Electronic Supplementary Material (ESI) for Molecular BioSystems
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Supplemental Table 2 Summary of expression data from all *Arabidopsis* probe sets. Averaged log2 estimates from the three biological replicates of the experiment for each contrast statement are presented with associated *p*-values and *q* -values for all 22,810 probe sets on the ATH1 GeneChip microarray. Raw data files are categorized under accession number AT42 and can be analyzed online using tools in PLEXdb (plexdb.org), or results can be directly downloaded. Raw data may also be downloaded from the Gene Expression Omnibus (GEO), accession number GSE20278 (ncbi.nlm.nih.gov/geo/).

Probeset	Locus	Description	poly RNA; TuMV vs. Control			total RNA; TuMV vs. Control			TuMV; poly RNA vs. total RNA			Control; poly RNA vs. total RNA		
			est	*p*-value	*q*-value	est	*p*-value	*q*-value	est	*p*-value	*q*-value	est	*p*-value	*q*-value
244901_at	ATMG00640	encodes a plant b subunit of mitochondrial ATP syn	-0.03204	0.9137	0.555	-0.729	0.0585	0.1202	-1.7022	0.0032	0.0251	-2.3992	9.00E-04	0.0114
244902_at	ATMG00650	Encodes NADH dehydrogenase subunit 4L.	0.2637	0.8034	0.525	-0.6876	0.5261	0.3946	-2.5767	0.0449	0.0887	-3.528	0.0169	0.0415
244903_at	ATMG00660	hypothetical protein	-1.4485	0.0922	0.176	-0.3786	0.5954	0.4216	-3.9885	0.0037	0.0268	-2.9186	0.0113	0.0334
244904_at	ATMG00670	hypothetical protein	0.7365	0.396	0.3733	-0.06482	0.9374	0.5284	-1.3868	0.1482	0.1778	-2.1881	0.0477	0.0771
244905_at	ATMG00680	hypothetical protein	-0.1257	0.8887	0.5481	-0.5067	0.5803	0.4164	0.1537	0.8643	0.4826	-0.2273	0.8008	0.429
244906_at	ATMG00690	hypothetical protein	0.1718	0.796	0.5226	-0.1605	0.8091	0.4927	-2.5692	0.0092	0.0385	-2.9015	0.006	0.024
244907_at	ATMG00710	hypothetical protein	0.4437	0.6832	0.4869	-0.5793	0.597	0.4221	-0.364	0.7367	0.4438	-1.387	0.2416	0.208
244908_at	ATMG00720	hypothetical protein	0.9732	0.5604	0.445	0.1622	0.9112	0.5219	0.3979	0.8082	0.4661	-0.3931	0.8105	0.4319
244909_at	ATMG00740	hypothetical protein	0.09658	0.8855	0.5472	-0.256	0.705	0.4606	-0.8567	0.245	0.238	-1.2093	0.127	0.1396
244910_s_at	ATMG00750;AT2G07686	[ATMG00750, hypothetical protein];[AT2G07686, tr	0.3675	0.5421	0.4378	-1.0374	0.1335	0.1856	1.0075	0.0818	0.1254	-0.3975	0.4132	0.2897
244911_at	ATMG00760	hypothetical protein	0.6792	0.1757	0.2452	-0.8808	0.4374	0.3585	-2.4156	0.0773	0.1214	-1.6172	0.1887	0.1786
244912_at	AT2G07783;ATMG00830	[AT2G07783, pseudogene, similar to Ccl1, blastp m	0.3621	0.2195	0.2748	1.1193	0.0109	0.056	-2.093	4.00E-04	0.0147	-1.3358	0.0024	0.0162
244913_at	ATMG00840	hypothetical protein	-0.3372	0.492	0.4166	-0.3653	0.459	0.3676	-0.5236	0.2467	0.2391	-0.5517	0.2264	0.1996
244914_at	ATMG00850;AT2G07682	[ATMG00850, hypothetical protein];[AT2G07682, tr	0.2779	0.0619	0.1428	-1.2944	0.1845	0.2229	1.0444	0.2659	0.2497	-2.328	0.045	0.0744
244915_s_at	ATMG00860;AT2G07682	[ATMG00860, hypothetical protein];[AT2G07682, tr	0.09768	0.9238	0.558	-0.2618	0.7985	0.4891	0.3913	0.6734	0.422	0.03174	0.9724	0.4761
244916_at	ATMG00880;AT2G07682	[ATMG00880, hypothetical protein];[AT2G07682, tr	-0.9104	0.4272	0.3881	1.0195	0.3788	0.3314	-1.836	0.1496	0.1787	0.09379	0.9319	0.4662
244917_at	ATMG00870	hypothetical protein	-0.1729	0.7612	0.512	-0.1513	0.79	0.4861	-0.9439	0.1214	0.1573	-0.9223	0.1278	0.1401
244918_at	ATMG00890	hypothetical protein	0.9413	0.422	0.386	-2.5164	0.0752	0.1376	1.8974	0.146	0.1761	-1.5603	0.2126	0.1922
244919_at	AT2G07768;ATMG00960	[AT2G07768, pseudogene, similar to Ccl1, blastp m	0.02395	0.9785	0.5719	-2.0994	0.0658	0.1283	1.4619	0.1549	0.1822	-0.6614	0.4726	0.3147
244920_s_at	AT2G07751;ATMG00990	[AT2G07751, NADH-ubiquinone oxidoreductase ch	0.1313	0.7176	0.4987	0.05605	0.8764	0.5121	-1.6291	0.0085	0.0371	-1.7044	0.0073	0.0266
244921_s_at	ATMG01000	hypothetical protein	0.5954	0.2618	0.3007	-0.8382	0.14	0.1906	-0.8613	0.132	0.1653	-2.2948	0.0073	0.0267
244922_s_at	AT2G07674;ATMG01010	[AT2G07674, similar to hypothetical protein BmapM	-0.9799	0.2971	0.3214	-1.143	0.2348	0.2547	-1.4414	0.1528	0.1807	-1.6046	0.1213	0.136
244923_s_at	ATMG01020	hypothetical protein	0.0318	0.9555	0.5662	-0.6241	0.3083	0.2965	-0.7917	0.2131	0.2198	-1.4476	0.0538	0.0829
244924_at	ATMG01040	hypothetical protein	1.5164	0.1091	0.1912	0.06127	0.9378	0.5285	-0.7961	0.3414	0.2889	-2.2513	0.038	0.0667
244925_at	ATMG00510	NADH dehydrogenase subunit 7	-0.5444	0.335	0.3429	0.006059	0.9909	0.5419	-0.563	0.3207	0.2786	-0.01251	0.9811	0.4783
244926_s_at	AT2G07712; pseudogene, similar to maturase-rela	[AT2G07712, pseudogene, similar to maturase-rela	1.7303	0.2084	0.2672	-1.8129	0.1916	0.2271	0.9366	0.4629	0.3444	-2.6066	0.087	0.1104
244927_at	ATMG00530;AT2G07776	[ATMG00530, hypothetical protein];[AT2G07776, id	0.6624	0.4168	0.3833	0.01792	0.9816	0.5396	-0.09345	0.9046	0.4936	-0.7379	0.3706	0.2715
244928_s_at	ATMG00570;AT2G07716	[ATMG00570, encodes a protein of unknown functi	-0.108	0.7956	0.5226	-0.451	0.3119	0.2983	-0.5697	0.0192	0.0555	-0.9127	0.0037	0.0197
244929_at	ATMG00580	NADH dehydrogenase subunit 4	0.2047	0.3397	0.3451	-0.1805	0.3936	0.3385	-2.1626	3.00E-04	0.0141	-2.5478	2.00E-04	0.0074
244930_at	ATMG00600	hypothetical protein	-0.4341	0.6672	0.4817	1.4111	0.2065	0.2371	0.4415	0.662	0.4186	2.2868	0.0712	0.0978
244931_at	ATMG00630	hypothetical protein	-0.6169	0.4517	0.399	-1.2516	0.1663	0.21	-2.516	0.0263	0.0659	-3.1506	0.0126	0.0354
244932_at	ATCG01060	Encodes the PsaC subunit of photosystem I.	-0.1552	0.564	0.4465	-0.07955	0.7637	0.4785	-4.2473	1.00E-04	0.0101	-4.1716	1.00E-04	0.0058
244933_at	ATCG01070	NADH dehydrogenase ND4L	-0.3046	0.585	0.4544	-0.4399	0.4399	0.3595	-3.271	0.0031	0.0251	-3.4063	0.0027	0.0171
244934_at	ATCG01080	NADH dehydrogenase ND6	-0.2884	0.5983	0.459	-1.0238	0.1125	0.1694	-3.3263	0.0014	0.0193	-4.0617	6.00E-04	0.0103
244935_at	ATCG01090	Encodes subunit of the chloroplast NAD(P)H dehyd	-0.08427	0.6422	0.4737	-0.4833	0.0451	0.1053	-2.8579	0	0.0092	-3.2569	0	0.0047
244936_at	ATG01100	NADH dehydrogenase ND1	-0.1799	0.3559	0.3526	-0.18	0.3556	0.3207	-4.859	0	0.0049	-4.8592	0	0.0033
244937_at	ATG01110	Encodes the 49KDa plastid NAD(P)H dehydrogenas	0.1169	0.8459	0.5373	-0.5886	0.3556	0.3207	-4.873	0.001	0.0175	-5.5786	6.00E-04	0.0101
244938_at	ATG01120	encodes a chloroplast ribosomal protein S15, a cor	-0.4475	0.0746	0.1569	-0.2797	0.2084	0.2385	-3.0937	1.00E-04	0.0101	-2.9259	1.00E-04	0.0061
244939_at	ATG00065	chloroplast gene encoding ribosomal protein s12. T	0.8798	0.335	0.3429	0.6992	0.4333	0.3569	-3.9166	0.0017	0.0204	-4.0972	0.0014	0.0135
244940_at	ATCG01230;ATCG00905	[ATCG01230, chloroplast gene encoding ribosomal	0.2595	0.2689	0.3048	0.2156	0.3466	0.3163	-4.0479	0	0.0049	-4.0917	0	0.0033
244941_at	ATG00010	hypothetical protein	0.3472	0.3164	0.3323	-0.4683	0.1977	0.2314	0.04198	0.8199	0.4698	-0.7735	0.011	0.0328
244942_at	ATG00050	hypothetical protein	-0.8796	0.5148	0.4271	1.3578	0.3323	0.3096	-1.711	0.2373	0.2336	0.5264	0.6912	0.3944
244943_at	ATG00070	NADH dehydrogenase subunit 9	-0.1978	0.5876	0.4554	-0.6514	0.1244	0.1788	-1.9979	0.004	0.0274	-2.4516	0.0019	0.0149
244944_s_at	ATMG00080;ATMG00090	[ATMG00080, encodes a mitochondrial ribosomal p	0.1748	0.0039	0.0463	0.3133	0.2432	0.26	-1.8511	3.00E-04	0.0158	-2.9126	1.00E-04	0.0061
244945_at	ATG00110	Encodes a mitochondria-encoded cytochrome c bio	-0.2988	0.4166	0.3832	-0.7041	0.0999	0.1593	-0.9303	0.0479	0.0919	-1.3355	0.0155	0.0398
244946_at	no_match	no_match	-0.1984	0.8769	0.5456	-1.14	0.3965	0.3397	-1.4081	0.3064	0.2718	-2.3498	0.1222	0.1366
244947_at	ATG00130	hypothetical protein	0.2709	0.4416	0.3944	0.4143	0.2619	0.2709	-0.2086	0.2425	0.2364	-0.06521	0.6905	0.3941
244948_at	ATG00140	hypothetical protein	1.2633	0.3576	0.3533	-0.6239	0.635	0.4365	1.3254	0.3371	0.2869	-0.5619	0.6681	0.3868
244949_at	ATG00150	hypothetical protein	-0.2054	0.7507	0.5087	-0.7519	0.2807	0.2813	-0.6425	0.347	0.2917	-1.1891	0.1201	0.135
244950_at	ATG00160	cytochrome c oxidase subunit 2	1.4316	0.0891	0.173	-0.4025	0.5638	0.4097	-3.5114	0.0054	0.0308	-5.3455	0.0011	0.0126
244951_s_at	AT2G07723;ATMG00180	[AT2G07723, pseudogene, similar to orf454~homol	-0.2287	0.3073	0.327	-0.464	0.0767	0.1387	-1.7076	9.00E-04	0.0173	-1.9428	6.00E-04	0.01
244952_at	ATG00260	hypothetical protein	-0.8253	0.3922	0.3712	-0.1883	0.8377	0.5009	-1.7675	0.076	0.1202	-1.1304	0.2027	0.1868
244953_s_at	ATMG00270;AT2G07731	[ATMG00270, NADH dehydrogenase subunit 6];[AT	0.1355	0.7327	0.5031	0.02387	0.9517	0.5323	-0.8718	0.078	0.1221	-0.7124	0.1265	0.1392
244954_s_at	ATMG00280;AT2G07732	[ATMG00280, hypothetical protein];[AT2G07732, pr	-0.8974	0.5905	0.4563	-1.5492	0.3704	0.3277	-1.684	0.3346	0.2858	-2.3357	0.2031	0.1869
244955_at	ATMG00320	hypothetical protein	-0.4361	0.462	0.4038	-0.1334	0.8159	0.4948	0.9371	0.1219	0.1578	1.2398	0.0607	0.0891
244956_s_at	ATMG00310;AT2G07737	[ATMG00310, hypothetical protein];[AT2G07737, tr	-0.1707	0.8879	0.5478	1.0085	0.4253	0.3531	-1.0088	0.3393	0.2881	0.1703	0.8637	0.4488
244957_at	ATMG00400	hypothetical protein	1.258	0.031	0.1022	0.239	0.569	0.4115	0.1089	0.7917	0.4606	-0.91	0.0777	0.103
244958_at	ATMG00450	hypothetical protein	0.94	0.5158	0.4276	-0.4899	0.7294	0.4684	-0.00816	0.9947	0.5164	-1.4381	0.2797	0.228
244959_s_at	AT2G07698; ATMG00500;A	[AT2G07698, identical to Uncharacterized mitochor	-0.0486	0.8853	0.5472	0.3235	0.3641	0.3248	-2.3197	0.0018	0.0206	-1.9476	0.0035	0.0194
244960_at	ATCG01020	encodes a chloroplast ribosomal protein L32, a core	-0.03269	0.9365	0.5613	-0.142	0.7311	0.4688	-1.8384	0.0067	0.0335	-1.9478	0.0054	0.023
244961_at	ATCG01040	hypothetical protein	-0.1003	0.633	0.4706	-0.4474	0.0828	0.1446	-2.2591	1.00E-04	0.0102	-2.6062	0	0.0055
244962_at	ATCG01050	Represents a plastid-encoded subunit of a NAD(P)H	0.07233	0.7804	0.518	-0.1818	0.4952	0.3826	-2.9641	0	0.0092	-3.2182	0	0.0047
244963_at	ATCG00570	PSII cytochrome b559	0.05394	0.9023	0.5519	-0.341	0.4552	0.3662	-4.2872	5.00E-04	0.0148	-4.6821	3.00E-04	0.0087
244964_at	ATCG00580	PSII cytochrome b559. There have been many spec	0.1581	0.7593	0.5115	-0.2589	0.6196	0.4304	-4.9569	5.00E-04	0.0152	-5.3739	4.00E-04	0.0088
244965_at	ATCG00590	hypothetical protein	0.2861	0.5809	0.4525	-0.1779	0.7281	0.4683	-2.2688	0.0089	0.0378	-2.7328	0.0046	0.0214
244966_at	ATCG00600	Cytochrome b6-f complex, subunit V. Disruption of	0.1132	0.785	0.5193	-1.0586	0.0525	0.1136	-2.4511	0.0032	0.0252	-3.6229	7.00E-04	0.0108
244967_at	ATCG00630	Encodes subunit J of photosystem I.	-0.6206	0.2909	0.3179	-0.4084	0.4685	0.3714	-2.2292	0.012	0.0435	-2.017	0.0168	0.0414
244968_at	ATCG00640	encodes a chloroplast ribosomal protein L33, a cor	-0.4254	0.3195	0.3342	-0.87	0.0809	0.1426	-3.65	6.00E-04	0.0158	-4.0945	4.00E-04	0.0089
244969_at	ATCG00650	chloroplast-encoded ribosomal protein S18	-0.154	0.5913	0.4565	-0.2528	0.393	0.3383	-3.1022	3.00E-04	0.0138	-3.201	3.00E-04	0.0081
244970_at	ATCG00660	encodes a chloroplast ribosomal protein L20, a cor	0.4289	0.1917	0.2566	-0.678	0.0682	0.1309	-2.1213	0.0015	0.0199	-3.2282	3.00E-04	0.0083
244971_at	ATCG00670	Encodes the only ClpP (caseinolytic protease) enco	0.1595	0.6031	0.4605	0.05907	0.8448	0.503	-3.5636	2.00E-04	0.0129	-3.664	2.00E-04	0.0078
244972_at	ATCG00680	encodes for CF47, subunit of the photosystem II re	-0.6518	0.4293	0.3887	-0.7822	0.3512	0.3186	-3.8016	0.0032	0.0252	-3.932	0.0028	0.0174
244973_at	ATCG00690	Encodes photosystem II 5 kD protein subunit PSII-1	-0.3511	0.639	0.4726	-0.5292	0.4875	0.3793	-3.3734	0.0076	0.0352	-3.5515	0.0063	0.0247
244974_at	ATCG00700	PSII low MW protein	-1.713	0.1264	0.2058	-0.02835	0.9761	0.5384	-4.6604	0.0052	0.0303	-2.9758	0.0242	0.051
244975_at	ATCG00710	Encodes a 8 kD phosphoprotein that is a componer	-0.5681	0.0954	0.1784	-0.2188	0.4496	0.3637	-5.4451	0	0.0092	-5.0958	0	0.0054
244976_at	ATCG00720	Encodes the cytochrome b(6) subunit of the cytoch	0.0258	0.9358	0.5612	-0.4356	0.2216	0.2469	-3.07	3.00E-04	0.0134	-3.5314	2.00E-04	0.007
244977_at	ATCG00730	A chloroplast gene encoding subunit IV of the cytoc	-0.9208	0.2513	0.2942	-0.2211	0.7637	0.4785	-2.8261	0.0147	0.0483	-2.1265	0.0364	0.0649
244978_at	ATCG00740	RNA polymerase alpha subunit	0.05359	0.8705	0.5442	-0.1944	0.5628	0.4093	-3.5166	3.00E-04	0.0141	-3.7646	3.00E-04	0.008
244979_at	ATCG00750	30S chloroplast ribosomal protein S11	-0.09469	0.7485	0.5084	-0.4787	0.1574	0.2039	-5.2605	0	0.0092	-5.6745	0	0.0053
244980_at	ATCG00760	encodes a chloroplast ribosomal protein L36, a cor	-0.1638	0.6655	0.4811	-0.2865	0.4609	0.3683	-5.4191	0	0.007	-5.5418	0	0.0043
244981_at	ATCG00770	chloroplast 30S ribosomal protein S8	0.5057	0.2447	0.2904	-0.2931	0.4739	0.3737	-4.5782	2.00E-04	0.0133	-5.377	1.00E-04	0.0065
244982_at	ATCG00780	encodes a chloroplast ribosomal protein L14, a cor	0.0491	0.9459	0.5636	-0.1528	0.8358	0.5004	-4.8734	0.0021	0.0218	-5.0761	0.0018	0.0148
244983_at	ATCG00790	chloroplast gene encoding a ribosomal protein L16,	0.3372	0.1175	0.1982	0.0111	0.9509	0.5321	-4.6328	0	0.0062	-4.9588	0	0.0043
244984_at	ATCG00800	encodes a chloroplast ribosomal protein S3, a cons	0.06822	0.8241	0.5307	-0.3182	0.3114	0.2982	-4.6443	1.00E-04	0.0101	-5.0278	1.00E-04	0.0055
244985_at	ATCG00810	encodes a chloroplast ribosomal protein L22, a cor	0.0278	0.9437	0.5633	-0.6271	0.1654	0.2093	-5.5422	1.00E-04	0.0118	-6.1972	1.00E-04	0.0058
244986_at	ATCG00820	Encodes a 6.8-kDa protein of the small ribosomal s	0.3093	0.1256	0.2052	-0.5635	0.0245	0.0786	-3.3295	0	0.0092	-4.2023	0	0.0047
244987_s_at	ATCG01310;ATCG00830	[ATCG01310, encodes a chloroplast ribosomal prot	0.1296	0.5922	0.4568	-0.6801	0.038	0.0965	-2.1698	5.00E-04	0.0148	-2.9795	1.00E-04	0.0065
244988_s_at	ATCG00840;ATCG01300	[ATCG00840, One of two chloroplast genes that enc	-0.3485	0.2786	0.3106	-0.984	0.0241	0.0781	-3.5141	2.00E-04	0.0129	-4.1497	1.00E-04	0.0062
244989_s_at	ATCG00860;ATCG01280	[ATCG00860, Encodes an unknown protein. This ge	-0.7377	0.208	0.267	-0.175	0.74	0.4713	-1.6587	0.028	0.068	-1.096	0.0897	0.1126
244990_s_at	ATCG00870;ATCG01270	[ATCG00870, hypothetical protein];[ATCG01270, ho	-0.04109	0.9326	0.5604	-0.8811	0.1257	0.1798	-0.2523	0.6098	0.4013	-1.0923	0.0749	0.1007
244991_s_at	ATCG00910;ATCG00890	[ATCG00910, NADH dehydrogenase N22];[ATCG0	0.2803	0.7184	0.4989	-0.3682	0.6378	0.4374	-0.9111	0.1646	0.1882	-1.5596	0.0438	0.0732
244992_s_at	ATCG00900;ATCG01240	[ATCG00900, encodes a chloroplast ribosomal prot	0.3848	0.2172	0.2733	0.106	0.7076	0.4613	-2.7889	0	0.0073	-3.0678	0	0.0043
244993_s_at	ATCG01000;ATCG01130	[ATCG01000, hypothetical protein];[ATCG01130, hy	-0.3587	0.2182	0.274	-0.03797	0.8847	0.5145	-4.744	0	0.0092	-4.4233	0	0.0052
244994_at	ATG01010	Chloroplast encoded NAD(P)H dehydrogenase unit.	0.7029	0.4317	0.39	0.4218	0.6278	0.4336	-2.3243	0.0446	0.0883	-2.6053	0.0317	0.06
244995_at	ATCG00150	Encodes a subunit of ATPase complex CF0, which	0.7821	0.1092	0.1913	-0.5655	0.2117	0.2408	-3.6366	7.00E-04	0.0159	-4.9842	2.00E-04	0.0077
244996_at	ATCG00160	Chloroplast ribosomal protein S2	-0.2261	0.5136	0.4266	-0.3123	0.3786	0.3313	-5.1344	0	0.006	-5.2206	0	0.0043
244997_at	ATCG00170	RNA polymerase beta' subunit 2	1.0677	0.2455	0.2908	-0.04438	0.9576	0.5336	-3.8166	9.00E-04	0.0169	-4.9287	3.00E-04	0.0086
244998_at	ATCG00180	RNA polymerase beta' subunit-1	0.1224	0.7768	0.5169	-0.2381	0.587	0.4187	-4.0278	1.00E-04	0.0101	-4.3883	0	0.0055
244999_at	ATCG00190	Chloroplast DNA-dependent RNA polymerase B su	0.6857	0.2348	0.2843	-0.6486	0.2567	0.2682	-1.1405	0.0807	0.1244	-2.4748	0.0073	0.0265
245000_at	ATCG00210	hypothetical protein	0.0158	0.9726	0.5705	-1.1363	0.0582	0.12	-0.2183	0.6401	0.4111	-1.3704	0.0338	0.0621
245001_at	ATCG00220	PSII low MW protein	0.6961	0.2738	0.3079	-0.4681	0.4422	0.3604	-0.6884	0.2784	0.2571	-1.8526	0.028	0.0558
245002_at	ATCG00270	PSII D2 protein	-0.1809	0.6497	0.4762	-0.2648	0.5128	0.3898	-4.9365	2.00E-04	0.0126	-5.0204	2.00E-04	0.0073
245003_at	ATCG00280	chloroplast gene encoding a CP43 subunit of the p	-0.665	0.0998	0.1823	-0.01966	0.9527	0.5325	-6.0036	0	0.0092	-5.3583	1.00E-04	0.0055
245004_at	ATCG00300	encodes PsbZ, which is a subunit of photosystem II	-0.3063	0.6006	0.4599	-0.5963	0.3311	0.309	-4.2375	0.0014	0.0197	-4.5275	0.0011	0.0124
245005_at	ATCG00330	30S chloroplast ribosomal protein S14	1.1114	0.3232	0.3362	-0.2945	0.7803	0.4836	-1.4936	0.2048	0.2146	-2.8995	0.0425	0.0719
245006_at	ATCG00340	Encodes the D1 subunit of cytochosystem I and II re	0.06788	0.8001	0.5241	-0.4325	0.1599	0.2058	-2.9226	0	0.0092	-3.423	0	0.0044
245007_at	ATCG00350	Encodes psaA protein comprising the reaction cente	0.3371	0.7489	0.5084	-0.4286	0.6853	0.4539	-7.0552	8.00E-04	0.0165	-7.8209	5.00E-04	0.0098
245008_at	ATCG00360	Encodes a protein required for photosystem I asser	-0.06883	0.8823	0.5469	-0.3256	0.497	0.3832	-2.7741	0.0031	0.0251	-3.0309	0.0023	0.0158
245009_at	ATCG00380	Chloroplast encoded ribosomal protein S4	0.2741	0.0964	0.1795	-0.2453	0.5041	0.3863	-3.1996	1.00E-04	0.012	-4.1689	0	0.0055
245010_at	ATCG00420	Encodes NADH dehydrogenase subunit J. Its trans	-0.05644	0.8906	0.5484	-0.4811	0.2797	0.2808	-3.372	1.00E-04	0.012	-3.7967	1.00E-04	0.006
245011_at	ATCG00430	Encodes a protein which was originally thought to b	-0.321	0.3899	0.3699	-0.7187	0.0972	0.1572	-3.3017	4.00E-04	0.0147	-3.6994	2.00E-04	0.0079
245012_at	ATCG00440	Encodes NADH dehydrogenase D3 subunit of the c	-0.04497	0.8822	0.5469	-0.3489	0.2879	0.2853	-1.4914	0.0042	0.0279	-1.7954	0.0021	0.0156
245013_at	ATCG00470	ATPase epsilon subunit	-0.1414	0.5398	0.4367	-0.5552	0.0583	0.1201	-1.8897	1.00E-04	0.012	-2.3034	1.00E-04	0.0056
245014_at	ATCG00480	chloroplast-encoded gene for beta subunit of ATP s	-0.3043	0.1211	0.2015	-0.5206	0.0283	0.0836	-2.8209	1.00E-04	0.0095	-3.0373	0	0.0053
245015_at	ATCG00490	large subunit of RUBISCO	0.04606	0.916	0.5559	-0.2016	0.6486	0.4411	-3.925	1.00E-04	0.012	-4.1727	1.00E-04	0.0061
245016_at	ATCG00500	Encodes the carboxyltransferase beta subunit of the	0.3407	0.4131	0.3816	0.2702	0.5092	0.3884	-4.5881	0	0.007	-4.6585	0	0.0043
245017_at	ATCG00510	Encodes subunit I of photosystem I.	0.2482	0.4884	0.4152	-0.2687	0.4557	0.3663	-3.6677	0	0.0092	-4.1846	0	0.0047
245018_at	ATCG00520	Encodes a protein required for photosystem I asser	0.7571	0.0518	0.1307	-0.6418	0.0808	0.1426	-5.1157	0	0.0092	-6.5146	0	0.0047
245019_at	ATCG00530	hypothetical protein	-0.4571	0.2078	0.2669	-0.5423	0.1495	0.1977	-5.6523	0	0.0092	-5.7376	0	0.0047
245020_at	ATCG00540	Encodes cytochrome f apoprotein; involved in phot	0.06472	0.8294	0.5322	-0.2938	0.3555	0.3206	-3.7186	1.00E-04	0.0098	-4.0771	0	0.0053
245021_at	ATCG00550	PSII component	0.2547	0.6084	0.4626	-0.1894	0.7009	0.4594	-3.1604	0.0023	0.0226	-3.6046	0.0014	0.0136
245022_at	ATCG00560	PSII L protein	-0.05951	0.9215	0.5574	-0.2254	0.7113	0.4626	-3.6393	0.003	0.0248	-3.8052	0.0026	0.0168
245023_at	ATCG00080	PSII I protein	-0.00576	0.9864	0.5735	-0.9322	0.0426	0.1026	-0.3012	0.1037	0.1439	-1.2277	0.001	0.0122
245024_at	ATCG00120	Encodes the ATPase alpha subunit, which is a subu	-0.1081	0.5383	0.4362	-0.5885	0.0216	0.0747	-3.3887	0	0.0049	-3.8691	0	0.003
245025_at	ATCG00130	ATPase F subunit.	0.02265	0.9417	0.5629	-0.607	0.1053	0.1639	-4.0903	1.00E-04	0.012	-4.7199	1.00E-04	0.0058
245026_at	ATCG00140	ATPase III subunit	0.4914	0.518	0.4285	-0.77	0.3295	0.3083	-2.8813	0.0067	0.0335	-4.1427	0.0018	0.0147
245027_at	AT2G26650	HO2 (HEME OXYGENASE 2); heme oxygenase (d	-0.4239	0.0111	0.066	-0.2794	0.0422	0.1021	0.009749	0.8768	0.4859	0.1543	0.0592	0.0878
245028_at	AT2G26570	similar to unknown protein [Arabidopsis thaliana] (T	0.1619	0.3768	0.3626	0.1975	0.2924	0.2878	-0.06747	0.7001	0.4313	-0.03189	0.8544	0.444
245029_at	AT2G26580	YAB5 (YABBY5); transcription factor	-0.6796	0.0156	0.0754	-0.2101	0.2797	0.2808	0.2312	0.1142	0.1519	0.7008	0.0036	0.0196
245030_at	AT2G26620	glycoside hydrolase family 28 protein / polygalactur	0.02865	0.9775	0.5716	0.8887	0.4046	0.3433	2.3253	0.0715	0.1162	3.2427	0.0274	0.055
245031_at	AT2G26360	binding	-0.03078	0.9474	0.564	-1.0409	0.0763	0.1384	0.6231	0.228	0.2283	-0.3871	0.4269	0.2954
245032_at	AT2G26630	transposable element gene	-0.9093	0.3

245090_at	AT2G40900	nodulin MtN21 family protein	-0.09052	0.7124	0.4971	-0.7245	0.0339	0.091	0.0246	0.9156	0.4965	-0.6093	0.0491	0.0785
245091_at	AT2G40910	F-box protein-related	-0.0163	0.9756	0.5711	0.1674	0.7553	0.4768	-1.7157	0.0105	0.0406	-1.5321	0.0154	0.0395
245092_at	AT2G40950	BZIP17; DNA binding / transcription activator/ transc	0.5675	0.1422	0.2192	0.2672	0.4389	0.3591	0.2361	0.3635	0.2998	-0.06426	0.7942	0.4272
245093_at	AT2G40820	3'-5'-exoribonuclease/ RNA binding	-0.1441	0.5578	0.4441	0.02996	0.9008	0.5192	0.5104	0.0865	0.1297	0.6845	0.0387	0.0676
245094_at	AT2G40840	DPE2 (DISPROPORTIONATING ENZYME 2); 4-alp	0.373	0.1512	0.2267	0.1417	0.5378	0.3996	-0.9002	5.00E-04	0.0148	-1.1316	2.00E-04	0.0076
245095_at	AT2G40860	protein kinase family protein / protein phosphatase	-1.4599	0.1037	0.186	-0.1709	0.8179	0.4953	-2.847	0.0149	0.0487	-1.558	0.0885	0.1116
245096_at	AT2G40880	FL3-27; cysteine protease inhibitor	-0.03245	0.9465	0.5637	0.0757	0.8757	0.5118	0.05813	0.9043	0.4935	0.1663	0.7327	0.4079
245097_at	AT2G40935	unknown protein [Arabidopsis thaliana] (T	0.3339	0.1933	0.2578	0.4102	0.1274	0.1811	-0.2313	0.1933	0.2076	-0.1549	0.3545	0.2646
245098_at	AT2G40940	ERS1 (ETHYLENE RESPONSE SENSOR 1); recep	0.5702	0.0044	0.0482	0.4698	0.0088	0.0516	0.2771	0.033	0.0742	0.1767	0.1111	0.1285
245099_at	AT2G40830	RHC1A (RING-H2 finger C1A); protein binding / zin	0.4744	0.0728	0.1554	0.3928	0.1156	0.1716	0.003966	0.9848	0.5138	-0.07762	0.7124	0.4018
245100_at	AT2G40930	UBP5 (UBIQUITIN-SPECIFIC PROTEASE 5); ubiq	0.5181	0.0471	0.1248	0.3057	0.1695	0.2122	-0.5776	0.0341	0.0755	-0.7899	0.0124	0.0352
245101_at	AT2G40890	CYP98A3 (CYTOCHROME P450, FAMILY 98, SUB	-0.3682	0.2472	0.2919	-0.4846	0.1494	0.1977	-0.2436	0.1196	0.1559	-0.36	0.0434	0.0727
245102_at	AT2G41580	transposable element gene	-1.1427	0.4242	0.3869	-0.3538	0.7967	0.4886	-0.7611	0.471	0.348	0.0278	0.9782	0.4777
245103_at	AT2G41590	similar to unknown protein [Arabidopsis thaliana] (T	-0.3641	0.7228	0.5003	-0.5508	0.5966	0.4217	1.1828	0.2839	0.2601	0.9961	0.3565	0.2654
245104_at	AT2G41600	similar to hypothetical protein [Vitis vinifera] (GB:CA	-0.3122	0.2945	0.3201	0.184	0.5168	0.3913	-0.2592	0.3736	0.3045	0.237	0.4121	0.2891
245105_at	AT2G41610	similar to unnamed protein product [Vitis vinifera] (G	-0.1873	0.5181	0.4285	0.3973	0.2078	0.2381	0.008206	0.9768	0.5118	0.5928	0.0887	0.1117
245106_at	AT2G41650	unknown protein	-0.5471	0.0753	0.1579	-0.05225	0.8308	0.4991	0.6444	0.0322	0.0731	1.1392	0.0047	0.0217
245107_at	AT2G41690	AT-HSFB3 (Arabidopsis thaliana heat shock transc	2.4397	0.0817	0.1653	1.9296	0.1412	0.1916	0.1422	0.8992	0.4921	-0.3679	0.7447	0.4119
245108_at	AT2G41510	ATCKX1/CKX1 (CYTOKININ OXIDASE/DEHYDRO	0.08295	0.7718	0.5152	0.4331	0.1805	0.2199	-0.07829	0.7581	0.4507	0.2718	0.3161	0.2465
245109_at	AT2G41520	DNAJ heat shock N-terminal domain-containing pro	-0.2141	0.3776	0.3632	-0.08455	0.7154	0.4639	-0.9323	0.0125	0.0443	-0.8027	0.0205	0.0463
245110_at	AT2G41550	transcription termination factor	1.266	0.0643	0.1453	0.3315	0.5432	0.402	0.4257	0.3393	0.2881	-0.5089	0.2647	0.2202
245111_at	AT2G41570	transposable element gene	1.5489	0.1826	0.2501	-0.9607	0.3744	0.3296	0.614	0.5579	0.3819	-1.8956	0.12	0.135
245112_at	AT2G41540	GPDHC1; NAD binding / glycerol-3-phosphate deh	-0.02521	0.9429	0.5631	-0.07981	0.8211	0.4962	-0.02443	0.8643	0.4826	-0.07903	0.5874	0.3588
245113_at	AT2G41660	MIZ1 (MIZU-KUSSEI 1)	-0.5041	0.5393	0.4366	-0.8906	0.3017	0.2923	2.2909	0.0381	0.0807	1.9044	0.0645	0.0923
245114_at	AT2G41630	TFIIB (TRANSCRIPTION FACTOR II B); RNA polyr	1.1968	0.1443	0.2208	0.5204	0.0087	0.0513	-0.262	0.0034	0.0257	0.06165	0.2167	0.1945
245115_at	AT2G41530	ATSFGH (ARABIDOPSIS THALIANA S-FORMYLG	0.6751	0.0077	0.058	0.4576	0.0281	0.0835	0.1389	0.2073	0.2161	-0.07867	0.4427	0.3027
245116_at	AT2G41620	nucleoporin interacting component family protein	0.128	0.4737	0.4094	0.08174	0.6404	0.4384	-0.9629	7.00E-04	0.0159	-1.0091	5.00E-04	0.0098
245117_at	AT2G41560	ACA4 (AUTO-INHIBITED CA(2+)-ATPASE, ISOFO	0.4923	0.1075	0.1896	0.4353	0.1415	0.1918	-1.0113	0.0053	0.0306	-1.0684	0.0044	0.0209
245118_at	AT2G41680	thioredoxin reductase, putative / NADPH-dependen	-0.3965	0.002	0.0396	-0.5783	5.00E-04	0.0252	-0.09282	0.1448	0.1752	-0.2746	0.0059	0.0238
245119_at	AT2G41640	similar to unknown protein [Arabidopsis thaliana] (T	0.5505	0.3848	0.3672	0.6011	0.3471	0.3166	-0.04298	0.2319	0.2305	0.007529	0.8174	0.4336
245120_at	AT2G39810	HOS1 (High expression of osmotically responsive g	0.6151	0.0121	0.0682	0.05983	0.6935	0.4567	-0.6261	0.0114	0.0423	-1.1814	0.0011	0.0125
245121_at	AT2G47610	60S ribosomal protein L7A (RPL7aA)	0.1076	0.5543	0.4425	0.0274	0.8776	0.5124	0.1557	0.0484	0.0924	0.07556	0.2447	0.2096
245122_at	AT2G47420	dimethyladenosine transferase, putative	0.5253	0.1902	0.2556	0.5174	0.1956	0.2298	-1.3004	0.0065	0.0331	-1.3083	0.0063	0.0246
245123_at	AT2G47450	CAO (CHLOROPLAST BIOGENESIS, CHLOROPLAST	-0.3396	0.194	0.2583	-0.2581	0.3018	0.2923	-0.99	0.0105	0.0406	-0.9085	0.014	0.0376
245124_at	AT2G47580	U1A (SPLICEOSOMAL PROTEIN U1A); RNA bindi	-0.08416	0.4251	0.3873	-0.01772	0.8609	0.5074	0.5061	0.0059	0.0321	0.5725	0.0038	0.02
245125_at	AT2G47430	CKI1 (CYTOKININ-INDEPENDENT 1); protein histi	0.5454	0.471	0.4078	0.9875	0.2233	0.2478	-1.5116	0.0857	0.1291	-1.0695	0.1834	0.1755
245126_at	AT2G47460	ATMYB12/MYB12 (MYB DOMAIN PROTEIN 12); D	1.4354	0.0299	0.1005	-0.7412	0.1636	0.2083	-0.7448	0.1621	0.1868	-0.05043	0.9133	0.4607
245127_at	AT2G47600	ATMHX (MAGNESIUM/PROTON EXCHANGER); c	-0.4108	0.0987	0.1813	-0.2064	0.3422	0.3145	-1.2146	0.003	0.0248	-1.0102	0.0059	0.0239
245128_at	AT2G45380	similar to calcium ion binding [Arabidopsis thaliana]	-0.3078	0.769	0.5143	0.6119	0.566	0.4104	-0.8597	0.4297	0.3295	0.05999	0.9541	0.4721
245129_at	AT2G45350	CRR4 (CHLORORESPIRATORY REDUCTION 4);	0.1391	0.7019	0.4931	-0.198	0.5895	0.4194	-0.7964	0.078	0.1221	-0.8554	0.0647	0.0925
245130_at	AT2G45340	leucine-rich repeat transmembrane protein kinase,	-0.178	0.3306	0.3403	-0.4964	0.0367	0.0947	-0.2777	0.1482	0.1778	-0.5961	0.0185	0.0436
245131_s_at	AT2G45330;AT5G23600	[AT2G45330, EMB1067 (EMBRYO DEFECTIVE 10	0.559	0.0034	0.0447	0.3261	0.0221	0.0751	0.03408	0.7234	0.4397	-0.1988	0.091	0.1136
245132_at	no_match	binding / catalytic	0.4706	0.1121	0.194	0.04713	0.8487	0.504	0.08536	0.7312	0.4422	-0.3381	0.2183	0.1953
245133_at	AT2G45310	GAE4 (UDP-D-GLUCURONATE 4-EPIMERASE 4);	-0.4679	0.0303	0.1009	-0.307	0.0972	0.1572	-0.1667	0.0318	0.0726	-0.00573	0.9168	0.4619
245134_s_at	AT4G38280;AT2G45250	[AT4G38280, similar to unknown protein [Arabidops	0.1949	0.2976	0.3219	0.3858	0.077	0.1391	-0.7638	0.0094	0.0388	-0.573	0.0245	0.0515
245135_at	AT2G45230	transposable element gene	-0.5183	0.4792	0.4116	0.06218	0.93	0.5266	0.05066	0.9273	0.4999	0.6311	0.2926	0.2349
245136_at	AT2G45210	auxin-responsive protein-related	0.2086	0.0599	0.1399	2.2508	0.0446	0.1047	-0.0778	0.8269	0.4718	0.1444	0.6872	0.3929
245137_at	AT2G45460	forkhead-associated domain-containing protein / FH	0.3875	0.2788	0.3107	0.5572	0.1462	0.1955	-0.3352	0.3397	0.2883	-0.1655	0.6212	0.3706
245138_at	AT2G45190	AFO (ABNORMAL FLORAL ORGANS); transcriptio	-0.04694	0.8068	0.5258	-0.1252	0.5242	0.3938	0.5362	0.0117	0.0428	0.4579	0.0198	0.0452
245139_at	AT2G45430	DNA-binding protein-related	-0.9074	0.1009	0.1835	-0.4328	0.3684	0.3268	-1.3774	0.0322	0.073	-0.9028	0.1021	0.1221
245140_at	AT2G45420	LBD18 (LOB DOMAIN-CONTAINING PROTEIN 18	0.4277	0.1814	0.2492	0.06218	0.8258	0.4976	0.3811	0.2233	0.2256	0.01558	0.9559	0.4725
245141_at	AT2G45400	BEN1; oxidoreductase, acting on CH-OH group of c	2.4964	0.003	0.0436	-2.223	0.0046	0.0416	0.1974	0.6382	0.4106	0.4708	0.2923	0.2348
245142_at	AT2G45270	glycoprotease M22 family protein	-0.3954	0.0498	0.1282	-0.4627	0.0312	0.0878	-0.04162	0.7241	0.4399	-0.1089	0.3776	0.2747
245143_at	AT2G45450	ZIPR1 (LITTLE ZIPPER 1); protein binding	0.9311	0.1639	0.2368	1.2856	0.0785	0.1404	0.8841	0.0568	0.1018	1.2386	0.0205	0.0463
245144_at	AT2G45240	MAP1A (METHIONINE AMINOPEPTIDASE 1A); m	0.7098	0.0015	0.0383	0.7666	0.0012	0.0294	0.044	0.645	0.4127	0.1028	0.3287	0.2527
245145_at	AT2G45440	DHDPS2 (DIHYDRODIPICOLINATE SYNTHASE);	-0.1677	0.532	0.4337	0.04438	0.8653	0.5086	-0.189	0.0791	0.1231	0.02309	0.7889	0.4254
245146_at	AT2G45200	GOS12 (GOLGI SNARE 12); SNARE binding	0.1039	0.2815	0.3122	0.2578	0.0367	0.0946	0.258	0.0366	0.0788	0.4119	0.0079	0.0277
245147_at	AT2G45280	ATRAD51C (Arabidopsis thaliana Rad Associated v	0.3967	0.1255	0.2051	-0.1109	0.6177	0.4298	-0.5758	0.0486	0.0927	-1.0834	0.0062	0.0244
245148_at	AT2G45220	peclinesterase family protein	1.2468	0.2006	0.2625	1.3746	0.1668	0.2103	0.278	0.2809	0.2586	0.4058	0.1431	0.1502
245149_at	AT2G47620	ATSWI3A (Arabidopsis thaliana switching protein 3	1.0274	0.0764	0.1592	0.1254	0.7863	0.485	0.1466	0.7382	0.4443	-0.7554	0.1387	0.1473
245150_at	AT2G47560	PHR2 (PHOTOLYASE/BLUE-LIGHT RECEPTOR 2	0.1626	0.0863	0.1704	-0.5453	0.0016	0.0317	0.1918	0.0558	0.1008	-0.1909	0.0566	0.0854
245151_at	AT2G47550	peclinesterase family protein	0.3701	0.5815	0.4528	0.4969	0.4663	0.3705	0.148	0.7019	0.4319	0.2749	0.4874	0.3208
245152_at	AT2G47490	mitochondrial substrate carrier family protein	-0.548	0.1258	0.2052	-0.787	0.0502	0.1112	-0.1204	0.6534	0.4157	-0.3593	0.2216	0.1969
245153_at	AT2G47450	similar to syntaxin-related family protein [Arabidops	-0.8354	0.4123	0.3812	-1.4243	0.194	0.2287	2.1628	0.077	0.1212	1.5739	0.16	0.1612
245154_at	AT2G47460	similar to fringe-related protein [Arabidopsis thaliana	0.5285	0.5474	0.4399	-0.9578	0.2999	0.2913	1.6002	0.1178	0.1545	0.1139	0.8944	0.4555
245155_at	AT5G12470	similar to unknown protein [Arabidopsis thaliana] (T	-0.8819	0.0127	0.0696	-1.2879	0.0033	0.0371	-0.4166	0.0269	0.0666	-0.8226	0.0025	0.0166
245156_at	AT5G12480	CPK7 (CALMODULIN-DOMAIN PROTEIN KINASE	0.377	0.1505	0.226	0.6807	0.0327	0.0896	-0.889	0.0138	0.0469	-0.5853	0.0511	0.0804
245157_at	AT2G33160	glycoside hydrolase family 28 protein / polygalactur	-0.02365	0.9877	0.5738	-1.5036	0.355	0.3204	0.6711	0.6652	0.4196	-0.8089	0.604	0.3646
245158_at	AT2G33130	RALFL18 (RALF-LIKE 18)	0.484	0.3644	0.3564	2.2998	0.0083	0.0505	0.874	0.0302	0.0708	2.6898	5.00E-04	0.0097
245159_at	AT2G33100	ATCSLD1 (Cellulose synthase-like D1); cellulose sy	0.4514	0.5762	0.4511	-0.8147	0.3343	0.3105	0.478	0.3372	0.2869	-0.7881	0.1469	0.1527
245160_at	AT2G33080	leucine-rich repeat family protein	2.2051	0.0411	0.1168	1.2652	0.1635	0.2083	-0.3466	0.6	0.3982	-1.2865	0.1024	0.1223
245161_at	AT2G33070	jacalin lectin family protein	0.4388	0.0318	0.1033	0.4739	0.025	0.0791	0.04109	0.7769	0.4564	0.07618	0.6042	0.3646
245162_at	AT2G33240	XID (Myosin-like protein XID); motor/ protein binding	1.4046	0.4073	0.379	-2.9554	0.1235	0.1784	1.8133	0.2984	0.2679	-2.5467	0.1688	0.1665
245163_at	AT2G33230	flavin-containing monooxygenase, putative / FMO,	-0.4407	0.671	0.4829	1.0157	0.3511	0.3186	0.2687	0.7582	0.4507	1.7251	0.1018	0.1219
245164_at	AT2G33210	chaperonin, putative	0.6165	0.0244	0.0909	0.3312	0.1316	0.184	-0.2539	0.2207	0.224	-0.5392	0.037	0.0655
245165_at	AT2G33180	similar to unnamed protein product [Vitis vinifera] (G	-0.3168	0.2962	0.3211	-0.8183	0.0362	0.094	0.4897	0.1372	0.1691	-0.01182	0.9664	0.4748
245166_at	AT2G33170	leucine-rich repeat transmembrane protein kinase,	0.4825	0.0958	0.1788	0.3614	0.1794	0.2192	0.03204	0.7937	0.4613	-0.08907	0.4804	0.3177
245167_s_at	AT2G33120;AT2G33110	[AT2G33120, SAR1 (SYNAPTOBREVIN-RELATED	0.4495	0.0183	0.0804	0.5948	0.007	0.0473	0.3478	0.0402	0.0831	0.4931	0.0132	0.0365
245168_at	AT2G33150	KAT2/PED1 (PEROXISOME DEFECTIVE 1); acety	0.1212	0.0958	0.053	0.9058	0.0088	0.0516	-0.1312	0.3777	0.3067	-0.2466	0.1359	0.1456
245169_at	AT2G33220	similar to MEE4 (maternal effect embryo arrest 4) [A	-0.4421	0.0203	0.0839	-0.02779	0.8261	0.4978	0.4505	0.0191	0.0554	0.8648	0.0019	0.0149
245170_at	AT2G47570	60S ribosomal protein L18 (RPL18A)	1.2374	0.2072	0.2666	-1.7905	0.0952	0.1555	1.8102	0.0311	0.0717	-1.2177	0.0934	0.1156
245171_at	AT2G47560	zinc finger (C3HC4-type RING finger) family protein	-1.8792	0.0527	0.1317	-2.9606	0.0127	0.0602	1.5767	0.0842	0.1276	0.4953	0.5123	0.3306
245172_at	AT2G47540	pollen Ole e 1 allergen and extensin family protein	0.008465	0.9851	0.5733	-0.6607	0.1961	0.2302	0.1683	0.7047	0.433	-0.5009	0.2923	0.2348
245173_at	AT2G47520	AP2 domain-containing transcription factor, putative	-0.5186	0.6828	0.4868	-0.2654	0.8329	0.4996	-0.07624	0.9515	0.5058	0.1769	0.888	0.4537
245174_at	AT2G47500	microtubule motor	-0.2621	0.4174	0.3836	-0.4218	0.2197	0.2457	-0.0189	0.9512	0.5058	-0.1786	0.5715	0.3531
245175_at	AT2G47470	ATPDIL2-1/MEE30/UNE5 (PDI-LIKE 2-1); thiol-disu	1.1276	0.0019	0.0391	1.0573	0.0024	0.0339	0.1896	0.2411	0.2356	0.1193	0.4358	0.2995
245176_at	AT2G47440	DNAJ heat shock N-terminal domain-containing pro	0.3092	0.522	0.4297	-0.0325	0.9448	0.5306	0.179	0.1857	0.2027	-0.1627	0.2204	0.1962
245177_at	AT5G12380	annexin, putative	-0.1027	0.9302	0.56	0.08489	0.9423	0.5298	0.2608	0.7895	0.46	0.4484	0.6493	0.3806
245178_at	AT5G12390	binding	0.8867	0.0107	0.0651	0.7447	0.0193	0.0715	0.3054	0.1951	0.2088	0.1634	0.4523	0.307
245179_at	AT5G12400	PHD finger transcription factor, putative	0.8396	0.0015	0.038	0.3921	0.0226	0.0759	-0.9447	3.00E-04	0.0141	-1.3923	1.00E-04	0.0058
245180_at	AT5G12410	THUMP domain-containing protein	0.4491	0.0068	0.0558	0.4162	0.0089	0.0518	0.04423	0.64	0.4111	0.01134	0.9032	0.4582
245181_at	AT5G12420	similar to unknown protein [Arabidopsis thaliana] (T	0.4914	0.121	0.2014	0.5808	0.081	0.1428	-0.4858	0.0829	0.1265	-0.3964	0.1337	0.1441
245182_at	AT5G12430	DNAJ heat shock N-terminal domain-containing pro	-0.3194	0.1275	0.2063	0.08705	0.6287	0.434	-0.8103	0.0082	0.0364	-0.4039	0.0723	0.0986
245183_at	AT5G12440	zinc finger (CCCH-type) family protein	0.06905	0.7167	0.5116	0.04329	0.8474	0.5037	-0.7973	0.0166	0.0514	-0.8231	0.015	0.0389
245184_at	AT1G67790	similar to unknown protein [Arabidopsis thaliana] (T	0.9949	0.3522	0.3509	-0.2322	0.8182	0.4953	-0.5564	0.588	0.3937	-1.7835	0.1324	0.1433
245185_at	AT1G67760	ATP binding / protein binding / unfolded protein bind	0.2605	0.3113	0.3295	-0.1401	0.567	0.4108	0.3419	0.2032	0.2137	-0.05874	0.8069	0.4307
245186_at	AT1G67750	ARR11 (RESPONSE REGULATOR 11); transcriptio	-0.2439	0.465	0.4052	0.3213	0.3477	0.3169	0.3607	0.2988	0.2682	0.9259	0.0376	0.0662
245187_s_at	AT1G67650;AT1G67680	[AT1G67650, 7S RNA binding];[AT1G67680, 7S RI	0.8464	0.0039	0.0464	0.7821	0.0053	0.0429	-0.08682	0.573	0.3878	-0.1511	0.3462	0.2608
245188_at	AT1G67660	DNA binding / magnesium ion binding / nuclease	0.5971	0.0651	0.1463	0.5987	0.0647	0.127	-0.2373	0.3727	0.3042	-0.2357	0.3756	0.2738
245189_at	AT1G67670	unknown protein	-0.5226	0.5765	0.4512	0.507	0.5874	0.4187	0.2143	0.8156	0.4685	1.2439	0.2219	0.197
245190_at	AT1G67690	peptidase M3 family protein / thimet oligopeptidase	0.108	0.5195	0.4289	-0.2146	0.2337	0.254	-0.4242	0.0503	0.095	-0.7467	0.0082	0.0281
245191_at	AT1G67710	TEL2 (TERMINAL EAR1-LIKE 2); RNA binding	0.4583	0.5799	0.4522	-0.6278	0.4562	0.3666	-1.2497	0.0159	0.0504	-2.3358	0.0017	0.0145
245192_at	AT1G67780	similar to unknown protein [Arabidopsis thaliana] (T	1.1268	0.1024	0.1044	0.6684	0.5295	0.3961	0.9507	0.3835	0.3094	-1.5076	0.1959	0.1825
245193_at	AT1G67810	Fe-S metabolism associated domain-containing pro	1.3065	0.0531	0.1323	1.2543	0.0595	0.1212	0.3438	0.011	0.0415	0.2916	0.0191	0.0443
245194_at	AT1G67820	protein phosphatase 2C, putative / PP2C, putative	0.6806	0.0346	0.1076	0.4465	0.1079	0.1656	-0.114	0.4996	0.3596	-0.348	0.0863	0.11
245195_at	AT1G67740	PSBY (photosystem II 8Y)	-0.5878	0.0255	0.0925	-0.7396	0.012	0.0587	0.3545	0.0374	0.0798	0.2026	0.1545	0.1577
245196_at	AT1G67750	pectate lyase family protein	-0.3565	0.0966	0.1796	-0.1254	0.4894	0.3801	0.4353	0.0576	0.1026	0.6665	0.0156	0.0398
245197_at	AT1G67800	copine-related	0.8505	0.0016	0.0383	0.6939	0.0033	0.0371	0.2666	0.0743	0.1187	0.11	0.3779	0.2748
245198_at	AT1G67700	similar to unknown [Populus trichocarpa] (GB:ABK9	-0.7818	0.0015	0.038	-0.7427	0.0018	0.0323	0.2254	0.0603	0.1054	0.2645	0.0381	0.0669
245199_at	AT1G67730	YBR159; ketoreductase/ oxidoreductase	-0.1456	0.497	0.4192	-0.06112	0.7697	0.4804	0.3092	0.044	0.0876	0.3936	0.0209	0.0469
245200_at	AT1G67850	similar to unknown protein [Arabidopsis thaliana] (T	0.494	0.0404	0.116	0.3017	0.142	0.1923	0.02306	0.8958	0.4913	-0.1692	0.3639	0.2686
245201_at	AT1G67840	ATP-binding region, ATPase-like domain-containing	-0.3407	0.0314	0.1027	-0.7147	0.0024	0.0339	0.2043	0.1143	0.1519	-0.1698	0.1696	0.1696
245202_at	AT1G67720	leucine-rich repeat family protein / protein kinase fa	0.6104	0.048	0.1261	0.3655	0.167	0.2104	0.3261	0.2068	0.2159	0.08127	0.7267	0.4061
245203_at	AT3G33080	transposable element gene	-0.2348	0.4486	0.3974	-0.3911	0.2347	0.2546	0.2477	0.1426	0.1734	0.2632	0.3168	0.2468
245204_at	AT5G12270	oxidoreductase, 2OG-Fe(II) oxygenase family prote	0.5394	0.1765	0.2457	-1.397	0.0132	0.0613	0.4264	0.2648	0.2492	-1.51	0.0101	0.0314
245205_at	AT5G12280	RNA binding	0.1854	0.8063	0.5257	-0.3446	0.6519	0.4424	1.1887	0.1684	0.1907	0.6587	0.0407	0.286
245206_at	AT5G12290	similar to expressed protein [Oryza sativa (japonica	0.5743	0.0061	0.0538	0.1871	0.1589	0.2051	-0.1966	0.0215	0.959	-0.7838	0.0019	0.0151
245207_at	AT5G12310	zinc finger (C3HC4-type RING finger) family protein	-0.3036	0.0473	0.1252	-0.4295	0.0161	0.066	0.004225	0.9705	0.5101	-0.1216	0.32	0.2483
245208_at	AT5G12330	LRP1 (LATERAL ROOT PRIMORDIUM 1)	-1.0004	0.2847	0.3141	0.383	0.6613	0.4455	-1.5923	0.121	0.157	-0.209	0.8093	0.4315
245209_at	AT5G12340	similar to unknown protein [Arabidopsis thaliana] (T	0.9262	0.3223	0.3396	0.04937	0.9549	0.5331	0.3988	0.3027	0.2699	1.2757	0.0194	0.0447
245210_at	AT5G12350	no_match	0.1245	0.3405	0.3456	0.173	0.2073	0.2378	-0.2721	0.0774	0.1215	-0.2235	0.1242	0.1378
245211_at	AT5G12370	SEC10 (EXOCYST COMPLEX COMPONENT SEC	0.5451	0.0068	0.0555	0.08113	0.4865	0.3789	-0.3857	0.022	0.0598	-0.8496	0.0013	0.0133
245212_at	no_match	no_match	0.1806	0.1392	0.2167	1.0428	0.4281	0.3544	-0.07959	0.9496	0.5055	3.1439	0.0566	0.0854
245213_at	AT1G44575	NPQ4 (NONPHOTOCHEMICAL QUENCHING)	-0.7027	0.0049	0.0501	-0.9965	0.0013	0.0312	0.1579	0.1392	0.1705	-0.1359	0.1881	0.1782
245214_at	no_match	no_match	0.02114	0.9867	0.5735	-0.4567	0.7201	0.4655	-0.01779	0.9886	0.515	-0.4957	0.6925	0.3949
245215_at	AT1G67830	ATFXG1 (ALPHA-FUCOSIDASE 1); alpha-L-fucos	-0.2283	0.2831	0.3134	-0.3277	0.1499	0.198	-0.01477	0.964	0.5034	-0.1142	0.5689	0.3523
245216_at	AT4G16143	importin alpha-2, putative (IMPA-2)	-0.06439	0.6637	0.4806	0.0507	0.7308	0.4687	-1.0138	0.0018	0.0206	-0.8987	0.0028	0.0174
245217_at	AT1G38340	transposable element gene	0.3031	0.6853	0.4877	-1.2609	0.1439	0.1936	1.0918	0.1762	0.1961	-0.4722	0.5172	0.3324
245218_at	AT1G58218;AT1G58848	[AT1G58218, disease resistance protein (CC-NBS-(	0.339	0.4277	0.3883	0.002496	0.9951	0.5429	-0.903	0.0142	0.0475	-1.2396	0.0047	0.0216
245219_at	AT1G58807;AT1G59124	[AT1G58807, disease resistance protein (CC-NBS-(	0.6775	0.0111	0.066	0.1678	0.3305	0.3087	-0.7659	0.002	0.0212	-1.2755	3.00E-04	0.0083
245220_at	AT1G59171	similar to unknown protein [Arabidopsis thaliana] (T	0.199	0.8946	0.5499	-1.7208	0.2894	0.2862	0.7887	0.5926	0.3956	-1.1311	0.4517	0.3067
245221_s_at	AT1G59889;AT1G59265	[AT1G59889, transposable element gene];[AT1G

245290_at	AT4G16490	armadillo/beta-catenin repeat family protein	-1.0841	0.0184	0.0807	-0.9328	0.0297	0.0856	-0.8543	0.0098	0.0395	-0.7029	0.0189	0.044
245291_at	AT4G16155	dihydrolipoamide dehydrogenase 2, plastidic / lipoa	-0.4798	0.125	0.2047	-0.6677	0.0545	0.1158	-0.5242	0.06	0.1051	-0.7121	0.0242	0.051
245292_at	AT4G15093	catalytic LigB subunit of aromatic ring-opening dioxe	0.2346	0.321	0.335	0.2179	0.3525	0.3193	0.1741	0.3619	0.2991	0.1574	0.4051	0.2862
245293_at	AT4G16660	heat shock protein 70, putative / HSP70, putative	1.3753	0.0012	0.036	1.3528	0.0013	0.0306	-0.4286	0.0309	0.0716	-0.451	0.0264	0.0538
245294_at	AT4G14340	CK1 (CASEIN KINASE I); casein kinase I/ kinase	-0.1833	0.35	0.3497	-0.2901	0.1695	0.2122	-0.4953	0.009	0.0378	-0.6021	0.0045	0.0212
245295_at	AT4G16100	similar to unknown protein [Arabidopsis thaliana] (T	0.424	0.0046	0.049	0.4534	0.0036	0.0378	-0.4053	0.0011	0.0183	-0.3758	0.0015	0.0137
245296_at	AT4G16370	ATOPT3 (OLIGOPEPTIDE TRANSPORTER); oligo	0.9958	0.004	0.0468	0.5649	0.0281	0.0835	-0.00936	0.9277	0.5	-0.4403	0.0105	0.032
245297_at	AT4G16510	Ybak/prolyl-RNA synthetase-related	0.1615	0.5084	0.4244	-0.04557	0.8445	0.5028	-0.03303	0.8892	0.4895	-0.241	0.3398	0.258
245298_at	AT4G15010	mitochondrial substrate carrier family protein	0.4245	0.0616	0.1425	0.6461	0.0173	0.0681	-0.4761	0.0446	0.0884	-0.2546	0.1974	0.1833
245299_at	AT4G17530	RAB1C; GTP binding	-0.1815	0.0923	0.176	-0.3481	0.0134	0.0616	0.693	0.0011	0.0182	0.5264	0.0031	0.018
245300_at	AT4G16360	CBL6 (CALCINEURIN B-LIKE PROTEIN 6)	-0.9148	0.2336	0.2839	-1.7012	0.0596	0.1213	0.485	0.3262	0.2814	-0.3015	0.5253	0.336
245301_at	AT4G17190	FPS2 (FARNESYL DIPHOSPHATE SYNTHASE 2);	-0.2104	0.3921	0.3711	-0.1818	0.4541	0.3656	0.2893	0.2053	0.215	0.3179	0.1721	0.1685
245302_at	AT4G17695	KAN3 (KANADI 3); DNA binding / transcription facto	0.9805	0.0182	0.0804	0.6662	0.0587	0.1204	0.3993	0.1912	0.2063	0.08498	0.7548	0.4151
245303_at	AT4G17010	similar to Os04g0431800 [Oryza sativa (japonica cu	0.5765	0.0044	0.0482	0.9554	7.00E-04	0.027	0.3497	0.0247	0.0637	0.7286	0.0019	0.0149
245304_at	AT4G15630	integral membrane family protein	-0.7016	0.0039	0.0464	-0.5504	0.0094	0.0529	0.6195	0.002	0.0211	0.7707	9.00E-04	0.0114
245305_at	AT4G17215	similar to unknown protein [Arabidopsis thaliana] (T	-0.3316	0.429	0.3886	-0.2446	0.5521	0.4056	0.04444	0.8988	0.492	0.1315	0.709	0.4005
245306_at	AT4G14690	ELIP2 (EARLY LIGHT-INDUCIBLE PROTEIN 2); ch	-2.0108	0.0012	0.036	-1.5754	0.003	0.0355	0.3796	0.1949	0.2087	0.815	0.0289	0.0569
245307_at	AT4G16770	oxidoreductase, 2OG-Fe(II) oxygenase family prote	-0.2838	0.286	0.3148	0.06248	0.7999	0.4896	-0.2097	0.0751	0.1193	0.1365	0.1944	0.1816
245308_at	AT4G17486	Identical to UPF0326 protein At4g17486 [Arabidops	0.4439	0.0522	0.1312	0.5579	0.0264	0.0813	-0.5018	0.0365	0.0787	-0.3878	0.0753	0.1009
245309_at	AT4G15140	similar to unknown [Populus trichocarpa] (GB:ABK9	-0.2147	0.4857	0.414	0.3513	0.2775	0.2795	0.6696	0.0136	0.0464	1.2356	0.0015	0.0137
245310_at	AT4G13950	RALFL31 (RALF-LIKE 31)	-0.1508	0.2462	0.2914	0.08701	0.4774	0.3753	0.3295	0.0414	0.0845	0.5673	0.007	0.026
245311_at	AT4G16440	60S ribosomal protein L36a/L44 (RPL36aB)	0.09657	0.4136	0.3817	0.2175	0.1093	0.1689	0.5183	0.0081	0.0361	0.6392	0.0038	0.02
245312_at	AT4G14600	Identical to Bet1-like protein At4g14600 [Arabidops	0.1155	0.445	0.3956	0.7721	0.0048	0.042	-0.00074	0.9959	0.5166	0.6559	0.0086	0.0289
245313_at	AT4G15420	PRLI-interacting factor K	0.5871	0.0046	0.0492	0.632	0.0035	0.0375	0.06777	0.5455	0.3775	0.1128	0.3339	0.2552
245314_at	AT4G16745	exostosin family protein	-0.1796	0.3288	0.3392	-0.3079	0.1295	0.1826	-0.3727	0.0825	0.1261	-0.501	0.0363	0.0647
245315_at	AT4G14800	PBD2 (20S PROTEASOME BETA SUBUNIT 2); pe	0.859	0.0155	0.0753	0.8665	0.0151	0.0646	0.4675	0.0226	0.0607	0.475	0.0214	0.0476
245316_at	AT4G14000	similar to unknown protein [Arabidopsis thaliana] (T	-0.05754	0.7539	0.5097	0.195	0.3186	0.3022	-0.1129	0.4915	0.3563	0.1397	0.4021	0.2851
245317_at	AT4G15610	integral membrane family protein	0.7471	0.2516	0.2943	1.203	0.0973	0.1572	0.2455	0.2305	0.2298	0.7014	0.0156	0.0399
245318_at	AT4G16980	arabinogalactan-protein family	-1.1616	0.002	0.0398	-1.4993	7.00E-04	0.0275	0.7648	0.0031	0.0249	0.4271	0.0234	0.0499
245319_at	AT4G16146	similar to unknown protein [Arabidopsis thaliana] (T	0.8498	0.0362	0.1097	1.4053	0.0068	0.0467	0.2909	0.3483	0.2923	0.8464	0.0366	0.0651
245320_at	AT4G16444	similar to unnamed protein product [Vitis vinifera] (G	0.5238	0.0098	0.0636	0.8644	0.0016	0.0316	0.4202	0.0206	0.0578	0.7608	0.0026	0.0168
245321_at	AT4G15545	similar to unknown protein [Arabidopsis thaliana] (T	-0.3509	0.1279	0.2067	-0.5996	0.0307	0.087	-0.1119	0.243	0.2368	-0.3606	0.0116	0.0338
245322_at	AT4G14815	protease inhibitor/seed storage/lipid transfer protein	-1.7352	0.0573	0.1372	2.5164	0.0185	0.0704	-3.451	0.0063	0.0328	0.8006	0.2894	0.2331
245323_at	AT4G16500	cysteine protease inhibitor family protein / cystatin fa	0.6587	0.1233	0.2035	-0.1211	0.7394	0.4708	0.7948	0.0029	0.0246	1.3324	4.00E-04	0.0089
245324_at	AT4G17260	L-lactate dehydrogenase, putative	-0.2044	0.2475	0.2921	-0.3968	0.0584	0.1202	0.1204	0.4703	0.3478	-0.07197	0.6587	0.3837
245325_at	AT4G14130	XTR7 (XYLOGLUCAN ENDOTRANSGLYCOSYLA	-0.6153	0.2841	0.3139	-0.7795	0.1925	0.2277	0.4401	0.0486	0.0928	0.276	0.1536	0.1572
245326_at	AT4G14100	transferase, transferring glycosyl groups	0.7477	0.0081	0.0411	0.5402	0.4007	0.402	-0.142	0.5388	0.3748	-0.07347	0.7459	0.4123
245327_at	AT4G16850	similar to unknown protein [Arabidopsis thaliana] (T	0.0537	0.8247	0.531	0.4911	0.0967	0.1566	-0.3791	0.0435	0.087	0.05836	0.6769	0.3897
245328_at	AT4G14465	DNA-binding protein-related	-0.01566	0.9847	0.5732	-0.9867	0.2666	0.2736	1.4709	0.1268	0.1616	0.4999	0.5491	0.3448
245329_at	AT4G14365	zinc finger (C3HC4-type RING finger) family protein	1.1483	0.0161	0.1359	1.0853	0.0655	0.1279	0.2096	0.1915	0.2064	0.1465	0.3339	0.2552
245330_at	AT4G14930	acid phosphatase survival protein SurE, putative	0.1893	0.502	0.4214	-0.03703	0.8923	0.5164	-0.3577	0.035	0.0767	-0.5841	0.0069	0.0259
245331_at	AT4G14410	basic helix-loop-helix (bHLH) family protein	0.1859	0.2585	0.2988	0.3751	0.0567	0.1184	0.3769	0.0559	0.1009	0.5662	0.016	0.0404
245332_at	AT4G15490	fumarylacetoacetate hydrolase family protein	0.1332	0.4498	0.3979	-0.141	0.426	0.3534	0.745	0.0095	0.0389	0.4708	0.0417	0.071
245333_at	AT4G14615	similar to unknown protein [Arabidopsis thaliana] (T	0.281	0.0798	0.1628	0.2188	0.1431	0.1931	0.08261	0.2474	0.2396	0.02041	0.7549	0.4151
245334_at	AT4G15800	RALFL33 (RALF-LIKE 33)	-0.797	0.0223	0.0875	-0.5612	0.0632	0.1252	0.5015	0.0584	0.1034	0.7373	0.0181	0.0432
245335_at	AT4G16500	ATOEP16-2/ATOEP16-S; P-P-bond-hydrolysis-driv	0.6587	0.1233	0.2035	-0.5925	0.5117	0.3893	0.6456	0.1897	0.2054	1.3324	4.00E-04	0.0089
245336_at	AT4G16515	unknown protein	-0.8676	0.0157	0.0756	-1.0269	0.0088	0.0516	1.3038	0.0025	0.0234	1.1445	0.0041	0.0206
245337_at	AT4G16566	histidine triad family protein / HIT family protein	-0.1365	0.2849	0.3142	-0.1799	0.1792	0.2191	0.4144	0.0135	0.0461	0.3709	0.0194	0.0447
245338_at	AT4G16642	integral membrane family protein	-0.9613	0.0073	0.0572	-0.6109	0.0054	0.0432	0.3727	0.0037	0.0266	0.3231	0.0061	0.0243
245339_at	AT4G16120	ATSEB1	-0.4169	0.0774	0.1602	-0.3572	0.1129	0.1699	-0.09836	0.6069	0.4003	-0.03866	0.8373	0.4393
245340_at	AT4G14420	lesion inducing protein-related	1.0611	0.0106	0.0647	1.3787	0.0042	0.04	-0.0656	0.7653	0.4528	0.2519	0.287	0.2318
245341_at	AT4G16447	unknown protein	0.1254	0.7667	0.7494	0.1306	0.1833	0.1406	0.4484	0.3186	0.2777	1.0734	0.0531	0.0823
245342_at	AT4G16720	60S ribosomal protein L15 (RPL15A)	0.2689	0.0564	0.1361	0.4072	0.0157	0.0653	-0.09213	0.4135	0.3224	0.04617	0.6715	0.3879
245343_at	AT4G15830	binding	0.4823	0.4089	0.3795	0.3724	0.5159	0.391	0.4424	0.0383	0.0809	0.3326	0.0842	0.1083
245344_at	AT4G15475	F-box family protein (FBL4)	0.2641	0.0835	0.1672	0.3284	0.0493	0.1067	-0.4047	0.0183	0.0541	-0.3404	0.0317	0.06
245345_at	AT4G16640	matrix metalloproteinase, putative	0.3785	0.7216	0.4999	0.9367	0.3976	0.3403	-0.198	0.8512	0.4788	0.3602	0.7344	0.4086
245346_at	AT4G17090	CT-BMY (BETA-AMYLASE 3, BETA-AMYLASE 8);	-0.5772	0.305	0.3256	-0.5964	0.2914	0.2873	-0.5484	0.0124	0.0443	-0.5675	0.0111	0.0329
245347_at	AT4G14890	ferredoxin family protein	-0.2792	0.1355	0.2137	-0.2497	0.1705	0.2129	0.5712	0.0188	0.055	0.6007	0.0159	0.0403
245348_at	AT4G17770	ATTPS5 (Arabidopsis thaliana trehalose phosphata	0.3244	0.0489	0.1271	-0.04752	0.7028	0.46	0.4061	0.0248	0.0639	0.0342	0.7826	0.4236
245349_at	AT4G16690	esterase/lipase/thioesterase family protein	0.01506	0.9422	0.563	-0.1808	0.4066	0.3443	-0.2939	0.0139	0.0471	-0.4898	0.0022	0.0158
245350_at	AT4G16830	nuclear RNA-binding protein (RBGA)	0.06816	0.7918	0.5214	0.2405	0.3759	0.3301	0.2914	0.0332	0.0743	0.4637	0.0071	0.0262
245351_at	AT4G17640	CKB2 (casein kinase II beta chain 2); protein kinase	0.2267	0.0342	0.1071	0.3353	0.0095	0.0534	-0.1139	0.1878	0.2042	-0.00523	0.9454	0.4697
245352_at	AT4G15490	UGT84A3; UDP-glycosyltransferase/ sinapate 1-glu	0.5239	0.0715	0.1541	0.3374	0.1917	0.2272	0.3305	0.199	0.2112	0.144	0.5397	0.341
245353_at	AT4G16000	similar to unknown protein [Arabidopsis thaliana] (T	-0.04364	0.9412	0.5628	0.495	0.4235	0.3523	0.8269	0.1242	0.1595	1.3656	0.0327	0.0611
245354_at	AT4G17600	LIL3:1; transcription factor	-0.7368	0.0038	0.0462	-0.8793	0.002	0.033	0.4397	0.0227	0.0609	0.2971	0.0717	0.0982
245355_at	AT4G17390	60S ribosomal protein L15 (RPL15B)	-0.1446	0.5555	0.443	0.03353	0.8887	0.5155	-0.03114	0.8371	0.4748	0.1469	0.3591	0.2666
245356_at	AT4G13940	HOG1 (HOMOLOGY-DEPENDENT GENE SILENC	0.04858	0.8096	0.5266	-0.06292	0.7556	0.4768	-0.6227	0.0144	0.0479	-0.7342	0.0082	0.0281
245357_at	AT4G17560	ribosomal protein L19 family protein	-0.6721	0.0273	0.0957	-0.7169	0.0222	0.0753	-0.1707	0.3654	0.3007	-0.2155	0.2673	0.2213
245358_at	AT4G15900	PRL1 (PLEIOTROPIC REGULATORY LOCUS 1); r	0.3681	0.1047	0.1869	0.2589	0.2155	0.2431	-0.08231	0.6402	0.4111	-0.1916	0.3051	0.2411
245359_at	AT4G14430	enoyl-CoA hydratase/isomerase family protein	1.2181	0.0021	0.0404	0.9959	0.0044	0.0409	0.04414	0.8095	0.4664	-0.178	0.3576	0.2659
245360_at	AT4G16330	oxidoreductase, 2OG-Fe(II) oxygenase family prote	0.6162	0.0482	0.1265	0.5063	0.0819	0.1436	-0.1639	0.319	0.2778	-0.2738	0.1303	0.1417
245361_at	AT4G17790	similar to unknown protein [Arabidopsis thaliana] (T	0.3643	0.0761	0.1586	0.02569	0.8749	0.5116	-0.3151	0.0464	0.0903	-0.6537	0.0041	0.0205
245362_at	AT4G17460	HAT1 (homeobox-leucine zipper protein 1); DNA bi	-0.2839	0.0797	0.1628	-0.7143	0.0042	0.0401	0.7215	0.004	0.0274	0.291	0.0748	0.1006
245363_at	AT4G15120	VQ motif-containing protein	-0.2587	0.3094	0.3282	0.1526	0.5303	0.3964	0.2234	0.3721	0.3039	0.6347	0.0462	0.0756
245364_at	AT4G15790	similar to unnamed protein product [Vitis vinifera] (G	-0.5475	0.0546	0.1341	-0.2817	0.2383	0.2567	0.7002	0.0262	0.0659	0.966	0.009	0.0296
245365_at	AT4G17720	RNA recognition motif (RRM)-containing protein	0.84	0.0015	0.038	0.9937	8.00E-04	0.0277	0.4223	0.0061	0.0325	0.576	0.002	0.0151
245366_at	AT4G14965	ATMAPR4 (ARABIDOPSIS THALIANA MEMBRAN	0.01921	0.9043	0.5525	0.04531	0.7776	0.4829	0.06764	0.6754	0.4228	0.09374	0.5658	0.3512
245367_at	AT4G16265	DNA-directed RNA polymerase II, putative	0.3962	0.1468	0.2229	0.3173	0.2236	0.2479	1.4726	0.0026	0.0235	1.3937	0.0032	0.0184
245368_at	AT4G15510	photosystem II reaction center PsbP family protein	-0.2834	0.1202	0.2005	-0.5215	0.0223	0.0754	0.00426	0.9778	0.512	-0.2338	0.1794	0.173
245369_at	no_match	no_match	-0.4145	0.5398	0.4367	-0.08663	0.8955	0.5173	0.6974	0.2342	0.2318	1.0252	0.1087	0.1267
245370_at	AT4G16840	similar to unknown protein [Arabidopsis thaliana] (T	0.06538	0.7392	0.5054	-0.2602	0.2285	0.2506	0.2226	0.291	0.2641	-0.1029	0.6041	0.3646
245371_at	AT4G15750	invertase/pectin methylesterase inhibitor family prot	-0.5678	0.3676	0.3582	-0.4376	0.4778	0.3754	-0.2648	0.6607	0.4181	-0.1347	0.8216	0.4346
245372_at	AT4G15000	60S ribosomal protein L27 (RPL27C)	-0.2027	0.1559	0.2302	0.08673	0.4967	0.3831	0.4175	3.00E-04	0.0138	0.7069	0	0.0053
245373_s_at	AT4G14716;AT4G14710	[AT4G14716, ATARD1; acireductone dioxygenase	0.2208	0.2705	0.3057	0.4505	0.0596	0.1213	0.3226	0.0012	0.0187	0.5523	1.00E-04	0.0069
245374_at	AT4G17620	glycine-rich protein	0.5733	5.00E-04	0.032	0.3791	0.0023	0.0336	0.1972	0.0126	0.0446	0.003016	0.9507	0.4711
245375_at	AT4G17660	protein kinase, putative	2.5803	0.0071	0.0567	1.3949	0.0516	0.1127	0.1849	0.7343	0.443	-1.0004	0.1203	0.1352
245376_at	AT4G17690	peroxidase, putative	0.5225	0.211	0.269	-1.1561	0.0302	0.0863	0.5493	0.1772	0.1967	-1.1293	0.0282	0.0561
245377_at	no_match	no_match	-2.6139	0.0586	0.1387	0.7479	0.4948	0.3825	-2.0531	0.0308	0.0714	1.3087	0.1054	0.1242
245378_at	AT4G17710	homeobox-leucine zipper family protein / lipid-bindi	0.8381	0.3993	0.375	-1.25	0.2325	0.2532	-0.3365	0.6027	0.3992	-2.4246	0.0153	0.0394
245379_at	AT4G17750	HSF1 (ARABIDOPSIS HEAT SHOCK FACTOR 1);	0.1201	0.3328	0.3417	0.02375	0.8384	0.501	0.2312	0.1015	0.1423	0.1348	0.2842	0.2305
245380_at	AT4G17760	damaged DNA binding / exonuclease	-0.21	0.7833	0.5187	0.445	0.5669	0.4107	0.14	0.8541	0.4795	0.795	0.3279	0.2523
245381_at	AT4G17785	MYB39 (MYB DOMAIN PROTEIN 39); DNA binding	0.4067	0.6996	0.4923	-1.4406	0.2157	0.2432	1.4442	0.2147	0.2207	-0.4031	0.7021	0.398
245382_at	AT4G17800	DNA-binding protein-related	0.2496	0.8241	0.5307	-1.1816	0.3242	0.3055	0.2597	0.7023	0.432	-1.1715	0.1375	0.1465
245383_at	AT4G17810	nucleic acid binding / transcription factor/ zinc ion bi	-0.7759	5.00E-04	0.032	-0.8196	4.00E-04	0.0251	0.2833	0.0141	0.0473	0.2396	0.0243	0.0513
245384_at	AT4G16790	hydroxyproline-rich glycoprotein family protein	0.4024	0.097	0.1798	0.6816	0.0216	0.0747	0.2902	0.1374	0.1693	0.5694	0.022	0.0484
245385_at	AT4G14020	rapid alkalinization factor (RALF) family protein	0.5215	0.3035	0.325	1.2356	0.049	0.1097	1.2651	3.00E-04	0.0134	1.9792	0	0.0055
245386_at	AT4G14010	RALFL32 (RALF-LIKE 32)	-0.1378	0.3473	0.3486	-0.03449	0.8032	0.4905	0.02707	0.8447	0.477	0.1304	0.3711	0.2716
245387_at	AT4G17520	nuclear RNA-binding protein, putative	0.1122	0.3504	0.3498	0.3077	0.0442	0.1041	0.7306	0.0018	0.0206	0.9261	7.00E-04	0.0108
245388_at	AT4G16410	similar to hypothetical protein [Vitis vinifera] (GB:CA	-0.4235	0.0137	0.0719	-0.1716	0.1645	0.2087	-0.3918	0.0178	0.0534	-0.1398	0.2382	0.2062
245389_at	AT4G17480	palmitoyl protein thioesterase family protein	0.192	0.7807	0.518	1.3876	0.0977	0.1575	0.3326	0.6332	0.4088	1.5281	0.0768	0.1022
245390_at	AT4G17650	aromatic-rich family protein	0.2534	0.2571	0.2978	-0.05748	0.7794	0.4834	0.3231	0.0516	0.0962	0.01224	0.9222	0.4636
245391_at	AT4G16520	ATG8F (AUTOPHAGY 8F); microtubule binding	0.1754	0.6048	0.4612	0.4007	0.2694	0.2751	0.6767	0.026	0.0656	0.902	0.01	0.0312
245392_at	AT4G15680	glutaredoxin family protein	-1.5499	0.0077	0.058	-0.7781	0.0672	0.1298	0.3844	0.2735	0.2543	1.1561	0.0189	0.044
245393_at	AT4G16260	glycosyl hydrolase family 17 protein	1.0079	0.3294	0.3396	0.7947	0.431	0.3557	0.5269	0.048	0.092	0.3138	0.1688	0.1665
245394_at	AT4G16450	similar to unknown [Populus trichocarpa] (GB:ABK9	-0.0955	0.6199	0.4665	-0.06243	0.7434	0.4725	0.8929	0.0074	0.0348	0.926	0.0065	0.025
245395_at	AT4G17420	similar to unknown protein [Arabidopsis thaliana] (T	0.4732	0.022	0.0872	0.1538	0.3028	0.2929	0.3478	0.0232	0.0616	0.02838	0.7847	0.4243
245396_at	AT4G14870	P-P-bond-hydrolysis-driven protein transmembrane	-0.161	0.398	0.3744	-0.04511	0.8042	0.4909	0.5507	0.0097	0.0393	0.6667	0.0049	0.022
245397_at	AT4G14560	IAA1 (INDOLE-3-ACETIC ACID INDUCIBLE); trans	-0.7224	0.0278	0.0966	-0.2267	0.3487	0.3175	0.3896	0.0069	0.0339	0.8853	3.00E-04	0.0084
245398_at	AT4G14900	hydroxyproline-rich glycoprotein family protein	0.4491	0.0236	0.0897	0.2609	0.1075	0.1653	0.6211	0.0079	0.0358	0.4329	0.0265	0.054
245399_at	AT4G17340	DELTA-TIP2/TIP2;2 (tonoplast intrinsic protein 2;2);	-1.3094	0.0023	0.0414	-1.4704	0.0015	0.0313	0.4086	0.0966	0.1382	0.2476	0.2603	0.2179
245400_at	AT4G17040	ATP-dependent Clp protease proteolytic subunit, pu	-0.01657	0.9199	0.557	-0.2308	0.2104	0.2399	-0.4493	0.0182	0.054	-0.6635	0.0047	0.0217
245401_at	AT4G17760	senescence-associated protein-related	1.5627	5.00E-04	0.032	1.8638	2.00E-04	0.0249	0.1279	0.4375	0.333	0.429	0.0446	0.0741
245402_at	AT4G17585	similar to unknown protein [Arabidopsis thaliana] (T	-1.6577	0.0923	0.176	-1.6773	0.0897	0.1509	0.2395	0.7662	0.453	0.2199	0.7847	0.4243
245403_at	AT4G17590	nucleolar protein-related	0.2165	0.8352	0.5339	-0.6325	0.5521	0.4056	0.5295	0.616	0.4031	0.1136	0.9729	0.4607
245404_at	AT4G17610	RNA/rRNA methyltransferase (SpoU) family protein	0.2372	0.3058	0.326	0.2077	0.3623	0.324	-0.3062	0.0373	0.0797	-0.3357	0.0282	0.056
245405_at	AT4G17150	similar to unknown protein [Arabidopsis thaliana] (T	0.4818	0.133	0.2116	0.4764	0.1363	0.1879	-0.2654	0.3263	0.2814	-0.2708	0.3178	0.2473
245406_at	AT4G17160	ARABB1a/ARab2b (Arabidopsis Rab GTPase hor	-1.7204	0.0855	0.1696	0.6264	0.4546	0.3659	-1.7764	0.0148	0.0482	0.5703	0.2562	0.2158
245407_at	AT4G17170	AT-RAB2 (Arabidopsis Rab GTPase homolog B1c);	-0.1657	0.3316	0.3409	-0.06669	0.6798	0.4518	-0.2353	0.192	0.2067	-0.1363	0.4151	0.2904
245408_at	AT4G17180	glycosyl hydrolase family 17 protein	0.06345	0.8558	0.54	-0.05534	0.874	0.5113	-0.0826	0.8133	0.4676	-0.2014	0.5718	0.3532
245409_at	AT4G17200	F-box family protein	0.02132	0.9816	0.5725	-1.5981	0.1399	0.1905	0.3982	0.0707	0.4213	-1.2212	0.2329	0.2031
245410_at	AT4G17220	ATMAP70-5 (microtubule-associated proteins 70-5);	-0.188	0.6152	0.4645	-0.3004	0.4337	0.3569	0.6124	0.151	0.1796	0.5001	0.2213	0.1968
245411_at	AT4G17240	similar to hypothetical protein 31.t00013 [Brassica c	-0.5281	0.4715	0.4081	1.5015	0.0869	0.1485	-0.5339	0.4437	0.3357	1.4957	0.0761	0.1016
245412_at	AT4G17280	auxin-responsive family protein	1.3143	0.2215	0.2761	0.6895	0.4902	0.3805	0.1678	0.8624	0.4819	-0.457	0.6414	0.3777
245413_at	AT4G17300	NS1 (OVULE ABORTION 8)	-0.2767	0.0369	0.1107	-0.311	0.0258	0.0803	-0.1894	0.1027	0.143	-0.2237	0.0675	0.0948
245414_at	AT4G17310	similar to unknown protein [Arabidopsis thaliana] (T	0.09901	0.5353	0.4352	0.09165	0.5646	0.41	0.7808	0.0059	0.032	0.7734	0.0061	0.0243
245415_at	AT4G17340	ATG2248-1 (Arabidopsis thaliana G2484-1 protein);	0.381	0.0451	0.1324	-0.1976	0.2097	0.2393	0.06619	0.5313	0.3718	-0.5125	0.0061	0.0242
245416_at	AT4G17350	similar to unknown protein [Arabidopsis thaliana] (T	-0.9909	0.0139	0.0723	-1.1662	0.0079	0.0496	0.7376	0.0359	0.0778	0.5622	0.0768	0.1022
245417_at	AT4G17360	formyltetrahydrofolate deformylase, putative	-0.99	0.0089	0.0609	-1.3232	0.0031	0.0363	-0.3264	0.1914	0.2063	-0.6596	0.0337	0.0621
245418_at	AT4G17370	oxidoreductase family protein	0.1311	0.4626	0.4041	0.1212	0.4947	0.3824	-0.3694	0.0675	0.1125	-0.2763	0.6628	0.091
245419_at	AT4G17380	MSH4 (MUTS-LIKE PROTEIN 4); ATP binding / da	-1.2386	0.421	0.3854	-0.9665	0.523	0.3933	0.2697	0.8548	0.4797	0.5418	0.7151	0.4025
245420_at	AT4G17410	similar to unknown protein [Arabidopsis thaliana] (T	0.4091	0.0781	0.161	0.102	0.5887	0.4189	0.08909	0.4918	0.3564	-0.218	0.138	0.1469
245421_at	AT4G17430	similar to hypothetical protein 31.t00055 [Brassica c	0.05282	0.5894	0.4559	-0.3298	0.0216	0.0747	-0.1289	0.0358	0.0777	-0.4059	6.00E-04	0.0103
245422_at	AT4G17470	palmitoyl protein thioesterase family protein	-0.8553	0.039	0.114	-0.7304	0.0612

245490_at	AT4G16310	LDL3 (LSD1-LIKE3); amine oxidase	-0.5745	0.6809	0.4863	1.2922	0.3758	0.3301	-2.5578	0.0599	0.105	-0.6911	0.5207	0.3341
245491_at	no_match	no_match	-0.06087	0.7253	0.5012	-0.04526	0.7931	0.4871	-0.3291	0.1111	0.1492	-0.3135	0.1241	0.1377
245492_at	AT4G16340	SPK1 (SPIKE1); GTP binding / GTPase binding / bi	0.1038	0.6424	0.4737	0.08375	0.7066	0.4611	-0.0776	0.7269	0.4408	-0.09768	0.6617	0.3848
245493_at	no_match	no_match	0.04187	0.8958	0.5502	-0.6068	0.1133	0.1702	-0.08382	0.7939	0.4614	-0.7325	0.0712	0.0978
245494_at	AT4G16390	chloroplastic RNA-binding protein P67, putative	0.08568	0.5266	0.4318	-0.1861	0.2064	0.2371	-0.3305	0.019	0.0553	-0.6022	0.0023	0.0159
245495_at	AT4G16400	similar to unknown protein [Arabidopsis thaliana] (T	0.9836	0.1323	0.2107	-0.3327	0.5581	0.4076	0.411	0.4746	0.3495	-0.9053	0.1575	0.1597
245496_at	AT4G16440	iron hydrogenase family protein	0.5119	0.0185	0.0809	0.5009	0.0199	0.0722	0.03106	0.8274	0.472	0.02	0.8881	0.4537
245497_at	AT4G16460	unknown protein	-1.6498	0.1543	0.2293	0.8247	0.4301	0.3553	-1.7804	0.1313	0.1649	0.6941	0.5014	0.3264
245498_at	AT4G16470	binding	-0.00027	0.9988	0.5763	0.1245	0.4988	0.3841	-1.0314	0.0035	0.0262	-0.9066	0.0057	0.0234
245499_at	AT4G16480	ATINT4 (INOSITOL TRANSPORTER 4); carbohydr	0.1424	0.5556	0.4431	0.3313	0.2094	0.2392	-0.09651	0.6858	0.4264	0.09242	0.6962	0.3968
245500_at	AT4G15590	transposable element gene	-1.4391	0.2082	0.2671	-0.4996	0.6302	0.4346	-0.4338	0.6748	0.4225	0.5057	0.6262	0.3724
245501_at	AT4G15620	integral membrane family protein	-0.5908	0.0232	0.0892	-0.3997	0.0728	0.1351	0.3289	0.0358	0.0777	0.5199	0.0079	0.0277
245502_at	AT4G15640	similar to unknown protein [Arabidopsis thaliana] (T	0.3958	0.0249	0.0915	0.2594	0.0835	0.1452	-0.1295	0.3162	0.2763	-0.2658	0.0785	0.1036
245503_at	AT4G15660	protein kinase-related	0.3121	0.8083	0.5263	-1.0291	0.4409	0.3599	0.6002	0.4244	0.3272	-0.741	0.3341	0.2552
245504_at	AT4G15660	glutaredoxin family protein	-1.0474	0.0165	0.0772	-0.7884	0.0403	0.0995	0.631	0.0748	0.1191	0.89	0.0279	0.0557
245505_at	AT4G15690	glutaredoxin family protein	-0.5177	0.2451	0.2906	-0.2885	0.4904	0.3805	1.3252	0.0253	0.0645	1.5544	0.015	0.039
245506_at	AT4G15700	glutaredoxin family protein	-0.3185	0.4987	0.4199	0.4794	0.326	0.3065	0.7509	0.0637	0.1087	1.5488	0.0063	0.0246
245507_at	AT4G15710	unknown protein	-0.1219	0.8787	0.5462	-0.1386	0.8623	0.5078	-0.1048	0.8942	0.4909	-0.1215	0.8775	0.4506
245508_at	AT4G15720	pentatricopeptide (PPR) repeat-containing protein	-0.1778	0.8635	0.5419	0.1757	0.8651	0.5086	0.9029	0.4048	0.3184	1.2565	0.2651	0.2203
245509_at	AT4G15730	zinc ion binding	0.1759	0.5513	0.4417	0.2021	0.4907	0.3831	-0.1609	0.5779	0.3898	-0.1346	0.6394	0.377
245510_at	AT4G15740	C2 domain-containing protein	-0.6447	0.4372	0.3925	-1.0684	0.2263	0.2494	0.9306	0.2225	0.225	0.5068	0.4759	0.316
245511_at	AT4G15755	C2 domain-containing protein	-1.517	0.2293	0.2816	-2.0675	0.1255	0.1796	0.886	0.4542	0.3405	0.3356	0.7695	0.4197
245512_at	AT4G15770	60S ribosome subunit biogenesis protein, putative	0.3448	0.0132	0.0708	0.4627	0.0047	0.0418	0.2291	0.0434	0.087	0.347	0.0115	0.0337
245513_at	AT4G15780	ATVAMP724 (Arabidopsis thaliana vesicle-associat	0.5604	0.093	0.1767	1.162	0.0104	0.0552	-1.5933	0.0034	0.0256	-0.9917	0.0177	0.0427
245514_at	no_match	no_match	-0.4222	0.5176	0.4282	0.0921	0.8946	0.5145	-0.01258	0.9768	0.5118	0.5017	0.2847	0.2307
245515_at	AT4G15810	chloroplast outer membrane protein, putative	0.4581	0.61	0.463	-0.3574	0.6886	0.4552	-1.7794	0.0592	0.1044	-2.5949	0.0189	0.0441
245516_at	AT4G15820	wound-responsive protein-related	0.3917	0.1723	0.243	0.5614	0.0761	0.1382	-0.5768	0.0312	0.0719	-0.4071	0.0832	0.1076
245517_at	AT4G15840	protein binding	0.4301	0.0762	0.1589	0.3449	0.1293	0.1825	-0.04108	0.815	0.4683	-0.1263	0.4852	0.3197
245518_at	AT4G15850	ATRH1 (Arabidopsis thaliana RNA helicase 1); ATP	0.000416	0.9989	0.5763	0.5313	0.13	0.1828	-1.2649	0.0106	0.0409	-0.734	0.0583	0.0871
245519_at	AT4G15860	transposable element gene	-0.5757	0.2541	0.296	-2.8004	0.0029	0.0355	-0.508	0.3054	0.2714	-2.7327	0.0032	0.0184
245520_at	AT4G15870	ATTS1 (Arabidopsis thaliana terpene synthase 1); t	0.6666	0.2698	0.4621	-0.4335	0.746	0.4736	0.4226	0.7521	0.4488	-0.7075	0.6014	0.3638
245521_at	AT4G15880	ESD4 (EARLY IN SHORT DAYS 4); cysteine-type p	0.03695	0.6874	0.4884	-0.02686	0.7687	0.4801	0.2285	0.0253	0.0646	0.2386	0.0221	0.0484
245522_at	AT4G15890	binding	-0.2959	0.0829	0.1666	-0.2173	0.1664	0.21	-0.1269	0.3795	0.3076	-0.04834	0.7261	0.406
245523_at	AT4G15910	ATDI21 (Arabidopsis thaliana drought-induced 21)	0.7842	0.0907	0.1745	1.5224	0.0126	0.06	-1.3254	0.0019	0.0208	-0.5873	0.0322	0.0606
245524_at	AT4G15920	nodulin MtN3 family protein	-0.422	0.1093	0.1914	-0.5062	0.0695	0.1321	0.1591	0.4719	0.3483	0.07489	0.7278	0.4065
245525_at	AT4G15930	dynein light chain, putative	0.04687	0.8254	0.5311	-0.07174	0.7368	0.4703	1.0916	0.0054	0.0308	0.973	0.0081	0.028
245526_at	AT4G15950	similar to unknown protein [Arabidopsis lyrata] (GB:	-0.1755	0.4226	0.3863	-0.1277	0.5515	0.4054	0.1686	0.4399	0.334	0.2163	0.3332	0.2549
245527_at	AT4G15955	epoxide hydratase-related	0.4943	0.2148	0.2715	0.5608	0.17	0.2126	-0.4247	0.2539	0.2431	-0.3581	0.3244	0.2504
245528_at	AT4G15530	PPDK (PYRUVATE ORTHOPHOSPHATE DIKINAS	0.4369	0.1766	0.2458	0.3008	0.3222	0.3043	-0.2431	0.0412	0.0842	-0.3791	0.0098	0.0309
245529_at	AT4G15570	tRNA-splicing endonuclease positive effector-relate	0.2025	0.1718	0.2427	-0.1134	0.4046	0.3433	-0.4003	0.0303	0.0709	0.7163	0.0042	0.0207
245530_at	AT4G15590	transposable element gene	-0.08323	0.8681	0.5433	-0.7356	0.1928	0.2278	0.3784	0.4662	0.3458	-0.274	0.5913	0.3603
245531_at	AT4G15100	SCPL30 (serine carboxypeptidase-like 30); serine c	0.1223	0.91	0.554	0.36	0.7409	0.4715	-0.3284	0.7627	0.4519	-0.09064	0.9332	0.4665
245532_at	AT4G15110	CYP97C1 (cytochrome P450, family 97, subfamily	-0.3646	0.0195	0.0826	-0.5959	0.0035	0.0374	-0.04547	0.6624	0.4187	-0.2768	0.0457	0.0755
245533_at	AT4G15130	cholinephosphate cytidylyltransferase, putative / ph	-0.4977	7.00E-04	0.0334	-0.2656	0.0076	0.0488	0.07726	0.2204	0.2238	0.3093	0.0044	0.021
245534_at	AT4G15150	glycine-rich protein	0.5413	0.5478	0.4401	-0.3781	0.6707	0.4488	0.1129	0.8978	0.4917	-0.8065	0.3839	0.2776
245535_at	AT4G15160	protease inhibitor/seed storage/lipid transfer protein	-0.02311	0.9462	0.5636	0.1312	0.704	0.4605	0.09585	0.7804	0.4576	0.2502	0.4799	0.3175
245536_at	no_match	no_match	0.1037	0.5296	0.433	-0.2254	0.2095	0.2393	-0.3378	0.0887	0.1315	-0.6669	0.0115	0.0337
245537_at	no_match	no_match	-0.6277	0.2374	0.2861	0.3665	0.4632	0.3694	-2.2959	0.0071	0.0341	-1.3017	0.0451	0.0744
245538_at	AT4G15200	formin homology 2 domain-containing protein / FH2	-0.1363	0.9106	0.5542	0.5996	0.6269	0.4334	1.1625	0.3656	0.3008	1.8994	0.1713	0.168
245539_at	AT4G15230	ATPDR2/PDR2 (PLEIOTROPIC DRUG RESISTAN	-0.3864	0.4286	0.3885	-0.134	0.7755	0.4823	0.1627	0.7216	0.4391	0.4151	0.3845	0.2778
245540_at	AT4G15230	ATPDR2/PDR2 (PLEIOTROPIC DRUG RESISTAN	-0.05741	0.8523	0.5389	-0.4194	0.2205	0.2462	-0.2924	0.3691	0.3023	-0.6545	0.0864	0.1101
245541_at	no_match	no_match	-0.2182	0.5909	0.4565	0.4586	0.2874	0.2851	-0.6315	0.0421	0.0855	0.04528	0.843	0.4408
245542_at	AT4G15250	zinc finger (B-box type) family protein	-0.6359	0.4037	0.3772	-0.1667	0.8188	0.4955	0.5788	0.4117	0.3216	1.0479	0.1728	0.1689
245543_at	AT4G15260	UDP-glucoronosyl/UDP-glucosyl transferase family	0.6291	0.0493	0.1276	0.9222	0.015	0.0644	-0.1913	0.2735	0.2543	0.1019	0.5365	0.3401
245544_at	AT4G15270	glucosyltransferase-related	0.0008683	0.9992	0.5764	0.7843	0.3731	0.3291	-0.4373	0.6061	0.4001	0.3459	0.6815	0.391
245545_at	AT4G15280	UDP-glucoronosyl/UDP-glucosyl transferase family	0.7335	0.4011	0.3758	3.4416	0.0117	0.0581	-0.6673	0.4413	0.3346	2.0408	0.0593	0.0879
245546_at	AT4G15290	ATCSLB06 (Cellulose synthase-like B5); transferase	-0.3082	0.7392	0.5054	1.193	0.2392	0.2572	-0.03716	0.9677	0.5095	1.464	0.1652	0.1644
245547_at	AT4G15300	CYP702A2 (cytochrome P450, family 702, subfamil	0.6554	0.1592	0.4289	0.3146	0.7518	0.4756	0.2711	0.7848	0.4587	-0.06972	0.9437	0.4693
245548_at	AT4G15310	CYP702A3 (cytochrome P450, family 702, subfamil	0.8987	0.3759	0.3623	-2.4475	0.0535	0.1147	2.2032	0.0712	0.116	-1.1429	0.2743	0.2252
245549_at	AT4G15320	ATCSLB06 (Cellulose synthase-like B6); transferase	-0.2264	0.7916	0.5213	-1.1304	0.2311	0.2522	0.5235	0.5491	0.3788	-0.3805	0.6596	0.384
245550_at	AT4G15330	CYP705A1 (cytochrome P450, family 705, subfamil	-0.7846	0.3554	0.3525	1.0024	0.2531	0.2658	0.0273	0.9725	0.5106	1.8143	0.0714	0.0979
245551_at	AT4G15350	CYP705A2 (cytochrome P450, family 705, subfamil	-1.6493	0.2918	0.3184	0.787	0.5937	0.4209	-1.4144	0.3559	0.2961	1.0219	0.493	0.3232
245552_at	AT4G15360	CYP705A3 (cytochrome P450, family 705, subfamil	-0.2638	0.688	0.4885	0.7822	0.2695	0.2752	0.04182	0.9487	0.5053	1.0878	0.1495	0.1543
245553_at	AT4G15370	BARS1 (BARLOL SYNTHASE 1); catalytic	-1.5099	0.0413	0.1171	-1.5974	0.035	0.0923	0.1779	0.6364	0.41	0.09044	0.8079	0.431
245554_at	AT4G15380	CYP705A4 (cytochrome P450, family 705, subfamil	-0.00227	0.996	0.5761	-1.4289	0.0287	0.0842	0.09651	0.8299	0.4727	-1.3301	0.0342	0.0625
245555_at	AT4G15390	transferase family protein	-0.374	0.7389	0.5053	0.8847	0.4454	0.362	-0.9259	0.4262	0.3281	0.3328	0.7664	0.4188
245556_at	AT4G15400	transferase family protein	1.1409	0.4259	0.3875	-0.443	0.7483	0.4745	0.7099	0.611	0.4016	-0.8741	0.5347	0.3397
245557_at	AT4G15410	UBX domain-containing protein	0.3266	0.112	0.194	0.3347	0.1058	0.1642	0.3537	0.0926	0.1348	0.3618	0.0876	0.1109
245558_at	AT4G15430	similar to early-responsive to dehydration protein-re	-0.618	0.2023	0.2638	-0.5457	0.2497	0.2636	-0.1036	0.6816	0.4248	-0.03133	0.9002	0.4573
245559_at	AT4G15460	glycine-rich protein	1.4971	0.2319	0.2831	0.8468	0.4704	0.3723	-0.2677	0.8136	0.4677	-0.918	0.4366	0.2999
245560_at	AT4G15480	UGT84A1; UDP-glycosyltransferase/ sinapate 1-glu	-0.4285	0.677	0.4849	-1.3258	0.2375	0.2562	-0.06685	0.8528	0.4792	-0.9642	0.0462	0.0755
245561_at	AT4G15500	UGT84A4; UDP-glycosyltransferase/ sinapate 1-glu	0.1021	0.6948	0.491	-0.108	0.6785	0.4514	0.5593	0.082	0.1256	0.3492	0.2226	0.1974
245562_at	AT4G15520	tRNA/rRNA methyltransferase (SpoU) family protein	0.9084	2.00E-04	0.0312	0.7641	4.00E-04	0.0249	-0.3864	2.00E-04	0.0126	-0.5306	0	0.0055
245563_at	AT4G14580	CIPK4 (CBL-INTERACTING PROTEIN KINASE 4);	0.3529	0.4852	0.414	0.6071	0.2568	0.2683	-0.674	0.1917	0.2065	-0.4198	0.3837	0.2775
245564_at	AT4G14590	EMB2739 (EMBRYO DEFECTIVE 2739)	0.1027	0.7591	0.5115	0.01904	0.9544	0.5329	-0.03585	0.9143	0.4962	-0.1195	0.7218	0.4046
245565_at	AT4G14605	mitochondrial transcription termination factor-relate	-0.1189	0.406	0.3784	-0.2656	0.1068	0.1649	-0.4305	0.0283	0.0683	-0.5773	0.0108	0.0325
245566_at	AT4G14610	pseudogene, disease resistance protein (CC-NBS-L	0.9945	0.0164	0.0771	0.785	0.0347	0.0921	0.2904	0.1129	0.1505	0.08086	0.603	0.3642
245567_at	AT4G14630	GLP9 (GERMIN-LIKE PROTEIN 9); manganese ior	2.1337	0.0861	0.1702	0.882	0.4019	0.3421	0.8184	0.3548	0.2957	-0.4332	0.6094	0.3665
245568_at	AT4G14650	unknown protein	-0.3994	0.4391	0.3932	-0.3895	0.4498	0.3638	0.3285	0.3181	0.2774	0.3385	0.3054	0.2412
245569_at	AT4G14660	RNA polymerase Rpb7 N-terminal domain-containir	0.3352	0.0607	0.1413	0.228	0.153	0.2004	-0.0015	0.9913	0.5155	-0.1087	0.4483	0.3054
245570_at	AT4G14670	CLPB2; ATP binding / nucleoside-triphosphatase/ n	-0.8035	0.5797	0.4521	-0.0353	0.9802	0.5393	1.2211	0.4121	0.3217	1.9893	0.2104	0.1911
245571_at	AT4G14695	similar to unknown protein [Arabidopsis thaliana] (T	0.3429	0.611	0.463	-1.1525	0.1377	0.189	2.1686	0.0199	0.0567	0.6733	0.309	0.2429
245572_at	AT4G14720	PPD2 (PEAPOD 2)	0.275	0.1938	0.2582	0.1758	0.3752	0.33	-0.1508	0.4406	0.3343	-0.25	0.2291	0.2011
245573_at	no_match	no_match	-0.4719	0.5769	0.4513	-0.5683	0.5057	0.3869	-0.5433	0.5216	0.3676	-0.6397	0.4552	0.308
245574_at	AT4G14750	IQD19 (IQ-DOMAIN 19); calmodulin binding	-0.6297	0.0755	0.1582	-1.6103	0.0037	0.038	0.568	0.0799	0.1237	-0.4126	0.1653	0.1644
245575_at	AT4G14760	M protein repeat-containing protein	-0.3157	0.1839	0.251	-0.4033	0.1097	0.1672	-1.011	0.0068	0.0337	-1.0986	0.005	0.0222
245576_at	AT4G14770	tesmin/TSO1-like CXC domain-containing protein	-0.9818	0.3516	0.3505	-1.1602	0.2812	0.2816	-0.2686	0.7875	0.4594	-0.447	0.6566	0.383
245577_at	AT4G14780	protein kinase, putative	-0.6933	0.5778	0.4517	-0.7992	0.5239	0.3937	0.06797	0.9555	0.5067	-0.03789	0.9752	0.4769
245578_at	AT4G14790	ATSUV3 (embryo sac development arrest 15)	-0.2066	0.4987	0.4199	-0.3789	0.2446	0.2608	-0.6929	0.0614	0.1066	-0.8652	0.0323	0.0607
245579_at	AT4G14810	unknown protein	0.8536	0.3437	0.3465	-0.6961	0.431	0.3557	1.6619	0.1049	0.1449	0.1122	0.8946	0.4556
245580_at	AT4G14820	pentatricopeptide (PPR) repeat-containing protein	-0.4333	0.4075	0.3791	0.07328	0.8833	0.514	-0.3376	0.511	0.3636	0.1689	0.7367	0.4093
245581_at	AT4G14840	similar to unknown protein [Arabidopsis thaliana] (T	-0.1266	0.8337	0.5336	1.0941	0.125	0.1792	-0.2593	0.6703	0.4211	0.9614	0.1642	0.1638
245582_at	AT4G14850	LOI1 (LOVASTATIN INSENSITIVE 1)	0.184	0.7868	0.5197	0.3376	0.6238	0.4323	-0.2437	0.7212	0.439	-0.09009	0.8942	0.4555
245583_at	AT4G14920	PHD finger transcription factor, putative	0.2909	0.3078	0.3274	0.1194	0.6569	0.4441	-0.6173	0.0668	0.1117	-0.7888	0.0331	0.0614
245584_at	AT4G14940	ATAO1 (Arabidosis thaliana amine oxidase 1); copp	-0.5892	0.4659	0.4056	-1.3369	0.1418	0.1921	1.0138	0.2236	0.2258	0.2661	0.7249	0.4056
245585_at	AT4G14970	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.2059	0.8745	0.5451	0.02847	0.9825	0.5398	-0.9357	0.4868	0.3541	-1.1131	0.4141	0.29
245586_at	AT4G14980	DC1 domain-containing protein	-1.5913	0.2107	0.2687	-0.1008	0.9294	0.5265	-1.174	0.3202	0.2784	0.3165	0.775	0.4215
245587_at	AT4G15020	similar to hAT dimerisation domain-containing prote	-0.05703	0.8017	0.5246	0.1975	0.4052	0.3436	-1.3124	0.0019	0.0207	-1.0578	0.0042	0.0207
245588_at	AT4G15030	similar to Phytr1 [Pimpinella brachycarpa] (GB:AAC	0.2293	0.3984	0.3746	0.768	0.0341	0.0911	-0.08427	0.7459	0.4468	0.4544	0.1345	0.1447
245589_at	AT4G15040	sulfotase family protein	-0.02003	0.9852	0.5733	-0.5178	0.6367	0.4371	0.9559	0.3994	0.3164	0.4582	0.6749	0.389
245590_at	AT4G15060	F-box protein-related	-0.1208	0.7786	0.5175	0.6648	0.1733	0.2151	-0.3912	0.3854	0.3102	0.3945	0.3817	0.2765
245591_at	AT4G14530	similar to AGL97, DNA binding / transcription factor	-0.4839	0.8116	0.5273	-0.6495	0.7497	0.4748	0.6559	0.6715	0.4215	0.4903	0.7499	0.4138
245592_at	AT4G14540	CCAAT-box binding transcription factor subunit B (H	0.0387	0.8214	0.53	0.29	0.1453	0.1948	0.2995	0.0074	0.0348	0.5468	8.00E-04	0.0108
245593_at	AT4G14550	IAA14 (SOLITARY ROOT); transcription factor	-0.6359	0.0361	0.1097	-0.378	0.1389	0.1899	0.9847	0.0033	0.0254	1.2427	0.0014	0.0133
245594_at	AT4G14570	acylaminoacyl-peptidase-related	-0.08384	0.6833	0.4869	-0.1447	0.4908	0.3806	-1.4136	0.0018	0.0206	-1.4745	0.0015	0.0138
245595_at	AT4G14170	pentatricopeptide (PPR) repeat-containing protein	-1.0975	0.3447	0.3472	0.552	0.6188	0.4302	-0.3694	0.6091	0.401	1.2801	0.1273	0.1398
245596_at	AT4G14180	initiation DEFECT 1); protein binding / protein hom	0.1949	0.7768	0.5169	-0.6701	0.356	0.3209	-0.346	0.6189	0.4042	-1.211	0.1327	0.1435
245597_at	AT4G14190	binding	9.50E-05	0.9997	0.5765	-0.01775	0.9525	0.5324	0.06304	0.8188	0.4695	0.0452	0.8693	0.4481
245598_at	AT4G14200	similar to unnamed protein product [Vitis vinifera] (G	0.8236	0.3119	0.3297	0.1941	0.7987	0.4892	0.05938	0.9376	0.5029	-0.5702	0.4683	0.3131
245599_at	AT4G14220	zinc finger (C3HC4-type RING finger) family protein	0.4496	0.0785	0.1615	0.05816	0.7762	0.4825	0.05952	0.7418	0.4454	-0.3319	0.1203	0.1352
245600_at	AT4G14230	CBS domain-containing protein-related	0.8618	0.0033	0.0446	0.4693	0.0272	0.0825	-0.09627	0.4707	0.3479	-0.4887	0.0156	0.0399
245601_at	AT4G14240	similar to CBS domain-containing protein-related [A	-0.4944	0.0561	0.1359	-1.0062	0.0056	0.0434	-0.1081	0.5914	0.3952	-0.6198	0.0288	0.0568
245602_at	AT4G14270	Protein containing PAM2 motif which mediates inter	1.285	0.0264	0.0939	1.6165	0.0124	0.0597	0.2863	0.1516	0.18	0.6177	0.0188	0.044
245603_at	no_match	no_match	0.6491	0.4837	0.4174	0.7112	0.4561	0.3665	0.8389	0.4002	0.3167	1.9963	0.0419	0.0712
245604_at	AT4G14290	similar to unknown protein [Arabidopsis thaliana] (T	0.2883	0.7534	0.5095	0.4972	0.5929	0.4206	-1.0709	0.2795	0.2578	-0.8621	0.3713	0.2718
245605_at	AT4G14300	heterogeneous nuclear ribonucleoprotein, putative /	-0.05827	0.6775	0.485	-0.2304	0.1513	0.1992	-0.1271	0.1744	0.195	-0.2992	0.0178	0.0427
245606_at	no_match	no_match	-0.1339	0.5353	0.4353	-0.2922	0.2137	0.2417	0.1329	0.2309	0.2299	-0.02535	0.8011	0.429
245607_at	AT4G14330	phragmoplast-associated kinesin-related protein 2 (	-0.5315	0.6892	0.4888	-0.9947	0.4658	0.3703	0.6779	0.3372	0.2869	0.2147	0.7474	0.4129
245608_at	AT4G14350	protein kinase family protein	-0.2893	0.1863	0.253	-0.07789	0.6901	0.4557	-0.3122	0.1607	0.186	-0.1007	0.6086	0.3663
245609_at	AT4G14370	disease resistance protein (TIR-NBS-LRR class), pa	-0.4425	0.3726	0.3608	-0.2964	0.8488	0.5035	-0.7884	0.6258	0.4065	0.3878	0.8008	0.429
245610_at	AT4G14380	similar to hypothetical protein [Vitis vinifera] (GB:CA	-1.3777	0.2032	0.2642	-0.3022	0.7556	0.4768	-1.1281	0.2812	0.2588	-0.05262	0.9565	0.4725
245611_at	AT4G14390	ankyrin repeat family protein	0.5437	0.1746	0.2445	0.259	0.4761	0.3746	0.02922	0.909	0.4951	-0.2555	0.3473	0.2612
245612_at	AT4G14440	enoyl-CoA hydratase/isomerase family protein	-0.1748	0.772	0.5153	-0.2872	0.6372	0.4372	0.4752	0.134	0.1668	0.3627	0.2256	0.1992
245613_at	no_match	no_match	-0.649	0.0936	0.1772	-0.04494	0.8868	0.515	-0.00857	0.9693	0.5097	0.5955	0.0467	0.076
245614_at	AT4G14460	transposable element gene	0.3444	0.7804	0.518	-1.0666	0.408	0.3449	1.4103	0.2891	0.2631	-0.00065	0.9996	0.4829
245615_at	AT4G14470	transposable element gene	-0.5463	0.1478	0.2236	-0.5018	0.1763	0.2164	0.153	0.6422	0.4119	0.1975	0.5527	0.346
245616_at	AT4G14480	protein kinase family protein	-0.2682	0.4318	0.3901	-0.6563	0.0994	0.159	-0.3582	0.1533	0.1811	-0.7463	0.0215	0.0477
245617_at	AT4G14490	forkhead-associated domain-containing protein / FH	-0.3191	0.7415	0.5064	-1.1564	0.2693	0.275	0.212	0.8258	0.4714	-0.6253	0.5265	0.3365
245618_at	AT4G14510	forkhead-associated domain-containing protein / FH	-0.2946	0.0377	0.1121	-0.6522	0.0025	0.0339	-0.4767	0.0078	0.0354	-0.8342	0.001	0.0121
245619_at	AT4G13990	exostosin family protein	-0.2267	0.6005	0.4599	0.4276	0.3445	0.3154	0.3974	0.2382	0.2342	1.0517	0.0215	0.0476
245620_at	AT4G14050	pentatricopeptide (PPR) repeat-containing protein	0.4651	0.7285	0.502	1.6506	0.2569	0.2683	-0.918	0.5032	0.3606	0.2675	0.8409	0.4403
245621_at	AT4G14070	AAE15 (ACYL-ACTIVATING ENZYME 15); long-ch	0.3528	0.0613	0.1421	0.1529	0.3262	0.3065	-0.3101	0.0355	0.0773	-0.51	0.0068	0.0257
245622_at	AT4G14080	MEE48 (maternal effect embryo arrest 48); hydrolas	-0.0764	0.9525	0.5653	0.1571	0.9026	0.5195	0.686	0.5997	0.3981	0.9196	0.488	0.3211
245623_s_at	AT4G14096;AT4G14103	[AT4G14096, F-box family protein];[AT4G14103, F-	-1.0063	0.0119	0.0681	0.2171	0.3987	0.3408	-1.3594	0.0017	0.0205	-0.136	0.4961	0.3243
245624_at	AT4G14090	UDP-glucoronosyl/UDP-glucosyl transferase family	-0.09409	0.8078	0.5262	-1.379	0.019	0.071	0.6848	0.1316	0.165	-0.6001	0.1728	0.1689
245625_at	AT4G14160	transport protein, putative	0.1233	0.4966	0.419	-0.00548	0.9751	0.5381	-0.7946	0.0086	0.0371	-0.9234	0.005	0.0222
245626_at	AT4

245690_at	AT5G04230	PAL3 (PHENYL ALANINE AMMONIA-LYASE 3); pl	-0.7945	0.0297	0.1	-0.6967	0.044	0.1038	0.482	0.0331	0.0743	0.5798	0.0185	0.0436
245691_at	AT5G04240	ELF6 (EARLY FLOWERING 6); transcription factor	0.3445	0.082	0.1657	-0.02562	0.872	0.5106	-0.1495	0.2242	0.2262	-0.5196	0.0075	0.027
245692_at	AT5G04150	BHLH101; DNA binding / transcription factor	-0.5599	0.495	0.4181	0.1815	0.8199	0.4958	0.2231	0.349	0.2927	0.9645	0.0102	0.0315
245693_at	AT5G04260	thioredoxin family protein	0.1218	0.3145	0.3311	0.3153	0.0409	0.1003	0.3864	0.0154	0.0493	0.58	0.0037	0.0197
245694_at	AT5G04170	calcium-binding EF hand family protein	0.2943	0.0073	0.0574	0.6444	4.00E-04	0.0251	0.1743	0.0277	0.0678	0.5244	5.00E-04	0.0096
245695_at	AT5G04270	zinc ion binding	0.06111	0.754	0.5097	-0.1546	0.4437	0.3612	0.2323	0.271	0.2528	0.01662	0.9316	0.4661
245696_at	AT5G04190	PKS4 (PHYTOCHROME KINASE SUBSTRATE 4)	-0.849	0.0176	0.0794	-0.6019	0.0506	0.1116	0.1855	0.2544	0.2433	0.4326	0.0362	0.0647
245697_at	AT5G04200	ATMC9 (METACASPASE 9); caspase/ cysteine-ty	0.1131	0.7748	0.5163	0.5678	0.1993	0.2324	0.278	0.4937	0.3571	0.7327	0.1184	0.1337
245698_at	AT5G04160	phosphate translocator-related	-0.6249	0.0761	0.1586	-0.9678	0.0211	0.074	0.2846	0.3396	0.2882	-0.05835	0.8351	0.4386
245699_at	AT5G04250	OTU-like cysteine protease family protein	0.112	0.7569	0.5108	0.02372	0.9474	0.5313	0.1635	0.5559	0.3812	0.0753	0.7823	0.4236
245700_at	AT5G04180	carbonic anhydrase family protein	0.2784	0.479	0.4115	-0.2722	0.4882	0.3797	0.5458	0.2009	0.2122	-0.00474	0.99	0.4802
245701_at	AT5G04140	GLS1/GLU1/GLUS (FERREDOXIN-DEPENDENT (	-0.7199	0.005	0.0504	-0.9108	0.0021	0.0331	-0.6117	0.0089	0.0378	-0.8026	0.0034	0.0189
245702_at	AT5G04220	ATSYTC/NTMC2T1.3/NTMC2T1PE1.3/SYTC	0.6122	0.2149	0.2715	0.3521	0.4449	0.3618	-0.8269	0.0963	0.138	-1.0871	0.0466	0.0759
245703_at	AT5G04360	S-adenosyl-L-methionine:carboxyl methyltransferas	0.575	0.5284	0.4326	-1.614	0.125	0.1792	2.5604	0.0373	0.0797	0.3714	0.679	0.3902
245704_at	AT5G04290	KOW domain-containing transcription factor family	0.6282	0.0341	0.1068	0.4139	0.1056	0.1641	-0.3171	0.0299	0.0704	-0.5314	0.0052	0.0226
245705_at	AT5G04390	zinc finger (C2H2 type) family protein	-0.501	0.2797	0.3111	-0.4731	0.3036	0.2933	-0.7761	0.1251	0.1601	-0.7482	0.1355	0.1454
245706_at	AT5G04310	pectate lyase family protein	0.3452	0.3413	0.3459	0.002555	0.994	0.5427	0.6055	0.1314	0.1649	0.2629	0.4575	0.309
245707_at	AT5G04400	ANAC077 (Arabidopsis NAC domain containing pro	0.2239	0.6629	0.4803	-0.5632	0.3026	0.2928	0.5337	0.3254	0.281	-0.2534	0.623	0.3712
245708_at	AT5G04310	pectate lyase family protein	-0.05218	0.9624	0.5679	-1.3597	0.2613	0.2705	0.2652	0.8114	0.467	-1.0423	0.3731	0.2727
245709_at	AT5G04320	similar to unknown protein [Arabidopsis thaliana] (T	-0.02147	0.8782	0.5461	0.01766	0.8996	0.5188	-0.1467	0.327	0.2819	-0.1075	0.4592	0.3097
245710_at	AT5G04330	cytochrome P450, putative / ferulate-5-hydroxylase	-0.2724	0.3959	0.3733	0.08932	0.7709	0.4807	-0.8167	0.0226	0.0608	-0.455	0.1148	0.1311
245720_at	AT5G04340	C2H2 (ZINC FINGER OF ARABIDOPSIS THALIAN	0.9441	0.0977	0.1805	-0.7523	0.1958	0.23	0.3889	0.0152	0.0492	0.6807	0.0021	0.0154
245712_at	AT5G04360	ATLDAATPU1 (PULLULANASE 1); alpha-amylase	-0.1179	0.3901	0.37	-0.2848	0.0806	0.1424	-0.9268	0.0016	0.0204	-1.0937	9.00E-04	0.0115
245713_at	AT5G04370	NAMT1; S-adenosylmethionine-dependent methyltr	-0.7973	0.3985	0.3747	-3.657	0.0123	0.0595	1.9763	0.028	0.0681	-0.8834	0.2063	0.1887
245714_at	AT5G04280	glycine-rich RNA-binding protein	0.5108	0.0398	0.1151	0.3887	0.0943	0.1461	0.229	0.1622	0.1868	0.1069	0.4691	0.3134
245715_s_at	AT5G08670;AT5G08690	ATP synthase beta chain 1, mitochon	0.08694	0.5374	0.4359	0.09017	0.5232	0.3934	0.08065	0.4259	0.328	0.08388	0.4092	0.2879
245716_at	AT5G08740	NDC1 (NAD(P)H DEHYDROGENASE C1); NADH (	-0.09211	0.1885	0.2543	-0.3331	0.0046	0.0416	-0.7469	2.00E-04	0.0129	-0.988	1.00E-04	0.0058
245717_at	AT5G03390	glycine-rich protein	0.6656	0.1689	0.2405	0.2492	0.5642	0.4098	0.3196	0.4659	0.3456	-0.09678	0.8194	0.4339
245718_at	AT5G04110	DNA topoisomerase II family protein	-0.1916	0.3716	0.3602	-0.1225	0.5554	0.4068	-0.09135	0.5478	0.3784	-0.02224	0.8809	0.4516
245719_at	AT5G04110	DNA topoisomerase II family protein	-1.7263	0.1261	0.2055	-0.5574	0.5673	0.4108	-2.5627	0.0256	0.065	-1.3938	0.1322	0.1431
245720_at	AT5G04130	RNA recognition motif (RRM)-containing protein	-0.6204	0.5694	0.4488	0.0379	0.9716	0.5371	-0.2622	0.6102	0.4013	0.408	0.4187	0.292
245721_s_at	AT1G73460;AT1G73450	[AT1G73460, protein kinase family protein];[AT1G7	-0.1985	0.1656	0.238	0.01056	0.9325	0.5271	-0.06827	0.5424	0.3763	0.1407	0.2422	0.2083
245722_at	AT73430	sec34-like family protein	0.1478	0.5459	0.4394	0.3003	0.2517	0.2651	-0.7004	0.0354	0.0772	-0.548	0.071	0.0977
245723_at	AT73400	pentatricopeptide (PPR) repeat-containing protein	0.351	0.2705	0.3057	0.4223	0.1992	0.2324	-0.6563	0.0133	0.0459	-0.585	0.0195	0.0448
245724_at	AT73390	similar to unknown protein [Arabidopsis thaliana] (T	-0.6668	0.0452	0.1225	-0.511	0.0923	0.1533	-0.5808	0.0131	0.0455	-0.4249	0.0357	0.0641
245725_at	AT73370	SUS6; UDP-glycosyltransferase/ sucrose synthase	-0.1057	0.6973	0.4918	0.2338	0.4073	0.3446	0.1063	0.6643	0.4193	0.4458	0.1214	0.136
245726_at	AT73360	HDG11 (HOMEODOMAIN GLABROUS11); DNA bi	-0.6649	0.0848	0.1687	-0.1119	0.675	0.4501	-0.5005	0.0875	0.1306	-0.05296	0.8262	0.4358
245727_at	AT73350	similar to Os02g0637900 [Oryza sativa (japonica c	0.1489	0.3538	0.3515	0.02033	0.8931	0.5167	-0.8376	0.0041	0.0277	-0.9662	0.0024	0.0164
245728_at	AT73340	oxygen binding	-0.00633	0.9936	0.5754	-1.5043	0.1125	0.1695	2.0674	0.0046	0.0289	0.5694	0.1897	0.1791
245729_at	AT73490	RNA recognition motif (RRM)-containing protein	0.2874	0.1084	0.1907	0.1996	0.2256	0.2489	-0.1855	0.0397	0.0825	-0.2732	0.0114	0.0335
245730_at	AT73470	similar to unknown protein product [Vitis vinifera] (G	0.2836	0.2454	0.2908	0.09159	0.6831	0.4532	-0.1372	0.5464	0.3779	-0.3292	0.1895	0.179
245731_at	AT73500	ATMKK9 (Arabidopsis thaliana MAP kinase kinase	-0.7685	0.017	0.0782	-0.2614	0.2516	0.265	0.2163	0.1516	0.18	0.7233	0.0041	0.0205
245732_at	AT73440	calmodulin-related	-0.05894	0.5802	0.4523	0.1225	0.7797	0.2808	0.4623	0.0092	0.0385	0.6438	0.0028	0.0173
245733_at	AT73380	similar to unnamed protein product [Vitis vinifera] (G	0.7067	0.0053	0.0519	0.6679	0.0065	0.046	-0.4519	0.0246	0.0636	-0.4908	0.0188	0.044
245734_at	AT73480	hydrolase, alpha/beta fold family protein	-0.4151	0.0898	0.1735	-0.2825	0.2041	0.2355	-0.774	0.0077	0.0354	-0.6413	0.0148	0.0387
245735_at	AT73410	MYB54 (myb domain protein 54); DNA binding / tra	0.9154	0.5596	0.4448	-1.2377	0.4386	0.359	0.897	0.5672	0.3856	-1.2661	0.4324	0.2978
245736_at	AT73330	ATDR4 (Arabidopsis thaliana drought-repressed 4)	0.8889	0.1289	0.2074	1.0503	0.0871	0.1488	0.8991	0.0076	0.0352	1.0604	0.0042	0.0207
245737_at	AT44160	DNAJ chaperone C-terminal domain-containing pro	1.2151	0.2718	0.3065	-0.3574	0.727	0.4678	0.5247	0.5849	0.3926	-1.0478	0.3018	0.2395
245738_at	AT44130	nucellin protein, putative	2.2644	0.0113	0.0666	2.5258	0.0078	0.049	-0.04224	0.9379	0.503	0.2191	0.6897	0.3938
245739_at	AT44110	CYCA1;1 (CYCLIN A1;1); cyclin-dependent protein	0.375	0.3704	0.3597	-0.9253	0.0676	0.1303	0.826	0.0187	0.0548	-0.4743	0.093	0.1152
245740_at	AT44100	AAP5 (amino acid permease 5); amino acid transm	-0.5419	0.0212	0.0855	-0.7161	0.0083	0.0504	0.1098	0.0811	0.1248	-0.06436	0.2456	0.21
245741_at	AT44120	C2 domain-containing protein / armadillo/beta-cat	-0.00222	0.9975	0.5763	0.2414	0.7393	0.471	0.005695	0.9935	0.5162	0.2495	0.731	0.4075
245742_at	AT44170	ALDH3H1 (ALDEHYDE DEHYDROGENASE 3); 3-	-0.04227	0.821	0.5299	0.2269	0.2644	0.2722	-0.4761	0.0177	0.0533	-0.2069	0.1664	0.165
245743_at	AT5G01080	similar to unnamed protein product [Vitis vinifera] (G	-1.4096	0.0014	0.038	-0.756	0.0137	0.062	-0.7644	0.01	0.0398	-0.1109	0.541	0.3413
245744_at	AT5G01110	plastid-lipid associated protein PAP / fibrillin family p	-1.1773	0.003	0.0435	-1.0742	0.042	0.04	-0.9567	0.0063	0.0328	-0.8536	0.0094	0.0303
245745_at	AT5G01110	plastid-lipid associated protein PAP / fibrillin family p	-0.6285	0.0153	0.0747	-0.8527	0.0053	0.0429	-0.2188	0.2297	0.2293	-0.443	0.0456	0.075
245746_at	AT5G01070	basic helix-loop-helix (bHLH) family protein	0.4363	0.0392	0.1143	0.3048	0.1026	0.1616	1.0562	0.0019	0.0207	0.9248	0.0031	0.018
245747_at	AT5G01100	similar to unnamed protein product [Vitis vinifera] (G	-0.6807	0.1065	0.1888	-0.7454	0.0854	0.1471	0.3767	0.1143	0.1519	0.312	0.1707	0.1676
245748_at	AT5G01140	basic helix-loop-helix (bHLH) family protein	0.1197	0.4645	0.405	0.367	0.0685	0.1313	-0.08198	0.5015	0.3601	0.1653	0.2109	0.1913
245749_at	AT5G01090	heavy-metal-associated domain-containing protein	-1.7966	0.0204	0.0842	-1.6275	0.028	0.0833	0.6154	0.0103	0.0403	0.7846	0.0043	0.0209
245750_at	AT5G01060	HTA10; DNA binding	-0.06081	0.7297	0.5025	-0.07977	0.7611	0.478	1.2018	0.008	0.0359	1.0313	0.0136	0.037
245751_s_at	AT1G25682;AT1G25988	[AT1G25682, cell cycle control protein-related];[AT1	0.1843	0.2038	0.2645	0.5585	0.0101	0.0545	-0.1496	0.2896	0.261	0.2246	0.1382	0.147
245752_at	AT5G35150	similar to hAT dimerisation domain-containing prote	-0.6007	0.5939	0.4575	-3.2621	0.0348	0.0921	1.5671	0.2058	0.2153	-1.0943	0.3514	0.2633
245753_at	AT5G35143	transposable element gene	0.9754	0.5477	0.4401	0.05651	0.9715	0.537	-2.1521	0.2215	0.2245	-3.071	0.1079	0.126
245754_at	AT5G35183	unknown protein	-1.193	0.2265	0.2795	0.5143	0.5715	0.4125	0.453	0.6165	0.4033	2.1604	0.061	0.0894
245755_at	AT5G35210	similar to unknown protein [Arabidopsis thaliana] (T	0.1366	0.7268	0.5015	0.07172	0.8536	0.5057	0.2672	0.3566	0.2964	0.2022	0.4747	0.3156
245756_at	AT5G35190	oxidoreductase, 2OG-Fe(II) oxygenase family prote	0.2482	0.1543	0.2293	0.3603	0.0636	0.1257	0.5905	0.0039	0.0273	0.7025	0.0021	0.0154
245757_at	AT5G35140	PHI-1 (PHOSPHATE-INDUCED 1)	-1.372	0.2258	0.279	-1.2608	0.259	0.2695	0.1998	0.6069	0.4003	0.311	0.4345	0.2988
245758_at	AT5G32240	KAN2 (KANADI 2); DNA binding / transcription facto	-0.413	0.4143	0.382	-0.07626	0.8747	0.5115	-0.3372	0.0451	0.089	-4.00E-04	0.9975	0.4822
245759_at	AT1G66900	similar to unknown protein [Arabidopsis thaliana] (T	0.1053	0.676	0.4847	-0.02171	0.9306	0.5267	-0.2069	0.3025	0.2698	-0.334	0.1289	0.1408
245760_s_at	AT1G66920;AT1G66910	[AT1G66920, serine/threonine protein kinase, putat	0.7004	0.0041	0.0468	0.7402	0.0034	0.0371	-0.1268	0.3357	0.2863	-0.08702	0.4949	0.3239
245761_at	AT1G66890	similar to 50S ribosomal protein-related [Arabidopsi	-0.06012	0.8276	0.5318	0.279	0.3416	0.3143	0.3809	0.0767	0.121	0.72	0.011	0.0328
245762_at	AT1G27880	ATP-dependent DNA helicase, putative	-0.00163	0.9961	0.5761	-0.885	0.0755	0.1378	0.07479	0.8501	0.4785	-0.8083	0.0949	0.1167
245763_at	AT1G27850	similar to unknown protein [Arabidopsis thaliana] (T	-0.195	0.2926	0.3187	-0.2659	0.174	0.2154	-0.02209	0.8975	0.4917	-0.09302	0.5944	0.3614
245764_s_at	AT1G19750;AT1G27840	[AT1G19750, transducin family protein / WD-40 rep	-0.1422	0.5297	0.433	-0.5462	0.0575	0.1192	0.08856	0.5539	0.3804	-0.3155	0.083	0.1075
245765_at	AT1G33600	leucine-rich repeat family protein	-1.2229	2.00E-04	0.0312	-1.1485	2.00E-04	0.0249	0.09658	0.3528	0.2946	0.1711	0.1363	0.1458
245766_at	AT1G33580	transposable element gene	-0.8157	0.3286	0.3392	-1.2661	0.1595	0.2055	0.7878	0.2777	0.2568	0.3374	0.6194	0.3702
245767_at	AT1G33610	leucine-rich repeat family protein	-0.5528	0.094	0.1775	-0.4013	0.1876	0.2249	-0.1115	0.6818	0.4249	0.04005	0.8818	0.4519
245768_at	AT1G33590	disease resistance protein-related / LRR protein-rel	-0.3857	0.0212	0.0855	-0.3672	0.0248	0.079	0.3718	0.0084	0.0369	0.3903	0.0071	0.0263
245769_at	AT1G30220	ATINT2 (INOSITOL TRANSPORTER 2); carbohydr	0.4544	0.1056	0.1878	0.1057	0.6533	0.4428	0.04316	0.7854	0.4589	-0.3055	0.1083	0.1264
245770_at	AT1G30240	binding	0.1475	0.5065	0.4236	0.5461	0.0542	0.1154	-0.4495	0.0905	0.133	-0.05086	0.814	0.4327
245771_at	no_match	no_match	-0.06134	0.8023	0.5248	0.3252	0.2292	0.2511	1.0774	0.0054	0.0309	1.4639	0.0018	0.0147
245772_at	AT1G30300	similar to phosphonate metabolism protein-related [	-0.06682	0.792	0.5214	-0.05256	0.8354	0.5003	-0.3908	0.1745	0.1951	-0.3765	0.1873	0.1777
245773_at	AT1G30290	pseudogene of unknown protein	-0.1122	0.3175	0.3328	-0.1434	0.2186	0.2449	-0.3399	0.0259	0.0653	-0.3711	0.0195	0.0448
245774_at	AT1G30210	TCP24; transcription factor	0.5085	0.0142	0.0728	0.0205	0.8752	0.5116	0.4321	0.0243	0.0631	-0.05589	0.6719	0.388
245775_at	AT1G30270	CIPK23 (CBL-INTERACTING PROTEIN KINASE 2	0.4524	0.0261	0.0933	0.9681	0.0018	0.0323	-0.06634	0.6292	0.4077	0.4494	0.0241	0.051
245776_at	AT1G30260	AGL79 (AGAMOUS-LIKE 79)	-0.3721	0.2179	0.2737	-0.03295	0.9033	0.5197	1.0212	0.0022	0.0219	1.3604	7.00E-04	0.0108
245777_at	AT1G30210	ATNUDT21 (Arabidopsis thaliana Nudix hydrolase 6	-1.4568	0.0285	0.0976	-1.5047	0.0257	0.0802	0.3199	0.1157	0.1529	0.272	0.1638	0.1635
245778_at	AT1G73530	RNA recognition motif (RRM)-containing protein	-0.459	0.013	0.0701	-0.3929	0.0217	0.0747	-0.3817	0.0238	0.0625	-0.3156	0.0426	0.0719
245779_at	AT1G73510	unknown protein	-0.2051	0.891	0.5486	0.2774	0.8531	0.5055	0.5165	0.7318	0.4423	0.9991	0.5164	0.3322
245780_at	AT1G45688	similar to unknown protein [Arabidopsis thaliana] (T	-0.6227	0.1023	0.1849	-0.8054	0.0524	0.1135	0.1352	0.5529	0.3801	-0.04748	0.8314	0.4375
245781_at	AT1G45976	SBP1 (S-RIBONUCLEASE BINDING PROTEIN 1);	0.7636	0.001	0.035	0.7591	0.001	0.0291	-0.4438	0.0073	0.0343	-0.4483	0.007	0.0261
245782_at	AT1G35200	60S ribosomal protein L4/L1 (RPL4B), pseudogene	-1.4481	0.1661	0.2384	0.413	0.6549	0.4435	-0.6395	0.4968	0.3585	1.2216	0.2269	0.1999
245783_s_at	AT1G35180;AT1G35170	[AT1G35180, similar to unknown protein [Arabidops	-0.7358	0.0372	0.1113	-0.8609	0.0229	0.0763	0.5091	0.028	0.068	0.384	0.0637	0.0917
245784_at	AT1G32190	similar to unknown protein [Arabidopsis thaliana] (T	0.07642	0.8349	0.5339	0.1609	0.6639	0.4462	-0.09737	0.7909	0.4604	-0.01286	0.9719	0.476
245785_at	AT1G32180	ATCSLD6 (Cellulose synthase-like D6); cellulose sy	0.1945	0.7719	0.5152	-0.9598	0.2007	0.2331	0.8726	0.2124	0.2194	-0.2817	0.6573	0.3832
245786_at	AT1G32150	bZIP transcription factor family protein	-0.108	0.3031	0.3248	-0.1607	0.1538	0.201	-0.05112	0.606	0.4001	-0.1038	0.3198	0.2483
245787_at	AT1G32130	similar to IWS1 C-terminus family protein [Arabidop	0.3216	0.0095	0.0626	0.5486	0.0013	0.0312	-0.22	0.0331	0.0742	0.007007	0.9239	0.4638
245788_at	AT1G32120	similar to unknown protein [Arabidopsis thaliana] (T	0.9871	0.0387	0.1134	0.7629	0.0791	0.141	0.2373	0.5065	0.3619	0.01306	0.9699	0.4754
245789_at	AT1G32090	early-responsive to dehydration protein-related / ER	-0.2141	0.5026	0.4216	-0.3334	0.3158	0.3006	-0.4065	0.0918	0.134	-0.5247	0.046	0.0754
245790_at	AT1G32200	ATS1 (ACYLTRANSFERASE 1)	-0.1125	0.213	0.2703	-0.6472	0.001	0.0293	0.1874	0.008	0.0359	-0.3472	8.00E-04	0.0111
245791_at	AT1G32210	ATDAD1 (DEFENDER AGAINST APOPTOTIC DEA	0.5948	0.0202	0.0838	0.6243	0.0172	0.0681	0.3529	0.091	0.1334	0.3823	0.0743	0.1001
245792_at	AT1G32100	jasmonoid-isoleucinoid reductase, putative	0.00802	0.9713	0.5702	0.01814	0.9351	0.5278	0.2853	0.2156	0.2212	0.2752	0.2293	0.2011
245793_at	AT1G32220	binding / catalytic/ coenzyme binding	-0.5849	0.0061	0.0539	-0.9527	0.001	0.0291	0.3798	0.0038	0.027	0.01199	0.8582	0.4453
245794_at	AT1G32170	XTR4 (XYLOGLUCAN ENDOTRANSGLYCOSYLA	0.1308	0.6722	0.4834	0.1959	0.5323	0.397	0.5236	0.1095	0.148	0.5887	0.0824	0.1069
245795_at	AT1G32160	similar to unknown protein [Arabidopsis thaliana] (T	0.02352	0.9096	0.5527	-0.3781	0.1122	0.169	0.1995	0.2995	0.2685	-0.1557	0.4068	0.2869
245796_at	AT1G32230	RCD1 (RADICAL-INDUCED CELL DEATH1)	0.4597	0.0153	0.0748	0.6369	0.0049	0.0422	-0.3429	0.0388	0.0814	-0.1658	0.2168	0.1945
245797_at	AT1G45230	defective chloroplasts and leaves protein-related / D	0.02459	0.8951	0.55	0.1498	0.4403	0.3596	-0.8716	0.0061	0.0325	-0.7463	0.0106	0.0322
245798_at	AT1G45545	similar to unknown protein [Arabidopsis thaliana] (T	-0.9778	0.4494	0.3978	0.9636	0.4555	0.3662	-0.7551	0.5418	0.3761	-1.1863	0.3544	0.2646
245799_at	AT1G45616	leucine-rich repeat family protein	-0.2129	0.8343	0.5338	0.1521	0.881	0.5134	-2.8815	0.0391	0.0817	-2.5165	0.0576	0.0864
245800_at	AT1G46264	AT-HSFB4 (Arabidopsis thaliana heat shock transc	0.9163	0.0024	0.0421	0.5318	0.0165	0.0667	0.3353	0.0664	0.1115	-0.04912	0.7322	0.4078
245801_at	AT1G46912	F-box family protein-related	0.09384	0.8598	0.54	0.1408	0.7857	0.4848	0.2534	0.6284	0.4074	0.3004	0.5687	0.3522
245802_at	AT1G46840	F-box family protein	-1.0564	0.3571	0.3532	-0.2095	0.8467	0.5035	-1.8299	0.0919	0.1341	-0.983	0.3014	0.2394
245803_at	AT1G47128	RD21 (RESPONSIVE TO DEHYDRATION 21); cys	-0.7935	0.4517	0.399	-0.1119	0.3092	0.2945	0.0012235	0.9903	0.5153	-0.03133	0.7587	0.4162
245804_at	AT1G46696	similar to myosin heavy chain-related [Arabidopsis t	-0.9264	0.3041	0.3253	0.03059	0.9708	0.5369	0.1045	0.9007	0.4926	1.0614	0.2484	0.2115
245805_at	AT1G46536	unknown protein	-1.2877	0.3548	0.3522	1.3413	0.3373	0.3122	-1.4828	0.295	0.2661	1.1462	0.4047	0.286
245806_at	AT1G45474	LHCA5 (Photosystem I light harvesting complex ge	0.1179	0.0079	0.0684	-1.1574	0.005	0.0424	-0.07877	0.7224	0.4394	-0.2182	0.3504	0.2628
245807_at	AT1G46768	RAP2.1 (related to AP2 1); DNA binding / transcript	-0.4463	0.1031	0.1855	0.2662	0.2777	0.2796	-0.3359	0.1611	0.1862	0.3766	0.1265	0.1392
245808_at	AT1G58470	ATRBP1 (ARABIDOPSIS THALIANA RNA-BINDIN	-1.10E-04	0.9997	0.5765	0.4019	0.1235	0.1784	0.006711	0.9756	0.5115	0.4087	0.119	0.134
245809_at	AT1G58440	XF1 (XANTHALENE EPOXIDASE 1); oxidoreductase	-0.7153	0.0182	0.0804	-0.6921	0.0203	0.0727	-0.5034	4.00E-04	0.0148	-0.4802	6.00E-04	0.0099
245810_at	AT1G38065;AT1G38131	[AT1G38065, similar to unknown protein [Arabidops	-0.7511	0.008	0.0586	-0.9077	0.004	0.0395	-0.2406	0.1105	0.1488	-0.3972	0.0279	0.0558
245811_at	AT137537	transposable element gene	2.2352	0.1093	0.1914	-0.7042	0.553	0.4059	2.3831	0.0938	0.1358	-0.5562	0.6364	0.3759
245812_at	no_match	no_match	0.2318	0.868	0.5433	0.7542	0.5953	0.4216	0.6492	0.0491	0.4142	1.1651	0.4236	0.294
245813_at	AT1G49920	zinc finger protein-related	0.2366	0.8388	0.535	-1.6901	0.1959	0.23	0.3423	0.2483	0.2401	-1.5844	0.0033	0.0188
245814_at	AT1G49910	WD-40 repeat family protein / mitotic checkpoint pr	0.7555	0.3708	0.3599	1.5062	0.1151	0.1712	0.3753	0.454	0.3405	1.126	0.0678	0.0951
245815_at	AT1G26090	ATP binding	0.6511	0.9001	0.5511	-0.6527	0.017	0.0677	-0.2292	0.2398	0.2346	-0.8597	0.0066	0.0252
245816_at	AT1G26210	similar to unknown protein [Arabidopsis thaliana] (T	-1.1858	0.0339	0.1063	-1.4158	0.0194	0.0716	0.3626	0.2775	0.2566	0.1326	0.6698	0.3873
245817_at	AT1G26160	metal-dependent phosphohydrolase HD domain-co	-0.1606	0.3762	0.3624	-0.1729	0.3444	0.3153	-0.1402	0.2831	0.2598	-0.1526	0.2489	0.2119
245818_at	AT1G26100	cytochrome B561 family protein	-0.4005	0.1154	0.1966	-0.5063	0.0643	0.1265	0.04774	0.8139	0.4678	-0.05813	0.7748	0.4215
245819_at	AT1G26310	CAL (CAULIFLOWER); DNA binding / transcription	0.8226	0.4097	0.3798	-0.6283	0.5211	0.3926	1.2065	0.2486	0.2402	-0.2443	0.7982	0.4282
245820_at	AT1G26320	NADP-dependent oxidoreductase, putative	-0.843	0.4278	0.3883	-0.3371	0.7422	0.4721	-0.3836	0.7088	0.4343	0.1223	0.9044	0.4586
245821_at	AT1G26270	phosphatidylinositol 3- and 4-kinase family protein	0.01058	0.9676	0.5692	-0.1597	0.55	0.4048	-0.3255	0.0061	0.0325	-0.4958	0.0013	0.0132
245822_at	AT1G26110	similar to unknown protein [Arabidopsis thaliana] (T	0.3432	0.0383	0.1128	0.2771	0.07	0.1324	0.3003	0.0553	0.1003	0.2342	0.

245890_at	AT5G09490	40S ribosomal protein S15 (RPS15B)	2.2474	0.0905	0.1743	-1.2399	0.2877	0.2852	1.3751	0.2458	0.2385	-2.1121	0.1052	0.1241
245891_at	AT5G09220	AAP2 (AMINO ACID PERMEASE 2); amino acid tra	-0.5462	0.1619	0.2352	-0.4014	0.2764	0.279	-0.5933	0.012	0.0434	-0.4486	0.0298	0.058
245892_at	AT5G09370	protease inhibitor/seed storage/lipid transfer protein	-0.3613	0.7118	0.4969	-2.048	0.0878	0.1492	2.2489	0.069	0.1139	0.5622	0.5705	0.3528
245893_at	AT5G09270	similar to hypothetical protein Osl_004420 [Oryza s	0.781	0.0227	0.0882	0.5028	0.0812	0.1429	0.2306	0.3473	0.2918	-0.04752	0.8372	0.4393
245894_at	AT5G09310	identical to Gamma-secretase subunit PEN2-like pr	0.0835	0.3093	0.3281	0.2415	0.0282	0.0835	0.3732	0.0065	0.0331	0.5312	0.0018	0.0147
245895_at	AT5G09230	SRT2; DNA binding	-0.4917	0.1304	0.2089	-0.6363	0.0699	0.1323	0.191	0.5016	0.3601	0.04653	0.8661	0.4472
245896_at	AT5G09250	KIWI; DNA binding / transcription coactivator	-0.05798	0.7204	0.4995	-0.1388	0.4099	0.3459	0.7282	0.0085	0.037	0.6474	0.0127	0.0357
245897_at	AT5G09400	KUP7 (K+ uptake permease 7); potassium ion trans	1.2651	0.2338	0.2839	0.4796	0.6234	0.4322	-2.4121	0.0357	0.1007	-3.1977	0.024	0.0509
245898_at	AT5G11020	kinase	-0.08278	0.6376	0.4722	-0.4392	0.0541	0.1153	0.005667	0.9739	0.511	-0.3508	0.0972	0.1185
245899_at	AT5G11030	ALF4 (ABERRANT LATERAL ROOT FORMATION	0.5426	0.0379	0.1121	0.6353	0.0232	0.0769	0.007485	0.9684	0.5096	0.1002	0.6028	0.3642
245900_at	AT5G11040	similar to hypothetical protein Osl_015984 [Oryza s	0.5857	0.0116	0.0672	0.387	0.0434	0.1033	-0.3113	0.0736	0.1181	-0.5101	0.0169	0.0415
245901_at	AT5G11060	KNAT4 (KNOTTED1-LIKE HOMEOBOX GENE 4);	0.161	0.2076	0.2669	0.4048	0.0195	0.0719	-0.2386	0.0565	0.1015	0.005171	0.9568	0.4726
245902_at	AT5G11080	ubiquitin family protein	0.3434	0.6454	0.4748	0.8546	0.2839	0.2831	-0.05078	0.945	0.5045	0.4605	0.5417	0.3415
245903_at	AT5G11100	ATSYTDNTMC2T2.2/NTMC2TYPE2.2/SYTD	-0.06765	0.8513	0.5385	-0.4308	0.2718	0.2765	0.2099	0.4447	0.336	-0.1532	0.57	0.3526
245904_at	AT5G11110	ATSPS2F/SPS1 (SUCROSE PHOSPHATE SYNTH	0.7074	0.0177	0.0796	0.5308	0.0433	0.1032	0.01604	0.8338	0.4737	-0.1606	0.0885	0.1116
245905_at	AT5G11090	serine-rich protein-related	-0.3105	0.1635	0.2366	-0.1237	0.5344	0.3981	-0.04026	0.8195	0.4697	0.1465	0.4254	0.2947
245906_at	AT5G11070	similar to unknown protein [Arabidopsis thaliana] (T	-0.7938	0.053	0.1322	-0.39	0.2525	0.2655	0.6384	0.0387	0.0813	1.0421	0.0078	0.0275
245907_at	AT5G09340	ubiquitin, putative	0.4403	0.7343	0.5037	-1.0495	0.4346	0.3574	0.3655	0.7776	0.4565	-1.1243	0.4053	0.2863
245908_at	AT5G09360	LAC14 (laccase 14); copper ion binding / oxidoredu	-1.3447	0.0171	0.0783	-1.2787	0.0201	0.0725	1.044	0.0379	0.0805	1.11	0.0315	0.0598
245909_at	AT5G09380	DNA-directed RNA polymerase III RPC4 family prot	0.05064	0.8349	0.5339	0.7338	0.0322	0.0889	-0.5306	0.0802	0.1239	0.1526	0.5394	0.3409
245910_at	AT5G09410	EICBP.B (ETHYLENE INDUCED CALMODULIN BI	0.2392	0.0764	0.1592	-0.01307	0.903	0.5196	-0.7269	0.002	0.021	-0.9792	6.00E-04	0.0103
245911_at	AT5G09460	STT3A (STAUROSPORIN AND TEMPERATURE S	0.9012	0	0.0007	0.706	0	0.0249	-0.2242	1.00E-04	0.012	-0.4194	0	0.0045
245912_at	AT5G19600	SULTR3;5; sulfate transmembrane transporter	-0.4581	0.0655	0.1468	-0.3047	0.1693	0.2121	0.001184	0.9951	0.5164	0.1546	0.4435	0.3032
245913_at	AT5G19860	similar to unknown protein [Arabidopsis thaliana] (T	0.3239	0.1078	0.1899	0.1693	0.341	0.314	0.7498	0.0088	0.0375	0.5952	0.0192	0.0444
245914_at	AT5G19620	OEP80 (ARABIDOPSIS THALIANA OUTER ENVE	0.1447	0.4362	0.3921	-0.08688	0.6313	0.435	-0.3587	0.0465	0.0904	-0.3008	0.0753	0.101
245915_s_at	AT5G19780/AT5G19770	[AT5G19780, TUA5 (tubulin alpha-5)][AT5G19770,	-0.1342	0.5145	0.427	-0.3006	0.1848	0.2231	0.0811	0.4955	0.358	-0.08531	0.4748	0.3156
245916_at	no_match	no_match	0.4408	0.626	0.4684	0.4128	0.6474	0.4406	-0.3454	0.7008	0.4315	-0.3733	0.6784	0.39
245917_at	AT5G26740	transcription-coupled DNA repair protein-related	0.2471	0.2888	0.3166	0.3696	0.1415	0.1918	-0.5671	0.0121	0.0436	-0.4445	0.0289	0.0545
245918_at	AT5G26760	transposable element gene	-1.0057	0.4974	0.4194	-0.5495	0.7046	0.4606	-0.09869	0.9452	0.5045	0.3574	0.8041	0.4299
245919_at	AT5G26780	similar to unknown protein [Arabidopsis thaliana] (T	0.5946	0.6274	0.4688	-0.1148	0.9242	0.5252	-0.2172	0.8573	0.4803	-0.9266	0.4594	0.3098
245920_at	AT5G26790	transposable element gene	-0.1313	0.5975	0.4587	0.1854	0.4641	0.3698	0.1256	0.5827	0.3917	0.4421	0.1032	0.1229
245921_at	AT5G26800	unknown protein	-0.3908	0.3502	0.3497	-1.2266	0.0295	0.0853	0.5858	0.0446	0.0883	-0.25	0.285	0.2308
245922_at	AT5G26810	similar to Ulp1 protease family protein [Arabidopsis	-1.0315	0.5571	0.4438	-2.9639	0.1398	0.1905	2.1198	0.2588	0.2457	0.1873	0.9131	0.4607
245923_at	AT5G26820	similar to unknown protein [Arabidopsis thaliana] (T	0.1473	0.8015	0.5446	0.7672	0.2342	0.2544	-0.3417	0.4251	0.3276	0.5733	0.2103	0.1911
245924_at	AT5G26780	thylakoid assembly protein, putative	-0.7578	0.0143	0.0729	-0.6126	0.0285	0.0838	0.2456	0.25	0.241	0.3909	0.0992	0.1199
245925_at	AT5G26770	BZO2H3 (ARABIDOPSIS THALIANA BASIC LEUC	-0.806	0.0352	0.1084	-0.4829	0.134	0.1861	0.2832	0.2599	0.2464	0.6063	0.0484	0.0778
245926_at	AT5G26740	similar to unknown protein [Arabidopsis thaliana] (T	0.4622	0.0944	0.1777	0.2919	0.24	0.2577	-1.288	0.0097	0.0267	-1.4584	0.0023	0.0161
245927_at	AT5G26750	similar to UDP-glucose:sterol glucosyltransferase, p	0.6798	0.1381	0.2159	0.4058	0.3316	0.3092	-0.8964	0.0713	0.1161	-1.1704	0.0334	0.0617
245928_s_at	AT5G24770/AT5G24780	[AT5G24770, VSP2 (VEGETATIVE STORAGE PR	-0.6814	0.0168	0.0777	-0.7181	0.0141	0.0628	0.2033	0.2919	0.2645	0.1665	0.3766	0.2741
245929_at	AT5G24760	alcohol dehydrogenase, putative	-0.268	0.4797	0.4117	-0.259	0.4936	0.3819	0.0868	0.6271	0.4069	0.0955	0.593	0.3609
245930_at	AT5G09240	transcriptional coactivator p15 (PC4) family protein	-1.6007	4.00E-04	0.032	-1.1254	0.0014	0.0123	0.7024	0.0079	0.0358	1.1777	0.0012	0.0127
245931_at	AT5G09280	pectate lyase family protein	0.74	0.4506	0.3984	-0.537	0.5772	0.4148	1.0206	0.3135	0.2751	-0.2564	0.7867	0.4248
245932_at	AT5G09290	3'(2'),5'-bisphosphate nucleotidase, putative / inositl	1.7568	0.0016	0.0388	1.0747	0.0098	0.0538	0.3173	0.243	0.2368	-0.3648	0.1909	0.1797
245933_at	AT5G09320	vacuolar sorting protein 9 domain-containing protein	-0.09579	0.5067	0.4237	0.1621	0.2851	0.2839	-0.8331	0.0032	0.0251	-0.5752	0.0119	0.0343
245934_at	AT5G09330	ANAC082 (Arabidopsis NAC domain containing pro	0.6692	0.002	0.04	0.703	0.0017	0.032	-0.1558	0.1715	0.193	-0.122	0.2625	0.219
245935_at	AT5G19840	transcription factor jumonji (jmj) domain-containing	0.4666	0.2821	0.3241	0.3127	0.3234	0.4379	0.3588	-0.8561	0.0191	0.0554	-0.9993	0.0114	0.0334
245936_at	AT5G19850	hydrolase, alpha/beta fold family protein	-0.6124	0.0695	0.152	-0.9177	0.021	0.074	-0.1289	0.6315	0.4084	-0.4342	0.1557	0.1586
245937_at	AT5G19750	peroxisomal membrane 22 kDa family protein	0.6017	0.0265	0.0941	0.6091	0.0255	0.0799	-0.2884	0.1409	0.172	-0.281	0.1488	0.1538
245938_at	AT5G19860	leucine-rich repeat family protein	0.3362	0.0206	0.0845	0.223	0.0695	0.1321	-0.09595	0.7346	0.4432	-0.1327	0.0774	0.1028
245939_at	AT5G19760	dicarboxylate/tricarboxylate carrier (DTC)	-0.7853	0.0101	0.064	-0.6444	0.0197	0.072	-0.767	0.0105	0.0406	-0.6261	0.0207	0.0466
245940_at	AT5G19630	similar to unnamed protein product [Vitis vinifera] (G	0.2211	0.3385	0.3447	0.02754	0.8989	0.5186	0.3901	0.1278	0.1624	0.1965	0.3889	0.2795
245941_at	AT5G19820	EMB2734 (EMBRYO DEFECTIVE 2734); unk	0.1474	0.3422	0.3461	-0.03434	0.8143	0.4945	-1.184	2.00E-04	0.0126	-1.3657	1.00E-04	0.0061
245942_at	AT5G19490	DNA binding / sequence-specific DNA binding	1.4049	0.114	0.1956	1.771	0.0639	0.126	-0.3135	0.6761	0.4231	0.05258	0.9435	0.4693
245943_at	AT5G19500	tryptophan/tyrosine permease family protein	-0.158	0.4783	0.4111	-0.4036	0.1167	0.1726	-0.293	0.221	0.2242	-0.5386	0.0562	0.0851
245944_at	AT5G19520	mechanosensitive ion channel domain-containing p	0.05189	0.9695	0.5697	1.9148	0.2073	0.2378	-1.0617	0.3471	0.2917	0.8011	0.4668	0.3126
245945_at	AT5G19560	ATROPGEF10/ROPGEF10 (KINASE PARTNER PF	0.06838	0.952	0.5652	0.8676	0.4617	0.3687	-0.08426	0.9373	0.5028	0.715	0.5166	0.3322
245946_at	AT5G19580	glycoxal oxidase-related	-0.5542	0.0548	0.1344	-0.1939	0.4005	0.3413	-0.3551	0.1602	0.1857	0.005216	0.981	0.4783
245947_at	AT5G19530	ACLS (ACAULIS 5)	0.3327	0.1679	0.2397	0.5466	0.0507	0.1116	-0.03062	0.8289	0.4724	0.1833	0.2395	0.2068
245948_at	AT5G19540	similar to unknown [Brassica napus] (GB:AAY21212	0.2793	0.0961	0.179	-0.08549	0.5433	0.402	-0.3024	0.0788	0.1227	-0.6671	0.0066	0.0253
245949_at	AT5G19510	elongation factor 1B alpha-subunit 2 (eEF1Balpha2	0.2786	0.1184	0.1989	0.03943	0.7929	0.487	-0.3363	0.0378	0.0804	-0.5755	0.0064	0.0248
245950_at	AT5G19570	similar to hypothetical protein Osl_018061 [Oryza s	0.248	0.3421	0.3461	0.2972	0.2634	0.2734	0.2683	0.3948	0.1615	0.1864	0.4441	0.126	0.1389
245951_at	AT5G19550	ASP2 (ASPARTATE AMINOTRANSFERASE 2)	0.7105	8.00E-04	0.0345	0.5192	0.0027	0.0347	-0.04878	0.5677	0.3858	-0.2401	0.0376	0.0663
245952_at	AT5G28500	similar to unknown protein [Arabidopsis thaliana] (T	-0.3605	0.0907	0.1744	-0.3932	0.0727	0.135	0.2203	0.2465	0.239	0.1876	0.3124	0.2446
245953_at	AT5G28520	similar to jacalin lectin family protein [Arabidopsis th	-0.5801	0.2572	0.2978	-0.08556	0.8551	0.506	-0.5168	0.3047	0.271	-0.02228	0.962	0.4737
245954_at	AT5G28530	FRS10 (FAR1-RELATED SEQUENCE 10); zinc ion	-0.1385	0.4519	0.3991	-0.5743	0.026	0.0807	-0.1671	0.372	0.3039	-0.6029	0.0223	0.0486
245955_at	AT5G28510	glycosyl hydrolase family 1 protein	1.1616	0.3275	0.3387	0.4797	0.6693	0.4483	0.3926	0.7256	0.4403	-0.2894	0.7951	0.4275
245956_s_at	AT5G42020,AT5G28540	ACLS (ACAULIS 5)	1.3187	0.0012	0.036	1.156	0.002	0.033	0.175	0.338	0.2873	0.01219	0.9433	0.4692
245957_at	AT5G19590	similar to unknown [Brassica napus] (GB:AAY21212	0.04989	0.7934	0.522	0.04729	0.8039	0.4909	0.8442	6.00E-04	0.0158	0.8416	6.00E-04	0.0101
245958_at	AT5G19610	sec7 domain-containing protein	-0.5287	0.5843	0.4541	-0.3727	0.6968	0.4578	0.8978	0.3271	0.2819	1.0539	0.2605	0.2181
245959_at	AT5G19640	proton-dependent oligopeptide transport (POT) fam	1.178	0.3038	0.3252	1.4189	0.2287	0.2508	0.9046	0.4166	0.3236	1.1455	0.3156	0.2463
245960_at	AT5G19660	ATS1P/ATSBT6.1/S1P (SITE-1 PROTEASE); endo	0.6215	0.0064	0.0547	0.5229	0.0117	0.0583	-0.3834	0.0019	0.021	-0.4819	8.00E-04	0.0112
245961_at	AT5G19670	exostosin family protein	0.1952	0.6111	0.463	0.2335	0.546	0.4029	-0.156	0.6825	0.4251	-0.1177	0.7565	0.4156
245962_at	AT5G19700	MATE efflux protein-related	-1.8552	0.0627	0.1436	-1.4306	0.1197	0.1751	-0.4643	0.48	0.3514	-0.03968	0.9502	0.4709
245963_at	AT5G19710	similar to AHP4 (HPT PHOSPHOTRANSMITTER 4	-0.4734	0.6512	0.4766	1.5826	0.1783	0.2185	-0.2342	0.8212	0.4701	1.8218	0.1337	0.1442
245964_at	AT5G19720	tRNA synthetase class I (E and Q) family protein	-0.2008	0.5344	0.4349	0.1386	0.6637	0.4461	0.07936	0.7666	0.4532	0.4187	0.169	0.1666
245965_at	AT5G19730	sec5/exocyst family protein	-1.9249	0.0208	0.085	-1.7024	0.0307	0.087	-0.4505	0.4355	0.3321	-0.228	0.6839	0.3919
245966_at	AT5G19790	RAP2.11 (related to AP2 11); DNA binding / transcr	0.02788	0.973	0.5705	-2.4588	0.0336	0.0906	1.1393	0.2148	0.2207	-1.3474	0.1565	0.159
245967_at	AT5G19800	hydroxyproline-rich glycoprotein family protein	-0.1066	0.8651	0.5423	-1.1467	0.1232	0.1782	1.5106	0.0402	0.083	0.4704	0.4038	0.2857
245968_at	AT5G19810	proline-rich extensin-like family protein	-0.6853	0.3449	0.3473	-1.4477	0.0866	0.1484	0.8409	0.2594	0.2461	0.07846	0.9084	0.4595
245969_at	AT5G19830	aminoacyl-tRNA hydrolase	0.1747	0.6923	0.49	0.8045	0.1215	0.1768	0.118	0.7879	0.4595	0.7479	0.1425	0.1498
245970_at	AT5G20710	BGAL7 (beta-galactosidase 7); beta-galactosidase	0.1728	0.9181	0.5566	-0.6697	0.6933	0.4567	0.4818	0.7755	0.4559	-0.3607	0.8305	0.4373
245971_at	AT5G20730	NPH4 (NON-PHOTOTROPHIC HYPOCOTYL3); trar	0.6024	1.00E-04	0.0312	0.7876	0	0.0249	0.127	0.0374	0.0798	0.3122	0.0017	0.0144
245972_at	AT5G20680	similar to unknown protein [Arabidopsis thaliana] (T	-0.05301	0.7726	0.5155	-0.4652	0.0534	0.1146	-0.0273	0.7977	0.4627	-0.4395	0.0116	0.0338
245973_at	AT5G32490	transposable element gene	1.3139	0.3693	0.3593	-2.3146	0.1496	0.1978	0.5889	0.674	0.4223	-3.0397	0.0795	0.1046
245974_at	no_match	no_match	-1.7643	0.1414	0.2186	0.6449	0.5405	0.4009	-1.2285	0.1594	0.1853	1.1806	0.1725	0.1687
245975_at	AT5G13070	MSF1-like family protein	0.09299	0.3392	0.3449	0.3957	0.0099	0.0542	0.4162	0.001	0.0175	0.7189	1.00E-04	0.0062
245976_at	AT5G13080	WRKY75 (WRKY DNA-BINDING PROTEIN 75); tra	1.4333	0.0754	0.158	2.4941	0.0142	0.0631	0.6318	0.0606	0.1056	1.6926	0.0023	0.0158
245977_at	AT5G13110	GEPD2 (GLUCOSE-6-PHOSPHATE DEHYDROGE	-0.1126	0.5668	0.4476	-0.4083	0.0867	0.1484	-0.01731	0.9195	0.4977	-0.313	0.1238	0.1375
245978_at	AT5G13130	ATP binding	-0.7231	0.3334	0.342	-0.829	0.2761	0.2788	0.2476	0.6692	0.4208	0.1416	0.8053	0.4302
245979_at	AT5G13150	ATEXO70C1 (exocyst subunit EXO70 family protein	-1.043	0.3492	0.3495	0.8101	0.4569	0.3668	-0.999	0.0985	0.1397	0.854	0.1406	0.1486
245980_at	AT5G13140	similar to unknown protein [Arabidopsis thaliana] (T	-0.3925	0.2718	0.3065	-0.5742	0.1359	0.1876	-0.4578	0.0458	0.0895	-0.6395	0.0161	0.0406
245981_at	AT5G13100	oxidoreductase	-0.6404	0.0163	0.0771	-0.9539	0.004	0.0395	-0.408	0.003	0.0248	-0.7215	3.00E-04	0.0087
245982_at	AT5G13170	nodulin MtN3 family protein	1.0631	0.2376	0.2861	1.2401	0.1809	0.2202	-1.0163	0.2554	0.2438	-0.8394	0.3348	0.2555
245983_at	AT5G13050	5-FCL; 5-formyltetrahydrofolate cyclo-ligase	-0.07907	0.5509	0.4415	0.008335	0.9486	0.5316	0.06022	0.581	0.3912	0.1476	0.2155	0.1939
245984_at	AT5G13090	similar to unknown protein [Arabidopsis thaliana] (T	-0.5087	0.0369	0.1107	-0.3905	0.0773	0.1394	0.4146	0.0237	0.0624	0.5328	0.0103	0.0317
245985_at	AT5G13120	peptidyl-prolyl cis-trans isomerase cyclophilin-type f	-0.3544	0.0598	0.1399	-0.5121	0.0197	0.072	0.4576	0.0283	0.0683	0.2999	0.0923	0.1146
245986_at	AT5G13160	PBS1 (AVRPPHB SUSCEPTIBLE 1); kinase	0.0309	0.8404	0.5357	0.2928	0.1115	0.1685	-0.223	0.1961	0.2093	0.03898	0.7998	0.4287
245987_at	AT5G13180	ANAC083 (Arabidopsis NAC domain containing pro	-0.3516	0.0458	0.1232	-0.04673	0.723	0.4664	0.1111	0.2961	0.2667	0.416	0.0109	0.0326
245988_at	AT5G20610	similar to unknown protein [Arabidopsis thaliana] (T	0.589	0.0038	0.0462	0.4699	0.0086	0.0511	-0.3458	3.00E-04	0.0133	-0.4649	1.00E-04	0.0058
245989_s_at	AT5G20620	UBQ4 (ubiquitin 4); protein binding	0.5135	0.0148	0.0737	0.6903	0.0053	0.0429	0.1437	0.3149	0.2759	0.3206	0.0626	0.0908
245990_at	AT5G20640	similar to unknown protein [Arabidopsis thaliana] (T	-0.05212	0.8055	0.5256	-0.1358	0.5307	0.3965	0.1032	0.5142	0.3647	0.01947	0.8992	0.4569
245991_at	AT5G20660	24 kDa vacuolar protein, putative	1.1873	9.00E-04	0.0349	0.9265	0.0024	0.0338	-0.0805	0.557	0.3816	-0.3413	0.0534	0.0825
245992_at	AT5G20690	leucine-rich repeat transmembrane protein kinase,	-0.107	0.7271	0.5015	-0.2933	0.3629	0.3243	0.9607	0.0283	0.0683	0.7745	0.0536	0.0827
245993_at	AT5G20700	senescence-associated protein-related	0.09169	0.7607	0.5119	0.2049	0.5065	0.3873	-1.5043	0.0025	0.0232	-1.3911	0.0034	0.0189
245994_at	AT5G20760	transposable element gene	0.09329	0.8327	0.5332	0.4288	0.3586	0.3222	0.4407	0.3469	0.2917	0.7761	0.1339	0.1443
245995_at	AT5G20770	transposable element gene	-0.7195	0.4237	0.3868	1.1254	0.2362	0.2555	-0.4789	0.5774	0.3896	1.366	0.1591	0.1606
245996_at	AT5G20800	transposable element gene	2.5131	0.0303	0.1009	-0.5374	0.5208	0.3925	1.4282	0.005	0.0298	-1.6223	0.0031	0.0182
245997_at	AT5G20810	auxin-responsive protein, putative / small auxin up f	-0.3474	0.1593	0.2329	-0.1082	0.6194	0.4303	0.05039	0.7491	0.4479	0.2897	0.1202	0.1351
245998_at	AT5G20270	SUS1 (SUCROSE SYNTHASE 1); UDP-glycosyltra	0.3434	0.097	0.1798	0.2392	0.2071	0.2377	-0.2217	0.2359	0.2327	-0.3259	0.1098	0.1276
245999_at	AT5G20650	COPT5 (copper transporter 5); copper ion transmer	0.2236	0.1247	0.2045	0.3977	0.0261	0.0809	0.432	0.0114	0.0423	0.6061	0.0034	0.019
246000_at	AT5G20820	auxin-responsive protein-related	-1.0482	0.0896	0.1734	-1.9005	0.0156	0.0652	1.229	0.0592	0.1043	0.3767	0.4679	0.3129
246001_at	AT5G20790	similar to unknown protein [Arabidopsis thaliana] (T	-0.9172	0.4257	0.3874	0.3647	0.7425	0.4722	1.1691	0.1607	0.186	2.442	0.0224	0.0487
246002_at	AT5G20740	invertase/pectin methylesterase inhibitor family prot	-0.3578	0.546	0.4394	-0.1263	0.8276	0.4982	0.2926	0.3967	0.315	0.5242	0.1646	0.1641
246003_at	AT5G20720	CPN20 (CHAPERONIN 20); calmodulin binding	-0.4147	0.0067	0.0551	-0.4137	0.0087	0.0464	-0.01201	0.8746	0.4852	-0.01123	0.885	0.4529
246004_at	AT5G20630	GLP3 (GERMIN-LIKE PROTEIN 3); manganese ion	-1.578	0.0585	0.1386	-1.344	0.089	0.1504	0.1094	0.7332	0.4427	0.3434	0.3149	0.2459
246005_at	AT5G08415	lipoic acid synthase family protein	-0.5782	0.011	0.0657	-0.5004	0.0179	0.0693	-0.109	0.0999	0.1409	-0.03123	0.5742	0.354
246006_at	AT5G08290	YLS8 (yellow-leaf-specific gene 8); catalytic	0.2264	0.0769	0.1595	0.2483	0.0601	0.1218	0.3927	0.016	0.0505	0.4047	0.0133	0.0366
246007_at	AT5G08410	FTRA2 (ferredoxin/thioredoxin reductase subunit A	-0.7144	0.0063	0.0542	-0.4295	0.0341	0.0911	0.04951	0.7339	0.4429	0.3343	0.0695	0.0965
246008_at	AT5G08320	similar to unnamed protein product [Vitis vinifera] (G	0.2629	0.3558	0.3525	0.1461	0.5932	0.4207	0.4669	0.1247	0.1598	0.3501	0.2198	0.196
246009_at	AT5G08335	ATSTE14B (PRENYLCYSTEINE ALPHA-CARBOX	0.3866	0.0309	0.1019	0.3196	0.0181	0.1198	0.1554	0.2698	0.2521	0.07834	0.554	0.3465
246010_at	AT5G08440	similar to unknown protein [Arabidopsis thaliana] (T	0.02379	0.8502	0.5382	-0.3041	0.0617	0.1234	-0.4274	0.0224	0.0604	-0.7553	0.0031	0.018
246011_at	AT5G08330	TCP family transcription factor, putative	-0.4364	0.2874	0.3157	-0.101	0.7907	0.4863	-0.1584	0.245	0.238	0.177	0.203	0.1868
246012_at	AT5G08450	zinc finger (C3HC4-type RING finger) family protein	-0.7405	0.0325	0.1046	0.5649	0.0704	0.1327	0.005668	0.9794	0.5124	-0.1696	0.4791	0.3171
246013_at	AT5G10660	calmodulin-binding protein-related	-0.474	0.4249	0.3872	0.6487	0.2912	0.2873	-0.5456	0.3647	0.3003	0.5771	0.3406	0.2584
246014_at	AT5G10680	calmodulin-binding protein-related	-0.1878	0.3002	0.3229	0.7317	0.0098	0.0538	-0.6291	0.0083	0.0365	0.2903	0.0883	0.1114
246015_at	AT5G10700	protein tyrosine phosphatase	0.05473	0.7603	0.5117	-0.03257	0.9554	0.606	-0.8554	0.1181	0.0199	0.367	-0.09991	0.5977	0.3627
246016_at	AT5G10720	AHK5 (CYTOKININ INDEPENDENT 2)	1.0316	0.0965	0.1795	-0.5836	0.2881	0.2855	0.765	0.0078	0.0356	-0.8501	0.0054	0.0229
246017_at	AT5G10730	binding / catalytic/ coenzyme binding	0.1083	0.5162	0.4276	-0.1377	0.4167	0.3491	0.02467	0.8791	0.4864	-0.2213	0.2196	0.1959
246018_at	AT5G10695	similar to unknown protein [Arabidopsis thaliana] (T	1.1395	0.2085	0.2672	1.9389	0.0634	0.1255	0.7052	0.0582	0.1032	1.5045	0.005	0.0221
246019_at	AT5G10690	pentatricopeptide (PPR) repeat-containing protein /	-0.2261	0.1156	0.1967	-0.3121	0.0505	0.1115	-0.5255	0.0049	0.0297	-0.6115	0.0028	0.0174
246020_at	AT5G10710	similar to unnamed protein product [Vitis vinifera] (G	0.3499	0.1288	0.2073	0.1954	0.3463	0.3161	-0.1197	0.5493	0.3788	-0.2742	0.2089	0.1902
246021_at	AT5G10740	L-ascorbate oxidase, putative	-0.5346	0.0071	0.0567	-0.7416	0.0021	0.0333	-0.3299	0.0343	0.0757	-0.5369	0.0068	0.0257
246022_at	AT5G21110	unknown protein	-0.3201

246090_at	AT5G20520	WAV2 (WAVY GROWTH 2)	0.285	0.3442	0.3469	0.1469	0.6102	0.427	-1.1807	0.0028	0.0244	-1.3168	0.0019	0.0149
246091_at	AT5G20590	similar to unknown protein [Arabidopsis thaliana] (T	0.05533	0.8458	0.5373	0.09179	0.7481	0.4745	-0.5743	0.0693	0.1141	-0.5379	0.0822	0.1068
246092_at	AT5G20500	glutaredoxin, putative	0.3532	0.0556	0.1355	0.4735	0.0231	0.0768	-0.2519	0.1112	0.1493	-0.1317	0.3469	0.2611
246093_at	AT5G20550	oxidoreductase, 2OG-Fe(II) oxygenase family prote	1.3436	0.2719	0.3065	0.3303	0.7699	0.4804	-0.0529	0.9624	0.5083	-1.0661	0.3695	0.2709
246094_at	AT5G19300	similar to unnamed protein product [Vitis vinifera] (G	-0.01992	0.9425	0.5631	0.7367	0.047	0.1076	-0.1378	0.6238	0.4059	0.6188	0.0757	0.1014
246095_at	AT5G19310	homeotic gene regulator, putative	0.211	0.4376	0.3927	0.5039	0.1089	0.1664	-0.5843	0.0756	0.1197	-0.2915	0.3	0.2386
246096_at	AT5G20330	BETA(2 (BETA-1,3-GLUCANASE 4); hydrolase, hy	0.003178	0.9981	0.5763	1.294	0.3675	0.3263	0.179	0.8952	0.4912	1.4698	0.3132	0.245
246097_at	AT5G20270	HHP1 (HEPTAHELICAL TRANSMEMBRANE PRO	-1.2966	0.0644	0.1453	-1.5314	0.0402	0.0995	0.3976	0.1101	0.1485	0.1628	0.4492	0.3057
246098_at	AT5G20400	oxidoreductase, 2OG-Fe(II) oxygenase family prote	1.8334	0.003	0.0437	1.4893	0.0065	0.0459	0.2991	0.1338	0.1666	-0.04496	0.7919	0.4265
246099_at	AT5G20230	ATBCB (ARABIDOPSIS BLUE-COPPER-BINDING	1.2071	0.0523	0.1313	1.6309	0.021	0.074	0.3386	0.2093	0.2174	0.7623	0.0282	0.056
246100_at	no_match	no_match	-0.1858	0.8841	0.5471	-0.06431	0.9597	0.5341	0.6736	0.6034	0.3994	0.7951	0.5426	0.3419
246101_at	no_match	no_match	-1.2231	0.283	0.3133	-1.6084	0.1785	0.2186	-0.4605	0.6615	0.4184	-0.8458	0.4349	0.299
246102_at	AT5G32590	myosin heavy chain-related	0.1619	0.8809	0.5465	0.469	0.6678	0.4477	-0.6404	0.562	0.3833	-0.3333	0.7589	0.4163
246103_at	AT5G28640	AN3 (ANGUSTIFOLIA3)	0.2861	0.6094	0.4628	0.4974	0.3904	0.337	-0.3407	0.401	0.3171	-0.1295	0.7393	0.4102
246104_at	AT5G28650	WRKY74 (WRKY DNA-binding protein 74); transcri	2.1428	0.0208	0.0849	2.6884	0.0097	0.0537	-0.218	0.7255	0.4403	0.3276	0.6016	0.3638
246105_at	AT5G28670	transposable element gene	0.9039	0.4625	0.4041	-0.03585	0.9759	0.5383	0.2436	0.8376	0.4749	-0.6962	0.5658	0.3512
246106_at	AT5G28680	protein kinase family protein	-1.8263	0.1166	0.1973	1.8452	0.1139	0.1704	-1.9954	0.0946	0.1365	1.6762	0.1409	0.1487
246107_at	AT5G28700	transposable element gene	-0.532	0.5711	0.4494	-0.5042	0.5906	0.4197	-1.2569	0.2192	0.2232	-1.2291	0.2277	0.2003
246108_at	AT5G28630	glycine-rich protein	-1.6681	0.0213	0.0857	-1.2277	0.0539	0.1152	1.7816	0.0013	0.0192	2.222	6.00E-04	0.01
246109_at	AT5G20120	similar to unnamed protein product [Vitis vinifera] (G	0.4898	0.0388	0.1136	0.4131	0.063	0.125	-0.3833	0.0768	0.121	-0.46	0.0467	0.0076
246110_at	AT5G20140	SOUL heme-binding family protein	-0.5264	0.0204	0.0842	-0.8715	0.0035	0.0374	0.1885	0.2534	0.2428	-0.1566	0.3301	0.2533
246111_at	AT5G20170	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.2271	0.126	0.2055	0.3732	0.0339	0.0909	-0.6622	0.0012	0.0185	-0.4161	0.0036	0.0194
246112_at	AT5G20200	nucleoporin-related	0.2796	0.0324	0.1043	0.0839	0.3889	0.3363	-0.02658	0.7749	0.4558	-0.2222	0.6628	0.091
246113_at	no_match	no_match	0.02174	0.9565	0.5664	0.2835	0.4918	0.3811	0.2311	0.571	0.3869	0.4929	0.2591	0.2173
246114_at	AT5G20250	DIN10 (DARK INDUCIBLE 10); hydrolase, hydroly	-0.05146	0.8717	0.5444	0.01868	0.9532	0.5326	-0.5444	0.0098	0.0395	-0.4742	0.0157	0.0399
246115_at	AT5G20300	chloroplast outer membrane protein, putative	0.3268	0.1608	0.2341	0.2279	0.2969	0.2902	-0.1083	0.5965	0.3969	-0.2072	0.3336	0.2551
246116_at	AT5G20310	similar to kinase [Arabidopsis thaliana] (TAIR:AT2G	1.2325	0.128	0.2067	1.1439	0.1501	0.1981	0.642	0.2746	0.255	0.5533	0.3369	0.2564
246117_at	AT5G20320	DCL4 (DICER-LIKE 4); RNA binding / ribonuclease	0.9319	0.0104	0.0646	0.7549	0.0211	0.074	-0.9155	0.0111	0.0417	-1.0926	0.006	0.0239
246118_at	AT5G20340	BG5 (BETA-1,3-GLUCANASE 5); hydrolase, hydrol	-1.885	0.1135	0.1952	-0.337	0.7363	0.4701	-1.3284	0.1226	0.1585	0.2196	0.7631	0.4178
246119_at	AT5G20350	TIP1 (TIP GROWTH DEFECTIVE 1)	0.6621	0.004	0.0468	0.2105	0.1321	0.1845	-0.226	0.0733	0.1178	-0.6776	0.0019	0.0151
246120_at	AT5G20360	octicosapeptide/Phox/Bem1p (PB1) domain-contair	0.1337	0.7032	0.4936	-0.16	0.6499	0.4417	-0.6523	0.0324	0.0733	-0.6786	0.0287	0.0566
246121_at	AT5G20370	serine-rich protein-related	-0.2023	0.6056	0.4616	-0.1346	0.7286	0.4683	-0.2081	0.5597	0.3967	-0.1404	0.7176	0.4033
246122_at	AT5G20380	transporter-related	-0.5789	0.028	0.097	-0.7721	0.0109	0.056	-1.0251	0.004	0.0273	-1.2183	0.0021	0.0154
246123_at	AT5G20390	beta-1,3-glucanase, putative	1.6306	0.1559	0.2302	0.4756	0.6376	0.4374	0.2045	0.8375	0.4749	-0.9505	0.3666	0.2698
246124_at	AT5G20060	phospholipase/carboxylesterase family protein	-0.1565	0.3936	0.3719	-0.2385	0.2192	0.2454	0.424	0.0178	0.0535	0.342	0.0352	0.0635
246125_at	AT5G19875	similar to unknown protein [Arabidopsis thaliana] (T	0.1794	0.2455	0.2908	0.5948	0.0107	0.0558	1.0656	0.0013	0.019	1.481	4.00E-04	0.0088
246126_at	AT5G20070	ATNUDT9 (Arabidopsis thaliana Nudix hydrolase	-0.5536	0.0787	0.1616	-0.955	0.0155	0.065	-0.1043	0.6046	0.3997	-0.5059	0.0532	0.0824
246127_s_at	no_match	no_match	-0.3624	0.7386	0.5053	-0.5933	0.5895	0.4194	0.08495	0.9208	0.4981	-0.146	0.8646	0.4469
246128_at	AT5G32540	transposable element gene	-0.3459	0.796	0.5226	-0.676	0.6178	0.4298	-0.9216	0.4454	0.3363	-1.2518	0.3148	0.2459
246129_at	no_match	no_match	-0.1342	0.8495	0.5479	0.5492	0.4115	0.2692	-0.7642	0.4355	0.3321	-0.08319	0.9295	0.4655
246130_at	AT5G32540	transposable element gene	1.008	0.4699	0.4072	-1.6418	0.2639	0.2719	1.4567	0.3134	0.2751	-1.1931	0.3987	0.2837
246131_at	AT5G20990	B73 (CHLORATE RESISTANT 6); molybdenum ion	0.7713	0.01	0.064	0.5331	0.0334	0.0905	-0.6175	0.0013	0.0188	-0.8557	4.00E-04	0.0088
246132_at	AT5G20850	ATRAN1 (Arabidopsis thaliana Ras Associated wit	0.957	0.2703	0.3055	1.3804	0.139	0.1899	-0.3841	0.5388	0.3748	0.03923	0.9486	0.4705
246133_at	AT5G20960	AAO1 (ALDEHYDE OXIDASE 1)	1.001	0.0807	0.164	1.2976	0.0394	0.0983	-0.4933	0.2612	0.2472	-0.1967	0.6297	0.3736
246134_at	AT5G20930	TSL (TOUSLED); kinase	0.221	0.2027	0.2641	0.4855	0.0288	0.0844	-0.5032	0.0257	0.0651	-0.2387	0.1755	0.1704
246135_at	AT5G20885	zinc finger (C3HC4-type RING finger) family protein	-0.6313	0.0488	0.1271	-0.7184	0.0333	0.0904	0.3705	0.1757	0.1958	0.2834	0.2771	0.2267
246136_at	AT5G28470	transporter	-0.2684	0.8166	0.5287	-0.6247	0.5952	0.4216	0.314	0.7864	0.4592	-0.04226	0.9708	0.4757
246137_at	AT5G28490	LSH1 (LIGHT-DEPENDENT SHORT HYPOCOTYL	0.1418	0.4913	0.4163	-0.1389	0.4995	0.3843	0.274	0.2175	0.2221	-0.00678	0.9729	0.4763
246138_at	AT5G19870	similar to unknown protein [Arabidopsis thaliana] (T	0.396	0.5251	0.4312	-0.9704	0.1635	0.2083	0.4356	0.4859	0.3539	-0.9308	0.1766	0.1711
246139_at	AT5G19900	PRLI-interacting factor, putative	-0.6689	0.0094	0.0624	-0.1788	0.2789	0.2803	-0.2859	0.0643	0.1094	0.2042	0.1445	0.1512
246140_at	AT5G19910	SOH1 family protein	-0.1089	0.4792	0.4116	-0.00633	0.966	0.5355	0.1568	0.3086	0.2727	0.2593	0.1262	0.139
246141_at	AT5G19920	transducin family protein / WD-40 repeat family prot	-0.1791	0.8057	0.5257	1.083	0.1874	0.2247	-0.3307	0.5795	0.3906	0.9314	0.1652	0.1644
246142_at	AT5G19970	similar to unnamed protein product [Vitis vinifera] (G	-1.3831	0.2104	0.2685	-2.4535	0.0574	0.119	1.1333	0.1768	0.1964	0.0629	0.9319	0.4662
246143_at	AT5G19980	integral membrane family protein	0.7125	0.0117	0.0677	0.3563	0.0929	0.1538	0.04516	0.7944	0.4616	-0.311	0.1276	0.1399
246144_at	AT5G20110	dynein light chain, putative	0.06091	0.6928	0.4902	-0.1864	0.4466	0.3623	1.221	6.00E-04	0.0159	0.9407	0.0017	0.0147
246145_at	AT5G19880	peroxidase, putative	0.5787	0.6342	0.4709	1.4406	0.2698	0.2754	1.0183	0.1787	0.1977	1.8802	0.0397	0.0687
246146_at	AT5G20050	protein kinase family protein	-0.2764	0.2206	0.2756	0.04306	0.8323	0.4995	0.5954	0.0354	0.0771	0.9148	0.0086	0.0289
246147_s_at	AT5G19990;AT5G20000	AT5G19990; RPT5A; ATPase[s];AT5G20000; (REG	0.7108	0.038	0.1482	0.0012	0.0294	-0.193	0.6672	0.1123	-0.1555	0.1148	0.1311	
246148_at	AT5G19960	RNA recognition motif (RRM)-containing protein	0.3638	0.1672	0.2392	0.3321	0.1987	0.2322	0.1946	0.2841	0.2602	0.1628	0.3594	0.2667
246149_at	AT5G19890	peroxidase, putative	0.8355	0.5148	0.4271	-0.4282	0.733	0.4691	-0.1978	0.874	0.4851	-1.4615	0.2799	0.2281
246150_at	AT5G19930	integral membrane family protein	0.5478	0.0423	0.1183	0.4584	0.0695	0.1321	-0.3954	0.0108	0.0414	-0.4848	0.0053	0.0227
246151_at	AT5G19950	similar to unknown protein [Arabidopsis thaliana] (T	0.8898	0.0122	0.0685	0.3011	0.2157	0.2432	-0.4903	0.075	0.1192	-1.079	0.0062	0.0245
246152_at	AT5G20040	ATIPT9 (Arabidopsis thaliana isopentenyltransferas	-0.2167	0.4861	0.4141	0.07887	0.794	0.4874	-0.7266	0.0106	0.0409	-0.431	0.055	0.0839
246153_s_at	AT5G20010;AT5G20020	AT5G20010; RAN-1 (RAS RELATED NUCLEAR P	0.3866	0.0246	0.0911	0.8254	0.0017	0.032	-0.3623	0.0183	0.0541	0.07651	0.4618	0.3108
246154_at	AT5G19940	plastid-lipid associated protein PAP-related / fibrilin	-0.5366	0.0062	0.0542	-0.571	0.005	0.0424	-0.2989	0.0427	0.086	-0.3333	0.0307	0.059
246155_at	AT5G20030	agenet domain-containing protein	-0.1432	0.5087	0.4245	-0.4204	0.1004	0.1598	0.4153	0.1034	0.1437	0.1381	0.523	0.335
246156_at	AT5G20090	similar to unknown protein [Arabidopsis thaliana] (T	-0.02433	0.7979	0.5233	0.09315	0.3538	0.3201	0.3472	0.0067	0.0335	0.4647	0.0023	0.016
246157_at	AT5G20080	NADH-cytochrome b5 reductase, putative	-0.3109	0.0384	0.1128	-0.08486	0.4532	0.3653	-0.2304	0.0676	0.1127	-0.00435	0.9648	0.4744
246158_at	AT5G19855	similar to unnamed protein product [Vitis vinifera] (G	-0.8146	0.0028	0.0431	-0.5899	0.0091	0.0522	0.3209	0.0618	0.1068	0.5456	0.0119	0.0343
246159_at	AT5G20935	similar to unnamed protein product [Vitis vinifera] (G	-0.7141	0.003	0.0436	-1.0593	7.00E-04	0.027	1.132	1.00E-04	0.0118	0.7868	5.00E-04	0.0095
246160_at	AT5G21040	F-box family protein / WD-40 repeat family protein	0.1111	0.3416	0.346	0.1295	0.2769	0.2792	-0.3094	0.0398	0.0826	-0.2909	0.0476	0.077
246161_at	AT5G20900	JAZ12/TIFY3B (JASMONATE-ZIM-DOMAIN PROT	-0.01961	0.8852	0.5471	0.08859	0.5251	0.3941	0.5013	9.00E-04	0.0169	0.6095	4.00E-04	0.009
246162_at	AT5G36400	FAD linked oxidase family protein	-0.1581	0.437	0.3925	0.1255	0.5313	0.3967	-0.3628	0.0606	0.1057	-0.07918	0.602	0.3639
246163_at	AT5G32600	transposable element gene	0.2737	0.6631	0.4804	-0.6364	0.3363	0.3116	-0.04006	0.9485	0.5053	-0.9502	0.1784	0.1723
246164_at	AT5G32610	transposable element gene	-2.8673	0.0716	0.1542	-0.6536	0.6084	0.4265	-0.3806	0.7493	0.448	1.833	0.1745	0.17
246165_at	no_match	no_match	-1.1179	0.2797	0.3111	1.0704	0.2977	0.2905	0.1299	0.8916	0.4901	2.3182	0.0607	0.0891
246166_at	no_match	no_match	1.1806	0.082	0.1657	1.4527	0.0467	0.1072	0.7119	0.236	0.2328	0.984	0.1265	0.1392
246167_at	no_match	no_match	-1.4143	0.1755	0.2452	-0.4659	0.6169	0.4295	-0.5333	0.5688	0.3863	0.4151	0.6546	0.3824
246168_at	AT5G32460	pseudogene, transcriptional factor B3 family, low si	-0.03749	0.9792	0.572	-0.07776	0.957	0.5335	-0.9103	0.5229	0.3681	-0.9505	0.5058	0.3281
246169_at	AT5G32470	similar to unnamed protein product [Vitis vinifera] (G	-0.01602	0.8607	0.5413	-0.237	0.0505	0.1115	0.01172	0.8978	0.4917	-0.2093	0.071	0.0977
246170_at	AT5G32450	RNA recognition motif (RRM)-containing protein	-0.4641	0.0177	0.0798	-0.3873	0.0315	0.0883	0.2091	0.0361	0.0781	0.2858	0.0132	0.0364
246171_at	AT5G32440	similar to unknown protein [Arabidopsis thaliana] (T	0.5402	0.0286	0.0981	0.3952	0.0705	0.1328	-0.01526	0.9237	0.4989	-0.1603	0.3448	0.2602
246172_s_at	AT3G61510;AT5G28360	(AT3G61510; ACS1 (ACC SYNTHASE 1); 1-amino	-0.8612	0.4041	0.3773	-0.7089	0.4858	0.3786	-0.4767	0.6332	0.4088	-0.3243	0.7433	0.4114
246173_s_at	AT5G28370;AT5G28460;A	(AT5G28370, pentatricopeptide (PPR) repeat-conta	0.009525	0.9688	0.5694	0.01101	0.964	0.535	-0.5066	0.03	0.0705	-0.5651	0.0302	0.0584
246174_s_at	AT5G28340;AT5G28380	(AT5G28340, pentatricopeptide (PPR) repeat-conta	-0.9987	0.5144	0.427	-1.0885	0.4796	0.3759	-0.6056	0.519	0.3666	-0.6955	0.4629	0.3112
246175_s_at	AT5G28400;AT5G28320	(AT5G28400, similar to EMB1703 (EMBRYO DEFE	-0.3495	0.4738	0.4094	0.005142	0.9913	0.542	-1.7682	0.0098	0.0395	-1.4136	0.0208	0.0467
246176_at	AT5G28410	unknown protein	-1.1215	0.235	0.2844	1.4017	0.1558	0.2026	-1.7653	0.0162	0.0508	0.7578	0.1618	0.1623
246177_at	AT5G28420	similar to unknown protein [Arabidopsis thaliana] (T	0.03273	0.9782	0.5718	0.7194	0.0577	0.4075	-1.0401	0.408	0.3199	-0.2879	0.8108	0.4319
246178_s_at	AT5G28430;AT3G60930	(AT5G28430, transposable element gene);[AT3G60	1.0778	0.1941	0.2583	0.8145	0.3041	0.2937	-0.3202	0.6674	0.4203	-0.5835	0.4463	0.3045
246179_at	AT5G28440	similar to unknown protein [Arabidopsis thaliana] (T	0.2936	0.7029	0.4935	-0.6147	0.4392	0.3592	-0.07	0.9269	0.4998	-0.9783	0.2437	0.2092
246180_at	AT5G20940	phosphoinositide phosphatase family protein	-0.07443	0.7295	0.5024	-0.2175	0.3393	0.3132	-0.3833	0.1288	0.1631	-0.5264	0.0586	0.0873
246181_at	AT5G20860	pectinesterase family protein	1.056	0.0457	0.1229	-1.8627	0.0072	0.0479	1.436	0.0075	0.0351	-1.4827	0.0067	0.0255
246182_at	AT5G20870	glycosyl hydrolase family 17 protein	-0.1536	0.4522	0.3992	-1.2408	0.0025	0.034	1.212	0.0027	0.0237	0.1247	0.5318	0.3386
246183_at	AT5G20940	glycosyl hydrolase family 3 protein	0.68	0.2182	0.274	0.06193	0.9007	0.5191	-0.1413	0.7769	0.4563	-0.7593	0.1785	0.1723
246184_at	AT5G20950	glycosyl hydrolase family 3 protein	0.8926	0.0019	0.0391	0.913	0.0017	0.0321	-0.6597	0.0016	0.0204	-0.6394	0.0018	0.0148
246185_at	AT5G20980	ATMS3 (METHIONINE SYNTHASE 3); 5-methyltet	-0.00658	0.9647	0.5684	-0.1942	0.2369	0.2559	-0.3552	0.0638	0.1089	-0.5428	0.0178	0.0427
246186_at	no_match	no_match	1.8677	0.1034	0.1858	2.8131	0.034	0.0911	-0.3288	0.7301	0.4418	0.6166	0.5259	0.3362
246187_at	no_match	no_match	-1.0054	0.1375	0.2154	-0.1284	0.8245	0.4974	-0.9974	0.1398	0.171	-0.1205	0.8351	0.4386
246188_at	AT5G21050	similar to unknown protein [Arabidopsis thaliana] (T	0.6988	0.2556	0.2968	-0.8745	0.1725	0.2145	0.4602	0.432	0.3304	-1.1131	0.1023	0.1222
246189_at	AT5G20910	zinc finger (C3HC4-type RING finger) family protein	0.8972	0.0056	0.0521	0.8611	0.0065	0.0458	0.2895	0.0248	0.0639	0.2534	0.0374	0.0661
246190_at	AT5G21010	ATBPM5 (BTB-POZ AND MATH DOMAIN 5); prote	0.0524	0.7969	0.5229	0.1067	0.6051	0.4251	-0.03972	0.845	0.4771	0.01463	0.9425	0.4691
246191_at	AT5G20890	chaperonin, putative	0.5956	0.0068	0.0556	0.4242	0.0216	0.0747	-0.1469	0.1543	0.1819	-0.3183	0.0191	0.0443
246192_at	AT5G20920	EIF2 BETA (EMBRYO DEFECTIVE 1401)	0.3014	0.0107	0.0649	0.412	0.0035	0.0374	0.06695	0.2214	0.2244	0.1776	0.0185	0.0436
246193_at	AT5G20880	transposable element gene	0.8556	0.014	0.0723	0.7872	0.0184	0.0702	-0.00883	0.9677	0.5095	-0.07724	0.7254	0.4058
246194_at	AT4G37000	ACD2 (ACCELERATED CELL DEATH 2)	-0.07992	0.5335	0.4344	-0.4358	0.0206	0.0733	0.4467	0.0178	0.0533	0.0909	0.4735	0.3151
246195_at	AT4G36410	UBC17 (UBIQUITIN-CONJUGATING ENZYME 17);	-0.6368	0.0166	0.0775	-0.2765	0.1603	0.2061	0.3252	0.113	0.1506	0.6854	0.013	0.0361
246196_at	AT4G37090	similar to unnamed protein product [Vitis vinifera] (G	0.6338	0.0039	0.0463	0.7204	0.0024	0.0339	0.6743	0.0031	0.025	0.7609	0.002	0.0151
246197_at	AT4G37010	caltractin, putative / centrin, putative	1.8328	0.0264	0.0939	1.6146	0.0389	0.0978	0.1293	0.5201	0.367	-0.08889	0.6536	0.382
246198_at	AT4G36810	GGPS1 (GERANYLGERANYL PYROPHOSPHATE	-0.2527	0.1666	0.2387	-0.608	0.0153	0.0649	0.1285	0.4389	0.3336	-0.2268	0.2042	0.1874
246199_at	AT4G36530	hydrolase, alpha/beta fold family protein	-0.761	9.00E-04	0.0348	-0.88	5.00E-04	0.0257	0.1414	0.0353	0.077	0.02232	0.6475	0.3799
246200_at	AT4G37240	similar to unknown protein [Arabidopsis thaliana] (T	-1.3641	0.1391	0.2165	-1.1663	0.1902	0.2265	0.3252	0.2123	0.2193	0.5231	0.0756	0.1013
246201_at	AT4G36750	quinone reductase family protein	0.4987	0.0098	0.0635	0.4744	0.016	0.0581	0.6148	4.00E-04	0.0147	0.5905	5.00E-04	0.0093
246202_at	AT4G37040	MAP1D (METHIONINE AMINOPEPTIDASE 1D); m	-0.2394	0.0414	0.1172	-0.417	0.0067	0.0463	0.3969	0.0023	0.0223	0.2194	0.0184	0.0436
246203_at	AT4G36610	hydrolase, alpha/beta fold family protein	0.08292	0.8328	0.5332	0.6925	0.1326	0.1848	0.4326	0.2236	0.2258	1.0912	0.0311	0.0595
246204_at	AT4G37020	similar to unknown protein product [Vitis vinifera] (G	0.1133	0.4136	0.3817	-0.1527	0.2866	0.2847	-0.4063	0.0308	0.0715	-0.6722	0.0057	0.0234
246205_at	AT4G36970	remorin family protein	0.6465	0.0159	0.0763	0.7278	0.0107	0.0557	0.3872	0.074	0.1184	0.4685	0.0437	0.0731
246206_at	no_match	no_match	0.012	0.9865	0.5735	0.9376	0.2318	0.2527	-0.8182	0.0261	0.2426	0.1074	0.8695	0.4482
246207_at	AT4G36960	RNA recognition motif (RRM)-containing protein	0.141	0.0762	0.1589	-0.01711	0.7873	0.4853	-0.0593	0.326	0.2814	-0.2174	0.0148	0.0388
246208_at	AT4G36490	SEC14 cytosolic factor, putative / phosphoglyceride	-0.3225	0.7677	0.5138	-1.033	0.3686	0.3268	1.0663	0.355	0.2957	0.3558	0.7449	0.4119
246209_at	AT4G36870	BLH2 (BEL1-LIKE HOMEODOMAIN 2, SAWTOOT	0.3156	0.1457	0.2218	0.1888	0.3415	0.3143	0.1615	0.1162	0.1533	0.03076	0.6843	0.3855
246210_at	AT4G36420	ribosomal protein L12 family protein	0.3542	0.0519	0.1307	0.7265	0.0049	0.0424	-0.3563	0.0174	0.0527	0.01589	0.87	0.4484
246211_at	AT4G36730	GBF1 (G-box binding factor 1); transcription factor	-0.5681	0.0341	0.1067	-0.2138	0.2997	0.2912	-0.5958	0.0068	0.0337	-0.2414	0.1056	0.1244
246212_at	AT4G36930	SPT (SPATULA); DNA binding / transcription factor	0.3208	0.3217	0.3352	0.2373	0.3099	0.2973	0.2966	0.1878	0.2042	0.3022	0.1803	0.1734
246213_at	AT4G36480	ATLCB1 (LONG-CHAIN BASE1); protein binding / s	0.04022	0.8811	0.5465	-0.05216	0.8464	0.5034	-0.3054	0.2882	0.2627	-0.3978	0.1862	0.1771
246214_at	AT4G36988;AT4G36990	(AT4G36988, CPuORF49 (Conserved peptide upst	1.3965	0.0042	0.0468	1.6627	0.0022	0.0333	0.03514	0.7609	0.4514	0.3014	0.0491	0.0785
246215_at	AT4G36920	myb family transcription factor	0.7763	0.1044	0.1866	1.0878	0.0427	0.1027	-0.1353	0.5357	0.3735	0.1762	0.4278	0.2958
246216_at	AT4G36380	ROT3 (ROTUNDIFOLIA 3); oxygen binding / steroid	1.7654	0.0127	0.0697	1.5285	0.0206	0.0732	0.4864	0.2307	0.2299	0.2496	0.5088	0.3293
246217_at	AT4G36920	AP2 (APETALA 2); transcription factor	0.4211	0.0597	0.1399	0.7466	0.0099	0.0541	-0.3229	0.0717	0.1164	0.002626	0.9852	0.4791
246218_at	AT4G36800	RCE1 (RUB1 CONJUGATING ENZYME 1); small p	-0.173	0.3787	0.3637	0.2257	0.2666	0.2736	-0.03908	0.8342	0.4738	0.3596	0.109	0.127
246219_at	AT4G36760	ATAPP1 (aminopeptidase P1)	0.6734	0.0075	0.0579	0.7249	0.0058	0.0439	-0.6693	0.0077	0.0353	-0.6177	0.0101	0.0315
246220_at	AT4G37210	tetratricopeptide repeat (TPR)-containing protein	0.182	0.1223	0.2026	0.2189	0.0784	0.1404	0.1064	0.2929	0.2651	0.1433	0.1786	0.1724
246221_at	AT4G37120	SMP2 (swollmp 2)	0.3621	0.0746	0.157	0.6207	0.0147	0.064	0.3598	0.0758	0.12	0.6185	0.0149	0.0388
246222_at	AT4G36900	RAP2.10 (related to AP2 10); DNA binding / transcr	-0.5499	0.5048	0.4225	-0.07413	0.9262	0.5257	-0.9551	0.1203	0.1564	-0.4793	0.3791	0.2753
246223_at	AT4G36890	IRX14 (IRREGULAR XYLEM 14); transferase, trans	0.1467	0.2916	0.3182	0.04839	0.7094	0.4619	-0.32	0.5571	0.1021	-0.4184	0.0258	0.0532
246224_at	AT4G36590	MAD5 protein (AGL40

246290_at	AT3G56800	CAM3 (CALMODULIN 3); calcium ion binding	-0.02657	0.8801	0.5464	0.2748	0.1718	0.214	0.5623	0.0023	0.0226	0.8637	4.00E-04	0.0093
246291_at	AT3G56820	similar to unnamed protein product [Vitis vinifera] (G	0.3968	0.21	0.2683	0.1506	0.6016	0.4242	0.479	0.1461	0.1762	0.2328	0.4309	0.2972
246292_at	AT3G56860	UBA2A; RNA binding	0.1024	0.5804	0.4523	0.09683	0.6003	0.4236	0.02934	0.8716	0.4846	0.02382	0.8956	0.4559
246293_at	AT3G56710	SIB1 (SIGMA FACTOR BINDING PROTEIN 1); bin	0.4601	0.1078	0.1899	0.5786	0.0602	0.1218	0.7721	0.0022	0.0219	0.8906	0.0013	0.013
246294_at	AT3G56910	PSRP5 (PLASTID-SPECIFIC 50S RIBOSOMAL PR	-0.5418	0.0597	0.1399	-0.7327	0.0244	0.0783	0.4541	0.0944	0.1363	0.2632	0.2744	0.2252
246295_at	AT3G56690	CIP111 (CAM INTERACTING PROTEIN 111); ATP	0.8966	0.0092	0.0618	0.798	0.0137	0.062	-0.3884	0.0034	0.0259	-0.487	0.0015	0.0137
246296_at	AT3G56750	similar to unknown protein [Arabidopsis thaliana] (T	0.1547	0.5178	0.4284	0.3546	0.1797	0.2194	-0.4445	0.1115	0.1495	-0.2446	0.3253	0.2509
246297_at	AT3G51760	unknown protein	0.5883	0.4083	0.3793	0.9145	0.2247	0.2483	-0.2442	0.5685	0.3862	-1.747	0.0113	0.0334
246298_at	AT3G51770	ETO1 (ETHYLENE OVERPRODUCER 1)	0.3314	0.2074	0.2668	0.5116	0.0812	0.1429	-0.7142	0.0317	0.0725	-0.534	0.0727	0.0989
246299_at	AT3G51810	ATEM1 (Early methionine labelled)	-0.9884	0.444	0.3952	0.7214	0.5693	0.4116	-1.1675	0.373	0.3043	0.5423	0.6658	0.3861
246300_at	AT3G51830	ATG5 (Gtp-related protein); phosphoinositide 5-phc	0.2155	0.232	0.2831	0.2991	0.1225	0.1776	-0.7601	0.0072	0.0343	-0.6765	0.0108	0.0326
246301_at	AT3G51850	CPK13 (calcium-dependent protein kinase 13); calc	0.09625	0.2325	0.2833	0.06721	0.3818	0.3328	-0.2787	0.0152	0.0492	-0.3078	0.0109	0.0326
246302_at	AT3G51860	CAX3 (cation exchanger 3); cation:cation antiporter	2.6666	0.0059	0.0534	2.4401	0.008	0.0499	-0.237	0.1397	0.1709	-0.4636	0.0228	0.0492
246303_at	AT3G51870	mitochondrial substrate carrier family protein	0.185	0.5249	0.4311	0.2583	0.3887	0.3362	-0.3472	0.1501	0.179	-0.7914	0.0154	0.0397
246304_at	AT3G51840	ACX4 (ACYL-COA OXIDASE 4); oxidoreductase	0.4244	0.028	0.097	0.5412	0.0126	0.0601	-0.6136	0.0082	0.0363	-0.4968	0.0169	0.0415
246305_at	AT3G51890	protein binding / protein transporter/ structural molec	1.2337	0.0019	0.0391	1.5152	9.00E-04	0.0284	1.0469	7.00E-04	0.016	1.3283	3.00E-04	0.0083
246306_at	AT3G51900	ATBAG4 (ARABIDOPSIS THALIANA BCL-2-ASSO	0.2389	0.0405	0.116	0.1748	0.0942	0.1546	0.5531	0.0023	0.0224	0.4889	0.0036	0.0196
246307_at	**AT3G51800**	**ATG2 (G2p-related protein); metalloexopeptidas**	**0.3064**	**0.1383**	**0.216**	**0.2576**	**0.1962**	**0.2295**	**0.1639**	**0.1942**	**0.2081**	**0.1151**	**0.3353**	**0.2557**
246308_at	AT3G51820	ATG4/CHLG/G4 (CHLOROPHYLL SYNTHASE); ch	-0.5692	0.0252	0.092	-0.8406	0.0067	0.0464	-0.2758	0.0787	0.1227	-0.5472	0.0096	0.0305
246309_at	AT3G51840	ATG1 (G1p-related protein)	0.2505	0.3024	0.3244	0.4616	0.0948	0.1552	-0.1901	0.4201	0.3254	0.02106	0.9256	0.4643
246310_at	AT3G51895	SULTR3;1 (SULFATE TRANSPORTER 1); sulfate	-0.453	0.0764	0.1592	-0.277	0.2202	0.246	-0.3183	0.0557	0.1007	-0.1423	0.2983	0.2378
246311_at	AT3G51880	HMG81 (HIGH MOBILITY GROUP B 1); transcripte	-0.04651	0.7707	0.5148	0.8404	0.0049	0.0422	0.02147	0.8464	0.4775	0.9084	9.00E-04	0.0119
246312_at	AT1G31930	XLG3 (EXTRA-LARGE GTP-BINDING PROTEIN 3	0.00079	0.996	0.5761	0.1276	0.4378	0.3588	-0.3586	0.0728	0.1173	-0.2302	0.1954	0.1821
246313_at	AT1G31920	pentatricopeptide (PPR) repeat-containing protein	-0.3244	0.0829	0.1666	-0.4828	0.0267	0.0816	-0.3962	0.0203	0.0573	-0.5546	0.0064	0.0249
246314_at	AT3G56850	AREB3 (ABA-RESPONSIVE ELEMENT BINDING F	0.09883	0.6143	0.4642	0.07644	0.6947	0.457	-0.03758	0.8368	0.4747	-0.05997	0.7434	0.4114
246315_at	AT3G56870	similar to unnamed protein product [Vitis vinifera] (G	-0.5795	0.3456	0.3476	0.1953	0.737	0.4703	0.3199	0.5871	0.3934	1.0947	0.1137	0.1304
246316_at	AT3G56890	F-box family protein related	-0.2175	0.8182	0.5291	-1.5491	0.1554	0.2024	-0.0165	0.986	0.5141	-1.3481	0.2029	0.1868
246317_at	AT3G56900	aladin-related / adracalin-related	0.282	0.6948	0.4868	0.03012	0.8197	0.4958	-0.1789	0.154	0.1617	-0.4308	0.0134	0.0367
246318_at	AT3G56740	ubiquitin-associated (UBA)/TS-N domain-containing	0.3278	0.0672	0.1489	0.07161	0.6148	0.4288	-0.03666	0.7741	0.4555	-0.2928	0.0702	0.0971
246319_at	AT3G56680	nucleic acid binding	0.04024	0.8342	0.5337	-0.03003	0.8757	0.5118	-0.8601	0.0032	0.0251	-0.9304	0.0024	0.0161
246320_at	AT1G16560	Per1-like family protein	0.386	0.0296	0.0999	0.2871	0.0894	0.132	-0.1799	0.1041	0.1442	-0.2788	0.0314	0.0598
246321_at	AT1G16640	transcriptional factor B3 family protein	-0.8154	0.0997	0.1823	-0.07579	0.8524	0.5052	-0.1653	0.6822	0.425	0.5743	0.2004	0.1853
246322_at	AT1G16680	DNAJ heat shock N-terminal domain-containing pro	0.07173	0.6278	0.4689	-0.1829	0.2523	0.2654	-0.42	0.0373	0.0797	-0.6746	0.0079	0.0277
246323_at	AT1G16690	transcription factor-related	-0.01944	0.8162	0.5286	-0.7547	6.00E-04	0.027	0.6869	2.00E-04	0.0125	0.04835	0.3865	0.2785
246324_at	AT1G16610	SR45 (arginine/serine-rich 45); RNA binding	0.6059	0.0209	0.085	0.1044	0.5588	0.4079	0.4964	0.0388	0.0814	-0.00507	0.9768	0.4773
246325_at	AT1G16540	ABA3/ATABA3/LOS5/SIR3 (ABA DEFICIENT 3); M	0.3965	0.475	0.4098	0.09555	0.8587	0.5068	-1.0464	0.1062	0.1459	-1.3473	0.0555	0.0844
246326_at	AT1G16590	REV7 (Reversionless 7); DNA binding	-0.6773	0.0225	0.0876	-0.7308	0.0175	0.0686	-0.3691	0.1202	0.1564	-0.4225	0.0872	0.1106
246327_at	AT1G16670	protein kinase family protein	0.5442	0.103	0.1855	0.5144	0.1174	0.1732	-0.07597	0.6122	0.4019	-0.1058	0.4873	0.3208
246328_at	AT3G43590	zinc knuckle (CCHC-type) family protein	0.4904	0.0865	0.1704	-0.02717	0.9063	0.5205	0.3519	0.0509	0.0956	-0.1657	0.2638	0.2196
246329_at	AT3G43610	tubulin binding	-0.3489	0.1778	0.2465	-0.4885	0.0492	0.146	-0.9443	0.0112	0.042	-1.0839	0.0069	0.026
246330_at	AT3G43600	AAO2 (ALDEHYDE OXIDASE 2)	-0.3074	0.2489	0.293	-0.5308	0.0804	0.1422	-0.3331	0.1025	0.1429	-0.5565	0.0243	0.0513
246331_at	AT3G44820	phototropic-responsive NPH3 family protein	-0.176	0.5463	0.4395	0.007075	0.9802	0.5393	-0.9307	0.0253	0.0646	-0.7477	0.0489	0.0783
246332_at	AT3G44830	lecithin:cholesterol acyltransferase family protein / L	0.1373	0.8842	0.5471	-0.6239	0.5197	0.3922	0.5012	0.6014	0.3987	-0.2599	0.7836	0.424
246333_at	AT3G44840	S-adenosyl-L-methionine:carboxyl methyltransfera	1.2531	0.2761	0.3094	0.174	0.8696	0.5098	1.7734	0.1491	0.1784	0.6943	0.5235	0.3353
246334_at	AT3G44850	protein kinase-related	0.1387	0.3533	0.3515	0.1716	0.2641	0.272	-0.1505	0.3185	0.2776	-0.1176	0.424	0.2941
246335_at	AT3G44880	ACD1 (ACCELERATED CELL DEATH 1)	0.4075	0.0563	0.136	0.216	0.2311	0.2522	0.1949	0.2594	0.2461	0.003404	0.9828	0.4787
246336_at	AT3G44900	ATCHX4 (CATION/H+ EXCHANGER 4); monovalet	0.587	0.7339	0.5036	0.682	0.6937	0.4567	-0.1825	0.9152	0.4965	-0.08754	0.9592	0.4732
246337_at	AT3G44910	ATCHX12 (cation/H+ exchanger 12); monovalent c	1.2589	0.2631	0.3015	-0.3936	0.7049	0.4606	0.0855	0.9338	0.5018	-1.567	0.1806	0.1737
246338_s_at	AT3G44930;AT3G44920	ACD1 (ACCELERATED CELL DEATH 1); CATION/H+ EXCHANGES	-0.4024	0.6971	0.4918	-0.5665	0.5875	0.4187	0.1406	0.891	0.4901	-0.02365	0.9816	0.4784
246339_at	AT3G44890	RPL9 (ribosomal protein L9); structural constituent	-0.8982	0.0135	0.0715	-1.0377	0.0082	0.0503	0.5819	0.0071	0.0341	0.4424	0.0181	0.0432
246340_s_at	AT3G44860;AT3G44870	[AT3G44860, FAMT (FARNESOIC ACID CARBOX	-0.3535	0.363	0.3559	-0.1384	0.7085	0.4616	-0.01552	0.9012	0.4928	0.1995	0.1644	0.1639
246341_x_at	AT3G43150	similar to unknown protein [Arabidopsis thaliana] (T	-0.9785	0.1388	0.2163	0.7643	0.223	0.2476	-0.3233	0.7931	0.4611	-0.3629	0.5314	0.3385
246342_at	AT3G56700	male sterility protein, putative	1.2747	0.4553	0.4006	-0.2335	0.8871	0.515	-0.7008	0.1786	0.1977	-2.209	0.0068	0.0257
246343_at	AT3G56720	similar to unnamed protein product [Vitis vinifera] (G	1.0013	0.0463	0.1237	1.4062	0.016	0.0659	0.2785	0.4719	0.3483	0.6835	0.1233	0.1372
246344_at	AT3G56730	similar to unknown protein [Arabidopsis thaliana] (T	-0.237	0.7511	0.5088	0.6727	0.3895	0.3365	0.5212	0.4965	0.3584	1.4309	0.1095	0.1274
246345_at	AT3G56760	calcium-dependent protein kinase, putative / CDPK	-0.1764	0.5072	0.424	-0.6103	0.0655	0.128	0.3187	0.1607	0.186	-0.1152	0.5678	0.3519
246346_at	AT3G56810	unknown protein	-0.2117	0.6027	0.4604	-0.4131	0.3327	0.3097	0.5749	0.1023	0.1428	0.3735	0.2421	0.2083
246347_at	AT3G56830	similar to unknown protein [Arabidopsis thaliana] (T	0.05698	0.8335	0.5335	0.07603	0.8755	0.4824	-0.5193	0.1059	0.1456	-0.4963	0.116	0.1319
246348_at	AT3G56840	FAD-dependent oxidoreductase family protein	0.07856	0.6839	0.4871	-0.05028	0.7931	0.4871	-0.2473	0.105	0.1449	-0.3762	0.0336	0.062
246349_at	AT1G51915	cryptdin protein-related	1.4167	0.1126	0.1943	2.1535	0.0369	0.0949	0.7586	0.3137	0.2752	1.4954	0.0857	0.1096
246350_at	AT1G16650	similar to unnamed protein product [Vitis vinifera] (G	0.7769	0.1649	0.2374	0.3386	0.5006	0.3848	-0.6504	0.2284	0.2286	-1.0888	0.0761	0.1016
246351_at	AT1G16570	glycosyl transferase family 1 protein	0.4457	0.029	0.0986	0.3639	0.0529	0.114	-0.2653	0.1181	0.1547	-0.3472	0.0602	0.0887
246352_at	no_match	no_match	-0.8512	0.3679	0.3583	-0.5679	0.5358	0.3988	-0.8756	0.3558	0.296	-0.5923	0.5193	0.3333
246353_s_at	AT4G08010;AT1G39190;A	[AT4G08010, transposable element gene];[AT1G39	-0.3875	0.6694	0.4824	-2.6102	0.0363	0.0941	0.793	0.3998	0.3165	-1.4297	0.1649	0.1643
246354_at	AT1G38950	unknown protein	-0.8314	0.5092	0.4246	-0.1657	0.8922	0.5164	0.4108	0.7386	0.4443	1.0765	0.4016	0.2848
246355_at	no_match	no_match	0.8312	0.4235	0.3868	0.2728	0.7847	0.4847	0.5405	0.5936	0.396	-0.01794	0.9856	0.4792
246356_x_at	AT1G40150	transposable element gene	1.8464	0.0445	0.1216	0.8207	0.268	0.2744	-0.1712	0.4305	0.3298	-1.197	0.0036	0.0195
246357_x_at	no_match	no_match	0.5684	0.5528	0.4421	-0.5436	0.5695	0.4117	0.01529	0.9847	0.5138	-1.0967	0.2161	0.1941
246358_x_at	no_match	no_match	0.1934	0.873	0.5449	0.1644	0.8919	0.5163	-0.5753	0.6392	0.4108	-0.6043	0.6229	0.3712
246359_x_at	AT1G41690;AT1G41600;A	[AT1G41690, transposable element gene];[AT1G41	0.06966	0.9333	0.5606	-1.4316	0.141	0.1914	1.4167	0.1441	0.1746	-0.08451	0.9191	0.4625
246360_at	no_match	no_match	-1.0375	0.5339	0.4346	-0.7029	0.669	0.4481	0.3033	0.8521	0.4791	0.6379	0.6974	0.3966
246361_s_at	AT1G41600;AT1G41115;A	[AT1G41600, transposable element gene];[AT1G41	0.7333	0.6001	0.4597	2.6671	0.1075	0.1653	-1.4882	0.3129	0.2749	0.4456	0.7472	0.4128
246362_at	no_match	no_match	-0.7302	0.6074	0.4622	0.2264	0.8714	0.5104	-1.8525	0.2308	0.2299	-0.8959	0.5321	0.3387
246363_at	AT1G40390	similar to unknown protein [Arabidopsis thaliana] (T	-1.0519	0.4223	0.3861	-0.4414	0.7269	0.4678	0.1193	0.9242	0.499	0.7298	0.5691	0.3523
246364_at	AT1G40230	transposable element gene	-0.09085	0.9246	0.5582	0.5907	0.5484	0.4041	0.4778	0.6245	0.4061	1.1593	0.2682	0.2218
246365_at	AT1G39750	transposable element gene	1.6172	0.3016	0.324	-1.0236	0.4949	0.3825	0.5255	0.6623	0.4187	-2.1153	0.131	0.1422
246366_at	AT1G51850	leucine-rich repeat protein kinase, putative	2.7661	0.0214	0.0859	0.3858	0.6358	0.4369	0.05365	0.9467	0.5048	-2.3267	0.0367	0.0652
246367_at	AT1G51880	leucine-rich repeat protein kinase, putative	-0.01945	0.9848	0.5733	-2.9276	0.0381	0.0966	2.7158	0.0475	0.0914	-0.1923	0.8511	0.443
246368_at	AT1G51890	leucine-rich repeat protein kinase, putative	2.1705	0.0095	0.0626	1.9922	0.0128	0.0603	-0.02861	0.8452	0.4771	-0.2069	0.2067	0.1888
246369_at	AT1G51910	protein kinase family protein	0.06807	0.9073	0.5531	-0.5167	0.3997	0.3411	0.3203	0.5907	0.3949	-0.2645	0.655	0.3825
246370_at	AT1G51920	unknown protein	1.5234	0.0271	0.0953	1.3108	0.0428	0.1027	0.7908	0.0274	0.0674	0.5782	0.0681	0.0953
246371_at	AT1G51940	protein kinase family protein / peptidoglycan-binding	0.5789	0.3329	0.3417	0.688	0.261	0.2703	-0.4115	0.0779	0.122	-0.3024	0.1582	0.1601
246372_at	AT1G51900	similar to unknown protein [Arabidopsis thaliana] (T	1.1155	0.341	0.3457	-0.3831	0.7296	0.4685	0.6523	0.3887	0.3116	-0.8463	0.2783	0.2273
246373_at	AT1G51860	leucine-rich repeat protein kinase, putative	3.1504	0.038	0.1123	2.7819	0.0544	0.1158	0.3313	0.6301	0.4079	-0.0372	0.9562	0.4725
246374_at	AT1G51840	protein kinase-related	0.7404	0.5599	0.4449	0.3491	0.7795	0.4834	0.2849	0.819	0.4695	-0.1063	0.9317	0.4661
246375_at	AT1G51830	ATP binding / kinase/ protein serine/threonine kinase	1.0096	0.4434	0.3951	-0.5498	0.6676	0.4477	-1.0023	0.4464	0.3368	-2.5617	0.0973	0.1185
246376_at	AT1G51950	IAA18 (indoleacetic acid-induced protein 18); transc	-0.287	0.4021	0.3763	-0.1525	0.645	0.4399	0.1662	0.2257	0.2269	0.3007	0.0608	0.0892
246377_at	AT1G51750	hydrophobic protein, putative / low temperature and	-0.4549	0.2454	0.2458	-0.6369	0.1296	0.1826	0.3761	0.1652	0.1885	0.194	0.431	0.2973
246378_at	AT1G57620	emp24/gp25L/p24 family protein	0.3096	0.0253	0.0923	0.5459	0.0036	0.0377	0.114	0.2691	0.2517	0.3504	0.017	0.0416
246379_s_at	AT1G57660;AT1G57860	[AT1G57660, 60S ribosomal protein L21 (RPL21E)]	-0.3311	0.5284	0.4326	0.1832	0.7222	0.4661	0.237	0.6475	0.4136	0.7514	0.1927	0.1806
246380_at	AT1G57750	CYP86A15/MAH1 (MID-CHAIN ALKANE HYDROX	-1.2743	0.1413	0.2185	-0.9222	0.2561	0.2678	-0.165	0.7347	0.4432	0.1871	0.7014	0.3978
246381_at	AT1G39430	transposable element gene	-0.3615	0.7077	0.4952	-0.488	0.6155	0.429	-0.04821	0.9579	0.5071	-0.1747	0.8487	0.4424
246382_at	AT1G39350	transposable element gene	-0.5797	0.5867	0.455	0.8776	0.422	0.3515	0.01411	0.9892	0.5152	1.4715	0.2084	0.1899
246383_at	AT1G77360	pentatricopeptide (PPR) repeat-containing protein	0.413	0.3662	0.3575	-0.4408	0.3383	0.3128	1.4746	0.0221	0.06	0.6209	0.2006	0.1855
246384_at	AT1G77370	glutaredoxin, putative	0.8041	0.0056	0.0523	0.9717	0.0028	0.0352	-0.277	0.0872	0.1304	-0.1094	0.4235	0.2939
246385_at	AT1G77390	CYCA1;2 (CYCLIN A1;2); cyclin-dependent protein	-0.01966	0.9553	0.5661	0.2698	0.4592	0.3676	-0.1708	0.6318	0.4084	0.1186	0.7373	0.4094
246386_at	AT1G77410	BGAL10 (BETA-GALACTOSIDASE 10); beta-galac	-0.1519	0.6637	0.4806	-0.1265	0.7162	0.464	-0.6074	0.1343	0.167	-0.582	0.1471	0.1528
246387_at	AT1G77400	similar to hydroxyproline-rich glycoprotein family pr	0.514	0.0599	0.1399	0.2007	0.367	0.3261	0.3275	0.1726	0.1936	0.0142	0.9461	0.4699
246388_at	AT1G77405	binding	0.1684	0.8826	0.547	-0.03215	0.9775	0.5386	-0.3744	0.7441	0.4462	-0.5749	0.6196	0.3702
246389_at	AT1G77380	AAP3 (amino acid permease 3); amino acid transm	0.00321	0.9971	0.5763	1.5557	0.1301	0.1829	0.3729	0.6501	0.4145	1.9317	0.0642	0.0922
246390_at	AT1G77330	1-aminocyclopropane-1-carboxylate oxidase, putati	-0.6578	0.5317	0.4335	-1.2141	0.2755	0.2785	1.1053	0.3147	0.2757	0.549	0.5988	0.363
246391_at	AT1G77350	similar to unnamed protein product [Vitis vinifera] (G	0.08194	0.7218	0.5	0.3701	0.1594	0.2054	0.3555	0.021	0.0583	0.6436	0.0026	0.0169
246392_at	AT1G58120;AT1G58122	[AT1G58120, similar to unnamed protein product [V	-0.6136	0.5458	0.4394	-0.7619	0.4591	0.3676	0.5346	0.5965	0.3969	0.3863	0.6994	0.3972
246393_at	AT1G58150	unknown protein	-0.2177	0.5012	0.4211	-0.2331	0.4733	0.3734	-0.8427	0.046	0.0897	-0.8582	0.0436	0.073
246394_at	AT1G58160	jacalin lectin family protein	-0.4647	0.0404	0.1159	-0.297	0.1287	0.1819	-0.3627	0.08	0.1237	-0.195	0.2781	0.2271
246395_at	AT1G58170	disease resistance-responsive protein-related / dirig	0.05404	0.8427	0.5364	-0.2143	0.5178	0.3916	0.845	0.0074	0.0347	0.5687	0.0281	0.056
246396_at	AT1G58180	carbonic anhydrase family protein / carbonate dehy	0.454	0.0525	0.1314	0.621	0.0202	0.0727	-0.3889	6.00E-04	0.0159	-0.2219	0.0053	0.0226
246397_at	AT1G58190	leucine-rich repeat family protein	1.2295	0.3171	0.3327	1.5353	0.227	0.2497	-1.0217	0.3963	0.3149	-0.7159	0.5424	0.3418
246398_at	AT1G58100	TCP family transcription factor, putative	0.2563	0.1442	0.2208	0.1766	0.2797	0.2808	0.1157	0.4661	0.3458	0.03211	0.8284	0.4367
246399_at	AT1G58110	bZIP family transcription factor	0.3825	0.1836	0.2508	0.5341	0.0884	0.1499	0.252	0.1594	0.1853	0.4036	0.0506	0.0799
246400_at	AT1G57540	similar to unknown protein (Oryza sativa (japonica c	0.5046	0.0102	0.064	0.531	0.0085	0.051	0.1795	0.1367	0.1688	0.2058	0.1	0.1206
246401_at	AT1G57560	AMY950 (myb domain protein 50); DNA binding /	0.6577	0.8689	0.5435	-0.143	0.6855	0.454	0.5021	0.2006	0.2121	0.3014	0.4102	0.2883
246402_at	AT1G57570	jacalin lectin family protein	-0.9014	0.3881	0.3689	1.7851	0.1279	0.1815	-0.7313	0.4765	0.3501	1.9553	0.1039	0.1233
246403_at	AT1G57590	carboxylesterase	0.1842	0.6381	0.4724	-0.1526	0.6954	0.4572	-0.0559	0.8521	0.4791	-0.3928	0.235	0.2044
246404_at	AT1G57600	membrane bound O-acyl transferase (MBOAT) fam	0.1029	0.6055	0.4615	0.1438	0.4779	0.3754	0.01163	0.9466	0.5048	0.05248	0.7637	0.4179
246405_at	AT1G57630	disease resistance protein (TIR class), putative	2.2859	5.00E-04	0.0325	1.6105	0.0021	0.0331	1.0319	0.0103	0.0404	0.3566	0.1903	0.1794
246406_at	AT1G57650	disease resistance protein (NBS-LRR class), putativ	2.9521	0.0041	0.0468	4.4557	9.00E-04	0.0284	-0.4196	0.4474	0.3373	1.0839	0.0954	0.1172
246407_at	AT1G57670	Toll-Interleukin-Resistance (TIR) domain-containing	-0.9553	0.224	0.2777	0.8073	0.2912	0.2873	1.3052	0.0488	0.0931	0.0678	0.0028	0.0172
246408_at	AT1G57680	similar to unnamed protein product [Vitis vinifera] (G	-0.3046	0.5377	0.4359	-0.1512	0.755	0.4767	-1.0021	0.0034	0.0259	-0.8487	0.0063	0.0245
246409_at	AT1G57700	protein kinase family protein	-0.1921	0.2951	0.2527	-0.3102	0.0973	0.1572	-0.4414	0.0118	0.0431	-0.5328	0.0049	0.022
246410_at	no_match	no_match	0.194	0.3613	0.3552	0.2656	0.2313	0.2524	-0.04629	0.818	0.4692	0.02535	0.8994	0.457
246411_at	AT1G57770	amine oxidase family	-0.8929	0.0086	0.0605	-1.2598	0.0025	0.0339	-0.09804	0.467	0.3462	-0.4649	0.019	0.0441
246412_at	AT1G57780	phosphoglucosamine mutase family protein	0.3122	0.0457	0.1229	-0.1637	0.2074	0.2378	-0.7124	0.0028	0.0244	-0.5639	0.0066	0.0253
246413_at	AT1G77310	wound-responsive protein, putative	0.1898	0.5761	0.4511	-0.9077	0.0438	0.1036	0.2439	0.4783	0.3508	-0.8536	0.0522	0.0814
246414_at	AT1G77340	pentatricopeptide (PPR) repeat-containing protein	-1.5812	0.3118	0.3297	-1.8174	0.2545	0.2669	0.7377	0.6181	0.4039	0.5014	0.7323	0.4079
246415_at	AT1G77160	similar to unknown protein [Arabidopsis thaliana] (T	-0.102	0.7676	0.5138	0.05074	0.8826	0.5138	-0.6826	0.0179	0.0575	0.4803	0.09099	0.7918	0.4265
246416_at	AT3G16920	similar to unknown protein [Arabidopsis thaliana] (T	0.7122	0.6472	0.4754	-1.8158	0.2763	0.2789	0.6616	0.6497	0.4144	-1.8665	0.2388	0.2064
246417_at	AT3G16990	NADP-dependent oxidoreductase, putative	-0.2758	0.0524	0.1313	-0.249	0.6693	0.132	0.1143	0.3211	0.2788	0.1411	0.2349	0.2044
246418_at	AT3G16960	NADP-dependent oxidoreductase, putative	1.4082	0.1447	0.2221	-0.02121	0.9796	0.5393	-0.3722	0.6427	0.412	-1.8015	0.0724	0.0987
246419_at	AT5G17030	UDP-glucuronosyl/UDP-glucosyl transferase family	-0.5159	0.6699	0.4825	-0.3595	0.765	0.4789	-1.3223	0.3044	0.2709	-1.1659	0.3579	0.266
246420_at	AT3G16870	similar to unknown protein [Arabidopsis thaliana] (T	0.1793	0.5013	0.4212	-0.1338	0.611	0.4272	-0.2482	0.3646	0.3003	-0.5613	0.0819	0.1066
246421_at	AT3G16880	VHS domain-containing protein / GAT domain-conta	0.9829	0.002	0.04	1.0841	0.0014	0.0312	-0.8126	0.0041	0.0276	-0.7115	0.0067	0.0254
246422_at	AT5G17060	ATARFB1B; GTP binding	0.3799	0.0426	0.1188	0.376	0.044	0.1037	0.3739	0.0114	0.0423	0.3699	0.0119	0.0342
246423_at	AT3G16950	similar to unnamed protein product [Vitis vinifera] (G	0.6414	0.1288	0.2073	1.1334	0.0279	0.0832	0.4585	0.0345	0.076	0.9505	0.0028	0.0174
246424_at	AT5G17020	XPO1A (exportin 1A); protein transporter

246490_at	AT5G15950;AT5G15948	[AT5G15950, adenosylmethionine decarboxylase fa	-1.003	0.084	0.1678	-1.1555	0.0578	0.1195	0.03158	0.913	0.496	-0.121	0.679	0.3902
246491_at	AT5G16100	similar to hypothetical protein [Cleome spinosa] (GE	-0.0953	0.726	0.5013	0.2201	0.4342	0.3571	0.1253	0.647	0.4134	0.4407	0.1571	0.1594
246492_at	AT5G16140	peptidyl-tRNA hydrolase family protein	-0.6566	0.006	0.0538	-0.8405	0.0024	0.0339	-0.02822	0.8305	0.4729	-0.2122	0.161	0.1618
246493_at	AT5G16180	ATCRS1/CRS1 (ARABIDOPSIS ORTHOLOG OF M	0.3254	0.0883	0.1723	0.1591	0.3344	0.3105	-0.09462	0.5498	0.379	-0.261	0.1464	0.1523
246494_at	AT5G16190	ATCSLA11 (Cellulose synthase-like A11); transfera	-0.7615	0.0985	0.1811	-0.5051	0.2279	0.2502	-0.3062	0.437	0.3328	-0.04979	0.8952	0.4558
246495_at	AT5G16200	50S ribosomal protein-related	-0.2385	0.3506	0.3499	-0.2735	0.2927	0.288	0.2214	0.3825	0.309	0.1865	0.4555	0.3082
246496_at	AT5G16210	HEAT repeat-containing protein	0.4768	0.075	0.1575	0.07973	0.7096	0.462	-0.5851	0.0426	0.0859	-0.9821	0.0079	0.0277
246497_at	AT5G16220	cotocsapeptide/Phox/Bem1p (PB1) domain-contain	0.3028	0.0398	0.115	0.1562	0.1961	0.2302	0.01628	0.8432	0.4766	-0.1303	0.1663	0.165
246498_at	AT5G16230	acyl-(acyl-carrier-protein) desaturase, putative / ste	-0.07453	0.8479	0.5378	0.6187	0.1647	0.2088	0.008695	0.9821	0.5133	0.702	0.1263	0.1391
246499_at	AT5G16260	RNA recognition motif (RRM)-containing protein	0.1724	0.5082	0.4244	0.2448	0.3611	0.3234	-0.5912	0.0655	0.1106	-0.5188	0.0917	0.1141
246500_at	AT5G16270	ATRAD21.3/SYN4 (ARABIDOPSIS HOMOLOG OF	0.6741	0.0246	0.0911	0.3504	0.1418	0.1922	-0.3124	0.0268	0.0666	-0.6361	0.0022	0.0158
246501_at	AT5G16280	binding	0.2557	0.1343	0.2128	0.1074	0.4754	0.3744	-0.5148	0.0147	0.0483	-0.6631	0.0061	0.0242
246502_at	AT5G16420	acyl-(acyl-carrier-protein) desaturase, putative / ste	-0.5892	0.0145	0.0731	-0.8969	0.0033	0.037	0.09853	0.4589	0.3426	-0.2091	0.1573	0.1595
246503_at	AT5G16430	40S ribosomal protein S7 (RPS7C)	-0.00998	0.9488	0.5645	-0.04778	0.76	0.4778	-0.05313	0.6529	0.4156	-0.09093	0.453	0.3072
246504_at	AT5G16160	similar to hypothetical protein [Cleome spinosa] (GE	0.6668	0.3586	0.3537	-0.03259	0.962	0.5345	0.5959	0.3923	0.3131	-0.1035	0.8759	0.4501
246505_at	AT5G16250	similar to unknown protein [Arabidopsis thaliana] (T	-0.5588	0.1112	0.1933	-0.3518	0.2687	0.2749	0.1331	0.513	0.3643	0.3401	0.1409	0.1487
246506_at	AT5G16110	similar to unknown protein [Arabidopsis thaliana] (T	0.2757	0.0317	0.1031	0.3838	0.0107	0.0958	-0.9354	4.00E-04	0.0147	-0.8273	6.00E-04	0.0103
246507_at	AT5G16120	hydrolase, alpha/beta fold family protein	0.28	0.1004	0.1831	0.635	0.0085	0.0509	-0.3082	0.0792	0.1231	0.04679	0.7401	0.4105
246508_at	AT5G16150	GLT1/PGLCT (GLUCOSE TRANSPORTER 1); carr	0.5142	0.0032	0.0442	-0.02819	0.746	0.4736	0.02095	0.7817	0.4579	-0.5214	0.0018	0.0148
246509_at	AT5G16715	EMB2247 (EMBRYO DEFECTIVE 2247); ATP bind	-0.4641	0.0764	0.1592	-0.793	0.0154	0.0649	-0.9369	0.0054	0.0307	-1.2659	0.0018	0.0147
246510_at	AT5G15410	DND1 (DEFENSE NO DEATH 1); calcium channel/	-0.2576	0.337	0.3438	-0.5186	0.0932	0.1539	-0.1256	0.6232	0.4057	-0.3866	0.1772	0.1715
246511_at	AT5G15490	UDP-glucose 6-dehydrogenase, putative	0.07707	0.7909	0.495	-0.2039	0.3454	0.3157	0.1411	0.4139	0.3225	0.01424	0.9312	0.466
246512_at	AT5G15630	COBL4/IRX6 (COBRA-LIKE4)	0.2521	0.3954	0.3729	0.02751	0.9223	0.5247	-0.2898	0.2909	0.2641	-0.5143	0.0971	0.1183
246513_at	AT5G15680	binding	0.677	0.0171	0.0785	0.3893	0.0868	0.1485	-0.6897	0.0022	0.0219	-0.9775	6.00E-04	0.01
246514_at	AT5G15700	DNA-directed RNA polymerase (RPOT2)	1.7443	0.0182	0.0804	0.6743	0.21	0.2396	-1.395	0.0163	0.051	-2.465	0.0021	0.0156
246515_at	AT5G15710	F-box family protein	0.1898	0.3653	0.357	0.05025	0.8004	0.4897	-0.00119	0.9952	0.5164	-0.1407	0.4915	0.3225
246516_at	AT5G15740	similar to unknown protein [Arabidopsis thaliana] (T	-1.0535	0.0244	0.0908	-1.1776	0.017	0.0677	-0.05663	0.8166	0.4687	-0.1808	0.4734	0.3151
246517_at	AT5G15760	plastid-specific 30S ribosomal protein 3, putative / P	0.5112	0.195	0.2551	-0.1058	0.7638	0.4785	0.3797	0.3136	0.2751	0.7842	0.0796	0.1013
246518_at	AT5G15770	ATGNA1 (ARABIDOPSIS THALIANA GLUCOSE-6	0.5443	0.0198	0.0832	1.0162	0.0022	0.0333	0.9363	0.003	0.0247	1.4081	6.00E-04	0.0103
246519_at	AT5G15780	pollen Ole e 1 allergen and extensin family protein	-0.4654	0.4749	0.4097	-1.8783	0.0336	0.0906	0.05342	0.9108	0.4955	-1.3595	0.0385	0.0674
246520_at	AT5G15790	zinc finger (C3HC4-type RING finger) family protein	0.1883	0.7608	0.6119	-0.4457	0.4835	0.3774	-0.5603	0.3073	0.2722	-1.1944	0.0674	0.0947
246521_at	AT5G15810	N2,N2-dimethylguanosine tRNA methyltransferase	0.4713	0.1132	0.1949	0.07724	0.757	0.4773	-0.1719	0.3332	0.2849	-0.566	0.0223	0.0487
246522_at	AT5G15830	ATBZIP3 (ARABIDOPSIS THALIANA BASIC LEUC	-0.3977	0.3942	0.3723	-0.1578	0.7243	0.4667	1.7053	0.0051	0.03	1.9452	0.0031	0.0182
246523_at	AT5G15850	COL1 (CONSTANS-LIKE 1); transcription factor/ zir	0.1191	0.6423	0.4737	-0.2203	0.4059	0.344	0.2149	0.1706	0.1922	0.1137	0.4271	0.2955
246524_at	AT5G15860	ATPCME (PRENYLCYSTEINE METHYLESTERAS	0.9236	0.0022	0.041	0.9304	0.0021	0.0332	0.1693	0.0031	0.0251	-0.1625	0.0036	0.0196
246525_at	AT5G15840	CO (CONSTANS); transcription factor/ zinc ion bind	0.4408	0.6789	0.4857	0.3448	0.745	0.4732	1.7056	0.1598	0.1856	1.6096	0.1791	0.1727
246526_at	AT5G15720	GLIP7 (GDSL-motif lipase 7); carboxylesterase	-0.4808	0.7447	0.6073	-0.4505	0.76	0.4778	-0.1066	0.9356	0.5022	-0.07826	0.9536	0.4719
246527_at	AT5G15750	RNA-binding S4 domain-containing protein	0.7255	0.0087	0.0605	0.6306	0.014	0.0627	0.2872	0.1168	0.1538	0.1924	0.2525	0.2138
246528_at	AT5G15640	mitochondrial substrate carrier family protein	-0.03745	0.8479	0.5378	0.2204	0.2951	0.2893	-0.2019	0.3319	0.2842	0.0559	0.7753	0.4216
246529_at	AT5G15730	serine/threonine protein kinase, putative	0.4121	0.112	0.194	0.8323	0.0148	0.0642	-0.2633	0.2325	0.2309	0.1568	0.4496	0.3059
246530_at	AT5G15725	unknown protein	-1.6251	0.3224	0.3357	0.5497	0.7222	0.4661	-2.1913	0.0846	0.1281	-0.01654	0.9871	0.4795
246531_at	AT5G15800	SEP1 (SEPALLATA1); DNA binding / transcription f	0.7832	0.1903	0.2556	1.236	0.0678	0.1304	0.3286	0.5447	0.3773	0.7815	0.1911	0.1798
246532_at	AT5G15870	glycosyl hydrolase family 81 protein	0.5292	0.0611	0.1417	0.8384	0.0149	0.0643	-0.6007	0.0273	0.0671	-0.2915	0.1742	0.1698
246533_at	AT5G15880	similar to hypothetical protein [Cleome spinosa] (GE	0.458	0.0195	0.0826	0.616	0.0071	0.0476	-0.3987	0.0303	0.0709	-0.2406	0.1183	0.1336
246534_at	AT5G15890	similar to unknown protein [Arabidopsis thaliana] (T	-0.8138	0.4638	0.4047	-0.6076	0.5784	0.4153	0.4956	0.5958	0.3968	0.7019	0.4609	0.3104
246535_at	AT5G15900	similar to unknown protein [Arabidopsis thaliana] (T	-1.1257	0.1469	0.223	-0.8612	0.2414	0.2587	0.1089	0.8544	0.4796	0.3734	0.5392	0.3409
246536_at	AT5G15920	structural maintenance of chromosomes (SMC) fam	-0.1446	0.3303	0.3402	-0.06959	0.6224	0.4317	-0.6343	0.0037	0.0268	-0.5593	0.0059	0.0238
246537_at	AT5G15940	oxidoreductase	0.477	0.376	0.3623	-0.3411	0.516	0.391	0.04725	0.9059	0.4939	-0.7709	0.1093	0.1272
246538_at	AT5G15520	40S ribosomal protein S19 (RPS19B)	-0.1505	0.6598	0.4792	-0.152	0.6566	0.4441	0.6043	0.1706	0.1922	0.1137	0.4271	0.2955
246539_at	AT5G15460	MUB2 (MEMBRANE-ANCHORED UBIQUITIN-FOL	0.3553	0.0897	0.1734	0.4461	0.0489	0.1097	0.3344	0.1039	0.1441	0.4252	0.0559	0.0848
246540_at	AT5G15600	SP1L4 (SPIRAL1-LIKE4)	-2.2409	0.0069	0.0558	-2.9341	0.0026	0.0341	0.9267	0.09	0.1326	0.2335	0.6047	0.3648
246541_at	AT5G15400	U-box domain-containing protein	0.7153	0.0148	0.0737	0.4982	0.046	0.1063	0.05757	0.6465	0.4132	-0.1595	0.2421	0.2083
246542_at	AT5G15020	similar to unknown protein [Arabidopsis thaliana] (T	0.05354	0.8151	0.5284	0.2594	0.2929	0.2881	-0.5831	0.045	0.0887	-0.3773	0.1358	0.1456
246543_at	AT5G15060	Identical to Putative LOB domain-containing protein	0.1845	0.6709	0.4829	0.3908	0.3872	0.3354	-0.4918	0.2894	0.2632	-0.2855	0.5178	0.3327
246544_at	AT5G15100	PINE (PIN-FORMED II); auxin:hydrogen symporter/	-1.4222	0.1293	0.2079	1.076	0.2227	0.2475	-1.6149	0.0964	0.138	0.8833	0.302	0.2397
246545_at	AT5G15110	pectate lyase family protein	0.2696	0.8571	0.5405	-1.3596	0.3877	0.3357	0.255	0.7882	0.4595	-1.3742	0.1965	0.1828
246546_at	AT5G15090	porin, putative / voltage-dependent anion-selective	-0.2326	0.0809	0.1643	-0.6825	0.0024	0.0339	0.7674	5.00E-04	0.0151	0.3175	0.013	0.0361
246547_at	AT5G14970	amine oxidase/ copper ion binding / quinone binding	-0.7238	0.0024	0.0421	-0.7705	0.0019	0.033	0.05094	0.6563	0.4166	0.004296	0.9697	0.4754
246548_at	AT5G14910	heavy-metal-associated domain-containing protein	-0.3647	0.0155	0.0751	-0.4404	0.0081	0.0501	0.2642	0.0156	0.0497	0.1886	0.0448	0.0742
246549_at	AT5G15050	glycosyltransferase family 14 protein / core-2/I-bran	-0.5063	0.0054	0.0519	-0.6057	0.0028	0.0351	0.1467	0.1873	0.2038	0.04729	0.6354	0.3755
246550_at	AT5G14920	gibberellin-regulated family protein	1.283	0.0091	0.0616	1.373	0.0072	0.0479	0.8428	0.0103	0.0403	0.9328	0.0072	0.0285
246551_at	AT5G15070	acid phosphatase/ oxidoreductase/ transition metal	1.9136	0.3272	0.3385	0.5384	0.7693	0.4802	-0.7429	0.6639	0.4192	-2.1181	0.2527	0.2139
246552_at	AT5G15420	unknown protein	1.5979	0.1113	0.1934	-0.4428	0.6026	0.4246	0.6824	0.4334	0.3311	-1.3583	0.1584	0.1603
246553_at	AT5G15440	EDL1 (EID1-LIKE 1)	-0.3254	0.1031	0.1855	-0.1384	0.4211	0.3512	-0.3936	0.0635	0.1086	-0.2067	0.2522	0.2137
246554_at	AT5G15450	APG6/CLPB-P/CLPB3 (ALBINO AND PALE GREE	-0.4569	0.0521	0.131	-0.6207	0.0205	0.0732	-0.5127	0.0373	0.0797	-0.6765	0.0155	0.0397
246555_at	AT5G15470	GAUT14 (Galacturonosyltransferase 14); polygalac	-0.5349	0.0601	0.1403	-0.5628	0.0522	0.1133	-0.2996	0.1486	0.1782	-0.3275	0.1227	0.1369
246556_at	AT5G15480	zinc finger (C2H2 type) family protein	0.3193	0.8365	0.5343	-0.9398	0.5523	0.4057	-0.1994	0.8875	0.489	-1.4584	0.3322	0.2545
246557_at	AT5G15510	similar to unknown protein [Arabidopsis thaliana] (T	-1.4021	0.2303	0.2822	0.4218	0.6925	0.4564	-0.4285	0.6679	0.4206	1.3953	0.2067	0.1888
246558_at	AT5G15540	EMB2773 (EMBRYO DEFECTIVE 2773); binding /	0.4282	0.0053	0.0517	0.03417	0.6831	0.4532	-0.7547	6.00E-04	0.0158	-1.1487	1.00E-04	0.0063
246559_at	AT5G15550	transducin family protein / WD-40 repeat family prot	0.992	4.00E-04	0.032	0.6683	0.002	0.033	0.1014	0.3395	0.2882	-0.2222	0.0765	0.1021
246560_at	AT5G15560	similar to unknown protein [Arabidopsis thaliana] (T	1.5872	0.245	0.2906	-1.2521	0.3433	0.3149	1.9494	0.1698	0.1917	-0.8899	0.4878	0.321
246561_at	AT5G15570	similar to DNA binding [Arabidopsis thaliana] (TAIR	-0.0488	0.7482	0.5083	0.07645	0.6185	0.4301	-0.3781	0.0561	0.101	-0.2528	0.1493	0.1541
246562_at	AT5G15580	LNG1 (LONGIFOLIA1)	0.1836	0.5311	0.4334	0.1864	0.5252	0.3941	0.001161	0.9954	0.5164	0.00395	0.9845	0.4791
246563_at	AT5G15581	unknown protein	1.2171	0.0556	0.1355	-0.95	0.1052	0.1639	0.2857	0.5643	0.3844	-1.8814	0.0145	0.0383
246564_at	AT5G15610	proteasome family protein	0.1705	0.6177	0.4656	-0.01356	0.9678	0.536	-0.2136	0.1519	0.1802	-0.3978	0.0302	0.0584
246565_at	AT5G15530	BCCP2 (biotin carboxyl carrier protein 2); biotin bin	-1.1384	0.0362	0.1097	-0.9219	0.0659	0.1284	0.409	0.0811	0.1248	0.6255	0.0238	0.0506
246566_at	AT5G14940	proton-dependent oligopeptide transport (POT) fam	0.4914	0.0509	0.1298	0.2694	0.2051	0.2362	0.6392	1.00E-04	0.012	0.4171	7.00E-04	0.0106
246567_at	AT5G14950	ATGMII/GMII (GOLGI ALPHA-MANNOSIDASE II);	0.2188	0.1983	0.2616	0.3676	0.0608	0.1225	-0.4314	0.0385	0.081	-0.2826	0.1175	0.133
246568_at	AT5G14960	DEL2/EZF/DE2L1 (DP-E2F-LIKE 2); DNA binding /	0.1719	0.7309	0.5027	0.5992	0.2678	0.2743	-0.4698	0.3492	0.2928	-0.04251	0.9283	0.4651
246569_at	AT5G14980	esterase/lipase/thioesterase family protein	1.2097	0.323	0.336	1.0044	0.4026	0.3424	-0.8704	0.3361	0.2864	-1.0757	0.2484	0.2115
246570_at	AT5G14990	similar to myosin heavy chain-related [Arabidopsis t	-1.3447	0.3443	0.347	-0.6978	0.6079	0.4263	-0.3594	0.7841	0.4586	0.2875	0.8262	0.436
246571_at	no_match	no_match	0.7287	0.5562	0.4433	-1.9716	0.1577	0.2042	1.2569	0.3307	0.2837	-1.4434	0.2729	0.2244
246572_at	AT5G15010	pentatricopeptide (PPR) repeat-containing protein	1.3398	0.2456	0.2908	0.3835	0.717	0.4643	-1.8514	0.1251	0.1601	-2.8077	0.0426	0.072
246573_at	AT3G31690	copper ion binding	0.1496	0.844	0.5369	-2.9175	0.0149	0.0643	0.301	0.6945	0.4292	-2.7661	0.0178	0.0427
246574_at	AT1G31670	copper amine oxidase, putative	-0.4542	0.2999	0.3229	-0.05761	0.8873	0.5151	-0.6062	0.1524	0.1806	-0.2097	0.5747	0.3541
246575_at	AT3G31660	similar to unknown [Populus trichocarpa] (GB:ABK9	0.3635	0.1885	0.2543	0.2904	0.2746	0.2778	-0.1938	0.2796	0.2578	-0.267	0.1604	0.1614
246576_at	AT1G31650	ATROPGEF14/ROPGEF14 (KINASE PARTNER PI	-0.1417	0.6175	0.4655	-0.4578	0.1557	0.2026	-0.1343	0.46	0.3431	-0.4503	0.052	0.0812
246577_at	AT1G31640	AGL92; DNA binding / transcription factor	-0.708	0.4679	0.4063	0.7364	0.4516	0.3647	-1.4209	0.1832	0.201	0.02352	0.98	0.4782
246578_at	AT1G31630	AGL86; DNA binding / transcription factor	1.9436	0.1317	0.21	-0.8599	0.45	0.3639	0.2727	0.8039	0.4647	-2.5308	0.0696	0.0966
246579_at	AT1G31620	unknown protein	-0.8105	0.4178	0.3838	-2.682	0.0405	0.0997	1.5482	0.1598	0.1856	-0.3233	0.737	0.4094
246580_at	AT1G31770	ABC transporter family protein	0.3531	0.2031	0.2642	0.235	0.3687	0.3269	-0.02924	0.9059	0.4939	-0.1473	0.5605	0.349
246581_at	AT1G31760	SWIB complex BAF60b domain-containing protein	0.1264	0.7628	0.5124	0.9794	0.0665	0.1291	-0.1864	0.6586	0.4175	0.6666	0.1636	0.1635
246582_at	AT1G31750	proline-rich family protein	0.07544	0.9571	0.5665	0.791	0.5807	0.4165	2.0422	0.196	0.2092	2.7577	0.1044	0.1236
246583_at	AT5G14720	protein kinase family protein	-0.3639	0.1634	0.2366	-0.07877	0.7308	0.4687	-0.8051	0.0076	0.0352	-0.52	0.0323	0.0607
246584_at	AT5G14730	similar to unknown protein [Arabidopsis thaliana] (T	-0.5112	0.4737	0.4094	-0.03691	0.9572	0.5335	-0.09594	0.7891	0.4599	0.3783	0.3225	0.2495
246585_at	AT5G14750	ATMYB66/WER/WER1 (WEREWOLF 1); DNA bind	-0.6157	0.6496	0.4762	-1.6985	0.2476	0.2623	-1.244	0.3779	0.3068	-2.3267	0.1375	0.1466
246586_at	AT5G14770	pentatricopeptide (PPR) repeat-containing protein	2.3288	0.0389	0.1137	0.04214	0.9589	0.534	-0.369	0.6565	0.4167	-2.6557	0.026	0.0534
246587_at	AT5G14830	transposable element gene	-1.5267	0.1047	0.1869	-0.1789	0.8185	0.4954	-0.8104	0.0975	0.1389	0.5374	0.2263	0.1996
246588_at	no_match	no_match	-0.07908	0.8913	0.5487	0.6518	0.2966	0.29	-0.2105	0.7063	0.4334	0.5204	0.3735	0.2728
246589_at	AT5G14860	transferase, transferring glycosyl groups	-1.4204	0.2101	0.2683	0.3418	0.3143	-0.7599	0.3941	0.3139	0.1898	1.6868	0.1016	0.1218
246590_at	AT5G14870	ATCNGC18/CNGC18 (CYCLIC NUCLEOTIDE-GA	0.03741	0.9688	0.5694	0.6354	0.5184	0.3919	-1.1072	0.2852	0.2608	-0.5092	0.6011	0.3638
246591_at	AT5G14880	potassium transporter, putative	-0.00424	0.9901	0.5745	-0.2496	0.4803	0.3763	0.03413	0.8161	0.4686	-0.2112	0.1991	0.1844
246592_at	AT5G14890	NHL repeat-containing protein	-0.882	0.4937	0.4154	-0.05558	0.9645	0.5351	-1.1317	0.2503	0.2412	-0.3052	0.7354	0.4089
246593_at	AT5G14790	binding	-0.3667	0.1654	0.2378	-0.2508	0.3109	0.2979	0.3227	0.1054	0.1452	0.4386	0.0472	0.0765
246594_at	AT5G14800	PSCR (PYRROLINE-5-CARBOXYLATE (P5C) REI	0.6259	0.0727	0.1554	0.7062	0.0524	0.1135	-0.9758	0.0059	0.032	-0.8955	0.008	0.0278
246595_at	AT5G14840	FDH (FORMATE DEHYDROGENASE); NAD bind	0.6724	0.0188	0.0814	0.7576	0.0126	0.06	-0.07935	0.6045	0.3996	0.005877	0.9688	0.4752
246596_at	AT1G14740	CA2 (BETA CARBONIC ANHYDRASE 2); carbonat	-0.5555	0.0087	0.0606	-0.7439	0.003	0.0358	-0.2544	0.0454	0.0892	-0.4428	0.0075	0.027
246597_at	AT5G14760	AO (L-ASPARTATE OXIDASE); L-aspartate oxidas	-1.3212	0.0133	0.0709	-0.9361	0.0398	0.0989	-0.2936	0.0256	0.0649	0.09149	0.3402	0.2581
246598_at	AT1G14850	mannosyltransferase, putative	0.1645	0.1118	0.1939	-0.06135	0.7494	0.4747	-0.218	0.2908	0.2641	-0.6439	0.0229	0.0493
246599_at	AT5G14900	helicase associated (HA2) domain-containing prote	0.4789	0.3034	0.325	-0.9179	0.0865	0.1483	0.1101	0.7996	0.4633	-0.3289	0.4632	0.3113
246600_at	AT5G14930	SAG101 (SENESCENCE-ASSOCIATED GENE 10	1.5001	0.0055	0.052	1.717	0.0033	0.0371	-0.3278	0.1693	0.1913	-0.1109	0.6013	0.3638
246601_at	AT1G31710	copper amine oxidase, putative	-1.6324	0.0058	0.053	-1.3021	0.0127	0.0602	0.1885	0.4124	0.3218	0.5188	0.0657	0.0933
246602_at	AT1G31710	copper amine oxidase, putative	0.6143	0.4514	0.3988	-0.9085	0.2851	0.2839	-0.3654	0.602	0.3989	-1.8882	0.0432	0.0726
246603_at	AT1G31690	copper ion binding	-0.4088	0.0088	0.0609	-2.6757	0.0061	0.045	0.2466	0.6522	0.4153	-0.02026	0.9699	0.4754
246604_at	no_match	no_match	0.4501	0.6183	0.4658	-1.2345	0.2132	0.2415	-0.4401	0.6258	0.4065	-2.1247	0.0636	0.0916
246605_at	AT5G35340	transposable element gene	-0.2079	0.8051	0.5255	0.4871	0.5703	0.412	-0.3537	0.6771	0.4235	0.3414	0.6875	0.393
246606_at	no_match	no_match	0.2448	0.5795	0.4521	-0.7666	0.1324	0.1847	0.1324	0.6411	0.1899	0.2055	-0.3703	0.4139	0.29
246607_at	AT5G35370	carbohydrate binding / kinase	0.3511	0.0229	0.0885	0.4224	0.0124	0.0597	0.485	0.0077	0.0354	0.5563	0.0047	0.0217
246608_at	AT5G35380	protein kinase family protein	1.1397	0.4204	0.3851	-0.669	0.6263	0.4334	0.1121	0.934	0.5018	-1.6967	0.2526	0.2139
246609_at	AT5G35390	leucine-rich repeat transmembrane protein kinase,	0.8542	0.3906	0.3702	0.6755	0.4892	0.3801	0.2825	0.7325	0.4425	0.1468	0.8767	0.4504
246610_at	no_match	no_match	-0.2641	0.1217	0.2021	-0.0387	0.7883	0.4857	-0.3246	0.0737	0.1182	-0.09918	0.5027	0.3268
246611_at	AT5G35330	MBD02 (methyl-CpG-binding domain 2); DNA bind	0.5706	0.0517	0.1306	0.7735	0.0205	0.073	-0.4288	0.1081	0.1472	-0.2259	0.3383	0.2571
246612_at	AT5G35350	similar to hypothetical protein [Vitis vinifera] (GB:C	0.4104	0.0327	0.1049	0.4902	0.0186	0.0706	0.155	0.1772	0.1967	0.2349	0.0683	0.0955
246613_at	AT5G35360	CAC2 (acetyl co-enzyme A carboxylase biotin carbo	-0.6799	0.0264	0.0939	-0.5203	0.0582	0.12	-0.4515	0.002	0.021	-0.292	0.0095	0.0304
246614_at	AT5G35410	SOS2 (SALT OVERLY SENSITIVE 2); kinase	1.1317	0.0022	0.041	0.7814	0.0084	0.0507	0.07063	0.5946	0.3963	-0.2797	0.0842	0.1083
246615_at	AT5G35420	transposable element gene	1.1259	0.1686	0.2404	-0.9393	0.234	0.2543	0.3916	0.56	0.3826	-1.6736	0.0533	0.0825
246616_at	AT5G36260	aspartyl protease family protein	-0.2911	0.461	0.4035	-0.3518	0.3806	0.3323	-0.4152	0.3099	0.2734	-0.4759	0.2538	0.2145
246617_at	AT5G36270	pseudogene of dehydroascorbate reductase	-1.5015	0.0965	0.1795	-0.7484	0.3416	0.3143	-0.4572	0.2488	0.2403	0.2959	0.432	0.2977
246618_at	AT5G36280	similar to MTACP2 (MITOCHONDRIAL ACYL CARR	-1.1474	0.1966	0.2602	-0.9953	0.2509	0.2643	-1.5779	0.1004	0.1414	-1.4258	0.1268	0.1395
246619_at	AT5G36290	similar to unknown protein [Arabidopsis thaliana] (T	-0.08577	0.5018	0.4213	0.1144	0.3811	0.3324	-0.1436	0.2846	0.2605	0.05656	0.6522	0.3816
246620_at	AT5G36220	CYP81D1 (CYTOCHROME P450 81A1); oxygen bi	0.4512	0.0619	0.1428	0.1404	0.4684	0.3714	0.1384	0.1494	0.1785	-0.1724	0.0906	0.1134
246621_at	AT5G36230	eIF4-gamma/eIF5/eIF2-epsilon domain-containing p	0.1314	0.241	0.2883	0.1438	0.2067	0.2373	0.2954	0.0365	0.0786	0.3078	0.0322	0.0606
246622_at	AT5G36250	protein phosphatase 2C, putative / PP2C, putative	-0.01681	0.9088	0.5536	-0.2835	0.1089	0.1664	0.09924	0.5114	0.3637	-0.1674	0.2913	0.2343
246623_at	AT1G48920	ATNUC-L1/PARL1 (PARALLE

246690_at	no_match	no_match	-2.0043	0.0381	0.1123	-0.8399	0.2705	0.2758	-1.0656	0.1804	0.199	0.0988	0.8878	0.4537
246691_at	AT5G34790	transposable element gene	-0.0079	0.9779	0.5717	-0.765	0.0462	0.1066	0.5712	0.0222	0.0602	-0.1859	0.3028	0.24
246692_at	no_match	no_match	-0.1134	0.8505	0.5383	0.2726	0.6543	0.4432	-0.03805	0.9495	0.5054	0.348	0.5709	0.3529
246693_at	AT5G29070	similar to nucleic acid binding / zinc ion binding [Ara	-0.7882	0.0909	0.1747	-0.2696	0.4905	0.3805	-0.5744	0.1391	0.1705	-0.05584	0.8665	0.4472
246694_at	no_match	no_match	1.7268	0.1717	0.2427	-1.7627	0.1649	0.209	1.4592	0.2328	0.2309	-2.0303	0.1223	0.1366
246695_at	AT5G29090	transposable element gene	-0.09285	0.933	0.5605	-0.09519	0.9313	0.5269	0.02469	0.971	0.5102	0.02234	0.9738	0.4765
246696_at	AT5G29100	transposable element gene	0.3931	0.6179	0.4657	-0.9598	0.2579	0.2688	0.09073	0.902	0.493	-1.2621	0.1422	0.1496
246697_at	AT5G29210	unknown protein	-0.3231	0.7115	0.4968	-1.5492	0.1295	0.1826	2.0453	0.0657	0.1108	0.8192	0.3708	0.2716
246698_at	AT5G30480	transposable element gene	0.2936	0.835	0.5339	1.6711	0.2744	0.2777	-0.4027	0.7406	0.4449	0.9749	0.4387	0.3008
246699_at	AT5G27990	similar to unknown protein [Arabidopsis thaliana] (T	0.2369	0.2789	0.3107	0.4071	0.0978	0.1576	0.01142	0.9413	0.5037	0.1817	0.2809	0.2286
246700_at	AT5G28030	cysteine synthase, putative / O-acetylserine (thiol)-l	-0.9109	0.0308	0.1018	-1.2091	0.0123	0.0593	0.2357	0.3701	0.3029	-0.06242	0.8025	0.4294
246701_at	AT5G28020	ATCYSD2 (Arabidopsis thaliana cysteine synthase	-0.8192	0.0329	0.1053	-0.659	0.0618	0.1236	-0.1517	0.0436	0.0871	0.008454	0.8789	0.451
246702_at	AT5G28050	cytidine/deoxycytidylate deaminase family protein	-0.2312	0.0347	0.1076	-0.107	0.2193	0.2455	0.2467	0.0077	0.0354	0.3709	0.0017	0.0147
246703_at	AT5G28080	WNK9 (Arabidopsis WNK kinase 9); kinase	1.4395	0.2104	0.2685	-0.01427	0.9889	0.5413	0.3813	0.7132	0.4359	-1.0724	0.3292	0.253
246704_at	AT5G28090	unknown protein	-0.1482	0.7216	0.4999	-0.5593	0.2223	0.2473	0.2547	0.5468	0.3781	-0.1564	0.7071	0.3998
246705_x_at	AT5G28120;AT5G28110	[AT5G28120, transposable element gene];[AT5G28	1.8009	0.2234	0.2772	-0.2007	0.8803	0.5133	0.7289	0.5914	0.3952	-1.2728	0.3665	0.2698
246706_at	AT5G28130	transposable element gene	-1.4808	0.316	0.3321	-1.1211	0.4377	0.3587	0.6611	0.6349	0.4094	1.0308	0.4685	0.3132
246707_at	AT5G28140	transposable element gene	-0.8242	0.4714	0.4081	-0.4405	0.693	0.4566	-1.1802	0.3188	0.2777	-0.7965	0.4854	0.3198
246708_at	AT5G28150	similar to unknown protein [Arabidopsis thaliana] (T	0.09766	0.5203	0.4291	-0.3104	0.0889	0.1504	0.2534	0.1121	0.15	-0.1546	0.2831	0.2298
246709_s_at	AT5G28160;AT5G28180	[AT5G28160, ketch repeat-containing F-box family	1.2878	0.5365	0.4356	-0.1614	0.9366	0.5283	0.583	0.7751	0.4558	-0.8661	0.6733	0.3885
246710_at	AT5G28170	transposable element gene	0.6764	0.5996	0.4595	1.2058	0.3675	0.3263	-0.9641	0.4626	0.3443	-0.4346	0.733	0.408
246711_at	AT5G28190	unknown protein	-0.09664	0.8684	0.5434	-1.3039	0.0757	0.1379	-0.2677	0.6503	0.4145	-1.4749	0.0543	0.0834
246712_at	no_match	no_match	0.7225	0.4633	0.4045	2.0379	0.0843	0.1461	0.3745	0.6961	0.4299	1.6899	0.131	0.1423
246713_at	AT5G28210	mRNA capping enzyme family protein	-0.1826	0.7372	0.5049	-0.6358	0.2786	0.2802	0.5629	0.3296	0.2831	0.1098	0.8394	0.4398
246714_at	AT5G28220	binding	0.4367	0.1261	0.2055	-0.02571	0.9151	0.5227	0.633	0.0252	0.0644	0.1705	0.4005	0.2944
246715_at	AT5G28230	pseudogene, similar to glucose-6-phosphate/phosp	-1.4282	0.2896	0.317	-0.1384	0.9116	0.5219	-0.5102	0.6855	0.4263	0.7796	0.542	0.3416
246716_s_at	AT5G28960;AT5G28910	[AT5G28960, similar to unknown protein [Arabidops	0.9138	0.2844	0.3139	-0.8612	0.3091	0.2969	0.2431	0.759	0.451	-1.5319	0.1072	0.1255
246717_at	AT5G28920	unknown protein	1.9786	0.1021	0.1847	0.4713	0.6412	0.4385	1.1627	0.2822	0.2593	-0.3446	0.7315	0.4076
246718_at	AT5G28930	transposable element gene	-0.9818	0.28	0.3113	1.7717	0.0874	0.1489	-1.5886	0.1124	0.1502	1.1649	0.2111	0.1914
246719_at	AT5G28940	transposable element gene	-1.709	0.1354	0.2136	1.6816	0.1401	0.1907	-1.6723	0.088	0.1309	1.7184	0.0822	0.1068
246720_at	AT5G28950	similar to unknown protein [Arabidopsis thaliana] (T	-0.002256	0.9984	0.5763	-1.6899	0.0273	0.2498	2.9874	0.0049	0.0295	1.3201	0.0673	0.0946
246721_at	no_match	no_match	-0.4853	0.5195	0.4289	0.1174	0.8728	0.5108	0.3957	0.596	0.3968	0.207	0.7785	0.4225
246722_at	AT5G29020	transposable element gene	-0.8655	0.4293	0.3887	1.3435	0.2444	0.2607	-0.7126	0.3599	0.298	1.4963	0.0959	0.1174
246723_at	AT5G29030	pseudogene, hypothetical protein	-0.6927	0.3869	0.3682	-0.4944	0.5268	0.3949	0.6886	0.4022	0.3175	0.8667	0.2916	0.2344
246724_at	AT5G29000	myb family transcription factor	0.2402	0.1262	0.2056	0.5616	0.0108	0.0559	-0.06531	0.5783	0.39	0.2561	0.0769	0.1024
246725_at	AT5G29040	pseudogene, hypothetical protein	0.1638	0.8587	0.5407	0.04296	0.9627	0.5347	1.0073	0.3078	0.2724	0.8865	0.3622	0.2679
246726_at	AT5G29050	similar to unknown protein [Arabidopsis thaliana] (T	0.1721	0.8747	0.5451	1.9548	0.1289	0.1821	-0.654	0.6578	0.3819	1.4729	0.2238	0.1982
246727_at	AT5G28010	Bet v I allergen family protein	1.3922	0.6387	0.4725	1.7917	0.0814	0.143	0.1555	0.8505	0.4786	1.5549	0.1147	0.1311
246728_at	AT5G28040	transcription regulator	0.2496	0.1794	0.2475	0.3685	0.0744	0.1368	-0.00096	0.9953	0.5164	0.1179	0.4852	0.3197
246729_at	AT5G28070	unknown protein	-1.9865	0.2143	0.2711	-0.238	0.8684	0.5095	-2.9979	0.0242	0.0631	-1.2494	0.2152	0.1938
246730_at	AT5G28060	40S ribosomal protein S24 (RPS24B)	0.0298	0.8369	0.5344	0.3522	0.0603	0.1219	-0.5448	0.0159	0.0504	-0.2224	0.1765	0.1711
246731_at	AT5G27630	ACBP5 (ACYL-COA BINDING PROTEIN 5); acyl-C	0.02958	0.9143	0.5552	-0.1998	0.4821	0.377	-0.3567	0.209	0.2172	-0.5862	0.0699	0.0968
246732_at	AT5G27650	PWWP domain-containing protein	0.3207	0.2385	0.2866	0.08574	0.73	0.4686	0.1417	0.5474	0.3783	-0.09325	0.688	0.3931
246733_at	AT5G27660	serine-type peptidase/ trypsin	0.5848	0.5212	0.4294	1.6522	0.1182	0.1738	0.3381	0.7007	0.4315	1.4056	0.161	0.1618
246734_at	AT5G27680	RECQSIM (Arabidopsis RecQ helicase sim); ATP-d	1.4538	0.2302	0.2822	-2.5251	0.07	0.1324	1.5409	0.2083	0.2168	-2.438	0.0767	0.1021
246735_at	AT5G27670	HTA7; DNA binding	-0.2792	0.0145	0.0731	-0.08409	0.2815	0.2818	0.6328	1.00E-04	0.0101	0.8279	0	0.0052
246736_at	AT5G27560	similar to unnamed protein product [Vitis vinifera] (G	-0.4545	0.0037	0.0459	-0.4966	0.0027	0.0346	0.2903	0.0175	0.053	0.2482	0.029	0.057
246737_at	AT5G27710	similar to unnamed protein product [Vitis vinifera] (G	-0.05127	0.7675	0.5138	-0.2032	0.2781	0.2799	-0.2338	0.1623	0.1868	-0.3857	0.0477	0.0771
246738_at	AT5G27740	EMB2775 (EMBRYO DEFECTIVE 2775); DNA binc	0.3333	0.1002	0.1828	0.1443	0.4086	0.3453	0.2778	0.1462	0.1763	0.08886	0.5957	0.3619
246739_at	AT5G27800	ATP binding / aminoacyl-tRNA ligase/ nucleotide bi	0.1383	0.8238	0.5307	-0.04763	0.9387	0.5287	0.8552	0.093	0.1352	0.6693	0.1607	0.1617
246740_at	AT5G27810	sequence-specific DNA binding / transcription factor	-2.8202	0.0446	0.1218	0.03876	0.9702	0.5368	-0.4925	0.6405	0.4112	2.3664	0.0725	0.0988
246741_at	AT5G27720	EMB1644 (EMBRYO DEFECTIVE 1644);	0.004571	0.9657	0.5686	0.4244	0.0131	0.0611	0.3902	0.007	0.034	0.8001	4.00E-04	0.0091
246742_at	AT5G27840	TOPP8 (Type one serine/threonine protein phospha	0.4634	0.0043	0.0476	0.2898	0.0218	0.0748	0.0354	0.618	0.4039	-0.1382	0.1028	0.1225
246743_at	AT5G27750	F-box family protein	0.5008	0.0106	0.0647	1.1728	4.00E-04	0.0251	-0.6034	0.0055	0.0309	0.06857	0.5685	0.3522
246744_at	AT5G27760	hypoxia responsive family protein	-0.05405	0.7431	0.5067	-0.2703	0.1539	0.201	0.9469	0.0035	0.0262	0.7307	0.009	0.0296
246745_at	AT5G27770	60S ribosomal protein L22 (RPL22C)	-0.07398	0.4994	0.4202	0.195	0.1222	0.1775	-0.2333	0.0794	0.1232	0.03566	0.7387	0.41
246746_at	AT5G27820	ribosomal protein L18 family protein	-0.1514	0.2961	0.321	0.3718	0.042	0.1019	0.1863	0.2135	0.22	0.7095	0.0049	0.022
246747_at	AT5G27700	40S ribosomal protein S21 (RPS21C)	0.2685	0.1674	0.2393	0.4646	0.0435	0.1034	-0.1687	0.2712	0.2529	0.02741	0.8459	0.4416
246748_at	AT5G27730	similar to unknown protein [Arabidopsis thaliana] (T	-0.04521	0.8954	0.55	-0.5214	0.1815	0.2208	-1.2526	0.0115	0.0423	-1.7287	0.0036	0.0196
246749_at	AT5G27830	similar to hypothetical protein [Vitis vinifera] (GB:CA	1.0394	0.003	0.0435	1.3521	0.0011	0.0294	-0.363	0.0248	0.0638	-0.05028	0.6527	0.3817
246750_at	no_match	no_match	0.294	0.354	0.3517	0.7341	0.0591	0.1209	-0.7282	0.0604	0.1055	-0.2881	0.3627	0.2681
246751_at	AT5G27870	peclinesterase family protein	1.5168	0.1089	0.1911	3.0706	0.0141	0.0629	0.4537	0.5718	0.3873	2.0075	0.0529	0.0821
246752_at	no_match	no_match	-1.4333	0.1788	0.2472	-0.8041	0.4127	0.3473	-1.5017	0.1633	0.1874	-0.8724	0.3778	0.2748
246753_at	no_match	no_match	0.2129	0.8487	0.5379	0.8406	0.4669	0.3707	0.02981	0.9747	0.5112	0.6576	0.4985	0.3254
246754_at	AT5G27910	CCAAT-box binding transcription factor Hap5a, puta	-0.3715	0.5894	0.4559	-1.5014	0.077	0.1391	0.8484	0.029	0.0691	-0.2815	0.3307	0.2537
246755_at	AT5G27920	F-box family protein	0.8244	0.0071	0.0567	1.0905	0.0026	0.0341	-0.5732	0.0053	0.0303	-0.3071	0.0416	0.0708
246756_at	AT5G27930	protein phosphatase 2C, putative / PP2C, putative	0.7384	0.0032	0.0445	0.4724	0.0157	0.0653	-0.3361	0.0456	0.0894	-0.6021	0.0068	0.0257
246757_at	AT5G27940	WIPP3 (WPP domain protein 3)	0.3168	0.6548	0.4775	0.4717	0.5125	0.3896	1.001	0.0894	0.1321	1.1558	0.0615	0.0899
246758_at	AT5G27850	60S ribosomal protein L18 (RPL18C)	0.05771	0.4442	0.3952	0.4582	0.0025	0.034	-0.3281	9.00E-04	0.0169	0.07246	0.1213	0.1359
246759_at	AT5G27950	kinesin motor protein-related	0.6923	0.0437	0.1206	1.0642	0.0111	0.0564	-2.3471	0	0.0092	-1.9753	0	0.0053
246760_at	AT5G27970	binding	0.03659	0.8884	0.5479	0.05272	0.84	0.5015	-0.688	0.0483	0.0924	-0.6718	0.0517	0.081
246761_at	AT5G27980	seed maturation family protein	-0.07952	0.9481	0.5643	-1.2022	0.3538	0.32	-0.1859	0.8791	0.4864	-1.3085	0.3176	0.2472
246762_at	AT5G27620	CYCH;1 (CYCLIN H;1); cyclin-dependent protein kir	-0.03958	0.8659	0.5425	-0.2521	0.3154	0.3004	0.1754	0.065	0.11	-0.03716	0.821	0.3706
246763_at	AT5G27150	NHX1 (NA+/H+ EXCHANGER); sodium ion transme	-0.1299	0.4078	0.3792	-0.3444	0.0705	0.1328	-0.3241	0.0825	0.1262	-0.5385	0.0186	0.0438
246764_s_at	AT2G27780;AT2G13640;A	elongation factor, TFIIS/CRSP70, N-terminal, sub-b	-0.06983	0.9501	0.5646	-1.4008	0.2528	0.2657	1.9371	0.0988	0.14	0.6061	0.5393	0.3409
246765_at	AT5G27160	similar to unknown protein [Arabidopsis thaliana] (T	-0.07178	0.8727	0.5448	0.185	0.6826	0.453	-0.05122	0.8651	0.4827	0.2056	0.5077	0.3288
246766_at	AT5G27340	unknown protein	-0.8489	0.3125	0.3301	-0.5986	0.4613	0.3685	-0.4678	0.2197	0.2234	-0.2174	0.5363	0.3401
246767_at	AT5G27395	P-P-bond-hydrolysis-driven protein transmembrane	0.4803	0.0283	0.0974	0.6015	0.0136	0.0618	-0.2399	0.1686	0.1908	-0.1186	0.4532	0.3073
246768_at	AT5G27400	similar to unnamed protein product [Vitis vinifera] (G	-0.01032	0.9591	0.567	0.03408	0.8657	0.5087	-1.0607	6.00E-04	0.0158	-1.0163	7.00E-04	0.0108
246769_at	AT5G27440	unknown protein	0.2011	0.7985	0.5235	0.7381	0.3735	0.3292	-0.3697	0.6425	0.412	0.1673	0.8317	0.4377
246770_at	AT5G27460	pentaticopeptide (PPR) repeat-containing protein	0.5131	0.0137	0.0719	0.8991	0.0018	0.0325	-0.5753	0.0092	0.0385	-0.1893	0.1961	0.1826
246771_at	no_match	no_match	0.3962	0.6856	0.4878	-2.0205	0.0904	0.1517	0.1087	0.8606	0.4812	-2.308	0.0165	0.041
246772_at	AT5G27490	integral membrane Yip1 family protein	-0.2192	0.4118	0.3811	-0.03882	0.8791	0.5129	0.1091	0.6404	0.4112	0.2895	0.2518	0.2135
246773_at	AT5G27510	protein kinase family protein	-0.1404	0.8578	0.5406	0.06164	0.9372	0.5284	0.3678	0.5849	0.3926	0.5698	0.4099	0.2882
246774_at	AT5G27530	glycoside hydrolase family 28 protein / polygalacturo	-0.27	0.8	0.5241	0.7186	0.511	0.3891	-0.3309	0.7567	0.4502	0.6576	0.5456	0.3432
246775_at	AT5G27540	EMB2473 (EMBRYO DEFECTIVE 2473); GTP bind	0.5824	0.0141	0.0725	0.4668	0.0288	0.0847	-0.3276	0.0745	0.1188	-0.4432	0.0315	0.0598
246776_at	AT5G27550	pseudogene of kinesin motor protein-related	-0.3631	0.2642	0.302	-0.4978	0.1498	0.1979	-0.05152	0.8616	0.4816	-0.1862	0.5385	0.3407
246777_at	AT5G27420	zinc finger (C3HC4-type RING finger) family protein	0.4149	0.5235	0.4304	1.0874	0.1412	0.1916	-0.2882	0.039	0.0816	0.3843	0.0157	0.0399
246778_at	AT5G27450	MK/MVK; mevalonate kinase	-0.8847	0.006	0.0538	-0.6552	0.017	0.0677	-0.05357	0.7123	0.4357	0.1758	0.2635	0.2194
246779_at	AT5G27520	mitochondrial substrate carrier family protein	-0.3344	0.5608	0.4451	0.01274	0.9819	0.5397	-0.3946	0.0247	0.0637	-0.0475	0.6944	0.3956
246780_at	AT5G27470	seryl-tRNA synthetase / serine--tRNA ligase	0.4381	0.0017	0.0391	0.3866	0.0024	0.0339	-0.05472	0.4015	0.3172	-0.05629	0.1743	0.1699
246781_at	AT5G27350	SFP1; carbohydrate transmembrane transporter/ su	-0.2555	0.1374	0.2154	-0.2199	0.1858	0.2236	-0.4142	0.0398	0.0825	-0.3786	0.0516	0.0809
246782_at	AT5G27320	ATGID1C;GID1C (GA INSENSITIVE DWARF1C); h	0.9591	0.0031	0.0438	0.5889	0.0172	0.068	-0.2875	0.0537	0.0985	-0.6577	0.0035	0.0191
246783_at	AT5G27283	SFP2; carbohydrate transmembrane transporter/ su	-0.4893	0.0269	0.0949	-0.5698	0.0164	0.0666	-0.7178	0.0012	0.0188	-0.7983	8.00E-04	0.0112
246784_at	AT5G27430	signal peptidase subunit family protein	0.4046	0.0084	0.06	0.4879	0.0043	0.0407	-0.5355	0.0031	0.0248	-0.4523	0.0057	0.0234
246785_at	AT5G27380	GSH2/GSHB (GLUTATHIONE SYNTHETASE 2); g	0.3663	0.0928	0.1764	0.5551	0.0291	0.0848	-0.5632	8.00E-04	0.0165	-0.3745	0.0038	0.02
246786_at	AT5G27410	aminotransferase class IV family protein	-2.1698	0.009	0.0612	-0.3252	0.516	0.391	-2.8893	0.0032	0.0252	-1.0448	0.0842	0.1084
246787_s_at	AT5G27570;AT5G27945	[AT5G27570, WD-40 repeat family protein];[AT5G2	-0.1131	0.908	0.5535	1.2829	0.2354	0.255	-0.1433	0.8297	0.4726	1.2527	0.1151	0.1313
246788_at	AT5G27580	AGL89; transcription factor	-0.8038	0.3342	0.3424	0.4449	0.5765	0.4145	-1.3604	0.1369	0.169	-0.1117	0.8862	0.4532
246789_at	AT5G27600	LACS7 (LONG-CHAIN ACYL-COA SYNTHETASE	1.095	0.0028	0.0431	0.9167	0.0054	0.0433	0.2124	0.274	0.2546	0.03413	0.8486	0.4424
246790_at	AT5G27610	DNA binding / transcription factor	-0.1238	0.828	0.5318	-0.4367	0.4593	0.3676	-0.2626	0.6486	0.4142	-0.5755	0.3418	0.2588
246791_at	AT5G27280	zinc finger (DNL type) family protein	0.8426	0.1134	0.1951	0.7971	0.1285	0.1819	0.8858	0.0164	0.0511	0.8403	0.0196	0.0449
246792_at	AT5G27290	similar to unknown protein [Arabidopsis thaliana] (T	-0.8924	0.0019	0.0391	-0.972	0.0013	0.0312	-0.03112	0.8111	0.467	-0.1107	0.4151	0.2904
246793_at	AT5G27210	similar to transmembrane protein, putative [Arabido	0.2521	0.3497	0.3496	0.2176	0.4127	0.3473	0.3482	0.2043	0.2143	0.3137	0.2439	0.2092
246794_s_at	AT5G27010;AT5G06350	[AT5G27010, binding];[AT5G06350, binding]	0.4699	0.2317	0.283	0.4222	0.2742	0.2776	-0.1896	0.6001	0.3982	-0.2372	0.5162	0.3321
246795_at	AT5G27020	unknown protein	-1.9132	0.0269	0.0949	-0.7834	0.2347	0.2546	-1.2062	0.0977	0.1391	-0.07644	0.8981	0.4566
246796_at	AT5G26770	similar to unknown protein [Arabidopsis thaliana] (T	-0.6022	0.0841	0.1678	0.2634	0.3736	0.3293	-0.453	0.1604	0.1858	0.4126	0.1921	0.1803
246797_at	AT5G26790	unknown protein	-0.9072	0.281	0.3119	-1.898	0.0597	0.1214	0.5991	0.2363	0.233	-0.3918	0.4141	0.29
246798_at	AT5G26930	zinc finger (GATA type) family protein	1.8706	0.1982	0.2615	-1.2932	0.3488	0.3164	2.0517	0.1663	0.1893	-1.112	0.4115	0.2889
246799_at	AT5G26940	exonuclease family protein	0.03763	0.6755	0.4846	-0.1	0.2969	0.2902	0.04389	0.6268	0.4069	-0.09376	0.3242	0.2503
246800_at	AT5G26780	SHM2 (SERINE HYDROXYMETHYLTRANSFERA	-0.1958	0.1362	0.2143	0.1356	0.2669	0.2737	-0.7619	0.0019	0.0209	-0.4306	0.0149	0.0388
246801_at	AT5G26830	threonyl-tRNA synthetase / threonine--tRNA ligase	-0.3925	0.0556	0.2172	0.2131	0.2415	-0.1091	0.4656	0.3455	-0.2843	0.1036	0.1232	
246802_at	AT5G27000	ATK4 (ARABIDOPSIS THALIANA KINESIN 4); mic	-0.00037	0.9982	0.5763	0.6386	0.014	0.0627	0.08621	0.6033	0.3994	0.7251	0.009	0.0296
246803_at	AT5G26980	SYP41 (SYNTAXIN OF PLANTS 41); SNAP recepto	0.4271	0.0527	0.1316	0.9144	0.0043	0.0407	-0.8565	0.0054	0.0309	-0.3693	0.0779	0.1032
246804_at	no_match	no_match	-0.4324	0.3129	0.3303	-0.07028	0.8604	0.5072	-0.3876	0.2649	0.2492	-0.02548	0.9362	0.4673
246805_at	AT5G27050	AGL101; transcription factor	1.7259	0.128	0.2067	-1.2984	0.223	0.2476	2.7317	0.0387	0.0813	-0.2926	0.7617	0.4172
246807_at	AT5G27080	WD-40 repeat family protein	-0.2227	0.8087	0.5264	-1.2379	0.224	0.248	-0.4382	0.637	0.4101	-1.4545	0.1666	0.1652
246808_at	AT5G27100	ATGLR2.1 (Arabidopsis thaliana glutamate receptor	0.3626	0.4331	0.3908	-0.1577	0.7242	0.4667	-0.2344	0.6035	0.3994	-0.7547	0.1442	0.151
246809_at	AT5G27110	pentaticopeptide (PPR) repeat-containing protein	0.1899	0.3487	0.3492	0.4208	0.0786	0.1405	0.1457	0.4617	0.344	0.3765	0.1034	0.123
246810_s_at	AT5G27120;AT5G27120	[AT5G27120, SAR DNA-binding protein, putative];[A	0.03338	0.8932	0.5495	0.2523	0.3408	0.314	-0.4896	0.0192	0.0556	-0.6871	0.0461	0.0755
246810_at	AT5G27160	transposable element gene	0.4115	0.7843	0.519	-1.2536	0.4229	0.352	1.3674	0.0446	0.0883	-0.2977	0.5635	0.3503
246811_at	AT5G27170	unknown protein	-0.4328	0.7321	0.503	-0.1224	0.9223	0.5247	0.2926	0.8161	0.4686	0.6031	0.6358	0.3757
246812_at	AT4G07023;AT1G43205;A	[AT4G07523, transposable element gene];[AT1G43	1.2298	0.3789	0.3638	-1.6337	0.2695	0.2697	0.6355	0.6366	0.41	-2.2283	0.1478	0.1533
246813_at	AT5G27190	transposable element gene	0.7412	0.7151	0.4977	-1.5452	0.4597	0.3678	1.4244	0.3964	0.3149	-0.862	0.5965	0.3623
246814_at	AT5G27200	ACP5 (ACYL CARRIER PROTEIN 5); acyl carrier	0.9943	0.3053	0.3257	-1.4781	0.1557	0.2026	2.7067	0.014	0.0472	0.2343	0.7361	0.4091
246815_at	AT5G27220	protein transport protein-related	0.1699	0.8301	0.5326	0.125	0.6577	0.4443	0.03156	0.9098	0.4962	-0.0967	0.7305	0.4073
246816_at	AT5G27230	similar to hydroxyproline-rich glycoprotein family pr	-0.4689	0.5596	0.4448	-0.3632	0.6483	0.441	-0.4026	0.6143	0.4024	-0.2969	0.708	0.4002
246817_at	AT5G27240	DNA/ heat shock N-terminal domain-containing pro	-0.02173	0.8982	0.5507	0.1892	0.3009	0.2919	-0.3618	0.0858	0.1292	-0.1508	0.3978	0.2833
246818_at	AT5G27270	EMB976 (EMBRYO DEFECTIVE 976)	0.3578	0.0249	0.0915	-0.08879	0.434	0.357	-0.4432	0.0015	0.0198	-0.8898	1.00E-04	0.0061
246819_at	AT5G26900	WD-40 repeat family protein	-2.3828	0.3128	0.3303	-1.3628	0.5454	0.4028	0.2288	0.9089	0.495	1.2488	0.5424	0.3418
246820_at	AT5G26910	similar to unknown protein [Arabidopsis thaliana] (T	-0.288	0.2437	0.2898	-0.1487	0.5195	0.3922	-0.5456	0.0276	0.0676	-0.4063	0.0652	0.093
246821_at	AT5G26920	calmodulin binding	0.9755	0.0182	0.0804	1.1482	0.0105	0.0554	-0.4308	0.1321	0.1654	-0.2581	0.3213	0.249
246822_at	AT5G26960	kelch repeat-containing F-box family protein	0.7724	0.0737	0.1562	0.5508	0.1611	0.2066	-0.2361	0.5025	0.3604	-0.4577	0.2268	0.1998
246823_at	AT5G26970	unknown protein	1.2703	0.4592	0.4025	0.4892	0.7684	0.48	0.1809	0.9129	0.496	-0.6001	0.7188	0.4036
246824_at	AT5G26990	drought responsive family protein	0.0773	0.5203	0.4291	0.2233	0.1119	0.1688	-0.1972	0.0675	0.1126	-0.05126	0.5529	0.3461
246825_at	AT5G26260	meprin and TRAF homology domain-containing pro	-0.9552	0.2573	0.2978	-1.4856	0.1093	0.1669	0.8582	0.3012	0.2694	0.3277	0.6741	0.3888
246826_at	AT5G26310	UGT72E3; UDP-glycosyltransferase/ coniferyl-alcot	-0.2749	0.3023	0.3244	-0.3482	0.2084	0.2385	-0.4099	0.0762	0.1203

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246890_at	AT5G25410	similar to unknown protein [Arabidopsis thaliana] (T	-0.7575	0.37	0.3595	-0.1981	0.8074	0.4921	-1.3708	0.1458	0.176	-0.8014	0.3515	0.2633
246891_at	AT5G25490	zinc finger (Ran-binding) family protein	-0.785	0.0209	0.085	-0.1178	0.6084	0.4265	-0.4377	0.019	0.0553	0.2295	0.1167	0.1325
246892_at	AT5G25500	similar to unnamed protein product [Vitis vinifera] (G	0.7554	0.2086	0.2672	0.3598	0.5151	0.3906	-0.04938	0.8771	0.4859	-0.4449	0.2118	0.1918
246893_at	AT5G25520	elongation factor-related	0.1219	0.3354	0.343	-0.1853	0.1715	0.2139	-0.3214	0.0016	0.0202	-0.6286	1.00E-04	0.0062
246894_at	AT5G25530	DNAJ heat shock protein, putative	1.1393	0.2078	0.2669	-1.1949	0.1905	0.2267	1.3426	0.1516	0.1801	-0.9916	0.2615	0.2185
246895_at	AT5G25540	CID6 (CTC-Interacting Domain 6); protein binding	0.289	0.0561	0.1359	0.4668	0.0126	0.06	0.6312	0.0043	0.0282	0.809	0.0017	0.0147
246896_at	AT5G25550	leucine-rich repeat family protein / extensin family p	-0.00885	0.9918	0.575	-0.775	0.3934	0.3384	0.1084	0.9001	0.4924	-0.6577	0.4629	0.3112
246897_at	AT5G25560	zinc finger (C3HC4-type RING finger) family protein	0.3024	0.2462	0.2914	0.09008	0.8332	0.4997	-2.4783	3.00E-04	0.0143	-2.7306	2.00E-04	0.0078
246898_at	AT5G25580	similar to aminoacyl-tRNA synthetase family [Arabic	-1.0429	0.3435	0.3465	0.9624	0.378	0.331	0.3515	0.6638	0.4192	2.3568	0.0348	0.0631
246899_at	AT5G25590	similar to unknown protein [Arabidopsis thaliana] (T	-0.1796	0.5658	0.4472	-0.2974	0.3592	0.3225	-0.2617	0.2823	0.2594	-0.3794	0.1463	0.1523
246900_at	AT5G25620	YUC6 (YUCCA6); monooxygenase	-0.8072	0.4462	0.3962	0.8364	0.4312	0.3958	-0.9126	0.394	0.3139	0.731	0.4872	0.3207
246901_at	AT5G25630	pentatricopeptide (PPR) repeat-containing protein	-0.02892	0.7922	0.5214	0.03483	0.7516	0.4755	-0.2821	0.0515	0.0962	-0.2184	0.1006	0.1211
246902_at	AT5G25640	similar to rhomboid family protein [Arabidopsis thali	-1.3287	0.2653	0.3023	1.1614	0.3213	0.3037	-1.2318	0.2965	0.2669	1.2583	0.2876	0.2322
246903_at	AT5G25750	unknown protein	2.469	0.0753	0.1579	0.008209	0.994	0.5427	1.0342	0.2194	0.2233	-1.4266	0.1152	0.1313
246904_at	AT5G25480	DNMT2 (DNA METHYLTRANSFERASE-2); DNA b	0.3047	0.234	0.2839	-0.06934	0.766	0.4792	0.463	0.1005	0.1415	0.08896	0.7037	0.3986
246905_at	AT5G25570	similar to unnamed protein product [Vitis vinifera] (G	-0.7594	0.0789	0.1618	0.06707	0.8461	0.5033	-0.1179	0.7342	0.443	0.7086	0.0939	0.1159
246906_at	AT5G25475	DNA binding	-0.3078	0.2226	0.2768	-0.2617	0.2872	0.285	-0.3025	0.1306	0.1643	-0.2564	0.1831	0.1753
246907_at	AT5G25510	serine/threonine protein phosphatase 2A (PP2A) re	-0.0511	0.6823	0.4867	0.3069	0.0573	0.119	-0.2553	0.0868	0.1299	0.1026	0.4151	0.2904
246908_at	AT5G25610	RD22 (RESPONSIVE TO DESSICATION 22)	-0.4047	0.0164	0.0771	-0.3822	0.0198	0.072	0.5757	0.0048	0.0293	0.5982	0.0042	0.0207
246909_at	AT5G25770	unknown protein product [Vitis vinifera] (G	0.8055	0.0966	0.1796	1.0093	0.0536	0.1148	-0.501	0.0155	0.0494	-0.2972	0.0741	0.1
246910_at	AT5G25800	exonuclease family protein	0.6636	0.0745	0.1569	0.7978	0.0449	0.105	-0.3886	0.2103	0.218	-0.2544	0.3844	0.2778
246911_at	AT5G25810	TNY (TINY); DNA binding / transcription factor	-1.4095	0.0041	0.0468	-0.5783	0.0726	0.1349	0.1868	0.2498	0.2409	0.1189	0.0018	0.0148
246912_at	AT5G25820	exostosin family protein	1.0378	0.1559	0.2302	2.7718	0.0096	0.0535	-0.896	0.0935	0.1356	-0.8381	0.1096	0.1274
246913_at	AT5G25830	zinc finger (GATA type) family protein	-0.6046	0.1738	0.244	-0.03946	0.9193	0.5239	-0.2859	0.3074	0.2722	0.2792	0.3173	0.2471
246914_at	AT5G25860	F-box family protein	0.5286	0.6209	0.4667	0.5506	0.6077	0.4262	-0.2242	0.832	0.4733	-0.2034	0.8472	0.4421
246915_at	AT5G25880	ATNADP-ME3 (NADP-MALIC ENZYME 3); malate	-1.4633	0.2065	0.2662	-0.6155	0.5608	0.4087	-0.6732	0.4679	0.3466	0.1746	0.8456	0.4416
246916_at	AT5G25910	disease resistance family protein	0.9555	0.0182	0.0804	1.0813	0.012	0.0589	-0.5077	0.1098	0.1483	-0.3819	0.1981	0.1838
246917_at	AT5G25280	serine-rich nitrilase-related protein [Arabidops	0.06075	0.76	0.5117	0.3845	0.1072	0.1651	0.2456	0.2542	0.2433	0.5694	0.0368	0.0653
246918_at	AT5G25340	similar to unknown protein [Arabidopsis thaliana] (T	-0.5391	0.5847	0.4541	-1.0928	0.2951	0.2893	-0.06745	0.9444	0.5043	-0.6212	0.5315	0.3385
246919_at	AT5G25460	similar to unknown protein [Arabidopsis thaliana] (T	0.02829	0.8203	0.5296	0.04092	0.7434	0.4725	0.2306	0.0586	0.1036	0.2432	0.0505	0.0798
246920_at	AT5G25590	plastocyanin-like domain-containing protein	-0.365	0.5397	0.4367	-1.3404	0.1637	0.1322	1.0943	0.0866	0.1297	0.1189	0.818	0.4337
246921_at	AT5G25080	similar to unnamed protein product [Vitis vinifera] (G	0.237	0.3048	0.3255	0.09831	0.6511	0.4421	-0.00166	0.9874	0.5146	-0.1403	0.23	0.2015
246922_at	AT5G25110	CIPK25 (CBL-INTERACTING PROTEIN KINASE 2	-0.8562	0.5662	0.4474	2.1379	0.194	0.2287	-1.2137	0.4058	0.3189	1.7804	0.2449	0.2097
246923_at	AT5G25100	endomembrane protein 70, putative	-0.2463	0.1295	0.2081	-0.2217	0.1616	0.2069	-0.1377	0.3471	0.2917	-0.113	0.4316	0.2975
246924_at	AT5G25060	RNA recognition motif (RRM)-containing protein	0.4384	0.1371	0.2151	0.6051	0.0626	0.1242	-0.4535	0.0826	0.1262	-0.2869	0.2187	0.1954
246925_at	AT5G25180	CYP71B14 (cytochrome P450, family 71, subfamily	0.8352	0.4498	0.3979	0.7542	0.492	0.3812	-0.5061	0.0932	0.1353	-0.5872	0.0636	0.0916
246926_at	AT5G25240	similar to NHL repeat-containing protein [Arabidops	0.3817	0.5444	0.4388	0.1246	0.8396	0.5014	0.3456	0.214	0.2203	0.0883	0.7251	0.4057
246927_s_at	AT5G25260;AT5G25250	[AT5G25260, similar to unknown protein [Arabidop	1.3777	0.0308	0.1017	2.2914	0.0055	0.0434	-0.4546	0.1091	0.1478	0.4591	0.1065	0.125
246928_at	AT5G25270	similar to ubiquitin family protein [Arabidopsis thalia	0.6767	0.0035	0.0452	0.3779	0.0264	0.0813	-0.4712	0.0128	0.045	-0.7699	0.0022	0.0157
246929_at	AT5G25210	similar to unknown protein [Arabidopsis thaliana] (T	0.9969	0.0114	0.0691	1.2673	0.0049	0.0422	0.000398	0.982	0.5133	0.2757	0.2879	0.2323
246930_at	AT5G25220	KNAT3 (KNOTTED1-LIKE HOMEOBOX GENE 3);	0.0271	0.7742	0.5161	0.2551	0.0446	0.1046	-0.382	0.0124	0.0442	-0.154	0.1562	0.159
246931_at	AT5G25170	similar to unknown protein [Arabidopsis thaliana] (T	-0.1258	0.672	0.4833	0.02373	0.9356	0.5279	-0.1635	0.5853	0.3928	-0.01391	0.9622	0.4737
246932_at	AT5G25190	ethylene-responsive element binding protein, putati	0.2547	0.5486	0.4405	0.2628	0.5366	0.3991	0.000637	0.9575	0.5071	0.01792	0.9226	0.4636
246933_at	AT5G25160	ZFP3 (ZINC FINGER PROTEIN 3); nucleic acid bin	0.9359	0.4416	0.3944	1.0158	0.4068	0.3444	2.1733	0.1186	0.1551	2.2533	0.1092	0.1271
246934_at	AT5G25290	F-box family protein	0.3682	0.7563	0.5106	0.07861	0.9468	0.5312	-0.6007	0.6165	0.4033	-0.8903	0.4667	0.3126
246935_at	AT5G25300	EBF2 (EIN3-BINDING F BOX PROTEIN 2)	0.5309	0.0733	0.1559	0.2662	0.2928	0.288	-0.9542	0.0013	0.0193	-1.2188	5.00E-04	0.0096
246936_at	AT5G25360	similar to unknown protein [Arabidopsis thaliana] (T	-0.3013	0.0924	0.176	-0.2196	0.1837	0.2223	0.08847	0.4971	0.3585	0.1702	0.2246	0.1985
246937_at	AT5G25370	PLDALPHA3 (PHOSPHLIPASE D ALPHA 3); phos	-1.1175	0.1178	0.1985	0.03924	0.9477	0.5313	-0.03261	0.9565	0.507	1.1241	0.1163	0.1322
246938_at	AT5G25380	CYCAZ1 (CYCLIN A2;1); cyclin-dependent kinin	-0.2005	0.7388	0.5053	0.1009	0.8659	0.5088	0.4237	0.4921	0.3564	0.7251	0.2657	0.2207
246939_at	AT5G25390	SHN2 (SHINE2); DNA binding / transcription factor	0.6479	0.5711	0.4494	0.8537	0.4625	0.3691	0.208	0.4582	0.3423	0.4137	0.1781	0.1721
246940_at	AT5G25400	phosphate translocator-related	1.9267	0.0601	0.1402	1.504	0.1124	0.1693	-0.498	0.4915	0.3563	-0.9207	0.2345	0.2042
246941_at	AT5G25415	similar to unknown protein [Arabidopsis thaliana] (T	-0.858	0.4816	0.4126	0.6338	0.5977	0.4224	-1.0633	0.328	0.2824	0.4083	0.6964	0.3964
246942_at	AT5G25430	anion exchange protein family	1.3037	0.216	0.2723	0.1358	0.8858	0.5147	-0.2731	0.7738	0.4555	-1.441	0.18	0.1733
246943_at	AT5G25440	protein kinase family protein	0.9163	0.074	0.1564	0.8426	0.0915	0.1526	-0.2737	0.1071	0.1466	-0.3474	0.0583	0.0871
246944_at	AT5G25450	ubiquinol-cytochrome C reductase complex 14 kDa	0.7674	0.0137	0.0719	0.9376	0.0098	0.0467	0.6906	6.00E-04	0.0158	1.1248	3.00E-04	0.0085
246945_s_at	AT5G25050	integral membrane transporter family protein	-0.03814	0.7031	0.4936	0.02204	0.8245	0.4974	-0.2276	0.0233	0.0617	-0.1674	0.0582	0.087
246946_at	AT5G25070	similar to unnamed protein product [Vitis vinifera] (G	0.06692	0.7306	0.5027	0.5074	0.0488	0.1096	-0.7041	0.0066	0.0333	-0.2636	0.1241	0.1377
246947_at	AT5G25120	CYP71B11 (cytochrome P450, family 71, subfamily	0.5456	0.0593	0.1394	0.5296	0.0643	0.1266	-0.2537	0.1989	0.2111	-0.2696	0.1774	0.1717
246948_at	AT5G25130	CYP71B12 (cytochrome P450, family 71, subfamily	0.05444	0.882	0.5468	0.1451	0.695	0.4571	-0.7582	0.0691	0.1139	-0.6676	0.0955	0.1172
246949_at	AT5G25140	CYP71B13 (cytochrome P450, family 71, subfamily	-0.2047	0.5781	0.4518	-0.09683	0.7891	0.4858	-1.4389	0.0132	0.0457	-1.331	0.0171	0.0418
246950_at	no_match	no_match	0.1016	0.6486	0.476	0.1227	0.5846	0.4179	-0.469	0.0282	0.0683	-0.4479	0.0325	0.0609
246951_at	AT5G04880	pseudogene of ABC transporter family protein	1.457	0.163	0.2363	0.9035	0.3495	0.3178	-1.6152	0.0887	0.1315	-2.1687	0.0397	0.0687
246952_at	AT5G04820	ATOFP13/OFP13 (Arabidopsis thaliana ovate famil	-0.4866	0.2778	0.3101	-0.8003	0.1079	0.1656	0.7646	0.0553	0.1003	0.4508	0.1894	0.179
246953_at	AT5G04850	VPS29.2	0.161	0.2767	0.3099	0.3948	0.0367	0.0946	0.8135	0.0031	0.0251	1.0474	0.0012	0.0129
246954_at	AT5G04830	similar to unknown [Populus trichocarpa x Populus	-0.04154	0.685	0.4876	0.02141	0.833	0.4996	0.4191	0.0021	0.0218	0.482	0.0012	0.013
246955_at	AT5G04870	CPK1 (calcium-dependent protein kinase isoform A	0.1624	0.5088	0.4245	0.2665	0.3002	0.2914	-0.02002	0.8652	0.4827	0.08409	0.4895	0.3217
246956_at	AT5G04890	RTM2 (RESTRICTED TEV MOVEMENT 2)	-0.3017	0.3367	0.3436	0.6005	0.0957	0.1559	0.248	0.3255	0.2811	1.1502	0.0065	0.0251
246957_at	AT5G24670	hydrolase; zinc ion binding	0.5607	0.0736	0.1561	0.1783	0.4863	0.3789	-1.9903	7.00E-04	0.016	-2.3727	4.00E-04	0.0088
246958_at	AT5G24690	similar to RER1 (RETICULATA-RELATED 1) [Arabi	0.001936	0.9927	0.5752	-0.00264	0.99	0.5416	-0.9204	0.0027	0.0236	-0.925	0.0026	0.0169
246959_at	AT5G24690	similar to RER1 (RETICULATA-RELATED 1) [Arabi	-0.4894	0.1404	0.218	-0.1092	0.6916	0.456	-2.4672	5.00E-04	0.0159	-2.107	0.0012	0.0128
246960_at	AT5G24710	similar to hypothetical protein Osl_003062 [Oryza s	0.08624	0.4855	0.414	0.1207	0.3431	0.3148	-0.5909	0.0063	0.0328	-0.5564	0.0077	0.0275
246961_at	AT5G24710	similar to hypothetical protein Osl_003062 [Oryza s	-0.1324	0.5968	0.4586	-0.04259	0.8625	0.5078	-0.971	0.0136	0.0465	-0.8811	0.0188	0.044
246962_s_at	AT5G24800	ATBZIP18;BZO2H2 (BASIC LEUCINE ZIPPER O2-I	0.7925	0.003	0.0437	1.0357	0.0011	0.0294	-0.1695	0.2425	0.2364	0.07373	0.5832	0.3573
246963_at	AT5G24820	aspartyl protease family protein	-1.6238	0.145	0.2213	-0.7792	0.4348	0.3574	-0.3025	0.7533	0.4491	0.5421	0.5788	0.3556
246964_at	AT5G24830	pentatricopeptide (PPR) repeat-containing protein	0.05491	0.7112	0.4967	0.1412	0.3645	0.325	-0.7503	0.0056	0.0311	-0.6641	0.0086	0.0288
246965_at	AT5G24840	methyltransferase	0.4514	0.0386	0.1133	0.479	0.0323	0.089	0.1681	0.3218	0.2791	0.1957	0.2588	0.2173
246966_at	AT5G24850	CRY3 (CRYPTOCHROME 3); DNA binding / DNA p	-1.0729	0.0075	0.0579	-1.3374	0.0034	0.0373	-0.1182	0.5677	0.3858	-0.3828	0.1144	0.1309
246967_at	AT5G24860	FPF1 (FLOWERING PROMOTING FACTOR 1)	-1.7972	0.1176	0.1983	-0.2643	0.7845	0.4847	-1.8542	0.1005	0.1415	-0.3212	0.7312	0.4075
246968_at	AT5G24870	zinc finger (C3HC4-type RING finger) family protein	0.07582	0.9802	0.5721	0.1179	0.7025	0.46	0.1927	0.4607	0.3434	0.3031	0.2691	0.2223
246969_at	AT5G24880	similar to calmodulin-binding protein-related [Arabid	-0.6003	0.6688	0.4822	0.1237	0.9289	0.5265	-0.4304	0.7395	0.4446	0.2936	0.8198	0.4341
246970_at	AT5G24900	CYP714A2 (cytochrome P450, family 714, subfamil	2.3724	0.0613	0.1421	0.1391	0.8871	0.515	0.6318	0.5298	0.3712	-1.6015	0.1566	0.159
246971_at	AT5G24940	protein phosphatase 2C, putative / PP2C, putative	-0.2653	0.7245	0.5009	1.498	0.0996	0.1591	0.0678	0.9276	0.5	1.8311	0.0594	0.0879
246972_s_at	AT5G24950;AT5G24960	[AT5G24950, CYP71A15 (cytochrome P450, family	0.255	0.7464	0.5078	0.3071	0.6978	0.4582	-1.061	0.2228	0.2252	-1.0088	0.2423	0.2083
246973_at	AT5G24970	ABC1 family protein	-0.08057	0.6255	0.4683	0.0618	0.7063	0.4611	-0.2983	0.0179	0.0535	-0.1559	0.1127	0.1295
246974_at	no_match	no_match	0.5465	0.2083	0.2671	0.3007	0.4559	0.3663	-0.08085	0.8354	0.4742	-0.3266	0.421	0.2929
246975_at	AT5G24890	similar to unknown protein [Arabidopsis thaliana] (T	-0.1487	0.4203	0.385	0.5458	0.0302	0.0863	-0.4875	0.0119	0.0434	0.2071	0.1369	0.1461
246976_s_at	AT5G24810	ABC1 family protein	0.2014	0.1118	0.1939	-0.06926	0.523	0.3933	-0.328	0.0296	0.07	-0.5987	0.0038	0.0199
246977_at	AT5G24930	zinc finger (B-box type) family protein	-0.5324	0.0831	0.1668	-0.5952	0.062	0.1238	-0.01809	0.9393	0.5032	-0.08084	0.7353	0.4089
246978_at	AT5G24910	CYP714A1 (cytochrome P450, family 714, subfami	-0.7588	0.5162	0.4276	-0.8445	0.4729	0.3733	0.1336	0.8954	0.4912	0.04784	0.9624	0.4738
246979_s_at	AT5G25020;AT5G24990	[AT5G25020, similar to unknown protein [Arabidops	-1.7841	0.0991	0.1816	0.2287	0.7974	0.4887	-1.5076	0.1448	0.1752	0.5052	0.5772	0.3549
246980_at	AT5G07530	peptidyl-prolyl cis-trans isomerase cyclophilin-type f	0.3994	0.0462	0.1237	0.4469	0.0331	0.0902	-0.5603	0.0161	0.0506	-0.5128	0.0215	0.0477
246981_at	AT5G04840	bZIP protein	-0.05941	0.8842	0.5471	-0.3225	0.4468	0.3624	0.3727	0.3853	0.3102	0.1096	0.7888	0.4254
246982_s_at	AT5G04860;AT2G10560	[AT5G04860, similar to unknown protein [Arabidops	0.2112	0.0794	0.1624	1.0269	3.00E-04	0.0249	-0.08924	0.3788	0.3072	0.7264	0.0013	0.0132
246983_at	AT5G67200	leucine-rich repeat transmembrane protein kinase,	0.4517	0.3196	0.3343	-0.238	0.5819	0.4169	0.6575	0.0758	0.12	-0.03221	0.9127	0.4607
246984_at	AT5G67310	CYP81G1 (cytochrome P450, family 81, subfamily	0.5513	0.328	0.339	0.6072	0.2875	0.2852	-0.1259	0.5967	0.3969	-0.07009	0.7653	0.4185
246985_at	AT5G67290	FAD-dependent oxidoreductase family protein	0.6157	0.0209	0.085	0.6894	0.0144	0.0634	-0.6039	0.0223	0.0603	-0.5303	0.0334	0.0617
246986_at	AT5G67280	RLK (RECEPTOR-LIKE KINASE); ATP binding / kir	-0.4831	0.0937	0.1772	-0.6139	0.0497	0.1105	0.2965	0.219	0.223	0.1658	0.4611	0.3105
246987_at	AT5G67300	ATMYB44/ATMYBR1/MYBR1 (MYB DOMAIN PRO	-0.3962	0.5209	0.4293	-0.1755	0.7711	0.4807	0.2804	0.0862	0.1295	0.5011	0.0155	0.0397
246988_at	AT5G67340	armadillo/beta-catenin repeat family protein / U-box	1.3622	0.0032	0.0442	1.5722	0.0019	0.0329	-0.0111	0.9503	0.5056	0.1989	0.3001	0.2387
246989_at	AT5G67360	unknown protein	-0.3901	0.1755	0.2452	-0.3982	0.1687	0.2116	0.4205	0.1511	0.1796	0.4125	0.1572	0.1595
246990_at	AT5G67360	ARA12; subtilase	0.2624	0.1922	0.257	0.5057	0.0392	0.0981	-0.7544	0.0099	0.0396	-0.5111	0.0351	0.0634
246991_at	AT5G67400	peroxidase 73 (PER73) (P73) (PRXR11)	-0.134	0.8582	0.5406	-0.912	0.2647	0.2724	-0.09789	0.8961	0.4913	-0.8759	0.2812	0.2287
246992_at	AT5G67430	GCN5-related N-acetyltransferase (GNAT) family pr	-1.1687	0.1433	0.2202	0.9133	0.2286	0.2507	-0.7805	0.2916	0.2644	1.3015	0.113	0.1298
246993_at	AT5G67450	AZF1 (ARABIDOPSIS ZINC-FINGER PROTEIN 1);	-0.03875	0.9448	0.5635	0.4349	0.4549	0.366	0.3914	0.2078	0.2165	0.865	0.0295	0.0576
246994_at	AT5G67460	glycosyl hydrolase family protein 17	-0.2721	0.517	0.428	0.09076	0.8245	0.4974	-0.00668	0.9869	0.5144	0.3562	0.4054	0.2863
246995_at	AT5G67470	formin homology 2 domain-containing protein / FH2	-0.4829	0.0653	0.1466	0.5498	0.0455	0.1057	0.3816	0.1173	0.1541	0.4485	0.0793	0.1044
246996_at	AT5G67420	LBD37 (LOB DOMAIN-CONTAINING PROTEIN 37	-0.05229	0.8555	0.5399	-0.4961	0.1393	0.1901	0.3573	0.0284	0.0684	-0.08654	0.4617	0.3107
246997_at	AT5G67390	similar to unknown protein [Arabidopsis thaliana] (T	-0.4823	0.4213	0.3856	-0.1567	0.7856	0.4848	-0.02213	0.9494	0.5054	0.3035	0.407	0.2869
246998_at	AT5G67370	similar to unknown protein [Arabidopsis thaliana] (T	-0.6461	0.0211	0.0855	-0.5547	0.0341	0.0912	-0.2577	0.1864	0.2033	-0.1663	0.3621	0.2679
246999_at	AT5G67440	phototropic-responsive NPH3 family protein	-0.2366	0.0966	0.1796	-0.1466	0.2512	0.2647	-0.4004	0.0012	0.0187	-0.3105	0.0031	0.0179
247000_at	AT5G67380	CKA1 (CASEIN KINASE ALPHA 1); kinase	0.4079	0.0139	0.0722	0.5488	0.0049	0.0422	-0.7318	0.0017	0.0205	-0.5909	0.0037	0.0199
247001_at	AT5G67300	ATNRAMP4 (Arabidopsis natural resistance-associ	0.3539	0.0577	0.1376	0.398	0.0413	0.1009	-0.3614	0.0544	0.0993	-0.3173	0.0772	0.1026
247002_at	AT5G67320	WD-40 repeat family protein	0.5595	0.0204	0.0841	0.5857	0.0175	0.0686	-0.3423	0.0848	0.1282	-0.3161	0.103	0.1228
247003_at	AT5G67560	similar to unknown protein [Arabidopsis thaliana] (T	-0.2767	0.7426	0.5096	-0.7018	0.4223	0.3517	0.9837	0.2789	0.2575	0.5586	0.5165	0.3322
247004_at	AT5G67570	EMB1408 (EMBRYO DEFECTIVE 1408)	1.2426	0.3404	0.3455	0.7846	0.5322	0.397	-2.1809	0.1024	0.1428	-2.6389	0.063	0.0911
247005_at	AT5G67520	adenylylsulfate kinase, putative	-0.3238	0.4018	0.3761	-0.5578	0.1818	0.2211	0.105	0.6906	0.428	-0.129	0.6269	0.3727
247006_at	AT5G67490	similar to unnamed protein product [Vitis vinifera] (G	0.4408	0.0074	0.0578	0.7609	0.001	0.0291	0.2691	0.0609	0.106	0.5353	0.003	0.0178
247007_at	AT5G67500	porin, putative	0.09466	0.5296	0.433	0.07728	0.6046	0.425	0.5078	0.0211	0.0584	0.4904	0.0236	0.0502
247008_at	AT5G67560	ATARLA1D (ADP-ribosylation factor-like A1D); GTF	0.0587	0.6784	0.4855	0.2067	0.191	0.2268	-0.04811	0.733	0.4426	0.09993	0.4895	0.3217
247009_at	AT5G67600	unknown protein	0.3272	0.2961	0.321	0.7507	0.0511	0.1122	1.1401	0.0037	0.0268	1.5536	0.0011	0.0126
247010_at	AT5G67510	60S ribosomal protein L26 (RPL26B)	0.1961	0.5621	0.4456	0.3508	0.3217	0.3041	-0.1119	0.5808	0.3911	0.04287	0.8294	0.437
247011_at	AT5G67590	FRO1 (FROSTBITE1)	-0.1164	0.2704	0.3056	0.05242	0.5958	0.4217	0.5826	0.0031	0.0249	0.7514	0.0012	0.0127
247012_at	AT5G67610	ATTRB1/TRB2 (TELOMERE REPEAT BINDING FA	0.0177	0.8632	0.5418	0.14	0.2199	0.2458	-0.4208	0.012	0.0435	-0.263	0.0525	0.0817
247013_at	AT5G67480	BT4 (BTB AND TAZ DOMAIN PROTEIN 4); protein	0.9435	0.2632	0.3016	0.938	0.2656	0.2729	-0.5363	0.0166	0.0514	-0.5417	0.016	0.0404
247014_at	AT5G67630	DNA helicase, putative	0.7605	0.0346	0.1075	0.6041	0.0667	0.1292	-0.4262	0.1206	0.1567	-0.5826	0.0547	0.0837
247015_at	AT5G66960	prolyl oligopeptidase family protein	0.1783	0.4778	0.4059	0.1893	0.4787	0.4371	-0.2421	0.5495	0.379	0.1254	0.7622	0.4144
247016_at	AT5G66970	GTP binding	0.5729	0.7	0.4925	-1.4132	0.3647	0.3251	1.7033	0.2856	0.261	-0.2827	0.848	0.4423
247017_at	AT5G66980	transcriptional factor B3 family protein	0.4949	0.2182	0.274	-0.6853	0.1134	0.1702	0.8347	0.0343	0.0757	-0.3455	0.2614	0.2185
247018_at	AT5G67000	DNA binding / transcription factor	0.7698	0.4611	0.4035	0.8947	0.3975	0.3403	0.7531	0.4702	0.3477	0.8779	0.4056	0.2864
247019_at	AT5G67010	AP2 domain-containing transcription factor, putative	0.5034	0.6637	0.4806	0.9151	0.4423	0.3605	0.8462	0.4287	0.3291	1.2579	0.261	0.2184
247020_at	AT5G67020	similar to unknown protein [Arabidopsis thaliana] (T	1.602	0.1321	0.2106	-0.8616	0.3675	0.3263	0.2611	0.7737	0.4555	-2.2025	0.0604	0.0888
247021_at	AT5G67040	similar to unknown protein [Arabidopsis thaliana] (T	-0.6292	0.2193	0.2747	-0.3482	0.4658	0.3703	0.2446	0.6018	0.3989	0.5257	0.2909	0.234
247022_at	AT5G67050	lipase class 3 family protein	-0.4871	0.1134	0.1951	-0.6398	0.0567	0.1184

247090_at	AT5G66370	metal ion binding	-1.0423	0.4754	0.41	0.4318	0.7608	0.478	-0.8308	0.531	0.3717	0.6433	0.624	0.3715
247091_at	AT5G66390	peroxidase 72 (PER72) (P72) (PRXR8)	0.444	0.6451	0.4748	-0.284	0.7663	0.4793	0.137	0.8774	0.486	-0.591	0.5175	0.3326
247092_at	AT5G66380	ATFOLT1 (ARABIDOPSIS THALIANA FOLATE TR	0.6599	0.0099	0.0638	0.6409	0.011	0.0563	-0.7297	0.006	0.0321	-0.7487	0.0055	0.0231
247093_at	AT5G66350	SHI (SHORT INTERNODES); transcription factor	0.4172	0.2706	0.3057	1.0448	0.0329	0.0899	-0.24	0.5033	0.3606	0.3877	0.301	0.2391
247094_at	AT5G66280	GMD1 (GDP-D-MANNOSE 4,6-DEHYDRATASE 1)	2.0479	0.056	0.1359	-0.91	0.3017	0.2923	1.2594	0.1765	0.1962	-1.6985	0.0915	0.114
247095_at	AT5G66400	RAB18 (RESPONSIVE TO ABA 18)	0.4736	0.5168	0.428	1.3079	0.1214	0.1767	-0.6058	0.0801	0.1238	0.2285	0.4286	0.2962
247096_at	AT5G66430	S-adenosyl-L-methionine:carboxyl methyltransferas	0.09491	0.8481	0.5379	-0.5351	0.3136	0.2992	-0.3978	0.4402	0.3341	-1.0277	0.0914	0.114
247097_at	AT5G66460	(1-4)-beta-mannan endohydrolase, putative	0.2628	0.2486	0.2928	-0.04281	0.8368	0.5007	-0.6868	0.0243	0.0632	-0.9925	0.007	0.0261
247098_at	AT5G66470	GTP binding / RNA binding	-0.3051	0.1877	0.2539	-1.0409	0.0056	0.0434	0.5472	0.0466	0.0905	-0.1886	0.3822	0.2767
247099_at	AT5G66500	pentatricopeptide (PPR) repeat-containing protein	0.2477	0.8277	0.5318	2.893	0.0534	0.1146	-0.5735	0.6193	0.4044	2.0718	0.124	0.1377
247100_at	AT5G66520	pentatricopeptide (PPR) repeat-containing protein	-0.7635	1.00E-04	0.0312	-0.5722	2.00E-04	0.0249	-0.6546	1.00E-04	0.0118	-0.4632	5.00E-04	0.0093
247101_at	AT5G66530	aldose 1-epimerase family protein	-0.2133	0.2866	0.3152	-0.6716	0.018	0.0694	0.4102	0.0722	0.1168	-0.04812	0.7899	0.4257
247102_at	AT5G66550	Maf family protein	-0.7844	0.0405	0.116	-0.5069	0.1258	0.1798	0.1918	0.5021	0.3603	0.4693	0.1458	0.152
247103_at	AT5G66610	zinc ion binding	0.8389	0.0352	0.1084	0.01903	0.9468	0.5312	-0.7395	0.0509	0.0956	-1.5974	0.004	0.0203
247104_at	AT5G66620	LIM domain-containing protein	-0.9047	0.1992	0.2619	-0.358	0.576	0.4142	-0.7171	0.0256	0.065	-0.1704	0.4562	0.3085
247105_at	AT5G66630	LIM domain-containing protein	1.1963	0.0259	0.093	1.2977	0.0199	0.0723	-1.0335	0.0405	0.0834	-0.9321	0.0544	0.0834
247106_at	AT5G66640	transducin family protein / WD-40 repeat family prot	0.2676	0.1855	0.2522	0.03809	0.8313	0.4992	-0.6185	0.021	0.0583	-0.848	0.0072	0.0264
247107_at	AT5G66040	STR16 (SULFURTRANSFERASE PROTEIN 16)	-0.3553	0.0524	0.1314	-0.6527	0.0074	0.0485	-0.2416	0.137	0.1691	-0.539	0.0144	0.0381
247108_at	AT5G66160	JR700 (Arabidopsis thaliana receptor homology reg	0.1471	0.4764	0.4102	-0.06829	0.7339	0.4695	-0.519	0.0503	0.095	-0.7344	0.0173	0.042
247109_at	AT5G66570	ATPBKS (PHYTOSULFOKINE 5 PRECURSOR); gr	-0.4538	0.1463	0.2223	-0.25	0.3775	0.3308	0.9015	0.003	0.0248	1.1053	0.0014	0.0135
247110_at	AT5G65830	leucine-rich repeat family protein	-0.1776	0.3167	0.3325	-0.7381	0.009	0.0518	0.3855	0.0563	0.1012	-0.1751	0.2932	0.2352
247111_at	AT5G65960	unknown protein	0.2647	0.1427	0.2197	0.4907	0.0279	0.0832	0.5368	0.0211	0.0584	0.7617	0.0063	0.0247
247112_at	AT5G65950	binding	0.4958	0.0027	0.0426	0.4999	0.0026	0.0342	-0.9019	3.00E-04	0.0134	-0.8979	3.00E-04	0.0082
247113_at	AT5G65960	similar to CM0216.310.nc [Lotus japonicus] (GB:BA	0.399	0.0408	0.1163	0.6573	0.008	0.0498	-0.5864	0.0106	0.0408	-0.3281	0.0643	0.0922
247114_at	AT5G65910	BSD domain-containing protein	0.2702	0.3348	0.3428	0.3095	0.2778	0.2796	0.4731	0.1274	0.1621	0.5124	0.1062	0.1248
247115_at	AT5G65930	ZW9 (ZWICHEL); calmodulin binding / microtubule r	0.2746	0.0316	0.103	0.4385	0.0066	0.0461	-0.7648	0	0.0092	-0.6008	1.00E-04	0.0061
247116_at	AT5G65970	MLO10 (MILDEW RESISTANCE LOCUS O 10); ca	0.3041	0.7294	0.5024	0.8324	0.3673	0.3263	-0.07132	0.9348	0.5021	0.4569	0.6069	0.3657
247117_at	AT5G65940	CHY1 (BETA-HYDROXYISOBUTYRYL-COA HYDI	0.3911	0.0366	0.1104	-0.1205	0.3954	0.3392	-0.4228	0.0289	0.069	-0.9344	0.0018	0.0148
247118_at	AT5G65890	ACR1 (ACT DOMAIN REPEAT 1)	-0.5538	0.1244	0.2043	-0.825	0.0446	0.1046	-0.06991	0.7048	0.433	-0.3411	0.118	0.1334
247119_at	AT5G65900	DEAD/DEAH box helicase, putative	0.2797	0.2595	0.2994	-0.2171	0.366	0.3256	-0.3639	0.1629	0.1872	-0.8607	0.0156	0.0399
247120_at	AT5G65980	amino acid transporter family protein	0.1663	0.3326	0.3416	-0.0048	0.9762	0.5384	-0.00569	0.9589	0.5074	-0.1768	0.1633	0.1633
247121_at	AT5G66010	RNA binding	0.4294	0.0465	0.1241	0.2782	0.1389	0.1898	-0.4316	0.0458	0.0896	-0.5828	0.0181	0.0432
247122_at	AT5G66020	ATSAC1B/IBS2 (IMPAIRED IN BABA-INDUCED S	0.8114	0.355	0.3523	-0.7317	0.3994	0.3409	1.0124	0.0554	0.1004	-0.5307	0.2333	0.2033
247123_at	AT5G66060	similar to wound-responsive family protein [Arabid	0.0361	0.8245	0.5309	-0.09251	0.5768	0.4147	-0.1498	0.3697	0.3026	-0.2784	0.1337	0.1442
247124_at	AT5G66060	oxidoreductase, 2OG-Fe(II) oxygenase family protei	0.0909	0.6183	0.4658	-0.2057	0.2893	0.2862	-0.08046	0.4286	0.3291	-0.3771	0.0146	0.0384
247125_at	AT5G66070	zinc finger (C3HC4-type RING finger) family protein	0.5164	0.0718	0.1545	0.2747	0.2654	0.2728	-0.2227	0.3361	0.2864	-0.4643	0.085	0.109
247126_at	AT5G66080	protein phosphatase 2C family protein / PP2C fami	0.2439	0.7494	0.6085	-0.08285	0.913	0.5222	0.04882	0.9382	0.503	-0.2779	0.663	0.3852
247127_at	AT5G66100	La domain-containing protein	-0.137	0.665	0.481	-0.5266	0.1472	0.1961	0.0246	0.8957	0.4913	-0.365	0.1069	0.1253
247128_at	AT5G66110	metal ion binding	0.6415	0.173	0.2435	0.4662	0.2951	0.2893	1.1589	0.0207	0.0579	0.9836	0.0346	0.0629
247129_at	AT5G66150	glycosyl hydrolase family 38 protein	1.3578	0.3455	0.3476	-1.0293	0.4634	0.3695	1.7558	0.2392	0.2348	-0.6313	0.6454	0.3792
247130_at	AT5G66180	similar to NOL1/NOP2/sun family protein [Arabidop	0.5379	0.02	0.0834	0.6111	0.0131	0.0611	-0.5259	6.00E-04	0.0157	-0.4527	0.001	0.0121
247131_at	AT5G66190	ATLFNR1 (LEAF FNR 1); NADPH dehydrogenase/	-0.2064	0.134	0.2124	-0.7035	0.0031	0.0359	0.5671	0.0067	0.0336	0.06994	0.5596	0.3487
247132_at	AT5G66200	armadillo/beta-catenin repeat family protein	0.2794	0.4041	0.3773	-0.09268	0.7727	0.4813	0.174	0.1957	0.2091	-0.1981	0.152	0.1561
247133_at	AT5G66220	chalcone isomerase	-0.419	0.6577	0.4782	1.6632	0.1307	0.1833	-0.5221	0.5835	0.392	1.56	0.1498	0.1544
247134_at	AT5G66230	similar to unknown protein [Arabidopsis thaliana] (T	0.0818	0.8336	0.5335	0.5747	0.1904	0.2266	0.2828	0.4816	0.3518	0.7757	0.1007	0.1211
247135_at	AT5G66260	auxin-responsive protein, putative	0.06168	0.9606	0.6675	0.07419	0.9435	0.5302	0.8274	0.4474	0.3373	0.8499	0.4361	0.2997
247136_at	AT5G66170	similar to unknown protein [Arabidopsis thaliana] (T	0.3138	0.1497	0.2254	0.6605	0.02	0.0724	-0.6923	0.0172	0.0524	-0.3456	0.1216	0.1361
247137_at	AT5G66210	CPK28 (calcium-dependent protein kinase 28); calm	0.4501	0.2344	0.284	0.2489	0.4825	0.3772	-0.1621	0.1452	0.1755	-0.3634	0.0155	0.0397
247138_at	AT5G66120	3-dehydroquinate synthase, putative	0.2319	0.1483	0.2241	0.03776	0.7855	0.4848	0.5175	4.00E-04	0.0145	0.3232	0.0022	0.0157
247139_at	AT5G66090	similar to unnamed protein product [Vitis vinifera] (G	-0.1765	0.1641	0.2368	-0.3358	0.0318	0.0885	0.3452	0.0207	0.058	0.1859	0.1167	0.1325
247140_at	AT5G66250	kinectin-related	0.36	0.1019	0.1845	0.527	0.0364	0.0942	-0.09768	0.1709	0.1926	0.06931	0.3024	0.2399
247141_at	AT5G65560	pentatricopeptide (PPR) repeat-containing protein	0.01326	0.9663	0.6688	0.06956	0.8252	0.4975	-0.5599	0.1306	0.1643	-0.5036	0.163	0.1631
247142_at	AT5G65570	pentatricopeptide (PPR) repeat-containing protein	0.3051	0.4668	0.4059	-0.02664	0.9474	0.5313	0.5257	0.2385	0.2344	0.194	0.6364	0.3759
247143_at	AT5G65580	unknown protein	1.5473	0.137	0.215	0.2064	0.8167	0.495	0.7404	0.4246	0.3274	-0.6005	0.5112	0.3302
247144_at	AT5G65590	Def-type zinc finger domain-containing protein	-1.2478	0.1955	0.2695	0.3788	0.6619	0.4458	-2.4377	0.0387	0.0812	-0.8111	0.37	0.2713
247145_at	AT5G65600	legume lectin family protein / protein kinase family p	0.1328	0.0376	0.1119	1.8582	0.1435	0.1934	1.3819	0.1107	0.1489	0.1073	0.8817	0.4519
247146_at	AT5G65610	unknown protein	-0.9699	0.3139	0.3308	-0.3386	0.7083	0.4616	0.5017	0.4768	0.3502	1.1329	0.1513	0.1556
247147_at	AT5G65630	GTE7 (GLOBAL TRANSCRIPTION FACTOR GRO	-0.4218	0.1881	0.254	-0.29	0.337	0.312	-0.4919	0.0256	0.065	-0.3601	0.064	0.0921
247148_at	AT5G65670	IAA9 (indoleacetic acid-induced protein 9); transcrip	0.1426	0.023	0.0886	0.4523	3.00E-04	0.0249	0.2278	0.0046	0.0288	0.5376	2.00E-04	0.0073
247149_at	AT5G65660	hydroxyproline-rich glycoprotein family protein	0.5242	0.1258	0.2052	0.3396	0.2792	0.2805	0.3651	0.0582	0.1032	0.1806	0.2633	0.2194
247150_at	AT5G65650	similar to unknown protein [Arabidopsis thaliana] (T	0.4417	0.0316	0.1029	-0.03064	0.833	0.4996	0.4162	0.0378	0.0804	-0.0561	0.7015	0.3978
247151_at	AT5G65640	BHLH093 (BETA HLH PROTEIN 93); DNA binding	-0.1981	0.339	0.3449	-0.09543	0.6289	0.434	-0.02367	0.9031	0.4932	0.07901	0.6876	0.393
247152_at	AT5G65620	peptidase M3 family protein / thimet oligopeptidase	0.4777	0.0038	0.0461	0.2234	0.0474	0.108	-0.06099	0.4831	0.3525	-0.3153	0.0162	0.0407
247153_at	AT5G65610	BAM1 (big apical meristem 1); ATP binding / kinase	-0.4351	0.2509	0.2939	-0.6281	0.1249	0.1792	-0.024	0.8733	0.4851	-0.217	0.1992	0.1845
247154_at	AT5G65710	HSL2 (HAESA-LIKE 2); ATP binding / kinase/ protein	-0.3102	0.1023	0.1849	-0.4106	0.049	0.1097	0.506	0.0149	0.0487	0.4055	0.0305	0.0587
247155_at	AT5G65750	2-oxoglutarate dehydrogenase E1 component, putat	0.4706	0.1745	0.2445	0.4641	0.1793	0.2191	-0.6666	0.0652	0.1101	-0.6731	0.0635	0.0916
247156_at	AT5G65760	serine carboxypeptidase S28 family protein	0.528	0.0124	0.0687	0.4298	0.0244	0.0763	0.06558	0.2408	0.2355	-0.03265	0.531	0.3384
247157_at	AT5G65770	LINC4 (LITTLE NUCLEI4)	0.02897	0.908	0.5535	-0.07074	0.7787	0.4832	-0.3933	0.17	0.1919	-0.493	0.1043	0.1236
247158_at	AT5G65780	ATBCAT-5; branched-chain-amino-acid transamina	-0.6145	0.0519	0.1307	-0.4524	0.1139	0.1704	-0.3273	0.2183	0.2226	-0.1651	0.5025	0.3267
247159_at	AT5G65800	ACS5 (ACC SYNTHASE 5); 1-aminocyclopropane-	0.3799	0.4371	0.3925	-1.7414	0.2002	0.2329	1.5318	0.2489	0.2404	-1.1895	0.3543	0.2646
247160_at	AT5G65820	pentatricopeptide (PPR) repeat-containing protein	-1.7638	0.1901	0.2555	-0.2818	0.8136	0.4942	-1.0415	0.4047	0.3184	0.4405	0.7139	0.4022
247161_at	AT5G65810	similar to unknown protein [Arabidopsis thaliana] (T	-0.3086	0.1193	0.1997	-0.6609	0.0133	0.0615	0.5444	0.0252	0.0644	0.1921	0.286	0.2314
247162_at	AT5G65730	xyloglucan:xyloglucosyl transferase, putative / xylog	-1.5104	0.0024	0.0421	-2.0534	8.00E-04	0.0276	0.6985	0.0061	0.0325	0.1554	0.3042	0.2408
247163_at	AT5G65685	soluble glycogen synthase-related	-0.2541	0.0418	0.1176	-0.3149	0.0216	0.0747	-0.519	0.002	0.0211	-0.5798	0.0013	0.0133
247164_at	AT5G65720	ATNFS1/ATNIFS1/NFS1/NIFS1 (ARABIOPSIS TH	-0.04592	0.746	0.5078	0.07428	0.6044	0.425	-0.47	0.0237	0.0624	-0.3498	0.0573	0.0862
247165_at	AT5G65790	MYB88 (myb domain protein 88); DNA binding / tra	0.827	0.6451	0.4748	0.9145	0.6116	0.4274	-1.2569	0.4918	0.3564	-1.1694	0.5207	0.3341
247166_at	AT5G65840	similar to antioxidant/ oxidoreductase [Arabidopsis t	-0.3205	0.035	0.1082	-0.8284	0.0013	0.0305	0.2111	0.103	0.1433	-0.2968	0.0415	0.0707
247167_at	AT5G65850	F-box family protein	0.7274	0.0015	0.038	0.748	0.0014	0.0312	0.1393	0.1996	0.2116	0.1598	0.153	0.1568
247168_at	AT5G65860	ankyrin repeat family protein	-0.2181	0.507	0.4239	0.06148	0.8474	0.5037	-0.7808	0.002	0.0214	-0.5012	0.0102	0.0316
247169_at	AT5G65520	binding	0.2268	0.3173	0.3328	0.2535	0.2709	0.2759	-0.2274	0.3052	0.2713	-0.2007	0.3585	0.2663
247170_at	AT5G65530	protein kinase, putative	-1.8648	0.1589	0.2326	-2.3946	0.0906	0.1518	0.5615	0.5944	0.3962	0.03176	0.9755	0.477
247171_at	AT5G65440	similar to unknown protein [Vitis vinifera] (G	0.03748	0.8862	0.5474	-0.06521	0.804	0.4909	0.2923	0.2592	0.246	0.1896	0.4422	0.3024
247172_at	AT5G65550	UDP-glucuronosyl/UDP-glucosyl transferase family	0.1193	0.7832	0.5187	0.467	0.3135	0.2992	-0.03611	0.9333	0.5016	0.3116	0.485	0.3196
247173_at	AT5G65260	polyadenylate-binding protein family protein / PABP	0.02377	0.8595	0.5409	0.2167	0.1605	0.2063	-0.2104	0.1702	0.192	-0.0175	0.8962	0.4561
247174_at	AT5G65250	similar to unnamed protein product [Vitis vinifera] (G	1.504	0.3736	0.3612	-0.281	0.1349	0.1868	0.06427	0.282	0.2592	-0.3672	0.0021	0.0154
247175_at	AT5G65280	GCL1 (GCR2-LIKE 1); catalytic	0.6968	0.0027	0.0427	0.8004	0.0016	0.0317	-0.01074	0.9232	0.4987	0.09291	0.4246	0.2944
247176_at	AT5G65110	ACX2 (ACYL-COA OXIDASE 2); acyl-CoA oxidase	0.5269	0.0539	0.1332	0.5967	0.0376	0.096	-0.0441	0.6869	0.4267	0.02565	0.8133	0.4326
247177_at	AT5G65300	unknown protein	-0.8835	0.0362	0.1097	-0.6826	0.0747	0.1371	0.3505	0.1986	0.211	0.5514	0.0727	0.0989
247178_at	AT5G65205	short-chain dehydrogenase/reductase (SDR) family	0.2464	0.3337	0.3422	-0.08838	0.7137	0.4633	0.152	0.5351	0.3733	-0.1827	0.4611	0.3105
247179_at	AT5G65320	basic helix-loop-helix (bHLH) family protein	0.2455	0.5751	0.4508	0.1437	0.7393	0.471	-0.1884	0.6644	0.4193	-0.2902	0.5111	0.3302
247180_at	AT5G65350	histone H3	-0.00192	0.9987	0.6763	0.9827	0.4101	0.346	-0.8364	0.2641	0.2489	0.1482	0.8294	0.437
247181_at	AT5G65370	epsin N-terminal homology (ENTH) domain-contain	-0.1878	0.4893	0.4156	-0.868	0.0246	0.0787	0.1825	0.501	0.3599	-0.4977	0.1141	0.1306
247182_at	AT5G65410	ATHB25/ZFHD2 (ZINC FINGER HOMEODOMAIN	-0.05951	0.8438	0.5369	0.01894	0.9499	0.5319	-0.1936	0.2866	0.2616	-0.1152	0.5054	0.3279
247183_at	AT5G65440	similar to unknown protein [Arabidopsis thaliana] (T	0.2691	0.0556	0.1354	0.8061	0.0368	0.0947	-0.5737	0.0196	0.0563	-0.4668	0.0374	0.0681
247184_at	AT5G65450	ubiquitin carboxyl-terminal hydrolase family protein	0.1667	0.5623	0.4457	-0.02653	0.9248	0.5253	-0.6842	0.0579	0.1028	-0.8774	0.0278	0.0556
247185_at	AT5G65460	kinesin motor protein-related	-0.3889	0.0269	0.0948	-0.5372	0.0092	0.0524	-0.7809	0.0024	0.0228	-0.9292	0.0012	0.0129
247186_at	AT5G65470	similar to unknown protein [Arabidopsis thaliana] (T	-0.7533	0.0889	0.1729	-1.139	0.0277	0.083	0.3272	0.196	0.2092	-0.05849	0.7954	0.4275
247187_at	AT5G65490	identical to SGT1 protein homolog AtSg65490 [Arab	0.4615	0.0599	0.14	0.4947	0.0493	0.1101	-0.01401	0.9408	0.5037	0.0192	0.919	0.4625
247188_at	AT5G65430	GRF8 (GENERAL REGULATORY FACTOR 8); pro	-0.06311	0.7148	0.4976	0.03243	0.8501	0.5044	-0.03202	0.8188	0.4695	0.06353	0.6529	0.3818
247189_at	AT5G65390	AGP7 (Arabinogalactan protein 7)	-0.6359	0.0486	0.1499	-0.7981	0.4037	0.3429	0.5096	0.0484	0.0925	0.3475	0.1281	0.1402
247190_at	AT5G65420	CYCD4;1 (CYCLIN D4;1); cyclin-dependent protein	0.04265	0.9173	0.5563	-0.1531	0.7117	0.4627	-0.4396	0.0863	0.1296	-0.55	0.0472	0.0765
247191_at	AT5G65310	ATHB5 (ARABIDOPSIS THALIANA HOMEOBOX P	-0.4788	0.0832	0.1669	0.3169	0.203	0.2347	-0.8208	0.0069	0.0339	-0.02508	0.8835	0.4525
247192_at	AT5G65360	histone H3	-0.1986	0.5087	0.4245	0.02901	0.9208	0.5242	0.9877	0.0187	0.0547	1.2153	0.0092	0.03
247193_at	AT5G65380	ripening-responsive protein, putative	0.2213	0.3532	0.3514	0.1108	0.6271	0.4334	-0.9585	0.002	0.0211	-1.069	0.0013	0.0133
247194_at	AT5G65480	similar to unknown protein [Arabidopsis thaliana] (T	0.4615	0.2504	0.2937	0.2976	0.4353	0.3577	0.146	0.3551	0.2957	-0.01785	0.9045	0.4586
247195_at	AT5G65500	protein kinase family protein	1.2342	0.3114	0.3295	0.8085	0.4905	0.3805	0.8393	0.4752	0.3496	0.4136	0.7778	0.4033
247196_at	AT5G65510	AIL7 (AINTEGUMENTA-LIKE 7); DNA binding / tra	-0.1347	0.8392	0.5351	-0.00333	0.996	0.5432	-2.4178	0.0177	0.0533	-2.2864	0.0213	0.0474
247197_at	AT5G65240	leucine-rich repeat family protein / protein kinase fa	0.105	0.6057	0.4616	0.9223	0.008	0.0497	-0.8624	0.0047	0.0292	-0.04508	0.7812	0.4233
247198_at	AT5G65260	LMBR1 integral membrane family protein	0.1179	0.5186	0.4287	-0.02861	0.8721	0.5105	-0.2841	0.1636	0.1877	-0.4306	0.0612	0.0896
247199_at	AT5G65210	TGA1; DNA binding / calmodulin binding / transcript	0.8388	0.014	0.0723	1.1361	0.0048	0.0421	-0.4673	0.0149	0.0487	-0.17	0.2108	0.1913
247200_at	AT5G65120	similar to unknown protein [Arabidopsis thaliana] (T	-0.5197	0.3804	0.3646	-0.7053	0.2523	0.2654	0.2665	0.64	0.4111	0.08095	0.8855	0.4531
247201_at	AT5G65220	ribosomal protein L29 family protein	-0.4989	0.0038	0.0463	-0.4296	0.0066	0.0461	-0.1341	0.0051	0.0957	-0.06479	0.2537	0.2145
247202_at	AT5G65270	AtRABA4a (Arabidopsis Rab GTPase homolog A4a	0.1597	0.2841	0.3139	0.3325	0.0618	0.1236	0.3648	0.0202	0.0571	0.5375	0.0053	0.0227
247203_at	AT5G65180	similar to unknown protein [Arabidopsis thaliana] (T	0.1415	0.4186	0.3841	0.1033	0.5486	0.4032	-0.1918	0.2381	0.2342	0.05305	0.721	0.4043
247204_at	AT5G64990	AtRABH1a (Arabidopsis Rab GTPase homolog H1a	-0.6671	0.0466	0.1242	0.09644	0.7019	0.4597	-0.1187	0.6392	0.4108	0.6448	0.0514	0.0807
247205_at	AT5G64890	PROPEP2 (Elicitor peptide 2 precursor)	0.9095	0.4819	0.4127	1.4566	0.2843	0.2834	0.8648	0.5023	0.3604	1.4059	0.2973	0.2372
247206_at	AT5G64960	mitochondrial transcription termination factor-relate	0.06552	0.8457	0.5373	-0.4534	0.2242	0.248	0.4462	0.482	0.352	-0.2745	0.4334	0.2982
247207_at	AT5G65000	nucleotide-sugar transporter family protein	0.5961	0.0298	0.1003	0.1099	0.575	0.4139	-0.1184	0.5474	0.3783	-0.6046	0.0285	0.0564
247208_at	AT5G64870	similar to unknown protein [Arabidopsis thaliana] (T	1.2697	0.0667	0.1482	1.3477	0.0567	0.1184	0.08477	0.8438	0.4768	0.1628	0.7071	0.3998
247209_at	AT5G64830	programmed cell death 2 C-terminal domain-contain	0.068322	0.5617	0.4455	0.4015	0.0206	0.0732	-0.02888	0.2481	0.0561	0.101	0.045	0.0968
247210_at	AT5G65020	ANNAT2 (ANNEXIN ARABIDOPSIS 2); calcium ion	0.6992	0.0025	0.0424	0.5356	0.0067	0.0462	0.2868	0.0136	0.0464	0.1233	0.1446	0.1512
247211_at	AT5G64880	unknown protein	0.1841	0.2524	0.2949	0.5938	0.0125	0.06	-0.3939	0.0087	0.0375	0.01581	0.857	0.445
247212_at	AT5G64850	senescence-associated protein-related	-1.0359	0.0918	0.1757	-0.1649	0.7429	0.4724	-0.4846	0.2314	0.2301	0.3864	0.3238	0.2901
247213_at	AT5G64900	ATPEP1/PROPEP1 (Elicitor peptide 1 precursor)	-0.8347	0.0794	0.1624	-0.2296	0.5549	0.4066	0.5331	0.2094	0.2174	1.1383	0.0332	0.0615
247214_at	AT5G64850	similar to unknown protein [Arabidopsis thaliana] (T	-1.3453	0.0102	0.064	-0.9926	0.0277	0.0831	0.9853	0.0063	0.0328	1.338	0.002	0.0154
247215_at	AT5G64905	PROPEP3 (Elicitor peptide 3 precursor)	0.2303	0.8053	0.5255	1.0677	0.2892	0.2862	1.0093	0.2024	0.2132	1.8466	0.0495	0.0788
247216_at	AT5G64860	DPE1 (DISPROPORTIONATING ENZYME); 4-alph	0.8464	0.0123	0.0687	0.611	0.0353	0.0927	-0.6493	0.0293	0.0696	-0.8846	0.0106	0.0322
247217_s_at	AT5G65050,AT5G65060	[AT5G65050, AGL31 (AGAMOUS LIKE MADS-BO	-2.2601	0.4978	0.4195	-0.1877	0.6195	0.4304	-0.1696	0.5898	0.3947	-0.09722	0.7542	0.4149
247218_at	AT5G65010	ASN2 (ASPARAGINE SYNTHETASE 2); glutamin	-0.8922	0.0422	0.1181	-0.9023	0.0408	0.1002	-0.4752	0.024	0.0629	-0.4852	0.0225	0.0487
247219_at	AT5G64920	CIP8 (COP1-INTERACTING PROTEIN 8); protein b	0.3931	0.0667	0.1484	0.13	0.4548	0.3659	-0.2498	0.0682	0.1133	-0.5129	0.007	0.0261
247220_at	AT5G64960	CDKC.2 (CYCLIN-DEPENDENT KINASE C.2); kina	0.3333	0.0313	0.1027	0.2865	0.0491	0.1097	-0.2054	0.1156	0.1528	-0.2522	0.0697	0.0967
247221_at	AT5G64813	LIP1 (LIGHT INSENSITIVE PERIOD1); GTPase	-0.06385	0.668	0.482	-0.158	0.3167	0.3011	-0.1365	0.2326	0.2309	-0.2306	0.0765	0.102
247222_at	AT5G64840	ATGCN5 (Arabidopsis thaliana general control non-	-0.3

247290_at	AT5G64450	similar to unknown protein [Arabidopsis thaliana] (T	0.5702	0.191	0.2561	0.2281	0.5634	0.4096	-1.0915	0.0396	0.0823	-1.4335	0.0168	0.0414
247291_at	AT5G64480	similar to hypothetical protein MrBRAFT_AC14839	0.2159	0.3481	0.349	0.2693	0.2559	0.2678	-0.03925	0.8563	0.4802	0.01416	0.9478	0.4703
247292_at	AT5G64490	binding	-0.6184	0.0574	0.1373	0.7038	0.0396	0.0986	-0.7446	0.0334	0.0747	0.5777	0.069	0.0962
247293_at	AT5G64510	similar to unnamed protein product [Vitis vinifera] (G	1.709	0.0028	0.0431	1.5406	0.0041	0.0399	0.181	0.0436	0.0872	0.01256	0.8498	0.4427
247294_at	no_match	no_match	0.01445	0.9781	0.5717	0.6544	0.2569	0.2683	-0.1525	0.7735	0.4554	0.4874	0.3808	0.2761
247295_at	AT5G64180	similar to unnamed protein product [Vitis vinifera] (G	0.9118	0.0038	0.0463	0.5079	0.0286	0.084	-0.2453	0.1809	0.1993	-0.6492	0.0128	0.0358
247296_at	AT5G64160	similar to unnamed protein product [Vitis vinifera] (G	0.2232	0.1792	0.2475	0.1151	0.4487	0.3634	0.5436	0.0167	0.0514	0.4355	0.0337	0.0621
247297_at	AT5G64100	peroxidase, putative	0.6474	0.4222	0.386	0.3477	0.6564	0.444	0.7706	0.3476	0.292	0.4709	0.5512	0.3455
247298_at	AT5G63840	RSW3 (RADIAL SWELLING 3); hydrolase, hydrolyz	0.6682	0	0.0312	0.4579	2.00E-04	0.0249	-0.00497	0.8814	0.4871	-0.2153	0.0023	0.0161
247299_at	AT5G63900	PHD finger family protein	-0.00647	0.9956	0.576	0.02335	0.984	0.5402	-0.873	0.47	0.3476	-0.8432	0.4842	0.3193
247300_at	AT5G63910	FCLY; prenylcysteine oxidase	0.6949	0.019	0.0819	0.3863	0.1019	0.161	0.1158	0.5414	0.3759	-0.1927	0.3295	0.2531
247301_at	AT5G63920	DNA topoisomerase III alpha, putative	-0.00344	0.9944	0.5756	-0.7811	0.1677	0.211	-0.127	0.798	0.4627	-0.9046	0.1231	0.1371
247302_at	AT5G63880	VPS20.1	1.1546	0.0168	0.0777	0.9628	0.03	0.0862	0.5597	0.1281	0.1626	0.3673	0.2769	0.2266
247303_at	AT5G63890	ATHDH (HISTIDINOL DEHYDROGENASE)	-0.1983	0.1008	0.1835	-0.2181	0.0796	0.1415	-0.07424	0.4708	0.348	-0.09411	0.3703	0.2714
247304_at	AT5G63850	AAP4 (amino acid permease 4); amino acid transm	-1.1398	0.0037	0.0459	-0.8051	0.0126	0.06	0.0795	0.5988	0.3977	0.4142	0.041	0.0701
247305_at	AT5G63905	unknown protein	0.2807	0.53	0.4331	0.6241	0.2013	0.2335	0.551	0.0273	0.0672	0.8948	0.0053	0.0226
247306_at	AT5G63870	PP7 (protein phosphatase 7); protein serine/threon	-0.2059	0.0836	0.1673	-0.03072	0.7494	0.4747	-0.3603	0.016	0.0505	-0.1851	0.1082	0.1263
247307_at	AT5G63860	UVR8 (UVB-RESISTANCE 8)	0.3392	0.0397	0.115	0.2059	0.1421	0.1923	0.04884	0.6369	0.4101	-0.08449	0.4275	0.2957
247308_at	AT5G63930	leucine-rich repeat transmembrane protein kinase,	0.6269	0.0191	0.082	0.4353	0.0577	0.1193	-0.8054	0.0081	0.0362	-0.997	0.0038	0.0199
247309_at	AT5G63940	protein kinase family protein	-0.5636	0.0138	0.072	-0.1336	0.3769	0.3305	-0.602	0.0047	0.0292	-0.172	0.18	0.1733
247310_at	AT5G63950	CHR24 (chromatin remodeling 24); ATP binding / D	0.07255	0.7742	0.5161	0.6424	0.0531	0.1143	-0.1581	0.5402	0.3753	0.4118	0.1565	0.159
247311_at	no_match	no_match	0.2856	0.1528	0.2279	-0.02663	0.6774	0.5124	-0.05084	0.7175	0.4375	-0.3631	0.0504	0.0797
247312_at	AT5G63970	copine-related	0.4764	0.0365	0.1102	0.4915	0.0333	0.0903	-0.0372	0.8212	0.4701	-0.0221	0.8929	0.4551
247313_at	AT5G63980	SAL1 (FIERY1); 3'(2'),5'-bisphosphate nucleotidase	-0.2414	0.0729	0.1555	-0.2909	0.0435	0.1034	0.1243	0.1493	0.1785	0.07478	0.3438	0.2598
247314_at	AT5G64000	SAL2; 3'(2'),5'-bisphosphate nucleotidase/ inositol	0.2235	0	0.0312	2.9544	0	0.0249	0.1497	0.3125	0.2746	0.4807	0.0207	0.0466
247315_at	AT5G64010	similar to unnamed protein product [Vitis vinifera] (G	-0.2471	0.2403	0.2877	0.702	0.0173	0.0681	-0.2601	0.2205	0.2239	0.689	0.0184	0.0436
247316_at	AT5G64030	dehydration-responsive protein-related	0.2037	0.3639	0.3562	-0.1382	0.5257	0.3944	-0.04217	0.8426	0.4765	-0.3841	0.1259	0.1388
247317_at	AT5G64060	ANAC102 (Arabidopsis NAC domain containing pro	1.905	0.1282	0.2069	1.5093	0.2578	0.2688	0.4384	0.7212	0.439	-0.2427	0.8424	0.4407
247318_at	AT5G63990	3'(2'),5'-bisphosphate nucleotidase, putative / inosit	0.5548	0.1176	0.1983	0.5873	0.1031	0.162	0.4098	0.1601	0.1857	0.4422	0.1366	0.1459
247319_at	AT5G64050	ATERS/ERS/OVA3 (OVULE ABORTION 3); glutam	0.4728	0.2167	0.273	0.3142	0.3853	0.3344	0.5249	0.0863	0.1296	0.3663	0.1893	0.179
247320_at	AT5G64040	PSAN (photosystem I reaction center subunit PSI-N	0.8252	0.0064	0.0546	-0.8576	0.002	0.033	0.3761	0.0017	0.0205	0.1436	0.0485	0.0758
247321_s_at	AT5G64070;AT5G09350	[AT5G64070, phosphatidylinositol 4-kinase (PI4K)]	0.2743	0.0086	0.0604	0.2572	0.0107	0.0558	-1.048	0	0.0092	-1.0651	0	0.0055
247322_at	AT5G64090	similar to unknown protein [Arabidopsis thaliana] (T	-0.2545	0.0818	0.1655	-0.4053	0.0212	0.0741	0.1301	0.1609	0.1861	-0.02075	0.7976	0.4281
247323_at	AT5G64110	dentin sialophosphoprotein-related	0.5874	0.0264	0.0939	-0.1241	0.5079	0.3877	-0.2365	0.2076	0.2336	0.2373	0.2538	0.2145
247324_at	AT5G64190	similar to unknown protein [Arabidopsis thaliana] (T	0.402	0.6154	0.4646	0.3864	0.6287	0.434	0.06732	0.8275	0.472	0.0518	0.8667	0.4472
247325_at	AT5G64200	ATSC35 (ARABIDOPSIS THALIANA ARGININE/SE	0.1852	0.5048	0.4225	0.3505	0.2381	0.2567	-0.1761	0.237	0.2335	-0.01075	0.9365	0.4674
247326_at	AT5G64120	peroxidase, putative	2.3954	0.0595	0.1396	1.6326	0.1501	0.1981	0.1641	0.6997	0.4312	-0.598	0.2068	0.1889
247327_at	AT5G64120	peroxidase, putative	0.8716	0.0208	0.085	0.9027	0.0186	0.0704	0.3378	0.0567	0.1017	0.369	0.0441	0.0736
247328_at	AT5G64130	similar to unknown protein [Arabidopsis thaliana] (T	0.3636	0.0874	0.1713	0.4904	0.0385	0.0972	0.178	0.0819	0.1256	0.3048	0.0167	0.0413
247329_at	AT5G64150	methyltransferase family protein	-0.4601	0.1008	0.1835	-0.271	0.279	0.2804	-0.1494	0.5283	0.3706	0.03974	0.8633	0.4467
247330_at	AT5G63510	GAMMA CAL1 (GAMMA CARBONIC ANHYDRASE	0.1798	0.2877	0.316	0.35	0.0756	0.1379	-0.5093	0.0147	0.0483	-0.3391	0.0519	0.0811
247331_at	AT5G63530	ATFP3 (Arabidopsis thaliana farnesylated protein 3	0.5379	0.0584	0.1385	0.8672	0.0133	0.0615	0.3804	0.0139	0.047	0.7097	0.0015	0.0137
247332_at	AT5G63440	similar to hypothetical protein [Vitis vinifera] (GB:CA	-0.5909	0.0113	0.0666	-0.3429	0.0615	0.1232	0.226	0.1508	0.1794	0.484	0.022	0.0484
247333_at	AT5G63600	flavonol synthase, putative	0.178	0.8787	0.5462	0.1514	0.8966	0.5178	-0.5641	0.6335	0.4089	-0.5906	0.6181	0.3696
247334_at	AT5G63610	HEN3 (HUA ENHANCER 3); kinase	0.04514	0.83	0.5325	0.254	0.2668	0.2736	-0.5791	0.0424	0.0857	-0.3702	0.1334	0.1439
247335_at	AT5G63630	DEAD box RNA helicase, putative	0.3535	0.0628	0.1437	0.2811	0.1117	0.1687	0.2085	0.206	0.2154	0.1361	0.3805	0.276
247336_at	AT5G63640	VHS domain-containing protein / GAT domain-conta	0.3229	0.1431	0.22	0.3332	0.1338	0.1859	0.09489	0.6214	0.405	0.1052	0.5853	0.3582
247337_at	AT5G63660	LCR74/PDF2.5 (Low-molecular-weight cysteine-rich	-0.3182	0.786	0.5196	-0.9745	0.4242	0.3527	0.3629	0.7095	0.4346	-0.2934	0.7625	0.4176
247338_at	AT5G63680	pyruvate kinase, putative	1.972	6.00E-04	0.0325	0.9782	0.0012	0.0302	-0.09704	0.4637	0.3448	-0.316	0.0579	0.0866
247339_at	AT5G63690	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.9533	0.1875	0.2537	-0.6023	0.3725	0.3286	0.3854	0.5558	0.3811	-1.1701	0.123	0.137
247340_at	AT5G63700	zinc finger (C3HC4 type RING finger) family protein	-0.3297	0.1655	0.2378	-0.5798	0.0408	0.1001	-0.4433	0.004	0.0273	-0.6934	7.00E-04	0.0108
247341_at	AT5G63720	unknown protein	-0.6714	0.6495	0.4762	-0.6042	0.6817	0.4526	0.6817	-0.4113	0.7779	0.4565	-0.3458	0.813
247342_at	AT5G63730	IBR domain-containing protein	-1.2008	0.1298	0.2084	-0.5047	0.4686	0.3714	-0.4444	0.5201	0.367	0.2516	0.7105	0.401
247343_at	AT5G63740	zinc finger protein-related	-0.7135	0.2047	0.2651	-0.5613	0.2997	0.2912	-0.1817	0.7196	0.4383	-0.02949	0.9531	0.4718
247344_at	AT5G63750	IBR domain-containing protein	1.9076	0.087	0.1708	1.7906	0.1015	0.1608	-0.14143	0.827	0.4718	-0.2583	0.6917	0.3946
247345_at	AT5G63760	IBR domain-containing protein	0.4605	0.067	0.1487	0.6236	0.0278	0.0831	-0.6259	0.0274	0.0674	-0.4628	0.0661	0.0936
247346_at	AT5G63770	ATDGK2 (DIACYLGLYCEROL KINASE 2); diacylgl	-0.3234	0.1302	0.2087	-0.4737	0.0497	0.1104	-0.2294	0.2489	0.2404	-0.3797	0.0895	0.1124
247347_at	AT5G63440	SHA1 (SHOOT APICAL MERISTEM ARREST 1); p	-0.1295	0.5671	0.4478	-0.2296	0.3315	0.3091	0.4626	0.0323	0.0733	0.3625	0.0652	0.093
247348_at	AT5G63810	BGAL10 (beta-galactosidase 10); beta-galactosida	0.558	0.4652	0.4053	0.593	0.4398	0.3595	-0.7288	0.0503	0.095	-0.6939	0.0577	0.0865
247349_at	AT5G63820	similar to unknown protein [Arabidopsis thaliana] (T	0.8242	0.1796	0.2476	-1.014	0.1163	0.1722	0.17	0.6197	0.4045	-1.6683	0.0062	0.0244
247350_at	AT5G63830	zinc finger (HIT type) family protein	0.5171	0.1026	0.1851	0.259	0.3504	0.3182	0.3506	0.226	0.227	0.09246	0.7253	0.4057
247351_at	AT5G63790	ANAC102 (Arabidopsis NAC domain containing pro	-0.5672	0.0258	0.093	-0.2138	0.262	0.271	0.01548	0.9133	0.4961	0.3689	0.0507	0.0799
247352_at	AT5G63650	SNRK2.5/SNRK2.5/SRK2H (SNF1-RELATED PRO	-0.4571	0.1937	0.2581	-0.766	0.0591	0.1209	0.3458	0.2633	0.2483	0.03693	0.8963	0.4561
247353_at	AT5G63620	oxidoreductase, zinc-binding dehydrogenase family	0.5073	0.1443	0.2208	0.618	0.0919	0.153	-0.1551	0.4804	0.3516	-0.0443	0.8351	0.4386
247354_at	AT5G63590	FLS (Flavonol synthase); flavonol synthase	-0.157	0.9017	0.5517	-0.9	0.4928	0.3815	0.3307	0.7281	0.4412	-0.4123	0.6661	0.3861
247355_at	AT5G63670	elongation factor/ zinc ion binding	0.1855	0.0765	0.1592	0.4518	0.0044	0.041	-0.5461	0.0021	0.0217	-0.2798	0.0222	0.0485
247356_at	AT5G63800	BGAL6/MUM2 (MUCILAGE-MODIFIED 2); beta-gal	-0.08398	0.8577	0.5406	-0.0788	0.8663	0.5088	-0.1975	0.4791	0.3511	-0.1924	0.4899	0.3219
247357_at	AT5G63710	leucine-rich repeat transmembrane protein kinase,	-0.2841	0.2086	0.2672	0.1557	0.458	0.3672	-0.06983	0.7314	0.4422	0.37	0.1229	0.137
247358_at	AT5G63580	flavonol synthase, putative	0.4422	0.2103	0.2684	0.3266	0.3327	0.3097	-0.05332	0.7208	0.4389	-0.169	0.2909	0.2341
247359_at	AT5G63560	transferase family protein	0.7347	0.2234	0.2772	-0.7195	0.2314	0.2524	0.9092	0.1494	0.1785	-0.545	0.3457	0.2606
247360_at	AT5G63450	CYP94B1 (cytochrome P450, family 94, subfamily $	-1.603	0.1262	0.2056	-1.208	0.2201	0.2459	0.2184	0.5962	0.3969	0.6133	0.1817	0.1744
247361_at	AT5G63480	similar to unknown [Populus trichocarpa] (GB:ABK9	0.04542	0.8545	0.5394	0.2652	0.3171	0.3014	0.5622	0.0687	0.1137	0.782	0.0263	0.0538
247362_at	AT5G63140	ATPAP29/APAP29 (purple acid phosphatase 29); ac	-0.847	0.0473	0.1251	-0.8997	0.0396	0.0986	0.1617	0.5949	0.3964	0.109	0.7172	0.4032
247363_at	AT5G63200	tetratricopeptide repeat (TPR)-containing protein	-0.0437	0.7239	0.5006	0.04891	0.6932	0.4567	-1.0691	8.00E-04	0.016	-0.9765	0.0011	0.0123
247364_at	AT5G63200	tetratricopeptide repeat (TPR)-containing protein	0.4082	0.1087	0.1909	0.07734	0.7165	0.4641	-0.1551	0.3438	0.2903	-0.486	0.0283	0.0561
247365_at	AT5G63220	similar to unnamed protein product [Vitis vinifera] (G	-0.1107	0.5195	0.4289	0.1088	0.5227	0.3932	-0.199	0.2738	0.2544	0.02158	0.8973	0.4585
247366_at	AT5G63260	zinc finger (CCCH-type) family protein	0.3255	0.0346	0.1075	0.3189	0.0368	0.0947	0.1453	0.2328	0.231	0.1386	0.2512	0.2132
247367_at	AT5G63290	coproporphyrinogen oxidase-related	0.3173	0.0548	0.1344	-0.2625	0.0902	0.1515	0.1865	0.1669	0.1896	-0.3934	0.0236	0.0503
247368_at	AT5G63330	DNA-binding bromodomain-containing protein	-0.3696	0.0162	0.077	-0.2755	0.0409	0.1004	-0.4097	0.0076	0.0353	-0.3156	0.0186	0.0438
247369_at	AT5G63340	unknown protein	-0.3871	0.6756	0.4846	-0.895	0.3563	0.321	-0.4717	0.6121	0.4018	-0.9795	0.3178	0.2473
247370_at	AT5G63320	similar to unknown protein [Arabidopsis thaliana] (T	-0.00266	0.9943	0.5756	0.06701	0.8574	0.5066	-1.2565	0.022	0.0598	-1.1868	0.0264	0.0538
247371_at	AT5G63110	HDA6 (HISTONE DEACETYLASE 6); histone deac	0.3774	0.0777	0.1605	0.178	0.328	0.3076	-0.0769	0.6557	0.4164	-0.2763	0.1591	0.1606
247372_at	AT5G63280	zinc finger (C2H2 type) family protein	0.2269	0.109	0.1912	0.3734	0.0277	0.083	-0.3778	0.0029	0.0245	-0.2313	0.0164	0.0409
247373_at	AT5G63150	contains InterPro domain Protein of unknown functi	-0.04014	0.645	0.4748	-0.08887	0.3326	0.3097	0.5032	0.0034	0.0257	0.4545	0.0049	0.022
247374_at	AT5G63190	MA3 domain-containing protein	0.5343	0.0125	0.0691	0.8789	0.0021	0.0331	-0.9605	0.0015	0.0199	-0.616	0.0076	0.0271
247375_at	AT5G63135	similar to unnamed protein product [Vitis vinifera] (G	-0.07836	0.7911	0.5212	0.3118	0.3229	0.3048	0.3412	0.0863	0.1296	0.7314	0.0083	0.0284
247376_at	AT5G63310	NDPK2 (NUCLEOSIDE DIPHOSPHATE KINASE 2	-0.7643	0.0104	0.0646	-0.9824	0.0043	0.0406	0.419	0.0673	0.1123	0.2009	0.2979	0.2375
247377_at	AT5G63180	pectate lyase family protein	-0.4417	0.1287	0.2073	-0.4821	0.1055	0.1641	0.6755	6.00E-04	0.0158	0.6351	8.00E-04	0.0109
247378_at	AT5G63120	ethylene-responsive DEAD box RNA helicase, puta	0.282	0.252	0.2945	0.009457	0.9664	0.5356	-0.5953	0.0477	0.0916	-0.3038	0.2231	0.1977
247379_at	no_match	no_match	-0.01259	0.9851	0.5733	-0.03774	0.9554	0.5332	-2.411	0.019	0.0553	-2.4361	0.0184	0.0436
247380_at	AT5G63380	4-coumarate--CoA ligase family protein / 4-coumarc	-0.329	0.0868	0.1707	-0.4291	0.0422	0.1021	0.1001	0.5299	0.3713	4.10E-05	0.9998	0.483
247381_at	AT5G63390	similar to unknown protein [Arabidopsis thaliana] (T	-0.1337	0.6074	0.4622	-0.5161	0.0982	0.1579	0.08396	0.6718	0.4215	-0.2984	0.1801	0.1734
247382_at	AT5G63400	ADK1 (ADENYLATE KINASE 1); adenylate kinase	0.2686	0.29	0.3173	0.6443	0.0431	0.1032	-0.03654	0.7602	0.4512	0.3391	0.0387	0.0676
247383_at	AT5G63410	leucine-rich repeat transmembrane protein kinase,	0.2178	0.1092	0.1913	0.2266	0.0995	0.1591	0.1702	0.085	0.1284	0.179	0.0748	0.1006
247384_at	AT5G63370	protein kinase family protein	-0.1495	0.16	0.2335	-0.07656	0.4274	0.3542	-0.4545	0.0063	0.0329	-0.3816	0.0117	0.0339
247385_at	AT5G63420	EMB2746 (EMBRYO DEFECTIVE 2746); catalytic	-0.0025	0.9946	0.5756	-0.03991	0.9143	0.5225	-1.6603	0.0048	0.0294	-1.6977	0.0044	0.0211
247386_at	AT5G63420	EMB2746 (EMBRYO DEFECTIVE 2746); catalytic	0.5202	0.1784	0.2469	0.306	0.3919	0.3377	-0.2688	0.2395	0.235	-0.483	0.0681	0.0953
247387_at	no_match	no_match	-0.5486	0.0112	0.0661	-0.4402	0.0232	0.0768	-0.07389	0.4233	0.3268	0.03451	0.6987	0.397
247388_s_at	AT5G63470;AT3G48590	[AT5G63470, CCAAT-box binding transcription fact	-0.08066	0.6958	0.4914	0.1235	0.5549	0.4066	0.2244	0.1299	0.1638	0.4285	0.0221	0.0484
247389_at	AT5G63480	CBS domain-containing protein / octicosapeptide/P	0.3506	0.0973	0.1801	0.07107	0.6846	0.4537	-0.04647	0.7431	0.4459	-0.326	0.0694	0.0965
247390_at	AT5G63520	identical to F-box/LRR-repeat protein At5g63520 [A	0.4454	0.0613	0.1421	0.4188	0.0722	0.1347	-0.1217	0.46	0.3431	-0.1482	0.3763	0.274
247391_at	AT5G63540	similar to hypothetical protein OsJ_014026 [Oryza s	0.5726	0.5205	0.4292	2.9107	0.0232	0.0769	-0.2258	0.7952	0.4619	2.1124	0.0603	0.0888
247392_at	AT5G63610	GSA1 (GLUTAMATE-1-SEMIALDEHYDE-2,1-AMIN	0.00888	0.9641	0.5682	-0.2238	0.2943	0.2888	-0.3366	0.1093	0.1478	-0.5516	0.0282	0.056
247393_at	AT5G63130	octicosapeptide/Phox/Bem1p (PB1) domain-contair	0.02473	0.901	0.5514	0.09511	0.6373	0.4372	0.3091	0.1123	0.1501	0.3794	0.0674	0.0947
247394_at	AT5G62860	F-box family protein-related	0.2728	0.5288	0.4327	0.2872	0.5085	0.388	0.2821	0.5155	0.3652	0.2965	0.4956	0.3241
247395_at	AT5G62910	protein binding / zinc ion binding	0.2614	0.296	0.3209	0.4011	0.1391	0.1899	0.01259	0.9168	0.497	0.1523	0.2499	0.2125
247396_at	AT5G62930	GDSL-motif lipase/hydrolase family protein	-0.01803	0.9327	0.5604	0.06822	0.751	0.4753	-0.2977	0.212	0.2192	-0.2115	0.3514	0.2633
247397_at	AT5G62940	Dof-type zinc finger domain-containing protein	-0.01844	0.9517	0.5651	0.05592	0.8545	0.5059	0.07304	0.6322	0.4085	0.1474	0.3554	0.2651
247398_at	AT5G62950	catalytic/ nucleotide binding	0.558	0.1436	0.2004	0.8011	0.0139	0.0625	-0.08644	0.4622	0.3442	0.1567	0.2149	0.1936
247399_at	AT5G62960	similar to unknown protein [Arabidopsis thaliana] (T	-0.826	0.1239	0.2039	-0.6217	0.2174	0.2442	-0.2533	0.4394	0.3338	-0.04893	0.8764	0.4503
247400_at	AT5G62840	phosphoglycerate/bisphosphoglycerate mutase fam	-0.9186	0.0033	0.0446	-1.1517	0.0014	0.0312	-0.06438	0.6699	0.421	-0.2975	0.1011	0.1214
247401_at	AT5G62790	DXR (1-DEOXY-D-XYLULOSE 5-PHOSPHATE RE	-0.302	0.105	0.1872	-0.5192	0.0229	0.0764	-0.2355	0.1787	0.1977	-0.4527	0.0351	0.0635
247402_at	AT5G62750	unknown protein	-1.1581	0.3078	0.3274	-0.2563	0.8089	0.4926	-2.486	0.0663	0.1114	-1.5841	0.1855	0.1766
247403_at	AT5G62740	band 7 family protein	1.0902	0.0184	0.0807	1.1306	0.0163	0.0664	0.1263	0.5878	0.3937	0.1673	0.4811	0.318
247404_at	AT5G62890	permease, putative	-0.02484	0.9253	0.5584	-0.1992	0.4683	0.3714	-0.3358	0.0633	0.1083	-0.5101	0.0179	0.0429
247405_at	AT5G62880	ARAC10/ATRAC10/ATROP11 (RHO-RELATED PR	0.2296	0.3017	0.324	-0.000587	0.9773	0.5386	-0.1111	0.597	0.397	-0.3466	0.1482	0.1535
247406_at	AT5G62820	ARR6 (RESPONSE REGULATOR 6); transcription	0.4773	0.0634	0.1443	-1.3054	0.0874	0.1489	-0.1065	0.4795	0.3512	0.06542	0.6572	0.3832
247407_at	AT5G62900	similar to unknown protein [Arabidopsis thaliana] (T	1.0503	0.0393	0.1144	1.2305	0.0241	0.0781	-0.2961	0.1045	0.1445	-0.1158	0.4589	0.3096
247408_at	AT5G62760	nuclear protein ZAP-related	-0.534	0.0394	0.1145	-0.382	0.0973	0.1572	-0.5696	0.0324	0.0734	-0.4177	0.0779	0.1032
247409_at	AT5G62980	ethylene-responsive jasmonate, putative	0.4348	0.0081	0.059	0.7446	0.0011	0.0294	-0.1388	0.1914	0.2063	0.1701	0.1287	0.1406
247410_at	AT5G62990	EMB1692 (EMBRYO DEFECTIVE 1692)	0.2085	0.5805	0.4523	0.1367	0.7139	0.4633	-0.1167	0.2681	0.2511	-0.1885	0.1065	0.125
247411_at	AT5G63000	similar to hypothetical protein OsJ_001206 [Oryza s	0.4797	0.0164	0.0771	0.2352	0.1228	0.1778	0.3753	0.01	0.0398	0.1308	0.1837	0.1757
247412_at	AT5G63010	WD-40 repeat family protein	0.4659	0.2447	0.2905	0.9358	0.0521	0.1132	-0.859	0.0659	0.111	-0.3891	0.3187	0.2477
247413_at	no_match	no_match	0.1541	0.6332	0.4707	0.5025	0.1678	0.211	-0.1441	0.5493	0.3788	0.2043	0.4069	0.2869
247414_at	AT5G63050	EMB2759 (EMBRYO DEFECTIVE 2759)	-0.3272	0.2768	0.3099	-0.4445	0.1626	0.2078	-0.1691	0.5509	0.3794	-0.2864	0.3326	0.2546
247415_at	AT5G63060	transporter	-1.0578	0.0018	0.0391	-1.2748	9.00E-04	0.0284	0.2792	0.0383	0.0809	0.06219	0.535	0.3398
247416_at	AT5G63070	40S ribosomal protein S15, putative	-0.06506	0.9567	0.5664	-0.1378	0.9084	0.5211	1.5795	0.233	0.231	1.5067	0.2515	0.2133
247417_at	AT5G63040	similar to unknown protein [Arabidopsis thaliana] (T	-0.9688	0.005	0.0507	-1.883	4.00E-04	0.0251	0.06137	0.7415	0.4452	-0.8528	0.008	0.0278
247418_at	AT5G63030	glutaredoxin, putative	0.8499	0.0022	0.041	0.4888	0.0158	0.0655	0.3389	0.0356	0.0775	-0.0222	0.8481	0.4423
247419_at	AT5G63080	transcription factor jumonji (jmjC) domain-containi	0.6469	0.0456	0.1227	0.3747	0.172	0.2142	-0.5267	0.0644	0.1095	-0.7989	0.0184	0.0436
247420_at	AT5G63100	similar to unknown protein [Arabidopsis thaliana] (T	-0.4492	0.0791	0.1621	-1.0047	0.0063	0.0456	0.6996	0.0218	0.0596	0.1441	0.4942	0.3237
247421_at	AT5G62800	seven in absentia (SINA) family protein	1.0367	0.32	0.3344	-1.7649	0.1257	0.1797	0.6998	0.4866	0.3541	-2.1018	0.083	0.1075
247422_at	AT5G62810	PEX14 (PEROXISOME DEFECTIVE 2)	0.01946	0.7813	0.518	-0.3114	0.009	0.0519	0.5397	7.00E-04	0.016	0.2089	0.0221	0.0484
247423_at	AT5G62830	F-box family protein-related	-0.4495	0.4816	0.4126	-0.05421	0.93	0.5266	-0.2479	0.691	0.4282	0.1474	0.812	0.4323
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247490_at	AT5G61850	LFY (LEAFY); transcription factor	1.9166	0.076	0.1585	-1.3833	0.1609	0.2065	2.0307	0.0652	0.1102	-1.2692	0.1901	0.1793
247491_at	AT5G61880	signaling molecule-related	0.1638	0.5655	0.4471	0.5583	0.1	0.1593	-0.1684	0.3125	0.2747	0.2261	0.196	0.1825
247492_at	AT5G61890	AP2 domain-containing transcription factor family p	0.6945	0.0265	0.0941	0.03226	0.8811	0.5134	0.7609	0.0198	0.0565	0.09872	0.6514	0.3813
247493_at	AT5G61900	BON1 (BONZAI1); calcium-dependent phospholipid	1.0621	0.009	0.0612	0.9859	0.0116	0.0581	0.01012	0.9601	0.5076	-0.06607	0.7455	0.4121
247494_at	AT5G61790	calnexin 1 (CNX1)	1.0636	5.00E-04	0.032	0.8627	0.0011	0.0293	0.2079	0.1112	0.1493	0.006999	0.9486	0.4705
247495_at	AT5G61760	ATIPK2BETA (Arabidopsis thaliana inositol hexakis	0.1532	0.4987	0.4199	0.1694	0.4575	0.3672	0.1943	0.2657	0.2497	0.2105	0.234	0.2038
247496_at	AT5G61840	GUT1; catalytic	0.2319	0.0407	0.1162	0.1595	0.1096	0.1671	0.2506	0.0322	0.0731	0.1782	0.0837	0.108
247497_at	AT5G61770	PPAN (PETER PAN-LIKE PROTEIN)	0.3436	0.1139	0.1955	0.259	0.203	0.2347	0.08684	0.4244	0.3273	0.00226	0.9827	0.4787
247498_at	AT5G61810	mitochondrial substrate carrier family protein	-0.6866	0.2611	0.3003	-0.7069	0.2495	0.2636	0.04779	0.5778	0.3898	0.02753	0.7451	0.412
247499_at	AT5G61865	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.09598	0.9445	0.5635	-0.05598	0.9676	0.536	-0.233	0.8261	0.4715	-0.3849	0.7181	0.4034
247500_at	AT5G61910	similar to unknown protein [Arabidopsis thaliana] (T	0.001112	0.9959	0.5761	0.003097	0.9886	0.5413	-0.3998	0.0941	0.136	-0.3978	0.0953	0.1171
247501_at	AT5G61920	similar to unknown protein [Arabidopsis thaliana] (T	-0.328	0.4437	0.3952	0.213	0.6108	0.4271	-0.2373	0.5724	0.3875	0.3038	0.4758	0.316
247502_at	AT5G61940	ubiquitin carboxyl-terminal hydrolase-related	-0.04949	0.9269	0.5589	-0.1659	0.7596	0.4778	-0.9717	0.1275	0.1621	-1.0881	0.0982	0.1192
247503_at	AT5G61980	AGD1 (ARF-GAP DOMAIN 1); ARF GTPase activa	-1.2358	0.2063	0.2661	-1.775	0.0964	0.1564	0.2158	0.8005	0.4651	-0.3234	0.7135	0.4021
247504_at	AT5G61990	pentatricopeptide (PPR) repeat-containing protein	-0.1004	0.8467	0.5375	-0.1337	0.7974	0.4887	-1.2203	0.0353	0.0771	-1.2535	0.0326	0.0609
247505_at	AT5G61970	signal recognition particle-related / SRP-related	0.4004	0.0617	0.1425	0.4707	0.0389	0.0977	-0.2231	0.0973	0.1388	-0.1527	0.2139	0.1929
247506_at	AT5G61960	AML1 (ARABIDOPSIS MEI2-LIKE PROTEIN 1); RN	-0.1887	0.3777	0.3633	0.06057	0.7663	0.4793	-0.642	0.0449	0.0297	-0.3927	0.0263	0.0537
247507_at	AT5G61930	APO3 (ACCUMULATION OF PHOTOSYSTEM ON	0.5062	0.0724	0.155	0.2394	0.3155	0.3004	0.125	0.4423	0.3351	-0.1418	0.3886	0.2793
247508_at	AT5G62000	ARF2 (AUXIN RESPONSE FACTOR 2); transcripti	-0.7613	0.0611	0.1418	-0.3479	0.3033	0.2933	-2.1642	0.0012	0.0187	-1.7508	0.0026	0.0169
247509_at	AT5G62020	AT-HSFB2A (Arabidopsis thaliana heat shock trans	-0.1417	0.6454	0.4748	0.09337	0.7598	0.4778	-0.07186	0.6982	0.4001	0.1632	0.2734	0.2247
247510_at	AT5G62030	diphthamide synthesis DPH2 family protein	0.02755	0.9054	0.5526	0.1362	0.5658	0.4103	-0.1994	0.2104	0.2181	-0.09076	0.5347	0.3397
247511_at	AT5G61310	brother of FT and TFL1 protein (BFT)	-0.3811	0.5356	0.4353	0.2577	0.6705	0.4489	0.01055	0.9725	0.5106	0.6494	0.0866	0.1102
247512_at	AT5G61720	similar to unknown protein [Arabidopsis thaliana] (T	-0.7694	0.2644	0.3021	-1.5921	0.055	0.1165	-0.5289	0.2535	0.2428	-1.3516	0.0271	0.0547
247513_at	AT5G61510	NADP-dependent oxidoreductase, putative	0.8736	0.0012	0.0363	0.6531	0.0037	0.038	0.2421	0.0428	0.0862	0.02162	0.8066	0.4306
247514_at	AT5G61640	PMSR1 (PEPTIDEMETHIONINE SULFOXIDE REC	0.4883	0.0598	0.1399	0.7074	0.0195	0.0719	0.09752	0.4576	0.3421	0.3167	0.056	0.0848
247515_at	AT5G61740	ATATH14 (ABC2 homolog 14); ATPase, coupled to	0.8118	0.2223	0.2766	0.008137	0.9891	0.5414	-0.4055	0.5108	0.3635	-1.2092	0.0979	0.1189
247516_at	AT5G61750	cupin family protein	-0.01265	0.9686	0.5694	1.5329	0.0071	0.0476	0.6278	0.1063	0.1459	2.1734	0.002	0.0151
247517_at	AT5G61780	tudor domain-containing protein / nuclease family p	-0.1457	0.6091	0.4427	-0.1886	0.5128	0.3898	-0.353	0.1187	0.1551	-0.3959	0.0904	0.1132
247518_at	AT5G61800	pentatricopeptide (PPR) repeat-containing protein	-0.2701	0.7423	0.5065	1.0343	0.2484	0.2628	-0.8001	0.0523	0.097	0.5043	0.1601	0.1613
247519_at	AT5G61430	ANAC100/ATNAC5 (Arabidopsis NAC domain cont	1.1563	0.1326	0.2112	-0.111	0.8653	0.5086	-0.1507	0.8182	0.4693	-1.418	0.082	0.1066
247520_at	AT5G61310	cytochrome c oxidase subunit Vc, putative / COX5C	0.02343	0.873	0.5449	0.228	0.1726	0.2146	0.7853	0.0047	0.0291	1.0368	0.0017	0.0144
247521_at	AT5G61450	2-phosphoglycerate kinase-related	0.4526	0.1221	0.2024	0.3682	0.1868	0.2242	0.04389	0.7459	0.4468	-0.04054	0.7644	0.4181
247522_at	AT5G61340	similar to unknown protein [Arabidopsis thaliana] (T	-0.09129	0.7466	0.5079	-0.8283	0.0348	0.0921	0.03518	0.9003	0.4924	-0.7019	0.0563	0.0851
247523_at	AT5G61410	RPE (EMBRYO DEFECTIVE 2728); ribulose-phosp	-0.6039	0.0312	0.1025	-0.8024	0.0124	0.0597	-0.3174	0.1622	0.1868	-0.5159	0.0497	0.0791
247524_at	AT5G61440	thioredoxin family protein	-1.2127	0.1255	0.2051	-1.0772	0.1612	0.2067	0.1197	0.858	0.4805	0.2552	0.7051	0.3992
247525_at	AT5G61380	TOC1 (TIMING OF CAB EXPRESSION 1); transcrip	0.8448	0.0374	0.1115	1.3348	0.0084	0.0507	-0.4761	0.0728	0.1173	0.01399	0.9467	0.47
247526_at	AT5G61470	zinc finger (C2H2 type) family protein	0.9052	0.0908	0.1746	0.1002	0.8181	0.4953	-0.7462	0.1415	0.1725	0.2592	0.5598	0.3487
247527_at	AT5G61480	leucine-rich repeat transmembrane protein kinase,	0.3883	0.3269	0.3384	0.09129	0.806	0.4915	0.5344	0.045	0.0888	0.2374	0.2699	0.2226
247528_at	AT5G61460	MIM (HYPERSENSITIVE TO MMS, IRRADIATION	0.6622	0.4609	0.4034	-0.8313	0.3641	0.3248	0.1505	0.8595	0.4809	-1.343	0.1675	0.1658
247529_at	AT5G61520	hexose transporter, putative	1.3358	0.0015	0.0381	1.3581	0.0014	0.0313	-0.4181	0.0152	0.0492	-0.3958	0.0183	0.0434
247530_at	AT5G61540	L-asparaginase, putative / L-asparagine amidohydr	0.2823	0.2632	0.3016	0.557	0.0622	0.124	-0.8103	0.0202	0.0572	-0.5356	0.0691	0.0963
247531_at	AT5G61550	protein kinase family protein	-0.9212	0.3616	0.3553	0.03282	0.9725	0.5372	-0.2148	0.8068	0.4656	0.7392	0.4194	0.2923
247532_at	AT5G61560	protein kinase family protein	0.1464	0.3802	0.3646	0.5274	0.0238	0.0776	-0.7874	0.0014	0.0196	-0.4064	0.0154	0.0395
247533_at	AT5G61570	protein kinase family protein	-0.2986	0.392	0.3711	-0.975	0.0351	0.0926	0.2038	0.5485	0.3786	-0.4726	0.2037	0.1872
247534_at	AT5G61580	phosphofructokinase family protein	0.6268	0.0199	0.0833	0.5208	0.0355	0.0929	-0.3031	0.1154	0.1527	-0.4091	0.0537	0.0828
247535_at	AT5G61620	myb family transcription factor	1.1693	0.2248	0.2784	1.4386	0.1497	0.1978	0.9317	0.242	0.2362	1.211	0.1492	0.1541
247536_at	AT5G61650	CYCP4;2 (CYCLIN P4;2); cyclin-dependent protein	1.0813	0.4049	0.3778	-1.4964	0.2674	0.274	0.5277	0.4925	0.3566	-2.05	0.0427	0.0721
247537_s_at	AT5G61730;AT5G61690	[AT5G61730, ATATH11 (ABC2 homolog 11); ATPa	0.791	0.2651	0.3022	0.6708	0.3339	0.3102	0.4708	0.4839	0.3529	0.3506	0.5968	0.3624
247538_at	AT5G61670	ATATH16 (ABC2 homolog 16); ATPase, coupled to	0.532	0.2952	0.3205	-1.0626	0.0741	0.1366	0.6698	0.2045	0.2145	-0.9252	0.1045	0.1237
247539_at	AT5G61710	similar to unknown protein [Arabidopsis thaliana] (T	0.4391	0.5613	0.4454	0.4154	0.5816	0.4168	-0.4455	0.208	0.2166	-0.4691	0.1894	0.179
247540_at	AT5G61590	AP2 domain-containing transcription factor family p	-0.1969	0.3406	0.3456	-0.2672	0.2163	0.2436	0.3655	0.0812	0.1248	0.2952	0.1343	0.1446
247541_at	AT5G61600	glycine-rich protein	-1.1918	0.0104	0.0646	-1.6775	0.0031	0.0359	1.5072	0.0019	0.0209	1.0216	0.008	0.0278
247542_at	AT5G61500	autophagy 3 (APG3)	0.08483	0.5814	0.4527	0.1232	0.4332	0.3569	0.2277	0.0649	0.11	0.2661	0.0419	0.0712
247543_at	AT5G61600	ethylene-responsive element-binding family protein	-0.5034	0.3688	0.359	-0.0119	0.9821	0.5397	0.5133	8.00E-04	0.0163	1.0048	1.00E-04	0.0056
247544_at	AT5G61610	heat shock protein binding / unfolded protein binding	-0.3334	0.1272	0.206	-0.9203	0.0061	0.0449	0.4776	0.0258	0.0653	-0.1092	0.4737	0.3152
247545_at	AT5G61530	small G protein family protein / RhoGAP family prot	1.2713	6.00E-04	0.0332	1.1512	9.00E-04	0.0286	-0.3536	0.0075	0.0351	-0.4737	0.0026	0.0169
247546_at	AT5G61605	similar to unknown protein [Arabidopsis thaliana] (T	-0.3314	0.7524	0.5091	1.2952	0.2572	0.2684	0.5161	0.6266	0.4068	2.1428	0.0943	0.1162
247547_at	AT5G61360	similar to unknown protein [Arabidopsis thaliana] (T	0.5988	0.0293	0.0992	0.09811	0.6092	0.4268	0.02974	0.8748	0.4853	-0.461	0.6599	0.0884
247548_at	AT5G61400	pentatricopeptide (PPR) repeat-containing protein	2.3542	0.0329	0.1053	2.6539	0.0226	0.076	-0.4792	0.5504	0.3792	-0.1796	0.8192	0.4339
247549_at	AT5G61420	MYB28 (MYB DOMAIN PROTEIN 28); DNA binding	-0.01201	0.9774	0.5716	-0.1642	0.701	0.4594	-0.4561	0.1666	0.1895	-0.6083	0.0875	0.1108
247550_at	AT5G61370	pentatricopeptide (PPR) repeat-containing protein	0.6716	0.0833	0.1671	0.3777	0.2662	0.2733	-0.1193	0.7043	0.4328	-0.4132	0.2306	0.2018
247551_at	AT5G60980	nuclear transport factor 2 (NTF2) family protein / R	0.03335	0.8123	0.5275	0.2115	0.1829	0.2218	-0.4878	0.0207	0.0579	-0.3096	0.0781	0.1033
247552_at	AT5G60920	COB (COBRA)	-0.1818	0.318	0.3331	-0.5262	0.03	0.0861	-0.08081	0.5757	0.3887	-0.4252	0.0328	0.0612
247553_at	AT5G60910	AGL6 (AGAMOUS-LIKE 6); transcription factor	1.083	0.0187	0.0813	0.5883	0.1063	0.1645	0.2993	0.0988	0.14	-0.1977	0.227	0.1999
247554_at	AT5G61010	ATEXO70E2 (EXOCYST SUBUNIT EXO70 FAMIL	0.4937	0.0097	0.0631	0.1808	0.1639	0.2085	0.2414	0.0386	0.0811	-0.07146	0.4198	0.2924
247555_at	AT5G61020	ECT3 (evolutionary conserved C-terminal 3)	0.8029	0.1386	0.2161	0.3822	0.4291	0.3549	-0.1067	0.5166	0.3658	-0.5273	0.0246	0.0516
247556_at	AT5G61040	similar to unknown protein [Arabidopsis thaliana] (T	-0.0502	0.849	0.5379	-0.2179	0.428	0.3544	-0.6134	0.0497	0.0943	-0.781	0.024	0.0508
247557_at	AT5G61050	histone deacetylase-related / HD-related	-0.02795	0.9796	0.572	-0.6754	0.5463	0.403	1.2658	0.2848	0.2606	0.6183	0.5792	0.3558
247558_at	AT5G61060	HDA05 (HISTONE DEACETYLASES); histone deac	0.5489	0.02	0.0834	0.846	0.0045	0.041	-0.8803	0.0039	0.0271	-0.5832	0.0164	0.0409
247559_at	AT5G61070	HDA18 (histone deacetylase 18); histone deacetyla	1.0849	0.3831	0.3663	2.5391	0.0838	0.1455	-1.087	0.25	0.241	0.3672	0.6733	0.3885
247560_at	AT5G61090	proline-rich family protein	0.2437	0.7309	0.5027	-1.3855	0.1041	0.1629	0.7493	0.3202	0.2784	-0.8799	0.2538	0.2145
247561_at	AT5G61110	protein binding / zinc ion binding	-0.8621	0.2742	0.308	-0.8503	0.2799	0.2808	-0.668	0.3822	0.3088	-0.6561	0.3898	0.2799
247562_at	AT5G61130	zinc ion binding	2.0584	0.0953	0.1783	0.1367	0.8922	0.5164	0.1841	0.8553	0.4798	-1.7376	0.1403	0.1484
247563_at	AT5G61130	glycosyl hydrolase family protein 17	-0.6795	0.0446	0.1217	-1.2649	0.0058	0.044	0.6999	4.00E-04	0.0147	0.1145	0.1509	0.1553
247564_at	AT5G61140	DEAD box RNA helicase, putative	0.405	0.0753	0.1579	0.5121	0.0392	0.0981	-1.1051	0.002	0.021	-0.998	0.0029	0.0175
247565_at	AT5G61150	VIP4 (VERNALIZATION INDEPENDENCE 4)	-0.249	0.1645	0.2371	0.2785	0.1301	0.1829	-0.3854	0.0553	0.1002	0.142	0.3794	0.2755
247566_at	AT5G61170	40S ribosomal protein S19 (RPS19C)	0.1611	0.267	0.3034	0.09047	0.5093	0.3884	0.4564	0.0119	0.0433	0.3858	0.0209	0.0469
247567_at	AT5G61190	zinc finger protein-related	0.7964	0.0151	0.0743	1.4768	0.0016	0.0318	-0.5502	0.0479	0.0918	0.1303	0.541	0.3413
247568_at	AT5G61260	chromosome scaffold protein-related	3.5704	0.005	0.0506	0.8396	0.2591	0.2695	0.6053	0.3634	0.2997	-2.1255	0.0228	0.0491
247569_at	AT5G61240	protein binding	-0.5252	0.0126	0.0692	-0.5764	0.0091	0.0522	0.5052	0.0143	0.0477	0.454	0.0204	0.0461
247570_at	AT5G61250	ATGUS1 (ARABIDOPSIS THALIANA GLUCURON	1.1318	7.00E-04	0.0334	0.9121	0.0017	0.0319	-0.01857	0.8853	0.4883	-0.2382	0.12	0.135
247571_at	AT5G61210	SNAP33 (synaptosomal-associated protein 33); SN	0.6512	0.019	0.0818	1.019	0.004	0.0394	0.1449	0.1592	0.1852	0.5128	0.0036	0.0196
247572_at	AT5G61220	complex 1 family protein / LVR family protein	-0.1293	0.4054	0.3781	0.3256	0.0794	0.1413	0.6275	0.0108	0.0412	1.0825	0.0015	0.0137
247573_at	AT5G61160	AACT1 (ANTHOCYANIN 5-AROMATIC ACYLTRAN	-2.1053	0.1766	0.2458	-1.045	0.4616	0.3686	-0.1974	0.8567	0.4802	0.8629	0.4475	0.305
247574_at	AT5G61230;AT5G61228	[AT5G61230, ankyrin repeat family protein];[AT5G6	0.3021	0.0126	0.0692	0.42	0.0039	0.0392	0.03062	0.6851	0.4261	0.1484	0.1019	0.122
247575_at	AT5G61030	GR-RBP3 (glycine-rich RNA-binding protein 3); RN	0.9578	0.0307	0.1016	0.7088	0.0726	0.1349	1.1037	0.0052	0.0302	0.8548	0.0127	0.0357
247576_at	AT5G61280	nemorin family protein	-0.6994	0.3567	0.353	0.4365	0.5514	0.4054	0.1813	0.8007	0.4636	1.3172	0.1215	0.1361
247577_at	AT5G61290	flavin-containing monooxygenase family protein / FI	1.9181	0.0517	0.1306	0.9482	0.2465	0.2618	0.04856	0.948	0.5051	-0.9213	0.258	0.2169
247578_at	AT5G61300	similar to unknown protein [Arabidopsis thaliana] (T	-0.1838	0.009	0.0612	0.001784	0.9655	0.5354	-0.456	3.00E-04	0.0138	-0.2704	0.0022	0.0157
247579_at	AT5G61320	CYP89A3 (cytochrome P450, family 89, subfamily A	-0.7119	0.3883	0.3689	0.9739	0.2564	0.268	-0.03761	0.9617	0.5081	1.6481	0.0887	0.1118
247580_at	AT5G61330	rRNA processing protein-related	0.4809	0.1736	0.244	0.4576	0.1908	0.2268	-0.1298	0.4692	0.3472	-0.153	0.3997	0.2841
247581_at	AT5G61350	protein kinase family protein	-3.1281	0.0145	0.0731	-3.4351	0.0105	0.0554	0.857	0.3207	0.2786	0.55	0.5077	0.3288
247582_at	AT5G60760	2-phosphoglycerate kinase-related	0.5125	0.2542	0.296	0.3526	0.4119	0.347	-0.237	0.3897	0.312	-0.397	0.1818	0.1744
247583_at	AT5G60750	CAAX amino terminal protease family protein	-0.2187	0.0409	0.1164	-0.1537	0.1047	0.1634	-0.03126	0.4712	0.3481	0.03375	0.4392	0.301
247584_at	AT5G60670	60S ribosomal protein L12 (RPL12C)	0.1338	0.3943	0.3723	0.1426	0.367	0.3261	0.1298	0.3534	0.2949	0.1385	0.3255	0.2509
247585_at	AT5G60680	similar to unknown protein [Arabidopsis thaliana] (T	0.1574	0.6419	0.4736	0.48	0.2003	0.233	-0.04936	0.4388	0.3336	0.2733	0.0089	0.0295
247586_at	AT5G60660	PIP2;4/PIP2F (plasma membrane intrinsic protein 2	-0.4043	0.4127	0.3815	-0.06974	0.8824	0.5138	0.2952	0.4199	0.3253	0.6298	0.1279	0.1402
247587_at	AT5G60620	phosphoglid/glycerol acyltransferase family protein	0.4177	0.0208	0.0848	0.412	0.0217	0.0748	-0.00233	0.9845	0.5138	-0.00807	0.9464	0.4699
247588_at	AT5G60640	ATPDIL1-4 (PDI-LIKE 1-4); thiol-disulfide exchange	0.4365	0.0187	0.0813	0.1839	0.1825	0.2215	0.1347	0.2583	0.2454	-0.118	0.313	0.2449
247589_at	AT5G60690	REV (REVOLUTA); DNA binding / lipid binding / tra	0.9234	0.0037	0.0459	0.8887	0.0043	0.0406	-0.6078	0.0162	0.0507	-0.6425	0.0134	0.0367
247590_at	AT5G60720	similar to unknown protein [Arabidopsis thaliana] (T	-0.3245	0.26	0.2997	0.0493	0.8518	0.505	-0.1256	0.5705	0.3869	0.2483	0.2893	0.233
247591_at	AT5G60770	ATNRT2.4 (Arabidopsis thaliana high affinity nitrate	-0.6469	0.1732	0.2437	0.0563	0.8924	0.5164	-0.452	0.3118	0.2743	0.2511	0.5555	0.3471
247592_at	ATNRT2.3 (Arabidopsis thaliana high affinity nitrate	2.4088	0.0235	0.0897	0.9706	0.2244	0.2482	0.2606	0.7195	0.4383	-1.1776	0.1565	0.159	
247593_at	ATGCN1 (Arabidopsis thaliana general control non-	0.2707	0.4134	0.3817	0.3888	0.2604	0.27	-0.8701	0.0095	0.039	-0.752	0.0157	0.0399	
247594_at	AT5G60800	heavy-metal-associated domain-containing protein	1.1365	0.0067	0.0552	1.5325	0.0022	0.0334	0.3658	0.0466	0.0906	0.7618	0.0041	0.0205
247595_at	AT5G60820	zinc finger (C3HC4-type RING finger) family protein	0.02179	0.9297	0.5599	0.1181	0.6376	0.4374	0.08016	0.7471	0.4472	0.22	0.3967	0.2828
247596_at	AT5G60840	unknown protein	0.3563	0.2731	0.3073	0.06163	0.8369	0.5007	1.0628	0.0027	0.0237	0.7682	0.0086	0.0289
247597_at	AT5G60860	ARABA1f (Arabidopsis Rab GTPase homolog A1f);	-0.6289	0.0442	0.1213	-0.6316	0.0437	0.1036	0.8029	7.00E-04	0.016	0.8002	7.00E-04	0.0108
247598_at	AT5G60870	regulator of chromosome condensation (RCC1) fam	0.02595	0.9462	0.5636	-0.057	0.8824	0.5138	-0.3009	0.4523	0.3396	-0.3838	0.3484	0.2617
247599_at	AT5G60880	unknown protein	-0.3096	0.8201	0.5296	-0.3017	0.8246	0.4974	-0.8311	0.3735	0.3045	-0.8233	0.3776	0.2747
247600_at	ATMYB34/ATR1/MYB34 (ALTERED TRYPTOPHAN	-1.401	0.0058	0.0534	-1.4005	0.0059	0.0442	0.2398	0.0492	0.0935	0.2403	0.0489	0.0782	
247601_at	OBP4 (OBF BINDING PROTEIN 4); DNA binding /	-0.5347	0.0647	0.1457	-0.1523	0.5111	0.3891	-0.7774	0.0125	0.0444	-0.395	0.0936	0.1157	
247602_at	AT5G60900	RLK1 (RECEPTOR-LIKE PROTEIN KINASE 1); ca	0.5838	0.0374	0.1115	0.557	0.0429	0.1029	-0.1855	0.0166	0.0514	-0.2122	0.0105	0.0321
247603_at	AT5G60930	chromosome-associated kinesin, putative	-0.2604	0.5521	0.442	-0.2175	0.6034	0.4247	-0.3941	0.1997	0.2117	-0.3612	0.2324	0.2029
247604_at	AT5G60950	Dof-type zinc finger domain-containing protein	1.7882	1.00E-04	0.0312	1.9491	1.00E-04	0.0249	-0.2339	0.1334	0.1662	0.3948	0.0338	0.0621
247605_at	AT5G60970	TCP5 (TEOSINTE BRANCHED1, CYCLOIDEA AN	-0.05607	0.8358	0.5341	0.2445	0.3894	0.3364	-0.1431	0.336	0.2864	0.1575	0.2954	0.2363
247606_at	AT5G61000	replication protein, putative	0.1167	0.8928	0.5493	-0.1523	0.2604	0.27	0.466	0.016	0.0505	0.2969	0.0631	0.0912
247607_at	AT5G61960	pentatricopeptide (PPR) repeat-containing protein	0.1128	0.4092	0.3795	0.213	0.157	0.2036	0.03388	0.6551	0.4162	0.6797	0.1341	0.1293
247608_at	AT5G60990	DEAD/DEAH box helicase, putative (RH10)	0.3219	0.2672	0.3035	0.4049	0.1805	0.2199	-0.5243	0.0057	0.0314	-0.4413	0.0104	0.0319
247609_at	AT5G60940	transducin family protein / WD-40 repeat family prot	0.459	0.0109	0.0655	0.1762	0.1614	0.2069	-0.6649	0.0012	0.0187	-0.9486	3.00E-04	0.0083
247610_at	AT5G60630	unknown protein	-0.2145	0.6519	0.4766	-0.78	0.1514	0.1993	0.1441	0.7601	0.4512	-0.4215	0.393	0.2813
247611_at	AT5G60710	zinc finger (C3HC4-type RING finger) family protein	0.1339	0.4436	0.3951	0.4424	0.0486	0.1094	-0.5954	2.00E-04	0.0126	-0.287	0.0029	0.0175
247612_at	AT5G60730	anion-transporting ATPase family protein	0.5234	0.4402	0.3938	-0.0777	0.905	0.5201	0.0427	0.1979	0.2104	0.2416	0.6812	0.3909
247613_at	AT5G60740	ABC transporter family protein	0.06143	0.9073	0.5531	0.007699	0.9883	0.5413	-0.2287	0.6389	0.4108	-0.2825	0.5653	0.351
247614_at	AT5G60240	unknown protein	-0.5162	0.6583	0.4786	0.7494	0.5268	0.3949	-0.6607	0.5746	0.3883	0.6049	0.6061	0.3654
247615_at	AT5G60250	zinc finger (C3HC4-type RING finger) family protein	1.7662	0.0017	0.091	0.698	0.0413	0.101	0.605	0.0339	0.0752	-0.4633	0.2722	0.0986
247616_at	AT5G60260	unknown protein	0.28	0.8018	0.5246	0.9346	0.4212	0.3512	-0.4098	0.6433	0.4122	0.2448	0.78	0.423
247617_at	AT5G60270	lectin protein kinase family protein	0.1239	0.7481	0.5083	-0.1457	0.7064	0.4611	-0.2142	0.4884	0.3549	-0.4838	0.1603	0.1614
247618_at	AT5G60280	lectin protein kinase family protein	2.8974	0.0293	0.0993	1.477	0.1657	0.2095	0.1697	0.8478	0.478	-1.2507	0.2058	0.1883
247619_at	AT5G60290	unknown protein	0.3823	0.7445	0.5073	0.007077	0.9952	0.5429	0.6074	0.6086	0.4009	-0.9826	0.4202	0.2926
247620_at	AT5G60310	lectin protein kinase, putative	0.8574	0.1706	0.2419	-0.2865	0.607	0.426	0.7339	0.2265	0.2274	-0.4099	0.4698	0.3136
247621_at	AT5G60340	macC-like dehydratase domain-containing protein	-1.4583	0.1551	0.2299	-0.6411	0.4847	0.378	0.1588	0.8582	0.4805	0.976	0.3066	0.2418
247622_at	AT5G60350	unknown protein	0.684	0.4447	0.3955	0.453	0.6048	0.425	0.93	0.2328	0.231	0.6989	0.3507	0.2629
247623_at	AT5G60320	lectin protein kinase family protein	0.5209	0.3249	0.3372	0.1

247690_at	AT5G59800	MBD7 (METHYL-CPG-BINDING DOMAIN 7); DNA	-0.4814	0.0579	0.1379	-0.2656	0.2197	0.2457	-0.355	0.1218	0.1577	-0.1392	0.4853	0.3197
247691_at	AT5G59720	HSP18.2 (HEAT SHOCK PROTEIN 18.2)	-0.7098	0.2216	0.2761	2.665	0.0056	0.0434	0.1198	0.8192	0.4696	3.4946	0.0021	0.0154
247692_s_at	AT5G59970;AT5G59690	[AT5G59970, histone H4];[AT5G59690, histone H4	-0.6326	0.0182	0.0804	-0.4431	0.054	0.1153	1.1432	0.0022	0.0222	1.3327	0.0012	0.013
247693_at	AT5G59730	ATEXO70H7 (EXOCYST SUBUNIT EXO70 FAMIL	-1.2653	0.0035	0.0451	-1.0104	0.0079	0.0496	0.03266	0.8578	0.4804	0.2876	0.1677	0.1658
247694_at	AT5G59750	riboflavin biosynthesis protein, putative	-0.3432	0.0519	0.1307	-0.3771	0.0395	0.0985	-0.2979	0.0294	0.0696	-0.3318	0.0209	0.0468
247695_at	AT5G59710	VIP2 (VIRE2 INTERACTING PROTEIN2); transcrip	0.2257	0.2698	0.3053	-0.05974	0.7518	0.4756	-0.05892	0.629	0.4077	-0.3444	0.0379	0.0666
247696_at	AT5G59780	MYB59 (myb domain protein 59); DNA binding / tra	0.1546	0.7092	0.4959	-0.03546	0.9312	0.5269	-0.5552	0.0539	0.0987	-0.7453	0.0222	0.0485
247697_at	AT5G59810	ATSBT5.4; subtilase	0.3737	0.4711	0.4079	-0.6069	0.2662	0.2733	0.5541	0.2394	0.2349	-0.4265	0.3478	0.2614
247698_at	AT5G59830	similar to unknown protein [Arabidopsis thaliana] (T	0.708	0.0028	0.0431	0.7029	0.0029	0.0355	-0.06579	0.4999	0.3596	-0.07085	0.4696	0.3136
247699_at	AT5G59840	Ras-related GTP-binding family protein	0.2979	0.0206	0.0845	0.3467	0.0124	0.0597	-0.07067	0.4281	0.3288	-0.02189	0.7984	0.4283
247700_at	AT5G59860	RNA recognition motif (RRM)-containing protein	-0.4836	0.7626	0.1	-0.6205	0.6811	0.4823	0.5918	0.6948	0.4293	0.4249	0.7771	0.422
247701_at	AT5G59900	pentatricopeptide (PPR) repeat-containing protein	0.3563	0.3913	0.3706	-0.8591	0.0815	0.1431	0.2529	0.5329	0.3724	-0.9625	0.0604	0.0889
247702_at	AT5G59500	protein-S-isoprenylcysteine O-methyltransferase	-0.08367	0.6708	0.4829	-0.3427	0.134	0.1861	-0.102	0.6066	0.4002	-0.361	0.1194	0.1344
247703_at	AT5G59560	SRR1 (SENSITIVITY TO RED LIGHT REDUCED 1	0.2894	0.2209	0.2757	0.7091	0.0238	0.0776	-0.6835	0.0267	0.0665	-0.2638	0.2571	0.2163
247704_at	AT5G59510	DVL18/RTFL5 (ROTUNDIFOLIA LIKE 5)	-1.1599	0.0793	0.1623	-0.9602	0.1247	0.179	-0.2427	0.6499	0.4144	-0.04306	0.9349	0.467
247705_at	AT5G59460	scarecrow-like transcription factor 11 (SCL11)	-0.00597	0.9635	0.5681	0.5802	0.0091	0.0522	0.1722	0.2328	0.2309	0.7583	0.0035	0.0192
247706_at	AT5G59480	haloacid dehalogenase-like hydrolase family protein	-1.4298	0.0097	0.0631	-1.1821	0.0184	0.0702	-0.2327	0.23	0.2295	0.01509	0.9313	0.466
247707_at	AT5G59450	scarecrow-like transcription factor 11 (SCL11)	-0.1835	0.2089	0.2674	0.2123	0.1584	0.2047	-0.8192	6.00E-04	0.0158	-0.4235	0.007	0.0261
247708_at	AT5G59550	zinc finger (C3HC4-type RING finger) family protein	-0.6226	0.0385	0.1131	-0.547	0.0558	0.1174	0.1226	0.436	0.3323	0.1982	0.2348	0.2043
247709_at	AT5G59250	sugar transporter family protein	-0.6596	0.0308	0.1018	-0.5542	0.0515	0.1126	-1.1119	0.0049	0.0296	-1.0065	0.007	0.0261
247710_at	AT5G59260	lectin protein kinase, putative	-0.344	0.5289	0.4327	0.449	0.4195	0.3505	0.2116	0.6937	0.4289	1.0046	0.1147	0.1311
247711_at	AT5G59270	lectin protein kinase family protein	-2.0975	0.0337	0.1062	-0.86	0.263	0.2715	-0.2858	0.5865	0.3932	0.9516	0.1207	0.1355
247712_at	AT5G59300	UBC7 (UBIQUITIN-CONJUGATING ENZYME 31);	-0.08177	0.6923	0.49	0.6145	0.0329	0.0899	-0.4398	0.0839	0.1274	0.2565	0.2527	0.2139
247713_at	AT5G59330	Encodes a Protease inhibitor/seed storage/LTP fam	1.7592	0.2113	0.2691	-1.2964	0.3348	0.3107	2.3879	0.1138	0.1514	-0.6677	0.6027	0.3642
247714_at	AT5G59340	WOX2 (WUSCHEL-related homeobox 2); transcript	-0.7186	0.0238	0.0897	-0.8084	0.0161	0.066	0.3757	0.1364	0.1686	0.2858	0.2299	0.2014
247715_at	AT5G59360	unknown protein	-0.8546	0.0585	0.1386	-0.6479	0.1175	0.1733	0.05387	0.8531	0.4793	0.2605	0.3937	0.2816
247716_at	AT5G59350	similar to unnamed protein product [Vitis vinifera] (G	-0.5632	0.211	0.269	-0.5479	0.2213	0.2467	-0.02947	0.8802	0.4868	-0.01424	0.9419	0.469
247717_at	AT5G59320	LTP3 (LIPID TRANSFER PROTEIN 3); lipid binding	1.3619	0.0184	0.0806	2.1381	0.0038	0.0388	0.5725	0.1067	0.1463	1.3488	0.0081	0.028
247718_at	AT5G59310	LTP4 (LIPID TRANSFER PROTEIN 4); lipid binding	0.5538	0.277	0.3099	1.4636	0.0293	0.0851	0.3053	0.3002	0.2688	1.2151	0.0091	0.0297
247719_at	AT5G59305	similar to unknown [Populus trichocarpa] (GB:ABK9	-1.2816	0.2712	0.3062	-1.2035	0.2972	0.2902	-1.892	0.0437	0.0872	-1.8139	0.0493	0.0786
247720_at	AT5G59290	UXS3 (UDP-GLUCURONIC ACID DECARBOXYLA	-0.3949	0.1235	0.2038	-0.3985	0.121	0.1763	-0.148	0.2271	0.2277	-0.1486	0.2177	0.1949
247721_at	AT5G59140	SKP1 family protein	0.4249	0.0958	0.1788	0.8045	0.0148	0.0641	-0.05353	0.7756	0.456	0.326	0.1368	0.1461
247722_at	AT5G59150	AtRABA2d (Arabidopsis Rab GTPase homolog A2d	0.1151	0.4255	0.3874	0.1508	0.3101	0.2974	-0.166	0.237	0.2335	-0.1303	0.3367	0.2564
247723_at	AT5G59220	protein phosphatase 2C, putative / PP2C, putative	0.6301	0.1514	0.2269	1.2029	0.0278	0.0831	-1.2911	0.0026	0.0236	-0.6283	0.0252	0.0525
247724_at	AT5G59380	MBD6 (methyl-CpG-binding domain 6); DNA binding	0.3643	0.1042	0.1866	0.2695	0.1961	0.2302	0.01672	0.928	0.5	-0.0781	0.6766	0.3896
247725_at	AT5G59410	similar to Rab5-interacting family protein [Arabidops	0.1472	0.293	0.319	-0.04316	0.7408	0.4715	0.8727	5.00E-04	0.0153	0.6823	0.0013	0.0133
247726_at	AT5G59430	ATTRF (TELOMERE REPEAT BINDING PROTEI	0.01025	0.966	0.5687	-0.1233	0.6147	0.4287	-0.2182	0.0508	0.0955	-0.3528	0.0113	0.0334
247727_at	AT5G59490	haloacid dehalogenase-like hydrolase family protein	2.7716	0.048	0.1261	-0.3664	0.7285	0.4683	1.2731	0.2654	0.2494	-1.865	0.131	0.1422
247728_at	no_match	no_match	1.9019	0.11	0.1921	-0.8212	0.4265	0.3536	1.3793	0.1875	0.204	-1.3438	0.1968	0.183
247729_at	AT5G59530	2-oxoglutarate-dependent dioxygenase, putative	1.6299	0.2596	0.2988	1.086	0.4302	0.3553	1.0068	0.3758	0.3057	0.4629	0.6709	0.3877
247730_at	AT5G59580	UDP-glucuronosyl/UDP-glucosyl transferase family	1.5403	0.1946	0.2588	1.1035	0.3273	0.3072	0.3798	0.0942	0.136	-0.05697	0.7595	0.4165
247731_at	AT5G59590	UDP-glucuronosyl/UDP-glucosyl transferase family	-0.05545	0.7315	0.5028	-0.02142	0.8938	0.5169	-0.3135	0.1059	0.1456	-0.2794	0.1372	0.1463
247732_at	AT5G59600	pentatricopeptide (PPR) repeat-containing protein	-0.3069	0.3632	0.3559	0.2177	0.5072	0.3875	-0.3712	0.2827	0.2596	0.1534	0.6352	0.3755
247733_at	AT5G59610	DNAJ heat shock N-terminal domain-containing pro	-0.2677	0.3199	0.3343	-0.2092	0.4253	0.3531	0.2709	0.0827	0.1264	0.3294	0.0488	0.0782
247734_at	AT5G59400	similar to hypothetical protein [Vitis vinifera] (GB:CA	-0.5023	0.0418	0.1176	-0.669	0.017	0.0677	-0.4798	0.0038	0.027	-0.6464	0.0012	0.013
247735_at	AT5G59440	thymidine kinase family protein	0.8178	0.0013	0.0376	0.5386	0.0063	0.0453	-0.3796	0.0066	0.0333	-0.6589	8.00E-04	0.0113
247736_at	AT5G59370	ACT4 (ACTIN 4)	-0.9574	0.3284	0.3392	0.07073	0.9385	0.5286	-2.0177	0.0216	0.0591	-0.9896	0.147	0.1528
247737_at	AT5G59200	pentatricopeptide (PPR) repeat-containing protein	-1.0864	0.134	0.2124	0.2923	0.6403	0.4384	-0.8547	0.2141	0.2204	0.524	0.4169	0.2912
247738_at	AT5G59210	myosin heavy chain-related	0.3397	0.0737	0.1562	0.5054	0.0231	0.0768	0.3744	0.0568	0.1018	0.5401	0.0186	0.0438
247739_at	AT5G59240	40S ribosomal protein S8 (RPS8B)	-0.322	0.4144	0.382	0.3306	0.4032	0.3427	-0.0217	0.9374	0.5028	0.631	0.072	0.0984
247740_at	AT5G58940	CRCK1 (CALMODULIN-BINDING RECEPTOR-LIK	1.0377	0.0563	0.136	0.8877	0.0851	0.1469	0.09137	0.7236	0.4398	-0.05855	0.8198	0.4341
247741_at	AT5G58960	GIL1 (GYM/ATIROPIC IN THE LIGHT)	-0.2677	0.2464	0.2915	0.0747	0.7242	0.4667	-0.1558	0.3861	0.3104	0.1866	0.3089	0.2429
247742_at	AT5G58980	ceramidase family protein	2.3141	0.0257	0.0929	-0.2795	0.697	0.4579	-1.8249	0.0523	0.097	-4.4185	0.0027	0.0171
247743_at	AT5G59010	protein kinase-related	0.3637	0.275	0.3085	0.2679	0.3927	0.3381	-0.1782	0.4183	0.3245	-0.2639	0.2526	0.2139
247744_at	AT5G59020	similar to unknown protein [Arabidopsis thaliana] (T	0.54604	0.8498	0.5381	-0.6281	0.0511	0.1122	0.5721	0.0661	0.1112	-0.102	0.6777	0.3899
247745_at	AT5G59030	COPT1 (COPPER TRANSPORTER 1); copper ion	-0.2075	0.1571	0.2311	-0.2039	0.1627	0.2078	-0.255	0.0285	0.0685	-0.2514	0.0297	0.0579
247746_at	AT5G58970	ATUCP2 (UNCOUPLING PROTEIN 2); oxidative pl	-0.2851	0.0895	0.1733	-0.1986	0.1951	0.2295	-0.1393	0.0462	0.0901	-0.05277	0.3403	0.2582
247747_at	AT5G59000	zinc finger (C3HC4-type RING finger) family protein	-0.5831	0.0667	0.1482	-0.0148	0.9524	0.5324	0.7362	0.0342	0.0757	1.3045	0.005	0.0222
247748_at	AT5G58920	similar to hypothetical protein Osl_001858 [Oryza s	0.2229	0.1405	0.218	0.5203	0.0128	0.0604	-0.3665	0.0393	0.082	-0.0691	0.6	0.3634
247749_at	AT5G58850	MYB119 (myb domain protein 119); DNA binding /	0.3254	0.4514	0.3988	1.976	0.0072	0.0478	0.1525	0.7159	0.4369	1.8031	0.0099	0.031
247750_at	AT5G58950	protein kinase family protein	0.06302	0.6995	0.4923	0.07481	0.7554	0.4768	-0.5453	0.0718	0.1164	-0.5635	0.0658	0.0934
247751_at	AT5G59050	similar to unknown [Populus trichocarpa] (GB:ABK9	-0.9519	0.0165	0.0774	-0.8771	0.0216	0.0747	-0.1911	0.2396	0.235	-0.1164	0.4479	0.3052
247752_at	AT5G59060	similar to glucose transmembrane transporter [Arab	-1.8958	0.0332	0.1056	-0.1557	0.8062	0.4916	-1.8859	0.0206	0.0577	-0.1458	0.7882	0.4252
247753_at	AT5G59070	glycosyl transferase family 1 protein	1.3086	0.1063	0.1885	3.279	0.0065	0.0459	-0.1825	0.7451	0.4466	1.7879	0.027	0.0546
247754_at	AT5G59080	similar to unknown protein [Arabidopsis thaliana] (T	-0.833	0.0744	0.1568	-0.4276	0.2856	0.2841	0.1636	0.4055	0.3188	0.5691	0.032	0.0602
247755_at	AT5G59090	ATSBT4.12; subtilase	-0.3352	0.6384	0.4724	-1.6716	0.0645	0.1268	0.8155	0.1052	0.1451	-0.5209	0.2534	0.2144
247756_at	AT5G59100	subtilase family protein	-2.6316	0.0396	0.1089	-0.2046	0.8204	0.496	-2.5545	0.0389	0.0815	-0.1274	0.8873	0.4536
247757_at	no_match	no_match	-2.2609	0.0619	0.1429	0.1844	0.8442	0.5028	-1.2849	0.0735	0.118	1.1604	0.095	0.1168
247758_at	AT5G59120	ATSBT4.13; subtilase	0.3829	0.6896	0.489	0.7932	0.4238	0.3524	-0.04393	0.9585	0.5073	0.3663	0.6683	0.3868
247759_at	AT5G59040	COPT3 (Copper transporter 3); copper ion transme	-0.4837	0.6663	0.4814	-1.4575	0.234	0.2543	-0.07733	0.9438	0.5042	-1.0511	0.3655	0.2694
247760_at	AT5G59130	subtilase family protein	-0.9394	0.0083	0.0599	-1.5495	0.0013	0.0312	-0.01316	0.9491	0.5053	-0.6232	0.0324	0.0607
247761_at	AT5G59160	TOPP2 (Type one serine/threonine protein phospha	0.07875	0.511	0.4253	-0.0927	0.4441	0.3613	0.2918	0.0212	0.0585	0.1203	0.2035	0.1871
247762_at	AT5G59170	proline-rich family protein	0.04537	0.9183	0.5566	-0.1107	0.803	0.4905	0.05066	0.9088	0.495	-0.1054	0.8122	0.4323
247763_at	AT5G59180	DNA-directed RNA polymerase II	0.09324	0.4768	0.4105	0.4394	0.0209	0.0738	-0.01471	0.9055	0.4938	0.3314	0.0465	0.0758
247764_at	AT5G59190	subtilase family protein	0.1307	0.8469	0.5375	-0.3152	0.6453	0.4401	-0.3762	0.4768	0.3502	-0.8221	0.1618	0.1623
247765_at	AT5G58860	CYP86A1 (cytochrome P450, family 86, subfamily A	0.9657	0.4281	0.3876	-0.02272	0.9844	0.5402	0.2571	0.8253	0.4713	-0.7314	0.5394	0.3409
247766_at	AT5G58870	FTSH9 (FtsH protease 9); ATP-dependent peptidas	-0.2215	0.2168	0.2731	-0.7326	0.0094	0.0507	-0.0553	0.5908	0.3949	-0.5664	0.0039	0.0202
247767_at	AT5G58890	AGL82; DNA binding / transcription factor	-0.7942	0.1299	0.2085	-0.2035	0.6515	0.4422	-0.4688	0.3243	0.2805	0.1219	0.7849	0.4243
247768_at	AT5G58900	myb family transcription factor	-1.1356	0.0194	0.0824	-1.1984	0.0163	0.0664	0.1203	0.5226	0.368	0.05756	0.7546	0.415
247769_at	AT5G58910	LAC16 (laccase 16); copper ion binding / oxidoredu	0.2749	0.8052	0.5255	-0.05992	0.9569	0.5335	0.3954	0.7239	0.4399	0.06064	0.9564	0.4725
247770_at	AT5G58930	similar to unknown protein [Arabidopsis thaliana] (T	0.5947	0.0119	0.0679	0.461	0.0274	0.0827	-0.06125	0.441	0.3345	-0.195	0.053	0.0821
247771_at	AT5G58590	RANBP1 (RAN BINDING PROTEIN 1)	0.137	0.4666	0.4058	0.5538	0.0314	0.0881	0.4031	0.0398	0.0825	0.8199	0.0036	0.0196
247772_at	AT5G58610	PHD finger transcription factor, putative	0.6449	0.6673	0.4817	0.4175	0.7792	0.4834	0.07661	0.882	0.4873	-0.1508	0.7712	0.4203
247773_at	AT5G58630	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.519	0.5701	0.4491	-0.4369	0.6304	0.4346	-0.03503	0.9687	0.5096	-0.9909	0.3035	0.2404
247774_at	AT5G58660	oxidoreductase, 2OG-Fe(II) oxygenase family prote	0.594	0.5792	0.4521	-0.1709	0.8708	0.5101	1.1358	0.3133	0.2751	0.3709	0.7257	0.4058
247775_at	AT5G58690	phosphoinositide-specific phospholipase C family p	-0.2097	0.6512	0.4766	-0.1975	0.6699	0.4486	-0.035	0.939	0.5031	-0.02277	0.9603	0.4733
247776_at	AT5G58700	phosphoinositide-specific phospholipase C family p	0.8333	0.0401	0.1156	0.4268	0.1997	0.2327	0.1883	0.5354	0.3733	-0.2182	0.4766	0.3164
247777_at	AT5G58740	nuclear movement family protein	-0.04262	0.8171	0.5288	-0.228	0.24	0.2577	0.7733	0.0021	0.0218	0.5779	0.0062	0.0244
247778_at	AT5G58750	wound-responsive protein-related	-1.1066	0.3785	0.3637	2.1078	0.1326	0.1848	-1.5971	0.2265	0.2274	1.6172	0.2217	0.197
247779_at	AT5G58760	DDB2 (DAMAGED DNA-BINDING 2); nucleotide bi	-0.07903	0.8528	0.5389	-0.413	0.3597	0.3226	-0.148	0.6513	0.415	-0.482	0.1875	0.1778
247780_at	AT5G58770	dehydrodolichyl diphosphate synthase, putative / DI	-1.4329	0.0017	0.0391	-1.395	0.0019	0.0329	-0.4621	0.0155	0.0496	-0.4242	0.0206	0.0465
247781_at	AT5G58784	dehydrodolichyl diphosphate synthase, putative / DI	-0.5377	0.5215	0.4296	-1.8575	0.0724	0.1349	2.4001	0.0351	0.0768	1.0803	0.2314	0.2022
247782_at	AT5G58790	unknown protein	0.2022	0.6525	0.4769	-0.291	0.5229	0.3933	-0.3866	0.3693	0.3024	-0.8798	0.0829	0.1074
247783_at	AT5G58800	quinone reductase family protein	0.302	0.0394	0.1145	0.1796	0.1476	0.1963	-0.00335	0.9748	0.5112	-0.1258	0.2759	0.226
247784_at	AT5G58810	subtilisin-like serine protease, pseudogene, contain	1.245	0.2391	0.2871	-1.7402	0.1255	0.1796	1.1953	0.2552	0.2438	-1.7899	0.1178	0.1333
247785_at	AT5G58820	subtilase family protein	0.02169	0.9904	0.5747	-1.0742	0.5623	0.4091	0.1233	0.9383	0.503	-0.9726	0.5514	0.3456
247786_at	AT5G58600	PMR5 (POWDERY MILDEW RESISTANT 5)	0.3257	0.3219	0.3354	0.5161	0.148	0.1967	-0.1113	0.7069	0.4336	0.07904	0.7886	0.4254
247787_at	AT5G58640	selenoprotein-related	0.6169	0.0053	0.0517	0.251	0.0883	0.1498	0.3451	0.0368	0.0791	-0.02075	0.862	0.4464
247788_at	AT5G58730	pfkB-type carbohydrate kinase family protein	0.4667	0.0268	0.0946	0.4248	0.0357	0.0932	-0.02853	0.8446	0.477	-0.07037	0.6332	0.3748
247789_at	AT5G58680	armadillo/beta-catenin repeat family protein	-0.5771	0.4326	0.3907	0.5845	0.4273	0.3541	-0.7185	0.3389	0.2878	0.4431	0.54	0.341
247790_at	AT5G58720	PRLI-interacting factor, putative	0.2425	0.0472	0.1251	0.3395	0.0166	0.0669	-0.1524	0.0691	0.1139	-0.05545	0.42	0.2925
247791_at	AT5G58710	ROC7 (rotamase CyP 7); peptidyl-prolyl cis-trans is	0.7205	0.0036	0.0457	0.7962	0.0025	0.034	0.3837	0.0095	0.0389	0.4594	0.005	0.0222
247792_at	AT5G58787	zinc finger (C3HC4-type RING finger) family protein	0.632	0.1067	0.189	0.7095	0.0804	0.1422	-0.1165	0.4864	0.354	-0.03895	0.8105	0.4319
247793_at	AT5G58650	PSY1 (PLANT PEPTIDE CONTAINING SULFATED	-0.741	0.0419	0.1177	-0.3581	0.2269	0.2497	0.7388	0.0348	0.0765	1.1218	0.0088	0.0293
247794_at	AT5G58670	ATPLC1 (PHOSPHOLIPASE C 1); phospholipase C	0.3261	0.3581	0.3535	0.181	0.5956	0.4217	-0.2422	0.0388	0.0814	-0.3873	0.0084	0.0285
247795_at	AT5G58620	zinc finger (CCCH-type) family protein	0.2785	0.1892	0.2548	0.3646	0.1074	0.1653	-0.4691	0.0563	0.1013	-0.3831	0.0955	0.1172
247796_at	AT5G58782	dehydrodolichyl diphosphate synthase, putative / DI	0.7864	0.1151	0.1963	0.1273	0.8931	0.5167	1.7512	0.0483	0.0924	0.09205	0.8897	0.4541
247797_at	AT5G58780	dehydrodolichyl diphosphate synthase, putative / DI	0.1814	0.7304	0.5027	0.6802	0.2379	0.2565	-0.6233	0.2728	0.2539	-0.1245	0.8122	0.4323
247798_at	AT5G58830	subtilase family protein	-1.8099	0.1747	0.2446	-1.5545	0.2298	0.2514	-0.4637	0.6584	0.4174	-0.2083	0.8409	0.4403
247799_at	AT5G58840	subtilase family protein	-0.1265	0.8944	0.5498	-0.4559	0.637	0.4372	0.4598	0.6342	0.4092	0.1304	0.8911	0.4545
247800_at	AT5G58570	unknown protein	1.5671	0.0067	0.0553	1.3652	0.0109	0.056	-0.2149	0.2566	0.2445	-0.4169	0.0623	0.0906
247801_at	AT5G58560	phosphatidate cytidylyltransferase family protein	-0.2901	0.3699	0.3595	-0.6012	0.1046	0.1634	0.1183	0.6093	0.4011	-0.1928	0.4179	0.2917
247802_at	AT5G58580	ATL63; protein binding / zinc ion binding	-0.6	0.1607	0.2341	-0.6356	0.1427	0.1928	-0.625	0.1479	0.1775	-0.6605	0.1314	0.1425
247803_at	no_match	no_match	0.4244	0.2327	0.2834	0.7831	0.0605	0.1222	-0.1418	0.6632	0.4189	0.2168	0.6126	0.3307
247804_at	AT5G58170	glycerophosphoryl diester phosphodiesterase family	-0.5656	0.5002	0.4206	0.8104	0.3487	0.3175	0.2389	0.7546	0.4495	1.6149	0.0864	0.1101
247805_at	AT5G58180	ATYKT62	-2.8062	0.02	0.0834	-0.9604	0.2689	0.2749	-1.4366	0.1275	0.1621	0.4091	0.6138	0.368
247806_at	AT5G58270	STA1 (STARIK 1); ATPase, coupled to transmembr	-0.03256	0.8371	0.5344	-0.3319	0.089	0.1504	-0.09233	0.9345	0.5027	0.6546	0.5885	0.3594
247807_at	AT5G58360	ATOFP3/OFP3 (Arabidopsis thaliana ovate family p	-2.9732	0.0166	0.0775	0.1768	0.8251	0.4975	-2.6475	0.0242	0.063	0.5026	0.5392	0.3409
247808_at	AT5G58190	ECT10	0.401	0.0442	0.1212	0.6962	0.0073	0.0483	0.09062	0.4525	0.3397	0.3859	0.024	0.0509
247809_at	AT5G58200	transcriptional factor B3 family protein	0.06025	0.9603	0.5674	0.8086	0.5165	0.3912	-0.09373	0.937	0.5027	0.6546	0.5885	0.3594
247810_at	AT5G58250	RPT3 (root phototropism 3); ATPase	0.9149	1.00E-04	0.0312	0.8213	2.00E-04	0.0249	0.1875	0.0349	0.0766	0.09393	0.191	0.1798
247811_at	AT5G58430	ATEXO70B1 (exocyst subunit EXO70 family protein	-0.01875	0.9263	0.5586	0.06959	0.7335	0.4693	-0.3726	0.0237	0.0624	-0.2843	0.0534	0.0826
247812_at	AT5G58390	peroxidase, putative	0.2206	0.6733	0.4838	0.2886	0.5844	0.4179	1.1128	0.0267	0.0664	1.1808	0.0221	0.0484
247813_at	AT5G58330	malate dehydrogenase (NADP), chloroplast, putativ	0.1368	0.2417	0.2887	-0.1807	0.144	0.1937	0.26	0.0254	0.0647	-0.05758	0.4842	0.3193
247814_at	AT5G58310	hydrolase, alpha/beta fold family protein	-0.5901	0.1151	0.1963	-1.3152	0.011	0.0563	0.7131	0.0109	0.0414	-0.01198	0.9435	0.4693
247815_at	AT5G58420	40S ribosomal protein S4 (RPS4D)	0.296	0.1638	0.2367	0.4633	0.0561	0.1177	0.08486	0.6042	0.3996	0.2522	0.1703	0.1674
247816_at	AT5G58260	Encodes subunit NDH-N of NAD(P)H:plastoquinone	-1.2629	1.00E-04	0.0312	-1.5193	1.00E-04	0.0249	0.6714	0.0016	0.0204	0.415	0.0095	0.0303
247817_at	AT5G58375	similar to unknown protein [Arabidopsis thaliana] (T	0.802	0.0149	0.0739	0.4968	0.0641	0.1263	0.2568	0.2514	0.2415	-0.04839	0.8131	0.4326
247818_at	AT5G58370	GTP binding	-0.2968	0.0994	0.1819	-0.496	0.0396	0.0985	-0.03104	0.8161	0.4686	-0.1524	0.2912	0.2342
247819_at	AT5G58350	WNK4 (Arabidopsis WNK kinase 4); kinase	-0.05909	0.7656	0.5132	0.11	0.5844	0.4179	-0.3881	0.0364	0.0784	-0.219	0.1556	0.1585
247820_at	AT5G58380	CIPK10 (CBL-INTERACTING PROTEIN KINASE 1	-0.04928	0.754	0.5097	0.1478	0.3711	0.3278	-0.5229	0.0235	0.0622	-0.3258	0.0906	0.1134
247821_at	AT5G58230	MIS1 (MULTICOPY SUPPRESSOR OF IRA1)	0.3042	0.0937	0.1772	0.1137	0.4591	0.3676	0.05536	0.593	0.3958	-0.1352	0.2297	0.2013
247822_at	AT5G58440	phox (PX) domain-containing protein	-0.1322	0.1278	0.2066	-0.1471	0.1	0.1593	0.208	0.0388	0.0814	0.1931	0.0482	0.0775
247823_at	AT5G58450	binding	0.5327	0.0282

247890_at	AT5G57940	ATCNGC5 (CYCLIC NUCLEOTIDE GATED CHAN	-0.1004	0.5626	0.4458	-0.3887	0.0711	0.1334	-0.1641	0.29	0.2636	-0.4524	0.0283	0.0562
247891_at	AT5G57960	GTP-binding family protein	-0.5153	0.0157	0.0756	-0.8614	0.0025	0.034	-0.4781	0.0042	0.0278	-0.8242	5.00E-04	0.0097
247892_at	AT5G57970	methyladenine glycosylase family protein	-0.3946	0.453	0.3996	0.4843	0.3658	0.3256	-0.0733	0.8849	0.4882	0.8056	0.1653	0.1644
247893_at	AT5G57980	eukaryotic rpb5 RNA polymerase subunit family pro	-1.0854	0.1407	0.2182	-0.06441	0.9186	0.5237	-0.535	0.4173	0.324	0.486	0.4579	0.3092
247894_at	AT5G58003	CPL4 (C-TERMINAL DOMAIN PHOSPHATASE-LI	0.1375	0.4178	0.3838	0.2163	0.2288	0.2508	0.06894	0.6745	0.4224	0.1477	0.3873	0.2789
247895_at	AT5G58010	basic helix-loop-helix (bHLH) family protein	-0.1425	0.8647	0.5423	-0.3828	0.6513	0.4422	-0.7185	0.4118	0.3216	-0.9587	0.289	0.2329
247896_at	AT5G57950	26S proteasome regulatory subunit, putative	0.08901	0.6622	0.4801	0.1537	0.4617	0.3687	0.4313	0.0046	0.0288	0.496	0.0027	0.0172
247897_at	AT5G57810	TET15 (TETRASPANIN15)	-0.09146	0.9315	0.5602	-0.01141	0.9914	0.542	-0.9047	0.4165	0.3236	-0.8247	0.4556	0.3082
247898_at	AT5G57360	ZTL (ZEITLUPE); ubiquitin-protein ligase	0.0646	0.6461	0.4751	0.2706	0.1065	0.1646	-0.5393	0.0144	0.0479	-0.3332	0.0629	0.091
247899_at	AT5G57345	similar to unknown [Populus trichocarpa x Populus	-0.1176	0.4717	0.4082	-0.2683	0.1442	0.1939	0.3092	0.0205	0.0576	0.1584	0.1293	0.1409
247900_at	AT5G57290	60S acidic ribosomal protein P3 (RPP3B)	0.1608	0.3474	0.3486	0.4955	0.0305	0.0868	0.4534	0.012	0.0434	0.7881	0.0016	0.0142
247901_at	AT5G57300	UbiE/COQ5 methyltransferase family protein	0.2056	0.0413	0.1171	0.3015	0.0121	0.0591	0.255	0.0212	0.0586	0.351	0.0072	0.0264
247902_at	AT5G57350	AHA3 (Arabidopsis H(+)-ATPase 3); ATPase	-0.3167	0.2508	0.2939	-0.202	0.4404	0.3596	-0.8314	0.0049	0.0297	-0.7167	0.0084	0.0285
247903_at	AT5G57340	similar to hypothetical protein MIKDRAFT_AC15528	0.6774	0.1782	0.2468	0.497	0.2975	0.2904	0.02767	0.9121	0.4957	-0.1526	0.552	0.3458
247904_at	AT5G57390	AIL5 (AINTEGUMENTA-LIKE 5); DNA binding / trar	0.3849	0.4375	0.3926	-0.4491	0.3716	0.3281	0.615	0.1766	0.1963	-0.219	0.5908	0.3602
247905_at	AT5G57400	unknown protein	-0.7266	0.6672	0.4817	-2.663	0.1647	0.2089	0.06404	0.9405	0.5036	-1.8723	0.0808	0.1057
247906_at	AT5G57420	IAA33 (INDOLEACETIC ACID-INDUCED 33); transc	1.0877	0.3835	0.3665	-1.5863	0.227	0.2497	0.9329	0.4488	0.338	-1.7412	0.1925	0.1806
247907_at	AT5G57460	protein binding / protein transporter	0.2986	0.1138	0.1955	0.1814	0.2877	0.2852	-0.0993	0.5391	0.375	-0.2166	0.2173	0.1948
247908_at	AT5G57440	GS1 (GLYCEROL-3-PHOSPHATASE 2); hydrolase	-0.2894	0.4469	0.3966	-0.447	0.263	0.2715	-0.5981	0.1068	0.1463	-0.7557	0.0588	0.0874
247909_at	AT5G57370	similar to unnamed protein product [Vitis vinifera] (G	0.2443	0.442	0.3945	0.8734	0.0381	0.0966	-0.3222	0.2793	0.2576	0.307	0.2993	0.2383
247910_at	AT5G57410	similar to unknown protein [Arabidopsis thaliana] (T	-0.2336	0.303	0.3248	0.2684	0.2464	0.2618	-0.3885	0.1009	0.1418	0.1135	0.5686	0.3522
247911_at	AT5G57430	XRCC3 (Arabidopsis thaliana homolog of XRCC3);	0.3082	0.216	0.2723	-0.179	0.8394	0.501	0.3866	0.6629	0.4189	-1.0006	0.2909	0.234
247912_at	AT5G57480	AAA-type ATPase family protein	-0.1288	0.849	0.5379	0.6294	0.3773	0.3307	-1.0077	0.1315	0.165	-0.2496	0.6639	0.3855
247913_at	AT5G57510	unknown protein	0.04395	0.9071	0.5531	0.2609	0.5015	0.3853	0.1084	0.7702	0.4543	0.3253	0.4011	0.2846
247914_at	AT5G57540	xyloglucan:xyloglucosyl transferase, putative / xylog	1.3871	0.0723	0.155	1.8578	0.0314	0.0881	-0.7949	0.0874	0.1306	-0.3242	0.4103	0.2883
247915_at	AT5G57570	similar to unknown protein [Arabidopsis thaliana] (T	-1.1893	0.2984	0.3224	0.004877	0.9963	0.5432	-1.907	0.1281	0.1626	-0.7128	0.5138	0.3312
247916_at	AT5G57590	BIO1 (BIOTIN AUXOTROPH 1)	-0.403	0.2695	0.3051	-0.4469	0.2286	0.2507	-0.1573	0.5899	0.3947	-0.2012	0.4959	0.3242
247917_at	AT5G57590	BIO1 (BIOTIN AUXOTROPH 1)	-1.3955	0.1446	0.2209	0.6899	0.4215	0.3513	-2.9793	0.0181	0.0539	-0.8939	0.3108	0.2438
247918_at	AT5G57610	protein kinase family protein	-0.1599	0.3315	0.3408	-0.04745	0.7596	0.4778	0.2408	0.1716	0.1931	0.3532	0.0713	0.0978
247919_at	AT5G57650	initiation factor-related	-0.04364	0.9606	0.5675	0.8035	0.3879	0.3358	-1.4068	0.0642	0.1093	-0.5596	0.3701	0.2713
247920_at	AT5G57670	protein kinase family protein	-0.4078	0.6815	0.5491	0.4385	0.5839	0.4177	-0.2364	0.8081	0.4661	0.7174	0.4803	0.3177
247921_at	AT5G57660	zinc finger (B-box type) protein	-0.3116	0.0314	0.1027	-0.3167	0.0299	0.0859	0.2493	0.0601	0.1053	0.2442	0.0636	0.0916
247922_at	AT5G57500	transferase, transferring glycosyl groups	0.02448	0.9484	0.5644	-0.3832	0.3418	0.3143	0.7678	0.0764	0.1205	0.3601	0.3276	0.2523
247923_at	AT5G57490	porin, putative	0.00602	0.9975	0.5763	-0.3797	0.1114	0.1685	0.2692	0.1102	0.1486	-0.1111	0.4461	0.3045
247924_at	AT5G57655	xylose isomerase family protein	0.6411	0.0738	0.1562	1.2624	0.009	0.0521	-1.2282	0.0099	0.0398	-0.6068	0.0849	0.1089
247925_at	AT5G57560	TCH4 (TOUCH 4); hydrolase, acting on glycosyl bo	-0.7093	0.4097	0.3798	-0.7575	0.3816	0.3327	0.252	0.2972	0.2672	0.2038	0.3875	0.279
247926_at	AT5G57280	methyltransferase	0.7573	0.0372	0.1113	0.1059	0.6897	0.4555	-0.2093	0.2893	0.2632	-0.8719	0.0085	0.0287
247927_at	AT5G57310	unknown protein	-0.6063	0.4617	0.4037	1.5401	0.1077	0.1655	-0.585	0.287	0.2619	1.5613	0.0306	0.0589
247928_at	AT5G57320	villin, putative	0.069	0.7712	0.515	-0.06436	0.7861	0.4849	-0.1438	0.5519	0.3797	-0.2772	0.2794	0.2279
247929_at	AT5G57330	aldose 1-epimerase family protein	0.6164	0.0065	0.0549	0.4666	0.0171	0.0677	0.6823	0.001	0.0178	0.5327	0.0026	0.0169
247930_at	AT5G57060	similar to unknown protein [Arabidopsis thaliana] (T	0.08419	0.7779	0.5173	0.5162	0.138	0.1891	0.3822	0.0524	0.0971	0.8143	0.0043	0.0209
247931_at	AT5G57040	lactoylglutathione lyase family protein / glyoxalase I	-0.2599	0.0935	0.1772	-0.3719	0.035	0.0923	-0.1059	0.2866	0.2616	-0.2179	0.0648	0.0926
247932_at	AT5G56920	cysteine protease inhibitor	-1.9513	0.1038	0.1862	0.07429	0.9402	0.5291	-0.8116	0.4248	0.3274	1.2139	0.2549	0.2151
247933_at	AT5G56980	similar to unknown protein [Arabidopsis thaliana] (T	-1.5363	0.0088	0.0607	-0.6629	0.1083	0.1658	-0.5744	0.0515	0.0962	0.299	0.2258	0.1993
247934_at	AT5G57000	similar to unknown protein [Arabidopsis thaliana] (T	-0.7701	0.0123	0.0685	-0.5753	0.0316	0.0884	0.4918	0.0116	0.0427	0.6866	0.0035	0.0194
247935_at	AT5G56970	ribosomal protein S16 family protein	-0.5367	0.0079	0.0585	0.6496	0.0046	0.0416	0.8055	0.001	0.0179	0.898	7.00E-04	0.0105
247936_at	AT5G57030	LUT2 (LUTEIN DEFICIENT 2); lycopene epsilon cy	-0.6446	0.0012	0.036	-1.0576	2.00E-04	0.0249	0.2777	0.0239	0.0628	-0.1353	0.1592	0.1607
247937_at	AT5G57110	ACA8 (AUTOINHIBITED CA2+ -ATPASE, ISOFOR	0.2789	0.399	0.3749	0.1743	0.5873	0.4187	-0.2097	0.3006	0.269	-0.3143	0.1496	0.1544
247938_at	AT5G57440	ATPAP28/PAP28 (purple acid phosphatase 28); ac	-0.833	0.0088	0.0607	-0.1534	0.4285	0.3547	-1.4401	0.0011	0.0181	-0.7605	0.0112	0.0331
247939_at	AT5G57160	ATLIG4 (ARABIDOPSIS THALIANA DNA LIGASE	0.5355	0.1027	0.1852	0.665	0.0589	0.1207	-0.2195	0.4363	0.3324	-0.08998	0.741	0.4108
247940_at	AT5G57190	PSD2 (PHOSPHATIDYLSERINE DECARBOXYLAS	0.07569	0.8279	0.5318	-0.6281	0.1264	0.1803	0.2403	0.5021	0.3603	-0.4634	0.2284	0.2006
247941_at	AT5G57200	epsin N-terminal homology (ENTH) domain-contain	-1.0017	0.3292	0.3395	-1.0133	0.3243	0.3056	-1.7885	0.1185	0.1551	-1.8002	0.1168	0.1325
247942_at	AT5G57120	similar to unnamed protein product [Vitis vinifera] (G	0.4721	0.0108	0.0654	0.3274	0.0354	0.0929	-0.5341	0.007	0.034	-0.6787	0.0029	0.0176
247943_at	AT5G57170	macrophage migration inhibitory factor family protei	-0.9721	0.001	0.0358	-0.778	0.0024	0.0339	0.3833	0.0281	0.0681	0.5774	0.0071	0.0263
247944_at	AT5G57260	transporter-related	-0.08616	0.7557	0.5104	0.03385	0.9022	0.5195	-0.4394	0.1646	0.1882	-0.3193	0.2845	0.2306
247945_at	AT5G57150	basic helix-loop-helix (bHLH) family protein	1.1056	0.0011	0.036	0.9532	0.002	0.033	0.2561	0.1253	0.1602	0.1036	0.4777	0.3167
247946_at	AT5G57180	CIA2 (CHLOROPLAST IMPORT APPARATUS 2)	0.1137	0.6393	0.4726	-0.1999	0.4238	0.3524	-0.00402	0.9795	0.5124	-0.3176	0.0962	0.1176
247947_at	AT5G57090	EIR1 (ETHYLENE INSENSITIVE ROOT 1); auxin/h	0.5514	0.5853	0.4545	-0.447	0.4929	0.3815	0.5313	0.2087	0.217	-0.2672	0.4933	0.3233
247948_at	AT5G57130	protein binding	-0.1012	0.7955	0.5226	0.436	0.2987	0.2909	0.004417	0.9909	0.5154	0.5416	0.2124	0.192
247949_at	AT5G57220	CYP81F2 (cytochrome P450, family 81, subfamily F	-0.1849	0.7743	0.5161	0.339	0.6038	0.4247	-0.3295	0.374	0.3047	0.1945	0.5868	0.3587
247950_at	AT5G57230	similar to unknown [Populus trichocarpa x Populus	0.3248	0.1777	0.2465	0.5014	0.0653	0.1277	0.3897	0.0104	0.0404	0.5662	0.0027	0.0171
247951_at	AT5G57240	oxysterol-binding family protein	-0.6709	0.5143	0.427	1.3826	0.2148	0.2426	-1.9207	0.1102	0.1486	0.1327	0.8944	0.4556
247952_at	AT5G57250	similar to pentatricopeptide (PPR) repeat-containing	-0.1378	0.6006	0.4599	-0.6915	0.0464	0.1068	-0.6372	0.0585	0.1034	-1.1909	0.008	0.0278
247953_at	AT5G57260	CYP71B10 (cytochrome P450, family 71, subfamily	1.8722	0.1609	0.2341	0.2776	0.8115	0.4934	-0.1242	0.9147	0.4964	-1.7188	0.1898	0.1791
247954_at	AT5G56870	BGAL4 (beta-galactosidase 4); beta-galactosidase	1.1346	0.116	0.197	1.8196	0.0326	0.0895	-0.825	0.0492	0.0936	-0.1401	0.6602	0.3843
247955_at	AT5G56950	NAP1;3/NFA3 (NUCLEOSOME ASSEMBLY PROT	-0.3637	0.3962	0.3734	-0.2096	0.6134	0.4282	-0.8138	0.0677	0.1128	-0.6597	0.114	0.1306
247956_at	AT5G56970	CKX3 (CYTOKININ OXIDASE 3); cytokinin dehydr	0.5912	0.3035	0.325	0.8474	0.1661	0.2099	0.07557	0.8874	0.489	0.3318	0.5441	0.3425
247957_at	AT5G57050	ABI2 (ABA INSENSITIVE 2); protein serine/threonine	0.7066	0.0125	0.0692	0.8556	0.0064	0.0457	-0.5152	0.0326	0.0736	-0.3661	0.0846	0.1086
247958_at	AT5G57070	hydroxyproline-rich glycoprotein family protein	0.7271	0.25	0.2936	-0.08324	0.8851	0.5147	0.5054	0.0885	0.1313	-0.3049	0.2477	0.2111
247959_at	AT5G57080	similar to unknown protein [Arabidopsis thaliana] (T	0.6683	0.3783	0.3636	1.1956	0.1512	0.1992	0.259	0.7208	0.4389	0.7863	0.3088	0.2429
247960_at	AT5G57020	NMT1 (N-MYRISTOYLTRANSFERASE 1)	0.5249	0.0166	0.0775	0.5669	0.0129	0.0605	-0.09463	0.305	0.2712	-0.05261	0.5491	0.3448
247961_at	AT5G56570	Identical to F-box/FBDLRR-repeat protein At5g565	-0.1774	0.7866	0.5197	-0.8397	0.2424	0.2594	-1.0176	0.1721	0.1934	-1.68	0.0518	0.0811
247962_at	AT5G56580	ATMKI9 (ARABIDOPSIS MDK1); kinase	0.2411	0.2636	0.3017	0.6305	0.0273	0.0826	0.1137	0.5731	0.3878	0.5031	0.0535	0.0826
247963_at	AT5G56590	glycosyl hydrolase family 17 protein	-0.3096	0.1414	0.2186	-0.5797	0.0267	0.0816	0.2626	0.0347	0.0764	-0.00749	0.9328	0.4664
247964_at	AT5G56600	PFN3/PRF3 (PROFILIN 3); actin binding	-0.7325	0.0193	0.0823	-0.2152	0.3284	0.3078	0.6518	0.0045	0.0287	1.1691	5.00E-04	0.0095
247965_at	AT5G56540	AGP14 (ARABINOGALACTAN PROTEIN 14)	-0.71	0.1304	0.2089	-0.9236	0.0689	0.1317	0.25	0.4236	0.3269	0.03637	0.9032	0.4582
247966_at	AT5G56610	dual specificity protein phosphatase family protein	0.3019	0.2554	0.2966	0.4077	0.1477	0.1965	-0.06207	0.7986	0.4629	0.04371	0.8571	0.445
247967_at	AT5G56620	ANAC099 (Arabidopsis NAC domain containing pro	1.7104	0.2316	0.283	-0.4896	0.7073	0.4613	0.9399	0.3874	0.311	-1.2601	0.2637	0.2195
247968_at	AT5G56670	40S ribosomal protein S30 (RPS30C)	0.154	0.166	0.2381	0.2607	0.0458	0.106	0.3756	0.0132	0.0457	0.4822	0.0055	0.0231
247969_at	AT5G56700	F-box protein-related	-1.7406	0.2229	0.277	-1.0256	0.4436	0.3611	-0.908	0.3559	0.2961	-0.193	0.8355	0.4387
247970_at	AT5G56720	malate dehydrogenase, cytosolic, putative	-0.3316	0.7006	0.4928	0.3994	0.6448	0.4399	0.8652	0.3314	0.2839	1.5963	0.1112	0.1286
247971_at	AT5G56730	peptidase M16 family protein / insulinase family pro	0.3041	0.2857	0.3148	-0.2115	0.4403	0.3596	0.4683	0.0863	0.1296	-0.04729	0.8304	0.4372
247972_at	AT5G56740	HAG2 (HISTONE ACETYLTRANSFERASE OF TH	0.1154	0.7092	0.4959	-0.05853	0.849	0.5041	-0.2373	0.3279	0.2823	-0.4113	0.1259	0.1388
247973_at	AT5G56770	similar to unknown protein [Arabidopsis thaliana] (T	-0.4517	0.6585	0.4786	1.1079	0.3073	0.2959	-1.3198	0.2361	0.2329	0.2397	0.8128	0.4325
247974_at	AT5G56780	similar to unknown protein [Arabidopsis thaliana] (T	0.1431	0.5785	0.452	0.2418	0.365	0.3252	0.01588	0.9498	0.5055	0.4008	0.1659	0.1648
247975_at	AT5G56800	similar to F-box family protein [Arabidopsis thaliana	-0.6087	0.6776	0.4851	0.4807	0.7416	0.4718	0.7946	0.5904	0.3948	1.884	0.2382	0.2061
247976_at	AT5G56830	transposable element gene	0.724	0.0291	0.0989	-0.3495	0.1833	0.222	0.3813	0.1544	0.1819	-0.6923	0.0334	0.0617
247977_at	AT5G56850	similar to unknown [Populus trichocarpa x Populus	-0.2296	0.4176	0.3836	-0.4869	0.1279	0.1815	-0.5952	0.0583	0.1033	-0.8525	0.0197	0.045
247978_at	AT5G56710	60S ribosomal protein L31 (RPL31C)	-0.00797	0.9507	0.5648	0.2148	0.1508	0.1989	0.4209	0.0011	0.0181	0.6437	2.00E-04	0.0078
247979_at	AT5G56750	Ndr family protein	-0.4665	0.2604	0.2998	-0.2989	0.4484	0.3633	-1.5894	4.00E-04	0.0145	-1.4219	6.00E-04	0.01
247980_at	AT5G56860	GNC (GATA, NITRATE-INDUCIBLE, CARBON ME	-0.5787	0.0022	0.041	-0.141	0.1635	0.2083	-0.6664	0.0013	0.0191	-0.2287	0.0506	0.0799
247981_at	AT5G56640	MIOX5 (MYO-INOSITOL OXYGENASE 5)	-0.7576	0.3954	0.3729	-2.0252	0.0638	0.126	1.3564	0.1638	0.1877	0.08889	0.9165	0.4617
247982_at	AT5G56760	AtSerat1;1 (SERINE ACETYLTRANSFERASE 52);	0.0465	0.822	0.5301	0.1601	0.4548	0.3659	-0.1117	0.5006	0.3598	0.001928	0.9904	0.4803
247983_at	AT5G56630	phosphofructokinase family protein	0.5131	0.0106	0.0649	0.5871	0.0066	0.0461	-0.01968	0.7907	0.4604	0.05436	0.477	0.3165
247984_s_at	AT5G56650;AT5G56660	[AT5G56650, ILL1 (IAA-leucine resistant (ILR)-like	-0.05236	0.7653	0.5131	0.3765	0.0832	0.1449	-0.1941	0.2588	0.2457	0.2347	0.1869	0.1775
247985_at	AT5G56790	protein kinase family protein	-0.1191	0.5788	0.4521	-0.1796	0.4143	0.3479	-0.2972	0.2065	0.2157	-0.3577	0.1441	0.151
247986_at	AT5G56800	unknown protein	1.8524	0.0818	0.1654	1.3794	0.1601	0.206	0.4898	0.4344	0.3317	0.01685	0.9776	0.4775
247987_at	AT5G56900	CwfJ-like family protein / zinc finger (CCCH-type) fa	0.4354	0.1348	0.2132	0.4119	0.1516	0.1995	-0.8638	0.0012	0.0187	-0.8873	0.0011	0.0123
247988_at	AT5G56910	cysteine protease inhibitor	0.1811	0.0455	0.1227	-0.103	0.178	0.2183	0.6588	5.00E-04	0.0148	0.3747	0.004	0.0204
247989_at	AT5G56360	pyruvate kinase, putative	0.7106	0.0062	0.0542	0.4492	0.029	0.0848	0.2278	0.1662	0.1893	-0.03352	0.8158	0.4331
247990_at	AT5G56360	calmodulin-binding protein	0.3523	0.1941	0.2583	0.7279	0.0323	0.0889	-0.3378	0.1488	0.1782	0.03783	0.8513	0.4431
247991_at	AT5G56320	ATEXPA14 (ARABIDOPSIS THALIANA EXPANSIN	-0.1911	0.8748	0.5451	-0.8781	0.4836	0.3775	0.3251	0.7894	0.46	-0.3619	0.7665	0.4188
247992_at	AT5G56520	similar to unknown protein [Arabidopsis thaliana] (T	0.5057	0.1774	0.1981	0.9655	0.0191	0.0712	-0.3429	0.2485	0.2402	0.1168	0.6597	0.3873
247993_at	AT5G56130	transducin family protein / WD-40 repeat family prot	-0.1381	0.1755	0.2452	-0.00724	0.9354	0.5279	0.1405	0.1224	0.1583	0.2714	0.0195	0.0448
247994_at	AT5G56140	KH domain-containing protein	0.03139	0.8151	0.5284	-0.1376	0.3352	0.3109	-0.6367	0.0072	0.0342	-0.8057	0.003	0.0179
247995_at	AT5G56160	transporter	0.2738	0.6313	0.4702	-0.2302	0.6853	0.4539	-0.2012	0.6998	0.4312	-0.7052	0.2199	0.196
247996_at	AT5G56170	similar to unknown protein [Arabidopsis thaliana] (T	-0.5566	0.0362	0.1097	-0.4396	0.0706	0.1328	0.5117	0.0057	0.0314	0.6288	0.0027	0.017
247997_at	AT5G56180	ATARP8 (ACTIN-RELATED PROTEIN 8); structura	0.7127	0.0138	0.0719	0.6633	0.0175	0.0686	-0.05519	0.7617	0.4516	-0.1047	0.5714	0.3531
247998_at	AT5G56200	zinc finger (C2H2 type) family protein	-0.01219	0.9833	0.5728	-0.3791	0.5263	0.3946	0.156	0.7896	0.4601	-0.2109	0.7193	0.4038
247999_at	AT5G56150	UBC30 (UBIQUITIN-CONJUGATING ENZYME 30)	0.912	0.0221	0.0872	0.9103	0.0222	0.0753	0.9667	0.0037	0.0268	0.9649	0.0038	0.0199
248000_at	AT5G56190	WD-40 repeat family protein	0.6026	0.018	0.0804	0.5847	0.0199	0.0722	-0.2614	0.0588	0.1039	-0.2794	0.0489	0.0782
248001_at	AT5G56860	CBL2 (calcineurin B-like protein 2); calcium ion bin	0.07727	0.6028	0.4604	-0.1783	0.2629	0.2715	0.169	0.2848	0.2606	-0.08654	0.5618	0.3496
248002_at	AT5G56180	ATARP8 (ACTIN-RELATED PROTEIN 8); structura	0.0706	0.7875	0.5199	0.6497	0.0568	0.1186	-1.2616	8.00E-04	0.0163	-0.6825	0.0078	0.0275
248003_at	AT5G56220	nucleoside-triphosphatase/ nucleotide binding	-0.01146	0.9779	0.5717	0.5766	0.2123	0.241	-0.2514	0.2433	0.2369	0.3365	0.1415	0.1492
248004_at	AT5G56230	prenylated rab acceptor (PRA1) family protein	0.001193	0.9975	0.5763	-0.1547	0.6842	0.4536	-0.04456	0.7839	0.4586	-0.2005	0.2576	0.2166
248005_at	AT5G56240	similar to unknown protein [Arabidopsis thaliana] (T	0.7176	0.012	0.0681	0.6917	0.0136	0.0618	-0.3041	0.0686	0.1137	-0.3299	0.055	0.0839
248006_at	AT5G56250	similar to unknown protein [Arabidopsis thaliana] (T	0.6272	0.0114	0.0668	0.4252	0.0397	0.0988	0.03387	0.8226	0.4704	-0.1681	0.3005	0.2389
248007_at	AT5G56260	dimethylmenaquinone methyltransferase family pro	0.3574	0.0478	0.1259	0.4651	0.0214	0.0745	0.126	0.3763	0.3059	-0.2337	0.139	0.1475
248008_at	AT5G56270	WRKY2 (WRKY DNA-binding protein 2); transcripte	0.3454	0.1131	0.1949	0.4547	0.0563	0.1179	-0.04512	0.6885	0.4273	0.0641	0.5731	0.3536
248009_at	AT5G56280	CSN4 (COP9 SIGNALOSOME SUBUNIT 4);	0.1927	0.0364	0.1099	0.3536	0.0047	0.0418	-0.0222	0.0113	0.0421	-0.05927	0.2976	0.2374
248010_at	AT5G56290	PEX5 (PEROXIN 5); peroxisome matrix targeting si	-0.02789	0.849	0.5379	-0.1708	0.2814	0.2818	-0.2678	0.1229	0.1586	-0.4108	0.0403	0.0694
248011_at	AT5G56300	GAMT2; S-adenosylmethionine-dependent methyltr	-0.8773	0.301	0.3235	-1.8388	0.0677	0.1304	0.4605	0.5671	0.3856	-0.501	0.5352	0.3398
248012_at	AT5G56310	pentatricopeptide (PPR) repeat-containing protein	0.8786	0.5524	0.442	1.6314	0.2944	0.2888	1.0339	0.4874	0.3544	-1.4741	0.3372	0.2566
248013_at	AT5G56330	carbonic anhydrase family protein	0.005402	0.9909	0.5748	0.06546	0.8907	0.5159	-0.7745	0.1583	0.1845	-0.7144	0.1854	0.1765
248014_at	AT5G56340	zinc finger (C3HC4-type RING finger) family protein	0.2722	0.3604	0.3548	-0.1161	0.6825	0.453	-0.03847	0.8911	0.4901	-0.4268	0.1809	0.1739
248015_at	AT5G56370	F-box family protein	-0.3945	0.8167	0.5287	-0.4025	0.813	0.494	1.1361	0.5153	0.3651	1.1282	0.5181	0.3328
248016_at	AT5G56380	F-box family protein	0.6701	0.0307	0.1016	0.1866	0.4133	0.3476	-0.7566	1.00E-04	0.0101	-1.24	0	0.0043
248017_at	AT5G56460	protein kinase, putative	0.222	0.4167	0.3832	0.4768	0.1238	0.1785	-0.01177	0.964	0.5085	0.243	0.3779	0.2748
248018_at	AT5G56470	FAD-dependent oxidoreductase family protein	-2.3369	0.0313	0.1027	-0.5395	0.4945	0.3824	0.6384	0.3359	0.2864	2.4359	0.014	0.0376
248019_at	AT5G56480	protease inhibitor/seed storage/lipid transfer protein	1.1365	0.2888	0.3166	-1.4664	0.19	0.2264	1.702	0.1412	0.1723	-0.9008	0.3876	0.279
248020_at	AT5G56490	FAD-binding domain-containing protein	-2.0317	0.0927	0.1764	-0.3194	0.7469	0.4738	-0.801	0.4347	0.3318	0.9113	0.3796	0.2756
248021_at	AT5G56500	ATP binding / protein binding / unfolded protein bind	0.6847	0.0644	0.1453	0.4645	0.1607	0.2063	-0.00418	0.9835	0.5135	-0.2244	0.3034	0.2404
248022_at	AT5G56510	APUM12 (ARABIDOPSIS PUMILIO 12); RNA bindi	1.6749	0.

248090_at	AT5G55090	MAPKKK15 (Mitogen-activated protein kinase kinas	-0.9305	0.5963	0.4585	-0.5997	0.7299	0.4686	-0.4816	0.7809	0.4577	-0.1509	0.9302	0.4657
248091_at	AT5G55120	VTC5; galactose-1-phosphate guanylyltransferase (	-0.7804	0.0292	0.0991	-0.3329	0.229	0.251	-1.1325	0.0056	0.0311	-0.685	0.0303	0.0586
248092_at	AT5G55170	SUM3 (SMALL UBIQUITIN-LIKE MODIFIER 3)	1.0601	0.0086	0.0604	1.198	0.0055	0.0434	0.4826	0.0936	0.1356	0.6205	0.048	0.0774
248093_at	AT5G55210	similar to unknown protein [Arabidopsis thaliana] (T	-0.2168	0.3506	0.35	-0.02035	0.9258	0.5256	0.2864	0.0292	0.0693	0.4828	0.005	0.0221
248094_at	AT5G55220	trigger factor type chaperone family protein	-0.4906	0.0907	0.1744	-0.3037	0.2415	0.2587	-0.3301	0.1094	0.1479	-0.1432	0.4235	0.2939
248095_at	AT5G55230	ATMAP65-1 (MICROTUBULE-ASSOCIATED PRO	0.2354	0.0879	0.1719	-0.02372	0.8319	0.4994	0.0229	0.8376	0.4749	-0.2362	0.0871	0.1105
248096_at	AT5G55240	calexcin-related family protein / embryo-specific pro	-0.3762	0.4135	0.3817	0.2631	0.5584	0.4078	-0.09083	0.7745	0.4557	0.5485	0.1378	0.1468
248097_at	AT5G55260	PP2A2 (protein phosphatase x-2); protein serine/thre	-0.3952	0.2924	0.3186	-0.1792	0.6154	0.429	-1.134	0.0263	0.0659	-0.914	0.0501	0.0795
248098_at	AT5G55290	ATP synthase subunit H family protein	0.3547	0.09	0.1737	0.2498	0.1921	0.2275	0.2859	0.0934	0.1355	0.181	0.2375	0.2059
248099_at	AT5G55300	TOP1BETA (DNA TOPOISOMERASE 1 BETA); DN	0.08574	0.6264	0.4685	0.2554	0.1918	0.2272	-0.416	0.063	0.1079	-0.2464	0.2049	0.1878
248100_at	AT5G55180	glycosyl hydrolase family 17 protein	0.771	0.1468	0.2228	0.1629	0.7236	0.4666	1.2087	0.0011	0.0184	0.2748	0.1312	0.1424
248101_at	AT5G55200	co-chaperone grpE protein, putative	0.2519	0.2009	0.2626	0.1549	0.4001	0.3412	0.6415	0.0176	0.0531	0.5445	0.0298	0.0579
248102_at	AT5G55140	ribosomal protein L30 family protein	0.3208	0.1335	0.2121	0.5386	0.0343	0.0915	0.1731	0.3681	0.302	0.3909	0.0839	0.1081
248103_at	AT5G55160	SUM2 (SMALL UBIQUITIN-LIKE MODIFIER 2)	0.09349	0.5061	0.4233	0.2505	0.1223	0.1775	0.3384	0.0048	0.0294	0.4954	0.0012	0.0127
248104_at	AT5G55250	IAMT1 (IAA CARBOXYLMETHYLTRANSFERASE	-0.2527	0.4028	0.3767	-0.4279	0.1886	0.2255	-0.08514	0.7686	0.4537	-0.2603	0.3901	0.28
248105_at	AT5G55280	FTSZ1-1 (FtsZ1-1); structural molecule	-0.06084	0.6354	0.4714	-0.5009	0.0135	0.0617	0.7825	0.0025	0.0234	0.3424	0.0422	0.0716
248106_at	AT5G55160	SWAP (Suppressor-of-White-APricot)/surp domain-	0.2811	0.0768	0.1595	0.4037	0.0272	0.0825	-1.2735	1.00E-04	0.0095	-1.1509	1.00E-04	0.0058
248107_at	AT5G55190	RAN3; GTP binding	0.3147	0.1657	0.2381	0.5304	0.0462	0.1066	0.1259	0.5352	0.3733	0.3416	0.1399	0.1481
248108_at	AT5G55130	CNX5 (SIRTINOL RESISTANT 1); Mo-molybdopter	1.1089	1.00E-04	0.0312	0.6783	6.00E-04	0.027	-0.2017	0.0447	0.0884	-0.6323	8.00E-04	0.0112
248109_at	AT5G55310	TOP1alpha (TOPOISOMERASE I)	0.5208	0.0119	0.0679	0.401	0.0279	0.0832	-0.2226	0.1344	0.167	-0.3423	0.045	0.0744
248110_at	AT5G55320	membrane bound O-acyl transferase (MBOAT) fam	0.204	0.8146	0.5283	-1.5439	0.1309	0.1835	0.8706	0.3453	0.2908	-0.8773	0.3421	0.259
248111_at	AT5G55330	membrane bound O-acyl transferase (MBOAT) fam	-0.09166	0.9027	0.6521	-1.0722	0.2022	0.2341	0.7964	0.3209	0.2787	-0.1842	0.8084	0.4306
248112_at	AT5G55350	membrane bound O-acyl transferase (MBOAT) fam	-0.7764	0.3873	0.3683	-0.5838	0.5065	0.3873	0.3607	0.6759	0.423	0.5533	0.5278	0.337
248113_at	AT5G55360	long-chain-alcohol O-fatty-acyltransferase family pr	-0.07434	0.929	0.5597	0.9743	0.2818	0.282	0.4018	0.6353	0.4095	1.4504	0.138	0.1469
248114_at	AT5G55370	long-chain-alcohol O-fatty-acyltransferase family pr	0.564	0.2509	0.4159	-0.1743	0.6998	0.459	0.04884	0.9131	0.496	0.4385	0.3559	0.2652
248115_at	AT5G54870	similar to unknown protein [Arabidopsis thaliana] (T	0.2361	0.1729	0.2435	0.0948	0.5423	0.4015	0.1483	0.3088	0.2728	0.006975	0.9589	0.4731
248116_at	AT5G55020	MYB120 (myb domain protein 120); DNA binding / t	1.4148	0.404	0.3773	-1.6184	0.3463	0.3161	1.3727	0.378	0.3068	-1.6605	0.297	0.2371
248117_at	AT5G55000	FIP2 (FH protein interacting protein 2); voltage-gate	0.2294	0.3329	0.3417	0.2125	0.3656	0.3256	0.3897	0.3225	0.0231	0.0615	0.3728	0.0266
248118_at	AT5G55050	GDSL-motif lipase/hydrolase family protein	-0.08392	0.7765	0.5168	-0.1125	0.7048	0.4606	0.2205	0.3206	0.2785	0.1919	0.3799	0.2757
248119_at	AT5G54590	protein kinase family protein	-0.7929	0.1731	0.2435	-0.2562	0.6209	0.4309	-0.6537	0.2439	0.2374	-0.117	0.819	0.4338
248120_at	AT5G54540	similar to unknown protein [Arabidopsis thaliana] (T	0.2441	0.05	0.1285	0.3663	0.0141	0.0628	0.1242	0.2304	0.2296	0.2464	0.0486	0.0779
248121_at	AT5G54690	GAUT12/IRX8/LGT6 (GALACTURONOSYLTRANS	0.2347	0.5743	0.4506	0.07395	0.8568	0.5064	-0.01143	0.9708	0.5102	-0.1722	0.5892	0.3597
248122_at	AT5G54700	ankyrin repeat family protein	-0.1348	0.8615	0.5415	0.2505	0.747	0.4739	0.4388	0.5775	0.3897	0.824	0.3189	0.2478
248123_at	AT5G54720	ankyrin repeat family protein	-1.5215	0.0704	0.1529	0.2049	0.7579	0.4774	-2.7056	0.0096	0.039	-0.9792	0.1667	0.1652
248124_at	AT5G54730	AIATG18f (Arabidopsis thaliana homolog of yeast a	0.04847	0.6169	0.4652	0.2334	0.0596	0.1213	-0.6521	3.00E-04	0.0133	-0.4672	0.001	0.012
248125_at	AT5G54740	protease inhibitor/seed storage/lipid transfer protein	-0.412	0.4832	0.4132	-0.3166	0.585	0.4181	0.3384	0.5605	0.3828	0.4339	0.4619	0.3108
248126_at	AT5G54760	initiation factor SUI1, putative	0.3118	0.2696	0.3051	0.4973	0.1107	0.1679	0.6305	0.0049	0.0297	0.8212	0.0019	0.015
248127_at	AT5G54750	transport protein particle (TRAPP) component Bet3	0.5672	0.0033	0.0446	0.5719	0.0032	0.037	0.4674	0.0068	0.0336	0.4721	0.0065	0.0251
248128_at	AT5G54770	THI1 (THIAZOLE REQUIRING)	-0.3505	0.0531	0.1322	-0.6153	0.0088	0.0516	0.0823	0.4114	0.3214	-0.1825	0.1119	0.129
248129_at	AT5G54780	RAB GTPase activator	0.1039	0.6845	0.4874	0.1847	0.4803	0.3763	-0.1459	0.5725	0.3876	-0.06503	0.7979	0.4282
248130_at	AT5G54790	similar to unknown protein [Arabidopsis thaliana] (T	0.7565	0.4384	0.3929	2.0678	0.0785	0.1404	1.3473	0.2005	0.212	-1.4769	0.1685	0.1664
248131_at	AT5G54830	DOMON domain-containing protein / dopamine beta	0.2348	0.3101	0.3286	0.1445	0.5143	0.3904	0.1678	0.3842	0.3098	0.07743	0.6756	0.3892
248132_at	AT5G54840	GTP-binding family protein	0.5581	0.0418	0.1176	0.4196	0.0906	0.1518	-0.3398	0.084	0.1274	-0.4783	0.0322	0.0606
248133_at	AT5G54850	unknown protein	-0.4003	0.3336	0.3421	-0.1389	0.7224	0.4661	0.09537	0.6068	0.4003	0.3568	0.1053	0.1241
248134_at	AT5G54860	integral membrane transporter family protein	1.2933	0.0274	0.0958	1.2328	0.0318	0.0885	-0.1289	0.5307	0.3715	-0.1894	0.3707	0.2716
248135_at	AT5G54890	identical to CRS2-associated factor 2, mitochondria	0.2427	0.4432	0.3951	-0.05377	0.8598	0.5071	0.5519	0.1254	0.1603	0.2554	0.4215	0.2931
248136_at	AT5G54910	DEAD/DEAH box helicase, putative	-0.03276	0.9077	0.5534	0.4244	0.1851	0.2232	-0.5282	0.0046	0.0289	-0.07097	0.4849	0.3196
248137_at	AT5G54950	aconitate hydratase-related / citrate hydro-lyase-rel	-1.0147	0.2941	0.3198	-0.01259	0.9888	0.5413	-0.8283	0.3805	0.308	0.1739	0.8463	0.4418
248138_at	AT5G54960	PDC2 (PYRUVATE DECARBOXYLASE-2); pyruvat	0.3933	0.2647	0.3021	0.4263	0.2328	0.2533	-0.2698	0.3727	0.3042	-0.2367	0.4286	0.2962
248139_at	AT5G54970	similar to unknown protein [Arabidopsis thaliana] (T	-0.4707	0.0243	0.0908	-0.5223	0.0173	0.0681	1.1524	0.001	0.0175	1.1007	0.0012	0.0127
248140_at	AT5G54980	integral membrane family protein	0.6122	0.1375	0.2154	-0.2252	0.5329	0.3973	0.4708	0.0927	0.1348	-0.3666	0.1619	0.1623
248141_at	AT5G55010	unknown protein	1.1811	0.3557	0.3525	-0.7113	0.5639	0.4097	0.09447	0.9327	0.5014	-1.7979	0.1625	0.1627
248142_at	AT5G55040	DNA binding	0.5863	0.0443	0.1213	0.07991	0.7131	0.4631	-0.6166	0.003	0.0248	-1.1229	3.00E-04	0.0083
248143_at	no_match	no_match	0.7254	0.4797	0.4117	-0.3874	0.6989	0.4585	-1.4166	0.203	0.2136	-2.5294	0.0533	0.0825
248144_at	AT5G54800	GPT1 (glucose-6-phosphate transporter 1); antiport	0.06268	0.6219	0.4672	0.1092	0.5637	0.4097	0.1986	0.3161	0.2763	0.2152	0.2826	0.2295
248145_at	AT5G54880	DTW domain-containing protein	-0.4509	0.0404	0.116	0.1471	0.385	0.3341	-0.5836	0.018	0.0538	0.0144	0.9286	0.4653
248146_at	AT5G54940	initiation factor SUI1, putative	-0.3317	0.2702	0.3055	-0.1548	0.5829	0.4174	0.6752	0.0141	0.0474	0.8522	0.0063	0.0246
248147_at	AT5G54990	ATRBP45A (RNA-BINDING PROTEIN 45A); RNA b	0.361	0.0713	0.1539	0.5639	0.0189	0.071	0.465	0.0348	0.0765	0.6679	0.0107	0.0302
248148_at	AT5G54930	AT hook motif-containing protein	-0.2171	0.6208	0.4667	0.04534	0.9164	0.5231	0.2802	0.1458	0.1759	0.5426	0.0251	0.0523
248149_at	AT5G54855	pollen Ole e 1 allergen and extensin family protein	-0.08221	0.5543	0.4425	-0.01157	0.932	0.527	0.6105	0.0013	0.0191	0.6811	9.00E-04	0.0114
248150_at	AT5G54670	ATK3 (ARABIDOPSIS THALIANA KINESIN 3); mic	-0.2803	0.4392	0.3933	-0.5372	0.1742	0.2155	0.1008	0.498	0.3589	-0.1581	0.308	0.2424
248151_at	AT5G54270	LHCB3 (LIGHT-HARVESTING CHLOROPHYLL BI	-0.356	0.0934	0.1771	-0.523	0.0322	0.0889	-0.22	0.0534	0.0983	-0.387	0.0088	0.0293
248152_at	AT5G54260	MRE11 (MEIOTIC RECOMBINATION 11); protein s	0.8813	0.3255	0.3376	0.6059	0.4843	0.3778	-0.1063	0.8991	0.4921	-0.3816	0.6531	0.3818
248153_at	AT5G54250	ATCNGC4 (DEFENSE, NO DEATH 2); calmodulin	-0.1106	0.781	0.518	-0.6805	0.1414	0.1917	-0.2057	0.0606	0.1057	-0.7756	6.00E-04	0.0103
248154_at	AT5G54400	methyltransferase	1.1637	0.0424	0.1185	0.08002	0.8497	0.5043	-0.09215	0.7636	0.4523	-1.1758	0.0148	0.0386
248155_at	AT5G54390	AHL (HAL2-LIKE); 3'(2'),5'-bisphosphate nucleotida	-0.3872	0.0554	0.1352	-0.2537	0.1542	0.2014	-1.0026	0.0023	0.0224	-0.8691	0.0039	0.0201
248156_at	AT5G54410	unknown protein	1.3692	0.4175	0.3836	0.7102	0.6638	0.4462	0.9054	0.5825	0.3917	0.2464	0.8788	0.451
248157_at	AT5G54420	similar to unknown protein [Arabidopsis thaliana] (T	-1.9497	0.2555	0.2967	-0.8167	0.6083	0.4265	0.9229	0.5643	0.3844	2.056	0.2346	0.2042
248158_at	AT5G54440	binding	0.3356	0.0766	0.1593	0.338	0.0752	0.1375	-0.1636	0.3116	0.2743	-0.1612	0.3179	0.2473
248159_at	AT5G54460	wound-responsive protein-related	-0.386	0.7218	0.5	0.3277	0.7619	0.4781	0.3628	0.7376	0.4442	1.0765	0.3466	0.2609
248160_at	AT5G54470	zinc finger (B-box type) family protein	-1.2537	0.3101	0.3286	-1.8171	0.1676	0.2109	0.6123	0.23	0.2295	0.04887	0.9155	0.4616
248161_at	AT5G54480	similar to unknown protein [Arabidopsis thaliana] (T	-1.0503	0.3722	0.3606	0.423	0.7067	0.4611	-2.2979	0.0792	0.1231	-0.8246	0.448	0.3052
248162_at	AT5G54500	FQR1 (FLAVODOXIN-LIKE QUINONE REDUCTAS	0.8721	0.0196	0.0827	1.0545	0.0103	0.0551	0.9321	0.0082	0.0362	1.1145	0.0043	0.0209
248163_at	AT5G54510	DFL1/GH3.6 (DWARF IN LIGHT 1); indole-3-acetic	0.8118	0.1522	0.2276	0.8749	0.1298	0.1828	-0.3512	0.1237	0.1592	-0.2881	0.1858	0.1768
248164_at	AT5G54490	PBP1 (PINOID-BINDING PROTEIN 1); calcium ion	0.2367	0.6047	0.4611	0.4051	0.3913	0.3373	0.9938	0.0147	0.0483	1.1622	0.0086	0.0288
248165_at	AT5G54430	universal stress protein (USP) family protein	0.2755	0.1206	0.2008	0.3559	0.0639	0.1262	0.3338	0.0262	0.0659	0.4142	0.0129	0.0361
248166_at	AT5G54520	WD-40 repeat family protein	0.3577	0.0577	0.1376	0.35	0.0612	0.1229	-0.08924	0.5464	0.3779	-0.09695	0.5141	0.3313
248167_at	AT5G54530	similar to unknown protein [Arabidopsis thaliana] (T	-0.5332	0.1147	0.1963	0.2187	0.456	0.3664	-0.5954	0.0111	0.0417	0.1565	0.3056	0.2413
248168_at	AT5G54570	glycosyl hydrolase family 1 protein	0.1445	0.8461	0.5471	-0.6034	0.552	0.4056	0.6005	0.5508	0.3794	-0.1474	0.8808	0.4516
248169_at	AT5G54610	ANK (ANKYRIN); protein binding	1.229	0.0253	0.0923	0.7788	0.0921	0.1531	0.4419	0.0339	0.0752	-0.000837	0.955	0.4723
248170_at	AT5G54620	ankyrin repeat family protein	1.3484	0.2529	0.2952	0.03072	0.9772	0.5386	0.7696	0.4887	0.3549	-0.548	0.6164	0.3689
248171_at	AT5G54680	ILR3 (IAA-LEUCINE RESISTANT3); DNA binding /	0.2763	0.1324	0.2109	-0.4815	0.0303	0.0864	1.0466	0.002	0.0213	0.2888	0.12	0.135
248172_at	AT5G54660	heat shock protein-related	-0.0663	0.8464	0.5374	-0.04913	0.8857	0.5147	0.6135	0.0015	0.02	0.6306	0.0014	0.0133
248173_at	AT5G54580	RNA recognition motif (RRM)-containing protein	0.2251	0.1941	0.2583	-0.09435	0.5492	0.4045	0.7198	0.0076	0.0352	0.4003	0.0502	0.0796
248174_at	AT5G54600	50S ribosomal protein L24, chloroplast (CL24)	-0.4503	0.0137	0.0719	-0.6366	0.004	0.0395	0.2557	0.0756	0.1197	0.06943	0.5527	0.346
248175_at	AT5G54640	HTA1/RAT5 (RESISTANT TO AGROBACTERIUM	0.153	0.4419	0.3945	0.1451	0.4642	0.3698	0.9142	0.007	0.034	0.9063	0.0072	0.0265
248176_at	AT5G54650	Fh5 (FORMIN HOMOLOGY5); actin binding	0.02928	0.8898	0.5483	0.1428	0.5116	0.3893	-0.3392	0.1626	0.1869	-0.2257	0.3189	0.2477
248177_at	AT5G54630	zinc finger protein-related	-0.6068	0.0054	0.0519	-0.1625	0.2166	0.2438	0.07965	0.4204	0.3256	0.5239	0.0041	0.0206
248178_at	AT5G54370	late embryogenesis abundant protein-related / LEA	2.8643	0.0397	0.1149	-0.6063	0.559	0.4079	0.8741	0.3385	0.2877	-2.5966	0.0321	0.0604
248179_at	AT5G54380	THE1 (THESEUS1); kinase/ protein kinase	-0.3851	0.4696	0.4071	-0.3391	0.5209	0.3925	-0.121	0.2559	0.2442	-0.07509	0.4574	0.309
248180_at	AT5G54310	AGD5 (ARF-GAP DOMAIN 5); DNA binding	0.5013	0.0041	0.0468	0.3005	0.0239	0.0779	0.05463	0.5117	0.3638	-0.1462	0.1265	0.1392
248181_at	AT5G54290	cytochrome c biogenesis protein family	0.02317	0.7136	0.4972	-0.346	0.0042	0.04	0.398	0.0017	0.0205	0.02879	0.6169	0.3692
248182_at	AT5G54030	DC1 domain-containing protein	-1.2896	0.4599	0.403	0.8432	0.6216	0.4313	-0.8419	0.6222	0.4054	1.2909	0.4595	0.3098
248183_at	AT5G54040	DC1 domain-containing protein	1.2774	0.2265	0.2795	-3.4468	0.0183	0.0698	2.5723	0.0452	0.0891	-2.1519	0.0739	0.0999
248184_at	AT5G54050	DC1 domain-containing protein	-1.8651	0.2067	0.2662	-0.9299	0.4947	0.3825	-1.2994	0.2272	0.2278	-0.3641	0.71	0.4009
248185_at	AT5G54060	UF3GT (UDP-GLUCOSE:FLAVONOID 3-O-GLUCO	-0.7634	0.0407	0.1162	-1.4555	0.0047	0.0418	0.3045	0.3002	0.2688	-0.3876	0.2046	0.1877
248186_at	AT5G53880	similar to unknown [Populus trichocarpa] (GB:ABK9	-1.0582	0.005	0.0507	-0.7216	0.019	0.071	1.1656	0.0035	0.0262	1.5022	0.0014	0.0133
248187_at	AT5G53940	yippee family protein	-0.1063	0.3976	0.3742	0.1367	0.2904	0.2868	0.3045	0.0534	0.0983	0.5475	0.0082	0.0281
248188_at	AT5G54070	AT-HSFA9 (ARABIDOPSIS THALIANA HEAT SHO	-0.02578	0.9818	0.5725	0.3305	0.7709	0.4807	-0.6252	0.5499	0.379	-0.2689	0.793	0.427
248189_at	AT5G54090	DNA mismatch repair MutS family protein	0.7432	0.0205	0.0842	0.7776	0.0177	0.0688	-1.3086	0.0018	0.0206	-1.2743	0.002	0.0153
248190_at	AT5G54130	calcium-binding EF hand family protein	-1.8274	0.0592	0.1393	-1.6881	0.0733	0.1357	-1.2039	0.0228	0.0611	-1.0646	0.0335	0.0619
248191_at	AT5G54130	calcium-binding EF hand family protein	-1.5087	0.0762	0.1589	-1.5892	0.0665	0.1291	-0.2787	0.2155	0.2212	-0.3591	0.1311	0.1423
248192_at	AT5G54140	IL3 (IAA-amino acid hydrolase ILR1-like 3); metall	0.7378	0.0095	0.0626	0.7861	0.0076	0.0488	0.2415	0.2008	0.2122	0.2897	0.1403	0.1484
248193_at	AT5G54080	HGO (HOMOGENTISATE 1,2-DIOXYGENASE); ho	0.3994	0.2754	0.3088	0.2518	0.4706	0.3723	-0.07494	0.6498	0.4144	-0.2225	0.2194	0.1958
248194_at	AT5G54095	similar to unknown protein [Arabidopsis thaliana] (T	-1.586	0.0821	0.1658	-0.3075	0.6776	0.4511	-0.7738	0.2255	0.2267	0.5047	0.4033	0.2855
248195_at	AT5G54100	ATMAM1(ARABIDOPSIS THALIANA MEMBRANE	0.3904	0.0025	0.0423	0.1732	0.0397	0.0986	0.1819	0.0255	0.0649	0.03525	0.538	0.3406
248196_at	AT5G54150	similar to unknown protein [Arabidopsis thaliana] (T	-0.4141	0.3417	0.346	0.3267	0.443	0.3608	-0.4706	0.1513	0.1798	0.2702	0.3668	0.2699
248197_at	AT5G54190	PORA (Protochlorophyllide reductase A); oxidoredu	1.2931	0.0564	0.1361	1.3962	0.0454	0.1055	-0.5212	0.052	0.0966	-0.418	0.093	0.1152
248198_at	AT5G54200	WD-40 repeat family protein	0.8353	0.0883	0.1724	-0.6228	0.1698	0.2124	-0.5025	0.0382	0.0807	-0.29	0.1536	0.1573
248199_at	AT5G54170	similar to CP5 [Arabidopsis thaliana] (TAIR:AT1G64	-0.5185	0.1719	0.2427	-0.3232	0.3589	0.3224	-0.3205	0.0181	0.0538	-0.1252	0.2057	0.1883
248200_at	AT5G54160	ATOMT1 (O-METHYLTRANSFERASE 1	-0.2101	0.2085	0.2672	-0.6534	0.0096	0.0536	0.2333	0.1716	0.1931	-0.2101	0.2086	0.19
248201_at	AT5G54180	PTAC16 (PLASTID TRANSCRIPTIONALLY ACTIV	-0.5953	0.0017	0.0391	-0.567	0.002	0.033	-0.3714	0.0094	0.0388	-0.3432	0.0123	0.0351
248202_at	AT5G54220	Encodes a defensin-like (DEFL) family protein.	1.0648	0.2097	0.268	0.6618	0.406	0.344	0.3739	0.6278	0.4072	-0.02903	0.9695	0.4754
248203_at	AT5G54230	MYB49 (myb domain protein 49); transcription facto	0.5055	0.5728	0.45	0.8493	0.361	0.3234	-0.5457	0.5441	0.377	-0.2019	0.8185	0.4338
248204_at	AT5G54280	ATM2 (ARABIDOPSIS THALIANA MYOSIN 4)	0.1244	0.4561	0.401	0.3923	0.0601	0.1217	-0.3568	0.0381	0.0806	-0.08884	0.4901	0.322
248205_at	AT5G54300	similar to unknown protein [Arabidopsis thaliana] (T	-0.7625	0.117	0.1977	-0.6971	0.1424	0.1925	0.1725	0.1723	0.1934	0.2379	0.0839	0.1082
248206_at	AT5G54350	similar to zinc finger (C2H2 type) family protein-rela	1.1094	0.3087	0.3278	-0.2984	0.7696	0.4804	1.4176	0.2108	0.2183	0.009692	0.9924	0.4807
248207_at	AT5G53970	aminotransferase, putative	0.08941	0.6263	0.4685	-0.4907	0.0446	0.1046	-0.6734	0.0166	0.0514	-1.2535	0.0018	0.0148
248208_at	AT5G53980	ATH852 (ARABIDOPSIS THALIANA HOMEOBOX	1.6554	0.135	0.2133	0.1402	0.8819	0.5137	1.0904	0.2857	0.261	-0.4248	0.6566	0.383
248209_at	AT5G53990	glycosyltransferase family protein	0.06986	0.7688	0.5143	-0.1063	0.6572	0.4442	-0.00477	0.8403	0.4757	-0.2109	0.2622	0.2189
248210_at	AT5G54000	oxidoreductase, 2OG-Fe(II) oxygenase family prote	0.2936	0.5678	0.448	-0.1592	0.753	0.4761	-0.3569	0.4919	0.3564	-0.8097	0.1616	0.1623
248211_at	AT5G54010	glycosyltransferase family protein	-1.2552	0.1537	0.2287	-0.9888	0.2385	0.2568	-0.2753	0.6918	0.4283	-0.00886	0.9897	0.4801
248212_at	AT5G54020	zinc ion binding	0.8729	0.446	0.3962	0.3236	0.7899	0.4804	1.0351	0.2485	0.2049	0.4898	0.5609	0.3492
248213_at	AT5G53660	AtGRF7 (GROWTH-REGULATING FACTOR 7)	0.4888	0.2352	0.2845	-0.29	0.4542	0.3657	0.3585	0.3638	0.2999	-0.4203	0.2963	0.2368
248214_at	AT5G53670	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.3585	0.655	0.4775	-1.1945	0.1835	0.2222	0.1303	0.8695	0.4841	-1.4227	0.1283	0.1404
248215_at	AT5G53680	RNA recognition motif (RRM)-containing protein	-0.8814	0.1988	0.2618	0.4799	0.4494	0.3637	-0.446	0.2838	0.2599	0.7154	0.2423	0.2084
248216_at	AT5G53690	unknown protein	-0.1506	0.8455	0.5372	-1.1371	0.1917	0.2272	-0.322	0.6798	0.4243	-1.3085	0.1453	0.1518
248217_at	AT5G53560	ATB5-A (Cytochrome b5 A)	0.197	0.1307	0.2091	0.5757	0.0052	0.0429	0.0157	0.7534	0.4492	0.3945	0.0011	0.0123
248218_at	AT5G53700	unknown protein	0.07833	0.8162	0.5286	1.1225	0.0236	0.0773	0.2295	0.27	0.2523	1.2733	0.0021	0.0154
248219_at	AT5G53650	similar to unnamed protein product [Vitis vinifera] (G	0.4718	0.1186	0.1991	0.2229	0.4022	0.3422	0.2996	0.2768	0.2562	0.05073	0.8417	0.4406
248220_at	AT5G53540	MSP1 protein, putative / intramitochondrial sorting p	0.4901	0.0233	0.0893	0.436	0.0335	0.0905	-0.1613	0.1508	0.1795	-0.2154	0.0769	0.1024
248221_at	AT5G53530	vacuolar protein sorting-associated protein 26, puta	0.4128	0.0553	0.1351	0.4806	0.0356	0.093	0.004735	0.9762	0.5116	0.0725	0.6521	0.3816
248222_at	AT5G53570	RabGAP/TBC domain-containing protein	0.4674	0.0314	0.1027	0.5803	0.0157

248290_at	no_match	no_match	0.4456	0.3729	0.3609	0.584	0.2593	0.2696	-1.4281	0.0325	0.0735	-1.2897	0.0441	0.0736
248291_at	AT5G53020	similar to unknown protein [Arabidopsis thaliana] (T	-0.4888	0.173	0.2435	-0.4526	0.1998	0.2327	0.0961	0.5426	0.3764	0.1322	0.4121	0.2892
248292_at	AT5G53030	similar to unknown protein [Arabidopsis thaliana] (T	-0.7705	0.1162	0.1971	-0.02713	0.9473	0.5313	0.08922	0.7726	0.4551	0.8326	0.0447	0.0742
248293_at	AT5G53050	hydrolase, alpha/beta fold family protein	-0.5418	0.1359	0.214	-0.8233	0.0473	0.108	-0.5079	0.1092	0.1478	-0.7894	0.0332	0.0615
248294_at	AT5G53060	KH domain-containing protein	-0.6101	0.0625	0.1436	-0.6741	0.0473	0.108	0.07425	0.7708	0.4544	0.0102	0.9679	0.475
248295_at	AT5G53070	ribosomal protein L9 family protein	0.3173	0.2594	0.2993	0.1305	0.6179	0.4298	0.04397	0.8645	0.4826	-0.1429	0.5862	0.3584
248296_at	AT5G53090	oxidoreductase	-0.6281	0.0109	0.0655	-0.3854	0.0511	0.1122	-1.0862	8.00E-04	0.0165	-0.8436	0.0022	0.0157
248297_at	AT5G53100	oxidoreductase, putative	-0.4942	0.707	0.495	-0.9497	0.481	0.3766	-0.1869	0.886	0.4884	-0.6424	0.6273	0.3728
248298_at	AT5G53110	similar to zinc finger (C3HC4-type RING finger) fam	1.2751	0.0284	0.0976	1.052	0.0504	0.1114	-0.1196	0.7072	0.4337	-0.3427	0.3119	0.2443
248299_at	AT5G53080	kinesin light chain-related	-0.6963	0.0816	0.1652	-0.4404	0.2171	0.244	-0.6967	0.0815	0.1252	-0.4408	0.2167	0.1945
248300_at	AT5G53000	TAP46 (2A PHOSPHATASE ASSOCIATED PROTE	0.3009	0.0019	0.0391	0.6258	0.0016	0.0319	0.07619	0.4096	0.3206	0.1011	0.2891	0.2329
248301_at	AT5G53150	heat shock protein binding / unfolded protein bindin	0.2722	0.1586	0.2323	0.3696	0.0785	0.1404	-0.7245	0.01	0.0398	-0.627	0.0163	0.0408
248302_at	AT5G53160	similar to unknown protein [Arabidopsis thaliana] (T	0.06587	0.8115	0.5273	0.7025	0.0532	0.1144	-0.7595	0.0202	0.0572	-0.1229	0.5782	0.3554
248303_at	AT5G53170	FTSH11 (FtsH protease 11); ATP-dependent peptid	0.4096	0.008	0.0587	0.1479	0.1513	0.1993	-0.5513	0.0027	0.0237	-0.813	6.00E-04	0.0103
248304_at	AT5G53180	polypyrimidine tract-binding protein, putative / heter	0.1344	0.3191	0.3339	-0.2314	0.1221	0.1773	-0.09449	0.3084	0.2727	-0.4603	0.0047	0.0217
248305_at	AT5G52560	ATUSP (ARABIDOPSIS THALIANA UDP-SUGAR F	-0.3293	0.0074	0.0578	-0.2754	0.0138	0.0621	-0.3064	0.0096	0.039	-0.2525	0.0184	0.0436
248306_at	AT5G52630	WRKY27 (WRKY DNA-binding protein 27); transcri	-0.9533	0.1257	0.2052	-0.6658	0.2487	0.2831	0.5148	0.3559	0.2961	0.8022	0.1795	0.173
248307_at	AT5G52850	pentatricopeptide (PPR) repeat-containing protein	0.4866	0.6808	0.4863	0.9316	0.4444	0.3615	-0.3398	0.7726	0.4551	0.1052	0.9283	0.4652
248308_at	AT5G52530	dentin sialophosphoprotein-related	-0.0994	0.6211	0.4668	0.03908	0.8437	0.5027	-0.6898	0.0066	0.0334	-0.5513	0.0145	0.0383
248309_at	AT5G52540	similar to unknown protein [Arabidopsis thaliana] (T	0.2348	0.102	0.1847	0.2409	0.0959	0.156	-0.06709	0.3805	0.308	-0.06099	0.4214	0.293
248310_at	AT5G52550;AT5G52552	[AT5G52550, similar to unknown protein [Arabidops	-0.1239	0.4611	0.4035	0.008767	0.9568	0.5335	-0.00791	0.9576	0.5071	0.1247	0.4232	0.2938
248311_at	AT5G52570	BETA-OHASE 2 (BETA-CAROTENE HYDROXYLA	-2.2046	0.0022	0.041	-2.1183	0.0025	0.034	-0.01766	0.8193	0.4696	0.06866	0.3966	0.2828
248312_at	AT5G52580	RAB GTPase activator	-0.3947	0.1165	0.1973	-0.1405	0.5165	0.3912	-0.9808	0.0077	0.0354	-0.7266	0.0213	0.0474
248313_at	AT5G52590	RAB GTPase activator	0.3821	0.0538	0.1331	0.1156	0.4589	0.3676	0.2048	0.2204	0.2238	-0.06166	0.6847	0.3922
248314_at	AT5G52620	F-box family protein	0.7468	0.6296	0.4697	0.2249	0.8828	0.5139	0.461	0.7636	0.4523	-0.06087	0.9681	0.475
248315_at	AT5G52630	pentatricopeptide (PPR) repeat-containing protein	0.3751	0.1077	0.1899	0.4268	0.0784	0.1404	-0.5011	0.0508	0.0955	-0.4493	0.0686	0.0958
248316_at	AT5G52670	heavy-metal-associated domain-containing protein	-1.2012	0.1498	0.2254	-0.4638	0.5299	0.3963	0.007399	0.9918	0.5156	0.7448	0.3319	0.2543
248317_at	AT5G52680	heavy-metal-associated domain-containing protein	-0.1865	0.8297	0.5324	0.2668	0.0637	0.1268	1.3527	0.1711	0.1928	3.606	0.0113	0.0334
248318_at	AT5G52690	heavy-metal-associated domain-containing protein	-0.2328	0.7118	0.4969	-2.3686	0.0157	0.0652	-0.2785	0.4599	0.4179	-2.4143	0.0147	0.0386
248319_at	AT5G52710	heavy-metal-associated domain-containing protein	0.9558	0.4013	0.3759	0.02913	0.9786	0.539	0.6403	0.5348	0.3731	-0.2864	0.7767	0.422
248320_at	no_match	no_match	-0.4107	0.7134	0.4972	0.3845	0.7307	0.4687	-1.0416	0.2953	0.2662	-0.2465	0.79	0.4258
248321_at	AT5G52740	heavy-metal-associated domain-containing protein	2.2752	0.001	0.036	2.1127	0.0014	0.0312	1.075	0.0021	0.0217	0.9125	0.0039	0.0201
248322_at	AT5G52760	heavy-metal-associated domain-containing protein	1.4995	0.0183	0.0806	1.7509	0.0109	0.056	1.1011	0.0089	0.0377	1.3526	0.0042	0.0208
248323_at	AT5G52770	heavy-metal-associated protein-related	1.6963	0.0709	0.1536	0.07155	0.9228	0.5248	0.3101	0.6782	0.4238	-1.4578	0.1036	0.1231
248324_at	no_match	no_match	-1.4568	0.0891	0.173	0.1175	0.8657	0.5087	-2.0361	0.0354	0.0771	-0.4617	0.5177	0.3327
248325_at	no_match	no_match	0.5236	0.4096	0.3797	-0.4529	0.4707	0.3724	0.04135	0.9456	0.5046	-0.9352	0.1757	0.1706
248326_at	AT5G52820	WD-40 repeat family protein / notchless protein, put	0.7652	0.0537	0.1331	0.7966	0.0475	0.1086	-0.4067	0.0267	0.0664	-0.3773	0.0341	0.0624
248327_at	AT5G52750	heavy-metal-associated domain-containing protein	1.3072	0.1374	0.2154	1.7046	0.073	0.1353	0.9131	0.041	0.0277	1.3106	0.0011	0.0123
248328_at	AT5G52660	myb family transcription factor	-0.5563	0.0035	0.0451	-0.4014	0.0113	0.0572	0.1029	0.318	0.2773	0.2579	0.0461	0.0755
248329_at	AT5G52780	similar to unknown protein [Arabidopsis thaliana] (T	0.09554	0.6474	0.4208	0.2008	0.2702	0.2016	0.3115	0.0056	0.0311	0.4243	0.0019	0.0151
248330_at	AT5G52810	ornithine cyclodeaminase/mu-crystallin family protei	1.0967	0.0201	0.0837	0.856	0.0433	0.1032	0.5015	0.0792	0.1231	0.2608	0.2901	0.2336
248331_at	AT5G52650	40S ribosomal protein S10 (RPS10C)	0.4553	0.021	0.0853	0.2004	0.1797	0.2194	0.3569	0.0445	0.0882	0.102	0.4551	0.3079
248332_at	AT5G52640	HSP81-1 (HEAT SHOCK PROTEIN 81-1); ATP bin	1.0016	0.0178	0.08	1.7883	0.0123	0.0595	-0.6658	0.0497	0.0943	-0.4791	0.1158	0.1317
248333_at	AT5G52390	photoassimilate-responsive protein, putative	1.6022	0.0014	0.038	1.5368	0.0017	0.032	0.3463	0.165	0.1885	0.2809	0.2409	0.2076
248334_s_at	AT5G58990;AT5G52370	[AT5G58990, similar to unknown protein [Arabidops	0.2333	0.3639	0.3562	0.6751	0.0415	0.1011	-0.348	0.2016	0.2126	0.09379	0.7019	0.3979
248335_at	AT5G52410	MATE efflux protein-related	0.2888	0.2893	0.3169	0.5021	0.1012	0.1605	-0.7657	0.0103	0.0403	-0.5724	0.0292	0.0573
248336_at	AT5G52420	similar to unknown protein [Arabidopsis thaliana] (T	-0.5103	0.0258	0.093	-0.6065	0.0147	0.064	-0.1251	0.4084	0.3201	-0.2212	0.178	0.1719
248337_at	AT5G52310	COR78 (COLD REGULATED 78)	-0.8815	0.3464	0.3481	-1.0952	0.2559	0.2678	0.6476	0.0128	0.045	0.4339	0.0455	0.0748
248338_at	AT5G52440	HCF135 (High chlorophyll fluorescence 106)	-1.9379	0.1712	0.2424	-0.3425	0.0386	0.0973	-0.2533	0.0574	0.1024	-0.4079	0.0131	0.0363
248339_at	AT5G52520	OVA6/PRORS1 (OVULE ABORTION 6); ATP bindi	-0.1125	0.3567	0.353	-0.3136	0.044	0.1038	-0.3395	0.0348	0.0765	-0.5407	0.0075	0.0269
248340_at	AT5G52180	similar to hypothetical protein [Vitis vinifera] (GB:CA	-0.1834	0.1138	0.1955	-0.3325	0.0216	0.0747	-0.1136	0.2748	0.2551	-0.2627	0.0431	0.0724
248341_at	AT5G52220	similar to unnamed protein product [Vitis vinifera] (G	-0.01172	0.9823	0.5725	-0.1536	0.7719	0.4811	0.7705	0.1131	0.1507	0.6287	0.1742	0.1698
248342_at	AT5G52230	MBD13 (methyl-CpG-binding domain 13)	-0.122	0.62	0.4665	-0.3942	0.158	0.2044	0.1081	0.5303	0.3713	-0.1641	0.3564	0.2654
248343_at	AT5G52260	AtMYB19 (myb domain protein 19); DNA binding / tr	1.3258	0.3929	0.3715	0.1036	0.944	0.5303	0.8919	0.5293	0.371	-0.3303	0.8115	0.4322
248344_at	AT5G52280	protein transport protein-related	-0.1359	0.6039	0.4608	-0.2579	0.346	0.316	0.3385	0.1144	0.1519	0.2165	0.2673	0.2213
248345_at	AT5G52290	similar to unnamed protein product [Vitis vinifera] (G	-0.9974	0.5076	0.4241	-0.732	0.622	0.4315	-0.08704	0.9324	0.5014	0.1783	0.8623	0.4464
248346_at	AT5G52210	ATARLB1/ATGB1 (ARABIDOPSIS THALIANA GTP	0.4753	0.0269	0.0948	0.3967	0.0463	0.1067	0.2276	0.1772	0.1967	0.149	0.3446	0.2601
248347_at	AT5G52250	transducin family protein / WD-40 repeat family prot	-1.0995	0.0093	0.0621	-0.7752	0.0295	0.0854	0.2498	0.2397	0.235	0.5741	0.0338	0.0621
248348_at	AT5G52190	sugar isomerase (SIS) domain-containing protein	0.04611	0.8101	0.5268	0.1387	0.4833	0.3774	0.1061	0.5552	0.3809	0.1986	0.2947	0.236
248349_at	AT5G52240	MSBP1 (MEMBRANE STEROID BINDING PROTE	0.138	0.2377	0.2861	0.2641	0.0567	0.1184	0.2766	0.0498	0.0944	0.4027	0.0155	0.0397
248350_at	AT5G52160	protease inhibitor/seed storage/lipid transfer protein	-1.2925	0.2546	0.2962	0.8603	0.4264	0.3536	-0.9211	0.3973	0.3153	1.2318	0.2741	0.2251
248351_at	AT5G52200	phosphatase inhibitor/ protein phosphatase inhibitor	0.3452	0.1272	0.206	0.1931	0.3433	0.3149	0.8427	0.0094	0.0388	0.6905	0.0184	0.0436
248352_at	AT5G52300	LTI65/RD29B (RESPONSIVE TO DESSICATION 2	1.3767	0.3535	0.3515	1.527	0.3094	0.2971	0.263	0.851	0.4788	0.4133	0.7686	0.4194
248353_at	AT5G52320	CYP96A4 (cytochrome P450, family 96, subfamily A	-1.3949	0.0094	0.0624	-1.1129	0.0201	0.0724	-0.00451	0.9476	0.505	0.2775	0.0126	0.0356
248354_at	AT5G52330	meprin and TRAF homology domain-containing pro	-0.01294	0.989	0.5743	0.718	0.4604	0.3681	-1.3114	0.2105	0.2181	-0.5805	0.5456	0.3431
248355_at	AT5G52340	ATEXO70A2 (exocyst subunit EXO70 family protein	1.325	0.1827	0.2501	-0.2956	0.7377	0.4705	1.6077	0.1225	0.1583	-0.01281	0.9883	0.4798
248356_at	AT5G52350	ATEXO70A3 (exocyst subunit EXO70 family protei	-0.05721	0.9489	0.5645	-2.1701	0.0609	0.1226	0.04665	0.9583	0.5072	-2.0662	0.0695	0.0965
248357_at	AT5G52380	zinc knuckle (CCHC-type) family protein	0.5499	0.0058	0.0529	0.6636	0.0029	0.0355	0.285	0.0399	0.0827	0.3987	0.0137	0.0372
248358_at	AT5G52400	CYP715A1 (cytochrome P450, family 715, subfami	-0.6747	0.2015	0.2632	-0.03644	0.9382	0.5286	-0.1987	0.6763	0.4231	0.4396	0.3761	0.274
248359_at	AT5G52410	similar to unknown protein [Arabidopsis thaliana] (T	-0.4944	0.3528	0.3513	-0.1705	0.7355	0.4698	-0.5118	0.338	0.2874	-0.1879	0.7101	0.4009
248360_at	AT5G52430	hydroxyproline-rich glycoprotein family protein	-0.2388	0.1215	0.2018	-0.6713	0.0053	0.0429	0.3896	0.0329	0.0741	-0.04293	0.7423	0.4112
248361_at	AT5G52460	EDA41 (embryo sac development arrest 41)	0.2168	0.7515	0.5088	-1.5126	0.0771	0.1392	1.0345	0.1615	0.1864	-0.6949	0.3134	0.2451
248362_at	AT5G52470	FIB1 (FIBRILLARIN 1)	0.3263	0.0242	0.0906	0.2831	0.0375	0.0958	-0.1846	0.1164	0.1535	-0.2278	0.0692	0.0964
248363_at	AT5G52480	protein binding	-1.352	0.1567	0.2308	-1.7094	0.0925	0.1535	0.151	0.8299	0.4727	-0.2064	0.7698	0.4199
248364_at	AT5G52490	fibrillarin, putative	-0.2883	0.6739	0.4839	-0.06565	0.9228	0.5248	-1.1801	0.1372	0.1691	-0.9574	0.2068	0.1889
248365_at	AT5G52500	similar to unknown protein [Arabidopsis thaliana] (T	-0.02722	0.9744	0.5709	-1.927	0.0732	0.1356	1.204	0.2058	0.2153	-0.6957	0.4325	0.2979
248366_at	AT5G52510	scarecrow-like transcription factor 8 (SCL8)	-0.1943	0.2111	0.269	-0.4339	0.0293	0.0851	0.2793	0.0379	0.0804	0.03968	0.6867	0.3928
248367_at	AT5G52360	actin-depolymerizing factor, putative	0.1872	0.7834	0.5188	-0.3693	0.5932	0.4207	0.398	0.5575	0.3819	-0.1585	0.8116	0.4322
248368_at	AT5G51950	glucose-methanol-choline (GMC) oxidoreductase fa	-0.2542	0.7028	0.4935	-0.9231	0.2107	0.2402	-0.09927	0.8805	0.4869	-0.7682	0.283	0.2298
248369_at	AT5G52040	ATRSP41 (Arabidopsis thaliana arginine/serine-rich	-0.01191	0.9198	0.557	0.0353	0.7666	0.4793	-0.275	0.0152	0.0492	-0.2278	0.028	0.0558
248370_at	AT5G52170	HDG7 (HOMEODOMAIN GLABROUS7); DNA bind	0.02014	0.9797	0.572	-0.6519	0.43	0.3553	-1.3886	0.1352	0.1676	-2.0606	0.0502	0.0796
248371_at	AT5G51810	ATZ33/ATGA20OX2/GA20OX8 (GIBBERELLIN 20	-0.6355	0.5938	0.4575	-1.4432	0.259	0.2695	-1.0126	0.3531	0.2948	-1.8203	0.1322	0.1431
248372_at	AT5G51850	similar to unknown protein [Arabidopsis thaliana] (T	-0.6104	0.362	0.3554	-1.2872	0.096	0.1561	0.8954	0.206	0.2154	0.2187	0.7313	0.4075
248373_at	AT5G51860	MADS-box protein (AGL72)	-0.7812	0.3325	0.3416	0.7782	0.3341	0.3104	-0.1629	0.812	0.4672	1.3966	0.0949	0.1167
248374_at	AT5G51870	AGL71; transcription factor	-0.8097	0.5446	0.4389	-0.1107	0.9397	0.529	-0.9515	0.5221	0.3678	-0.1525	0.916	0.4617
248375_at	AT5G51710	KEA5 (K+ efflux antiporter 5); potassium/hydrogen	0.2805	0.1418	0.2189	0.3281	0.0994	0.159	-0.2279	0.2118	0.2191	-0.1803	0.3055	0.2412
248376_at	AT5G51880	oxidoreductase, acting on paired donors, with incor	-0.02016	0.8592	0.5409	0.01882	0.8684	0.5095	-0.09995	0.3219	0.2791	-0.06097	0.5288	0.3374
248377_at	AT5G51720	similar to Os07g0467200 [Oryza sativa (japonica cu	-2.744	0.0016	0.0388	-2.7696	0.0016	0.0316	0.8663	0.0068	0.0338	0.8407	0.0076	0.0271
248378_at	AT5G51840	similar to unnamed protein product [Vitis vinifera] (G	0.2635	0.3018	0.3241	0.6953	0.0353	0.0928	0.5534	0.0051	0.0301	0.9852	6.00E-04	0.0101
248379_at	AT5G51700	PBS2 (PPHB SUSCEPTIBLE 2); protein binding / z	0.2405	0.1708	0.242	0.5781	0.016	0.0659	0.227	0.1908	0.206	0.5645	0.0174	0.0421
248380_at	AT5G51820	PGM (PHOSPHOGLUCOMUTASE)	-0.4009	0.2564	0.2973	-0.6833	0.0872	0.1488	-0.7055	0.0043	0.028	-0.9878	0.0012	0.0129
248381_at	AT5G51830	pfkB-type carbohydrate kinase family protein	0.3488	0.2064	0.2661	0.4292	0.1373	0.1887	-0.2937	0.1592	0.1852	-0.2133	0.2781	0.2271
248382_at	AT5G51890	peroxidase	-0.2745	0.4333	0.3909	-0.4988	0.1889	0.2257	0.6263	0.0542	0.0991	0.402	0.1584	0.1603
248383_at	AT5G51900	cytochrome P450 family	-1.2492	0.4153	0.3824	-0.7089	0.5336	0.4358	-1.0649	0.4805	0.3516	-0.5246	0.7213	0.4044
248384_at	AT5G51930	glucose-methanol-choline (GMC) oxidoreductase fa	-0.2944	0.7783	0.5174	1.677	0.1614	0.2069	-1.0856	0.3204	0.2785	0.8857	0.4075	0.2872
248385_at	AT5G51910	TCP family transcription factor, putative	-0.4936	0.1988	0.2618	-0.2269	0.5184	0.3919	0.09766	0.4454	0.3363	0.3643	0.0343	0.0627
248386_at	AT5G51940	DNA-directed RNA polymerase II, putative	0.06163	0.5778	0.4517	-0.06219	0.5745	0.4137	1.0015	6.00E-04	0.0158	0.8776	0.001	0.0121
248387_at	AT5G51960	similar to unknown [Brassica juncea] (GB:ABM5445	0.4074	0.1042	0.1866	0.4288	0.0922	0.1531	0.06704	0.6921	0.4284	0.0884	0.6044	0.3647
248388_at	AT5G51980	WD-40 repeat family protein / ztwd2 protein (ZFWD	0.01709	0.9314	0.5602	0.3836	0.1087	0.1663	-0.5308	0.0039	0.0273	-0.1643	0.137	0.1462
248389_at	AT5G51990	CBF4/DREB1D (C- REPEAT/DRE BINDING FACTOR 4	0.03438	0.962	0.5678	-0.581	0.4399	0.3595	0.8798	0.2643	0.2489	0.2644	0.7165	0.403
248390_at	AT5G52000	importin alpha-1 subunit, putative	-1.432	0.3058	0.326	0.9268	0.49	0.3804	-1.9241	0.1134	0.151	0.4346	0.6718	0.388
248391_at	AT5G52030	TraB protein-related	-0.4589	0.0676	0.1493	-0.6576	0.0235	0.0771	-0.3605	0.0912	0.1335	-0.5591	0.0264	0.0538
248392_at	AT5G52050	MATE efflux protein-related	-0.7854	0.195	0.2591	-1.3737	0.053	0.1142	0.3981	0.1691	0.1912	-0.1903	0.468	0.3129
248393_at	AT5G52060	ATBAG1 (ARABIDOPSIS THALIANA BCL-2-ASSO	-1.3883	0.0116	0.0672	-1.5218	0.0084	0.0507	0.3268	0.1151	0.1525	0.1933	0.3007	0.239
248394_at	AT5G52070	agenet domain-containing protein	0.353	0.0623	0.1433	0.325	0.0775	0.1395	-0.7058	8.00E-04	0.0167	-0.7337	7.00E-04	0.0108
248395_at	AT5G52120	ATPP2-A14 (Phloem protein 2-A14); carbohydrate	-0.7779	0.0265	0.0941	0.1077	0.6597	0.4449	-0.685	9.00E-04	0.0172	0.2006	0.0621	0.0904
248396_at	AT5G52130	unknown protein	0.002516	0.9982	0.5763	0.8522	0.4628	0.3692	-3.1983	0.0382	0.0808	-2.3486	0.0891	0.112
248397_at	AT5G52140	protein binding / zinc ion binding	0.1444	0.8606	0.5412	0.3172	0.7019	0.4597	0.3099	0.6872	0.4268	0.4827	0.5369	0.3403
248398_at	AT5G51970	sorbitol dehydrogenase, putative / L-iditol 2-dehydr	0.4962	0.0743	0.1567	0.2679	0.2647	0.2724	0.291	0.0569	0.1019	0.06264	0.5987	0.3629
248399_at	AT5G52010	zinc finger (C2H2 type) family protein	-0.1499	0.6006	0.4599	-0.292	0.3308	0.3088	-0.3976	0.2065	0.2157	-0.5397	0.1104	0.128
248400_at	AT5G52020	AP2 domain-containing protein	-2.0357	0.2274	0.2801	0.6713	0.663	0.446	0.025	0.9817	0.5132	2.732	0.0557	0.0846
248401_at	AT5G52100	HCF208 (HIGH CHLOROPHYLL FLUORESCENCE	-0.4722	0.0987	0.1813	-0.02698	0.9084	0.5211	0.09905	0.5298	0.3712	0.5443	0.0195	0.0448
248402_at	AT5G52100	CRR1 (CHLORORESPIRATION REDUCTION 1); c	-0.7242	0.0105	0.0647	-0.6598	0.0145	0.0635	-0.949	0.004	0.0274	-0.8847	0.0052	0.0225
248403_at	AT5G51410	LUC7 N_terminus domain-containing protein	0.2327	0.0841	0.1678	0.4968	0.0081	0.0503	-0.1956	0.1083	0.1473	0.06847	0.5105	0.33
248404_at	AT5G51460	ATTPPA (Arabidopsis thaliana trehalose-6-phospha	-1.8153	0.0182	0.0804	-2.5578	0.0056	0.0434	0.298	0.4433	0.3355	-0.4445	0.2737	0.2249
248405_at	AT5G51480	SKS2 (SKU5 SIMILAR 2); copper ion binding	0.2195	0.8253	0.5311	1.2519	0.2502	0.2641	-0.3968	0.6921	0.4284	0.6366	0.5326	0.3389
248406_at	AT5G51490	pectinesterase family protein	0.5144	0.3565	0.3529	0.1451	0.7836	0.4844	-0.2634	0.5969	0.397	-0.6527	0.2569	0.2162
248407_at	AT5G51500	pectinesterase family protein	0.417	0.6712	0.483	-0.01129	0.9907	0.5419	0.8338	0.4097	0.3206	0.4055	0.6777	0.3899
248408_at	AT5G51520	invertase/pectin methylesterase inhibitor family prot	1.1363	0.3669	0.3578	-0.8853	0.4728	0.3733	1.2398	0.3296	0.2831	-0.7818	0.5229	0.335
248409_at	AT5G51545	LPA2 (LOW PHOSPHATE ACCUMULATION2)	-0.6151	0.003	0.0435	-0.2839	0.0408	0.1001	0.5438	0.0039	0.0273	0.8749	6.00E-04	0.0105
248410_at	AT5G51570	band 7 family protein	1.4105	0.0165	0.0772	1.417	0.0162	0.0663	-0.3653	0.041	0.084	0.3589	0.0432	0.0726
248411_at	AT5G51580	unknown protein	1.0177	0.2992	0.3225	1.7344	0.1121	0.169	-0.5594	0.3415	0.2889	0.1573	0.7769	0.422
248412_at	AT5G51590	DNA-binding protein-related	0.7326	0.1687	0.2404	1.0197	0.0798	0.1417	0.1442	0.5684	0.3861	0.4313	0.137	0.1462
248413_at	AT5G51600	PLE (PLEIADE)	0.406	0.6815	0.4865	0.2904	0.7678	0.4799	0.945	0.3619	0.2991	0.8294	0.4178	0.2916
248414_at	AT5G51610	ribosomal protein L11 family protein	0.9715	0.5299	0.4331	-0.769	0.6155	0.429	0.9979	0.497	0.3585	-0.7426	0.6083	0.3662
248415_at	AT5G51620	similar to EMB2731 (EMBRYO DEFECTIVE 2731)	0.2775	0.3606	0.355	0.3261	0.2877	0.2921	0.1895	0.3019	0.2696	0.3672	0.244	0.2093
248416_at	AT5G51630	disease resistance protein (TIR-NBS-LRR class), p	1.1425	0.033	0.1053	-0.01027	0.9785	0.539	-0.291	0.4613	0.3437	-1.4438	0.0156	0.0399
248417_at	AT5G51650	unknown protein	0.6175	0.6725	0.4835	-0.06085	0.9664	0.5356	0.02545	0.9846	0.5138	-0.6529	0.6271	0.3727
248418_at	AT5G51660	CPSF160 nucleic acid binding	0.05037	0.7292	0.5023	-0.167	0.2858	0.2842	-0.714	0.0062	0.0328	-0.9314	0.0024	0.0161
248419_at	AT5G51550	phosphate-responsive 1 family protein	-0.3769	0.6618	0.48	-0.08448	0.9209	0.5242	0.02547	0.923	0.4987	0.3179	0.2687	0.2221
248420_at	AT5G51560	leucine-rich repeat transmembrane protein kinase,	-0.9675	0.0786	0.1616	-0.9948	0.0731	0.1355	-0.1709	0.3318	0.2842	-0.1982	0.27	0.2227
248421_at	AT5G51510	similar to Os10g0508600 [Oryza sativa (japonica cu	0.6002	0.0298	0.1003	0.5563	0.0375	0.0959	0.04137	0.6862	0.4265	-0.00256	0.9798	0.4781
248422_at	AT5G51640	YLS7 (yellow-leaf-specific gene 7)	0.4023	0.0102	0.064	0.5415	0.0035	0.0374	0.1232	0.0898	0.1325	0.2624	0.009	0.0296
248423_at	AT5G51670	similar to unknown protein [Arabidopsis thaliana] (T	-0.6047	0.4874	0.4148	0.1451	0.8634	0.5081	-0.6617	0.3243	0.2805	0.

248490_at	AT5G50940	pseudogene of unknown protein	-0.03864	0.8962	0.5503	0.4599	0.1736	0.2153	-0.3244	0.2513	0.2415	0.1742	0.5117	0.3304
248491_at	AT5G51010	subredoxin family protein	-1.2185	1.00E-04	0.0312	-1.2683	1.00E-04	0.0249	0.676	1.00E-04	0.012	0.6261	2.00E-04	0.0078
248492_at	AT5G51040	similar to unnamed protein product [Vitis vinifera] (G	-0.2112	0.1444	0.2208	0.2492	0.0993	0.159	0.2503	0.0699	0.1147	0.7107	0.0022	0.0158
248493_at	AT5G51100	FSD2 (FE SUPEROXIDE DISMUTASE 2); iron sup	-0.5825	0.0814	0.165	-0.7117	0.0473	0.108	0.328	0.0425	0.0858	0.1988	0.1497	0.1544
248494_at	AT5G50770	ATHSD6 (HYDROXYSTEROID DEHYDROGENA	-0.1213	0.7411	0.5062	-0.4372	0.271	0.2759	-0.1939	0.2539	0.2431	-0.5098	0.0249	0.052
248495_at	AT5G50780	ATP-binding region, ATPase-like domain-containing	1.0309	0.1497	0.2254	0.4263	0.5025	0.3857	-0.5981	0.3601	0.2982	-1.2027	0.1065	0.125
248496_at	AT5G50790	nodulin MtN3 family protein	-0.05613	0.9242	0.5581	0.3023	0.6143	0.4286	0.2484	0.6771	0.4235	0.6068	0.3349	0.2556
248497_at	AT5G50380	ATEXO70F1 (exocyst subunit EXO70 family protein	0.6803	0.0037	0.0459	0.4662	0.0141	0.0629	-0.1909	0.1634	0.1875	-0.405	0.0224	0.0487
248498_at	AT5G50390	pentatricopeptide (PPR) repeat-containing protein	0.1219	0.8125	0.5275	0.06523	0.8987	0.5185	-0.5379	0.3261	0.2814	-0.5946	0.2841	0.2304
248499_at	AT5G50400	ATPAP27/PAP27 (purple acid phosphatase 27); ac	0.5455	0.0375	0.1117	0.6072	0.027	0.0822	-0.3341	0.0994	0.1405	-0.2725	0.1563	0.159
248500_at	AT5G50410	similar to unnamed protein product [Vitis vinifera] (G	0.029	0.8452	0.5372	0.04767	0.7494	0.4747	0.4456	0.0329	0.0741	0.4642	0.029	0.057
248501_at	AT5G50440	MEMB12 (Golgi SNARE protein membrin 12); SNA	-0.2044	0.3142	0.331	0.06367	0.7383	0.4707	0.2078	0.3072	0.2721	0.4759	0.0554	0.0843
248502_at	AT5G50450	zinc finger (MYND type) family protein	0.5473	0.3813	0.3652	0.8814	0.1886	0.2255	-0.7532	0.1079	0.147	-0.4192	0.3146	0.2458
248503_at	AT5G50470	CCAAT-box binding transcription factor Hap5a, put	0.989	0.401	0.3758	-0.7288	0.5272	0.395	1.4902	0.2301	0.2295	-0.2276	0.8395	0.4398
248504_at	AT5G50480	CCAAT-box binding transcription factor Hap5a, put	-0.1095	0.9055	0.5526	0.6943	0.4678	0.3712	0.1198	0.8967	0.4915	0.9236	0.3464	0.2609
248505_at	AT5G50360	similar to unknown protein [Arabidopsis thaliana] (T	1.2072	0.2064	0.2661	2.8315	0.0242	0.0781	-1.5031	0.1339	0.1667	0.1213	0.887	0.4535
248506_at	AT5G50370	adenylate kinase, putative	-0.3468	0.0427	0.1189	-0.2611	0.0918	0.1529	0.2384	0.0076	0.0352	0.3241	0.0025	0.0165
248507_at	AT5G50420	similar to unknown protein [Arabidopsis thaliana] (T	-0.2286	0.0972	0.1801	-0.5402	0.007	0.0473	-0.02718	0.7894	0.46	-0.3387	0.0236	0.0503
248508_at	AT5G50320	ELO3/HAC8/HAG3 (ELONGATA 3); N-acetyltransfe	0.6771	0.005	0.0506	0.3781	0.0354	0.0929	-0.7363	0.0037	0.0267	-1.0353	0.001	0.0122
248509_at	AT5G50335	unknown protein	-0.6169	0.1716	0.2426	-0.8479	0.0842	0.146	0.06238	0.8746	0.4852	-0.1686	0.673	0.3885
248510_at	AT5G50315	transposable element gene	0.3327	0.6213	0.4669	1.1741	0.1323	0.1846	0.5326	0.4329	0.3309	1.374	0.088	0.1112
248511_at	AT5G50375	CPI1 (CYCLOPROPYL ISOMERASE)	0.07888	0.6415	0.4735	0.03562	0.8315	0.4993	0.03248	0.8461	0.4775	-0.08202	0.6287	0.3733
248512_at	AT5G50460	protein transport protein SEC61 gamma subunit, pu	0.5509	0.0382	0.1125	0.8658	0.0087	0.0514	0.5946	0.0303	0.0709	0.9094	0.0073	0.0267
248513_at	AT5G50500	unknown protein	-0.4369	0.5224	0.43	0.523	0.4491	0.3636	-0.7672	0.2863	0.2614	0.1927	0.7729	0.4209
248514_s_at	AT5G50620;AT5G50510	[AT5G50620, heat shock protein binding];[AT5G50	0.04941	0.9449	0.5635	-1.5952	0.0764	0.1385	-0.2214	0.7582	0.4507	-1.7672	0.0581	0.0869
248515_at	AT5G50530;AT5G50640	[AT5G50530, CBS domain-containing protein / octo	-0.699	0.022	0.0871	-0.9676	0.0073	0.0482	-0.5652	0.0423	0.0856	-0.8338	0.0122	0.0349
248516_at	AT5G50645;AT5G50540	[AT5G50645, similar to unknown protein [Arabidops	0.4832	0.684	0.4872	-0.8348	0.4914	0.3809	-1.6586	0.2072	0.2161	-2.9767	0.0542	0.0833
248517_at	AT5G50550;AT5G50650	[AT5G50550, WD-40 repeat family protein / SH12p (	0.4655	0.0611	0.1418	0.3865	0.0986	0.1582	-0.2279	0.2748	0.2551	-0.3069	0.1638	0.1636
248518_at	AT5G50660;AT5G50560	[AT5G50660, similar to unknown protein [Arabidops	0.786	0.1721	0.2429	0.6687	0.2306	0.2519	0.08134	0.867	0.4833	-0.03596	0.9409	0.4687
248519_at	AT5G50590;AT5G50690	[AT5G50590, ATHSD4 (HYDROXYSTEROID DEH	0.1011	0.8831	0.5471	1.427	0.0916	0.1527	-2.1481	0.014	0.0472	-0.8222	0.1853	0.1765
248520_at	AT5G50700;AT5G50600	[AT5G50700, short-chain dehydrogenase/reductase	0.0485	0.8981	0.5507	0.1077	0.7771	0.4827	-0.01793	0.9195	0.4977	0.1383	0.4532	0.3073
248521_s_at	AT5G50630;AT5G50520	[AT5G50630, nodulin family protein];[AT5G50520, n	0.8168	0.0011	0.036	0.6639	0.0025	0.0339	0.2688	0.0269	0.0668	-0.4217	0.0059	0.0238
248522_at	AT5G50565;AT5G50665	[AT5G50565, similar to unknown protein [Arabidops	-0.1927	0.512	0.4257	0.2638	0.3808	0.3323	-0.3612	0.2492	0.2405	0.09534	0.7401	0.4105
248523_s_at	AT5G50680;AT5G50580	[AT5G50680, SUMO activating enzyme 1b (SAE1b)	1.563	0.1367	0.2147	0.2845	0.0277	0.083	-0.03806	0.6744	0.4224	0.09021	0.3438	0.2598
248524_s_at	AT5G50670;AT5G50570	[AT5G50670, squamosa promoter-binding protein,	0.3837	0.2082	0.2671	0.5275	0.1083	0.1659	-0.3675	0.0193	0.0557	-0.2237	0.0823	0.1069
248525_s_at	AT5G50610;AT5G50710	[AT5G50610, similar to unknown protein [Arabidops	-2.5255	0.1154	0.1966	-0.8183	0.5513	0.4054	-1.7402	0.015	0.0488	-0.03297	0.942	0.469
248526_at	AT5G50740	metal ion binding	-1.5858	0.0011	0.036	-1.6432	9.00E-04	0.0288	0.9381	0.0028	0.0241	0.8808	0.0035	0.0193
248527_at	AT5G50740	metal ion binding	-2.1522	5.00E-04	0.0323	-1.3178	0.0032	0.0366	-0.4817	0.0453	0.0891	0.3527	0.1032	0.1229
248528_at	AT5G50760	auxin-responsive family protein	0.3027	0.5871	0.4552	0.1029	0.8509	0.5047	0.7702	0.1676	0.1901	0.5703	0.2806	0.2284
248529_at	AT5G50780	protein kinase, putative	0.1652	0.1422	0.2192	0.1871	0.1077	0.1655	0.1536	0.0152	0.0492	0.1755	0.0097	0.0306
248530_at	AT5G49945	identical to Uncharacterized protein At5g49945 pre	0.422	0.1726	0.2431	0.5118	0.1146	0.1708	-0.2633	0.2759	0.2557	-0.1735	0.4528	0.3071
248531_at	AT5G49950	embryogenesis-associated protein-related	0.2566	0.0637	0.1446	-0.1911	0.131	0.1835	0.001865	0.984	0.5137	-0.4459	0.007	0.0261
248532_at	AT5G49940	NFU2 (NFU domain protein 2)	-0.2522	0.0626	0.1436	-0.0851	0.4362	0.3581	0.05266	0.6212	0.405	0.2197	0.0895	0.1124
248533_at	AT5G50020	zinc finger (DHHC type) family protein	-1.1106	0.0029	0.0434	-0.3017	0.1531	0.2004	-0.4923	0.0453	0.0891	0.3166	0.1383	0.1471
248534_at	AT5G50030	invertase/pectin methylesterase inhibitor family prot	-0.6214	0.1909	0.256	0.007239	0.9863	0.5406	-1.0402	0.0301	0.0707	-0.4116	0.2623	0.219
248535_at	AT5G50120	transducin family protein / WD-40 repeat family prot	-0.1227	0.7471	0.5031	-0.1354	0.7224	0.4661	-0.2605	0.3608	0.2732	0.4846	0.0229	0.0195
248536_at	AT5G50140	ankyrin repeat family protein	0.2131	0.7101	0.4962	1.7292	0.0317	0.0884	-0.1391	0.8072	0.4656	1.377	0.0613	0.0897
248537_at	AT5G50100	similar to PBng143 [Vigna radiata] (GB:BAB82450;	-1.3541	2.00E-04	0.0312	-1.2888	2.00E-04	0.0249	0.2089	0.1057	0.1455	0.2742	0.0523	0.0814
248538_at	AT5G50110	methyltransferase-related	-0.613	0.0076	0.0579	-0.6663	0.0065	0.0434	0.1096	0.2802	0.2582	0.05621	0.5566	0.3476
248539_at	AT5G50130	short-chain dehydrogenase/reductase (SDR) family	-0.2702	0.1385	0.2161	-0.1207	0.4557	0.3663	0.2628	0.1469	0.1769	0.4122	0.0479	0.0773
248540_at	AT5G50160	ATFRO8/FRO8 (FERRIC REDUCTION OXIDASE 8	0.1566	0.585	0.4544	0.1749	0.544	0.4022	-0.4172	0.1654	0.1887	-0.399	0.1804	0.1735
248541_at	AT5G50180	protein kinase, putative	-0.1204	0.3246	0.3246	-0.04849	0.6588	0.4446	-0.3322	0.031	0.0717	-0.2603	0.0629	0.0911
248542_at	AT5G50190	similar to EMB1353 (EMBRYO DEFECTIVE 1353)	1.6964	0.2062	0.2661	-1.1918	0.3494	0.3178	1.3344	0.3014	0.2694	-1.5538	0.2396	0.2068
248543_at	AT5G50230	nucleotide binding	0.1973	0.0563	0.136	-0.04786	0.5536	0.406	0.1004	0.0912	0.1335	-0.1447	0.0332	0.0616
248544_at	no_match	no_match	-0.5454	0.1267	0.2058	-0.8191	0.1046	0.2159	-0.4899	0.3556	-0.05831	0.8471	0.442	
248545_at	AT5G50260	cysteine proteinase, putative	1.528	0.1988	0.2618	0.9933	0.3738	0.3294	0.2445	0.8177	0.4692	-0.2902	0.7847	0.4243
248546_at	no_match	no_match	-0.00158	0.9984	0.5763	0.4622	0.569	0.4115	0.05495	0.9307	0.5009	0.5187	0.4316	0.2975
248547_at	AT5G50280	EMB1006 (EMBRYO DEFECTIVE 1006)	-0.7653	0.0108	0.0652	-0.3783	0.0898	0.1511	-0.5969	0.0019	0.0207	-0.3791	0.0226	0.0489
248548_at	AT5G50300	xanthine/uracil/vitamin C permease family protein	-0.6316	0.3593	0.3542	-0.4507	0.5014	0.3852	0.3901	0.5576	0.3819	0.5711	0.4025	0.2853
248549_at	AT5G50310	kelch repeat-containing protein	-0.1456	0.7115	0.4968	0.2741	0.4962	0.3829	-0.852	0.0134	0.0461	-0.4322	0.0988	0.1197
248550_at	AT5G50210	QS (QUINOLINATE SYNTHASE); quinolinate synth	-0.4336	0.009	0.0612	-0.6222	0.0024	0.0339	-0.3117	0.027	0.0668	-0.5003	0.0054	0.023
248551_at	AT5G50200	WR3 (WOUND-RESPONSIVE 3); nitrate transmem	1.3478	1.00E-04	0.0312	1.6127	0	0.0249	0.5695	0.0015	0.0198	0.8344	3.00E-04	0.0086
248552_at	AT5G50250	31 kDa ribonucleoprotein, chloroplast, putative / RN	-0.4514	0.0696	0.1521	-0.3229	0.1531	0.2004	0.3184	0.1573	0.1839	0.4469	0.0713	0.0979
248553_at	AT5G50170	C2 domain-containing protein / GRAM domain-cont	-0.04585	0.8975	0.5505	-0.0337	0.9245	0.5252	-0.07906	0.7384	0.4443	-0.0669	0.777	0.422
248554_at	AT5G50330	ATP binding / protein kinase	1.3661	0.1779	0.2465	1.0723	0.2692	0.275	-1.0703	0.2142	0.2204	-1.3641	0.1333	0.1439
248555_at	AT5G50340	ATP binding / ATP-dependent peptidase/ damaged-	0.3316	0.185	0.2519	0.5788	0.0492	0.1099	-0.5704	0.0513	0.0961	-0.3231	0.1941	0.1815
248556_at	AT5G50350	similar to unnamed protein product [Vitis vinifera] (G	0.1228	0.0049	0.05	1.0626	0.0042	0.0403	0.3715	0.058	0.1031	0.4112	0.0435	0.0729
248557_at	AT5G49980	AFB5 (AUXIN F-BOX PROTEIN 5); ubiquitin-protei	-0.1072	0.6617	0.48	0.2406	0.3494	0.3178	-0.8147	0.0088	0.0376	-0.4669	0.0521	0.0813
248558_at	AT5G49990	xanthine/uracil permease family protein	0.8718	0.0202	0.0838	0.8297	0.0237	0.0774	-0.4119	0.1069	0.1464	-0.454	0.0844	0.1085
248559_at	A[AT5G50012 CFu;ORF36 (Conserved peptide upst	0.4403	0.6836	0.487	-2.0966	0.105	0.1637	2.3192	0.0369	0.0792	-0.2177	0.7869	0.4249	
248560_at	AT5G49970	ATPPOX (A. THALIANA PYRIDOXAL (PYRIDOXA	-0.3225	0.0229	0.0885	-0.3669	0.015	0.0645	0.001523	0.9443	0.5043	-0.04289	0.1042	0.1236
248561_at	AT5G49680	cell expansion protein, putative	0.8922	0.086	0.17	0.9723	0.0689	0.1317	-0.6801	0.0283	0.0684	-0.5999	0.0414	0.0706
248562_at	AT5G49660	cell expansion protein, putative	0.4362	0.3821	0.3656	1.0494	0.0776	0.1397	-0.531	0.2643	0.2489	0.08218	0.8507	0.4429
248563_at	AT5G49690	UDP-glucuronosyl/UDP-glucosyl transferase family	-0.7534	0.5717	0.4495	0.4506	0.7316	0.4688	-2.2942	0.0838	0.1273	-1.0903	0.3375	0.2567
248564_at	AT5G49700	DNA-binding protein-related	1.7348	0.0737	0.1561	2.6798	0.0205	0.073	-0.1002	0.8961	0.4913	0.8448	0.3059	0.2414
248565_at	AT5G49710	similar to unknown protein [Arabidopsis thaliana] (T	-0.4545	0.0463	0.1237	0.4527	0.0488	0.1073	-0.04447	0.7722	0.4549	-0.0463	0.7632	0.4178
248566_s_at	AT5G49740;AT5G49730	[AT5G49740, ATFRO7/FRO7 (FERRIC REDUCTIC	0.1372	0.5829	0.4534	-0.165	0.5128	0.3898	-0.325	0.095	0.1368	-0.6273	0.0137	0.0371
248567_at	AT5G49750	leucine-rich repeat family protein	2.0168	0.0756	0.1583	-0.06909	0.9388	0.5287	0.7787	0.0619	0.1069	-1.3071	0.0125	0.0353
248568_at	AT5G49760	leucine-rich repeat family protein / protein kinase fa	0.6738	0.004	0.0466	0.5146	0.0104	0.0552	0.3798	0.0283	0.0684	0.2206	0.1228	0.1369
248569_at	AT5G49770	leucine-rich repeat transmembrane protein kinase,	0.2608	0.7598	0.5116	2.2206	0.0494	0.1102	-1.4804	0.0206	0.0577	0.4694	0.307	0.242
248570_at	AT5G49780	ATP binding / kinase/ protein serine/threonine kinas	-0.6016	0.6142	0.4642	0.09222	0.9373	0.5284	-0.9949	0.34	0.2884	-0.3011	0.7597	0.4165
248571_at	AT5G49790	transposable element gene	1.4499	0.2485	0.2927	-0.7871	0.5044	0.3864	1.8425	0.0518	0.0964	-0.3945	0.5887	0.3594
248572_at	AT5G49800	similar to unnamed protein product [Vitis vinifera] (G	-0.4545	0.539	0.4365	0.1946	0.7882	0.4857	0.2218	0.7597	0.4512	0.8709	0.2679	0.2217
248573_at	AT5G49720	AtGH9A1 (ARABIDOPSIS THALIANA GLYCOSYL	-0.3109	0.0528	0.1318	-0.3922	0.0264	0.0813	-0.1995	0.1555	0.1826	-0.2808	0.0697	0.0967
248574_at	AT5G49830	similar to unknown protein [Arabidopsis thaliana] (T	0.2963	0.1679	0.2397	0.08429	0.6573	0.4442	-0.6133	0.0065	0.0331	-0.8253	0.0022	0.0157
248575_at	AT5G49840	ATP-dependent Clp protease ATP-binding subunit	-0.02238	0.8436	0.5369	0.1011	0.3958	0.3394	-1.1637	1.00E-04	0.0118	-1.0403	2.00E-04	0.0076
248576_at	AT5G49810	MMT (methionine S-methyltransferase); S-adenosyl	0.2035	0.1508	0.2262	-0.03504	0.7753	0.4822	-0.5743	0.0075	0.0349	-0.8129	0.0021	0.0154
248577_at	AT5G49870	jacalin lectin family protein	-0.5455	0.6818	0.4865	-0.9042	0.5051	0.3867	0.7634	0.4784	0.3508	0.4047	0.7001	0.3975
248578_at	AT5G49820	EMB1879 (EMBRYO DEFECTIVE 1879)	0.05721	0.7587	0.5114	-0.3922	0.0872	0.1488	0.148	0.4429	0.3354	-0.3014	0.1582	0.1601
248579_at	AT5G49880	mitotic checkpoint family protein	0.869	0.0174	0.0789	0.9059	0.0151	0.0646	-0.515	0.0428	0.0862	-0.4781	0.053	0.0821
248580_at	AT5G49890	CLC-C (chloride channel C); anion channel/ voltage	0.1263	0.6075	0.4622	-0.1342	0.5859	0.4184	-0.2158	0.1859	0.2028	-0.4763	0.0244	0.0514
248581_at	AT5G49900	catalytic	-0.3132	0.2752	0.3087	0.2312	0.4039	0.343	-0.5496	0.091	0.1334	-0.00511	0.9846	0.4791
248582_at	AT5G49910	cpHSC70-2 (HEAT SHOCK PROTEIN 70-7); ATP b	-0.4546	0.0554	0.1352	-0.9851	0.0044	0.0409	0.2456	0.0381	0.0806	-0.2849	0.0241	0.051
248583_at	AT5G49930	EMB1441 (EMBRYO DEFECTIVE 1441); nucleic ac	0.5585	0.048	0.1261	0.2605	0.2693	0.2696	-0.4235	0.0302	0.0708	-0.7216	0.005	0.0221
248584_at	AT5G49960	binding / catalytic	-0.02556	0.9068	0.553	-0.3635	0.1509	0.1989	-0.7207	0.0245	0.0635	-1.0586	0.0067	0.0254
248585_at	AT5G49640	unknown protein	0.2671	0.8663	0.5425	0.9245	0.5682	0.4112	-2.6133	0.154	0.1817	-1.9558	0.2592	0.2174
248586_at	AT5G49610	F-box family protein	0.05928	0.7525	0.5091	0.246	0.1738	0.2153	-0.04457	0.7795	0.4571	0.1511	0.3674	0.2702
248587_at	AT5G49550	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.686	0.0403	0.1159	0.8038	0.0248	0.079	0.2557	0.1194	0.1558	0.3735	0.0448	0.0742
248588_at	AT5G49540	similar to unknown [Picea sitchensis] (GB:ABK2676	0.32	0.0304	0.1012	0.3422	0.0247	0.0788	0.7444	0.0016	0.0202	0.7666	0.0014	0.0135
248589_at	AT5G49510	VHL binding protein, putative / prefoldin, putative	0.02858	0.6042	0.4609	0.145	0.0463	0.1067	0.07379	0.2032	0.2137	0.1902	0.0173	0.042
248590_at	AT5G49660	leucine-rich repeat transmembrane protein kinase,	-0.3586	0.0715	0.1541	-0.4246	0.0448	0.105	0.08218	0.6509	0.4001	0.01619	0.9176	0.462
248591_at	AT5G49650	xylulose kinase, putative	0.5308	0.0056	0.0523	0.4177	0.013	0.0609	0.09857	0.3655	0.3007	-0.01457	0.8874	0.4536
248592_at	AT5G49280	hydroxyproline-rich glycoprotein family protein	0.02719	0.9416	0.5629	-0.1635	0.6636	0.4461	0.8007	0.0559	0.1009	0.6099	0.1118	0.1289
248593_at	AT5G49180	pectinesterase family protein	0.3545	0.6183	0.4658	2.0338	0.0364	0.0942	-0.6674	0.1465	0.1766	1.0119	0.0526	0.0818
248594_at	AT5G49210	similar to unknown [Brassica rapa] (GB:ABP80728.	0.01892	0.8964	0.5503	0.55	0.0157	0.0653	-0.09617	0.5198	0.3669	0.4349	0.0333	0.0616
248595_at	AT5G49230	HRB1 (HYPERSENSITIVE TO RED AND BLUE)	-0.1526	0.1457	0.2218	-0.3043	0.0228	0.0763	0.2837	0.0188	0.0549	0.132	0.1502	0.1547
248596_at	AT5G49330	AtMYB111 (myb domain protein 111); DNA binding	0.2882	0.8066	0.5258	1.3443	0.2896	0.2863	-0.7902	0.5131	0.3643	0.2659	0.8212	0.4346
248597_at	AT5G49160	MET1 (DECREASED METHYLATION 2DNA)	-0.7349	0.0462	0.1236	-0.7672	0.0407	0.1001	-0.6135	0.0757	0.1198	-0.6458	0.0661	0.0936
248598_at	AT5G49370	hydrogen ion transporting ATP synthase, rotational	-0.2572	0.8999	0.5511	-0.7286	0.7237	0.4666	-0.03069	0.9867	0.5143	-0.5021	0.7867	0.4248
248599_at	AT5G49380	hydrogen ion transporting ATP synthase, rotational	0.01048	0.9909	0.5748	1.0111	0.3078	0.2962	-1.1236	0.2642	0.2489	-0.123	0.8939	0.4554
248600_at	AT5G49390	binding	-0.7768	0.0417	0.1176	-0.4506	0.1614	0.2069	-0.769	0.0429	0.0864	-0.4428	0.1672	0.1655
248601_at	AT5G49400	zinc knuckle (CCHC-type) family protein	0.6558	0.0218	0.0867	0.8742	0.0083	0.0504	-0.335	0.1358	0.1683	-0.1167	0.5515	0.3456
248602_s_at	AT5G49420;AT5G38620	[AT5G49420, MADS-box protein (AGL84)];[AT5G38	-0.7458	0.6667	0.4815	1.2968	0.465	0.37	0.476	0.7647	0.4527	2.5186	0.1653	0.1644
248603_at	AT5G49430	transducin family protein / WD-40 repeat family prot	0.302	0.3743	0.3617	0.4569	0.2053	0.2362	-0.04867	9.00E-04	0.0169	-0.7939	0.0018	0.0147
248604_at	AT5G49470	protein kinase family protein	-0.2245	0.496	0.4186	-0.3138	0.3548	0.3203	-0.6169	0.0903	0.1328	-0.7062	0.0636	0.0917
248605_at	AT5G49410	similar to unknown protein [Arabidopsis thaliana] (T	1.0656	0.0727	0.1553	1.2601	0.0458	0.106	0.2761	0.5334	0.3725	0.4706	0.3104	0.2436
248606_at	AT5G49490;AT5G49448	[AT5G49450, ATB2IP1 (ARABIDOPSIS THALIANA	0.08563	0.8479	0.5573	0.2539	0.2664	-0.03625	0.869	0.484	0.6067	0.0423	0.0717	
248607_at	AT5G49480	ATCP1 (CA2+-BINDING PROTEIN 1); calcium ion	-0.6244	0.0482	0.1265	-0.5655	0.0635	0.1256	0.8035	0.0224	0.0604	0.8624	0.0178	0.0427
248608_at	AT5G49460	ACLB-2 (ATP-citrate lyase B-2)	-0.7763	0.0432	0.1199	-0.9404	0.024	0.078	0.242	0.0236	0.0623	0.07789	0.3159	0.2464
248609_at	AT5G49440	unknown protein	0.5068	0.1426	0.2196	0.5481	0.0438	0.4022	-1.2758	0.1978	0.2104	0.7791	0.3995	0.2841
248610_at	AT5G49500	signal recognition particle 54 kDa protein 2 / SRP54	-0.1954	0.6287	0.4691	0.351	0.4008	0.3415	-0.05969	0.8395	0.4755	0.4867	0.1528	0.1567
248611_at	AT5G49520	WRKY48 (WRKY DNA-binding protein 48); transcri	0.2048	0.7563	0.5106	-0.3985	0.5532	0.4059	0.2686	0.3954	0.3145	-0.3347	0.3016	0.2394
248612_at	AT5G49530	SIN-like family protein	0.4307	0.0548	0.1344	0.4678	0.0433	0.1032	-0.2025	0.1982	0.2107	-0.1654	0.2767	0.2265
248613_at	AT5G49555	amine oxidase-related	0.2371	0.2891	0.3168	0.1308	0.5374	0.3994	-0.1873	0.3894	0.3119	-0.2936	0.2051	0.1879
248614_at	AT5G49560	similar to unknown protein [Arabidopsis thaliana] (T	-0.6861	0.5074	0.4241	0.6044	0.5567	0.4071	-0.6394	0.5352	0.3733	0.6512	0.5281	0.3372
248615_at	AT5G49570	ATPNG1 (ARABIDOPSIS THALIANA PEPTIDE-N-	0.1521	0.0042	0.0468	0.787	0.0117	0.0581	-0.04549	0.6169	0.3659	-0.3106	0.0084	0.0284
248616_at	AT5G49580	DNAJ heat shock N-terminal domain-containing pro	0.6122	0.0106	0.0649	0.4561	0.0281	0.0835	-0.3125	0.0822	0.1258	-0.4686	0.0258	0.0532
248617_at	AT5G49590	unknown protein	-2.1933	0.225	0.2785	-3.1601	0.1078	0.1655	-1.2013	0.4762	0.35	-2.1681	0.2294	0.2012
248618_at	AT5G49620	AMYB371 (myb domain protein 78); DNA binding / tr	-0.8965	0.365	0.3573	1.1125	0.1694	-0.125	1.7847	0.2934	0.2654	1.8092	0.0662	0.0937
248619_at	AT5G49630	AAP6 (AMINO ACID PERMEASE 6); amino acid tra	-0.817	0.0095	0.0626	-1.0674	0.0036	0.0379	0.3028	0.1061	0.1458	0.05241	0.7371	0.4094
248620_at	AT5G49320	similar to unknown protein [Vitis vinifera] (GB:CA	-0.3698	0.1945	0.2587	-0.7991	0.0282	0.0835	0.1312	0.6101	0.4013	-0.2981	0.2777	0.2269
248621_at	AT5G49350	similar to unknown protein [Arabidopsis thaliana] (T	1.3151	0.3626	0.3557	0.8922	0.5245	0.3939	0.746	0.5916	0.3952	0.3231	0.8133	0.4326
248622_at	AT5G49360	BXL1 (BETA-XYLOSIDASE

248690_at	AT5G48230	ACAT2/EMB1276 (ACETOACETYL-COA THIOLAS	-0.1621	0.5706	0.4493	-0.1777	0.5359	0.3988	0.06897	0.6519	0.4152	0.05337	0.7255	0.4058
248691_at	AT5G48310	similar to unknown protein [Arabidopsis thaliana] (T	-0.06469	0.8851	0.5471	-0.1099	0.8065	0.4918	-0.02544	0.9546	0.5066	-0.07067	0.8746	0.4498
248692_s_at	AT4G15070;AT5G48320	[AT4G15070, DC1 domain-containing protein]-[AT5	-0.1633	0.4057	0.3782	0.9411	0.0059	0.0442	-0.8316	0.0065	0.0332	0.2728	0.1635	0.1634
248693_at	AT5G48330	regulator of chromosome condensation (RCC1) fam	0.394	0.0625	0.1435	0.007346	0.9642	0.535	0.1996	0.264	0.2488	-0.187	0.2907	0.2339
248694_at	AT5G48340	similar to unnamed protein product [Vitis vinifera] (G	0.2127	0.2084	0.2672	0.1937	0.2442	0.2606	-0.2029	0.2262	0.2271	-0.2219	0.193	0.1809
248695_at	AT5G48350	nucleic acid binding	0.8886	0.3829	0.3662	-1.7817	0.1211	0.1764	1.0873	0.2969	0.2671	-1.5829	0.156	0.1589
248696_at	AT5G48360	formin homology 2 domain-containing protein / FH2	-0.5477	0.0916	0.1756	-0.8014	0.0319	0.0886	-0.1164	0.4552	0.3409	-0.3701	0.0584	0.0871
248697_at	AT5G48370	thioesterase family protein	-0.02003	0.9258	0.5585	0.2376	0.3046	0.294	-0.2106	0.2633	0.2483	0.0471	0.7856	0.4245
248698_at	AT5G48380	leucine-rich repeat family protein / protein kinase fa	1.1822	0.0247	0.0912	1.1533	0.0267	0.0816	0.1039	0.3263	0.2814	0.07495	0.4653	0.3121
248699_at	AT5G48390	binding	-0.4142	0.5634	0.4461	-0.6895	0.354	0.3201	-0.09712	0.8898	0.4897	-0.3724	0.6018	0.3639
248700_at	AT5G48400	ATGLR1.2 (Arabidopsis thaliana glutamate recepto	0.746	0.0577	0.1376	0.9208	0.0312	0.0877	0.2755	0.385	0.3101	0.4503	0.1865	0.1772
248701_at	AT5G48410	ATGLR1.3 (Arabidopsis thaliana glutamate recepto	0.4666	0.2498	0.2935	0.8787	0.0645	0.1267	-0.2689	0.1729	0.1938	0.1432	0.4274	0.2957
248702_at	AT5G48420	unknown protein	-0.1855	0.5452	0.439	-0.2997	0.3461	0.316	-0.7275	0.0607	0.1057	-0.8417	0.0401	0.0691
248703_at	AT5G48430	aspartic-type endopeptidase/ pepsin A	-0.2974	0.6089	0.4627	-0.2373	0.6811	0.4523	0.02445	0.9658	0.5089	0.08453	0.8824	0.4521
248704_at	AT5G48450	SKS3 (SKU5 Similar 3); copper ion binding	-0.03112	0.9233	0.558	0.1836	0.5781	0.4153	-0.3544	0.0911	0.1335	-0.1397	0.4319	0.2977
248705_at	AT5G48520	similar to predicted protein [Physcomitrella patens s	-0.3747	0.0218	0.0867	-0.3428	0.0289	0.0847	-0.123	0.2565	0.2445	-0.0911	0.3828	0.277
248706_at	AT5G48530	similar to unknown protein [Arabidopsis thaliana] (T	1.2855	0.1547	0.2296	0.6501	0.4258	0.3834	-0.4752	0.4917	0.3564	-2.4108	0.0185	0.0437
248707_at	AT5G48550	F-box family protein-related	0.05083	0.9562	0.5664	1.2563	0.2223	0.2473	-0.6015	0.5274	0.3702	0.6039	0.5259	0.3362
248708_at	AT5G48560	basic helix-loop-helix (bHLH) family protein	2.4006	0.0084	0.06	0.7056	0.228	0.2502	0.01974	0.9639	0.5085	-1.6753	0.015	0.039
248709_at	AT5G48570	similar to unnamed protein product [Vitis vinifera] (G	-0.1319	0.6547	0.4775	-0.2541	0.4053	0.3436	0.3805	0.0217	0.0595	0.2583	0.0683	0.0955
248710_at	AT5G48480	Identical to Uncharacterized protein At5g48480 [Ara	0.8157	0.0161	0.0768	0.8628	0.0134	0.0615	0.5705	0.0489	0.0932	0.6177	0.0388	0.0678
248711_at	AT5G48270	similar to unknown protein [Arabidopsis thaliana] (T	0.5996	0.7129	0.4972	-0.7029	0.6673	0.4475	0.2719	0.7876	0.4594	-1.0306	0.3362	0.2562
248712_at	AT5G48280	unknown protein	1.0289	0.5579	0.4441	-0.9022	0.6054	0.4253	-0.5726	0.7403	0.4449	-2.5037	0.1952	0.182
248713_at	AT5G48180	kelch repeat-containing protein	-0.01192	0.9566	0.5664	-0.1413	0.5304	0.3964	0.5435	0.0577	0.1027	0.4141	0.1148	0.1311
248714_at	AT5G48140	polygalacturonase, putative / pectinase, putative	0.3822	0.6483	0.4759	0.09628	0.9073	0.5207	-0.5451	0.5213	0.3675	-0.831	0.3447	0.2602
248715_at	AT5G48290	heavy-metal-associated domain-containing protein	1.4265	0.0967	0.1796	0.4306	0.5496	0.4047	0.5473	0.4534	0.3402	-0.4486	0.5339	0.3394
248716_at	AT5G48210	similar to unknown protein [Arabidopsis thaliana] (T	0.412	0.7387	0.5053	2.035	0.1521	0.1998	-1.3884	0.072	0.1167	0.2346	0.7024	0.3981
248717_at	AT5G48175	unknown protein	-1.1819	0.0105	0.0647	-0.3501	0.2503	0.2641	-0.4656	0.1485	0.1781	0.3661	0.2328	0.2031
248718_at	AT5G48770	FPS1 (FARNESYL DIPHOSPHATE SYNTHASE 1);	0.3697	0.1605	0.2338	0.1871	0.433	0.3567	-0.1642	0.2788	0.2575	-0.3467	0.0574	0.0862
248719_at	AT5G47910	RBOHD (RESPIRATORY BURST OXIDASE PROT	-0.2968	0.0078	0.0583	-0.1817	0.0389	0.0977	-0.1889	0.0065	0.0331	-0.07384	0.1113	0.1286
248720_at	AT5G47750	protein kinase, putative	0.1985	0.3977	0.3743	0.448	0.1697	0.1592	-0.2873	0.2431	0.2368	-0.03765	0.8664	0.4472
248721_at	AT5G47780	GAUT4 (Galacturonosyltransferase 4); polygalactur	-0.0047	0.9622	0.5679	-0.1512	0.1796	0.2193	0.2441	0.0587	0.1037	0.09757	0.3538	0.2644
248722_at	AT5G47810	phosphofructokinase family protein	1.1935	7.00E-04	0.0334	0.7108	0.0052	0.0429	-0.3524	0.0509	0.0956	-0.8352	0.0028	0.0174
248723_at	AT5G47950	transferase family protein	0.1729	0.7251	0.5011	-2.1958	0.0087	0.0513	1.9039	0.0142	0.0475	-0.4647	0.3678	0.2703
248724_at	AT5G47970	nitrogen regulation family protein	-0.1234	0.3547	0.3521	-0.1293	0.3347	0.3107	-0.704	0.004	0.0273	-0.7099	0.0038	0.02
248725_at	AT5G47980	transferase family protein	-2.1967	0.0449	0.1221	-0.1961	0.8096	0.4928	-2.0628	0.0537	0.0986	-0.06215	0.9389	0.4681
248726_at	AT5G47960	SMC1 (SMALL MOLECULAR WEIGHT G-PROTEI	0.727	0.0418	0.1176	0.9145	0.0205	0.0732	0.42	0.163	0.1872	0.6075	0.069	0.0963
248727_at	AT5G47990	CYP705A5 (cytochrome P450, family 705, subfamil	1.6717	0.1325	0.211	-0.04595	0.9612	0.5343	0.5185	0.1197	0.156	-1.1991	0.0103	0.0317
248728_at	AT5G48000	CYP708A2 (cytochrome P450, family 708, subfami	0.7996	0.4567	0.4012	0.1597	0.8774	0.5124	-0.5034	0.6317	0.4084	-1.1433	0.3045	0.2408
248729_at	AT5G48010	pentacyclic triterpene synthase, putative	-1.8515	0.0996	0.1786	-0.6582	0.4831	0.3773	-0.8429	0.3787	0.3072	0.3504	0.7021	0.398
248730_at	AT5G48050	similar to unknown protein [Arabidopsis thaliana] (T	-1.241	0.3338	0.3422	-0.8992	0.4708	0.3724	-0.3703	0.7596	0.4512	-0.02848	0.9811	0.4783
248731_at	AT5G48060	C2 domain-containing protein	0.032	0.9479	0.5642	0.1075	0.8269	0.498	0.5913	0.0997	0.1407	0.6668	0.0738	0.0998
248732_at	AT5G48070	ATXTH20 (XYLOGLUCAN ENDOTRANSGLUCOS	-0.588	0.4774	0.4107	-1.5327	0.1108	0.1681	0.7005	0.4037	0.3181	-0.2442	0.7613	0.4171
248733_at	AT5G48080	similar to EDM2, transcription factor [Arabidopsis th	-0.1086	0.8989	0.5508	-0.2393	0.7804	0.4836	0.524	0.4713	0.3481	0.3934	0.583	0.3573
248734_at	AT5G48090	ELP1 (EDM2-LIKE PROTEIN1); protein binding / zi	0.8729	0.1569	0.231	-0.5133	0.3641	0.3248	-0.1884	0.7263	0.4406	-1.5746	0.0349	0.0632
248735_at	AT5G48100	TT10 (TRANSPARENT TESTA 10); laccase	-1.8979	0.2139	0.2707	-1.0866	0.4455	0.3621	0.3692	0.7838	0.4586	1.1805	0.4013	0.2847
248736_at	AT5G48110	terpene synthase/cyclase family protein	-1.0809	0.2195	0.2748	-0.6313	0.4434	0.361	-0.8677	0.3078	0.2724	-0.4181	0.6037	0.3645
248737_at	AT5G48120	binding	0.2046	0.2397	0.2875	0.3838	0.0607	0.1225	-1.3321	6.00E-04	0.0158	-1.1529	0.0011	0.0123
248738_at	AT5G48020	similar to unnamed protein product [Vitis vinifera] (G	0.4632	0.0094	0.0624	0.2841	0.0454	0.1055	0.1863	0.1317	0.1651	0.00778	0.9411	0.4688
248739_at	AT5G48030	GFA2 (GAMETOPHYTIC FACTOR 2); heat shock p	0.5916	0.001	0.0354	0.08903	0.2637	0.2719	-0.2142	0.0068	0.0338	-0.7168	1.00E-04	0.0058
248740_at	AT5G48130	phototropic-responsive NPH3 family protein	0.5531	0.5838	0.4539	-0.9514	0.364	0.3248	0.6334	0.533	0.3725	-0.8711	0.4018	0.2849
248741_at	AT5G48170	SLY2 (SLEEPY2)	-0.2963	0.3252	0.3374	-0.3026	0.3205	0.3034	0.3561	0.223	0.2254	0.3547	0.2265	0.1997
248742_at	AT5G48200	unknown protein	0.1578	0.8869	0.5475	0.4288	0.7017	0.4597	-1.6076	0.1977	0.156	-1.1991	0.0103	0.0317
248743_at	no_match	no_match	1.0468	0.0023	0.0418	0.3737	0.0696	0.1322	0.7082	9.00E-04	0.0169	0.03511	0.6826	0.3914
248744_at	AT5G48250	zinc finger (B-box type) family protein	1.1508	0.2426	0.2891	1.3603	0.1809	0.2201	-0.4412	0.1393	0.1706	-0.2317	0.3882	0.2792
248745_at	no_match	no_match	-0.1589	0.5855	0.4546	-0.1724	0.5555	0.4068	-0.2367	0.3892	0.3118	-0.2502	0.3654	0.2693
248746_at	AT5G47890	NADH-ubiquinone oxidoreductase B8 subunit, putat	0.03945	0.7276	0.5017	0.4106	0.0177	0.0689	0.05986	0.6011	0.3985	0.4311	0.0151	0.039
248747_at	AT5G48030	40S ribosomal protein S27 (RPS27D)	0.05994	0.7788	0.5175	0.398	0.1168	0.1727	0.1783	0.422	0.3263	0.5163	0.0608	0.0892
248748_at	AT5G47840	AMK2 (ADENOSINE MONOPHOSPHATE KINASE	-0.3971	0.0744	0.1568	-0.5634	0.0272	0.0825	-0.5367	0.0035	0.026	-0.7029	0.0013	0.013
248749_at	AT5G47880	release factor/release factor	0.5824	0.0137	0.0719	0.3136	0.0867	0.1484	0.1047	0.4928	0.3567	-0.1641	0.3025	0.2399
248750_at	AT5G47530	auxin-responsive protein, putative	-0.00312	0.9912	0.5748	0.03144	0.9118	0.5219	0.06742	0.8127	0.4675	0.102	0.7214	0.4044
248751_at	AT5G47540	Mo25 family protein	0.3428	0.3293	0.3395	-0.3467	0.3245	0.3057	-0.1938	0.5643	0.3844	-0.8832	0.0459	0.0753
248752_at	AT5G47600	heat shock protein-related	0.5627	0.5386	0.4363	0.525	0.5648	0.41	-0.07882	0.6736	0.422	-0.1165	0.5391	0.3409
248753_at	AT5G47630	ATMCP2 (MITOCHONDRIAL ACYL CARRIER PRO	-0.3179	0.2419	0.2887	-0.2116	0.4126	0.3473	0.4219	0.1245	0.1598	0.5282	0.0722	0.0985
248754_at	AT5G47670	CCAAT-box binding transcription factor family prote	0.3611	0.5755	0.451	-0.3725	0.564	0.4097	1.5286	0.0571	0.102	0.795	0.2405	0.2074
248755_at	no_match	no_match	-0.02671	0.8884	0.5479	0.1804	0.3695	0.3273	-0.4357	0.0712	0.116	-0.2286	0.2698	0.2226
248756_at	AT5G47560	ATSDA1/ATTDT (TONOPLAST DICARBOXYLATE	-0.2025	0.1595	0.2331	-0.514	0.0119	0.0585	-0.2181	0.073	0.1176	-0.5297	0.0042	0.0208
248757_at	AT5G47680	RNA binding / tRNA methyltransferase	0.4112	0.1381	0.2159	0.578	0.0601	0.1217	-0.4739	0.0288	0.0689	-0.3071	0.0963	0.1177
248758_at	AT5G47620	heterogeneous nuclear ribonucleoprotein, putative /	0.3585	0.0487	0.1271	0.4554	0.0236	0.0773	0.09317	0.5069	0.3621	0.1901	0.2115	0.1916
248759_at	AT5G47610	zinc finger (C3HC4-type RING finger) family protein	-0.4823	0.3904	0.3701	-0.1982	0.7127	0.463	-0.1329	0.4629	0.3444	0.1512	0.4083	0.2875
248760_at	AT5G47570	similar to unknown [Populus trichocarpa] (GB:ABK9	-0.03284	0.7178	0.4987	0.2686	0.0337	0.0908	0.6181	0.0019	0.0207	0.9195	4.00E-04	0.0089
248761_at	AT5G47635	similar to unknown protein [Arabidopsis thaliana] (T	1.5569	0.255	0.2964	1.1678	0.3757	0.3301	1.5366	0.2603	0.2466	1.1474	0.3833	0.2773
248762_at	AT5G47455	similar to unknown protein [Arabidopsis thaliana] (T	0.7373	0.0229	0.0885	0.8527	0.0142	0.0631	0.3239	0.1898	0.2054	0.4393	0.0991	0.1199
248763_at	AT5G47550	cysteine protease inhibitor, putative / cystatin, putat	-0.5096	0.1749	0.2448	-0.29	0.4017	0.3421	0.5424	0.0179	0.0536	0.762	0.0055	0.0232
248764_at	AT5G47640	CCAAT-box binding transcription factor subunit B (N	-1.0318	0.0052	0.0513	-0.6816	0.0216	0.0747	0.2456	0.2352	0.2323	0.5958	0.0276	0.0553
248765_at	AT5G47650	ATNUDT2 (Arabidopsis thaliana Nudix hydrolase hc	0.6674	0.0021	0.0406	-0.7061	9.00E-04	0.0286	0.385	0.0053	0.0306	0.2463	0.0246	0.0515
248766_at	AT5G47580	similar to unknown protein [Arabidopsis thaliana] (T	0.6669	0.0019	0.0391	0.8447	8.00E-04	0.0277	0.01687	0.7918	0.4606	0.1946	0.0312	0.0595
248767_at	AT5G47710	C2 domain-containing protein	-0.0955	0.6289	0.4693	-0.1498	0.4586	0.3675	0.9783	0.0059	0.032	0.9241	0.0072	0.0264
248768_at	AT5G47700	60S acidic ribosomal protein P1 (RPP1C)	0.05774	0.7893	0.5204	0.2606	0.2668	0.2736	0.1116	0.6101	0.4013	0.3145	0.1947	0.1818
248769_at	AT5G47730	SEC14 cytosolic factor, putative / polyphosphoinosi	0.1482	0.5846	0.4541	-0.04016	0.88	0.5131	0.3297	0.1202	0.1564	0.1414	0.4459	0.3044
248770_at	AT5G47740	similar to protein kinase family protein / U-box doma	0.9707	0.492	0.4166	1.2741	0.3775	0.3308	-0.7398	0.4624	0.3442	-0.4364	0.657	0.3832
248771_at	AT5G47790	forkhead-associated domain-containing protein / FH	0.03932	0.8485	0.5379	0.208	0.3417	0.3143	-0.1394	0.4404	0.3342	0.02933	0.8659	0.4472
248772_at	AT5G47800	phototropic-responsive NPH3 family protein	-0.06351	0.8067	0.5258	-0.2636	0.3391	0.3131	-0.06206	0.7409	0.445	-0.2621	0.2087	0.1901
248773_at	AT5G47820	FRA1 (FRAGILE FIBER 1); microtubule motor	-0.4981	0.0031	0.044	-0.04215	0.6182	0.4299	-1.0046	2.00E-04	0.0129	-0.5487	0.0022	0.0157
248774_at	AT5G47830	similar to hypothetical protein MtDRAFT_AC15020	-0.02406	0.9294	0.5598	0.6621	0.0603	0.1219	-0.6255	0.0016	0.0202	0.06068	0.4995	0.3257
248775_at	AT5G47850	protein kinase, putative	1.0487	0.2095	0.2678	-0.5684	0.4635	0.3696	1.111	0.1887	0.2047	-0.506	0.5109	0.3302
248776_at	AT5G47900	similar to unknown protein [Arabidopsis thaliana] (T	-0.01776	0.9294	0.5598	-0.16	0.4431	0.3608	-0.5776	0.0099	0.0396	-0.7199	0.0045	0.0213
248777_at	AT5G47920	similar to unknown protein [Arabidopsis thaliana] (T	1.1081	0.02	0.0834	1.2964	0.0324	0.0891	0.6684	0.0828	0.1264	0.4556	0.1917	0.1801
248778_at	AT5G47940	similar to unknown protein [Arabidopsis thaliana] (T	0.8419	0.0134	0.0715	0.4849	0.0718	0.1341	0.04589	0.8292	0.4725	-0.3111	0.1936	0.1812
248779_at	AT5G47720	acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-(	0.6435	0.036	0.1096	-0.2099	0.3682	0.3267	1.0502	0.0071	0.0342	0.1968	0.3959	0.2826
248780_at	AT5G47760	ATPGLP2/ATPK5/PGLP2 (ARABIDOPSIS THALIA	0.45	0.051	0.1298	0.4657	0.0462	0.1066	-0.2445	0.2084	0.2169	-0.2288	0.2336	0.2035
248781_at	AT5G47870	similar to unknown protein [Arabidopsis thaliana] (T	-0.4169	0.1076	0.1897	-0.5173	0.0623	0.124	0.475	0.0409	0.084	0.3745	0.0789	0.104
248782_at	AT5G47340	palmitoyl protein thioesterase family protein	-0.2431	0.8	0.5241	0.5599	0.5666	0.4106	0.8756	0.3736	0.3045	1.6785	0.1275	0.1399
248783_at	AT5G47360	pentatricopeptide (PPR) repeat-containing protein	-0.9555	0.0919	0.1758	-0.5171	0.2983	0.2907	-0.4091	0.3982	0.3158	0.0293	0.9493	0.4707
248784_at	AT5G47380	similar to unknown protein [Arabidopsis thaliana] (T	-0.2557	0.4787	0.4114	-0.3836	0.3067	0.2955	-0.04392	0.8853	0.4883	-0.1718	0.5802	0.3562
248785_at	AT5G47400	similar to hypothetical protein 25.t00068 [Brassica c	0.1835	0.3471	0.3485	0.2873	0.1709	0.2133	-0.3482	0.1134	0.151	-0.2444	0.2291	0.2011
248786_at	AT5G47410	similar to hypothetical protein 25.t00068 [Brassica c	0.659	6.00E-04	0.0332	0.5363	0.0014	0.0312	-0.06168	0.4746	0.3495	-0.1743	0.0565	0.0853
248787_at	AT5G47420	similar to unknown protein [Arabidopsis thaliana] (T	0.6509	0.0513	0.1301	0.5014	0.1014	0.1607	-0.1092	0.6188	0.4042	-0.2587	0.2713	0.2234
248788_at	AT5G47430	similar to unknown protein [Arabidopsis thaliana] (T	0.9597	0.0109	0.0655	0.7623	0.0216	0.0747	0.2924	0.1499	0.1788	0.115	0.5227	0.335
248789_at	AT5G47440	similar to unknown protein [Arabidopsis thaliana] (T	-1.7418	9.00E-04	0.0349	-2.0289	5.00E-04	0.0259	0.1448	0.3466	0.2915	-0.1423	0.354	0.2645
248790_at	AT5G47450	ATTIP2;3 (Arabidopsis thaliana tonoplast intrinsic pr	-0.4423	0.422	0.386	-0.691	0.2352	0.2549	-0.06758	0.8825	0.4874	-0.3162	0.5022	0.3267
248791_at	AT5G47360	palmitoyl protein thioesterase family protein	-0.1522	0.6315	0.4702	0.09916	0.7526	0.4759	-0.198	0.5371	0.3741	0.05336	0.8646	0.447
248792_at	AT5G47200	ARABIDOPSIS ATH A (Arabidopsis Rab GTPase hor	-0.03495	0.7807	0.518	0.28	0.0756	0.1379	0.6817	0.0044	0.0283	0.9966	0.0011	0.0123
248793_at	AT5G47240	ATNUDT8 (Arabidopsis thaliana Nudix hydrolase hc	-0.8496	0.2269	0.2797	-0.6151	0.3601	0.3228	0.3495	0.2308	0.2299	0.584	0.0777	0.103
248794_at	AT5G47220	ATERF-2/ATERF2/ERF2 (ETHYLENE RESPONSE	-0.04217	0.8491	0.5379	0.06501	0.7701	0.4805	0.2897	0.2358	0.2327	0.3969	0.1289	0.1408
248795_at	AT5G47390	myb family transcription factor	0.01401	0.9363	0.5613	-0.02274	0.8968	0.5178	0.3012	0.0349	0.0767	0.2644	0.0511	0.0805
248796_at	AT5G47180	vesicle-associated membrane family protein / VAMI	0.4937	0.1932	0.2578	0.6852	0.0959	0.156	-0.3974	0.0625	0.1074	-0.2058	0.2551	0.2152
248797_at	AT5G47210	nuclear RNA-binding protein, putative	0.02265	0.9221	0.5576	0.06899	0.7671	0.4795	0.5382	0.0127	0.0447	0.5845	0.0095	0.0304
248798_at	AT5G47190	ribosomal protein L15 family protein	-0.799	0.002	0.0398	-0.5056	0.0104	0.0552	0.2098	0.1319	0.1652	0.5032	0.0106	0.0322
248799_at	AT5G47230	ERF5 (ETHYLENE RESPONSIVE ELEMENT BIND	-1.2986	0.0081	0.0587	-0.9645	0.022	0.075	0.5359	0.0028	0.0241	0.8699	4.00E-04	0.0091
248800_at	AT5G47320	RPS19 (40S ribosomal protein S19); RNA binding	0.0701	0.4256	0.3874	0.1957	0.0687	0.1315	0.2862	0.0224	0.0604	0.4117	0.0065	0.025
248801_at	AT5G47370	HAT2; transcription factor	-0.4832	0.0549	0.1344	-0.3308	0.1397	0.1905	0.2193	0.257	0.2448	0.3716	0.0887	0.1117
248802_at	AT5G47435	formyltetrahydrofolate deformylase, putative	0.4565	0.0376	0.1119	0.04929	0.7576	0.4774	-1.3356	3.00E-04	0.0138	-1.7429	1.00E-04	0.0061
248803_at	AT5G47460	pentatricopeptide (PPR) repeat-containing protein	0.1654	0.6057	0.4616	-0.4333	0.2165	0.2437	0.4126	0.8725	0.2323	0.1446	0.6502	0.3809
248804_at	AT5G47470	nodulin MtN21 family protein	1.3095	0.1987	0.2618	0.9938	0.3078	0.2962	-0.1116	0.8725	0.4848	-0.4273	0.5484	0.3445
248805_at	AT5G47480	similar to unknown protein [Arabidopsis thaliana] (T	0.6111	0.0228	0.0882	0.3878	0.0844	0.1462	-0.2818	0.1723	0.1934	-0.5051	0.0409	0.07
248806_at	AT5G47490	similar to unknown protein [Arabidopsis thaliana] (T	0.03201	0.9063	0.5528	0.03919	0.8855	0.5147	-0.3936	0.293	0.2652	-0.2377	0.4046	0.286
248807_at	AT5G47500	pectinesterase family protein	0.3865	0.5912	0.4565	-0.3975	0.5811	0.4166	-0.2608	0.6556	0.4163	-1.0448	0.1262	0.139
248808_at	AT5G47510	SEC14 cytosolic factor family protein / phosphoglyc	0.1477	0.7	0.4925	-0.3117	0.4315	0.356	0.3732	0.3545	0.2955	-0.08619	0.821	0.4345
248809_at	AT5G47520	ARA8/ARA4 (Arabidopsis Rab GTPase homolog A5e	0.06382	0.5904	0.4563	0.4545	0.0131	0.0611	-0.302	0.0506	0.0954	0.09866	0.4175	0.2915
248810_at	AT5G47280	ADR1-L3 (ADR1-LIKE 3); ATP binding / nucleoside	-2.1536	0.0979	0.1807	-0.4589	0.6705	0.4488	-3.2098	0.0327	0.0738	-1.5151	0.2049	0.1878
248811_at	AT5G47310	similar to unknown protein [Arabidopsis thaliana] (T	0.1071	0.5019	0.4214	-0.1287	0.426	0.3534	-0.3364	0.0816	0.1252	-0.5721	0.017	0.0416
248812_at	AT5G47330	palmitoyl protein thioesterase family protein	-0.4279	0.1201	0.2004	-0.318	0.2168	0.2439	0.2866	0.2572	0.2448	0.3965	0.1419	0.1494
248813_at	AT5G46860	VAM3 (syntaxin 22); SNAP receptor	0.6319	0.0427	0.1189	0.7406	0.0264	0.0813	0.2229	0.069	0.1139	0.3316	0.0214	0.0475
248814_at	AT5G46910	transcription factor jumonji (jmj) family protein	-0.3505	0.2493	0.2932	-0.3382	0.2635	0.2718	-0.6027	0.0044	0.0284	-0.5905	0.0048	0.0218
248815_at	AT5G46690	nitron maturase, type II family protein	0.7655	0.0321	0.1038	0.8033	0.0276	0.0829	-0.567	0.0751	0.1193	-0.5287	0.0896	0.1125
248816_at	AT5G47010	LBA1/UPF1 (LOW-LEVEL BETA-AMYLASE 1); RN	0.03633	0.7775	0.5172	0.1531	0.2718	0.2765	-0.1758	0.1763	0.1961	-0.059	0.6112	0.3672
248817_at	AT5G47020	glycine-rich protein	0.2927	0.0885	0.1724	-0.1132	0.435	0.3576	-0.6033	0.0031	0.0251	-1.0091	4.00E-04	0.0091
248818_at	AT5G47040	1-cys peroxiredoxin homolog 1, mitochondrial (LON	-0.1269	0.5427	0.439	-0.2326	0.2899	0.2865	-0.8529	0.0111	0.0417	-0.9587	0.0074	0.0267
248819_at	AT5G47050	ATP binding / protein binding / shikimate kinase/ zir	-0.3604	0.1527	0.2279	-0.2014	0.3804	0.3322	-0.04432	0.7542	0.4494	0.1147	0.4343	0.2988
248820_at	AT5G47060	senescence-associated protein-related	0.681	0.0379	0.1122	1.1904	0.0059	0.0444	0.03843	0.8716	0.4846	0.5478	0.07	0.097
248821_at	AT5G47070	protein kinase, putative	0.6559	0.0439	0.1209	1.0267	0.0105	0.0553	-0.34	0.0154	0.0493	0.03079	0.7319	0.4077
248822_at	AT5G47000	peroxidase, putative	-0.7586	0.3149	0.3313	-0.9703	0.2159	0.2433	-0.8858	0.2272	0.2278	-1.0975

248890_at	AT5G46270	ATP binding / nucleoside-triphosphatase/ nucleotide	0.458	0.1639	0.2367	-0.08168	0.7766	0.4826	-0.536	0.1172	0.154	-1.0757	0.0162	0.0406
248891_at	AT5G46280	DNA replication licensing factor, putative	-0.06285	0.7825	0.5184	-0.3787	0.1498	0.1979	0.4008	0.0717	0.1163	0.08503	0.6329	0.3747
248892_at	AT5G46300	unknown protein	-0.6212	0.6847	0.4875	0.3295	0.8281	0.4984	-0.7713	0.5709	0.3869	0.1793	0.8929	0.4551
248893_at	AT5G46310	WRKY family transcription factor	-0.262	0.8162	0.5286	-0.6226	0.5871	0.4187	-0.5737	0.599	0.3978	-0.9343	0.4057	0.2864
248894_at	AT5G46320	similar to AGL102, DNA binding / transcription facto	2.2599	0.036	0.1095	-0.02994	0.9691	0.5365	-0.102	0.8952	0.4912	-2.3918	0.0302	0.0585
248895_at	AT5G46330	FLS2 (FLAGELLIN-SENSITIVE 2); ATP binding / ki	1.2622	0.0131	0.0705	1.1064	0.0203	0.0727	-0.2532	0.0385	0.0811	-0.409	0.008	0.0278
248896_at	AT5G46350	WRKY8 (WRKY DNA-binding protein 8); transcriptio	0.5338	0.0255	0.0926	0.6259	0.0152	0.0648	0.1716	0.1268	0.1615	0.2638	0.0418	0.0711
248897_at	AT5G46360	KCO3 (CA2+ activated outward rectifying K+ channe	-1.5666	0.0588	0.1388	-0.6946	0.31	0.2974	-0.9224	0.1978	0.2104	-0.05036	0.9369	0.4676
248898_at	AT5G46370	KCO2 (CA2+ ACTIVATED OUTWARD RECTIFYIN	0.6337	0.6796	0.486	0.1344	0.9294	0.5265	-1.3708	0.3906	0.3124	-1.87	0.2597	0.2176
248899_at	AT5G46390	peptidase S41 family protein	-0.4213	0.0789	0.1618	-0.2614	0.2192	0.2454	-0.9473	0.0039	0.0273	-0.7875	0.0077	0.0272
248900_at	AT5G46400	AT PRP39-2	0.5142	0.0771	0.1598	0.288	0.2556	0.2676	-0.4345	0.1162	0.1533	-0.6607	0.0384	0.0672
248901_at	AT5G46410	NLI interacting factor (NIF) family protein	0.1923	0.0784	0.1613	0.202	0.0689	0.1317	-1.0316	2.00E-04	0.0129	-1.0219	2.00E-04	0.0078
248902_at	AT5G46440	similar to pentatricopeptide (PPR) repeat-containing	0.0595	0.9519	0.5652	1.665	0.147	0.196	-0.1907	0.8471	0.4778	1.4148	0.2017	0.1861
248903_at	AT5G46290	KAS I (3-KETOACYL-ACYL CARRIER PROTEIN S	-0.5291	0.0675	0.1492	-0.9611	0.0106	0.0956	0.1833	0.0821	0.1257	-0.2486	0.0351	0.0634
248904_at	AT5G46295	unknown protein	-0.594	0.4667	0.4058	0.6423	0.434	0.357	0.1173	0.8606	0.4812	1.3536	0.0969	0.1181
248905_at	AT5G46250	RNA recognition motif (RRM)-containing protein	0.07751	0.4227	0.3863	0.01413	0.8787	0.5128	-0.9401	4.00E-04	0.0147	-1.0035	3.00E-04	0.0085
248906_at	AT5G46420	18S rRNA processing protein Rrm4 family	-0.345	0.0783	0.1613	-0.4467	0.0381	0.0967	-0.3973	0.0536	0.0984	-0.499	0.0272	0.0548
248907_at	AT5G46340	O-acetyltransferase-related	0.449	0.0438	0.1207	-0.1316	0.442	0.3603	-0.1016	0.5465	0.378	-0.6822	0.0115	0.0337
248908_at	AT5G45800	MEE62 (maternal effect embryo arrest 62); ATP bin	1.5382	1.00E-04	0.0312	1.4011	1.00E-04	0.0249	0.265	0.0065	0.0331	0.1279	0.066	0.0936
248909_at	AT5G45810	CIPK18 (SNF1-RELATED PROTEIN KINASE 3.5);	0.2198	0.824	0.5307	-0.1616	0.8699	0.5098	0.6173	0.536	0.3736	0.236	0.8088	0.4313
248910_at	AT5G45820	CIPK20 (CBL-INTERACTING PROTEIN KINASE 2	-1.6281	0	0.0312	-1.7996	0	0.0249	-0.2148	0.0615	0.1067	-0.3864	0.0098	0.0309
248911_at	AT5G45930	DOG1 (DELAY OF GERMINATION 1)	-1.0094	0.2489	0.2917	0.2428	0.7608	0.478	-0.5389	0.3517	0.2941	0.7133	0.2358	0.2049
248912_at	AT5G45670	GDSL-motif lipase/hydrolase family protein	-1.9342	0.0535	0.1328	-1.5112	0.1016	0.1608	0.1454	0.3852	0.3102	0.5684	0.019	0.0441
248913_at	AT5G45760	transducin family protein / WD-40 repeat family prot	0.2919	0.061	0.1417	-0.00052	0.9966	0.5432	-0.7348	0.0029	0.0245	-1.0272	8.00E-04	0.0111
248914_at	AT5G45750	ARABA1c (Arabidopsis Rab GTPase homolog A1c	0.8896	0.0622	0.1432	0.79	0.0849	0.1466	0.5441	0.0178	0.0534	0.4444	0.0339	0.0622
248915_at	AT5G45690	similar to unknown protein [Arabidopsis thaliana] (T	0.5989	0.4437	0.3952	0.8883	0.2765	0.279	0.2267	0.7632	0.4522	0.5161	0.5035	0.3272
248916_at	AT5G45840	leucine-rich repeat transmembrane protein kinase,	-0.1721	0.5092	0.4246	-0.2341	0.3804	0.3322	-0.04591	0.8562	0.4802	-0.1079	0.6733	0.3885
248917_at	AT5G45850	similar to unknown protein [Arabidopsis thaliana] (T	-1.7497	0.0713	0.1539	-0.02913	0.9696	0.5365	0.08419	0.9122	0.4957	1.8048	0.0656	0.0933
248918_at	AT5G45890	SAG12 (SENESCENCE-ASSOCIATED GENE 12);	1.1493	0.395	0.3726	0.1765	0.8908	0.516	-0.4734	0.5736	0.3879	-1.4462	0.1348	0.1449
248919_at	AT5G45920	carboxylesterase	-0.4135	0.6447	0.4747	-1.2433	0.2087	0.2387	1.1484	0.2217	0.2245	0.3186	0.7088	0.4005
248920_at	AT5G45930	CHL12; magnesium chelatase	-0.5831	0.0135	0.0716	-0.7922	0.0046	0.0416	0.2196	0.0138	0.0469	0.0104	0.8524	0.4434
248921_at	AT5G45950	GDSL-motif lipase/hydrolase family protein	-0.7501	0.057	0.137	-1.0075	0.0236	0.0773	0.7326	0.0507	0.0954	0.4752	0.1477	0.1532
248922_at	AT5G45980	WOX8 (WUSCHEL-related homeobox 8); DNA binc	1.6937	0.2725	0.307	-1.8538	0.2365	0.2557	1.44	0.3406	0.2886	-2.1074	0.1888	0.1787
248923_at	AT5G45940	ATNUDT11 (Arabidopsis thaliana Nudix hydrolase	0.1171	0.4795	0.41	0.1881	0.2752	0.2783	0.7086	0.0078	0.0354	1.0138	0.0021	0.0155
248924_at	AT5G45960	GDSL-motif lipase/hydrolase family protein	0.377	0.7232	0.5005	0.8584	0.4357	0.3578	1.2249	0.2008	0.2122	-1.7063	0.1001	0.1206
248925_at	AT5G45910	GDSL-motif lipase/hydrolase family protein	0.276	0.818	0.5291	-1.4798	0.2581	0.269	0.5574	0.6457	0.4129	-1.1984	0.3461	0.2608
248926_at	AT5G45880	exo1in-2e e 1 allergen and extensin family protein	0.03739	0.9731	0.5705	-0.3416	0.7598	0.4778	-1.9241	0.1273	0.162	-2.3031	0.0831	0.1076
248927_at	AT5G45900	APG7 (AUTOPHAGY 7)	0.3109	0.205	0.2653	0.3333	0.1802	0.2196	-0.1553	0.4919	0.3564	-0.1329	0.5531	0.3461
248928_at	AT5G45970	ARAC2 (RHO-RELATED PROTEIN FROM PLANT	0.2522	0.5362	0.4355	0.1341	0.7376	0.4705	0.2861	0.486	0.3539	0.1679	0.676	0.3894
248929_at	AT5G46000	jacalin lectin family protein	-0.2774	0.8087	0.5264	0.776	0.5094	0.3884	0.8828	0.4113	0.3214	1.9359	0.1148	0.1311
248930_at	AT5G46010	homeobox-leucine zipper transcription factor family	0.6142	0.5894	0.4559	0.9519	0.4152	0.3485	0.05389	0.9532	0.5063	0.3916	0.6733	0.3885
248931_at	AT5G46040	proton-dependent oligopeptide transport (POT) fam	-0.7547	0.6421	0.4737	-1.2039	0.4681	0.3714	0.2518	0.8751	0.4854	-0.1974	0.9019	0.4579
248932_at	AT5G46050	ATPTR3/PTR3 (PEPTIDE TRANSPORTER PROTE	2.5075	3.00E-04	0.0312	2.1284	5.00E-04	0.0261	0.02587	0.6533	0.4157	-0.3532	0.0027	0.0171
248933_at	AT5G46070	GTP binding / GTPase	0.4114	0.3065	0.3264	0.3648	0.3577	0.3218	-1.5981	0.0031	0.0249	-1.6447	0.0028	0.0172
248934_at	AT5G46080	protein kinase family protein	0.2402	0.3426	0.3463	-0.1221	0.6134	0.4282	0.2387	0.3451	0.2908	-0.1236	0.6094	0.3665
248935_at	AT5G46100	pentatricopeptide (PPR) repeat-containing protein	-0.06407	0.8726	0.5448	-0.1094	0.785	0.4847	-1.2505	0.029	0.0691	-1.2958	0.0259	0.0534
248936_at	AT5G45710	AT-HSFA4C (Arabidopsis thaliana heat shock trans	0.01226	0.9287	0.5596	0.09645	0.4953	0.3826	0.06066	0.662	0.4186	0.1449	0.3234	0.2499
248937_at	AT5G45770	leucine-rich repeat family protein	0.5219	0.615	0.4645	1.0634	0.3294	0.3083	0.549	0.5975	0.3972	1.0905	0.3187	0.2477
248938_at	AT5G45780	leucine-rich repeat transmembrane protein kinase,	0.07677	0.8164	0.5287	0.506	0.1865	0.224	-0.3421	0.3423	0.2895	0.08513	0.802	0.4293
248939_at	AT5G45790	similar to RPD1 (ROOT PRIMORDIUM DEFECTIVE	-0.6122	0.5376	0.4359	0.9146	0.3713	0.3279	-2.5758	0.0014	0.0193	-1.049	0.0317	0.06
248940_at	AT5G45400	replication protein, putative	0.0841	0.7636	0.5126	-0.5261	0.1143	0.1707	0.203	0.4805	0.3516	-0.4072	0.194	0.1815
248941_s_at	AT5G45460, similar to unknown protein [Arabidops	AT5G45460	0.7972	0.0199	0.2833	0.7242	0.0271	0.0823	-0.4624	0.0951	0.1369	-0.5356	0.0653	0.0931
248942_at	AT5G45480	similar to unknown protein [Arabidopsis thaliana] (T	0.3267	0.0518	0.1307	0.2547	0.0994	0.159	-0.3369	0.0361	0.0781	-0.4089	0.0196	0.045
248943_s_at	AT5G45490, AT5G45440	[AT5G45490, disease resistance protein-related];[A	-0.08684	0.7617	0.5121	-0.2803	0.3537	0.32	-0.5263	0.0208	0.058	-0.7197	0.0072	0.0264
248944_at	AT5G45500	similar to unknown protein [Arabidopsis thaliana] (T	1.4051	2.00E-04	0.0312	1.1691	4.00E-04	0.0251	-0.2137	0.0708	0.1157	-0.4497	0.0068	0.0256
248945_at	AT5G45510	leucine-rich repeat family protein	1.0755	0.0013	0.0366	0.7278	0.0054	0.0432	-0.4548	0.0108	0.0413	-0.8025	0.0014	0.0133
248946_at	AT5G45530	similar to unknown protein [Arabidopsis thaliana] (T	-0.1684	0.7489	0.5084	-0.01852	0.9717	0.5371	0.4053	0.4319	0.3304	0.5551	0.2978	0.2375
248947_at	AT5G45540	similar to unknown protein [Arabidopsis thaliana] (T	-2.2677	0.1934	0.2579	-0.9388	0.0054	0.0432	0.5276	0.0065	0.0331	-0.1435	0.2299	0.2015
248948_at	AT5G45560	pleckstrin homology (PH) domain-containing protein	-1.4795	0.1527	0.2279	-0.01018	0.9909	0.5419	-2.5619	0.0379	0.0805	-1.0926	0.2629	0.2192
248949_at	AT5G45570	Ulp1 protease family protein	-1.4344	0.4382	0.3929	-1.2322	0.5009	0.385	-1.1226	0.5377	0.3744	-0.9204	0.6104	0.3669
248950_at	AT5G45390	CLPP4 (Clp protease proteolytic subunit 4); endope	-0.1705	0.7249	0.5045	-0.5163	0.0042	0.0403	0.3516	0.0138	0.0468	0.005863	0.9476	0.4703
248951_at	AT5G45550	mob1/phocein family protein	0.5574	0.0083	0.0597	0.6664	0.0044	0.0409	0.501	0.012	0.0435	0.6099	0.006	0.0241
248952_at	AT5G45410	similar to unknown protein [Arabidopsis thaliana] (T	-0.01481	0.924	0.558	-0.2092	0.2245	0.2482	0.06513	0.3629	0.2995	-0.1293	0.1113	0.1286
248953_at	AT5G45430, protein kinase, putative];[AT5G45428	[AT5G45430, protein kinase, putative];[AT5G45428	0.1585	0.6088	0.4627	-0.16	0.6055	0.4253	-0.4484	0.0349	0.0766	-0.7669	0.0058	0.0237
248954_at	AT5G45420	myb family transcription factor	0.06036	0.6061	0.4618	0.243	0.0877	0.1491	-0.0969	0.4204	0.3256	0.08576	0.4717	0.3144
248955_at	AT5G45600	GAS41 (TBP-ASSOCIATED FACTOR 14B)	0.3509	0.0349	0.108	0.4029	0.0227	0.0761	0.1603	0.1349	0.1674	0.2122	0.0685	0.0957
248956_at	AT5G45610	binding	0.2652	0.3999	0.3752	-0.04406	0.8833	0.514	-0.5299	0.1332	0.1661	-0.8392	0.0408	0.0699
248957_at	AT5G45620	26S proteasome regulatory subunit, putative (RPN6	0.3655	0.0827	0.1664	0.1591	0.373	0.329	-0.1936	0.2002	0.2119	-0.4	0.034	0.0623
248958_at	AT5G45590	structural constituent of ribosome	-0.4662	0.1016	0.1843	-0.6129	0.0496	0.1104	0.4662	0.1016	0.1424	0.3194	0.2204	0.1962
248959_at	AT5G45630	similar to unknown protein [Arabidopsis thaliana] (T	-0.736	0.0153	0.0748	-0.2891	0.1858	0.2236	0.07793	0.6893	0.4276	0.5248	0.0443	0.0738
248960_at	AT5G45640	subtilase family protein	0.3937	0.6659	0.4812	0.6697	0.4729	0.3733	-2.0639	0.0712	0.116	-1.7879	0.1021	0.1221
248961_at	AT5G45650	subtilase family protein	-0.4024	0.1755	0.2452	-0.6469	0.0574	0.1191	-0.3733	0.1176	0.1544	-0.6178	0.0302	0.0584
248962_at	AT5G45680	FK506-binding protein 1 (FKBP13)	-0.8103	0.0017	0.0391	-0.6736	0.0034	0.0374	0.04418	0.7044	0.4328	0.1809	0.1703	0.1674
248963_at	AT5G45700	NLI interacting factor (NIF) family protein	-2.0998	0.1643	0.237	-1.2155	0.3807	0.3323	0.5102	0.7007	0.4315	1.3945	0.3219	0.2492
248964_at	AT5G45340	CYP707A3 (cytochrome P450, family 707, subfami	-1.5049	0.0626	0.1436	-1.7283	0.0424	0.1022	0.1737	0.6787	0.4241	-0.04975	0.9045	0.4586
248965_at	AT5G45370	nodulin-related / integral membrane family protein	0.4902	0.0342	0.1069	0.2192	0.2304	0.2517	0.01804	0.8905	0.4899	-0.2529	0.1092	0.1271
248966_at	AT5G45360	F-box family protein	0.2553	0.4415	0.3944	0.5716	0.1286	0.1819	-0.6323	0.102	0.1426	-0.3161	0.3502	0.2627
248967_at	AT5G45350	proline-rich family protein	-0.2171	0.2987	0.3224	0.2047	0.3235	0.3051	0.9794	0.0032	0.0253	1.4012	8.00E-04	0.0113
248968_at	AT5G45260	pectinacetylesterase, putative	-0.673	0.0584	0.1386	-1.1677	0.0104	0.0552	0.4632	0.0241	0.0629	-0.03153	0.8215	0.4346
248969_at	AT5G45310	similar to unnamed protein product [Vitis vinifera] (G	-0.00111	0.9967	0.5762	0.1704	0.5406	0.4009	-0.2108	0.4548	0.3408	-0.03933	0.8849	0.4529
248970_at	AT5G45380	sodium:solute symporter family protein	1.1253	0.0242	0.0906	0.9573	0.0398	0.0988	-0.05916	0.7284	0.4413	-0.2271	0.2259	0.1994
248971_at	AT5G45000	transmembrane receptor	1.3195	0.0072	0.057	1.0517	0.0157	0.0653	-0.1232	0.54	0.3752	-0.3909	0.1009	0.1212
248972_at	AT5G45010	ATDSS1(V) (ARABIDOPSIS DSS1 HOMOLOG ON	0.8023	0.0182	0.0804	0.9358	0.0109	0.056	0.5298	0.0636	0.1086	0.6634	0.0333	0.0616
248973_at	AT5G45050	TTR1 (WRKY domain family protein 16); transcriptic	0.1755	0.4291	0.3887	-0.07257	0.7347	0.4696	-0.3487	0.065	0.11	-0.5967	0.0124	0.0353
248974_at	AT5G45060	disease resistance protein (TIR-NBS-LRR class), pu	-0.06633	0.7238	0.5006	0.1787	0.3647	0.3251	-1.1959	0.0014	0.0193	-0.9508	0.0032	0.0185
248975_at	AT5G45040	cytochrome c6 (ATC6)	-0.4109	0.0843	0.168	-0.2684	0.2098	0.2394	0.2371	0.1326	0.1657	0.3796	0.0393	0.0683
248976_at	AT5G45930	ARAD2 (ARABINAN DEFICIENT 2); catalytic	-0.04432	0.8817	0.5466	0.4371	0.1928	0.2278	-0.9278	0.0272	0.0671	-0.4464	0.177	0.1713
248977_at	AT5G45020	similar to unknown protein [Arabidopsis thaliana] (T	-0.129	0.5038	0.4221	0.2965	0.1669	0.2104	-0.0787	0.6775	0.4237	0.3468	0.1198	0.1348
248978_at	AT5G45070	ATPP2-A8 (Phloem protein 2-A8); transmembrane	1.5401	0.1474	0.2234	0.5819	0.5353	0.3986	0.0466	0.9593	0.5076	-0.9116	0.3484	0.2617
248979_at	AT5G45080	ATPP2-A6 (Phloem protein 2-A6); transmembrane	-0.08502	0.815	0.5283	-0.2014	0.5858	0.4183	-0.2388	0.5125	0.3641	-0.3552	0.3458	0.2606
248980_at	AT5G45090	ATPP2-A7 (Phloem protein 2-A7); transmembrane	1.0241	0.112	0.194	0.1286	0.8112	0.4934	0.2326	0.6684	0.4207	-0.6628	0.2588	0.2173
248981_at	AT5G45110	NPR3 (NPR1-LIKE PROTEIN 3); protein binding	0.5536	0.124	0.2039	0.3564	0.2791	0.2804	-0.061	0.6709	0.4213	-0.2581	0.1248	0.1382
248982_at	AT5G45120	aspartyl protease family protein	0.5952	0.3938	0.3721	0.707	0.3202	0.3032	-0.2701	0.6028	0.3992	-0.1583	0.7576	0.416
248983_at	AT5G45130	RHA1	0.5639	9.00E-04	0.0349	0.6043	7.00E-04	0.027	0.2875	4.00E-04	0.0147	0.3079	2.00E-04	0.0078
248984_at	AT5G45140	NRPC2 (nuclear RNA polymerase C 2); DNA bindi	0.4479	0.0126	0.0692	0.4143	0.0163	0.0664	-0.428	0.0147	0.0483	-0.4615	0.0113	0.0334
248985_at	AT5G45160	root hair defective 3 GTP-binding (RHD3) family pro	0.4817	0.0167	0.0776	0.6124	0.0073	0.0484	-0.5681	0.0054	0.0309	-0.4374	0.0136	0.0369
248986_at	AT5G45170	CbbY protein-related	-0.4517	0.0086	0.0605	-0.6948	0.0018	0.0323	0.0934	0.3765	0.3059	-0.1497	0.1864	0.1772
248987_at	AT5G45180	flavin-containing monooxygenase family protein / FI	0.6648	0.4771	0.4106	-0.1615	0.8583	0.5067	0.7541	0.4243	0.3272	-0.07213	0.9363	0.4674
248988_at	AT5G45190	cyclin family protein	0.3833	0.1014	0.1842	0.5864	0.0316	0.0883	-0.1226	0.535	0.3733	0.08048	0.6793	0.3902
248989_at	AT5G45200	disease resistance protein (TIR-NBS-LRR class), pu	-0.7381	0.4989	0.4192	0.1752	0.868	0.5094	0.04144	0.9686	0.5096	0.9547	0.3886	0.2793
248990_at	AT5G45210	disease resistance protein (TIR-NBS-LRR class), pu	-2.5885	0.0841	0.1678	-1.5782	0.2356	0.255	0.4973	0.5181	0.3662	1.5077	0.0984	0.1194
248991_at	AT5G45220	Toll-Interleukin-Resistance (TIR) domain-containing	-0.8018	0.5117	0.4256	-0.01685	0.9887	0.5413	-1.0666	0.3928	0.3133	-0.2816	0.813	0.4326
248992_at	AT5G45230	disease resistance protein (TIR-NBS-LRR class), pu	0.1169	0.5727	0.4465	0.4456	0.3621	-0.3846	0.708	0.434	0.3451	0.7364	0.4092	
248993_at	AT5G45240	disease resistance protein (TIR-NBS-LRR class), pu	-0.6246	0.4195	0.3847	-1.1139	0.1842	0.2226	-1.6668	0.0745	0.1188	-2.1561	0.0361	0.0646
248994_at	AT5G45250	RPS4 (RESISTANT TO P. SYRINGAE 4)	0.9142	0.0076	0.0579	1.1955	0.0029	0.0355	-0.3748	0.076	0.1202	-0.09348	0.5848	0.358
248995_at	AT5G45261	RRS1 (RESISTANT TO RALSTONIA SOLANACEA	0.8705	0.1242	0.2042	0.3845	0.4395	0.3594	-0.9664	0.0074	0.1184	-1.4523	0.0225	0.0488
248996_at	AT5G45260	RRS1 (RESISTANT TO RALSTONIA SOLANACEA	0.009369	0.9502	0.5646	0.3178	0.0873	0.1488	-0.7705	0.0055	0.0309	-0.4621	0.0306	0.0588
248997_at	AT5G45300	BAMB/BMY2 (BETA-AMYLASE 8); beta-amylase	-0.04362	0.6879	0.4885	-0.2754	0.0525	0.1136	-0.04475	0.6804	0.4245	-0.2765	0.0519	0.0812
248998_at	AT5G45320	similar to unknown protein [Arabidopsis thaliana] (T	-0.1836	0.6137	0.464	-0.1686	0.642	0.4389	0.08081	0.82	0.4698	0.09579	0.7877	0.425
248999_at	AT5G44970	similar to F-box family protein [Arabidopsis thaliana	-2.1174	0.06	0.14	-2.0722	0.0636	0.1258	-0.9397	0.3127	0.2748	-0.8944	0.3337	0.2551
249000_at	AT5G44980	F-box family protein	-0.00893	0.9869	0.5736	-0.1939	0.723	0.4664	-0.00523	0.9908	0.5154	-0.1902	0.6779	0.3899
249001_at	AT5G44990	similar to unknown protein [Arabidopsis thaliana] (T	3.5645	0.0213	0.0856	2.3827	0.0698	0.1323	-0.4637	0.628	0.4073	-1.6455	0.1365	0.1459
249002_at	AT5G44520	ribose 5-phosphate isomerase-related	-0.1918	0.2297	0.2819	-0.4939	0.0218	0.0748	-0.315	0.0406	0.0836	-0.6172	0.0043	0.0208
249003_at	AT5G44500	small nuclear ribonucleoprotein associated protein	-0.00843	0.9734	0.5706	-0.4648	0.1222	0.1775	0.5528	0.0807	0.1244	0.09624	0.7063	0.3996
249004_at	AT5G44570	unknown protein	3.0254	0.0098	0.0636	2.4059	0.0212	0.0742	1.1178	0.1624	0.1869	0.4983	0.4884	0.3212
249005_at	AT5G44630	terpene synthase/cyclase family protein	0.383	0.6987	0.4922	1.6745	0.1431	0.193	-0.5723	0.4571	0.3418	0.7192	0.3598	0.2669
249006_at	AT5G44660	similar to unknown protein [Arabidopsis thaliana] (T	0.9344	0.2052	0.2656	-0.5961	0.3895	0.3365	-3.0035	0.0015	0.0199	-4.556	3.00E-04	0.0084
249007_at	AT5G44650	similar to unnamed protein product [Vitis vinifera] (G	-0.3201	0.0442	0.1212	-0.6095	0.0053	0.0429	0.6209	0.0049	0.0297	0.3315	0.0399	0.0689
249008_at	AT5G44680	methyladenine glycosylase family protein	-0.4442	0.1987	0.2618	-0.2874	0.3758	0.3301	0.6125	8.00E-04	0.0163	0.7693	3.00E-04	0.0085
249009_at	AT5G44610	MAP1B (MICROTUBULE-ASSOCIATED PROTEIN	0.5397	0.5804	0.4523	0.9227	0.3624	0.324	0.6462	0.6171	0.4036	0.8682	0.3881	0.2792
249010_at	AT5G44580	similar to unknown protein [Arabidopsis thaliana] (T	-0.0969	0.7752	0.5165	-0.1001	0.7681	0.4799	0.3849	0.2917	0.2644	0.3817	0.2952	0.2362
249011_at	AT5G44670	similar to unknown protein [Arabidopsis thaliana] (T	-0.9131	0.0237	0.0898	-1.0286	0.0161	0.066	0.3523	0.2424	0.2364	0.2368	0.4091	0.2879
249012_at	AT5G44620	CYP706A5 (cytochrome P450, family 706, subfami	0.9366	0.3636	0.3561	0.9344	0.3646	0.325	-0.4473	0.6429	0.4121	-0.4494	0.6413	0.3777
249013_at	AT5G44700	EDA23 (embryo sac development arrest 23); ATP b	-1.1643	0.0398	0.115	0.04228	0.9184	0.5237	-0.7839	0.0247	0.0637	0.4227	0.1314	0.1425
249014_at	AT5G44710	similar to unnamed protein product [Vitis vinifera] (G	-0.1309	0.613	0.4637	0.02951	0.9077	0.5208	0.7225	0.039	0.0816	0.883	0.0209	0.0469
249015_at	AT5G44720	haloacid dehalogenase-like hydrolase family protein	0.9817	0.0014	0.038	1.4748	3.00E-04	0.0249	0.1794	0.2265	0.2274	-0.6725	0.0059	0.0238
249016_at	AT5G44750	REV1 (Reversionless 1); damaged DNA binding / m	1.7036	0.029	0.0988	0.1884	0.7312	0.4688	-1.8276	0.0233	0.0617	-3.3428	0.0028	0.0174
249017_at	AT5G44760	C2 domain-containing protein	0.2593	0.7966	0.5226	-1.7541	0.1343	0.1863	-0.1705	0.8644	0.4826	-2.1839	0.0801	0.1051
249018_at	AT5G44770	DC1 domain-containing protein	0.5412	0.6726	0.4835	2.0012	0.1676	0.2109	1.6776	0.3443	0.2904	0.1863	0.8831	0.4523
249019_at	AT5G44780	similar to unknown protein [Arabidopsis thaliana] (T	0.1616	0.6801	0.4861	-0.5758	0.1889	0.2257	0.4053	0.2761	0.2558	-0.3322	0.36	0.267
249020_at	AT5G44840	CHR4/MI-2-LIKE (chromatin remodeling 4); ATP bir	0.1837	0.4055	0.3781	0.1616	0.4596	0.3678	-0.4271	0.0241	0.0629	-0.4492	0.0205	0.0463
249021_at	AT5G44820	similar to unknown protein [Arabidopsis thaliana] (T	-1.4961	0.0709	0.1536	0.6764	0.029	0.0848	-0.3651	0.1185	0.155	-0.1948	0.3725	0.2723
249022_s_at	AT5G44830, AT5G44840	[AT5G44830, glycoside hydrolase family 28 protein	-2.269	0.1025

249090_at	AT5G43745	phosphotransferase-related	-0.9219	0.0039	0.0463	-1.2348	0.0013	0.0309	-0.54	0.0204	0.0574	-0.8529	0.0042	0.0207
249091_at	AT5G43860	ATCLH2 (Chlorophyll-chlorophyllido hydrolase 2)	1.7987	0.006	0.0535	1.8326	0.0056	0.0434	-0.249	0.3492	0.2928	-0.2152	0.4118	0.289
249092_at	AT5G43710	glycoside hydrolase family 47 protein	0.3944	0.0022	0.041	0.3293	0.0043	0.0406	-0.596	5.00E-04	0.0148	-0.6611	3.00E-04	0.0083
249093_at	AT5G43880	similar to unknown protein [Arabidopsis thaliana] (T	-0.7512	0.0033	0.0446	-0.8033	0.0026	0.0342	0.3312	0.0363	0.0784	0.2791	0.0594	0.088
249094_at	AT5G43890	SUPER1/VUCCA5 (SUPPRESSOR OF ER1); mone	-0.717	0.5749	0.4508	-0.8234	0.5223	0.393	-0.1235	0.9057	0.4939	-0.2299	0.8259	0.4399
249095_at	AT5G43900	MYA2 (ARABIDOPSIS MYOSIN)	0.463	0.0369	0.1106	-0.07504	0.6436	0.4394	-0.9299	0.003	0.0247	-1.4679	5.00E-04	0.0096
249096_at	AT5G43910	pfkB-type carbohydrate kinase family protein	1.4661	0.0165	0.0771	1.8211	0.0078	0.0493	-0.5464	0.2126	0.2194	-0.1915	0.631	0.374
249097_at	AT5G43920	DC1 domain-containing protein	0.4293	0.0508	0.1296	0.4409	0.0471	0.1078	-0.3352	0.0782	0.1223	-0.3236	0.0855	0.1094
249098_at	AT5G43530	SNF2 domain-containing protein / helicase domain-	-1.5572	0.3852	0.3674	1.7342	0.3391	0.3131	-0.9264	0.5934	0.3959	2.3649	0.2132	0.1925
249099_at	AT5G43550	similar to unknown protein [Arabidopsis thaliana] (T	-0.1699	0.8521	0.5389	-0.7104	0.4527	0.3651	-0.6356	0.4984	0.359	-1.1761	0.2409	0.2076
249100_at	AT5G43560	meprin and TRAF homolog domain-containing pro	0.1693	0.0781	0.1611	0.04762	0.5439	0.4022	-0.4412	0.0019	0.0209	-0.5629	8.00E-04	0.0108
249101_at	AT5G43580	serine-type endopeptidase inhibitor	0.1415	0.8981	0.5507	0.8709	0.4484	0.3633	0.8636	0.071	0.1159	1.593	0.0108	0.0325
249102_at	AT5G43590	patatin, putative	-0.2691	0.7822	0.5184	0.05241	0.9568	0.5335	0.02552	0.979	0.5123	0.347	0.7224	0.4049
249103_at	AT5G43600	N-carbamyl-L-amino acid hydrolase, putative	-0.1108	0.572	0.4496	-0.3357	0.1361	0.1877	0.01648	0.8692	0.4841	-0.2084	0.0907	0.1134
249104_at	AT5G43610	ATSUC6 (SUCROSE-PROTON SYMPORTER 6); c	-0.6806	0.4773	0.4107	-0.2104	0.8206	0.4961	-0.3748	0.654	0.4159	0.09542	0.908	0.4594
249105_at	AT5G43640	40S ribosomal protein S15 (RPS15E)	-1.8004	0.1	0.1825	-0.6212	0.5027	0.3857	-1.323	0.1922	0.2069	-0.1437	0.8731	0.4494
249106_at	AT5G43670	transport protein, putative	0.4293	0.0508	0.1296	0.4409	0.0471	0.1078	-0.3352	0.0782	0.1223	-0.3236	0.0855	0.1094
249107_at	AT5G43680	similar to unnamed protein product [Vitis vinifera] (G	0.2316	0.4808	0.4123	0.03369	0.9155	0.5229	-0.03449	0.9135	0.4961	-0.2324	0.4794	0.3173
249108_at	AT5G43690	sulfotransferase family protein	-0.9733	0.3544	0.352	2.0447	0.0928	0.1538	-1.319	0.1974	0.2101	1.699	0.1175	0.133
249109_at	AT5G43700	ATAUX2-11 (indoleacetic acid-induced protein 4); t	-0.9547	0.0026	0.0426	-0.0972	0.5326	0.3972	-0.5679	0.0163	0.051	0.2896	0.1119	0.129
249110_at	AT5G43730	disease resistance protein (CC-NBS-LRR class), p	0.8767	0.4524	0.3993	1.0496	0.3759	0.3301	-0.7791	0.5009	0.3599	-0.6063	0.5961	0.3621
249111_at	AT5G43770	proline-rich family protein	0.6459	0.5402	0.4368	-0.06111	0.9526	0.5325	0.1578	0.8752	0.4854	-0.5492	0.5913	0.3603
249112_at	AT5G43780	APS4	0.3334	0.1018	0.1844	-0.03688	0.8265	0.4979	0.3834	0.0457	0.0895	0.01309	0.9268	0.4647
249113_at	AT5G43790	pentatricopeptide (PPR) repeat-containing protein	-0.3772	0.1969	0.2605	-0.5467	0.0885	0.1499	-0.189	0.4817	0.3519	-0.3585	0.2155	0.1939
249114_at	AT5G43800	transposable element gene	1.3821	0.1556	0.2302	1.0153	0.2687	0.2749	-0.6202	0.477	0.3503	-0.9869	0.2803	0.2284
249115_at	AT5G43810	ZLL (ZWILLE)	0.5833	0.06	0.14	0.807	0.0228	0.0762	-0.04301	0.8568	0.4802	0.1807	0.4642	0.3117
249116_at	AT5G43820	pentatricopeptide (PPR) repeat-containing protein	1.2701	0.0083	0.0597	0.8177	0.0353	0.0927	0.09998	0.7216	0.4391	-0.3524	0.2489	0.2119
249117_at	AT5G43840	AT-HSFA6A (Arabidopsis thaliana heat shock trans	1.8833	0.1082	0.1904	1.5421	0.1666	0.2102	0.04434	0.958	0.5071	0.2668	0.7264	0.4061
249118_at	AT5G43870	similar to unknown protein [Arabidopsis thaliana] (T	-0.3391	0.1518	0.2272	-0.2064	0.3425	0.3145	0.1578	0.3721	0.3039	0.2905	0.1382	0.147
249119_at	AT5G43720	similar to unknown protein [Arabidopsis thaliana] (T	-0.08734	0.4738	0.4094	0.2146	0.1242	0.1787	-0.4388	0.0166	0.0514	-0.1368	0.2836	0.2301
249120_at	AT5G43750	similar to unknown protein product [Vitis vinifera] (G	-1.2434	0.0019	0.0391	-1.2283	0.002	0.033	0.1356	0.0702	0.1149	0.1506	0.0526	0.0818
249121_at	AT5G43830	similar to unknown protein [Arabidopsis thaliana] (T	0.4322	0.0479	0.1261	0.4546	0.0414	0.1011	0.0628	0.5896	0.3946	0.08517	0.4716	0.3143
249122_at	AT5G43850	ATARD4; acireductone dioxygenase [iron(II)-requir	-0.2421	0.1606	0.234	-0.2797	0.1178	0.1735	0.6497	8.00E-04	0.0162	0.6121	0.001	0.012
249123_at	AT5G43760	beta-ketoacyl-CoA synthase, putative	-0.616	0.1552	0.2299	-0.6321	0.1471	0.1961	0.2539	0.0685	0.0235	0.2378	0.0348	0.0631
249124_at	AT5G43740	disease resistance protein (CC-NBS-LRR class), p	0.3665	0.454	0.4	0.1723	0.7167	0.4642	-0.3614	0.1842	0.2016	-0.5555	0.0694	0.0965
249125_at	AT5G43450	2-oxoglutarate-dependent dioxygenase, putative	0.237	0.3688	0.359	0.1103	0.6623	0.4458	0.1671	0.3018	0.2695	0.04031	0.7892	0.4255
249126_at	AT5G43460	TOPP8 (TYPE ONE SERINE/THREONINE PROTEIN PHOSPHA	0.9225	0.1504	0.2226	1.5013	0.0446	0.1046	0.01823	0.9728	0.5106	0.5969	0.2997	0.2385
249127_at	AT5G43500	ATARP9 (ACTIN-RELATED PROTEIN 9); protein b	0.3391	0.1891	0.2547	0.07023	0.7598	0.4778	0.0324	0.8444	0.477	-0.2365	0.2011	0.1858
249128_at	AT5G43440	2-oxoglutarate-dependent dioxygenase, putative	1.04	0.0688	0.151	0.9478	0.0874	0.1489	0.1342	0.5857	0.3929	0.04203	0.862	0.4464
249129_at	AT5G43080	CYCA2;4 (CYCLIN A3;1); cyclin-dependent protein	-0.9876	0.1062	0.1885	-0.238	0.4472	0.3626	-0.5452	0.1077	0.1469	-0.1996	0.4544	0.3237
249130_at	AT5G43100	aspartyl protease family protein	0.6123	0.0201	0.0836	0.5691	0.0254	0.0797	-0.2016	0.28	0.2581	-0.2448	0.2043	0.1875
249131_at	AT5G43110	APUM14 (ARABIDOPSIS PUMILIO 14); RNA bindi	-0.09909	0.8943	0.5498	-0.07829	0.9164	0.5231	-0.7327	0.3545	0.2955	-0.7119	0.3669	0.2699
249132_at	AT5G43120	tetratricopeptide repeat (TPR)-containing protein	-0.4942	0.6809	0.4863	-0.2767	0.8165	0.495	0.153	0.8976	0.4917	0.3705	0.7567	0.4156
249133_at	AT5G43130	initiation factor	0.484	0.0077	0.058	0.5523	0.0048	0.042	-0.3957	0.0153	0.0493	-0.3274	0.0283	0.0562
249134_at	AT5G43150	similar to unnamed protein product [Vitis vinifera] (G	-0.3913	0.021	0.0851	-0.4619	0.0121	0.0589	-0.4579	0.0124	0.0443	-0.5285	0.0076	0.027
249135_at	AT5G43160	similar to unknown protein [Arabidopsis thaliana] (T	-0.9421	0.3146	0.3312	-0.1862	0.8315	0.4993	-1.6038	0.1218	0.1577	-0.8479	0.3589	0.2665
249136_at	AT5G43180	similar to unknown protein [Arabidopsis thaliana] (T	-0.7064	0.1876	0.2538	-0.8418	0.1315	0.1839	1.1827	0.0565	0.1015	1.0473	0.0782	0.1034
249137_at	AT5G43140	peroxisomal membrane 22 kDa family protein	-0.00836	0.9681	0.5693	-0.3393	0.1593	0.2053	-0.01562	0.9405	0.5036	-0.3466	0.1526	0.1565
249138_at	AT5G43070	WPP1 (WPP domain protein 1)	-0.1266	0.4591	0.4025	-0.3207	0.1068	0.1649	1.2022	0.0015	0.0198	1.0081	0.0029	0.0175
249139_at	AT5G43170	AZF3 (ARABIDOPSIS ZINC-FINGER PROTEIN 3);	-0.8426	0.0934	0.1771	-0.9021	0.0787	0.1406	0.538	0.2341	0.2318	0.4785	0.2811	0.2287
249140_at	AT5G43190	F-box family protein (FBX6)	-0.1451	0.5339	0.4346	-0.05438	0.8114	0.4934	-0.2041	0.1389	0.1705	-0.1134	0.3635	0.2684
249141_at	AT5G43230	zinc finger (C3HC4-type RING finger) family protein	0.3724	0.692	0.4899	-0.4483	0.635	0.4365	0.9175	0.3531	0.2948	0.09673	0.9172	0.4619
249142_at	AT5G43230	similar to unknown protein [Arabidopsis thaliana] (T	0.3562	0.6711	0.4829	-0.1964	0.8133	0.4941	0.547	0.5211	0.3675	-0.0056	0.9946	0.4814
249143_at	AT5G43230	similar to unknown protein [Arabidopsis thaliana] (T	-0.5618	0.5638	0.4463	1.0842	0.2919	0.2876	-0.5699	0.4328	0.3309	1.076	0.1753	0.1704
249144_at	AT5G43270	SPL2 (SQUAMOSA PROMOTER BINDING PROTE	0.8733	0.0265	0.0941	-0.2495	0.3626	0.3331	-0.5042	0.1077	0.1469	-0.1996	7.00E-04	0.0107
249145_at	AT5G43280	ATDC1 (DELTA(3,5),DELTA(2,4)-DIENOYL-COA	0.2973	0.1046	0.1867	0.3743	0.0579	0.1196	0.3482	0.0315	0.0721	0.4253	0.0166	0.0411
249146_at	AT5G43310	COP1-interacting protein-related	0.3675	0.0516	0.1304	0.1603	0.2971	0.2902	0.3465	4.00E-04	0.0147	0.1392	0.0115	0.0337
249147_at	AT5G43330	malate dehydrogenase, cytosolic, putative	0.1749	0.5448	0.4389	0.2592	0.3828	0.3331	-0.2861	0.3405	0.2886	-0.2018	0.4882	0.3212
249148_at	AT5G43260	chaperone protein dnaJ-related	-0.3037	0.0946	0.1778	-0.1003	0.5112	0.3891	0.778	4.00E-04	0.0145	0.9814	1.00E-04	0.0068
249149_at	AT5G43320	CKL8 (Casein Kinase I-like 8); casein kinase I/ kina	0.1006	0.434	0.391	0.2391	0.1078	0.1656	-0.2792	0.0608	0.1058	-0.1407	0.2621	0.2189
249150_at	AT5G43340	PHT6 (phosphate transporter 6); carbohydrate trans	-0.1853	0.7033	0.4936	-0.3453	0.4969	0.3832	-0.118	0.8112	0.467	-0.274	0.5856	0.3582
249151_at	AT5G43360	PHT3 (phosphate transporter 3); carbohydrate trans	-0.4987	0.419	0.3844	-0.5592	0.3699	0.3275	-0.6011	0.3029	0.27	-0.6616	0.2633	0.2194
249152_s_at	AT5G43350,AT5G43370	ATPT1 (PHOSPHATE TRANSPORTER	0.7869	0.2289	0.2813	-0.6489	0.3069	0.2956	1.3216	0.013	0.0454	-0.1142	0.7312	0.4075
249153_s_at	AT5G43350,AT5G43390	ATSDA400, similar to unknown protein [Arabidopsi	-1.0539	0.2778	0.3101	-0.1659	0.8531	0.5055	-0.713	0.347	0.2917	0.1751	0.8067	0.4306
249154_at	AT5G43410	ethylene-responsive factor, putative	1.3663	0.2893	0.3169	-0.8496	0.4901	0.3805	1.1148	0.3407	0.2886	-1.1011	0.3459	0.2607
249155_at	AT5G43480	unknown protein	0.403	0.6919	0.4899	-2.0568	0.0952	0.1555	3.2527	0.0263	0.0659	0.7929	0.4489	0.3056
249156_s_at	AT5G43490,AT5G48610	similar to unnamed protein product [V	0.04701	0.7421	0.5065	-0.135	0.3684	0.3268	0.0184	0.8566	0.4802	-0.1636	0.1618	0.1623
249157_at	AT5G43510,AT5G43518,A	ATS5G43510, Encodes a defensin-like (DEFL) famil	1.8988	0.1423	0.2194	-0.6102	0.5894	0.4193	0.1635	0.859	0.4807	-2.3455	0.0532	0.0824
249158_at	AT5G43430	ETFBETA; electron carrier	-0.00827	0.9705	0.5701	0.0219	0.9219	0.5245	0.5982	0.0127	0.0448	0.6284	0.0108	0.0325
249159_at	AT5G43460	lesion inducing protein-related	0.6551	0.0209	0.085	0.6446	0.022	0.075	-0.9448	0.0088	0.0377	-0.8552	0.0085	0.0286
249160_at	AT5G42660	similar to unknown protein [Arabidopsis thaliana] (T	0.538	0.1219	0.2022	0.1924	0.5224	0.393	0.3277	0.2991	0.2682	-0.01782	0.9514	0.4713
249161_at	AT5G42790	PAF1 (proteasome alpha subunit F1); peptidase	0.673	0.0026	0.0426	0.6143	0.0036	0.0378	-0.01295	0.9036	0.4933	-0.07166	0.5149	0.3316
249162_at	AT5G42765	similar to unnamed protein product [Vitis vinifera] (G	-0.7849	6.00E-04	0.0334	-0.7824	6.00E-04	0.027	0.05163	0.5593	0.3824	0.05406	0.6419	0.3416
249163_at	AT5G42740	glucose-6-phosphate isomerase, cytosolic (PGIC)	0.1817	0.4031	0.3769	-0.1008	0.6317	0.4352	-0.1552	0.4698	0.3475	-0.4377	0.0877	0.111
249164_at	AT5G42820	ATU2AF35B; RNA binding	0.138	0.5161	0.4276	0.87	0.0109	0.0561	-0.8303	0.0128	0.0451	-0.09836	0.6388	0.3767
249165_at	AT5G42810	ATIPK1 (inositol-pentakisphosphate 2-kinase 1); ino	-0.3286	0.2154	0.2719	-0.2586	0.3116	0.2983	-0.464	0.0247	0.0637	-0.394	0.0408	0.0699
249166_at	AT5G42840	DC1 domain-containing protein	0.08015	0.95	0.5646	0.1395	0.9131	0.5222	0.1982	0.8295	0.4726	0.2575	0.78	0.423
249167_at	AT5G42860	similar to unknown protein [Arabidopsis thaliana] (T	-0.8443	0.0769	0.1596	-0.4519	0.2737	0.2774	0.1479	0.6867	0.4266	0.5403	0.1881	0.1782
249168_at	AT5G42870	lipin family protein	0.4312	0.0589	0.1389	0.4059	0.0693	0.132	0.147	0.4225	0.3265	0.1217	0.501	0.3263
249169_at	AT5G42880	similar to unknown protein [Arabidopsis thaliana] (T	-0.5268	0.667	0.4816	1.7807	0.1921	0.2275	-0.771	0.3166	0.2766	1.5364	0.0849	0.1089
249170_at	AT5G42910	basic leucine zipper transcription factor (BZIP15)	0.9761	0.3652	0.3569	-1.351	0.2307	0.252	0.9371	0.3827	0.3091	-1.39	0.2198	0.196
249171_at	AT5G42940	zinc finger (C3HC4-type RING finger) family protein	0.3566	0.0221	0.0872	0.4828	0.0079	0.0496	0.02147	0.8032	0.4645	0.1477	0.1411	0.1489
249172_at	AT5G42950	GYF domain-containing protein	0.1609	0.3452	0.3474	0.6813	0.0106	0.0556	-1.0873	0.0019	0.021	-0.5668	0.0197	0.045
249173_at	AT5G43000	unknown protein	0.1104	0.854	0.5392	-0.9448	0.1685	0.2115	0.6703	0.1894	0.2051	-0.3849	0.4156	0.2907
249174_at	AT5G42900	similar to unknown protein [Arabidopsis thaliana] (T	0.6182	0.5301	0.4331	1.4514	0.1823	0.2214	-0.4599	0.6364	0.41	0.3734	0.6996	0.3973
249175_at	AT5G42970	COP8 (CONSTITUTIVE PHOTOMORPHOGENIC	0.548	0.0153	0.0747	-0.5292	0.0171	0.0679	-0.3692	0.0073	0.0346	-0.388	0.0061	0.0243
249176_at	AT5G42980	ATTRX3 (thioredoxin H-type 3); thiol-disulfide excha	-0.2104	0.3667	0.3577	-0.07449	0.737	0.4703	0.729	0.0055	0.031	0.8649	0.0029	0.0176
249177_at	AT5G42850	electron carrier/ protein disulfide oxidoreductase	0.279	0.1082	0.2179	0.4997	0.021	0.0739	0.2911	0.0978	0.1391	0.5118	0.0194	0.0447
249178_at	AT5G42890	sterol carrier protein 2 (SCP-2) family protein	0.02981	0.8461	0.5374	0.5526	0.0185	0.0703	0.6037	0.0039	0.0273	1.1265	4.00E-04	0.0088
249179_at	AT5G42955	similar to unknown protein [Arabidopsis thaliana] (T	-0.3478	0.7782	0.5174	-0.4882	0.6941	0.4568	0.6421	0.6077	0.4006	0.5017	0.6863	0.3928
249180_at	AT5G43010	RPT4A (regulatory particle triple-A 4A); ATPase	-0.3042	0.0014	0.038	0.4401	0.0024	0.0338	-0.05486	0.8408	0.3344	-0.1196	0.1359	0.1456
249181_at	AT5G42920	similar to unknown protein [Arabidopsis thaliana] (T	0.4218	0.0794	0.1624	0.5369	0.0408	0.1002	-0.4847	0.0059	0.032	-0.3697	0.0152	0.0392
249182_at	AT5G42960	similar to unknown protein [Arabidopsis thaliana] (T	0.0065	0.9822	0.5725	-0.1595	0.5914	0.4201	0.09834	0.7376	0.4442	-0.06769	0.8169	0.4334
249183_at	AT5G42990	UBC18 (UBIQUITIN-CONJUGATING ENZYME 18)	0.1586	0.1935	0.2579	0.1506	0.2122	0.241	0.3511	0.0154	0.0494	0.3431	0.0166	0.0411
249184_at	AT5G43020	leucine-rich repeat transmembrane protein kinase,	-0.5172	0.1526	0.2278	-0.2689	0.4112	0.3466	-0.1973	0.4368	0.3327	0.0511	0.834	0.4383
249185_at	AT5G43030	DC1 domain-containing protein	0.6075	0.3617	0.3553	-0.46	0.4795	0.3759	0.9241	0.1926	0.2071	-0.1433	0.8202	0.4342
249186_at	AT5G43040	DC1 domain-containing protein	-0.5696	0.1724	0.243	-1.1479	0.0287	0.0844	-0.4802	0.2345	0.2319	-1.0584	0.0368	0.0653
249187_at	AT5G43060	cysteine proteinase, putative / thiol protease, putati	0.455	0.1755	0.2452	0.6526	0.0778	0.1398	-0.2264	0.3212	0.2788	-0.02872	0.8928	0.4551
249188_at	AT5G42830	transferase family protein	1.868	2.00E-04	0.0312	1.5213	5.00E-04	0.0252	0.2431	0.1688	0.191	-0.1037	0.5139	0.3312
249189_at	AT5G42750	ATHB27 (ARABIDOPSIS THALIANA HOMEOBOX	-0.7539	0.1739	0.2441	-1.0829	0.0766	0.1386	1.0393	0.085	0.1284	0.7103	0.1946	0.1817
249190_at	AT5G42750	BKI1 (BRI1 KINASE INHIBITOR 1); protein heterod	0.1317	0.586	0.4547	-0.1387	0.5674	0.4109	0.4146	0.1155	0.1527	0.1442	0.524	0.3355
249191_at	AT5G42760	similar to unknown [Populus trichocarpa] (GB:ABK9	-1.1945	0.014	0.0723	-1.656	0.0044	0.041	0.1942	0.1378	0.1695	-0.2673	0.0634	0.0915
249192_at	AT5G42470	similar to unnamed protein product [Vitis vinifera] (G	0.7631	0.0084	0.06	0.7913	0.0074	0.0485	0.05836	0.7302	0.4418	0.08652	0.8126	0.3676
249193_at	AT5G42480	ARC6 (ACCUMULATION AND REPLICATION OF	-0.2603	0.0671	0.1488	-0.5571	0.0059	0.0444	-0.1552	0.0418	0.085	-0.4519	0.001	0.0121
249194_at	AT5G42490	kinesin motor family protein	-0.478	0.6532	0.4771	0.8852	0.4201	0.3506	-0.172	0.87	0.4841	1.1912	0.2936	0.2354
249195_s_at	AT5G42500,AT5G42510	ATS5G42500, disease resistance-responsive family	-0.4985	0.7256	0.5012	0.3754	0.7908	0.4863	-0.2406	0.8646	0.4826	0.6334	0.6573	0.3832
249196_at	AT5G42560	abscisic acid-responsive HVA22 family protein	0.5501	0.0027	0.0426	0.4665	0.0049	0.0422	-0.0969	0.3067	0.272	-0.1806	0.0946	0.1164
249197_at	AT5G42380	CML37/CML39; calcium ion binding	0.3191	0.3535	0.3515	0.7176	0.0778	0.1398	0.8216	0.0152	0.0492	1.22	0.0038	0.0199
249198_s_at	AT5G42350,AT5G42360	ATS5G42350, kelch repeat-containing F-box family	0.08018	0.7045	0.4942	0.08969	0.6722	0.4492	-0.4307	0.0299	0.0705	-0.2608	0.1163	0.1322
249199_at	AT5G42520	ATBPC6/BBR/BPC6/BPC6 (BASIC PENTACYSTE	0.5724	0.01	0.064	0.1879	0.2052	0.2362	0.03612	0.6258	0.4065	-0.3483	0.0071	0.0262
249200_at	AT5G42540	XRN2 (EXORIBONUCLEASE 2); 5'-3' exonuclease	0.2346	0.1186	0.199	0.4961	0.0138	0.0621	-0.9257	3.00E-04	0.0143	-0.6641	0.0013	0.013
249201_at	AT5G42370	similar to unnamed protein product [Vitis vinifera] (G	0.2224	0.454	0.4	0.3659	0.2447	0.2699	-0.02921	0.8813	0.4871	0.1142	0.5677	0.3518
249202_at	AT5G42580	CYP705A12 (cytochrome P450, family 705, subfam	-0.7114	0.3818	0.3655	-1.2461	0.1606	0.2063	0.4603	0.5598	0.3826	-0.0744	0.9232	0.4636
249203_at	AT5G42590	CYP71A16 (cytochrome P450, family 71, subfamily	-1.7842	0.0978	0.1806	0.41	0.6471	0.4405	-2.4135	0.0069	0.0339	-0.2233	0.6618	0.3848
249204_at	AT5G42570	similar to unknown protein [Arabidopsis thaliana] (T	0.1124	0.7684	0.5141	0.05604	0.8827	0.5138	0.4342	0.1283	0.1627	0.3778	0.1712	0.168
249205_at	AT5G42600	MRN (MARNERAL SYNTHASE); catalytic	-0.3727	0.4082	0.3793	-0.2859	0.5181	0.3917	0.1496	0.6788	0.4241	0.2365	0.5199	0.3337
249206_at	AT5G42630	ATSKAN4 (ABERRANT TESTA SHAPE); DNA bin	0.8244	0.4548	0.4004	0.1908	0.8578	0.5066	1.5296	0.2215	0.2245	0.659	0.5017	0.3265
249207_at	AT5G42640	zinc finger (C2H2 type) family protein	-1.0317	0.2783	0.3104	1.4283	0.1577	0.2042	-1.4617	0.1504	0.1792	0.9983	0.2919	0.2346
249208_at	AT5G42650	AOS (ALLENE OXIDE SYNTHASE); hydro-lyase/ o	-1.2101	0.0109	0.0655	-1.2143	0.0107	0.0558	-0.3128	0.226	0.227	-0.317	0.2209	0.1965
249209_at	AT5G42670	metalloendopeptidase/ zinc ion binding	-0.6449	0.0248	0.0914	-0.08058	0.684	0.4535	-1.6645	8.00E-04	0.0165	-1.1001	0.0039	0.0202
249210_at	AT5G42670	agenet domain-containing protein	-0.2123	0.1227	0.203	-0.4271	0.0172	0.0679	-0.1305	0.2963	0.2668	-0.3453	0.0337	0.062
249211_at	AT5G42680	similar to unknown protein [Arabidopsis thaliana] (T	0.5588	0.0182	0.0804	0.2524	0.1567	0.2033	0.6536	0.0074	0.0347	0.3472	0.0559	0.0848
249212_at	AT5G42690	similar to unknown protein [Arabidopsis thaliana] (T	0.0994	0.0801	0.1633	-0.655	0.2371	0.2561	-0.9231	0.1315	0.165	-0.4477	0.3962	0.2827
249213_at	AT5G42700	transcriptional factor B3 family protein	-1.105	0.3721	0.3605	0.4471	0.7053	0.4607	-1.3027	0.302	0.2696	0.2493	0.8318	0.4377
249214_at	AT5G42720	glycosyl hydrolase family 17 protein	0.8211	0.0028	0.0431	0.7174	0.0046	0.0416	1.1358	8.00E-04	0.0165	1.0321	0.0012	0.0128
249215_at	AT5G42750	DFR (DIHYDROFLAVONOL 4-REDUCTASE); dihy	0.7157	0.0241	0.0906	0.7603	0.0199	0.0721	-0.5581	0.051	0.0956	-0.5135	0.0642	0.0921
249216_at	AT5G42240	SCPL42 (serine carboxypeptidase-like 42); serine c	0.09575	0.3218	0.3353	-0.282	0.0292	0.0849	-0.1166	0.2408	0.2355	-0.4944	0.0043	0.0209
249217_at	AT5G42300	UBL5 (UBIQUITIN-LIKE PROTEIN 5)	0.28	0.2412	0.2885	0.4899	0.0739	0.1365	0.5836	0.011	0.0415	0.7935	0.0037	0.0196
249218_at	AT5G42390	metalloendopeptidase	-0.1246	0.4756	0.41	-0.1003	0.5609	0.4087	-0.7917	0.0075	0.035	-0.7674	0.0084	0.0285
249219_at	AT5G42400	SET domain-containing protein (TXR7)	0.02049	0.8847	0.5471	0.7603	0.0046	0.0416	-0.6142	0.0098	0.0395	0.1255	0.3972	0.2831
249220_at	AT5G42420	transporter-related	0.4368	0.1859	0.2527	0.3479	0.2728	0.277	-0.3905	0.1601	0.1857	-0.4794	0.102	0.122
249221_at	AT5G42440	protein kinase family protein	0.4029	0.2033	0.2643	0.7984	0.0395	0.0985	-0.06

249290_at	AT5G41060	zinc finger (DHHC type) family protein	-0.2365	0.4914	0.4164	-0.2231	0.5149	0.3906	0.06008	0.8197	0.4697	0.0735	0.7807	0.4232
249291_at	AT4G41210	ATGSTT1 (Arabidopsis thaliana Glutathione S-trans	0.3709	0.0686	0.1506	0.1544	0.3611	0.3234	0.0826	0.6005	0.3984	-0.1338	0.4096	0.288
249292_at	AT5G41150	UVH1 (ULTRAVIOLET HYPERSENSITIVE 1)	-0.5851	0.0514	0.1302	-0.2647	0.2815	0.2818	-0.9781	0.0101	0.0398	-0.6577	0.0366	0.0651
249293_at	AT5G41260	protein kinase family protein	0.03191	0.9017	0.5517	0.7048	0.0439	0.1037	-1.4584	5.00E-04	0.0148	-0.7855	0.005	0.0221
249294_at	no_match	no_match	0.6053	0.1135	0.1952	1.2267	0.0149	0.0643	-0.8493	0.0259	0.0654	-0.2278	0.4063	0.2867
249295_at	AT5G41280	Identical to Cysteine-rich repeat secretory protein 5	0.1306	0.8723	0.5447	-0.3369	0.6816	0.4526	1.1466	0.2072	0.2161	0.6791	0.4236	0.294
249296_at	AT5G41310	kinesin motor protein-related	1.6862	0.1285	0.2071	-2.1707	0.6696	0.1322	1.7084	0.1249	0.1599	-2.1485	0.0715	0.098
249297_at	AT5G41320	unknown protein	-0.1479	0.6997	0.4924	-0.08544	0.8226	0.4966	0.1674	0.4714	0.3481	0.2299	0.3365	0.2563
249298_at	AT5G41330	potassium channel tetramerisation domain-containi	-0.5583	0.1425	0.2196	0.1128	0.7314	0.4688	-1.3438	0.0107	0.041	-0.6727	0.0866	0.1102
249299_at	AT5G41340	UBC4 (UBIQUITIN CONJUGATING ENZYME 4); u	-0.5607	1.00E-04	0.0312	-0.1951	0.0047	0.0418	-0.1199	0.025	0.064	0.2457	0.002	0.0152
249300_at	no_match	no_match	0.2455	0.8515	0.5386	0.6876	0.606	0.4255	0.708	0.5957	0.3967	1.1501	0.4027	0.2853
249301_at	AT5G41440	zinc finger (C3HC4-type RING finger) family protein	1.278	0.3796	0.3643	-2.4744	0.1287	0.1819	3.6783	0.0469	0.0907	-0.07404	0.9572	0.4727
249302_at	AT5G41450	zinc finger (C3HC4-type RING finger) family protein	0.3388	0.6859	0.4878	-1.9189	0.6693	0.132	0.9997	0.2684	0.2512	-1.2579	0.1814	0.1743
249303_at	AT5G41460	fringe-related protein	-0.6645	0.1484	0.2242	-1.052	0.0474	0.108	0.1701	0.5289	0.3708	-0.2174	0.4284	0.2961
249304_at	AT5G41480	GLA1 (GLOBULAR ARREST1); tetrahydrofolylpolyg	0.3474	0.0322	0.1041	-0.3293	0.0379	0.0964	-0.08119	0.4934	0.3569	-0.7578	0.0022	0.0157
249305_at	AT5G41490	F-box family protein	0.227	0.8363	0.5343	0.3983	0.7185	0.4648	1.4318	0.1724	0.1934	1.6032	0.1367	0.146
249306_at	AT5G41400	zinc finger (C3HC4-type RING finger) family protein	0.6578	0.1151	0.1963	0.2287	0.5236	0.3936	0.5438	0.0692	0.114	0.1147	0.6304	0.3737
249307_s_at	AT5G41360;AT5G41370	[AT5G41360, XP82 (ARABIDOPSIS HOMOLOG O	0.05801	0.7168	0.4983	-0.04294	0.7875	0.4853	-0.9023	0.0023	0.0224	-1.0033	0.0015	0.0138
249308_at	AT5G41350	zinc finger (C3HC4-type RING finger) family protein	-0.06494	0.6573	0.4781	0.2226	0.1764	0.2173	-0.2382	0.1541	0.1818	0.04932	0.7348	0.4087
249309_at	AT5G41410	BEL1 (BELL 1); DNA binding / transcription factor	0.617	0.0686	0.1506	0.6362	0.0632	0.1252	-0.04118	0.8018	0.4641	-0.02193	0.8933	0.4553
249310_at	AT5G41520	40S ribosomal protein S10 (RPS10B)	0.3339	0.013	0.0704	-0.0216	0.7965	0.4885	0.203	0.0606	0.1057	-0.1525	0.1235	0.1374
249311_at	AT5G41540	disease resistance protein (TIR-NBS-LRR class), p	0.6663	0.6111	0.463	-0.06474	0.6599	0.5341	-0.5969	0.6475	0.4136	0.00464	0.9971	0.4821
249312_at	AT5G41550	disease resistance protein (TIR-NBS-LRR class), p	0.9402	0.1753	0.2451	2.6216	0.0101	0.0547	0.07276	0.9049	0.4937	1.7541	0.0373	0.0659
249313_at	AT5G41560	similar to unnamed protein product [Vitis vinifera] (G	0.6678	0.015	0.0741	0.5947	0.0219	0.075	0.3026	0.1375	0.1693	0.2296	0.2325	0.2029
249314_at	AT5G41580	leucine-rich repeat protein kinase, putative	0.3632	0.294	0.3197	0.2911	0.3882	0.3359	-0.167	0.6086	0.4009	-0.2391	0.4714	0.3142
249315_at	AT5G41190	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.6714	0.0475	0.1254	0.3433	0.2218	0.247	-0.06746	0.7162	0.4369	-0.3955	0.084	0.1082
249316_s_at	AT5G41220;AT5G41240	[AT5G41220, ATGSTT3 (Arabidopsis thaliana Glut	0.4679	0.1475	0.2235	0.7683	0.0422	0.1022	-0.7973	0.0379	0.0804	-0.4968	0.1297	0.1413
249317_at	AT5G41240	ATGSTT2 (Arabidopsis thaliana Glutathione S-trans	0.4775	0.1316	0.21	-0.02109	0.9374	0.5284	-1.6489	0.0028	0.0244	-1.1926	0.0092	0.0298
249318_at	AT5G40870	ATUK/UPRT1 (URIDINE KINASE/URACIL PHOSPI	0.5282	5.00E-04	0.032	0.2992	0.004	0.0395	-0.01046	0.8453	0.4771	-0.2395	0.0089	0.0294
249319_s_at	AT5G40880;AT5G49200	[AT5G40880, WD-40 repeat family protein / zfwd3 p	0.3205	0.1423	0.2193	0.3829	0.0949	0.1552	-0.533	0.0387	0.0812	-0.4706	0.0554	0.0843
249320_at	AT5G40910	disease resistance protein (TIR-NBS-LRR class), p	0.9761	0.0169	0.0778	0.8715	0.0532	0.1144	-2.0638	0.0011	0.0183	-2.3684	7.00E-04	0.0105
249321_at	AT5G40920	pseudogene, disease resistance protein (TIR-NBS-L	0.4256	0.1416	0.2187	0.3558	0.2013	0.2334	-0.2414	0.1542	0.1818	-0.3113	0.0865	0.1101
249322_at	AT5G40930	TOM20-4 (TRANSLOCASE OF OUTER MEMBRAN	-0.3307	0.0648	0.1458	-0.16	0.2884	0.2857	0.6393	0.008	0.0359	0.81	0.0034	0.019
249323_at	AT5G40940	FLA20 (FUTILE FASCICLIN-LIKE ARABINOGA	-1.4538	0.2492	0.2932	0.6895	0.6577	0.4074	-2.601	0.0693	0.114	-0.5177	0.6565	0.383
249324_at	AT5G40810	cytochrome c1, putative	0.3196	0.0114	0.0669	0.08606	0.299	0.291	-0.2642	0.0092	0.0385	-0.4977	9.00E-04	0.0116
249325_at	AT5G40850	UPM1 (UROPHORPHYRIN METHYLASE 1); uropc	-1.8908	0.0067	0.0553	-1.8361	0.0075	0.0486	-0.4483	0.0324	0.0735	-0.3935	0.0477	0.0771
249326_at	AT5G40840	SYN2 (Sister chromatid cohesion 1 (SCC1) protein	0.8286	0.1183	0.1989	0.1174	0.7926	0.487	0.2625	0.5643	0.3844	-0.4491	0.3428	0.2593
249327_at	AT5G40890	ATCLC-A (CHLORIDE CHANNEL A); anion channe	0.07236	0.5915	0.4566	0.004044	0.9756	0.5383	-0.4432	0.0049	0.0297	-0.5115	0.0029	0.0176
249328_at	AT5G40820	ATRAD3 (ATAXIA TELANGIECTASIA-MUTATED A	-0.1576	0.5893	0.4559	-0.3734	0.2373	0.2562	0.5287	0.0905	0.133	0.3129	0.259	0.2173
249329_at	AT5G40960	similar to unknown protein [Arabidopsis thaliana] (T	0.6594	0.1424	0.1185	0.5419	0.0731	0.1355	0.2198	0.3827	0.3091	0.1022	0.6722	0.3881
249330_at	AT5G40970	similar to unknown protein [Arabidopsis thaliana] (T	-0.6194	0.0362	0.1084	-0.05684	0.7883	0.4857	-0.08069	0.5799	0.3906	0.4818	0.0229	0.0493
249331_at	AT5G40950	RPL27; structural constituent of ribosome	-0.5919	0.0414	0.1171	-0.7561	0.0193	0.0715	0.4311	0.0777	0.1218	0.267	0.2178	0.195
249332_at	AT5G40980	similar to unknown protein [Arabidopsis thaliana] (T	0.7975	0.0211	0.0853	0.6118	0.0474	0.108	-0.8968	0.0143	0.0477	0.711	0.0303	0.0585
249333_at	AT5G40990	GLIP1 (GDSL LIPASE1); carboxylesterase	1.0518	0.4153	0.3824	0.115	0.9257	0.5255	0.8838	0.488	0.3546	-0.05299	0.9657	0.4747
249334_at	AT5G41000	YSL4 (YELLOW STRIPE LIKE 4); oligopeptide tran	0.0436	0.8009	0.5244	-0.3151	0.1233	0.1782	0.1837	0.1204	0.1565	-0.175	0.1341	0.1444
249335_at	AT5G41010	DNA-directed RNA polymerase I, II, and III 7 kDa s	0.3257	0.024	0.0903	0.619	0.0025	0.034	0.5437	0.0025	0.0233	0.8369	9.00E-04	0.0094
249336_at	AT5G41070	DRB5 (DSRNA-BINDING PROTEIN 5); double-stra	-0.7014	0.415	0.3823	-1.6165	0.1044	0.1633	0.6238	0.4644	0.345	-0.2912	0.7252	0.4057
249337_at	AT5G41080	glycerophosphoryl diester phosphodiesterase family	0.3649	0.3543	0.3519	0.1372	0.714	0.4633	-0.2495	0.5137	0.3645	-0.4772	0.2429	0.2086
249338_at	AT5G41090	DNA-directed DNA polymerase I, II, and III 7 kDa s	0.9832	0.2815	0.2122	-0.8452	0.3452	0.3157	0.9678	0.1019	0.1426	-0.8605	0.1332	0.1438
249339_at	AT5G41100	DNA binding	0.3393	0.0434	0.1201	0.2674	0.0831	0.1448	0.1146	0.3801	0.3078	0.04277	0.7317	0.4077
249340_at	AT5G41140	similar to unknown protein [Arabidopsis thaliana] (T	-0.5861	0.1572	0.2311	-0.6645	0.1201	0.1754	0.2857	0.4445	0.336	0.2073	0.5719	0.3532
249341_at	AT5G41170	pentatricopeptide (PPR) repeat-containing protein	-0.1288	0.7099	0.4962	-0.5179	0.1835	0.2221	0.1733	0.6195	0.4044	-0.2158	0.5399	0.341
249342_at	AT5G40660	ATP12 protein-related	0.3196	0.1112	0.1933	0.327	0.1054	0.164	-0.2325	0.2122	0.2193	-0.2252	0.2244	0.1984
249343_at	AT5G40650	SDH2-2 (succinate dehydrogenase 2-2)	0.617	0.0174	0.0792	0.6667	0.0135	0.0617	0.2926	0.1376	0.1694	0.3413	0.0968	0.1181
249344_at	AT5G40770	ATPHB3 (PROHIBITIN 3)	0.5143	0.0072	0.0572	0.694	0.0024	0.0339	-0.1619	0.1869	0.2036	0.0177	0.8704	0.4485
249345_at	AT5G40740	similar to Os02g0329300 [Oryza sativa (japonica cu	-0.007	0.9693	0.5697	-0.1303	0.4889	0.3799	-0.5693	0.0255	0.0649	-0.6927	0.0134	0.0367
249346_at	AT5G40780	LHT1 (LYSINE HISTIDINE TRANSPORTER 1); am	1.7415	0.0034	0.0448	1.8548	0.0027	0.0349	-0.1243	0.4524	0.3397	-0.01105	0.9446	0.4695
249347_at	AT5G40830	(ARABIDOPSIS THALIANA RAS ASSOCIATED WI	-0.3074	0.1524	0.2277	-0.2739	0.191	0.2269	-0.01375	0.9409	0.5037	0.01978	0.9151	0.4614
249348_at	no_match	no_match	1.3733	0.3451	0.3474	0.3166	0.8174	0.4951	1.0423	0.4625	0.3442	-0.01447	0.9915	0.4805
249349_at	AT5G40350	MYB24 (myb domain protein 24); DNA binding / tra	-0.8037	0.4941	0.4176	0.9429	0.4277	0.3543	-0.8559	0.4683	0.3468	0.8906	0.4518	0.3067
249350_at	AT5G40360	MYB115 (myb domain protein 115); DNA binding /	-2.3302	0.1152	0.1964	-0.2892	0.8155	0.4947	-0.3808	0.7593	0.4511	1.6602	0.2259	0.1994
249351_at	AT5G40440	ATMKK3 (MITOGEN-ACTIVATED KINASE KINASE	0.2982	0.3297	0.3398	0.1894	0.5202	0.3923	-0.2563	0.1566	0.1827	-0.3651	0.0676	0.0948
249352_at	AT5G40430	MYB22 (myb domain protein 22); DNA binding / tra	-0.8262	0.6044	0.4609	-0.165	0.9161	0.523	-0.9146	0.5678	0.3858	-0.2535	0.8715	0.4489
249353_at	AT5G40420	OLE02 (OLEOSIN 2)	-0.2513	0.8579	0.5406	0.9309	0.5186	0.3919	0.09725	0.919	0.4975	1.2794	0.2274	0.2001
249354_at	AT5G40480	EMB3012 (EMBRYO DEFECTIVE 3012)	0.666	0.0182	0.0804	0.3785	0.0934	0.1539	-0.4086	0.0278	0.0679	-0.6962	0.0045	0.0213
249355_at	AT5G40500	similar to unnamed protein product [Vitis vinifera] (G	-0.3956	0.2552	0.2964	-0.5212	0.1553	0.2023	0.6883	0.0427	0.0861	0.5628	0.0746	0.1005
249356_at	AT5G40520	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.06065	0.4009	0.3758	0.09857	0.4159	0.3488	-0.2391	0.0194	0.0558	-0.2412	0.0188	0.044
249357_at	AT5G40490	RNA recognition motif (RRM)-containing protein	0.2478	0.7401	0.5058	-0.4518	0.5521	0.4056	0.874	0.2221	0.2247	0.1745	0.7873	0.4249
249358_at	AT5G40510	similar to unknown protein [Arabidopsis thaliana] (T	0.5179	0.6515	0.4766	-0.3544	0.7555	0.4768	1.6916	0.0577	0.1027	0.8192	0.2705	0.2229
249359_at	AT5G40470	similar to F-box family protein (FBL4) [Arabidopsis t	-0.1398	0.434	0.391	0.05953	0.7302	0.4686	-0.363	0.0871	0.1303	-0.1636	0.3669	0.2699
249360_at	AT5G40530	similar to unnamed protein product [Vitis vinifera] (G	0.4071	0.0193	0.0823	0.4204	0.0173	0.0681	0.3293	0.0374	0.0798	0.3427	0.0332	0.0615
249361_at	AT5G40540	protein kinase, putative	-1.104	0.155	0.2298	-1.0627	0.1673	0.2108	0.1508	0.6972	0.4302	0.192	0.6225	0.3711
249362_at	AT5G40560	similar to unknown protein [Arabidopsis thaliana] (T	0.1207	0.7942	0.5223	-0.06095	0.8948	0.5171	0.4571	0.2422	0.2363	0.2755	0.455	0.3079
249363_at	AT5G40560	DEGP13 (DEGP PROTEASE 13); serine-type peptid	-0.4206	0.7915	0.5213	-1.6287	0.3354	0.3111	0.9476	0.275	0.2552	-0.2604	0.7459	0.4123
249364_at	AT5G40590	DC1 domain-containing protein	-0.1464	0.8895	0.5483	0.4442	0.6766	0.4508	0.1447	0.8868	0.4887	0.7353	0.4839	0.3193
249365_at	AT5G40600	similar to unknown protein [Arabidopsis thaliana] (T	-0.4474	0.061	0.1417	-0.06403	0.7302	0.4686	-0.5696	0.0302	0.0708	-0.1863	0.3424	0.2591
249366_at	AT5G40610	glycerol-3-phosphate dehydrogenase (NAD+) / GP	-0.9741	0.0053	0.0519	-1.1926	0.0025	0.034	-0.09534	0.3824	0.3089	-0.3138	0.032	0.0603
249367_at	AT5G40630	ubiquitin family protein	-2.0231	0.0882	0.1722	-1.5458	0.1615	0.2069	1.4495	0.1831	0.201	1.9268	0.0994	0.1201
249368_at	AT5G40640	similar to unknown protein [Arabidopsis thaliana] (T	-0.447	0.2946	0.3201	-0.178	0.6564	0.444	-0.2525	0.5335	0.3726	0.01647	0.9667	0.4748
249369_at	AT5G40680	kelch repeat-containing F-box family protein	-0.5235	0.631	0.4701	-1.7658	0.1548	0.2019	0.6244	0.5693	0.3864	-0.6178	0.5732	0.3536
249370_at	AT5G40710	zinc finger (C2H2 type) family protein	-0.1321	0.404	0.3773	0.2651	0.1346	0.1865	-0.5339	0.0047	0.0292	-0.1368	0.2193	0.1957
249371_at	AT5G40750	similar to F-box family protein [Arabidopsis thaliana	1.9815	0.1296	0.2082	0.9591	0.4088	0.3454	-0.5714	0.6121	0.4018	-1.5938	0.2003	0.1853
249372_at	AT5G40760	G6PD6 (GLUCOSE-6-PHOSPHATE DEHYDROGE	1.3957	2.00E-04	0.0312	1.2903	2.00E-04	0.0249	0.1223	0.3063	0.2718	0.01691	0.8792	0.4511
249373_at	AT5G40670	PQ-loop repeat family protein / transmembrane fam	-0.3386	0.2289	0.2813	-0.4156	0.1565	0.2032	0.01644	0.8382	0.4751	-0.06056	0.4673	0.3128
249374_at	AT5G40580	PBB2 (20S proteasome beta subunit B 2); peptidase	1.102	0.0015	0.038	0.9559	0.0026	0.0342	0.2019	0.0505	0.0952	0.04763	0.5496	0.3449
249375_at	AT5G40730	AGP24 (ARABINOGALACTAN PROTEIN 24)	-0.2033	0.2268	0.2797	-0.1535	0.3421	0.3145	-0.2156	0.1924	0.207	-0.1657	0.295	0.2361
249376_at	AT5G40645	nitrate-responsive NOI protein, putative	2.8492	0.157	0.231	-0.03104	0.9858	0.5405	-0.3058	0.8327	0.4734	-3.1861	0.0787	0.1038
249377_at	AT5G40690	similar to unknown protein [Arabidopsis thaliana] (T	1.0627	0.0314	0.1027	1.3891	0.0132	0.0612	0.1703	0.4577	0.3421	0.4967	0.0748	0.1006
249378_at	AT5G40450	similar to unknown protein [Arabidopsis thaliana] (T	0.09552	0.7826	0.5184	-0.2831	0.4311	0.3557	0.01807	0.9227	0.4987	-0.3605	0.1084	0.1265
249379_at	AT5G40460	similar to unknown protein [Arabidopsis thaliana] (T	-0.5487	0.3522	0.3509	-0.5435	0.3563	0.321	0.6473	0.15	0.1788	0.6526	0.1475	0.1531
249380_at	AT5G40370	glutaredoxin, putative	-0.1089	0.5781	0.4518	0.1996	0.3301	0.3085	0.7691	0.0023	0.0223	1.0776	6.00E-04	0.0103
249381_at	AT5G40440	60S acidic ribosomal protein P2 (RPP2E)	1.8629	0.0631	0.1441	-0.2587	0.7409	0.4715	0.8947	0.2567	0.2446	-1.2269	0.1441	0.151
249382_at	AT5G40050	F-box family protein	0.02231	0.9627	0.568	-0.635	0.2296	0.2512	0.7766	0.0936	0.1356	0.1193	0.7533	0.4146
249383_at	AT5G39983	PRE1 (ACLOBUTRAZOL RESISTANCE1); DNA b	-1.2466	0.0445	0.1217	-1.4305	0.0295	0.0853	1.2437	0.003	0.0248	1.1098	0.0054	0.0229
249384_at	AT5G39890	similar to unknown protein [Arabidopsis thaliana] (T	-0.1258	0.7949	0.5224	-0.1324	0.7845	0.4847	-0.0995	0.8063	0.4655	-0.1061	0.7938	0.4271
249385_at	AT5G39950	ATTRX2 (ARABIDOPSIS THIOREDOXIN H2); thiol	0.5279	0.0015	0.0383	0.6926	5.00E-04	0.0263	0.7081	5.00E-04	0.0149	0.8727	2.00E-04	0.0078
249386_at	AT5G40060	pseudogene of disease resistance protein (TIR-NBS	0.03078	0.887	0.5476	-0.3412	0.1687	0.2116	-0.6968	0.0266	0.0663	-1.0687	0.0063	0.0246
249387_at	AT5G40070	similar to AGL81/EMB3008 (EMBRYO DEFECTIVE	-0.6541	0.5803	0.4523	-0.1717	0.8823	0.5138	0.3831	0.7427	0.4457	0.8655	0.4711	0.3141
249388_at	AT5G40090	ATP binding / nucleoside-triphosphatase/ nucleotide	-0.8265	0.3341	0.3424	-1.0886	0.2219	0.247	0.2693	0.7387	0.4444	0.00717	0.9929	0.4809
249389_at	AT5G40100	disease resistance protein (TIR-NBS-LRR class), p	1.0313	0.4449	0.3955	1.5684	0.2673	0.274	-0.3342	0.7974	0.4627	0.2029	0.8758	0.4501
249390_at	AT5G40130	60S ribosomal protein L5 (RPL5C), pseudogene, 6	-0.4593	0.7898	0.5205	0.1452	0.9325	0.5271	-0.2747	0.8729	0.4849	0.3298	0.8479	0.4422
249391_at	AT5G40140	armadillo/beta-catenin repeat family protein / U-box	0.3461	0.2083	0.2671	-0.1113	0.6549	0.4435	0.7039	0.0381	0.0806	0.2465	0.3459	0.2607
249392_at	AT5G40150	peroxidase, putative	-0.3192	0.1334	0.212	-0.4781	0.0481	0.1088	0.6969	0.0148	0.0485	0.538	0.0339	0.0622
249393_at	AT5G40170	disease resistance family protein	0.7104	0.0061	0.0541	0.5141	0.0187	0.0706	-0.08378	0.3114	0.2742	-0.2801	0.018	0.043
249394_at	AT5G40180	similar to unknown protein [Arabidopsis thaliana] (T	0.6013	0.6459	0.475	1.6122	0.2543	0.2667	-1.1759	0.387	0.3108	-0.1649	0.8984	0.4567
249395_at	AT5G40190	calmodulin-binding protein	0.8597	0.0045	0.0482	0.5572	0.0082	0.0503	0.4118	0.0227	0.0608	0.3093	0.0537	0.0828
249396_at	AT5G40200	DEGP9 (DEGP PROTEASE 9); serine-type peptida	0.3471	0.1155	0.1966	0.3742	0.0968	0.1568	-0.2592	0.0913	0.1336	-0.2321	0.1186	0.1337
249397_at	AT5G40230	nodulin-related	-0.416	0.2462	0.2913	1.1877	0.0179	0.0693	-0.9675	0.0343	0.0757	0.6363	0.1065	0.125
249398_at	AT5G40250	zinc finger (C3HC4-type RING finger) family protein	-0.05944	0.8593	0.5409	0.09954	0.117	0.1728	-0.2735	0.0054	0.0308	-0.1645	0.0301	0.0583
249399_at	AT5G40290	metal-dependent phosphohydrolase HD domain-co	-1.2894	0.1827	0.2501	-0.3355	0.6968	0.4578	-1.4352	0.1476	0.1773	-0.4812	0.5803	0.3562
249400_at	AT5G40300	integral membrane protein, putative	0.8669	0.0164	0.0771	0.8428	0.0181	0.0694	0.3654	0.0528	0.0975	0.3412	0.0638	0.0918
249401_at	AT5G40260	nodulin MtN3 family protein	0.01214	0.9855	0.5733	-0.03851	0.9539	0.5326	0.2594	0.7002	0.4313	0.2087	0.7558	0.4153
249402_at	AT5G40155	Encodes a defensin-like (DEFL) family protein.	0.6494	0.5149	0.4272	-0.9919	0.337	0.312	0.3787	0.6987	0.4308	-1.2626	0.2376	0.2059
249403_at	AT5G40270	metal-dependent phosphohydrolase HD domain-co	0.8407	0.0769	0.1593	-0.9125	0.0278	0.0831	0.03848	0.8936	0.4907	-0.2333	0.4363	0.2997
249404_at	AT5G40160	EMB506 (EMBRYO DEFECTIVE 506); protein bind	-0.864	0.005	0.0504	-0.6374	0.0144	0.0634	-0.2447	0.1872	0.2038	-0.01807	0.9122	0.4606
249405_at	AT5G40280	ERA1 (ENHANCED RESPONSE TO ABA 1); prote	0.4391	0.0172	0.0787	0.5854	0.0064	0.0457	-0.5847	0.0064	0.033	-0.4385	0.0173	0.0421
249406_at	AT5G40210	nodulin MtN21 family protein	-1.1475	0.0051	0.0508	-1.0641	0.0086	0.0461	-0.146	0.517	0.3659	-0.06261	0.776	0.4217
249407_at	AT5G40320	DC1 domain-containing protein	-0.198	0.8832	0.5471	-0.01514	0.991	0.5419	-0.1316	0.9222	0.4985	0.05135	0.9696	0.4754
249408_at	AT5G40330	MYB23 (myb domain protein 23); DNA binding / tra	-2.4782	0.0034	0.0446	-1.6808	0.0133	0.0615	-0.2083	0.5584	0.3819	0.5892	0.1456	0.1518
249409_at	AT5G40340	PWWP domain-containing protein	0.05221	0.8349	0.5339	0.1054	0.6788	0.4508	-0.5921	0.0413	0.0844	-0.5389	0.0541	0.0831
249410_at	AT5G40380	protein kinase family protein	-1.4699	0.0163	0.0771	-1.4472	0.0172	0.0679	0.269	0.115	0.1524	0.2917	0.0949	0.1167
249411_at	AT5G40390	SIP1 (SEED IMBIBITION 1-LIKE); galactinol-sucros	-1.2599	0.012	0.0681	-1.2716	0.0116	0.0581	-0.1589	0.6031	0.3993	-0.1705	0.5779	0.3552
249412_at	AT5G40410	binding	0.3751	0.7634	0.5125	0.6179	0.6237	0.4322	-1.4588	0.2781	0.257	-0.4669	0.7089	0.4005
249413_at	AT5G39620	ARABG1 (Arabidopsis Rab GTPase homolog G1);	-0.2276	0.8199	0.5295	-0.2367	0.8129	0.4939	-0.5109	0.6143	0.4024	-0.52	0.6083	0.3662
249414_at	AT5G39700	MYB89 (myb domain protein 89); DNA binding / tra	1.3765	0.2565	0.2974	0.9508	0.4126	0.3473	-1.0602	0.366	0.3008	-1.4859	0.2266	0.1997
249415_at	AT5G39660	CDF2 (CYCLING DOF FACTOR 2); DNA binding /	-0.9621	0.0427	0.1189	-0.4097	0.0994	0.159	0.06037	0.3765	0.3069	0.2127	0.0249	0.0519
249416_at	AT5G39570	unknown protein	0.06507	0.6513	0.4766	0.004108	0.9769	0.5385	0.6334	0.0033	0.0254	0.5724	0.0047	0.0217
249417_at	AT5G39670	calcium-binding EF hand family protein	1.5664	0.0209	0.085	1.6828	0.0165	0.0668	0.2165	0.4519	0.3395	0.3329	0.2698	0.2226
249418_at	AT5G39785	structural constituent of ribosome	-0.8971	0.1367	0.2147	0.04837	0.925	0.5253	-0.8162	0.1059	0.1456	0.1293	0.7581	0.4161
249419_s_at	AT5G39750;AT5G39810	[AT5G39750, AGL81/EMB3008 (EMBRYO DEFEC	0.298	0.8585	0.5406	-0.5141	0.7593	0.4778	0.04072	0.9731	0.5107	-0.7714	0.5343	0.3396
249420_at	AT5G39820	ANAC094 (ARABIDOPSIS NAC domain containing pro	0.6867	0.3416	0.346	-0.6355	0.3748	0.3298	-0.00641	0.9923	0.5158	-1.3287	0.1001	0.1206
249421_at	AT5G39830	SEGA/

249490_s_at	AT5G39110:AT5G39150:A	[AT5G39110, germin-like protein, putative];[AT5G3	1.1722	0.0268	0.0943	1.2642	0.0209	0.0739	-0.3639	0.0835	0.1272	-0.2718	0.1618	0.1623
249491_at	AT5G39130	germin-like protein, putative	-1.2334	0.6304	0.4699	-0.6296	0.8037	0.4908	-0.5157	0.8385	0.4752	0.08811	0.9721	0.476
249492_at	no_match	no_match	-1.4301	0.5068	0.4238	-0.2119	0.9193	0.5239	-0.9322	0.368	0.302	0.286	0.7713	0.4203
249493_at	AT5G39080	transferase family protein	-0.6741	0.0254	0.0923	-0.958	0.0078	0.0491	0.2641	0.1004	0.1414	-0.01978	0.8811	0.4517
249494_at	AT5G39050	transferase family protein	0.9917	0.0179	0.0801	1.103	0.0125	0.0599	-0.2444	0.3933	0.3134	-0.1331	0.6301	0.3737
249495_at	AT5G39100	GLP6 (GERMIN-LIKE PROTEIN 6); manganese ion	-0.01645	0.9816	0.5725	-0.1613	0.8214	0.4962	-0.1941	0.7505	0.4485	-0.339	0.5839	0.3576
249496_s_at	AT5G39200:AT5G39140:A	[AT5G39200, similar to unknown protein [Arabidops	0.6992	0.2601	0.2997	-0.04589	0.9356	0.5279	1.1742	0.0905	0.133	0.4291	0.4625	0.3111
249497_at	AT5G39220	hydrolase, alpha/beta fold family protein	-1.7703	0.0367	0.1105	-0.3527	0.5719	0.4127	-0.7825	0.2391	0.2348	0.6351	0.3248	0.2506
249498_at	AT5G39230	initiation factor-related	-0.06202	0.9638	0.5682	-1.4286	0.3282	0.3076	1.0671	0.4526	0.3398	-0.2994	0.827	0.4363
249499_at	AT5G39250	F-box family protein	0.3848	0.0639	0.1448	0.2851	0.1329	0.1852	0.2644	0.1557	0.1829	0.1648	0.3378	0.2569
249500_at	AT5G39260	ATEXPA21 (ARABIDOPSIS THALIANA EXPANSIN	-1.6924	0.0803	0.1635	1.5296	0.0979	0.1577	-1.4602	0.048	0.092	1.7178	0.0295	0.0576
249501_s_at	AT5G39270:AT5G39290	[AT5G39270, ATEXPA22 (ARABIDOPSIS THALIAN	-0.2116	0.8757	0.5454	-0.1473	0.9132	0.5222	-0.4302	0.7516	0.4486	-0.3659	0.7873	0.4249
249502_s_at	AT5G39280:AT5G39300	[AT5G39280, ATEXPA23 (ARABIDOPSIS THALIAN	0.04901	0.9623	0.5679	0.2755	0.7916	0.4866	0.5095	0.629	0.4077	0.7359	0.4925	0.323
249503_at	AT5G39310	ATEXPA24 (ARABIDOPSIS THALIANA EXPANSIN	0.9676	0.4858	0.414	0.4503	0.7392	0.471	0.115	0.8951	0.4912	-0.4023	0.649	0.3805
249504_at	AT5G38850	disease resistance protein (TIR-NBS-LRR class), p	-0.2054	0.0405	0.116	0.02511	0.7335	0.4693	-0.7645	0	0.0092	-0.5339	2.00E-04	0.0076
249505_at	AT5G38870	transposable element gene	-0.4985	0.4804	0.412	-0.8946	0.2355	0.255	-0.2088	0.7538	0.4493	-0.6049	0.3856	0.2782
249506_at	AT5G38880	similar to unnamed protein product [Vitis vinifera] (G	0.03601	0.8907	0.5485	0.3621	0.215	0.2427	-0.2873	0.2355	0.2324	-0.6854	0.0291	0.0572
249507_at	AT5G38370	zinc ion binding	-1.0428	0.184	0.251	0.373	0.5969	0.4221	-1.2457	0.1279	0.1624	0.1701	0.8066	0.4306
249508_at	AT5G38380	similar to cation efflux family protein [Arabidopsis th	0.5342	0.0173	0.0788	0.6108	0.011	0.0563	-0.595	0.012	0.0436	-0.5183	0.0191	0.0443
249509_at	AT5G38390	F-box family protein	-0.6132	0.5335	0.4345	-0.4226	0.6635	0.4461	-0.1168	0.9032	0.4932	0.07384	0.9386	0.468
249510_at	AT5G38510	rhomboid family protein	-0.2347	0.2648	0.3021	-0.2613	0.2226	0.2474	-0.1945	0.134	0.1667	-0.2211	0.1	0.1206
249511_at	AT5G38530	DNA binding	-0.3405	0.8088	0.5264	1.4277	0.3394	0.3132	-0.8777	0.6417	0.376	0.8906	0.536	0.34
249512_at	AT5G38470	DNA repair protein RAD23, putative	0.2772	0.0187	0.0813	0.2767	0.0188	0.0708	0.4275	0.0041	0.0277	0.427	0.0042	0.0207
249513_at	AT5G38460	ALG6, ALG8 glycosyltransferase family protein	0.1836	0.326	0.338	0.03562	0.8389	0.5012	-0.1884	0.3152	0.2759	-0.3364	0.1099	0.1276
249514_at	AT5G38480	GRF3 (GENERAL REGULATORY FACTOR 3); pro	0.1473	0.3448	0.3472	-0.04823	0.7436	0.4726	0.5536	0.0099	0.0396	0.358	0.0404	0.0695
249515_at	AT5G38530	tryptophan synthase-related	0.1342	0.4901	0.4159	0.04409	0.8153	0.4947	-0.1385	0.4773	0.3504	-0.2286	0.2657	0.2207
249516_s_at	AT5G38550:AT5G38540	[AT5G38550, jacalin lectin family protein];[AT5G38	-0.9053	0.5035	0.422	-1.6778	0.2452	0.2611	1.2335	0.3737	0.3045	0.4609	0.7275	0.4064
249517_at	AT5G38580	similar to F-box family protein [Arabidopsis thaliana]	-0.7549	0.545	0.439	-0.3141	0.797	0.4887	-1.0046	0.429	0.3292	-0.5639	0.6476	0.3799
249518_at	AT5G38610	invertase/pectin methylesterase inhibitor family prot	-0.269	0.5865	0.4549	-0.7755	0.1638	0.2085	0.3869	0.4435	0.3356	-0.1197	0.8057	0.4304
249519_at	AT5G38660	APE1 (ACCLIMATION OF PHOTOSYNTHESIS TO	-0.4286	0.0452	0.1225	-0.6247	0.0138	0.0621	-0.00841	0.9577	0.5071	-0.2045	0.2419	0.2082
249520_at	AT5G38670	F-box family protein	0.2491	0.016	0.0764	0.2529	0.0464	0.4403	2.534	0.0077	0.0354	0.7378	0.222	0.197
249521_at	AT5G38690	similar to unknown protein [Arabidopsis thaliana] (T	-0.4177	0.0526	0.1316	0.1069	0.5237	0.3936	-0.5005	0.0308	0.0715	0.02408	0.8827	0.4522
249522_at	AT5G38700	similar to unknown protein [Arabidopsis thaliana] (T	-1.5675	0.015	0.0743	-1.5294	0.0163	0.0664	0.4066	0.0902	0.1328	0.4446	0.0718	0.0983
249523_at	AT5G38720	ACYB-1 (Arabidopsis cytochrome b561-1); carbon-	0.5439	0.0298	0.093	0.3787	0.0736	0.1362	0.03709	0.6915	0.4283	-0.1279	0.2178	0.195
249524_at	AT5G38520	hydrolase, alpha/beta fold family protein	-1.2341	9.00E-04	0.0349	-1.2138	9.00E-04	0.0288	-0.5359	0.018	0.0537	-0.5156	0.0204	0.0461
249525_at	AT5G38650	proteasome maturation factor UMP1 family protein	0.8595	2.00E-04	0.0312	0.8662	2.00E-04	0.0249	-0.1343	0.1091	0.1478	-0.1276	0.1226	0.1369
249526_at	AT5G38560	protein kinase family protein	-0.02859	0.8641	0.5422	-0.02311	0.8895	0.5157	-0.252	0.183	0.2009	-0.2465	0.1907	0.1796
249527_at	AT5G38710	proline oxidase, putative / osmotic stress-responsiv	-0.3836	0.2838	0.3137	0.1238	0.7102	0.4621	-0.2423	0.4783	0.3508	0.2651	0.4409	0.3018
249528_at	AT5G38720	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.5077	0.0461	0.1235	0.1842	0.3585	0.3222	0.4546	0.0215	0.059	0.1311	0.3505	0.2628
249529_at	AT5G38730	pentatricopeptide (PPR) repeat-containing protein	0.1077	0.7779	0.5173	0.3845	0.3418	0.3143	-0.1656	0.6288	0.4076	0.1113	0.7431	0.4114
249530_at	AT5G38750	asparaginyl-tRNA synthetase family	1.6532	0.1784	0.2469	-0.1169	0.9138	0.5224	0.6756	0.1548	0.1822	-1.0945	0.047	0.0763
249531_at	AT5G38770	ATGDU7 (ARABIDOPSIS THALIANA GLUTAMINE	-0.6566	0.0529	0.1319	-0.3004	0.2809	0.2814	0.5834	0.0729	0.1174	0.9396	0.0176	0.0425
249532_at	AT5G38780	S-adenosyl-L-methionine:carboxyl methyltransferas	0.7819	0.0564	0.1361	0.1088	0.7302	0.4686	0.4638	0.096	0.1377	-0.2094	0.383	0.2771
249533_at	AT5G38790	unknown protein	1.2273	0.1397	0.2173	-0.7301	0.3353	0.311	1.4468	0.0732	0.1178	-0.5106	0.4422	0.3024
249534_at	AT5G38800	ATBZIP43 (ARABIDOPSIS THALIANA BASIC LEU	0.5056	0.6606	0.4795	-0.9036	0.4451	0.3619	0.1218	0.9058	0.4939	-1.2874	0.2537	0.2145
249535_at	AT5G38820	amino acid transporter family protein	0.4535	0.114	0.1956	-0.3317	0.3641	0.3248	-0.4158	0.2395	0.2349	-0.094	0.7705	0.4201
249536_at	AT5G38760	similar to unknown protein [Arabidopsis thaliana] (T	0.3927	0.7911	0.5212	-0.3015	0.8385	0.501	-0.4527	0.7605	0.4513	-1.1469	0.4547	0.3079
249537_at	AT5G38830	tRNA synthetase class I (C) family protein	0.5437	0.0414	0.1172	0.3765	0.1095	0.167	0.09676	0.4907	0.3559	-0.07045	0.6105	0.367
249538_at	AT5G38840	forkhead-associated domain-containing protein / FH	0.234	0.0715	0.1541	0.3744	0.0176	0.0686	0.308	0.0198	0.0565	0.4484	0.0054	0.0223
249539_at	no_match	no_match	0.6869	0.4104	0.3801	-0.3243	0.6869	0.4545	0.1322	0.8682	0.4837	-0.8789	0.3051	0.241
249540_at	AT5G38120	4-coumarate--CoA ligase family protein / 4-coumarc	-0.6822	0.1551	0.2299	-0.7309	0.1342	0.1862	-0.0825	0.6483	0.414	-0.1313	0.4772	0.3165
249541_at	AT5G38130	transferase family protein	-1.0446	0.0559	0.1358	-1.3414	0.0266	0.0816	0.04913	0.9614	0.1096	0.1946	0.3649	0.269
249542_at	AT5G38140	histone-like transcription factor (CBF/NF-Y) family p	0.08262	0.7381	0.5052	-0.734	0.0334	0.0905	-1.877	0.0012	0.0188	-2.6936	3.00E-04	0.0083
249543_at	AT5G38035	transposable element gene	0.1787	0.6411	0.4734	-0.3677	0.3587	0.3223	-0.2558	0.4946	0.3575	-0.8022	0.0782	0.1034
249544_at	AT5G38260	serine/threonine protein kinase, putative	0.1136	0.5779	0.4517	-0.1578	0.448	0.363	-0.7063	0.0176	0.053	-0.9777	0.0057	0.0235
249545_at	AT5G38030	MATE efflux family protein	0.1227	0.8288	0.532	0.1088	0.8479	0.5039	0.3073	0.5944	0.3962	0.2933	0.6106	0.367
249546_at	AT5G38150	PMI15 (plastid movement impaired 15)	-0.4229	0.1126	0.1943	-0.7674	0.0212	0.0742	-0.3199	0.1999	0.2118	-0.6644	0.0334	0.0617
249547_at	AT5G38160	protease inhibitor/seed storage/lipid transfer protein	1.063	0.3073	0.327	0.3367	0.73	0.4686	0.1567	0.8715	0.4846	-0.5696	0.5651	0.3509
249548_at	AT5G38170	protease inhibitor/seed storage/lipid transfer protein	-0.1692	0.8538	0.5392	-1.3526	0.1914	0.227	2.1896	0.0638	0.1089	1.0061	0.3076	0.2422
249549_at	AT5G38180	protease inhibitor/seed storage/lipid transfer protein	0.1306	0.9049	0.5526	-2.3416	0.0846	0.1465	-0.2444	0.8202	0.4698	-2.7166	0.0542	0.0833
249550_at	AT5G38210	serine/threonine protein kinase family protein	1.0332	0.0242	0.0906	1.3541	0.0098	0.0538	-0.2597	0.4248	0.3274	0.06121	0.8445	0.4412
249551_at	AT5G38220	similar to unknown protein [Arabidopsis thaliana] (T	0.05589	0.8065	0.5257	0.155	0.5082	0.3879	0.0564	0.7485	0.4476	0.1555	0.3972	0.2831
249552_s_at	AT5G38250:AT5G38240	[AT5G38250, serine/threonine protein kinase, putat	0.8317	0.0199	0.0833	1.0082	0.0104	0.0552	0.3917	0.1109	0.1491	0.5682	0.0416	0.0708
249553_at	AT5G38260	serine/threonine protein kinase, putative	0.5447	0.5803	0.4523	-0.136	0.888	0.5153	2.3654	0.0182	0.054	1.6846	0.0515	0.0808
249554_at	AT5G38290	peptidyl-tRNA hydrolase family protein	-0.2265	0.2545	0.2962	-0.1472	0.4363	0.3581	-0.2544	0.1341	0.1668	-0.1751	0.2664	0.221
249555_at	AT5G38300	similar to unknown protein [Arabidopsis thaliana] (T	-0.2799	0.5917	0.4567	-0.3366	0.5225	0.3931	0.2245	0.665	0.4195	0.1677	0.7448	0.4119
249556_at	AT5G38195	protease inhibitor/seed storage/lipid transfer protein	1.3628	0.2066	0.2662	-0.09368	0.9225	0.5247	1.1563	0.231	0.23	-0.3002	0.7326	0.4079
249557_at	AT5G38280	PR5K (PR5-like receptor kinase); kinase/ transmem	0.6038	0.1827	0.2501	0.6931	0.1383	0.1893	-0.4538	0.2929	0.2651	-0.3645	0.3861	0.2783
249558_at	AT5G38310	unknown protein	-0.4624	0.0725	0.1551	-0.5199	0.0527	0.1139	0.6195	0.0315	0.0721	0.5619	0.0422	0.0716
249559_at	AT5G38320	similar to unknown protein [Arabidopsis thaliana] (T	-0.4883	0.4659	0.4056	1.1729	0.1253	0.1795	-0.7665	0.275	0.2552	0.8948	0.2142	0.1931
249560_at	AT5G38330	LCR80 (Low-molecular-weight cysteine-rich 80)	0.4792	0.6908	0.4895	-1.4207	0.2735	0.2773	0.9759	0.4329	0.3309	-0.924	0.4558	0.3083
249561_at	AT5G38340	disease resistance protein (TIR-NBS-LRR class), p	-0.8726	0.1624	0.2357	-0.3836	0.494	0.3821	-0.3021	0.5856	0.3929	0.1869	0.7327	0.4079
249562_at	AT5G38350	disease resistance protein (NBS-LRR class), putati	0.4834	0.8322	0.5331	-0.1435	0.7171	0.4643	0.423	0.2082	0.2167	0.3629	0.2678	0.2216
249563_at	AT5G38360	catalytic	-0.4294	0.2075	0.2669	-0.2914	0.3657	0.3256	-0.2724	0.3946	0.3141	-0.1344	0.6628	0.3852
249564_at	AT5G38400	unknown protein	-1.8038	0.0817	0.1654	-1.156	0.2124	0.241	-0.08897	0.8928	0.4905	0.5588	0.4183	0.2918
249565_at	AT5G38440	self-incompatibility protein-related	1.1409	0.2327	0.2835	-0.7225	0.4239	0.3525	0.66	0.251	0.2415	-1.2033	0.0708	0.0976
249566_at	AT5G38450	CYP735A1 (cytochrome P450, family 735, subfamil	-1.4206	0.1403	0.2179	1.0208	0.2577	0.2688	-0.8048	0.3571	0.2966	1.6366	0.102	0.122
249567_at	AT5G38020	S-adenosyl-L-methionine:carboxyl methyltransferas	0.2516	0.8331	0.5334	1.549	0.2386	0.2569	-1.1269	0.3188	0.2777	0.1705	0.8717	0.4489
249568_at	AT5G38460	UDP-glucuronosyl/UDP-glucosyl transferase family	-0.3949	0.7332	0.5033	-1.0019	0.4061	0.3441	-0.3969	0.7319	0.4423	-1.0039	0.4053	0.2863
249569_at	AT5G38070	zinc finger (C3HC4-type RING finger) family protein	-0.09311	0.8452	0.5372	-0.3999	0.4218	0.3514	-1.4301	0.022	0.0598	-1.7368	0.0115	0.0337
249570_at	AT5G38080	similar to unknown protein [Arabidopsis thaliana] (T	-0.5603	0.6496	0.4762	0.7629	0.5409	0.401	-0.8085	0.5183	0.3663	0.5148	0.6757	0.3892
249571_at	AT5G37620	DC1 domain-containing protein	0.3546	0.5563	0.4433	-0.7747	0.2339	0.2541	0.8931	0.1624	0.1868	-0.2361	0.6746	0.3889
249572_at	AT5G37630	EMB2656 (EMBRYO DEFECTIVE 2656); binding	0.0717	0.8189	0.5293	-0.474	0.1813	0.2206	0.3229	0.3327	0.2846	-0.2228	0.4897	0.3218
249573_at	AT5G37640	UBQ9 (ubiquitin 9)	0.2755	0.7722	0.5153	-0.3078	0.7467	0.4737	0.9834	0.3309	0.2837	0.4	0.6762	0.3894
249574_at	AT5G37650	receptor-like protein kinase-related	0.2977	0.4928	0.417	0.1883	0.6582	0.4444	0.3451	0.2419	0.2361	0.2357	0.4016	0.2848
249575_at	AT5G37670	15.7 kDa class I-related small heat shock protein-lik	1.3779	0.0249	0.0915	1.7954	0.0103	0.0551	0.5495	0.0831	0.1268	0.9669	0.0156	0.0398
249576_at	AT5G37690	GDSL-motif lipase/hydrolase family protein	0.2756	0.7212	0.4998	-0.1413	0.8538	0.5058	0.7987	0.3292	0.283	0.3818	0.6238	0.3715
249577_at	AT5G37710	lipase class 3 family protein / calmodulin-binding he	0.2341	0.5044	0.4223	0.5214	0.1781	0.2183	-0.1385	0.5293	0.371	0.1488	0.5007	0.3262
249578_at	AT5G37730	similar to unknown protein [Arabidopsis thaliana] (T	-0.1582	0.9107	0.5542	-2.4728	0.1356	0.1873	1.0262	0.4161	0.3234	-1.2884	0.3187	0.2477
249579_at	AT5G37680	ATARLA1A (ADP-ribosylation factor-like A1A); GTP	-0.1024	0.3046	0.3254	-0.1145	0.2587	0.2694	0.07747	0.4237	0.3269	0.06539	0.4942	0.3237
249580_at	AT5G37740	C2 domain-containing protein	1.1652	0.0113	0.0666	1.1992	0.0103	0.0551	0.5361	0.0012	0.0187	0.57	9.00E-04	0.0119
249581_at	AT5G37600	ATGSR1 (Arabidopsis thaliana glutamine synthase	2.1604	0.0014	0.038	2.0353	0.0018	0.0325	0.2731	0.1048	0.1448	0.148	0.3206	0.2486
249582_at	AT5G37780	CAM1 (CALMODULIN 1); calcium ion binding	0.5577	0.0442	0.1213	1.1766	0.0036	0.0379	0.4323	0.0176	0.053	1.0511	7.00E-04	0.0106
249583_at	AT5G37770	TCH2 (TOUCH 2); calcium ion binding	-1.1292	0.033	0.1053	-0.8192	0.0812	0.1429	0.8325	0.0028	0.0243	1.1424	8.00E-04	0.0113
249584_s_at	AT5G37810:AT5G37820	[AT5G37810, NIP4;1/NLM4 (NOD26-LIKE INTRINS	-1.28	0.3001	0.3229	0.8168	0.4902	0.3805	-1.333	0.2832	0.2599	0.7638	0.5171	0.3324
249585_at	AT5G37830	OXP1 (OXOPROLINASE 1); hydrolase	0.5147	0.0216	0.0862	0.4967	0.0242	0.0781	-0.5972	0.0132	0.0457	-0.6151	0.0119	0.0343
249586_at	AT5G37840	similar to PMI2 (plastid movement impaired 2) [Arat	-0.1431	0.8721	0.5445	-0.4144	0.6452	0.4401	0.4333	0.289	0.2631	0.162	0.6717	0.388
249587_at	AT5G37860	copper-binding family protein	-1.0912	0.5031	0.4218	-1.8271	0.2859	0.2843	1.1332	0.3913	0.3126	0.3973	0.7533	0.4146
249588_at	AT5G37790	protein kinase family protein	-1.2603	0.0014	0.038	-0.872	0.0056	0.0434	-0.09303	0.5941	0.3961	0.2952	0.1404	0.1484
249589_at	AT5G37850	SOS4 (SALT OVERLY SENSITIVE 4); kinase/ pyric	-0.06326	0.6427	0.4738	0.1568	0.282	0.2821	-0.4884	0.0104	0.0405	-0.2683	0.0667	0.0941
249590_at	AT5G37870	seven in absentia (SINA) family protein	-2.0045	0.0959	0.1789	0.4439	0.6561	0.4439	-1.3698	0.1664	0.1894	1.0786	0.2542	0.2148
249591_at	AT5G37880	transposable element gene	0.5057	0.4736	0.4094	-0.9821	0.1997	0.2327	1.1647	0.0898	0.1324	-0.3231	0.5699	0.3526
249592_at	AT5G37890	seven in absentia (SINA) protein, putative	-0.37	0.1572	0.2311	-0.3944	0.1376	0.1889	0.1526	0.3024	0.2698	0.1282	0.3765	0.274
249593_at	AT5G37900	seven in absentia (SINA) family protein	-1.5824	0.2425	0.2891	-1.7086	0.2131	0.2415	0.09271	0.9399	0.5034	-0.03343	0.9783	0.4777
249594_at	AT5G37910	seven in absentia (SINA) family protein	-0.1211	0.831	0.5327	-0.5431	0.3648	0.3251	-0.03459	0.9503	0.5056	-0.4566	0.4307	0.2971
249595_at	AT5G37930	seven in absentia (SINA) family protein	0.3989	0.0367	0.1104	0.1952	0.2055	0.2364	0.2555	0.0404	0.0834	0.05173	0.5778	0.3552
249596_s_at	AT5G38010:AT5G37950	[AT5G38010, UDP-glucuronosyl/UDP-glucosyl tran	-0.7016	0.3787	0.3637	-1.0483	0.2136	0.2417	0.2676	0.7252	0.4402	-0.0791	0.9166	0.4617
249597_at	AT5G37960	oxidoreductase-related	-1.9861	0.0803	0.1635	-0.4983	0.5903	0.4196	0.7327	0.4385	0.3334	2.2206	0.0597	0.0883
249598_at	AT5G37970	S-adenosyl-L-methionine:carboxyl methyltransferas	1.1053	0.2878	0.3161	-0.6171	0.5316	0.3968	-0.5382	0.5829	0.3918	-0.05003	0.9584	0.4731
249599_at	AT5G37990	S-adenosylmethionine-dependent methyltransferase	0.3211	0.7576	0.511	2.4915	0.0623	0.124	-0.8544	0.4288	0.3292	1.316	0.247	0.2108
249600_s_at	AT5G37940:AT5G38000	[AT5G37940, NADP-dependent oxidoreductase, pu	-3.2496	0.0471	0.1248	-1.0691	0.4036	0.3429	-1.4868	0.1025	0.1429	0.6937	0.3807	0.2761
249601_at	AT5G37980	NADP-dependent oxidoreductase, putative	-0.3738	0.2988	0.3224	-0.2278	0.5075	0.3876	0.449	0.2251	0.2265	0.595	0.1304	0.1418
249602_at	AT5G37610	voltage-gated anion channel	-0.9039	0.4745	0.4096	1.1608	0.3685	0.3268	-1.2745	0.3285	0.2826	0.7901	0.5286	0.3373
249603_at	AT5G37210	DC1 domain-containing protein	-0.9465	0.2489	0.293	-1.0092	0.224	0.248	-0.7673	0.1874	0.2039	-0.8462	0.1614	0.1621
249604_x_at	AT5G37230	zinc finger (C3HC4-type RING finger) family protein	0.01116	0.9773	0.5716	-0.1976	0.6201	0.4306	0.07687	0.5671	0.3856	-0.1319	0.3455	0.2605
249605_at	AT5G37240	unknown protein	0.07291	0.9536	0.5657	-1.8753	0.1869	0.2242	0.4832	0.6779	0.4238	-1.4651	0.2466	0.2105
249606_at	AT5G37260	CIR1/RVE2 (CIRCADIAN 1); DNA binding / transcri	0.3346	0.6536	0.4771	-0.05639	0.9389	0.5287	-0.9684	0.2338	0.2316	-1.3594	0.1206	0.1354
249607_at	AT5G37280	zinc finger (C3HC4-type RING finger) family protein	-1.8964	0.0888	0.1728	-1.4005	0.1737	0.2153	0.8387	0.3783	0.307	1.3346	0.1904	0.1794
249608_at	AT5G37310	transporter	0.3069	0.3627	0.3557	0.1573	0.6266	0.4334	-0.3471	0.2514	0.2415	-0.4967	0.1277	0.1401
249609_at	no_match	no_match	1.8209	0.1714	0.2425	-2.2406	0.0826	0.1446	2.68	0.0513	0.096	-1.1815	0.2918	0.2345
249610_at	AT5G37360	similar to unnamed protein product [Vitis vinifera] (G	-0.578	0.01	0.064	-0.8288	0.0027	0.0349	0.5717	0.0077	0.0354	0.3209	0.0498	0.0791
249611_at	AT5G37370	ATSRL1; binding	0.08218	0.6339	0.4709	0.3234	0.1128	0.1698	-0.7077	5.00E-04	0.0155	-0.4665	0.0026	0.0169
249612_at	AT5G37380	armadillo/beta-catenin repeat family protein	-0.2753	0.2902	0.3175	-0.2544	0.3234	0.305	0.2366	0.138	0.1697	0.3869	0.1222	0.1366
249613_at	AT5G37380	DNAJ heat shock N-terminal domain-containing pro	0.02916	0.8803	0.5465	0.5709	0.0348	0.0922	-0.7874	9.00E-04	0.0172	-0.2456	0.0523	0.0814
249614_at	AT5G37300	similar to unknown protein [Arabidopsis thaliana] (T	-1.5125	0.2465	0.2915	-0.5615	0.641	0.4384	0.114	0.7933	0.4612	1.0649	0.0589	0.0876
249615_s_at	AT5G37420	ATHB40; transcription factor	0.5897	0.6789	0.4849	-0.3984	0.7769	0.4827	0.3598	0.7979	0.4527	-0.6284	0.6576	0.3833
249616_s_at	AT5G37750:AT5G37440	[AT5G37750, heat shock protein binding / unfolded	0.1476	0.7049	0.4943	0.825	0.0853	0.1469	-0.2316	0.5578	0.3819	0.4459	0.2863	0.2314
249617_at	AT5G37450	leucine-rich repeat transmembrane protein kinase,	1.3608	0.3601	0.3547	-1.0431	0.4729	0.3733	0.1939	0.8901	0.4897	-2.21	0.1688	0.1665
249618_at	AT5G37490	U-box domain-containing protein	-0.428	0.53	0.4331	-0.9787	0.1914	0.2271	0.4707	0.3631	0.2996	-0.0799	0.8703	0.4485
249619_at	AT5G37500	GORK (GATED OUTWARDLY-RECTIFYING K+ C	-1.1697	0.1482	0.224	-0.05984	0.9315	0.5269	-1.9436	0.0411	0.0841	-0.8338	0.2714	0.2235
249620_at	AT5G37520	similar to unknown protein [Arabidopsis thaliana] (T	0.7195	0.5697	0.4489	0.4279	0.7316	0.4688	0.3721	0.765	0.4527	0.08056	0.9481	0.4704
249621_at	AT5G37530	thiF family protein	-0.3561	0.5287	0.4327	-0.2044	0.7126	0.463	-0.6678	0.2659	0.2497	-0.5161	0.3744	0.2732
249622_at	AT5G37550	similar to unknown protein [Arabidopsis thaliana] (T	-1.2247	0.1829	0.2503	-1.9283	0.0644	0.1267	1.19	0.193	0.2073	0.4864	0.5576	0.3479
249623_at	AT5G37560	nucleic acid binding / zinc ion binding	-1.4468	0.3591	0.3541	-1.5667	0.3254	0.3062	-1.09	0.4791	0.3511	1.9225	0.241

249690_at	AT5G36210	serine-type peptidase	0.04529	0.6825	0.4867	0.4007	0.0176	0.0687	-0.2964	0.045	0.0887	0.05901	0.5969	0.3624
249691_at	AT5G36170	release factor	-0.2369	0.0558	0.1357	-0.4703	0.0061	0.0449	0.045	0.5796	0.3906	-0.1883	0.0654	0.0931
249692_s_at	AT5G36740;AT5G36670	[AT5G36740, PHD finger family protein];[AT5G366	0.7638	0.4284	0.3884	0.4082	0.6625	0.4458	0.8872	0.1329	0.1659	0.5316	0.3223	0.2494
249693_at	AT5G35750	AHK2 (ARABIDOPSIS HISTIDINE KINASE 2)	-0.5341	0.1785	0.2469	-0.5582	0.1637	0.2084	-0.8428	0.0319	0.0726	-0.867	0.0292	0.0572
249694_at	AT5G35790	G6PD1 (GLUCOSE-6-PHOSPHATE DEHYDROGE	-0.2171	0.1279	0.2066	-0.3756	0.0295	0.0854	-0.2658	0.0788	0.1227	-0.4243	0.02	0.0455
249695_at	AT5G35800	transposable element gene	1.8255	0.1066	0.1888	1.4618	0.1719	0.2141	-0.2108	0.8224	0.4704	-0.5745	0.5494	0.3449
249696_at	AT5G35820	transposable element gene	-0.585	0.687	0.4882	-1.83	0.2465	0.2618	1.1621	0.2881	0.2626	-0.08294	0.9346	0.4669
249697_at	AT5G35510	unknown protein	1.1103	0.2416	0.2886	-0.5634	0.5242	0.3938	-2.1783	0.0544	0.0993	-3.8519	0.0089	0.0294
249698_at	AT5G35520	kinetochore protein-related	-0.3313	0.1498	0.2254	-0.3368	0.1447	0.1943	0.4899	0.0581	0.1032	0.4844	0.06	0.0885
249699_at	AT5G35540	similar to unknown protein [Arabidopsis thaliana] (T	-0.8763	0.4715	0.4081	-1.0087	0.4123	0.3472	0.9393	0.4426	0.3352	0.8069	0.5051	0.3278
249700_at	AT5G35530	40S ribosomal protein S3 (RPS3C)	0.007147	0.9632	0.568	0.06359	0.7312	0.4688	-0.2117	0.1186	0.1551	-0.1653	0.1968	0.183
249701_at	AT5G35460	similar to unknown [Populus trichocarpa] (GB:ABK9	0.0076	0.968	0.5693	0.1461	0.4585	0.3674	-0.6085	0.0269	0.0668	-0.47	0.0578	0.0866
249702_at	AT5G35570	similar to unknown protein [Arabidopsis thaliana] (T	-0.4489	0.177	0.2462	-0.04007	0.8909	0.516	-1.5317	0.0027	0.0241	-1.1228	0.0084	0.0286
249703_at	AT5G35560	DENN (AEX-3) domain-containing protein	0.7489	0.0563	0.136	0.4865	0.1727	0.2146	-0.38	0.0012	0.0187	-0.6425	1.00E-04	0.0063
249704_at	AT5G35550	TT2 (TRANSPARENT TESTA 2); DNA binding / tra	1.4145	0.1548	0.2297	-0.1006	0.9069	0.5207	1.328	0.1755	0.1956	-0.187	0.8282	0.4367
249705_at	AT5G35580	kinase	-0.7395	0.5682	0.4482	0.9606	0.4651	0.37	0.06042	0.9617	0.5081	1.7605	0.2104	0.1911
249706_at	AT5G35600	HDA7 (HISTONE DEACETYLASE7); histone deace	0.4948	0.63	0.4698	0.0029	0.9977	0.5435	-0.4348	0.6709	0.4214	-0.9267	0.3846	0.2778
249707_at	AT5G35640	similar to nucleic acid binding / zinc ion binding [Ara	1.0819	0.322	0.3354	0.04327	0.9661	0.5355	1.5482	0.1682	0.1906	0.5097	0.6097	0.3666
249708_at	AT5G35660	pseudogene similar to protease inhibitor/seed stora	2.1495	0.05	0.1285	0.6273	0.4631	0.3694	1.2522	0.1376	0.1694	-0.2699	0.7101	0.4009
249709_at	AT5G35670	IQD33 (IQ-domain 33); calmodulin binding	0.7167	0.102	0.1847	0.6158	0.1435	0.1934	0.1764	0.6304	0.408	0.0754	0.8349	0.4386
249710_at	AT5G35630	GS2 (GLUTAMINE SYNTHETASE 2); glutamate-an	-0.6577	0.0156	0.0754	-0.9947	0.0036	0.0379	0.1649	0.1994	0.2115	-0.1721	0.1841	0.1758
249711_at	AT5G35680	initiation factor 1A, putative / eIF-1A, putative / eIF-	0.1661	0.0698	0.1523	0.56	0.0018	0.0323	0.5265	5.00E-04	0.3833	0.02717	1.00E-04	0.0058
249712_at	AT5G35620	initiation factor	-0.2916	0.2155	0.272	0.1322	0.5415	0.4012	0.3565	0.0194	0.0599	0.7803	0.0012	0.0127
249713_at	no_match	no_match	-0.637	0.2545	0.2962	-0.1814	0.7243	0.4667	-0.419	0.4313	0.3301	0.03657	0.9428	0.4691
249714_at	AT5G35710	transposable element gene	1.6015	0.2499	0.2936	0.9708	0.4608	0.3683	-1.714	0.2235	0.2257	0.8583	0.511	0.3302
249715_at	AT5G35760	beta-galactosidase	0.3887	0.5772	0.4515	-0.06694	0.9219	0.5245	0.3783	0.5871	0.3934	-0.07741	0.9098	0.4599
249716_at	AT5G35770	SAP (STERILE APETALA); transcription factor	0.6318	0.4819	0.4127	-0.4469	0.613	0.4281	-0.1019	0.9066	0.4942	-1.1806	0.2214	0.1968
249717_at	AT5G35730	EXS family protein / ERD1/XPR1/SYG1 family prote	0.3579	0.007	0.058	0.4537	0.0033	0.037	-0.4435	0.0035	0.0262	-0.3477	0.0085	0.0287
249718_at	AT5G35740	glycosyl hydrolase family protein 17	-0.3284	0.1905	0.2558	-0.3784	0.1438	0.1935	-0.01735	0.9184	0.4973	-0.06733	0.6937	0.3953
249719_at	AT5G35735	auxin-responsive family protein	0.7785	0.0744	0.1568	0.6074	0.1345	0.1864	0.4334	0.0333	0.0745	0.2624	0.1258	0.1388
249720_at	AT5G35700	FIM2 (FIMBRIN-LIKE PROTEIN 2); actin binding	0.2384	0.3154	0.3318	0.3968	0.1289	0.1821	-0.1313	0.562	0.3833	0.02717	0.9023	0.458
249721_at	AT5G24655	similar to unknown protein [Arabidopsis thaliana] (T	-0.08028	0.8738	0.5451	0.05976	0.9058	0.5204	0.6098	0.037	0.0793	0.7498	0.0193	0.0446
249722_at	AT5G35430	binding	-0.2739	0.6716	0.4831	-0.3921	0.5489	0.4043	-1.5546	0.0605	0.1056	-1.6728	0.0493	0.0786
249723_at	AT5G35430	binding	0.3687	0.0837	0.1674	0.2172	0.2483	0.2628	-0.3264	0.0195	0.0561	-0.477	0.0052	0.0226
249724_at	AT5G35450	disease resistance protein (CC-NBS-LRR class), p	-0.3185	0.2536	0.2956	-0.2864	0.297	0.2902	-0.01662	0.9336	0.5017	0.01548	0.9381	0.4678
249725_at	AT5G35470	unknown protein	-1.3081	0.3499	0.3497	-1.2294	0.3765	0.3303	-0.155	0.8045	0.4648	-0.07636	0.9026	0.458
249726_at	AT5G35480	unknown protein	-0.5135	0.395	0.3726	-0.3927	0.5089	0.3874	-0.543	0.371	0.3034	-0.4223	0.4775	0.3166
249727_at	AT5G35490	unknown protein	-0.2441	0.3966	0.3735	-0.4395	0.163	0.2081	-0.1646	0.4811	0.3517	-0.3599	0.1649	0.1643
249728_at	AT5G24390	RabGAP/TBC domain-containing protein	-0.2514	0.5864	0.4549	0.06542	0.8853	0.5147	-0.1403	0.6267	0.4068	0.1766	0.5442	0.3426
249729_at	AT5G24410	glucosamine/galactosamine-6-phosphate isomerase	0.7974	0.1154	0.1966	-0.6294	0.1885	0.2255	-0.06855	0.8577	0.4804	-1.4954	0.014	0.0376
249730_at	AT5G24430	calcium-dependent protein kinase, putative / CDPK	0.283	0.1017	0.1843	0.5073	0.0192	0.0713	-0.3252	0.0055	0.031	-0.1008	0.1662	0.1649
249731_at	AT5G24440	CID13 (CTC-Interacting Domain 13); RNA binding	1.2227	0.2721	0.3067	-0.1549	0.8797	0.5131	1.4755	0.1085	0.1474	0.09784	0.898	0.4566
249732_at	AT5G24420	glucosamine/galactosamine-6-phosphate isomerase	-0.3453	0.2214	0.2761	-0.5881	0.0694	0.132	0.3248	0.0016	0.0202	0.08203	0.1252	0.1384
249733_at	AT5G24400	EMB2024 (EMBRYO DEFECTIVE 2024); catalytic	-0.06301	0.8006	0.5243	-0.07203	0.773	0.4815	-0.1218	0.6294	0.4077	-0.1308	0.6051	0.365
249734_at	AT5G24360	protein kinase family protein / Ire1 homolog-1 (IRE1	-0.03785	0.8844	0.5471	-0.2447	0.3735	0.3292	-0.1551	0.5603	0.3827	-0.3619	0.2129	0.1923
249735_at	AT5G24430	similar to unknown protein [Arabidopsis thaliana] (T	0.5868	0.0346	0.1075	0.3056	0.1765	0.2173	-0.04049	0.8386	0.4752	-0.3218	0.1594	0.1608
249736_at	AT5G24460	hydrolase	0.4485	0.319	0.3339	0.4106	0.3566	0.3212	-0.1641	0.4334	0.3311	-0.202	0.3447	0.2601
249737_at	AT5G24480	beta-galactosidase	0.02813	0.9204	0.5571	-0.7087	0.0552	0.1166	0.4337	0.1762	0.1961	-0.3031	0.3154	0.2462
249738_at	AT5G24510	60s acidic ribosomal protein P1, putative	0.7926	0.0615	0.1799	1.5544	0.407	0.3445	0.5493	0.76	0.4512	1.3111	0.4786	0.317
249739_at	AT5G24520	TTG1 (TRANSPARENT TESTA GLABRA 1); nucle	0.1532	0.3485	0.3492	0.2044	0.2299	0.2514	-0.02641	0.8377	0.4749	0.02476	0.8477	0.4422
249740_at	AT5G24500	similar to unnamed protein product [Vitis vinifera] (G	0.4956	0.1911	0.2562	0.2301	0.5059	0.3871	0.4432	0.2326	0.2309	0.1777	0.6031	0.3642
249741_at	AT5G24470	APRR5*PSEUDO-RESPONSE REGULATOR 5); t	0.7961	0.5973	0.4586	1.8172	0.261	0.2703	0.6599	0.5687	0.3863	1.681	0.1893	0.1789
249742_at	AT5G24490	30S ribosomal protein, putative	0.1547	0.396	0.3733	0.1205	0.5003	0.3847	-0.03983	0.8188	0.4695	-0.07398	0.6732	0.3885
249743_at	AT5G24540	glycosyl hydrolase family 1 protein	2.9495	0.0131	0.0705	0.3372	0.6518	0.4424	0.3153	0.6726	0.4218	-2.2969	0.0295	0.0576
249744_at	AT5G24550	glycosyl hydrolase family 1 protein	-2.6987	0.1008	0.1835	0.2775	0.8378	0.5009	-1.3471	0.1618	0.1866	1.629	0.107	0.1254
249745_at	AT5G24560	ATPP2-B12 (Phloem protein 2-B12); carbohydrate	-0.01433	0.9804	0.5721	0.3769	0.5304	0.3964	-0.3511	0.4168	0.3238	0.04017	0.9225	0.4636
249746_at	AT5G24590	ANAC091/TIP (TCV-INTERACTING PROTEIN); tra	0.009844	0.9666	0.5688	0.1285	0.5922	0.4204	-0.08258	0.6956	0.4296	0.03603	0.8633	0.4467
249747_at	AT5G24600	similar to unknown protein [Arabidopsis thaliana] (T	1.2341	0.1155	0.1966	-0.2818	0.6709	0.4489	0.5727	0.3832	0.3093	-0.9431	0.1824	0.1749
249748_at	AT5G24620	thaumatin-like protein, putative	-0.3617	0.0341	0.1068	-0.093	0.4618	0.3687	-3.4942	0	0.0062	-3.2255	0	0.0043
249749_at	no_match	no_match	-0.1116	0.7832	0.5187	-0.1919	0.6396	0.4381	0.1681	0.6806	0.4245	0.08784	0.8282	0.4367
249750_at	AT5G24570	unknown protein	0.6356	0.0234	0.0895	-0.707	0.0165	0.0667	1.4585	0.0012	0.0187	1.387	0.0015	0.0137
249751_at	AT5G24650	mitochondrial import inner membrane translocase s	-0.1197	0.0783	0.1613	-0.2449	0.0086	0.051	0.486	7.00E-04	0.0159	0.3608	0.0021	0.0154
249752_at	AT5G24660	similar to unknown protein [Arabidopsis thaliana] (T	-0.4886	0.6074	0.4622	-0.8869	0.3694	0.3273	1.371	0.005	0.0297	0.9726	0.0164	0.0409
249753_at	AT5G24610	similar to unknown protein [Arabidopsis thaliana] (T	0.7174	8.00E-04	0.0345	0.9074	3.00E-04	0.0249	-0.05204	0.5118	0.3638	0.1379	0.1293	0.1409
249754_at	AT5G24530	oxidoreductase, 2OG-Fe(II) oxygenase family prote	1.499	0.0027	0.0426	1.2299	0.0056	0.0434	0.1707	0.309	0.273	-0.09836	0.5391	0.3409
249755_at	AT5G24580	copper-binding family protein	-0.6063	0.0353	0.1085	-0.4259	0.093	0.1539	0.6067	0.0352	0.0769	0.7871	0.0154	0.0395
249756_at	AT5G24313	unknown protein	-0.5174	0.6535	0.4771	-0.829	0.4811	0.3766	-0.8054	0.4929	0.3567	-1.117	0.3548	0.2648
249757_at	AT5G24316	proline-rich family protein	1.3558	0.2016	0.2632	1.9074	0.0983	0.1579	-1.0183	0.3155	0.276	-0.4667	0.627	0.3727
249758_at	AT5G24350	similar to unnamed protein product [Vitis vinifera] (G	0.713	0.0246	0.0911	0.1062	0.6283	0.4338	-1.0075	0.0077	0.0354	-1.6143	0.0014	0.0133
249759_at	AT5G24380	YSL2 (YELLOW STRIPE LIKE 2); oligopeptide tran	-0.02153	0.9355	0.5611	-0.4451	0.1495	0.1977	0.08951	0.4378	0.3331	-0.3341	0.0325	0.0608
249760_at	AT5G23960	terpene synthase/cyclase family protein	-1.8917	0.2359	0.285	-2.2472	0.1732	0.215	-0.7159	0.6258	0.4065	-1.0714	0.4741	0.3154
249761_at	AT5G23970	transferase family protein	0.1262	0.8851	0.5471	-1.6971	0.1072	0.1652	1.5078	0.1398	0.171	-0.3155	0.7199	0.4039
249762_at	AT5G24000	similar to unknown protein [Arabidopsis thaliana] (T	-0.402	0.0379	0.1121	-0.1408	0.345	0.3156	-0.7775	0.0036	0.0265	-0.5163	0.0153	0.0395
249763_at	AT5G24010	protein kinase family protein	0.4356	0.2601	0.2997	0.6663	0.1155	0.1715	-0.08795	0.6583	0.4174	0.1428	0.482	0.3184
249764_at	AT5G24020	MIND (ACCUMULATION AND REPLICATION OF C	-0.1711	0.4852	0.414	-0.6425	0.0448	0.1049	0.5611	0.0654	0.1104	0.08965	0.7078	0.4001
249765_at	AT5G24030	SLAH3 (SLAC1 HOMOLOGUE 3); transporter	-0.5355	0.3083	0.3276	-1.2112	0.0577	0.1194	0.08816	0.7662	0.453	-0.5876	0.1012	0.1215
249766_at	AT5G24070	peroxidase family protein	-1.375	0.2501	0.2937	-1.0882	0.3474	0.3167	-0.8223	0.4666	0.346	-0.5355	0.6283	0.3731
249767_at	AT5G24090	acidic endochitinase (CHIB1)	0.3868	0.4071	0.379	1.0959	0.0587	0.1204	-0.7393	0.0363	0.0784	-0.03026	0.9053	0.4589
249768_at	AT5G24100	leucine-rich repeat transmembrane protein kinase,	-0.01369	0.9805	0.5721	1.0002	0.1298	0.1827	-0.7242	0.0137	0.0466	0.2897	0.1682	0.1662
249769_at	AT5G24120	SIGE (RNA polymerase sigma subunit E); DNA bin	-1.2093	0.0105	0.0647	-1.5238	0.0046	0.0416	-0.000059	0.9961	0.5166	-0.315	0.0497	0.079
249770_at	AT5G24110	WRKY30 (WRKY DNA-binding protein 30); transcri	0.8579	0.0386	0.1132	1.0628	0.0198	0.072	0.4932	0.1045	0.1445	0.6982	0.0414	0.0706
249771_at	AT5G24080	protein kinase family protein	0.8834	0.0688	0.1508	0.4928	0.2399	0.2577	-0.4255	0.2995	0.2684	-0.8161	0.0844	0.1085
249772_at	AT5G24130	similar to unnamed protein product [Vitis vinifera] (G	-0.7369	0.2731	0.3073	0.3521	0.5769	0.4147	-1.1056	0.1295	0.1636	-0.01658	0.9786	0.4778
249773_at	AT5G24140	SQP2 (Squalene monooxygenase 2); oxidoreductac	0.8494	0.5196	0.4289	0.3058	0.8121	0.4935	-0.06283	0.9609	0.5079	-0.6064	0.6411	0.3776
249774_at	AT5G24150	SQP1 (Squalene monooxygenase 1)	-0.7727	0.0044	0.048	-1.4264	4.00E-04	0.0251	0.2411	0.144	0.1745	-0.4126	0.0361	0.0647
249775_at	AT5G24160	squalene monooxygenase 1,2 / squalene epoxidase	0.3789	0.2891	0.3168	0.2528	0.4609	0.3683	-0.4087	0.0297	0.0701	-0.5347	0.0124	0.0351
249776_at	AT5G24170	similar to unknown protein [Arabidopsis thaliana] (T	-0.2036	0.3263	0.3381	-0.1354	0.4986	0.3839	0.01577	0.9352	0.5021	0.08397	0.6687	0.3869
249777_at	AT5G24210	lipase class 3 family protein	0.1853	0.0639	0.1448	0.8272	0.1248	0.1792	0.1672	0.5612	0.383	-0.09081	0.7484	0.4132
249778_at	AT5G24165	similar to unknown protein [Arabidopsis thaliana] (T	-0.2885	0.2612	0.3004	-0.1269	0.5962	0.422	0.6893	0.0354	0.0772	0.8509	0.0182	0.0434
249779_at	AT5G24230	similar to triacylglycerol lipase [Arabidopsis thaliana	0.06947	0.9259	0.5585	0.9209	0.2597	0.2697	0.541	0.4554	0.341	1.3923	0.1007	0.1211
249780_at	AT5G24240	phosphatidylinositol 3- and 4-kinase family protein	1.3985	0.1239	0.2039	0.2642	0.7321	0.4689	0.1216	0.874	0.4851	-1.0127	0.232	0.2027
249781_at	AT5G24250	unknown protein	0.7503	0.5453	0.439	-1.3588	0.2979	0.2906	1.9431	0.1625	0.1869	-0.1661	0.8909	0.4545
249782_at	AT5G24260	prolyl oligopeptidase family protein	0.6501	0.1376	0.2155	0.4289	0.2888	0.286	-0.2161	0.269	0.2517	-0.4373	0.0604	0.0888
249783_at	AT5G24270	SOS3 (SALT OVERLY SENSITIVE 3)	-1.2461	0.2221	0.2764	-1.5436	0.148	0.1967	0.4884	0.4805	0.3516	0.1909	0.7765	0.4219
249784_at	AT5G24280	ATP binding	1.2027	0.1863	0.253	1.8299	0.0724	0.1349	-0.156	0.8211	0.4701	0.4712	0.5064	0.3283
249785_at	AT5G24300	ATSS1/SSI (STARCH SYNTHASE I); transferase, t	-0.4674	0.0023	0.0417	-0.8323	3.00E-04	0.0249	-0.1409	0.1058	0.1455	-0.5059	0.0017	0.0146
249786_at	AT5G24310	ABIL3 (ABIL INTERACTOR-LIKE PROTEIN 3)	0.4581	0.1592	0.2328	0.04953	0.8609	0.5074	0.4181	0.1901	0.2055	0.009534	0.973	0.4763
249787_at	AT5G24320	WD-40 repeat family protein	-0.1201	0.672	0.4833	-0.2806	0.3467	0.3163	0.01868	0.9468	0.5049	-0.1418	0.6188	0.3699
249788_at	AT5G24330	ATXR6 (Arabidopsis thaliana Trithorax- related prot	0.7775	0.3949	0.3726	0.6319	0.4822	0.377	0.9318	0.2573	0.2448	0.7862	0.3278	0.2523
249789_at	AT5G24340	3'-5' exonuclease domain-containing protein	-0.1963	0.4012	0.3758	0.3549	0.1651	0.2091	-0.115	0.6119	0.4018	0.4363	0.1054	0.1242
249790_at	AT5G24290	integral membrane family protein	0.1969	0.2137	0.2707	0.6194	0.0097	0.0537	-0.07246	0.6156	0.4029	0.3501	0.0584	0.0871
249791_at	AT5G23810	AAP7 (amino acid permease 7); amino acid transm	1.043	0.0365	0.1101	0.8145	0.0731	0.1355	-0.1134	0.7422	0.4455	-0.3418	0.3476	0.2614
249792_at	AT5G23720	SH3 (PROPYZAMIDE-HYPERSENSITIVE 1); pro	0.2	0.341	0.3458	0.4836	0.0594	0.1211	-0.3303	0.1492	0.1784	-0.04678	0.8131	0.4326
249793_at	AT5G23680	sterile alpha motif (SAM) domain-containing protein	-0.7222	0.2619	0.3007	-0.06744	0.9089	0.5212	-0.6105	0.3319	0.2842	0.04431	0.94	0.4685
249794_at	AT5G23530	ATCXE18 (ARABIDOPSIS THALIANA CARBOXYE	0.002385	0.9961	0.5761	0.8111	0.1546	0.2016	-0.253	0.5105	0.3634	0.5557	0.1882	0.1782
249795_at	AT5G23740	RPS11-BETA (RIBOSOMAL PROTEIN S11-BETA	0.02617	0.8006	0.5243	-0.316	0.0311	0.0876	-0.04051	0.6933	0.4288	-0.3304	0.0258	0.0533
249796_at	AT5G23540	26S proteasome regulatory subunit, putative	1.1144	2.00E-04	0.0312	1.0606	3.00E-04	0.0249	0.0419	0.6008	0.3984	-0.01191	0.8797	0.4512
249797_at	AT5G23750	remorin family protein	-1.1958	0.0032	0.0442	-0.769	0.0151	0.0646	0.5796	0.0371	0.0794	1.0064	0.0059	0.0239
249798_at	AT5G23730	nucleotide binding	-1.403	0.0181	0.0804	-1.0179	0.0487	0.1095	-0.9989	0.0297	0.0701	-0.6139	0.1117	0.1289
249799_at	AT5G23670	LCB2 (Serine palmitoyltransferase LCB2 (long chai	0.01238	0.949	0.5645	-0.05062	0.7947	0.4877	-0.6443	0.024	0.0629	-0.7073	0.0177	0.0427
249800_at	AT5G23660	MTN3 (ARABIDOPSIS HOMOLOG OF MEDICAGO	0.1912	0.6797	0.486	0.5841	0.2461	0.2616	0.2706	0.4262	0.3281	0.6636	0.0958	0.1174
249801_at	AT5G23580	CDPK6 (CALCIUM-DEPENDENT PROTEIN KINAS	0.7237	0.0054	0.0519	0.8099	0.0036	0.0378	-0.6403	0.0084	0.0368	-0.5541	0.0138	0.0374
249802_at	AT5G23770	agenet domain-containing protein	0.188	0.8275	0.5318	1.1225	0.2372	0.2562	0.243	0.7536	0.4492	1.1775	0.1786	0.1724
249803_at	AT5G23780	agenet domain-containing protein	-0.3186	0.4263	0.3877	-0.6668	0.2465	0.2618	-0.05975	0.9091	0.4951	-0.2916	0.585	0.3581
249804_at	AT5G23790	ATGOLS5 (ARABIDOPSIS THALIANA GALACTIN	-0.01832	0.9894	0.5744	-0.8435	0.552	0.4056	1.2108	0.4047	0.3184	0.3856	0.7817	0.4233
249805_at	AT5G23800	agenet domain-containing protein	0.7765	0.0271	0.0953	-0.1	0.6833	0.4532	-0.3202	0.2327	0.2309	-1.1966	0.0063	0.0246
249806_at	AT5G23810	similar to unknown protein [Arabidopsis thaliana] (T	0.8981	0.0194	0.0826	0.8056	0.0275	0.0828	0.2926	0.0718	0.1165	0.2001	0.1716	0.1682
249807_at	AT5G23870	pectinacetylesterase family protein	-0.2426	0.1399	0.2175	-0.06215	0.6622	0.4458	-0.2882	0.0944	0.1363	-0.1077	0.4604	0.3101
249808_at	AT5G23890	similar to unknown protein [Arabidopsis thaliana] (T	0.3389	0.0554	0.1352	-0.03442	0.7992	0.4894	-0.4761	0.0033	0.0256	-0.8494	4.00E-04	0.0088
249809_at	AT5G23910	microtubule motor	0.3527	0.6276	0.4689	1.2464	0.1374	0.1888	-0.5374	0.3369	0.2868	0.3563	0.5098	0.3297
249810_at	AT5G23920	similar to unknown protein [Arabidopsis thaliana] (T	-0.2318	0.4576	0.4018	-0.4505	0.1857	0.2235	0.4439	0.0011	0.0183	0.2252	0.0132	0.0364
249811_at	AT5G23760	heavy-metal-associated domain-containing protein	-0.09933	0.6789	0.4857	0.2858	0.2689	0.2749	0.9915	0.0113	0.042	1.3766	0.0035	0.0193
249812_at	AT5G23840	MD-2-related lipid recognition domain-containing pr	-0.2512	0.7557	0.6104	1.5368	0.1111	0.1682	-0.06411	0.9363	0.5024	1.7238	0.0842	0.1083
249813_at	AT5G23940	EMB3009 (EMBRYO DEFECTIVE 3009); transferase	0.6716	0.3558	0.3525	-0.3756	0.5909	0.4198	-0.04085	0.9202	0.4979	-1.0881	0.0469	0.0762
249814_at	AT5G23840	MD-2-related lipid recognition domain-containing pr	-2.063	0.0351	0.1083	-0.3917	0.584	0.4178	-1.0563	0.184	0.2014	0.615	0.4032	0.2855
249815_at	AT5G23900	60S ribosomal protein L13 (RPL13D)	0.3195	0.2494	0.2932	0.3208	0.2478	0.2624	-0.3062	0.0103	0.0404	-0.3048	0.0105	0.0321
249816_at	AT5G23880	ATCPSF100/CPSF100/EMB1265/ESP5 (CLEAVAG	1.2765	2.00E-04	0.0312	0.8703	9.00E-04	0.0286	-0.1035	0.3137	0.2752	-0.5096	0.0048	0.0218
249817_at	AT5G23820	MD-2-related lipid recognition domain-containing pr	-0.9073	0.0012	0.036	-0.7066	0.003	0.0356	0.763	0.0016	0.0203	0.9636	7.00E-04	0.0105
249818_at	AT5G23860	TUB8 (tubulin beta-8)	-0.7045	0.0684	0.1504	-0.4159	0.2174	0.2442	0.0822	0.7227	0.4395	0.3709	0.1609	0.1618
249819_at	AT5G23640	unknown protein	1.6637	0.1764	0.2457	2.2718	0.0887	0.1501	-0.0075	0.9945	0.5163	0.6006	0.5857	0.3583
249820_at	AT5G23650	myb family transcription factor	0.1007	0.9313	0.5602	-0.4453	0.7059	0.4609	0.0119	0.9919	0.5156	-0.5342	0.6522	0.3816
249821_at	AT5G23690	polynucleotide adenylyltransferase family protein	1.1904	0.0079	0.0585	0.2748	0.3191	0.3026	-0.3531	0.2179	0.2224	-1.2687	0.0063	0.0246
249822_at	AT5G23710	DNA binding / DNA-directed RNA polymerase	0.4183	0.006	0.0538	0.6589	0.0011	0.0294	0.1999	0.0641	0.1092	0.4404	0.005	0.0222
249823_s_at	AT5G23350;AT5G23360	[AT5G23350, GRAM domain-containing protein / AS	-0.6332	0.0058	0.053	-0.1589	0.2486	0.263	1.2289	4.00E-04	0.0147	1.7032	1.00E-04	0.0063
249824_at	AT5G23380	similar to unknown protein [Arabidopsis tha

249890_at	AT5G22570	WRKY38 (WRKY DNA-binding protein 38); transcri	1.1259	0.0142	0.0727	1.1421	0.0135	0.0617	0.5625	0.04	0.0828	0.5787	0.0368	0.0653
249891_at	AT5G22590	similar to F-box family protein [Arabidopsis thaliana	1.7886	0.1719	0.2427	-0.3983	0.7301	0.4686	2.0005	0.1366	0.1688	-0.1864	0.8709	0.4486
249892_at	AT5G22600	similar to F-box family protein [Arabidopsis thaliana	-0.95	0.1559	0.2302	-0.4495	0.4553	0.3662	0.1883	0.7469	0.4472	0.6887	0.2744	0.2252
249893_at	AT5G22555	unknown protein	-0.473	0.5648	0.4469	-0.2108	0.7938	0.4874	0.5655	0.4953	0.3579	0.8276	0.3344	0.2553
249894_at	AT5G22580	identical to Uncharacterized protein At5g22580 [Ara	-0.2845	0.3915	0.3708	0.09409	0.7668	0.4794	1.1809	0.0014	0.0197	1.3713	8.00E-04	0.0111
249895_at	AT5G22500	acyl CoA reductase, putative / male-sterility protein,	0.6054	0.1536	0.2287	0.7851	0.0848	0.1465	0.199	0.388	0.3112	0.3788	0.1394	0.1477
249896_at	AT5G22530	similar to unknown protein [Arabidopsis thaliana] (T	1.9607	0.003	0.0435	1.4474	0.0088	0.0516	1.2315	0.0138	0.0469	0.7181	0.071	0.0977
249897_at	AT5G22550	similar to unknown protein [Arabidopsis thaliana] (T	1.4238	0.3287	0.3392	2.0889	0.1783	0.2185	0.8059	0.5634	0.3841	1.4711	0.3149	0.2459
249898_at	AT5G22510	beta-fructofuranosidase, putative / invertase, putati	0.2171	0.0742	0.1566	-0.1229	0.2454	0.2613	-0.1384	0.2006	0.2121	-0.4784	0.0061	0.0242
249899_at	AT5G22620	phosphoglycerate/bisphosphoglycerate mutase fam	-1.0088	0.0048	0.0496	-1.2942	0.0019	0.0329	-0.4589	0.0612	0.1062	-0.7443	0.0138	0.0374
249900_at	AT5G22640	EMB1211 (EMBRYO DEFECTIVE 1211)	-0.3672	0.0306	0.1015	0.3767	0.0283	0.0836	-0.8338	9.00E-04	0.0167	-0.8432	8.00E-04	0.0112
249901_at	AT5G22650	HD2B (HISTONE DEACETYLASE 2B)	0.3501	0.3651	0.3569	0.3848	0.3248	0.3058	0.03088	0.832	0.4733	0.06552	0.6561	0.3829
249902_at	AT5G22680	similar to F-box family protein [Arabidopsis thaliana	0.4295	0.463	0.4044	-1.459	0.0511	0.1122	0.9856	0.1363	0.1686	-0.9029	0.1635	0.1634
249903_at	AT5G22690	disease resistance protein (TIR-NBS-LRR class), p	-0.1946	0.6277	0.4689	-0.2671	0.5114	0.3892	-0.4827	0.0883	0.1312	-0.5552	0.0613	0.0897
249904_at	AT5G22700	F-box family protein	0.2653	0.3779	0.3634	-0.1001	0.7274	0.468	-1.9603	0.0014	0.0194	-2.3257	7.00E-04	0.0107
249905_at	AT5G22710	similar to F-box family protein [Arabidopsis thaliana	0.5381	0.0289	0.0985	-0.1373	0.4421	0.3604	-0.4838	0.0071	0.0342	-1.1592	3.00E-04	0.0081
249906_at	AT5G22730	F-box family protein	0.2739	0.1472	0.2231	0.2746	0.1464	0.1957	-0.2216	0.2202	0.2237	-0.2209	0.2214	0.1968
249907_at	AT5G22750	RAD5; ATP binding / DNA binding / helicase/ prote	1.151	0.4666	0.4058	-0.3466	0.8207	0.4961	0.453	0.6751	0.4227	-1.0446	0.3567	0.2655
249908_at	AT5G22760	PHD finger family protein	0.1462	0.5656	0.4471	0.257	0.3332	0.3098	-0.7658	0.0065	0.0331	-0.6549	0.0112	0.0332
249909_s_at	[AT5G22770,AT5G22780	[AT5G22770, ALPHA-ADR (ALPHA-ADAPTIN); bin	0.447	0.0683	0.1503	0.2836	0.1909	0.2268	-0.2817	0.0472	0.0911	-0.4451	0.011	0.0328
249910_at	AT5G22630	ADT5 (AROGENATE DEHYDRATASE 5); arogenat	-0.5601	0.0879	0.1719	-0.2935	0.3042	0.2938	0.07191	0.2117	0.219	0.3385	0.0022	0.0157
249911_at	AT5G22620	ATCSLA02 (Cellulose synthase-like A2); transferas	-0.3898	0.3523	0.3559	-0.4969	0.2511	0.2647	-0.4744	0.1042	0.1444	-0.5815	0.0621	0.0904
249912_at	AT5G22790	RER1 (RETICULATA-RELATED 1)	0.02999	0.914	0.5551	0.4015	0.1987	0.2321	-0.2951	0.3213	0.2788	0.07641	0.7842	0.4242
249913_at	AT5G22810	GDSL-motif lipase, putative	1.9493	0.0148	0.0737	-0.488	0.3623	0.324	0.6553	0.2398	0.235	-1.782	0.0199	0.0453
249914_at	AT5G22850	aspartyl protease family protein	0.2831	0.0774	0.1602	0.1531	0.2704	0.2757	0.03466	0.7867	0.4592	-0.09531	0.4709	0.3141
249915_at	AT5G22870	harpin-induced protein-related / HIN1-related / harp	-0.5643	0.2404	0.2877	-1.1987	0.043	0.103	0.6803	0.1721	0.1934	0.04587	0.9162	0.4617
249916_at	AT5G22880	H2B/HTB2 (HISTONE H2B); DNA binding	-0.512	0.0278	0.0966	-0.2248	0.2118	0.2408	0.7991	0.0062	0.0327	1.0863	0.002	0.0152
249917_at	AT5G22890	esterase/lipase/thioesterase family protein	0.04118	0.9512	0.565	0.0505	0.9402	0.5291	0.1543	0.4976	0.3587	0.1636	0.4736	0.3152
249918_at	AT5G19240	Identical to Uncharacterized GPI-anchored protein /	-0.5034	0.255	0.2964	-0.5849	0.1979	0.2316	0.79	0.0117	0.0429	0.7085	0.0169	0.0416
249919_at	AT5G19250	Identical to Uncharacterized GPI-anchored protein /	0.07147	0.7154	0.4979	-0.2576	0.231	0.2522	0.8888	0.0018	0.0206	0.5597	0.0098	0.0309
249920_at	AT5G19260	similar to unknown protein [Arabidopsis thaliana] (T	-1.7822	0.011	0.036	-1.6659	0.0015	0.0313	0.9081	0.0133	0.0449	1.0244	0.0088	0.0292
249921_at	AT5G19270	nucleic acid binding	0.1976	0.7089	0.4959	0.1989	0.7072	0.4613	-0.475	0.3898	0.312	-0.4738	0.3909	0.2804
249922_at	AT5G19140	auxin/aluminum-responsive protein, putative	-0.1497	0.4697	0.4071	0.05728	0.7754	0.4822	0.07546	0.5111	0.3636	0.2824	0.0543	0.0833
249923_at	AT5G19120	aspartic-type endopeptidase pepsin A	0.1801	0.5827	0.4534	0.1119	0.7295	0.4685	0.03732	0.864	0.4592	0.3293	0.1585	0.1603
249924_at	AT5G19280	KAPP (Kinase-associated protein phosphatase); pr	0.3507	0.2205	0.2755	0.3474	0.2241	0.248	-0.4891	0.1131	0.1507	-0.4925	0.1113	0.1286
249925_at	AT5G19150	carbohydrate kinase family	0.5409	0.0095	0.0626	0.0562	0.6528	0.4427	-0.1683	0.2198	0.2235	-0.653	0.0049	0.022
249926_at	AT5G19160	ECR1 (E1 C-TERMINAL RELATED 1); small protei	0.7623	0.0173	0.0788	0.8619	0.0114	0.0577	-0.9386	0.0065	0.037	-0.839	0.0125	0.0354
249927_at	AT5G19220	ADG2 (ADPG PYROPHOSPHORYLASE 2); glucos	-0.792	0.0075	0.0579	-0.7587	0.0088	0.0515	-0.4889	0.0101	0.0399	-0.4556	0.0128	0.0359
249928_at	AT5G22250	CCR4-NOT transcription complex protein, putative	-1.1805	0.006	0.0535	-0.973	0.0117	0.0583	0.717	0.0317	0.0724	0.9246	0.014	0.0375
249929_at	AT5G22340	similar to unnamed protein product [Vitis vinifera] (	-0.4454	0.169	0.189	-0.7899	0.0212	0.0742	-0.7317	0.0096	0.0391	-1.0816	0.0024	0.0162
249930_at	AT5G22360	ATVAMP714 (Vesicle-associated membrane protein	0.3011	0.0337	0.1062	0.3866	0.0151	0.0646	0.2228	0.0785	0.1225	0.3084	0.0313	0.0596
249931_at	AT5G22370	EMB1705/QQT1 (QUATRE-QUART1); ATP binding	0.2115	0.2929	0.3189	0.03585	0.8475	0.5037	0.004167	0.9799	0.5126	-0.1715	0.3312	0.254
249932_at	AT5G22390	similar to unnamed protein product [Vitis vinifera] (	-1.49	0.0011	0.036	-1.3878	0.0014	0.0313	-0.1563	0.0555	0.1005	-0.0541	0.407	0.2869
249933_at	AT5G22400	rac GTPase activating protein, putative	-0.4464	0.1733	0.2437	-0.4127	0.2008	0.2331	-0.2445	0.3952	0.3144	-0.2107	0.4582	0.3093
249934_at	AT5G22410	peroxidase, putative	-1.3302	0.2749	0.3085	0.5514	0.628	0.4337	-1.388	0.1687	0.1909	0.4936	0.5829	0.3572
249935_at	AT5G22420	acyl CoA reductase, putative	-0.7734	0.4105	0.3802	-1.8799	0.0894	0.1507	1.6388	0.1236	0.1591	0.5322	0.5618	0.3496
249936_at	AT5G22450	similar to unknown protein [Arabidopsis thaliana] (T	0.3125	0.0709	0.1536	0.2026	0.1882	0.2254	-0.3172	0.0681	0.1132	-0.4271	0.0288	0.0568
249937_at	AT5G22470	NAD+ ADP-ribosyltransferase	0.6453	0.316	0.3321	-1.9568	0.0255	0.0799	0.9054	0.1834	0.2011	-1.6967	0.0395	0.0685
249938_at	AT5G22330	ATTIP49A(RIN1 (RESISTANCE TO PSEUDOMON	0.5682	0.0328	0.1049	0.08843	0.6442	0.4396	0.09279	0.864	0.4074	-0.387	0.0945	0.1164
249939_at	AT5G22430	similar to unknown protein [Arabidopsis thaliana] (T	-0.00977	0.984	0.573	0.703	0.1992	0.2324	-0.4877	0.296	0.2667	0.2251	0.6088	0.3663
249940_at	AT5G22380	ANAC090 (Arabidopsis NAC domain containing pro	0.3377	0.575	0.4508	0.492	0.4246	0.3528	0.3564	0.2938	0.2655	0.5107	0.1587	0.1604
249941_at	AT5G22270	similar to unknown protein [Arabidopsis thaliana] (T	-0.1353	0.4838	0.4135	0.02239	0.9047	0.52	0.8365	0.0017	0.0204	0.994	9.00E-04	0.0114
249942_at	AT5G22300	NIT4 (NITRILASE 4)	-0.3636	0.2514	0.2942	-0.4216	0.1953	0.2296	0.1454	0.5006	0.3598	0.08745	0.6795	0.3903
249943_at	AT5G22280	similar to unknown protein [Arabidopsis thaliana] (T	0.2107	0.3502	0.3497	0.1555	0.4791	0.3757	0.5422	0.0531	0.0978	0.487	0.0711	0.0977
249944_at	AT5G22290	ANAC089 (Arabidopsis NAC domain containing pro	0.7413	0.0715	0.1541	0.7395	0.072	0.1343	0.1248	0.4966	0.3584	0.123	0.5025	0.3267
249945_at	AT5G22440	60S ribosomal protein L10A (RPL10aC)	-0.2169	0.217	0.2733	-0.1234	0.4518	0.3648	-0.3807	0.0064	0.033	-0.2871	0.0169	0.0415
249946_at	AT5G19170	similar to unknown protein [Arabidopsis thaliana] (T	-0.1491	0.5964	0.4585	0.01952	0.9437	0.5302	-0.1248	0.3559	0.2961	0.04385	0.7326	0.4079
249947_at	AT5G19200	short-chain dehydrogenase/reductase (SDR) family	0.3707	0.0198	0.0832	0.5353	0.1069	0.1649	0.03342	0.8856	0.4884	-0.402	0.139	0.1475
249948_at	AT5G19210	DEAD/EAH box helicase, putative	0.2107	0.1617	0.235	-0.04173	0.7513	0.4754	-0.6935	0.0049	0.0295	-0.9459	0.0015	0.0139
249949_at	AT5G18880	glucose transmembrane transporter	-0.8748	0.1018	0.1844	-0.8989	0.0953	0.1556	-0.2561	0.5691	0.3863	-0.2802	0.5351	0.3398
249950_at	AT5G18910	protein kinase family protein	-1.265	0.3593	0.3542	0.5314	0.6863	0.4544	-0.8514	0.5246	0.369	0.9449	0.4828	0.3188
249951_at	AT5G18930	BUD2/SAMDC4 (BUSHY AND DWARF 2); adenos	-0.3685	0.6098	0.4629	-1.8866	0.0473	0.108	1.1002	0.1597	0.1855	-0.4178	0.5482	0.3444
249952_at	AT5G18950	pentatricopeptide (PPR) repeat-containing protein	0.1187	0.7885	0.5201	0.1951	0.6618	0.4457	-0.2938	0.5169	0.3659	-0.2174	0.6272	0.3728
249953_at	AT5G18960	ERS12 (F-BAR-RELATED SEQUENCE 12); zinc ion	-0.1825	0.47	0.4094	-0.06904	0.8538	0.5058	-0.649	0.0626	0.1075	-0.5356	0.1021	0.1221
249954_at	AT5G18920	similar to Os05g0404300 [Oryza sativa (japonica cu	0.2634	0.3844	0.367	0.1522	0.6031	0.4247	0.2596	0.3907	0.3124	0.1483	0.6119	0.3674
249955_at	AT5G18840	sugar transporter, putative	-0.6737	0.3381	0.3446	1.2418	0.1156	0.1716	-0.4722	0.4682	0.3467	1.4434	0.0706	0.0974
249956_at	AT5G18850	Mo25 family protein	0.01366	0.9462	0.5636	-0.2597	0.2438	0.2605	-0.1483	0.2885	0.2627	-0.4217	0.0254	0.0527
249957_at	AT5G18900	oxidoreductase, 2OG-Fe(II) oxygenase family protei	0.5769	0.0121	0.0682	0.5521	0.014	0.0627	0.2933	0.0123	0.0441	0.2684	0.0166	0.0411
249958_at	AT5G18970	AWPM-19-like membrane family protein	-0.4663	0.1245	0.2043	-0.09388	0.7161	0.464	0.869	0.0119	0.0433	1.2414	0.0033	0.0188
249959_at	AT5G18800	NADH-ubiquinone oxidoreductase 19 kDa subunit (	0.298	0.0219	0.087	0.6891	0.0201	0.0293	0.109	0.7253	0.4603	0.5001	9.00E-04	0.0116
249960_at	AT5G18830	SPL7 (SQUAMOSA PROMOTER BINDING PROTE	0.2868	0.2031	0.2642	0.05136	0.7989	0.4893	-0.3976	0.0306	0.0713	-0.6331	0.0064	0.0249
249961_at	AT5G18770	F-box family protein	-0.6091	0.1914	0.2563	-0.7221	0.1361	0.1877	-0.8386	0.0967	0.1382	-0.9516	0.0702	0.0971
249962_at	AT5G18990	zectineesterase family protein	-0.8565	0.4079	0.3792	0.02777	0.9775	0.5386	-1.9606	0.1019	0.1426	-1.0764	0.3102	0.2435
249963_at	no_match	no_match	0.03481	0.7411	0.5062	0.08205	0.4507	0.3643	-0.07923	0.4653	0.3454	-0.03199	0.7611	0.4171
249964_at	AT5G19010	MPK16 (mitogen-activated protein kinase 16); MAP	0.04929	0.7938	0.5222	-0.1668	0.3981	0.3404	-0.3179	0.146	0.1762	-0.5339	0.0389	0.0679
249965_at	AT5G19020	pentaticopeptide (PPR) repeat-containing protein	-0.1081	0.8528	0.5389	1.037	0.1306	0.1833	-0.5792	0.3452	0.2908	0.5659	0.3551	0.2649
249966_at	AT5G19030	RNA recognition motif (RRM)-containing protein	0.4905	0.0095	0.0626	0.2832	0.0543	0.1156	0.2559	0.0613	0.1065	0.04861	0.6497	0.3808
249967_at	AT5G19050	similar to unnamed protein product [Vitis vinifera] (G	0.232	0.2704	0.3056	0.1828	0.371	0.3278	0.04799	0.8046	0.4649	-0.00123	0.9949	0.4814
249968_at	AT5G19070	similar to unknown protein [Arabidopsis thaliana] (T	-0.2491	0.1872	0.2536	-0.08538	0.6149	0.4288	-0.1898	0.2925	0.2649	-0.02615	0.8756	0.4501
249969_at	AT5G19090	heavy-metal-associated domain-containing protein	0.01898	0.9426	0.5631	-0.1675	0.5362	0.399	0.4541	0.1408	0.1719	0.2677	0.3408	0.2584
249970_at	AT5G19100	extracellular dermal glycoprotein-related / EDGP-re	-0.4611	0.4227	0.3863	-1.0679	0.1077	0.1655	0.5779	0.1937	0.2078	-0.02889	0.9416	0.4689
249971_at	AT5G19110	extracellular dermal glycoprotein-related / EDGP-re	-2.3548	0.1748	0.2448	-1.9797	0.2383	0.2567	0.01387	0.9868	0.5143	0.3889	0.6465	0.3796
249972_at	AT5G19040	ATIPT5 (Arabidopsis thaliana isopentenyltransferas	0.7276	0.4116	0.3809	-0.3797	0.6576	0.4443	1.0916	0.2414	0.2358	-0.0158	0.9851	0.4791
249973_at	AT5G19130	GPI transamidase component family protein / Gaa1	0.8337	0.0081	0.0588	0.8757	0.0068	0.0467	-0.4382	0.0619	0.1069	-0.3961	0.0807	0.1056
249974_at	AT5G19180	F-box family protein	1.2219	0.0066	0.0549	1.7428	0.0018	0.0323	-0.8551	0.0223	0.0603	-0.3343	0.2294	0.2012
249975_s_at	[AT3G06320,AT5G18790	[AT3G06320, ribosomal protein L33 family protein];	0.09141	0.6665	0.4814	0.3231	0.176	0.217	0.2258	0.3152	0.2759	0.4575	0.0807	0.1056
249976_at	AT5G18810	SCL28 (SC35-like splicing factor 28); RNA binding	0.01551	0.9781	0.5717	-0.3795	0.5141	0.3903	-0.08172	0.8405	0.4758	-0.4768	0.2786	0.2274
249977_at	AT5G18820	EMB3007 (EMBRYO DEFECTIVE 3007); ATP bind	0.5944	0.1545	0.2294	-0.01938	0.9572	0.5335	0.2241	0.4885	0.3549	-0.3897	0.2557	0.2155
249978_at	AT5G18850	similar to hypothetical protein [Vitis vinifera] (GB:CA	-0.2205	0.2251	0.2786	0.05661	0.7315	0.4688	-0.06	0.7164	0.437	0.2171	0.231	0.202
249979_s_at	[AT5G18860,AT5G18890	[AT5G18860, inosine-uridine preferring nucleoside	-0.3667	0.1414	0.2186	-0.8108	0.0156	0.0652	0.1898	0.3974	0.3154	-0.2542	0.2736	0.2248
249980_at	AT5G18870	inosine-uridine preferring nucleoside hydrolase-rela	0.06252	0.9519	0.5652	-1.9907	0.1104	0.1677	0.1414	0.8916	0.4901	-1.9118	0.1211	0.1358
249981_at	AT5G18510	similar to unknown protein [Arabidopsis thaliana] (T	-1.7123	0.1009	0.1835	0.005821	0.9946	0.5428	-1.2936	0.1838	0.2013	0.4245	0.6263	0.3725
249982_at	AT5G18520	similar to unknown protein [Arabidopsis thaliana] (T	0.006424	0.9349	0.561	-0.1045	0.2306	0.2519	-0.2414	0.031	0.0716	-0.3523	0.0089	0.0294
249983_at	AT5G18470	curculin-like (mannose-binding) lectin family protein	1.7849	0.0123	0.0687	1.8288	0.0114	0.0575	0.6138	0.0411	0.0842	0.6576	0.0334	0.0617
249984_at	AT5G18400	similar to unknown protein [Arabidopsis thaliana] (T	0.1868	0.4689	0.4067	-0.1041	0.6791	0.4516	0.9226	0.0019	0.0207	0.6318	0.0075	0.027
249985_at	AT5G18500	protein kinase family protein	-0.4359	0.0869	0.1707	-0.5876	0.0382	0.0968	-0.2622	0.1128	0.1504	-0.414	0.033	0.0613
249986_at	AT5G18460	similar to unknown protein [Arabidopsis thaliana] (T	0.2429	0.1086	0.1909	-0.5373	0.1605	0.2062	0.2279	0.4466	0.3369	0.3335	0.2848	0.2307
249987_at	AT5G18490	similar to unknown protein [Arabidopsis thaliana] (T	0.3632	0.1605	0.2338	0.2982	0.2306	0.2519	0.08859	0.5903	0.3948	0.02362	0.8837	0.4525
249988_at	AT5G18310	similar to unknown protein [Arabidopsis thaliana] (T	1.1103	0.0641	0.1449	1.1423	0.0593	0.121	0.6744	0.003	0.0247	0.7064	0.0025	0.0165
249989_at	AT5G18525	WD-40 repeat family protein	0.4189	0.0475	0.1254	0.6823	0.01	0.0544	-0.7433	0.0074	0.0348	-0.4799	0.0317	0.06
249990_at	AT5G18540	similar to hypothetical protein [Vitis vinifera] (GB:CA	-0.2263	0.7701	0.5147	1.3993	0.1254	0.1795	-0.7821	0.3407	0.2886	0.8435	0.3086	0.2428
249991_at	AT5G18550	nucleic acid binding	-0.2202	0.3749	0.3618	-0.4912	0.0901	0.1514	0.4795	0.0347	0.0764	0.2085	0.2432	0.2089
249992_at	AT5G18560	PUCHI; DNA binding / transcription factor	0.3311	0.6495	0.4762	-0.1578	0.8266	0.4979	0.9986	0.093	0.1351	0.5097	0.3249	0.2506
249993_at	AT5G18570	GTP1/OBG family protein	-0.1316	0.4135	0.3817	-0.2016	0.2352	0.2549	-0.2802	0.1242	0.1596	-0.3502	0.0723	0.0987
249994_at	AT5G18590	kelch repeat-containing protein	0.1096	0.453	0.3996	-0.08466	0.556	0.4068	0.1274	0.2637	0.2486	-0.06681	0.5331	0.339
249995_at	AT5G18610	protein kinase family protein	-0.06095	0.9565	0.5664	0.3351	0.7655	0.479	-0.5254	0.643	0.4121	-0.1293	0.9079	0.4594
249996_at	AT5G18600	glutaredoxin family protein	-0.5694	0.0798	0.1629	-0.202	0.4541	0.3656	0.7683	0.0043	0.028	1.1357	0.001	0.0121
249997_at	AT5G18620	CHR17 (CHROMATIN REMODELING FACTOR17)	0.3184	0.1277	0.2065	0.1781	0.344	0.3151	-0.5566	0.0178	0.0533	-0.6969	0.0083	0.0282
249998_at	AT5G18580	FASS (FASS 1)	0.08699	0.5428	0.438	0.1144	0.4316	0.356	-0.2028	0.0538	0.0987	-0.1754	0.0794	0.1045
249999_at	AT5G18640	lipase class 3 family protein	0.4251	0.2685	0.3045	0.4468	0.2485	0.263	-0.338	7.00E-04	0.016	-0.3163	9.00E-04	0.0117
250000_at	AT5G18650	zinc finger (C3HC4-type RING finger) family protein	-0.03328	0.8269	0.5316	0.219	0.1993	0.2324	-0.05464	0.721	0.439	0.1977	0.2379	0.206
250001_at	AT5G18680	AITLP11 (TUBBY LIKE PROTEIN 11); phosphoric-d	0.2115	0.1027	0.1852	0.3906	0.0176	0.0688	-0.05768	0.5019	0.3602	0.1214	0.1957	0.1824
250002_at	AT5G18690	AGP25/ATAGP25 (ARABINOGALACTAN PROTEI	0.2901	0.3133	0.3305	-0.00063	0.9981	0.5435	1.4409	0.0042	0.0278	1.1502	0.0094	0.0302
250003_at	AT5G18710	similar to unknown protein [Arabidopsis thaliana] (T	0.03982	0.9805	0.5721	-0.5006	0.7589	0.4778	1.163	0.4014	0.3172	0.7039	0.6013	0.3638
250004_at	AT5G18750	DNAJ heat shock N-terminal domain-containing pro	0.632	0.0639	0.1448	0.5326	0.099	0.1587	0.08268	0.7513	0.4486	-0.01668	0.9487	0.4705
250005_at	AT5G18760	zinc finger (C3HC4-type RING finger) family protein	-0.03619	0.857	0.5405	-0.2535	0.2495	0.2636	0.2177	0.0856	0.129	0.000322	0.9975	0.4822
250006_at	AT5G18680	DVR (PALE-GREEN AND CHLOROPHYLL B RED	-1.8845	0.0027	0.0426	-2.0305	0.002	0.033	0.4039	0.0636	0.1086	0.258	0.1793	0.1729
250007_at	AT5G18670	BMY3 (BETA-AMYLASE 9); beta-amylase	-0.7546	0.064	0.1448	-1.0313	0.0256	0.08	0.09358	0.6887	0.4273	-0.183	0.4467	0.3047
250008_at	AT5G18630	lipase class 3 family protein	0.4062	0.172	0.2427	0.3121	0.2709	0.2759	-0.252	0.0348	0.0764	-0.3461	0.0125	0.0353
250009_at	AT5G18440	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.2769	0.2241	0.2779	0.3095	0.1835	0.2222	0.0078	0.6251	0.4063	0.1004	0.4774	0.3166
250010_at	AT5G18450	AP2 domain-containing transcription factor, putative	-0.1958	0.7423	0.5065	-0.2169	0.7162	0.464	0.5482	0.3797	0.3077	0.5271	0.3965	0.2828
250011_at	AT5G18475	pentaticopeptide (PPR) repeat-containing protein	-0.445	0.1524	0.2277	-0.4101	0.1792	0.2191	-0.201	0.2599	0.2464	-0.1662	0.3393	0.2577
250012_s_at	AT5G18460	auxin-responsive protein, putative	1.2071	0.0836	0.1673	1.3506	0.0623	0.124	0.7447	0.077	0.1212	0.6012	0.1285	0.1405
250013_at	AT5G18040	similar to unknown protein [Arabidopsis thaliana] (T	0.9513	0.0016	0.0389	0.8943	0.0021	0.0331	-0.6793	0.0057	0.0314	-0.7363	0.0043	0.0208
250014_at	AT5G17990	TRP1 (TRYPTOPHAN BIOSYNTHESIS 1); anthran	0.2008	0.268	0.3042	0.1188	0.4893	0.3801	-0.158	0.1536	0.1815	-0.2401	0.0559	0.0848
250015_at	AT5G18070	DRT100 (DNA-DAMAGE-REPAIR/TOLERATION 1	0.2841	0.1703	0.2416	0.0812	0.6581	0.4444	0.2761	0.1256	0.1605	0.07319	0.8356	0.3756
250016_at	AT5G18100	CSD3 (COPPER/ZINC SUPEROXIDE DISMUTASE	-0.5119	0.0196	0.0827	-0.4733	0.0252	0.0794	0.07394	0.6149	0.4025	0.1125	0.4539	0.3075
250017_at	AT5G18140	DNAJ heat shock N-terminal domain-containing pro	0.3218	0.1432	0.2201	0.01759	0.9256	0.5255	-0.6348	0.0223	0.0603	-0.9391	0.0058	0.0237
250018_at	AT5G18160	similar to unknown protein [Arabidopsis thaliana] (T	-0.5519	0.079	0.1619	-0.6214	0.0576	0.1193	0.0576	0.08174	0.7164	0.437	0.0123	0.956	0.4725
250019_at	AT5G18160	F-box family protein	0.6506	0.4254	0.3874	0.6686	0.4138	0.3477	-0.2547	0.7381	0.4443	-0.2366	0.7558	0.4153
250020_at	AT5G18180	Gar1 RNA-binding region family protein	0.119	0.6654	0.4811	1.0356	0.0154	0.0649	-0.1124	0.6826	0.4251	0.8043	0.0345	0.0628
250021_at	AT5G18190	protein kinase family protein	0.1778	0.2904	0.3175	0.1538	0.3517	0.3189	-0.4163	0.0464	0.0903	-0.4403	0.0394	0.0684
250022_at	AT5G18210	short-chain dehydrogenase/reductase (SDR) family	0.7

250090_at	AT5G17330	GAD (Glutamate decarboxylase 1); calmodulin bind	3.1814	0.0096	0.0627	3.8762	0.0047	0.0418	-0.01206	0.9846	0.5138	0.6827	0.3088	0.2429
250091_at	AT5G17340	similar to unknown protein [Arabidopsis thaliana] (T	-1.2526	0.1122	0.1941	0.4398	0.5154	0.3908	-0.852	0.2395	0.235	0.8404	0.2449	0.2096
250092_at	AT5G17360	similar to ATP dependent DNA ligase family protein	-1.3888	0.2503	0.2937	-0.3047	0.7829	0.4844	-0.326	0.7683	0.4536	0.7582	0.504	0.3273
250093_at	AT5G17370	WD-40 repeat family protein	0.6974	0.0101	0.064	0.1434	0.3985	0.3407	-0.07165	0.6616	0.4184	-0.6257	0.0146	0.0384
250094_at	AT5G17380	pyruvate decarboxylase family protein	0.5381	0.0244	0.0908	0.661	0.0124	0.0597	0.08611	0.2115	0.2189	0.209	0.0226	0.0489
250095_at	AT5G17230	PSY (PHYTOENE SYNTHASE); geranylgeranyl-dp	-0.7205	0.0047	0.0492	-0.7852	0.0034	0.0373	-0.2368	0.0947	0.1366	-0.3014	0.05	0.0793
250096_at	AT5G17190	similar to unknown protein [Arabidopsis thaliana] (T	1.2353	3.00E-04	0.0312	1.6472	1.00E-04	0.0249	0.445	0.012	0.0435	0.8568	0.0011	0.0124
250097_at	AT5G17350	similar to Os03g0530900 [Oryza sativa (japonica cu	0.09326	0.6565	0.4779	0.2153	0.3302	0.3085	-0.00957	0.9631	0.5084	0.1125	0.5938	0.3612
250098_at	AT5G17350	similar to unknown protein [Arabidopsis thaliana] (T	-1.6803	0.0581	0.1382	-1.5931	0.0672	0.1298	0.6223	0.3402	0.2885	0.7095	0.285	0.2308
250099_at	AT5G17300	myb family transcription factor	-0.7531	0.2457	0.2909	-0.9866	0.1496	0.1978	-0.259	0.0475	0.0914	-0.4925	0.0058	0.0236
250100_at	AT5G16570	GLN1;4 (Glutamine synthetase 1;4); glutamate-amr	-0.5123	0.172	0.2427	-0.6969	0.0807	0.1484	0.9129	0.125	0.0443	0.7283	0.0262	0.0536
250101_at	no_match	no_match	-1.8599	0.1264	0.2058	-0.7051	0.5058	0.387	-1.3399	0.1475	0.1771	-0.1851	0.8165	0.4333
250102_at	AT5G16590	leucine-rich repeat transmembrane protein kinase,	-0.9588	0.0238	0.0899	-1.1545	0.0129	0.0606	-0.3092	0.2706	0.2526	-0.5049	0.1054	0.1242
250103_at	AT5G16600	MYB43 (myb domain protein 43); DNA binding / tra	-0.3201	0.3445	0.3471	-0.2194	0.5034	0.386	0.1391	0.6557	0.4198	0.2397	0.4673	0.3128
250104_at	AT5G16610	similar to unnamed protein product [Vitis vinifera] (C	0.1026	0.6332	0.4707	-0.07684	0.7189	0.4649	-0.4211	0.1016	0.1424	-0.6005	0.0392	0.0682
250105_at	AT5G16630	DNA repair protein Rad4 family	0.4591	0.0537	0.1331	0.2913	0.1611	0.2066	-0.7658	0.002	0.0211	-0.9337	9.00E-04	0.0118
250106_at	AT5G16640	pentatricopeptide (PPR) repeat-containing protein	0.453	0.2128	0.2702	-0.09318	0.7759	0.4824	-0.4337	0.2293	0.2291	-0.9798	0.0328	0.0611
250107_at	AT5G15330	SPX (SYG1/Pho81/XPR1) domain-containing protein	-0.1069	0.3481	0.349	-0.3965	0.017	0.0677	-0.3524	0.013	0.0453	-0.6421	0.0015	0.0137
250108_at	AT5G15150	ATH8-3 (ARABIDOPSIS THALIANA HOMEOBOX	-1.1026	0.4651	0.4053	-0.1568	0.9142	0.5225	0.2613	0.8577	0.4804	1.2072	0.4271	0.2955
250109_at	AT5G15230	GASA4 (GAST1 PROTEIN HOMOLOG 4)	1.05	0.1141	0.1957	0.967	0.137	0.1885	0.4899	0.3394	0.0821	-0.572	0.0243	0.0513
250110_at	AT5G15350	plastocyanin-like domain-containing protein	-1.2988	0.0178	0.0799	-1.1693	0.025	0.0791	0.5532	0.0475	0.0915	0.6827	0.0252	0.0524
250111_at	AT5G16290	acetolactate synthase small subunit, putative	-0.4197	0.0305	0.1012	-0.2652	0.1069	0.1649	-0.5215	0.0051	0.0301	-0.3671	0.0173	0.0421
250112_at	AT5G16300	similar to hypothetical protein Osl_003871 [Oryza s	0.757	0.0011	0.036	0.3781	0.0133	0.0615	0.1585	0.0948	0.1366	-0.2204	0.0387	0.0677
250113_at	AT5G16320	FRL1 (FRIGIDA LIKE 1)	0.7386	0.0194	0.0823	0.4275	0.0937	0.1541	0.456	0.0797	0.1235	0.145	0.4989	0.3255
250114_s_at	AT5G16370:AT5G16340	[AT5G16370, AMP-binding protein, putative]:[AT5G	0.09641	0.6431	0.474	0.3913	0.1121	0.169	-0.3474	0.1457	0.1759	-0.05246	0.7989	0.4284
250115_at	AT5G16420	pentatricopeptide (PPR) repeat-containing protein	-0.07203	0.8334	0.5335	-0.3398	0.3495	0.3178	0.3221	0.3185	0.2776	0.05441	0.8569	0.445
250116_at	AT5G16430	similar to DC1 domain-containing protein [Arabidops	-0.365	0.6513	0.4766	-1.034	0.2392	0.2572	0.808	0.3411	0.2887	0.1389	0.8618	0.4463
250117_at	AT5G16440	IPP1 (ISOPENTENYL DIPHOSPHATE ISOMERAS	0.9285	0.0019	0.0391	0.7883	0.0035	0.0374	0.1569	0.2647	0.2491	0.0167	0.897	0.4564
250118_at	AT5G16460	similar to unknown protein [Arabidopsis thaliana] (T	0.08277	0.9402	0.5625	-0.3639	0.7433	0.4725	0.8455	0.4449	0.3361	0.3988	0.71	0.4009
250119_at	AT5G16470	zinc finger (C2H2 type) family protein	0.327	0.0216	0.0862	0.7322	0.0012	0.03	0.5536	0.0017	0.0205	0.9588	2.00E-04	0.0078
250120_at	AT5G16490	RIC4 (ROP-INTERACTIVE CRIB MOTIF-CONTAIN	-0.2422	0.1218	0.2202	0.2148	0.1674	0.2039	0.4123	0.029	0.0691	0.8693	0.0022	0.0157
250121_at	AT5G16500	protein kinase family protein	0.4136	0.647	0.4753	-0.2267	0.7999	0.4896	-0.4245	0.6386	0.4107	-1.0648	0.2721	0.2239
250122_at	AT5G16520	similar to unknown [Populus trichocarpa] (GB:ABK9	0.303	0.1188	0.1992	0.0783	0.6359	0.4369	-0.1578	0.3608	0.2985	-0.3826	0.0668	0.0942
250123_at	AT5G16530	PINE (PIN-FORMED I); auxin hydrogen symporter/	0.5937	0.248	0.2924	-0.8169	0.1365	0.1881	0.07675	0.8698	0.4841	-0.1464	0.7557	0.4153
250124_at	AT5G16480	tyrosine specific protein phosphatase family protein	-0.4361	0.074	0.1564	-0.8389	0.0098	0.0539	-0.2543	0.2043	0.2143	-0.6571	0.0173	0.0421
250125_at	AT5G16390	BCCP/BCCP-1/BCCP1/CAC1-A/CAC1A (BIOTIN C	-0.7184	0.0053	0.0519	-0.8985	0.0023	0.0337	0.7666	0.0013	0.0188	0.5865	0.0034	0.0191
250126_at	AT5G16310	UCH1; ubiquitin thiolesterase	0.4469	0.0177	0.0798	0.3755	0.0309	0.0873	-0.3322	0.0448	0.0883	-0.4036	0.0246	0.0516
250127_at	AT5G16380	similar to unknown protein [Arabidopsis thaliana] (T	0.4652	0.2168	0.2731	0.2633	0.4536	0.3655	0.3722	0.0499	0.0945	0.1704	0.2724	0.2241
250128_at	AT5G16540	ZFN3 (ZINC FINGER PROTEIN 3); nucleic acid bin	0.2821	0.4607	0.4034	-0.4143	0.2972	0.2902	-0.9155	0.0198	0.0565	-1.6119	0.0027	0.0171
250129_at	AT5G16450	dimethylmenaquinone methyltransferase family pro	0.7901	0.0029	0.0431	0.8078	0.0026	0.0343	1.1174	1.00E-04	0.0101	1.1351	1.00E-04	0.0058
250130_at	AT5G16510	reversibly glycosylated polypeptide, putative	0.5492	0.0082	0.0595	0.5125	0.0105	0.0554	0.1711	0.2043	0.2143	0.1343	0.3001	0.2387
250131_at	AT5G16550	similar to unknown [Gossypium hirsutum] (GB:ABO	0.04688	0.7921	0.5214	0.09718	0.5905	0.4197	0.1506	0.4165	0.3236	0.2009	0.2937	0.2354
250132_at	AT5G16560	KAN (KANADI) transcription factor	0.6273	0.3241	0.3368	-0.04264	0.9428	0.5299	0.5612	0.199	0.2112	-0.1088	0.7805	0.4231
250133_at	AT5G16400	ATF2/TRXF2 (THIOREDOXIN F2); thiol-disulfide ex	-0.7093	0.0332	0.1056	-0.5314	0.0751	0.1374	0.5179	0.0285	0.0685	0.6958	0.0108	0.0325
250134_at	AT5G16505	transposable element gene	0.4038	0.0785	0.1615	0.4054	0.0777	0.1397	-0.3962	0.0551	0.1001	-0.3946	0.0558	0.0846
250135_at	AT5G16530	unknown protein	-0.8749	0.0511	0.1299	-2.2759	0.002	0.033	1.8468	2.00E-04	0.013	0.4458	0.0391	0.0681
250136_at	AT5G15380	DRM1 (DOMAINS REARRANGED METHYLASE 1	0.1012	0.8339	0.5336	-0.5749	0.2724	0.2768	0.4963	0.1362	0.1685	-0.1797	0.5373	0.3403
250137_at	AT5G15390	tRNA=RNA methyltransferase (SpoU) family protein	-0.2666	0.2017	0.2632	-0.6325	0.0224	0.0755	-0.1834	0.0345	0.076	-0.5493	7.00E-04	0.0107
250138_at	AT5G14610	ATP binding / ATP-dependent helicase	-0.1965	0.5049	0.2226	0.08861	0.758	0.4774	-1.1596	0.0125	0.0443	-0.8745	0.0312	0.0595
250139_at	AT5G14620	DRM2 (DOMAINS REARRANGED METHYLTRANS	0.4082	0.1271	0.206	0.6065	0.0462	0.1066	-0.4389	0.1078	0.1469	-0.2407	0.3206	0.2486
250140_at	AT5G14620	DRM2 (DOMAINS REARRANGED METHYLTRANS	0.1522	0.6991	0.4922	0.1123	0.7743	0.4819	-1.134	0.0364	0.0784	-1.1738	0.0328	0.0611
250141_at	AT5G14540	protein kinase family protein	-0.2871	0.1754	0.2451	-0.2684	0.1989	0.2323	-0.03045	0.8086	0.4662	-0.01176	0.9252	0.4643
250142_at	AT5G14650	polygalacturonase, putative / pectinase, putative	0.5002	0.5839	0.4539	0.4969	0.5864	0.4185	-0.2573	0.7749	0.4557	-0.2607	0.772	0.4206
250143_at	AT5G14670	ATARFA1B (ADP-RIBOSYLATION FACTOR A1B);	0.198	0.7097	0.4962	-0.751	0.2039	0.2354	1.4513	0.0428	0.0861	0.5023	0.3677	0.2703
250144_at	AT5G14680	universal stress protein (USP) family protein	0.1367	0.0496	0.128	0.1992	0.0154	0.0649	-0.2232	0.0105	0.0406	-0.1607	0.0307	0.059
250145_at	AT5G14690	similar to unknown protein [Arabidopsis thaliana] (T	0.8806	0.3761	0.3623	0.4121	0.6657	0.4469	0.2108	0.8234	0.4706	-0.2577	0.7854	0.4244
250146_at	AT5G14660	PDF1B (PEPTIDE DEFORMYLASE 1B); peptide de	-0.6682	0.0128	0.0698	-0.9429	0.0038	0.0388	0.01966	0.8216	0.4702	-0.2551	0.0355	0.0638
250147_at	AT5G14600	similar to unnamed protein product [Vitis vinifera] (C	-0.188	0.3356	0.2431	-0.4132	0.0741	0.1366	0.2286	0.2545	0.2434	0.00336	0.9853	0.4791
250148_at	AT5G14530	transducin family protein / WD-40 repeat family prot	0.3882	0.2045	0.2651	0.2681	0.3547	0.3203	-0.7007	0.0523	0.097	-0.8208	0.0329	0.0612
250149_at	AT5G14700	cinnamoyl-CoA reductase-related	-0.5868	0.0835	0.1672	-0.6683	0.0593	0.121	-0.2215	0.0153	0.0493	-0.303	0.0051	0.0224
250150_at	AT5G14710	similar to unnamed protein product [Vitis vinifera] (C	0.5495	0.7525	0.5091	0.1615	0.3323	0.3096	0.4456	0.0384	0.0809	0.5576	0.019	0.0442
250151_at	AT5G14570	ATNRT2.7 (ARABIDOPSIS THALIANA HIGH AFFI	-0.7817	0.0141	0.0725	-0.8105	0.0125	0.0598	-0.0571	0.7762	0.4562	-0.08589	0.6711	0.3878
250152_at	AT5G15120	similar to unknown protein [Arabidopsis thaliana] (T	1.4611	0.1518	0.2273	1.99	0.0737	0.1364	0.05999	0.9286	0.5002	0.5889	0.4021	0.2851
250153_at	AT5G15130	WRKY72 (WRKY DNA-binding protein 72); transcri	1.5157	0.0905	0.1743	-0.598	0.4304	0.3854	-0.7089	0.2213	0.2244	-2.8226	0.0045	0.0213
250154_at	AT5G15140	aldose 1-epimerase family protein	0.03098	0.977	0.5715	-1.1576	0.315	0.3003	1.7388	0.1201	0.1563	0.5503	0.5667	0.3515
250155_at	AT5G15160	bHLH family protein	0.4122	0.0493	0.1276	0.5647	0.0187	0.0706	0.4376	0.005	0.0298	0.5901	0.0016	0.0143
250156_at	AT5G15170	tyrosyl-DNA phosphodiesterase-related	0.06785	0.7935	0.522	0.06552	0.8004	0.4897	-0.3677	0.204	0.2142	-0.37	0.2017	0.1861
250157_at	AT5G15180	peroxidase, putative	-1.0477	0.3526	0.3511	-1.1869	0.2997	0.2912	-0.7135	0.481	0.3517	-0.8527	0.4061	0.2866
250158_at	AT5G15190	unknown protein	0.3241	0.3701	0.3596	0.5982	0.1361	0.1877	0.2963	0.272	0.2535	0.5704	0.0704	0.0972
250159_at	AT5G15200	40S ribosomal protein S9 (RPS9B)	0.07143	0.5831	0.4534	0.0513	0.6905	0.4658	-0.0501	0.6043	0.3996	-0.07022	0.4751	0.3157
250160_at	AT5G15210	ATHB30/ZFHD3 (ZINC FINGER HOMEODOMAIN	-0.273	0.3207	0.3348	0.1112	0.6685	0.4479	-0.2108	0.2283	0.2286	0.1733	0.3075	0.2422
250161_at	AT5G15240	amino acid transporter family protein	-1.1965	0.0012	0.036	-0.6717	0.0096	0.0536	-0.146	0.2832	0.2599	0.3788	0.0325	0.0608
250162_at	AT5G15250	ATFTSH6/FTSH6 (FtsH protease 6); ATP-depende	-0.5948	0.5261	0.4316	-0.2999	0.7442	0.4728	-0.7039	0.4578	0.3421	-0.4091	0.6582	0.3835
250163_at	no_match	no_match	0.4673	0.1744	0.2445	0.02656	0.9298	0.5266	-0.09612	0.7515	0.4486	-0.5368	0.131	0.1423
250164_at	AT5G15280	pentatricopeptide (PPR) repeat-containing protein	0.1857	0.5949	0.458	0.3962	0.2858	0.2842	-0.7703	0.0749	0.1192	-0.5598	0.157	0.1593
250165_at	AT5G15290	integral membrane family protein	-0.1766	0.5889	0.4559	0.1337	0.6798	0.4518	-0.4781	0.1873	0.2039	-0.1678	0.6068	0.3656
250166_at	AT5G15300	pentatricopeptide (PPR) repeat-containing protein	-0.851	0.3257	0.3377	0.1584	0.8451	0.5031	-0.3853	0.5025	0.3604	0.6241	0.299	0.2381
250167_at	AT5G15310	AtMIXTA/AtMYB16 (myb domain protein 16); DNA	-0.8226	0.0301	0.1007	-0.6612	0.0572	0.1189	0.2712	0.1078	0.147	0.4327	0.0301	0.0583
250168_at	AT5G15320	similar to unknown protein [Arabidopsis thaliana] (T	0.3001	0.3428	0.3463	-0.05703	0.848	0.5039	0.53	0.1242	0.1595	0.1729	0.561	0.3492
250169_at	AT5G15340	pentatricopeptide (PPR) repeat-containing protein	1.1961	0.2579	0.2983	1.1965	0.2577	0.2688	-0.5762	0.1245	0.1598	-0.5758	0.1247	0.1381
250170_at	AT5G14260	SET domain-containing protein	-0.3505	0.0019	0.0391	-0.3995	0.0011	0.0294	-0.6018	2.00E-04	0.0126	-0.6509	1.00E-04	0.0068
250171_at	AT5G14300	ATPHB5 (PROHIBITIN 5)	-0.6569	0.6076	0.4623	0.4666	0.7128	0.4831	-1.1102	0.4003	0.3167	0.01331	0.9915	0.4805
250172_at	AT5G14330	unknown protein	-1.5205	0.1669	0.2389	-0.2816	0.7703	0.4805	-0.5062	0.6043	0.3996	1.2959	0.2238	0.1982
250173_at	AT5G14340	AtMYB40 (myb domain protein 40); DNA binding / t	0.2643	0.8446	0.5371	-0.8729	0.5279	0.3953	-0.884	0.5229	0.3681	-2.0212	0.1851	0.1764
250174_at	AT5G14380	AGP6 (ARABINOGALACTAN PROTEIN 6)	0.1156	0.1683	0.2402	-0.06531	0.8419	0.502	-0.5803	0.1317	0.1651	-1.1612	0.0194	0.0447
250175_at	AT5G14390	similar to unknown protein [Arabidopsis thaliana] (T	0.328	0.2431	0.2895	0.6358	0.0569	0.1186	-0.7867	0.0268	0.0666	-0.4789	0.1059	0.1245
250176_at	AT5G14400	CYP724A1 (cytochrome P450, family 724, subfami	0.4762	0.5921	0.4568	0.235	0.7884	0.4857	1.0578	0.266	0.2498	0.8167	0.3751	0.2735
250177_at	AT5G14420	RGLG2 (RING DOMAIN LIGASE2); ubiquitin-protei	0.02181	0.8462	0.5374	-0.01316	0.9067	0.5206	0.006261	0.94	0.5034	-0.02871	0.7318	0.4077
250178_at	AT5G14430	dehydration-responsive protein-related	0.2854	0.0505	0.1292	0.2748	0.0562	0.1177	-0.6698	0.0017	0.0205	-0.6803	0.0016	0.0141
250179_at	AT5G14440	similar to surfeit locus protein 2 family protein / SUR	0.01983	0.9143	0.5552	-0.1156	0.5406	0.4009	0.4972	0.0453	0.0891	0.3618	0.1046	0.1238
250180_at	AT5G14450	GDSL-motif lipase/hydrolase family protein	0.07679	0.6958	0.4914	0.011	0.9549	0.5331	0.05432	0.6964	0.42	-0.01147	0.9265	0.4647
250181_at	AT5G14460	pseudouridylate synthase TruB family protein	-0.2474	0.1163	0.1972	-0.1199	0.3875	0.3356	-0.4312	0.0155	0.0495	-0.3038	0.0463	0.0757
250182_at	AT5G14470	GHMP kinase-related	0.6199	0.43	0.389	1.3494	0.1289	0.1821	-0.5487	0.481	0.3517	0.1809	0.8107	0.4319
250183_at	AT5G14510	armadillo/beta-catenin repeat family protein	-0.3062	0.0901	0.1737	-0.5658	0.0147	0.064	0.3588	0.0595	0.1047	0.0992	0.5108	0.3301
250184_at	AT5G14240	similar to unnamed protein product [Vitis vinifera] (C	0.219	0.2229	0.277	0.5295	0.0252	0.0794	-0.2395	0.1068	0.1464	0.07109	0.5715	0.3531
250185_at	AT5G14310	ATCXE16 (ARABIDOPSIS THALIANA CARBOXYE	0.5197	0.0487	0.1271	0.3895	0.1036	0.1625	0.1849	0.3753	0.3055	0.05464	0.783	0.4238
250186_at	AT5G14500	aldose 1-epimerase family protein	-0.6222	0.0186	0.0812	-0.1227	0.4921	0.3812	-0.3688	0.0532	0.098	0.1307	0.3903	0.2801
250187_at	AT5G14370	similar to CIL [Arabidopsis thaliana] (TAIR:AT4G25	-0.1693	0.2739	0.308	0.01298	0.9273	0.526	0.255	0.1291	0.1633	0.4373	0.0307	0.059
250188_at	AT5G14250	COP13 (CONSTITUTIVE PHOTOMORPHOGENIC	0.7622	0.0024	0.0421	0.5995	0.0058	0.044	0.01002	0.8903	0.4898	-0.1528	0.0887	0.1117
250189_at	AT5G14410	unknown protein	-0.4134	0.0982	0.181	-0.3415	0.1507	0.1988	0.3233	0.1683	0.1906	0.3952	0.1093	0.1272
250190_at	AT5G14320	30S ribosomal protein S13, chloroplast (CS13)	-0.4008	0.0082	0.0591	-0.57	0.0023	0.0334	0.3877	0.0092	0.0384	0.2185	0.0565	0.0853
250191_at	AT5G14270	ATBET9 (ARABIDOPSIS THALIANA BROMODOM	0.4472	0.0804	0.1637	0.8958	0.0096	0.0535	-0.4686	0.0712	0.116	-0.01997	0.9222	0.4636
250192_at	AT5G14520	descalllo-related	0.8855	0.0313	0.1027	0.5237	0.1288	0.1806	-0.5633	0.008	0.0358	-0.9251	0.0013	0.0131
250193_at	AT5G14540	proline-rich family protein	0.4594	0.0452	0.1225	0.3564	0.0895	0.1508	-0.1071	0.5392	0.375	-0.2101	0.2586	0.2172
250194_at	AT5G14550	similar to unknown protein [Arabidopsis thaliana] (T	0.6527	0.2177	0.2736	0.3121	0.5231	0.3933	-0.33	0.1347	0.1673	-0.6706	0.0191	0.0442
250195_at	AT5G14560	unknown protein	0.4696	0.7714	0.515	-1.5363	0.3666	0.3259	0.9306	0.5711	0.387	-1.0754	0.5158	0.332
250196_at	AT5G14580	polyribonucleotide nucleotidyltransferase, putative	0.2405	0.0385	0.1131	0.8139	0.363	0.3243	-0.2633	0.5929	0.3958	-1.8599	0.0149	0.0388
250197_at	AT5G14590	isocitrate dehydrogenase, putative / NADP+ isocitra	0.4852	0.0141	0.0725	0.3071	0.0578	0.1194	0.1455	0.2044	0.2144	-0.03253	0.7519	0.4144
250198_at	AT5G14100	ATNAP14 (Non-intrinsic ABC protein 14)	0.8503	0.0083	0.0595	-0.9527	0.0011	0.0293	-0.1979	0.1551	0.1824	-0.6003	0.0061	0.0241
250199_at	AT5G14180	MPL1 (MYZUS PERSICAE-INDUCED LIPASE 1); c	0.558	0.3121	0.3298	0.3007	0.5671	0.4108	-0.4836	0.1157	0.1529	-0.7408	0.0374	0.0659
250200_at	AT5G14130	peroxidase, putative	1.2537	0.2121	0.2697	0.5583	0.545	0.4025	0.5933	0.3345	0.2857	-0.1021	0.8595	0.4457
250201_at	AT5G14230	ankyrin repeat family protein	-0.5868	0.2445	0.2903	0.4973	0.3122	0.2986	-0.7607	0.1519	0.1802	0.3235	0.4942	0.3237
250202_at	AT5G13970	similar to unknown protein [Arabidopsis thaliana] (T	0.3484	0.0655	0.1468	0.5698	0.0146	0.0638	-0.00082	0.994	0.5163	0.2205	0.0985	0.1194
250203_at	AT5G13980	glycosyl hydrolase family 38 protein	0.3762	0.0445	0.1216	0.09096	0.5229	0.3933	-0.252	0.1247	0.1599	-0.5373	0.0145	0.0383
250204_at	AT5G13990	ATEXO70C2 (exocyst subunit EXO70 family protein	0.9027	0.2406	0.2879	-1.3711	0.1047	0.1634	1.5548	0.0602	0.1054	-0.719	0.2958	0.2365
250205_at	AT5G14020	similar to unknown protein [Arabidopsis thaliana] (T	0.9772	0.3611	0.3551	0.09974	0.9213	0.5243	-0.7777	0.4583	0.3423	-1.6552	0.1559	0.1588
250206_at	AT5G14040	mitochondrial phosphate transporter	0.1215	0.5973	0.4586	-0.1267	0.5824	0.4171	-0.04851	0.8258	0.4714	-0.2967	0.224	0.1983
250207_at	AT5G13930	ATCHS/CHS/TT4 (CHALCONE SYNTHASE); narin	-1.3497	0.0185	0.081	-1.3307	0.0194	0.0717	-0.2297	0.2054	0.2151	-0.2107	0.238	0.206
250208_at	AT5G14000	ANAC084 (ARABIDOPSIS NAC domain containing pro	-0.1265	0.9087	0.5536	0.2374	0.83	0.4988	-0.1965	0.8588	0.4806	0.1673	0.8795	0.4512
250209_at	AT5G14030	translocon-associated protein beta (TRAPB) family	0.4664	0.003	0.0436	0.1993	0.0516	0.1127	0.7516	6.00E-04	0.0158	0.4431	0.0036	0.0196
250210_at	AT5G13890	similar to unknown [Populus trichocarpa] (GB:ABK9	0.6542	0.0094	0.0623	0.5622	0.0157	0.0653	-0.1522	0.3363	0.2865	-0.2441	0.1548	0.1579
250211_at	AT5G13880	similar to unknown protein [Arabidopsis thaliana] (T	2.135	5.00E-04	0.0325	2.6474	2.00E-04	0.0249	0.04252	0.7995	0.4632	0.5548	0.024	0.0509
250212_at	AT5G13960	SUVH4 (SUVAR(3-9 HOMOLOG 4)	0.6438	0.0023	0.0417	0.6327	0.0025	0.0339	-0.1998	0.0977	0.139	-0.2009	0.0855	0.1094
250213_at	AT5G13820	TBP1 (TELOMERIC DNA BINDING PROTEIN 1); D	0.1776	0.4056	0.3781	0.5027	0.0583	0.1201	-0.223	0.3084	0.2727	0.102	0.6221	0.3709
250214_at	AT5G13870	EXGT-A4 (ENDOXYLOGLUCAN TRANSFERASE	-0.4565	0.234	0.2839	-0.2127	0.5497	0.4048	-1.2247	0.0198	0.0565	-0.9809	0.0396	0.0686
250215_at	AT5G14080	pentatricopeptide (PPR) repeat-containing protein	0.8481	0.0142	0.0727	0.7716	0.0194	0.0717	-0.657	0.0148	0.0485	-0.7336	0.0102	0.0315
250216_at	AT5G14090	similar to hypothetical protein [Vitis vinifera] (GB:CA	-0.1387	0.7969	0.5229	0.186	0.7309	0.4687	0.6773	0.0549	0.0998	1.002	0.0165	0.041
250217_at	AT5G14120	nodulin family protein	-0.4748	0.2063	0.2661	-0.3872	0.2864	0.2846	-0.4727	0.0063	0.0328	-0.3851	0.0128	0.0358
250218_at	AT5G14170	CHC1	0.2857	0.0462	0.1236	0.1468	0.1765	0.2174	-0.9072	0.0048	0.0293	-0.6161	0.0023	0.0161
250219_at	AT5G14180	MPL1 (MYZUS PERSICAE-INDUCED LIPASE 1); c	0.5732	0.4599	0.403	0.817	0.3091	0.2969	-0.831	0.2534	0.2428	-0.5871	0.3996	0.2841
250220_at	AT5G14210	leucine-rich repeat transmembrane protein kinase,	-0.5728	0.0101	0.064	-0.1572	0.2765	0.279	-0.4626	0.0208	0.058	-0.04696	0.7259	0.4059
250221_at	AT5G14220	HEMCGPAEE1 (maternal effect embryo arrest 61);	-0.6068	0.0719	0.1546	-0.3985	0.1285	0.1819	-0.1186	0.5

250290_at	AT5G13310	similar to unknown protein [Arabidopsis thaliana] (T	0.2373	0.1202	0.2005	-0.00224	0.986	0.5406	0.4974	0.0024	0.023	0.2578	0.024	0.0509
250291_at	AT5G13280	AK-LYS1 (ASPARTATE KINASE 1)	-0.111	0.5999	0.4583	-0.2833	0.2158	0.2433	-0.2947	0.0042	0.0279	-0.4671	8.00E-04	0.0108
250292_at	AT5G13220	JAS1/JAZ10/TIFY9 (JASMONATE-ZIM-DOMAIN P	-0.6374	0.3093	0.3281	-0.03765	0.9485	0.5316	0.213	0.5312	0.3718	0.8128	0.0593	0.0879
250293_s_at	AT5G13370;AT5G13360	[AT5G13370, auxin-responsive GH3 family protein]	0.4723	0.0827	0.1664	0.2893	0.2313	0.2524	-0.06698	0.657	0.4169	-0.25	0.1483	0.1535
250294_at	AT5G13380	auxin-responsive GH3 family protein	1.0528	0.1549	0.2298	0.7141	0.3008	0.2918	0.2223	0.7305	0.4419	-0.1165	0.8558	0.4446
250295_at	AT5G13390	NEF1 (NO EXINE FORMATION 1)	0.4133	0.0248	0.0915	0.07448	0.5621	0.4091	-0.09769	0.0935	0.1356	-0.4365	6.00E-04	0.0103
250296_at	AT5G12020	HSP17.6II (17.6 KDA CLASS II HEAT SHOCK PRO	0.2375	0.789	0.5203	0.6216	0.4957	0.3828	-0.3419	0.6607	0.4181	0.04215	0.9563	0.4725
250297_at	AT5G11980	conserved oligomeric Golgi complex component-rel	0.4623	0.0937	0.1772	0.212	0.3721	0.3284	0.2549	0.2143	0.2204	0.004559	0.9802	0.4782
250298_at	AT5G11860	NLI interacting factor (NIF) family protein	0.4047	0.0092	0.0618	0.2225	0.0604	0.1221	-0.02739	0.7655	0.4529	-0.2096	0.0709	0.0976
250299_at	AT5G11910	esterase/lipase/thioesterase family protein	0.7399	8.00E-04	0.0342	0.622	0.0016	0.0316	-0.1616	0.1177	0.1544	-0.2795	0.0263	0.0538
250300_at	AT5G11890	similar to unknown protein [Arabidopsis thaliana] (T	0.5693	0.0844	0.1682	0.5089	0.1107	0.168	-0.1115	0.5707	0.3869	-0.1719	0.3956	0.2825
250301_at	AT5G11970	similar to unknown protein [Arabidopsis thaliana] (T	0.3335	0.2402	0.2877	0.8638	0.0234	0.077	0.743	0.0071	0.0341	1.2733	0.001	0.0119
250302_at	AT5G11920	ATCWINV6 (6-&1-FRUCTAN EXOHYDROLASE); h	2.6048	4.00E-04	0.032	2.4216	6.00E-04	0.0265	0.1678	0.5258	0.3694	-0.0155	0.9519	0.4715
250303_at	AT5G12100	pentatricopeptide (PPR) repeat-containing protein	0.4733	0.3424	0.3461	0.6978	0.1877	0.225	-0.5383	0.2881	0.2626	-0.3138	0.515	0.3316
250304_at	AT5G12110	elongation factor 1B alpha-subunit 1 (eEF1Balpha1	-0.873	0.0367	0.1105	-0.7543	0.0561	0.1177	0.2782	0.0478	0.0918	0.3969	0.0158	0.0401
250305_at	AT5G12150	pleckstrin homology (PH) domain-containing protein	-0.4025	0.0193	0.0823	-0.9845	8.00E-04	0.0276	0.3049	0.0272	0.0671	-0.2771	0.0365	0.065
250306_at	AT5G12170	conserved oligomeric Golgi complex component-rel	-0.456	0.1892	0.2548	-0.05437	0.8597	0.5071	-0.5766	0.1119	0.1497	-0.1749	0.5709	0.3529
250307_at	AT5G12170	similar to unknown protein [Arabidopsis thaliana] (T	0.0965	0.627	0.4687	-0.5145	0.0487	0.1096	0.2995	0.0619	0.1069	-0.3116	0.0555	0.0844
250308_at	AT5G12180	CPK17 (calcium-dependent protein kinase 17); calm	0.09374	0.9216	0.5574	-0.2453	0.0661	0.1286	1.5608	0.1559	0.1829	-0.7782	0.4334	0.2982
250309_at	AT5G12220	tas1-like family protein	0.752	0.0187	0.0813	0.3587	0.1422	0.1923	0.08065	0.7027	0.4322	-0.3126	0.1871	0.1777
250310_at	AT5G12230	similar to unknown protein [Arabidopsis thaliana] (T	0.09773	0.4881	0.4151	0.1808	0.231	0.2522	-0.6409	0.0023	0.0227	-0.5578	0.0039	0.0202
250311_at	AT5G12240	similar to unknown protein [Oryza sativa (japonica c	-0.06683	0.9095	0.5538	-0.3128	0.6012	0.424	-0.1932	0.5573	0.3818	-0.4392	0.2196	0.1959
250312_at	AT5G12260	similar to glycosyltransferase family protein 2 [Arabi	-0.1677	0.2252	0.2787	0.1575	0.2497	0.2636	-0.4955	0.0133	0.046	-0.1703	0.2195	0.1959
250313_at	AT5G12210	geranylgeranyl transferase type II beta subunit, put	1.2062	0.0137	0.0719	1.0287	0.0231	0.0768	-0.8553	0.0408	0.0839	-1.0328	0.0228	0.0492
250314_at	AT5G12190	RNA recognition motif (RRM)-containing protein	0.7432	0.0093	0.0621	0.6389	0.0158	0.0653	1.2102	0.0016	0.0202	1.1029	0.0022	0.0157
250315_at	AT5G12130	PDE149 (PIGMENT DEFECTIVE 149)	-0.4685	0.0319	0.1035	-0.5766	0.0164	0.0666	-0.4223	0.0435	0.087	-0.5304	0.0216	0.0478
250316_at	AT5G12140	ATCYS1 (A. THALIANA CYSTATIN-1); cysteine pro	-0.3397	0.1671	0.2391	0.4835	0.0744	0.1368	0.8432	0.0097	0.0392	1.6664	8.00E-04	0.0109
250317_at	AT5G12250	TUB6 (BETA-6 TUBULIN)	-0.7051	0.0089	0.061	-0.6044	0.0151	0.0646	-0.06703	0.6743	0.4224	0.03369	0.8312	0.4375
250318_at	AT5G12200	dihydropyrimidinase / DHPase / dihydropyrimidine p	0.5945	0.0364	0.1099	0.6393	0.0291	0.0849	-0.05641	0.6512	0.415	-0.01162	0.9248	0.4641
250319_at	AT5G12120	ubiquitin-associated (UBA)/TS-N domain-containing	0.3572	0.0352	0.1084	0.3964	0.0255	0.08	-0.1716	0.1063	0.1459	-0.1324	0.1843	0.176
250320_at	AT5G12240	HAP2A (EMBRYO DEFECTIVE 2272); transcription	0.1644	0.174	0.2442	0.223	0.3886	0.15	-0.2673	0.0403	0.0832	0.12	0.2504	0.2128
250321_at	AT5G12850	zinc finger (CCCH-type) family protein	-0.1335	0.594	0.4575	-0.2464	0.3457	0.3159	-0.1991	0.2704	0.2525	-0.312	0.1157	0.1317
250322_at	AT5G12870	AtMYB46/MYB46 (myb domain protein 46); DNA bi	1.164	0.1823	0.25	1.0441	0.2218	0.247	0.7053	0.0134	0.046	0.5854	0.0246	0.0516
250323_at	AT5G12880	proline-rich family protein	0.0735	0.013	0.0703	0.3353	0.0761	0.2637	0.2664	0.612	0.4098	0.1166	0.1263	0.6424
250324_at	AT5G12040	carbon-nitrogen hydrolase family protein	0.3864	0.0358	0.1093	0.1641	0.2569	0.2683	0.2556	0.0891	0.1319	0.0332	0.786	0.4246
250325_s_at	AT5G12060;AT5G12070	[AT5G12060, self-incompatibility protein-related] [A	-0.5359	0.5268	0.4318	-0.6532	0.4462	0.3623	-1.8547	0.0747	0.119	-1.972	0.0635	0.0916
250326_at	AT5G12080	mechanosensitive ion channel domain-containing p	0.1824	0.2859	0.148	0.04929	0.7562	0.477	-0.12	0.4637	0.3448	-0.2531	0.163	0.1631
250327_at	AT5G12050	similar to unnamed protein product [Vitis vinifera] (G	-1.942	2.00E-04	0.0312	-1.9702	2.00E-04	0.0249	0.1532	0.3011	0.2693	0.125	0.3879	0.2791
250328_at	AT5G11780	similar to hypothetical protein [Vitis vinifera] (GB:CA	-0.00092	0.999	0.5763	-0.3088	0.6633	0.446	-0.08151	0.8925	0.4904	-0.3894	0.5295	0.3378
250329_at	AT5G11800	KEAE (K+ efflux antiporter 6); potassium:hydrogen	0.1133	0.7095	0.4961	-0.3467	0.288	0.2854	-0.6995	0.0804	0.124	-1.1195	0.0168	0.0414
250330_at	AT5G11810	similar to Os02g0135600 [Oryza sativa (japonica cu	0.282	0.1645	0.2372	0.1262	0.4191	0.3503	0.4129	0.004	0.0274	0.3008	0.0124	0.0353
250331_at	AT5G11820	similar to unknown protein [Arabidopsis thaliana] (T	-0.8867	0.336	0.3433	-2.1146	0.0597	0.1214	2.7348	0.0136	0.0465	1.507	0.0814	0.1061
250332_at	AT5G11680	similar to hypothetical protein Os_031621 [Oryza s	0.2902	0.2001	0.2622	0.3502	0.138	0.1892	0.4018	0.0405	0.0834	0.4618	0.0265	0.0539
250333_at	AT5G11690	ATTIM17-3 (Arabidopsis thaliana translocase inner	-0.5257	0.0377	0.112	-0.3432	0.1165	0.1724	0.2851	0.1298	0.1637	0.4675	0.0355	0.0638
250334_at	AT5G11770	NADH-ubiquinone oxidoreductase 20 kDa subunit,	0.09873	0.5147	0.4271	0.0395	0.7893	0.4859	0.09715	0.5211	0.3675	0.03792	0.7975	0.4281
250335_at	AT5G11650	hydrolase, alpha/beta fold family protein	-0.6847	0.0385	0.1131	-0.6261	0.0499	0.1108	-0.2207	0.2646	0.2491	-0.1615	0.3954	0.2825
250336_at	AT5G11720	alpha-glucosidase 1 (AGLU1)	0.1957	0.4187	0.3842	0.3156	0.2201	0.2459	-0.6009	0.0392	0.0818	-0.4811	0.0729	0.0991
250337_at	AT5G11790	Ndr family protein	-1.2115	0.0069	0.0558	-1.5987	0.0025	0.034	0.3048	0.2667	0.2501	-0.0824	0.745	0.4119
250338_at	AT5G11760	similar to hypothetical protein [Oryza sativa (japonic	0.3499	0.0281	0.097	0.4593	0.0115	0.0578	0.5175	0.0076	0.0352	0.6269	0.0038	0.02
250339_at	AT5G11670	ATNADP-ME2 (NADP-MALIC ENZYME 2); malate	0.5939	0.076	0.1585	0.5796	0.0809	0.1426	0.08718	0.5744	0.3883	0.07287	0.6366	0.3759
250340_at	AT5G11840	similar to unknown protein [Arabidopsis thaliana] (T	-0.03031	0.91	0.554	-0.4242	0.1673	0.2108	0.3176	0.0673	0.1123	-0.07631	0.5815	0.3566
250341_at	AT5G11850	protein kinase family protein	0.288	0.3829	0.3662	0.3537	0.2954	0.2894	-0.9743	0.0296	0.07	-0.9086	0.0366	0.0651
250342_at	AT5G11870	similar to SAG18 (SENESCENCE ASSOCIATED G	2.2158	0.1253	0.2049	-0.7668	0.5401	0.4007	1.2258	0.345	0.2908	-1.7568	0.2001	0.1851
250343_at	AT5G11900	initiation factor SUI1 family protein	0.3377	0.0625	0.1435	0.4076	0.0365	0.0943	0.5438	0.0145	0.0481	0.6137	0.0096	0.0305
250344_at	AT5G11930	glutaredoxin family protein	-0.03297	0.9428	0.5631	-0.1953	0.6743	0.45	1.0769	0.0026	0.0235	0.9146	0.0048	0.0218
250345_at	AT5G11940	subtilase family protein	1.848	0.107	0.1892	-0.5097	0.5983	0.4227	1.1086	0.1965	0.2095	-1.2491	0.156	0.1589
250346_at	AT5G11950	Encodes a protein of unknown function. It has been	0.2153	0.1244	0.2043	0.03164	0.7898	0.486	0.6384	7.00E-04	0.016	0.4547	0.0026	0.0169
250347_at	AT5G11960	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.2743	0.0393	0.1145	0.1989	0.0941	0.1545	-0.4711	7.00E-04	0.0159	-0.9465	5.00E-04	0.0094
250348_at	AT5G11990	proline-rich family protein	-0.2164	0.7985	0.5235	-0.1803	0.8314	0.4993	1.4745	0.1366	0.1688	1.5106	0.1296	0.1412
250349_at	AT5G12000	kinase	-0.2554	0.7209	0.4997	-0.6958	0.3552	0.3205	0.5779	0.4346	0.3317	0.1376	0.8465	0.4418
250350_at	AT5G12010	similar to unknown protein [Arabidopsis thaliana] (T	-0.3911	0.1576	0.2313	-0.1021	0.674	0.4499	-0.3497	0.1575	0.184	-0.06068	0.7782	0.4224
250351_at	AT5G12030	AT-HSP17.6A (Arabidopsis thaliana heat shock pro	1.0303	0.0495	0.1278	2.7808	0.0017	0.032	-0.1858	0.5309	0.3717	1.5646	0.0045	0.0212
250352_at	AT5G11490	adaptin family protein	0.2987	0.1218	0.2022	0.1487	0.3849	0.3341	-0.5884	0.0182	0.054	-0.7385	0.0084	0.0285
250353_at	AT5G11500	similar to unknown protein [Arabidopsis thaliana] (T	-0.02365	0.8862	0.5474	0.215	0.2381	0.2566	0.1593	0.3626	0.2994	0.3979	0.0623	0.0906
250354_at	AT5G11640	similar to unnamed protein product [Vitis vinifera] (G	-0.1829	0.3835	0.3665	0.1843	0.3803	0.3321	-0.6393	0.0268	0.0666	-0.2721	0.2195	0.1959
250355_at	AT5G11700	glycine-rich protein	-0.2039	0.4684	0.4065	-0.1445	0.6011	0.424	-1.0402	0.0151	0.0489	-0.9807	0.0183	0.0435
250356_at	AT5G11710	(EPSIN1); binds	-0.02318	0.8714	0.5443	0.1521	0.3206	0.3035	-0.03292	0.7844	0.4586	0.1424	0.2745	0.2252
250357_at	AT5G11730	similar to unknown protein [Arabidopsis thaliana] (T	0.4678	0.0029	0.0435	0.5281	0.0019	0.0329	-0.2113	0.0343	0.0757	-0.151	0.087	0.1104
250358_at	AT5G11740	AGP15 (ARABINOGALACTAN PROTEIN 15)	-0.4164	0.1166	0.1973	-0.4553	0.0945	0.1548	0.3753	0.0028	0.0243	0.3364	0.0042	0.0208
250359_at	AT5G11650	endonuclease/exonuclease/phosphatase family pro	0.4011	0.0503	0.129	0.4144	0.0458	0.106	-0.4096	0.0473	0.0913	-0.3963	0.052	0.0813
250360_at	AT5G11360	ATP binding / protein kinase	0.7644	0.3923	0.3712	2.4319	0.0381	0.0966	-2.2118	0.0502	0.0949	-0.5443	0.5326	0.3389
250361_at	AT5G11370	similar to F-box family protein [Arabidopsis thaliana	-0.6898	0.1894	0.255	-1.3606	0.0357	0.0931	0.7863	0.0504	0.095	0.1154	0.7052	0.3993
250362_at	AT5G11380	DXPS3 (1-DEOXY-D-XYLULOSE 5-PHOSPHATE	-0.08912	0.5518	0.4419	-0.5601	0.0151	0.0646	-0.08686	0.5615	0.3831	-0.5578	0.0153	0.0395
250363_at	AT5G11390	similar to unknown protein [Arabidopsis thaliana] (T	1.2118	0.0093	0.0621	1.0867	0.0135	0.0617	0.03518	0.8283	0.4721	-0.08985	0.5861	0.3584
250364_at	AT5G11400	protein kinase-related	0.2611	0.7133	0.4972	0.07837	0.9114	0.5219	-0.6917	0.3549	0.2957	-0.8745	0.2569	0.2162
250365_at	AT5G11410	protein kinase family protein	1.6559	0.0163	0.0771	1.9753	0.0089	0.0518	0.1432	0.4095	0.3206	0.4626	0.0411	0.0702
250366_at	AT5G11420	similar to unknown protein [Arabidopsis thaliana] (T	-0.2741	0.0671	0.1488	-0.4777	0.0122	0.0591	0.405	0.0069	0.0338	0.2014	0.0635	0.0916
250367_s_at	AT5G11170;AT5G11200	[AT5G11170, DEAD/DEAH box helicase, putative (	0.841	0.0047	0.0493	0.3392	0.0829	0.1447	0.01227	0.8195	0.4697	-0.4896	6.00E-04	0.0103
250368_at	AT5G11280	similar to unknown protein [Arabidopsis thaliana] (T	0.4237	0.1039	0.1862	0.2681	0.255	0.2673	0.04039	0.7612	0.4515	-0.1152	0.406	0.2866
250369_at	AT5G11300	CYC3B (MITOTIC-LIKE CYCLIN 3B FROM ARABI	1.6312	0.0735	0.1561	0.2243	0.7569	0.4773	-0.4944	0.4039	0.3181	-1.9013	0.023	0.0495
250370_at	AT5G11430	elongation factor-related	0.3174	0.4522	0.3992	-0.6146	0.1825	0.2215	0.1211	0.6496	0.4144	-0.8108	0.0304	0.0587
250371_at	AT5G11450	oxygen-evolving complex-related	-0.6035	0.0159	0.0763	-0.6802	0.0106	0.0556	-0.2931	0.1229	0.1586	-0.3699	0.0696	0.0966
250372_at	AT5G11460	senescence-associated protein-related	-0.0307	0.9315	0.5602	0.2074	0.5701	0.4119	-0.9883	0.0422	0.0856	-0.7502	0.0891	0.1121
250373_at	AT5G11470	bromo-adjacent homology (BAH) domain-containing	-0.1865	0.6687	0.4822	-0.9307	0.0828	0.1446	-0.02776	0.9486	0.5053	-0.772	0.129	0.1408
250374_at	AT5G11530	EMF1 (EMBRYONIC FLOWER 1)	0.1887	0.3446	0.3472	0.7265	0.0146	0.0637	-0.3477	0.1197	0.156	0.1902	0.3411	0.2585
250375_at	AT5G11540	FAD-binding domain-containing protein	-0.8184	0.3129	0.3303	-1.0527	0.212	0.2409	0.4684	0.5452	0.3774	0.2341	0.758	0.4161
250376_at	AT5G11550	binding	0.4581	0.3084	0.3277	0.4255	0.3397	0.3133	0.2148	0.2078	0.2165	0.1822	0.2719	0.2238
250377_at	AT5G11560	catalytic	0.701	7.00E-04	0.0334	0.2984	0.0164	0.0665	0.5078	0.0025	0.0232	0.1063	0.2303	0.2017
250378_at	AT5G11570	proton-dependent oligopeptide transport (POT) fam	-0.2978	0.6382	0.4724	-2.3595	0.0158	0.0654	1.9965	0.0271	0.067	-0.6608	0.3226	0.2495
250379_at	AT5G11590	TINY2 (TINY2); DNA binding / transcription factor	-1.1767	0.0346	0.1075	0.1119	0.7797	0.4834	-0.01249	0.975	0.5113	1.2761	0.0269	0.0546
250380_at	AT5G11600	similar to unknown protein [Arabidopsis thaliana] (T	0.6497	0.0848	0.1687	0.4795	0.1678	0.211	0.2934	0.2811	0.2587	0.1232	0.6286	0.3733
250381_at	AT5G11610	exostosin family protein	0.7586	0.1285	0.2071	0.6683	0.1675	0.2109	-0.2564	0.3031	0.2701	-0.3467	0.1856	0.1767
250382_at	AT5G11580	UVB-resistance protein-related / regulator of chrom	0.3899	0.0594	0.1394	0.264	0.1519	0.1997	-1.1881	0.0011	0.0183	-1.3141	8.00E-04	0.0108
250383_at	AT5G11483	GTP binding	0.2163	0.1557	0.2302	-0.3056	0.0691	0.1319	0.3614	0.0042	0.0279	0.2721	0.0116	0.0338
250384_at	AT5G11500	similar to unknown [Brassica juncea] (GB:ABX1074	0.4535	0.0317	0.1031	0.5689	0.0153	0.0649	-0.6287	0.0109	0.0414	-0.5133	0.0215	0.0476
250385_at	AT5G11520	ASP3 (ASPARTATE AMINOTRANSFERASE 3)	0.4285	0.0675	0.1492	0.3827	0.0903	0.1516	0.129	0.4022	0.3175	0.08319	0.5786	0.3555
250386_at	AT5G11510	MYB3R-4 (C-MYB-LIKE TRANSCRIPTION FACTO	0.6096	0.2749	0.3085	-0.5716	0.2292	0.2511	0.1861	0.6684	0.4207	0.124	0.7737	0.4212
250387_at	AT5G11290	similar to unknown protein [Arabidopsis thaliana] (T	0.1698	0.8804	0.5465	-0.6813	0.5553	0.4068	-1.145	0.3407	0.2886	-1.9962	0.1327	0.1435
250388_at	AT5G11310	pentatricopeptide (PPR) repeat-containing protein	2.0174	0.0734	0.156	0.1131	0.8989	0.5186	-0.04466	0.96	0.5076	-1.9489	0.0802	0.1053
250389_at	AT5G11320	YUC4 (YUCCA4); monooxygenase	-0.5028	0.6269	0.4687	-1.8242	0.1292	0.1823	0.8381	0.4304	0.3298	-0.4832	0.64	0.3772
250390_at	AT5G11340	GCN5-related N-acetyltransferase (GNAT) family pr	0.4138	0.0178	0.0799	0.4307	0.0156	0.0652	-0.1052	0.3795	0.3075	-0.08828	0.4539	0.3075
250391_at	AT5G10850	transposable element gene	-0.9225	0.5441	0.4386	-1.2105	0.434	0.357	-0.1256	0.9325	0.5014	-0.4136	0.7814	0.4233
250392_at	AT5G10880	RNA synthetase-related / RNA ligase-related	-0.4932	0.573	0.4501	-0.3481	0.6875	0.4547	-0.9752	0.2921	0.2647	-0.8301	0.3604	0.2672
250393_at	AT5G10900	calcineurin-like phosphoesterase family protein	-0.5167	0.1563	0.2305	-0.4069	0.2418	0.2589	-0.1258	0.6931	0.4287	-0.01601	0.9595	0.4732
250394_at	AT5G10910	mraW methylase family protein	0.0485	0.7266	0.5014	-0.05224	0.7069	0.4612	-0.0301	0.8274	0.472	-0.1308	0.3688	0.2707
250395_at	AT5G10950	cylicin-related	-0.06464	0.7011	0.4929	0.04068	0.808	0.4923	-0.98	0.0021	0.0218	-0.8747	0.0033	0.0186
250396_at	AT5G10970	zinc finger (C2H2 type) family protein	-0.2921	0.5864	0.4549	-1.0864	0.093	0.1538	0.7827	0.1886	0.2047	-0.01153	0.9825	0.4786
250397_at	AT5G10980	histone H3	-0.01769	0.8787	0.5462	0.1529	0.2327	0.2533	0.5879	0.0057	0.0314	0.7585	0.0022	0.0158
250398_at	AT5G11000	similar to unknown protein [Arabidopsis thaliana] (T	0.06406	0.8526	0.5389	0.2439	0.4927	0.3815	-0.3307	0.058	0.103	-0.1509	0.2958	0.2365
250399_at	AT5G10750	similar to unknown protein [Arabidopsis thaliana] (T	0.03697	0.7951	0.5224	-0.02509	0.8598	0.5071	0.1215	0.3859	0.3104	0.05941	0.6591	0.3838
250400_at	AT5G10740	protein phosphatase 2C-related / PP2C-related	1.3002	0.0019	0.0391	0.8154	0.0104	0.0552	0.2658	0.2118	0.2191	-0.219	0.2885	0.2326
250401_at	AT5G10760	disease resistance protein (TIR-NBS-LRR class), p	0.7087	0.0042	0.047	0.9346	0.0015	0.0314	-0.0703	0.5911	0.3951	0.1557	0.2662	0.2209
250402_at	AT5G10940	transducin family protein / WD-40 repeat family prot	0.1371	0.2268	0.2797	0.1638	0.1634	0.2083	-0.6203	0.0017	0.0205	-0.5936	0.002	0.0151
250403_at	AT5G10920	argininosuccinate lyase, putative / arginosuccinase,	0.09776	0.6877	0.4885	-0.02081	0.9311	0.5268	-0.1105	0.522	0.3678	-0.229	0.2199	0.196
250404_at	AT5G10960	CCR4-NOT transcription complex protein, putative	0.1367	0.1414	0.2186	0.2627	0.0246	0.0787	-0.29	0.0169	0.0519	-0.164	0.0896	0.1125
250405_at	AT5G10790	UBP22 (UBIQUITIN-SPECIFIC PROTEASE 22); ub	0.2563	0.1183	0.1989	0.648	0.0074	0.0485	-0.3096	0.0747	0.119	0.08218	0.5593	0.3486
250406_at	AT5G10810	ATER (Arabidopsis thaliana enhancer of rudimentar	0.4325	0.0338	0.1063	0.4527	0.0294	0.0852	0.647	0.009	0.038	0.6672	0.008	0.028
250407_at	AT5G10870	ATCM2 (CHORISMATE MUTASE 2); chorismate m	0.3698	0.3138	0.3308	0.594	0.1382	0.1893	0.1496	0.5439	0.3769	0.3737	0.1733	0.1692
250408_at	AT5G10930	CIPK5 (CBL-INTERACTING PROTEIN KINASE 5);	0.3307	0.479	0.4115	0.3946	0.4048	0.3434	-0.2568	0.0079	0.0357	-0.1929	0.0207	0.0466
250409_at	AT5G10800	CBS domain-containing protein	0.6643	0.0035	0.0402	0.7721	0.002	0.033	-0.3662	0.0162	0.0508	-0.2873	0.0439	0.0734
250410_at	AT5G11010	pre-mRNA cleavage complex-related	-0.1021	0.699	0.4922	-0.09412	0.721	0.4658	-0.7023	0.0037	0.0267	-0.6944	0.0038	0.02
250411_at	AT5G11120	unknown protein	-2.2608	0.0605	0.141	1.6092	0.1388	0.1898	-2.0699	0.0766	0.1208	1.8001	0.108	0.1261
250412_at	AT5G11130	ATVAM3 (Arabidopsis thaliana vesicle-associat	-0.376	0.3863	0.3461	-0.3611	0.4036	0.3429	0.2668	0.213	0.2197	0.2818	0.1931	0.1809
250413_at	AT5G11160	APT5 (ADENINE PHOSPHORIBOSYLTRANSFER	-1.2207	0.037	0.1108	-0.8936	0.0873	0.1488	0.05826	0.8668	0.4832	0.3854	0.3025	0.2399
250414_at	AT5G11180	ATGLR2.6 (Arabidopsis thaliana glutamate recepto	-0.5019	0.4246	0.387	0.247	0.6846	0.4538	0.1543	0.7983	0.4628	0.9032	0.1852	0.1765
250415_at	AT5G11210	ATGLR2.5 (Arabidopsis thaliana glutamate recepto	2.1106	0.1542	0.2293	1.8289	0.2031	0.2348	-0.5746	0.4793	0.3511	-0.8562	0.31	0.2434
250416_at	AT5G11220	similar to unknown protein [Arabidopsis thaliana] (T	0.2356	0.7388	0.5053	-0.1713	0.8077	0.4922	0.2959	0.6328	0.4087	-0.1111	0.8557	0.4446
250417_at	AT5G11230	phosphate translocator-related	-0.2304	0.2789	0.3107	-0.3026	0.1756	0.2166	-0.1942	0.3509	0.2938	-0.2664	0.2214	0.1968
250418_at	AT5G11240	transducin family protein / WD-40 repeat family prot	0.8863	0.0297	0.1001	0.5189	0.1249	0.1792	-0.2083	0.3686	0.3023	-0.5757	0.0489	0.0783
250419_at	AT5G11250	disease resistance protein (TIR-NBS-LRR class), p	-0.2381	0.351	0.3501	0.3627	0.1833	0.222	-1.2182	0.0057	0.0315	-0.6174	0.0521	0.0814
250420_at	AT5G11260	HY5 (ELONGATED HYPOCOTYL 5); DNA binding	-0.4699	0.2423	0.2889	-0.03286	0.9282	0.5263	-0.1991	0.4434	0.3355	0.2379	0.3673	0.2701
250421_at	AT5G11270	OCP3 (OVEREXPRESSER OF CATIONIC PEROX	-0.3649	0.1207	0.2009	-0.4219	0.0854	0.1471	0.003479	0.9761	0.5116	-0.05351	0.6498	0.3808
250422_at	AT5G10840	endomembrane protein 70, putative	0.

250490_at	AT5G09760	pectinesterase family protein	-1.201	0.0017	0.0391	-1.0369	0.003	0.0357	0.3317	0.1088	0.1476	0.4958	0.0371	0.0657
250491_at	AT5G09780	transcriptional factor B3 family protein	0.06165	0.899	0.5508	0.3793	0.4525	0.365	0.2083	0.6417	0.4215	0.526	0.3132	0.245
250492_at	AT5G09790	ATXR5 (SETDOMAIN GROUP 15); DNA binding	0.9865	0.079	0.1619	0.2603	0.5697	0.4117	0.118	0.7931	0.4611	-0.6082	0.222	0.197
250493_at	AT5G09800	U-box domain-containing protein	0.01036	0.9758	0.5712	-0.1336	0.6988	0.4585	0.1351	0.6956	0.4296	-0.00885	0.9793	0.478
250494_at	AT5G09740	HAM2 (HISTONE ACETYLTRANSFERASE OF TH	-0.0606	0.696	0.4914	0.08525	0.5863	0.4185	0.1498	0.3577	0.2968	0.2956	0.1097	0.1275
250495_at	AT5G09770	ribosomal protein L17 family protein	0.6084	0.0032	0.0442	0.5988	0.0034	0.0371	-0.1662	0.1582	0.1845	-0.1758	0.1408	0.1487
250496_at	AT5G09650	ATPPA6 (ARABIDOPSIS THALIANA PYROPHOSF	-1.043	0.0012	0.036	-0.9714	0.0016	0.0316	-0.119	0.2095	0.2175	-0.04747	0.5833	0.3574
250497_at	AT5G09930	protein binding / zinc ion binding	0.4771	0.0498	0.1282	1.4165	0.0012	0.0296	-0.279	0.1792	0.198	0.6603	0.0183	0.0435
250498_at	AT5G09660	PMDH2 (PEROXISOMAL NAD-MALATE DEHYDR	-0.4277	0.0028	0.0431	-0.6949	4.00E-04	0.0251	0.0215	0.4458	0.3366	-0.2458	6.00E-04	0.0104
250499_at	AT5G09730	BXL3 (BETA-XYLOSIDASE 3); hydrolase, hydrolyz	-0.198	0.5082	0.4244	-0.3258	0.2984	0.2908	-0.2186	0.4679	0.3466	-0.3464	0.2731	0.2245
250500_at	AT5G09530	hydroxyproline-rich glycoprotein family protein	0.6407	0.2722	0.3067	1.1567	0.0832	0.145	-0.3338	0.2409	0.2356	0.1823	0.4943	0.3237
250501_at	AT5G09640	SNG2 (SINAPOYLGLUCOSE ACCUMULATOR 2);	-0.3591	0.7029	0.4935	-0.0741	0.9367	0.5283	0.3377	0.7195	0.4383	0.6227	0.5165	0.3322
250502_at	AT5G09590	mtHSC70-2 (HEAT SHOCK PROTEIN 70); ATP bir	0.8225	0.0301	0.1007	0.5009	0.1152	0.1713	-0.1513	0.4351	0.3319	-0.4729	0.0537	0.0828
250503_at	AT5G09820	plastid-lipid associated protein PAP / fibrillin family p	0.6622	0.0059	0.0534	-0.4564	0.0211	0.074	-0.9213	0.0017	0.0206	-0.7155	0.0045	0.0212
250504_at	AT5G09840	similar to unknown protein [Arabidopsis thaliana] (T	1.4589	0.147	0.223	-0.2485	0.775	0.4821	-0.3103	0.7219	0.4392	-2.0177	0.068	0.0952
250505_at	AT5G09870	CESA5 (CELLULOSE SYNTHASE 5); transferase,	-1.4587	0.0076	0.0579	-1.3291	0.0105	0.0554	-0.433	0.109	0.1477	-0.3034	0.2232	0.1978
250506_at	AT5G09930	protein binding / zinc ion binding	0.4771	0.0498	0.1282	1.4165	0.0012	0.0296	-0.279	0.1792	0.198	0.6603	0.0183	0.0435
250507_at	AT5G09940	similar to unknown protein [Arabidopsis thaliana] (T	0.9373	0.1406	0.2182	0.1181	0.8286	0.4985	1.4215	0.0498	0.0943	0.6023	0.304	0.2407
250508_at	AT5G09950	pentaticopeptide (PPR) repeat-containing protein	-0.8849	0.4133	0.3817	1.2012	0.2834	0.2827	0.07121	0.945	0.5045	2.1573	0.0902	0.113
250509_at	AT5G09970	CYP78A7 (cytochrome P450, family 78, subfamily A	1.4875	0.2314	0.283	-0.3851	0.7336	0.4693	1.5443	0.2172	0.2219	-0.3282	0.7713	0.4203
250510_at	AT5G09920	RPB15.9 (RNA polymerase II 15.9)	-0.09192	0.6888	0.4887	0.3381	0.1882	0.2254	0.44	0.069	0.1139	0.8701	0.0081	0.028
250511_at	AT5G09960	similar to unknown protein [Arabidopsis thaliana] (T	0.1072	0.4386	0.393	0.365	0.043	0.103	0.7598	7.00E-04	0.016	1.0176	2.00E-04	0.0078
250512_at	AT5G09995	similar to unknown protein [Arabidopsis thaliana] (T	-0.4726	0.0722	0.1549	-0.4538	0.0802	0.142	0.03591	0.8446	0.477	0.05467	0.7662	0.4187
250513_at	AT5G09890	protein kinase, putative	0.3038	0.2195	0.2748	0.1036	0.6459	0.4402	-0.7082	0.0219	0.0598	-0.9083	0.0095	0.0304
250514_at	AT5G09550	RAB GDP-dissociation inhibitor	0.8409	0.0618	0.1427	-0.3776	0.3123	0.2686	0.2754	0.4469	0.337	-0.9431	0.0448	0.0742
250515_at	AT5G09570	similar to unknown protein [Arabidopsis thaliana] (T	-0.2403	0.5074	0.4241	-0.1846	0.6062	0.4256	0.01078	0.9723	0.5106	0.06646	0.8309	0.4374
250516_at	AT5G09620	octicosapeptide/Phox/Bem1p (PB1) domain-contair	0.5124	0.0274	0.0959	0.6784	0.0109	0.056	0.146	0.2005	0.212	0.3119	0.0307	0.059
250517_at	AT5G09260	SCPL35 (serine carboxypeptidase-like 35); serine c	0.3378	0.3485	0.3491	0.0314	0.9268	0.5259	-0.1587	0.6443	0.4124	-0.4654	0.2176	0.1949
250518_at	AT5G08139	zinc finger (C3HC4-type RING finger) family protein	0.3001	0.1773	0.2463	0.0091	0.9628	0.5347	0.1744	0.3957	0.3146	-0.1166	0.5598	0.3487
250519_at	AT5G08460	GDSL-motif lipase/hydrolase family protein	-0.6873	0.3704	0.3597	-2.0744	0.0383	0.0969	0.09335	0.8977	0.4917	-1.2938	0.1305	0.1419
250520_at	AT5G08470	PEX1 (PEROXISOME 1); ATPase	0.6236	0.0532	0.133	0.2913	0.2732	0.2772	-0.4193	0.1425	0.1733	-0.7505	0.0308	0.0591
250521_at	AT5G08490	pentaticopeptide (PPR) repeat-containing protein	1.2383	0.2121	0.2697	-1.3221	0.1884	0.2254	0.1743	0.6965	0.4299	-2.3861	0.0046	0.0214
250522_at	AT5G08500	transmembrane CLPTM1 family protein	0.4229	0.0576	0.1375	0.4879	0.0382	0.0967	-0.6104	0.0189	0.0552	-0.5454	0.0272	0.0548
250523_at	AT5G08510	pentaticopeptide (PPR) repeat-containing protein	-0.09633	0.7122	0.4971	0.6079	0.0668	0.1293	-0.1915	0.4751	0.3496	0.5128	0.1027	0.1224
250524_at	AT5G08520	myb family transcription factor	0.4878	0.0319	0.1035	0.4734	0.0349	0.0923	-0.03329	0.7323	0.4424	-0.04771	0.6268	0.3727
250525_at	AT5G08550	ILP1 (INCREASED LEVEL OF POLYPLOIDY1-1D)	0.4661	0.1381	0.2159	0.1193	0.6607	0.4453	-0.405	0.0936	0.1356	-0.7519	0.0153	0.0394
250526_at	AT5G08570	pyruvate kinase, putative	0.03154	0.7807	0.518	-0.1008	0.3953	0.3392	-0.01087	0.9247	0.4991	-0.07988	0.4926	0.323
250527_at	AT5G08590	ASK2 (ARABIDOPSIS SERINE/THREONINE KINA	0.1303	0.2697	0.3052	0.07822	0.4849	0.3781	-0.2369	0.804	0.1241	-0.289	0.4649	0.0762
250528_at	AT5G08600	U3 ribonucleoprotein (Utp) family protein	-0.2063	0.3948	0.3726	-0.1506	0.5252	0.3941	-0.00127	0.9908	0.5154	0.05443	0.625	0.372
250529_at	AT5G08610	DEAD box RNA helicase (RH26)	0.2488	0.0953	0.183	-0.00599	0.9608	0.5343	-0.538	0.0051	0.03	-0.7927	0.0012	0.0128
250530_at	AT5G08630	DDT domain-containing protein	0.1545	0.4175	0.3836	0.4823	0.0479	0.1086	-0.6929	0.003	0.0248	-0.3651	0.0278	0.0556
250531_at	AT5G08650	GTP-binding protein LepA, putative	-0.5744	0.0033	0.0446	-0.7071	0.0015	0.0315	-0.02224	0.7992	0.4631	-0.1549	0.1313	0.1424
250532_at	AT5G08540	similar to unknown protein product [Vitis vinifera] (G	0.1084	0.1106	0.1928	0.372	0.0893	0.132	-0.4585	0.0385	0.081	-0.3948	0.0591	0.0877
250533_at	AT5G08640	FLS (FLAVONOL SYNTHASE)	1.2383	0.2121	0.2697	-1.3221	0.1884	0.2254	0.1743	0.6965	0.4299	-2.3861	0.0046	0.0214
250534_at	AT5G08530	CI51 (51 KDA SUBUNIT OF COMPLEX I); NADH d	-0.3016	0.2413	0.2885	-0.01248	0.9574	0.5336	-0.6095	0.0308	0.0715	-0.3204	0.1609	0.1618
250535_at	AT5G08480	VQ motif-containing protein	-0.1039	0.9258	0.6585	-1.2569	0.2864	0.2899	0.5115	0.3129	0.2749	-0.6416	0.2215	0.1968
250536_at	AT5G08535	D111/G-patch domain-containing protein	0.4393	0.0196	0.0827	0.4186	0.0229	0.0763	0.3786	0.0313	0.0719	0.3579	0.0371	0.0657
250537_at	AT5G08565	elongation factor/ zinc ion binding	0.1513	0.6112	0.463	0.301	0.3348	0.3107	0.09387	0.6919	0.4284	0.2436	0.3308	0.2537
250538_at	AT5G08620	STRS2 (STRESS RESPONSE SUPPRESSOR 2);	0.3351	0.157	0.231	0.31	0.3707	0.3278	-0.2181	0.2929	0.2651	-0.4432	0.0698	0.0967
250539_at	AT5G08560	transducin family protein / WD-40 repeat family prot	0.3688	0.0245	0.0909	0.2373	0.0863	0.1481	0.1405	0.2512	0.2415	0.008928	0.9362	0.4673
250540_at	AT5G08580	calcium-binding EF hand family protein	0.366	0.0032	0.0442	0.2654	0.0101	0.0547	0.3046	0.0062	0.0328	0.2041	0.0243	0.0513
250529_at	AT5G08610	DEAD box RNA helicase (RH26)	0.2488	0.0953	0.183	-0.00599	0.9608	0.5343	-0.538	0.0051	0.03	-0.7927	0.0012	0.0128
250542_at	AT5G08270	similar to unknown protein [Arabidopsis thaliana] (T	-0.255	0.0666	0.1481	-0.5335	0.0064	0.0456	0.2556	0.0661	0.1113	-0.02287	0.8334	0.4381
250543_at	AT5G08190	TATA-binding protein-associated phosphoprotein D	0.2479	0.1881	0.254	0.6709	0.0127	0.0603	-0.0069	0.9669	0.5093	0.4161	0.0564	0.0852
250544_at	AT5G08660	identical to UPF0139 protein At5g07960 [Arabidops	-0.4864	0.0511	0.1299	0.008471	0.964	0.535	-0.09858	0.6065	0.4002	0.3963	0.0882	0.1114
250545_at	AT5G08160	mitochondrial transcription termination factor family	0.002778	0.9905	0.5747	-0.2164	0.3809	0.3324	0.09806	0.6788	0.4241	-0.1211	0.6113	0.3672
250546_at	AT5G08180	ATPK3 (Arabidopsis thaliana serine/threonine prote	0.05493	0.7262	0.5013	0.2253	0.1982	0.2318	0.01761	0.8989	0.492	0.188	0.2223	0.1972
250547_at	AT5G08100	ribosomal protein L7Ae/L30e/S12e/Gadd45 family p	-0.1662	0.4407	0.394	-0.02893	0.8888	0.5155	0.2344	0.2541	0.2432	0.3717	0.1025	0.1223
250548_at	AT5G08120	MBP2C; protein binding	0.302	0.0799	0.1629	0.2722	0.1032	0.1621	-0.6529	0.0025	0.0232	-0.6827	0.0021	0.0155
250549_at	AT5G07860	transferase family protein	-0.1046	0.5959	0.4583	0.07097	0.7162	0.464	-0.2655	0.2181	0.2225	-0.0899	0.647	0.3797
250550_at	AT5G07870	transferase family protein	0.2509	0.3684	0.3587	0.1343	0.6164	0.4294	0.1568	0.4546	0.3407	0.04022	0.8423	0.4407
250551_at	AT5G07880	SNAP29 (Synaptosomal-associated protein SNAP2	0.4658	0.6865	0.4881	-0.03808	0.9734	0.5374	0.01568	0.9879	0.5148	-0.4882	0.6423	0.378
250552_at	AT5G07890	myosin heavy chain-related	-0.4403	0.0526	0.1316	-0.0666	0.7011	0.4595	-0.6301	0.0175	0.053	-0.2564	0.1876	0.1779
250553_at	AT5G07960	identical to UPF0139 protein At5g07960 [Arabidops	-0.4714	0.0193	0.0823	0.8676	0.0022	0.0334	0.222	0.1494	0.1785	0.6179	0.0077	0.0274
250554_at	AT5G07900	mitochondrial transcription termination factor family	0.002778	0.9905	0.5747	-0.2164	0.3809	0.3324	0.09806	0.6788	0.4241	-0.1211	0.6113	0.3672
250555_at	AT5G07950	similar to unknown protein product [Vitis vinifera] (G	0.4641	0.0575	0.1374	0.5978	0.0272	0.0825	-0.6584	0.02	0.0567	-0.5247	0.0405	0.0695
250556_at	AT5G07620	DGK1 (DIACYLGLYCEROL KINASE 1, DIACYLGL	0.056977	0.7825	0.5184	0.2003	0.7385	0.3313	-0.1381	0.3931	0.3134	0.002499	0.987	0.4795
250557_at	AT5G07842;AT5G07840	[AT5G07842; CPuORF16 (Conserved peptide upstr	0.1134	0.4075	0.3791	0.02736	0.8344	0.5	0.03359	0.5333	0.3725	-0.05244	0.3477	0.2614
250558_at	AT5G07990	TT7 (TRANSPARENT TESTA 7); flavonoid 3'-mono	0.07891	0.8412	0.536	-0.2801	0.4904	0.3805	-0.4754	0.2674	0.2506	-0.8344	0.0867	0.1103
250559_at	AT5G08010	similar to unknown protein [Arabidopsis thaliana] (T	0.09494	0.4288	0.3885	0.1066	0.3792	0.3315	0.02577	0.8231	0.4706	0.03747	0.7461	0.4123
250560_at	AT5G08020	replication protein, putative	-0.3422	0.1519	0.2274	-0.1762	0.4144	0.348	-0.01844	0.9287	0.5002	0.1476	0.4884	0.3212
250561_at	AT5G08030	glycerophosphoryl diester phosphodiesterase famil	-0.2837	0.0318	0.1034	-0.468	0.5077	0.3877	-0.9428	0.2082	0.2167	0.6728	0.3449	0.2603
250562_at	AT5G08040	TOM5 (MITOCHONDRIAL IMPORT RECEPTOR SI	-0.02314	0.8798	0.5464	0.002443	0.9872	0.5409	0.664	0.0046	0.0289	0.6896	0.004	0.0204
250563_at	AT5G08050	similar to unknown protein product [Vitis vinifera] (G	-1.2005	4.00E-04	0.032	-1.0758	7.00E-04	0.027	0.2286	0.1113	0.1493	0.3533	0.0346	0.0629
250564_at	AT5G08060	similar to unknown [Populus trichocarpa] (GB:ABK9	0.1429	0.0319	0.1035	0.2728	0.0035	0.0374	0.4215	7.00E-04	0.0159	0.5513	2.00E-04	0.0078
250565_at	AT5G08065	E13L3 (GLUCAN ENDO-1,3-BETA-GLUCOSIDASE	0.4156	0.3232	0.3362	0.2174	0.5876	0.4187	0.4253	0.1285	0.163	0.227	0.3652	0.2692
250566_at	AT5G08070	TCP17 (TCP domain protein 17); transcription facto	-0.3949	0.3594	0.3543	-0.1943	0.6376	0.4374	0.1996	0.4788	0.351	0.4001	0.1927	0.1807
250567_at	AT5G08090	unknown protein	-0.1419	0.8894	0.5483	-0.7157	0.4963	0.3829	0.4157	0.6865	0.4266	-0.1582	0.8768	0.4504
250568_at	AT5G08110	DEAD/DEAH box helicase, putative	0.59	0.4979	0.4195	-0.03133	0.9704	0.5368	-0.5363	0.5357	0.3735	-1.1577	0.2179	0.195
250569_at	AT5G08130	BIM1 (BES1-interacting Myc-like protein 1); DNA bi	0.04437	0.8347	0.5339	-0.369	0.1376	0.189	0.2223	0.3269	0.2818	-0.191	0.3919	0.2807
250570_at	AT5G08170	ATAIH/EMB1873 (ASPARTATE IMINOHYDROLASE	-0.1207	0.4577	0.4018	0.0146	0.9256	0.5255	-0.06629	0.6753	0.4228	0.06898	0.6632	0.3852
250571_at	AT5G08200	peptidoglycan-binding LysM domain-containing prot	-0.4226	0.0487	0.1271	-0.0741	0.649	0.4413	-0.2418	0.1843	0.2016	0.1067	0.5183	0.3329
250572_at	AT5G08210	MIR834a; miRNA	1.3737	0.1425	0.2196	0.03016	0.97	0.5367	-1.971	0.0591	0.1042	-3.3145	0.0117	0.0339
250573_at	AT5G08220	unknown protein	-1.3215	0.2354	0.2847	0.8478	0.4213	0.3512	-1.3695	0.2058	0.2153	0.7998	0.4279	0.2958
250574_at	AT5G08230	PWWP domain-containing protein	0.5805	0.464	0.4048	0.03655	0.9618	0.5345	-0.4181	0.5914	0.3952	-0.9621	0.2511	0.2132
250575_at	AT5G08240	similar to unknown protein [Arabidopsis thaliana] (T	1.2973	0.0448	0.122	1.6905	0.0198	0.072	0.4537	0.0781	0.1222	0.8469	0.0117	0.034
250576_at	AT5G08250	cytochrome P450 family protein	-0.3095	0.4802	0.4119	-0.234	0.5882	0.4188	0.5264	0.2565	0.2445	0.602	0.205	0.1878
250577_at	AT5G07910	leucine-rich repeat family protein	0.3625	0.0637	0.1446	0.3725	0.0592	0.1209	0.1181	0.4539	0.3404	0.128	0.4197	0.2924
250578_at	AT5G07850	transferase family protein	0.8506	0.3516	0.3505	-0.3624	0.6769	0.4508	0.9916	0.2868	0.2617	-0.2214	0.7976	0.4281
250579_at	AT5G07930	MCT2 (mei2 C-Terminal RRM only like 2); nucleic a	0.4282	0.4826	0.4131	0.7018	0.2739	0.2775	-0.8331	0.207	0.216	-0.5596	0.3696	0.271
250580_at	AT5G07440	GDH2 (GLUTAMATE DEHYDROGENASE 2); oxid	0.5281	0.0581	0.1382	0.8158	0.0153	0.0649	0.1616	0.3343	0.2856	0.4482	0.038	0.0688
250581_at	AT5G07300	BON2 (BONZAI 2)	0.7853	0.0053	0.0514	0.5333	0.0199	0.0723	-0.8189	0.0028	0.0242	-1.0709	0.001	0.0122
250582_at	AT5G07580	DNA binding / transcription factor	-0.4685	0.0781	0.161	0.07948	0.7099	0.462	-0.1288	0.3209	0.2787	0.4191	0.0212	0.0472
250583_at	AT5G07500	PEI1; nucleic acid binding / transcription factor	-0.3847	0.6407	0.4734	0.0317	0.9689	0.5364	-0.303	0.7116	0.4354	0.1134	0.889	0.454
250584_at	AT5G07590	WD-40 repeat protein family	-0.3283	0.2062	0.2661	-0.1479	0.5343	0.3981	0.1164	0.6122	0.4019	0.2968	0.2342	0.204
250585_at	AT5G07620	protein kinase family protein	-0.4098	0.6265	0.4685	0.7371	0.3973	0.3402	-0.8956	0.3124	0.2746	0.2513	0.762	0.4174
250586_at	AT5G07630	nuclear division RFT family protein	-0.05157	0.7699	0.5146	-0.2589	0.1911	0.227	-1.1742	6.00E-04	0.0156	-1.3816	3.00E-04	0.0083
250587_at	AT5G07640	zinc finger (C3HC4-type RING finger) family protein	-0.6496	0.5024	0.4215	2.99	0.0275	0.0829	-1.8456	0.0849	0.1283	1.7941	0.0911	0.1136
250588_at	AT5G07660	structural maintenance of chromosomes (SMC) fam	0.9673	0.4302	0.3892	1.6225	0.2155	0.2431	-0.4083	0.7302	0.4418	0.2469	0.834	0.4383
250589_at	AT5G07700	MYB76 (myb domain protein 76); DNA binding / tra	-1.4113	0.0379	0.1121	-1.0437	0.0888	0.1485	0.09765	0.7031	0.4323	0.4652	0.1228	0.1369
250590_at	AT5G07710	exonuclease family protein	0.1255	0.5427	0.438	-0.05186	0.7973	0.4887	0.02905	0.8852	0.4883	-0.1484	0.4762	0.3162
250591_at	AT5G07720	galactosyl transferase GMA12/MNN10 family protei	-0.8607	0.0307	0.1016	0.03417	0.9029	0.5196	-0.5835	0.0454	0.0892	0.3114	0.2001	0.1851
250592_at	AT5G07740	pseudogene, formin homology 2 (FH2) domain-cont	1.3739	0.0564	0.1361	0.8893	0.1603	0.2061	-0.9371	0.1439	0.1745	1.4217	0.0513	0.0806
250593_at	AT5G07740	pseudogene, formin homology 2 (FH2) domain-cont	0.1623	0.8593	0.5409	-0.8781	0.3642	0.3249	0.7176	0.4502	0.3386	-0.3228	0.726	0.4059
250594_at	AT5G07760	formin homology 2 domain-containing protein / FH2	2.2261	0.0845	0.1683	0.5584	0.5975	0.4224	-1.7504	0.147	0.1769	-3.4181	0.0248	0.0518
250595_at	AT5G07770	formin homology 2 domain-containing protein / FH2	1.3722	0.0022	0.041	0.7895	0.0156	0.0652	-0.4133	0.0845	0.128	-0.996	0.0053	0.0228
250596_at	AT5G07780	formin homology 2 domain-containing protein / FH2	0.4349	0.6407	0.4734	1.5382	0.1491	0.1976	0.08578	0.9256	0.4994	1.1891	0.2401	0.2072
250597_at	AT5G07680	ANAC079/ANAC080/ATNAC4 (Arabidopsis NAC do	0.5599	0.3365	0.3434	1.3621	0.0567	0.1184	-0.6913	0.2491	0.2404	0.1109	0.8394	0.4398
250598_at	AT5G07690	MYB29 (myb domain protein 29); DNA binding / tra	-0.0636	0.9635	0.5443	-1.0926	0.0433	0.1032	-0.01873	0.9405	0.5036	-0.1577	0.5404	0.3411
250599_at	AT5G07730	similar to unknown protein [Arabidopsis thaliana] (T	0.2123	0.4559	0.4008	-0.1434	0.6072	0.4261	0.2039	0.236	0.2328	-0.1518	0.3584	0.2663
250600_at	AT5G07800	rhomboid family protein	-0.4329	0.0822	0.1658	0.02196	0.9124	0.5221	0.209	0.3274	0.282	0.6638	0.024	0.0509
250601_at	AT5G07810	SNF2 domain-containing protein / helicase domain-	0.1129	0.3145	0.3311	0.769	0.4129	0.3474	-0.8939	0.3484	0.2924	-1.0931	0.2642	0.2199
250602_s_at	AT5G07940;AT5G07980	[AT5G07940; similar to dentin sialophosphoprotein-	0.445	0.0374	0.1116	0.5419	0.0202	0.0727	-0.2385	0.1404	0.1716	-0.1416	0.3371	0.2565
250603_at	AT5G07820	similar to chromosome scaffold protein-related [Ara	1.092	0.0133	0.0709	1.4222	0.0053	0.0429	-0.1023	0.7111	0.4352	0.2277	0.4268	0.2954
250604_at	AT5G07830	ATGUS2 (ARABIDOPSIS THALIANA GLUCURON	1.2248	0.0047	0.0496	1.2299	0.0047	0.0417	-0.07367	0.6842	0.4257	-0.06854	0.7047	0.3991
250605_at	AT5G07570	glycine/proline-rich protein	0.07311	0.9313	0.5602	-0.7818	0.3822	0.3329	0.0874	0.918	0.4972	-0.7675	0.3901	0.28
250606_s_at	AT5G07410	[AT1G69940, ATPPME1; pectinesterase];[AT5G07	0.4426	0.7541	0.5097	-1.1954	0.4161	0.3488	1.788	0.2468	0.2391	0.15	0.915	0.4614
250607_at	AT5G07370	IPK2a (INOSITOL POLYPHOSPHATE KINASE 2 A	0.5467	0.0057	0.0525	0.2998	0.0414	0.1011	0.2504	0.0619	0.1069	0.003467	0.9733	0.4764
250608_at	AT5G07420	pectinesterase family protein	-0.163	0.9068	0.553	-0.3726	0.7898	0.4861	1.0484	0.4675	0.3465	0.8389	0.556	0.3473
250609_at	AT5G07470	PMSR5 (PEPTIDEMETHIONINE SULFOXIDE REDU	0.5148	0.0167	0.0775	0.5257	0.0156	0.0652	0.1977	0.203	0.2136	0.2086	0.1838	0.1758
250610_at	AT5G07550	GRP19 (Glycine rich protein 19)	1.4889	0.4272	0.3881	1.425	0.4458	0.3621	-1.8295	0.2615	0.2473	-1.8934	0.2477	0.2112
250611_at	AT5G07200	YAP169 (GIBBERELLIN 20 OXIDASE 3); gibberelli	1.2788	0.3358	0.3432	0.7733	0.5448	0.4025	0.8509	0.488	0.3546	0.3455	0.7722	0.4206
250612_s_at	AT5G07210;AT2G27070	[AT5G07210, ARR21 (ARABIDOPSIS RESPONSE	1.23	0.3608	0.355	-0.1216	0.9237	0.5251	1.1112	0.4043	0.3183	0.2404	0.8501	0.4428
250613_at	AT5G07240	IQD24 (IQ-domain 24); calmodulin binding	-0.7392	0.0054	0.0519	-0.8984	0.0026	0.0342	0.1209	0.3522	0.2944	-0.0383	0.7557	0.4153
250614_at	AT5G07260	homeobox protein-related	0.8807	0.4315	0.3899	0.5424	0.6189	0.4302	-0.2513	0.8153	0.4683	-0.5896	0.5899	0.3599
250615_at	AT5G07270	ankyrin repeat family protein	0.5061	0.0833	0.1671	0.07883	0.7387	0.4708	-0.5595	0.0641	0.1092	-0.9867	0.011	0.0328
250616_at	AT5G07280	EMS1 (EXCESS MICROSPOROCYTES1); kinase	1.1722	0.0938	0.1772	0.03683	0.9485	0.5316	-0.1139	0.8419	0.4763	-1.2493	0.0799	0.105
250617_at	AT5G07290	AML4 (ARABIDOPSIS MEI2-LIKE); RNA binding	-0.1176	0.611	0.463	-0.0698	0.7601	0.4778	-0.2995	0.2333	0.2313	-0.2517	0.3038	0.2405
250618_at	AT5G07220	ATBAG3 (ARABIDOPSIS THALIANA BCL-2-ASSO	-0.4773	0.0797	0.1627	-0.1446	0.6181	0.3917	-0.2043	0.3672	0.3016	0.1284	0.6579	0.3481
250619_at	AT5G07230	proteasome inhibitor/seed storage/lipid transfer protein	0.3543	0.1588	0.2325	0.2208	4.00E-04	0.0251	-1.069	0.0064	0.0331	0.7974	0.0177	0.0426
250620_at	AT5G07190	ATS3 (ARABIDOPSIS THALIANA SEED GENE 3)	-0.3773	0.6031	0.4605	-0.3833	0.5976	0.4224	0.8906	0.1868	0.2035	0.8847	0.1892	0.1789
250621_at	AT5G07250	rhomboid family protein	-0.6011	0.0444	0.1215	-0.3477	0.1151	0.1712	0.1804	0.282	0.2593	0.3337	0.0831	0.1076
250622_at	AT

250690_at	AT5G06530	ABC transporter family protein	0.3164	0.3868	0.3682	-0.04227	0.9031	0.5196	-0.3362	0.0404	0.0833	-0.6949	0.0035	0.0193
250691_at	AT5G06580	FAD linked oxidase family protein	0.2381	0.3041	0.3253	0.1118	0.6095	0.4268	-0.3629	0.147	0.1769	-0.4891	0.0727	0.099
250692_at	AT5G06560	similar to unknown protein [Arabidopsis thaliana] (T	-0.02704	0.9163	0.5559	0.02122	0.9343	0.5277	-0.04491	0.7421	0.4455	0.003359	0.9802	0.4782
250693_at	AT5G06600	UBP12 (UBIQUITIN-SPECIFIC PROTEASE 12); ub	0.1906	0.3487	0.3492	0.05629	0.7698	0.4804	-0.5934	0.0299	0.0704	-0.7277	0.0155	0.0397
250694_at	AT5G06710	HAT14 (homeobox-leucine zipper protein 14); DNA	-0.4172	0.2514	0.2942	-0.2471	0.4719	0.3729	0.1154	0.7297	0.4417	0.2855	0.4112	0.2887
250695_at	AT5G06740	lectin protein kinase family protein	1.6179	0.2493	0.2932	1.0541	0.4298	0.3552	0.1132	0.9295	0.5004	-0.4506	0.7267	0.4061
250696_at	AT5G06790	similar to unknown protein [Arabidopsis thaliana] (T	-0.5963	0.3403	0.3454	-0.6401	0.3102	0.2974	0.1143	0.8161	0.4686	0.07047	0.8857	0.4531
250697_at	AT5G06800	myb family transcription factor	-0.7736	0.0482	0.1275	-0.8366	0.0391	0.0981	0.01318	0.9359	0.5023	-0.04983	0.7623	0.4175
250698_at	AT5G06810	mitochondrial transcription termination factor-relate	0.1784	0.4024	0.3765	0.2379	0.2802	0.281	-0.1673	0.4299	0.3295	-0.1078	0.6021	0.3639
250699_at	AT5G06820	SRF2 (STRUBBELIG-RECEPTOR FAMILY 2); ATP	-1.1499	0.3211	0.335	0.6883	0.5354	0.3987	-2.6371	0.0604	0.1055	-0.7989	0.4758	0.316
250700_at	AT5G06830	Identical to CDKSRAP3-like protein [Arabidopsis Tha	0.7095	0.0471	0.1248	0.5314	0.1009	0.1693	-0.337	0.0431	0.0866	-0.5151	0.0111	0.033
250701_at	AT5G06839	bZIP family transcription factor	-1.4134	0.0994	0.1819	0.4645	0.5212	0.3926	-0.3896	0.5875	0.3935	1.4882	0.0876	0.1109
250702_at	AT5G06730	peroxidase, putative	2.4536	0.0059	0.0534	3.595	0.0014	0.0313	-0.2133	0.5839	0.3921	0.9281	0.0608	0.0892
250703_at	AT5G06360	ribosomal protein S8e family protein	0.5324	0.0428	0.1191	0.4954	0.0526	0.1137	-0.1251	0.3271	0.2819	-0.162	0.222	0.197
250704_at	AT5G06265	hyaluronan mediated motility receptor-related	0.5001	0.2326	0.2833	0.0984	0.7958	0.4882	0.04152	0.9127	0.4959	-0.3602	0.3686	0.2707
250705_at	AT5G06340	diadenosine 5',5''-P1,P4-tetraphosphate hydrolase,	0.02638	0.882	0.5468	0.1189	0.5151	0.3906	-1.2642	3.00E-04	0.0133	-1.1716	4.00E-04	0.0088
250706_at	AT5G05920	DHS (embryo sac development arrest 22)	0.08252	0.6257	0.4684	0.2379	0.2029	0.2347	-0.3486	0.0898	0.1324	-0.1932	0.2844	0.2306
250707_at	AT5G05950	MEE60 (maternal effect embryo arrest 60)	0.4124	0.0029	0.0433	0.261	0.0147	0.064	0.1396	0.0928	0.1349	-0.01173	0.8624	0.4465
250708_at	AT5G06070	RBE (RABBIT EARS); nucleic acid binding / transcr	1.5488	0.2967	0.3212	-1.2135	0.4007	0.3414	0.9784	0.491	0.356	-1.7839	0.2394	0.2067
250709_at	AT5G06080	LBD33 (LOB DOMAIN-CONTAINING PROTEIN 33)	-0.1963	0.888	0.5478	0.865	0.5449	0.4025	-0.6974	0.6224	0.4055	0.3639	0.7948	0.4274
250710_at	AT5G06100	ATMYB33/MYB33 (myb domain protein 33); DNA b	-0.6926	0.0217	0.0866	0.3245	0.1623	0.2075	-2.3301	3.00E-04	0.0133	-1.313	0.0023	0.016
250711_at	AT5G06110	DNAJ heat shock N-terminal domain-containing pro	0.5236	0.0654	0.1467	0.6296	0.0388	0.0977	-0.168	0.3297	0.2831	-0.06205	0.7031	0.3984
250712_at	AT5G06120	Ran-binding protein, putative	-0.02868	0.8855	0.5472	-0.02276	0.909	0.5212	-1.038	0.0052	0.0301	-1.0321	0.0053	0.0226
250713_at	AT5G06130	chaperone protein dnaJ-related	0.06296	0.6629	0.4803	-0.2848	0.1007	0.16	0.2259	0.0688	0.1137	-0.1218	0.2534	0.2144
250714_at	AT5G06140	phox (PX) domain-containing protein	0.2745	0.3461	0.3478	0.8587	0.0289	0.0847	-0.6175	0.0744	0.1188	-0.03329	0.9033	0.4582
250715_at	AT5G06160	splicing factor-related	0.631	0.0202	0.0837	0.2171	0.2678	0.2743	-0.21	0.2814	0.2589	-0.624	0.0209	0.0469
250716_at	AT5G06170	ATSUC9 (SUCROSE-PROTON SYMPORTER 9);	-0.642	0.1172	0.1979	-0.4123	0.27	0.2754	-0.1689	0.6281	0.4073	0.06085	0.8595	0.4457
250717_at	AT5G06200	integral membrane family protein	0.3547	0.1728	0.4972	0.2113	0.8253	0.4975	0.1203	0.8998	0.4924	-0.02305	0.9807	0.4783
250718_at	AT5G06240	EMB2735 (EMBRYO DEFECTIVE 2735)	0.6954	0.0151	0.0744	0.9857	0.0045	0.041	-0.2278	0.2526	0.2423	0.06251	0.7326	0.4079
250719_at	AT5G06250	transcription factor	0.3484	0.4102	0.3801	0.6016	0.1879	0.2251	-0.0928	0.4259	0.328	0.1603	0.2008	0.1856
250720_at	AT5G06180	similar to unknown protein [Arabidopsis thaliana] (T	0.2973	0.3883	0.3689	0.1983	0.5542	0.4062	-0.6119	0.0647	0.1097	-0.711	0.0424	0.0718
250721_at	AT5G06210	RNA-binding protein, putative	0.005024	0.975	0.571	0.2815	0.1349	0.1868	-0.5532	0.0213	0.0587	-0.2767	0.1399	0.1481
250722_at	AT5G06190	unknown protein	0.4161	0.1698	0.2412	0.1609	0.5531	0.4059	1.2874	0.0066	0.0334	1.0322	0.0143	0.0379
250723_at	AT5G06300	carboxy-lyase	-0.2021	0.4933	0.4173	0.2501	0.4702	0.3432	0.2238	0.2829	0.2598	0.676	0.0201	0.0456
250724_at	AT5G06330	hairpin-responsive protein, putative (HIN1)	-0.1536	0.7597	0.5116	-0.438	0.4031	0.3427	-0.083	0.7386	0.4443	-0.3674	0.1885	0.1785
250725_at	AT5G06400	pentatricopeptide (PPR) repeat-containing protein	0.0934	0.7171	0.4984	-0.1113	0.667	0.4474	-0.1325	0.6104	0.4014	-0.3372	0.2328	0.2031
250726_at	AT5G06410	DNAJ heat shock N-terminal domain-containing pro	0.2958	0.0945	0.1777	0.635	0.0572	0.119	-0.06908	0.6345	0.4093	0.04219	0.7693	0.4197
250727_at	AT5G06430	thioredoxin-related	-0.9181	0.0116	0.0672	-0.3701	0.15	0.198	-0.6998	0.0182	0.0683	-0.1517	0.5063	0.3283
250728_at	AT5G06440	similar to unknown protein [Arabidopsis thaliana] (T	0.09587	0.6541	0.4773	0.3209	0.181	0.2203	-0.3398	0.0123	0.0441	-0.1147	0.2171	0.1947
250729_at	AT5G06450	ATUBA2 (Arabidopsis thaliana ubiquitin activating e	0.6492	0.0368	0.1105	0.6351	0.0393	0.0982	-0.5879	0.0237	0.0624	-0.6017	0.022	0.0483
250730_at	AT5G06490	zinc finger (C3HC4-type RING finger) family protein	0.379	0.6536	0.4771	0.3667	0.6639	0.4462	0.5036	0.555	0.3809	0.4912	0.5643	0.3506
250731_at	AT5G06500	ACL96; DNA binding / transcription factor	-0.4633	0.6758	0.4846	-0.3335	0.762	0.4781	-0.6833	0.3507	0.2937	-0.5535	0.4406	0.3017
250732_at	AT5G06480	MD-2-related lipid recognition domain-containing pr	-0.05128	0.7482	0.5083	-0.1588	0.3469	0.3164	0.3411	0.0291	0.0692	0.2336	0.0847	0.1087
250733_at	AT5G06290	2-cys peroxiredoxin, chloroplast, putative	-0.5944	0.0028	0.0431	-0.96	5.00E-04	0.0252	0.127	0.089	0.1317	-0.2386	0.0137	0.0371
250734_at	AT5G06270	similar to unknown protein [Arabidopsis thaliana] (T	-1.5088	0.0144	0.0731	-1.0874	0.0406	0.1	0.06375	0.8028	0.4644	0.4852	0.1121	0.1291
250735_at	AT5G06280	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.4221	0.1988	0.2618	0.3477	0.2738	0.2775	0.6559	0.0329	0.0741	0.5815	0.047	0.0763
250736_s_at	AT1G01350;AT5G06420	[AT1G01350, nucleic acid binding];[AT5G06420, zi	0.2392	0.3087	0.3278	0.6345	0.0365	0.0943	-0.3107	0.0621	0.1071	0.08465	0.5227	0.335
250737_at	AT5G06370	NC domain-containing protein	1.3753	3.00E-04	0.0312	1.4377	2.00E-04	0.0249	0.1327	0.1037	0.1439	0.1951	0.0367	0.0652
250738_at	AT5G05730	ASA1 (ANTHRANILATE SYNTHASE ALPHA SUBU	0.3071	0.1925	0.2572	0.4006	0.1106	0.1679	0.2192	0.19	0.2055	0.3127	0.0677	0.111
250739_at	AT5G05740	ATEGY2; metalloendopeptidase	-0.2304	0.3442	0.347	-0.4701	0.0941	0.1545	-0.1167	0.6163	0.4032	-0.3563	0.1729	0.169
250740_at	AT5G05760	SYP31 (T-SNARE SED 5); SNAP receptor	0.3604	0.1998	0.2621	0.4575	0.1233	0.1782	0.7571	0.0065	0.0332	0.8541	0.0042	0.0208
250741_at	AT5G05790	myb family transcription factor	-1.2475	0.0082	0.0591	-0.9791	0.0186	0.0705	0.4852	0.1285	0.163	0.7541	0.0412	0.0704
250742_at	AT5G05800	similar to unknown protein [Arabidopsis thaliana] (T	-0.1488	0.0682	0.1501	-0.00395	0.9507	0.5321	-0.8158	2.00E-04	0.0126	-0.6709	4.00E-04	0.0088
250743_at	AT5G05820	phosphate translocator-related	-0.08501	0.6648	0.4809	-0.6604	0.0222	0.0753	0.02007	0.9097	0.4952	-0.5554	0.0288	0.0568
250744_at	AT5G05840	similar to unknown protein [Arabidopsis thaliana] (T	-1.5979	0.061	0.1417	-0.6837	0.3309	0.3089	-1.3224	0.0992	0.1403	-0.4082	0.5452	0.343
250745_at	AT5G05850	leucine-rich repeat family protein	0.2734	0.3599	0.3545	-0.00561	0.9841	0.5402	0.1227	0.4135	0.3224	-0.1563	0.31	0.2434
250746_at	AT5G05880	UDP-glucuronosyl/UDP-glucosyl transferase family	-0.3537	0.8233	0.5306	-0.2391	0.8798	0.5131	-0.9812	0.1537	0.1814	-0.8666	0.1956	0.1823
250747_at	AT5G05900	UDP-glucuronosyl/UDP-glucosyl transferase family	-0.7097	0.3523	0.3509	-1.345	0.117	0.1729	-0.4065	0.5794	0.3905	-1.0418	0.1975	0.1834
250748_at	AT5G05710	pleckstrin homology (PH) domain-containing protein	0.3875	0.0013	0.0366	0.5726	3.00E-04	0.0249	0.08916	0.0175	0.053	0.2742	3.00E-04	0.0082
250749_at	AT5G05780	AE3/ATHMOV34 (ASYMMETRIC LEAVES ENHAN	0.298	0.0347	0.1076	0.2756	0.0437	0.1036	-0.09198	0.3866	0.3106	-0.1145	0.2936	0.2354
250750_at	AT5G05870	UGT76C1 (UDP-GLUCOSYL TRANSFERASE 76C	-0.2243	0.0407	0.1163	-0.347	0.01	0.0543	-0.4542	0.0038	0.027	-0.5768	0.0016	0.0139
250751_at	AT5G05890	UDP-glucuronosyl/UDP-glucosyl transferase family	-0.8219	0.1216	0.2021	-1.5251	0.022	0.0751	-0.1299	0.7656	0.4529	-0.8331	0.1101	0.1278
250752_at	AT5G05690	CPD (CABBAGE 3); oxygen binding	0.3328	0.3363	0.3434	-0.05753	0.8595	0.507	0.07808	0.3936	0.3136	-0.3123	0.0188	0.044
250753_at	AT5G05860	UGT76C2 (UDP-glucosyl transferase 76C2); UDP-g	-0.4156	0.3	0.3229	-0.8143	0.0802	0.1421	-0.02982	0.8971	0.4916	-0.4285	0.1188	0.1339
250754_at	AT5G05700	ATE1 (DELAYED LEAF SENESCENCE 1); arginyl	0.1121	0.2779	0.3102	0.09018	0.3699	0.3275	-0.08702	0.3852	0.3102	-0.1089	0.2898	0.2334
250755_at	AT5G05750	DNAJ heat shock N-terminal domain-containing pro	0.1046	0.4518	0.3991	0.514	0.0149	0.0643	-1.1725	7.00E-04	0.016	-0.7631	0.0037	0.0197
250756_at	AT5G05940	ATROPGEF5/ROPGEF5 (RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR	0.8462	0.3348	0.3428	-0.1509	0.8546	0.5059	0.444	0.4323	0.3306	-0.5531	0.3384	0.2572
250757_at	AT5G05980	ATDFB (A. THALIANA DHFS-FPGS HOMOLOG B)	0.3228	0.072	0.1547	0.3076	0.0816	0.1431	-0.5193	0.0067	0.0336	-0.5345	0.0061	0.0242
250758_at	AT5G06000	initiationinitiation factor	-0.08781	0.7067	0.4949	-0.1993	0.4108	0.3464	0.3887	0.1481	0.1777	0.2772	0.271	0.2232
250759_at	AT5G06020	self-incompatibility protein-related	1.4961	0.2657	0.3026	-1.2348	0.3461	0.316	0.5982	0.6325	0.4086	-2.1327	0.1392	0.1476
250760_at	AT5G06040	self-incompatibility protein-related	-1.2029	0.1384	0.216	1.7954	0.051	0.112	-2.6301	0.0096	0.039	0.3683	0.5495	0.3449
250761_at	AT5G06050	dehydration-responsive protein-related	-0.1167	0.6701	0.4826	0.05475	0.84	0.5015	-0.2773	0.2511	0.2415	-0.1059	0.6357	0.3756
250762_at	AT5G05990	mitochondrial glycoprotein family protein / MAM33 f	-0.1116	0.6073	0.4622	-0.2119	0.35	0.318	0.2898	0.0254	0.0646	0.1895	0.0853	0.1092
250763_at	AT5G06060	tropinone reductase, putative / tropine dehydrogena	-0.3978	0.0102	0.064	-0.6433	0.0018	0.0323	0.05818	0.5398	0.3752	-0.1873	0.0973	0.1185
250764_at	AT5G05960	protease inhibitor/seed storage/lipid transfer protein	0.003073	0.9917	0.575	0.3107	0.3233	0.305	0.9764	0.0134	0.046	1.284	0.0051	0.0224
250765_at	AT5G05930	guanylyl cyclase-related (GC1)	0.3198	0.0241	0.0905	0.2851	0.0344	0.0917	-0.5548	2.00E-04	0.0126	-0.5895	2.00E-04	0.007
250766_at	AT5G05550	transcription factor	0.5753	0.1161	0.1971	0.6184	0.098	0.1579	-0.7634	0.04	0.0828	-0.7202	0.0474	0.0767
250767_at	AT5G05660	transcription factor	-0.2973	0.1822	0.2499	0.2909	0.1899	0.2264	-0.6016	4.00E-04	0.0147	-0.01333	0.8231	0.4351
250768_at	AT5G05670	signal recognition particle binding	0.03586	0.8843	0.5471	0.3773	0.1783	0.2184	-0.4765	0.0908	0.1332	-0.135	0.5637	0.3503
250769_at	AT5G05680	nuclear pore complex protein-related	0.9011	0.0338	0.1063	0.8381	0.042	0.1018	-0.6979	0.0699	0.1147	-0.7609	0.0553	0.0843
250770_at	AT5G05390	LAC12 (laccase 12); copper ion binding / oxidoredu	1.132	0.2062	0.2661	-0.6309	0.4481	0.3631	0.8189	0.297	0.2672	-0.944	0.2394	0.2067
250771_at	AT5G05400	disease resistance protein (CC-NBS-LRR class), pu	-1.3532	0.1908	0.256	-0.9935	0.3124	0.2987	-0.7248	0.4469	0.337	-0.3651	0.6931	0.3951
250772_at	AT5G05420	immunophilin, putative / FKBP-type peptidyl-prolyl c	-1.0916	0.1732	0.2437	-0.3664	0.6081	0.4264	-1.9265	0.0432	0.0867	-1.2012	0.1426	0.1498
250773_at	AT5G05430	nucleotide binding	-1.0997	0.486	0.414	-0.6828	0.6589	0.4446	-0.0618	0.9677	0.5095	0.3551	0.8166	0.4333
250774_at	AT5G05450	DEAD/DEAH box helicase, putative (RH18)	-0.07113	0.5441	0.4386	0.5461	0.0071	0.0475	-0.4214	0.0083	0.0366	0.1959	0.087	0.1105
250775_at	AT5G05460	hydrolase, acting on glycosyl bonds	1.3307	0.0551	0.1349	1.2801	0.0613	0.123	-0.3616	0.5065	0.3619	-0.4121	0.4528	0.3071
250776_at	AT5G05320	monooxygenase, putative (MO3)	1.2348	0.0116	0.0672	1.0811	0.0181	0.0695	-0.5841	0.0438	0.0874	-0.7379	0.0214	0.0475
250777_at	AT5G05440	similar to unknown protein [Arabidopsis thaliana] (T	-1.0806	0.128	0.2067	-0.7096	0.2769	0.2792	0.5151	0.0145	0.048	0.8861	0.0021	0.0154
250778_at	AT5G05500	pollen Ole e 1 allergen and extensin family protein	-0.3021	0.7194	0.4992	0.4325	0.6102	0.427	-1.1054	0.231	0.23	-0.3708	0.6606	0.3844
250779_at	AT5G05470	initiation factor 2 alpha subunit); RNA binding	0.009682	0.9607	0.5675	0.0721	0.7164	0.4641	-0.1594	0.4372	0.3329	-0.09694	0.6277	0.3729
250780_at	AT5G05290	ATEXPA2 (ARABIDOPSIS THALIANA EXPANSIN	0.9838	0.3391	0.3449	0.3426	0.7249	0.4669	-0.08759	0.9277	0.5	-0.7288	0.4668	0.3126
250781_at	AT5G05410	DREB2A (DRE-BINDING PROTEIN 2A); DNA bind	0.7198	0.2209	0.2757	1.6807	0.0277	0.083	-0.7146	0.0477	0.0917	0.2463	0.3858	0.2782
250782_at	AT5G05490	DIF1/SYN1	-0.4465	0.7557	0.5104	0.581	0.687	0.4545	-0.6226	0.6664	0.42	0.4049	0.7776	0.4222
250783_at	AT5G05260	CYP79A2 (CYTOCHROME P450 79A2); oxygen bi	0.2299	0.582	0.453	-0.00505	0.9924	0.5422	-0.8589	0.1609	0.1861	-1.1629	0.0806	0.1055
250784_at	AT5G05480	similar to unknown protein [Arabidopsis thaliana] (T	0.5568	0.045	0.1222	0.603	0.0355	0.0929	-0.3687	0.1291	0.1633	-0.3225	0.1705	0.1675
250785_at	AT5G05510	protein kinase-related	0.9809	0.2423	0.2889	-2.0816	0.0437	0.1036	1.7946	0.0356	0.0774	-1.2679	0.0923	0.1146
250786_at	AT5G05540	exonuclease family protein	0.1199	0.5078	0.4243	0.4793	0.044	0.1037	-0.7819	0.0091	0.0381	-0.4226	0.0626	0.0908
250787_at	AT5G05560	APC1 (EMBRYO DEFECTIVE 2771); ubiquitin-prot	0.6447	0.1716	0.2426	0.7076	0.142	0.1923	-0.7199	0.026	0.0655	-0.657	0.0344	0.0628
250788_at	AT5G05570	transducin family protein / WD-40 repeat family prot	0.3597	0.1979	0.2613	0.2216	0.3958	0.3394	0.1424	0.5056	0.3615	0.004354	0.9833	0.4788
250789_at	AT5G05630	amino acid permease family protein	-0.4104	0.2638	0.3018	-0.8981	0.0407	0.1072	0.2808	0.2943	0.2658	-0.2069	0.4245	0.2944
250790_at	AT5G05640	nucleoprotein-related	-0.06293	0.8739	0.5451	0.4084	0.334	0.3103	-0.3251	0.4317	0.3303	0.1463	0.7143	0.4023
250791_at	AT5G05610	PHD finger family protein	0.07692	0.5217	0.4297	0.6329	0.0045	0.0412	-0.6074	0.0018	0.0206	-0.0515	0.5678	0.3519
250792_at	AT5G05520	outer membrane OMP85 family protein	0.3349	0.0494	0.1276	0.4271	0.0237	0.0773	0.1289	0.3437	0.2902	0.221	0.1395	0.1478
250793_at	AT5G05600	oxidoreductase, 2OG-Fe(II) oxygenase family prote	-0.5284	0.3071	0.3269	-0.3522	0.4792	0.3757	0.369	0.12	0.1562	0.5452	0.0436	0.073
250794_at	AT5G05270	chalcone-flavanone isomerase family protein	-2.456	0.0314	0.1027	-3.2526	0.0126	0.06	1.5768	0.1053	0.1451	0.7802	0.3603	0.2672
250795_at	AT5G05280;AT5G05282	[AT5G05280, zinc finger (C3HC4-type RING finger)	-0.9762	0.3833	0.3664	-1.595	0.1852	0.2232	0.01466	0.989	0.5151	-0.6041	0.5776	0.3551
250796_at	AT5G05300	similar to unknown protein [Arabidopsis thaliana] (T	0.07424	0.9186	0.5566	0.3444	0.6404	0.4384	0.7496	0.0666	0.1116	1.0198	0.0272	0.0548
250797_at	AT5G05310	similar to unnamed protein product [Vitis vinifera] (G	0.559	0.0051	0.0511	0.2694	0.0551	0.1165	-0.6781	8.00E-04	0.0163	-0.9677	2.00E-04	0.0078
250798_at	AT5G05340	peroxidase, putative	0.5701	0.2716	0.3065	0.3493	0.4787	0.3757	0.6871	0.166	0.1891	0.4662	0.315	0.246
250799_at	AT5G05350	similar to unknown protein [Arabidopsis thaliana] (T	-0.1314	0.6269	0.4687	-0.3765	0.2065	0.2371	0.1611	0.5544	0.3806	-0.084	0.7537	0.4148
250800_at	AT5G05370	ubiquinol-cytochrome C reductase complex ubiquin	0.09275	0.5946	0.4578	0.7122	0.0114	0.0576	0.236	0.2157	0.2212	0.8555	0.006	0.024
250801_at	AT5G04960	pectinesterase family protein	-0.2193	0.8396	0.5353	-0.01197	0.9912	0.5419	0.41	0.7071	0.4337	0.6174	0.5761	0.3545
250802_at	AT5G04970	pectinesterase, putative	-0.1601	0.3369	0.3437	-0.00568	0.971	0.5369	-0.9191	0.0013	0.0191	-0.7647	0.0026	0.0169
250803_at	AT5G04980	endonuclease/exonuclease/phosphatase family pro	0.178	0.2502	0.2937	-0.2359	0.1495	0.1977	-0.1894	0.1982	0.2107	-0.5979	0.0075	0.0269
250804_at	AT5G05030	myb family transcription factor	0.9683	0.4372	0.3925	-0.4506	0.7087	0.4616	1.568	0.2351	0.2323	0.1491	0.9008	0.4575
250805_at	AT5G05050	peptidase C1A papain family protein	-0.00192	0.9984	0.5763	-1.9033	0.1053	0.1639	1.1455	0.2776	0.2567	-0.7559	0.4539	0.3075
250806_at	AT5G05070	zinc ion binding	-0.3414	0.6229	0.4675	-0.4053	0.6619	0.409	-0.2739	0.6841	0.4257	-0.3378	0.6179	0.3695
250807_at	AT5G05130	SNF2 domain-containing protein / helicase domain-	0.2641	0.1636	0.2366	0.5418	0.025	0.0791	-0.2909	0.1231	0.1588	-0.01315	0.934	0.4667
250808_at	AT5G05150	AATG18e (Arabidopsis thaliana homolog of yeast A	-1.489	0.2282	0.2808	-1.0147	0.3875	0.3356	1.4087	0.2498	0.2409	1.8829	0.1466	0.1525
250809_at	AT5G05140	elongation factor-related	-0.3688	0.2586	0.2974	0.07624	0.7981	0.489	-0.9616	0.0037	0.0269	-0.5165	0.0313	0.0596
250810_at	AT5G05090	myb family transcription factor	0.2252	0.4442	0.3952	0.9623	0.0223	0.0754	-0.2619	0.2003	0.2119	0.4753	0.0498	0.0791
250811_at	AT5G05110	cysteine protease inhibitor, putative / cystatin, putat	0.5814	0.0588	0.1389	0.6178	0.0497	0.1104	0.1568	0.4046	0.3183	0.1931	0.3155	0.2463
250812_at	AT5G05080	short-chain dehydrogenase/reductase (SDR) family	0.8328	0.0033	0.0446	-1.1424	0.001	0.0282	0.4049	0.0386	0.0811	0.09429	0.5176	0.3326
250813_at	AT5G05000	ATTOC34/OEP34 (Translocase of chloroplast 34);	0.197	0.3192	0.334	-0.01755	0.9242	0.5252	0.009791	0.8493	0.4784	-0.2048	0.0133	0.0365
250814_at	AT5G05080	UBC22 (UBIQUITIN-CONJUGATING ENZYME 22)	0.3636	0.0673	0.1489	0.2971	0.1114	0.1685	0.6131	0.0137	0.0465	0.5466	0.02	0.0455
250815_s_at	AT5G05040;AT5G05060	[AT5G05040, cysteine protease inhibitor];[AT5G05	0.4158	0.0392	0.1143	0.361	0.0587	0.1205	-0.4862	0.0242	0.0631	-0.541	0.0171	0.0419
250816_at	AT5G05010	dathrin adaptor complexes medium subunit-related	0.5129	0.0438	0.1207	0.2923	0.173	0.2148	0.09378	0.6232	0.4057	-0.1268	0.5121	0.3306
250817_at	AT5G04940	SUVH1 (SU(VAR)3-9 HOMOLOG 1)	0.0711	0.2971	0.3214	-0.1666	0.0485	0.1094	-0.1901	0.0237	0.0624	-0.4277	0.0013	0.0133
250818_at	AT5G04930	ALA1 (AMINOPHOSPHOLIPID ATPASE1); ATPase	0.4024	0.0086	0.0604	0.6086	0.0083	0.0504	-0.3571	0.0445	0.0882	-0.3509	0.0468	0.0761
250819_at	AT5G05100	nucleic acid binding	0.6621	0.0146	0.0732	0.5403	0.0282	0.0835	0.05029	0.7469	0.4472	-0.07148	0.6488	0.3804
250820_at	AT5G05160	leucine-rich repeat transmembrane protein kinase,	0.215	0.3802	0.3646	-0.2215	0.3674	0.3263	0.8478	0.0167	0.0514	0.4113	0.127	0.1396
250821_at	AT5G05190	Identical to Uncharacterized protein At5g05190 (Y-	-0.3022	0.4206	0.3852	-0.2675	0.4718	0.3729	0.103	0.4809	0.3517	0.1377	0.358	0.2661
250822_at	AT5G05230	ubiquitin-protein ligase	0.3793	0.0681	0.1499	0.6472	0.0133	0.0615	-0.2798	0.1092	0.1478	-0.01183	0.9349	0.467
250823_at	AT5G05180	similar to unknown protein [Arabidopsis thaliana] (T	0.1

250890_at	AT5G04520	oxidoreductase/ transition metal ion binding	0.9338	0.0015	0.038	0.806	0.0026	0.0342	-0.2548	0.1026	0.143	-0.3826	0.034	0.0623
250891_at	AT5G04530	beta-ketoacyl-CoA synthase family protein	-0.1936	0.7808	0.518	-0.213	0.7597	0.4778	0.2077	0.0899	0.1325	0.1883	0.1136	0.1302
250892_at	AT5G03760	ATCSLA09 (RESISTANT TO AGROBACTERIUM T	-1.9407	0.0029	0.0435	-2.0792	0.0023	0.0334	-0.2761	0.1754	0.1956	-0.4146	0.069	0.0962
250893_at	AT5G03795	oxidoreductase	-0.2713	0.7502	0.5086	0.6616	0.4524	0.365	0.1912	0.8219	0.4703	1.1242	0.2305	0.2017
250894_s_at	AT5G03810;AT5G03820	GDS_motif lipase/hydrolase family protein (AT5G03820, GDS	1.463	0.2233	0.2772	0.4728	0.6659	0.447	-0.3792	0.714	0.4362	-1.3694	0.2283	0.2006
250895_at	AT5G03850	40S ribosomal protein S28 (RPS28B)	-0.1477	0.3253	0.3375	-0.02354	0.867	0.509	0.3325	0.0652	0.1101	0.4566	0.0257	0.0531
250896_at	AT5G03860	nucleobase:cation symporter	0.3074	0.106	0.1884	-0.1922	0.2633	0.2717	-0.4631	0.0177	0.0533	-0.9626	0.0013	0.0131
250897_at	AT5G03430	phosphoadenosine phosphosulfate (PAPS) reducta	0.1513	0.4862	0.4141	0.1356	0.5301	0.3964	-0.6275	0.0143	0.0477	-0.6432	0.0132	0.0364
250898_at	AT5G03300	ADK2 (ADENOSINE KINASE 2); kinase	-0.1286	0.4832	0.4132	-0.4554	0.0522	0.1133	0.4394	0.0164	0.0511	0.1126	0.3656	0.2694
250899_at	AT5G03340	(Cell division control protein 48 homolog E); ATPase	0.7513	0.0131	0.0706	1.0717	0.0037	0.0386	-0.3798	0.0335	0.0747	-0.05938	0.6451	0.3791
250900_at	AT5G03470	ATB' ALPHA (PP2A_B' subunit, alpha isoform); pro	0.4529	0.0534	0.1326	0.6708	0.0159	0.0655	-0.5386	0.0321	0.073	-0.3207	0.127	0.1396
250901_at	AT5G03530	ATRAB ALPHA (Arabidopsis Rab GTPase homolog	-0.4954	0.1039	0.1862	0.04652	0.8534	0.5057	0.1291	0.6136	0.4022	0.671	0.0468	0.0761
250902_at	AT5G03590	GDSL-motif lipase/hydrolase protein-related	-0.1111	0.9303	0.56	-1.4879	0.2805	0.2811	0.2761	0.8151	0.4683	-1.1007	0.3758	0.2738
250903_at	AT5G03600	GDSL-motif lipase/hydrolase family protein	0.4371	0.3044	0.3254	0.177	0.6585	0.4445	0.3931	0.3494	0.2929	0.133	0.7383	0.4098
250904_at	AT5G03620	subtilase family protein	-0.716	0.5341	0.4347	-0.8464	0.4668	0.3707	0.5977	0.2906	0.2639	0.4673	0.3953	0.2824
250905_at	AT5G03640	protein kinase family protein	-0.4351	0.4529	0.3995	-1.3163	0.0659	0.1284	0.2511	0.6568	0.4168	-0.6301	0.2954	0.2363
250906_at	AT5G03650	SBE2.2 (STARCH BRANCHING ENZYME 2.2); 1,4	0.07911	0.5414	0.4374	-0.6044	0.007	0.0473	-0.197	0.1721	0.1934	-0.8806	0.0018	0.0147
250907_at	AT5G03670	similar to unknown protein [Arabidopsis thaliana] (T	0.09424	0.8796	0.5464	-0.9203	0.1902	0.2265	0.205	0.7433	0.4459	-0.8096	0.238	0.206
250908_at	AT5G03680	PTL (PETAL LOSS); transcription factor	1.1608	0.1309	0.2092	1.8926	0.0365	0.0943	-0.22	0.52	0.367	0.5118	0.1766	0.1711
250909_at	AT5G03700	PAN domain-containing protein	-0.451	0.1627	0.236	-0.2632	0.3751	0.33	-0.05728	0.8388	0.4752	0.1305	0.647	0.3797
250910_at	AT5G03720	AT-HSFA3 (Arabidopsis thaliana heat shock transc	2.2593	0.0239	0.09	2.5573	0.0159	0.0658	-0.3258	0.6075	0.4005	-0.02771	0.9645	0.4744
250911_at	AT5G03730	CTR1 (CONSTITUTIVE TRIPLE RESPONSE 1); ke	0.7613	0.0102	0.064	0.6208	0.0202	0.0727	-0.4205	0.0648	0.1098	-0.561	0.028	0.0558
250912_at	AT5G03740	HDZC (HISTONE DEACETYLASE 2C); nucleic acid	0.4246	0.0851	0.1691	0.2852	0.201	0.2332	0.4179	0.0213	0.0587	0.2785	0.0705	0.0973
250913_at	AT5G03770	3-deoxy-D-manno-octulosonic acid transferase-rela	2.1672	0.0138	0.0719	0.7454	0.2226	0.2474	-0.2643	0.6359	0.4098	-1.6861	0.031	0.0593
250914_at	AT5G03780	TRFL10 (TRF-LIKE 10); DNA binding	1.2262	0.0382	0.124	1.1381	0.0475	0.1081	-0.07393	0.8071	0.4656	-0.162	0.5982	0.3629
250915_at	AT5G03790	ATHB51/ATMI1 (LATE MERISTEM IDENTITY1); DN	0.3845	0.7332	0.5033	-1.2038	0.3163	0.3009	1.5757	0.2085	0.2169	-0.01251	0.9911	0.4804
250916_at	AT5G03630	ATMDAR2; monodehydroascorbate reductase (NA	0.5094	0.0454	0.1226	0.5852	0.0299	0.086	-0.04325	0.744	0.4462	0.03262	0.8048	0.4301
250917_at	AT5G03690	fructose-bisphosphate aldolase, putative	0.1828	0.1121	0.1941	0.04724	0.6275	0.4335	0.1414	0.9193	0.2063	0.005844	0.9514	0.4713
250918_at	AT5G03610	GDSL-motif lipase/hydrolase family protein	0.6963	0.0565	0.1362	0.7225	0.0509	0.112	0.5278	0.1022	0.1428	0.554	0.0909	0.1135
250919_at	AT5G03660	similar to unknown protein [Arabidopsis thaliana] (T	-0.2222	0.3494	0.3495	0.4534	0.0968	0.1568	0.05436	0.8084	0.4661	0.7299	0.0254	0.0526
250920_at	AT5G03390	similar to unknown protein [Arabidopsis thaliana] (T	-0.3572	0.5664	0.4474	-1.1705	0.1103	0.1676	1.0703	0.1348	0.2157	0.1674	0.257	0.1896
250921_at	AT5G03460	similar to unknown [Populus trichocarpa] (GB:ABK9	0.9749	0.0062	0.0542	1.4865	0.0013	0.0309	0.4189	0.0503	0.095	0.9305	0.0035	0.0194
250922_at	AT5G03345	similar to unknown protein product [Vitis vinifera] (G	0.4105	0.0251	0.0919	0.5128	0.0121	0.0589	0.1385	0.1308	0.1645	0.2407	0.03	0.0582
250923_at	AT5G03455	CDC26	0.7795	1.00E-04	0.0312	0.7809	3.00E-04	0.0249	-0.03721	0.5966	0.3969	-0.3359	0.0086	0.0252
250924_at	AT5G03440	similar to unknown protein [Arabidopsis thaliana] (T	0.3055	0.3917	0.3709	0.3537	0.329	0.3081	0.8268	0.0603	0.1055	0.875	0.0515	0.0809
250925_at	AT5G03370	acylphosphatase family	-0.3767	0.0094	0.0624	-0.04169	0.6316	0.4351	0.3785	0.0028	0.0241	0.7135	2.00E-04	0.0079
250926_at	AT5G03555	permease, cytosine/purines, uracil, thiamine, allanto	-0.3003	0.2397	0.2874	-0.6624	0.0382	0.0968	-0.1077	0.6043	0.3996	-0.4697	0.0704	0.0972
250927_at	AT5G03270	similar to unknown protein [Arabidopsis thaliana] (T	-0.6816	0.162	0.2354	-0.8997	0.0867	0.1484	-0.252	0.3204	0.2785	-0.4701	0.102	0.122
250928_at	AT5G03280	EIN2 (ETHYLENE INSENSITIVE 2); transporter	0.7371	0.0146	0.0734	0.3205	0.1478	0.1965	-0.1588	0.263	0.2481	-0.5754	0.0092	0.0299
250929_at	AT5G03630	isocitrate dehydrogenase, putative / NAD+ isocitrate	0.658	0.0148	0.0737	0.6864	0.0129	0.0605	-0.2181	0.0642	0.1093	-0.1897	0.0919	0.1143
250930_at	AT5G03160	DNAJ heat shock N-terminal domain-containing pro	0.7857	0.0606	0.141	0.7026	0.0813	0.1429	0.309	0.1057	0.1455	0.2259	0.2025	0.1866
250931_at	AT5G03200	zinc finger (C3HC4-type RING finger) family protein	0.8474	4.00E-04	0.032	0.9208	3.00E-04	0.0249	0.1817	0.08	0.1238	0.2552	0.0306	0.0589
250932_s_at	AT5G03220, AT5G03500	[AT5G03220, transcriptional co-activator-related];[A	0.1954	0.1843	0.2513	0.3217	0.0577	0.1194	0.3326	0.0431	0.0867	0.4589	0.0157	0.0399
250933_at	AT5G03170	FLA11 (fasciclin-like arabinogalactan-protein 11)	-0.4084	0.0736	0.1561	-0.4976	0.0426	0.1026	0.4651	0.0517	0.0964	0.3759	0.0909	0.1135
250934_at	AT5G03030	DNAJ heat shock N-terminal domain-containing pro	-0.5947	0.1075	0.1896	-0.6292	0.0939	0.1544	0.9614	0.0163	0.051	0.9269	0.0184	0.0436
250935_at	AT5G03240	UBQ3 (POLYUBIQUITIN 3); protein binding	0.8221	0.0161	0.0768	1.6712	0.0012	0.0303	-1.456	2.00E-04	0.013	-0.6099	0.0064	0.0247
250936_at	AT5G03120	similar to hypothetical protein [Vitis vinifera] (GB:CA	-1.6054	0.0393	0.1143	-1.7515	0.0301	0.0863	1.3852	0.0046	0.0289	1.2391	0.0069	0.0258
250937_at	AT5G03230	similar to unknown protein [Arabidopsis thaliana] (T	0.7506	0.2789	0.3107	0.8519	0.2285	0.2606	0.2828	0.0475	0.0915	0.384	0.0185	0.0436
250938_at	AT5G03180	zinc finger (C3HC4-type RING finger) family protein	0.05301	0.7826	0.5184	-0.07982	0.6798	0.4518	-0.02059	0.9139	0.4962	-0.1534	0.4393	0.301
250939_at	AT5G03040	IQD2 (IQ-domain 2); calmodulin binding	-1.0351	0.0062	0.0542	-0.9122	0.0097	0.0537	-0.7954	0.0011	0.0183	-0.6725	0.0021	0.0156
250940_at	AT5G03310	auxin-responsive family protein	0.3159	0.7662	0.5133	-2.2126	0.0897	0.1509	0.9388	0.3978	0.3155	-1.5896	0.1845	0.176
250941_at	AT5G03320	protein kinase, putative	0.3876	0.0121	0.0682	0.5834	0.0028	0.0351	-0.1927	0.0154	0.0494	0.003003	0.9527	0.4717
250942_at	AT5G03350	legume lectin family protein	0.002603	0.9918	0.575	-0.296	0.2819	0.282	0.6189	0.0098	0.0396	0.3203	0.0749	0.1006
250943_at	AT5G03360	DC1 domain-containing protein	-0.7458	0.5985	0.4591	0.5128	0.7146	0.4635	0.9096	0.5171	0.3659	2.1682	0.166	0.1648
250944_at	AT5G03660	heavy-metal-associated domain-containing protein	-0.4418	0.0392	0.1142	-0.3183	0.0952	0.1555	0.1268	0.2812	0.2588	0.2503	0.0699	0.0968
250945_at	AT5G03400	unknown protein	1.7661	0.0862	0.1703	-0.00597	0.9943	0.5427	0.5191	0.5421	0.3762	-1.253	0.1834	0.1755
250946_at	AT5G03420	dentin sialophosphoprotein-related	-0.4892	0.0103	0.0642	-0.1667	0.1945	0.229	-0.4337	0.0025	0.0234	-0.1112	0.1594	0.1609
250947_at	AT5G03450	zinc finger (C3HC4-type RING finger) family protein	0.04398	0.8215	0.53	0.2993	0.1767	0.2174	-0.2739	0.2082	0.2167	-0.01858	0.9239	0.4638
250948_at	AT5G03490	UDP-glucuronosyl/UDP-glucosyl transferase family	-0.1994	0.355	0.3523	-0.07136	0.7274	0.468	-0.3009	0.19	0.2055	-0.1728	0.4164	0.2911
250949_at	AT5G03510	zinc finger (C2H2 type) family protein	0.09479	0.7462	0.5078	-0.6071	0.0905	0.1517	1.0284	0.0197	0.0564	0.3265	0.2982	0.2377
250950_at	no_match	no_match	0.3715	0.2342	0.2839	0.6922	0.0596	0.1213	-0.2691	0.1209	0.157	0.05162	0.7254	0.4058
250951_at	AT5G03550	similar to meprin and TRAF homology domain-conta	-2.0783	0.0879	0.1719	-0.4426	0.6572	0.4442	-1.2776	0.2392	0.2348	0.3581	0.7183	0.4034
250952_at	AT5G03570	iron-responsive transporter-related	-0.0266	0.9454	0.5635	0.07812	0.8411	0.5017	-0.08019	0.7367	0.4438	0.02453	0.9175	0.462
250953_at	AT5G03415	SPB	-0.05913	0.6567	0.4779	0.09646	0.4779	0.3754	0.1546	0.1737	0.1945	0.3102	0.0295	0.0576
250954_at	AT5G03520	ATRABE1/AtRab8C; GTP binding	-0.6183	0.0093	0.0622	-0.3351	0.0636	0.1257	0.07537	0.2155	0.2212	0.3585	0.0022	0.0157
250955_at	AT5G03190	CPuORF47 (Conserved peptide upstream open rea	-0.3936	0.054	0.1332	-0.09798	0.538	0.3996	-0.5987	0.0147	0.0484	-0.3031	0.1059	0.1246
250956_at	AT5G03210	unknown protein	-0.1608	0.7915	0.5213	0.2308	0.7058	0.4609	-0.3376	0.585	0.3927	0.05405	0.9289	0.4653
250957_at	AT5G03250	phototropic-responsive NPH3 family protein	0.1408	0.8985	0.5508	-0.4384	0.694	0.4568	-1.0385	0.373	0.3043	-1.6178	0.1935	0.1811
250958_at	AT5G03260	LAC11 (laccase 11); copper ion binding / oxidoredu	0.02153	0.9429	0.5631	-0.4772	0.1662	0.2099	0.1689	0.5578	0.3819	-0.3298	0.2805	0.2284
250959_at	AT5G03520	ubiquitin-protein ligase	0.655	0.427	0.3881	-0.3008	0.7058	0.4609	0.7558	0.5843	0.4749	0.3495	-0.3715	0.6427	0.3781
250960_at	AT5G02940	similar to phosphotransferase-related [Arabidopsis t	-0.1891	0.5193	0.4289	-0.7677	0.0457	0.1059	-0.4313	0.0054	0.0308	-1.0099	2.00E-04	0.0078
250961_at	AT5G02980	kelch repeat-containing F-box family protein	0.07413	0.8914	0.5487	-0.03466	0.949	0.5318	0.4823	0.328	0.2824	0.3735	0.4372	0.3001
250962_at	AT5G03000	kelch repeat-containing F-box family protein	0.06257	0.8686	0.5434	-0.3712	0.3545	0.3202	0.8584	0.0728	0.1173	0.4246	0.2974	0.2373
250963_at	AT5G03000	kelch repeat-containing F-box family protein	1.0679	0.1284	0.2071	-0.6063	0.3387	0.313	0.3539	0.4905	0.3558	-0.1077	0.8289	0.4368
250964_at	no_match	no_match	-1.3112	0.2722	0.3067	-0.07569	0.945	0.5306	-1.228	0.1646	0.1882	0.007463	0.9923	0.4807
250965_at	AT5G03020	kelch repeat-containing F-box family protein	0.9201	0.2845	0.314	0.5961	0.4686	0.3714	0.282	0.7244	0.44	-0.042	0.9578	0.4729
250966_at	AT5G02910	F-box family protein	-0.0489	0.7405	0.506	0.1487	0.3411	0.314	-0.3161	0.0506	0.0954	-0.1186	0.3584	0.2663
250967_at	AT5G02790	In2-1 protein, putative	-0.02456	0.9243	0.5581	0.1367	0.6034	0.4247	0.2699	0.3256	0.2811	0.4311	0.1482	0.1535
250968_at	AT5G02890	transferase family protein	-1.2443	0.0533	0.1325	-1.0156	0.0911	0.1523	0.4636	0.2164	0.2215	0.6923	0.0937	0.1158
250969_at	AT5G02740	nucleotide binding	0.1231	0.5631	0.446	0.3491	0.1488	0.1973	0.3396	0.1574	0.184	0.5656	0.0445	0.074
250970_at	AT5G02770	similar to unknown protein product [Vitis vinifera] (G	-1.1125	0.0248	0.0915	-0.221	0.5248	0.394	-2.362	0.0017	0.0206	-1.4706	0.0098	0.0309
250971_at	AT5G02810	PRR7 (PSEUDO-RESPONSE REGULATOR 7); tra	0.4625	0.1923	0.2571	0.3321	0.3236	0.3052	-0.8721	4.00E-04	0.0147	-1.0025	2.00E-04	0.0078
250972_at	AT5G02840	LCL1 (LHY/CCA1-LIKE 1); DNA binding / transcript	-0.4012	0.0309	0.1019	-0.3833	0.0355	0.0929	-1.2165	6.00E-04	0.0158	-1.1986	6.00E-04	0.0103
250973_at	AT5G02870	60S ribosomal protein L4/L1 (RPL4D)	0.2045	0.1846	0.2514	-0.3453	0.0539	0.1152	0.6697	0.0063	0.0328	0.1199	0.401	0.2846
250974_at	AT5G02820	RHL2 (ROOT HAIRLESS 2); ATP binding / DNA bi	0.492	0.06	0.14	0.799	0.0134	0.0617	-0.4334	0.0837	0.1273	-0.1264	0.5407	0.3412
250975_at	AT5G03050	similar to hypothetical protein [Vitis vinifera] (GB:CA	-0.2372	0.5277	0.4322	0.345	0.3719	0.3283	-0.04743	0.8866	0.4887	0.5348	0.1618	0.1623
250976_at	AT5G03060	similar to unknown protein [Arabidopsis thaliana] (T	0.09953	0.7912	0.5212	0.2561	0.5068	0.3873	0.1662	0.435	0.3319	0.3227	0.1677	0.1658
250977_at	AT5G03070	binding	0.04648	0.8395	0.5352	-0.04746	0.8362	0.5005	0.1118	0.6306	0.4081	0.01788	0.9377	0.4678
250978_at	AT5G03080	phosphatidic acid phosphatase-related / PAP2-relat	0.1695	0.5631	0.446	0.4129	0.1998	0.2327	-0.3862	0.2247	0.2264	-0.1428	0.6239	0.3715
250979_at	AT5G03090	similar to unknown protein [Arabidopsis thaliana] (T	0.3875	0.694	0.4908	-1.4374	0.1916	0.2272	1.342	0.21	0.2178	-0.4829	0.6198	0.3703
250980_at	AT5G03130	unknown protein	-0.1571	0.6735	0.4838	-1.239	0.0232	0.0768	0.6246	0.0974	0.1389	-0.4573	0.1896	0.179
250981_at	AT5G03140	lectin protein kinase family protein	-0.8748	0.0136	0.0717	-1.0329	0.0076	0.0489	0.05013	0.8211	0.4701	-0.108	0.6305	0.3737
250982_at	AT5G03150	JKD (JACKDAW); nucleic acid binding / protein bind	0.5116	0.3999	0.3752	-0.9227	0.1649	0.209	0.515	0.3971	0.3152	-0.9193	0.1661	0.1649
250983_at	AT5G02780	In2-1 protein, putative	2.0825	0.0495	0.1278	1.8501	0.0686	0.1314	0.5279	0.4421	0.335	0.2955	0.6582	0.3835
250984_at	AT5G02800	protein kinase family protein	0.09405	0.5962	0.4584	0.02212	0.899	0.5186	0.0937	0.376	0.3057	0.02177	0.8285	0.4367
250985_at	AT5G02830	pentaticopeptide (PPR) repeat-containing protein	-0.3977	0.2727	0.307	-0.4308	0.2407	0.2583	-0.9532	0.0065	0.0331	-0.9862	0.0057	0.0235
250986_at	AT5G02850	hydroxyproline-rich glycoprotein family protein	0.6278	0.0029	0.0431	0.2982	0.0363	0.0941	0.2603	0.0187	0.0548	-0.06935	0.3658	0.2695
250987_at	AT5G02860	pentaticopeptide (PPR) repeat-containing protein	0.8118	0.0541	0.1334	0.8126	0.0539	0.1152	-0.2228	0.4998	0.3596	-0.2219	0.5014	0.3264
250988_at	AT5G02880	UPL4 (ubiquitin-protein ligase 4)	0.602	0.0398	0.1151	0.4787	0.0753	0.1377	-0.9886	0.0066	0.0334	-1.1118	0.0043	0.0209
250989_at	AT5G02900	CYP86A13 (cytochrome P450, family 86, subfamily	0.2203	0.8657	0.5425	-1.2804	0.354	0.3201	1.1433	0.4026	0.3176	-0.3574	0.7845	0.4242
250990_at	AT5G02290	NAK; kinase	0.7404	0.0251	0.0919	0.7443	0.0247	0.0788	0.05808	0.4798	0.3513	0.06202	0.4525	0.307
250991_at	AT5G02380	MT2B (METALLOTHIONEIN 2B)	-0.3478	0.0655	0.1467	-0.3829	0.0502	0.1111	0.4386	0.0022	0.0221	0.4034	0.003	0.0178
250992_at	AT5G02400	ATEXPA9 (ARABIDOPSIS THALIANA EXPANSIN,	-0.5689	0.0164	0.0771	-0.3068	0.0983	0.158	-0.31	0.0959	0.1376	-0.04788	0.7544	0.415
250993_at	AT5G02280	synbindin, putative	-0.00391	0.975	0.571	0.2821	0.0736	0.1362	0.4292	0.0144	0.0479	0.7152	0.0023	0.0161
250994_at	AT5G02490	heat shock cognate 70 kDa protein 2 (HSC70-2) (H	2.1524	0.0032	0.0445	1.7926	0.0063	0.0456	0.08253	0.7059	0.4333	-0.2773	0.2448	0.2096
250995_at	AT5G02500	HSC70-1 (heat shock cognate 70 kDa protein 1); A	0.04285	0.8061	0.5257	-0.2406	A 215	0.2427	-0.5277	0.0059	0.0321	-0.8111	0.0012	0.0128
250996_at	AT5G02530	RNA and export factor-binding protein, putative	0.3242	0.1013	0.1841	0.4787	0.0351	0.0926	0.2098	0.0569	0.1018	0.3643	0.01	0.0312
250997_at	AT5G02570	histone H2B, putative	-0.583	0.3651	0.3569	0.927	0.18	0.2195	0.7327	0.2689	0.2516	2.2426	0.0172	0.0419
250998_at	AT5G02620	ankyrin repeat family protein	0.6392	0.0012	0.036	0.5272	0.0025	0.0339	0.05025	0.5527	0.38	-0.06172	0.4711	0.3141
250999_at	AT5G02630	similar to unknown protein [Arabidopsis thaliana] (T	0.5793	0.0446	0.1217	0.6317	0.0345	0.0918	-0.2669	0.0931	0.1352	-0.2145	0.1524	0.1563
251000_at	AT5G02650	similar to unknown protein [Arabidopsis thaliana] (T	0.02727	0.9203	0.5571	-0.02659	0.9223	0.5247	-0.4925	0.0119	0.0433	-0.5464	0.0083	0.0283
251001_at	AT5G02670	similar to polynucleotide adenylyltransferase/ protei	-0.3275	0.5972	0.4586	0.5632	0.3801	0.3321	-1.2832	0.0881	0.131	-0.3925	0.5299	0.3379
251002_at	AT5G02680	ATP binding / aminoacyl-tRNA ligase/ nucleotide bi	0.6904	0.2688	0.3047	0.224	0.6986	0.4585	-1.1287	0.0684	0.1135	-1.5951	0.0249	0.052
251003_at	AT5G02690	unknown protein	0.7042	0.097	0.1799	0.5217	0.165	0.2231	-2.519	7.00E-04	0.016	-1.2931	0.0087	0.0289
251004_at	AT5G02720	similar to unknown protein [Arabidopsis thaliana] (T	0.3287	0.4974	0.4194	0.304	0.5285	0.3956	0.2668	0.5778	0.3898	0.242	0.6122	0.3675
251005_at	AT5G02590	chloroplast lumen common family protein	-0.2787	0.5708	0.4494	0.01712	0.9716	0.5371	0.1206	0.8027	0.4644	0.4164	0.4089	0.2878
251006_at	AT5G02600	heavy-metal-associated domain-containing protein	-0.3038	0.1403	0.2178	-0.02742	0.8764	0.5121	0.6824	0.0146	0.0482	0.9587	0.0044	0.0211
251007_at	AT5G02610	60S ribosomal protein L35 (RPL35D)	0.3934	0.0518	0.1307	0.6537	0.0104	0.0552	-0.2208	0.1272	0.1619	0.03941	0.7491	0.4134
251008_at	AT5G02710	similar to unknown protein product [Vitis vinifera] (G	-0.2852	0.1481	0.2238	-0.2397	0.207	0.2376	0.1445	0.4159	0.3234	0.19	0.2992	0.2382
251009_at	AT5G02640	similar to unknown protein [Arabidopsis thaliana] (T	0.2362	0.6382	0.4724	-0.4931	0.3486	0.3175	1.7305	0.0204	0.0575	1.0014	0.0976	0.1187
251010_at	AT5G02550	unknown protein	-0.6438	0.2191	0.2745	-0.1587	0.7378	0.4706	0.58	0.1226	0.1585	1.0652	0.0231	0.0495
251011_at	AT5G02560	HTA12; DNA binding	-0.5171	0.0355	0.1087	-0.3493	0.1026	0.1616	0.9615	7.00E-04	0.016	1.1292	4.00E-04	0.0089
251012_at	AT5G02580	similar to unknown protein [Arabidopsis thaliana] (T	-1.442	0.3495	0.3495	1.8708	0.1971	0.231	0.4011	0.7294	0.4416	0.9277	0.4391	0.301
251013_at	AT5G02540	short-chain dehydrogenase/reductase (SDR) family	-0.9796	0.0025	0.0421	-1.0945	0.0016	0.0317	0.181	0.2737	0.2544	0.0661	0.6674	0.3866
251014_at	AT5G02520	unknown protein	-0.06113	0.8981	0.5507	0.4906	0.3352	0.3109	-0.1731	0.719	0.4382	0.3786	0.4458	0.3044
251015_at	AT5G02510	similar to SLT1 (SODIUM- AND LITHIUM-TOLERA	0.7114	0.0288	0.0983	-0.3449	0.1806	0.2199	-0.6771	0.0335	0.0748	-0.3105	0.2184	0.1953
251016_at	AT5G02730	allergen V5/Tpx-1-related family protein	0.5192	0.6566	0.4779	-0.8746	0.4646	0.3698	1.17	0.3407	0.2886	-0.2237	0.8464	0.4418
251017_at	AT5G02760	protein phosphatase 2C family protein / PP2C famil	-1.3797	0.0015	0.038	-1.1146	0.0033	0.0371	-0.2411	0.1123	0.1502	0.02409	0.8492	0.4426
251018_at	AT5G02450	60S ribosomal protein L36 (RPL36C)	0.4244	0.0397	0.115	1.0177	0.002	0.033	-0.07043	0.6441	0.4123	0.5229	0.0208	0.0467
251019_at	AT5G02420	similar to unknown protein [Arabidopsis thaliana] (T	-0.5096	0.2068	0.2663	0.05887	0.8704	0.51	-0.1135	0.5677	0.3858	0.4549	0.0673	0.0946
251020_at	AT5G02270	ATNAP9 (Non-intrinsic ABC protein 9)	-0.5436	0.1534	0.2286	-0.5084	0.1753	0.2164	0.1031	0.6412	0.4115	0.1382	0.5367	0.3402
251021_at	AT5G02440	thaumatin-like protein, putative	0.4255	0.2466	0.2915	1.1823	0.3915	0.3374	-0.106	0.9241	0.4989	-0.5942	0.6	0.3634
251022_at	AT5G02150	binding	0.9468	0.0012	0.036	1.023	9.00E-04	0.0284	-0.9552	0	0.0092	-0.879	1.00E-04	0.0056
251023_at	AT5G02170	amino acid transporter family protein	0.1541	0.6983	0.492	0.2077	0.6045	0.425	-0.7951	0.0525	0.0972	-0.7415	0.0636	0.0916
251024_at	AT5G

251090_at	AT5G01340	mitochondrial substrate carrier family protein	0.03166	0.9058	0.5527	0.2837	0.3217	0.3041	-0.3745	0.2101	0.2179	-0.1225	0.6513	0.3813
251091_at	AT5G01410	PDX1 (PYRIDOXINE BIOSYNTHESIS 1 3); protein	-0.4085	0.0449	0.1222	-0.6739	0.0089	0.0518	0.2038	0.0448	0.0886	-0.06158	0.4328	0.298
251092_at	AT5G01470	similar to unnamed protein product [Vitis vinifera] (G	0.2366	0.267	0.3034	-0.1965	0.3447	0.3155	-0.1194	0.5508	0.3794	-0.5525	0.0396	0.0686
251093_at	AT5G01360	similar to unknown protein [Arabidopsis thaliana] (T	-0.07918	0.7591	0.5115	-0.1952	0.4637	0.3697	0.4084	0.128	0.1626	0.2924	0.2423	0.2083
251094_at	AT5G01350	similar to predicted protein [Physcomitrella patens s	0.3892	0.0995	0.182	0.1872	0.3623	0.324	-0.07183	0.7135	0.436	-0.2738	0.2072	0.1892
251095_at	AT5G01510	similar to unknown protein [Arabidopsis thaliana] (T	-0.7519	0.0101	0.064	-0.6834	0.014	0.0627	-1.1461	0.0011	0.0181	-1.0776	0.0013	0.0133
251096_at	AT5G01550	lectin protein kinase, putative	0.9027	0.014	0.0723	0.9408	0.0122	0.0591	0.2053	0.3522	0.2943	0.2435	0.2803	0.2284
251097_at	AT5G01560	lectin protein kinase, putative	1.6175	0.266	0.3028	-0.1244	0.9257	0.5255	0.09563	0.9024	0.4931	-1.6462	0.0879	0.1112
251098_at	AT5G01650	macrophage migration inhibitory factor family protei	-0.02919	0.83	0.5325	-0.3588	0.048	0.1088	0.6108	0.0018	0.0206	0.2812	0.0269	0.0545
251099_at	AT5G01660	kelch repeat-containing protein	1.994	0.082	0.1657	-0.8062	0.4032	0.3427	1.8259	0.0973	0.1388	-0.9743	0.314	0.2455
251100_at	AT5G01670	aldose reductase, putative	-0.05828	0.6338	0.4708	-0.1487	0.2591	0.2695	-0.8489	0.0017	0.0205	-0.9394	0.0012	0.0127
251101_at	AT5G01680	ATCHX26 (cation/hydrogen exchanger 26); monova	-0.5252	0.6838	0.4871	-2.3152	0.1255	0.1796	1.5262	0.2717	0.2532	-0.2638	0.8365	0.4391
251102_at	AT5G01690	ATCHX27 (cation/hydrogen exchanger 27); monova	-0.8716	0.3633	0.356	-0.3414	0.7086	0.4616	-1.1432	0.1789	0.1978	-0.6131	0.432	0.2977
251103_at	AT5G01700	protein phosphatase 2C, putative / PP2C, putative	0.3301	0.5128	0.4262	-0.9258	0.1146	0.1708	-0.4676	0.3583	0.2971	-1.7235	0.0187	0.0439
251104_at	AT5G01720	F-box family protein (FBL3)	-0.08778	0.6407	0.4734	-0.00476	0.9795	0.5393	-0.5906	0.0063	0.0328	-0.5076	0.0106	0.0323
251105_at	AT5G01730	WAVE3	-0.2974	0.3504	0.3498	-0.6098	0.0963	0.1563	0.1943	0.0574	0.1024	-0.1181	0.1836	0.1756
251106_at	AT5G01500	mitochondrial substrate carrier family protein	-0.4298	0.0384	0.1128	-0.3998	0.0474	0.108	0.06755	0.4889	0.3542	0.09751	0.3314	0.254
251107_at	AT5G01610	Identical to Uncharacterized protein At5g01610 [Ara	0.5953	0.051	0.1299	0.8622	0.0162	0.0663	0.4012	0.0932	0.1353	0.6681	0.0217	0.0479
251108_at	AT5G01620	similar to unknown protein [Arabidopsis thaliana] (T	0.1682	0.4239	0.3868	0.02281	0.9098	0.5215	-0.1375	0.4164	0.3236	-0.2829	0.1359	0.1456
251109_at	AT5G01600	ATFER1 (FERRETIN 1); ferric iron binding	-0.02525	0.8664	0.5425	0.01669	0.9113	0.5219	0.4176	0.0118	0.0429	0.4595	0.0084	0.0286
251110_at	AT5G01260	glycoside hydrolase starch-binding domain-contain	-0.6975	0.2056	0.2658	-0.5497	0.2999	0.2913	-0.1471	0.6948	0.4293	0.000812	0.9983	0.4825
251111_at	AT5G01310	basic helix-loop-helix (bHLH) family protein	0.198	0.5703	0.4492	-0.1184	0.7282	0.4683	0.03386	0.9028	0.4931	-0.2805	0.3417	0.2588
251112_s_at	AT5G01320;AT5G01330	[AT5G01320, pyruvate decarboxylase, putative];[AT	-0.2092	0.211	0.269	-0.2539	0.1454	0.1948	-0.4987	0.2239	0.0627	-0.5434	0.0181	0.0432
251113_at	AT5G01370	unknown protein	0.6781	0.0075	0.0579	0.4845	0.0234	0.077	0.6716	0.0036	0.0265	0.478	0.0121	0.0347
251114_at	AT5G01380	transcription factor	-0.4671	0.4062	0.3794	-0.2567	0.637	0.4372	0.01931	0.9431	0.504	0.2296	0.4177	0.2916
251115_at	AT5G01400	ESP4 (ENHANCED SILENCING PHENOTYPE 4);	0.22	0.1925	0.2572	0.3321	0.0773	0.1394	-0.9289	1.00E-04	0.012	-0.8167	2.00E-04	0.0078
251116_at	AT5G03470	SCPL40 (serine carboxypeptidase-like 40); serine c	-1.5913	0.2011	0.2628	-1.4159	0.2454	0.2613	-0.3312	0.7663	0.453	-0.1558	0.8883	0.4537
251117_at	AT5G03390	similar to unnamed protein product [Vitis vinifera] (G	0.03706	0.769	0.6143	-0.2201	0.1353	0.187	-0.01798	0.7475	0.4474	-0.2751	0.0062	0.0244
251118_at	AT3G63410	APG1 (ALBINO OR PALE GREEN MUTANT 1); me	-0.2041	0.0735	0.1561	-0.5656	0.0026	0.0342	0.06923	0.4594	0.3428	-0.2922	0.026	0.0534
251119_at	AT5G03510	FAD binding / catalytic/ tRNA dihydrouridine synthe	-0.7156	0.1537	0.2287	-0.961	0.0776	0.1397	-0.7567	0.1084	0.1473	-1.0022	0.0525	0.0817
251120_at	AT5G03490	ribosomal protein L1 family protein	-0.1657	0.0562	0.136	-0.4022	0.0029	0.0355	0.004433	0.9424	0.5038	-0.2321	0.0158	0.04
251121_at	AT3G63420	AGG1 (ARABIDOPSIS GGAMMA-SUBUNIT 1)	0.3939	0.1035	0.1859	0.6331	0.0278	0.0831	-0.1258	0.4092	0.3205	0.1134	0.4533	0.3073
251122_at	AT5G01020	protein kinase family protein	-0.17	0.3309	0.3404	-0.00767	0.9626	0.5347	-0.5639	0.0069	0.0339	-0.4015	0.0219	0.0482
251123_at	AT5G01030	similar to proline-rich family protein [Arabidopsis tha	0.09655	0.5704	0.4492	0.0267	0.8727	0.5108	0.01184	0.8967	0.4915	-0.05821	0.5275	0.337
251124_s_at	AT5G01050;AT5G01040	[AT5G01050, laccase family protein / diphenol oxid	-2.3199	0.0066	0.0549	-3.2402	0.0019	0.033	0.7626	0.1235	0.159	-0.1577	0.708	0.4002
251125_at	AT5G01060	protein kinase family protein	-0.2258	0.2242	0.2779	-0.9811	0.0034	0.0371	0.1314	0.4502	0.3386	-0.624	0.0165	0.0411
251126_at	AT5G01070	zinc finger (C3HC4-type RING finger) family protein	0.7831	0.268	0.3042	-0.5786	0.396	0.3395	1.804	0.0415	0.0447	0.4423	0.5081	0.329
251127_at	AT5G01080	beta-galactosidase	0.3019	0.8118	0.5273	-0.2606	0.8371	0.5008	-0.3648	0.774	0.4555	-0.9273	0.4785	0.317
251128_at	AT5G01110	pentatricopeptide (PPR) repeat-containing protein	0.387	0.7812	0.518	0.2729	0.8443	0.5028	-2.5405	0.102	0.1426	-2.6546	0.0917	0.1141
251129_at	AT5G01150	similar to unknown protein [Arabidopsis thaliana] (T	0.04574	0.8757	0.5454	-0.2483	0.4165	0.349	0.5506	0.1152	0.1526	0.2565	0.4027	0.2853
251130_at	AT5G01180	proton-dependent oligopeptide transport (POT) fam	-0.2799	0.601	0.46	-1.6598	0.0282	0.0836	1.369	0.0501	0.0949	-0.01091	0.9834	0.4788
251131_at	AT5G01190	LAC10 (laccase 10); copper ion binding / oxidoredu	-0.3883	0.5486	0.4405	-0.6773	0.3174	0.3016	-0.03618	0.935	0.5021	-0.3252	0.4789	0.3171
251132_at	AT5G01200	myb family transcription factor	-0.9222	0.4363	0.3921	-0.2686	0.668	0.4478	0.6891	0.2408	0.2355	0.9227	0.1392	0.1477
251133_at	AT5G01240	amino acid permease, putative	-0.4832	0.0144	0.0731	-0.596	0.007	0.0471	0.2475	0.0256	0.065	0.1346	0.1323	0.1432
251134_at	AT5G01270	CPL2 (CTD phosphatase-like 2); double-stranded R	-0.1391	0.3645	0.3564	0.1855	0.2444	0.2607	-0.7299	0.0058	0.0319	-0.4053	0.0408	0.0699
251135_at	AT5G01280	similar to proline-rich family protein [Arabidopsis tha	0.3125	0.8156	0.5285	-1.1795	0.4004	0.3413	2.1906	0.1572	0.1838	0.6886	0.6123	0.3675
251136_at	AT5G01290	mRNA guanylyltransferase	0.27	0.3158	0.332	0.3458	0.2162	0.2435	-0.02861	0.8471	0.4778	0.0472	0.7515	0.4143
251137_at	AT5G01300	phosphatidylethanolamine-binding family protein	-0.0625	0.8624	0.5416	-0.05082	0.8879	0.5153	0.3233	0.3934	0.3135	0.335	0.3782	0.2749
251138_at	AT5G01310	e-cadherin binding protein-related	0.0703	0.1528	0.2515	0.5502	0.1111	0.2222	0.1909	0.2061	-0.1599	0.317	0.2469	
251139_at	AT5G01230	FtsJ-like methyltransferase family protein	0.6396	7.00E-04	0.0334	0.3006	0.0112	0.0569	0.3336	0.0078	0.0355	-0.00537	0.9404	0.4686
251140_at	AT5G01090	legume lectin family protein	-0.5017	0.0219	0.0869	-0.4658	0.0277	0.083	0.05002	0.5673	0.3857	0.08588	0.3453	0.2605
251141_at	AT5G01075	beta-galactosidase	-1.7703	0.0015	0.0383	-1.4428	0.0033	0.0371	0.05338	0.62	0.4046	0.3809	0.0186	0.0438
251142_at	AT5G01015	unknown protein	-1.5642	3.00E-04	0.0312	-1.8162	2.00E-04	0.0249	-0.1756	0.1816	0.1999	-0.4276	0.0171	0.0417
251143_at	AT5G01220	SQD2 (SULFOQUINOVOSYLDIACYLGLYCEROL	-1.1464	0.0061	0.0539	-0.9064	0.0138	0.0623	-0.4256	0.0414	0.0846	-0.1856	0.2658	0.2207
251144_at	AT5G01210	transferase family protein	-0.3182	0.0699	0.1523	0.08057	0.5674	0.4109	0.5764	0.4375	0.333	0.5103	0.0169	0.0416
251145_at	AT3G63500	similar to unknown protein [Arabidopsis thaliana] (T	0.3051	0.0591	0.1391	0.5782	0.0077	0.049	-0.7359	0.0032	0.0253	-0.4628	0.0166	0.0411
251146_at	AT3G63520	CCD1 (CAROTENOID CLEAVAGE DIOXYGENAS	0.2488	0.0438	0.1207	0.1156	0.248	0.2626	-0.454	0.0061	0.0324	-0.5872	0.0024	0.0161
251147_at	AT3G63480	kinesin motor, putative	1.4397	0.0672	0.1489	1.5666	0.0534	0.1146	0.7867	0.2448	0.2379	0.9135	0.1888	0.1787
251148_at	AT3G63180	ATTKL/TKL (TICKLE)	0.4779	0.0258	0.093	0.3829	0.0501	0.1111	-0.3728	0.0541	0.0989	-0.4678	0.0276	0.0553
251149_at	AT3G62940	OTU-like cysteine protease family protein	0.1972	0.078	0.161	0.1926	0.0829	0.1446	0.4411	0.0062	0.0328	0.4365	0.0065	0.0249
251150_at	AT3G63120	CYCP1;1 (cyclin P1;1); cyclin-dependent protein kir	0.4698	0.0312	0.1025	-0.9932	0.0061	0.0449	0.006021	0.9703	0.5101	-0.3774	0.0682	0.0953
251151_at	AT3G63170	similar to unknown protein [Arabidopsis thaliana] (T	-0.6557	0.0575	0.1374	-0.8546	0.0262	0.081	0.1624	0.0853	0.1287	-0.03656	0.6356	0.3756
251152_at	AT3G63130	RANGAP1 (RAN GTPASE ACTIVATING PROTEIN	-0.04025	0.8513	0.5385	0.2937	0.2186	0.2449	-0.3079	0.2011	0.2123	0.02602	0.9034	0.4583
251153_at	AT3G63000	NPL41 (NPL4-LIKE PROTEIN 1)	0.3612	0.0245	0.0911	0.2519	0.0703	0.1326	0.3315	0.0321	0.073	0.2222	0.0966	0.1179
251154_at	AT3G63110	ATIPT3 (Arabidopsis thaliana isopentenyltransferas	-0.7356	0.2034	0.2643	-0.1895	0.7156	0.4639	-0.2278	0.0146	0.0483	0.3183	0.0045	0.0213
251155_at	AT3G63160	unknown protein	-0.8045	0.2131	0.2704	-0.4794	0.4277	0.3543	0.1426	0.5583	0.3819	0.4676	0.1046	0.1238
251156_at	AT3G63060	EDL3 (EID1-LIKE 3)	0.8562	0.5105	0.425	0.9086	0.4866	0.3789	0.9493	0.4686	0.3468	1.0017	0.4462	0.3045
251157_at	AT3G63140	mRNA-binding protein, putative	-1.0293	3.00E-04	0.0312	-1.3648	1.00E-04	0.0249	-0.02844	0.7575	0.4506	-0.364	0.0134	0.0366
251158_at	AT3G63150	GTP-binding protein-related	0.704	0.0075	0.0579	0.278	0.1193	0.1748	0.4176	0.0224	0.0604	-0.00837	0.9457	0.4698
251159_at	AT3G63230	senescence-associated protein-related	0.2074	0.8402	0.5356	0.3402	0.742	0.472	-0.6127	0.5316	0.3718	-0.4799	0.6206	0.3705
251160_at	AT3G63240	endonuclease/exonuclease/phosphatase family pro	-1.8386	0.0448	0.122	0.2208	0.7464	0.4737	-2.1911	0.014	0.0472	-0.1317	0.8143	0.4327
251161_at	AT3G63290	similar to unknown protein [Arabidopsis thaliana] (T	-0.00592	0.9841	0.5731	-0.306	0.3359	0.3114	-0.4424	0.108	0.1471	-0.7425	0.0257	0.0531
251162_at	AT3G63300	similar to unknown protein [Arabidopsis thaliana] (T	-1.4254	0.0712	0.1538	-0.06145	0.9213	0.5243	-1.3556	0.0246	0.0636	0.008396	0.9837	0.4789
251163_at	AT3G63310	glutamate binding /	0.4306	0.0559	0.1358	0.2109	0.2614	0.2705	-0.3736	0.0816	0.1252	-0.5933	0.0213	0.0474
251164_s_at	AT3G63340;AT3G63320	[AT3G63340, protein phosphatase 2C-related / PP2	-0.896	0.4498	0.3979	-0.1043	0.9271	0.526	-2.1036	0.0224	0.0604	-1.3119	0.0871	0.1105
251165_at	AT3G63350	protein kinase family protein	-0.5391	0.1957	0.2596	0.2193	0.5622	0.4091	-0.8277	0.0758	0.12	-0.06931	0.8516	0.4431
251166_at	AT3G63350	AT-HSFA7B (Arabidopsis thaliana heat shock trans	-0.2318	0.8314	0.5329	-0.4426	0.6868	0.4545	0.3392	0.7562	0.4501	0.1285	0.9059	0.459
251167_at	AT3G63360	defensin-related	-1.6305	0.1531	0.2282	-0.109	0.912	0.522	-0.1885	0.8486	0.4783	1.333	0.2234	0.1979
251168_at	AT3G63370	pentatricopeptide (PPR) repeat-containing protein	-0.9924	0.4685	0.4065	-1.2358	0.3755	0.3301	0.0695	0.9555	0.5067	-0.1739	0.889	0.454
251169_at	AT3G63210	MARD1 (MEDIATOR OF ABA-REGULATED DORM	1.1802	0.0243	0.0908	1.1803	0.0243	0.0783	-0.5934	0.0222	0.0603	-0.5933	0.0222	0.0486
251170_at	AT3G63260	ATMRK1 (Arabidopsis thaliana MLK/Raf-related pro	-0.1256	0.5652	0.447	-0.02109	0.9213	0.5243	0.1293	0.0363	0.0784	0.2337	0.005	0.0221
251171_at	AT3G63220	kelch repeat-containing F-box family protein	0.2961	0.1162	0.1971	0.2222	0.2079	0.2382	0.159	0.2959	0.2666	0.08507	0.5553	0.3471
251172_at	AT3G63190	RRF (RIBOSOME RECYCLING FACTOR, CHLOR	-0.3332	0.0257	0.0929	-0.6283	0.0028	0.0352	0.2406	0.052	0.0966	-0.05451	0.5685	0.3522
251173_at	AT3G63270	similar to unknown protein [Arabidopsis thaliana] (T	0.6823	0.0178	0.0798	0.3724	0.1013	0.1605	-0.3372	0.1273	0.1619	-0.6471	0.0211	0.0472
251174_at	AT3G63200	PLA IIIBP/LP9 (Patatin-like protein 9); nutrient rese	-1.9373	0.0089	0.0611	-2.6438	0.0029	0.0355	0.6299	0.0305	0.0712	-0.0766	0.7105	0.401
251175_at	AT3G63250	ATHMT-2/HMT-2/HMT2 (HOMOCYSTEINE METH	0.2901	0.232	0.2831	0.4998	0.0723	0.1348	-0.2841	0.1406	0.1718	-0.07432	0.6564	0.3829
251176_at	AT3G63380	calcium-transporting ATPase, plasma membrane-ty	2.0273	8.00E-04	0.0336	1.3705	0.0033	0.0371	-0.3373	0.198	0.2106	-0.9941	0.0105	0.032
251177_at	AT3G63400	peptidyl-prolyl cis-trans isomerase cyclophilin-type f	0.72118	0.6258	0.4684	0.3325	0.072	0.1344	-0.7411	0.0056	0.0313	-0.4808	0.0246	0.0516
251178_at	AT3G63440	ATCKX6/ATCKX7/CKX6 (CYTOKININ OXIDASE/D	-0.974	0.0104	0.0646	-0.9012	0.0136	0.0618	0.3301	0.1758	0.1959	0.4028	0.1155	0.1316
251179_at	AT3G63460	WD-40 repeat family protein	0.006019	0.9836	0.573	0.4361	0.1891	0.2258	-0.5581	0.0944	0.1363	-0.128	0.6427	0.3781
251180_at	AT3G62940	similar to unknown protein [Arabidopsis thaliana] (T	-0.5757	0.6482	0.4759	0.8518	0.5066	0.3873	-0.03499	0.9776	0.5119	1.3925	0.2995	0.2383
251181_at	AT3G62820	invertase/pectin methylesterase inhibitor family prot	-0.2371	0.3458	0.3478	-0.4743	0.0996	0.1591	0.1495	0.5378	0.3744	-0.08769	0.7131	0.402
251182_at	AT3G62600	DNAJ heat shock family protein	1.2982	1.00E-04	0.0312	1.1522	1.00E-04	0.0249	0.1794	0.0932	0.1353	0.03348	0.7032	0.3984
251183_at	AT3G62630	similar to calmodulin-binding protein [Arabidopsis th	-0.2877	0.4798	0.4117	-0.3514	0.3645	0.325	0.4642	0.0737	0.1181	0.3804	0.1196	0.1346
251184_at	AT3G62840	similar to small nuclear ribonucleoprotein D2, putat	0.2817	0.1179	0.1985	0.4909	0.0258	0.0803	0.7869	0.0052	0.0301	0.996	0.0022	0.0157
251185_at	AT3G62870	60S ribosomal protein L7A (RPL7aB)	0.0391	0.4679	0.4063	0.09611	0.1202	0.1755	-0.3719	0.0016	0.0203	-0.3149	0.003	0.0177
251186_at	AT3G62790	NADH-ubiquinone oxidoreductase-related	-0.00767	0.9723	0.5704	0.3715	0.1483	0.1968	0.09636	0.6669	0.4202	0.4755	0.084	0.1082
251187_at	AT3G62770	AtATG18a (Arabidopsis thaliana homolog of yeast A	0.3072	0.2095	0.2678	0.3059	0.211	0.2404	-0.2744	0.253	0.2425	-0.2756	0.2512	0.2132
251188_at	AT3G62730	similar to unknown protein [Arabidopsis thaliana] (T	1.0631	0.2415	0.2886	-0.238	0.7738	0.4817	-0.2643	0.746	0.4468	-1.5654	0.1089	0.1269
251189_at	AT3G62650	binding	0.6214	0.0697	0.1521	0.7163	0.047	0.1077	-0.2167	0.4069	0.3194	-0.1218	0.8303	0.3737
251190_at	AT3G62590	ATL5 (Arabidopsis T?xicos en Levadura 5); protein	-0.4373	0.2939	0.3197	-0.2134	0.5874	0.4187	-0.02775	0.9426	0.5039	0.1961	0.6171	0.3693
251191_at	AT3G62590	lipase class 3 family protein	0.8527	0.0036	0.0457	0.5253	0.0197	0.072	0.1797	0.1991	0.2113	-0.1477	0.2749	0.2254
251192_at	AT3G62720	ATXT1 (ODP-xylosyltransferase/ transferase/ transfe	0.8235	0.1238	0.2039	-1.0995	0.0758	0.1379	0.4585	0.0568	0.1018	0.2726	0.1899	0.1791
251193_at	AT3G62930	release factor	-0.244	0.0507	0.1296	-0.4065	0.01	0.0544	-0.485	0.0034	0.0259	-0.6476	0.0012	0.0127
251194_at	AT3G62920	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.06538	0.8203	0.5296	0.4089	0.2039	0.2354	0.1907	0.5133	0.3644	0.5342	0.1152	0.1314
251195_at	AT3G62900	glutaredoxin family protein	-2.0812	0.0046	0.0492	-1.5589	0.0129	0.0605	0.8626	0.0547	0.0996	1.3849	0.0125	0.0353
251196_at	AT3G62950	glutaredoxin family protein	-1.4657	0.0055	0.052	-0.5508	0.1093	0.1669	0.3033	0.3215	0.2789	1.2182	0.0105	0.0321
251197_at	AT3G62960	glutaredoxin family protein	-1.084	0.0664	0.148	-0.8107	0.1343	0.1863	0.7617	0.0439	0.0875	1.036	0.0169	0.0415
251198_at	AT3G62970	protein binding / zinc ion binding	0.02503	0.8605	0.5412	-0.04857	0.7346	0.4696	-0.2475	0.1008	0.1417	-0.3211	0.051	0.0804
251199_at	AT3G62980	TIR1 (TRANSPORT INHIBITOR RESPONSE 1); ub	-0.1274	0.5457	0.4393	0.5417	0.0486	0.1095	-1.09	0.0037	0.0268	-0.4208	0.079	0.104
251200_at	AT3G63010	ATGID1B/GID1B (GA INSENSITIVE DWARF1B); h	0.2394	0.4917	0.4165	0.9316	0.0423	0.1022	-0.8091	0.063	0.1079	-0.1169	0.7307	0.4074
251201_at	AT3G63020	unknown protein	-0.5176	0.7417	0.5065	-0.03672	0.9812	0.5395	-0.07349	0.9533	0.5063	0.4074	0.7471	0.4128
251202_at	AT3G63040	unknown protein	-0.4963	0.7253	0.5012	-0.7258	0.6107	0.4271	0.6151	0.6253	0.4064	0.3855	0.7572	0.4158
251203_at	AT3G63070	PWWP domain-containing protein	0.1136	0.4339	0.391	-0.1061	0.4628	0.3692	0.4459	0.0185	0.0544	-0.6633	0.0046	0.0214
251204_at	no_match	no_match	0.2398	0.8244	0.5308	0.5695	0.6038	0.4247	0.06276	0.9535	0.5064	0.3925	0.718	0.4034
251205_at	AT3G63080	ATGPX5 (GLUTATHIONE PEROXIDASE 5); glutat	0.6984	0.0143	0.073	0.6514	0.0181	0.0694	0.4092	0.0087	0.0373	0.3623	0.0132	0.0364
251206_at	AT3G63090	similar to unknown protein [Arabidopsis thaliana] (T	0.1016	0.0462	0.1237	1.5493	0.0119	0.0586	-0.2091	0.5882	0.3938	0.3306	0.4034	0.2855
251207_at	AT3G63050	similar to unknown protein [Arabidopsis thaliana] (T	0.156	0.6238	0.4678	0.3986	0.2467	0.2619	0.4276	0.2195	0.2233	0.6702	0.0848	0.1088
251208_at	AT3G62880	AtOEP16-4; P-P-bond-hydrolysis-driven protein tra	0.2009	0.2194	0.2748	0.2767	0.1156	0.1716	-0.7067	0.001	0.0179	-0.6309	0.0016	0.0142
251209_at	AT3G62890	binding	0.5688	0.5091	0.4246	1.2246	0.1947	0.2292	-0.7391	0.3555	0.2969	-0.08429	0.911	0.4602
251210_at	AT3G62810	complex 1 family protein / LVR family protein	0.6777	0.0066	0.0549	1.152	9.00E-04	0.0286	0.4171	0.0333	0.0745	0.8914	0.0024	0.0163
251211_s_at	AT3G62470;AT3G62540;A	[AT3G62470, pentatricopeptide (PPR) repeat-conta	0.03818	0.8995	0.551	0.4265	0.2073	0.2378	-0.819	0.004	0.0273	-0.4306	0.035	0.0633
251212_at	AT3G62480	transposable element gene	-1.4324	0.145	0.2213	-0.8103	0.3645	0.325	0.3476	0.6836	0.4255	0.9698	0.2883	0.2326
251213_at	AT3G62490	transposable element gene	-0.2338	0.9193	0.5568	-1.5364	0.5176	0.3915	0.7856	0.7354	0.4434	-0.517	0.8233	0.4351
251214_at	AT3G62500	similar to DNA binding [Arabidopsis thaliana] (TAIR	-0.5813	0.5657	0.4472	0.08785	0.9293	0.5265	-1.3437	0.2219	0.2247	-0.6745	0.5083	0.329
251215_at	AT3G62510	cell division cycle protein-related	0.6955	0.2146	0.2712	0.8974	0.1299	0.1828	-1.55	0.0303	0.0709	-1.3481	0.0461	0.0754
251216_at	AT4G27597;AT3G62520	[AT4G27597, transposable element gene];[AT3G62	-1.4113	0.1686	0.2404	0.6918	0.457	0.3669	-1.6211	0.1262	0.161	0.482	0.5973	0.3625
251217_at	AT3G62560	GTP-binding protein, putative	0.08313	0.575	0.4508	-0.0706	0.6319	0.4353	0.6233	0.001	0.0174	0.4696	0.0028	0.0174
251218_at	AT3G62410	CP12-2	-0.5652	0.002	0.04	-0.4962	0.0033	0.0371	0.6052	0.001	0.0179	0.6742	7.00E-04	0.0105
251219_at	AT3G62390	similar to unknown protein [Arabidopsis thaliana] (T	0.07341	0.7146	0.4974	-0.12	0.5558	0.4068	-0.05844	0.6225	0.4055	-0.2519	0.0834	0.1077
251220_at	AT3G62400	unknown protein	-0.1429	0.4911	0.4163	0.3621	0.1275	0.1812	0.2356	0.2801	0.2581	0.7406	0.0172	0.0419
251221_at	AT3G62550	universal stress protein (USP) family protein	0.7802	0.2982	0.3223	1.0002	0.2004	0.233	0.434	0.1311	0.1646	0.6539	0.0462	0.0755
251222_at	AT3G62580	similar to late embryogenesis abundant domain-cor	0.3706	0.0267	0.0945	0.3757	0.0256	0.08	0.4563	0.0047	0.0291	0.4614	0.0045	0.0212
251223_at	AT3G62610	AtMYB11 (myb domain protein 11); DNA binding / tr	-1.2599	0.1316	0.21	0.6001	0.4187	0.3501	-0.3085	0.6314	0.4084	1.5515	0.0595	0.0881
251224_at	AT3

251290_at	AT3G61850	DAG1 (DOF AFFECTING GERMINATION 1); DNA	0.9063	0.0109	0.0655	0.4261	0.1024	0.1614	-0.06875	0.7483	0.4476	-0.549	0.0516	0.0809
251291_at	AT3G61900	auxin-responsive family protein	-0.08749	0.8845	0.5471	-0.02525	0.9665	0.5357	0.479	0.2783	0.2571	0.5413	0.2296	0.2013
251292_at	AT3G61920	similar to unnamed protein product [Vitis vinifera] (C	-1.0959	0.0326	0.1048	-0.06454	0.8593	0.5069	-0.5103	0.2094	0.2174	0.5211	0.2017	0.1861
251293_at	AT3G61930	unknown protein	0.7164	0.5811	0.4526	2.4826	0.1063	0.1645	0.2466	0.6798	0.4243	2.0128	0.0222	0.0485
251294_at	AT3G61940	MTPA1; efflux transmembrane transporter/ zinc ion	1.5824	0.3053	0.3257	-0.7679	0.5991	0.4231	-0.236	0.8694	0.4841	-2.5863	0.1273	0.1398
251295_at	AT3G62000	O-methyltransferase family 3 protein	-0.7553	0.0104	0.0646	-0.6407	0.0181	0.0695	-0.7289	0.0117	0.0429	-0.6143	0.0208	0.0467
251296_at	AT3G62010	metal ion binding / oxidoreductase	0.09061	0.4939	0.4175	-0.1782	0.2132	0.2415	-0.2275	0.0599	0.105	-0.4963	0.0047	0.0217
251297_at	AT3G62020	GLP10 (GERMIN-LIKE PROTEIN 10); manganese	-0.2147	0.5824	0.4533	-0.3642	0.3692	0.3267	0.5079	0.1705	0.1922	0.3584	0.3043	0.2408
251298_at	AT3G62040	hydrolase	-0.2353	0.697	0.4918	-0.2538	0.6751	0.4502	0.9308	0.1731	0.194	0.9123	0.1799	0.1733
251299_at	AT3G61950	basic helix-loop-helix (bHLH) family protein	-0.3067	0.5681	0.4482	-0.3514	0.516	0.391	-0.1727	0.6452	0.4127	-0.2174	0.5654	0.3511
251300_at	AT3G61980	serine protease inhibitor, Kazal-type family protein	0.3401	0.0982	0.181	0.5418	0.0267	0.0817	0.1934	0.0547	0.0996	0.3961	0.0054	0.0229
251301_at	AT3G61880	CYP78A9 (CYTOCHROME P450 78A9); oxygen bi	0.109	0.8625	0.5416	-0.2896	0.6496	0.4415	1.1311	0.0099	0.0397	0.7325	0.0404	0.0695
251302_at	AT3G61970	NGA2 (NGATHA2); transcription factor	-0.2649	0.427	0.3881	-0.4545	0.2042	0.2356	-0.1553	0.4259	0.328	-0.3449	0.1206	0.1354
251303_at	AT3G61910	NST2 (NAC SECONDARY WALL THICKENING PR	0.2466	0.8154	0.5284	-1.528	0.1973	0.2312	0.6191	0.5653	0.3849	-1.1555	0.3076	0.2422
251304_at	AT3G61990	O-methyltransferase family 3 protein	0.5194	0.2882	0.3163	0.3451	0.4618	0.3687	-0.2314	0.3627	0.2994	-0.4057	0.1462	0.1523
251305_at	AT3G62030	ROC4 (ROTAMASE CYP 4); peptidyl-prolyl cis-tran	-0.5633	0.0012	0.036	-0.911	2.00E-04	0.0249	0.3508	0.0067	0.0335	0.00318	0.9649	0.4744
251306_at	AT3G61260	DNA-binding family protein / remorin family protein	-0.7932	0.0077	0.0582	-0.5098	0.0333	0.0904	0.3136	0.0045	0.1095	0.597	0.0085	0.0287
251307_at	AT3G61200	thioesterase family protein	0.8658	0.0056	0.0521	0.2605	0.1776	0.218	-0.6644	0.0047	0.0292	-1.2697	4.00E-04	0.0089
251308_at	AT3G61130	GAUT1/LGT1 (Galacturonosyltransferase 1); polyga	-1.121	0.0129	0.0699	-1.2763	0.0082	0.0504	-0.2211	0.184	0.2014	-0.3765	0.0524	0.0816
251309_at	AT3G61220	short-chain dehydrogenase/reductase (SDR) family	-0.6614	0.0206	0.0846	-0.611	0.0266	0.0816	-0.1444	0.4633	0.3446	-0.09396	0.6259	0.3724
251310_at	AT3G61150	HDG1 (HOMEODOMAIN GLABROUS1); DNA bind	0.4122	0.1808	0.2486	0.4006	0.1908	0.2268	-0.3899	0.0949	0.1367	-0.4016	0.0882	0.1114
251311_at	AT3G61140	FUS6 (FUSCA 6)	0.5616	0.0215	0.0862	0.1285	0.4492	0.3637	-0.2668	0.158	0.1844	-0.699	0.0103	0.0318
251312_at	AT3G61120	AGL13 (AGAMOUS-LIKE 13); DNA binding / transc	-0.7837	0.4072	0.379	0.04608	0.9592	0.534	-1.4041	0.1727	0.1937	-0.5744	0.5349	0.3398
251313_at	AT3G61360	pentatricopeptide (PPR) repeat-containing protein	-0.09782	0.7513	0.5088	-0.3574	0.2826	0.2824	0.4948	0.161	0.1862	0.2353	0.46	0.31
251314_at	AT3G61180	zinc finger (C3HC4-type RING finger) family protein	0.4389	0.0033	0.0446	0.5611	0.0013	0.0312	-1.0035	1.00E-04	0.012	-0.8813	2.00E-04	0.0078
251315_at	AT3G61410	similar to protein kinase family protein / U-box doma	-0.8921	0.2551	0.2964	-0.7544	0.3245	0.3057	-0.2793	0.699	0.431	-0.1416	0.8434	0.4409
251316_s_at	AT5G28350,AT3G61480	[AT5G28350, similar to unknown protein [Arabidops	0.6268	0.0116	0.0674	0.07037	0.6468	0.4404	-0.4649	0.0076	0.0352	-1.0213	4.00E-04	0.0089
251317_at	AT3G61490	glycoside hydrolase family 28 protein / polygalacturo	-0.05406	0.8399	0.5341	-0.2882	0.3345	0.3105	0.0137	0.9437	0.5042	-0.3085	0.1669	0.1648
251318_at	AT3G61570	GC3/GDAP1 (GRIP-RELATED ARF-BINDING DOM	0.1592	0.4274	0.3881	-0.4533	0.0659	0.1284	0.01375	0.9429	0.504	-0.5987	0.0294	0.0575
251319_at	AT3G61610	aldose 1-epimerase family protein	0.01898	0.9616	0.5677	-0.1665	0.6763	0.4507	-0.1064	0.7881	0.4595	-0.2919	0.4746	0.3155
251320_at	AT3G61630	PANB2; 2-methyl-2-oxobutanoate hydroxymethyltra	0.3248	0.1552	0.2299	0.5685	0.0377	0.0961	-0.03116	0.8398	0.4756	0.2121	0.216	0.1941
251321_at	AT3G61460	BRH1 (BRASSINOSTEROID-RESPONSIVE RING-	0.04876	0.7917	0.5214	-0.1518	0.4292	0.3549	0.4886	0.0121	0.0437	0.2288	0.0623	0.0906
251322_at	AT3G61440	ATCYSC1 (BETA-SUBSTITUTED ALA SYNTHASE	-0.09848	0.3206	0.3347	-0.2807	0.032	0.0887	-0.07336	0.3913	0.3126	-0.2556	0.0287	0.0566
251323_at	AT3G61680	delta-8 sphingolipid desaturase (SLD1)	0.4101	0.1606	0.234	-0.1422	0.583	0.4174	-1.4503	2.00E-04	0.0124	-1.1824	4.00E-04	0.0088
251324_at	AT3G61430	PIP1A (PLASMA MEMBRANE INTRINSIC PROTEI	-0.6084	0.0018	0.0391	-0.794	7.00E-04	0.027	0.1863	0.0412	0.0843	0.000703	0.9916	0.4805
251325_s_at	AT3G61470,AT5G28450	[AT3G61470, LHCA2 (Photosystem I light harvestin	-0.3349	0.1163	0.1972	-0.6223	0.0206	0.0732	0.1912	0.1955	0.209	-0.09619	0.4785	0.317
251326_at	AT3G61590	HSI/WIG (HAWAIIAN SKIRT); ubiquitin-protein liga	-0.4009	0.0151	0.0744	-0.7516	0.0016	0.0316	0.158	0.183	0.2009	-0.1927	0.1214	0.136
251327_at	AT3G61540	peptidase family protein	1.0583	0.0148	0.0737	1.024	0.0166	0.0668	-0.3336	0.0575	0.1025	-0.368	0.0435	0.0729
251328_at	AT3G61600	ATPDB1 (Arabidopsis thaliana POZ/BTB containing	0.1804	0.2301	0.2821	0.239	0.1342	0.1862	-0.325	0.0175	0.053	-0.2664	0.033	0.0613
251329_at	AT3G61450	SYP73 (SYNTAXIN OF PLANTS 73)	1.4151	0.3061	0.3262	1.9608	0.1796	0.2193	0.3493	0.7867	0.4592	0.8949	0.4996	0.3258
251330_at	AT3G61550	zinc finger (C3HC4-type RING finger) family protein	-0.5549	0.0171	0.0783	-0.6721	0.0089	0.0517	-0.1609	0.2234	0.2256	-0.2781	0.1676	0.0949
251331_s_at	AT3G61650,AT5G05620	[AT3G61650, TUBG1 (GAMMA-TUBULIN); structur	-0.04972	0.7735	0.5159	0.05531	0.7491	0.4747	-0.5268	0.031	0.0716	-0.4217	0.0593	0.0879
251332_at	AT3G61670	similar to unknown protein [Arabidopsis thaliana] (T	0.059665	0.8339	0.5336	0.4824	0.1446	0.1942	-0.1609	0.4059	0.3189	0.2618	0.2057	0.1883
251333_at	AT3G61690	nucleotidyltransferase	0.3241	0.0634	0.1443	0.3098	0.0715	0.1338	-0.5777	0.0053	0.0306	-0.592	0.0049	0.022
251334_at	AT3G61390	U-box domain-containing protein	0.366	0.4079	0.3792	0.08869	0.8338	0.4999	0.1588	0.6486	0.4141	-0.1185	0.7322	0.4078
251335_at	AT3G61660	2-oxoglutarate-dependent dioxygenase, putative	-0.7797	0.4636	0.4046	-1.1759	0.2892	0.2862	0.3173	0.7414	0.4452	-0.07888	0.9342	0.4988
251336_at	AT3G61190	BAP1 (BON ASSOCIATION PROTEIN 1)	0.2195	0.7314	0.5028	0.5926	0.3764	0.3303	0.7992	0.0772	0.1214	1.1723	0.0256	0.053
251337_at	AT3G60820	PBF1 (20S proteasome beta subunit F1); peptidase	0.5155	0.0151	0.0744	0.4307	0.0271	0.0824	0.2377	0.1291	0.1633	0.1529	0.287	0.2318
251338_at	AT3G60600	VAP27-1 (VAMP-ASSOCIATED PROTEINS-VN-ASSOCIATED	0.3763	0.0329	0.1052	0.457	0.0177	0.0689	-0.134	0.2481	0.24	-0.05323	0.6199	0.3703
251339_at	AT3G60780	similar to unknown protein [Arabidopsis thaliana] (T	-1.2153	0.1512	0.2267	0.5738	0.45	0.3639	-2.0875	0.0383	0.0809	-0.2984	0.6861	0.3927
251340_at	AT3G60830	ATARP7 (ACTIN-RELATED PROTEIN 7); structura	-0.07954	0.6744	0.4841	-0.1076	0.5736	0.4133	0.05734	0.7606	0.4513	0.0293	0.8757	0.4501
251341_at	AT3G60770	40S ribosomal protein S13 (RPS13A)	0.2055	0.1536	0.2287	0.4661	0.0163	0.0664	0.3367	0.0085	0.0371	0.5973	0.001	0.0122
251342_at	AT3G60690	auxin-responsive family protein	0.228	0.411	0.3805	0.4678	0.133	0.1853	0.3138	0.0454	0.0891	0.5536	0.0071	0.0264
251343_at	AT3G60620	phosphatidate cytidylyltransferase family protein	-0.5057	0.0313	0.1027	-0.6123	0.017	0.0677	-0.1368	0.4286	0.3291	-0.2434	0.1925	0.1806
251344_at	AT3G60800	beige/BEACH domain-containing protein	-2.4472	0.0888	0.1728	-0.00544	0.9963	0.5432	-2.5014	0.084	0.1275	-0.05963	0.9591	0.4731
251345_at	AT3G60940	similar to unknown protein [Arabidopsis thaliana] (T	1.3069	0.3133	0.3305	-0.5234	0.6684	0.4479	1.5953	0.0513	0.0961	-0.235	0.7061	0.3995
251346_at	AT3G60980	pentatricopeptide (PPR) repeat-containing protein	0.3672	0.2515	0.2942	0.5791	0.1022	0.1613	-0.4589	0.0129	0.0452	-0.247	0.0829	0.1074
251347_at	AT3G61010	glycosyl hydrolase family protein 85	0.525	0.1147	0.1962	0.02247	0.9355	0.5279	-1.917	0.0018	0.0206	-2.4195	8.00E-04	0.0108
251348_at	no_match	no_match	0.2654	0.2473	0.2919	0.2568	0.2605	0.27	-0.7937	0.0143	0.0477	-0.8023	0.0138	0.0373
251349_s_at	AT3G61020,AT3G11030	[AT3G61020, pseudogene, similar to P0034A04.28	0.4931	0.1718	0.2427	0.4031	0.2457	0.2614	-0.9328	0.0182	0.0541	-1.0228	0.0134	0.0367
251350_at	AT3G61070	CYP76C7 (cytochrome P450, family 76, subfamily C	0.07619	0.8832	0.5471	-0.4293	0.4276	0.3543	0.3576	0.2329	0.231	0.004518	0.9867	0.4794
251351_s_at	AT3G61030,AT3G60950,A	[AT3G61030, C2 domain-containing protein];[AT3G	0.0967	0.2628	0.3014	0.2056	0.0504	0.1114	-0.4401	0.0041	0.0275	-0.3312	0.0112	0.0331
251352_at	AT3G61070	PEX11E	0.1153	0.4556	0.4007	-0.03859	0.7961	0.4884	-0.01507	0.9193	0.4976	-0.169	0.2931	0.2352
251353_at	AT3G61080	fructosamine kinase family protein	-0.9574	0.0017	0.0391	-1.3029	5.00E-04	0.0201	-0.04581	0.7365	0.4437	-0.3913	0.0369	0.0654
251354_at	AT3G61090	similar to unknown protein [Arabidopsis thaliana] (T	-1.5284	0.0818	0.1654	-2.8117	0.0131	0.0611	0.5862	0.4251	0.3276	-0.6971	0.351	0.2631
251355_at	AT3G61100	similar to unknown protein [Arabidopsis thaliana] (T	-0.3046	0.0287	0.0982	-0.4517	0.0077	0.049	-0.4068	0.0044	0.0282	-0.5539	0.0014	0.0134
251356_at	AT3G61060	ATPP2-A13	0.4602	0.0951	0.1782	-0.3411	0.4464	0.3623	-0.7289	0.0029	0.0244	-0.1898	0.1648	0.1642
251357_at	AT3G61110	ARS27A (ARABIDOPSIS RIBOSOMAL PROTEIN S	0.09124	0.3151	0.3315	0.1392	0.155	0.202	0.772	6.00E-04	0.0158	0.8199	5.00E-04	0.0095
251358_at	AT3G61160	shaggy-related protein kinase beta / ASK-beta (ASK	0.5552	0.0946	0.1778	-0.04479	0.8689	0.5096	-0.2752	0.2926	0.2649	-0.8752	0.0183	0.0434
251359_at	AT3G61170	pentatricopeptide (PPR) repeat-containing protein	-0.3273	0.2087	0.2672	-0.7299	0.0289	0.0847	-0.2197	0.3718	0.3038	-0.6223	0.0466	0.0759
251360_at	AT3G61210	embryo-abundant protein-related	-0.306	0.3212	0.3352	-0.4093	0.2048	0.236	-0.2705	0.374	0.3047	-0.3738	0.2392	0.2067
251361_at	AT3G61230	LIM domain-containing protein	0.5354	0.5542	0.4425	2.5125	0.0389	0.0978	-0.2343	0.7548	0.4496	1.7428	0.0676	0.0949
251362_at	AT3G61240	DEAD/DEAH box helicase, putative (RH12)	-0.2351	0.2903	0.3175	-0.143	0.5002	0.3847	-0.432	0.0086	0.0372	-0.3398	0.0195	0.0448
251363_at	AT3G61250	AtMYB17 (myb domain protein 17); DNA binding / tr	0.2822	0.4901	0.4159	0.3893	0.3541	0.3201	-0.3476	0.0744	0.1188	-0.2405	0.1723	0.1686
251364_at	AT3G61300	C2 domain-containing protein	2.2999	0.012	0.0681	-0.7057	0.2515	0.265	2.5007	0.0021	0.0218	-0.5049	0.2273	0.2001
251365_at	AT3G61310	DNA-binding family protein	-0.09546	0.7243	0.5009	-0.106	0.6959	0.4574	-0.3027	0.2428	0.2366	0.2922	0.2568	0.2182
251366_at	AT3G61340	F-box family protein	0.2049	0.762	0.5121	1.1041	0.1556	0.2025	-0.5533	0.2849	0.2606	0.3458	0.4838	0.3192
251367_at	AT3G61350	SKIP4 (SKP1 INTERACTING PARTNER 4)	0.08942	0.4227	0.3863	0.3973	0.0166	0.0669	-0.3705	0.0209	0.0581	-0.06266	0.5657	0.3512
251368_at	AT3G61360	similar to unknown protein [Arabidopsis thaliana] (T	-0.00197	0.9927	0.5752	-0.0811	0.7076	0.4613	0.3351	0.1713	0.1929	0.256	0.2724	0.2241
251369_at	AT3G60480	hydrolase, acting on carbon-nitrogen (but not peptid	0.4954	0.0054	0.0519	0.4381	0.0084	0.0507	0.3976	0.0113	0.0421	0.3402	0.019	0.0442
251370_at	AT3G60450	similar to unknown protein [Arabidopsis thaliana] (T	1.1505	0.001	0.0354	1.3305	6.00E-04	0.0265	0.1479	0.2227	0.2252	0.3279	0.033	0.0613
251371_at	AT3G60360	EDA14/ATP11 (EMBRYO SAC DEVELOPMENT AI	0.7103	0.1172	0.1979	0.671	0.133	0.1852	0.239	0.0027	0.0238	0.1997	0.0052	0.0226
251372_at	AT3G60520	zinc ion binding	0.5394	0.127	0.206	0.9682	0.0261	0.0808	0.4191	0.0016	0.0204	0.8478	1.00E-04	0.0061
251373_at	AT3G60530	zinc finger (GATA type) family protein	-0.1693	0.5596	0.4448	-0.01343	0.9622	0.5346	-0.1818	0.329	0.2829	-0.02595	0.8817	0.4519
251374_at	AT3G60390	HAT3 (homeobox-leucine zipper protein 3); transcri	0.3541	0.2437	0.2898	-0.1111	0.6902	0.4557	-0.09184	0.5396	0.3752	0.1511	0.3323	0.2545
251375_at	AT3G60410	similar to unknown protein [Arabidopsis thaliana] (T	0.2056	0.4564	0.4011	0.09351	0.727	0.4678	-0.231	0.2961	0.2667	-0.3431	0.149	0.154
251376_at	AT3G60630	scarecrow transcription factor family protein	0.1141	0.3525	0.351	-0.5142	0.009	0.0521	0.001286	0.99	0.5153	-0.627	0.0029	0.0176
251377_at	AT3G60650	unknown protein	-0.9069	0.0919	0.1758	-3.1404	0.0016	0.0316	-0.07053	0.872	0.4847	-2.304	0.005	0.0221
251378_at	AT3G60660	similar to unknown protein [Arabidopsis thaliana] (T	-0.09503	0.8806	0.5465	-1.2747	0.0982	0.1579	1.0481	0.1522	0.1805	-0.1316	0.8353	0.4387
251379_at	AT3G60680	similar to unknown protein [Arabidopsis thaliana] (T	-0.1052	0.5104	0.425	0.3237	0.0906	0.1518	-0.09947	0.5326	0.3723	0.3295	0.0867	0.1103
251380_at	AT3G60700	similar to unknown protein [Arabidopsis thaliana] (T	-0.756	0.5592	0.4446	0.2492	0.8441	0.5028	-1.4545	0.2881	0.2626	-0.4493	0.7246	0.4055
251381_at	AT3G60720	receptor-like protein kinase-related	-0.03707	0.8809	0.5465	-0.6054	0.0596	0.1213	0.5445	0.0789	0.1228	-0.02391	0.9229	0.4636
251382_at	AT3G60730	pectinesterase family protein	-2.2857	0.0914	0.1753	0.751	0.5076	0.3877	-1.735	0.1684	0.1907	1.3017	0.2762	0.2262
251383_at	AT3G60740	TTN1 (TITAN 1)	0.3074	0.1623	0.2357	0.2484	0.239	0.2571	-0.666	0.0207	0.0579	-0.725	0.0157	0.0399
251384_at	AT3G60760	unknown protein	2.4367	0.1262	0.2056	0.8865	0.5218	0.3929	0.5054	0.6542	0.4159	-1.0448	0.3743	0.2732
251385_at	AT3G60790	F-box protein-related	-0.9036	0.3618	0.3554	2.0994	0.0752	0.1375	-1.0824	0.2854	0.2609	1.9205	0.0941	0.1161
251386_at	AT3G60800	zinc finger (DHHC type) family protein	0.5937	0.0031	0.0441	0.314	0.0281	0.0835	-0.06504	0.4546	0.3407	-0.3447	0.0118	0.0341
251387_at	AT3G60810	similar to unnamed protein product [Vitis vinifera] (C	-0.2693	0.1409	0.2183	-0.4777	0.0314	0.0881	0.3621	0.0695	0.1142	0.1537	0.3549	0.2648
251388_at	AT3G60840	microtubule associated protein (MAP65/ASE1) fam	0.2259	0.2994	0.3226	-0.1831	0.389	0.3363	0.3758	0.0107	0.0411	-0.03361	0.7067	0.3997
251389_at	AT3G60850	similar to unnamed protein product [Vitis vinifera] (C	0.1386	0.3264	0.3382	0.1541	0.2819	0.2821	0.01406	0.9073	0.4945	0.001444	0.9904	0.4803
251390_at	AT3G60860	guanine nucleotide exchange family protein	0.7693	9.00E-04	0.0349	0.6511	0.0017	0.0321	-0.5264	0.0028	0.0244	-0.6446	0.0013	0.0133
251391_at	AT3G60910	catalytic	0.3896	0.1042	0.1866	0.1871	0.3711	0.3278	-0.6312	0.0088	0.0375	-0.8336	0.0032	0.0185
251392_at	AT3G60880	dihydrodipicolinate synthase 1 (DHDPS1) (DHDPS)	0.08139	0.7753	0.5165	-0.0634	0.8236	0.4971	-0.4666	0.1198	0.1561	-0.6114	0.061	0.0894
251393_at	AT3G60640	ATG8G (AUTOPHAGY 8G); microtubule binding	0.6995	0.0995	0.182	0.7305	0.0895	0.1508	1.0935	0.0033	0.0255	1.1246	0.003	0.0177
251394_at	AT3G60900	FLA10 (fasciclin-like arabinogalactan-protein 10)	-0.8626	0.0537	0.1331	-1.1482	0.0227	0.076	0.2916	0.4119	0.3216	0.005848	0.9862	0.4793
251395_at	AT3G60470	FLA8 (Arabinogalactan protein 8)	-1.4714	0.0011	0.036	-2.0232	3.00E-04	0.0249	0.7048	0.0086	0.0372	0.153	0.3555	0.2651
251396_at	AT3G60750	transketolase, putative	-0.387	0.0075	0.0579	-0.8485	4.00E-04	0.0251	-0.2084	0.0013	0.019	-0.6698	0	0.0047
251397_at	AT3G60570	ATEXP5 (ARABIDOPSIS THALIANA EXPANSIN	-0.5527	0.2953	0.3206	-0.9059	0.12	0.1752	-0.1222	0.8034	0.4645	-0.4754	0.3593	0.2667
251398_at	AT3G60580	zinc finger (C2H2 type) family protein	0.9545	0.109	0.1912	0.7285	0.1918	0.2272	-0.082	0.8684	0.4838	-0.308	0.5434	0.3422
251399_at	AT3G60590	similar to unknown protein [Arabidopsis thaliana] (T	0.2718	0.2379	0.2862	0.1298	0.5442	0.4023	-0.1272	0.4978	0.3588	-0.2692	0.19	0.1792
251400_at	AT3G60420	similar to unknown protein [Arabidopsis thaliana] (T	1.892	1.00E-04	0.0312	1.8664	1.00E-04	0.0249	0.1468	0.1645	0.1882	0.1212	0.2333	0.2034
251401_at	AT3G60270	ucbcyanin, putative	-0.1267	0.8866	0.5475	-1.4101	0.1661	0.2099	2.5931	0.0069	0.0338	1.3096	0.0607	0.0892
251402_at	AT3G60290	oxidoreductase, acting on paired donors, with incor	-1.3544	0.0133	0.0709	-1.4834	0.0097	0.0537	-0.1728	0.6173	0.4036	-0.3019	0.3983	0.2835
251403_at	AT3G60300	RWD domain-containing protein	0.5132	0.011	0.0656	0.4387	0.0361	0.0939	-0.6505	0.0098	0.0394	-0.8501	0.0038	0.0201
251404_at	AT3G60340	TTN1 (TITAN 1)	-0.1545	0.6875	0.4884	-0.4244	0.3003	0.2914	-0.857	0.0743	0.1187	-1.1269	0.0343	0.0626
251405_at	AT3G60330	AHA7 (ARABIDOPSIS H(+)-ATPASE 7); hydrogen-	2.0614	0.1832	0.2504	-0.6058	0.6612	0.4455	1.0566	0.4562	0.3413	-1.6106	0.2774	0.2268
251406_at	AT3G60260	phagocytosis and cell motility protein ELMO1-relate	0.1502	0.6585	0.4779	0.1102	0.7428	0.4722	-0.1534	0.2459	0.2386	-0.1903	0.1607	0.1617
251407_at	AT3G60350	armadillo/beta-catenin repeat family protein / F-box	0.4772	0.009	0.0612	0.0334	0.7564	0.477	-0.3349	4.00E-04	0.0147	-0.7787	0	0.0047
251408_at	AT3G60340	palmitoyl protein thioesterase family protein	0.3929	0.0236	0.0897	0.2908	0.058	0.1196	0.1258	0.3181	0.2774	0.02365	0.8409	0.4403
251409_at	AT3G60245	60S ribosomal protein L37a (RPL37aC)	0.09725	0.3892	0.3695	0.1012	0.3723	0.3285	0.4248	0.0098	0.0396	0.644	0.0026	0.0169
251410_at	AT3G60280	UCC3 (UCLACYANIN 3); copper ion binding	0.07591	0.9424	0.5631	0.1787	0.8652	0.5086	-0.5935	0.5804	0.3909	-0.4907	0.6455	0.3792
251411_at	AT3G60250	CKB3 (casein kinase II beta chain 3); protein kinase	0.6672	0.0042	0.0471	0.684	0.0039	0.0391	-0.4992	0.0118	0.0431	-0.4823	0.0133	0.0365
251412_at	AT3G60290	ATL4 (Arabidopsis T?xicos en Levadura 4); protein	0.4994	0.4737	0.4094	-0.666	0.1536	0.2009	0.5055	0.0611	0.1062	0.1388	0.5173	0.3325
251413_at	AT3G60320	DNA binding	-0.1952	0.485	0.414	-0.3802	0.2088	0.2387	-0.1515	0.0244	0.0633	-0.3365	0.0014	0.0137
251414_at	AT3G60370	immunophilin / FKBP-type peptidyl-prolyl cis-trans i	-0.08313	0.4488	0.3975	0.05488	0.6092	0.4268	-0.8329	4.00E-04	0.0145	-0.6949	7.00E-04	0.0108
251415_at	AT3G60380	similar to hydroxyproline-rich glycoprotein family pr	0.08566	0.5716	0.4495	0.3828	0.0512	0.1123	-0.1979	0.1369	0.1683	0.09933	0.4026	0.2853
251416_at	AT3G60400	mitochondrial transcription termination factor-relate	-0.3585	0.2009	0.2627	-0.1198	0.6363	0.437	-0.632	0.0543	0.0992	-0.3933	0.1687	0.1665
251417_at	no_match	no_match	-1.5583	0.2307	0.2825	-0.1932	0.8695	0.5098	-1.4024	0.019	0.0553	-0.03735	0.9241	0.4638
251418_at	AT3G60440	similar to unknown protein [Arabidopsis thaliana] (T	0.4758	0.2139	0.2707	0.1663	0.633	0.4357	0.3723	0.2746	0.2746	0.06285	0.8549	0.4442
251419_at	AT3G60470	similar to unknown protein [Arabidopsis thaliana] (T	1.3894	0.0345	0.1073	1.7146	0.0177	0.0689	0.4907	0.3281	0.2824	0.8159	0.1379	0.1468
251420_at	AT3G60490	AP2 domain-containing transcription factor TINY, p	-0.245	0.8302	0.5325	1.3763	0.2678	0.2743	0.5416	0.5118	0.3638	2.1628	0.0454	0.0747
251421_at	AT3G60510	enoyl-CoA hydratase/isomerase family protein	-0.3644	0.1772	0.2463	0.008866	0.9702	0.5368	-0.3742	0.0215	0.059	-0.00093	0.9931	0.481
251422_at	AT3G60540	sec61beta family protein

251490_at	AT3G59490	similar to unnamed protein product [Vitis vinifera] (G	0.3971	0.0211	0.0853	0.3672	0.027	0.0822	-0.727	0.0025	0.0232	-0.7569	0.0022	0.0157
251491_at	AT3G59480	pNB-type carbohydrate kinase family protein	-0.07753	0.9384	0.5618	-2.2248	0.0776	0.1397	1.2481	0.2561	0.2443	-0.8992	0.3942	0.2819
251492_at	AT3G59280	TXR1 (THAXTOMIN A RESISTANT 1)	0.05486	0.569	0.4485	0.2272	0.0622	0.124	0.6744	3.00E-04	0.0133	0.8467	1.00E-04	0.0061
251493_at	AT3G59300	similar to unknown protein [Arabidopsis thaliana] (T	-0.1385	0.4839	0.4135	-0.2515	0.2344	0.2546	-0.3562	0.0473	0.0912	-0.4691	0.0203	0.0459
251494_at	AT3G59350	serine/threonine protein kinase, putative	-0.4893	0.4257	0.3874	-0.03859	0.9477	0.5313	-0.6062	0.0153	0.0493	-0.1555	0.3564	0.2654
251495_at	AT3G59020	protein transporter	0.6844	0.0109	0.0655	0.5828	0.0188	0.0707	-0.827	0.0048	0.0292	-0.9286	0.0031	0.0181
251496_at	AT3G59040	pentatricopeptide (PPR) repeat-containing protein	0.08551	0.6007	0.4599	0.002281	0.9886	0.5413	-0.6807	0.0031	0.0251	-0.7639	0.002	0.0153
251497_at	AT3G59060	PILE (PHYTOCHROME-INTERACTING FACTOR 3	-0.3878	0.0842	0.1678	-0.3722	0.0932	0.1539	-0.4217	0.0573	0.1024	-0.4061	0.0636	0.0916
251498_at	AT3G59070	auxin-responsive protein, putative	-0.4678	0.6876	0.4885	0.3888	0.7374	0.4704	-0.2905	0.8015	0.464	0.5661	0.6283	0.3731
251499_at	AT3G59100	ATGSL11 (GLUCAN SYNTHASE-LIKE 11); 1,3-bet	1.4927	0.0027	0.0426	1.4386	0.0031	0.0363	-0.4867	0.0977	0.1391	-0.5408	0.0751	0.1008
251500_at	AT3G59110	protein kinase family protein	-0.1953	0.3046	0.3254	0.1135	0.5317	0.3968	-0.7039	0.0083	0.0366	-0.3952	0.0526	0.0818
251501_at	AT3G59120	DC1 domain-containing protein	1.3344	0.108	0.1902	0.8793	0.2454	0.2613	-0.09068	0.8952	0.4912	-0.5458	0.4461	0.3045
251502_at	AT3G59130	similar to DC1 domain-containing protein [Arabidops	-0.3222	0.6384	0.4724	-0.7086	0.3267	0.3069	-1.1977	0.1322	0.1654	-1.5842	0.067	0.0944
251503_at	AT3G59140	ATMRP14 (Arabidopsis thaliana multidrug resistanc	-0.1516	0.3069	0.3267	0.1548	0.2981	0.2907	-0.365	0.0479	0.0919	-0.05866	0.6741	0.3888
251504_at	AT3G59030	TT12 (TRANSPARENT TESTA 12); antiporter/ solu	1.1281	0.1369	0.2149	-1.1552	0.13	0.1829	0.5748	0.3976	0.3155	-1.7085	0.0482	0.0775
251505_at	AT3G59052;AT3G59050	CPuORF18 (Conserved peptide upst	-0.581	0.1051	0.1872	-0.5485	0.12	0.1752	-0.03979	0.8409	0.4758	-0.00737	0.9703	0.4755
251506_at	AT3G59590	similar to TOM1 (TOBAMOVIRUS MULTIPLICATIC	-0.00276	0.9856	0.5733	-0.06327	0.6832	0.4532	-0.4457	0.0191	0.0554	-0.5062	0.0125	0.0353
251507_at	AT3G59080	aspartyl protease family protein	-0.3001	0.4547	0.4003	-0.172	0.6603	0.4451	0.03555	0.8589	0.4807	0.1637	0.4322	0.2977
251508_at	AT3G59970	magnesium transporter CorA-like family protein	0.6573	0.0156	0.0753	0.2345	0.2225	0.2474	-0.03034	0.8515	0.4789	-0.4531	0.0406	0.0697
251509_at	AT3G59160	pectinesterase family protein	-0.7559	0.0396	0.1149	-0.9138	0.022	0.0751	0.2618	0.2833	0.2599	0.1039	0.6488	0.3804
251510_at	AT3G59170	F-box family protein	0.7966	0.3289	0.3393	0.05604	0.9415	0.5295	-0.2261	0.7684	0.4536	-0.9666	0.249	0.2119
251511_at	AT3G59180	similar to F-box family protein [Arabidopsis thaliana	0.6141	0.0312	0.1434	-0.7555	0.4471	0.3625	0.4753	0.5908	0.3949	-0.8939	0.3343	0.2553
251512_at	AT3G59190	F-box family protein	0.3771	0.6111	0.463	-0.3743	0.6137	0.4283	0.9837	0.2242	0.2262	0.2323	0.7515	0.4143
251513_at	AT3G59220	PRN (PIRIN); calmodulin binding	0.3279	0.3848	0.3672	-0.08117	0.8211	0.4962	0.5283	0.1913	0.2063	0.1192	0.7409	0.4107
251514_at	AT3G59260	pirin, putative	-0.446	0.3944	0.3724	-0.8685	0.1369	0.1884	-0.1837	0.6202	0.4047	-0.2389	0.5239	0.3354
251515_at	AT3G59270	syntaxin-related family protein	1.7345	0.1792	0.2475	0.495	0.6667	0.4473	0.6307	0.5861	0.393	-0.6089	0.5986	0.3629
251516_s_at	AT3G59310;AT3G59320	[AT3G59310, similar to unknown protein [Arabidops	-0.3174	0.1387	0.2162	-0.2141	0.281	0.2814	-0.5912	0.0026	0.0234	-0.4879	0.0052	0.0225
251517_at	AT3G59370	contains domain PTHR22683 (PTHR22683);	0.7092	0.5514	0.4417	-1.2007	0.3332	0.3098	1.2362	0.3208	0.2786	-0.6736	0.3706	0.3528
251518_at	AT3G59390	similar to unknown [Populus trichocarpa] (GB:ABK9	-0.1405	0.2381	0.2863	0.1624	0.1845	0.2228	0.3069	0.0389	0.0815	0.6098	0.038	0.0201
251519_at	AT3G59400	GUN4 (Genomes uncoupled 4)	-0.6635	0.0026	0.0426	-0.8886	9.00E-04	0.0284	0.2109	0.0127	0.0448	-0.01423	0.7865	0.4247
251520_at	AT3G59410	protein kinase family protein	0.4962	0.0097	0.0633	0.4721	0.0116	0.058	-0.7123	0.0026	0.0236	-0.7364	0.0023	0.0161
251521_at	AT3G59420	ACR4 (ARABIDOPSIS CRINKLY4); kinase	-0.6894	0.3265	0.3382	-0.5705	0.4075	0.3447	-0.2826	0.6707	0.4213	-0.1638	0.8038	0.4299
251522_at	AT3G59430	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.6374	0.1084	0.1907	0.4837	0.193	0.2278	-0.2507	0.4631	0.3445	-0.4045	0.2612	0.2184
251523_at	AT3G59975	pseudogene of F-box family protein	-0.1758	0.888	0.4885	0.3042	0.4963	0.383	-0.5553	0.2193	0.2232	-0.07522	0.8533	0.4437
251524_at	AT3G58990	aconitase C-terminal domain-containing protein	-1.1556	0.0198	0.0832	-1.2718	0.0144	0.0635	0.7854	0.0264	0.066	0.6691	0.0429	0.0723
251525_at	AT3G59000	F-box family protein	0.3494	0.1	0.1825	0.4479	0.0523	0.1134	-0.6838	0.0124	0.0442	-0.5853	0.0207	0.0467
251526_at	AT3G58940	protein kinase family protein	0.6703	0.0094	0.0624	0.3507	0.0701	0.1325	-0.2468	0.1594	0.1853	-0.5662	0.0166	0.0412
251527_at	AT3G58650	similar to unknown protein [Arabidopsis thaliana] (T	0.1543	0.8165	0.5287	0.7072	0.3196	0.3029	0.1803	0.7866	0.4592	0.7332	0.3044	0.2408
251528_at	AT3G58600	similar to ATNAP4 (ARABIDOPSIS THALIANA NOI	0.4153	0.0542	0.1336	0.5856	0.019	0.071	0.4831	0.0059	0.0321	0.6534	0.002	0.0151
251529_at	AT3G58570	DEAD box RNA helicase, putative	0.9123	0.0281	0.097	0.982	0.0223	0.0754	-0.1513	0.3647	0.3003	-0.08215	0.6098	0.3666
251530_at	AT3G58520	similar to unknown protein [Arabidopsis thaliana] (T	0.358	0.7105	0.4964	1.864	0.1066	0.1647	-0.5982	0.5418	0.3761	0.9078	0.3693	0.2709
251531_at	AT3G58550	protease inhibitor/seed storage/lipid transfer protein	-0.5589	0.408	0.3792	-0.4251	0.5211	0.3926	0.1199	0.8526	0.4792	0.2537	0.6966	0.3964
251532_at	AT3G58530	F-box family protein-related	0.7443	2.00E-04	0.0312	0.5982	4.00E-04	0.0251	-0.09197	0.0834	0.1271	-0.2381	0.004	0.0204
251533_at	AT3G58460	rhomboid family protein / ubiquitin-associated (UBA	0.104	0.5058	0.4231	0.1241	0.4327	0.3567	-0.2637	0.1378	0.1695	-0.2435	0.1625	0.1627
251534_at	AT3G58510	DEAD box RNA helicase, putative (RH11)	0.5641	0.0658	0.1471	0.165	0.5029	0.3858	0.005282	0.9824	0.5133	-0.3937	0.1542	0.1576
251535_at	AT3G58540	similar to unknown protein [Arabidopsis thaliana] (T	-0.3853	0.2404	0.2877	-0.3211	0.3149	0.3002	0.03309	0.9115	0.4957	0.09728	0.7455	0.4121
251536_at	AT3G58610	ketol-acid reductoisomerase	-0.2231	0.2252	0.2787	-0.311	0.1164	0.1724	-0.3015	0.1249	0.1599	-0.3895	0.0667	0.0941
251537_at	AT3G58470	similar to Os03g0749900 [Oryza sativa (japonica cu	0.3331	0.0943	0.1777	0.07168	0.6628	0.446	-0.107	0.5214	0.3675	-0.3685	0.0731	0.0992
251538_at	AT3G58500	60S ribosomal protein-related	0.07282	0.6972	0.4918	0.4691	0.0544	0.1157	-0.2226	0.187	0.2037	0.1737	0.2825	0.2295
251539_at	AT3G58690	protein kinase family protein	0.08662	0.6387	0.4725	-0.1062	0.5678	0.411	0.09446	0.6097	0.4012	-0.09835	0.5956	0.3619
251540_at	AT3G58740	CSY1 (CITRATE SYNTHASE 1); citrate (Si)-syntha	-0.9887	0.3174	0.3328	-1.1865	0.2426	0.2595	0.8763	0.3689	0.3023	0.6785	0.4772	0.3165
251541_at	AT3G58750	CSY2 (CITRATE SYNTHASE 2); citrate (Si)-syntha	-0.9347	0.0017	0.0391	0.7958	6.00E-04	0.0265	-0.4253	0.0059	0.0321	-0.2242	0.0482	0.0775
251542_at	AT3G58760	ankyrin protein kinase, putative	0.0477	0.8057	0.5257	0.4315	0.0762	0.1383	-0.2616	0.1232	0.1588	0.1222	0.4143	0.2901
251543_at	AT3G58770	similar to hypothetical protein [Vitis vinifera] (GB:CA	-0.09066	0.893	0.5494	0.8375	0.256	0.2678	-0.0084	0.99	0.5153	0.9198	0.2173	0.1948
251544_at	AT3G58710	GAUT15 (Galacturonosyltransferase 15); polygalac	-0.5322	0.0773	0.16	-0.3758	0.1702	0.2127	-0.2285	0.1904	0.2058	-0.07211	0.6453	0.3791
251545_at	AT3G58810	MTPA2; efflux transmembrane transporter/ zinc ion	-1.5484	0.1802	0.2482	-0.272	0.7899	0.4861	-1.9807	0.0905	0.133	-0.7043	0.4739	0.3153
251546_at	AT3G58830	haloacid dehalogenase (HAD) superfamily protein	-0.5697	0.0264	0.0939	-0.5448	0.0303	0.0864	0.08547	0.5513	0.3796	0.1104	0.4487	0.3056
251547_at	AT3G58860	F-box family protein	-0.1804	0.8206	0.5297	-0.8172	0.3344	0.3105	0.7241	0.3863	0.3105	0.08732	0.8124	0.4606
251548_at	no_match	no_match	0.8742	0.011	0.0656	0.03237	0.8762	0.512	0.4987	0.0128	0.0449	-0.3431	0.0419	0.0713
251549_at	AT3G58890	syntaxin-related family protein	0.05365	0.9493	0.5646	-1.1655	0.2155	0.2431	-0.4031	0.497	0.3585	-1.6222	0.0398	0.0689
251550_at	AT3G58800	similar to unnamed protein product [Vitis vinifera] (G	-0.7163	0.0264	0.0939	-0.4458	0.0992	0.1588	0.092	-0.332	0.073	0.1175	-0.0615	0.6775	0.3899
251551_at	AT3G58680	ATMBF1B/MBF1B (MULTIPROTEIN BRIDGING FA	0.2519	0.1636	0.2366	0.4848	0.0305	0.0868	0.7426	0.0074	0.0347	0.9754	0.0027	0.0172
251552_at	AT3G58700	60S ribosomal protein L11 (RPL11B)	0.4828	0.0229	0.0885	0.5044	0.0199	0.0722	0.3576	0.0284	0.0684	0.3792	0.0236	0.0502
251553_at	AT3G58710	WRKY69 (WRKY DNA-binding protein 69); transcri	0.379	0.3711	0.3601	0.4261	0.321	0.3036	0.03736	0.9	0.4924	0.08446	0.7773	0.4221
251554_at	AT3G58670	similar to unknown protein [Arabidopsis thaliana] (T	0.3733	0.0473	0.1251	0.3687	0.049	0.1097	-0.7533	0.0027	0.0237	-0.7579	0.0026	0.0169
251555_at	AT3G58780	SHP1 (SHATTERPROOF 1); DNA binding / transcr	-0.00323	0.9966	0.5761	0.6928	0.381	0.3324	0.9456	0.2505	0.2413	1.6417	0.0802	0.1052
251556_at	AT3G58840	similar to myosin heavy chain-related [Arabidopsis t	0.1328	0.7286	0.502	0.1284	0.7372	0.4704	0.2215	0.4292	0.3293	0.217	0.4378	0.3004
251557_at	AT3G58730	(VACUOLAR ATP SYNTHASE SUBUNIT D); ATPa	0.0873	0.5132	0.4264	0.02751	0.8324	0.4995	0.2302	0.0043	0.028	0.1704	0.0124	0.0352
251558_at	AT3G57810	OTU-like cysteine protease family protein	-0.06196	0.7693	0.5143	-0.1197	0.5769	0.4147	-0.3614	0.0584	0.1034	-0.4192	0.0382	0.0669
251559_at	AT3G58010	Identical to Probable plastid-lipid-associated protein	-0.2103	0.1927	0.2574	-0.5641	0.0137	0.062	-0.06861	0.6038	0.3995	-0.4224	0.0257	0.0531
251560_at	AT3G57920	squamosa promoter-binding protein, putative	0.06807	0.9435	0.5632	-0.1551	0.8719	0.5105	-1.0715	0.301	0.2692	-1.2947	0.2249	0.1987
251561_at	AT3G57870	AHUS5 (SUMO CONJUGATION ENZYME 1); ubiq	-0.02216	0.9083	0.5536	0.2003	0.3296	0.3084	0.6189	6.00E-04	0.0158	0.8414	2.00E-04	0.0073
251562_at	AT3G57860	tubulin-specific chaperone C-related	0.2462	0.0521	0.131	0.03343	0.729	0.4683	0.2553	0.0449	0.0908	0.04258	0.6606	0.3844
251563_at	AT3G57880	C2 domain-containing protein	0.2541	0.2899	0.3172	0.6595	0.0341	0.0911	-0.1953	0.2571	0.2448	0.2101	0.2284	0.2007
251564_at	AT3G58160	XIU (Myosin-like protein XIU)	0.6278	0.342	0.3461	-0.1724	0.782	0.4841	-1.5831	0.0451	0.089	-2.3833	0.0123	0.0351
251565_at	AT3G58190	ASL16/LBD29 (LOB DOMAIN-CONTAINING PROT	1.7129	0.1012	0.1841	-1.0522	0.2626	0.2712	1.5689	0.1077	0.1469	-1.0963	0.2462	0.2103
251566_at	AT3G58210	meprin and TRAF homology domain-containing pro	-1.6703	0.4185	0.3841	0.5638	0.7762	0.4825	-1.4144	0.4879	0.3546	0.8198	0.6811	0.3909
251567_at	AT3G58230	similar to unknown protein [Arabidopsis thaliana] (T	-0.1535	0.9312	0.5601	-0.2004	0.9103	0.5216	-0.6315	0.7245	0.4401	-0.6783	0.7054	0.3994
251568_at	AT3G58280	similar to meprin and TRAF homology domain-conta	0.5533	0.3564	0.3564	-0.2229	0.7015	0.4597	0.2489	0.5327	0.3723	-0.5274	0.222	0.197
251569_at	AT3G58290	meprin and TRAF homology domain-containing pro	-0.09074	0.8846	0.5471	0.4183	0.5154	0.3908	0.6947	0.3021	0.2696	1.2038	0.1096	0.1274
251570_at	AT3G58300	similar to unknown protein [Arabidopsis thaliana] (T	-1.5924	0.3178	0.3329	-0.8509	0.5752	0.4139	-0.2511	0.8661	0.483	0.4904	0.7431	0.4114
251571_at	AT3G58330	similar to unknown protein [Arabidopsis thaliana] (T	0.7813	0.3494	0.3495	-1.8061	0.0707	0.1329	1.4137	0.1112	0.1493	-1.1736	0.166	0.1648
251572_at	AT3G58390	release factor 1 family protein / eRF1 family protein	-0.3218	0.7753	0.5165	-0.01524	0.9892	0.5414	-0.507	0.6555	0.4163	-0.2004	0.8584	0.4453
251573_at	AT3G58140	phenylalanyl-tRNA synthetase class IIc family prote	0.02022	0.8571	0.5405	-0.09166	0.4334	0.3569	-0.1811	0.1606	0.186	-0.293	0.0497	0.0791
251574_at	AT3G58100	glycosyl hydrolase family protein 17	-0.3934	0.1736	0.244	-0.3278	0.2403	0.258	-0.01063	0.9665	0.5092	0.05497	0.8286	0.4387
251575_at	AT3G58120	bZIP transcription factor family protein	-1.2257	0.0988	0.1814	-0.6922	0.2928	0.2881	0.02677	0.9134	0.4961	0.5602	0.0725	0.0988
251576_at	AT3G58200	meprin and TRAF homology domain-containing pro	-0.2786	0.6894	0.4889	1.1381	0.1538	0.201	0.2181	0.5354	0.3733	1.6348	0.0071	0.0263
251577_at	AT3G58350	meprin and TRAF homology domain-containing pro	1.8852	0.0748	0.1573	0.6618	0.448	0.363	-0.1519	0.8086	0.4662	-1.3753	0.0792	0.1042
251578_at	AT3G58180	PBS lyase HEAT-like repeat-containing protein	0.5489	0.0061	0.0541	0.2239	0.0973	0.1572	0.2598	0.0666	0.1116	-0.06522	0.5641	0.3505
251579_at	AT3G58170	ATBS14A; protein transporter	0.2219	0.2551	0.2964	0.1794	0.3437	0.315	0.8101	0.0084	0.0367	0.7676	0.0101	0.0314
251580_at	AT3G58450	universal stress protein (USP) family protein	0.5969	0.5747	0.4507	0.01105	0.9915	0.542	1.2935	0.2566	0.2445	0.7077	0.5094	0.3295
251581_at	AT3G58560	endonuclease/exonuclease/phosphatase family pro	0.47	0.0267	0.0945	0.2016	0.216	0.2433	0.2299	0.1694	0.1915	-0.03849	0.7931	0.427
251582_at	AT3G58580	hydrolase	0.4276	0.0063	0.0543	0.1448	0.1498	0.1979	0.1749	0.0981	0.1394	-0.1078	0.2559	0.2157
251583_at	AT3G58590	pentatricopeptide (PPR) repeat-containing protein	1.553	0.3502	0.3497	-0.2262	0.8462	0.5034	0.9841	0.4189	0.3248	-0.3973	0.7347	0.4086
251584_at	AT3G58620	TTL4 (TETRATRICOPEPTIDE-REPEAT THIOREDO	-1.1093	0.2426	0.2891	-0.7979	0.3802	0.3321	-0.3877	0.0189	0.0552	-0.07633	0.4948	0.3239
251585_at	AT3G58630	transcription factor	-0.4415	0.1385	0.2161	-0.1693	0.5179	0.3916	-0.1255	0.6275	0.4071	0.1467	0.5726	0.3534
251586_at	AT3G58070	GIS (GLABROUS INFLORESCENCE STEMS); nuc	-1.2245	0.017	0.0781	-1.8582	0.0039	0.0392	0.5862	0.1323	0.1655	-0.04751	0.8859	0.4531
251587_at	AT3G58080	unknown protein	0.98	0.2082	0.2671	-0.6288	0.3906	0.337	0.1561	0.823	0.4706	-1.4527	0.0904	0.1132
251588_at	AT3G58090	pseudogene, disease resistance response protein-r	-0.3356	0.2999	0.3229	-0.02479	0.9342	0.5277	-0.1423	0.6388	0.4107	0.1685	0.5806	0.3563
251589_at	AT3G58040	seven in absentia (SINA) family protein	-0.1363	0.3666	0.3576	0.1478	0.3319	0.3094	0.000385	0.9972	0.517	0.2845	0.0499	0.0792
251590_at	AT3G57690	AGP23/ATAGP23 (ARABINOGALACTAN-PROTEI	0.7497	0.016	0.0765	0.4392	0.0786	0.1405	-0.04367	0.8268	0.4718	-0.3542	0.1311	0.1423
251591_at	AT3G57680	peptidase S41 family protein	-0.3123	0.1027	0.1852	-0.3357	0.0861	0.1478	-0.00407	0.9646	0.5086	-0.02749	0.7656	0.4185
251592_at	AT3G57670	NTT (NO TRANSMITTING TRACT); nucleic acid bi	0.9661	0.025	0.0918	1.2789	0.0098	0.0539	2.1098	6.00E-04	0.0158	2.4225	4.00E-04	0.0089
251593_at	AT3G57660	NRPA1 (nuclear RNA polymerase A 1); DNA bindi	0.2973	0.5525	0.442	0.3578	0.4792	0.3757	-0.8111	0.0437	0.0872	-0.7506	0.0546	0.0836
251594_at	AT3G57630	exostosin family protein	-0.02447	0.9113	0.5543	0.06198	0.7787	0.4832	-0.2001	0.2149	0.2208	-0.1137	0.4501	0.306
251595_at	AT3G57620	glycoprotease-related	-0.1532	0.9137	0.555	0.9494	0.5138	0.3902	0.0511	0.9683	0.5096	1.1537	0.3937	0.2816
251596_at	AT3G57650	LPAT2 (Lysophosphatidyl acyltransferase 2); 1-acy	0.4116	0.0109	0.0655	-0.1214	0.2564	0.268	0.3022	0.2051	0.0642	-0.2308	0.056	0.0848
251597_at	AT3G57750	protein kinase, putative	-0.2141	0.3009	0.3235	0.02429	0.8994	0.5187	-0.2457	0.0249	0.0639	-0.00727	0.9225	0.4636
251598_at	AT3G57600	AP2 domain-containing transcription factor, putative	-0.4192	0.2029	0.2642	-0.4203	0.202	0.2339	-0.9916	0.014	0.0473	-0.9926	0.014	0.0376
251599_at	AT3G57610	ATPURA; adenylosuccinate synthase	0.1792	0.2584	0.2987	-0.2186	0.1835	0.2222	-0.2084	0.1976	0.2103	-0.6062	0.0109	0.0327
251600_at	AT3G57710	protein kinase family protein	0.246	0.2798	0.3112	0.4136	0.1036	0.1625	-0.5542	0.0481	0.0922	-0.3865	0.1212	0.1359
251601_at	AT3G57800	basic helix-loop-helix (bHLH) family protein	-0.1894	0.5204	0.4291	0.05818	0.8394	0.5013	0.1749	0.2705	0.2526	0.4225	0.0367	0.0652
251602_at	AT3G57785	similar to unknown protein [Arabidopsis thaliana] (T	-0.2317	0.2964	0.3212	-0.08531	0.6814	0.4525	0.6033	0.0305	0.0711	0.7497	0.0151	0.0392
251603_at	AT3G57760	protein kinase family protein	-0.424	0.2912	0.318	-0.09207	0.805	0.4912	-0.7781	0.0142	0.0475	-0.444	0.0761	0.1016
251604_at	AT3G57820	60S ribosomal protein L21 (RPL21F), pseudogene,	-0.1485	0.6559	0.4778	-0.5598	0.1441	0.1938	-0.1826	0.5862	0.3931	-0.594	0.1268	0.1395
251605_at	AT3G57830	leucine-rich repeat transmembrane protein kinase,	-0.7794	0.1566	0.2308	-0.7295	0.1784	0.2186	-0.2142	0.6492	0.4142	-0.1643	0.7256	0.4058
251606_at	AT3G57940	self-incompatibility protein-related	0.4969	0.6604	0.4794	0.6956	0.4579	0.4021	-0.1956	0.8612	0.4814	0.003178	0.9977	0.4823
251607_at	AT3G57850	similar to self-incompatibility protein-related [Arabid	0.4149	0.7808	0.518	-0.8868	0.5593	0.408	0.1679	0.7407	0.4449	-1.1338	0.0747	0.1006
251608_at	AT3G57860	UVI4-LIKE (UV-B-INSENSITIVE 4-LIKE)	-0.3675	0.5342	0.4348	-0.02594	0.964	0.535	-0.8684	0.1837	0.2013	-0.5269	0.3852	0.2781
251609_at	AT3G57900	unknown protein	0.4066	0.7524	0.5091	1.5689	0.2622	0.2711	-1.0704	0.4239	0.327	0.09187	0.9428	0.4691
251610_at	AT3G57930	similar to unknown protein [Arabidopsis thaliana] (T	0.144	0.7676	0.5138	0.4555	0.3738	0.3294	-0.1152	0.6238	0.4059	0.1963	0.4169	0.2912
251611_at	AT3G57940	identical to UPF0202 protein At3g57940 [Arabidopsis	0.3336	0.5027	0.4216	0.7818	0.1597	0.2057	-0.3995	0.428	0.3288	0.04873	0.9196	0.4626
251612_at	AT3G57950	similar to unknown protein [Arabidopsis thaliana] (T	0.9801	0.0098	0.0549	2.3709	0.0341	0.0911	0.8718	0.4208	0.3257	-0.8475	0.3214	0.249
251613_at	AT3G57960	emsy N terminus domain-containing protein / ENT c	0.156	0.7612	0.512	-1.5523	0.0317	0.0885	1.1903	0.068	0.1131	-0.518	0.3407	0.2584
251614_at	AT3G57970	emsy N terminus domain-containing protein / ENT c	1.0126	0.349	0.3492	-1.2167	0.2718	0.2765	0.8374	0.4302	0.3297	-1.3918	0.2189	0.1955
251615_at	AT3G57980	DNA-binding bromodomain-containing protein	-0.309	0.2476	0.2922	-0.8617	0.0196	0.0719	-0.3797	0.1718	0.1932	-0.9325	0.0151	0.039
251616_at	AT3G57990	similar to unnamed protein product [Vitis vinifera] (G	0.02923	0.8182	0.5291	-0.08776	0.5022	0.3856	-0.1043	0.2237	0.2258	-0.2213	0.038	0.0667
251617_at	AT3G58000	VQ motif-containing protein	-0.2612	0.5318	0.4336	-0.5216	0.244	0.2606	-0.4988	0.1481	0.1777	-0.7592	0.0528	0.0819
251618_at	no_match	no_match	0.1999	0.7498	0.5086	0.4743	0.4629	0.3692	-0.5035	0.4379	0.3331	-0.2291	0.7153	0.4026
251619_at	AT3G58050	similar to unknown protein [Arabidopsis thaliana] (T	0.2732	0.0049	0.05	-0.03114	0.5555	0.4068	-0.1279	0.0544	0.0993	-0.4322	8.00E-04	0.0111
251620_at	AT3G58060	cation efflux family protein / metal tolerance protein	0.6635	0.5322	0.4338	0.6904	0.5167	0.3912	-1.095	0.3229	0.2796	-1.0682	0.3334	0.255
251621_at	AT3G57700	protein kinase, putative	0.5544	0.165	0.2374	0.7253	0.0907	0.1518	0.02566	0.9095	0.4951	0.1965	0.4064	0.2867
251622_at	AT3G57340	DNAJ heat shock N-terminal domain-containing pro	0.5319	0.0463	0.1237	0.5619	0.0394	0.0983	-0.2201	0.2664	0.2499	-0.1901	0.3276	0.2523
251623_at	AT3G57390	AGL18 (AGAMOUS-LIKE 18); transcription factor	0.7258	0.0065	0.0549	0.6623	0.009	0.052	-0.1231	0.4275	0.3287	-0.1866	0.2519	0.

251690_at	AT3G56510	TBP-binding protein, putative	0.3419	0.2186	0.2742	0.2379	0.3677	0.3264	0.3791	0.1813	0.1997	0.2751	0.3059	0.2414
251691_at	AT3G56520	no apical meristem (NAM) family protein	-0.2619	0.7745	0.5162	-0.2577	0.778	0.483	0.5494	0.5553	0.381	0.5536	0.5524	0.3459
251692_s_at	AT3G52020;AT3G56540	[AT3G52020, SCPL39 (serine carboxypeptidase-lik	-0.9415	0.2887	0.3165	-1.9727	0.0626	0.1242	0.187	0.8022	0.4643	-0.8442	0.2934	0.2353
251693_at	AT3G56550	pentatricopeptide (PPR) repeat-containing protein	1.7527	0.1043	0.1866	0.02609	0.9766	0.5385	2.2036	0.058	0.103	0.477	0.5991	0.3631
251694_s_at	AT3G55210;AT3G56560	[AT3G55210, ANAC063 (Arabidopsis NAC domain	0.3822	0.6231	0.4675	-0.4832	0.5383	0.3997	0.5747	0.401	0.3171	-0.2908	0.6596	0.384
251695_at	AT3G56590	hydroxyproline-rich glycoprotein family protein	0.07456	0.8199	0.5295	-0.3563	0.3099	0.2973	0.2147	0.4354	0.3321	-0.2161	0.4328	0.298
251696_at	no_match	no_match	-0.07827	0.8794	0.5463	0.9169	0.131	0.1835	-0.345	0.4864	0.354	0.6502	0.2223	0.1972
251697_at	AT3G56600	inositol or phosphatidylinositol kinase	0.7631	0.5409	0.4372	-1.2017	0.3524	0.3193	-0.2564	0.8335	0.4736	-2.2212	0.1239	0.1376
251698_at	AT3G56610	unknown protein	-1.4994	0.2347	0.2843	-3.9378	0.0214	0.0745	1.1563	0.3417	0.289	-1.2822	0.298	0.2375
251699_at	AT3G56630	CYP94D2 (cytochrome P450, family 94, subfamily D	0.285	0.248	0.2924	0.2992	0.229	0.251	-0.04026	0.7652	0.4528	-0.02605	0.8463	0.4418
251700_at	AT3G56640	exocyst complex subunit Sec15-like family protein	0.259	0.3945	0.3724	0.1512	0.6076	0.4262	-0.4125	0.0416	0.0848	-0.5203	0.0202	0.0459
251701_at	AT3G56650	thylakoid lumenal 20 kDa protein	-0.9199	4.00E-04	0.032	-0.7211	0.001	0.0291	-0.08233	0.3819	0.3087	0.1164	0.2374	0.2058
251702_at	AT3G56660	BZIP49; DNA binding / transcription factor	0.4125	0.7601	0.5117	0.5892	0.6649	0.4466	0.8767	0.5255	0.3693	1.0533	0.4509	0.3063
251703_at	AT3G56670	similar to F-box family protein [Arabidopsis thaliana	0.1554	0.8869	0.5475	-2.2971	0.0886	0.15	1.8594	0.144	0.1745	-0.5932	0.594	0.3613
251704_at	AT3G56360	similar to unknown protein [Arabidopsis thaliana] (T	-0.2292	0.3909	0.3704	-0.1779	0.497	0.3832	-0.1949	0.0413	0.0844	-0.1437	0.0941	0.116
251705_at	AT3G56400	WRKY70 (WRKY DNA-binding protein 70); transcrip	0.4745	0.0957	0.1787	0.3634	0.1717	0.214	0.3995	0.0224	0.0604	0.284	0.0599	0.0884
251706_at	AT3G56680	integral membrane family protein / nodulin MtN21 /e	0.0372	0.8852	0.5471	-0.8106	0.0285	0.0838	-0.4627	0.0119	0.0433	-1.2361	3.00E-04	0.0083
251707_at	AT3G56490	zinc-binding protein, putative / protein kinase C inhi	0.2496	0.049	0.1274	0.03992	0.6778	0.4511	0.7683	0.001	0.0176	0.5587	0.0033	0.0188
251708_at	AT3G56580	zinc finger (C3HC4-type RING finger) family protein	0.3912	0.1018	0.1844	0.1198	0.5522	0.4057	0.3767	0.1112	0.1493	0.1053	0.5994	0.3632
251709_at	AT3G56360	ARR17 (response regulator 17); transcription regula	0.1609	0.2342	0.2839	-1.4982	0.2607	0.2701	1.835	0.1841	0.2015	-1.265	0.3311	0.2539
251710_at	AT3G56930	zinc finger (DHHC type) family protein	-0.4079	0.2331	0.2837	0.06499	0.834	0.4999	-0.1842	0.5607	0.3829	0.2887	0.3767	0.2741
251711_at	AT3G56960	PIP5K4 (PHOSPHATIDYL INOSITOL MONOPHOS	1.2814	0.1258	0.2052	-0.3777	0.5996	0.4234	0.03889	0.943	0.504	-1.6202	0.0339	0.0622
251712_at	AT3G56120	Met-10+ like family protein [Arabidopsis thaliana]	0.1786	0.5226	0.4301	-0.1557	0.5748	0.4138	-0.19	0.241	0.2356	-0.5243	0.0192	0.0444
251713_at	AT3G56080	dehydration-responsive protein-related	0.7323	0.0869	0.1708	0.1056	0.7611	0.478	-0.4277	0.0024	0.023	-1.0543	1.00E-04	0.0058
251714_at	AT3G56370	leucine-rich repeat transmembrane protein kinase,	-1.1491	0.0124	0.0688	-0.979	0.0211	0.074	-0.2922	0.192	0.2067	-0.1221	0.5481	0.3444
251715_at	AT3G56390	unknown protein	0.413	0.7207	0.4996	-1.8131	0.1674	0.2108	1.1421	0.3485	0.2924	-1.084	0.3709	0.2716
251716_at	AT3G55870	anthranilate synthase, alpha subunit, putative	0.2193	0.6645	0.4808	0.02867	0.9542	0.5329	0.7084	0.0753	0.1195	0.5178	0.1557	0.1587
251717_at	AT3G55850	LAF3(LAF3 ISF1;LAF3 ISF2 (LONG AFTER FAR-R	0.4459	0.0502	0.1289	0.3219	0.116	0.1719	-1.1304	0.0016	0.0203	-1.2545	0.0011	0.0123
251718_at	AT3G56100	MRLK (MERISTEMATIC RECEPTOR-LIKE KINAS	0.2512	0.6879	0.4885	-0.1535	0.8048	0.4911	-0.78	0.2508	0.2414	-1.1847	0.1112	0.1286
251719_at	AT3G56140	similar to unknown protein [Arabidopsis thaliana] (T	0.06386	0.7476	0.5081	-0.2109	0.3183	0.3021	-0.4058	0.0301	0.0707	-0.6806	0.0052	0.0226
251720_at	AT3G56160	bile acid:sodium symporter	-0.2483	0.4823	0.413	-1.6763	0.0064	0.0457	-0.2858	0.4234	0.3288	-1.7139	0.0059	0.0239
251721_s_at	AT3G56450;AT3G56190	[AT3G56450, ALPHA-SNAP1 (alpha-soluble NSF a	0.6333	0.0262	0.0937	0.5528	0.0398	0.0988	-0.1234	0.5393	0.375	-0.2039	0.3298	0.2532
251722_at	AT3G56200	amino acid transporter family protein	-1.4849	0.0191	0.0821	-1.9725	0.0073	0.0481	0.2384	0.4039	0.3181	-0.2492	0.385	0.2779
251723_at	AT3G56230	speckle-type POZ protein-related	-0.1594	0.6511	0.4766	-0.7679	0.4764	0.1404	0.6648	0.0742	0.1186	0.05601	0.8495	0.4426
251724_at	AT3G56250	unknown protein	-0.4611	0.4588	0.4023	0.07469	0.9009	0.5192	-0.2562	0.6231	0.4057	0.2796	0.5929	0.3609
251725_at	AT3G56260	unknown protein	-1.763	0.0042	0.0468	-1.306	0.0121	0.0589	0.6462	0.0046	0.0288	1.1032	6.00E-04	0.0103
251726_at	AT3G56280	pseudogene, protein kinase family, contains protein	0.018089	0.9897	0.6744	-1.1183	0.4612	0.3684	1.6197	0.3036	0.2704	0.5203	0.7241	0.4054
251727_at	AT3G56290	similar to hypothetical protein [Vitis vinifera] (GB:CA	-1.25	0.0017	0.0391	-1.2672	0.0016	0.0317	0.3124	0.081	0.1247	0.2952	0.0933	0.1155
251728_at	AT3G56300	tRNA synthetase class I (C) family protein	-0.5037	0.1827	0.2501	-0.7002	0.0888	0.1503	-1.329	0.0106	0.0409	-1.5255	0.0066	0.0251
251729_at	AT3G56310	similar to hypothetical protein [Vitis vinifera] (GB:C	0.7873	8.00E-04	0.0342	0.484	0.005	0.0424	0.001946	0.961	0.508	-0.3014	0.0013	0.0132
251730_at	AT3G56330	N2,N2-dimethylguanosine tRNA methyltransferase	0.2807	0.0894	0.1732	-0.1645	0.2607	0.2701	0.2484	0.1193	0.1558	-0.1968	0.1926	0.1806
251731_at	AT3G56350	superoxide dismutase (Mn), putative / manganese s	1.5775	0.176	0.2454	1.0714	0.3274	0.3072	0.03752	0.9685	0.5096	-0.4687	0.6275	0.3729
251732_at	AT3G56110	prenylated rab acceptor (PRA1) family protein	0.4312	0.0123	0.0686	0.3743	0.0197	0.072	0.353	0.016	0.0505	0.2962	0.0283	0.0561
251733_at	AT3G56240	CCH (COPPER CHAPERONE)	-0.4343	0.0775	0.1602	-0.3063	0.1711	0.2134	1.2024	0.0019	0.0209	1.3305	0.0013	0.0133
251734_at	AT3G56270	similar to unknown protein [Arabidopsis thaliana] (T	-0.03854	0.8877	0.5477	-0.3389	0.2563	0.268	-0.2342	0.2912	0.2643	-0.5346	0.0502	0.0795
251735_at	AT3G56090	ATFER3 (FERRITIN 3); ferric iron binding	-1.1693	0.0109	0.0655	-1.2589	0.0085	0.0508	0.4549	0.009	0.0378	0.3654	0.0188	0.044
251736_at	AT3G56130	biotin/lipoyl attachment domain-containing protein	-0.5549	0.0967	0.1797	-0.4195	0.1776	0.218	0.01212	0.9205	0.498	0.1475	0.2654	0.2206
251737_at	AT3G56340	40S ribosomal protein S26 (RPS26C)	0.09417	0.6304	0.4699	0.305	0.1674	0.2108	0.2236	0.2754	0.2554	0.4344	0.0703	0.0971
251738_at	AT3G56150	initiation FACTOR 3)	0.1885	0.5269	0.4318	0.01246	0.9657	0.5355	-0.9229	0.0103	0.0402	-1.0985	0.0055	0.0232
251739_at	AT3G56170	CAN (CA-2+ DEPENDENT NUCLEASE); nuclease	0.8488	0.004	0.0467	1.0732	0.0017	0.032	-0.03428	0.822	0.4703	0.1901	0.2538	0.2145
251740_at	AT3G56070	ROC2 (rotamase CyP 2); peptidyl-prolyl cis-trans is	0.2245	0.2603	0.2997	0.4689	0.0521	0.1132	-0.3604	0.0146	0.0483	-0.116	0.2556	0.2155
251741_at	AT3G56040	similar to hypothetical protein OsJ_018104 [Oryza s	-0.282	0.1265	0.2058	-0.6197	0.0134	0.0615	-0.4743	0.6386	0.4107	-0.412	0.0482	0.0775
251742_at	AT3G56050	protein kinase family protein	-0.1986	0.0847	0.1686	-0.06009	0.5281	0.3954	-0.1522	0.1167	0.1536	-0.01368	0.8663	0.4472
251743_at	AT3G55890	yippee family protein	0.5931	0.2771	0.3099	1.1721	0.0679	0.1306	-0.1874	0.649	0.4142	0.3916	0.3625	0.2681
251744_at	AT3G56310	similar to hypothetical protein [Vitis vinifera] (GB:CA	-0.1746	0.3291	0.3395	-0.3548	0.087	0.1487	-0.1552	0.3794	0.3075	-0.3354	0.0098	0.1204
251745_at	AT3G55980	zinc finger (CCCH-type) family protein	-1.0531	0.0381	0.1123	-0.7612	0.0923	0.1532	-0.1992	0.289	0.2631	0.09273	0.6001	0.3634
251746_at	AT3G56060	glucose-methanol-choline (GMC) oxidoreductase fa	-0.8269	0.0086	0.0605	-0.822	0.0088	0.0516	0.01609	0.9099	0.4952	0.02097	0.8827	0.4522
251747_at	AT3G55670	similar to F-box family protein [Arabidopsis thaliana	0.4032	0.7638	0.5126	-1.0956	0.4314	0.3559	0.6314	0.6306	0.4081	-0.8673	0.1146	0.3315
251748_at	AT3G55680	invertase/pectin methylesterase inhibitor family prot	-0.01122	0.9907	0.5747	0.2574	0.789	0.4858	-0.07698	0.9359	0.5023	0.1917	0.8417	0.4406
251749_at	AT3G55690	similar to unknown protein [Arabidopsis thaliana] (T	-0.3067	0.1807	0.2486	-0.303	0.1849	0.2231	0.5538	0.0249	0.0639	0.5575	0.0244	0.0514
251750_at	AT3G55710	UDP-glucuronosyl/UDP-glucosyl transferase family	-1.2262	0.0163	0.0771	-0.996	0.0318	0.0885	-0.8608	0.049	0.0932	-0.6305	0.1099	0.1276
251751_at	AT3G55720	similar to unknown protein [Arabidopsis thaliana] (T	0.411	0.5174	0.4282	-0.3984	0.5297	0.3962	0.821	0.2296	0.2293	0.01157	0.985	0.4791
251752_at	AT3G55740	Pro/T2 (PROLINE TRANSPORTER 2); amino acid t	0.4136	0.0269	0.0949	0.04032	0.756	0.4769	-0.1406	0.3105	0.2737	-0.5138	0.0133	0.0365
251753_at	AT3G55760	similar to unknown protein [Arabidopsis thaliana] (T	0.4463	0.181	0.2488	0.4362	0.189	0.2257	-0.1002	0.4505	0.3388	-0.1102	0.4099	0.2882
251754_at	AT3G55780	glycosyl hydrolase family 17 protein	-0.638	0.4045	0.3776	0.1806	0.8051	0.4912	-1.4152	0.0248	0.0639	-0.5966	0.2139	0.1929
251755_at	AT3G55790	unknown protein	0.5891	0.6657	0.4812	0.6681	0.6254	0.433	0.3185	0.5522	0.3799	0.3975	0.4639	0.3116
251756_at	AT3G55800	similar to Unknown protein [Oryza sativa (japonica c	0.09996	0.6691	0.4823	0.2393	0.3321	0.3096	0.419	0.1258	0.1607	0.5583	0.0618	0.0902
251757_at	AT3G55640	mitochondrial substrate carrier family protein	-0.1617	0.2102	0.2684	-0.2605	0.0742	0.1366	-0.6241	0.0017	0.0206	-0.7229	0.001	0.0121
251758_at	AT3G55770	LIM domain-containing protein	0.2171	0.1595	0.2331	0.1881	0.2093	0.2391	-0.137	0.3375	0.2871	-0.166	0.2575	0.2166
251759_at	AT3G55630	ATDFD (A. THALIANA DHFS-FPGS HOMOLOG D	-0.8901	8.00E-04	0.0336	-0.941	6.00E-04	0.027	-0.6458	0.0026	0.0234	-0.6968	0.0019	0.0151
251760_at	AT3G55605	mitochondrial glycoprotein family protein / MAM33 f	0.4262	0.0156	0.0754	0.6709	0.0031	0.0363	0.3238	0.0374	0.0798	0.5685	0.0057	0.0236
251761_at	AT3G55700	UDP-glucuronosyl/UDP-glucosyl transferase family	1.2114	0.2441	0.2901	0.1898	0.8412	0.5017	-0.3279	0.7297	0.4417	-1.3495	0.2019	0.1862
251762_at	AT3G55800	SBPASE (SEDOHEPTULOSE-BISPHOSPHATASE	-1.0224	4.00E-04	0.032	-1.146	2.00E-04	0.0249	0.06356	0.5123	0.364	-0.06007	0.5344	0.3396
251763_at	AT3G55730	MYB109 (myb domain protein 109); DNA binding / t	0.1664	0.5352	0.4352	0.2581	0.3524	0.3193	-0.0239	0.8409	0.4758	0.06787	0.576	0.3545
251764_at	AT3G55830	EPC1 (ECTOPICALLY PARTING CELLS); transfer	0.4248	0.0123	0.0685	0.5435	0.0052	0.0429	-0.2024	0.0151	0.0489	-0.08373	0.1667	0.1652
251765_at	no_match	no_match	-0.6983	0.3765	0.3626	1.2393	0.1525	0.2001	-0.2239	0.7659	0.453	1.7137	0.0713	0.0978
251766_at	AT3G55910	unknown protein	-0.05272	0.8842	0.5471	0.5199	0.2007	0.2331	-1.2017	0.0241	0.0629	-0.6291	0.1377	0.1468
251767_at	AT3G55930	RNA splicing factor-related	0.9364	0.2003	0.2624	1.5807	0.061	0.1226	0.9623	0.1906	0.2059	1.6066	0.0583	0.0871
251768_at	AT3G55940	phosphoinositide-specific phospholipase C, putative	-2.0246	0.0114	0.0669	-2.1605	0.0091	0.0522	-0.1441	0.5813	0.3912	-0.28	0.3089	0.2429
251769_at	AT3G55950	protein kinase family protein	0.4143	0.0552	0.135	-0.1275	0.4556	0.3662	0.2914	0.0904	0.1329	-0.2504	0.1287	0.1407
251770_at	AT3G55970	oxidoreductase, 2OG-Fe(II) oxygenase family prote	0.1378	0.6257	0.4684	0.1628	0.5671	0.4108	0.6836	0.0189	0.0552	0.7085	0.0168	0.0414
251771_at	AT3G56000	ATCSLA14 (Cellulose synthase-like A14); transfera	-0.3133	0.3933	0.3717	-0.3294	0.3717	0.3282	-0.624	0.0046	0.0288	-0.6401	0.0042	0.0207
251772_at	AT3G55920	peptidyl-prolyl cis-trans isomerase, putative / cyclop	0.2046	0.3116	0.3296	-0.07998	0.6744	0.45	0.09577	0.5531	0.3801	-0.1888	0.2715	0.2236
251773_at	AT3G55960	NLI interacting factor (NIF) family protein	0.08817	0.695	0.4911	-0.00338	0.9879	0.5411	0.1844	0.3299	0.2833	0.09285	0.6066	0.3656
251774_at	AT3G55840	similar to unknown protein [Arabidopsis thaliana] (T	-0.1001	0.0626	0.1436	-0.6141	0.2087	0.2387	-0.1186	0.708	0.434	0.3174	0.3423	0.259
251775_s_at	AT2G39800;AT3G55610	[AT2G39800, P5CS1 (DELTA1-PYRROLINE-5-CA	0.4534	0.1684	0.2402	0.4006	0.2121	0.2409	-1.3736	0.007	0.0341	-1.4264	0.0062	0.0243
251776_at	AT3G55620	initiation factor	0.2306	0.0946	0.1778	0.1495	0.2303	0.2517	0.4165	0.008	0.0359	0.3353	0.0167	0.0413
251777_s_at	AT3G55650;AT3G55810	[AT3G55650, pyruvate kinase, putative];[AT3G5581	0.2957	0.4154	0.3824	-0.4952	0.7461	0.4736	0.749	0.562	0.3833	-1.0419	0.4293	0.2965
251778_at	AT3G55660	ATROPGEF6/ROPGEF6 (KINASE PARTNER PRO	-0.7739	0.5403	0.4368	-0.3623	0.7699	0.4804	-0.5783	0.5532	0.3801	-0.1667	0.8612	0.4462
251779_at	AT3G55300	transposable element gene	1.4144	0.1105	0.1927	-0.00134	0.9986	0.5436	-0.2796	0.707	0.4336	-1.6953	0.0705	0.0973
251780_s_at	AT3G55310;AT3G55290	[AT3G55310, oxidoreductase];[AT3G55290, short-c	0.8912	0.0644	0.1453	0.7195	0.1102	0.1676	-0.1578	0.5809	0.3911	-0.3295	0.2786	0.2274
251781_at	AT3G55320	PGP20 (P-GLYCOPROTEIN 20); ATPase, coupled	-0.03097	0.8029	0.525	0.03901	0.7538	0.4763	-0.784	0.0025	0.0232	-0.714	0.0035	0.0194
251782_at	AT3G55260	ATHEX2/HEXO1 (BETA-HEXOSAMINIDASE 1); be	0.3622	0.0274	0.0958	0.1935	0.1438	0.1935	-0.3429	0.0195	0.056	-0.5115	0.0049	0.022
251783_at	AT3G55280	60S ribosomal protein L23A (RPL23aB)	-0.1778	0.155	0.2298	-0.01239	0.9088	0.5212	0.4936	1.00E-04	0.0101	0.6589	0	0.0047
251784_at	AT3G55330	PPL1 (PSBP-LIKE PROTEIN 1); calcium ion binding	-0.7161	0.0026	0.0426	-0.9331	0.001	0.0291	0.0494	0.6691	0.4208	-0.1677	0.1931	0.1809
251785_at	AT3G55130	ATWBC19 (WHITE-BROWN COMPLEX HOMOLOG	-0.128	0.3643	0.3564	-0.3839	0.0374	0.0957	-0.1554	0.1685	0.1908	-0.4113	0.0113	0.0334
251786_at	AT3G55270	MKP1; MAP kinase tyrosine/serine/threonine phosp	0.5196	0.0953	0.1783	0.4892	0.11	0.1674	-0.4173	0.0994	0.1404	-0.4477	0.0836	0.1078
251787_at	AT3G55410	2-oxoglutarate dehydrogenase E1 component, puta	0.336	0.0406	0.1161	0.4513	0.016	0.0659	-1.0341	6.00E-04	0.0158	-0.9189	9.00E-04	0.0119
251788_at	AT3G55420	similar to hypothetical protein [Vitis vinifera] (GB:CA	-0.911	0.0034	0.0446	-0.2955	0.113	0.1699	-0.2991	0.0634	0.1085	0.3163	0.0544	0.0834
251789_at	AT3G55450	protein kinase, putative	1.2757	8.00E-04	0.0336	1.3735	6.00E-04	0.0266	-0.2205	0.1868	0.2035	-0.1227	0.4261	0.2951
251790_at	AT3G55470	C2 domain-containing protein	0.8523	0.0079	0.0584	0.9879	0.0046	0.0416	0.9146	0.002	0.021	1.0502	0.0012	0.0127
251791_at	AT3G55500	ATEXPA16 (ARABIDOPSIS THALIANA EXPANSIN	0.002457	0.9938	0.5754	0.3003	0.3701	0.3275	-0.3549	0.299	0.2682	-0.05708	0.8572	0.445
251792_at	AT3G55550	lectin protein kinase, putative	-0.7642	0.509	0.4245	0.2385	0.8322	0.4995	-1.4052	0.2179	0.2224	-0.4025	0.6972	0.3965
251793_at	AT3G55580	regulator of chromosome condensation (RCC1) fam	-0.9039	0.4198	0.3848	-0.3242	0.7634	0.4784	-0.6387	0.0265	0.0662	-0.05898	0.7671	0.419
251794_at	AT3G55590	GDP-mannose pyrophosphorylase, putative	0.2635	0.6723	0.4834	-1.0519	0.1431	0.193	0.1858	0.7641	0.4524	-1.1296	0.1225	0.1368
251795_at	AT3G55390	integral membrane family protein	0.6687	0.0489	0.1271	0.1749	0.5047	0.3865	0.271	0.2969	0.2671	-0.2228	0.3804	0.276
251796_at	AT3G55360	ATTSC13/CER10/ECR/TSC13 (ENOYL-COA REDI	-0.6597	0.199	0.2619	-0.6713	0.1927	0.2278	-0.02979	0.9054	0.4938	-0.04143	0.8688	0.4479
251797_at	AT3G55560	AGF2 (AT-HOOK PROTEIN OF GA FEEDBACK 2)	0.17	0.4859	0.414	0.2351	0.3488	0.3175	-0.2364	0.3177	0.2771	-0.1714	0.4548	0.3079
251798_at	AT3G55460	SCL30 (SC35-like splicing factor 30); RNA binding	0.373	0.0532	0.1323	0.3579	0.0596	0.1213	-0.2171	0.1891	0.2049	-0.2322	0.1661	0.1649
251799_at	AT3G55520	immunophilin, putative / FKBP-type peptidyl-prolyl c	0.2657	0.1381	0.2159	0.5863	0.0152	0.0646	-0.05829	0.7058	0.4333	0.2613	0.1431	0.1502
251800_at	AT3G55510	similar to unknown protein [Arabidopsis thaliana] (T	0.4244	0.0079	0.0584	0.1244	0.2221	0.2471	-0.4504	0.0042	0.0277	-0.7504	6.00E-04	0.0103
251801_at	AT3G55440	ATCTIMC (CYTOSOLIC TRIOSE PHOSPHATE IS	0.1049	0.1398	0.2174	-0.1394	0.0709	0.1332	0.1477	0.0608	0.1058	-0.09665	0.1654	0.1645
251802_at	AT3G55380	UBC14 (ubiquitin-conjugating enzyme 14); ubiquitin	0.2562	0.1049	0.187	0.4284	0.025	0.0791	0.3337	0.0069	0.0339	0.506	0.0015	0.0138
251803_at	AT3G55350	similar to unknown protein [Arabidopsis thaliana] (T	0.7804	0.0671	0.1488	-0.3741	0.2976	0.2994	0.02628	0.9151	0.4964	0.4325	0.1349	0.145
251804_at	AT3G55430	glycosyl hydrolase family 17 protein / beta-1,3-gluca	-0.1715	0.7111	0.4967	-0.2094	0.6525	0.4426	0.3393	0.0612	0.1063	0.3014	0.0836	0.1078
251805_at	AT3G55530	SDIR1 (SALT- AND DROUGHT-INDUCED RING F	0.2823	0.0925	0.1761	0.1008	0.4758	0.3745	-0.3031	0.0774	0.1214	-0.4846	0.0194	0.0447
251806_at	AT3G55370	OBP3 (OBF-BINDING PROTEIN 3); DNA binding /	-0.2708	0.7588	0.6114	2.0347	0.0689	0.1317	-0.03242	0.9705	0.5101	2.2731	0.0509	0.0802
251807_at	AT3G55400	OVA1 (OVULE ABORTION 1); ATP binding / amino	-0.3083	0.1639	0.2368	-0.1377	0.4896	0.3802	-0.2723	0.0262	0.0658	-0.1016	0.2681	0.2218
251808_at	AT3G55480	adaptin family protein	0.5407	0.0106	0.0647	0.4043	0.0276	0.0829	-0.5894	0.0025	0.0232	-0.7258	0.0011	0.0126
251809_at	AT3G55600	similar to cation exchanger, putative (CAX10) [Ara	0.4628	0.0963	0.1763	0.5092	0.0757	0.1379	0.1588	0.4951	0.3578	0.2052	0.3876	0.279
251810_at	AT3G55250	similar to unnamed protein product [Vitis vinifera] (G	0.00492	0.9723	0.5704	-0.3613	0.0536	0.1148	-0.2324	0.1563	0.1832	-0.5987	0.0109	0.0327
251811_at	AT3G54990	SMZ (SCHLAFMUTZE); DNA binding / transcription	-0.3003	0.5675	0.4479	-0.6356	0.2583	0.2691	-0.4093	0.4443	0.3359	-0.7446	0.1978	0.1836
251812_at	AT3G55910	catalytic	0.4716	0.0758	0.1584	0.1635	0.4554	0.3662	-0.2544	0.2636	0.2512	-0.5625	0.0468	0.0761
251813_at	AT3G55000	TON1A (TONNEAU 1)	0.07572	0.4938	0.4174	0.1314	0.2619	0.2709	-0.4846	0.0036	0.0265	-0.429	0.0056	0.0234
251814_at	AT3G54890	LHCA1; chlorophyll binding	-0.3882	0.0333	0.1056	-0.7201	0.0041	0.0398	0.1751	0.1947	0.2085	-0.1568	0.2358	0.2049
251815_at	AT3G54900	CXIP1 (CAX INTERACTING PROTEIN 1)	-0.558	0.0265	0.0941	-0.8502	0.0064	0.0457	0.5313	0.0309	0.0715	0.2392	0.2153	0.1938
251816_at	AT3G55005	TON1B (TONNEAU 1B)	-1.0082	0.0076	0.0579	-0.5815	0.0454	0.1056	0.4602	0.0231	0.0616	0.8868	0.0023	0.016
251817_at	AT3G54840	ARA6; GTP binding	0.2324	0.0331	0.1055	0.351	0.0085	0.0509	0.3674	0.0014	0.0194	0.486	5.00E-04	0.0093
251818_at	AT3G54860	ATVPS23 (Arabidopsis thaliana vacuolar protein so	0.09357	0.5601	0.4449	0.1445	0.3827	0.3331	-0.3003	0.0282	0.0682	-0.2494	0.049	0.0784
251819_at	AT3G55030	PGPS2 (phosphatidylglycerolphosphate synthase 2	-0.1198	0.2936	0.3195	-0.1471	0.2123	0.241	-0.1191	0.2961	0.2667	-0.1464	0.2141	0.193
251820_at	AT3G55040	In2-1 protein, putative	0.2555	0.0173	0.0789	-0.7651	0.0042	0.0403	0.04603	0.7419	0.4454	-0.2087	0.1848	0.1762
251821_at	AT3G55050	serine/threonine protein phosphatase 2C (PP2C6)	0.1907	0.2435	0.2897	-0.2731

251890_at	AT3G54220	SCR (SCARECROW); transcription factor	0.1052	0.681	0.4863	-0.3938	0.1728	0.2147	0.00912	0.9644	0.5086	-0.4899	0.0634	0.0915
251891_at	AT3G54320	WRI1 (WRINKLED 1); DNA binding / transcription f	-0.7499	0.0639	0.1448	-0.357	0.2929	0.2881	-1.0038	0.0272	0.0671	-0.6109	0.1072	0.1255
251892_at	AT3G54320	WRI1 (WRINKLED 1); DNA binding / transcription f	0.8328	0.0049	0.0502	0.4678	0.0343	0.0915	0.8896	0.0038	0.0269	0.5246	0.0234	0.05
251893_at	AT3G54380	SAC3/GANP family protein	0.7318	0.0068	0.0558	0.7528	0.0062	0.0451	-0.2276	0.0138	0.0468	-0.2066	0.019	0.0442
251894_at	AT3G54380	SAC3/GANP family protein	0.1068	0.6507	0.4765	0.5685	0.06	0.1216	-1.3856	0.0032	0.0251	-0.9238	0.0134	0.0367
251895_at	AT3G54420	ATEP3 (Arabidopsis thaliana chitinase class IV); ch	0.1383	0.6503	0.4764	-0.05923	0.8443	0.5028	1.1446	0.0026	0.0236	0.947	0.0053	0.0226
251896_at	AT3G54360	transcription factor	-0.6762	0.0768	0.1595	-0.329	0.3131	0.2991	0.4394	0.1792	0.198	0.7866	0.0436	0.073
251897_at	AT3G54360	protein binding / zinc ion binding	0.4011	0.0195	0.0826	0.5599	0.0062	0.0451	-0.3799	0.0233	0.0617	-0.2211	0.1059	0.1246
251898_at	AT3G54340	AP3 (APETALA 3); DNA binding / transcription facto	0.7898	0.096	0.179	0.5555	0.202	0.2339	0.8579	0.068	0.1131	0.6236	0.1454	0.1518
251899_at	AT3G54400	aspartyl protease family protein	-0.8562	0.2348	0.2843	-0.8734	0.2271	0.2498	0.984	0.0334	0.0747	0.9668	0.0353	0.0635
251900_at	AT3G54430	SRS6 (SHI-RELATED SEQUENCE 6)	-0.6892	0.1484	0.2242	-0.09975	0.8086	0.4926	0.5789	0.1954	0.209	1.1683	0.035	0.0634
251901_at	AT3G54100	similar to unknown protein [Arabidopsis thaliana] (T	0.2683	0.1233	0.2035	0.6117	0.0113	0.0573	-0.6383	0.0093	0.0386	-0.2949	0.0953	0.1171
251902_at	AT3G54110	ATPUMP1; binding / oxidative phosphorylation unc	0.5302	0.0241	0.0906	0.1723	0.3148	0.3001	-0.03648	0.8074	0.4658	-0.3944	0.0481	0.0774
251903_at	AT3G54120	reticulon family protein (RTNLB12)	-0.1296	0.1891	0.2547	-0.6738	0.0012	0.0299	0.4906	0.0013	0.0191	-0.0536	0.4292	0.2964
251904_at	AT3G54130	josephin family protein	0.3012	0.0876	0.1715	0.4008	0.0401	0.0994	0.1725	0.2438	0.2373	0.2722	0.0975	0.1187
251905_at	AT3G53710	AGD6; DNA binding	0.03209	0.8588	0.5407	0.1189	0.5209	0.3925	-0.2299	0.1444	0.1748	-0.1431	0.3228	0.2496
251906_at	AT3G53720	ATCHX20 (CATION/H+ EXCHANGER 20); monova	-0.148	0.6522	0.4768	-0.4168	0.2426	0.2595	-0.6564	0.0251	0.0642	-0.9252	0.0079	0.0277
251907_at	AT3G53760	tubulin family protein	0.2883	0.2813	0.3121	0.2	0.4367	0.3583	-0.2573	0.3291	0.2829	-0.3456	0.2101	0.1909
251908_at	AT3G53770	late embryogenesis abundant protein-related / LEA	1.4612	0.2309	0.2826	-0.889	0.4388	0.359	1.7799	0.1606	0.186	-0.5703	0.6109	0.3672
251909_at	AT3G53790	TRFL4 (TRF-LIKE 4); DNA binding	-0.02353	0.9798	0.972	0.1807	0.846	0.5033	-0.1365	0.8332	0.4735	0.06775	0.9166	0.4617
251910_at	AT3G53810	lectin protein kinase, putative	0.4741	0.1257	0.2052	0.4779	0.1235	0.1784	0.1664	0.242	0.2362	0.1702	0.2332	0.2033
251911_at	AT3G53820	zinc finger (C2H2 type) family protein	0.2311	0.8385	0.535	-2.2879	0.0978	0.1576	1.6229	0.2016	0.2126	-0.8961	0.4467	0.3047
251912_at	AT3G53840	protein kinase family protein	0.6071	0.5495	0.4409	-1.2668	0.2448	0.2609	0.9389	0.217	0.2218	-0.935	0.2186	0.1954
251913_at	AT3G53910	malate dehydrogenase-related	1.749	0.1979	0.2613	0.7502	0.5445	0.4024	-0.4821	0.4987	0.3592	-1.4808	0.0846	0.1086
251914_at	AT3G53930	protein kinase family protein	-0.314	0.0485	0.1269	0.2728	0.0174	0.1338	-0.7781	0.0021	0.0217	-0.1912	0.1564	0.159
251915_at	AT3G53940	mitochondrial substrate carrier family protein	0.3084	0.3714	0.3602	-0.1306	0.692	0.4562	0.09957	0.6962	0.4299	-0.3394	0.2256	0.1992
251916_at	AT3G53960	proton-dependent oligopeptide transport (POT) fam	-0.1023	0.656	0.4778	0.09533	0.6774	0.4511	-0.1931	0.3325	0.2845	0.004458	0.9809	0.4783
251917_at	AT3G53970	proteasome inhibitor-related	0.6721	0.0118	0.0678	1.1053	0.0015	0.033	0.03677	0.8219	0.4703	0.47	0.0373	0.0658
251918_at	AT3G54040	photoassimilate-responsive protein-related	0.4327	0.2731	0.3073	0.1397	0.703	0.4601	0.9271	0.0437	0.0872	0.634	0.1174	0.1329
251919_at	AT3G53800	armadillo/beta-catenin repeat family protein	0.4158	0.2533	0.2954	0.1297	0.6989	0.4585	-0.6947	0.0068	0.0338	-0.9809	0.0019	0.0151
251920_at	AT3G53900	uracil phosphoribosyltransferase, putative / UMP py	-1.7895	0.0018	0.091	-1.9686	0.0012	0.0302	0.3737	0.1766	0.1963	0.1945	0.4417	0.3022
251921_at	AT3G53890	40S ribosomal protein S21 (RPS21B)	-0.1765	0.2046	0.2651	-0.09851	0.4457	0.3621	0.6066	0.0029	0.0247	0.6846	0.0019	0.0149
251922_at	AT3G54030	protein kinase family protein	0.5428	0.045	0.1223	0.5302	0.0482	0.109	0.2804	0.0205	0.0576	0.2678	0.0238	0.0505
251923_at	AT3G53880	aldo/keto reductase family protein	0.2431	0.2396	0.2874	-0.3863	0.1539	0.0933	0.1302	0.3577	0.2968	0.2158	0.1603	0.1614
251924_at	AT3G53730	histone H4	-0.2879	0.2391	0.2871	0.03774	0.8651	0.5086	0.8316	0.0162	0.0508	1.1572	0.0051	0.0224
251925_at	AT3G54000	similar to unknown protein [Arabidopsis thaliana] (T	0.9417	0.0382	0.1126	0.3578	0.3118	0.2983	0.3625	0.197	0.2099	-0.2214	0.3986	0.2837
251926_at	AT3G53740	60S ribosomal protein L36 (RPL36B)	0.1676	0.364	0.3562	0.1705	0.3566	0.3212	0.2802	0.1392	0.1705	0.2831	0.1361	0.1457
251927_at	AT3G53990	universal stress protein (USP) family protein	0.5047	0.127	0.206	0.9404	0.0232	0.0768	0.8338	0.0124	0.0443	1.2696	0.0028	0.0173
251928_at	AT3G53980	protease inhibitor/seed storage/lipid transfer protein	2.4532	0.0166	0.0775	3.5938	0.0044	0.0409	1.0312	0.0987	0.1398	2.1718	0.0107	0.0324
251929_at	AT3G53920	SIGC (RNA polymerase sigma subunit C); DNA bin	-0.4221	0.0165	0.0771	-0.5771	0.0056	0.0434	-0.3621	0.027	0.0668	-0.5171	0.0082	0.0282
251930_at	AT3G53780	rhomboid family protein	0.8121	0.008	0.0587	0.7155	0.0125	0.0598	0.1363	0.4569	0.3417	0.03977	0.8221	0.4348
251931_at	AT3G53950	glyoxal oxidase-related	0.2125	0.1666	0.2388	0.1875	0.2106	0.2401	0.2203	0.155	0.1823	0.1953	0.1958	0.1824
251932_at	AT3G54010	PAS1 (PASTICCINO 1); FK506 binding / peptidyl-pr	0.9163	9.00E-04	0.0349	0.8592	0.0012	0.0299	0.1049	0.1242	0.1595	0.0449	0.4528	0.3071
251933_at	AT3G54060	similar to unknown protein [Arabidopsis thaliana] (T	-0.2482	0.6038	0.4608	-0.9182	0.1059	0.1642	0.06001	0.8984	0.4919	-0.61	0.2389	0.2065
251934_at	AT3G54070	ankyrin repeat family protein	-1.4325	0.215	0.2716	-2.7191	0.0491	0.1098	1.0979	0.2848	0.2606	-0.1887	0.8425	0.4407
251935_at	AT3G54090	histone carbohydrate kinase family protein	0.3019	0.0737	0.1562	0.3875	0.0366	0.0943	0.1302	0.3577	0.2968	0.2158	0.1603	0.1614
251936_at	AT3G53700	MEE40 (maternal effect embryo arrest 40)	-0.03204	0.8497	0.5381	0.06597	0.6986	0.4585	-0.7514	8.00E-04	0.0165	-0.6534	0.0014	0.0135
251937_at	AT3G53400,AT3G53402	(AT3G53400, similar to CPuORF47 (Conserved pep	-0.3151	0.0304	0.1011	-0.1312	0.2434	0.2601	-0.1905	0.1181	0.1547	-0.00658	0.9486	0.4705
251938_at	AT3G53600	60S ribosomal protein L12 (RPL12B)	-0.1198	0.3516	0.4105	-0.07915	0.5247	0.394	0.4562	0.0047	0.0292	0.4968	0.0035	0.0192
251939_at	AT3G53440	DNA binding	0.06713	0.7185	0.4989	0.05833	0.7536	0.4763	-0.06111	0.6609	0.4182	-0.06991	0.6172	0.3693
251940_at	AT3G53450	similar to unknown protein [Arabidopsis thaliana] (T	-0.5914	0.5955	0.4581	0.6542	0.5587	0.4079	0.1319	0.904	0.4934	1.3774	0.2509	0.2131
251941_at	AT3G53470	similar to unknown protein [Arabidopsis thaliana] (T	-0.03066	0.7387	0.5053	-0.06362	0.4992	0.3842	0.1327	0.0646	0.1096	0.09914	0.1303	0.1417
251942_at	AT3G53480	ATPDR9/PDR9 (PLEIOTROPIC DRUG RESISTAN	0.9307	0.2076	0.2669	1.0588	0.1628	0.2079	0.3236	0.328	0.2824	0.4517	0.1951	0.182
251943_at	AT3G53500	RSZ32; nucleic acid binding	0.2496	0.1094	0.1915	0.5214	0.0128	0.0603	-0.1909	0.1916	0.2065	0.0809	0.5423	0.3418
251944_at	AT3G53510	ABC transporter family protein	0.2218	0.0322	0.104	-0.8729	0.2394	0.2557	1.1138	0.1504	0.1792	-1.7808	0.0469	0.0762
251945_at	AT3G53520	UXS1 (UDP-GLUCURONIC ACID DECARBOXYLA	0.1781	0.3412	0.3458	-0.1847	0.3255	0.3062	0.3648	0.0746	0.1189	0.001953	0.9904	0.4803
251946_at	AT3G53540	similar to unknown protein [Arabidopsis thaliana] (T	-0.1747	0.3721	0.3605	-0.0084	0.9638	0.535	-0.3802	8.00E-04	0.0165	-0.214	0.007	0.0261
251947_at	AT3G53550	similar to unknown protein [Arabidopsis thaliana] (T	0.9349	0.3658	0.3572	-2.2685	0.0687	0.1315	0.2676	0.785	0.4588	-2.9358	0.0329	0.0612
251948_at	AT3G53580	diaminopimelate epimerase family protein	0.1436	0.2631	0.3016	0.05413	0.6496	0.4415	0.4789	0.0123	0.0441	0.3894	0.0243	0.0512
251949_at	AT3G53590	leucine-rich repeat transmembrane protein kinase,	1.2755	0.2641	0.3019	0.9144	0.4048	0.3434	0.5166	0.4074	0.3197	0.1555	0.7945	0.4273
251950_at	AT3G53600	zinc finger (C2H2 type) family protein	1.4109	0.0777	0.1605	-1.3867	0.0812	0.1429	0.8017	0.2511	0.2415	0.8258	0.2394	0.2067
251951_s_at	AT3G53630,AT1G55710,A	(AT3G53630, similar to unknown protein [Arabidops	0.662	0.003	0.0436	0.6441	0.0033	0.0371	-0.3908	0.0191	0.0555	-0.4087	0.0165	0.0411
251952_at	AT3G53650	histone H2B, putative	-0.00545	0.9896	0.5744	0.1657	0.6945	0.457	1.2075	0.0272	0.067	1.3787	0.0177	0.0427
251953_at	AT3G53668,AT3G53670	(AT3G53668, CPuORF51 (Conserved peptide upst	-0.2826	0.4281	0.3884	0.1134	0.7415	0.4718	-0.328	0.3643	0.3002	0.06796	0.8426	0.4407
251954_at	AT3G53668,AT3G53670	(AT3G53668, CPuORF51 (Conserved peptide upst	0.2877	0.0147	0.0737	0.5149	0.0018	0.0325	-0.03168	0.6744	0.4224	0.1956	0.0491	0.0785
251955_at	AT3G53680	PHD finger transcription factor, putative	-0.409	0.2834	0.3136	-0.924	0.049	0.1097	-0.3256	0.2845	0.2604	-0.8405	0.0333	0.0616
251956_at	AT3G53460	CP29 (chloroplast 29 kDa ribonucleoprotein); RNA	0.4237	0.4017	0.3761	0.387	0.4402	0.3596	-0.4735	0.0761	0.1202	-0.5103	0.0624	0.0907
251957_at	AT3G53690	zinc finger (C3HC4-type RING finger) family protein	0.2134	0.3991	0.3749	0.4964	0.0934	0.1539	0.1862	0.4569	0.3417	0.4692	0.1069	0.1253
251958_at	AT3G53560	chloroplast lumen common family protein	-0.2522	0.1882	0.2541	-0.3587	0.0873	0.1488	0.2748	0.0016	0.0204	0.1683	0.0096	0.0306
251959_at	AT3G53410	zinc finger (C3HC4-type RING finger) family protein	0.8559	0.0093	0.0621	0.3454	0.1306	0.1833	0.7195	0.0151	0.0489	0.209	0.3013	0.2393
251960_at	AT3G53610	ATRAB8; GTP binding	0.4304	0.0261	0.0934	0.2188	0.1545	0.2015	-0.07393	0.5856	0.3929	-0.2855	0.8841	0.1083
251961_at	AT3G53620	ATPPA4 (ARABIDOPSIS THALIANA PYROPHOSP	-0.4255	0.1723	0.243	-0.5318	0.1067	0.1648	0.6926	0.0313	0.0719	0.5863	0.0512	0.0805
251962_at	AT3G53420	PIP2A (PLASMA MEMBRANE INTRINSIC PROTE	-0.6077	0.0291	0.099	-0.9293	0.007	0.0474	0.1941	0.0026	0.0235	-0.1275	0.0118	0.034
251963_at	AT3G53570	AFC1 (ARABIDOPSIS FUS3-COMPLEMENTING G	0.6175	0.0107	0.0649	0.3102	0.0857	0.1474	-0.1666	0.1021	0.1427	-0.4739	0.0339	0.0201
251964_at	AT3G53370	DNA-binding S1FA family protein	-0.9331	0.01	0.064	-0.08168	0.7076	0.4613	0.07606	0.5744	0.3883	0.9275	0.0017	0.0147
251965_at	AT3G53360	pentatricopeptide (PPR) repeat-containing protein	0.2198	0.5955	0.4581	-0.9987	0.059	0.1208	0.2628	0.5288	0.3708	-0.9556	0.0664	0.0939
251966_at	AT3G53380	lectin protein kinase family protein	-0.2355	0.7967	0.5228	-0.5147	0.5798	0.416	0.2359	0.6429	0.4121	-0.04334	0.9311	0.466
251967_at	AT3G53390	transducin family protein / WD-40 repeat family prot	0.3329	0.0637	0.1446	0.5149	0.017	0.0677	-0.5159	0.0125	0.0443	-0.3339	0.0491	0.0785
251968_at	AT3G53100	GDSL-motif lipase/hydrolase family protein	-0.8862	0.0054	0.0519	-0.5678	0.0246	0.0788	-0.4194	0.0604	0.1055	-0.1009	0.5662	0.3513
251969_at	AT3G53130	LUT1 (LUTEIN DEFICIENT 1); oxygen binding	-0.2136	0.2394	0.2873	-0.8442	0.0055	0.0434	0.09584	0.44	0.334	-0.5348	0.0088	0.0292
251970_at	AT3G53150	UGT73D1 (UDP-GLUCOSYL TRANSFERASE 73D	1.4711	0.2865	0.3151	2.2871	0.1287	0.1819	-0.1718	0.8928	0.4905	0.6442	0.619	0.37
251971_at	AT3G53160	UGT73C7 (UDP-GLUCOSYL TRANSFERASE 73C	0.1801	0.7419	0.5065	0.4175	0.4591	0.3676	-0.2739	0.6198	0.4045	-0.03653	0.9463	0.4699
251972_at	AT3G53170	pentatricopeptide (PPR) repeat-containing protein	-0.6036	0.2324	0.2833	-1.4789	0.0262	0.0809	0.2102	0.5791	0.3904	-0.665	0.1291	0.1409
251973_at	AT3G53180	glutamate-ammonia ligase	-0.3407	0.3914	0.3707	-0.5399	0.2029	0.2347	-0.7105	0.0162	0.0507	-0.9096	0.0069	0.0259
251974_at	AT3G53200	AMYB27 (myb domain protein 27); DNA binding / tr	-0.618	0.4028	0.3767	-1.7875	0.0539	0.1152	0.859	0.1761	0.1961	-0.08448	0.9045	0.4586
251975_at	AT3G53230	cell division cycle protein 48, putative / CDC48, puta	2.0956	1.00E-04	0.0312	2.328	1.00E-04	0.0249	-0.3323	0.0094	0.0388	-0.0999	0.2321	0.2028
251976_at	AT3G53240	leucine-rich repeat family protein	0.1001	0.9164	0.5559	-0.3287	0.7323	0.4689	-1.9218	0.0985	0.1397	-2.3507	0.0586	0.0873
251977_at	AT3G53250	auxin-responsive family protein	-1.2887	0.2966	0.3212	0.2095	0.8549	0.5059	1.0833	0.3646	0.3003	2.5815	0.0716	0.0981
251978_at	AT3G53290	CYP71B30P (cytochrome P450, family 71, subfami	-1.4767	0.1308	0.2091	-2.1863	0.0484	0.1093	-0.0308	0.9698	0.5099	-0.7404	0.3878	0.279
251979_at	AT3G53140,AT3G53130	(AT3G53140, O-diphenol-O-methyl transferase, put	1.4938	0.1246	0.2044	0.07226	0.9298	0.5266	-0.4197	0.615	0.4026	-1.8412	0.0753	0.1009
251980_at	AT3G53270	similar to unknown protein [Arabidopsis thaliana] (T	0.2479	0.3523	0.3509	0.4259	0.1451	0.1945	-0.4465	0.0806	0.1243	-0.2685	0.2345	0.2041
251981_at	AT3G53080	galactose-binding lectin family protein	-0.9231	0.5172	0.4281	-0.1384	0.9204	0.5241	-0.1073	0.9383	0.503	0.6775	0.6301	0.3737
251982_at	AT3G53190	pectate lyase family protein	0.4915	0.1416	0.2187	0.56	0.1057	0.1642	0.1063	0.4585	0.3424	0.1747	0.2491	0.212
251983_at	AT3G53210	nodulin MtN21 family protein	1.1204	0.0218	0.0867	1.3261	0.0125	0.0998	-0.656	0.0181	0.0539	-0.4503	0.057	0.0859
251984_at	AT3G53260	PAL2 (phenylalanine ammonia-lyase 2); phenylalan	-1.0054	0.0893	0.1732	-1.1045	0.0702	0.1325	-0.2072	7.00E-04	0.016	-0.3063	2.00E-04	0.007
251985_at	AT3G53220	thioredoxin family protein	-0.2222	0.1226	0.2029	-0.2747	0.0732	0.1356	0.9918	0.001	0.0173	0.9393	0.0012	0.0127
251986_at	AT3G53310	transcriptional factor B3 family protein	1.2765	0.0025	0.0424	1.2437	0.0027	0.035	0.01259	0.8853	0.4883	-0.02022	0.8172	0.4335
251987_at	AT3G53280	CYP71B5 (CYTOCHROME P450 71B5); oxygen bi	-0.1781	0.1979	0.2613	0.04043	0.7439	0.4727	-0.4272	0.0015	0.0199	-0.2087	0.0193	0.0445
251988_at	AT3G53300	CYP71B31 (cytochrome P450, family 71, subfamily	-1.6175	0.2804	0.3116	-1.9275	0.2115	0.2407	-0.851	0.3549	0.2957	-1.1609	0.227	0.1999
251989_at	AT3G53110	LOS4 (Low expression of osmotically responsive ge	0.2396	0.1818	0.2495	0.1253	0.4461	0.3622	-0.00985	0.9317	0.5012	-0.1241	0.3148	0.2459
251990_at	AT3G53320	similar to unknown protein [Arabidopsis thaliana] (T	-0.3796	0.2158	0.2723	-0.758	0.0427	0.1027	0.6872	0.0564	0.1015	0.3088	0.2981	0.2377
251991_at	AT3G53340	transcription factor	0.3285	0.0882	0.1722	0.4126	0.0479	0.1086	0.5996	0.0105	0.0407	0.6836	0.0066	0.0253
251992_at	AT3G53350	myosin heavy chain-related	-0.6694	0.0374	0.1115	0.1223	0.6051	0.4251	-0.08473	0.7177	0.4376	0.707	0.0317	0.06
251993_at	AT3G52960	peroxiredoxin type 2, putative	-1.0011	0.0033	0.0446	-1.2009	0.0017	0.032	0.4753	0.0411	0.0842	0.2755	0.1602	0.1613
251994_at	AT3G52890	KIPK (KCBP-INTERACTING PROTEIN KINASE); k	0.2031	0.4008	0.3758	0.1047	0.6536	0.4429	0.08482	0.7149	0.4365	-0.01357	0.953	0.4717
251995_at	AT3G52940	FK (FACKEL); sterol 14-demethylase reductase	-0.7076	0.0702	0.1527	-0.9374	0.0314	0.088	0.2759	0.1728	0.1938	0.04606	0.7957	0.4275
251996_at	AT3G52840	BGAL2 (beta-galactosidase 2); beta-galactosidase	-0.5236	0.0194	0.0825	-0.7251	0.0064	0.0457	-0.04398	0.7163	0.4369	-0.2454	0.095	0.1168
251997_at	AT3G53020	STV1 (SHORT VALVE1); structural constituent of ri	0.2051	0.2434	0.2897	0.6002	0.0161	0.066	0.4881	0.0313	0.0719	0.8832	0.0042	0.0207
251998_at	AT3G53090	UPL7 (ubiquitin-protein ligase 7); ubiquitin-protein li	0.5071	0.0196	0.0827	0.1301	0.3879	0.3358	-0.4743	0.0243	0.0631	-0.8512	0.0032	0.0183
251999_at	AT3G52700	unknown protein	-1.6981	0.1561	0.2304	-0.2766	0.7905	0.4862	-0.494	0.6386	0.4107	0.9276	0.3947	0.2821
252000_at	AT3G52710	similar to unknown protein [Arabidopsis thaliana] (T	0.673	0.0193	0.0823	0.9957	0.005	0.0424	-0.1996	0.1858	0.2028	0.1232	0.3805	0.276
252001_at	AT3G52720	FTSZ2-2; FtsZ-2; structural molecule	-1.2263	3.00E-04	0.0312	-1.2631	2.00E-04	0.0249	0.1063	0.3433	0.29	0.06954	0.5212	0.3343
252002_at	AT3G52760	integral membrane Yip1 family protein	0.02559	0.8812	0.5465	0.2108	0.2597	0.2697	0.1439	0.3897	0.312	0.3291	0.0922	0.1145
252003_at	AT3G52770	ZPR3 (LITTLE ZIPPER 3); protein binding	0.4836	0.7125	0.4972	2.949	0.0733	0.1358	0.5321	0.6857	0.4263	2.9975	0.0702	0.0971
252004_at	AT3G52780	ATPAP20/PAP20; acid phosphatase/ protein serine	-1.1809	0.2448	0.2905	0.4253	0.6494	0.4415	-0.4776	0.5272	0.3701	-1.1286	0.1775	0.1717
252005_at	AT3G52810	ATPAP21/PAP21 (purple acid phosphatase 21); ac	-1.0951	0.334	0.3424	0.4387	0.6829	0.4531	-1.2473	0.2794	0.2577	0.2866	0.7882	0.4252
252006_at	AT3G52830	ATPAP22/PAP22 (purple acid phosphatase 22); ac	0.8522	0.2871	0.3155	0.415	0.5622	0.4171	0.05187	0.944	0.5042	-0.3852	0.6086	0.3663
252007_at	AT3G52830	similar to ankyrin repeat family protein [Arabidopsis	-0.2299	0.8812	0.5465	0.2162	0.8882	0.5153	0.0215	0.9888	0.515	-0.4676	0.7623	0.4175
252008_at	AT3G52610	similar to hypothetical protein [Vitis vinifera] (GB:CA	-0.2029	0.2835	0.3136	-0.3494	0.1	0.1594	-0.07676	0.664	0.4192	-0.2233	0.2448	0.2096
252009_at	AT3G52800	zinc finger (AN1-like) family protein	0.1851	0.436	0.392	-0.1265	0.5864	0.4185	0.6619	0.0052	0.0303	0.7205	0.0038	0.0201
252010_at	AT3G52740	similar to unknown protein [Arabidopsis thaliana] (T	0.1574	0.7587	0.5114	-0.1087	0.8316	0.4993	1.3137	7.00E-04	0.016	1.0476	0.0017	0.0145
252011_at	AT3G52720	carbonic anhydrase family protein	-2.508	0	0.0312	-2.7598	0	0.0249	0.8995	0.0018	0.0206	0.6477	0.0061	0.0243
252012_at	AT3G52730	ubiquinol-cytochrome C reductase UQCRX/QCR9 (	0.9641	0.5211	0.4294	0.2417	0.163	0.2004	0.7658	0.0051	0.0299	0.9109	0.0027	0.017
252013_at	AT3G52860	similar to unnamed protein product [Vitis vinifera] (G	-0.04266	0.8414	0.536	0.1482	0.4993	0.3842	0.3968	0.1179	0.1546	0.5877	0.0423	0.0717
252014_at	AT3G52870	calmodulin-binding family protein	-0.4729	0.2066	0.2662	-0.3527	0.3242	0.3055	-0.00598	0.9385	0.503	0.1142	0.1916	0.1801
252015_at	no_match	no_match	0.4166	0.2642	0.302	0.4206	0.2694	0.27	-0.1489	0.5407	0.3755	-0.145	0.551	0.3455
252016_at	AT3G52950	CBS domain-containing protein / octicosapeptide/Ph	-0.3293	0.288	0.3162	-0.4913	0.1418	0.1921	-0.4153	0.0339	0.0752	-0.5772	0.0117	0.0339
252017_at	AT3G52970	CYP78G1 (cytochrome P450, family 76, subfamily	0.337	0.623	0.4675	-0.1061	0.8751	0.5116	0.8312	0.2598	0.2463	0.3881	0.5733	0.3536
252018_at	AT3G53000	ATPP2-A15 (PHloem protein 2-A15); carbohydrate	0.04468	0.8102	0.5268	0.1346	0.4828	0.3773	-0.01864	0.8595	0.4809	0.1606	0.1793	0.1729
252019_at	AT3G53040	late embryogenesis abundant protein, putative / LE	-0.2501	0.7944	0.5223	2.1286	0.0768	0.139	-1.4035	0.1081	0.1472	0.9753	0.2251	0.1989
252020_at	AT3G53060	ASK6 (ARABIDOPSIS SKP1-LIKE 6); ubiquitin-prot	0.6486	0.6225	0.4674	-0.2641	0.8389	0.5012	0.06485	0.9601	0.5076	-0.8478	0.5246	0.3357
252021_at	AT3G53070	beta-galactosidase-related	0.06274	0.887	0.5476	-0.04779	0.9416	0.5295	-0.4321	0.5197	0.3669	-0.5726	0.403	0.2854
252022_at	AT3G52930	fructose-bisphosphate aldolase, putative	0.3121	0.1032	0.1855	0.06464	0.6855	0.454	0.1591	0.3439	0.2903	-0.0884	0.5833	0.3574
252023_at	AT3G52920	similar to unknown protein [Arabidopsis thaliana] (T	-0.7321

252090_at	AT3G52130	protease inhibitor/seed storage/lipid transfer protein	-1.6684	0.1248	0.2045	-1.5827	0.14	0.1906	-0.4745	0.611	0.4016	-0.3867	0.6751	0.389
252091_at	AT3G51390	zinc finger (DHHC type) family protein	0.583	0.0042	0.0469	0.4864	0.0074	0.0486	0.08105	0.3998	0.3165	-0.00554	0.9518	0.4715
252092_at	AT3G51420	strictosidine synthase family protein	0.05206	0.7546	0.5099	-0.1596	0.3627	0.3242	-0.04859	0.7703	0.4543	-0.2602	0.1695	0.1669
252093_at	AT3G51500	unknown protein	0.1762	0.4821	0.4129	0.7301	0.0327	0.0896	0.6029	0.0571	0.102	1.1568	0.0071	0.0262
252094_at	AT3G51260	PAD1 (20S PROTEASOME ALPHA SUBUNIT PAD	0.4601	0.0684	0.1504	0.7223	0.0177	0.0689	-0.1086	0.5903	0.3948	0.1536	0.4547	0.3079
252095_at	AT3G51000	epoxide hydrolase, putative	0.973	9.00E-04	0.0349	1.15	5.00E-04	0.0257	-0.5273	0.0089	0.0378	-0.3503	0.0342	0.0625
252096_at	AT3G51180	zinc finger (CCCH-type) family protein	0.1394	0.2574	0.2979	-0.2896	0.0518	0.113	0.3151	0.0406	0.0836	-0.1139	0.3416	0.2588
252097_at	AT3G51090	similar to unknown protein [Arabidopsis thaliana] (T	-0.758	0.0571	0.137	-0.5756	0.1146	0.1708	-0.0601	0.8439	0.4768	0.1224	0.691	0.3944
252098_at	AT3G51330	aspartyl protease family protein	1.7789	0.0254	0.0923	1.1099	0.0957	0.1559	0.153	0.5003	0.3597	-0.5159	0.0671	0.0945
252099_at	AT3G51250	senescence/dehydration-associated protein-related	0.2746	0.0109	0.0655	0.2801	0.0102	0.0549	0.0849	0.1652	0.1885	0.09035	0.1455	0.1518
252100_at	AT3G51110	crooked neck protein, putative / cell cycle protein p	-0.3329	0.2534	0.2955	0.3028	0.2921	0.2877	-1.4105	5.00E-04	0.0148	-0.7748	0.0045	0.0213
252101_at	AT3G51300	ARAC11/ATRAC11/ATROP1/ROP1/ROP1AT (RHO	-0.3089	0.3976	0.3742	-0.4737	0.2203	0.2461	-0.5484	0.1682	0.1906	-0.7133	0.0942	0.1162
252102_at	AT3G50970	LTI30 (LOW TEMPERATURE-INDUCED 30)	-1.0937	0.0173	0.0787	-0.5005	0.1475	0.1963	0.7101	0.0244	0.0634	1.3034	0.003	0.0177
252103_at	AT3G51410	similar to unknown protein [Arabidopsis thaliana] (T	0.1944	0.6327	0.4705	0.1642	0.685	0.4538	-0.1193	0.767	0.4533	-0.1495	0.7114	0.4014
252104_at	AT3G51460	phosphoinositide phosphatase family protein	0.005073	0.9801	0.5721	-0.6919	0.0224	0.0756	0.3465	0.1443	0.1748	-0.3505	0.1409	0.1487
252105_at	AT3G51470	protein phosphatase 2C, putative / PP2C, putative	-1.2783	0.0084	0.06	-0.7685	0.0438	0.1036	-0.3331	0.2761	0.2558	0.1767	0.5404	0.3411
252106_at	AT3G51480	ATGLR3.6 (Arabidopsis thaliana glutamate receptor	-0.5357	0.0362	0.1097	-0.4859	0.0482	0.109	-0.08579	0.6086	0.4009	-0.03603	0.8272	0.4363
252107_at	AT3G51490	TMT3 (TONOPLAST MONOSACCHARIDE TRANS	-0.625	0.5978	0.4588	1.0167	0.4047	0.3434	-0.3167	0.7863	0.4591	1.325	0.2919	0.2346
252108_at	AT3G51530	F-box family protein	0.6784	0.046	0.1233	0.5486	0.0819	0.1436	-0.01939	0.9388	0.5031	-0.1492	0.5636	0.3503
252109_at	AT3G51540	similar to unknown protein [Arabidopsis thaliana] (T	-0.7385	0.5653	0.447	0.6489	0.6116	0.4274	-0.4999	0.6936	0.4288	0.8875	0.4938	0.3236
252110_at	AT3G51560	disease resistance protein (TIR-NBS-LRR class), p	-0.8258	0.3175	0.3328	-1.0233	0.2303	0.2517	-0.7161	0.2847	0.2606	-0.9136	0.1905	0.1795
252111_at	AT3G51570	disease resistance protein (TIR-NBS-LRR class), p	0.6154	0.3711	0.3601	0.01729	0.9788	0.539	-0.191	0.7703	0.4543	-0.7892	0.2663	0.221
252112_at	AT3G51580	similar to unknown [Populus trichocarpa] (GB:ABK9	-0.1061	0.3612	0.3551	0.328	0.0334	0.0905	-0.1574	0.2012	0.2124	0.2767	0.0549	0.0838
252113_at	AT3G51620	similar to nucleotidyltransferase family protein [Arab	0.7807	0.0163	0.0771	0.5122	0.0591	0.1209	0.06226	0.7557	0.45	-0.2062	0.3317	0.2542
252114_at	AT3G51450	strictosidine synthase family protein	0.1224	0.8344	0.5338	-0.05953	0.9189	0.5238	0.5282	0.007	0.0341	0.3462	0.029	0.057
252115_at	AT3G51600	LTP5 (LIPID TRANSFER PROTEIN 5); lipid transpo	-0.4697	0.0171	0.0783	-0.2971	0.0676	0.1303	0.7803	0.0028	0.0244	0.9529	0.0013	0.0133
252116_at	AT3G51510	similar to unnamed protein product [Vitis vinifera] (G	-0.4841	0.0176	0.0794	-0.4385	0.0242	0.0782	0.02844	0.7985	0.4629	0.07407	0.5166	0.3322
252117_at	AT3G51550	YLS2 (yellow-leaf-specific gene 2); strictosidine syn	1.5507	0.0032	0.0442	1.5966	0.0028	0.0353	-0.1118	0.4913	0.3562	-0.06598	0.6788	0.3902
252118_at	AT3G51400	similar to unknown protein [Arabidopsis thaliana] (T	1.0366	0.222	0.2763	-0.7092	0.3788	0.3314	0.8192	0.3143	0.2756	-0.9266	0.2633	0.2194
252119_at	AT3G51030	ATTRX1 (Arabidopsis thaliana thioredoxin H-type 1	-0.03268	0.9047	0.5526	0.7925	0.0366	0.0944	0.9202	0.023	0.0614	1.7454	0.0024	0.0164
252120_at	AT3G51130	identical to UPF0183 protein At3g51130 [Arabidopsis	0.3459	0.0933	0.1771	0.3324	0.1027	0.1617	0.1021	0.2976	0.2674	0.08864	0.3577	0.2659
252121_at	AT3G51160	MUR1 (MURUS 1)	0.3369	0.1445	0.2209	-0.02198	0.9117	0.5219	0.1031	0.6092	0.4011	-0.2558	0.2412	0.2078
252122_at	AT3G51140	heat shock protein binding	-0.382	0.0353	0.1084	-0.2403	0.1204	0.1757	-0.1178	0.2087	0.217	0.02384	0.777	0.422
252123_at	AT3G51240	F3H (TRANSPARENT TESTA 6); naringenin 3-dioxy	1.9913	0.0453	0.1225	1.85	0.0558	0.1174	-0.00888	0.9589	0.5074	0.1325	0.4597	0.3099
252124_at	AT3G51010	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.2869	0.1187	0.1992	0.265	0.1414	0.1917	0.2147	0.1523	0.1805	0.1928	0.1882	0.1782
252125_at	AT3G51040	RTH (RTE1-HOMOLOG)	0.2699	0.343	0.3463	0.05952	0.8243	0.4973	0.6574	0.0589	0.104	0.4471	0.1496	0.1544
252126_at	AT3G50950	disease resistance protein (CC-NBS-LRR class), p	0.6004	0.1858	0.2525	0.3579	0.3953	0.3392	-0.1466	0.5825	0.3917	-0.3923	0.1929	0.1808
252127_at	AT3G50960	PLP3A (PHOSDUCIN-LIKE PROTEIN 3 HOMOLO	-0.9532	0.0176	0.0794	-0.3704	0.2043	0.2357	0.03742	0.8858	0.4884	0.6203	0.0642	0.0921
252128_at	AT3G50870	MNP (MONOPOLE); transcription factor	-1.4762	0.0799	0.1629	-1.7501	0.0505	0.1115	0.8461	0.2519	0.2418	0.5723	0.4166	0.2911
252129_at	AT3G50890	ATHB26 (ARABIDOPSIS THALIANA HOMEOBOX	-1.4194	0.1733	0.2437	-0.2112	0.8176	0.4952	0.9156	0.3141	0.2754	2.1276	0.0563	0.0851
252130_at	AT3G50820	PSB0-2/PSB02 (PHOTOSYSTEM II SUBUNIT O-2	-0.3058	0.0583	0.1385	-0.5858	0.0073	0.0483	0.4443	0.0188	0.055	0.1644	0.2306	0.2018
252131_at	AT3G50930	AAA-type ATPase family protein	0.7087	0.1438	0.2205	1.0773	0.051	0.112	-0.146	0.6782	0.4238	0.2225	0.5334	0.3391
252132_at	AT3G50790	late embryogenesis abundant protein, putative / LE	-0.5949	0.0229	0.0885	-1.1552	0.0022	0.0334	-0.5474	0.0298	0.0703	-1.1076	0.0026	0.0169
252133_at	AT3G50900	similar to unknown protein [Arabidopsis thaliana] (T	0.7481	0.2335	0.2839	0.6997	0.2599	0.2698	1.4062	0.0071	0.0341	1.3578	0.008	0.0278
252134_at	AT3G50910	similar to unknown protein [Arabidopsis thaliana] (T	0.002865	0.9853	0.5733	-0.168	0.3155	0.3004	0.4715	0.0021	0.0214	0.3006	0.0105	0.032
252135_at	AT3G50830	COR413-PM2 (cold regulated 413 plasma membrar	0.07326	0.7197	0.4993	-0.116	0.5749	0.4139	0.3491	0.0165	0.0513	0.3064	0.0253	0.0525
252136_at	AT3G50770	calmodulin-related protein, putative	1.7074	0.0052	0.0513	1.7579	0.0047	0.0417	0.5893	0.0071	0.0341	0.6398	0.0053	0.0227
252137_at	AT3G50980	XERO1 (DEHYDRIN XERO 1)	-0.06583	0.9391	0.5621	1.1296	0.2354	0.255	-0.192	0.8242	0.4709	1.0034	0.2829	0.2297
252138_at	AT3G50960	peroxidase	0.07326	0.7197	0.4993	-0.116	0.5749	0.4139	0.3491	0.0165	0.0513	0.3064	0.0253	0.0525
252139_at	AT3G51050	FG-GAP repeat-containing protein	0.3594	0.0156	0.0754	0.3926	0.0116	0.058	-0.2518	0.042	0.0853	-0.2186	0.0626	0.0908
252140_at	AT3G51070	dehydration-responsive protein-related	0.4438	0.5472	0.4398	0.6307	0.4034	0.3428	-0.2231	0.7579	0.4507	-0.03614	0.9599	0.4733
252141_at	AT3G51100	similar to hypothetical protein Osl_023576 [Oryza s	0.209	0.035	0.1081	0.3223	0.0084	0.0507	0.1946	0.0433	0.0868	0.3079	0.0099	0.031
252142_at	AT3G51120	zinc finger (CCCH-type) family protein	0.5651	0.0555	0.1352	0.3562	0.1669	0.2104	-0.1009	0.6577	0.4171	-0.3098	0.2163	0.1942
252143_at	AT3G51150	kinesin motor family protein	-0.7536	0.0203	0.084	-1.2916	0.0031	0.036	0.02603	0.8336	0.4736	-0.5119	0.0116	0.0338
252144_at	AT3G51060	60S ribosomal protein L8 (RPL8B)	0.4047	0.3416	0.346	-0.2374	0.5614	0.4089	0.2792	0.4983	0.359	-0.3629	0.3884	0.2792
252145_at	AT3G51200	auxin-responsive family protein	1.1981	0.3387	0.3448	-0.06613	0.9551	0.5331	0.9553	0.4355	0.3321	-0.309	0.7934	0.427
252146_at	AT3G51210	flavonol 3-sulfotransferase-related	0.02088	0.982	0.5725	-0.9736	0.3263	0.3066	1.085	0.2786	0.2573	0.09059	0.9217	0.4634
252147_at	AT3G51270	ATP binding / protein serine/threonine kinase	0.1849	0.343	0.3463	0.5567	0.0318	0.0886	-0.2828	0.1327	0.1657	0.08892	0.5855	0.3582
252148_at	AT3G51280	male sterility MS5, putative	0.07124	0.7047	0.4942	0.2606	0.2105	0.24	0.1984	0.3202	0.2784	0.3878	0.0909	0.1135
252149_at	AT3G51290	proline-rich family protein	-0.2644	0.6419	0.4736	0.02805	0.9601	0.5341	-0.05892	0.9163	0.4968	0.2335	0.6803	0.3905
252150_at	AT3G51310	vacuolar protein sorting-associated protein 35 famil	0.5485	0.0014	0.038	0.4749	0.0024	0.0339	-0.3219	0.0099	0.0396	-0.3954	0.0048	0.0218
252151_at	AT3G51320	binding	-0.03284	0.8394	0.5352	0.1021	0.5382	0.3997	-0.5312	0.025	0.064	-0.3962	0.0596	0.0881
252152_at	no_match	no_match	0.5096	0.6765	0.4848	0.5208	0.6699	0.4486	-0.7731	0.5328	0.3724	-0.7619	0.5385	0.3407
252153_at	AT3G51360	aspartyl protease family protein	1.4002	0.1386	0.2161	-0.3466	0.6713	0.449	-0.2298	0.7279	0.4412	-1.9766	0.0326	0.0609
252154_at	AT3G50880	HhH-GPD base excision DNA repair family protein	0.3152	0.0604	0.1407	0.2611	0.0981	0.1579	0.4811	0.0167	0.0514	0.427	0.0246	0.0515
252155_at	AT3G50920	phosphatidic acid phosphatase-related / PAP2-relat	0.5916	0.0123	0.0685	0.05792	0.6929	0.4566	0.1068	0.4708	0.3479	-0.4269	0.0335	0.0618
252156_at	no_match	no_match	0.6511	0.4593	0.4025	1.3702	0.1603	0.2061	-0.5035	0.5217	0.3677	0.2156	0.7789	0.4226
252157_at	AT3G50430	similar to Os07g0120700 [Oryza sativa (japonica c	0.2343	0.2091	0.2675	0.2543	0.1798	0.2194	-0.6213	0.0166	0.0514	-0.6013	0.0185	0.0436
252158_at	AT3G50530	CRK (CDPK-RELATED KINASE); calcium ion bindi	0.005627	0.9756	0.5711	0.1249	0.51	0.3887	0.39	0.0205	0.0577	0.5093	0.0083	0.0284
252159_at	AT3G50540	unknown protein	-0.5379	0.6011	0.46	-2.2797	0.0742	0.1366	0.6595	0.5253	0.3692	-1.0822	0.3177	0.2473
252160_at	AT3G50570	hydroxyproline-rich glycoprotein family protein	-0.8738	0.0025	0.0425	-1.0225	0.0014	0.0312	0.7236	0.0051	0.03	0.5749	0.0115	0.0336
252161_at	AT3G50580	histamine receptor	0.706	0.285	0.3142	-0.2669	0.6653	0.4468	0.3005	0.6274	0.4071	-0.6725	0.3053	0.2412
252162_at	AT3G50590	transducin family protein / WD-40 repeat family prot	-0.486	0.274	0.308	-0.3504	0.4128	0.3473	-1.4225	0.02	0.0567	-1.2869	0.0275	0.0552
252163_at	AT3G50610	similar to unknown protein [Arabidopsis thaliana] (T	-0.5648	0.5226	0.4301	0.8752	0.3392	0.3131	-0.6968	0.4366	0.3326	0.7432	0.4093	0.2879
252164_at	AT3G50620	nodulation protein-related	-0.9624	0.0618	0.1427	-0.5762	0.1984	0.2319	-0.6608	0.1521	0.1804	-0.2746	0.5037	0.3273
252165_at	AT3G50650	unknown protein	-0.08299	0.804	0.5251	0.4645	0.2118	0.2408	0.2644	0.4446	0.326	0.8123	0.0601	0.0887
252166_at	AT3G50500	SPK-2-2 (SNF1-RELATED PROTEIN KINASE 2.2);	0.1054	0.0016	0.0383	1.0707	0.0015	0.0313	-0.3516	0.0629	0.1079	-0.3363	0.0709	0.0976
252167_at	AT3G50560	short-chain dehydrogenase/reductase (SDR) family	-1.2168	0.0028	0.0431	-1.1166	0.0039	0.0391	0.5185	0.0186	0.0546	0.6187	0.0102	0.0316
252168_at	AT3G50440	hydrolase	0.6597	0.0093	0.0621	0.9055	0.003	0.0355	0.2534	0.0092	0.0385	0.4992	8.00E-04	0.0108
252169_at	AT3G50520	phosphoglycerate/bisphosphoglycerate mutase fam	-0.1127	0.4674	0.4062	0.1627	0.3114	0.2982	-0.0089	0.886	0.4884	0.2665	0.0103	0.0317
252170_at	AT3G50480	HR4 (HOMOLOG OF RPW8 4)	1.2924	0.0016	0.0383	0.8924	0.0062	0.0451	0.5717	0.0014	0.0197	0.1717	0.0788	0.104
252171_at	AT3G50590	transducin family protein / WD-40 repeat family prot	0.5952	0.0048	0.0498	0.2475	0.0784	0.1404	-0.1412	0.2125	0.2194	-0.4889	0.0068	0.0257
252172_at	AT3G50640	similar to unknown protein [Arabidopsis thaliana] (T	1.3601	0.2583	0.2987	-1.689	0.1774	0.2179	1.9135	0.1376	0.1694	-1.1356	0.3333	0.255
252173_at	AT3G50650	scarecrow-like transcription factor 7 (SCL7)	0.169	0.7246	0.501	0.3257	0.5067	0.3873	0.08933	0.6716	0.4215	0.246	0.2769	0.2266
252174_at	AT3G50690	leucine-rich repeat family protein	0.03244	0.8629	0.5417	0.1886	0.3446	0.3154	-0.5305	0.0196	0.0562	-0.3744	0.0564	0.0852
252175_at	AT3G50700	ATIDD2 (ARABIDOPSIS THALIANA INDETERMIN	0.5484	0.0409	0.1165	1.034	0.005	0.0424	-0.2198	0.2023	0.2131	0.2659	0.1391	0.1476
252176_at	AT3G50720	protein kinase, putative	0.3496	0.5892	0.4559	-1.665	0.0492	0.1099	0.5872	0.2942	0.2657	-1.4273	0.0427	0.0721
252177_at	AT3G50730	protein kinase, putative	0.3025	0.789	0.5203	-0.163	0.8849	0.5146	0.07769	0.9415	0.5037	-0.3877	0.7166	0.403
252178_at	AT3G50750	brassinosteroid signalling positive regulator-related	-0.1739	0.5605	0.445	-0.4321	0.1902	0.2265	0.384	0.0318	0.0726	0.1257	0.3493	0.2622
252179_at	AT3G50760	GATL2 (Galacturonosyltransferase-like 2); polygala	-0.3135	0.4895	0.4157	-0.812	0.1203	0.1756	0.6187	0.0037	0.0268	0.1202	0.3042	0.2407
252180_at	AT3G50630	IKI2/KRP2 (KIP-RELATED PROTEIN 2); cyclin-de	-0.3301	0.2589	0.2991	-0.2595	0.3596	0.3226	0.1075	0.6599	0.4179	0.178	0.4759	0.316
252181_at	AT3G50685	similar to unnamed protein product [Vitis vinifera] (G	-0.946	0.0065	0.0549	-1.3747	0.0016	0.0319	0.7107	7.00E-04	0.016	0.2821	0.0199	0.0453
252182_at	AT3G50670	U1-70K (SPLICEOSOMAL PROTEIN U1A); RNA b	0.5015	0.0041	0.0468	-0.1115	0.2593	0.2696	-0.1312	0.1974	0.2101	-0.7441	9.00E-04	0.0118
252183_at	AT3G50740	UGT72E1 (UDP-glucosyl transferase 72E1); UDP-g	0.05193	0.8982	0.5507	0.2333	0.5734	0.4132	0.1015	0.6588	0.4175	0.2828	0.2551	0.2152
252184_at	AT3G50660	DWF4 (DWARF 4)	-0.7972	0.0175	0.0793	-0.4841	0.0768	0.139	-0.4291	0.0425	0.0858	-0.116	0.4715	0.3143
252185_at	AT3G50780	protein binding	-0.05337	0.8268	0.5316	0.4169	0.1421	0.1923	-0.1973	0.0313	0.0719	0.273	0.0108	0.0325
252186_at	AT3G50810	integral membrane protein, putative	1.3197	0.0034	0.0448	1.0601	0.0075	0.0488	-0.6573	0.0364	0.0785	-0.917	0.0125	0.0353
252187_at	AT3G50850	similar to unknown protein [Arabidopsis thaliana] (T	-0.06665	0.8577	0.5406	0.4205	0.2942	0.2888	-0.7307	0.0931	0.1352	-0.2436	0.5047	0.3276
252188_at	AT3G50860	clathrin adaptor complex small chain family protein	0.0255	0.918	0.5566	0.3063	0.2584	0.2692	0.2328	0.3738	0.3046	0.5136	0.0919	0.1143
252189_at	AT3G50970	CYCD3;3 (CYCLIN D3;3); cyclin-dependent protein	0.9903	0.0286	0.0981	0.5619	0.1303	0.183	0.000291	0.999	0.5176	-0.4281	0.1252	0.1384
252190_at	AT3G50170	similar to unknown protein [Arabidopsis thaliana] (T	-1.813	0.2297	0.2819	0.107	0.9374	0.5284	-1.1407	0.4233	0.3268	0.7793	0.5756	0.3544
252191_at	AT3G50180	similar to unknown protein [Arabidopsis thaliana] (T	0.04774	0.9592	0.5671	0.7543	0.4387	0.359	0.5971	0.4447	0.336	1.3036	0.1381	0.147
252192_at	AT3G50000	CKA2 (casein kinase II alpha chain 2); kinase	0.4504	0.0106	0.0647	0.4459	0.0109	0.056	-0.2916	0.0426	0.0859	-0.2961	0.0407	0.0698
252193_at	AT3G50060	MYB77; DNA binding / transcription factor	-0.4359	0.5037	0.422	-0.4936	0.4527	0.3651	0.5042	0.1253	0.1602	0.4465	0.1619	0.1623
252194_at	AT3G50110	phosphatase-related	-0.269	0.401	0.3758	-0.06869	0.8223	0.4965	-0.2133	0.498	0.3589	-0.01299	0.966	0.4748
252195_at	AT3G50190	similar to unknown protein [Arabidopsis thaliana] (T	-0.3739	0.6072	0.4622	-1.5406	0.0834	0.1452	0.1819	0.7999	0.4634	-0.9848	0.2163	0.1942
252196_at	AT3G50200	similar to unknown protein [Arabidopsis thaliana] (T	0.1362	0.8106	0.5269	0.2826	0.6235	0.4322	-0.3821	0.5123	0.364	-0.2357	0.6806	0.3907
252197_at	AT3G50230	leucine-rich repeat transmembrane protein kinase,	0.2141	0.7601	0.5117	-1.2151	0.1371	0.1886	0.199	0.7291	0.4415	-1.2302	0.0833	0.1077
252198_x_at	AT3G50250	similar to unknown protein [Arabidopsis thaliana] (T	-0.0581	0.8226	0.5303	0.06772	0.7941	0.4874	0.1258	0.6211	0.405	0.2516	0.345	0.2603
252199_at	AT3G50270	transferase family protein	-0.8324	0.0034	0.0448	-0.7929	0.0041	0.0399	-0.5041	0.0024	0.0229	-0.4647	0.0032	0.0185
252200_at	AT3G50280	transferase family protein	-0.3776	0.1994	0.2619	0.3159	0.2682	0.2745	-0.2716	0.3133	0.2751	0.422	0.1478	0.1533
252201_at	AT3G50295	transferase family protein	-0.07691	0.9432	0.5632	-0.5012	0.6473	0.4406	0.1821	0.8663	0.4831	-0.2422	0.8231	0.4351
252202_at	AT3G50300	transferase family protein	-0.3945	0.7643	0.5128	-0.3926	0.7654	0.4789	0.774	0.5117	0.3638	0.7759	0.5107	0.3301
252203_at	AT3G50320	unknown protein	0.5705	0.6185	0.4658	1.4541	0.2414	0.2587	-1.2772	0.1284	0.2656	-2.3936	0.7288	0.4067
252204_at	AT3G50340	similar to unknown protein [Arabidopsis thaliana] (T	-0.1642	0.4493	0.3978	-0.5402	0.0511	0.1122	-0.0336	0.8523	0.4792	-0.4096	0.0728	0.099
252205_at	AT3G50350	similar to unknown protein [Arabidopsis thaliana] (T	-1.1185	0.0024	0.0421	-0.9836	0.0039	0.0391	0.2774	0.0711	0.116	0.4124	0.0222	0.0485
252206_at	AT3G50360	ATCEN2 (CENTRIN2); calcium ion binding	0.185	0.3143	0.3311	0.2432	0.2053	0.2362	1.134	0.0018	0.0206	1.1922	0.0015	0.0138
252207_at	AT3G50370	similar to unnamed protein product [Vitis vinifera] (G	0.3954	0.256	0.2971	0.1895	0.5603	0.4084	-1.0655	0.0034	0.0257	-1.2715	0.0017	0.0147
252208_at	AT3G50380	similar to hypothetical protein Osl_037699 [Oryza s	0.799	0.0039	0.0463	0.2261	0.1652	0.2091	-1.0039	0.001	0.0179	-1.5768	2.00E-04	0.0075
252209_at	AT3G50400	GDSL-motif lipase/hydrolase family protein	0.5582	0.4538	0.3998	2.0249	0.0396	0.0986	0.174	0.8088	0.4662	1.6407	0.0714	0.0979
252210_at	AT3G50410	OBP1 (OBF BINDING PROTEIN 1); DNA binding /	-0.2498	0.6691	0.4823	-0.3099	0.5983	0.4228	0.3334	0.4741	0.3494	0.2732	0.5529	0.3461
252211_at	AT3G50220	nucleic acid binding / pancreatic ribonuclease	0.003605	0.9965	0.5761	1.4074	0.1462	0.1955	-0.5126	0.5478	0.3784	0.8912	0.3179	0.2473
252212_at	AT3G50310	MAPKKK20 (Mitogen-activated protein kinase kinas	-1.0674	0.2195	0.2748	1.1472	0.193	0.2278	-1.7812	0.0722	0.1168	0.4335	0.5865	0.3586
252213_at	AT3G50210	2-oxoacid-dependent oxidase, putative	1.0688	0.0021	0.0406	0.8032	0.006	0.0447	0.3628	0.0054	0.0308	0.09725	0.2158	0.194
252214_at	AT3G50260	ATERF#011/CEJ1 (COOPERATIVELY REGULATE	0.2054	0.8128	0.5275	0.2374	0.7846	0.4847	0.9482	0.1272	0.1619	0.9802	0.1181	0.1334
252215_at	AT3G50240	KICP-2 (KIP-1-like cyclin-dependent protein kinase	-0.3892	0.231	0.2827	-0.9076	0.0326	0.0896	-0.4367	0.1046	0.1446	-0.9451	0.0106	0.0322
252216_at	AT3G50420	pentatricopeptide (PPR) repeat-containing protein	0.1788	0.849	0.5379	-0.01725	0.9853	0.5405	-0.901	0.3641	0.3001	-1.0971	0.2809	0.2286
252217_at	AT3G50140	similar to unknown protein [Arabidopsis thaliana] (T	1.3441	0.2205	0.2755	0.3805	0.7024	0.46	0.7695	0.453	0.3399	-0.1942	0.8443	0.4412
252218_at	AT3G50160	similar to unknown protein [Arabidopsis thaliana] (T	0.5377	0.6972	0.4918	-2.1146	0.1752	0.2164	1.7752	0.6368	0.41	-1.1287	0.2679	0.2217
252219_at	AT3G50160	similar to unknown protein [Arabidopsis thaliana] (T	-0.8768	0.3288	0.3393	-0.3565	0.6749	0.4501	0.7368	0.359	0.2975	1.2571	0.1521	0.1562
252220_at	AT3G49940	LBD38 (LOB DOMAIN-CONTAINING PROTEIN 38	-0.05232	0.8742	0.5451	-0.08364	0.8007	0.4897	0.3175	0.0963	0.138	0.2861	0.1227	0.1369
252221_at	AT3G49830	DNA helicase-related	-0.5964	0.5166	0.4279	-0.832	0.3776	0.3308	-1.1429	0.2449	0.238	-1.3785	0.1758	0.1706
252222_at	AT3G49845	contains InterPro domain XYPPX repeat (InterPro:I	1.158	0.1912	0.2562	-0.7127	0.3882	0.3359	0.9378	0.2721	0.2535	-0.9329	0.2743	0.2252
252223_at	AT3G49850	ATTRB3/TRB3 (TELOMERE REPEAT BINDING FA	-0.2432	0.2845	0.314	-0.2348	0.

252290_at	AT3G49140	binding	0.02528	0.8238	0.5307	0.1529	0.2241	0.248	-0.8769	0.0012	0.0187	-0.7493	0.0021	0.0156
252291_s_at	AT3G49120;AT3G49110	AtPCB/AtPERX34/PERX34/PRXCB	0.9103	0.0538	0.1331	1.1386	0.0277	0.083	0.2014	0.2564	0.2444	0.4297	0.0477	0.077
252292_at	AT3G49000	RNA polymerase III subunit RPC82 family protein	-0.3597	0.1236	0.2038	-0.8592	0.0097	0.0537	0.1478	0.2795	0.2578	-0.3517	0.041	0.0701
252293_at	AT3G48990	AMP-dependent synthetase and ligase family protei	0.2625	0.3269	0.3384	0.03594	0.886	0.5147	0.07201	0.6389	0.4108	-0.1546	0.3377	0.2568
252294_at	AT3G49010	ATBBC1 (breast basic conserved 1); structural com	0.05205	0.685	0.4876	-0.1463	0.2872	0.285	0.2401	0.0577	0.1027	0.04175	0.6703	0.3875
252295_at	AT3G49100	signal recognition particle 9 kDa protein, putative / S	0.6471	0.0044	0.0482	1.1561	5.00E-04	0.0257	0.5583	0.0075	0.0351	1.0673	7.00E-04	0.0105
252296_at	AT3G48970	copper-binding family protein	-0.3238	0.4276	0.3882	-0.2306	0.564	0.4097	0.6384	0.157	0.1837	0.7316	0.1171	0.1327
252297_at	AT3G48930	EMB3160 (EMBRYO DEFECTIVE 1080); structural	0.1759	0.4364	0.3921	0.02219	0.9185	0.5237	0.5333	0.0146	0.0483	0.3796	0.0428	0.0722
252298_at	AT3G49060	protein kinase family protein / U-box domain-contai	0.1771	0.2143	0.271	-0.01827	0.8864	0.5148	-0.1932	0.1828	0.2008	-0.3886	0.0318	0.06
252299_at	AT3G49150	Identical to Putative F-box/LRR-repeat protein At3g	-1.4382	0.2722	0.3067	-0.506	0.6776	0.4511	-0.8385	0.4995	0.3595	0.09375	0.9379	0.4678
252300_at	AT3G49160	pyruvate kinase family protein	-1.0897	0.0471	0.1248	-0.5198	0.2475	0.2623	-0.7185	0.1348	0.1674	-0.1486	0.7186	0.4036
252301_at	AT3G49162	pseudogene of glycoside hydrolase family 28 protei	-3.4594	0.0116	0.0672	-0.9425	0.2957	0.2895	0.4373	0.5113	0.3637	2.9542	0.0083	0.0282
252302_at	AT3G49190	condensation domain-containing protein	1.1571	0.1986	0.2618	-0.177	0.8254	0.4975	1.7361	0.0821	0.1257	0.4019	0.6212	0.3706
252303_at	AT3G49210	similar to unknown protein [Arabidopsis thaliana] (T	1.0755	0.1269	0.2059	0.3637	0.551	0.4053	-0.1468	0.7467	0.4471	-0.8586	0.1128	0.1296
252304_at	AT3G49230	unknown protein	2.0229	0.0389	0.1137	-0.8977	0.2503	0.2641	0.5087	0.4889	0.355	-2.4119	0.0226	0.0489
252305_at	AT3G49240	EMB1796 (EMBRYO DEFECTIVE 1796); binding	0.1796	0.5895	0.456	0.2503	0.4602	0.3679	-0.03333	0.9143	0.4962	0.03738	0.9039	0.4585
252306_at	AT3G49270	similar to unknown protein [Arabidopsis thaliana] (T	0.1699	0.9232	0.5579	0.06743	0.8695	0.5365	0.1427	0.9182	0.4973	0.04032	0.9769	0.4773
252307_at	AT3G49280	transposable element gene	-2.6411	0.0696	0.1521	-1.6268	0.2041	0.2355	-0.7912	0.4027	0.3177	0.223	0.8052	0.4302
252308_at	AT3G49310	similar to unknown protein [Arabidopsis thaliana] (T	0.2866	0.1635	0.2366	0.5085	0.039	0.0978	-0.7006	0.0141	0.0473	-0.4786	0.0465	0.0759
252309_at	AT3G49340	systeine proteinase, putative	0.6451	0.0122	0.0685	0.3189	0.0981	0.1579	0.2609	0.1231	0.1588	-0.06531	0.6511	0.3812
252310_at	AT3G49350	RAB GTPase activator	0.1167	0.7	0.4925	0.5199	0.1386	0.1897	-0.6019	0.0241	0.0629	-0.1986	0.3083	0.2426
252311_at	AT3G49360	calcium-dependent protein kinase, putative / CDPK	0.5082	0.0262	0.0937	0.6781	0.0101	0.0546	-0.5747	0.0022	0.0221	-0.4049	0.0079	0.0277
252312_at	AT3G49380	IQD15 (IQ-domain 15); calmodulin binding	-0.1887	0.6956	0.4913	-1.1026	0.0698	0.1323	-0.2381	0.6237	0.4059	-1.152	0.0621	0.0904
252313_at	AT3G49390	CID10; RNA binding / protein binding	0.725	0.0149	0.0739	0.9969	0.0049	0.0422	0.02861	0.8795	0.4865	0.3005	0.1648	0.1642
252314_at	AT3G49400	transducin family protein / WD-40 repeat family prot	2.2159	0.0031	0.0438	-0.08967	0.8085	0.4925	-0.3593	0.3436	0.2901	-2.6649	0.0013	0.0133
252315_at	AT3G48690	ATCXE12 (ARABIDOPSIS THALIANA CARBOXYE	-0.04938	0.7519	0.5089	0.15	0.3618	0.3238	-0.523	0.023	0.0614	-0.3236	0.0907	0.1134
252316_at	AT3G48700	ATCXE13; hydrolase	-0.162	0.88	0.5464	-0.3848	0.7219	0.4661	0.2986	0.7816	0.4579	0.07583	0.9436	0.4693
252317_at	AT3G48720	transferase family protein	-1.1285	0.0103	0.0642	-1.2033	0.0082	0.0504	0.2722	0.0498	0.0943	0.1974	0.114	0.1305
252318_at	AT3G48730	GSA2 (GLUTAMATE-1-SEMIALDEHYDE 2,1-AMIN	-0.4148	0.0519	0.1307	-0.6272	0.0143	0.0631	-0.4094	0.0129	0.0452	-0.6225	0.0029	0.0175
252319_at	AT3G48710	GTP binding / RNA binding	-0.3802	0.4229	0.3865	0.175	0.7024	0.46	0.1504	0.7328	0.4426	0.7056	0.161	0.1618
252320_at	AT3G48580	xyloglucan:xyloglucosyl transferase, putative / xylog	0.1387	0.7236	0.5006	-0.3612	0.3786	0.3314	-0.4377	0.2972	0.2672	-0.6603	0.1451	0.1516
252321_at	AT3G48510	similar to unknown protein [Arabidopsis thaliana] (T	-0.3482	0.5863	0.4549	0.2532	0.6895	0.4555	-0.1595	0.8	0.4634	0.4419	0.4949	0.3239
252322_at	AT3G48550	similar to ATIDD15/SGR5 (ARABIDOPSIS THALIA	0.05189	0.8386	0.535	0.4661	0.1227	0.1777	1.1406	0.0038	0.027	1.5548	0.0012	0.0218
252323_at	AT3G48530	KINC1 (SNF1-RELATED PROTEIN KINASE CATEGOL	0.6182	0.1501	0.1288	0.7319	0.0303	0.0865	-0.3025	0.181	0.1994	-0.1888	0.3698	0.2711
252324_at	AT3G48570	protein transport protein SEC61 gamma subunit, pu	0.4948	0.1598	0.2333	0.7506	0.0591	0.1209	0.8886	0.0355	0.0773	1.1444	0.0159	0.0402
252325_at	AT3G48560	CSR1 (CHLORSULFURON/IMIDAZOLINONE RES	-0.3325	0.2129	0.2703	-0.7062	0.0347	0.0921	0.2027	0.3239	0.2802	-0.171	0.3967	0.2828
252326_at	AT3G48680	GAMMA-CAL2 (GAMMA CARBONIC ANHYDRASE	0.4946	0.0128	0.0698	0.3981	0.0262	0.0809	-0.5366	0.0032	0.0253	-0.633	0.0017	0.0147
252327_at	AT3G48740	nodulin MtN3 family protein	-0.705	0.0793	0.1623	-0.6212	0.1081	0.1657	0.7149	7.00E-04	0.016	0.7987	5.00E-04	0.0094
252328_at	AT3G48570	protein transport protein SEC61 gamma subunit, pu	0.1755	0.2112	0.269	0.334	0.0474	0.108	0.9362	0.0014	0.0194	1.0947	8.00E-04	0.0108
252329_at	AT3G48760	zinc finger (DHHC type) family protein	0.3479	0.0755	0.1582	0.2019	0.2385	0.2569	0.2344	0.1022	0.1428	0.08837	0.4704	0.3138
252330_at	AT3G48770	ATP binding / DNA binding	3.6474	0.0054	0.0519	3.7268	0.005	0.0425	-0.4903	0.4488	0.338	-0.4109	0.5209	0.3342
252331_s_at	AT3G48780;AT3G48790	[AT3G48780, serine C-palmitoyltransferase, putativ	0.7438	0.0151	0.0744	1.0555	0.0044	0.041	-0.314	0.1547	0.1822	-0.00229	0.9904	0.4803
252332_at	AT3G48810	pentatricopeptide (PPR) repeat-containing protein	0.1349	0.6744	0.4841	-0.09392	0.7885	0.4801	-0.4492	0.2065	0.2157	-0.678	0.0854	0.1093
252333_at	AT3G48830	polynucleotide adenylyltransferase family protein / P	0.7204	0.1905	0.2558	0.419	0.4116	0.3468	-0.1301	0.1157	0.1529	-0.4316	0.0027	0.017
252334_at	AT3G48850	mitochondrial phosphate transporter, putative	2.1677	0.0096	0.0628	1.3544	0.0437	0.1036	0.04888	0.9214	0.4983	-0.7644	0.176	0.1707
252335_at	AT3G48860	similar to unknown protein [Arabidopsis thaliana] (T	0.7709	0.0089	0.0609	0.8874	0.0054	0.0432	0.1235	0.4878	0.3546	0.24	0.2122	0.1919
252336_at	AT3G48880	F-box family protein	0.1295	0.2331	0.2837	0.1513	0.1765	0.2173	-0.1419	0.1168	0.1537	-0.1202	0.1665	0.1651
252337_at	AT3G48750	CDC2/CDC2A/CDC2AAT/CDK2/CDKA1/CDKA;1 (C	0.6511	0.0019	0.0391	0.478	0.0058	0.0441	0.07392	0.4531	0.34	-0.09912	0.328	0.2523
252338_at	AT3G48890	ATMP2 (MEMBRANE STEROID BINDING PROTE	0.3784	0.0677	0.1494	0.3301	0.0595	0.156	0.4755	0.0015	0.0197	0.4268	0.0022	0.0157
252339_at	AT3G48900	nuclease	0.08363	0.9431	0.5632	0.4982	0.6743	0.45	-1.1337	0.3432	0.2899	-0.7191	0.5331	0.339
252340_at	AT3G48920	AtMYB45 (myb domain protein 45); DNA binding / tr	0.9223	0.5704	0.4492	-0.6303	0.6948	0.457	0.6699	0.6578	0.4172	-0.8827	0.5633	0.3502
252341_at	AT3G48940	nemorin family protein	-0.1312	0.7863	0.5197	-0.3369	0.498	0.3837	0.3261	0.4812	0.3517	0.1205	0.7887	0.4254
252342_at	AT3G48950	glycoside hydrolase family 28 protein / polygalactur	-1.1612	0.3638	0.3562	-1.8083	0.1861	0.2238	0.1262	0.9111	0.4955	-0.521	0.6492	0.3806
252343_at	AT3G48610	phosphoesterase family protein	-0.7287	0.0181	0.0804	-1.4741	0.0014	0.0313	0.7085	0.0192	0.0556	-0.03684	0.8533	0.4437
252344_s_at	AT3G48620;AT3G44160	[AT3G48620, chloroplast outer membrane protein-r	-0.00999	0.97	0.6699	0.2352	0.3996	0.3411	-0.5002	0.037	0.0793	-0.305	0.1631	0.1632
252345_at	AT3G48640	similar to unknown protein [Arabidopsis thaliana] (T	1.601	0.0046	0.049	1.0324	0.021	0.074	0.1553	0.6076	0.4005	-0.4133	0.2128	0.1923
252346_at	AT3G48650	pseudogene, At14a-related protein, similar to At14a	0.4157	0.5208	0.4293	0.5508	0.4044	0.3432	-0.5651	0.0158	0.0502	-0.43	0.0376	0.0663
252347_at	AT3G48130	ribosomal protein L13 homolog	0.2983	0.6285	0.4691	-0.6438	0.3219	0.3042	0.5053	0.3965	0.315	-0.4368	0.4583	0.3093
252348_at	AT3G48140	senescence-associated protein, putative	0.2059	0.1381	0.2159	0.07111	0.8853	0.5147	0.09028	0.4378	0.3331	-0.09852	0.4007	0.2845
252349_at	AT3G48150	APC8 (anaphase-promoting complex/cyclosome 8);	0.7191	0.0478	0.1259	0.3112	0.2892	0.2862	0.04309	0.8445	0.477	-0.3648	0.1513	0.1556
252350_at	AT3G48190	ATM (ATAXIA-TELANGIECTASIA MUTATED)	0.3401	0.1245	0.2043	0.1955	0.3274	0.3072	-1.2422	0.0021	0.0217	-1.3868	0.0014	0.0134
252351_at	AT3G48210	similar to unnamed protein product [Vitis vinifera] (G	0.7027	0.0515	0.1303	0.9887	0.018	0.0694	0.02837	0.917	0.497	0.3143	0.2863	0.2315
252352_at	AT3G48185	unknown protein	0.2685	0.5448	0.4389	0.1553	0.7217	0.466	0.9914	0.0712	0.116	0.8782	0.0967	0.118
252353_at	AT3G48200	similar to hypothetical protein Osl_020499 [Oryza s	-0.01034	0.9501	0.6646	-0.2167	0.2354	0.255	-0.9353	0.0038	0.0271	-1.1417	0.0018	0.0148
252354_at	AT3G48170	ALDH10A9 (Aldehyde dehydrogenase 10A9); 3-chi	0.8862	0.0041	0.0468	0.853	0.0047	0.0418	-0.3154	0.0571	0.102	-0.3486	0.043	0.0724
252355_at	AT3G48250	pentatricopeptide (PPR) repeat-containing protein	0.4755	0.5893	0.4559	1.2156	0.2084	0.2385	-0.325	0.6892	0.4276	0.4151	0.6119	0.3674
252356_at	AT3G48370	transposable element gene	-0.5265	0.6502	0.4764	0.4059	0.7252	0.4671	-2.6584	0.0689	0.1137	-1.726	0.1839	0.1758
252357_at	AT3G48410	hydrolase, alpha/beta fold family protein	-0.5514	0.3868	0.3682	-0.00075	0.999	0.5438	-0.3039	0.6212	0.405	0.2467	0.6865	0.3928
252358_at	AT3G48425	endonuclease/exonuclease/phosphatase family pro	-0.1741	0.4746	0.4096	-0.4285	0.1243	0.1787	0.1651	0.3719	0.3039	-0.08939	0.6153	0.3685
252359_at	AT3G48440	zinc finger (CCCH-type) family protein	0.07431	0.6436	0.4743	0.02066	0.8962	0.5176	0.3196	0.0423	0.0857	0.266	0.0706	0.0974
252360_at	AT3G48480	cysteine-type peptidase	-1.1547	0.33	0.34	-0.3064	0.7834	0.4844	-0.9919	0.3952	0.3144	-0.1436	0.8971	0.4564
252361_at	AT3G48490	similar to unknown [Populus trichocarpa] (GB:ABK9	-0.1637	0.5676	0.4479	0.06514	0.8167	0.495	-0.3524	0.2516	0.2416	-0.1235	0.6633	0.3852
252362_at	AT3G48500	PDE312/PTAC10 (PIGMENT DEFECTIVE 312); RN	0.7012	0.0409	0.1164	0.8558	0.0221	0.0751	-0.3112	0.0595	0.1047	-0.1567	0.2594	0.2175
252363_at	AT3G48460	GDSL-motif lipase/hydrolase family protein	-1.7846	7.00E-04	0.0334	-2.0861	4.00E-04	0.0251	0.3725	0.0401	0.0828	0.07088	0.599	0.363
252364_at	AT3G48450	nitrate-responsive NOI protein, putative	-0.5321	0.4656	0.4054	0.8973	0.2459	0.2615	0.1744	0.7841	0.4586	1.6039	0.0545	0.0835
252365_at	AT3G48360	systeine proteinase, putative	-0.5922	0.0466	0.1242	-0.2196	0.3508	0.3184	0.2038	0.154	0.1817	0.5763	0.0077	0.0273
252366_at	AT3G48420	haloacid dehalogenase-like hydrolase family protein	-0.9536	4.00E-04	0.032	-1.3076	1.00E-04	0.0249	0.223	0.0548	0.0997	-0.131	0.1895	0.179
252367_at	AT3G48360	BT2 (BTB AND TAZ DOMAIN PROTEIN 2); protein	0.09891	0.8131	0.5277	0.9976	0.0636	0.1257	-0.8783	0.0884	0.1313	0.02035	0.9611	0.4734
252368_at	AT3G48520	CYP94B3 (cytochrome P450, family 94, subfamily B	-1.1289	0.222	0.2764	-1.0366	0.2553	0.2675	-0.04257	0.9231	0.4987	0.04972	0.9103	0.46
252369_at	no_match	no_match	-1.225	0.2776	0.3101	0.3483	0.7391	0.471	0.2132	0.7904	0.4603	1.0899	0.2199	0.196
252370_at	no_match	no_match	-0.19	0.4858	0.414	0.3881	0.1922	0.2275	-0.03624	0.8621	0.4818	0.5419	0.0504	0.0797
252371_at	AT3G48070	protein binding / zinc ion binding	0.06185	0.5439	0.4385	0.07779	0.4516	0.3647	0.1357	0.2198	0.2235	0.1516	0.1797	0.1731
252372_at	AT3G48000	ALDH2B4 (ALDEHYDE DEHYDROGENASE 2); 3-(	0.2693	0.1432	0.2201	0.2552	0.16	0.2059	-0.5515	6.00E-04	0.0158	-0.5656	5.00E-04	0.0096
252373_at	AT3G48090	EDS1 (ENHANCED DISEASE SUSCEPTIBILITY 1	1.2253	0.004	0.0466	1.2679	0.0035	0.0374	-0.2134	0.0349	0.0766	-0.1708	0.0659	0.0935
252374_at	AT3G48100	ARR5 (ARABIDOPSIS RESPONSE REGULATOR	-0.4388	0.1319	0.2103	-0.07583	0.7574	0.4774	-0.1453	0.217	0.2218	0.2166	0.6945	0.3164
252375_at	AT3G48040	ARAC8/ATROP10/ROP10 (rho-related protein from	-0.5668	0.028	0.097	-0.1866	0.3293	0.3083	-0.4814	0.0458	0.0895	-0.1012	0.5796	0.3559
252376_at	AT3G47930	ATGLDH (L-GALACTONO-1,4-LACTONE DEHYDI	-0.01963	0.8642	0.5422	-0.05999	0.6071	0.426	0.01677	0.8838	0.4879	-0.0236	0.8372	0.4393
252377_at	AT3G47960	proton-dependent oligopeptide transport (POT) fam	-0.8755	0.0873	0.1711	-0.9616	0.0686	0.1314	-0.3422	0.0125	0.0443	-0.4282	0.0057	0.0235
252378_at	AT3G47570	leucine-rich repeat transmembrane protein kinase, p	0.6433	0.0743	0.1567	0.3986	0.2111	0.2404	-0.2466	0.4096	0.3206	-0.4913	0.1407	0.1486
252379_at	AT3G47730	ATATH1 (ABC2 homolog 1); ATPase, coupled to tra	0.2294	0.1149	0.1963	0.375	0.0304	0.0865	-0.5803	0.0071	0.0341	-0.4347	0.019	0.0441
252380_at	AT3G47740	ATAH2 (ABC2 homolog 2); ATPase, coupled to tra	0.243	0.8052	0.5255	-1.1517	0.2799	0.2808	0.04484	0.9311	0.501	-1.3099	0.2286	0.2008
252381_s_at	AT3G47760;AT3G47750	[AT3G47760, ATATH4 (ABC2 homolog 4); ATPase	-0.8523	0.074	0.1564	-0.9794	0.0507	0.1116	-0.6587	0.056	0.101	-0.7858	0.0335	0.0618
252382_at	AT3G47770	ATATH5 (ABC2 homolog 5); ATPase, coupled to tra	0.5412	0.4887	0.4154	-1.5878	0.0892	0.1505	-0.06147	0.9189	0.4975	-2.1905	0.0181	0.0432
252383_at	AT3G47780	ATATH6 (ABC2 homolog 6); ATPase, coupled to tra	1.9493	0.0091	0.0615	1.5576	0.0194	0.0716	0.2447	0.3998	0.3165	-0.147	0.6019	0.3639
252384_at	no_match	no_match	0.2377	0.8656	0.5425	0.4068	0.773	0.4815	-1.587	0.2789	0.2575	-1.418	0.326	0.2512
252385_at	AT3G47810	MAG1 (MAIGO 1); protein serine/threonine phospha	0.3733	0.0167	0.0775	0.2961	0.0349	0.0923	0.5523	0.0023	0.0223	0.4751	0.0039	0.0202
252386_at	AT3G47840	pentatricopeptide (PPR) repeat-containing protein	1.3969	0.1948	0.259	1.0189	0.3199	0.3031	-0.166	0.8623	0.4819	0.4349	0.5774	0.355
252387_at	AT3G47800	aldose 1-epimerase family protein	1.1524	0.0101	0.064	1.3417	0.0059	0.0443	0.4182	0.0215	0.059	0.6075	0.006	0.024
252388_at	AT3G47850	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.7022	0.0126	0.0692	0.7051	0.0124	0.0597	0.4856	0.0409	0.084	0.4885	0.0402	0.0693
252389_at	AT3G47833	similar to unknown protein [Arabidopsis thaliana] (T	0.2723	0.1865	0.253	0.4079	0.0755	0.1378	0.8094	0.0091	0.0381	0.945	0.0052	0.0226
252390_at	AT3G47836	unknown protein	0.2697	0.1229	0.2033	0.1329	0.391	0.3372	-0.09892	0.5041	0.3609	-0.2357	0.1555	0.1585
252391_at	AT3G47860	apolipoprotein D-related	-0.659	0.1647	0.2373	-1.0434	0.0548	0.1161	-0.00778	0.9504	0.5056	-0.3922	0.0289	0.0569
252392_s_at	AT3G47890;AT3G47910	[AT3G47890, ubiquitin carboxyl-terminal hydrolase-	0.2646	0.1165	0.1973	0.01548	0.9126	0.5221	-1.0185	0.0015	0.0201	-1.2676	7.00E-04	0.0105
252393_at	no_match	no_match	-0.1727	0.6337	0.4708	-0.2138	0.5583	0.4078	-1.3306	0.0123	0.0441	-1.3718	0.0111	0.033
252394_at	AT3G47940	DNAJ heat shock protein, putative	0.1273	0.4921	0.4166	0.09085	0.6184	0.4301	-0.01518	0.9326	0.5014	-0.05162	0.7747	0.4214
252395_at	AT3G47950	AHA4 (Arabidopsis H(+)-ATPase 4); ATPase	1.5696	0.1614	0.2346	0.8205	0.4205	0.3509	0.4372	0.6577	0.4171	-0.3119	0.7503	0.4139
252396_at	AT3G47960	integral membrane HPP family protein	1.7053	0.0728	0.1554	-1.1341	0.1829	0.2217	0.5893	0.4337	0.3313	1.1605	0.1621	0.1624
252397_at	AT3G47980	integral membrane HPP family protein	-1.6634	0.1231	0.2034	-1.4543	0.1636	0.2083	1.5836	0.1371	0.1691	1.7927	0.1036	0.1231
252398_at	AT3G47990	zinc finger (C3HC4-type RING finger) family protein	0.2654	0.0357	0.1091	0.1672	0.1212	0.1766	-0.4508	0.005	0.0299	-0.5489	0.0024	0.0164
252399_at	AT3G48010	ATCNGC16 (cyclic nucleotide gated channel 16); c	-0.5067	0.749	0.5084	-1.3371	0.4169	0.3491	-1.136	0.371	0.3034	-1.9664	0.1564	0.159
252400_at	AT3G48020	similar to F-box family protein-related [Arabidopsis t	1.109	0.0499	0.1284	0.8752	0.0934	0.1539	0.1594	0.5195	0.3668	-0.0744	0.7585	0.4162
252401_at	AT3G48030	hypoxia-responsive family protein / zinc finger (C3H	0.08093	0.9045	0.5525	-1.1777	0.1364	0.188	1.1936	0.1325	0.1656	-0.06498	0.8232	0.4636
252402_s_at	AT3G48060;AT3G48050	[AT3G48060, bromo-adjacent homology (BAH) dom	0.2517	0.1222	0.2024	0.133	0.3598	0.3226	-0.5202	0.0095	0.0389	-0.6389	0.0046	0.0214
252403_at	AT3G48080	lipase class 3 family protein / disease resistance pr	0.5365	0.0087	0.0606	0.5825	0.0065	0.0459	-0.4245	0.0014	0.0196	-0.5646	0.001	0.0119
252404_at	AT3G48110	EDD1 (EMBRYO-DEFECTIVE-DEVELOPMENT 1);	0.09062	0.5854	0.4545	-0.2301	0.2069	0.2376	-0.7989	0.001	0.0176	-1.1196	3.00E-04	0.0081
252405_at	AT3G48120	similar to unnamed protein product [Vitis vinifera] (G	1.2296	0.0021	0.0407	0.5513	0.0341	0.0911	-0.2076	0.2994	0.2684	-0.886	0.0071	0.0262
252406_at	AT3G47670	pectinesterase inhibitor	0.216	0.0554	0.1352	0.2456	0.0383	0.0969	0.2202	0.0523	0.0971	0.25	0.0363	0.0648
252407_at	AT3G47520	MDH (MALATE DEHYDROGENASE); malate dehy	0.3928	0.0685	0.1505	-0.09858	0.568	0.4111	0.2869	0.1448	0.1752	-0.2044	0.267	0.2212
252408_at	AT3G47600	MYB94 (myb domain protein 94); DNA binding / tra	-0.2158	0.1084	0.1907	-0.1851	0.1521	0.1998	0.3263	0.0225	0.0232	0.3571	0.0018	0.0148
252409_at	AT3G47650	bundle sheath defective protein 2 family / tad2 fami	-0.3889	0.1237	0.2038	-0.7659	0.0202	0.0727	-0.4499	0.0838	0.1273	-0.1028	0.6423	0.378
252410_at	AT3G47450	ATNOA1/ATNOS1/NOA1/NOS1 (NO ASSOCIATED	-0.1896	0.401	0.3758	-0.05072	0.8141	0.4944	-0.3046	0.206	0.2154	-0.1657	0.4579	0.3092
252411_at	AT3G47430	PEX11B	-0.6452	0.0468	0.1245	-1.0598	0.0095	0.0535	0.1818	0.0579	0.103	-0.2328	0.028	0.0558
252412_at	AT3G47296	unknown protein	-0.817	0.0271	0.0952	-1.0825	0.0107	0.0557	0.2396	0.1796	0.1983	0.06427	0.7674	0.4191
252413_at	AT3G47370	40S ribosomal protein S20 (RPS20B)	-0.01146	0.9507	0.5648	0.2989	0.1613	0.2068	0.5719	0.0141	0.0475	0.8822	0.003	0.0179
252414_at	AT3G47420	glycerol-3-phosphate transporter, putative / glycerol	-0.2534	0.4083	0.3794	-0.599	0.0946	0.1549	-0.1822	0.4847	0.3533	-0.5278	0.0898	0.1126
252415_at	AT3G47460	ASN1 (DARK INDUCIBLE 6)	0.3106	0.6886	0.4887	0.5999	0.2887	0.2848	-0.5981	0.0394	0.0809	-0.2088	0.3484	0.2617
252416_at	AT3G47460	ATSMC2 (Arabidopsis thaliana structural maintenan	0.09654	0.8068	0.5258	0.6305	0.1632	0.2081	-0.2523	0.5323	0.3722	0.2817	0.4884	0.3212
252417_at	AT3G47480	calcium-binding EF hand family protein	2.3022	0.0129	0.0699	2.6979	0.0074	0.0486	0.37	0.0687	0.1137	0.7657	0.0069	0.0259
252418_at	AT3G47490	HNH endonuclease domain-containing protein	-0.06791	0.5571	0.4438	0.3659	0.0261	0.0809	-0.1206	0.3193	0.2779	0.3132	0.0419	0.0713
252419_at	AT3G47510	unknown protein	-0.6786	0.0563	0.136	-0.2855	0.3256	0.3062	0.3856	0.1924	0.207	0.7787	0.0341	0.0624
252420_at	AT3G47530	pentatricopeptide (PPR) repeat-containing protein	0.4975	0.1782	0.2468	0.7162	0.0787	0.1405	0.05539	0.8611	0.4814	0.2741	0.4082	0.2875
252421_at	AT3G47540	chitinase, putative	0.454	0.0099	0.0513	0.5123	0.0243	0.0783	0.4957	0.0071	0.0341	0.6929	0.0021	0.0154
252422_at	AT3G47550	zinc finger (C3HC4-type RING finger) family protein	0.1421	0.6014	0.46	0.4519	0.1461	0.1955	0.1184	0.6618	0.4185

252490_at	AT3G46720	UDP-glucuronosyl/UDP-glucosyl transferase family	-0.517	0.4085	0.3795	-1.038	0.1377	0.189	-0.07424	0.901	0.4927	-0.5953	0.3481	0.2615
252491_at	AT3G46730	disease resistance protein (CC-NBS class), putative	-3.5022	0.0533	0.1325	-0.5794	0.6766	0.4508	-1.6815	0.2624	0.2479	1.2413	0.3905	0.2802
252492_at	AT3G46740	TOC75-III (translocon outer membrane complex 75	0.08773	0.657	0.478	-0.2542	0.2375	0.2562	-0.3056	0.0817	0.1253	-0.6476	0.008	0.0279
252493_at	AT3G46750	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.3157	0.7614	0.512	-0.7673	0.4735	0.3735	1.2615	0.2407	0.2355	0.1786	0.855	0.4443
252494_at	AT3G46760	protein kinase family protein	-0.3253	0.5439	0.4385	-0.8677	0.1519	0.1997	0.07158	0.8776	0.4861	-0.4708	0.3411	0.2585
252495_at	AT3G46770	transcriptional factor B3 family protein	1.0495	0.0657	0.1469	0.8634	0.1073	0.1653	0.3796	0.4144	0.3228	0.1935	0.6669	0.3864
252496_at	AT3G46790	CRR2 (CHLORORESPIRATORY REDUCTION 2)	0.4013	0.0889	0.1729	0.303	0.1665	0.2101	-0.07269	0.7025	0.432	-0.1709	0.389	0.2795
252497_at	AT3G46800	DC1 domain-containing protein	-1.4924	0.3046	0.3254	-1.5082	0.3002	0.2914	-0.4018	0.7673	0.4533	-0.4175	0.7585	0.4162
252498_at	AT3G46810	DC1 domain-containing protein	-1.1182	0.1027	0.1852	-0.1725	0.7613	0.478	-0.9068	0.1625	0.1869	0.03898	0.9449	0.4696
252499_s_at	AT3G46840;AT3G46850	subtilase family protein;[AT3G46850	-0.95	0.4255	0.3874	0.3157	0.783	0.4844	-1.6977	0.1884	0.2046	-0.432	0.7075	0.4
252500_at	AT3G46860	serine protease inhibitor, potato inhibitor I-type fam	1.1482	0.3532	0.3514	-0.2662	0.8198	0.4958	0.6376	0.0931	0.1352	-0.7768	0.0555	0.0844
252501_at	AT3G46880	similar to unknown protein [Arabidopsis thaliana] (T	-1.6823	0.0145	0.0731	-0.89	0.0941	0.1545	-0.3367	0.4226	0.3266	0.4555	0.2939	0.2355
252502_at	AT3G46900	COPT2 (Copper transporter 2); copper ion transme	-0.01801	0.9714	0.5702	-0.1104	0.8269	0.498	0.9	0.0228	0.061	0.8076	0.032	0.0603
252503_at	AT3G46910	ubiquitin protein ligase binding	1.2499	0.3896	0.3697	-1.0081	0.4803	0.3763	2.0886	0.1825	0.2006	-0.1694	0.9024	0.458
252504_at	AT3G46590	TRFL1 (TRF-LIKE 1); DNA binding	0.09273	0.6129	0.4636	0.1382	0.4599	0.3679	0.1593	0.0317	0.0725	0.2048	0.0141	0.0377
252505_at	AT3G46170	short-chain dehydrogenase/reductase (SDR) family	-0.0612	0.8768	0.5456	-0.2312	0.5664	0.4105	0.4463	0.2947	0.266	0.2763	0.4972	0.3248
252506_at	AT3G46180	AT/UTR5/UTR5 (UDP-GALACTOSE TRANSPORTE	0.3402	0.2208	0.2757	0.4147	0.1519	0.1997	-0.6232	0.0566	0.1017	-0.5486	0.0796	0.1046
252507_at	AT3G46200	ATNUDT9 (Arabidopsis thaliana Nudix hydrolase h	-0.1471	0.2776	0.3101	-0.4247	0.0223	0.0754	-0.1393	0.3002	0.2688	-0.4169	0.0236	0.0503
252508_at	AT3G46210	3' exoribonuclease family domain 1-containing prote	0.1225	0.5793	0.4521	0.04467	0.8369	0.5007	-0.0365	0.6757	0.423	-0.1143	0.2311	0.202
252509_at	AT3G46240	protein kinase-related	0.1821	0.8489	0.5379	1.6457	0.14	0.1906	-0.6379	0.1557	0.3653	1.1899	0.2547	0.2151
252510_at	AT3G46270	receptor protein kinase-related	-0.5983	0.6423	0.4737	0.1003	0.937	0.5284	-1.2137	0.3657	0.3008	-0.5151	0.6876	0.393
252511_at	AT3G46280	protein kinase-related	-0.05993	0.899	0.6508	0.7079	0.1856	0.2235	-0.3044	0.5302	0.3713	0.4635	0.3549	0.2648
252512_at	AT3G46290	protein kinase, putative	-0.6103	0.0603	0.1406	-0.6023	0.0626	0.1242	-0.3346	0.2278	0.2282	-0.3266	0.2372	0.2057
252513_at	AT3G46220	similar to unnamed protein product [Vitis vinifera] (G	0.8349	9.00E-04	0.0347	0.2291	0.0696	0.1321	-0.04922	0.6249	0.4063	-0.6551	0.0021	0.0156
252514_at	AT3G46060	ARA3; GTP binding	0.3389	0.0097	0.0632	0.3903	0.0059	0.0443	-0.1256	0.1293	0.1634	-0.07423	0.323	0.2497
252515_at	AT3G46230	ATHSP17.4 (Arabidopsis thaliana heat shock protei	1.2754	0.0449	0.1222	2.5368	0.0046	0.0416	0.02175	0.9632	0.5084	1.2831	0.0442	0.0736
252516_at	AT3G46100	ATHRS1 (HISTIDYL-TRNA SYNTHETASE 1); histi	-0.1866	0.3675	0.3581	-0.02282	0.9072	0.5207	-0.4602	0.0665	0.1115	-0.2964	0.1822	0.1747
252517_at	AT3G46340	leucine-rich repeat protein kinase, putative	-0.5343	0.3565	0.3529	-1.2576	0.0703	0.1327	0.5934	0.3117	0.2743	-0.1299	0.8126	0.4325
252518_at	AT3G46350	leucine-rich repeat protein kinase, putative	-1.1753	0.4269	0.3881	-0.9906	0.4979	0.3837	0.9082	0.5099	0.3633	1.0928	0.4336	0.2983
252519_at	AT3G46360	similar to unknown protein [Arabidopsis thaliana] (T	0.2468	0.4844	0.4136	-0.5321	0.1724	0.2145	0.432	0.2492	0.2405	-0.3469	0.3401	0.2581
252520_at	AT3G46370	leucine-rich repeat protein kinase, putative	-0.7513	0.4139	0.3819	-0.7205	0.4316	0.356	-2.6605	0.0129	0.0452	-2.6297	0.0135	0.0368
252521_at	AT3G46380	unknown protein	0.3777	0.7614	0.512	-1.8103	0.1943	0.2289	1.5362	0.2567	0.2446	-0.6518	0.6048	0.3649
252522_at	AT3G46390	similar to unknown protein [Arabidopsis thaliana] (T	0.8398	0.6014	0.4601	0.8987	0.5772	0.4148	0.9153	0.2285	0.2287	0.9742	0.2051	0.1879
252523_at	AT3G46400	leucine-rich repeat protein kinase, putative	0.6231	0.3709	0.3558	0.6126	0.428	0.2754	0.9129	0.0497	0.0393	1.7954	0.0506	0.0799
252524_at	AT3G46430	similar to unknown protein [Arabidopsis thaliana] (T	-0.1388	0.3836	0.3665	-0.174	0.2874	0.2851	0.5905	0.0086	0.0372	0.5552	0.0107	0.0324
252525_at	AT3G46450	SEC14 cytosolic factor family protein / phosphoglyc	-0.08816	0.6626	0.4802	-0.02017	0.9195	0.5239	-0.3789	0.0599	0.105	-0.311	0.0996	0.1203
252526_at	AT3G46460	oxidoreductase, acting on paired donors, with incor	0.1868	0.8796	0.5464	0.4255	0.7317	0.4688	1.4257	0.2654	0.2609	-1.1869	0.363	0.2683
252527_at	AT3G46440	UXS5 (UDP-Xyl synthase 5); catalytic	1.0925	0.0492	0.1276	1.4374	0.0213	0.0744	-0.326	0.2159	0.2213	0.01891	0.9362	0.4673
252528_at	AT3G46460	UBC13 (ubiquitin-conjugating enzyme 13); ubiquitin	0.1324	0.348	0.349	0.3857	0.0364	0.0942	0.08497	0.4591	0.3427	0.3383	0.0311	0.0595
252529_at	AT3G46490	oxidoreductase, acting on paired donors, with incor	-2.8804	0.019	0.0819	-3.2492	0.0127	0.0602	-0.05601	0.9334	0.5016	-0.4248	0.537	0.3403
252530_at	AT3G46500	oxidoreductase, 2OG-Fe(II) oxygenase family prote	-1.7111	0.0714	0.154	0.1404	0.8512	0.5048	-1.9997	0.0048	0.0292	-0.1482	0.6957	0.396
252531_at	AT3G46520	ACT12 (ACTIN-12); structural constituent of cytoske	-0.9633	0.5484	0.4405	-1.3416	0.4135	0.3476	1.5608	0.3027	0.2699	1.1825	0.4212	0.2929
252532_at	AT3G46570	glycosyl hydrolase family 17 protein	-0.5189	0.6226	0.4479	-0.07796	0.9401	0.5291	-1.9738	0.1128	0.1504	-1.5329	0.1908	0.1797
252533_at	AT3G46110	signal transducer	-0.4948	0.2888	0.3166	-0.1519	0.7266	0.4677	-0.04183	0.5806	0.391	0.3011	0.0124	0.0353
252534_at	AT3G46130	MYB111 (myb domain protein 111); DNA binding / k	0.0604	0.9178	0.5565	-0.249	0.6742	0.4499	-1.008	0.0325	0.0735	-1.3174	0.0137	0.0372
252535_at	AT3G46150	unknown protein	1.3507	0.2761	0.3094	-2.5083	0.0794	0.1412	2.9686	0.0097	0.0393	-0.8901	0.2362	0.205
252536_at	AT3G45700	proton-dependent oligopeptide transport (POT) fam	-0.3715	0.7013	0.4929	-0.9658	0.3443	0.3153	-0.5469	0.3852	0.3102	-1.1412	0.1119	0.129
252537_at	AT3G45710	proton-dependent oligopeptide transport (POT) fam	0.5653	0.6343	0.4709	1.3711	0.2805	0.2811	0.7266	0.393	0.3134	1.5323	0.1139	0.1304
252538_at	AT3G45720	proton-dependent oligopeptide transport (POT) fam	0.5115	0.6536	0.4771	-0.6738	0.5583	0.4078	1.2646	0.2974	0.2673	1.1025	0.3556	0.2651
252539_at	AT3G45730	unknown protein	-0.3837	0.3466	0.3482	0.7565	0.1035	0.1624	0.4717	0.1194	0.1558	1.612	0.0025	0.0166
252540_at	AT3G45740	hydrolase family protein / HAD-superfamily protein	-0.2286	0.1178	0.1985	0.2289	0.1175	0.1734	-1.2032	5.00E-04	0.0148	-0.7457	0.0029	0.0176
252541_at	AT3G45750	similar to unknown protein [Arabidopsis thaliana] (T	-0.1152	0.52	0.429	0.1706	0.3555	0.3206	-1.0497	5.00E-04	0.0155	-0.7639	0.0018	0.0148
252542_at	AT3G45770	oxidoreductase, zinc-binding dehydrogenase family	0.4764	0.0417	0.1176	0.6001	0.0204	0.0729	-0.5018	0.0358	0.0777	-0.3781	0.0789	0.104
252543_at	AT3G45780	PHOT1 (phototropin 1); kinase	-0.0961	0.5488	0.4405	-0.02795	0.8584	0.5067	-0.1562	0.1203	0.1564	-0.08806	0.3292	0.253
252544_at	AT3G45810	ferric reductase-like transmembrane component fam	0.605	0.6425	0.4737	0.735	0.5755	0.414	0.5115	0.0312	0.501	0.2409	0.8515	0.4431
252545_at	AT3G45820	unknown protein	1.4502	0.1824	0.25	-2.0917	0.0808	0.1426	1.3512	0.2076	0.2164	-2.1906	0.0717	0.0981
252546_at	AT3G45830	similar to unknown protein [Arabidopsis thaliana] (T	0.15	0.6661	0.4813	0.3719	0.3132	0.2991	-0.9394	0.0046	0.029	-0.7175	0.012	0.0344
252547_at	no_match	no_match	0.178	0.895	0.55	0.9615	0.4899	0.3803	-0.1615	0.819	0.4695	0.6221	0.4001	0.2842
252548_at	AT3G45850	kinesin motor protein-related	-0.198	0.2337	0.2839	-0.3863	0.0522	0.1133	-0.4919	0.0179	0.0535	-0.6802	0.0058	0.0237
252549_at	AT3G45860	receptor-like protein kinase, putative	1.6474	0.0053	0.0519	1.4836	0.0078	0.049	-0.4054	0.0338	0.0752	-0.5691	0.0112	0.0332
252550_at	AT3G45870	integral membrane family protein / nodulin MtN21-re	0.1042	0.8764	0.5456	2.2161	0.0244	0.0783	-0.6718	0.3455	0.2909	1.44	0.0839	0.1081
252551_at	AT3G45880	similar to transcription factor jumonji (jmjC) domain-	0.3237	0.5541	0.4425	1.2022	0.0748	0.1371	-0.2182	0.428	0.3288	0.6603	0.056	0.0848
252552_at	AT3G45900	similar to unknown protein [Arabidopsis thaliana] (T	-0.4325	0.0104	0.0646	-0.3079	0.0316	0.0883	-0.223	0.0394	0.0821	-0.09841	0.2542	0.2148
252553_at	AT3G45910	unknown protein	-1.3476	0.2462	0.2914	-0.4525	0.6722	0.4492	0.5048	0.537	0.3741	1.3999	0.1348	0.1449
252554_s_at	AT3G46330;AT3G45920	[AT3G46330, MEE39 (maternal effect embryo arres	0.871	0.308	0.3274	-0.00275	0.9972	0.5434	0.648	0.4342	0.3315	-0.2257	0.7774	0.4221
252555_at	AT3G45940	alpha-xylosidase, putative	0.8842	0.4683	0.4065	-0.2633	0.8233	0.497	0.2793	0.8129	0.4675	-0.8682	0.4758	0.316
252556_at	AT3G45950	splicing factor-related	0.9905	0.1702	0.2415	-0.931	0.1915	0.2271	1.0728	0.1447	0.1751	-0.8487	0.2256	0.1992
252557_at	AT3G45960	ATEXLA3 (ARABIDOPSIS THALIANA EXPANSIN-A	1.1436	0.3628	0.3558	1.1552	0.3585	0.3222	0.9037	0.2623	0.2479	0.9153	0.2572	0.2164
252558_at	AT3G45990	actin-depolymerizing factor, putative	-0.8205	0.1192	0.1995	-0.0681	0.8776	0.5124	-0.7442	0.1474	0.1771	0.00813	0.9853	0.4791
252559_at	AT3G46020	RNA-binding protein, putative	-0.1147	0.4469	0.3966	0.3314	0.0716	0.1339	0.4128	0.0038	0.027	0.8589	2.00E-04	0.0078
252560_at	AT3G46030	HTB11; DNA binding	-0.2058	0.2687	0.3046	0.1225	0.4875	0.3793	0.7429	0.0098	0.0395	1.0712	0.0026	0.0169
252561_at	AT3G45980	HTB9; DNA binding	-0.2888	0.3009	0.3235	-0.107	0.6828	0.4531	0.8472	0.0253	0.0646	1.029	0.0134	0.0367
252562_s_at	AT3G46320;AT3G45930	AT3G46320, histone H4];[AT3G45930, histone H4]	-0.1376	0.6736	0.4147	-0.05737	0.7651	0.4789	0.479	0.0279	0.068	1.1592	0.0012	0.0129
252563_at	AT3G45970	ATEXLA1 (ARABIDOPSIS THALIANA EXPANSIN-A	-0.1553	0.8526	0.5389	-0.4456	0.6003	0.4236	1.0923	0.001	0.0176	0.8021	0.0032	0.0184
252564_at	AT3G46010	ADF1 (ACTIN DEPOLYMERIZING FACTOR 1)	-0.3731	0.1127	0.1945	-0.1078	0.5897	0.4194	0.3109	0.1667	0.1895	0.5762	0.0352	0.0635
252565_at	AT3G46000	ADF2 (ACTIN DEPOLYMERIZING FACTOR 2); act	-0.07117	0.6505	0.4765	0.4942	0.0274	0.0827	0.4247	0.0123	0.0441	0.9901	5.00E-04	0.0097
252566_at	AT3G46040	RPS15AD (Arabidopsis protein S15A D); structural co	0.04434	0.7634	0.5125	0.4473	0.0314	0.088	-0.297	0.0835	0.1271	0.1059	0.4591	0.3096
252567_at	AT3G46070	zinc finger (C2H2 type) family protein	1.2952	0.0509	0.1298	-0.3519	0.4952	0.3826	0.9961	0.1012	0.142	-0.651	0.2379	0.206
252568_at	AT3G45410	lectin protein kinase family protein	1.4453	0.1476	0.2236	0.6539	0.463	0.3693	-0.3445	0.5241	0.3687	-1.1359	0.0831	0.1075
252569_at	AT3G45420	lectin protein kinase family protein	0.2055	0.6434	0.4741	-0.0349	0.9364	0.5283	-0.9244	0.0878	0.1308	-1.1648	0.0472	0.0765
252570_at	AT3G45300	IVD (ISOVALERYL-COA-DEHYDROGENASE)	0.6761	0.1386	0.2161	1.1617	0.0338	0.0908	-0.5938	0.0255	0.0649	-0.1083	0.5611	0.3493
252571_at	AT3G45280	SYP72 (SYNTAXIN OF PLANTS 72)	-0.9133	0.4172	0.3835	-0.09245	0.9315	0.5269	0.7716	0.3414	0.2889	1.5925	0.09	0.1128
252572_at	AT3G45290	MLO3 (MILDEW RESISTANCE LOCUS O 3); calm	1.0348	9.00E-04	0.0349	0.9001	0.0016	0.0317	-0.3167	0.0551	0.1	-0.4514	0.0187	0.0439
252573_at	AT3G45260	zinc finger (C2H2 type) family protein	0.5188	0.0815	0.1651	0.3688	0.1751	0.2163	-0.2555	0.2111	0.2185	-0.4055	0.0776	0.103
252574_at	AT3G45430	lectin protein kinase family protein	-0.9827	0.0038	0.0461	-1.465	8.00E-04	0.0284	-0.2764	0.1493	0.1785	-0.7587	0.0081	0.028
252575_at	AT3G45440	lectin protein kinase family protein	0.1399	0.7312	0.5028	0.0579	0.8862	0.5148	0.4837	0.1468	0.1768	0.4017	0.21	0.1909
252576_s_at	AT3G45450;AT3G46870	[AT3G45450, Clp amino terminal domain-containing	-0.1275	0.7061	0.4948	-0.421	0.2519	0.2652	-1.3421	0.0053	0.0306	-1.6356	0.0026	0.0169
252577_at	AT3G45460	zinc ion binding	-0.9964	0.0141	0.0725	-1.1159	0.0096	0.0535	0.5285	0.0918	0.134	-1.5838	0.0027	0.0171
252578_at	AT3G45480	nucleic acid binding / protein binding / zinc ion bind	-1.1588	0.3276	0.3387	0.9863	0.3966	0.3398	-1.1679	0.2367	0.2333	0.9772	0.3093	0.243
252579_at	AT3G45510	zinc finger (C3HC4-type RING finger) family protein	-0.1665	0.7778	0.5173	-0.1484	0.8012	0.4898	0.3671	0.3252	0.281	0.3852	0.3049	0.241
252580_at	AT3G45490	similar to zinc finger protein-related [Arabidopsis tha	-0.729	0.4698	0.4072	-0.4547	0.645	0.4399	0.2561	0.7624	0.4519	0.5304	0.5392	0.3409
252581_at	AT3G45500	similar to zinc finger (C3HC4-type RING finger) fam	-0.1301	0.9002	0.5511	-0.9237	0.3964	0.3397	0.1442	0.8572	0.4803	-0.6494	0.4363	0.2997
252582_at	AT3G45530	DC1 domain-containing protein	1.7553	0.2158	0.2723	-1.321	0.331	0.3089	2.0024	0.1691	0.1912	-1.074	0.4196	0.2924
252583_at	AT3G45540	zinc finger (C3HC4-type RING finger) family protein	0.383	0.5985	0.4591	-0.6346	0.3976	0.3403	1.9526	0.0436	0.0872	0.9351	0.2357	0.2048
252584_at	AT3G45560	zinc finger (C3HC4-type RING finger) family protein	-1.0404	0.2427	0.2891	-0.2978	0.715	0.4638	0.8422	0.2105	0.2181	1.5848	0.0486	0.078
252585_s_at	AT3G45580;AT3G45570	[AT3G45580, zinc finger (C3HC4-type RING finger)	0.4972	0.7171	0.4984	-2.5509	0.1167	0.1726	1.4501	0.32	0.2783	-1.598	0.2794	0.2279
252586_at	AT3G45620	Dof-type zinc finger domain-containing protein	-1.1654	0.2121	0.2697	-0.1963	0.815	0.4947	1.483	0.1218	0.1577	2.4522	0.0317	0.06
252587_at	AT3G45620	transducin family protein / WD-40 repeat family prot	1.3075	0.0023	0.0418	1.1716	0.0035	0.0374	0.2242	0.1988	0.2111	0.08832	0.5772	0.3549
252588_at	AT3G45630	RNA recognition motif (RRM)-containing protein	0.05959	0.6512	0.4766	0.546	0.0111	0.0564	-0.9748	0.0013	0.0192	-0.4884	0.0161	0.0406
252589_s_at	AT3G45660;AT3G45650	[AT3G45660, proton-dependent oligopeptide transp	-0.246	0.3966	0.3735	0.6022	0.0809	0.1426	-1.2073	0.0043	0.0282	-0.3591	0.1585	0.1603
252590_at	AT3G45670	unknown protein	-0.3516	0.4653	0.4053	-1.0409	0.0754	0.1378	0.01024	0.9824	0.5133	-0.679	0.1944	0.1816
252591_at	AT3G45600	TET3 (TETRASPANIN3)	0.3927	0.1699	0.2413	0.5157	0.0931	0.1539	-0.02617	0.8118	0.4671	0.09689	0.3998	0.2841
252592_at	AT3G45640	ATMPK3 (MITOGEN-ACTIVATED PROTEIN KINA	0.05007	0.866	0.5425	0.06877	0.817	0.495	0.2993	0.15	0.1788	0.318	0.1318	0.1428
252593_at	AT3G45590	ATSEN1 (SPLICING ENDONUCLEASE 1); RNA-ir	0.8083	0.0041	0.0468	0.6227	0.0104	0.0552	-0.3325	0.0062	0.0328	-0.5182	0.0012	0.0128
252594_at	AT3G45680	proton-dependent oligopeptide transport (POT) fam	-0.6663	0.25	0.2936	-0.7375	0.211	0.2404	-0.06684	0.8871	0.4888	-0.138	0.7705	0.4201
252595_at	AT3G45690	proton-dependent oligopeptide transport (POT) fam	0.1936	0.801	0.5245	-0.0912	0.9051	0.5201	0.04813	0.9498	0.5055	0.1505	0.8443	0.4412
252596_at	AT3G45530	lectin protein kinase family protein	1.162	0.3261	0.338	0.8705	0.4493	0.3637	0.2407	0.8282	0.4721	-0.05077	0.9634	0.4741
252597_at	no_match	no_match	0.2078	0.9146	0.5553	0.4567	0.8143	0.4945	-0.9167	0.6411	0.4114	-0.6678	0.7324	0.4079
252598_at	AT3G45380	transposable element gene	-2.1377	0.2531	0.2953	1.1244	0.5216	0.3928	-0.8774	0.6131	0.4021	2.3848	0.2109	0.1913
252599_at	AT3G45390	lectin protein kinase family protein	0.4514	0.7556	0.5104	-0.17	0.9061	0.5204	0.6775	0.5981	0.3975	0.05618	0.9645	0.4744
252600_at	AT3G45000	VPS24-2	-0.872	0.5256	0.4315	-1.7566	0.2344	0.2546	0.1744	0.8948	0.4911	-0.7101	0.597	0.3624
252601_s_at	AT3G45020;AT5G62300	[AT3G45020, 40S ribosomal protein S20 (RPS20A);	-0.04005	0.6427	0.4738	-0.1156	0.2219	0.247	0.06884	0.4378	0.3331	-0.00666	0.9376	0.4678
252602_at	AT3G45040	phosphatidate cytidylyltransferase family protein	0.7724	0.0366	0.1104	0.2999	0.2966	0.29	-0.2703	0.0924	0.1346	-0.7428	0.0038	0.0199
252603_at	AT3G45050	similar to unnamed protein product [Vitis vinifera] (G	0.3667	0.0265	0.0941	0.09582	0.6137	0.4283	-0.00669	0.9509	0.5057	0.4069	0.0163	0.0408
252604_at	AT3G45060	ATNRT2.6 (Arabidopsis thaliana high affinity nitrate	2.2304	0.0233	0.0893	0.455	0.5063	0.3872	-0.3499	0.6049	0.3998	-2.1253	0.0271	0.0547
252605_s_at	AT3G45070;AT3G45080	[AT3G45070, sulfotransferase family protein];[AT3G	-0.1713	0.7774	0.5172	0.7881	0.2365	0.2557	-1.4157	0.0668	0.1118	-0.4563	0.4656	0.3122
252606_at	AT3G45010	SCPL48 (serine carboxypeptidase-like 48); serine c	-0.3492	0.1757	0.2452	-0.459	0.1569	0.0969	0.2545	0.0652	0.1101	0.2448	0.1467	0.1987
252607_at	AT3G44990	XTR6 (xyloglucan:xyloglucosyl transferase 6); hydr	-1.777	0.0281	0.0971	-2.3921	0.0106	0.0555	0.6709	0.0516	0.0962	-0.05567	0.8309	0.4374
252608_at	AT3G45090	2-phosphoglycerate kinase-related	0.09623	0.9304	0.56	1.1324	0.3357	0.3112	-0.9584	0.2056	0.2152	0.07781	0.9083	0.4594
252609_at	AT3G45110	unknown protein	-0.4935	0.1905	0.2558	-1.1864	0.5841	0.4178	0.3708	0.3024	0.2698	0.6779	0.0966	0.1179
252610_x_at	AT3G45120	transposable element gene	-0.9356	0.4906	0.4162	1.6707	0.2473	0.2622	-2.5445	0.0599	0.105	0.06177	0.9527	0.4717
252611_at	AT3G45130	LAS1 (Lanosterol synthase 1); lanosterol synthase	1.2127	0.0243	0.0908	0.9771	0.0468	0.1073	-0.1689	0.6491	0.4142	-0.4045	0.3048	0.241
252612_at	AT3G45140	contains domain PROKAR_LIPOPROTEIN (PS512	-0.816	0.0368	0.1105	-0.1659	0.5648	0.41	0.7922	0.0417	0.085	1.4324	0.0056	0.0234
252613_at	AT3G45190	SIT4 phosphatase-associated family protein	0.4489	0.0226	0.0879	0.1727	0.2376	0.2564	-0.5046	0.0088	0.0375	-0.7808	0.0018	0.0147
252614_at	AT3G45220	serpin, putative / serine protease inhibitor, putative	-0.655	0.6095	0.4628	-2.122	0.1475	0.1963	1.7377	0.216	0.2213	0.2707	0.8303	0.4372
252615_at	AT3G45230	hydroxyproline-rich glycoprotein family protein	-0.8257	0.1013	0.1841	-0.7646	0.0368	0.0947	0.6873	0.0382	0.0807	0.4484	0.1178	0.1333
252616_at	AT3G45242;AT3G45240	[AT3G45242, CPuORF51 (Conserved peptide upstr	0.187	0.5675	0.4479	0.436	0.2205	0.2462	-0.9582	0.0292	0.0693	-0.7093	0.0694	0.0965
252617_at	AT3G45100	SETH2; transferase, transferring glycosyl groups	0.63	0.0013	0.0376	0.1944	0.07	0.1324	-0.2772	0.0248	0.0639	-0.7128	8.00E-04	0.0113
252618_at	AT3G45140	LOX2 (LIPOXYGENASE 2)	-0.2118	0.1857	0.2526	-0.512	0.0182	0.0696	-0.1128	0.331	0.2838	-0.413	0.0155	0.0397
252619_at	AT3G45210	similar to unknown protein [Arabidopsis thaliana] (T	-0.07438	0.566	0.4473	0.1085	0.4138	0.3477	0.04738	0.6629	0.4189	0.2302	0.0845	0.1085
252620_at	AT3G45250	transposable element gene	0.6052	0.6737	0.4839	-1.8763	0.2324	0.2532	2.1818	0.1774	0.1967	-0.2997	0.8333	0.4381
252621_at	AT3G45270	transposable element gene	0.9742	0.415	0.4823	-0.4789	0.6782	0.4512	-0.5993	0.606	0.4001	-2.0525	0.1281	0.1403
252622_at	AT3G45310	cysteine proteinase, putative	0.3432	0.0095	0.0626	0.3029	0.0146	0.0637	0.08469	0.3132	0.2751	0.0444	0.5782	0.3554
252623_at	AT3G45320	similar to unknown protein [Arabidopsis thaliana] (T	-2.518	0.0551	0.1348	-1.4677	0.1929	0.2278	-1.388	0.2071

252690_at	no_match	no_match	-1.4996	0.0236	0.0897	0.5025	0.2987	0.2909	-1.0654	0.0647	0.1097	0.9367	0.0902	0.113
252691_at	AT3G44050	kinesin motor protein-related	0.6298	0.638	0.4724	0.1823	0.8901	0.5158	-0.2965	0.8226	0.4704	-0.7438	0.5805	0.3563
252692_at	AT3G43960	cysteine proteinase, putative	-0.2516	0.1905	0.2558	-0.5262	0.0301	0.0863	1.0256	0.0029	0.0247	0.751	0.0091	0.0297
252693_s_at	AT3G44010;AT3G43980	[AT3G44010, 40S ribosomal protein S29 (RPS29B)	-0.01282	0.9244	0.5581	0.3749	0.0418	0.1016	0.3632	0.0459	0.0896	0.7509	0.0041	0.0205
252694_at	AT3G43630	nodulin, putative	-0.7064	0.0348	0.1078	0.2676	0.2999	0.2913	-0.5965	0.0297	0.0702	0.3774	0.1045	0.1237
252695_s_at	AT1G36040;AT3G43640	[AT1G36040, transposable element gene];[AT3G43	1.0393	0.4017	0.3761	0.4478	0.707	0.4613	0.6146	0.6089	0.401	0.02317	0.9843	0.4791
252696_at	AT3G43650	transposable element gene	-2.0467	0.1953	0.2594	-1.2436	0.3987	0.3408	0.06923	0.9606	0.5078	0.8724	0.5441	0.3425
252697_at	AT3G43660	nodulin, putative	0.4508	0.6216	0.467	-0.7168	0.4436	0.3611	0.9289	0.3329	0.2847	-0.2388	0.7913	0.4263
252698_at	AT3G43670	copper amine oxidase, putative	0.3194	0.1837	0.2508	0.6027	0.0388	0.0977	0.004367	0.9634	0.5084	0.2876	0.0325	0.0609
252699_at	AT3G43680	transposable element gene	-0.9341	0.2504	0.2937	-1.1565	0.1717	0.214	0.2877	0.6672	0.4203	0.06527	0.9213	0.4632
252700_at	AT3G43690	transposable element gene	0.6014	0.1361	0.2142	0.1138	0.7424	0.4721	-0.06985	0.8394	0.4754	-0.5574	0.1594	0.1609
252701_at	AT3G43700	ATBPM6 (BTB-POZ AND MATH DOMAIN 6); prote	0.1116	0.625	0.4682	0.5685	0.0544	0.1158	-0.6238	0.0382	0.0808	-0.1669	0.4612	0.3105
252702_at	AT3G43730	transposable element gene	0.05511	0.9655	0.5686	-0.5055	0.6948	0.457	1.3844	0.3123	0.2746	0.8238	0.5296	0.3378
252703_at	AT3G43740	leucine-rich repeat family protein	-0.1107	0.5669	0.4477	0.05814	0.7598	0.4778	0.2968	0.1701	0.1919	0.4656	0.0587	0.0874
252704_at	AT3G43750	zinc finger (C3HC4-type RING finger) family protein	0.492	0.7188	0.499	-0.02766	0.9837	0.5401	1.2504	0.1661	0.1892	0.7307	0.379	0.2753
252705_at	AT3G43760	transposable element gene	0.4504	0.6329	0.4706	-1.144	0.2599	0.2698	1.6151	0.1378	0.1695	0.0207	0.9822	0.4786
252706_at	AT3G43770	transposable element gene	0.8054	0.6925	0.4901	0.674	0.7399	0.4713	-0.6296	0.7563	0.4501	-0.7611	0.7084	0.4004
252707_at	AT3G43790	ZIFL2 (ZINC INDUCED FACILITATOR-LIKE 2); car	0.2426	0.3085	0.3277	-0.01133	0.9592	0.534	-0.2796	0.072	0.1166	-0.5335	0.0098	0.0309
252708_at	AT3G43820	pseudogene, copper amine oxidase protein family,	-1.1197	0.277	0.3099	-0.3014	0.752	0.4756	-1.7375	0.1084	0.1473	-0.9192	0.3369	0.2564
252709_at	AT3G43840	oxidoreductase, acting on the CH-CH group of donc	-0.7605	0.1533	0.2284	-0.8697	0.1145	0.1708	-0.3628	0.4484	0.3378	-0.4721	0.336	0.2561
252710_at	AT3G43860	ATGH9A4 (ARABIDOPSIS THALIANA GLYCOSYL	0.09016	0.9421	0.563	-2.054	0.1532	0.2004	1.4674	0.277	0.2563	-0.6768	0.593	0.3609
252711_at	AT3G43870	protease inhibitor/seed storage/lipid transfer protein	-1.1184	0.0139	0.0722	-1.2531	0.01	0.0544	0.9466	0.009	0.038	0.8318	0.0141	0.0376
252712_at	AT3G43900	ATGSTU27 (Arabidopsis thaliana Glutathione S-tra	-0.2522	0.193	0.2576	-0.07333	0.673	0.4496	1.0674	0.0017	0.0205	1.2463	9.00E-04	0.0118
252713_at	AT3G43810	CAM7 (CALMODULIN 7); calcium ion binding	-0.1383	0.2613	0.3004	0.2504	0.0772	0.1393	0.7794	1.00E-04	0.0118	1.1681	0	0.005
252714_x_at	AT3G43880	similar to unknown protein [Arabidopsis thaliana] (T	-1.6548	0.4463	0.3963	-2.2787	0.1424	0.1925	1.5823	0.2801	0.2581	0.3364	0.8012	0.429
252715_x_at	AT3G43900	similar to unknown protein [Arabidopsis thaliana] (T	-0.3402	0.394	0.3722	-0.5781	0.1802	0.2196	-0.04963	0.8838	0.4879	-0.2876	0.4181	0.2918
252716_at	AT3G43920	DCL3 (DICER-LIKE 3); RNA binding / ribonuclease	0.2626	0.3876	0.3685	0.1376	0.6383	0.4376	-0.3566	0.2201	0.2237	-0.4816	0.1214	0.136
252717_at	AT3G43930	similar to unknown protein [Arabidopsis thaliana] (T	0.5166	0.1732	0.2437	2.444	0.056	0.1176	-0.2949	0.7637	0.4523	0.6325	0.528	0.3371
252718_at	AT3G43940	unknown protein	0.1402	0.9095	0.5538	-0.3454	0.7805	0.4837	0.693	0.5297	0.3712	0.2074	0.8471	0.442
252719_at	AT3G43950	phosphotransferase, alcohol group as acceptor	-0.6385	0.5016	0.4212	0.8027	0.4062	0.3441	-0.8839	0.3648	0.3003	0.5573	0.5547	0.3468
252720_at	AT3G43970	similar to unknown protein [Arabidopsis thaliana] (T	-0.3368	0.7578	0.511	-0.7879	0.4825	0.3773	-0.09701	0.9288	0.5002	-0.5482	0.6194	0.3702
252721_at	AT3G43990	bromo-adjacent homology (BAH) domain-containing	0.05782	0.9685	0.5694	0.1659	0.9098	0.5215	0.06384	0.9652	0.5088	0.1719	0.9066	0.4591
252722_at	no_match	no_match	0.01153	0.9898	0.5744	-1.781	0.1028	0.1617	0.06441	0.9411	0.5037	-1.7282	0.1025	0.1223
252723_at	AT3G43520	similar to unknown protein [Arabidopsis thaliana] (T	0.236	0.0972	0.1801	-0.1364	0.2806	0.2812	0.8076	0.0018	0.0206	0.4353	0.0164	0.0409
252724_at	AT3G43540	similar to unknown protein [Arabidopsis thaliana] (T	-0.0575	0.694	0.4908	-0.487	0.0231	0.0768	0.1233	0.4157	0.3233	-0.3062	0.0874	0.1107
252725_at	AT3G43050	transposable element gene	0.6527	0.5792	0.4521	-1.4687	0.2465	0.2618	0.3848	0.7204	0.4388	-1.7367	0.1579	0.16
252726_at	AT3G43560	transposable element gene	-1.7836	0.1444	0.2208	0.2241	0.8311	0.4992	0.5418	0.6116	0.4017	2.5493	0.0608	0.0892
252727_s_at	AT1G24938;AT4G03979;A	[AT1G24938, transposable element gene];[AT4G03	-0.4845	0.7887	0.5202	1.837	0.3383	0.3129	-0.2119	0.9063	0.4941	2.1096	0.2802	0.2283
252728_at	AT3G43080	transposable element gene	0.1095	0.9191	0.5567	0.3447	0.7507	0.4751	0.3872	0.7217	0.4391	0.6224	0.572	0.3532
252729_at	AT3G43100	transposable element gene	0.1257	0.9182	0.5566	0.2493	0.8369	0.5012	0.04894	0.9618	0.5081	0.1726	0.8661	0.4472
252730_at	AT3G43110	similar to unknown protein [Arabidopsis thaliana] (T	-0.3833	0.5891	0.4559	0.6114	0.4026	0.3424	-0.04712	0.946	0.5047	0.9476	0.2208	0.1964
252731_at	AT3G43130	transposable element gene	0.3587	0.6535	0.4771	-0.8447	0.3178	0.3018	0.2927	0.7129	0.4359	-0.9108	0.2863	0.2315
252732_at	AT3G43140	transposable element gene	-2.2174	0.0898	0.1735	0.5468	0.6119	0.4275	-1.675	0.1662	0.1893	1.0891	0.3334	0.255
252733_at	AT3G43120	auxin-responsive protein-related	0.7177	0.2176	0.2736	0.4177	0.4428	0.3608	-0.1814	0.6291	0.4077	-0.4814	0.238	0.206
252734_at	AT3G43160	MEE38 (maternal effect embryo arrest 38)	0.3693	0.7775	0.5172	2.4196	0.1187	0.1742	-1.8525	0.204	0.2142	0.1978	0.8792	0.4511
252735_at	AT3G43170	similar to unknown protein [Arabidopsis thaliana] (T	-0.6562	0.5301	0.4321	0.2782	0.7855	0.4848	-0.2622	0.7681	0.4536	0.6715	0.4653	0.3121
252736_at	AT3G43210	TES (TETRASPORE); microtubule motor	0.2124	0.6177	0.4656	-0.1313	0.7552	0.4768	0.1877	0.6556	0.4164	-0.1559	0.71	0.4009
252737_at	AT3G43220	phosphoinositide phosphatase family protein	-0.3044	0.1174	0.1981	-0.2308	0.2057	0.2366	-0.4018	0.0583	0.1033	-0.3282	0.0984	0.1194
252738_at	AT3G43240	ARID/BRIGHT DNA-binding domain-containing prot	0.478	0.0833	0.1671	0.4993	0.0745	0.1369	0.08198	0.6929	0.4286	0.1033	0.6209	0.3705
252739_at	AT3G43250	cell cycle control protein-related	0.1278	0.3022	0.3244	-0.8969	0.4	0.3412	0.8285	0.4338	0.3313	1.0594	0.3287	0.2527
252740_at	AT3G43270	pectinesterase family protein	0.5485	0.115	0.1963	0.8709	0.0332	0.0903	0.03818	0.7689	0.4537	0.3605	0.0411	0.0703
252741_at	AT3G43280	similar to unknown protein [Arabidopsis thaliana] (T	-1.1766	0.2719	0.3065	-2.0397	0.0919	0.153	0.90171	0.3845	0.3098	0.03859	0.9687	0.4752
252742_at	AT3G43290	unknown protein	-0.1049	0.742	0.5065	-0.605	0.1115	0.1685	-0.09789	0.673	0.422	-0.5981	0.05	0.0792
252743_at	AT3G43300	ATMIN7 (ARABIDOPSIS THALIANA HOPM INTER	1.0052	0.0084	0.06	0.6692	0.0323	0.0889	-0.5288	0.0637	0.1087	-0.8648	0.0141	0.0377
252744_at	AT3G43310	transposable element gene, hypothetical prot	1.3907	0.3604	0.3548	0.04417	0.9754	0.5382	0.9062	0.5381	0.3745	-0.4403	0.7603	0.4168
252745_at	AT3G43230	zinc finger (FYVE type) family protein	0.2738	0.1679	0.2397	0.2369	0.2193	0.2455	0.253	0.0663	0.1114	0.2161	0.099	0.1198
252746_at	AT3G43190	SUS4; UDP-glycosyltransferase/ sucrose synthase	0.05477	0.9453	0.5635	-0.5011	0.5405	0.4009	0.08283	0.916	0.4967	-0.473	0.5563	0.3474
252747_at	AT3G43320	transposable element gene	-0.0081	0.9844	0.5731	-0.7893	0.1127	0.1697	-0.867	0.0901	0.1327	-1.6482	0.0134	0.0366
252748_at	AT3G43330	transposable element gene	-1.5917	0.3632	0.3559	0.5017	0.7628	0.4782	-2.5559	0.1751	0.1954	-0.4624	0.7807	0.4232
252749_at	AT3G43390	transposable element gene	1.0192	0.4503	0.3983	0.7367	0.5784	0.4153	0.2027	0.876	0.4856	-0.07984	0.9509	0.4712
252750_at	AT3G43420	unknown protein	-0.03431	0.9706	0.5701	2.7611	0.0342	0.0912	-1.2623	0.222	0.2247	1.5331	0.1541	0.1575
252751_at	AT3G43430	zinc finger (C3HC4-type RING finger) family protein	0.7193	0.0129	0.07	0.7072	0.0137	0.062	0.2087	0.1233	0.1589	0.1967	0.1404	0.1484
252752_s_at	AT3G43470;AT3G43480	[AT3G43470, nucleic acid binding / zinc ion binding	-1.101	0.2991	0.3225	0.02127	0.9827	0.5399	-1.1397	0.2847	0.2606	-0.0174	0.9859	0.4792
252753_at	AT3G43500	similar to unknown protein [Arabidopsis thaliana] (T	0.3355	0.7004	0.4927	-1.1048	0.2449	0.261	0.6885	0.4158	0.3233	-0.7518	0.3781	0.2748
252754_at	AT3G43510	transposable element gene	0.5366	0.0111	0.066	0.4227	0.0244	0.0785	-0.1776	0.1134	0.151	-0.2915	0.0295	0.0576
252755_at	AT3G43530	transposable element gene	0.04221	0.9768	0.5715	-1.1033	0.4644	0.3698	-0.6806	0.6443	0.4124	-1.8261	0.2521	0.2136
252756_s_at	AT1G58480;AT3G43550;A	[AT1G58480, GDSL-motif lipase, putative];[AT3G43	-3.5456	0.0195	0.0825	-3.3166	0.0241	0.0781	-1.0034	0.3451	0.2908	-0.7744	0.4556	0.3082
252757_at	AT3G42700	transposable element gene	0.203	0.7141	0.4973	-0.7438	0.2229	0.2475	1.3091	0.0642	0.1093	0.3623	0.5213	0.3344
252758_at	AT3G42710	transposable element gene	-1.0308	0.3795	0.3643	1.0651	0.3655	0.3255	-0.9861	0.0464	0.0903	1.1097	0.0327	0.0611
252759_at	AT3G42630	pentatricopeptide (PPR) repeat-containing protein	0.4127	0.0577	0.1376	0.2269	0.2205	0.2462	-0.244	0.1699	0.1918	-0.4298	0.0422	0.0716
252760_x_at	AT3G42730	transposable element gene	0.2063	0.8346	0.5339	0.1711	0.8624	0.5078	1.218	0.2586	0.2457	1.1828	0.2705	0.2229
252761_at	AT3G42770	F-box family protein	-1.3557	0.1854	0.2522	-1.7695	0.1054	0.164	-0.2919	0.7482	0.4476	-0.7057	0.4525	0.307
252762_at	AT3G42780	similar to unknown protein [Arabidopsis thaliana] (T	0.02488	0.9832	0.5728	-0.8774	0.4727	0.3733	0.7912	0.4346	0.3317	-0.1111	0.9089	0.4596
252763_at	AT3G42725	similar to unknown [Olimarabidopsis pumila] (GB:Al	-0.8495	0.1264	0.2058	-0.6858	0.195	0.2294	-0.08244	0.8019	0.4642	0.0813	0.8046	0.4301
252764_at	AT3G42790	PHD finger family protein	0.5046	0.0334	0.1058	0.6211	0.0173	0.0681	-0.2052	0.159	0.1851	-0.08867	0.4967	0.3245
252765_at	AT3G42800	similar to unknown protein [Arabidopsis thaliana] (T	-2.1113	0.0233	0.0894	-1.1158	0.1321	0.1845	0.192	0.7616	0.4516	1.1875	0.1149	0.1312
252766_at	AT3G42820	transposable element gene	0.2004	0.5427	0.438	-0.1852	0.5723	0.4128	0.1138	0.6058	0.4	-0.2718	0.2524	0.2138
252767_at	AT3G42830	ring-box protein Roc1/Rbx1/Hrt1, putative	-0.127	0.9094	0.5538	0.7699	0.5031	0.3859	-0.7715	0.5023	0.3604	0.1254	0.9105	0.46
252768_at	no_match	no_match	-0.3001	0.6414	0.4735	-0.9303	0.194	0.2287	0.1835	0.7737	0.4555	-0.4466	0.4957	0.3241
252769_at	AT3G42850	galactokinase, putative	-0.6308	0.5533	0.4421	0.5971	0.5737	0.4133	-0.9103	0.4038	0.3181	0.3177	0.7611	0.4171
252770_at	AT3G42860	zinc knuckle (CCHC-type) family protein	0.3778	0.29	0.3173	2.6695	0.001	0.0291	0.3211	0.3589	0.2974	2.6128	0.0011	0.0124
252771_at	AT3G42880	leucine-rich repeat transmembrane protein kinase,	-0.2571	0.5496	0.4409	-0.3543	0.4194	0.3504	-0.2459	0.5136	0.3645	-0.343	0.3745	0.2732
252772_at	AT3G42900	transposable element gene	0.2585	0.7947	0.5223	-1.5519	0.1704	0.2128	2.0686	0.036	0.0781	0.2582	0.7181	0.4034
252773_at	AT3G42910	transposable element gene	0.1118	0.8568	0.5404	-1.7241	0.0412	0.1009	1.4574	0.0447	0.0884	-0.3785	0.4949	0.3239
252774_at	AT3G42920	transposable element gene	-0.2357	0.8531	0.5389	-0.1771	0.8893	0.5156	0.2637	0.836	0.4743	0.3223	0.8005	0.4289
252775_s_at	AT3G42930;AT5G30545	[AT3G42930, transposable element gene];[AT5G30	0.4705	0.8177	0.5291	2.6403	0.2395	0.2573	-1.4795	0.4823	0.352	0.6903	0.7363	0.4092
252776_at	AT3G42940	similar to zinc finger (C3HC4-type RING finger) fam	1.1543	0.2293	0.2817	-2.2773	0.049	0.1097	2.2893	0.0471	0.091	-1.1422	0.2301	0.2016
252777_at	AT3G42970	unknown protein	1.1983	0.4464	0.3963	0.1511	0.9204	0.5241	-0.05047	0.9634	0.5084	-1.0977	0.3481	0.2615
252778_at	AT3G42980	transposable element gene	-0.346	0.6886	0.4887	-0.864	0.3423	0.3145	2.4943	0.0359	0.0779	1.9763	0.0695	0.0965
252779_at	AT3G42990	unknown protein	0.5616	0.5775	0.4516	0.1284	0.8966	0.5178	0.7273	0.4767	0.3502	0.2941	0.767	0.419
252780_at	AT3G42960	ATA1 (ARABIDOPSIS TAPETUM 1); oxidoreductas	0.6109	0.2789	0.3107	-0.9033	0.1379	0.1891	0.3822	0.4774	0.3504	-1.132	0.0812	0.106
252781_at	AT3G42950	glycoside hydrolase family 28 protein / polygalactur	0.1421	0.6775	0.485	-0.02224	0.9475	0.5313	0.2523	0.1469	0.1769	0.08801	0.565	0.3509
252782_at	AT3G43020	transposable element gene	-1.2084	0.4121	0.3812	0.7187	0.6153	0.4289	1.6069	0.2907	0.2639	3.534	0.0555	0.0844
252783_at	AT3G43020	transposable element gene	-0.1388	0.8547	0.5395	-1.1566	0.1792	0.2191	-0.2112	0.6819	0.4249	-1.229	0.0622	0.0905
252784_at	AT3G43040	transposable element gene	-1.126	0.2433	0.2896	1.7007	0.1078	0.1656	-0.9602	0.2932	0.2653	1.8665	0.0785	0.1036
252785_at	AT3G42660	nucleotide binding	-0.1833	0.5209	0.4293	-0.2976	0.3175	0.3016	0.3902	0.1921	0.2068	0.2759	0.3299	0.2533
252786_at	AT3G42670	CHR38 (chromatin remodeling 38); ATP binding / D	-0.2502	0.3797	0.3643	-0.2324	0.4113	0.3466	-0.4915	0.1124	0.1502	-0.4738	0.1223	0.1366
252787_at	AT3G42680	transposable element gene	-0.4419	0.7829	0.5185	-0.9776	0.55	0.4048	0.3886	0.7525	0.449	-0.1471	0.9044	0.4586
252788_at	AT3G42690	transposable element gene	-0.6707	0.6514	0.4766	-0.4504	0.7598	0.4778	-0.8837	0.5556	0.3811	-0.6634	0.6548	0.3824
252789_s_at	AT1G21930;AT3G42150	[AT1G21930, similar to unknown protein [Arabidops	0.4196	0.0123	0.0685	0.4828	0.0075	0.0488	-0.03863	0.3896	0.3119	0.02456	0.573	0.3535
252790_at	AT3G42220	transposable element gene	2.3798	0.0632	0.1441	0.925	0.3774	0.3308	0.5631	0.5785	0.3901	-0.8917	0.3932	0.2813
252791_at	AT3G42230	transposable element gene	-0.05649	0.9714	0.5702	0.5907	0.71	0.462	-1.1884	0.3239	0.2802	-0.5412	0.6357	0.3756
252792_at	AT3G42240	transposable element gene	1.4328	0.0523	0.1312	-1.4431	0.0512	0.1123	2.0065	0.0187	0.0547	-0.8694	0.1725	0.1687
252793_at	AT3G42250	transposable element gene	2.6807	0.1602	0.2336	-2.9769	0.1284	0.1819	2.3284	0.1434	0.1741	-3.3292	0.0602	0.0887
252794_at	AT3G42260	transposable element gene	-1.26	0.2044	0.265	0.1984	0.8232	0.497	-2.2874	0.0514	0.0961	-0.8291	0.3753	0.2736
252795_at	no_match	no_match	-0.9915	0.4676	0.4063	-1.9704	0.1803	0.2239	0.7381	0.5827	0.3917	-0.2408	0.8551	0.4443
252796_at	AT3G42290	transposable element gene	-0.3003	0.7489	0.5084	-1.5379	0.1539	0.201	0.3926	0.6369	0.4101	-0.8449	0.334	0.2552
252797_at	AT3G42300	transposable element gene	-0.06797	0.932	0.5603	0.972	0.2637	0.2719	0.9685	0.2651	0.2493	2.0085	0.055	0.0839
252798_at	AT3G42310	unknown protein	-1.2129	0.3609	0.3551	-0.2963	0.8136	0.4942	0.4367	0.7294	0.4416	1.3533	0.3142	0.2456
252799_at	AT3G42320	transposable element gene	-0.5892	0.304	0.3253	0.2531	0.6394	0.438	-0.2384	0.6585	0.4174	0.6039	0.2937	0.2354
252800_at	AT3G42330	transposable element gene	0.3838	0.6294	0.4696	-1.6916	0.083	0.1447	0.7744	0.3519	0.2942	-1.3011	0.1517	0.1559
252801_at	AT3G42340	transposable element gene	-0.7396	0.4843	0.4136	1.5307	0.1863	0.2239	-1.0277	0.345	0.2908	1.2427	0.2655	0.2206
252802_at	AT3G42350	transposable element gene	-0.1255	0.9183	0.5566	-0.02177	0.9858	0.5405	-0.3355	0.7849	0.4588	-0.2318	0.85	0.4428
252803_at	AT3G42360	transposable element gene	-0.9189	0.1908	0.256	0.2144	0.7322	0.4689	-0.4983	0.337	0.2869	0.6349	0.2373	0.2057
252804_at	AT3G42360	transposable element gene	0.9532	0.2586	0.2988	-0.6405	0.4266	0.3536	1.3017	0.1468	0.1768	-0.292	0.7075	0.4
252805_at	AT3G42380	unknown protein	0.1807	0.8772	0.5457	1.0403	0.3968	0.3399	-0.622	0.6011	0.3986	0.2376	0.8392	0.4398
252806_at	AT3G42390	unknown protein	-0.3449	0.7644	0.5128	0.4488	0.6978	0.4582	-0.202	0.8601	0.4811	0.5917	0.6113	0.3672
252807_at	AT3G42400	transposable element gene	-0.1094	0.9474	0.564	0.5272	0.752	0.4756	0.04278	0.9794	0.5124	0.6793	0.6851	0.3923
252808_at	AT3G42420	transposable element gene	0.205	0.6284	0.4691	0.7427	0.1309	0.1835	-0.3994	0.2335	0.2314	0.1383	0.6526	0.3817
252809_at	AT3G42430	transposable element gene	-0.3775	0.6706	0.4828	0.8938	0.339	0.3131	0.004751	0.9957	0.5165	1.2761	0.1963	0.1828
252810_at	AT3G42440	transposable element gene	0.03201	0.9681	0.5693	-2.0643	0.0517	0.1128	1.8905	0.0658	0.1109	-0.2058	0.7979	0.4282
252811_at	AT3G42460	transposable element gene	0.2146	0.5664	0.4474	-0.4798	0.2354	0.255	0.1417	0.7014	0.4317	-0.5527	0.1832	0.1754
252812_at	AT3G42480	transposable element gene	-0.8092	0.5758	0.4511	0.4743	0.7394	0.4711	-1.9311	0.1928	0.2072	-0.6477	0.6276	0.3729
252813_at	no_match	no_match	1.1848	0.433	0.3908	-0.6392	0.6629	0.446	0.692	0.6219	0.4053	-1.132	0.432	0.2977
252814_at	AT3G42530	transposable element gene	0.2168	0.8368	0.5344	-1.4367	0.2189	0.2452	1.4219	0.2228	0.2252	-0.2316	0.8259	0.4359
252815_at	AT3G42540	transposable element gene	0.8317	0.2703	0.3056	-1.005	0.1974	0.2312	-0.05604	0.9351	0.5021	-0.2294	0.7407	0.4107
252816_at	AT3G42550	aspartyl protease family protein	1.2525	0.2893	0.3169	0.9646	0.4004	0.3413	-0.3661	0.7393	0.4446	-0.6539	0.5586	0.3483
252817_at	AT3G42580	transposable element gene	0.2445	0.8175	0.529	-0.1403	0.8944	0.517	-1.9061	0.1272	0.1619	-2.291	0.0822	0.1068
252818_at	AT3G42590	transposable element gene	-0.1086	0.8764	0.5456	0.01376	0.9843	0.5402	1.5437	0.0781	0.1222	1.6661	0.0639	0.092
252819_at	AT3G42600	transposable element gene	-0.4596	0.5841	0.454	-0.3068	0.7117	0.4627	-0.7445	0.39	0.3121	-0.5917	0.4867	0.3205
252820_at	AT3G42640	AHA8 (ARABIDOPSIS H(+)-ATPASE 8); ATPase	0.7663	0.0214	0.086	-0.02543	0.909	0.5212	-1.3291	0.0018	0.0206	-2.1209	3.00E-04	0.0083
252821_at	AT3G42650	similar to unknown protein [Arabidopsis thaliana] (T	0.2192	0.4818	0.4127	0.5798	0.1098	0.1672	0.5699	0.0689	0.1137	0.9305	0.0157	0.0399
252822_at	AT3G39955	hydrolase, alpha/beta fold family protein	0.785	0.0258	0.093	0.9242	0.0151	0.0646	0.3589	0.0456	0.0894	0.4982	0.0164	0.0409
252823_at	AT3G40045	similar to unnamed protein product [Vitis vinifera] (G	-0.8068	6.00E-04	0.0332	-0.8939	4.00E-04	0.0251	-0.04198	0.6392	0.4108	-0.1291	0.1943	0.1816
252824_at	AT3G40030	histone H3.2	-0.4448	0.0122	0.0684	-0.5891	0.0045	0.0413	0.6734	0.0028	0.0241	0.5291	0.0066	0.0253
252825_at	AT3G39890	AtRABH1c (Arabidopsis Rab GTPase homolog H1c	0.5322	0.2747	0.3084	0.644	0.2006	0.2331	0.3917	0.0498	0.0944	0.5036	0.0233	0.0499
252826_at	AT3G40050	signal transducer	0.2521	0.2571	0.2978	-0.1038	0.6155	0.429	-0.2413	0.0605	0.1056	-0.5973	0.003	0.0179
252827_at	AT3G39950	CYP79B2 (cytochrome P450, family 79, subfamily B	0.4474	0.3536	0.3515	0.5601	0.2832	0.2826	0.3326	0.0127	0.0449	0.4196	0.0057	0.0235
252828_at	AT3G39960	DNAJ heat shock family protein	-0.1625	0.4055	0.3781	-0.1581	0.4172	0.3493	-0.1907	0.306	0.2717	-0.1863	0.3158	0.2464
252829_at	AT3G40060	ATHB-16/ATHB16 (ARABIDOPSIS THALIANA HOI	0.4965	0.0136	0.0719	0.3523	0.0405	0.0998	-0.09405	0.3882	0.3113	-0.2383

252890_at	AT4G39400	BR1 (BRASSINOSTEROID INSENSITIVE 1); kinas	0.08594	0.5036	0.422	-0.04514	0.7194	0.4652	-0.3573	0.038	0.0805	-0.4884	0.014	0.0376
252891_at	AT4G39410	WRKY13 (WRKY DNA-binding protein 13); transcri	0.08206	0.8448	0.5371	0.6209	0.1894	0.226	-0.03519	0.933	0.5014	0.5036	0.2693	0.2224
252892_at	AT4G39420	similar to unnamed protein product [Vitis vinifera] (G	-0.01281	0.9791	0.572	-0.3973	0.4364	0.3581	0.3372	0.504	0.3609	-0.04724	0.9231	0.4636
252893_at	AT4G39430	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.3932	0.6762	0.4847	0.8324	0.395	0.3391	0.1766	0.8004	0.4636	0.6158	0.3995	0.2841
252894_at	AT4G39440	similar to unnamed protein product [Vitis vinifera] (G	-0.9098	0.2544	0.2961	1.2807	0.1345	0.1864	-0.07913	0.9135	0.4961	2.1113	0.0367	0.0652
252895_at	AT4G39450	similar to predicted protein [Physcomitrella patens s	0.6137	0.0526	0.1316	0.2975	0.2569	0.2683	-1.0763	0.0077	0.0353	-1.3926	0.003	0.0178
252896_at	AT4G39480	CYP96A9 (cytochrome P450, family 96, subfamily A	-0.8008	0.2042	0.2649	0.01385	0.9803	0.5393	-0.7925	0.1297	0.1637	0.02216	0.9601	0.4733
252897_at	AT4G39490	CYP96A10 (cytochrome P450, family 96, subfamily	-0.9161	0.555	0.4428	-1.5141	0.3475	0.3168	1.1531	0.4634	0.3447	0.555	0.7165	0.403
252898_at	AT4G39500	CYP96A11 (cytochrome P450, family 96, subfamily	-0.07172	0.9395	0.5622	-1.7969	0.1128	0.1697	1.1228	0.2744	0.2548	-0.6024	0.5344	0.3396
252899_at	AT4G39530	pentatricopeptide (PPR) repeat-containing protein	-0.2434	0.5254	0.4314	0.4173	0.2996	0.2912	-0.293	0.4157	0.3233	0.3678	0.3185	0.2476
252900_at	AT4G39540	shikimate kinase family protein	-0.3566	0.0471	0.1249	-0.1488	0.3022	0.2926	0.3211	0.0631	0.108	0.5289	0.0136	0.0371
252901_at	AT4G39550	kelch repeat-containing F-box family protein	0.3828	0.0378	0.1121	0.2291	0.1414	0.1918	-0.432	0.0156	0.0498	-0.5858	0.0054	0.023
252902_at	AT4G39560	kelch repeat-containing F-box family protein	-0.1981	0.5141	0.4269	-0.2964	0.3449	0.3156	-0.6445	0.0699	0.1147	-0.7428	0.0472	0.0765
252903_at	AT4G39570	kelch repeat-containing F-box family protein	-0.00313	0.9805	0.5721	-0.01096	0.9321	0.527	0.1405	0.3093	0.2731	0.1327	0.3336	0.2551
252904_at	AT4G39620	EMB2453 (EMBRYO DEFECTIVE 2453)	-0.4076	0.0045	0.0486	-0.2867	0.0155	0.0651	-0.3748	0.0011	0.0183	-0.2539	0.0048	0.0219
252905_at	AT4G39720	VQ motif-containing protein	-0.3329	0.1493	0.225	-0.5453	0.0433	0.1032	0.5746	0.0371	0.0794	0.3622	0.1245	0.1379
252906_at	AT4G39940	GGT1 (GAMMA-GLUTAMYL TRANSPEPTIDASE 1	-0.1783	0.3424	0.3461	-0.8416	0.6381	0.4375	-0.3103	0.1066	0.1462	-0.2162	0.2217	0.197
252907_at	AT4G39650	GGT2 (GAMMA-GLUTAMYL TRANSPEPTIDASE 2	0.4707	0.5967	0.4586	0.07692	0.9298	0.5266	0.2697	0.6502	0.4145	-0.1241	0.8328	0.438
252908_at	AT4G39670	glycolipid binding / glycolipid transporter	1.0024	0.0568	0.1367	1.7749	0.0093	0.0528	0.01666	0.9639	0.5085	0.7892	0.0847	0.1087
252909_at	AT4G39680	SAP domain-containing protein	0.08287	0.5568	0.4436	-0.3732	0.0449	0.105	-0.2077	0.0812	0.1249	-0.6638	0.0018	0.0147
252910_at	AT4G39590	kelch repeat-containing F-box family protein	-0.8587	0.5502	0.4412	-0.6596	0.643	0.4392	-0.4167	0.2246	0.2263	-0.2176	0.4953	0.324
252911_at	AT4G39510	CYP96A12 (cytochrome P450, family 96, subfamily	-0.4726	0.0134	0.0712	-1.3042	0.02	0.0724	-0.3625	0.118	0.1546	-0.1942	0.3474	0.2613
252912_at	AT4G39200	40S ribosomal protein S25 (RPS25E)	0.3491	0.196	0.2597	0.5126	0.0851	0.1469	-0.012	0.9601	0.5076	0.1515	0.5379	0.3406
252913_at	AT4G39220	ATRER1A (Arabidopsis thaliana endoplasmic reticu	0.5204	0.0122	0.0685	0.5809	0.0083	0.0506	0.5276	0.0089	0.0378	0.5881	0.0061	0.0242
252914_at	AT4G39130	dehydrin family protein	0.24	0.8152	0.5284	-1.1062	0.013	0.0608	1.4526	0.2056	0.2152	-2.4138	0.0661	0.0936
252915_at	AT4G38810	calcium-binding EF hand family protein	-0.9962	0.0082	0.0591	-0.7023	0.0263	0.0811	-0.1745	0.3931	0.3134	0.1195	0.5484	0.3445
252916_at	AT4G38950	kinesin motor family protein	-0.5877	0.0598	0.1399	-1.0607	0.0093	0.0528	-1.0134	0.0109	0.0414	-1.4864	0.0028	0.0172
252917_at	AT4G38960	zinc finger (B-box type) family protein	-0.8435	0.0158	0.0758	-0.618	0.0419	0.1018	-0.08386	0.7093	0.4346	0.1417	0.5359	0.34
252918_at	AT4G38980	unknown protein	0.2338	0.1137	0.1954	0.4147	0.0232	0.0768	-0.2488	0.095	0.1368	-0.06787	0.5844	0.3578
252919_at	AT4G38990	pseudogene of a glycosyl hydrolase family 9 protei	-1.2132	0.238	0.2863	-2.7735	0.0339	0.091	0.7979	0.4136	0.3224	-0.7623	0.4329	0.2981
252920_at	AT4G39030	ATGH9B7 (ARABIDOPSIS THALIANA GLYCOSY	0.2769	0.0823	0.1659	-0.943	0.354	0.3201	1.0635	0.1884	0.2046	-1.9564	0.0435	0.0729
252921_at	AT4G39033	EDS5 (ENHANCED DISEASE SUSCEPTIBILITY 5	0.3726	0.2803	0.3114	0.4232	0.2294	0.2511	-0.3159	0.3195	0.2781	-0.2653	0.3943	0.2819
252922_at	AT4G39040	similar to unknown protein [Arabidopsis thaliana] (T	-0.3912	0.0077	0.0582	-0.5263	0.0026	0.0342	0.07838	0.3768	0.3061	-0.05675	0.5119	0.3305
252923_at	no_match	no_match	-0.1198	0.4973	-0.1044	0.7488	0.4747	-0.6711	0.0922	0.1344	-0.6557	0.0976	0.1187	
252924_at	AT4G39070	zinc finger (B-box type) family protein	0.3918	0.2992	0.3225	0.01796	0.959	0.534	0.3758	0.3168	0.2766	0.001963	0.9955	0.4816
252925_at	AT4G39100	SHL1 (SHORT LIFE)	-0.1203	0.5187	0.4287	0.2029	0.2993	0.291	-0.2093	0.145	0.1753	0.1139	0.3812	0.2763
252926_at	AT4G39220	ATVHA-A3 (VACUOLAR-type H(+)-ATPase C2	0.9043	0.4913	0.4163	-0.1231	0.422	0.3515	-0.08446	0.6573	0.3878	-0.1033	0.495	0.3239
252927_at	AT4G39090	RD19 (RESPONSIVE TO DEHYDRATION 19); cys	0.3977	0.2035	0.2643	0.5138	0.1213	0.1766	0.4326	0.0306	0.0712	0.5488	0.0142	0.0378
252928_at	AT4G38940	kelch repeat-containing F-box family protein	0.2217	0.4442	0.3952	0.4467	0.1627	0.2078	-0.5476	0.0577	0.1026	-0.3225	0.1951	0.182
252929_at	AT4G38970	fructose-bisphosphate aldolase, putative	-0.497	0.0074	0.0576	-0.5935	0.0039	0.0391	-0.1041	0.3506	0.2936	-0.2006	0.1117	0.1288
252930_at	AT4G39010	ATGH9B18 (ARABIDOPSIS THALIANA GLYCOSY	-0.3312	0.5073	0.4241	-0.7562	0.1722	0.2143	-0.01161	0.9809	0.5129	-0.4366	0.392	0.2807
252931_at	AT4G38930	ubiquitin fusion degradation UFD1 family protein	0.1041	0.0974	0.1802	0.1464	0.0388	0.0977	0.2834	0.0042	0.0279	0.3256	0.0025	0.0167
252932_at	AT4G39080	VHA-A2 (VACUOLAR PROTON ATPASE A3); ATP	0.08088	0.9962	0.6761	-0.3778	0.0933	0.1539	-0.4097	0.0761	0.1202	-0.7866	0.0103	0.0317
252933_at	AT4G39110	protein kinase family protein	0.8631	0.4753	0.41	1.0101	0.4092	0.3455	-0.1595	0.8914	0.4901	-0.01242	0.9915	0.4805
252934_at	AT4G39120	inositol monophosphatase family protein	-0.5926	0.0954	0.1784	-0.6097	0.089	0.1504	-0.3137	0.259	0.2458	-0.3308	0.238	0.206
252935_at	AT4G39150	DNAJ heat shock N-terminal domain-containing pro	-0.08038	0.5359	0.4354	-0.1078	0.4156	0.3487	0.409	0.0243	0.0632	0.3816	0.0302	0.0584
252936_at	AT4G39160	DNA binding / transcription factor	0.2758	0.2571	0.2978	0.4213	0.1139	0.1704	-0.08003	0.6531	0.4156	0.06544	0.712	0.4016
252937_at	AT4G39180	SEC14 (secretion 14)	0.5345	0.081	0.1645	1.4811	0.003	0.0357	0.3443	0.1481	0.1777	1.2908	0.0026	0.0168
252938_at	AT4G39190	similar to unknown protein [Arabidopsis thaliana] (T	2.2328	0	0.0312	3.1595	0	0.0249	-0.1893	0.1487	0.1782	0.7373	0.0023	0.0158
252939_at	AT4G39230	isoflavone reductase, putative	0.498	0.1629	0.2361	0.7505	0.0617	0.1235	0.3698	0.1345	0.1671	0.6223	0.0345	0.0628
252940_at	AT4G39270	leucine-rich repeat transmembrane protein kinase,	1.3778	0.0281	0.0971	1.3363	0.0309	0.0873	-0.09756	0.8233	0.4706	-0.139	0.7512	0.4142
252941_at	AT4G39280	phenylalanyl-tRNA synthetase, putative / phenylala	0.3012	0.0312	0.1026	-0.03643	0.7139	0.4633	0.1727	0.1355	0.168	-0.165	0.1492	0.1541
252942_at	AT4G39300	similar to unknown protein [Arabidopsis thaliana] (T	0.1029	0.4288	0.3885	0.305	0.0595	0.1212	0.5667	0.0084	0.0367	0.7689	0.0028	0.0173
252943_at	AT4G39330	mannitol dehydrogenase, putative	-0.4668	0.2088	0.2673	-0.7311	0.0747	0.1371	0.6716	0.0172	0.0524	0.3973	0.081	0.1058
252944_at	AT4G39320	microtubule-associated protein, putative	0.1215	0.9247	0.6582	1.1129	0.4091	0.3455	1.2745	0.3509	0.2938	2.2659	0.134	0.1443
252945_at	AT4G39140	protein binding / zinc ion binding	0.6551	0.0019	0.0391	0.4267	0.0092	0.0524	-0.419	0.0035	0.026	-0.6474	7.00E-04	0.0105
252946_at	AT4G39235	similar to unknown protein [Arabidopsis thaliana] (T	-1.0593	0.0194	0.0823	-0.7766	0.0501	0.1111	0.3815	0.2446	0.2378	0.6642	0.0766	0.1021
252947_at	AT4G38600	KAK (KAKTUS)	0.577	0.0351	0.1082	0.3356	0.1425	0.1926	-0.6913	0.0199	0.0566	-0.9328	0.0072	0.0264
252948_at	AT4G38600	KAK (KAKTUS)	-2.3971	0.0181	0.0804	-0.2681	0.6879	0.4548	-3.6439	0.0033	0.0254	-1.5149	0.0592	0.0878
252949_at	AT4G38670	pathogenesis-related thaumatin family protein	0.2621	0.0388	0.1136	-0.3803	0.0117	0.0583	0.2818	0.0031	0.0249	-0.3606	0.0012	0.0129
252950_at	AT4G38690	1-phosphatidylinositol phosphodiesterase-related	-1.1966	0.0047	0.0496	-1.2501	0.004	0.0395	0.337	0.1179	0.1546	0.2835	0.17	0.1673
252951_at	AT4G38700	disease resistance-responsive family protein	0.1045	0.6414	0.4735	0.02007	0.9277	0.5261	0.5781	0.0162	0.0508	0.4937	0.027	0.0547
252952_at	AT4G38710	glycine-rich protein	-0.07549	0.7119	0.497	0.1109	0.5915	0.4201	0.232	0.2556	0.244	0.4183	0.0751	0.1009
252953_at	AT4G38570	PIS2 (PIG8ABLE CDP-DIACYLGLYCEROL--INOS	-0.293	0.0936	0.1772	-0.7588	0.0048	0.0419	0.05782	0.4686	0.3468	-0.408	0.0049	0.022
252954_at	AT4G38660	thaumatin, putative	-0.8441	0.0562	0.136	-0.951	0.0399	0.099	0.06797	0.6892	0.4276	-0.03893	0.8175	0.4336
252955_at	AT4G38630	RPN10 (REGULATORY PARTICLE NON-ATPASE	0.7704	0.006	0.0536	0.7562	0.0064	0.0457	-0.3403	0.0784	0.1224	-0.3545	0.0705	0.0973
252956_at	AT4G38580	ATFP6 (FARNESYLATED PROTEIN 6); metal ion	0.2763	0.0064	0.0547	0.9796	0.0022	0.0333	0.9853	0.0013	0.0188	1.2356	5.00E-04	0.0096
252957_at	AT4G38680	CSDP2/GRP2 (COLD SHOCK DOMAIN PROTEIN	-0.02498	0.9459	0.5636	0.2213	0.5569	0.4072	-0.0695	0.8505	0.4786	0.1768	0.636	0.3757
252958_at	AT4G38620	MYB4 (myb domain protein 4); transcription factor	-0.8121	0.0527	0.1317	-1.1552	0.0179	0.0693	0.8284	0.0305	0.0711	0.4854	0.127	0.1396
252959_at	AT4G38640	choline transporter-related	0.2386	0.0981	0.1809	0.1352	0.2903	0.2867	-0.2396	0.0971	0.1386	-0.343	0.0366	0.0651
252960_at	AT4G38750	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.375	0.0625	0.1436	-0.2504	0.1623	0.2076	-0.6892	0.0011	0.0181	-1.3146	1.00E-04	0.0058
252961_at	AT4G38760	similar to unnamed protein product [Vitis vinifera] (G	0.3787	0.5372	0.4358	-0.7989	0.228	0.2502	0.6675	0.3005	0.269	-0.5101	0.4152	0.2905
252962_at	AT4G38730	splicing factor, putative	-0.3059	0.3037	0.325	0.07146	0.7966	0.4886	-0.1495	0.5735	0.3879	0.2278	0.4037	0.2857
252963_at	AT4G38820	unknown protein	-0.06049	0.9382	0.5618	-1.2095	0.1743	0.2156	3.1006	8.00E-04	0.0162	1.9516	0.0044	0.0211
252964_at	AT4G38830	protein kinase family protein	-0.2499	0.5518	0.4419	0.09811	0.8115	0.4934	0.1735	0.6682	0.4207	0.5216	0.2374	0.2058
252965_at	AT4G38860	auxin-responsive protein, putative	-0.5136	0.0485	0.1268	-0.3056	0.1702	0.2127	0.2598	0.1507	0.1794	0.4678	0.0331	0.0614
252966_at	AT4G38870	F-box family protein	0.6465	0.3079	0.3274	0.03963	0.9464	0.531	0.3768	0.5336	0.3726	-0.2301	0.6991	0.3971
252967_at	AT4G38880	ATASE3 (GLN PHOSPHORIBOSYL PYROPHOSP	-0.5554	0.1241	0.2041	-0.5248	0.1405	0.191	-0.4955	0.1583	0.1845	-0.4649	0.1794	0.1729
252968_at	AT4G38890	dihydrouridine synthase family protein	0.706	5.00E-04	0.032	0.1817	0.0554	0.1169	0.1338	0.12	0.1562	-0.3905	0.0045	0.0213
252969_at	AT4G38900	bZIP protein	0.01004	0.9413	0.5629	0.4695	0.0215	0.0746	-0.1666	0.1579	0.1843	0.2929	0.0381	0.0668
252970_at	AT4G38850	SAUR_AC1 (SMALL AUXIN UP RNA 1 FROM ARA	-0.3484	0.5464	0.4396	-0.2036	0.7202	0.4655	0.5772	0.1504	0.1792	0.722	0.0905	0.1132
252971_at	AT4G38770	PRP4 (PROLINE-RICH PROTEIN 4)	-0.9985	0.0052	0.0514	-1.5221	0.0011	0.0293	0.5638	0.0014	0.0197	0.04017	0.6069	0.3657
252972_at	AT4G38840	auxin-responsive protein, putative	-0.724	0.0011	0.036	-0.7445	0.001	0.0291	-0.07343	0.4414	0.3347	-0.09393	0.3362	0.2562
252973_s_at	AT4G38740	ROC1 (rotamase CyP 1); peptidyl-prolyl cis-trans is	-0.5622	0.0101	0.064	-0.4703	0.0184	0.0702	0.6159	0.0071	0.0341	0.7077	0.0043	0.0208
252974_at	AT4G38800	ATMTN1; catalytic/ methylthioribose kinase/ nucleosida	0.199	0.3794	0.3642	0.2819	0.2346	0.2546	-1.1471	0.0047	0.0292	-1.0643	0.0062	0.0244
252975_s_at	AT4G38430	ATROPGEF1/ROPGEF1 (KINASE PARTNER PRO	-0.4057	0.1833	0.2506	-0.7495	0.0412	0.1008	0.2083	0.1017	0.1425	-0.1355	0.2406	0.2074
252976_s_at	AT4G38550	similar to unknown protein [Arabidopsis thaliana] (T	0.3687	0.406	0.3784	0.4678	0.3044	0.2938	0.008305	0.9766	0.5117	0.1074	0.7067	0.3997
252977_at	AT4G38560	similar to pEARL14 [Arabidopsis thaliana] (TAIR:AT2	1.0743	0.0371	0.111	1.7373	0.0076	0.0489	-0.2777	0.4711	0.3481	0.3853	0.3319	0.2543
252978_at	AT4G38590	BGAL14 (beta-galactosidase 14); beta-galactosidas	-0.9832	0.0998	0.1823	-0.928	0.1143	0.1707	-0.2965	0.555	0.3809	-0.2414	0.6281	0.3731
252979_at	AT4G38225	similar to unnamed protein product [Vitis vinifera] (G	-0.2602	0.1976	0.2611	-0.6168	0.0216	0.0747	0.2473	0.2162	0.2214	-0.1094	0.5518	0.3457
252980_at	AT4G38040	exostosin family protein	-0.02228	0.8135	0.5278	-0.303	0.0266	0.0816	0.1434	0.1575	0.184	-0.1373	0.1719	0.1684
252981_at	AT4G38260	similar to unknown protein [Arabidopsis thaliana] (T	0.7458	0.0091	0.0616	0.7915	0.0074	0.0485	-0.4127	0.0417	0.085	-0.367	0.0582	0.087
252982_at	AT4G38130	HD1 (HISTONE DEACETYLASE19); histone deace	0.2607	0.15	0.2255	0.2449	0.1702	0.2127	-0.00267	0.9864	0.5143	-0.01846	0.9059	0.459
252983_at	AT4G38970	ELI3-1 (ELICITOR-ACTIVATED GENE 3); binding	-1.5067	0.0037	0.0459	-1.498	0.0038	0.0389	0.3218	0.0924	0.1346	0.3305	0.0865	0.1101
252984_at	AT4G37990	ELI3-2 (ELICITOR-ACTIVATED GENE 3)	0.6175	0.1191	0.1995	0.9984	0.033	0.09	-0.03195	0.9196	0.4977	0.349	0.3057	0.2413
252985_at	AT4G38350	patched family protein	0.1361	0.5663	0.4474	-0.00843	0.971	0.5369	-1.1498	0.0062	0.0327	-1.2943	0.004	0.0204
252986_at	AT4G38380	MATE efflux protein-related	0.8564	0.3006	0.3233	0.2601	0.7363	0.4701	-0.3802	0.5851	0.3927	-0.9755	0.2028	0.1868
252987_at	AT4G38390	similar to unknown protein [Arabidopsis thaliana] (T	-1.2086	0.2176	0.2736	-0.8534	0.3603	0.3228	0.3288	0.7111	0.4352	0.6841	0.4545	0.3078
252988_at	AT4G38410	dehydrin, putative	0.2625	0.8453	0.5372	0.7929	0.5636	0.4097	0.2738	0.8387	0.4752	0.8043	0.5583	0.3482
252989_at	AT4G38420	Sk39 (SKU5 Similar 9); copper ion binding / oxidore	-0.2998	0.2612	0.3003	-1.0107	0.0116	0.0581	-0.3771	0.1754	0.1956	-1.0881	0.009	0.0296
252990_at	AT4G38440	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.2589	0.3564	0.3529	0.3794	0.2015	0.2336	-0.7206	0.0269	0.0667	-0.6001	0.0467	0.076
252991_at	AT4G38470	protein kinase family protein	-0.2051	0.3724	0.3607	-0.2638	0.2663	0.2734	0.04315	0.8431	0.4766	-0.01557	0.9429	0.4692
252992_at	AT4G38520	protein phosphatase 2C family protein / PP2C famil	0.3255	0.2135	0.2706	0.1496	0.5343	0.3981	-0.2395	0.1072	0.1466	-0.4154	0.023	0.0494
252993_at	AT4G38540	monooxygenase, putative (MO2)	1.2044	0.0711	0.1538	1.3982	0.0472	0.1079	-0.2903	0.4516	0.3394	-0.09654	0.7955	0.4275
252994_at	AT4G38480	transducin family protein / WD-40 repeat family prot	0.04613	0.8838	0.5471	0.4061	0.2423	0.2593	-0.09218	0.7712	0.4545	0.2678	0.4171	0.2913
252995_at	AT4G38370	phosphoglycerate/bisphosphoglycerate mutase fam	-0.4905	0.0331	0.1055	-0.4715	0.0373	0.0955	-0.284	0.0041	0.0274	-0.265	0.0052	0.0226
252996_s_at	AT4G38460	GGR (GERANYLGERANYL REDUCTASE); farnes	0.6771	0.026	0.0933	0.3773	0.1269	0.1806	0.4035	0.0748	0.1191	0.1037	0.5717	0.3531
252997_at	AT4G38400	ATEXLA2 (ARABIDOPSIS THALIANA EXPANSIN-L	-1.0209	0.2981	0.3222	-0.9201	0.3421	0.3145	0.1599	0.2149	0.2207	0.2607	0.0743	0.1002
252998_at	AT4G38510	VACUOLAR ATP SYNTHASE SUBUNIT B2); hydr	1.443	0.5265	0.4318	-0.2007	0.3897	0.3366	-0.06154	0.7823	0.4581	-0.4066	0.1226	0.1369
252999_at	AT4G38500	similar to unknown protein [Arabidopsis thaliana] (T	0.2845	0.1251	0.2047	0.05605	0.7224	0.4661	0.3296	0.0507	0.0954	0.1012	0.4439	0.3033
253000_at	AT4G38360	similar to unknown protein [Arabidopsis thaliana] (T	0.01782	0.9231	0.5579	0.1654	0.3944	0.3388	-0.7424	0.0129	0.0451	-0.5949	0.0266	0.054
253001_at	AT4G38630	similar to Os03g0455200 [Oryza sativa (japonica cu	0.3171	0.0178	0.08	0.1437	0.1534	0.2006	-0.4859	9.00E-04	0.0169	-0.6592	3.00E-04	0.0081
253002_at	AT4G38530	ATPLC1 (PHOSPHOLIPASE C 1); phosphoinositide C	0.1966	0.2778	0.3101	0.01798	0.9141	0.5225	-0.1267	0.4198	0.3253	-0.3053	0.0964	0.1178
253003_s_at	AT4G38530,AT4G38650	[AT4G38300, glycosyl hydrolase family 10 protein];[	0.01559	0.9714	0.5702	0.6313	0.1973	0.2312	-0.8097	0.0761	0.1202	-0.1628	0.6574	0.3833
253004_at	AT4G38280,AT4G38330,A	[AT4G38280, similar to unknown protein [Arabidops	0.2971	0.3286	0.3392	0.171	0.5571	0.4072	0.03727	0.8882	0.4891	-0.08886	0.739	0.4101
253005_at	AT4G38100	threonine endopeptidase	0.09723	0.6995	0.4923	0.02583	0.9175	0.5235	0.2061	0.1023	0.1428	0.1347	0.2397	0.2069
253006_at	AT4G38090	amino acid transporter family protein	-0.1874	0.1773	0.2463	-0.3785	0.0298	0.0858	-0.2753	0.0742	0.1186	-0.4863	0.0152	0.0393
253007_at	AT4G38080	similar to unnamed protein product [Vitis vinifera] (G	0.06612	0.6975	0.4918	0.1244	0.4759	0.3745	-0.329	0.1062	0.1458	-0.2707	0.1623	0.1626
253008_at	AT4G38210	ATEXPA20 (ARABIDOPSIS THALIANA EXPANSIN	2.225	0.0557	0.1355	1.6873	0.1127	0.1697	0.1667	0.5469	0.3781	-0.3711	0.2172	0.1948
253009_at	AT4G38220	SHM1 (SERINE HYDROXYMETHYLTRANSFERA	0.6028	0.0036	0.0465	0.8267	6.00E-04	0.027	0.009715	0.9277	0.5	-0.3171	0.0103	0.0317
253010_at	AT4G37750	ANT (AINTEGUMENTA); DNA binding / transcriptio	0.6521	0.0644	0.1453	0.1014	0.7136	0.4632	0.2266	0.1491	0.1784	-0.3241	0.0633	0.0914
253011_at	AT4G37890	EDA40 (embryo sac development arrest 40); protei	0.1953	0.5731	0.4501	0.07812	0.8185	0.4954	0.09808	0.7013	0.4317	-0.01914	0.9397	0.4684
253012_at	AT4G37900	glycine rich protein	0.4642	0.0566	0.1363	2.0755	0.0388	0.1503	0.03634	0.9706	0.5101	-0.3523	0.7233	0.4051
253013_at	AT4G37910	MTHSC70-1 (mitochondrial heat shock protein 70-1	0.4849	0.01	0.064	0.0942	0.4219	0.3514	-0.1999	0.1307	0.1644	-0.5906	0.005	0.0221
253014_at	AT4G37940	AGL21 (AGAMOUS-LIKE 21); transcription factor	0.2269	0.5993	0.4594	-0.05626	0.8945	0.5171	-0.1799	0.5388	0.3748	-0.4631	0.159	0.1606
253015_at	AT4G37950	lyase	0.2183	0.8741	0.6128	-0.102	0.478	0.3755	0.2108	0.8783	0.4862	-1.0177	0.475	0.3157
253016_at	AT4G37960	lyase	0.2212	0.6128	0.4636	-0.4899	0.2916	0.2874	0.3792	0.4007	0.3169	-0.3319	0.4571	0.3089
253017_at	AT4G37970	mannitol dehydrogenase, putative	0.1171	0.6497	0.4762	0.4341	0.1433	0.1932	0.06793	0.7902	0.4602	0.3849	0.1823	0.1748
253018_at	AT4G38000	Dof-type zinc finger domain-containing protein	0.07361	0.8663	0.5425	0.6365	0.1958	0.2299	-0.4432	0.0855	0.2886	0.1196	0.7851	0.4243
253019_at	AT4G38010	pentatricopeptide (PPR) repeat-containing protein	0.1421	0.7096	0.4961	0.1968	0.6092	0.4268	-0.7034	0.0855	0.129	-0.6487	0.1042	0.1236
253020_at	AT4G38020	tRNA/rRNA methyltransferase (SpoU) family protein	0.01759	0.9443	0.5635	0.3995	0.1668	0.2103	-0.00211	0.9829	0.5134	0.3798	0.0148	0.0386
253021_at	AT4G38060	transmembrane transporter	0.2447	0.2793	0.311	0.2562	0.2606	0.2701	0.01164	0.9443	0.5043	0.02315	0.8897	0.4541
253022_at	AT4G38060	similar to unknown protein [Arabidopsis thaliana] (T	0.2372	0.4432	0.3951	0.6465	0.0814	0.143	-0.

253090_at	AT4G36360	BGAL3 (beta-galactosidase 3); beta-galactosidase	-1.0114	0.044	0.121	-1.2005	0.0262	0.0809	-0.2963	0.1011	0.142	-0.4855	0.0254	0.0527
253091_at	AT4G37360	CYP81D2 (cytochrome P450, family 81, subfamily	0.402	0.5195	0.4289	-0.04508	0.9408	0.5293	0.09602	0.8744	0.4852	-0.3511	0.5712	0.353
253092_at	AT4G37380	pentatricopeptide (PPR) repeat-containing protein	-0.16	0.7332	0.5033	0.6973	0.1863	0.2239	-0.9846	0.0877	0.1307	-0.1272	0.7858	0.4245
253093_at	AT4G37460	binding	0.4795	0.0052	0.0514	0.208	0.0745	0.1369	-0.5566	0.003	0.0248	-0.8281	7.00E-04	0.0105
253094_at	AT4G37480	DNAJ heat shock N-terminal domain-containing pro	-0.1104	0.727	0.5015	0.6806	0.0822	0.1438	-1.4989	0.0071	0.0341	-0.7079	0.0743	0.1001
253095_at	AT4G37510	ribonuclease III family protein	-0.06405	0.3466	0.3482	-0.1957	0.0312	0.0877	0.3133	0.0065	0.0331	0.1816	0.0391	0.0681
253096_at	AT4G37330	CYP81D4 (cytochrome P450, family 81, subfamily [	-0.09016	0.6916	0.4898	-0.2034	0.3903	0.3369	-0.3274	0.0394	0.082	-0.4406	0.0154	0.0395
253097_at	AT4G37320	CYP81D5 (cytochrome P450, family 81, subfamily [	-0.08484	0.8018	0.5246	-0.2086	0.5458	0.4029	-0.1639	0.5965	0.3969	-0.2876	0.3705	0.2715
253098_at	AT37340	CYP81D3 (cytochrome P450, family 81, subfamily [	-0.5727	0.364	0.3562	-0.7166	0.2696	0.2753	0.6466	0.3123	0.2746	0.5027	0.4199	0.2925
253099_s_at	AT4G37530;AT4G37520	[AT4G37530, peroxidase, putative];[AT4G37520, pe	0.5518	0.3501	0.3497	1.1161	0.0993	0.159	0.4298	0.0836	0.1272	0.9942	0.0061	0.0242
253100_at	AT4G37400	CYP81F3 (cytochrome P450, family 81, subfamily F	-0.01039	0.9749	0.571	-0.1389	0.6776	0.4511	0.206	0.0193	0.0557	0.07746	0.2275	0.2002
253101_at	AT37430	CYP91A2 (CYTOCHROME P450 MONOOXYGEN	0.1442	0.7008	0.4929	0.3018	0.4361	0.358	-0.678	0.0303	0.0708	-0.5204	0.0651	0.0929
253102_at	AT4G36105	similar to unknown protein [Arabidopsis thaliana] (T	-1.0857	0.1092	0.1913	-1.3889	0.0583	0.1201	-0.1523	0.7875	0.4594	-0.4556	0.4373	0.3001
253103_at	AT4G36110	auxin-responsive protein, putative	-0.4408	0.2216	0.2761	-0.1215	0.7105	0.4623	-0.4647	0.041	0.0841	-0.1454	0.4049	0.286
253104_at	AT4G36010	pathogenesis-related thaumatin family protein	-0.3833	0.5897	0.456	-0.04087	0.9532	0.5326	0.2429	0.0726	0.1171	0.5853	0.0043	0.0208
253105_at	no_match	no_match	1.5236	8.00E-04	0.0336	1.4414	9.00E-04	0.0288	0.3159	0.1277	0.1624	0.2338	0.229	0.201
253106_at	AT4G35870	similar to early-responsive to dehydration protein-re	-0.1444	0.361	0.3551	-0.1728	0.2849	0.2838	0.09753	0.1841	0.2015	0.06907	0.3195	0.2481
253107_at	AT4G35880	aspartyl protease family protein	-0.4387	0.0397	0.1149	-0.1282	0.4291	0.3549	-0.231	0.1369	0.169	0.07955	0.5572	0.3478
253108_at	AT4G35900	FD; DNA binding / transcription factor	-0.5632	0.6355	0.4714	-0.5712	0.6308	0.4349	0.6623	0.5643	0.3844	0.6543	0.5688	0.3523
253109_at	AT4G35920	MCA1 (MID1-COMPLEMENTING ACTIVITY 1)	-0.8167	0.0143	0.073	-1.0032	0.007	0.0474	0.1816	0.3016	0.2694	-0.00488	0.9761	0.4772
253110_at	AT4G35930	Identical to F-box protein At4g35930 [Arabidopsis T	0.3482	0.518	0.4285	0.6366	0.2653	0.2728	-0.1674	0.5397	0.3752	0.121	0.6536	0.382
253111_at	AT4G35940	similar to unknown protein [Arabidopsis thaliana] (T	0.312	0.1154	0.1966	-0.04268	0.7974	0.4887	-0.1891	0.2854	0.2609	-0.5438	0.0239	0.0508
253112_at	AT4G35970	APX5; L-ascorbate peroxidase/ peroxidase	0.1805	0.2815	0.3122	0.1696	0.3074	0.2959	0.5349	0.0052	0.0303	0.524	0.0056	0.0234
253113_at	AT4G35985	senescence/dehydration-associated protein-related	0.1966	0.5993	0.4594	0.5	0.221	0.2465	-0.1281	0.3482	0.2923	0.1753	0.22	0.196
253114_at	AT4G35860	ATGB2/ATRAB2C/ATRAB81B (GTP-BINDING 2); [	0.4261	0.0395	0.1447	0.3101	0.0936	0.154	0.3486	0.0213	0.0587	0.2335	0.0701	0.0971
253115_at	AT4G35910	similar to unnamed protein product [Vitis vinifera] (G	0.0806	0.6338	0.4708	0.2405	0.1993	0.2324	-0.604	0.0047	0.0291	-0.4441	0.0137	0.0372
253116_at	AT4G35850	pentatricopeptide (PPR) repeat-containing protein	0.2753	0.088	0.172	0.3011	0.07	0.1324	-0.4743	0.018	0.0538	-0.4485	0.0216	0.0478
253117_at	AT4G35905	similar to unnamed protein product [Vitis vinifera] (G	0.2454	0.2478	0.2923	-0.3816	0.1034	0.1624	0.184	0.3681	0.302	0.04785	0.8051	0.4302
253118_at	AT4G35950	ARAC6/ATROP5/RAC2 (RHO-RELATED PROTEIN	-0.473	0.071	0.1537	-0.6105	0.0344	0.0917	0.2907	0.0864	0.1296	0.1532	0.299	0.2381
253119_at	AT4G35980	similar to unnamed protein product [Vitis vinifera] (G	-0.06142	0.6703	0.4827	0.2554	0.1292	0.1824	0.2674	0.1166	0.1535	0.5842	0.012	0.0345
253120_at	AT4G35790	ATPLDBETA (Arabidopsis thaliana phospholipase	0.2095	0.6996	0.5516	0.2295	0.7219	0.5193	-0.408	0.0177	0.0533	-0.2377	0.0861	0.1098
253121_at	AT4G35890	La domain-containing protein	0.416	0.0265	0.094	0.3905	0.0322	0.0889	0.04704	0.7177	0.4376	0.02153	0.8676	0.4476
253122_at	AT4G35990	similar to unnamed protein product [Vitis vinifera] (G	0.1077	0.4756	0.41	0.1663	0.2914	0.2873	-0.4412	0.0322	0.0731	-0.3825	0.0491	0.0785
253123_at	AT4G36000	pathogenesis-related thaumatin family protein	-0.2998	0.7992	0.5238	0.522	0.6606	0.4452	-0.8944	0.4675	0.3464	-0.06256	0.9576	0.4728
253124_at	AT4G36030	armadillo/beta-catenin repeat family protein	-0.4844	0.0601	0.1402	-0.03099	0.876	0.5119	0.06935	0.6895	0.4277	0.5228	0.0317	0.06
253125_at	AT4G36040	DNAJ heat shock N-terminal domain-containing pro	0.07357	0.8598	0.541	0.09202	0.8254	0.4975	0.4472	0.019	0.0553	0.4657	0.0166	0.0411
253126_at	AT4G36050	endonuclease/exonuclease/phosphatase family pro	0.2606	0.2956	0.3208	0.1462	0.537	0.3993	-0.7552	0.0163	0.0542	-0.8696	0.0114	0.0335
253127_at	no_match	no_match	-0.5258	0.2343	0.2839	-0.2784	0.4999	0.3845	0.1843	0.6231	0.4057	0.4317	0.2809	0.2286
253128_at	AT4G36070	CPK18 (calcium-dependent protein kinase 18); calr	0.3119	0.749	0.5084	-0.9565	0.3525	0.3193	1.2824	0.1371	0.1691	0.01399	0.9848	0.4791
253129_at	AT4G36020	CSDP1 (COLD SHOCK DOMAIN PROTEIN 1); bin	0.6473	0.0131	0.0705	0.3918	0.0615	0.1232	0.8335	0.0016	0.0203	0.5778	0.0062	0.0244
253130_at	AT4G35513	similar to unknown protein [Arabidopsis thaliana] (T	-0.1823	0.5204	0.4291	0.1545	0.583	0.4174	0.03852	0.8143	0.4679	0.3753	0.0708	0.0976
253131_at	AT4G35550	HB-4/WOX13 (WUSCHEL-RELATED HOMEOBOX	-0.4942	0.2214	0.276	-0.2831	0.4536	0.3655	0.1458	0.1281	0.1626	0.3569	0.0094	0.0302
253132_at	AT4G35580	no apical meristem (NAM) family protein	0.3163	0.1014	0.1842	0.4674	0.0351	0.0926	0.06974	0.6646	0.4193	0.2208	0.2131	0.1924
253133_at	AT4G35800	NRPB1 (RNA POLYMERASE II LARGE SUBUNIT);	0.2179	0.334	0.3423	0.02706	0.8982	0.5184	-0.4676	0.0169	0.0519	-0.6585	0.0051	0.0224
253134_at	AT4G35820	oxidoreductase, 2OG-Fe(II) oxygenase family prote	-0.05947	0.9647	0.5684	-0.944	0.4961	0.3829	1.1465	0.415	0.3231	0.262	0.8457	0.4416
253135_at	AT4G35830	aconitate hydratase, cytoplasmic / citrate hydro-lyas	0.3646	0.0523	0.1313	0.2017	0.2053	0.2362	-0.7516	6.00E-04	0.0158	-0.9148	3.00E-04	0.0083
253136_at	AT4G35470	leucine-rich repeat family protein	0.1062	0.691	0.4896	-0.1204	0.6531	0.4428	-0.3902	0.1828	0.2008	-0.6169	0.0637	0.0918
253137_at	AT4G35500	protein kinase family protein	0.5641	0.1962	0.2599	-0.08448	0.8279	0.4983	0.02999	0.9383	0.503	-0.6185	0.1646	0.164
253138_at	AT4G35490	MRPL12 (MITOCHONDRIAL RIBOSOMAL PROTE	0.2431	0.2412	0.2885	0.5821	0.0302	0.0863	-0.3819	0.0536	0.0984	-0.04295	0.7758	0.4217
253139_at	AT4G35450	AKR2 (ANKYRIN REPEAT-CONTAINING PROTEI	-0.8065	0.343	0.3463	-0.2687	0.0322	0.0889	0.1445	0.1583	0.1845	-0.03455	0.7	0.3974
253140_at	AT4G35480	RHA3B (RING-H2 finger A3B); protein binding / zinc	-0.6769	0.2027	0.2641	-0.4655	0.3544	0.3202	0.667	0.0465	0.0905	0.8784	0.02	0.0454
253141_at	AT4G35440	CLC-E (CHLORIDE CHANNEL E); voltage-gated ch	0.228	0.2017	0.2632	-0.06791	0.6729	0.4496	-0.8881	0.004	0.0274	-1.184	0.0014	0.0133
253142_at	AT4G35520	ATMLH3/MLH3 (MUTL PROTEIN HOMOLOG 3); A	0.01181	0.9877	0.5738	0.2319	0.7633	0.4784	0.741	0.3612	0.2987	0.9611	0.2525	0.2138
253143_at	AT4G35530	phosphatidylinositol/glycan-related	0.7334	0.005	0.0504	0.4627	0.0242	0.0781	-0.1086	0.4537	0.3403	-0.3793	0.0443	0.0738
253144_at	AT4G35600	transcription regulator/ zinc ion binding	-0.3162	0.2262	0.2792	-0.3901	0.1527	0.2002	-0.346	0.173	0.1939	-0.4199	0.1148	0.1311
253145_at	AT4G35560	similar to transducin family protein / WD-40 repeat f	-0.3756	0.2226	0.2768	-0.02079	0.9402	0.5291	-0.2042	0.4717	0.3482	0.1506	0.5897	0.3599
253146_at	AT4G35590	RWP-RK domain-containing protein	-0.02206	0.9598	0.5673	-0.4488	0.3369	0.312	0.2184	0.4489	0.338	-0.2083	0.4686	0.3132
253147_at	AT4G35600	CONNEXIN 32 kinase	0.4111	0.0598	0.1399	0.3185	0.1139	0.1704	-0.2057	0.2563	0.2444	-0.2982	0.1274	0.1399
253148_at	AT4G35620	CYCB2;2 (CYCLIN B2;2); cyclin-dependent protein	0.1002	0.8228	0.5304	-0.3549	0.445	0.3618	-0.7178	0.1083	0.1473	-1.1729	0.0281	0.056
253149_at	AT4G35650	isocitrate dehydrogenase, putative / NAD+ isocitrate	0.04266	0.952	0.5652	-0.1649	0.8166	0.495	1.0036	0.2062	0.2156	0.7961	0.2979	0.2375
253150_at	AT4G35660	similar to unknown protein [Arabidopsis thaliana] (T	-0.01625	0.9763	0.5713	-0.927	0.1457	0.1951	-0.2646	0.6339	0.4091	-1.1753	0.0842	0.1083
253151_at	AT4G35670	glycoside hydrolase family 28 protein / polygalactur	0.6924	0.3838	0.3666	-0.4702	0.5433	0.402	-0.2423	0.7496	0.4481	-1.4049	0.1184	0.1337
253152_at	AT4G35690	similar to unknown protein [Arabidopsis thaliana] (T	-0.2224	0.6309	0.47	2.6467	0.0035	0.0374	0.4701	0.3339	0.2854	3.3393	0.0015	0.0137
253153_at	AT4G35703	zinc finger (C2H2 type) family protein	0.4472	0.7023	0.4934	0.04354	0.97	0.5367	0.4546	0.6977	0.4304	0.9454	0.4342	0.2987
253154_at	AT4G35710	similar to unknown protein [Arabidopsis thaliana] (T	-0.3664	0.2892	0.3169	-0.169	0.6035	0.4247	0.3888	0.2649	0.2492	0.5863	0.1225	0.1368
253155_at	AT4G35720	similar to unknown protein [Arabidopsis thaliana] (T	-0.3699	0.5761	0.4511	-1.7902	0.0423	0.1022	-1.3315	0.0266	0.0663	-2.7518	0.0021	0.0154
253156_at	AT4G35730	similar to unknown protein [Arabidopsis thaliana] (T	0.1624	0.6535	0.4771	-0.00683	0.9847	0.5403	0.2464	0.4086	0.3202	0.0772	0.787	0.4249
253157_at	AT4G35740	RecQl3 (Recq-like 3); ATP binding / ATP-dependen	0.8949	0.018	0.0804	0.5396	0.08	0.1419	-0.1305	0.5333	0.3725	-0.4858	0.0644	0.0922
253158_at	AT4G35780	protein kinase family protein	-0.1608	0.477	0.4106	-0.09293	0.6741	0.4499	-0.3642	0.0094	0.0388	-0.2963	0.0188	0.044
253159_at	AT4G35570	HMGB5 (HIGH MOBILITY GROUP B 5); transcriptio	0.05357	0.8334	0.5335	0.6738	0.0477	0.1084	0.6436	0.0543	0.0992	1.2639	0.0061	0.0242
253160_at	AT4G35760	electron carrier/ protein disulfide oxidoreductase	-0.1113	0.53	0.4331	-0.1042	0.5552	0.4067	-0.4884	0.0348	0.0765	-0.4813	0.0364	0.0649
253161_at	AT4G35770	SEN1 (DARK INDUCIBLE 1)	0.1672	0.827	0.5316	0.4381	0.5741	0.4135	0.5978	0.1159	0.1531	0.8686	0.0437	0.0731
253162_at	AT4G35630	PSAT (phosphoserine aminotransferase); phosphoc	0.3421	0.2542	0.296	0.3685	0.2252	0.2485	0.134	0.0614	0.1065	0.1604	0.0367	0.0652
253163_at	AT4G35750	Rho-GTPase-activating protein-related	0.966	0.0275	0.0961	1.394	0.0081	0.0501	0.002738	0.9858	0.5141	0.4307	0.0407	0.0698
253164_at	AT4G35725	unknown protein	-1.292	0.3281	0.339	-0.7347	0.5612	0.4088	-0.9707	0.4501	0.3386	-0.4135	0.7397	0.4103
253165_at	AT4G35610	similar to unknown protein [Arabidopsis thaliana] (T	-1.905	0.0117	0.0676	-2.1075	0.0082	0.0504	1.0206	0.0039	0.0273	0.818	0.0086	0.0289
253166_at	AT4G35290	GLUR2 (Glutamate receptor 2)	-0.00953	0.9799	0.5721	-0.7691	0.0968	0.1568	-0.3076	0.2578	0.2451	-1.0671	0.0102	0.0316
253167_at	AT4G35310	CPK5 (CALMODULIN-DOMAIN PROTEIN KINASE	0.2218	0.3703	0.3597	0.3709	0.1669	0.2104	-0.6001	4.00E-04	0.0146	-0.4509	0.0012	0.0127
253168_at	AT4G35570	similar to SBP1 (S-RIBONUCLEASE BINDING PRO	0.6842	0.2427	0.2891	-0.4132	0.4547	0.3659	0.1063	0.8419	0.4763	-0.9912	0.1183	0.1336
253169_at	AT4G35120	kelch repeat-containing F-box family protein	0.0779	0.8254	0.5311	0.814	0.0697	0.1322	-0.3625	0.26	0.2464	0.3736	0.2479	0.2113
253170_at	AT4G35130	pentatricopeptide (PPR) repeat-containing protein	-1.5039	0.1842	0.2511	1.5909	0.1651	0.2091	-2.9227	0.015	0.0488	0.1721	0.8216	0.4346
253171_at	AT4G35030	bZIP transcription factor family protein	0.06176	0.66	0.4793	0.1322	0.2925	0.2879	0.3875	0.0081	0.036	0.468	0.0041	0.0205
253172_at	AT4G35060	heavy-metal-associated domain-containing protein	-0.8927	0.017	0.0782	-0.8395	0.0208	0.0737	1.3008	0.0046	0.0288	1.354	0.004	0.0202
253173_at	AT4G35110	similar to unknown protein [Arabidopsis thaliana] (T	0.1712	0.6325	0.4705	0.3694	0.3273	0.3072	-0.04035	0.713	0.4359	0.1578	0.1973	0.1833
253174_at	AT4G35090	CAT2 (CATALASE 2); catalase	-0.7159	0.0242	0.0906	-1.2144	0.0039	0.0391	0.02236	0.9156	0.4965	-0.4762	0.0741	0.1001
253175_at	AT4G35050	MSI3 (NUCLEOSOME/CHROMATIN ASSEMBLY F	0.2703	0.5015	0.4212	0.1792	0.6503	0.4419	-0.6912	0.1322	0.1654	-0.7823	0.0995	0.1202
253176_at	no_match	no_match	0.2118	0.3479	0.3489	-0.02297	0.9138	0.5224	0.3345	0.1686	0.1909	0.09973	0.6431	0.3783
253177_s_at	AT4G35150; AT4G35160	[AT4G35150, O-methyltransferase family 2 protein];	0.1314	0.7927	0.5216	0.09475	0.8494	0.5042	-0.2617	0.6058	0.4	-0.2984	0.5583	0.3482
253178_at	AT4G35170	similar to unknown protein [Arabidopsis thaliana] (T	0.3161	0.6428	0.4738	-0.4172	0.5447	0.4025	0.2635	0.6977	0.4304	-0.4698	0.498	0.3251
253179_at	AT4G35200	carrier	-0.8811	0.5983	0.459	-1.3647	0.4261	0.3534	-1.153	0.4537	0.3403	-1.6367	0.3045	0.2408
253180_at	AT4G35210	carrier	-0.5548	0.4877	0.4149	-1.3587	0.1348	0.1867	-0.1494	0.8471	0.4778	-0.9534	0.2597	0.2176
253181_at	AT4G35180	LHT7 (LYS/HIS TRANSPORTER 7); amino acid tra	0.07207	0.8834	0.5471	0.6482	0.2325	0.2532	0.1021	0.8357	0.4743	0.6782	0.2153	0.1938
253182_at	AT4G35190	similar to unknown protein [Arabidopsis thaliana] (T	0.9005	0.4459	0.3962	1.4546	0.2442	0.2606	0.2064	0.8205	0.4699	0.7604	0.4226	0.2936
253183_at	AT4G35220	cyclase family protein	0.3007	0.0726	0.1552	0.188	0.2044	0.2357	0.08176	0.4025	0.3176	-0.03091	0.7414	0.4109
253184_at	AT4G35230	protein kinase family protein	0.7261	0.0054	0.0519	0.9103	0.0023	0.0338	-0.3374	0.0056	0.0312	-0.1532	0.0694	0.0965
253185_at	AT4G35240	similar to unknown protein [Arabidopsis thaliana] (T	0.2033	0.5275	0.4322	0.1617	0.6117	0.4274	-0.7248	0.0049	0.0297	-0.7663	0.004	0.0204
253186_at	no_match	no_match	-0.2172	0.6645	0.4809	-0.6684	0.2238	0.248	-0.3236	0.2409	0.2356	-0.7748	0.0301	0.0583
253187_at	AT4G35280	zinc finger (C2H2 type) family protein	-0.2157	0.8505	0.5383	-1.4364	0.2518	0.2652	1.7532	0.1777	0.197	0.5326	0.6458	0.3793
253188_at	AT4G35300	TMT2 (TONOPLAST MONOSACCHARIDE TRANS	0.2646	0.0334	0.1057	-0.3034	0.0218	0.0748	-0.3481	0.0035	0.0262	-0.9161	1.00E-04	0.0058
253189_at	no_match	no_match	-0.3643	0.1895	0.255	-0.4486	0.1238	0.1785	-1.0284	1.00E-04	0.0105	-1.1127	1.00E-04	0.0058
253190_at	AT4G35335	nucleotide-sugar transporter family protein	-0.04797	0.7498	0.5086	-0.2087	0.2114	0.2407	-0.00938	0.9462	0.5047	-0.1701	0.2627	0.2191
253191_at	AT4G35360	XCP1 (XYLEM CYSTEINE PEPTIDASE 1); cysteine	-0.2957	0.5606	0.445	-0.8106	0.1572	0.2038	0.6426	0.1165	0.1535	0.1277	0.7117	0.4015
253192_at	AT4G35370	transducin family protein / WD-40 repeat family prot	0.1883	0.422	0.386	-0.0566	0.9614	0.5343	-0.5403	0.6491	0.4142	-1.5802	0.2243	0.1984
253193_at	AT4G35380	guanine nucleotide exchange family protein	-0.3796	0.7506	0.5087	0.002168	0.9985	0.5436	0.7618	0.3831	0.3093	1.1435	0.2157	0.194
253194_s_at	AT4G35400;AT1G48250;A	[AT4G35400, transposable element gene];[AT1G48	1.3303	0.1502	0.2258	-0.3944	0.6262	0.4334	0.08502	0.9151	0.4964	-1.6397	0.0937	0.1158
253195_at	AT4G35450	dihydrofolate reductase family / dihydrofolate reduc	0.4863	0.2829	0.3133	-0.741	0.132	0.1844	-1.5915	0.0154	0.0494	-1.8462	0.0093	0.03
253196_at	AT4G35260	IDH1 (ISOCITRATE DEHYDROGENASE 1); isocitr	0.5409	0.0074	0.0577	0.5403	0.0074	0.0485	0.2075	0.0642	0.1093	0.2069	0.0647	0.0926
253197_at	AT4G35250	vestitone reductase-related	-0.8903	0.0013	0.0376	-1.1175	6.00E-04	0.0265	0.03315	0.7185	0.438	-0.1941	0.0861	0.1098
253198_at	AT4G35360	pantothenate kinase family protein	0.2223	0.0514	0.1302	0.09352	0.3116	0.2983	0.2181	0.005	0.0298	0.08931	0.0834	0.1078
253199_at	AT4G35410	clathrin adaptor complex small chain family protein	0.07594	0.3459	0.3478	0.006154	0.9352	0.5279	0.4194	0.0041	0.0277	0.3496	0.008	0.0278
253200_at	AT4G34720	AVA-P1 (vacuolar H+-pumping ATPase 16 kDa pro	-0.5259	0.0177	0.0798	-0.6294	0.0096	0.0536	0.1005	0.4039	0.3181	-0.00305	0.9788	0.4778
253201_at	AT4G34620	SSR16 (ribosomal protein S16); structural constitue	-0.5326	0.0037	0.0459	-0.4415	0.0073	0.0484	-0.2762	0.004	0.0273	-0.185	0.6161	0.3406
253202_at	AT4G34555	40S ribosomal protein S25, putative	0.2435	0.2005	0.2624	0.2142	0.2493	0.2635	1.2777	0.0013	0.0191	1.2484	0.0014	0.0136
253203_at	AT4G34710	ADC2 (ARGININE DECARBOXYLASE 2)	0.1165	0.6147	0.4644	0.05337	0.8151	0.4947	-0.04454	0.6849	0.426	0.1245	0.2966	0.2369
253204_at	AT4G34460	AGB1 (GTP BINDING PROTEIN BETA 1); nucleotic	0.1586	0.3078	0.3274	0.2703	0.1174	0.1732	0.07262	0.5463	0.3779	0.1844	0.17	0.1673
253205_at	AT4G34490	ATCAP1 (CYCLASE ASSOCIATED PROTEIN 1)	-0.2721	0.1004	0.1831	-0.378	0.0417	0.1015	0.00341	0.98	0.5126	-0.1025	0.4679	0.3129
253206_at	AT4G34640	SQS1 (SQUALENE SYNTHASE 1); farnesyl-diphos	0.1595	0.2473	0.2919	0.03808	0.7628	0.4782	-0.7202	0.0454	0.0145	-0.8417	2.00E-04	0.0077
253207_at	AT4G34770	auxin-responsive family protein	0.1967	0.478	0.4109	0.3102	0.285	0.2838	0.2439	0.3871	0.3109	0.3574	0.2284	0.2006
253208_at	AT4G34830	binding	-0.8785	0.0243	0.0908	-0.5799	0.0804	0.1422	-1.2736	0.0069	0.0339	-0.9751	0.0173	0.0421
253209_at	AT4G34830	binding	-0.944	0.0172	0.0785	-0.5736	0.0755	0.1378	-2.2161	6.00E-04	0.0158	-1.8457	0.0011	0.0126
253210_at	AT4G34840	ATMTN2; methylthioadenosine nucleosidase	0.3437	0.2295	0.2818	0.1251	0.6332	0.4357	-0.5359	0.0917	0.134	-0.7545	0.0359	0.0643
253211_at	AT4G34880	amidase family protein	0.1441	0.9046	0.5526	0.282	0.8151	0.4947	2.0164	0.1487	0.1782	2.1543	0.1291	0.1409
253212_s_at	AT4G34890;AT4G34900	[AT4G34890, ATXDH1 (XANTHINE DEHYDROGE	0.6873	0.0069	0.0559	0.5421	0.0156	0.0652	-0.2308	0.1408	0.1719	-0.376	0.0405	0.0696
253213_at	AT4G34910	DEAD/DEAH box helicase, putative (RH16)	0.04384	0.8355	0.534	0.2969	0.2079	0.2382	-0.3852	0.1142	0.1519	-0.1321	0.5275	0.337
253214_at	AT4G34940	armadillo/beta-catenin repeat family protein	-1.6951	0.1119	0.194	-0.94	0.3227	0.3046	-0.9301	0.3272	0.2819	-0.175	0.844	0.4412
253215_at	AT4G34950	nodulin family protein	0.784	0.1032	0.1855	0.1193	0.7649	0.4789	-0.04953	0.7898	0.4601	-0.7143	0.0147	0.0386
253216_at	AT4G34960	peptidyl-prolyl cis-trans isomerase, putative / cyclop	-0.06526	0.6648	0.4809	0.2935	0.1036	0.1625	0.03681	0.781	0.4577	0.3956	0.033	0.0614
253217_at	AT4G34970	actin binding	0.169	0.4825	0.4131	0.6518	0.0406	0.1	0.04089	0.7595	0.4512	0.5237	0.0137	0.0372
253218_at	AT4G34980	SLP2 (subtilisin-like serine protease 2); subtilase	0.03413	0.909	0.5537	0.03815	0.8994	0.5184	-0.2256	0.2291	0.2291	-0.1533	0.3897	0.2799
253219_at	AT4G34990	AtMYB32 (myb domain protein 32); DNA binding / t	-0.2545	0.2385	0.2867	-0.3862	0.1036	0.1625	-0.1541	0.3523	0.2944	-0.2858	0.1229	0.137
253220_s_at	AT4G34930;AT4G34920	[AT4G34930, 1-phosphatidylinositol phosphodieste	-0.5712	0.0016	0.0388	-0.07256	0.3903	0.3369	-0.1899	0.0654	0.1104	0.3087	0.0149	0.0388
253221_at	AT4G34870	ROC5 (ROTAMASE CYP 5); peptidyl-prolyl cis-tran	0.2697	0.1411	0.2183	0.47	0.0332	0.0903	0.4208	0.0461	0.0899	0.621	0.0135	0.0368
253222_at	AT4G34850	chalcone and stilb

253290_at	AT4G34330	Identical to UPF0496 protein At4g34330 [Arabidopsi	1.1928	0.304	0.3253	0.2059	0.8488	0.504	0.6167	0.5417	0.376	-0.3702	0.7096	0.4008
253291_at	AT4G33865	40S ribosomal protein S29 (RPS29C)	0.1442	0.1979	0.2613	0.1415	0.2048	0.236	0.01824	0.8549	0.4797	0.01554	0.8761	0.4502
253292_at	AT4G33985	similar to unknown protein [Arabidopsis thaliana] (T	0.3412	0.0906	0.1743	1.261	0.0012	0.0299	0.6744	0.0012	0.0187	1.5941	0	0.0054
253293_at	AT4G33905	peroxisomal membrane protein 22 kDa, putative	-0.2472	0.6409	0.4734	-0.9251	0.1325	0.1848	0.8336	0.0177	0.0533	0.1557	0.5077	0.3288
253294_at	AT4G33750	unknown protein	-0.07434	0.6808	0.4795	-0.02913	0.8619	0.5077	0.133	0.4449	0.3361	0.1782	0.32	0.2483
253295_at	AT4G33760	tRNA synthetase class II (D, K and N) family protein	-0.109	0.5422	0.4378	-0.2745	0.1692	0.212	-0.6876	0.0012	0.0186	-0.8531	5.00E-04	0.0095
253296_at	AT4G33770	inositol 1,3,4-trisphosphate 5/6-kinase family protein	-0.8155	0.0138	0.0721	-0.4019	0.108	0.1656	-0.4309	0.0914	0.1336	-0.01729	0.9335	0.4666
253297_at	AT4G33810	glycosyl hydrolase family 10 protein	-0.2138	0.5914	0.4565	-0.7165	0.1226	0.1777	-0.483	0.1185	0.155	-0.9857	0.0155	0.0398
253298_at	AT4G33560	unknown protein	0.1713	0.8409	0.5358	0.8462	0.3497	0.3178	0.5532	0.3944	0.3139	1.2282	0.1017	0.1219
253299_at	AT4G33800	similar to hypothetical protein [Vitis vinifera] (GB:CA	-1.7027	0.2082	0.2671	0.7319	0.5544	0.4064	-1.4332	0.2721	0.2535	1.0013	0.4242	0.2942
253300_at	AT4G33580	carbon-sulfur lyase family protein / carbonate dehy	-0.8954	0.0037	0.0459	-0.6579	0.0095	0.0533	0.3343	0.046	0.0898	0.5319	0.0104	0.032
253301_at	AT4G33720	pathogenesis-related protein, putative	-0.529	0.5464	0.4396	0.1774	0.8362	0.5005	-1.0389	0.2658	0.2497	-0.3325	0.7003	0.3975
253302_at	AT4G33660	unknown protein	-0.7564	0.0326	0.1047	-1.1295	0.0087	0.0512	1.2034	6.00E-04	0.0156	0.8293	0.0023	0.016
253303_at	AT4G33780	similar to unknown protein [Arabidopsis thaliana] (T	0.3054	0.2465	0.2915	0.58	0.0616	0.1233	0.2065	0.1415	0.1725	0.4811	0.013	0.0362
253304_at	AT4G33640	similar to Os03g0690000 [Oryza sativa (japonica cu	0.1714	0.3322	0.3413	0.4249	0.0523	0.1134	0.5196	0.0189	0.0552	0.7731	0.0048	0.0218
253305_at	AT4G33666	unknown protein	-1.0726	0.0047	0.0493	-1.2073	0.003	0.0358	0.6508	0.0079	0.0357	0.5161	0.0174	0.0421
253306_at	AT4G33650	ADL2 (ARABIDOPSIS DYNAMIN-LIKE 2); GTP bin	0.4782	0.0343	0.1071	0.1092	0.511	0.3891	-0.2931	0.0954	0.1104	-0.6621	0.0047	0.0217
253307_at	AT4G33670	L-galactose dehydrogenase (L-GalDH)	0.2352	0.004	0.0466	0.1809	0.0101	0.0547	-0.4059	5.00E-04	0.0152	-0.4602	3.00E-04	0.0083
253308_at	AT4G33680	AGD2 (ABERRANT GROWTH AND DEATH 2); tra	0.04091	0.7502	0.5086	-0.256	0.0996	0.1591	0.2018	0.1153	0.1526	-0.09518	0.3975	0.2831
253309_at	AT4G33790	acyl CoA reductase, putative	-0.1162	0.7755	0.5166	-0.2706	0.5166	0.3912	0.2972	0.3178	0.2772	0.1428	0.6129	0.3677
253310_at	AT4G33630	EX1 (EXECUTER1)	0.1284	0.4491	0.3977	-0.2235	0.2183	0.2448	-0.1482	0.3836	0.3095	-0.5	0.03	0.0582
253311_s_at	AT4G33840,AT4G33830	(AT4G33840, glycosyl hydrolase family 10 protein);(	-0.05335	0.8583	0.6406	-0.8925	0.0437	0.1035	0.3263	0.3473	0.2918	-0.5079	0.173	0.169
253312_s_at	AT4G33860,AT4G33850	(AT4G33860, glycosyl hydrolase family 10 protein);(	0.1442	0.8531	0.5389	0.1764	0.821	0.4962	0.8369	0.2567	0.2446	0.8691	0.2418	0.2081
253313_at	AT4G33870	peroxidase, putative	0.223	0.7338	0.5035	-0.6463	0.3502	0.3181	0.4378	0.5136	0.3645	-0.4314	0.5194	0.3334
253314_at	AT4G33890	similar to unknown protein [Arabidopsis thaliana] (T	0.3782	0.0222	0.0875	0.4706	0.0108	0.0559	-0.8122	0.0042	0.0279	-0.5208	0.0076	0.0271
253315_at	AT4G33900	kelch repeat-containing F-box family protein	-0.739	0.2996	0.3227	0.09413	0.8868	0.515	-1.1421	0.1396	0.1708	-0.3089	0.6448	0.3789
253316_s_at	AT4G34300,AT4G33930	similar to unnamed protein product [Vitis vinifera] (G	0.6621	0.2315	0.283	-0.4175	0.4244	0.3527	0.3832	0.4605	0.3434	-0.6964	0.2124	0.192
253317_at	AT4G33940	[AT4G34300, glycine-rich protein];[AT4G33930, gly	0.9637	0.0167	0.0775	-0.6171	0.0643	0.1266	0.5382	0.0916	0.1338	0.8848	0.0221	0.0484
253318_at	AT4G33970	similar to unknown protein [Arabidopsis thaliana] (T	-0.5948	0.628	0.4689	-0.4364	0.7203	0.4656	1.3246	0.3082	0.2726	1.4831	0.2615	0.2185
253319_at	AT4G33990	leucine-rich repeat family protein / extensin family p	-0.4021	0.7825	0.5184	1.0481	0.4845	0.3779	-1.2801	0.3747	0.3051	0.1702	0.9009	0.4575
253320_at	AT4G34020	EMB2758 (EMBRYO DEFECTIVE 2758)	0.05072	0.8265	0.5316	-0.3608	0.1713	0.2137	-0.5862	0.0533	0.0982	-0.8983	0.0143	0.038
253321_at	AT4G33910	DJ-1 family protein	0.689	0.0103	0.0644	0.9039	0.0039	0.0392	0.2722	0.1228	0.1586	0.4872	0.0251	0.0523
253322_at	AT4G33980	oxidoreductase, 2OG-Fe(II) oxygenase family protei	-1.2884	0.4709	0.4078	2.2007	0.2458	0.2615	-2.4889	0.1703	0.192	1.0002	0.539	0.3409
253323_at	AT4G33920	similar to unknown protein [Arabidopsis thaliana] (T	0.02222	0.9412	0.6628	0.3633	0.2685	0.2747	-0.1727	0.4779	0.3506	0.2128	0.3898	0.2799
253324_at	AT4G33940	protein phosphatase 2C family protein / PP2C family	0.3311	0.029	0.0986	0.1286	0.2648	0.2725	0.5621	0.0048	0.0293	0.3596	0.0223	0.0486
253325_at	AT4G33925	zinc finger (C3HC4-type RING finger) family protein	-0.5953	0.4789	0.4115	0.5964	0.4781	0.3755	0.4904	0.5554	0.381	1.682	0.0922	0.1145
253326_at	AT4G33440	similar to unknown protein [Arabidopsis thaliana] (T	-0.2962	0.3951	0.3727	-0.4804	0.0909	0.1521	-0.0543	0.813	0.4675	-0.329	0.2035	0.1871
253327_at	AT4G33450	glycoside hydrolase family 28 protein / polygalactur	-0.5428	0.5568	0.4436	0.02921	0.9742	0.5378	-1.1402	0.2498	0.2409	-0.5682	0.5394	0.3409
253328_at	AT4G33460	AIMY89 (myb domain protein 89); DNA binding / tr	-0.2436	0.0912	0.1751	-0.1046	0.3955	0.3393	-0.1532	0.0452	0.0891	-0.01418	0.8033	0.4297
253329_at	AT4G33480	ATNAP13 (EMBRYO DEFECTIVE 2751)	0.3656	0.1918	0.2567	0.1707	0.5045	0.3864	-0.2015	0.3046	0.2709	-0.3964	0.0816	0.1063
253330_at	AT4G33530	similar to unknown protein [Picea sitchensis] (GB:ABK2482	-0.8043	0.0264	0.094	-0.7503	0.0328	0.0898	-0.6985	0.0311	0.0717	-0.6445	0.0396	0.0687
253331_at	AT4G33490	KUP5 (K+ uptake permease 5); potassium ion trans	-0.3563	0.0514	0.1302	0.1406	0.3387	0.313	-0.4441	0.0033	0.0256	0.05274	0.4989	0.3255
253332_at	AT4G33420	aspartic-type endopeptidase/ pepsin A	-0.7242	0.0632	0.1442	-0.8925	0.025	0.0791	1.0383	0.0216	0.0593	0.77	0.0534	0.0826
253333_at	AT4G33510	peroxisomal, putative	0.4215	0.0769	0.1595	0.1581	0.4243	0.3527	-0.246	0.0447	0.0884	-0.5093	0.0039	0.0202
253334_at	AT4G33360	DHS2 (3-DEOXY-D-ARABINO-HEPTULOSONATE	0.453	0.0087	0.0606	0.3839	0.0153	0.0649	0.7334	2.00E-04	0.0129	0.6643	3.00E-04	0.0086
253335_at	AT4G33500	terpene cyclase/mutase-related	-0.2566	0.2067	0.2662	-0.5302	0.0541	0.1153	-0.2423	0.0669	0.1118	-0.4769	0.0079	0.0277
253336_at	AT4G33250	protein phosphatase 2C-related / PP2C-related	0.3707	0.0143	0.0729	0.4436	0.0077	0.0489	-0.3758	0.0136	0.0465	-0.303	0.0275	0.0552
253337_at	AT4G33470	initiation factor 3K)	-0.8336	0.0027	0.0426	-0.9207	0.0019	0.0329	-0.6612	0.0064	0.0329	-0.7483	0.0041	0.0205
253338_at	AT4G33430	HDA14 (histone deacetylase 14); histone deacetyla	0.4237	0.0278	0.0966	0.473	0.0196	0.0719	0.2503	7.00E-04	0.016	0.2996	4.00E-04	0.0088
253339_at	AT4G33520	BAK1 (BRI1-ASSOCIATED RECEPTOR KINASE);	0.1332	0.6731	0.4837	-0.4229	0.2227	0.2474	-0.4972	0.1243	0.1596	-0.7868	0.0372	0.0658
253340_s_at	AT4G33270,AT4G33260	PAA1 (metal-transporting P-type ATPase 1)	-0.3429	0.5672	0.4478	0.0775	0.8949	0.5171	-1.7048	0.0213	0.0587	-1.2844	0.0503	0.0796
253341_at	AT4G33410	[AT4G33270, CDC20.1; signal transducer];[AT4G33	-0.2979	0.0511	0.1299	-0.215	0.1176	0.1734	0.01573	0.8913	0.4901	-0.4971	0.01	0.0313
253342_at	AT4G33520	signal peptide peptidase family protein	-1.201	0.0066	0.0549	-1.0581	0.0103	0.0551	-0.6731	0.0435	0.0871	-0.5303	0.0834	0.1077
253343_at	AT4G33540	PAA1 (metal-transporting P-type ATPase 1); ATPas	0.6582	0.0354	0.1085	0.6717	0.0332	0.0903	-0.1121	0.2856	0.261	-0.09851	0.34	0.258
253344_at	AT4G33550	metallo-beta-lactamase family protein	-0.01113	0.9765	0.6713	0.7339	0.1074	0.1653	1.043	0.0424	0.0857	1.788	0.0073	0.0266
253345_at	no_match	lipid binding	-0.6631	0.4102	0.38	-0.5944	0.4564	0.3666	-0.8681	0.2226	0.2251	-0.7994	0.2548	0.2151
253346_at	AT4G33600	no_match	-0.1313	0.8843	0.5471	-2.2677	0.0554	0.1169	0.3723	0.683	0.4252	-1.7641	0.1057	0.1244
253347_at	AT4G33610	similar to unknown protein [Arabidopsis thaliana] (T	1.3	0.3617	0.3553	1.0151	0.4668	0.3707	0.05259	0.9688	0.5096	-0.2323	0.8631	0.4467
253348_at	no_match	glycine-rich protein	0.9889	0.0922	0.176	0.6916	0.198	0.2316	-0.2452	0.5612	0.383	-0.5424	0.234	0.2038
253349_at	no_match	no_match	-0.7567	0.1567	0.2308	-0.3857	0.4251	0.353	0.441	0.3678	0.3019	0.812	0.1352	0.1451
253350_at	no_match	no_match	0.638	0.0074	0.0577	0.6357	0.0075	0.0487	-0.3663	0.045	0.0888	-0.3686	0.0442	0.0736
253351_at	AT4G33700	CBS domain-containing protein	0.5557	0.0344	0.1073	0.6412	0.022	0.075	0.2845	0.0339	0.0752	0.37	0.0146	0.0384
253352_at	AT4G33710	pathogenesis-related protein, putative	-1.0435	0.3616	0.3553	1.5622	0.1983	0.2318	-1.0146	0.3737	0.3045	1.5912	0.1917	0.1801
253353_at	AT4G33730	pathogenesis-related protein, putative	0.9958	0.4143	0.382	-1.1769	0.3427	0.3146	0.5124	0.664	0.4192	-1.6603	0.2038	0.1872
253354_at	AT4G33370	DEAD-box protein abstrakt, putative	0.2945	0.7731	0.5158	-1.3231	0.238	0.2565	1.3394	0.2242	0.2262	-0.2781	0.7803	0.4231
253355_at	no_match	no_match	0.3601	0.3325	0.3416	0.2455	0.4945	0.3824	-0.5334	0.1627	0.187	-0.648	0.1065	0.125
253356_at	AT4G33390	similar to unknown protein [Arabidopsis thaliana] (T	0.2177	0.8234	0.5306	2.1733	0.0761	0.1382	-0.2609	0.7776	0.4565	1.7047	0.1092	0.1272
253357_at	AT4G33400	dem protein-related / defective embryo and meriste	-0.1858	0.4683	0.4065	-0.3715	0.1848	0.2231	-0.05166	0.8348	0.474	-0.2373	0.3645	0.2689
253358_at	AT4G33940	GAMMA-VPE (Vacuolar processing enzyme gamm	0.419	0.3702	0.3597	0.2687	0.5531	0.4059	0.2339	0.0764	0.1205	0.08351	0.444	0.3034
253359_at	AT4G33080	protein kinase, putative	-0.4156	0.0952	0.1782	-0.08217	0.6892	0.4555	-0.4266	0.0333	0.0745	-0.09319	0.5247	0.3357
253360_at	AT4G33090	APM1 (AMINOPEPTIDASE M1)	0.694	0.0348	0.1077	0.4994	0.0866	0.1484	-0.3999	0.0133	0.0458	-0.5945	0.0032	0.0185
253361_at	AT4G33100	Identical to Uncharacterized protein At4g33100 [Ara	0.478	0.0832	0.1669	0.9972	0.0087	0.0513	-0.4125	0.1036	0.1439	0.1068	0.6155	0.3685
253362_s_at	AT4G33110,AT4G33120	(AT4G33110, cocaurine N-methyltransferase, puta	-0.3887	0.0345	0.1073	-0.5618	0.0104	0.0552	-0.1446	0.2587	0.2457	-0.3177	0.6445	0.074
253363_at	AT4G33130	similar to unknown protein [Arabidopsis thaliana] (T	-0.8787	0.4089	0.3795	1.0269	0.3421	0.3145	-0.2755	0.7341	0.443	1.6302	0.0974	0.1186
253364_at	AT4G33160	ubiquitin-protein ligase	0.7722	0.1308	0.2092	-0.8039	0.1196	0.1749	0.5983	0.2157	0.2212	-0.9777	0.0743	0.1001
253365_at	AT4G33180	pentatricopeptide (PPR) repeat-containing protein	-0.6008	0.303	0.3248	0.2138	0.6958	0.4574	-0.947	0.1025	0.1429	-0.1324	0.7826	0.4236
253366_at	AT4G33180	hydrolase, alpha/beta fold family protein	-0.3976	0.3762	0.3624	0.1944	0.6523	0.4426	-0.3016	0.4926	0.3567	0.2904	0.5078	0.3288
253367_at	AT4G33180	hydrolase, alpha/beta fold family protein	-0.812	0.0079	0.0585	-0.728	0.0116	0.0581	-0.2981	0.0872	0.1304	-0.214	0.1809	0.1738
253368_at	AT4G33200	XI-i (Myosin-like protein XI-i); motor/ protein binding	0.4428	0.0062	0.0542	-0.00139	0.9876	0.541	-0.2334	0.05	0.0946	-0.6775	0.0013	0.0132
253369_at	AT4G33210	F-box family protein (FBL15)	-0.1167	0.4336	0.391	0.07223	0.6189	0.4302	-0.7165	0.0038	0.0271	-0.5276	0.0114	0.0335
253370_at	AT4G33230	pectinesterase family protein	0.5196	0.6515	0.4766	0.8332	0.4782	0.3755	0.2379	0.8343	0.4738	0.5515	0.6322	0.3745
253371_at	AT4G33240	1-phosphatidylinositol-4-phosphate 5-kinase/ zinc ic	-0.3494	0.2276	0.2803	-0.06883	0.793	0.4871	-0.6393	0.0597	0.1049	-0.3587	0.2176	0.1949
253372_at	AT4G33220	pectinesterase family protein	0.244	0.165	0.2374	0.2979	0.107	0.165	0.3799	0.0575	0.1025	0.4338	0.0393	0.0683
253373_at	AT4G33150	LKR (SACCHAROPINE DEHYDROGENASE)	0.6546	0.1668	0.2389	0.9993	0.0616	0.1233	-0.4009	0.0641	0.1092	-0.05622	0.7398	0.4104
253374_at	AT4G33140	similar to unnamed protein product [Vitis vinifera] (G	-0.2763	0.2077	0.2669	-0.3481	0.1315	0.184	0.01256	0.9489	0.5053	-0.05924	0.7637	0.4179
253375_at	AT4G33280	DNA binding / transcription factor	0.04169	0.9653	0.5685	0.2379	0.8046	0.4911	0.2023	0.8332	0.4735	0.3984	0.6809	0.3908
253376_at	AT4G33290	F-box family protein	1.9675	0.0937	0.1772	0.1432	0.8811	0.5134	-0.4785	0.6226	0.4055	-2.3028	0.0624	0.0907
253377_at	AT4G33300	ADR1-L1 (ADR1-LIKE 1); ATP binding / protein bin	1.44	0.005	0.0504	1.282	0.0076	0.0488	-0.1088	0.3066	0.2719	-0.2668	0.0454	0.0747
253378_at	AT4G33310	unknown protein	-0.6329	0.2659	0.3026	0.6484	0.2561	0.2679	-0.775	0.1887	0.2047	0.5063	0.3597	0.2669
253379_at	AT4G33330	initiation PROTEIN 3); transferase, transferring glyc	-0.05606	0.9441	0.5634	0.9062	0.294	0.2887	0.02193	0.9765	0.5117	0.9842	0.2323	0.2029
253380_at	AT4G33330	initiation PROTEIN 3); transferase, transferring glyc	-0.1618	0.0713	0.1539	0.2325	0.6217	0.4313	-0.5933	0.2447	0.2378	-1.4226	0.0309	0.0592
253381_at	AT4G33350	chloroplast inner membrane import protein Tic22, p	-0.3148	0.0301	0.1007	-0.07908	0.4547	0.3659	0.3201	0.0286	0.0687	0.5558	0.0044	0.0209
253382_at	AT4G33040	glutaredoxin family protein	0.5475	0.2869	0.3154	0.3663	0.4576	0.3672	0.8948	0.0038	0.0271	0.7136	0.0086	0.0289
253383_at	AT4G32900	similar to unknown protein [Arabidopsis thaliana] (T	-0.1471	0.335	0.3429	-0.1996	0.2117	0.2408	0.2011	0.2089	0.2171	0.1486	0.3307	0.2537
253384_at	AT4G32915	glutamyl-tRNA(Gln) amidotransferase	-0.4099	0.0109	0.0655	-0.8814	6.00E-04	0.027	0.3466	0.0192	0.0556	-0.1249	0.2435	0.209
253385_at	AT4G32930	similar to unnamed protein product [Vitis vinifera] (G	0.4422	0.0383	0.1128	0.4928	0.0275	0.0828	0.516	0.0021	0.0218	0.5666	0.0015	0.0138
253386_at	AT4G33030	SQD1 (sulfoquinovosyldiacylglycerol 1); UDPsulfoq	0.2886	0.4173	0.3836	-0.09676	0.777	0.4827	-0.3649	0.051	0.0956	-0.7503	0.0048	0.0218
253387_at	AT4G33010	ATGLDP1 (ARABIDOPSIS THALIANA GLYCINE D	-0.5482	0.0084	0.06	-0.9232	0.0012	0.0302	-0.1119	0.3671	0.3015	-0.4869	0.0115	0.0337
253388_at	AT4G32910	similar to nucleoporin [Lotus japonicus] (GB:BAF45	0.9298	0.0044	0.0482	0.8936	0.0051	0.0428	-1.0888	0.0025	0.0232	-1.125	0.0022	0.0157
253389_at	AT4G32680	similar to unnamed protein product [Vitis vinifera] (G	0.5548	0.006	0.0538	0.6338	0.0037	0.0386	0.1572	0.1067	0.1463	0.2362	0.0356	0.064
253390_at	AT4G32750	similar to unnamed protein product [Vitis vinifera] (G	-0.1359	0.6412	0.4734	-0.02473	0.9314	0.5269	-0.6733	0.0673	0.1123	-0.5621	0.1058	0.1245
253391_at	AT4G32590	ferredoxin-related	-0.8763	0.0049	0.05	-0.7017	0.0107	0.0558	0.06735	0.6873	0.4268	0.2419	0.1947	0.1818
253392_at	AT4G32660	ATKC1 (ARABIDOPSIS THALIANA K+ RECTIFYIN	0.31	0.2695	0.3051	0.2817	0.3092	0.2969	-0.6123	0.02	0.0568	-0.6406	0.0173	0.042
253393_at	AT4G32690	GLB3 (2-on-2 hemoglobin like gene 3)	-0.0067	0.9587	0.5669	-0.00902	0.9443	0.5304	0.8412	0.0023	0.0224	0.8388	0.0023	0.016
253394_at	AT4G32770	VTE1 (VITAMIN E DEFICIENT 1)	-1.0716	0.0151	0.0743	-1.3584	0.0066	0.0461	-0.386	0.1131	0.1507	-0.6728	0.0243	0.0512
253395_at	AT4G32650	AME3; kinase	0.4107	0.1191	0.1995	-0.1787	0.438	0.3589	-0.754	0.0222	0.0602	-1.3434	0.0029	0.0176
253396_at	AT4G32720	ATLA1 (ARABIDOPSIS THALIANA LA PROTEIN 1	0.5672	0.0149	0.074	0.6415	0.0098	0.0538	-0.0488	0.6944	0.4292	0.02544	0.8365	0.4391
253397_at	AT4G32710	kinase	-0.2578	0.3858	0.3678	-0.1466	0.6096	0.4268	0.1001	0.7249	0.4402	0.2112	0.4701	0.3137
253398_at	no_match	no_match	-0.6326	0.2332	0.2838	-0.03591	0.9292	0.5265	-0.6635	0.1554	0.1825	-0.1668	0.683	0.3915
253399_at	AT4G32850	nPAP (NUCLEAR POLY(A) POLYMERASE); nucle	0.3587	0.203	0.2642	0.2276	0.3893	0.3364	-0.6612	0.0018	0.0206	-0.7922	9.00E-04	0.0118
253400_at	AT4G32860	similar to unknown [Populus trichocarpa x Populus	-0.2292	0.6449	0.4748	-0.5545	0.295	0.2892	0.1946	0.6782	0.4238	-0.1307	0.779	0.4226
253401_at	AT4G32870	similar to unknown protein [Arabidopsis thaliana] (T	0.8269	0.0014	0.038	1.1156	5.00E-04	0.0251	0.07997	0.2864	0.2615	0.3687	0.0048	0.0218
253402_at	AT4G32880	ATHB-8 (HOMEOBOX GENE 8); DNA binding / tra	0.3727	0.0875	0.1713	0.3123	0.1322	0.1845	-0.361	0.0824	0.1261	-0.4213	0.0546	0.0836
253403_at	AT4G32830	ATAURA1 (ATAURORA1); histone serine kinase/H3-	0.2547	0.5085	0.4244	-0.3626	0.3601	0.3228	0.2098	0.4264	0.3282	0.1009	0.6912	0.3944
253404_at	AT4G32840	phosphotidylcholine-sterol acyltransferase family	-0.03885	0.8464	0.5374	-0.3461	0.1394	0.1902	0.06728	0.7385	0.4443	-0.2399	0.2709	0.2232
253405_at	AT4G32800	AP2 domain-containing transcription factor TINY, p	-1.6244	0.1204	0.2007	-1.4262	0.159	0.2052	0.3056	0.1467	0.1767	0.5037	0.0414	0.0706
253406_at	AT4G32890	zinc finger (GATA type) family protein	-0.1649	0.6485	0.476	-0.1921	0.5973	0.4223	-0.2797	0.4517	0.3395	-0.3064	0.4124	0.2892
253407_at	AT4G32920	glycine-rich protein	-0.484	0.1958	0.2596	-0.736	0.0778	0.1398	-0.4131	0.0307	0.0714	-0.665	0.0062	0.0244
253408_at	AT4G32950	protein phosphatase 2C, putative / PP2C, putative	-0.3439	0.6988	0.4922	0.9406	0.3187	0.3024	0.1726	0.8166	0.4687	1.457	0.1047	0.1239
253409_at	AT4G32960	similar to unknown protein [Arabidopsis thaliana] (T	0.257	0.216	0.1384	0.4355	0.0352	0.0926	0.3424	0.0687	0.1137	0.5225	0.0198	0.0452
253410_at	AT4G32970	similar to unknown protein [Arabidopsis thaliana] (T	0.552	0.0365	0.1101	0.149	0.4508	0.3643	-0.3676	0.087	0.1301	-0.7706	0.0091	0.0297
253411_at	AT4G32980	ATH1 (ARABIDOPSIS THALIANA HOMEOBOX GE	-0.2526	0.5958	0.4583	0.09618	0.8373	0.5008	-0.7555	0.0617	0.1068	-0.4067	0.238	0.206
253412_at	AT4G33000	CBL10 (CALCINEURIN B-LIKE10); calcium ion bin	-0.836	0.003	0.0435	-0.6231	0.0086	0.051	-0.8538	8.00E-04	0.0165	-0.6409	0.0025	0.0164
253413_at	AT4G33020	ZIP9 (ZINC TRANSPORTER 9 PRECURSOR); cati	-0.5073	0.2894	0.317	-0.2936	0.519	0.392	0.3315	0.47	0.3476	0.5452	0.26	0.2177
253414_at	EDA39	EDA39 (embryo sac development arrest 39); calmo	0.5654	0.1636	0.2366	0.8097	0.0712	0.1335	-0.2838	0.2375	0.2338	-0.03947	0.8564	0.4448
253415_at	no_match	no_match	0.1052	0.7883	0.5201	-0.3726	0.3669	0.3261	0.6377	0.0888	0.1315	0.1599	0.6047	0.3648
253416_at	AT4G33070	pyruvate decarboxylase, putative	1.9221	0.1361	0.2142	1.5414	0.2096	0.2393	0.4029	0.7162	0.4369	0.02223	0.9838	0.4789
253417_at	AT4G32730	PC-MYB1 (myb domain protein 3R1); DNA binding	-0.1754	0.3237	0.3364	-0.2179	0.2348	0.2547	-0.3141	0.0705	0.1154	-0.3567	0.0498	0.0791
253418_at	AT4G32760	protein transporter	0.3025	0.0988	0.1814	0.1331	0.3992	0.3409	-0.1293	0.4116	0.3216	-0.2987	0.1018	0.122
253419_at	AT4G32780	similar to unknown protein [Arabidopsis thaliana] (T	-2.0023	0.0679	0.1496	0.7096	0.4283	0.3545	0.254	0.7684	0.4536	2.966	0.0212	0.0473
253420_at	AT4G32260	ATP synthase family	-0.556	0.0071	0.0567	-0.6776	0.0035	0.0374	-0.1176	0.3433	0.29	-0.2392	0.0942	0.1162
253421_at	AT4G32340	binding	0.07111	0.9041	0.5525	-0.02966	0.9599	0.5341	0.4595	0.1135	0.151	0.3588	0.1899	0.1791
253422_at	AT4G32240	unknown protein	0.5084	0.0301	0.1007	0.5218	0.0278	0.0831	-0.4255	0.0384	0.0809	-0.4122	0.0422	0.0716
253423_at	AT4G32280	IAA29 (indoleacetic acid-induced protein 29); transc	-1.5241	0.0089	0.0609	-1.7831	0.0

253490_at	AT4G31790	diphthine synthase, putative (DPH6)	0.3579	0.1074	0.1895	0.3461	0.1161	0.172	0.09475	0.5668	0.3855	0.08293	0.6144	0.3682
253491_at	AT4G31770	calcineurin-like phosphoesterase family protein	0.2957	0.1096	0.1917	-0.7203	0.0075	0.0487	0.07806	0.617	0.4035	-0.9379	0.0029	0.0175
253492_at	AT4G31810	enoyl-CoA hydratase/isomerase family protein	0.2609	0.1049	0.1871	0.3397	0.053	0.1142	-0.3237	0.0606	0.1056	-0.2449	0.1214	0.136
253493_at	AT4G31820	ENP (ENHANCER OF PINOID); signal transducer	-0.1778	0.0917	0.1757	-0.3702	0.01	0.0545	0.005003	0.9534	0.5064	-0.1874	0.0804	0.1054
253494_at	AT4G31830	similar to unnamed protein product [Vitis vinifera] (G	-0.1217	0.9112	0.5543	0.07028	0.9486	0.5316	-1.3229	0.2681	0.2498	-1.1309	0.3315	0.2541
253495_at	AT4G31850	PGR3 (PROTON GRADIENT REGULATION 3)	-0.173	0.2927	0.3188	-0.3523	0.0694	0.132	-0.3045	0.0441	0.0878	-0.4837	0.01	0.0312
253496_at	AT4G31870	ATGPX7 (GLUTATHIONE PEROXIDASE 7); glutat	-1.2755	0.0081	0.0588	-1.455	0.0051	0.0425	0.399	0.0076	0.0352	0.2194	0.052	0.0812
253497_at	AT4G31880	binding; no unknown protein [Arabidopsis thaliana] (T	0.1214	0.2188	0.2743	0.183	0.0928	0.1538	-0.2102	0.0593	0.1044	-0.1485	0.1387	0.1474
253498_at	AT4G31890	armadillo/beta-catenin repeat family protein	-0.5742	0.1439	0.2205	-0.2486	0.4761	0.3746	-0.2554	0.4649	0.3453	0.07012	0.8355	0.4388
253499_at	AT4G31900	chromatin remodeling factor, putative	0.3865	0.7241	0.5007	0.9122	0.4218	0.3514	-0.01158	0.9865	0.5143	0.5142	0.4698	0.3136
253500_at	AT4G31920	ARR10 (ARABIDOPSIS RESPONSE REGULATOR	0.3029	0.1883	0.2542	0.07304	0.7219	0.4661	0.1387	0.4153	0.3231	-0.09123	0.5824	0.357
253501_at	AT4G32010	HSI2-L1/HSL1 (HSI2-LIKE 1); transcription factor	0.1051	0.5672	0.4478	0.06213	0.7314	0.4688	-6.00E-04	0.997	0.517	-0.04356	0.7892	0.4255
253502_at	AT4G31940	CYP82C4 (cytochrome P450, family 82, subfamily	-0.939	0.4982	0.4197	0.7129	0.6023	0.4246	-0.8023	0.5595	0.3825	0.8497	0.5377	0.3405
253503_at	AT4G31950	CYP82C3 (cytochrome P450, family 82, subfamily	0.1137	0.913	0.5548	-1.9665	0.1145	0.1708	1.3217	0.2063	0.2156	-0.7586	0.4359	0.2995
253504_at	AT4G31960	unknown protein	0.4298	0.2864	0.3151	-0.3367	0.3902	0.3369	0.845	0.0731	0.1176	0.0785	0.8334	0.4381
253505_at	AT4G31970	CYP82C2 (cytochrome P450, family 82, subfamily	0.681	0.503	0.4217	0.5318	0.5966	0.4221	0.07577	0.4542	0.3405	-0.07346	0.4671	0.3128
253506_at	AT4G31980	binding; no unknown protein [Arabidopsis thaliana] (T	0.9217	0.0049	0.05	0.4569	0.049	0.1097	0.4231	0.0307	0.0714	-0.04167	0.7633	0.4178
253507_at	no_match	no_match	-0.6221	0.094	0.1775	-0.9185	0.032	0.0887	0.4976	0.1196	0.1559	0.2012	0.4694	0.3135
253508_at	AT4G31680	transcriptional factor B3 family protein	-0.5962	0.4906	0.4162	-1.5443	0.121	0.1763	-0.02421	0.9769	0.5118	-2.1647	0.0512	0.0806
253509_at	AT4G31520	ATGLR2.4 (Arabidopsis thaliana glutamate receptor	-0.08299	0.7227	0.5003	-0.5152	0.0773	0.1394	-0.1119	0.6348	0.4094	-0.544	0.067	0.0944
253510_at	AT4G31730	GDU1 (GLUTAMINE DUMPER 1)	0.8838	0.2367	0.2856	1.2104	0.1296	0.1826	0.9417	0.2125	0.2194	1.2682	0.1167	0.1325
253511_at	AT4G31410	similar to ATSLY1, protein transporter [Arabidopsis	1.6508	0.0245	0.0911	1.6577	0.0242	0.0782	1.8859	0.0125	0.0444	1.879	0.0127	0.0356
253512_at	AT4G31750	protein phosphatase 2C, putative / PP2C, putative	0.04376	0.8148	0.5283	0.278	0.1873	0.2247	0.09454	0.6176	0.4038	0.3287	0.1334	0.144
253513_at	AT4G31760	peroxidase, putative	1.3421	0.2561	0.2971	0.1471	0.8916	0.5162	0.4696	0.4802	0.3515	-0.7255	0.2958	0.2365
253514_at	AT4G31805	WRKY family transcription factor	-1.2979	0.0371	0.111	0.39868	0.4004	0.3413	-1.5436	0.0187	0.0548	0.1511	0.7271	0.4062
253515_at	AT4G31320	auxin-responsive protein, putative / small auxin up f	-0.2546	0.8307	0.5326	-0.9251	0.4536	0.3655	-0.9878	0.426	0.328	-1.6583	0.2114	0.1916
253516_at	AT4G31360	selenium binding	-0.5612	0.1366	0.2147	-0.5137	0.1641	0.2085	0.3926	0.0088	0.0375	0.4401	0.0058	0.0237
253517_at	AT4G31390	ABC1 family protein	-0.2411	0.3883	0.3689	-0.6305	0.0647	0.127	-0.9175	0.0044	0.0283	-1.3069	0.0012	0.0127
253518_at	AT4G31400	similar to unnamed protein product [Vitis vinifera] (G	-0.458	0.2987	0.3224	-0.2706	0.5197	0.3922	-0.7388	0.0591	0.1042	-0.5514	0.1228	0.1369
253519_at	AT4G31240	electron carrier	0.4013	0.084	0.1678	0.303	0.159	0.2051	-0.7774	0.0114	0.0423	-0.8756	0.0075	0.027
253520_at	AT4G31410	similar to unknown protein [Arabidopsis thaliana] (T	0.121	0.3886	0.369	0.2618	0.1048	0.1635	-0.2549	0.1115	0.1495	-0.1141	0.4137	0.2899
253521_at	AT4G31300	PBA1 (20S proteasome beta subunit A 1); peptidas	0.6348	0.0102	0.0641	0.3107	0.0886	0.15	0.7701	0.0052	0.0301	0.4461	0.0324	0.0608
253522_at	AT4G31290	ChaC-like family protein	-1.8956	0.0145	0.0731	-1.4887	0.0316	0.0883	-1.2933	3.00E-04	0.014	-0.8863	0.0014	0.0133
253523_at	AT4G31340	myosin heavy chain-related	0.07917	0.6301	0.4698	0.002297	0.9887	0.5413	-0.4089	0.0344	0.0758	-0.4858	0.02	0.0455
253524_at	AT4G31430	similar to unnamed protein product [Vitis vinifera] (G	0.376	0.0337	0.1062	0.3508	0.0415	0.1011	-0.1363	0.3138	0.2753	-0.1615	0.2443	0.2095
253525_at	AT4G31330	similar to unknown protein [Arabidopsis thaliana] (T	-0.5935	0.4279	0.3883	-1.2289	0.142	0.1923	0.8958	0.2541	0.2432	0.2603	0.7187	0.4036
253526_at	AT4G31420	zinc finger (C2H2 type) family protein	0.1653	0.3689	0.3678	0.1091	0.5559	0.4068	0.1652	0.3259	0.2813	0.1101	0.5	0.326
253527_at	AT4G31470	pathogenesis-related protein, putative	-0.1786	0.7624	0.5123	-0.5895	0.3455	0.3158	-0.2338	0.6935	0.4288	-0.6447	0.3075	0.2422
253528_s_at	AT4G31480;AT4G31490	(AT4G31480, coatomer beta subunit, putative / beta	0.1622	0.0567	0.1365	0.2715	0.0113	0.0573	-0.6109	6.00E-04	0.0158	-0.5016	0.0012	0.0128
253529_at	AT4G31520	SDA1 family protein	0.1539	0.8752	0.5453	0.6945	0.4921	0.3812	-0.1809	0.8536	0.4795	0.3597	0.7156	0.4027
253530_at	AT4G31530	binding / catalytic/ coenzyme binding	-0.1949	0.0815	0.1651	-0.3352	0.0164	0.0665	0.2592	0.0249	0.0639	0.1189	0.1837	0.1757
253531_at	AT4G31540	ATEX070G1 (exocyst subunit EXO70 family protei	0.2111	0.0898	0.1735	0.5237	0.0052	0.0429	-0.6777	0.002	0.0212	-0.3651	0.0183	0.0434
253532_at	AT4G31570	similar to myosin-related [Arabidopsis thaliana] (TA	0.7921	0.5394	0.4362	-0.677	0.5965	0.422	0.07065	0.9551	0.5066	-1.3984	0.3011	0.2392
253533_at	AT4G31590	ATCSLC05 (Cellulose synthase-like C5); transferas	-1.1937	0.0011	0.036	-1.1908	0.0011	0.0293	-0.2788	0.1201	0.1563	-0.276	0.123	0.137
253534_at	AT4G31500	CYP83B1 (CYTOCHROME P450 MONOOXYGEN	0.286	0.2672	0.3035	0.2539	0.3167	0.3011	-0.2437	0.1671	0.1898	-0.2758	0.129	0.1409
253535_at	AT4G31550	WRKY11 (WRKY DNA-binding protein 11); transcri	0.6551	0.0157	0.0755	-0.5687	0.0742	0.1366	0.3165	0.1776	0.1969	0.7029	0.0222	0.0485
253536_at	AT4G31580	SRZ-22 (SERINE/ARGININE-RICH 22)	0.2456	0.239	0.2871	0.04832	0.7992	0.4894	0.2943	0.0337	0.0749	0.09699	0.3543	0.2646
253537_at	AT4G31560	HCF163	-0.1821	0.1132	0.1949	-0.299	0.0294	0.0852	-0.2256	0.0664	0.1115	-0.3425	0.0191	0.0442
253538_at	AT4G31460	ribosomal protein L28 family protein	0.2884	0.2299	0.282	0.5688	0.0492	0.1099	-0.394	0.0817	0.1253	-0.1136	0.5412	0.3414
253539_at	AT4G31450	zinc finger (C3HC4-type RING finger) family protein	0.08514	0.6547	0.4775	-0.08869	0.6416	0.4388	0.006955	0.905	0.4937	0.003399	0.9534	0.4719
253540_at	AT4G31615	DNA binding / transcription factor	2.237	0.1434	0.2203	-0.7869	0.5576	0.4074	0.1695	0.8972	0.4916	-2.8544	0.0813	0.106
253541_at	AT4G31630	transcriptional factor B3 family protein	0.1261	0.9331	0.5605	1.256	0.4236	0.3523	-0.5319	0.7253	0.4403	0.598	0.6934	0.3953
253542_at	AT4G31670	ubiquitin carboxyl-terminal hydrolase family protein	0.2714	0.1664	0.2386	0.5188	0.032	0.0887	-0.02457	0.8858	0.4884	0.2229	0.2377	0.2059
253543_at	AT4G31270	transcription factor	0.5113	0.1226	0.2029	-0.1985	0.4905	0.3805	0.3084	0.1719	0.1933	-0.4014	0.0966	0.1179
253544_at	AT4G31280	unknown protein	-0.2312	0.4801	0.4119	0.3801	0.2701	0.2754	-0.04082	0.8769	0.4859	0.5705	0.0823	0.1069
253545_at	AT4G31310	avirulence-responsive protein-related / avirulence in	-1.2527	0.0033	0.0446	-1.3077	0.0028	0.0352	-0.2642	0.0794	0.1232	-0.3191	0.0475	0.0769
253546_at	AT4G31040	proton extrusion protein-related	-0.1957	0.3689	0.359	0.01169	0.9547	0.5331	-0.9031	0.0095	0.039	-0.6957	0.0228	0.0492
253547_at	AT4G30960	FAD6 (FATTY ACID DESATURASE 6); omega-6 fa	0.2494	0.048	-0.7605	0.0024	0.0339	-0.7985	7.00E-04	0.016	-0.9096	4.00E-04	0.0091	
253548_at	AT4G30993	similar to hypothetical protein [Vitis vinifera] (GB:CA	-0.5278	0.0197	0.0831	-0.7419	0.0061	0.0451	-0.1962	0.2344	0.2319	-0.4103	0.043	0.0724
253549_at	AT4G30930	NFD1 (NUCLEAR FUSION DEFECTIVE 1); structu	0.6463	0.0271	0.0953	0.8309	0.0119	0.0585	-0.3794	0.1161	0.1532	-0.1947	0.3625	0.2681
253550_at	AT4G30960	CIPK6 (CBL-INTERACTING PROTEIN KINASE 6);	-0.06064	0.766	0.5133	-0.01901	0.9253	0.5254	0.1879	0.0463	0.0902	0.2295	0.0253	0.0525
253551_at	AT4G30996	similar to unknown protein [Arabidopsis thaliana] (T	-0.3229	0.3003	0.323	-0.00459	0.9873	0.5409	0.5113	0.0181	0.0539	0.8297	0.0033	0.0187
253552_at	AT4G30890	UBP24 (UBIQUITIN-SPECIFIC PROTEASE 24); ub	0.6052	0.0077	0.0581	0.06444	0.6252	0.4329	-0.1997	0.1768	0.1965	-0.7405	0.0037	0.0198
253553_at	AT4G31050	lipoyltransferase (LIP2p)	0.828	0.0333	0.1056	-0.1655	0.5586	0.4078	0.1198	0.6685	0.4207	-0.8737	0.0282	0.056
253554_at	AT4G30940	potassium channel tetramerisation domain-containi	0.2259	0.4578	0.4018	-0.06543	0.8237	0.4971	0.2828	0.3621	0.2992	-0.00851	0.9768	0.4773
253555_at	AT4G31080	similar to unknown protein [Arabidopsis thaliana] (T	-0.07778	0.7779	0.5173	0.2682	0.357	0.3214	-0.9625	0.0139	0.0471	-0.6165	0.0554	0.0843
253556_at	AT4G31100	wall-associated kinase, putative	0.1362	0.9426	0.5631	0.9198	0.6321	0.4353	-0.7772	0.6845	0.4259	0.006428	0.9973	0.4822
253557_at	no_match	no_match	-0.1536	0.4816	0.4126	0.1048	0.625	0.4328	-1.0165	9.00E-04	0.0169	-0.7581	0.0027	0.0171
253558_at	AT4G31120	ATPRMT5/PRMT5/SKB1 (SHK1 BINDING PROTE	0.6233	0.0141	0.0726	0.2704	0.1452	0.1947	-0.2639	0.0654	0.1104	-0.6167	0.0042	0.0207
253559_at	AT4G31140	glycosyl hydrolase family 17 protein	-0.7467	0.0768	0.1594	-0.757	0.0741	0.1366	0.2606	0.3521	0.2943	0.2502	0.3694	0.2709
253560_at	AT4G31160	transducin family protein / WD-40 repeat family prot	0.7966	0.008	0.0587	0.5325	0.0306	0.0869	-0.4049	0.0383	0.0809	-0.6691	0.0073	0.0267
253561_at	AT4G31180	aspartyl-tRNA synthetase, putative / aspartate--tRN	0.5508	0.0028	0.0431	0.761	8.00E-04	0.0284	-0.1464	0.1576	0.1841	0.06376	0.4918	0.3227
253562_at	AT4G31130	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.5341	0.0024	0.0421	0.3599	0.0101	0.0545	0.5945	0.0016	0.0204	0.4204	0.0058	0.0237
253563_at	AT4G31150	endonuclease V family protein	0.725	0.0464	0.1238	0.2687	0.3505	0.3182	-0.1321	0.631	0.4083	-0.5884	0.0818	0.1064
253564_at	AT4G31170	protein kinase family protein	0.3968	0.0379	0.1122	0.7293	0.005	0.0424	-0.4619	0.0237	0.0624	-0.1294	0.3757	0.2738
253565_at	AT4G31200	SWAP (Suppressor-of-White-APricot)/surp domain-	0.5652	0.0025	0.0421	0.0577	0.5261	0.3946	0.21	0.0651	0.1101	-0.2976	0.0232	0.0498
253566_at	AT4G31210	DNA topoisomerase family protein	0.4767	0.0277	0.0966	0.1422	0.37	0.3275	-0.4846	0.0263	0.0659	-0.8191	0.0044	0.0209
253567_at	AT4G31230	protein kinase family protein	1.9414	0.1437	0.2205	0.03314	0.9768	0.5385	2.0129	0.133	0.166	0.1046	0.9268	0.4647
253568_at	no_match	no_match	0.1944	0.8686	0.5434	0.1758	0.881	0.5134	1.2587	0.3173	0.2769	1.2401	0.3236	0.25
253569_at	AT4G31250	leucine-rich repeat transmembrane protein kinase,	0.184	0.5111	0.4253	0.2363	0.4072	0.3446	-0.8205	0.0088	0.0375	-0.7682	0.011	0.0328
253570_at	AT4G31260	unknown protein	2.4202	0.1776	0.2464	0.5357	0.7359	0.4699	2.1664	0.2174	0.2221	0.2819	0.8583	0.4453
253571_at	AT4G31000	calmodulin-binding protein	-0.502	0.2601	0.2997	-0.4633	0.293	0.2881	-1.5213	0.0113	0.0421	-1.4826	0.0123	0.0351
253572_at	no_match	no_match	0.2619	0.0747	0.1571	0.2111	0.1256	0.1797	-0.2791	0.0439	0.0875	-0.3299	0.0265	0.0539
253573_at	AT4G31020	similar to unknown protein [Arabidopsis thaliana] (T	-0.2199	0.5218	0.4297	-0.3948	0.2765	0.279	-0.2798	0.4227	0.3266	-0.4546	0.2207	0.1964
253574_at	AT4G31030	contains domain PROKAR_LIPOPROTEIN (PS51	0.7171	5.00E-04	0.032	0.6102	9.00E-04	0.0286	-0.1389	0.0777	0.1218	-0.2459	0.014	0.0375
253575_at	AT4G31060	AP2 domain-containing transcription factor, putative	-0.1448	0.7745	0.5162	-0.2542	0.6191	0.4303	-0.7315	0.1965	0.2095	-0.8408	0.1497	0.1544
253576_at	AT4G31070	pentatricopeptide (PPR) repeat-containing protein	1.7723	0.0257	0.0929	1.2872	0.0656	0.1281	-0.2431	0.6003	0.3983	-0.7282	0.164	0.1637
253577_at	AT4G31080	similar to unknown protein [Arabidopsis thaliana] (T	-0.06219	0.7773	0.5172	0.2371	0.3129	0.2989	-1.6393	4.00E-04	0.0147	-1.34	9.00E-04	0.0114
253578_at	AT4G30340	ATDGK7 (DIACYLGLYCEROL KINASE 7); diacylgl	-0.5703	0.1988	0.2618	-0.5983	0.1819	0.2211	-0.3186	0.276	0.2558	-0.3465	0.2422	0.2083
253579_at	AT4G30610	BRS1 (BR1 SUPPRESSOR 1)	-2.0745	0.0076	0.0579	-2.4527	0.0042	0.04	0.3754	0.308	0.2725	-0.00272	0.9937	0.481
253580_at	AT4G30400	zinc finger (C3HC4-type RING finger) family protein	-0.567	0.0452	0.1225	-0.3719	0.1322	0.1846	0.644	0.0309	0.0715	0.8391	0.0131	0.0362
253581_at	AT4G30660	hydrophobic protein, putative / low temperature and	0.09439	0.7497	0.5086	0.601	0.0951	0.1554	0.8393	0.0229	0.0611	1.3459	0.0045	0.0213
253582_at	AT4G30670	contains domain PROKAR_LIPOPROTEIN (PS512	-0.8884	0.3345	0.3427	0.08275	0.9236	0.5251	0.1481	0.8639	0.4824	1.1193	0.2394	0.2067
253583_at	AT4G30680	MA3 domain-containing protein	0.1529	0.5897	0.456	-0.2164	0.4538	0.3655	-0.5806	0.0903	0.1328	-0.6442	0.0692	0.0964
253584_at	AT4G30700	pentatricopeptide (PPR) repeat-containing protein	0.3615	0.3356	0.3431	-0.1703	0.6335	0.4358	0.5148	0.0013	0.0192	-0.01702	0.8047	0.4301
253585_at	AT4G30720	oxidoreductase	-0.1505	0.6756	0.4846	-0.7125	0.0999	0.1593	-0.9745	0.0233	0.0618	-1.5365	0.0049	0.022
253586_s_at	AT4G30740;AT4G30710	(AT4G30740, similar to unknown protein [Arabidops	0.01184	0.9759	0.5712	0.1432	0.7178	0.4646	-0.4807	0.0431	0.0866	-0.3494	0.1008	0.1211
253587_at	AT4G30770	similar to Os11g0195700 [Oryza sativa (japonica cu	0.9903	0.3259	0.3379	-0.806	0.414	0.3478	2.4073	0.053	0.0977	0.611	0.528	0.3371
253588_at	AT4G30790	similar to protein transport protein-related [Arabidop	0.3543	0.0685	0.1505	0.3773	0.0578	0.1195	-0.4348	0.0385	0.081	-0.4118	0.0451	0.0745
253589_at	AT4G30825	pentatricopeptide (PPR) repeat-containing protein	0.04976	0.8458	0.5373	0.1216	0.639	0.4379	-0.6442	2.00E-04	0.0126	-0.5724	3.00E-04	0.0083
253590_at	no_match	no_match	0.1174	0.7859	0.5196	-0.303	0.4952	0.3826	0.1752	0.6871	0.4268	-0.2452	0.5768	0.3548
253591_at	no_match	no_match	-0.02889	0.9558	0.5663	0.9878	0.1138	0.1704	-0.4792	0.3732	0.3044	0.5375	0.3241	0.2503
253592_at	AT4G30940	WD-40 repeat protein family	0.7164	0.044	0.121	0.3232	0.2606	0.2701	0.1051	0.8245	0.4961	-0.2881	0.2202	0.1961
253593_at	AT4G30760	similar to unknown protein [Arabidopsis thaliana] (T	0.4654	0.0145	0.0731	0.5474	0.0083	0.0505	-0.03866	0.6475	0.4136	0.04339	0.609	0.3664
253594_at	AT4G30820	cyclin-dependent kinase-activating kinase assembly	0.211	0.2293	0.2817	-0.01654	0.9169	0.5232	0.2093	0.2209	0.2241	-0.01822	0.9057	0.459
253595_at	AT4G30830	similar to unknown protein [Arabidopsis thaliana] (T	-4.0137	0.0378	0.1121	-1.8372	0.2344	0.2545	-0.726	0.6098	0.4013	1.4505	0.3313	0.254
253596_s_at	AT4G30730;AT4G30750	(AT4G30730, similar to unknown protein [Arabidops	0.5491	0.003	0.0436	0.4665	0.0055	0.0434	0.2672	0.0316	0.0722	0.1846	0.0885	0.1116
253597_at	AT4G30690	initiation factor 3 (IF-3) family protein	0.2458	0.3168	0.3325	0.4201	0.1224	0.1776	-0.3736	0.0752	0.1195	-0.1993	0.2716	0.2236
253598_at	AT4G30800	40S ribosomal protein S11 (RPS11B)	0.1802	0.468	0.4064	-0.1395	0.5688	0.4115	1.1909	0.0061	0.0325	0.8713	0.0179	0.043
253599_at	AT4G30860	ASHR3 (ASH1-RELATED 3); protein binding / zinc	-0.7875	0.0335	0.1059	0.04443	0.8663	0.5088	-0.5816	0.0786	0.1227	0.2503	0.3692	0.2709
253600_at	AT4G30810	SCPL29 (serine carboxypeptidase-like 29); serine c	-0.291	0.0289	0.0985	-0.7553	0.001	0.0291	0.6837	0.0014	0.0197	0.2195	0.0655	0.0932
253601_at	AT4G30900	similar to unknown [Populus trichocarpa] (GB:ABK9	1.1836	0.0221	0.0872	0.4808	0.2139	0.2419	-0.6659	0.1104	0.1487	-1.3687	0.0137	0.0371
253602_s_at	AT4G30920;AT4G30910	(AT4G30920, cytosol aminopeptidase family protein	0.4227	0.1297	0.2083	0.1535	0.5274	0.3951	-0.7044	0.0146	0.0483	-0.9736	0.0047	0.0217
253603_at	AT4G30920	WRKY32 (WRKY DNA-binding protein 32); transcri	0.3217	0.0635	0.1444	0.08863	0.5221	0.393	0.4915	0.0177	0.0533	0.2583	0.1104	0.128
253604_at	AT4G30970	unknown protein	0.3573	0.7067	0.4949	0.955	0.3406	0.3139	-1.6542	0.1163	0.1534	-1.0565	0.2708	0.2231
253605_at	AT4G30991	binding	0.1757	0.8116	0.5273	0.0747	0.919	0.5239	-2.5967	0.0135	0.0462	-2.6977	0.0118	0.0341
253606_at	AT4G30530	defense-related protein, putative	0.423	0.0252	0.092	-0.5184	0.044	0.1038	0.335	0.0139	0.0471	0.4395	0.0054	0.023
253607_at	AT4G30330	small nuclear ribonucleoprotein E, putative / snRNP	-0.09827	0.7502	0.5086	0.02664	0.9308	0.5268	0.1847	0.2248	0.2264	0.3096	0.074	0.0999
253608_at	AT4G30290	ATXTH19 (XYLOGLUCAN ENDOTRANSGLUCOS	-1.1492	0.1335	0.2121	-2.0845	0.0271	0.0823	1.4098	0.0209	0.0582	0.4746	0.2814	0.2288
253609_at	AT4G30190	AHA2 (Arabidopsis H(+)-ATPase 2); ATPase,	0.8453	0.0184	0.0807	0.4648	0.1022	0.1613	-0.3095	0.1298	0.1638	-0.69	0.0132	0.0365
253610_at	AT4G30200	similar to VIN3 (VERNALIZATION INSENSITIVE 3);	0.1369	0.4483	0.3973	0.1475	0.417	0.3492	-1.0589	0.0024	0.0228	-1.0484	0.0025	0.0164
253611_at	AT4G30300	ATNAP15 (Arabidopsis thaliana non-intrinsic ABC p	-0.02188	0.9895	0.5744	-1.2432	0.4726	0.3733	-1.2918	0.1405	0.1718	-2.5131	0.0234	0.05
253612_at	AT4G30310	ribitol kinase, putative	0.3649	0.0087	0.0605	0.2355	0.0364	0.0942	-0.6512	0.001	0.0178	-0.7806	5.00E-04	0.0096
253613_at	AT4G30320	allergen V5/Tpx-1-related family protein	0.4499	0.7012	0.4929	1.0845	0.3765	0.3303	0.08584	0.938	0.503	0.7204	0.5253	0.336
253614_at	AT4G30350	heat shock protein-related	0.1123	0.8084	0.5263	-0.07979	0.8629	0.5079	0.4418	0.2129	0.2197	0.2497	0.4498	0.306
253615_at	AT4G30360	ATCNGC17 (cyclic nucleotide gated channel 17); c	0.1252	0.6248	0.4682	0.4242	0.1475	0.1963	-0.4276	0.0094	0.0388	-0.487	0.044	0.0734
253616_at	AT4G30380	EXL82 (EXPANSIN-LIKE B2 PRECURSOR)	-0.276	0.8327	0.5332	-0.3135	0.8106	0.4932	-1.5857	0.265	0.2493	-1.6232	0.2556	0.2155
253617_at	AT4G30410	transcription factor	0.574	0.0485	0.1269	0.3894	0.1297	0.1827	-0.04599	0.776	0.4561	-0.2306	0.2017	0.1861
253618_at	AT4G30420	nodulin MtN21 family protein	0.3207	0.5374	0.4359	-0.1496	0.769	0.4801	0.3198	0.5385	0.3747	-0.1505	0.7677	0.4192
253619_at	AT4G30460	glycine-rich protein	-0.6112	0.1884	0.2542	0.1523	0.7132	0.4632	0.6374	0.0958	0.1376	1.4009	0.0088	0.0293
253620_at	AT4G30520	leucine-rich repeat family protein / protein kinase fa	-0.3823	0.0191	0.082	-0.2931	0.0436	0.1034	0.07793	0.482	0.352	0.1671	0.1721	0.1685
253621_at	AT4G30540	glutamine amidotransferase class-I domain-contain	0.659	0.4935	0.4174	-1.2707	0.2203	0.2461	0.3941	0.6836	0.4254	-1.5456	0.1523	0.1563
253622_at	AT4G30560	ATCNGC6 (CYCLIC NUCLEOTIDE GATED CHANI	1.2304	0.2378	0.2862	-0.6293	0.5173	0.3914	0.09392	0.9208	0.4981	-1.7657	0.1174	0.1329
253623_at	AT4G30570	GDP-mannose pyrophosphorylase, putative	0.06751	0.8966	0.5503	-0.5247	0.3425	0.3145	-0.6055	0.1947	0.2085	-1.1977	0.037	0.0655

253690_at	AT4G29550	similar to unknown protein [Arabidopsis thaliana] (T	-0.1769	0.8829	0.5471	-0.1514	0.8996	0.5188	0.5458	0.6534	0.4157	0.5713	0.6388	0.3767
253691_at	AT4G29660	EMB2752 (EMBRYO DEFECTIVE 2752)	0.3609	0.0067	0.0553	0.8359	3.00E-04	0.0249	0.1902	0.0398	0.0826	0.6653	5.00E-04	0.0093
253692_at	AT4G29720	ATPAO5 (POLYAMINE OXIDASE 5); amine oxidas	-0.7595	0.0058	0.053	-0.9541	0.0025	0.034	-0.03184	0.8328	0.4735	-0.2264	0.1843	0.176
253693_at	AT4G29670	thioredoxin family protein	-0.5878	0.0139	0.0722	-0.4078	0.044	0.1038	-0.0359	0.8109	0.467	0.1441	0.3632	0.2683
253694_at	AT4G29735	similar to unknown [Populus trichocarpa] (GB:ABK9	0.4573	0.0307	0.1017	0.5154	0.0211	0.074	-0.1311	0.4015	0.3172	-0.07297	0.6293	0.3735
253695_at	AT4G29510	ATPRMT11/PRMT11 (ARABIDOPSIS ARGININE M	0.7786	0.0276	0.0963	0.613	0.056	0.1176	0.1211	0.3787	0.3072	-0.04456	0.7344	0.4086
253696_at	AT4G29740	CKX4 (CYTOKININ OXIDASE 4); cytokinin dehydro	-0.6485	0.3901	0.37	-0.8933	0.2553	0.2675	0.05104	0.6732	0.422	-0.1938	0.1597	0.1611
253697_at	AT4G29100	type I phosphodiesterase/nucleotide pyrophosphata	-1.666	0.0042	0.0468	-1.4558	0.0068	0.0465	0.2588	0.0289	0.069	0.4689	0.0038	0.0199
253698_at	AT4G29680	type I phosphodiesterase/nucleotide pyrophosphata	0.4022	0.112	0.194	0.07086	0.7385	0.4708	-0.1773	0.4211	0.3258	-0.5086	0.062	0.0904
253699_at	AT4G29800	PLA IVD/PLP8 (Patatin-like protein 8)	-0.5692	0.7476	0.5081	0.04231	0.9808	0.5394	-0.03047	0.9862	0.5142	0.5811	0.7426	0.4113
253700_at	AT4G29840	MTO2 (METHIONINE OVER-ACCUMULATOR); tha	-0.07723	0.7103	0.4963	0.03161	0.8782	0.5126	-0.3071	0.035	0.0767	-0.1982	0.1131	0.1298
253701_at	AT4G29890	choline monooxygenase, putative (CMO-like)	-0.3278	0.1336	0.2121	-0.1591	0.4136	0.3476	-0.731	0.0138	0.0469	-0.5622	0.0323	0.0606
253702_at	AT4G29900	ACA10 (autoinhibited Ca2+ -ATPase 10); calcium-t	1.0528	0.0036	0.0457	1.2262	0.0021	0.0331	-1.0959	0.0031	0.0249	-0.9225	0.0058	0.0236
253703_at	AT4G29910	ATORC5/ORC5 (origin recognition complex protein	0.2266	0.5101	0.4249	0.466	0.2116	0.2408	-0.4116	0.177	0.1965	-0.1721	0.5312	0.3384
253704_at	AT4G29490	X-Pro dipeptidase	0.6822	0.0106	0.0649	0.4252	0.0479	0.1086	-0.1145	0.4644	0.345	-0.3714	0.0587	0.0874
253705_at	AT4G29130	ATHXK1 (GLUCOSE INSENSITIVE 2); ATP binding	-0.05602	0.8235	0.5306	-0.4357	0.1376	0.189	0.1253	0.1287	0.163	-0.2544	0.0179	0.0428
253706_at	AT4G29120	6-phosphogluconate dehydrogenase NAD-binding;	0.1057	0.3977	0.3742	-0.08114	0.5079	0.3877	0.2261	0.113	0.1507	0.03923	0.7432	0.4114
253707_at	AT4G29200	beta-galactosidase	-0.4651	0.6483	0.4759	-2.0978	0.0906	0.1518	2.1595	0.0593	0.1045	0.5268	0.5587	0.3483
253708_at	AT4G29210	GGT3/GGT4 (GAMMA-GLUTAMYL TRANSPEPTI	0.6198	0.0029	0.0431	0.5523	0.0044	0.0409	-0.04911	0.271	0.2528	-0.1166	0.0388	0.0678
253709_at	AT4G29220	phosphofructokinase family protein	-0.4179	0.026	0.0933	-0.4706	0.0177	0.0689	0.01702	0.6848	0.426	-0.03571	0.4112	0.2887
253710_at	AT4G29230	ANAC075 (Arabidopsis NAC domain containing pro	-1.3648	0.2398	0.2875	-0.123	0.9071	0.5207	0.5314	0.6069	0.4003	1.7733	0.1364	0.1458
253711_at	no_match	no_match	-2.2349	0.0842	0.1678	1.2397	0.2734	0.2773	-0.6795	0.5252	0.3692	2.7951	0.0459	0.0753
253712_at	AT4G29330	DER1 (DERLIN-1)	0.8693	0.0064	0.0547	0.3277	0.1205	0.1758	0.2828	0.1438	0.1744	-0.2588	0.1722	0.1685
253713_at	AT4G29370	kelch repeat-containing F-box family protein	1.3072	0.2579	0.2983	0.1192	0.9101	0.5216	0.7115	0.5128	0.3642	-0.4765	0.656	0.3829
253714_at	AT4G29380	protein kinase family protein / WD-40 repeat family	1.0331	0.0024	0.0421	0.7785	0.0089	0.0468	-0.4921	0.0317	0.0725	-0.7468	0.008	0.0278
253715_at	AT4G29390	40S ribosomal protein S30 (RPS30B)	0.1642	0.3052	0.3257	0.2492	0.1491	0.1975	0.8041	0.0017	0.0205	0.8892	0.0012	0.0127
253716_at	AT4G29420	F-box family protein	-0.2705	0.2887	0.3165	0.2289	0.3594	0.3226	-1.0651	0.0086	0.0371	-0.5657	0.0629	0.0911
253717_at	AT4G29440	similar to unknown protein [Arabidopsis thaliana] (T	0.0030566	0.9083	0.5535	-0.1689	0.4282	0.3544	0.1107	0.5014	0.3601	-0.03475	0.8281	0.4367
253718_at	AT4G29450	leucine-rich repeat protein kinase, putative	1.611	0.2819	0.3126	-2.0168	0.1948	0.2293	2.4099	0.1332	0.1661	-1.2179	0.3957	0.2826
253719_at	AT4G29490	X-Pro dipeptidase	0.1437	0.5168	0.428	0.2081	0.3619	0.3239	-0.7104	0.0095	0.039	-0.646	0.0132	0.0364
253720_at	AT4G29270	acid phosphatase class B family protein	0.9967	0.3136	0.3307	0.6544	0.4917	0.3811	-1.3014	0.1146	0.1521	-1.6441	0.064	0.092
253721_at	AT4G29250	transferase family protein	-1.0465	0.2617	0.3006	-0.9604	0.2969	0.2902	-0.914	0.2408	0.2355	-0.8279	0.2806	0.2284
253722_at	AT4G29190	zinc finger (CCCH-type) family protein	-0.04641	0.8806	0.5465	0.02601	0.9328	0.5272	-0.2493	0.0622	0.1072	-0.1769	0.1427	0.1499
253723_at	AT4G29240	leucine-rich repeat family protein / extensin family p	-0.7184	0.1259	0.2053	-0.6862	0.1391	0.1899	0.3245	0.3963	0.3149	0.3567	0.3557	0.2651
253724_at	AT4G29285	LCR24 (Low-molecular-weight cysteine-rich 24)	0.03772	0.9783	0.5718	-1.5615	0.2967	0.2901	0.292	0.8336	0.4736	-1.3072	0.3723	0.2723
253725_at	AT4G29340	PRF4 (PROFILIN 4); actin binding	0.05143	0.9613	0.5676	0.8882	0.4235	0.3523	-0.8454	0.4444	0.336	-0.00861	0.9935	0.481
253726_at	AT4G29430	RPS15A/RPS15AC (RIBOSOMAL PROTEIN S15A E); structural co	0.0030566	0.9915	0.5749	0.454	0.1684	0.2115	0.5715	0.102	0.1426	1.025	0.0194	0.0447
253727_at	AT4G29350	PFN2/PRF2/PRO2 (PROFILIN 2); actin binding / pr	-0.4074	0.0164	0.0771	0.0531	0.6313	0.435	0.4959	0.0034	0.0256	0.8502	4.00E-04	0.0091
253728_at	AT4G29410	60S ribosomal protein L28 (RPL28C)	0.06937	0.7428	0.5067	0.1246	0.5619	0.409	0.1375	0.1796	0.1983	0.1928	0.0851	0.109
253729_at	AT4G29360	glycosyl hydrolase family 17 protein	-0.2149	0.6124	0.4635	-0.3141	0.4675	0.371	-0.2881	0.4781	0.3507	-0.3873	0.3526	0.2638
253730_at	AT4G29480	mitochondrial ATP synthase g subunit family protein	0.09472	0.3042	0.3253	0.2255	0.0486	0.1095	0.3519	0.0119	0.0433	0.4827	0.0039	0.0201
253731_at	AT4G29260	acid phosphatase class B family protein	-0.4089	0.0109	0.0655	-0.3296	0.0224	0.0757	0.4547	0.0076	0.0352	0.5339	0.0042	0.0208
253732_at	AT4G29440	MATE efflux protein-related	-0.3384	0.8154	0.5284	-0.5052	0.7287	0.4683	-0.474	0.7446	0.4464	-0.6408	0.6615	0.3947
253733_at	AT4G29170	ATMND1	0.2603	0.7381	0.5052	0.9305	0.2692	0.275	0.002245	0.9977	0.5172	0.6724	0.4067	0.2869
253734_at	AT4G29180	leucine-rich repeat protein kinase, putative	-0.04154	0.9449	0.5635	-1.5423	0.0524	0.1135	1.5472	0.0519	0.0965	0.0464	0.9385	0.468
253735_at	AT4G29600	SNF7.1	0.5635	0.0064	0.0547	0.9293	0.001	0.0291	1.0142	7.00E-04	0.016	1.38	2.00E-04	0.0078
253736_at	AT4G28780	GDSL-motif lipase/hydrolase family protein	-1.6871	0.0064	0.0547	-1.559	0.0085	0.0509	-0.02923	0.9322	0.5013	0.09884	0.7748	0.4215
253737_at	AT4G28703	similar to unknown protein [Arabidopsis thaliana] (T	0.4293	0.3304	0.3402	1.3371	0.0261	0.0809	0.7507	0.125	0.16	1.6584	0.0129	0.036
253738_at	AT4G28750	PSAE-1 (PSA E1 KNOCKOUT); catalytic	-0.4331	0.0062	0.136	-0.6525	0.016	0.0658	0.1569	0.2654	0.2494	-0.06246	0.6337	0.375
253739_at	AT4G28760	similar to unknown protein [Arabidopsis thaliana] (T	0.03713	0.8193	0.5294	0.2472	0.1799	0.2195	-0.4412	0.0168	0.0518	-0.2311	0.1074	0.1257
253740_at	AT4G28706	pfkB-type carbohydrate kinase family protein	-0.3728	0.1282	0.2069	-0.5733	0.0423	0.1022	-0.1586	0.1715	0.193	-0.3592	0.0196	0.045
253741_at	AT4G28890	protein binding / ubiquitin-protein ligase/ zinc ion bir	-0.6356	0.5169	0.428	0.3334	0.7284	0.4683	0.7604	0.4435	0.3356	1.7294	0.1255	0.1386
253742_at	AT4G28900	transposable element gene	0.5158	0.5414	0.4374	-0.6037	0.4788	0.3757	0.4613	0.3151	0.2759	-0.6582	0.1769	0.1713
253743_at	AT4G28940	catalytic	-0.08161	0.9448	0.5635	0.6635	0.5814	0.4167	-0.9232	0.4514	0.3393	-0.1782	0.88	0.4514
253744_s_at	AT4G28930/AT5G33230;A	[AT5G44415, transposable element gene];[AT5G33	-1.1539	0.4148	0.3822	-1.6268	0.2693	0.275	-0.2881	0.1149	0.4961	-0.358	0.7361	0.4091
253745_at	AT4G29090	reverse transcriptase, putative / RNA-dependent DN	-1.3944	0.3131	0.3304	1.1634	0.3905	0.337	-0.939	0.4808	0.3517	1.6188	0.2517	0.2135
253746_at	AT4G29100	ethylene-responsive family protein	-0.05112	0.7123	0.4971	0.06567	0.6377	0.4374	0.02423	0.773	0.4553	0.141	0.1469	0.1527
253747_at	AT4G29060	lectin protein kinase family protein	0.2119	0.3569	0.353	0.3747	0.1397	0.1905	-0.00402	0.9803	0.5127	0.1587	0.3585	0.2663
253748_at	AT4G28990	RNA-binding protein-related	0.1269	0.3749	0.3618	-0.1215	0.3932	0.3383	-0.03864	0.7764	0.4562	-0.287	0.0869	0.1104
253749_at	AT4G29080	PAP2 (PHYTOCHROME-ASSOCIATED PROTEIN	-0.3769	0.0943	0.1777	-0.2081	0.2943	0.2888	0.9255	0.0058	0.0319	1.0943	0.0032	0.0183
253750_at	AT4G29000	tesmin/TSO1-like CXC domain-containing protein	0.3324	0.8637	0.542	-0.04196	0.8243	0.4973	-0.3573	0.0898	0.1325	-0.4317	0.0545	0.0835
253751_at	AT4G29070	similar to unnamed protein product [Vitis vinifera] (G	-0.656	0.0019	0.0391	-0.9078	5.00E-04	0.0263	0.2622	0.0435	0.087	0.01043	0.9133	0.4607
253752_at	AT4G28910	similar to nuclear transport factor 2 (NTF2) family p	0.2	0.0742	0.1566	0.1572	0.1321	0.1845	0.2531	0.0384	0.0809	0.2103	0.065	0.0928
253753_at	AT4G29030	glycine-rich protein	-0.8168	0.3728	0.3608	-1.0692	0.2596	0.2697	-0.2201	0.6353	0.4095	-0.4725	0.333	0.2549
253754_at	AT4G29020	glycine-rich protein	-0.3475	0.0062	0.0542	-0.2424	0.0243	0.0783	-0.6194	0.0857	0.1291	0.3857	0.2304	0.2017
253755_at	AT4G29040	RPT2A (REGULATORY PARTICLE AAA-ATPASE	1.1476	0.0151	0.0743	1.1408	0.0154	0.0649	0.4426	0.071	0.1158	0.4357	0.0739	0.0999
253756_at	AT4G28980	CAK1AT/CDKF;1 (CDK-ACTIVATING KINASE 1AT	-0.1636	0.2431	0.2895	-0.03852	0.7487	0.4747	-0.574	0.0069	0.0339	-0.4589	0.015	0.0389
253757_at	AT4G28950	ARAC7/ATRAC7/ATROP9/RAC7/ROP9 (RHO-REL	-0.3717	0.6268	0.4686	0.07677	0.9187	0.5238	-0.7355	0.1896	0.2053	-0.287	0.5713	0.3531
253758_at	AT4G29060	elongation factor	-0.2182	0.226	0.2791	-0.4765	0.0355	0.0929	-0.7343	0.0086	0.0371	-0.9926	0.0029	0.0175
253759_at	AT4G29010	AIM1 (ABNORMAL INFLORESCENCE MERISTEM	0.5801	0.0064	0.0545	0.7814	0.0021	0.0332	-0.4244	0.0188	0.0546	-0.223	0.1143	0.1308
253760_at	no_match	no_match	-0.4064	0.7649	0.513	1.9681	0.196	0.2301	-1.5325	0.2939	0.2655	0.842	0.5434	0.3422
253761_at	no_match	no_match	0.8784	0.0493	0.1276	0.9487	0.0394	0.0983	-0.7248	0.0452	0.0891	-0.6546	0.0602	0.0887
253762_at	AT4G28830	methyltransferase	0.6435	0.086	0.17	0.4512	0.1871	0.2245	-0.3305	0.309	0.273	-0.5228	0.1393	0.1477
253763_at	AT4G28850	xyloglucan xyloglucosyl transferase, putative / xylog	-0.9759	0.1907	0.256	-0.5843	0.3994	0.341	-0.544	0.4299	0.3295	-0.1524	0.8179	0.4337
253764_s_at	AT4G28860;AT4G28880	[AT4G28860, CKL4 (Casein Kinase I-like 4); casein	-0.2179	0.4053	0.378	0.5315	0.086	0.1477	-1.3698	0.0043	0.028	-0.6204	0.0572	0.0861
253765_at	AT4G28740	similar to LPA1 (LOW PSII ACCUMULATION1), bin	-0.1255	0.531	0.4333	-0.4335	0.0772	0.1392	0.2246	0.0602	0.1054	0.08342	0.3893	0.2797
253766_at	AT4G28770	similar to unknown protein [Arabidopsis thaliana] (T	0.2739	0.1704	0.2417	0.1002	0.5746	0.4138	0.2274	0.1793	0.1981	0.05366	0.7208	0.4043
253767_at	AT4G28520	CRU3 (CRUCIFERIN 3); nutrient reservoir	-0.5303	0.6419	0.4736	0.3111	0.7829	0.4844	0.08018	0.9431	0.504	0.9216	0.4321	0.2977
253768_at	AT4G28560	RabGAP/TBC domain-containing protein	0.1203	0.8718	0.5444	0.6135	0.43	0.3552	0.7484	0.3449	0.2908	1.2415	0.1506	0.1551
253769_at	AT4G28560	RIC7 (ROP-INTERACTIVE CRIB MOTIF-CONTAIN	0.81	0.3396	0.3451	1.6912	0.0865	0.1483	-0.1435	0.8572	0.4803	0.7377	0.3797	0.2756
253770_at	AT4G28540	CKL6/PAPK1 (Casein Kinase I-like 6); casein kinase	0.2862	0.1591	0.2328	0.6067	0.0215	0.0747	-0.1379	0.3897	0.312	0.1826	0.271	0.2232
253771_at	AT4G28430	reticulon family protein	2.037	0.1274	0.2063	2.5125	0.0771	0.1392	-0.02791	0.9803	0.5127	0.4476	0.695	0.3959
253772_at	AT4G28395	ATA7 (Arabidopsis thaliana anther 7)	0.372	0.6707	0.4829	2.0009	0.0694	0.132	-1.0122	0.2626	0.248	0.6167	0.4718	0.3144
253773_s_at	AT4G28360;AT1G52370	[AT4G28360, ribosomal protein L22 family protein];	-0.2847	0.0778	0.1608	-0.3337	0.0506	0.1116	0.244	0.0592	0.1044	0.1949	0.1051	0.124
253774_at	AT4G28530	ANAC074 (Arabidopsis NAC domain containing pro	0.1574	0.3666	0.3576	-0.3534	0.0844	0.1462	0.3051	0.1199	0.1562	-0.2057	0.2545	0.215
253775_at	AT4G28440	DNA-binding protein-related	0.1838	0.3454	0.3475	0.4537	0.0577	0.1194	0.4619	0.0549	0.0998	0.7317	0.0131	0.0363
253776_at	AT4G28390	AAC3 (ADP/ATP CARRIER 3); ATP:ADP antiporter	2.1296	0.0039	0.0463	2.1269	0.0039	0.0392	-0.07986	0.634	0.4091	-0.08261	0.6227	0.3711
253777_at	AT4G28450	transducin family protein / WD-40 repeat family prot	1.1947	0.0037	0.0459	0.9338	0.0089	0.0518	-0.3794	0.0327	0.0738	-0.6403	0.0056	0.0234
253778_at	AT4G28480	DNAJ heat shock family protein	0.08281	0.5953	0.458	-0.00429	0.9776	0.5386	0.634	0.0053	0.0305	0.5469	0.009	0.0296
253779_at	AT4G28490	HAESA (RECEPTOR-LIKE PROTEIN KINASE 5);/	0.5939	0.2299	0.282	0.6005	0.2256	0.2489	-0.02421	0.9393	0.5032	-0.01759	0.9559	0.4725
253780_at	AT4G28400	protein phosphatase 2C, putative / PPDC, putative	0.6058	0.0505	0.1292	0.7229	0.0299	0.0859	0.2643	0.0849	0.1283	0.3814	0.0302	0.0585
253781_at	AT4G28580	magnesium transporter CorA-like family protein (MS	-0.5073	0.6681	0.482	-0.2449	0.8344	0.5	1.0268	0.4026	0.3176	1.2892	0.3055	0.2412
253782_at	AT4G28590	similar to unknown protein [Arabidopsis thaliana] (T	0.1533	0.5975	0.4587	0.01345	0.9623	0.5346	-0.4661	0.1366	0.1688	-0.6059	0.0731	0.0992
253783_at	AT4G28600	NPGR2 (NO POLLEN GERMINATION RELATED 2	0.1763	0.3274	0.3387	0.197	0.2809	0.2813	0.1032	0.5496	0.379	0.1239	0.477	0.3165
253784_at	AT4G28610	PHR1 (PHOSPHATE STARVATION RESPONSE 1	-0.1011	0.5531	0.4421	0.2129	0.245	0.261	-0.5289	0.0277	0.0678	-0.2149	0.2413	0.2079
253785_s_at	AT4G28620;AT4G28630	[AT4G28620, ATM2 (ABC TRANSPORTER OF TH	0.07605	0.7873	0.5199	0.3453	0.2604	0.27	-0.6616	0.0661	0.1112	-0.3924	0.2108	0.1913
253786_at	AT4G28650	leucine-rich repeat transmembrane protein kinase,	0.4209	0.5764	0.4512	-0.9634	0.2368	0.2559	1.1265	0.1793	0.1981	-0.2578	0.7287	0.4067
253787_at	AT4G28670	protein kinase family protein	-0.2646	0.8101	0.5268	-1.1891	0.3128	0.2989	1.6852	0.1773	0.1967	0.7607	0.5014	0.3264
253788_at	AT4G28680	tyrosine decarboxylase, putative	0.001139	0.9971	0.5763	-1.2104	0.014	0.0627	0.0339	0.8985	0.4919	-1.1777	0.0092	0.0298
253789_at	AT4G28570	alcohol oxidase-related	1.1985	9.00E-04	0.0349	0.9154	0.0025	0.034	-0.00544	0.8623	0.4818	-0.2885	6.00E-04	0.0103
253790_at	AT4G28660	PSB28 (PHOTOSYSTEM II REACTION CENTER P	-1.3652	0.0012	0.036	-1.5817	7.00E-04	0.027	0.8844	1.00E-04	0.0101	0.6678	2.00E-04	0.0078
253791_at	AT4G28640	IAA11 (indoleacetic acid-induced protein 11); transc	-0.0788	0.5242	0.4308	0.5247	0.0097	0.0537	0.2019	0.1487	0.1782	0.8054	0.0021	0.0154
253792_at	AT4G28700	ammonium transporter, putative	-0.9855	0.1646	0.2373	0.08271	0.8935	0.5169	-0.9283	0.1849	0.202	0.1399	0.8213	0.4346
253793_at	AT4G28710	XIH (Myosin-like protein XIH)	-0.7792	0.0187	0.0813	0.09542	0.6639	0.4462	-0.8247	0.0044	0.0284	0.04986	0.7443	0.4117
253794_at	AT4G28720	flavin-containing monooxygenase family protein / FI	-0.8967	0.3606	0.355	-1.385	0.1863	0.2239	0.4131	0.6594	0.4177	-0.07524	0.9352	0.4671
253795_at	AT4G28420	aminotransferase, putative	1.8948	0.1231	0.2034	0.2345	0.8212	0.4962	1.826	0.1336	0.1665	0.1657	0.8729	0.4493
253796_at	AT4G28460	unknown protein	0.3461	0.4272	0.3881	1.1721	0.0403	0.0995	0.6293	0.1837	0.2013	1.4553	0.0206	0.0465
253797_at	no_match	no_match	0.6105	0.0048	0.0498	0.1404	0.2634	0.2718	0.2011	0.1361	0.1685	-0.269	0.0674	0.0947
253798_at	AT4G28500	ANAC073 (Arabidopsis NAC domain containing pro	-1.4626	0.0769	0.1595	-0.8475	0.2418	0.2589	0.8554	0.2382	0.2342	1.4705	0.0759	0.1015
253799_at	AT4G28140	AP2 domain-containing transcription factor, putative	0.2771	0.762	0.5121	0.5255	0.5718	0.4126	0.3417	0.1337	0.1665	0.5901	0.0316	0.0599
253800_at	AT4G28160	hydroxyproline-rich glycoprotein family protein	0.8082	0.3109	0.3292	-0.227	0.761	0.478	0.771	0.3309	0.2837	-0.2642	0.724	0.4053
253801_at	no_match	no_match	-0.1704	0.7074	0.4951	-0.3659	0.4355	0.3577	0.2239	0.5987	0.3977	0.02813	0.9462	0.4699
253802_at	AT4G28180	unknown protein	0.1074	0.747	0.5081	0.2493	0.4673	0.371	-0.6806	0.0732	0.1177	-0.5387	0.1285	0.1405
253803_at	AT4G28200	similar to unnamed protein product [Vitis vinifera] (G	0.0926	0.0281	0.097	0.46	0.0368	0.0947	-0.4268	0.0281	0.0681	-0.4675	0.0207	0.0467
253804_at	AT4G28230	similar to unnamed protein product [Vitis vinifera] (G	-0.4747	0.5857	0.4546	1.2546	0.1927	0.2278	0.2472	0.7382	0.4443	1.9766	0.0457	0.0751
253805_at	AT4G28260	similar to unnamed protein product [Vitis vinifera] (G	0.4061	0.0546	0.1341	0.4694	0.0358	0.0934	-0.205	0.1209	0.1569	-0.1417	0.2459	0.2101
253806_at	AT4G28270	zinc finger (C3HC4-type RING finger) family protein	0.09661	0.7933	0.522	0.3986	0.3121	0.2984	0.09437	0.2346	0.2319	0.3967	0.0042	0.0208
253807_at	AT4G28280	similar to unknown protein [Arabidopsis thaliana] (T	0.3652	0.6929	0.4902	-0.8875	0.3604	0.3229	1.732	0.1143	0.1519	-0.4792	0.607	0.3657
253808_at	AT4G28300	hydroxyproline-rich glycoprotein family protein	0.1691	0.2116	0.2693	0.1205	0.3495	0.3178	-0.03698	0.7616	0.4516	-0.0856	0.494	0.3236
253809_at	AT4G28320	glycosyl hydrolase family 5 protein / cellulase family	0.2663	0.4351	0.3916	-0.1527	0.6454	0.4401	0.3807	0.2832	0.2599	-0.03829	0.9069	0.4591
253810_at	AT4G28220	NDB1 (NAD(P)H DEHYDROGENASE B1); NADH-(	-0.1024	0.6452	0.4748	-0.4684	0.0853	0.147	0.2183	0.2877	0.2624	-0.1478	0.4534	0.3074
253811_at	AT4G28190	ULT1 (ULTRAPETALA1); DNA binding / binding	-0.8101	0.1865	0.253	-0.4869	0.3926	0.3381	-0.3812	0.303	0.27	-0.05801	0.8661	0.4472
253812_at	AT4G28240	wound-responsive protein-related	-0.3109	0.4727	0.4088	0.08172	0.8453	0.5031	0.7097	0.0043	0.0282	0.9389	0.0015	0.0139
253813_at	AT4G28150	similar to unknown protein [Arabidopsis thaliana] (T	-0.1598	0.5303	0.4331	0.2377	0.3652	0.3254	-0.3391	0.2191	0.2231	0.05841	0.8143	0.4328
253814_at	AT4G28290	unknown protein	-1.0003	0.135	0.2133	-0.7747	0.2214	0.2468	1.0707	0.0315	0.0721	1.2964	0.0171	0.0418
253815_at	AT4G28210	ATEXPR1 (ARABIDOPSIS THALIANA EXPANSIN	-0.7912	0.0034	0.0448	-0.9242	0.0019	0.033	0.4383	0.0264	0.0661	0.3063	0.075	0.1008
253816_at	AT4G28210	EMB1923 (EMBRYO DEFECTIVE 1923)	0.06647	0.5267	0.4318	-0.3383	0.0243	0.0783	-0.03477	0.671	0.4214	-0.4396	0.0044	0.0211
253817_at	AT4G28310	similar to unknown protein [Arabidopsis thaliana] (T	-0.265	0.1907	0.256	-0.9415	0.005	0.0425	0.7674	0.0054	0.0309	0.09095	0.5523	0.3459
253818_at	AT4G28130	ATP binding / ATPase, coupled to transmembrane	-0.4426	0.3312	0.3407	0.09685	0.8209	0.4961	0.276	0.4152	0.3231	0.8155	0.055	0.084
253819_at	AT4G28350	lectin protein kinase family protein	-0.6578	0.1267	0.2058	0.03922	0.9142	0.5225	-0.1125	0.7014	0.4317	0.5845	0.0989	0.1198
253820_at	AT4G28370	zinc ion binding	0.06504	0.577	0.4513	0.5184	0.0084	0.0507	-0.1845	0.1606	0.186	0.2689	0.0663	0.0937
253821_at	AT4G28380	leucine-rich repeat family protein	-1.0855	0.3353	0.343	-1.0357	0.3554	0.3206	-0.7995	0.1633	0.1874	-0.7498	0.1849	0.1763
253822_at	AT4G28410	aminotransferase-related	0.9272	0.4661	0.4056	-0.7222	0.5648	0.41	0.8186	0.3645	0.3003	-0.8309	0.3581	0.2661
253823_at	AT4G28030	GCN5-related N-acetyltransferase (GNAT) family pr	-0.2243	0.0835	0

253890_s_at	[AT4G27585.AT5G54100	[AT4G27585, band 7 family protein];[AT5G54100;	0.4969	0.1718	0.2427	-0.4146	0.2378	0.2564	0.3201	0.2795	0.2578	-0.5914	0.0821	0.1067
253891_at	AT4G27720	similar to unknown protein [Arabidopsis thaliana] (T	-0.3297	0.2707	0.3057	-0.6112	0.077	0.1391	-0.1491	0.5512	0.3795	-0.4306	0.1337	0.1442
253892_at	AT4G27620	similar to unknown protein [Arabidopsis thaliana] (T	0.3096	0.3146	0.3312	0.4841	0.1469	0.196	-0.02782	0.9223	0.4986	0.1467	0.6134	0.3679
253893_at	AT4G27390	similar to unmamed protein product [Vitis vinifera] (G	-0.08165	0.7733	0.5159	-0.2428	0.4113	0.3466	0.4047	0.0038	0.0271	0.2436	0.0223	0.0486
253894_at	AT4G27150	2S seed storage protein 2 / 2S albumin storage prot	-0.6682	0.6858	0.4878	-0.1836	0.1068	0.1649	1.1674	0.4813	0.3518	-1.3479	0.4212	0.2929
253895_at	AT4G27160	AT2S3; lipid binding / nutrient reservoir	-1.022	0.4626	0.4042	-1.6106	0.2701	0.2755	-0.101	0.9399	0.5034	-0.6896	0.6131	0.3677
253896_at	AT4G27190	disease resistance protein (NBS-LRR class), putativ	-0.6184	0.5209	0.4293	-0.00952	0.9919	0.5421	-0.9926	0.3224	0.2793	-0.3837	0.6853	0.3924
253897_at	AT4G27200	unknown protein [Populus trichocarpa] (GB:ABK9	0.7065	0.0035	0.0452	0.6036	0.0063	0.0453	-0.08629	0.1654	0.1887	-0.1892	0.0205	0.0464
253898_s_at	AT5G54810.AT4G27070	[AT5G54810, TSB1 (TRYPTOPHAN SYNTHASE B	0.4568	0.0172	0.0787	0.2409	0.1075	0.1653	0.0697	0.5261	0.3695	-0.1462	0.2195	0.1959
253899_at	AT4G27080	ATPDL5-4 (PDI-LIKE 5-4)	0.05558	0.6193	0.4663	0.18	0.1566	0.2032	-0.1895	0.1407	0.1719	-0.06506	0.5632	0.3502
253900_at	AT4G27130	initiation factor SUI1, putative	0.4894	0.114	0.1956	0.274	0.3221	0.3043	-0.4636	0.0099	0.0396	-0.679	0.0025	0.0165
253901_at	AT4G27090	60S ribosomal protein L14 (RPL14B)	0.1639	0.3036	0.325	0.1158	0.4517	0.3648	-0.2027	0.1913	0.2063	-0.2508	0.1238	0.1375
253902_at	AT4G27170	2S seed storage protein 4 / 2S albumin storage prot	1.1567	0.4634	0.4045	0.3205	0.8334	0.4998	0.8913	0.5664	0.3853	0.05515	0.971	0.4758
253903_at	AT4G27180	ATK2 (ARABIDOPSIS THALIANA KINESIN 2); mic	-0.1611	0.2509	0.2939	-0.351	0.0431	0.1031	0.03894	0.6973	0.4302	-0.151	0.1802	0.1734
253904_at	AT4G27140	2S seed storage protein 1 / 2S albumin storage prot	-0.7606	0.6547	0.4775	-0.4719	0.7796	0.4834	0.1977	0.9063	0.494	0.4865	0.7731	0.4209
253905_s_at	AT4G27210.AT4G27200	[AT4G27210, transposable element gene];[AT4G27	-0.06083	0.9443	0.5635	-0.4997	0.5746	0.4138	-0.6426	0.4764	0.35	-1.0815	0.257	0.2163
253906_at	AT4G27220	disease resistance protein (NBS-LRR class), putativ	-1.8772	0.1087	0.0813	0.3689	0.4941	0.3822	-1.669	0.0273	0.0671	0.5771	0.305	0.241
253907_at	AT4G27250	dihydroflavonol 4-reductase family / dihydrokaempf	-0.5218	0.5598	0.4448	-0.4836	0.5876	0.4187	-0.4504	0.6126	0.402	-0.4122	0.6421	0.378
253908_at	AT4G27260	GH3.5/WES1; indole-3-acetic acid amido synthetas	0.407	0.0722	0.1549	0.7216	0.0126	0.06	-0.2281	0.1833	0.2011	0.08647	0.5754	0.3543
253909_at	AT4G27270	quinone reductase family protein	-0.02055	0.9346	0.5509	0.5921	0.0657	0.1282	0.343	0.1351	0.1676	0.9556	0.0065	0.025
253910_at	AT4G27290	S-locus protein kinase, putative	-1.2518	0.3718	0.3604	0.8076	0.5522	0.4056	-2.0318	0.0474	0.0914	0.02759	0.9712	0.4758
253911_at	AT4G27300	S-locus protein kinase, putative	0.1405	0.884	0.4872	-0.31	0.3887	0.3362	0.4187	0.0242	0.0631	-0.03188	0.8014	0.429
253912_at	no_match		0.01203	0.9655	0.5686	0.06531	0.815	0.4947	-0.525	0.0098	0.0395	-0.4717	0.0141	0.0377
253913_at	AT4G27370	VIIIB (Myosin-like protein VIIB); motor	1.3539	0.1404	0.218	-0.6639	0.4191	0.3503	0.2262	0.7745	0.4557	-1.7917	0.0721	0.0985
253914_at	AT4G27400	late embryogenesis abundant protein-related / LEA	0.8756	0.227	0.2798	-0.8315	0.2472	0.2621	1.1847	0.0578	0.1028	-0.5224	0.3095	0.2432
253915_at	AT4G27280	calcium-binding EF hand family protein	-0.7533	0.1585	0.2323	-0.5567	0.27	0.2754	0.8844	0.0094	0.0388	1.081	0.0046	0.0214
253916_at	AT4G27240	zinc finger (C2H2 type) family protein	0.4281	0.2247	0.2783	0.3425	0.3149	0.3002	0.5557	0.04	0.0827	0.4702	0.0641	0.0921
253917_at	AT4G27380	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.2711	0.3788	0.3638	0.5535	0.1137	0.1704	-0.09907	0.5591	0.3823	0.1833	0.3043	0.2408
253918_at	AT4G27320	universal stress protein (USP) family protein	0.363	0.0071	0.0567	0.3825	0.0059	0.0442	0.1494	0.0823	0.1259	0.1688	0.0595	0.0881
253919_at	AT4G27350	similar to unknown protein [Arabidopsis thaliana] (T	-0.3888	0.1537	0.2287	-0.309	0.235	0.2548	-0.02716	0.7004	0.4314	0.05261	0.468	0.3129
253920_at	AT4G27230	HTA2 (HISTONE H2A); DNA binding	0.6285	0.0209	0.085	-0.6955	0.0083	0.0504	0.992	8.00E-04	0.016	0.8191	0.0015	0.0138
253921_at	AT4G26900	AT-HF (ARABIDOPSIS THALIANA HISF PROTEIN	-0.01761	0.9145	0.5553	-0.1413	0.411	0.3465	0.005776	0.9675	0.5095	-0.1179	0.4266	0.2953
253922_at	AT4G26850	VTC2 (VITAMIN C DEFECTIVE 2)	-1.1897	0.0181	0.0804	-1.2132	0.0169	0.0676	-0.1867	0.1759	0.1959	-0.2102	0.1381	0.147
253923_at	AT4G27060	TOR1 (TORTIFOLIA 1)	0.09731	0.4219	-0.00899	0.5492	0.5318	0.4052	-0.2052	0.0538	0.0987	-0.3115	0.0148	0.0387
253924_at	AT4G27110	COBL11 (COBRA-LIKE PROTEIN 11 PRECURSOR	0.0657	0.9316	0.5602	-1.0123	0.2323	0.2531	0.847	0.1845	0.2017	-0.231	0.6848	0.3922
253925_at	AT4G26690	MRH5/SHV3 (morphogenesis of root hair 5); glycer	-0.3239	0.3426	0.3463	-0.7525	0.0668	0.1294	-0.03588	0.7353	0.4434	-0.4645	0.0094	0.0301
253926_at	AT4G26650	RNA recognition motif (RRM)-containing protein	0.1677	0.6409	0.4734	0.2379	0.5143	0.3904	-0.7508	0.0267	0.0665	-0.6806	0.0362	0.0647
253927_at	AT4G26710	ATP synthase subunit H family protein	0.05204	0.5215	0.4296	-0.2784	0.0199	0.0722	-0.2697	0.022	0.0599	-0.6001	0.0013	0.0131
253928_at	AT4G26720	PPX1 (protein phosphatase x-1); protein serine/thre	0.1721	0.2111	0.269	0.2287	0.1193	0.1748	-0.7075	0.0036	0.0265	-0.6509	0.0049	0.022
253929_s_at	AT4G26730, methylacetamidase];[AT2G16030.a		-0.3668	0.7132	0.4972	-1.8031	0.1747	0.1787	1.8631	0.1154	0.1527	0.4268	0.6698	0.3873
253930_at	AT4G26740	ATS1 (ARABIDOPSIS THALIANA SEED GENE 1);	-0.4927	0.5269	0.4318	-2.321	0.0311	0.0876	2.2312	0.035	0.0767	0.4029	0.6016	0.3638
253931_at	AT4G26770	phosphatidate cytidylyltransferase, putative / CDP-c	-0.7578	0.5546	0.4426	-0.3911	0.7563	0.477	0.4677	0.6969	0.4301	0.8343	0.4966	0.3245
253932_at	AT4G26800	pentatricopeptide (PPR) repeat-containing protein	-0.09292	0.9453	0.5635	1.5175	0.2992	0.291	-2.0255	0.1717	0.1931	-0.415	0.7504	0.414
253933_at	AT4G26820	contains InterPro domain Harpin-induced 1 (InterPr	-1.1272	0.3107	0.329	0.0138	0.9893	0.5415	-1.917	0.1199	0.1561	-0.776	0.4693	0.3135
253934_at	AT4G26830	hydrolase, hydrolyzing O-glycosyl compounds	-0.0167	0.9863	0.5735	-1.9804	0.0957	0.1559	1.4926	0.1771	0.1966	-0.471	0.6328	0.3747
253935_at	AT4G26870	aspartyl-tRNA synthetase, putative / aspartate--tRN	0.5239	0.0037	0.0459	0.5297	0.0035	0.0374	-0.2083	0.0229	0.0611	-0.9597	0.0125	0.0522
253936_at	AT4G26880	stigma-specific Stig1 family protein	-0.8279	0.199	0.2619	0.1448	0.8014	0.4898	-0.2504	0.5203	0.3671	0.7222	0.1122	0.1291
253937_at	AT4G26890	MAPKKK16 (Mitogen-activated protein kinase kinas	-0.09462	0.8791	0.5463	-0.8056	0.2396	0.2575	-0.1183	0.8388	0.4752	-0.8293	0.2029	0.1868
253938_at	AT4G26920	similar to homeobox protein-related [Arabidopsis tha	-0.3416	0.5371	0.4358	0.1229	0.8203	0.496	0.07301	0.8924	0.4904	0.5375	0.3486	0.2618
253939_at	AT4G26930	MYB97 (myb domain protein 97); DNA binding / tra	-1.5843	0.2959	0.3209	-1.0485	0.4711	0.3726	-0.6106	0.2877	0.2624	-0.07488	0.8878	0.4537
253940_at	AT4G26950	similar to unknown protein [Arabidopsis thaliana] (T	-0.3958	0.5025	0.4216	-0.1592	0.7818	0.484	-0.1267	0.4405	0.3343	0.1099	0.4995	0.3257
253941_at	AT4G26980	similar to unnamed protein product [Vitis vinifera] (G	0.02677	0.8777	0.5444	0.09669	0.5678	0.411	-0.09546	0.5725	0.3876	-0.02553	0.8775	0.4506
253942_at	AT4G27010	binding	0.9206	0.0126	0.0692	0.9246	0.0124	0.0597	-0.7719	0.0069	0.0338	-0.7679	0.007	0.0261
253943_at	AT4G27030	small conjugating protein ligase	-1.8053	0.001	0.0349	-2.176	5.00E-04	0.0252	0.2762	0.0784	0.1224	-0.09455	0.466	0.3123
253944_at	AT4G27040	similar to unknown protein [Arabidopsis thaliana] (T	-0.3668	0.7132	0.4972	-1.8031	0.1747	0.1787	1.8631	0.1154	0.1527	0.4268	0.6698	0.3873
253945_at	AT4G27050	F-box family protein	-0.4326	0.0279	0.0968	-0.6936	0.0056	0.0434	-0.2644	0.0599	0.105	-0.5255	0.0066	0.0253
253946_at	AT4G26790	GDSL-motif lipase/hydrolase family protein	-1.8117	0.0023	0.0414	-0.9942	0.019	0.071	-0.2181	0.206	0.2154	0.5994	0.0143	0.038
253947_at	AT4G26760	microtubule associated protein (MAP65/ASE1) fami	0.09152	0.726	0.5013	0.08847	0.7347	0.4696	0.08798	0.3864	0.3105	0.08492	0.4015	0.2848
253948_at	AT4G26940	galactosyltransferase family protein	-0.3793	0.0866	0.1705	-0.00524	0.9766	0.5385	-0.7923	0.0048	0.0292	-0.4183	0.0401	0.0691
253949_at	AT4G26780	AR192; adenyl-nucleotide exchange factor/ chapero	0.3357	0.249	0.293	-0.1613	0.5524	0.4057	0.6154	0.0689	0.1137	0.1184	0.6593	0.3839
253950_at	AT4G26910	2-oxoacid dehydrogenase family protein	0.6756	0.0217	0.0864	1.045	0.0048	0.0421	-0.2676	0.2212	0.2244	0.1018	0.6112	0.3672
253951_at	AT4G26860	alanine racemase family protein	-0.7797	0.0094	0.0624	-0.7603	0.0102	0.0549	-0.4816	0.0442	0.0879	-0.4622	0.0497	0.0791
253952_at	AT4G26840	SUM1 (SMALL UBIQUITIN-LIKE MODIFIER 1)	0.1134	0.0269	0.0949	0.4723	1.00E-04	0.0249	0.6433	0	0.0092	1.0022	0	0.0043
253953_at	AT4G26750	hydroxyproline-rich glycoprotein family protein	0.3123	0.0957	0.1787	0.2104	0.2175	0.2442	0.3735	0.0603	0.1055	0.2715	0.1322	0.1431
253954_at	AT4G26970	aconitate hydratase, cytoplasmic, putative / citrate h	0.6382	0.0306	0.1015	0.3862	0.1185	0.1741	-0.04378	0.7388	0.4444	-0.2959	0.0731	0.0992
253955_at	AT4G27000	ATRBP45C; RNA binding	0.1731	0.2872	0.3156	0.3474	0.0695	0.1321	-0.9549	0.0025	0.0232	-0.7806	0.0052	0.0226
253956_at	AT4G26700	ATFIM1 (Arabidopsis thaliana fimbrin 1); actin bindi	0.1375	0.5282	0.4325	-0.1934	0.3867	0.3351	-0.5	0.0658	0.1108	-0.8309	0.0139	0.0375
253957_at	AT4G26320	AGP13 (ARABINOGALACTAN PROTEIN 13)	0.8176	0.5351	0.4352	-0.665	0.6107	0.4271	0.6366	0.5826	0.3917	-0.8461	0.4719	0.3144
253958_at	AT4G26400	zinc finger (C3HC4-type RING finger) family protein	0.5038	0.1191	0.1995	0.2814	0.3312	0.309	-0.3825	0.0227	0.0609	-0.6049	0.0047	0.0217
253959_at	AT4G26410	similar to unknown protein [Arabidopsis thaliana] (T	-0.05055	0.575	0.4508	0.02489	0.779	0.4833	0.1865	0.0356	0.0774	0.262	0.0119	0.0342
253960_at	no_match		0.1969	0.8218	0.5301	-1.1768	0.2241	0.248	-1.9266	0.0783	0.1223	-3.3003	0.0157	0.0399
253961_at	AT4G26440	WRKY34 (MICROSPORE-SPECIFIC PROMOTER	-0.5733	0.2325	0.2833	0.4148	0.3666	0.3259	-0.1654	0.7058	0.4333	0.8227	0.1138	0.1304
253962_at	AT4G26460	similar to GAMT1 [Arabidopsis thaliana] (TAIR:AT4	-0.2474	0.0493	0.1276	-0.2082	0.6658	0.4469	-0.6175	0.1993	0.2115	0.4217	0.3534	0.2642
253963_at	AT4G26470	calcium ion binding	-0.2331	0.5191	0.4289	-0.02878	0.9347	0.5278	-0.4789	0.1373	0.1692	-0.2746	0.3477	0.2614
253964_at	AT4G26480	KH domain-containing protein	-0.1322	0.6446	0.4747	-0.3549	0.252	0.2652	-0.6386	0.0326	0.0736	-0.8614	0.0123	0.0351
253965_at	AT4G26490	similar to unknown protein [Arabidopsis thaliana] (T	0.02016	0.9384	0.5618	-0.05901	0.8216	0.4962	0.6296	0.0587	0.1038	0.5504	0.0837	0.108
253966_at	AT4G26520	fructose-bisphosphate aldolase, cytoplasmic	-0.1955	0.636	0.4716	-0.6751	0.1522	0.1998	-0.5027	0.123	0.1587	-0.9823	0.0189	0.0441
253967_at	AT4G26550	similar to unknown protein [Arabidopsis thaliana] (T	0.4917	0.0225	0.0876	0.6	0.0116	0.058	0.08054	0.5171	0.3659	0.1889	0.1714	0.1681
253968_at	AT4G26560	CBL7 (CALCINEURIN B-LIKE 7)	1.6885	0.0577	0.1376	-1.4144	0.0917	0.1527	1.953	0.038	0.0806	-1.1499	0.1469	0.1527
253969_at	AT4G26430	CSN6B (COP9 SIGNALOSOME SUBUNIT 6B)	0.7419	0.0162	0.0769	0.9425	0.0071	0.0476	0.2087	0.1928	0.2072	0.4092	0.0374	0.066
253970_at	AT4G26510	uracil phosphoribosyltransferase / UMP pyrophosph	0.5166	0.0089	0.061	0.3398	0.0352	0.0926	-0.306	0.0479	0.0919	-0.4828	0.0113	0.0333
253971_at	AT4G26530	fructose-bisphosphate aldolase, putative	-1.023	0.0499	0.1232	-0.88	0.0697	0.1322	-1.1523	0.0013	0.0188	-1.0092	0.0021	0.0154
253972_at	AT4G26500	ATSUFE/CPSUFE/EMB1374 (EMBRYO DEFECTI	0.101	0.3409	0.3457	-0.02469	0.8047	0.4911	-0.135	0.1947	0.2085	-0.2606	0.0397	0.0688
253973_at	AT4G26555	immunophilin / FKBP-type peptidyl-prolyl cis-trans i	-0.3599	0.1478	0.2236	-0.4098	0.111	0.1682	-0.4142	0.0158	0.0502	-0.464	0.0108	0.0325
253974_at	AT4G26540	protein kinase family protein	-1.8007	0.0936	0.1772	-1.1692	0.2279	0.2502	-2.7003	0.0303	0.0709	-2.0688	0.0656	0.0932
253975_at	AT4G26600	nucleolar protein, putative	-0.141	0.7913	0.5213	1.0825	0.0957	0.1559	-1.1597	0.0807	0.1244	0.06385	0.9043	0.4586
253976_at	AT4G26610	protein kinase, putative	0.03705	0.7965	0.5228	-0.04964	0.7307	0.4687	-0.1016	0.3789	0.3073	-0.1883	0.1409	0.1488
253977_at	AT4G26630	GTP binding / RNA binding	-0.05948	0.8032	0.525	-0.04963	0.8351	0.5002	-0.5411	0.0726	0.1171	-0.5313	0.0761	0.1016
253978_at	AT4G26660	similar to unknown protein [Arabidopsis thaliana] (T	0.1719	0.8896	0.5483	1.0997	0.3979	0.3403	-0.3216	0.7867	0.4592	0.6061	0.6145	0.3682
253979_at	AT4G26680	pentatricopeptide (PPR) repeat-containing protein	-0.4058	0.661	0.4796	0.4926	0.5967	0.4221	-0.5279	0.5718	0.3873	0.3706	0.6882	0.3932
253980_at	AT4G26620	sucrase-related	0.583	0.0017	0.0391	0.5971	0.0016	0.0316	-0.2924	0.0141	0.0473	-0.2782	0.0166	0.0411
253981_at	AT4G26670	mitochondrial import inner membrane translocase s	0.7845	0.1751	0.245	1.2954	0.0531	0.1143	0.1464	0.6816	0.4248	0.6573	0.1184	0.1337
253982_at	AT4G26570	ATCBL3 (CALCINEURIN B-LIKE 3)	0.08228	0.7434	0.5068	0.4407	0.1334	0.1856	-0.2023	0.4371	0.3329	0.1562	0.5419	0.3416
253983_at	AT4G26640	WRKY20 (WRKY DNA-binding protein 20); transcri	0.02181	0.7864	0.5197	-0.1539	0.7102	0.4676	0.04141	0.6114	0.4017	-0.1343	0.1488	0.1538
253984_at	AT4G26590	ATOPT5 (oligopeptide transporter 5); oligopeptide t	0.2408	0.776	0.5167	0.4212	0.6226	0.4318	0.3827	0.6538	0.4158	0.5631	0.5158	0.332
253985_at	AT4G26220	caffeoyl-CoA 3-O-methyltransferase, putative	-0.3072	0.7487	0.5084	0.05588	0.9532	0.5326	1.48	0.1735	0.1943	1.8431	0.1085	0.1265
253986_at	AT4G26210	mitochondrial ATP synthase g subunit family protein	0.5317	0.014	0.0723	0.622	0.0081	0.0503	0.3637	0.0376	0.0801	0.454	0.0188	0.044
253987_at	AT4G26270	phosphofructokinase family protein	1.4057	0.0041	0.0468	1.5642	0.0028	0.0351	0.3625	0.0722	0.1168	0.521	0.0252	0.0524
253988_at	AT4G26310	elongation factor P (EF-P) family protein	0.2117	0.2769	0.3099	0.3894	0.0817	0.1433	0.1304	0.1665	0.1894	0.3081	0.0163	0.0408
253989_at	AT4G26130	similar to unknown protein [Arabidopsis thaliana] (T	0.5659	0.105	0.1872	0.6289	0.0811	0.1428	0.2933	0.0721	0.1167	0.3562	0.042	0.0713
253990_at	AT4G26160	thioredoxin family protein	0.4696	0.0964	0.1795	0.2329	0.3434	0.3149	0.3401	0.0836	0.1272	0.1034	0.524	0.3355
253991_at	AT4G26000	PEP (PEPPER); nucleic acid binding	0.5867	0.0521	0.131	0.1525	0.5162	0.3911	0.4437	0.068	0.1131	0.009542	0.96	0.4733
253992_at	AT4G26060	similar to unknown protein [Arabidopsis thaliana] (T	1.1547	0.0319	0.1035	1.6107	0.0107	0.0958	0.0215	0.8656	0.4828	0.4775	0.0161	0.0404
253993_at	AT4G26070	MEK1 (mitogen-activated protein kinase kinase 1);	0.5518	0.2229	0.277	0.6401	0.1698	0.2124	0.197	0.3369	0.2868	0.2853	0.1894	0.179
253994_at	AT4G26080	ABI1 (ABA INSENSITIVE 1); calcium ion binding / p	0.2796	0.1268	0.2058	0.6368	0.0119	0.0585	-0.5692	0.0033	0.0256	-0.2036	0.0856	0.1094
253995_at	AT4G26100	CK1 (casein kinase 1-like protein 1); casein kinase	-0.03856	0.8573	0.5405	-0.104	0.6325	0.4355	-0.00092	0.9966	0.5168	-0.06634	0.7581	0.4161
253996_at	AT4G26110	NAP1;1 (NUCLEOSOME ASSEMBLY PROTEIN1;	0.2802	0.2644	0.3021	0.3882	0.1468	0.1959	-0.4422	0.0506	0.0954	-0.3342	0.1049	0.124
253997_at	AT4G26090	RPS2 (RESISTANT TO P. SYRINGAE 2)	0.687	0.0738	0.1563	0.4341	0.203	0.2347	-0.5325	0.0148	0.0484	-0.7855	0.0037	0.0199
253998_at	AT4G26010	peroxidase, putative	0.1597	0.8233	0.5306	1.033	0.1979	0.2316	-0.4351	0.4837	0.3528	0.4382	0.4808	0.3178
253999_at	AT4G26200	ACS7 (1-Amino-cyclopropane-1-carboxylate synthe	0.7022	0.0646	0.1454	0.8989	0.0317	0.0884	-0.4013	0.0906	0.133	-0.2046	0.321	0.2488
254000_at	AT4G26250	ATGOLS6 (ARABIDOPSIS THALIANA GALACTIN	1.859	0.086	0.1719	0.0533	0.9517	0.5323	1.0858	0.2597	0.2463	-0.72	0.4333	0.2982
254001_at	AT4G26260	MIOX4 (MYO-INOSITOL OXYGENASE 4)	2.5764	0.0639	0.1448	-0.5786	0.5989	0.423	0.7849	0.4821	0.352	-2.3701	0.0796	0.1047
254002_at	AT4G26280	sulfotransferase family protein	-0.8905	0.435	0.3916	-0.00213	0.9984	0.5436	-2.4514	0.0755	0.1197	-1.563	0.2028	0.1868
254003_at	AT4G26290	unknown protein	-0.2754	0.7982	0.5234	-0.3836	0.7229	0.4664	-0.2068	0.8376	0.4749	-0.3088	0.7533	0.4146
254004_at	AT4G26300	EMB1027 (EMBRYO DEFECTIVE 1027); ATP bind	0.007545	0.9434	0.5632	-0.2224	0.0899	0.1511	-0.07228	0.5093	0.3631	-0.3023	0.0389	0.0679
254005_at	AT4G26330	ATSBT3.18/UNE17 (UNFERTILIZED EMBRYO SA	-0.6455	0.4183	0.3841	-2.3991	0.0286	0.084	2.136	0.0406	0.0836	0.3824	0.6216	0.3707
254006_at	AT4G26340	F-box family protein	-0.5761	0.5817	0.4529	-1.3728	0.227	0.2497	0.84	0.4321	0.3305	0.04328	0.9663	0.4748
254007_s_at	AT1G60720.AT4G26360	[AT1G60720, similar to unknown protein [Arabidops	0.6728	0.4314	0.3899	-0.3849	0.6434	0.4393	0.844	0.3339	0.2854	-0.2137	0.7948	0.4274
254008_at	AT4G26380	DC1 domain-containing protein	0.5782	0.5249	0.4311	0.4931	0.5848	0.4181	-1.5144	0.0931	0.1352	-1.5995	0.0812	0.106
254009_at	AT4G26390	pyruvate kinase, putative	-0.7118	0.2215	0.2761	-2.227	0.0106	0.0556	1.2928	0.0583	0.1033	-0.2224	0.6747	0.389
254010_at	AT4G26240	similar to unnamed protein product [Vitis vinifera] (G	0.5532	0.0027	0.0426	0.4511	0.0056	0.0434	0.2446	0.0425	0.0858	0.1426	0.1621	0.1625
254011_at	AT4G26370	antitermination NusB domain-containing protein	0.01381	0.9341	0.5608	0.191	0.2905	0.2868	-0.06421	0.3587	0.2973	0.113	0.1423	0.1496
254012_at	AT4G26380	60S ribosomal protein L31 (RPL31B)	0.08738	0.7576	0.511	0.4048	0.2005	0.233	0.1043	0.6673	0.4203	0.4317	0.1551	0.1582
254013_at	AT4G26050	leucine-rich repeat family protein	0.4559	0.6276	0.4689	0.7572	0.4328	0.3567	0.03167	0.9707	0.5101	0.333	0.7018	0.3979
254014_at	AT4G26120	ankyrin repeat family protein / BTB/POZ domain-co	0.1049	0.0857	0.1697	1.4818	0.0313	0.088	-0.1357	0.2	0.2118	0.3112	0.0245	0.0515
254015_at	AT4G26140	BGAL10 (beta-galactosidase 10); beta-galactosidase	0.3405	0.0566	0.1362	0.1942	0.2289	0.2	-0.6477	0.005	0.0298	-1.1878	5.00E-04	0.0095
254016_at	AT4G26150	CGA1 (CYTOKININ-RESPONSIVE GATA FACTOR	-0.1694	0.2637	0.3018	-0.3978	0.038	0.0965	-0.00226	0.979	0.5123	-0.2307	0.0456	0.0749
254017_at	AT4G26170	similar to unknown protein [Arabidopsis thaliana] (T	-0.6593	0.6837	0.487	2.6838	0.1488	0.1973	-2.0149	0.2513	0.2415	1.3282	0.4269	0.2955
254018_at	AT4G26180	mitochondrial substrate carrier family protein	0.07504	0.7622	0.5122	0.1901	0.4578	0.3672	-0.4661	0.0495	0.0941	-0.351	0.1039	0.1234
254019_at	AT4G26190	similar to unknown protein [Arabidopsis thaliana] (T	0.01952	0.953	0.5655	-0.1441	0.6674	0.4475	-0.342	0.0972	0.1388	-0.5056	0.0333	0.0616
254020_at	AT4G25700	BETA-OHASE 1 (BETA-HYDROXYLASE 1); beta-c	-1.0531	0.0292	0.099	-1.3285	0.0137	0.062	-0.3422	0.0066	0.0333	-0.6176	7.00E-04	0.0108
254021_at	AT4G25650	ACD11 (ACCELERATED CELL DEATH 11); electron carrier	0.1308	0.2896	0.3171	-0.3296	0.0372	0.0953	0.2073	0.1254	0.1603	-0.2531

254090_at	AT4G25010	nodulin MtN3 family protein	-0.4903	0.668	0.482	0.0284	0.9799	0.5393	0.01406	0.9892	0.5152	0.5328	0.6155	0.3685
254091_at	AT4G25070	similar to unknown protein [Arabidopsis thaliana] (T	0.3948	0.4284	0.3884	0.5326	0.3006	0.2917	0.2262	0.4518	0.3395	0.364	0.2511	0.2132
254092_at	AT4G25090	respiratory burst oxidase, putative / NADPH oxidase	-0.7158	0.1418	0.2189	-0.9376	0.075	0.1373	0.0399	0.9238	0.4989	-0.1819	0.6667	0.3864
254093_at	AT4G25110	ATMC2 (METACASPASE 2); caspase	1.6709	9.00E-04	0.0349	1.1954	0.0033	0.0371	0.301	0.1443	0.1748	-0.1745	0.353	0.264
254094_at	AT4G25120	UvrD/REP helicase family protein	-0.1475	0.6174	0.4654	0.001559	0.9957	0.5431	-0.7886	0.0118	0.043	-0.6396	0.0236	0.0502
254095_at	AT4G25140	OLEO1 (OLEOSIN1)	-0.0295	0.9769	0.5715	0.3412	0.7399	0.4713	-1.5595	0.0436	0.0872	-1.1889	0.0907	0.1134
254096_at	AT4G25150	acid phosphatase, putative	-0.2605	0.3407	0.3456	-0.6555	0.053	0.1142	-0.1334	0.6095	0.4012	-0.5284	0.0935	0.1156
254097_at	AT4G25160	protein kinase family protein	1.5373	0.2036	0.2644	0.1323	0.9024	0.5195	-0.1281	0.9505	0.4938	-1.5331	0.2046	0.1877
254098_at	AT4G25100	FSD1 (FE SUPEROXIDE DISMUTASE 1); iron sup	-0.6726	0.0024	0.0421	-0.9388	7.00E-04	0.027	0.202	0.1092	0.1478	-0.06424	0.5493	0.3448
254099_at	AT4G25130	peptide methionine sulfoxide reductase, putative	-0.3406	0.0858	0.1699	-0.3252	0.0962	0.1562	0.1081	0.5112	0.3636	0.1235	0.4569	0.3088
254100_at	AT4G25020	KOW domain-containing protein / DYM1/KG-patch do	-0.3349	0.0812	0.1647	0.09184	0.5593	0.408	0.09775	0.6356	0.3734	0.5245	0.2221	0.0485
254101_at	AT4G25000	AMY1/ATAMY1 (ALPHA-AMYLASE-LIKE); alpha-a	0.9804	0.0204	0.0842	1.2957	0.0079	0.0496	0.1577	0.5123	0.364	0.4731	0.0975	0.1187
254102_at	AT4G25050	ACP4 (ACYL CARRIER PROTEIN 4)	-0.8361	0.0015	0.038	-0.8054	0.0017	0.0321	0.009678	0.9284	0.5002	0.04043	0.7099	0.4009
254103_at	AT4G25030	similar to unknown protein [Arabidopsis thaliana] (T	-0.07147	0.575	0.4508	0.01691	0.8923	0.5164	-0.06669	0.5998	0.3981	0.02169	0.8622	0.4464
254104_at	AT4G25040	integral membrane family protein	0.2959	0.6558	0.4778	1.086	0.1524	0.2	0.2182	0.7409	0.445	1.0083	0.1767	0.1712
254105_at	AT4G25080	CHLM (MAGNESIUM-PROTOPORPHYRIN IX MET	-0.892	0.0092	0.0618	-0.8766	0.0098	0.0538	-0.2821	0.1681	0.1905	-0.2667	0.1872	0.1777
254106_at	AT4G24990	ATGPI1 (ARABIDOPSIS thaliana glycerylcenalyated pl	1.5373	0.2036	0.2644	0.1323	0.9024	0.5195	-0.1281	0.9505	0.4938	-1.5331	0.2046	0.1877
254107_at	AT4G25220	transporter, putative	-0.3234	0.7603	0.5117	-0.8796	0.4245	0.3527	1.7713	0.137	0.1691	1.2152	0.2719	0.2238
254108_at	AT4G25230	RIN2 (RPM1 INTERACTING PROTEIN 2); protein b	0.06226	0.815	0.5283	0.1516	0.5756	0.414	-0.8131	0.0153	0.0492	-0.7237	0.0224	0.0487
254109_at	AT4G25240	SKS1 (SKU5 SIMILAR 1); copper ion binding	2.8345	0.0358	0.1093	0.1185	0.9028	0.5196	0.5097	0.6056	0.4	-2.2063	0.0726	0.0988
254110_at	AT4G25260	invertase/pectin methylesterase inhibitor family prot	-0.7245	0.0226	0.0879	-1.0096	0.0073	0.0484	0.226	0.3234	0.2799	-0.05909	0.7832	0.4239
254111_at	AT4G24890	ATPAP24/PAP24 (purple acid phosphatase 24); ac	-0.3778	0.6197	0.4665	0.3631	0.633	0.4357	1.2743	0.1444	0.1748	2.0153	0.0457	0.0751
254112_at	AT4G24970	ATP-binding region, ATPase-like domain-containing	0.1369	0.78	0.5179	-0.4108	0.4205	0.3509	0.1233	0.6715	0.4215	-0.4244	0.1911	0.1798
254113_at	AT4G24900	similar to hypothetical protein SDM1_56000018 [Sol	-0.1563	0.4831	0.4132	-0.2785	0.2407	0.2583	-1.0347	1.00E-04	0.0111	-1.157	1.00E-04	0.0058
254114_at	AT4G24980	nodulin MtN21 family protein	2.1196	0.0287	0.0982	1.5679	0.0686	0.1315	0.2131	0.4792	0.448	-0.3385	0.6163	0.3685
254115_at	AT4G24710	ATPase	0.1439	0.8417	0.5361	-0.318	0.6623	0.4458	-0.553	0.3686	0.3023	-1.0149	0.1367	0.146
254116_at	AT4G24730	calcineurin-like phosphoesterase family protein	0.09946	0.5361	0.4355	0.2081	0.2302	0.2517	0.07773	0.4869	0.3542	0.1863	0.1406	0.1485
254117_at	AT4G24750	similar to rhodanese-like domain-containing protein	-0.4363	0.0624	0.1433	-0.6204	0.0218	0.0748	-0.1644	0.2987	0.2682	-0.3486	0.0647	0.0925
254118_at	AT4G24790	ATP binding / DNA binding / DNA-directed DNA pol	-0.4332	0.1493	0.225	-0.6327	0.0599	0.1215	-0.5992	0.0156	0.0497	-0.7986	0.0057	0.0235
254119_at	AT4G24780	pectate lyase family protein	-0.01763	0.9665	0.5688	0.05104	0.9034	0.5197	-0.202	0.241	0.2356	-0.1334	0.4152	0.2905
254120_at	AT4G24570	mitochondrial substrate carrier family protein	-1.4594	0.018	0.0802	-1.7665	0.0094	0.053	1.0938	0.0102	0.0401	0.7866	0.0301	0.0583
254121_at	AT4G24760	similar to unknown protein [Arabidopsis thaliana] (T	-0.314	0.171	0.2421	-0.03832	0.8488	0.504	-0.2538	0.2493	0.2405	0.02189	0.9131	0.4607
254122_at	AT4G24510	CER2 (ECERIFERUM 2); transferase	-1.0834	0.0489	0.1271	-0.8673	0.0886	0.15	0.07591	0.3963	0.3149	0.292	0.0218	0.0481
254123_at	AT4G24640	APR81; pectinesterase inhibitor	-0.02676	0.9831	0.5728	-1.1546	0.3845	0.3339	0.4647	0.7146	0.4364	-0.6631	0.6051	0.365
254124_at	AT4G24500	hydroxyproline-rich glycoprotein family protein	-0.2909	0.1472	0.2232	0.1095	0.5365	0.3991	-0.5444	0.0284	0.0684	-0.144	0.4245	0.2944
254125_at	AT4G24670	allinase family protein	-1.5163	4.00E-04	0.032	-2.1845	1.00E-04	0.0249	0.2367	0.1581	0.1844	-0.4314	0.0342	0.0626
254126_at	AT4G24770	NBP73 (14-KDA RNA-BINDING PROTEIN); RNA b	-0.6707	0.0067	0.0552	-0.6361	0.0081	0.0501	-0.1658	0.2394	0.2331	-0.131	0.3327	0.2547
254127_at	AT4G24520	ATR1 (ARABIDOPSIS P450 REDUCTASE 1)	0.406	0.0425	0.1187	0.3045	0.0924	0.1534	-1.1819	0.001	0.0178	-1.2834	7.00E-04	0.0108
254128_at	AT4G24560	UBP16 (UBIQUITIN-SPECIFIC PROTEASE 16); ub	0.3698	0.0344	0.1073	0.05851	0.6441	0.4396	-0.3248	0.0504	0.095	-0.6361	0.0056	0.0234
254129_at	AT4G24650	ATIPT4 (ARABIDOPSIS thaliana isopentenyltransferase	1.8034	0.2157	0.2722	0.4009	0.7604	0.4778	-0.6004	0.6503	0.4145	1.6038	0.2614	0.2185
254130_at	AT4G24540	AGL24 (AGAMOUS-LIKE 24); protein binding / prot	-0.3487	0.1869	0.2534	-0.2064	0.3998	0.3411	-0.1361	0.2914	0.2643	0.006181	0.9587	0.4731
254131_at	AT4G24740	AFC2 (ARABIDOPSIS FUS3-COMPLEMENTING G	0.3255	0.0645	0.1454	0.4321	0.0283	0.0836	-0.1939	0.206	0.2154	-0.08725	0.5345	0.3396
254132_at	AT4G24610	ATHB22/MEE63 (ARABIDOPSIS THALIANA HOME	0.03721	0.8782	0.5461	0.2297	0.3704	0.3277	0.02619	0.8064	0.4655	0.2931	0.0429	0.0723
254133_at	AT4G24810	ABC1 family protein	-0.1942	0.4982	0.4197	-0.3998	0.2003	0.233	-0.4795	0.0303	0.0708	-0.6852	0.0093	0.0301
254134_at	AT4G24830	arginosuccinate synthase family	-0.4034	0.0897	0.1734	-0.568	0.0349	0.0923	0.2089	0.0687	0.1137	0.04428	0.6279	0.373
254135_at	AT4G24860	AAA-type ATPase family protein	1.0854	0.0513	0.1301	0.2566	0.5508	0.4052	0.3188	0.4645	0.3451	-0.5102	0.2655	0.2206
254136_at	no_match	no_match	-1.8359	0.2342	0.2839	2.0096	0.2003	0.233	-1.1809	0.4189	0.3248	2.6646	0.1121	0.1291
254137_at	AT4G24930	thylakoid lumenal 17.9-kDa protein, chloroplast	-1.2	0	0.0312	-1.4555	0	0.0249	0.6846	4.00E-04	0.0146	0.429	0.0023	0.016
254138_at	AT4G24950	unknown protein	0.5848	0.3384	0.3447	-0.6068	0.3226	0.3046	0.5535	0.3618	0.2991	-0.638	0.3015	0.2394
254139_at	AT4G24600	unknown protein	1.366	0.2601	0.2997	2.1898	0.1035	0.1624	-0.8234	0.3092	0.273	0.000415	0.9996	0.4829
254140_at	AT4G24610	similar to unknown protein [Arabidopsis thaliana] (T	1.1708	0.0337	0.1062	1.2101	0.0304	0.0866	-0.116	0.7687	0.4537	-0.07671	0.8453	0.4415
254141_at	AT4G24620	PGI1 (CHLOROPLASTIC PHOSPHOGLUCOSE IS	-0.4724	0.0517	0.1306	-0.5215	0.0388	0.0977	-0.4663	0.0191	0.0554	-0.5154	0.0137	0.0371
254142_at	AT4G24630	receptor/ zinc ion binding	0.5185	0.1624	0.2357	0.4351	0.2245	0.2482	-0.3849	0.2731	0.254	-0.4682	0.1973	0.1833
254143_at	AT4G24680	similar to unmarked protein product [Vitis vinifera] (G	-0.02501	0.8834	0.5471	-0.1887	0.3039	0.2936	-0.4491	0.0485	0.0927	-0.6128	0.0187	0.0438
254144_at	AT4G24650	ubiquitin-associated (UBA)/TS-N domain-containing	1.4085	0.003	0.0436	1.5296	0.0022	0.0334	-0.5336	6.00E-04	0.0158	-0.4127	0.0015	0.0138
254145_at	AT4G24700	unknown protein	-1.2275	0.0033	0.0446	-1.7517	9.00E-04	0.0284	0.2565	0.2617	0.2474	-0.2677	0.2447	0.2096
254146_at	AT4G24260	ATGH9A3/KOR3 (ARABIDOPSIS THALIANA GLYC	-0.333	0.2884	0.3164	0.04048	0.889	0.5155	-0.3461	0.2725	0.2538	0.0274	0.9247	0.4641
254147_at	AT4G24270	RNA recognition motif (RRM)-containing protein	0.7276	0.0376	0.1119	0.7817	0.0302	0.0864	-0.215	0.2193	0.2232	-0.1609	0.3373	0.2566
254148_at	AT4G24280	CPHSC70-1 (chloroplast heat shock protein 70-1);	-0.1302	0.2822	0.3128	-0.4746	0.0106	0.0556	-0.1703	0.1798	0.1985	-0.5146	0.008	0.0278
254149_at	AT4G24300	peptidase	-1.8576	0.1129	0.1947	0.3935	0.6901	0.4557	-0.9637	0.2784	0.2571	1.2873	0.1694	0.1668
254150_at	AT4G24350	phosphoesterase family protein	-1.2766	0.0232	0.0892	-1.4339	0.0159	0.0656	-0.6004	2.00E-04	0.0129	-0.7576	1.00E-04	0.0058
254151_at	AT4G24390	F-box family protein (FBX14)	0.02595	0.8765	0.5456	0.426	0.053	0.1142	-0.3767	0.074	0.1184	0.02332	0.8889	0.454
254152_at	AT4G24410	unknown protein	0.3533	0.8288	0.532	-2.0455	0.2525	0.2655	1.304	0.4423	0.3351	-1.0948	0.514	0.3312
254153_at	AT4G24450	AT6P/2GGWD3/PWD (PHOSPHOGLUCAN, WAT	0.6456	0.0757	0.1584	0.9947	0.7443	0.4728	-1.2408	0.0014	0.0193	-1.7916	3.00E-04	0.0085
254154_at	AT4G24460	similar to unknown protein [Arabidopsis thaliana] (T	0.1738	0.3869	0.3682	-0.2122	0.3017	0.2923	0.03851	0.8361	0.4744	-0.3475	0.1172	0.1328
254155_at	AT4G24480	serine/threonine protein kinase, putative	0.2216	0.4956	0.4184	-0.03658	0.9076	0.5208	-0.6766	0.0544	0.0993	-0.9349	0.0204	0.0461
254156_at	AT4G24490	protein binding / protein prenyltransferase	0.3147	0.053	0.1322	0.6366	0.0053	0.0431	-0.8111	0.0022	0.0219	-0.4892	0.0134	0.0367
254157_at	AT4G24220	VEP1 (VEIN PATTERNING 1); binding / catalytic	0.5296	0.0471	0.1249	0.3255	0.1564	0.2031	-0.6427	0.0114	0.0423	-0.8468	0.0043	0.0208
254158_at	AT4G24380	hydrolase, acting on ester bonds	-0.4991	0.1141	0.1957	-0.4762	0.1269	0.1806	0.5048	0.0789	0.1228	0.5277	0.0703	0.0972
254159_at	AT4G24240	WRKY7 (WRKY DNA-binding protein 7); transcriptio	0.09108	0.7532	0.5095	-0.1715	0.5606	0.4085	-0.163	0.5791	0.3904	-0.4256	0.1907	0.1796
254160_at	AT4G24210	SLY1 (SLEEPY1)	0.2654	0.2087	0.2672	0.5556	0.035	0.0925	0.4626	0.0594	0.1046	0.7528	0.0132	0.0364
254161_at	AT4G24370	unknown protein	0.2467	0.2376	0.2861	0.7235	0.0152	0.0648	-0.01385	0.9417	0.5037	0.4629	0.0598	0.0884
254162_at	AT4G24440	initiation factor IIA gamma chain / TFIIA-gamma (TF	0.9041	0.001	0.0349	0.6703	0.0029	0.0355	0.4093	0.0091	0.0383	0.1755	0.1128	0.1296
254163_s_at	AT4G24340;AT4G24350	[AT4G24340, phosphorylase family protein];[AT4G2	-1.2738	0.085	0.1688	-1.807	0.0319	0.0887	0.6269	0.0265	0.0662	0.09371	0.6351	0.3755
254164_at	AT4G24470	ZIM (ZINC-FINGER PROTEIN EXPRESSED IN INF	0.5874	0.0041	0.0468	0.4545	0.0102	0.0549	0.1831	0.0468	0.0907	0.05016	0.4798	0.3174
254165_at	AT4G24330	similar to unknown protein [Arabidopsis thaliana] (T	0.3794	0.0221	0.0872	0.2215	0.1012	0.1605	0.4039	0.009	0.0378	0.246	0.0444	0.0739
254166_at	AT4G24190	SHD (SHEPHERD); ATP binding	1.4321	0	0.0312	1.2505	0	0.0249	0.07928	0.1828	0.2008	-0.1023	0.1063	0.1249
254167_at	AT4G24400	CIPK8 (CBL-INTERACTING PROTEIN KINASE 8);	0.3999	0.082	0.1656	0.333	0.1266	0.1805	0.1375	0.1505	0.1792	0.07066	0.4132	0.2897
254168_at	AT4G24250	MLO13 (MILDEW RESISTANCE LOCUS O 13); cal	0.3841	0.6107	0.463	-0.7887	0.3208	0.3036	0.7489	0.3428	0.2898	-0.4239	0.5757	0.3544
254169_at	AT4G24290	similar to NSL1 (NECROTIC SPOTTED LESIONS	-0.07504	0.6207	0.4667	0.2697	0.1266	0.1805	-1.2508	9.00E-04	0.0169	-0.9061	0.0029	0.0176
254170_at	AT4G24430	lyase	-0.3345	0.6183	0.4658	-0.1586	0.8107	0.4932	-0.2818	0.6732	0.422	-0.1059	0.8727	0.4493
254171_at	AT4G24530	similar to unknown protein [Arabidopsis thaliana] (T	0.02068	0.82	0.5296	0.2389	0.0485	0.1094	-0.2084	0.0387	0.0812	0.05124	0.4972	0.3248
254172_at	AT4G24550	clathrin adaptor complexes medium subunit family p	0.6327	6.00E-04	0.0325	0.5108	0.0013	0.0309	0.007542	0.9111	0.4955	-0.1143	0.146	0.1521
254173_at	AT4G24580	pleckstrin homology (PH) domain-containing protein	0.3412	0.7916	0.5213	0.7897	0.5491	0.4044	-0.5152	0.6918	0.4283	-0.06672	0.9586	0.4731
254174_at	AT4G24120	YSL1 (YELLOW STRIPE LIKE 1); oligopeptide tran	0.4686	0.057	0.137	0.4205	0.0762	0.1383	-0.233	0.0662	0.1113	-0.2811	0.0389	0.0679
254175_at	AT4G24050	short-chain dehydrogenase/reductase (SDR) family	-0.8476	0.0529	0.1319	-0.5123	0.1753	0.2164	-0.4213	0.0724	0.1169	-0.08595	0.6467	0.3796
254176_at	AT4G24200	DNA binding / protein binding / transcription regulat	0.6219	0.1053	0.1875	0.5908	0.1186	0.1741	0.1921	0.4903	0.3557	0.161	0.5594	0.3486
254177_at	AT4G23860	PHD finger protein-related	-0.06416	0.7876	0.52	0.2182	0.3827	0.3331	-0.2187	0.3818	0.3087	0.0637	0.7891	0.4255
254178_at	AT4G23880	unknown protein	0.8231	0.0629	0.1438	1.1976	0.0205	0.073	0.006281	0.9737	0.5109	0.3808	0.101	0.1213
254179_at	AT4G23910	similar to unknown protein [Arabidopsis thaliana] (T	0.6305	0.0042	0.0472	0.02619	0.8198	0.4958	0.6448	0.0012	0.0187	0.04054	0.6315	0.3742
254180_at	AT4G23930	similar to proline-rich family protein [Arabidopsis tha	0.2116	0.8134	0.5278	1.1217	0.2523	0.2654	0.4378	0.6295	0.4077	1.3479	0.1835	0.1756
254181_at	AT4G23940	FtsH protease, putative	-0.1296	0.287	0.3155	-0.6119	0.0044	0.041	-0.4658	0.0116	0.0426	-0.9481	9.00E-04	0.0113
254182_at	AT4G23950	similar to unknown protein [Arabidopsis thaliana] (T	0.1792	0.3989	0.3748	-0.3815	0.115	0.1711	-0.1612	0.3122	0.2746	-0.7219	0.0066	0.0253
254183_at	AT4G23960	F-box family protein	1.621	0.0751	0.1576	-0.5328	0.4759	0.3745	1.0486	0.1968	0.2098	-1.1052	0.1784	0.1723
254184_at	AT4G23970	unknown protein	0.0995	0.8436	0.5369	-0.5454	0.3128	0.2989	0.2113	0.678	0.4238	-0.4336	0.4109	0.2886
254185_at	AT4G23990	ATCSLG3 (Cellulose synthase-like G3); transferase	-0.4283	0.2382	0.2864	-0.6685	0.0966	0.1566	-0.0516	0.6533	0.4157	-0.2918	0.0519	0.0812
254186_at	AT4G24010	ATCSLG1 (Cellulose synthase-like G1); transferase	-0.7495	0.2723	0.3067	-0.8534	0.2211	0.2466	0.9688	0.1755	0.1956	0.8648	0.2161	0.1941
254187_at	AT4G23890	similar to unmarked protein product [Vitis vinifera] (G	-0.1977	0.4362	0.3921	-0.4348	0.1301	0.1829	0.451	0.1199	0.1562	0.2139	0.4026	0.2853
254188_at	AT4G23920	UGE2 (UDP-D-GLUCOSE/UDP-D-GALACTOSE 4-	0.2491	0.1852	0.2521	-0.07289	0.6644	0.4464	0.1058	0.5344	0.373	-0.2162	0.2377	0.206
254189_at	AT4G24000	ATCSLG2 (Cellulose synthase-like G2); transferase	0.05457	0.8549	0.5396	1.0998	0.0193	0.0715	-1.8813	0.002	0.0211	-0.8761	0.0285	0.0564
254190_at	AT4G23885	similar to unknown protein [Arabidopsis thaliana] (T	0.9788	0.0318	0.1033	1.5201	0.0074	0.0484	0.9334	0.0113	0.0421	1.4747	0.0022	0.0157
254191_at	AT4G23900	nucleoside diphosphate kinase 4 (NDK4)	-0.4123	0.0315	0.1029	-0.09138	0.5119	0.3894	-0.2552	0.0772	0.1213	0.06576	0.575	0.3541
254192_at	AT4G23850	long-chain-fatty-acid--CoA ligase / long-chain acyl-C	0.6739	0.0021	0.0404	0.5799	0.0036	0.0378	0.025578	0.7991	0.4631	-0.06817	0.5118	0.3304
254193_at	AT4G23870	similar to unknown protein [Arabidopsis thaliana] (T	0.2838	0.4868	0.4145	0.3698	0.3752	0.33	-0.4652	0.1179	0.1546	-0.3792	0.1806	0.1737
254194_at	AT4G23980	ARF9 (AUXIN RESPONSE FACTOR 9); transcriptic	0.08679	0.683	0.4868	0.1574	0.4702	0.3722	-0.6888	0.0035	0.026	-0.6182	0.0051	0.0225
254195_at	AT4G24020	RWP-RK domain-containing protein	0.2163	0.0285	0.0977	-0.1809	0.0486	0.1095	-0.2552	0.0022	0.0219	-0.6524	1.00E-04	0.0056
254196_at	AT4G24030	unknown protein	-1.3953	0.2274	0.2801	0.7022	0.5131	0.3899	0.8083	0.4556	0.3411	2.9058	0.0413	0.0705
254197_at	AT4G24040	ATTRE1/TRE1 (TREHALASE 1); alpha,alpha-treha	1.2656	0.0172	0.0786	0.7647	0.0768	0.139	-0.1369	0.574	0.3881	-0.6378	0.0465	0.0759
254198_at	AT4G24090	similar to hypothetical protein [Vitis vinifera] (GB:CA	-0.2843	0.0135	0.0716	-0.323	0.0087	0.0513	0.3872	0.0046	0.0288	0.3485	0.0067	0.0254
254199_at	no_match	no_match	-1.0605	0.1341	0.2125	-0.7111	0.2772	0.2793	-0.3819	0.5367	0.3739	-0.03244	0.957	0.4727
254200_at	AT4G24110	similar to unmarked protein product [Vitis vinifera] (G	0.3641	0.7861	0.5196	-0.545	0.6864	0.4544	-1.0946	0.4322	0.3306	-2.0037	0.1855	0.1766
254201_at	AT4G24130	similar to unknown protein [Arabidopsis thaliana] (T	-0.3111	0.1439	0.2205	-0.3038	0.1512	0.1992	0.756	0.0116	0.0427	0.7633	0.0112	0.0332
254202_at	AT4G24140	hydrolase, alpha/beta fold family protein	-0.1552	0.8093	0.5266	-1.6996	0.0477	0.1084	0.2255	0.7271	0.4409	-1.3189	0.0937	0.1158
254203_at	AT4G24150	AtGRF8 (GROWTH-REGULATING FACTOR 8)	0.4362	0.0865	0.2024	0.4933	0.0816	0.1432	-0.3402	0.766	0.453	-0.2861	0.3037	0.4298
254204_at	AT4G24160	hydrolase, alpha/beta fold family protein	-0.2407	0.3319	0.3411	-0.1438	0.546	0.403	0.07952	0.6789	0.4241	0.1765	0.3786	0.275
254205_at	AT4G24170	kinesin motor family protein	-0.764	0.5996	0.4596	-3.1505	0.0788	0.1406	1.2415	0.4073	0.3197	-1.145	0.4417	0.3022
254206_at	AT4G24180	similar to thaumatin, putative [Arabidopsis thaliana]	1.905	0.0899	0.1735	1.8797	0.0929	0.1538	-0.4607	0.3691	0.3023	-0.8903	0.3567	0.2655
254207_at	AT4G24060	Def-type zinc finger domain-containing protein	0.05799	0.8072	0.526	0.4115	0.1381	0.1892	-0.01784	0.9273	0.4999	0.3357	0.1417	0.1493
254208_at	AT4G24175	similar to unmarked protein product [Vitis vinifera] (G	-0.5466	0.1559	0.2302	-0.5694	0.1432	0.1931	0.1605	0.6352	0.4095	0.1377	0.6828	0.3915
254209_at	AT4G24490	fringe-related protein	-0.7799	0.0286	0.0979	-0.9269	0.0164	0.0665	0.006407	0.9633	0.5084	-0.1387	0.4644	0.3118
254210_at	AT4G23450	zinc finger (C3HC4-type RING finger) family protein	1.5406	0.0402	0.1157	1.56	0.0387	0.0975	0.03093	0.938	0.503	0.05028	0.8994	0.457
254211_at	AT4G23570	SGT1A (Suppressor of G2 (Two) 1A); protein bindir	0.7022	0.0081	0.0588	0.5943	0.0144	0.0633	0.09538	0.5426	0.3764	-0.01255	0.9345	0.4669
254212_at	AT4G23580	kelch repeat-containing F-box family protein	0.9198	0.0031	0.0441	-1.0368	0.0043	0.1547	-2.3499	0.0078	0.0354	-0.3668	0.4828	0.3188
254213_at	AT4G23590	aminotransferase class I and II family protein	-0.5476	0.6658	0.4812	1.6797	0.2265	0.2496	-1.5763	0.2513	0.2415	0.651	0.6095	0.3665
254214_at	AT4G23640	TRH1 (TINY ROOT HAIR 1); potassium ion transm	0.2991	0.1833	0.2506	0.2257	0.2919	0.2876	0.007321	0.9612	0.5081	-0.06605	0.6652	0.3858
254215_at	AT4G23700	ATCHX17 (CATION/H+ EXCHANGER 17); antiport	2.138	0.0257	0.0929	1.8804	0.0381	0.0966	-0.4319	0.1239	0.1593	-0.6895	0.0361	0.0646
254216_at	AT4G23710	VAG2/VATG2/VHA-G2 (VACUOLAR ATP SYNTHA	-0.2295	0.1693	0.2409	0.1634	0.299	0.291	0.3598	0.0022	0.0219	0.7527	1.00E-04	0.0063
254217_at	AT4G23720	similar to unknown protein [Arabidopsis thaliana] (T	1.3926	0.1019	0.1845	0.7619	0.3116	0.2983	0.4586	0.5245	0.3689	-0.1722	0.8067	0.4306
254218_at	AT4G23740	leucine-rich repeat transmembrane protein kinase,	-0.6889	0.0135	0.0717	-0.6221	0.019	0.071	-0.00142	0.9883	0.5149	0.06537	0.5133	0.331
254219_at	AT4G23760	unknown protein	0.2234	0.853	0.5389	0.1675	0.8893	0.5156	0.842	0.4747	0.3495	0.7862	0.5026	0.3268
254220_at	AT4G23780	similar to unknown protein [Arabidopsis thaliana] (T	-1.4198	0.1053	0.1875	-0.3274	0.6556	0.4438	-2.3204	0.027	0.0668	-1.2279	0.1455	0.1518
254221_at	AT4G23820	glycosyl hydrolase family 28 protein / polygalacturo	-0.3824	0.288	0.3162	-0.08889	0.7901	0.4861	-0.1218	0.1668	0.1895	0.1717	0.0761	0.1016
254222_at	no_match	no_match	-0.0385	0.9349	0.561	0.03239	0.9452	0.5306	-0.5361	0.2925

254290_at	AT4G23000	protein serine/threonine phosphatase	-0.4336	0.2171	0.2733	0.7263	0.0703	0.1326	-1.1818	0.0111	0.0417	-0.02191	0.938	0.4678
254291_at	AT4G23010	ATUTR2/UTR2 (UDP-GALACTOSE TRANSPORTE	0.6009	0.1542	0.2292	0.3823	0.3268	0.3069	0.1997	0.3081	0.2725	-0.01889	0.9174	0.462
254292_at	AT4G23030	MATE efflux protein-related	2.1699	0.0884	0.1724	2.9636	0.0376	0.0959	-0.4209	0.4183	0.3245	0.3728	0.4694	0.3135
254293_at	AT4G23060	IQD22 (IQ-domain 22); calmodulin binding	-0.9861	0.0833	0.1671	-0.679	0.1891	0.2257	-0.9309	0.0036	0.0265	-0.6238	0.0147	0.0386
254294_at	AT4G23070	rhomboid family protein	-0.5596	0.6503	0.4764	-0.1886	0.877	0.5123	-0.7005	0.5733	0.3878	-0.3296	0.7875	0.425
254295_at	AT4G23080	similar to unknown protein [Arabidopsis thaliana] (T	-2.3769	0.0453	0.1225	0.08798	0.9204	0.5241	-2.5807	0.0355	0.0773	-0.1159	0.8953	0.4558
254296_at	AT4G23090	unknown protein	-1.7135	0.0923	0.176	0.5408	0.5251	0.3941	-1.4754	0.1307	0.1643	0.7789	0.3732	0.2727
254297_at	AT4G23100	insulin-like growth factor binding	2.5554	0.1381	0.2159	0.7547	0.614	0.4284	1.5054	0.3174	0.2769	-0.2953	0.8338	0.4383
254298_at	AT4G22890	PGR5-LIKE A	-0.4815	0.0048	0.0498	-0.6578	0.0015	0.0314	0.2099	0.0333	0.0745	0.03369	0.636	0.3757
254299_at	AT4G22920	ATNYE1/NYE1 (NON-YELLOWING 1)	0.03465	0.9088	0.5536	0.2452	0.4369	0.3583	-0.02508	0.9059	0.4939	0.1855	0.4045	0.286
254300_at	AT4G22780	ACR7 (ACT Domain Repeat 7)	-0.0484	0.899	0.5508	0.5556	0.1956	0.2298	-0.5417	0.0018	0.0206	0.06232	0.4465	0.3047
254301_at	AT4G22790	MATE efflux family protein	-0.2616	0.3997	0.3752	-0.1825	0.5472	0.4034	-0.1469	0.4842	0.3531	-0.06778	0.7403	0.4105
254302_at	AT4G22800	unknown protein	0.2256	0.834	0.5337	0.3618	0.738	0.4706	-1.2535	0.282	0.2592	-1.1173	0.3302	0.2534
254303_at	AT4G22830	similar to Os04g0379400 [Oryza sativa (japonica cu	-0.6531	0.051	0.1298	-0.8516	0.0228	0.0763	0.4193	0.0468	0.0907	0.2208	0.2088	0.1902
254304_at	AT4G22270	similar to unknown protein [Arabidopsis thaliana] (T	-0.7437	0.0066	0.0551	-0.5789	0.0158	0.0654	-0.2532	0.153	0.1808	-0.08845	0.5717	0.3531
254305_at	AT4G22200	AKT2 (Arabidopsis K+ transporter 2); cyclic nucleot	0.2819	0.3986	0.3747	0.2475	0.4538	0.3655	-0.4802	0.0351	0.0768	-0.5146	0.0284	0.0563
254306_at	AT4G22330	ATCES1; catalytic	2.5554	0.1381	0.2159	0.7547	0.614	0.4284	1.5054	0.3174	0.2769	-0.2953	0.8338	0.4383
254307_at	AT4G22400	similar to unknown protein [Arabidopsis thaliana] (T	-1.3667	0.3327	0.3416	0.3405	0.7974	0.4887	-2.1259	0.1619	0.1866	-0.4188	0.7528	0.4145
254308_at	AT4G22410	ubiquitin carboxyl-terminal hydrolase family protein	-0.2658	0.3336	0.3421	0.2965	0.2877	0.2852	-1.5782	0.0029	0.0244	-1.016	0.0137	0.0372
254309_s_at	AT4G22420,AT4G22390	AT4G22420, Identical to Putative F-box protein At4	-0.9242	0.4917	0.4165	0.7531	0.5712	0.4124	-1.8931	0.1332	0.1661	-0.2158	0.8407	0.4403
254310_at	AT4G22430	Identical to Putative F-box/Kelch-repeat protein At4	-0.89	0.483	0.4132	0.3623	0.7689	0.4801	-0.00231	0.9985	0.5174	1.2499	0.339	0.2575
254311_at	AT4G22440	unknown protein	-0.155	0.626	0.4684	-0.814	0.0509	0.112	0.2871	0.3842	0.3098	-0.3692	0.2777	0.2269
254312_s_at	AT4G22450,AT1G61510	[AT4G22450, transposable element gene];[AT1G61	-0.4993	0.4859	0.414	-0.8408	0.2661	0.2733	-0.5117	0.4076	0.3198	-0.8532	0.1981	0.1838
254313_at	AT4G22460	protease inhibitor/seed storage/lipid transfer protein	-0.4672	0.3903	0.37	-0.8561	0.1525	0.2001	0.4114	0.4443	0.3359	0.0225	0.9652	0.4745
254314_at	AT4G22470	protease inhibitor/seed storage/lipid transfer protein	0.1347	0.7972	0.523	-0.1097	0.834	0.4999	0.4126	0.2069	0.2159	0.1681	0.5729	0.3535
254315_at	no_match	no_match	-0.2087	0.7439	0.507	-0.1033	0.8708	0.5101	-0.857	0.2046	0.2145	-0.7516	0.255	0.2152
254316_at	no_match	no_match	-0.2068	0.8259	0.5313	2.1744	0.0691	0.1318	-0.6251	0.5171	0.3659	1.756	0.117	0.1326
254317_at	AT4G22510	unknown protein	0.45	0.6649	0.4809	0.534	0.609	0.4267	-1.0719	0.3284	0.2825	-0.9879	0.3633	0.2684
254318_at	AT4G22530	embryo-abundant protein-related	0.8722	0.1842	0.2511	1.0441	0.1274	0.1811	0.4854	0.142	0.173	0.6573	0.0688	0.0961
254319_at	AT4G22560	similar to unknown protein [Arabidopsis thaliana] (T	-0.9941	0.0195	0.0826	-0.9259	0.0245	0.0786	0.8164	0.0361	0.0781	0.8846	0.0282	0.056
254320_at	AT4G22580	exostosin family protein	-0.3432	0.1162	0.1971	-0.1198	0.5237	0.3936	-0.1121	0.4806	0.3516	0.1113	0.4835	0.3191
254321_at	AT4G22590,AT4G22592	[AT4G22590, trehalose-6-phosphate phosphatase,	-0.06187	0.8077	0.5262	-0.02254	0.9291	0.5265	0.2565	0.1527	0.1807	0.2958	0.1118	0.1289
254322_at	AT4G22600	similar to hypothetical protein [Vitis vinifera] (GB:CA	1.9342	0.1971	0.2606	-1.0492	0.449	0.3636	1.2545	0.3396	0.2882	-1.7289	0.2097	0.1908
254323_at	AT4G22620	auxin-responsive family protein	-2.3166	0.0873	0.1711	-2.3009	0.0891	0.1504	1.4186	0.2244	0.2159	1.4384	0.1208	0.1356
254324_at	AT4G22640	similar to unknown protein [Arabidopsis thaliana] (T	-0.292	0.7843	0.519	-0.3829	0.7207	0.4656	0.776	0.4801	0.3514	0.6852	0.5299	0.3379
254325_at	AT4G22650	similar to unknown protein [Arabidopsis thaliana] (T	0.04672	0.964	0.5682	-0.5087	0.6289	0.434	-0.513	0.6261	0.4066	-1.0685	0.334	0.2552
254326_at	AT4G22610	protease inhibitor/seed storage/lipid transfer protein	-0.1936	0.8041	0.6251	-0.422	0.5946	0.4213	-0.9863	0.1361	0.1685	-1.2152	0.0836	0.1079
254327_at	AT4G22490	protease inhibitor/seed storage/lipid transfer protein	-0.06624	0.8451	0.5372	0.04268	0.8997	0.5188	0.08255	0.7315	0.4422	0.1915	0.4414	0.302
254328_at	AT4G22570	APT3 (ADENINE PHOSPHORIBOSYL TRANSFER	-0.4179	0.056	0.1359	-0.6159	0.0171	0.0679	0.1439	0.4106	0.321	-0.05411	0.7473	0.4129
254329_at	AT4G22540	unknown protein	0.6753	0.007	0.0566	0.7654	0.0445	0.0413	-0.553	0.0141	0.0473	-0.4628	0.0252	0.0525
254330_at	AT4G22700	LBD32 (LOB DOMAIN-CONTAINING PROTEIN 32	1.5791	0.0297	0.1	-1.3134	0.0512	0.1123	1.889	0.0148	0.0486	-1.0035	0.0949	0.1167
254331_s_at	AT4G22710,AT4G22690	[AT4G22710, CYP706A2 (cytochrome P450, family	-0.3799	0.1021	0.1847	-0.3226	0.1471	0.1961	0.02623	0.8633	0.4822	0.08348	0.5904	0.3601
254332_at	AT4G22730	leucine-rich repeat transmembrane protein kinase,	-0.2658	0.3577	0.3533	-0.254	0.3606	0.3231	0.3362	0.2243	0.2262	0.338	0.2224	0.1972
254333_at	AT4G22753	SMO1-3 (STEROL 4-ALPHA METHYL OXIDASE);	-0.6396	0.0067	0.0552	-0.4356	0.0246	0.0787	-0.2493	0.066	0.1112	-0.04542	0.6712	0.3878
254334_at	AT4G22760	pentatricopeptide (PPR) repeat-containing protein	0.251	0.8367	0.5343	-1.0561	0.4072	0.3445	1.0275	0.4189	0.3248	-0.2796	0.8185	0.4338
254335_at	AT4G22200	IM (IMMUTANS)	0.3952	0.0326	0.1047	0.4146	0.0281	0.0835	-0.2192	0.0262	0.0658	-0.1998	0.0348	0.0631
254336_at	AT4G22050	aspartyl protease family protein	2.7742	0.0977	0.1805	-1.0164	0.4745	0.374	1.1311	0.4298	0.3295	-2.6595	0.1081	0.1262
254337_at	no_match	no_match	-1.2396	0.2229	0.277	1.8844	0.0936	0.154	-1.4768	0.161	0.1862	1.6471	0.128	0.1402
254338_s_at	AT4G22800,AT4G22090	[AT4G22800, pectate lyase family protein];[AT4G22	0.6708	0.5351	0.4352	-2.1445	0.0962	0.1562	1.0741	0.3389	0.2878	-1.7413	0.1534	0.1571
254339_at	AT4G22100	glycosyl hydrolase family 1 protein	-1.2774	0.175	0.2448	-0.4872	0.5641	0.4098	-0.8058	0.317	0.2767	-0.01561	0.9834	0.4788
254340_at	AT4G22120	early-responsive to dehydration protein-related / ER	0.2098	0.4182	0.384	-0.1173	0.6406	0.4384	-0.02136	0.9313	0.5011	-0.3485	0.2086	0.19
254341_at	AT4G22130	SRF8 (STRUBBELIG-RECEPTOR FAMILY 8); kina	-0.1574	0.4785	0.4112	-0.06989	0.7463	0.4737	-0.03633	0.8657	0.4828	0.05118	0.8121	0.4323
254342_at	AT4G22140	DNA binding	0.04826	0.7485	0.5084	-0.06331	0.6756	0.4504	-0.06241	0.4031	0.3178	-0.174	0.0598	0.0883
254343_at	AT4G21990	APR3 (APS REDUCTASE 3)	-1.7578	1.00E-04	0.0312	-1.8878	1.00E-04	0.0249	0.01751	0.8937	0.4908	-0.1125	0.4121	0.2892
254344_at	AT4G22110	alcohol dehydrogenase, putative	1.6188	0.0023	0.0418	0.4604	0.122	0.1773	0.3082	0.2604	0.2467	-0.8502	0.0225	0.0487
254345_at	AT4G22000	similar to hypothetical protein [Vitis vinifera] (GB:CA	-0.06761	0.7401	0.5058	0.2752	0.2213	0.2467	0.3452	0.1436	0.1742	0.688	0.0224	0.0487
254346_at	AT4G21980	APG8A (autophagy 8A)	0.7913	0.0312	0.1026	1.2597	0.0066	0.0461	0.6606	0.0061	0.0325	1.1291	8.00E-04	0.0112
254347_at	AT4G22070	WRKY31 (WRKY DNA-binding protein 31); transcri	0.032001	0.9573	0.6665	-0.1213	0.8395	0.5014	1.0707	0.1291	0.1634	0.9175	0.1775	0.1717
254348_at	AT4G22150	PUX3 (PLANT UBX DOMAIN-CONTAINING PROT	0.6024	0.0035	0.0448	0.733	0.0017	0.032	0.2369	0.0716	0.1163	0.3676	0.0195	0.0448
254349_at	AT4G22250	zinc finger (C3HC4-type RING finger) family protein	1.8495	0.053	0.1321	1.4206	0.1049	0.1636	-0.3591	0.5948	0.3964	-0.7879	0.2741	0.2251
254350_at	AT4G22280	F-box family protein	-0.8373	0.0246	0.0911	-0.6238	0.059	0.1209	0.01273	0.96	0.5076	0.2263	0.3963	0.2827
254351_at	AT4G22300	SOBER1 (SUPPRESSOR OF AVRBST-ELICITED	-0.166	0.2608	0.3001	-0.2698	0.1006	0.16	-0.2798	0.0921	0.1343	-0.3836	0.039	0.068
254352_at	AT4G22320	similar to unknown protein [Arabidopsis thaliana] (T	0.05669	0.8022	0.5248	-0.1939	0.4118	0.3469	0.3009	0.1528	0.1807	0.05035	0.7827	0.4237
254353_s_at	AT4G22285,AT4G22350	[AT4G22285, ubiquitin thiolesterase/ zinc ion bindin	0.3283	0.1649	0.2374	0.2089	0.3409	0.314	-0.2472	0.0874	0.1305	-0.3666	0.0288	0.0568
254354_at	no_match	no_match	0.04098	0.9688	0.5694	-0.06174	0.953	0.5325	1.5526	0.19	0.2055	1.4499	0.2149	0.1936
254355_at	AT4G22380	ribosomal protein L7Ae/L30e/S12e/Gadd45 family p	-0.5016	0.0206	0.0845	-0.3071	0.0853	0.147	0.5912	0.0119	0.0433	0.7856	0.0043	0.0209
254356_at	AT4G22190	similar to unknown [Populus trichocarpa] (GB:ABK9	-0.1322	0.5972	0.4586	-0.01159	0.9623	0.5346	0.00537	0.9329	0.5014	0.1259	0.1033	0.123
254357_at	AT4G22220	ISU1 (Iron-sulfur cluster assembly complex protein)	0.08934	0.353	0.3514	0.1117	0.2597	0.2697	0.4996	0.0015	0.0198	0.522	0.0012	0.013
254358_at	AT4G22310	similar to unknown protein [Arabidopsis thaliana] (T	-0.01583	0.9403	0.5625	-0.04366	0.8367	0.5007	0.7528	0.0151	0.049	0.725	0.0172	0.0419
254359_at	AT4G22360	SWIB complex BAF60b domain-containing protein	0.1873	0.2286	0.2811	0.2224	0.1671	0.2106	-0.03412	0.796	0.4621	0.000928	0.9944	0.4813
254360_at	AT4G22240	phosphatidate cytidylyltransferase, putative / CDP-c	-0.2124	0.0215	0.0861	-0.4945	0.001	0.0293	0.1512	0.0596	0.1047	-0.1309	0.0868	0.1104
254361_at	AT4G22212	Encodes a defensin-like (DEFL) family protein.	-0.7992	0.3328	0.3417	0.09021	0.9071	0.5207	-0.4683	0.2831	0.2599	0.4211	0.3276	0.2523
254362_at	AT4G22160	unknown protein	0.1914	0.4408	0.3941	0.3739	0.1703	0.2128	-0.04945	0.8361	0.4744	0.1331	0.5844	0.3578
254363_at	AT4G22010	SKS4 (SKU5 Similar 4); copper ion binding / oxidor	0.07841	0.7503	0.5086	-0.5908	0.0621	0.1239	0.3253	0.0915	0.1338	-0.187	0.2725	0.2242
254364_at	AT4G22020	pseudogene, hypothetical protein, similar to unchar	-1.3744	0.088	0.172	-0.9305	0.203	0.2347	0.1451	0.6744	0.4224	0.5891	0.1402	0.1483
254365_at	AT4G22030	F-box family protein	-0.7516	0.5355	0.4353	1.1588	0.0354	0.1834	0.3206	-1.3146	0.3018	0.2695	0.5958	0.6199	0.3703
254366_s_at	AT4G22040,AT5G25045,A	[AT4G22040, transposable element gene];[AT5G25	0.2771	0.6242	0.4679	0.02151	0.9692	0.5365	0.1028	0.8342	0.4738	-0.1528	0.7566	0.4156
254367_at	AT4G21700	similar to unknown protein [Arabidopsis thaliana] (T	0.6276	0.0815	0.1651	0.441	0.179	0.2189	0.2566	0.3638	0.2999	0.06995	0.794	0.4272
254368_at	AT4G21710	NHP6A2 (EMBRYO DEFECTIVE 1989); DNA binding	0.5758	0.0631	0.144	0.8125	0.0227	0.0761	-1.0273	0.0104	0.0404	-0.7906	0.0248	0.0518
254369_at	AT4G21720	similar to unknown [Picea sitchensis] (GB:ABK2330	0.4579	0.2137	0.2707	0.2755	0.4244	0.3527	-0.297	0.3553	0.2958	-0.4795	0.1671	0.1655
254370_at	AT4G21750	ATML1 (MERISTEM LAYER 1); DNA binding / tran	-1.1367	0.0093	0.0621	-0.9382	0.0178	0.069	-0.2946	0.1956	0.2091	-0.09612	0.6392	0.3769
254371_at	AT4G21760	BGLU47 (Beta-glucosidase 47); hydrolase, hydroly	-1.2778	0.0072	0.0572	-0.8189	0.0319	0.0886	-0.2003	0.0143	0.0477	0.2586	0.0059	0.0238
254372_at	AT4G21620	glycine-rich protein	0.03538	0.8061	0.5257	0.7411	0.0054	0.0432	0.395	0.0429	0.0864	1.1007	0.0012	0.0129
254373_at	AT4G21730	pseudogene of N-ethylmaleimide sensitive factor (N	1.466	0.0483	0.1265	1.0642	0.1108	0.1681	-1.4984	0.0024	0.023	-1.9002	0.001	0.0121
254374_at	AT4G21780	similar to unknown [Populus trichocarpa] (GB:ABK9	-1.1003	0.0336	0.1061	0.5563	0.1834	0.2221	0.6612	0.1288	0.1632	2.3178	0.0026	0.0169
254375_at	AT4G21800	QQT2 (QUARTE-QUART2); ATP binding	0.7277	0.0054	0.0519	0.8146	0.0036	0.0378	-0.4116	0.0365	0.0785	-0.3248	0.0711	0.0978
254376_at	AT4G21790	TOM1 (TOBAMOVIRUS MULTIPLICATION 1)	-0.1701	0.6011	0.46	-0.3075	0.3633	0.3244	-0.7255	0.0134	0.0461	-0.8629	0.0074	0.0267
254377_at	AT4G21650	subtilase family protein	-0.1681	0.7788	0.5175	-0.107	0.8577	0.5066	0.3479	0.2369	0.2334	0.409	0.1775	0.1717
254378_at	AT4G21810	DER2.1 (DERLIN-2.1)	0.4524	0.0215	0.0862	0.4555	0.0211	0.074	-0.0948	0.4429	0.3354	-0.09162	0.4572	0.3089
254379_at	AT4G21820	calmodulin-binding family protein	-2.824	0.0279	0.0968	-0.1853	0.8356	0.5003	-2.1723	0.0151	0.0489	0.4664	0.4304	0.297
254380_at	no_match	no_match	-0.2477	0.4717	0.4082	0.2681	0.4387	0.359	0.5598	0.1472	0.177	1.0756	0.0261	0.0535
254381_at	AT4G21880	pentatricopeptide (PPR) repeat-containing protein	0.8392	0.2958	0.3208	-0.2388	0.7496	0.4748	0.04041	0.9566	0.507	-1.0376	0.2116	0.1916
254382_at	AT4G21890	similar to unnamed protein product [Vitis vinifera] (G	-0.7256	0.0983	0.181	-1.2629	0.0202	0.0726	-1.217	0.0227	0.0609	-1.7543	0.0066	0.0252
254383_at	AT4G21950	unknown protein	1.0929	0.393	0.3716	-0.07568	0.9504	0.532	0.9156	0.4679	0.3466	-0.253	0.8356	0.4388
254384_at	AT4G21870	26.5 kDa class P-related heat shock protein (HSP2	-1.4544	0.1203	0.2006	-1.9249	0.0597	0.1213	1.27	0.0037	0.0267	0.7996	0.0186	0.0438
254385_s_at	AT4G21830,AT4G21840	[AT4G21830, methionine sulfoxide reductase doma	0.2854	0.0059	0.0534	1.8045	0.0135	0.0617	1.5331	0.0167	0.0516	1.0522	0.0533	0.0825
254386_at	AT4G21860	PRXR1 (peroxidase 42); peroxidase	-0.4856	0.0175	0.0793	-0.5032	0.0155	0.0652	0.003977	0.9709	0.5102	-0.01367	0.9003	0.4573
254387_at	AT4G21850	methionine sulfoxide reductase domain-containing p	2.0342	0.0025	0.0424	1.8376	0.0037	0.038	1.3761	0.0103	0.0403	1.1795	0.0173	0.0421
254388_at	AT4G21860	MSRB2 (METHIONINE SULFOXIDE REDUCTASE	-0.4407	0.0033	0.0446	-0.6034	0.001	0.0291	0.1223	0.1559	0.1829	-0.04045	0.5947	0.3615
254389_s_at	AT4G21903,AT4G21910	[AT4G21903, antiporter/ drug transporter];[AT4G21	0.828	0.0096	0.0628	0.9375	0.0062	0.0451	-0.8975	0.0063	0.0328	-0.788	0.0099	0.0311
254390_at	AT4G21940	CPK15 (calcium-dependent protein kinase 15); calm	0.1993	0.5416	0.4374	0.4197	0.2332	0.2535	-0.4093	0.2134	0.22	-0.189	0.5324	0.3388
254391_at	AT4G21590	ENDO3 (ENDONUCLEASE 3); T/G mismatch-spec	-0.2646	0.7672	0.5138	1.6127	0.1257	0.1797	-1.6081	0.1265	0.1613	0.2693	0.7633	0.4178
254392_at	AT4G21600	ENDO5 (ENDONUCLEASE 5); T/G mismatch-spec	-1.1992	0.1744	0.2445	-0.3118	0.6902	0.4557	-0.4092	0.5589	0.3822	0.4783	0.4981	0.3252
254393_at	AT4G21580	oxidoreductase, zinc-binding dehydrogenase family	0.5752	0.0061	0.0538	0.7709	0.0021	0.0331	-0.1566	0.2219	0.2247	0.03903	0.7369	0.4093
254394_at	AT4G21630	subtilase family protein	-0.6657	0.3663	0.3575	-0.09322	0.8936	0.5169	-0.1195	0.8639	0.4824	0.4529	0.5267	0.3366
254395_at	no_match	no_match	0.6506	0.4781	0.411	-1.729	0.1064	0.1645	0.6407	0.4844	0.3532	-1.7389	0.1049	0.124
254396_at	AT4G21680	proton-dependent oligopeptide transport (POT) fam	-0.7843	0.5348	0.4351	-0.8117	0.5214	0.3927	0.3761	0.7231	0.4396	0.3487	0.7422	0.4112
254397_at	AT4G21690	ATGA3OX3 (GIBBERELLIN 3-OXIDASE 3); iron ion	-1.3291	0.234	0.2839	-0.5096	0.6198	0.4305	-0.3374	0.7402	0.4448	0.482	0.6383	0.3766
254398_at	AT4G21750	PSBQ/PSBQ-1/PSBQA; calcium ion binding	-0.5132	0.0079	0.0584	-0.6392	0.0036	0.0377	0.2976	6.00E-04	0.0159	0.1716	0.0051	0.0224
254399_at	AT4G21110	G10 family protein	0.1172	0.4337	0.391	0.3362	0.6672	0.1298	0.3464	0.037	0.0794	0.5654	0.0074	0.0267
254400_at	AT4G21270	ATK1 (ARABIDOPSIS THALIANA KINESIN 1); mic	-1.1151	0.3177	0.3329	-1.0147	0.3579	0.3219	-0.8891	0.4087	0.3202	-0.7888	0.4593	0.3097
254401_at	AT4G21300	pentatricopeptide (PPR) repeat-containing protein	1.8972	0.0577	0.1376	0.06888	0.9283	0.5263	0.5728	0.4704	0.3478	-1.3933	0.1248	0.1382
254402_at	AT4G21310	similar to unknown protein [Arabidopsis thaliana] (T	0.3807	0.3434	0.3465	0.1846	0.6302	0.4346	0.3589	0.2115	0.2188	0.1628	0.5373	0.3403
254403_at	AT4G21323	subtilase family protein	1.06	0.394	0.3722	1.8675	0.1681	0.2113	-1.2603	0.1804	0.199	-0.4528	0.6916	0.3604
254404_at	AT4G21340	B70; transcription factor	-0.5554	0.5677	0.4479	0.6552	0.5039	0.3862	0.302	0.7101	0.4349	0.4018	0.6234	0.3714
254405_at	AT4G21350	B80/PUB8 (PLANT U-BOX8); binding / protein bind	0.3506	0.0406	0.1161	0.163	0.2376	0.2564	-0.2961	0.0183	0.0541	-0.4836	0.0033	0.0186
254406_at	AT4G21360	transposable element gene	0.4352	0.7336	0.5035	-0.598	0.6423	0.439	0.5093	0.6913	0.4282	-0.5239	0.6831	0.3915
254407_at	AT4G21370	S-locus protein kinase, putative	-1.0399	0.3452	0.3474	-0.9968	0.3634	0.3245	-0.2454	0.6493	0.4143	-0.2023	0.7065	0.3996
254408_at	AT4G21390	B120; protein kinase/ sugar binding	-0.2081	0.7302	0.5026	0.09991	0.8677	0.5093	-0.02322	0.8722	0.4847	0.2848	0.1033	0.123
254409_at	AT4G21400	protein kinase family protein	0.1521	0.5502	0.4412	0.04139	0.8482	0.5039	-0.1718	0.4443	0.3359	0.2625	0.265	0.2203
254410_at	AT4G21410	protein kinase family protein	-0.2804	0.3819	0.3655	0.004495	0.9882	0.5412	-0.6979	0.0535	0.0984	-0.413	0.1841	0.1758
254411_at	AT4G21420	transposable element gene	-1.5387	0.0569	0.1369	1.1547	0.1176	0.1734	-0.3031	0.6291	0.4077	2.3902	0.0146	0.0385
254412_at	AT4G21430	B160; transcription factor	0.1321	0.5502	0.4412	0.04139	0.8482	0.5039	-0.1718	0.4443	0.3359	0.2625	0.265	0.2203
254413_at	AT4G21440	ATM4/ATMYB102 (ARABIDOPSIS MYB-LIKE 102);	-0.1995	0.3829	0.3662	-0.5298	0.06	0.1216	0.03313	0.8787	0.4863	-0.2972	0.2183	0.1953
254414_at	no_match	no_match	0.06585	0.7277	0.5017	0.0269	0.8861	0.5148	0.1725	0.3832	0.3093	0.1335	0.4909	0.3222
254415_at	AT5G61325	AT5G61325; subtilase	0.5564	0.5628	0.4459	-0.1577	0.867	0.509	-2.4364	0.0562	0.0956	-3.1504	0.0234	0.05
254416_at	AT4G21380	ARK3 (Arabidopsis Receptor Kinase 3); kinase	1.4401	0.0059	0.0534	1.0161	0.0194	0.0717	0.3094	0.0562	0.1012	-0.1146	0.3797	0.2756
254417_at	AT4G21470	ATFMN/FHY (RIBOFLAVIN KINASE/FMN HYDRO	0.1618	0.0812	0.1647	-0.02566	0.7316	0.4688	-0.01722	0.8034	0.4645	-0.2047	0.0341	0.0624
254418_at	AT4G21480	glucose transporter, putative	0.2386	0.4979	0.4195	-0.01674	0.9608	0.5343	-0.444	0.1144	0.1519	-0.6993	0.0338	0.0621
254419_at	AT4G21490	NDB3; NADH dehydrogenase	-0.00246	0.9969	0.5763	-0.1073	0.8636	0.5081	-0.3465	0.586	0.393	-0.4513	0.484	0.3193
254420_at	AT4G21500	similar to unknown protein [Arabidopsis thaliana] (T	0.1043	0.8447	0.5371	-0.9602	0.1268	0.1806	0.9099	0.0531	0.0979	-0.1547	0.6681	0.3868
254421_at	AT4G21550	transcriptional factor B3 family protein	1.2858	0.0114	0.0667	0.68	0.0789	0.1408	-0.1068	0.6264	0.4067	-0.7126	0.0246	0.0516
254422_at	AT4G21560	vacuolar protein sorting-associated protein 28 famil	0.2843	0.3607	0.355	0.3595	0.2622	0.2711	-0.4106	0.0755	0.1197	-0.3354	0.1232	0.1371
254423_at	AT4G21610	LOL2 (LSD ONE LIKE 2); transcription factor	1.3036	6.00E-04	0.0332	0.971	0.0019

254490_at	AT4G20320	CTP synthase	2.871	0.0351	0.1083	1.308	0.2267	0.2496	-0.7435	0.3556	0.2959	-2.3066	0.0317	0.06
254491_at	AT4G20300	similar to unknown protein [Arabidopsis thaliana] (T	-0.06869	0.757	0.5108	-0.05835	0.7923	0.4869	0.2601	0.2258	0.227	0.2704	0.2111	0.1914
254492_at	AT4G20260	DREPP plasma membrane polypeptide family prote	0.06429	0.5894	0.4559	0.2199	0.1155	0.1715	0.5856	0.001	0.0173	0.7412	4.00E-04	0.0089
254493_at	AT4G20020	similar to unknown protein [Arabidopsis thaliana] (T	0.9664	0.0027	0.0426	0.4897	0.0283	0.0836	0.6119	0.0011	0.0184	0.1352	0.1398	0.148
254494_at	AT4G20050	QRT3 (QUARTET 3)	-0.298	0.5919	0.4568	-0.4466	0.4326	0.3566	-0.3059	0.4769	0.3502	-0.4544	0.3089	0.2429
254495_at	AT4G20060	EMB1895 (EMBRYO DEFECTIVE 1895); binding	-0.04	0.894	0.5498	-0.1646	0.5907	0.4197	-1.0267	0.011	0.0416	-1.1513	0.0074	0.0267
254496_at	AT4G20070	ATAAH (ARABIDOPSIS THALIANA ALLANTOATE	-1.365	0.0027	0.0426	-1.4352	0.0022	0.0334	-0.9121	0.0105	0.0406	-0.9823	0.0081	0.028
254497_at	AT4G20080	C2 domain-containing protein	-1.5993	0.2369	0.2857	-1.9582	0.164	0.2085	0.7133	0.5689	0.3863	0.3544	0.7735	0.4211
254498_at	AT4G20090	EMB1025 (EMBRYO DEFECTIVE 1025)	0.3311	0.6359	0.4716	1.1665	0.1458	0.1952	-1.3077	0.1027	0.143	-0.4723	0.4888	0.3214
254499_at	AT4G20100	PQ-loop repeat family protein / transmembrane fam	-1.0701	0.3788	0.3638	0.7934	0.5042	0.3863	-0.3663	0.752	0.4488	1.4971	0.2388	0.2064
254500_at	AT4G20110	vacuolar sorting receptor, putative	1.9338	0.0032	0.0443	1.6248	0.0061	0.0449	0.2056	0.1211	0.1571	-0.1035	0.3788	0.2751
254501_at	AT4G20130	PTAC14 (PLASTID TRANSCRIPTIONALLY ACTIV	-0.5076	0.2323	0.2833	-0.3823	0.3492	0.3177	-1.3016	0.0024	0.0229	-1.1763	0.0035	0.0193
254502_at	AT4G20130	PTAC14 (PLASTID TRANSCRIPTIONALLY ACTIV	0.03234	0.7788	0.5175	-0.05385	0.6432	0.4393	-0.5858	0.0023	0.0224	-0.672	0.0014	0.0133
254503_at	AT4G20010	OSB2/PTAC9 (PLASTID TRANSCRIPTIONALLY AC	0.1053	0.623	0.4675	-0.04792	0.8207	0.4961	0.1746	0.3984	0.3159	0.02142	0.9134	0.4607
254504_at	AT4G20030	RNA recognition motif (RRM)-containing protein	-0.3122	0.124	0.2039	-0.09846	0.5731	0.4131	0.1512	0.3396	0.2882	0.3649	0.0591	0.0878
254505_at	AT4G19985	GCN5-related N-acetyltransferase (GNAT) family pr	-0.2506	0.3643	0.3564	-0.4102	0.1695	0.2122	-0.3447	0.0779	0.122	-0.5043	0.0261	0.0535
254506_at	AT4G20140	leucine-rich repeat transmembrane protein kinase,	-0.6368	0.1929	0.2576	-1.0216	0.0661	0.1287	-0.4637	0.0067	0.0335	-0.8486	7.00E-04	0.0106
254507_at	AT4G20160	similar to protein binding / zinc ion binding [Arabido	-1.1153	0.0883	0.1723	-1.0906	0.0933	0.1539	0.2847	0.5976	0.3973	0.3094	0.5674	0.3517
254508_at	AT4G20170	similar to unknown protein [Arabidopsis thaliana] (T	-0.5164	0.0185	0.0809	-0.7286	0.0056	0.0434	0.1996	0.0412	0.0842	-0.01254	0.8611	0.4462
254509_at	AT4G20200	terpene synthase/cyclase family protein	1.062	0.0408	0.1164	-0.3291	0.4083	0.3451	-0.8466	0.0182	0.0541	-2.2378	5.00E-04	0.0096
254510_at	AT4G20210	terpene synthase/cyclase family protein	-1.4487	0.1506	0.2261	0.7393	0.4164	0.3489	-1.3849	0.165	0.1885	0.803	0.381	0.2762
254511_at	AT4G20220	contains InterPro domain Reverse transcriptase, Rt	-0.184	0.8944	0.6498	-0.107	0.9384	0.5286	-0.1877	0.8923	0.4904	-0.1107	0.9363	0.4674
254512_at	AT4G20230	terpene synthase/cyclase family protein	-2.4828	0.087	0.1708	-2.7473	0.067	0.1296	-0.06701	0.9544	0.5066	-0.3315	0.7782	0.4224
254513_at	AT4G20235	pseudogene of cytochrome P450	-0.3841	0.6922	0.49	0.6398	0.5175	0.3915	-0.9045	0.3729	0.3043	0.1194	0.9011	0.4576
254514_at	AT4G20250	unknown protein	-0.5659	0.3754	0.3621	0.7472	0.2585	0.2692	-0.5644	0.1487	0.1782	0.7487	0.0769	0.1024
254515_at	AT4G20270	BAM3 (big apical meristem 3); ATP binding / protein	0.09533	0.7267	0.5014	0.2626	0.36	0.3227	0.4614	0.0496	0.0941	0.6286	0.0192	0.0444
254516_at	AT4G20290	unknown protein	-0.5162	0.5379	0.436	-0.4015	0.6284	0.4339	-0.3402	0.56	0.3826	-0.2255	0.6955	0.396
254517_at	AT4G20310	metallocarboxypeptidase	0.05516	0.7052	0.4944	-0.1904	0.2333	0.2536	-0.5443	0.016	0.0505	-0.7899	0.0043	0.0209
254518_at	AT4G19910	Toll-Interleukin-Resistance (TIR) domain-containing	0.004846	0.9973	0.5763	0.8063	0.587	0.4187	-0.2824	0.8464	0.4775	0.519	0.7235	0.4052
254519_at	AT4G19940	F-box family protein	-0.4512	0.6474	0.4755	2.7925	0.0378	0.0963	-1.5149	0.1728	0.1937	1.7287	0.1315	0.1426
254520_at	AT4G19960	potassium ion transmembrane transporter	0.8702	0.0017	0.0391	0.2572	0.0463	0.1067	-0.09185	0.366	0.3008	-0.5048	0.005	0.0221
254521_at	AT5G44820	similar to unknown protein [Arabidopsis thaliana] (T	1.5946	0.0063	0.0542	1.1029	0.022	0.075	0.2702	0.4014	0.3172	-0.2215	0.4848	0.3196
254522_at	AT4G19980	unknown protein	-1.5294	0.2885	0.3164	0.05336	0.968	0.5361	-0.03921	0.9726	0.5106	1.5436	0.2242	0.1984
254523_at	no_match	no_match	0.3318	0.1979	0.2613	0.4214	0.1218	0.177	-0.7082	0.0302	0.0708	-0.6186	0.0452	0.0746
254524_at	AT4G20000	VQ motif-containing protein	0.9883	0.1908	0.256	2.7452	0.012	0.0587	0.822	0.0912	0.1335	2.5789	0.0023	0.0158
254525_at	AT4G19580	DNAJ heat shock N-terminal domain-containing pro	-1.8586	0.2063	0.2661	-0.6875	0.607	0.426	-0.05511	0.9665	0.5092	1.116	0.4168	0.2912
254526_at	AT4G19600	CYCT1;4; cyclin-dependent protein kinase	0.4075	0.1023	0.1849	0.4172	0.0987	0.1566	-0.4143	0.0983	0.1396	-0.4046	0.1041	0.1235
254527_at	AT4G19610	RNA binding	0.1918	0.3447	0.3472	0.5933	0.0296	0.0855	-0.5791	0.016	0.0505	-0.1777	0.2858	0.2312
254528_at	AT4G19620	unknown protein	-0.897	0.2594	0.2993	1.064	0.1943	0.2289	-0.7237	0.3491	0.2928	1.2374	0.1443	0.1511
254529_at	AT4G19540	similar to HCF101 (HIGH-CHLOROPHYLL-FLUOR	0.01662	0.9164	0.5559	-0.7837	0.0062	0.0452	-0.4731	0.0336	0.0748	-1.2734	0.001	0.0122
254530_at	AT4G19640	ARA7; GTP binding	0.3734	0.011	0.0658	0.06515	0.4786	0.3756	0.504	0.0308	0.027	0.1958	0.0788	0.104
254531_at	AT4G19650	similar to mitochondrial transcription termination fac	0.8331	0.2757	0.309	0.1448	0.8372	0.5008	-0.9683	0.2164	0.2215	-1.6567	0.0662	0.0936
254532_at	AT4G19660	NPR4 (NPR1-LIKE PROTEIN 4); protein binding	0.4499	0.0237	0.0898	0.4538	0.0301	0.0863	-0.3523	0.0629	0.1079	-0.3883	0.0773	0.1611
254533_at	AT4G19670	zinc finger (C3HC4-type RING finger) family protein	0.7333	0.0161	0.0767	0.704	0.0184	0.0702	-0.211	0.3135	0.2751	-0.2403	0.2598	0.2177
254534_at	AT4G19680	IRT2 (iron-responsive transporter 2); iron ion transm	-1.0783	0.4089	0.3795	-0.4956	0.6936	0.4567	0.5327	0.6725	0.4218	1.1153	0.3945	0.282
254535_at	AT4G19710	AK-HSDH/AK-HSDH II; aspartate kinase/ homoserin	-0.4513	0.0333	0.1057	-0.8984	0.0032	0.0365	-0.2929	0.0923	0.1344	-0.6563	0.0023	0.016
254536_at	AT4G19720	glycosyl hydrolase family 18 protein	-0.1536	0.8599	0.541	-0.0239	0.978	0.5388	1.2403	0.1522	0.1805	1.3699	0.1229	0.137
254537_at	AT4G19730	glycosyl hydrolase family 18 protein	-0.2058	0.7511	0.5088	1.2912	0.1	0.1593	-0.2406	0.7115	0.4354	1.2564	0.1067	0.1251
254538_at	AT4G19740	hydrolase, hydrolyzing O-glycosyl compounds	-1.6584	0.2131	0.2704	-1.15	0.3364	0.3116	-0.6101	0.5464	0.3779	-0.2016	0.8385	0.4396
254539_s_at	AT4G19750;AT4G19760	[AT4G19750, glycosyl hydrolase family 18 protein];[	-0.3396	0.4069	0.3789	-0.1675	0.6715	0.4491	0.1143	0.7396	0.4447	0.2863	0.4225	0.2936
254540_s_at	AT4G19800;AT4G19770	[AT4G19800, glycosyl hydrolase family 18 protein];[	-0.7714	0.6009	0.4599	1.1355	0.4507	0.3643	0.05105	0.9719	0.5104	1.9579	0.2233	0.1979
254541_at	AT4G19780	transposable element gene	2.8821	0.5187	0.4288	1.4878	0.0204	0.0729	0.5176	0.2255	0.2267	1.7773	0.0112	0.0332
254542_s_at	AT4G19790;AT4G17450	[AT4G19790, transposable element gene];[AT4G17	0.142	0.7641	0.5127	-0.08481	0.8572	0.5065	-0.02506	0.9575	0.5071	-0.2519	0.5993	0.3632
254543_at	AT4G19810	glycosyl hydrolase family 18 protein	0.227	0.5133	0.4264	0.2526	0.4699	0.3721	0.2016	0.3366	0.2866	0.2272	0.2862	0.2314
254544_at	AT4G19820	glycosyl hydrolase family 18 protein	-1.8272	0.0999	0.1486	-4.4235	0.0038	0.0387	2.7286	0.0203	0.0573	0.1326	0.8649	0.447
254545_at	AT4G19830	immunophilin / FKBP-type peptidyl-prolyl cis-trans i	-0.9729	0.0108	0.0654	-1.0079	0.0096	0.0535	-0.2823	0.1936	0.2078	-0.3172	0.1543	0.1576
254546_at	AT4G19850	ATPP2-A2 (Arabidopsis thaliana phloem protein 2-A	-2.7207	0.0862	0.1703	0.132	0.9178	0.5236	-1.4407	0.2966	0.267	1.4119	0.305	0.241
254547_at	AT4G19860	lecithin-cholesterol acyltransferase family protein / L	0.5561	0.103	0.1855	0.4477	0.1653	0.2091	-0.1679	0.3539	0.2952	-0.2764	0.1598	0.1611
254548_at	AT4G19865	kelch repeat-containing F-box family protein	-0.00559	0.9723	0.5704	0.09486	0.565	0.41	0.2052	0.1634	0.1875	0.3056	0.064	0.092
254549_at	AT4G19880	similar to unknown protein [Arabidopsis thaliana] (T	0.9875	0.0132	0.0708	0.7213	0.0361	0.0939	0.8947	0.0092	0.0384	0.6286	0.0295	0.0576
254550_at	AT4G19890	proline-rich family protein	0.1248	0.3351	0.3429	0.6329	0.0051	0.0429	0.8003	0.0022	0.0219	1.3085	3.00E-04	0.0085
254560_at	AT4G19110;AT4G19112	[AT4G19110, protein kinase, putative];[AT4G19112	0.1912	0.4846	0.4137	0.1631	0.5476	0.4037	-0.3844	0.1968	0.2098	-0.4126	0.1723	0.1686
254561_at	AT4G19160	binding	0.1996	0.5205	0.4292	0.0698	0.8178	0.4952	-0.7406	0.004	0.0273	-0.8704	0.0022	0.0157
254562_at	AT4G19230	CYP77A1 (cytochrome P450, family 707, subfamil	-0.2608	0.5972	0.4586	-0.2815	0.5697	0.4117	0.1314	0.7143	0.4363	0.1107	0.757	0.4158
254563_at	AT4G19120	ERD3 (EARLY-RESPONSIVE TO DEHYDRATION	-0.1885	0.3608	0.355	-0.1441	0.4745	0.374	0.1259	0.5289	0.3708	0.1702	0.4045	0.286
254564_at	AT4G19170	NCED4 (NINE-CIS-EPOXYCAROTENOID DIOXYG	0.1005	0.8186	0.5292	-0.2893	0.5198	0.3923	-0.1554	0.2279	0.2282	-0.5452	0.0075	0.027
254565_at	AT4G19130	DNA binding / nucleic acid binding / zinc ion binding	1.4544	0.0623	0.1433	1.337	0.0779	0.1398	0.4085	0.3476	0.292	0.2911	0.4908	0.3222
254566_at	AT4G19240	similar to unknown protein [Arabidopsis thaliana] (T	-1.1633	0.3996	0.3751	-2.2977	0.1363	0.1879	-0.1667	0.8955	0.4912	-1.3011	0.3361	0.2561
254567_s_at	AT4G19340;AT4G19260	[AT4G19340, similar to kelch repeat-containing prot	-1.52	0.1781	0.2468	0.01912	0.9846	0.5403	-2.1738	0.08	0.1237	-0.6347	0.5331	0.339
254568_x_at	AT1G35090;AT4G19300	[AT1G35090, transposable element gene];[AT4G19	0.9622	0.415	0.3823	0.1255	0.9114	0.5219	-1.6114	0.2028	0.2134	-0.5238	0.6468	0.3797
254569_s_at	AT5G36020;AT4G19320	[AT5G36020, transposable element gene];[AT4G19	-1.7534	0.1835	0.2507	-0.2508	0.8296	0.4987	-0.129	0.9116	0.4957	1.3736	0.2767	0.2265
254570_s_at	AT4G19250;AT4G19330	[AT4G19250, kelch repeat-containing protein];[AT4	-0.8883	0.2538	0.2958	-0.3767	0.6024	0.4246	0.0399	0.9552	0.5066	0.5514	0.4549	0.3079
254571_at	AT4G19370	similar to unknown protein [Arabidopsis thaliana] (T	0.4677	0.6941	0.4908	2.1511	0.1237	0.1785	-0.1105	0.9252	0.4993	1.5729	0.228	0.2005
254572_at	AT4G19380	alcohol oxidase-related	-0.1938	0.7734	0.5159	-0.8281	0.2585	0.2692	0.4074	0.2684	0.2512	-0.2269	0.514	0.3312
254573_at	AT4G19420	pectinacetylesterase family protein	0.2271	0.4613	0.4036	0.4798	0.1606	0.2063	-1.0726	0.0041	0.0276	-0.8199	0.0107	0.0324
254574_at	AT4G19430	unknown protein	-1.7754	0.0595	0.1396	-1.1183	0.1757	0.2167	0.1899	0.6601	0.418	0.847	0.102	0.122
254575_at	AT4G19460	glycosyl transferase family 1 protein	-0.3849	0.2613	0.3004	-0.6441	0.094	0.1545	0.5065	0.1358	0.1683	0.2472	0.4143	0.2901
254576_at	AT4G19350	EMB3006 (EMBRYO DEFECTIVE 3006)	-0.2502	0.2747	0.3084	0.2664	0.2494	0.2636	0.2957	0.2095	0.2174	0.8124	0.0148	0.0387
254577_at	AT4G19450	nodulin-related	-0.2379	0.2763	0.3095	-0.4283	0.0859	0.1476	-0.07745	0.5976	0.3973	-0.2679	0.1188	0.1338
254578_at	AT4G19410	pectinacetylesterase, putative	-0.1694	0.6792	0.4857	-0.1141	0.7792	0.4833	-0.5144	0.0506	0.0313	-0.4591	0.0085	0.0286
254579_at	AT4G19400	actin binding	1.3049	0.0129	0.07	1.1172	0.0216	0.0747	-0.8092	0.0026	0.0234	-0.9969	0.0012	0.0127
254580_at	AT4G19390	similar to unknown protein [Arabidopsis thaliana] (T	0.4898	0.1908	0.256	0.8705	0.049	0.1097	-0.3598	0.1053	0.1451	0.02088	0.9095	0.4598
254581_at	AT4G19440	pentatricopeptide (PPR) repeat-containing protein	1.1936	0.2845	0.314	0.2945	0.7759	0.4824	-0.5706	0.5868	0.3933	-1.4698	0.2031	0.1869
254582_at	AT4G19470	disease resistance protein-related	1.8719	0.2547	0.2964	0.3149	0.8341	0.4999	1.219	0.4358	0.3322	-0.338	0.8222	0.4348
254583_at	AT4G19480	unknown protein	0.2924	0.6246	0.4681	0.2043	0.7302	0.4686	-0.7085	0.1871	0.2037	-0.7966	0.1484	0.1535
254584_at	no_match	no_match	0.4696	0.1528	0.2279	0.3266	0.2876	0.2852	-0.8906	0.0288	0.0689	-1.0336	0.0179	0.0428
254585_at	AT4G19500	disease resistance protein (TIR-NBS-LRR class), p	0.068	0.615	0.4645	-0.1376	0.3324	0.3096	-0.6621	0.0037	0.0267	-0.8677	0.0013	0.0133
254586_at	AT4G19510	disease resistance protein (TIR-NBS-LRR class), p	0.1024	0.7502	0.5086	-0.276	0.4099	0.3459	-0.6462	0.0977	0.139	-1.0245	0.0269	0.0546
254587_at	no_match	no_match	-1.0115	0.2532	0.2954	-0.02427	0.976	0.5384	-1.1988	0.1891	0.205	-0.2116	0.794	0.4272
254588_at	AT4G18840	pentatricopeptide (PPR) repeat-containing protein	-0.1984	0.235	0.2844	-0.1699	0.2977	0.2905	0.3086	0.0364	0.0785	0.3371	0.0278	0.0556
254589_at	AT4G18850	unknown protein	-1.3566	0.3557	0.3525	-0.293	0.8328	0.4996	0.4062	0.7703	0.4543	1.4698	0.3215	0.249
254590_at	AT4G18860	unknown protein	-0.05359	0.9628	0.568	-0.6981	0.5537	0.406	-0.5817	0.6191	0.4043	-1.2262	0.3201	0.2484
254591_at	AT4G18870	heat shock transcription factor family protein	1.1379	0.1955	0.2595	1.0446	0.2272	0.2498	0.1475	0.8503	0.4786	0.05417	0.9446	0.4695
254592_at	AT4G18880	AT-HSFA4A (Arabidopsis thaliana heat shock trans	1.0237	0.033	0.1054	1.0014	0.0353	0.0927	-0.1108	0.4117	0.3216	-0.1331	0.3333	0.255
254593_s_at	AT4G18900;AT4G18905	[AT4G18900, transducin family protein / WD-40 rep	0.3496	0.1176	0.1983	0.2836	0.1819	0.2211	-0.6835	0.0177	0.0533	-0.7495	0.013	0.0362
254594_at	AT4G18930	cyclic phosphodiesterase	1.3775	0.0179	0.0802	1.0452	0.0424	0.1023	0.4891	0.1046	0.1446	0.1568	0.5391	0.3409
254595_at	AT4G18940	AG (AGAMOUS); transcription factor	-0.1366	0.5883	0.4558	-0.04429	0.8582	0.5067	0.4221	0.1436	0.1743	0.5144	0.0914	0.1139
254596_at	AT4G18975	pentatricopeptide (PPR) repeat-containing protein	-0.3646	0.113	0.1947	-0.1294	0.5123	0.3896	0.04738	0.5278	0.3703	0.2826	0.0146	0.0385
254597_at	AT4G18980	similar to unknown protein [Arabidopsis thaliana] (T	0.3393	0.6813	0.4865	2.8514	0.0206	0.0732	-0.9037	0.3043	0.2709	1.6085	0.1041	0.1235
254598_at	AT4G18990	xyloglucan:xyloglucosyl transferase, putative / xyloglu	0.9178	0.3638	0.3872	1.7226	0.1372	0.1886	-0.6088	0.5479	0.3784	0.1961	0.8431	0.4408
254599_at	AT4G19000	IWS1 C-terminus family protein	0.5777	0.616	0.4649	-0.2314	0.8385	0.501	0.6649	0.5659	0.3851	-0.1442	0.8988	0.4568
254600_at	AT4G19010	4-coumarate--CoA ligase family protein / 4-coumarc	0.3754	0.1594	0.233	0.223	0.3631	0.3244	-0.08723	0.7088	0.4343	-0.2396	0.3323	0.2545
254601_at	no_match	no_match	-0.5118	0.0723	0.155	-0.5713	0.0536	0.1149	-0.15	0.5164	0.3657	-0.2095	0.377	0.2743
254602_at	AT4G19040	EDR2 (enhanced disease resistance 2); lipid bindin	0.7014	0.0089	0.0611	0.5249	0.0236	0.0773	-0.3972	0.0545	0.0994	-0.5738	0.0177	0.0426
254603_at	AT4G19050	mob1/phocein family protein	0.1623	0.6228	0.4675	0.2091	0.5307	0.3965	0.3678	0.2944	0.2658	0.4145	0.2457	0.2101
254604_at	AT4G19070	cadmium-responsive protein / cadmium induced pro	-0.1776	0.4661	0.4056	-0.2693	0.2894	0.2862	-0.4869	0.092	0.1342	-0.5786	0.0587	0.0874
254605_at	AT4G18950	ankyrin protein kinase, putative	-0.5801	0.2208	0.2757	-0.4113	0.3622	0.324	-0.4259	0.0328	0.0739	-0.2572	0.1253	0.1385
254606_at	AT4G19030	NLM1 (NOD26-like intrinsic protein 1;1); water chan	-1.0743	0.4105	0.3802	0.3268	0.7939	0.4874	-0.3606	0.7613	0.4515	1.0205	0.4324	0.2978
254607_at	AT4G18920	similar to unknown protein [Arabidopsis thaliana] (T	1.3267	0.2796	0.3111	1.1012	0.3583	0.3221	-0.2703	0.8116	0.467	-0.4958	0.6648	0.3857
254608_at	AT4G18910	NIP1;2/NLM2 (NOD26-like intrinsic protein 1;2); wat	0.8842	0.034	0.1065	0.8747	0.0351	0.0925	-0.07419	0.3508	0.2937	-0.08375	0.2994	0.2383
254609_at	AT4G18970	GDSL-motif lipase/hydrolase family protein	1.9688	0.0021	0.0406	1.8062	0.0029	0.0355	0.3546	0.1515	0.18	0.5172	0.0613	0.0897
254610_at	AT4G18890	transcription factor-related	0.3282	0.1995	0.262	0.522	0.0711	0.1333	0.1448	0.3596	0.2979	0.3386	0.0729	0.0991
254611_at	AT4G19095	unknown protein	0.412	0.7786	0.5175	-0.07797	0.9574	0.5336	-0.3513	0.8103	0.4667	-0.8413	0.5724	0.3533
254612_at	AT4G19100	similar to unknown protein [Arabidopsis thaliana] (T	-0.206	0.0585	0.1386	-0.1266	0.1819	0.2211	0.2877	0.0215	0.059	0.3671	0.0095	0.0303
254613_at	AT4G19150	ankyrin repeat family protein	-0.1534	0.2109	0.2689	0.0881	0.441	0.3599	-0.0096	0.7532	0.4491	0.2319	0.0012	0.013
254614_at	AT4G19191	similar to pentatricopeptide (PPR) repeat-containing	0.6746	0.5215	0.4296	2.1105	0.0931	0.1539	-0.3863	0.4813	0.3518	1.0496	0.1028	0.1226
254615_at	AT4G19210	ATRLI2 (Arabidopsis thaliana RNase L inhibitor pro	0.003181	0.9855	0.5733	0.1108	0.5371	0.3993	-0.3172	0.0047	0.0292	-0.2096	0.0197	0.045
254616_at	AT4G18710	BIN2 (BRASSINOSTEROID-INSENSITIVE 2); kinas	-0.06278	0.5991	0.4594	-0.2143	0.1235	0.1784	-0.2237	0.1121	0.15	-0.3752	0.0271	0.0547
254617_s_at	AT5G45775;AT4G18730	[AT5G45775, 60S ribosomal protein L11 (RPL11D)];	-0.03089	0.8871	0.5476	0.2329	0.3178	0.3018	-0.4396	0.0379	0.0804	-0.1758	0.289	0.2329
254618_at	AT4G18780	CESA6 (CELLULOSE SYNTHASE 6); cellulose syn	0.02629	0.9008	0.5513	-0.09314	0.6625	0.4458	-0.00875	0.9656	0.5089	-0.1282	0.5379	0.3406
254619_at	AT4G18770	MYB98 (myb domain protein 98); DNA binding / tra	-1.6156	0.2551	0.2964	-1.1607	0.3943	0.3388	-0.678	0.6072	0.4004	-0.223	0.8636	0.4468
254620_at	AT4G18590	similar to unknown protein [Arabidopsis thaliana] (T	-0.3361	0.2508	0.2939	0.004478	0.9866	0.5407	-0.06103	0.753	0.4491	0.2796	0.1974	0.1833
254621_at	AT4G18600	WAVE-DAMPENED 2-LIKE PROTEIN (WDL2) / WAVE	-0.09479	0.5923	0.4569	-0.04588	0.7925	0.487	-0.4172	0.0628	0.1077	0.3683	0.0869	0.1104
254622_at	AT4G18375	KH domain-containing protein	-0.1718	0.8686	0.5434	1.1815	0.2921	0.2877	-0.1705	0.8696	0.4841	1.1828	0.2916	0.2344
254623_at	AT4G18480	CHL11 (CHLORINA 42); magnesium chelatase	-0.3935	0.0143	0.0729	-0.6565	0.0023	0.0335	0.1884	0.1181	0.1547	-0.0746	0.4757	0.316
254624_at	AT4G18580	unknown protein	0.5453	0.2133	0.2706	0.664	0.1462	0.1955	0.9079	0.0072	0.0343	1.0266	0.0046	0.0216
254625_at	AT4G18470	SNI1 (SUPPRESSOR OF NPR1-1, INDUCIBLE 1)	0.6357	0.4315	0.3899	0.1204	0.8766	0.5122	1.3376	0.102	0.1426	0.8223	0.2636	0.2195
254626_at	AT4G18400	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.6851	0.0211	0.0854	0.3775	0.1121	0.169	-0.1976	0.2804	0.2584	-0.5052	0.0333	0.0616
254627_at	AT4G18395	unknown protein	-1.878	0.0914	0.1753	-0.4194	0.6472	0.4406	-1.039	0.2665	0.2499	0.4197	0.6297	0.3736
254628_at	AT4G18593	dual specificity protein phosphatase-related	0.02317	0.8969	0.5504	0.1714	0.365	0.3252	0.5076	0.0305	0.0711	0.6557	0.0133	0.0365
254629_at	AT4G18425	similar to unknown protein [Arabidopsis thaliana] (T	0.5153	0.3353	0.343	0.6957	0.2136	0.2417	0.06636	0.8839	0.4879	0.2468	0.594	0.3613
254630_at	AT4G18360	(S)-2-hydroxy-acid oxidase, peroxisomal, putative /	0.5015	0.489	0.4155	1.9312	0.0428	0.1027	0.0428	-0.168	0.8113	0.467	1.2617	0.1281	0.1402
254631_at	AT4G18610	similar to unknown protein [Arabidopsis thaliana] (T	-0.2617	0.6688	0.4822	0.5886	0.3585	0.3222	0.4716	0.4529	0.3399	1.3219	0.0804	0.1054
254632_at	AT4G18630	similar to unknown protein [Arabidopsis thaliana] (T	0.4416	0.6217	0.4671

254690_at	AT4G17830	peptidase M20/M25/M40 family protein	0.7148	0.0421	0.1181	0.6376	0.0583	0.12	0.3414	0.0259	0.0653	0.2642	0.0554	0.0843
254691_at	AT4G17840	similar to unknown protein [Arabidopsis thaliana] (T	-0.4128	0.0686	0.1506	0.6186	0.0207	0.0734	-0.1021	0.3845	0.3098	-0.308	0.0422	0.0716
254692_at	AT4G17860	similar to unknown protein [Arabidopsis thaliana] (T	0.1192	0.8454	0.5372	-0.2533	0.6814	0.4525	-1.2844	0.0741	0.1185	-1.6569	0.0362	0.0647
254693_at	AT4G17880	basic helix-loop-helix (bHLH) family protein	-0.8927	0.0032	0.0442	-0.5055	0.0229	0.0764	-0.3842	0.0525	0.0972	0.002955	0.9843	0.4791
254694_at	no_match	no_match	0.4418	0.1244	0.2043	0.6798	0.0406	0.0999	0.4674	0.0039	0.0272	0.7054	8.00E-04	0.0112
254695_at	AT4G17905	ATL4H; protein binding / zinc ion binding	-0.3018	0.4418	0.3945	-0.8163	0.0823	0.1439	0.5759	0.179	0.1978	0.06141	0.8707	0.4486
254696_at	AT4G17930	unknown protein	-1.422	0.2796	0.3111	-1.0859	0.394	0.3388	-1.697	0.1776	0.1969	0.8109	0.4785	0.317
254697_at	AT4G17950	DNA-binding family protein	-0.4739	0.1993	0.2619	-0.7917	0.0622	0.124	-0.1736	0.5628	0.3837	-0.4913	0.149	0.154
254698_at	AT4G17980	ANAC071 (Arabidopsis NAC domain containing pro	0.4996	0.4478	0.3971	0.09643	0.879	0.5128	0.3269	0.4351	0.3319	-0.07632	0.8495	0.4426
254699_at	AT4G17990	similar to unknown protein [Arabidopsis thaliana] (T	-1.476	0.2624	0.3011	0.1464	0.9033	0.5197	-1.4385	0.2728	0.2539	0.1839	0.8788	0.451
254700_at	AT4G18000	unknown protein	1.5087	0.2424	0.289	-0.5325	0.6539	0.443	1.2151	0.2224	0.225	-0.8261	0.382	0.2766
254701_at	AT4G18030	dehydration-responsive family protein	-0.8637	0.0072	0.0572	-0.8306	0.0083	0.0505	-0.07048	0.6538	0.4158	-0.03735	0.8103	0.4319
254702_at	AT4G17940	binding	0.5232	0.1345	0.2131	0.6276	0.0881	0.1496	-0.1317	0.5426	0.3764	-0.02729	0.8971	0.4564
254703_at	AT4G17960	similar to unknown protein [Arabidopsis thaliana] (T	0.03449	0.821	0.5299	0.7199	0.0073	0.0481	-0.3168	0.0907	0.1331	0.3686	0.0612	0.0896
254704_at	AT4G18020	APRR2 (PSEUDO-RESPONSE REGULATOR 2); t	-0.2434	0.2066	0.2662	-0.2158	0.2528	0.2657	0.1165	0.5109	0.3636	0.1441	0.423	0.2937
254705_at	AT4G17970	similar to unknown protein [Arabidopsis thaliana] (T	-0.6502	4.00E-04	0.032	-0.4561	0.0015	0.0314	-0.04662	0.4747	0.3495	0.1475	0.0672	0.0945
254706_at	AT4G17950	DNA-binding family protein	0.4263	0.2806	0.3	0.6357	0.1227	0.1777	0.1317	0.695	0.4294	0.3411	0.3363	0.2562
254707_at	AT4G18010	IP5PII (INOSITOL POLYPHOSPHATE 5-PHOSPHA	0.369	0.4091	0.3795	0.4623	0.3128	0.2989	-0.05771	0.7039	0.4327	0.03558	0.8136	0.4326
254708_at	AT4G17895	UBP20 (UBIQUITIN-SPECIFIC PROTEASE 20); ub	-0.02806	0.9161	0.5559	-0.6178	0.0689	0.1317	0.09215	0.468	0.3466	-0.4976	0.0124	0.0352
254709_at	AT4G18050	ADB8 (ARF-GAP DOMAIN 8); DNA binding	-0.3326	0.0406	0.1161	-0.2081	0.1353	0.187	0.2168	0.0132	0.0457	0.3412	0.0026	0.0169
254710_at	AT4G18050	PGP9 (P-GLYCOPROTEIN 9); ATPase, coupled to	0.2236	0.5183	0.4286	-0.03487	0.9174	0.5235	0.03182	0.9246	0.4991	-0.2266	0.5129	0.3309
254711_at	AT4G18060	SH3 domain-containing protein 3 (SH3P3)	0.3077	0.0633	0.1442	0.1056	0.431	0.3557	0.3198	0.0081	0.0382	0.1776	0.1466	0.1525
254712_at	AT4G18080	similar to unknown protein [Arabidopsis thaliana] (T	0.4563	0.6732	0.4837	0.8921	0.4246	0.3528	-0.5994	0.5828	0.3917	-0.1636	0.8785	0.4509
254713_at	AT4G18090	unknown protein	-0.8205	0.1151	0.1963	0.5506	0.2491	0.2633	-0.4135	0.3689	0.3023	0.9576	0.0791	0.1041
254714_at	AT4G18480	AtMYB79 (myb domain protein 79); DNA binding / s	1.4997	0.274	0.308	0.4652	0.7144	0.4634	-1.8507	0.1931	0.2074	0.1142	0.9278	0.465
254715_at	AT4G13550	lipase class 3 family protein	0.171	0.5114	0.4254	-0.0308	0.9031	0.5196	-0.9249	8.00E-04	0.0165	-1.1267	4.00E-04	0.0089
254716_at	AT4G13560	UNE15 (unfertilized embryo sac 15)	0.2198	0.6178	0.4657	-0.1716	0.695	0.4571	-1.4221	0.0097	0.0392	-1.8135	0.0041	0.0205
254717_at	AT4G13570	HTA4; DNA binding	-0.153	0.7138	0.4972	-0.1865	0.6564	0.444	-0.07384	0.8585	0.4806	-0.1073	0.7961	0.4276
254718_at	AT4G13580	disease resistance-responsive family protein	-0.3436	0.6006	0.4599	0.2028	0.7544	0.4765	-0.1124	0.8617	0.4816	0.4341	0.5129	0.3309
254719_at	AT4G13600	glycosyl hydrolase family protein 17	-0.2377	0.6128	0.4636	-0.00961	0.9834	0.54	-0.1731	0.5852	0.3927	0.05501	0.8598	0.4458
254720_at	AT4G13610	MEE57 (maternal effect embryo arrest 57); DNA (c	0.1516	0.8546	0.5394	0.6716	0.4354	0.3577	0.2145	0.7959	0.4921	0.1377	0.2519	0.2136
254721_at	AT4G13620	SMAP1 (SMALL ACIDIC PROTEIN 1)	-0.1924	0.1605	0.2338	0.1165	0.3563	0.3211	0.3145	0.0482	0.0923	0.6234	0.0051	0.0223
254722_at	AT4G13530	similar to unknown protein [Arabidopsis thaliana] (T	0.03197	0.8502	0.5382	0.3	0.1317	0.1841	0.2094	0.1343	0.167	0.4773	0.0129	0.0361
254723_at	AT4G13510	AMT1;1 (AMMONIUM TRANSPORT 1); ammonium	0.6278	0.0212	0.0856	0.2901	0.1645	0.2087	-0.0449	0.9523	0.5061	-0.3427	0.0112	0.0332
254724_at	AT4G13630	similar to unknown protein [Arabidopsis thaliana] (T	0.3125	0.2324	0.2833	0.3995	0.1467	0.1958	-0.04314	0.8092	0.4663	0.04388	0.8061	0.4305
254725_at	AT4G13650	pentatricopeptide (PPR) repeat-containing protein	-0.1262	0.9296	0.5599	-0.3282	0.8189	0.4955	-1.2316	0.1971	0.2099	-1.4336	0.1463	0.1523
254726_at	AT4G13660	sinorespiratorial-lanosterol reductase, putative	0.9462	0.362	0.3554	0.1363	0.6989	0.071	0.03628	0.8585	0.42	2.6726	0.0315	0.0598
254727_at	AT4G13670	PTAC5 (PLASTID TRANSCRIPTIONALLY ACTIVE	-0.2737	0.1863	0.253	-0.8927	0.0065	0.046	0.2406	0.2339	0.2316	-0.3784	0.0923	0.1146
254728_at	AT4G13690	similar to hypothetical protein MtDRAFT_AC16186	-1.191	0.3042	0.3253	0.4091	0.7065	0.4611	-1.3519	0.2523	0.2421	0.2482	0.8182	0.4337
254729_at	AT4G13700	ATPAP23/PAP23 (purple acid phosphatase 23); ac	1.1821	0.4398	0.392	0.3291	0.8215	0.4962	-0.199	0.8912	0.4801	-1.0519	0.4843	0.3193
254730_at	AT4G13730	RabGAP/TBC domain-containing protein	0.2197	0.1041	0.1864	0.256	0.071	0.1333	0.203	0.1248	0.1599	0.2392	0.0846	0.1086
254731_at	AT4G13750	ATP binding	-0.3027	0.3423	0.3461	-0.5058	0.1465	0.1957	-0.4009	0.2271	0.2277	-0.604	0.0982	0.1192
254732_at	AT4G13750	ATP binding	0.2059	0.1687	0.2404	-0.1663	0.2489	0.2621	-0.6667	0.0056	0.0311	-1.039	0.0011	0.0123
254733_at	AT4G13760	polygalacturonase	-0.3758	0.7563	0.5106	0.4654	0.7017	0.4597	-0.6236	0.6106	0.4014	-0.7132	0.5624	0.3498
254734_at	AT4G13780	methionine--tRNA ligase, putative / methionyl-tRNA	0.7526	7.00E-04	0.0334	0.4379	0.0054	0.0432	-0.5251	0.0028	0.0241	-0.8398	5.00E-04	0.0093
254735_at	AT4G13810	disease resistance family protein / LRR family prote	1.2739	0.0406	0.1161	0.8747	0.1089	0.1673	-0.448	0.187	0.2037	-0.8452	0.0394	0.0684
254736_at	AT4G13820	disease resistance family protein / LRR family prote	0.3125	0.2324	0.2833	0.3995	0.1467	0.1958	-0.04314	0.8092	0.4663	0.04388	0.8061	0.4305
254737_at	AT4G13840	transferase family protein	-0.3476	0.06	0.14	-0.3872	0.0442	0.1041	0.09971	0.4971	0.3585	0.06005	0.6765	0.3895
254738_at	no_match	no_match	0.5923	0.1727	0.2432	-0.01942	0.9593	0.534	0.006474	0.9815	0.5132	-0.6052	0.0824	0.107
254739_at	AT4G13880	leucine-rich repeat family protein	-1.113	0.2775	0.3101	-0.07466	0.9369	0.5284	-0.8644	0.3846	0.3099	0.174	0.8539	0.4439
254740_s_at	AT4G13930/AT4G13890	[AT4G13930, SHM4 (SERINE HYDROXYMETHYL	-0.7112	0.2028	0.2642	-0.8015	0.1616	0.2069	0.09745	0.6118	0.4017	0.007155	0.9697	0.4754
254741_s_at	AT4G13920, AT4G13900	disease resistance family protein / LRR family prote	2.026	0.0038	0.0462	1.7053	0.0068	0.0467	0.2146	0.5535	0.3803	-3.08266	0.8158	0.4331
254742_at	AT4G13430	aconitase family protein / aconitate hydratase family	-0.4745	0.0515	0.1304	-0.2936	0.1644	0.2086	-0.2788	0.1057	0.1455	-0.09787	0.5053	0.3279
254743_at	AT4G13420	HAK5 (High affinity K+ transporter 5); potassium ior	0.4643	0.6713	0.483	-1.0924	0.3428	0.3147	0.5377	0.6246	0.4061	-1.019	0.3726	0.2724
254744_at	AT4G13440	MEE55 (maternal effect embryo arrest 55)	0.6571	0.065	0.1461	-0.6803	0.0368	0.0947	-0.6751	1.00E-04	0.0101	-0.7863	0	0.0053
254745_at	AT4G13460	SUVH9 (SU(VAR)3-9 HOMOLOG 9); histone-lysine	0.2717	0.3187	0.3337	0.2869	0.2959	0.2896	-0.2113	0.2445	0.2377	-0.1962	0.2743	0.2252
254746_at	AT4G12980	auxin-responsive protein, putative	-1.3005	6.00E-04	0.0325	-1.4535	4.00E-04	0.0251	0.007804	0.9441	0.5042	-0.1452	0.2372	0.2057
254747_at	AT4G13020	MHK; kinase	0.172	0.5607	0.4451	-0.1326	0.6508	0.442	-0.377	0.0396	0.0823	-0.6816	0.0055	0.0232
254748_at	AT4G13120	transposable element gene	-0.03382	0.9558	0.5663	-0.2766	0.6548	0.4434	0.4537	0.3864	0.3105	0.2109	0.6749	0.389
254749_at	AT4G13130	DC1 domain-containing protein	0.1585	0.5738	0.4504	0.1363	0.6267	0.4334	0.1475	0.5111	0.3636	0.1253	0.5735	0.3537
254750_at	AT4G13140	similar to unnamed protein product [Vitis vinifera] (G	0.2252	0.4295	0.3888	-0.0697	0.7993	0.4894	-0.4594	0.0101	0.04	-0.7543	0.0017	0.0144
254751_at	AT4G13150	unknown protein	1.3984	0.1255	0.2052	0.099	0.8978	0.5182	-0.7053	0.359	0.2975	-2.0047	0.0423	0.0716
254752_at	AT4G13160	similar to unknown protein [Arabidopsis thaliana] (T	0.0582	0.705	0.4943	0.3557	0.0678	0.1305	-0.5621	0.0171	0.0524	-0.2646	0.1381	0.147
254753_at	AT4G13190	kinase	0.833	0.4641	0.4048	1.9928	0.1251	0.1793	-1.1359	0.332	0.2843	0.02394	0.9826	0.4786
254754_at	AT4G13210	pectate lyase family protein	-0.1801	0.5227	0.4301	-0.6983	0.0534	0.1146	-0.0363	0.8947	0.4911	-0.5545	0.0976	0.1187
254755_at	AT4G13220	similar to hypothetical protein [Vitis vinifera] (GB:CA	-0.1291	0.5258	0.4316	-0.1477	0.4718	0.3729	0.3276	0.0477	0.0917	0.309	0.0562	0.0851
254756_at	no_match	no_match	0.3677	0.5995	0.4595	1.7638	0.0523	0.1134	0.04132	0.8936	0.4907	1.4374	0.0077	0.0274
254757_at	AT4G13240	ATROPGEF8/ROPGEF9 (KINASE PARTNER PRO	0.3111	0.7943	0.5223	0.7707	0.5279	0.3953	0.3631	0.7613	0.4515	0.8228	0.502	0.3266
254758_at	AT4G13260	YUC2 (YUCCA2); FAD binding / NADP binding / fla	-0.6517	0.0736	0.1561	0.2592	0.3922	0.3378	-0.4297	0.1103	0.1486	0.4812	0.0839	0.1081
254759_at	AT4G13180	short-chain dehydrogenase/reductase (SDR) family	0.2618	0.1237	0.2038	0.6254	0.0097	0.0537	-0.08424	0.53	0.3713	0.2794	0.085	0.109
254760_at	AT4G13200	Identical to Uncharacterized protein At4g13200, chl	-0.2392	0.1668	0.2389	-0.1536	0.3393	0.3132	-0.08761	0.5699	0.3867	-0.00209	0.9889	0.4799
254761_at	AT4G13195	CLE44 (CLAVATA3/ESR-RELATED 44)	0.9387	0.034	0.1065	0.194	0.5485	0.4042	0.976	0.0301	0.0708	0.2313	0.4788	0.317
254762_at	AT4G13230	late embryogenesis abundant domain-containing pr	-0.03417	0.9723	0.5704	-0.3571	0.7187	0.4648	0.7354	0.4704	0.3478	0.4125	0.6782	0.39
254763_at	AT4G13170	60S ribosomal protein L13A (RPL13aC)	-0.1473	0.2324	0.2833	-0.027	0.8093	0.4927	0.7102	1.00E-04	0.0101	0.8305	0	0.0053
254764_at	AT4G13250	short-chain dehydrogenase/reductase (SDR) family	0.2376	0.3857	0.3677	0.218	0.4225	0.3518	-0.4294	0.0093	0.0387	-0.449	0.008	0.0278
254765_at	AT4G13270	similar to unknown protein [Arabidopsis thaliana] (T	0.660301	0.555	0.4428	0.262	0.0491	0.1097	-0.1133	0.2935	0.2654	0.0884	0.3991	0.2838
254766_at	no_match	no_match	0.311	0.7813	0.518	0.5479	0.6285	0.4339	0.1238	0.9116	0.4957	0.3607	0.7479	0.413
254767_s_at	AT4G13310,AT4G13290	[AT4G13310, CYP71A20 (cytochrome P450, family	-0.7093	0.6124	0.4635	-1.0101	0.4783	0.3755	0.08488	0.9508	0.5057	-0.2158	0.8755	0.4501
254768_at	AT4G13320	similar to hypothetical protein [Vitis vinifera] (GB:CA	1.3048	0.14	0.2176	-0.5585	0.4755	0.3744	1.7055	0.0586	0.1036	-0.1578	0.8201	0.4342
254769_at	AT4G13330	similar to unnamed protein product [Vitis vinifera] (G	0.4057	0.6827	0.4868	0.5189	0.6037	0.4247	-0.6105	0.2838	0.2601	-0.4973	0.3707	0.2716
254770_at	AT4G13340	leucine-rich repeat family protein / extensin family p	0.07932	0.8799	0.5464	-0.7412	0.207	0.2376	0.6826	0.0258	0.0652	-0.1379	0.5228	0.335
254771_at	AT4G13380	MEE56 (maternal effect embryo arrest 56); metal io	0.5516	0.5971	0.4586	0.1705	0.8679	0.5094	1.0409	0.3401	0.2884	0.6598	0.5305	0.3382
254772_at	AT4G13390	proline-rich extensin-like family protein	0.008404	0.9966	0.5761	0.3192	0.8702	0.51	-0.4883	0.8032	0.4645	-0.1774	0.9276	0.465
254773_at	AT4G13410	ATCSLA15 (Cellulose synthase-like A15); transfera	-0.9184	0.0917	0.1757	-1.8812	0.0106	0.0556	-0.2685	0.4427	0.3353	-1.2312	0.0175	0.0423
254774_at	AT4G13440	calcium-binding EF hand family protein	-1.452	0.0209	0.085	-0.1967	0.6427	0.4391	-1.3815	0.0245	0.0634	-0.1263	0.7639	0.4179
254775_at	AT4G13450	universal stress protein (USP) family protein	-1.7994	0.069	0.1511	-0.6288	0.4368	0.3583	-1.3248	0.1432	0.174	-0.1541	0.8428	0.4408
254776_at	AT4G13360	catalytic	0.6852	0.0011	0.036	0.5722	0.0023	0.0334	0.02453	0.6998	0.4312	-0.08848	0.2092	0.1904
254777_at	AT4G12960	gamma interferon responsive lysosomal thiol reduct	-0.2864	0.6168	0.4652	-1.014	0.1276	0.1812	0.6486	0.1145	0.1521	-0.07909	0.8183	0.4338
254778_at	AT4G12750	sequence-specific DNA binding / transcription factor	0.8899	3.00E-04	0.0318	0.8791	3.00E-04	0.0249	-0.4052	0.0058	0.0319	-0.416	0.0053	0.0227
254779_at	AT4G12760	similar to Os05g0417300 [Oryza sativa (japonica cu	0.6983	0.0553	0.135	0.7132	0.0521	0.1132	-0.08719	0.6446	0.4125	-0.07225	0.701	0.3978
254780_s_at	AT4G12770,AT4G12780	[AT4G12770, heat shock protein binding];[AT4G12(	0.3441	0.2478	0.2923	0.2759	0.3394	0.3132	0.2238	0.4289	0.3292	0.1556	0.574	0.3539
254781_at	AT4G12840	similar to unknown protein [Arabidopsis thaliana] (T	-0.2412	0.4049	0.3778	-0.5299	0.1104	0.1677	0.514	0.1079	0.147	0.2253	0.4167	0.2911
254782_at	AT4G12860	UNE14 (unfertilized embryo sac 14); calcium ion bir	1.5767	0.1575	0.2313	-0.8077	0.424	0.3525	0.9477	0.3556	0.2959	-1.4367	0.1888	0.1787
254783_at	AT4G12810	hydrolase, alpha/beta fold family protein	-1.6432	0.0012	0.036	-2.0084	5.00E-04	0.0263	0.02509	0.8812	0.487	-0.3401	0.097	0.1182
254784_at	AT4G12720	AtNUDT7 (ARABIDOPSIS THALIANA NUDIX HYDI	0.6409	0.1198	0.2001	0.6554	0.1138	0.1704	0.3759	0.0068	0.0337	0.3904	0.0059	0.0239
254785_at	AT4G12730	FLA2	-2.4056	0.0078	0.0583	-2.5577	0.0063	0.0454	0.7518	0.0275	0.0675	0.5997	0.0539	0.0829
254786_at	AT4G12890	gamma interferon responsive lysosomal thiol reduct	-0.1222	0.9089	0.5536	-1.5035	0.208	0.2383	1.2939	0.2663	0.2499	-0.08742	0.9347	0.4689
254787_at	AT4G12690	similar to unknown protein [Arabidopsis thaliana] (T	-0.5798	0.0233	0.0894	-0.3651	0.0877	0.1492	-0.5078	0.0089	0.0378	-0.2931	0.0517	0.081
254788_at	AT4G12790	ATP-binding family protein	0.1475	0.424	0.3868	0.02392	0.8923	0.5164	0.1435	0.0849	0.1283	0.01999	0.7668	0.4189
254789_at	AT4G12880	elastin/ovarian-like domain-containing protein	-0.9575	0.0116	0.0672	-0.681	0.0348	0.0922	0.1237	0.5989	0.3977	0.4002	0.1388	0.1474
254790_at	AT4G12800	PSAL (photosystem I subunit L)	-0.4529	0.0571	0.137	-0.604	0.0242	0.0781	0.1585	0.1311	0.1646	0.007349	0.9342	0.4668
254791_at	AT4G12910	SCPL20 (serine carboxypeptidase-like 20); serine c	-0.5839	0.0089	0.0611	-0.5507	0.011	0.0562	0.1276	0.3575	0.2968	0.1608	0.2606	0.2181
254792_at	AT4G12920	aspartyl protease family protein	-1.1553	0.2613	0.3004	1.4098	0.3018	0.2923	-0.7213	0.4958	0.3581	2.2437	0.0804	0.1054
254793_at	AT4G12930	similar to unknown protein [Arabidopsis thaliana] (T	-1.5859	0.1838	0.2509	0.3918	0.712	0.4628	-1.4685	0.2114	0.2188	0.5091	0.6336	0.3749
254794_at	AT4G12970	similar to unnamed protein product [Vitis vinifera] (G	-0.9193	0.0133	0.0711	-0.5896	0.0533	0.1145	-0.5457	0.035	0.0767	-0.216	0.2826	0.2295
254795_at	AT4G12900	unknown protein	-0.316	0.3576	0.3533	0.06093	0.851	0.5048	-0.6373	0.1043	0.1444	-0.2603	0.4404	0.3015
254796_at	AT4G13000	protein kinase family protein	0.6005	0.031	0.1022	0.1731	0.4002	0.3412	-0.06165	0.7545	0.4495	-0.489	0.0566	0.0854
254797_at	AT4G13030	similar to unnamed protein product [Vitis vinifera] (G	-0.1642	0.5162	0.4276	-0.0262	0.9151	0.5227	-2.97E-06	1	0.5179	0.138	0.5822	0.357
254798_at	AT4G13050	acyl-(acyl carrier protein) thioesterase, putative / ac	-0.02328	0.9218	0.5575	-0.1792	0.4663	0.3705	-0.09451	0.6602	0.418	-0.2504	0.2774	0.2268
254799_at	AT4G13060	F-box family protein-related	-0.3182	0.7882	0.52	-0.135	0.9089	0.5212	-1.6851	0.0717	0.1164	-1.5018	0.096	0.1175
254800_at	AT4G13070	group II intron splicing factor CRS1-related	-0.971	0.0242	0.0906	-0.2347	0.4412	0.36	-0.4146	0.1347	0.1673	0.3217	0.2203	0.1962
254801_at	AT4G13080	xyloglucan:xyloglucosyl transferase, putative / xylog	0.607	0.3505	0.3505	-0.4721	0.4586	0.3675	0.2392	0.6994	0.4311	-0.8399	0.2187	0.1954
254802_at	AT4G13090	xyloglucan:xyloglucosyl transferase, putative / xylog	-0.8398	0.6286	0.4691	-1.9362	0.2943	0.2888	-0.5609	0.6353	0.4095	-1.6573	0.2045	0.1876
254803_at	AT4G13100	zinc finger (C3HC4-type RING finger) family protein	-0.4243	0.2831	0.3134	-0.6243	0.1424	0.1925	0.07714	0.807	0.4656	-0.1229	0.899	0.3971
254804_at	AT4G13010	oxidoreductase, zinc-binding dehydrogenase family	-0.0393	0.7978	0.5233	-0.09588	0.5408	0.401	0.1128	0.4475	0.3373	0.05621	0.6965	0.3964
254805_at	AT4G12480	pEARLI 1; lipid binding	1.025	0.1231	0.2034	1.3292	0.0648	0.1272	0.5611	0.0475	0.0915	0.8653	0.0121	0.0346
254806_at	AT4G12430	[AT4G12430, trehalose-6-phosphate phosphatase,	-0.5773	0.0709	0.1536	-1.1702	0.0077	0.049	-0.8651	0.0159	0.0503	-1.458	0.0026	0.0165
254807_at	AT4G12700	similar to unknown protein [Arabidopsis thaliana] (T	-0.4587	0.0743	0.1567	-0.6864	0.0229	0.0764	-0.02314	0.9095	0.4961	-0.2508	0.2596	0.2176
254808_at	AT4G12740	adenine-DNA glycosylase-related / MYH-related	0.3782	0.2256	0.2789	-0.575	0.0952	0.1555	0.1202	0.6729	0.422	-0.8331	0.0344	0.0628
254809_at	AT4G12410	auxin-responsive family protein	-0.7271	0.5336	0.4345	0.709	0.5433	0.402	0.6116	0.6978	0.3973	2.0477	0.1278	0.1402
254810_at	AT4G12390	PME1; pectinesterase inhibitor	-0.5263	0.1135	0.1952	-1.1697	0.0109	0.056	1.0343	0.0065	0.0331	0.3908	0.1206	0.1354
254811_at	AT4G12230	esterase/lipase/thioesterase family protein	0.3398	0.0614	0.1422	0.4548	0.026	0.0807	-0.04444	0.7529	0.4491	0.07048	0.6211	0.3706
254812_at	AT4G12260	GAE5 (UDP-D-GLUCURONATE 4-EPIMERASE 5);	0.4006	0.0018	0.0265	0.4625	0.0011	0.0293	-0.1729	0.0339	0.0752	0.111	0.1116	0.1288
254813_at	AT4G12350	MYB42 (myb domain protein 42); transcription facto	-0.8028	0.4921	0.4166	-0.9031	0.4434	0.361	0.2573	0.812	0.4672	0.1569	0.8844	0.4528
254814_at	AT4G12340	similar to unnamed protein product [Vitis vinifera] (G	0.3717	0.0224	0.0876	0.7414	0.002	0.033	-0.1286	0.279	0.2575	0.2411	0.0788	0.104
254815_at	AT4G12450	SKU5 (skewed 5) copper ion binding	-0.7816	0.1459	0.222	-1.2132	0.049	0.1097	-0.2989	0.1151	0.1525	-0.7306	0.008	0.0278
254816_at	AT4G12440	APT4; adenine phosphoribosyltransferase	0.9228	0.2467	0.2916	0.4514	0.5436	0.4021	0.4907	0.4869	0.3542	0.0193	0.9774	0.4775
254817_at	AT4G12460	oxysterol binding	-0.1968	0.5502	0.4412	-0.09604	0.7665	0.4793	-1.2905	0.0028	0.0241	-1.1897	0.0037	0.0198
254818_at	AT4G12470	protease inhibitor/seed storage/lipid transfer protein	0.3782	0.4448	0.3955	0.6091	0.2444	0.2607	0.435	0.0389	0.0816	0.6659	0.0098	0.0309
254819_at	AT4G12500	protease inhibitor/seed storage/lipid transfer protein	0.569	0.4665	0.4058	1.3308	0.1332	0.1854	0.3201	0.0448	0.0885	1.0819	6.00E-04	0.0103
254820_s_at	AT4G12510,AT4G12520	[AT4G12510, protease inhibitor/seed storage/lipid tr	-0.1663	0.6764	0.4848	-0.2446	0.5446	0.4024	0.5834	0.1899	0.2055	0.505	0.244	0.2093
254821_at	AT4G12540	similar to unnamed protein product [Vitis vinifera] (G	-0.4269	0.6953	0.4912	-0.4806	0.6601	0.4451	0.3045	0.7788	0.4568	0.2508	0.8167	0.4334
254822_at	AT4G12570	UPL5 (UBIQUITIN PROTEIN LIGASE 5); ubiquitin-p	0.3099	0.2342	0.2839	0.3062	0.2389	0.2571	-0.6362	0.0453	0.0891	-0.6399	0.0446	0.074
254823_at	AT4G12580	unknown protein	-0.6638	0.2935	0.3194	0.6551	0.299	0.291	1.1315	0.1085	0.1474	2.4504	0.0112	0.0331
254824_

254890_at	AT4G11600	ATQPX6 (GLUTATHIONE PEROXIDASE 6); glutat	0.6952	0.0594	0.1395	0.8295	0.0357	0.0932	0.5319	0.0042	0.0277	0.6662	0.0018	0.0148
254891_at	AT4G11740	SAY1	0.5784	0.0257	0.0929	0.5838	0.0249	0.0791	0.5633	0.011	0.0416	0.5687	0.0107	0.0324
254892_at	AT4G11800	protein serine/threonine phosphatase	0.2943	0.0214	0.0859	0.02077	0.8084	0.4925	-0.4228	0.0062	0.0327	-0.6963	0.001	0.012
254893_at	AT4G11830	PLDGAMMA2; phospholipase D	-0.08068	0.6254	0.4683	-0.4263	0.0493	0.1101	-1.8447	3.00E-04	0.0134	-2.1903	1.00E-04	0.0067
254894_at	AT4G11840	PLDGAMMA3 (phospholipase D gamma 3); phosph	1.5835	0.0048	0.0499	1.6777	0.0039	0.0392	-0.3955	0.2313	0.2301	-0.3014	0.343	0.2593
254895_at	AT4G11870	unknown protein	-0.8106	0.5953	0.458	0.2266	0.8798	0.5131	-0.2701	0.8571	0.4803	0.7672	0.6144	0.3682
254896_at	AT4G11880	AGL14 (AGAMOUS-LIKE 14); DNA binding / transc	0.3747	0.7161	0.4981	0.993	0.3592	0.3225	-0.2315	0.7856	0.459	0.3868	0.6524	0.3816
254897_at	AT4G11890	protein kinase family protein	0.1151	0.8615	0.5415	0.07456	0.9099	0.5215	0.03093	0.9589	0.5074	-0.00966	0.9872	0.4795
254898_at	AT4G11480	protein kinase family protein	1.1268	0.4992	0.4201	1.2243	0.4653	0.3701	-0.3289	0.6862	0.4265	-0.2314	0.775	0.4215
254899_at	AT4G11490	protein kinase family protein	-0.2	0.8124	0.5275	-1.1409	0.2217	0.247	0.9542	0.2886	0.2629	0.01329	0.9872	0.4785
254900_at	AT4G11510	RALFL28 (RALF-LIKE 28)	0.3064	0.7519	0.5089	1.1575	0.2698	0.2754	0.03762	0.9688	0.5096	0.8887	0.3815	0.2764
254901_at	AT4G11530	protein kinase family protein	0.5607	0.025	0.0918	0.2108	0.2592	0.2696	0.137	0.4415	0.3347	-0.2129	0.2553	0.2153
254902_at	AT4G11550	DC1 domain-containing protein	0.9863	0.5258	0.4316	-1.1799	0.453	0.3653	1.5814	0.3281	0.2824	-0.5848	0.7017	0.3979
254903_at	AT4G11150	TUF (VACUOLAR ATP SYNTHASE SUBUNIT E1)	0.08905	0.5266	0.4318	0.08108	0.5625	0.4092	0.3563	0.0035	0.026	0.3483	0.0038	0.0199
254904_at	AT4G11160	initiation factor IF-2, mitochondrial, putative	0.1899	0.3873	0.3683	0.4301	0.0932	0.1539	-0.5629	0.0453	0.0891	-0.3227	0.1749	0.1702
254905_at	AT4G11170	disease resistance protein (TIR-NBS-LRR class), p	1.2594	0.0588	0.1389	1.5596	0.0316	0.0883	-0.6475	0.1782	0.1974	-0.3473	0.4309	0.2972
254906_at	AT4G11180	disease resistance-responsive family protein / dirige	-1.8553	0.1807	0.2486	-1.2133	0.3494	0.3178	-0.4151	0.7351	0.4433	0.2269	0.8525	0.4434
254907_at	AT4G11190	disease resistance-responsive family protein / dirige	-1.0305	0.0631	0.1441	0.02152	0.96	0.5341	-0.475	0.3046	0.2709	0.577	0.2261	0.1995
254908_at	AT4G11200	transposable element gene	0.2473	0.7431	0.5067	-1.1027	0.1924	0.2276	-0.02004	0.9757	0.5115	-1.37	0.0907	0.1134
254909_at	AT4G11210	disease resistance-responsive family protein / dirige	0.2702	0.6627	0.4803	-0.4769	0.4533	0.3653	0.6956	0.2927	0.265	-0.05141	0.933	0.4664
254910_at	AT4G11175	initiation factor IF-1, chloroplast, putative	-0.7222	0.0044	0.0482	-0.391	0.035	0.0925	0.4284	0.0264	0.0661	0.7597	0.0037	0.0197
254911_at	AT4G11100	similar to unknown protein (Arabidopsis thaliana) (T	-0.02722	0.8287	0.532	-0.2761	0.0792	0.141	0.2036	0.1592	0.1852	-0.04528	0.7204	0.4041
254912_at	AT4G11230	respiratory burst oxidase, putative / NADPH oxidase	-0.4549	0.8094	0.5266	-0.04015	0.9829	0.5399	-1.2277	0.5252	0.3692	-0.813	0.6692	0.387
254913_at	AT4G11270	transducin family protein / WD-40 repeat family prot	0.1759	0.4217	0.3859	0.1434	0.5063	0.3872	-0.3905	0.0411	0.0841	-0.4229	0.0323	0.0607
254914_at	AT4G11290	peroxidase, putative	0.1924	0.8287	0.532	0.4061	0.6513	0.4422	0.8057	0.262	0.2477	1.0194	0.1741	0.1698
254915_s_at	AT4G11320;AT4G11310	AT4G11320, cysteine proteinase, putative;[AT4G1	-0.7304	0.0227	0.0881	-0.172	0.4436	0.3611	0.3524	0.1569	0.1837	0.9107	0.0109	0.0326
254916_at	AT4G11340	Toll-Interleukin-Resistance (TIR) domain-containing	0.05591	0.8646	0.5423	-1.1257	0.0216	0.0747	0.2525	0.4578	0.3421	-0.9291	0.0391	0.0681
254917_at	AT4G11350	transferase, transferring glycosyl groups	1.0247	0.0505	0.1292	1.5057	0.0153	0.0649	-0.3735	0.3703	0.303	0.1075	0.7861	0.4246
254918_at	AT4G11260	SGT1B (enhanced downy mildew 1b); protein bindi	0.3626	0.0809	0.1643	0.6802	0.0121	0.059	-0.3412	0.0391	0.136	-0.02363	0.887	0.4535
254919_at	AT4G11360	RHA1B (RING-H2 finger A1B); protein binding / zin	0.1269	0.7743	0.5161	0.4132	0.3709	0.3278	0.1864	0.0962	0.1378	0.4737	0.0053	0.0227
254920_at	AT4G11370	BTI2 (VIRB2-INTERACTING PROTEIN 2)	0.5141	0.0255	0.0926	0.5122	0.0259	0.0855	0.0814	0.6118	0.4017	-0.08336	0.6036	0.4041
254921_at	AT4G11300	similar to unknown protein (Arabidopsis thaliana) (T	0.03902	0.8182	0.5291	0.3591	0.0867	0.1485	-0.06085	0.6996	0.4312	0.2593	0.1519	0.1561
254922_at	AT4G11370	RHA1A (RING-H2 finger A1A); protein binding / zin	1.0215	0.0416	0.1175	1.2574	0.0219	0.075	0.3116	0.2925	0.2649	0.5476	0.1004	0.1209
254923_at	AT4G11240	TOPP7 (type one serine/threonine protein phospha	0.1787	0.4936	0.3796	0.3208	0.1739	0.2154	-1.0686	0.0016	0.0202	-0.9165	0.0027	0.0171
254924_at	AT4G11330	ATMPK6 (MAP KINASE 6); MAP kinase kinase	-0.1184	0.6014	0.46	-0.3132	0.2083	0.2385	0.1681	0.216	0.2213	-0.02679	0.8265	0.4361
254925_at	AT4G11380	beta-adaptin, putative	0.4655	0.001	0.036	0.2255	0.0146	0.0638	-0.3224	0.0042	0.0277	-0.5625	5.00E-04	0.0095
254926_at	AT4G11260	ACS6 (1-AMINOCYCLOPROPANE-1-CARBOXYLI	0.9366	0.045	0.1223	-0.8763	0.0152	0.1155	0.3742	0.0711	0.116	0.4342	0.0475	0.0768
254927_at	AT4G11400	ARID/BRIGHT DNA-binding domain-containing prot	-0.9841	0.3227	0.3359	-0.9815	0.3238	0.3052	0.297	0.7508	0.4485	0.2996	0.7488	0.4134
254928_at	AT4G11410	short-chain dehydrogenase/reductase (SDR) family	-0.2189	0.3483	0.3491	-0.1785	0.4354	0.3577	0.3958	0.0203	0.0573	0.4362	0.0147	0.0386
254929_at	AT4G11360	binding	-0.8887	0.5029	0.4217	0.599	0.6461	0.4402	-0.6344	0.6273	0.4071	0.8533	0.519	0.3332
254930_at	AT4G11450	similar to unknown protein (Arabidopsis thaliana) (T	0.2009	0.3167	0.3325	-0.333	0.1311	0.1836	0.1442	0.4581	0.3423	-0.3898	0.0909	0.1135
254931_at	AT4G11460	protein kinase family protein	0.8083	0.0955	0.1785	-1.3025	0.0249	0.0791	0.8336	0.0885	0.1314	-1.2773	0.0264	0.0539
254932_at	AT4G11120	elongation factor Ts (EF-Ts), putative	0.2819	0.2333	0.2838	0.2623	0.2617	0.2708	-0.4101	0.1108	0.1489	-0.4297	0.0992	0.12
254933_at	AT4G11130	RDR2 (RNA-DEPENDENT RNA POLYMERASE 2)	0.07525	0.7482	0.5083	0.1846	0.4463	0.3623	-0.09529	0.6592	0.4177	0.01402	0.9476	0.4703
254934_at	AT4G11140	CRF1 (CYTOKININ RESPONSE FACTOR 1); DNA	-0.8437	0.0839	0.1678	-1.1558	0.035	0.0923	-0.2181	0.5784	0.39	-0.5302	0.2159	0.1941
254935_at	AT4G11660	disease resistance protein (CC-NBS-LRR class), p	-0.6704	0.4936	0.4174	0.4611	0.6513	0.4353	-0.3403	0.6917	0.4283	0.7912	0.3775	0.2747
254936_at	AT4G10790	UBX domain-containing protein	0.3791	0.0593	0.1394	0.4631	0.0332	0.0903	-0.2547	0.1166	0.1536	-0.1707	0.2519	0.2136
254937_at	AT4G10750	HpcH/HpaI aldolase family protein	0.1705	0.3429	0.3463	0.2874	0.1442	0.1939	0.1421	0.4209	0.3257	0.2591	0.1778	0.1719
254938_at	AT4G10770	ATOPT7 (oligopeptide transporter 7); oligopeptide t	-0.9518	0.0224	0.0875	-1.5516	0.0041	0.04	0.0701	0.7195	0.4383	-0.5296	0.0437	0.073
254939_at	AT4G10800	similar to protein binding [Arabidopsis thaliana] (TA	-0.9941	0.0191	0.082	0.07034	0.8013	0.4898	-0.9897	0.0034	0.0256	0.07472	0.6621	0.3849
254940_at	AT4G10820	F-box family protein	0.1345	0.9291	0.5597	-1.3082	0.4091	0.3455	0.731	0.6192	0.4043	-0.7117	0.6281	0.3731
254941_s_at	AT1G30030;AT4G10830	AT1G30030, transposable element gene];[AT4G10	1.2485	0.3575	0.3533	-0.9328	0.701	0.4594	0.07723	0.9677	0.5095	-3.204	0.1483	0.1535
254942_at	AT4G10880	similar to unknown protein (Arabidopsis thaliana) (T	1.4277	0.2809	0.3118	0.224	0.8546	0.5059	1.2082	0.3513	0.2939	0.004504	0.9971	0.4821
254943_at	AT4G10890	similar to unknown protein [Arabidopsis thaliana] (T	-0.07993	0.5578	0.4441	0.04223	0.7528	0.476	0.5828	0.0089	0.0378	0.7049	0.0045	0.0213
254944_at	AT4G10930	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.4899	0.0868	0.1706	0.2126	0.3824	0.333	-0.4071	0.1337	0.1665	-0.6844	0.0343	0.0626
254945_at	AT4G10940	PHD finger family protein	0.05361	0.9414	0.5629	-0.5097	0.4984	0.3839	-0.8264	0.2836	0.26	-1.3898	0.1059	0.1246
254946_at	AT4G10950	GDSL-motif lipase/hydrolase family protein	-0.6469	0.026	0.0933	0.2878	0.1993	0.2324	-0.6775	0.0079	0.0358	0.2573	0.1352	0.1452
254947_at	AT4G10960	transposable element gene	0.9567	0.3794	0.3642	1.1785	0.2908	0.287	0.6101	0.5631	0.3839	0.832	0.439	0.301
254948_at	AT4G11000	ankyrin repeat family protein	0.2079	0.6138	0.4641	0.5527	0.2199	0.2458	-0.6466	0.1044	0.1445	-0.3018	0.3837	0.2775
254949_at	AT4G11020	similar to unknown protein [Arabidopsis thaliana] (T	0.5658	0.6255	0.4683	-0.4943	0.6686	0.4479	1.5018	0.2337	0.2316	0.4418	0.7013	0.3978
254950_at	AT4G10810	similar to unknown protein [Arabidopsis thaliana] (T	-0.04118	0.7273	0.5017	0.2395	0.0951	0.1554	0.9008	2.00E-04	0.0133	1.1815	1.00E-04	0.0058
254951_at	AT4G10840	kinesin light chain-related	0.1041	0.4652	0.4053	-0.1397	0.3398	0.3133	0.401	0.0319	0.0726	0.1573	0.2736	0.2248
254952_at	AT4G10955;AT4G10960	[AT4G10955, lipase class 3 family protein];[AT4G10	0.5634	0.0164	0.0771	0.922	0.0029	0.0355	0.08559	0.3691	0.3023	0.4441	0.0063	0.0246
254953_at	AT4G10925	F-box family protein	0.08821	0.2804	0.3116	0.4	0.0048	0.0421	-0.6212	1.00E-04	0.0119	-0.3094	0.0019	0.0149
254954_at	AT4G10910	unknown protein	-0.8826	0.0944	0.1777	-0.2752	0.5334	0.3977	0.2451	0.577	0.3895	0.8525	0.1026	0.1224
254955_at	AT4G10920	KELP; DNA binding / transcription coactivator	0.1771	0.2654	0.3024	0.5806	0.0132	0.0613	0.2093	0.0637	0.1087	0.6129	0.0017	0.0147
254956_at	AT4G10850	sodium:hydrogen antiporter, putative	-0.05141	0.9604	0.5674	0.3539	0.7344	0.4496	-0.578	0.5792	0.3904	-0.1727	0.8658	0.4472
254957_at	AT4G10970	similar to unknown protein [Arabidopsis thaliana] (T	0.4979	0.0394	0.1145	0.6885	0.0141	0.0628	0.4919	0.0016	0.0202	0.6824	4.00E-04	0.0092
254958_at	AT4G11010	NDPK3 (NUCLEOSIDE DIPHOSPHATE KINASE 3	0.3189	0.1805	0.2485	0.1633	0.4533	0.3653	0.3226	0.1765	0.1963	0.1671	0.4438	0.3033
254959_at	AT4G10955;AT4G10960	[AT4G10955, lipase class 3 family protein];[AT4G10	-0.2662	0.3315	0.3408	-0.4488	0.1252	0.1793	-0.2864	0.1806	0.1992	-0.4791	0.0536	0.0827
254960_at	AT4G10845	unknown protein	-1.4367	0.0729	0.1555	-0.541	0.414	0.3478	-1.1297	0.13	0.1639	-0.2339	0.7139	0.4022
254961_at	AT4G11030	long-chain-fatty-acid--CoA ligase, putative / long-ch	-0.2598	0.8267	0.5316	0.7856	0.5189	0.392	-0.3516	0.7599	0.4512	0.6938	0.5537	0.3464
254962_at	AT4G11050	ATGH9C3 (ARABIDOPSIS THALIANA GLYCOSYL	-1.2108	0.3502	0.3497	0.7084	0.5699	0.4118	0.5699	-1.4917	0.2157	0.2212	0.4275	0.6953	0.396
254963_at	no_match	no_match	0.4278	0.0548	0.1344	0.6909	0.0122	0.0593	0.04727	0.7608	0.4514	0.3104	0.0991	0.1199
254964_at	AT4G11080	high mobility group (HMG1/2) family protein	-0.114	0.7958	0.5226	-0.3349	0.4623	0.3689	0.2088	0.6302	0.4079	-0.01203	0.9775	0.4775
254965_at	AT4G11090	similar to unknown protein [Arabidopsis thaliana] (T	0.3019	0.1819	0.2496	0.5457	0.0434	0.1033	0.2658	0.2285	0.2287	0.5096	0.0528	0.0819
254966_at	AT4G11110	SPA2 (SPA1-RELATED 2); signal transducer	-0.06483	0.7767	0.5169	0.1936	0.4161	0.3488	-0.9141	0.0099	0.0398	-0.6557	0.0297	0.0579
254967_at	AT4G10410	similar to F-box family protein [Arabidopsis thaliana	-0.03315	0.9772	0.5716	0.3862	0.7408	0.4715	-0.2352	0.8395	0.4755	0.1841	0.8739	0.4495
254968_at	AT4G10420	similar to F-box family protein [Arabidopsis thaliana	-0.9455	0.0566	0.1363	-0.5488	0.198	0.2316	-0.7168	0.1143	0.1519	-0.3201	0.4193	0.2923
254969_at	AT4G10360	similar to unknown protein [Arabidopsis thaliana] (T	-0.2531	0.1614	0.2346	-0.3207	0.0954	0.1556	-0.08699	0.5747	0.3883	-0.1546	0.3392	0.2576
254970_at	AT4G10340	LHCB5 (LIGHT HARVESTING COMPLEX OF PHO	-0.2361	0.1886	0.2543	-0.5675	0.019	0.071	0.07201	0.5139	0.3646	-0.2593	0.0616	0.0899
254971_at	AT4G10380	NIP5;1/NLM6/NLM8 (NOD26-like intrinsic protein 5;	-0.3496	0.6396	0.4728	0.2843	0.7019	0.4597	-0.1806	0.7244	0.44	0.4532	0.3962	0.2827
254972_at	AT4G10440	dehydration-responsive family protein	1.7476	0.2041	0.2647	-1.2698	0.3325	0.3096	1.9397	0.1677	0.1902	-1.0777	0.4028	0.2853
254973_at	AT4G10460	transposable element gene	-2.44	0.099	0.1816	0.9361	0.4575	0.3672	-2.9874	0.0587	0.1037	0.3887	0.7502	0.4139
254974_at	AT4G10490	oxidoreductase, 2OG-Fe(II) oxygenase family prote	0.7889	0.3556	0.3525	-0.5182	0.5308	0.3965	0.05642	0.9441	0.5042	-1.2506	0.1734	0.1693
254975_at	AT4G10500	oxidoreductase, 2OG-Fe(II) oxygenase family prote	2.7905	5.00E-04	0.0325	2.67	6.00E-04	0.027	0.9455	0.0266	0.0663	0.825	0.0403	0.0694
254976_at	AT4G10510	subtilase family protein	0.1426	0.8652	0.5423	-1.7737	0.0875	0.1489	1.5755	0.1161	0.1533	-0.3408	0.6876	0.393
254977_s_at	AT4G10530;AT4G10520	AT4G10530, subtilase family protein];[AT4G10520;	-1.1327	0.3587	0.3538	-0.1497	0.8977	0.5182	0.3389	0.733	0.4426	1.322	0.2267	0.1997
254978_at	AT4G10540	subtilase family protein	0.2234	0.8409	0.5358	-1.6208	0.1953	0.2296	1.155	0.3304	0.2835	-0.6893	0.545	0.3429
254979_at	AT4G10550	subtilase family protein	-0.1879	0.5573	0.4439	0.0345	0.9122	0.522	-0.6013	0.1102	0.1485	-0.3789	0.2668	0.2211
254980_at	AT4G10450	60S ribosomal protein L9 (RPL90D)	0.008562	0.9737	0.5707	0.0834	0.75	0.4749	-0.04131	0.6808	0.4246	0.03351	0.7377	0.4096
254981_at	AT4G10480	nascent polypeptide associated complex alpha chai	0.04715	0.706	0.4948	0.2311	0.1179	0.1736	0.6432	3.00E-04	0.0141	0.8271	1.00E-04	0.0063
254982_at	AT4G10470	similar to unknown protein [Arabidopsis thaliana] (T	-0.4439	0.1751	0.245	-0.2948	0.3357	0.3112	-0.1799	0.3069	0.272	-0.0309	0.8506	0.4429
254983_at	AT4G10560	MEE53 (maternal effect embryo arrest 53); protein	0.3326	0.6361	0.4716	0.2962	0.8226	0.4966	1.3552	0.3349	0.286	1.0187	0.4566	0.3087
254984_s_at	AT4G10590;AT4G10570	[AT4G10590, ubiquitin carboxyl-terminal hydrolase	0.3326	0.0259	0.0931	0.5075	0.0062	0.0451	-0.8729	4.00E-04	0.0145	-0.6981	9.00E-04	0.0115
254985_x_at	AT4G10580;AT1G42605	[AT4G10580, transposable element gene];[AT1G42	0.1131	0.8178	0.5291	0.8825	0.1273	0.181	-1.1459	0.0035	0.0261	-0.3765	0.1124	0.1293
254986_at	AT4G10640	IQD16 (IQ-domain 16); calmodulin binding	-0.4178	0.6968	0.4918	-0.2971	0.7807	0.4837	0.07026	0.9472	0.505	0.191	0.8575	0.4451
254987_s_at	AT4G10700;AT4G10660	[AT4G10700, similar to unknown protein [Arabidops	0.3433	0.697	0.4918	0.5796	0.5186	0.3919	-0.7711	0.38	0.3078	-0.5348	0.5316	0.3386
254988_at	AT4G10670	GTC2 (GLOBAL TRANSCRIPTION FACTOR GRO	1.1422	0.3857	0.3678	-0.1472	0.9063	0.5205	1.4178	0.2343	0.2319	0.1283	0.9053	0.4589
254989_at	AT4G10690	transposable element gene	-0.3544	0.6847	0.4875	-0.4154	0.6355	0.4367	1.0595	0.2615	0.2474	0.9985	0.2858	0.2312
254990_at	AT4G10610	RBP37 (RNA-BINDING PROTEIN 37); RNA binding	0.7107	0.0034	0.0446	0.7389	0.0029	0.0355	0.0582	0.6365	0.41	0.08643	0.4904	0.3221
254991_at	AT4G10620	similar to GTP binding [Arabidopsis thaliana] (TAIR:	0.3604	0.2445	0.2904	0.1206	0.672	0.4492	0.2161	0.0339	0.0752	-0.02371	0.7456	0.4121
254992_at	AT4G10710	SPT16 (GLOBAL TRANSCRIPTION FACTOR C);	0.2903	0.2398	0.2875	0.2923	0.2371	0.2561	-0.4512	0.0986	0.1398	-0.4492	0.0997	0.1204
254993_at	AT4G10730	kinase	-0.1426	0.6256	0.4684	0.5876	0.0954	0.1556	-0.5881	0.0951	0.137	0.1421	0.6269	0.3727
254994_at	AT4G10760	EMB1706 (EMBRYO DEFECTIVE 1706); S-adenos	0.1644	0.4439	0.3952	0.1696	0.4565	0.3666	0.004155	0.9795	0.5124	-0.00071	0.9965	0.482
254995_at	AT4G10370	DC1 domain-containing protein	0.6574	0.3515	0.3505	0.01062	0.9849	0.5404	-0.8191	0.1339	0.1667	-0.2723	0.5666	0.3515
254996_at	AT4G10390	protein kinase family protein	-1.4086	0.0831	0.1668	-0.8322	0.2461	0.2616	-0.6792	0.0529	0.0976	-0.1028	0.7015	0.3978
254997_s_at	AT4G10400;AT4G09920	[AT4G10400, F-box family protein];[AT4G09920, F-	0.06087	0.8268	0.5316	-0.5294	0.1121	0.169	-0.1711	0.4865	0.354	-0.7614	0.0271	0.0547
254998_at	AT4G09760	choline kinase, putative	0.3666	0.294	0.3197	0.1759	0.5937	0.4209	-0.2606	0.0311	0.0718	-0.4514	0.0049	0.022
254999_at	AT4G09830	similar to unknown protein [Arabidopsis thaliana] (T	0.6678	0.0025	0.0424	0.2711	0.0517	0.1128	-0.2159	0.0068	0.0336	-0.6125	1.00E-04	0.0064
255000_at	AT4G09800	RPS18C (S18 RIBOSOMAL PROTEIN); structural c	0.3009	0.0098	0.0633	0.3359	0.0066	0.0461	-0.1061	0.1773	0.1967	-0.07118	0.3344	0.2553
255001_at	AT4G09930	avirulence-responsive family protein / avirulence in	-1.0938	0.3554	0.3525	0.2728	0.2.5304	0.1351	-2.4695	0.062	0.107	1.1597	0.2941	0.2356
255002_at	AT4G09940	avirulence-responsive family protein / avirulence in	0.1035	0.9164	0.5559	0.6746	0.5065	0.3873	-0.9188	0.3771	0.3063	-0.3476	0.7263	0.406
255003_at	AT4G09960	avirulence-responsive family protein / avirulence in	0.6956	0.963	0.568	0.7742	0.6124	0.4278	0.9777	0.5265	0.3697	1.6824	0.299	0.2381
255004_at	AT4G09970	unknown protein	-0.00412	0.9929	0.5752	0.2042	0.6623	0.4458	0.02953	0.9488	0.5053	0.2378	0.6112	0.3672
255005_at	AT4G09990	similar to unknown protein [Arabidopsis thaliana] (T	0.0857	0.822	0.5301	-0.6539	0.1408	0.1913	0.1814	0.62	0.4046	-0.5582	0.1741	0.1698
255006_at	AT4G10010	protein kinase family protein	0.076561	0.9537	0.5657	-0.5626	0.6731	0.4496	0.7813	0.5623	0.3835	0.2952	0.8232	0.4351
255007_at	AT4G10020	ATHSD5 (HYDROXYSTEROID DEHYDROGENAS	1.1442	0.2957	0.3208	-0.673	0.5186	0.3919	0.6722	0.5191	0.3666	-1.1449	0.2954	0.2363
255008_at	AT4G10060	catalytic	-0.2016	0.0631	0.144	-0.2657	0.0282	0.0835	-0.7782	3.00E-04	0.014	-0.8423	2.00E-04	0.0078
255009_at	AT4G10070	KH domain-containing protein	0.2275	0.5036	0.422	0.1681	0.6163	0.4293	-0.5402	0.0773	0.1214	-0.5995	0.0586	0.0873
255010_at	AT4G10050	histidine, alpha/beta fold family protein	0.6085	0.0205	0.0842	0.5904	0.0226	0.0759	-0.1522	0.4047	0.3184	-0.1703	0.3565	0.2654
255011_at	AT4G10040	CYTC-2 (CYTOCHROME C-2); electron carrier	-0.6509	0.0136	0.0719	-0.4115	0.0564	0.118	0.9631	0.0016	0.0202	1.2025	7.00E-04	0.0105
255012_at	AT4G10030	hydrolase, alpha/beta fold family protein	-0.1886	0.0872	0.171	-0.2421	0.0444	0.1043	0.01951	0.8218	0.4703	-0.03401	0.6966	0.3964
255013_at	AT4G10000	similar to unknown protein [Arabidopsis thaliana] (T	-0.00024	0.9987	0.5763	-0.5209	0.0223	0.0755	0.3748	0.0279	0.068	-0.1459	0.2595	0.2175
255014_at	AT4G09960	STK (SEEDSTICK); transcription factor	0.4855	0.615	0.4645	-1.529	0.1615	0.2069	0.7019	0.4751	0.3496	-1.3126	0.2149	0.1936
255015_at	AT4G09920	EMB1920 (EMBRYO DEFECTIVE 1691); S-adenos	0.2234	0.483	0.4132	0.02029	0.9474	0.5313	-0.4141	0.1548	0.1822	-0.6578	0.0497	0.0791
255016_at	AT4G10120	ATSPS4F; sucrose-phosphate synthase/ transferas	-1.1978	0.0012	0.036	-1.6373	4.00E-04	0.0251	-0.3726	0.0196	0.0563	-0.812	0.0012	0.0128
255017_at	AT4G10100	CNX7/SIR5; catalytic	0.1797	0.1988	0.2618	0.2215	0.131	0.1835	0.1939	0.1724	0.1934	0.2356	0.114	0.1305
255018_at	AT4G10090	similar to unnamed protein product [Vitis vinifera] (G	0.3596	0.0166	0.0775	0.2658	0.0429	0.1028	-0.2486	0.0519	0.0966	-0.3424	0.0196	0.0449
255019_at	AT4G10210	similar to unknown protein [Arabidopsis thaliana] (T	-0.634	0.6548	0.4775	-0.4901	0.7282	0.4683	-0.5287	0.7081	0.434	-0.3848	0.7843	0.4242
255020_at	no_match	no_match	0.3816	0.1419	0.219	0.6493	0.036	0.0937	-0.03766	0.8415	0.4761	0.23	0.2626	0.2191
255021_at	AT4G10330	glycine-rich protein	0.2251	0.3172	0.3327	0.4622	0.079	0.1409	-0.249	0.0614	0.1066	-0.01188	0.908	0.4594
255022_at	AT4G10350	ANAC070 (Arabidopsis NAC domain containing pro	-1.3353	0.2137	0.2707	-0.1892	0.8445	0.5028	-0.8265	0.4123	0.3218	0.3196	0.7415	0.411

255090_at	AT4G09360	disease resistance protein (NBS-LRR class), putati	2.0833	0.1369	0.2149	0.04078	0.9728	0.5372	0.3102	0.6538	0.4158	-1.7324	0.054	0.083	
255091_at	AT4G09390	transposable element gene	0.03194	0.9727	0.5705	-1.2444	0.2293	0.2511	0.7128	0.4624	0.3442	-0.5636	0.5558	0.3473	
255092_s_at	AT4G09400;AT2G14340;A	AT4G09400, transposable element gene];[AT2G14	-0.4393	0.7192	0.4992	1.717	0.2059	0.2367	-1.9916	0.1551	0.1823	0.1648	0.8919	0.4548	
255093_s_at	AT4G08580;AT5G17900	AT4G08580, microfibrillar-associated protein-relate	0.1359	0.1757	0.2452	0.2499	0.0391	0.098	-0.02423	0.7333	0.4427	0.08982	0.2469	0.2107	
255094_at	AT4G08590	zinc finger (C3HC4-type RING finger) family protein	-1.0785	0.0065	0.0549	-0.5254	0.0642	0.1265	-0.4862	0.0506	0.0954	0.06693	0.7229	0.405	
255095_at	AT4G08500	MEKK1 (MYTOGEN ACTIVATED PROTEIN KINAS	0.03733	0.8507	0.5383	0.5904	0.0337	0.0907	-0.3234	0.1569	0.1836	0.2297	0.2842	0.2305	
255096_at	AT4G08600	transposable element gene	-0.291	0.6771	0.4849	-0.01236	0.9857	0.5405	1.0547	0.1785	0.1977	1.3334	0.1085	0.1265	
255097_at	no_match	no_match	2.0639	0.0026	0.0426	-0.05245	0.8731	0.5109	-0.5598	0.0435	0.087	-2.6762	2.00E-04	0.007	
255098_at	no_match	no_match	0.8926	0.4351	0.3916	-0.2349	0.8308	0.4991	-0.5362	0.6301	0.4079	-1.6637	0.1815	0.1743	
255099_at	AT4G08650	transposable element gene	0.02527	0.9859	0.5734	0.2738	0.8488	0.504	0.3555	0.7909	0.4604	0.604	0.6552	0.3826	
255100_at	no_match	no_match	-0.2449	0.6251	0.4682	-0.9007	0.1238	0.1785	0.05363	0.9134	0.4961	-0.6022	0.2636	0.2194	
255101_at	AT4G08670	protease inhibitor/seed storage/lipid transfer protein	0.3474	0.8146	0.5283	1.3119	0.3979	0.3403	-0.4724	0.7506	0.4485	0.4922	0.7407	0.4107	
255102_s_at	AT4G08680;AT1G78095	AT4G08680, transposable element gene];[AT1G78	-1.9606	0.1568	0.2309	1.0437	0.4067	0.3443	-2.5562	0.0858	0.1292	0.4482	0.7111	0.4013	
255103_at	AT4G08690	SEC14 cytosolic factor family protein / phosphoglyc	0.6727	0.0349	0.1078	-0.1562	0.5063	0.3873	0.03684	0.8371	0.4748	-0.792	0.0092	0.0299	
255104_at	AT4G08685	SAH7	-0.3538	0.0273	0.0957	-0.3388	0.0312	0.0877	1.0502	5.00E-04	0.0156	1.0652	5.00E-04	0.0096	
255105_at	AT4G08620	SULTR1;1 (sulfate transporter 1;1); sulfate transme	0.4869	0.7289	0.5022	0.223	0.8731	0.5109	0.4643	0.6558	0.4164	0.2004	0.8458	0.4416	
255106_at	AT4G08710	transposable element gene	0.7816	0.5576	0.444	0.01647	0.9899	0.5416	1.4037	0.3001	0.2688	0.6385	0.6173	0.3693	
255107_at	AT4G08730	contains domain PTHR10432:SF61 (PTHR10432:S	0.0975	0.8834	0.5471	0.9434	0.2051	0.2362	-0.3418	0.6082	0.4008	0.5042	0.4586	0.3094	
255108_at	AT4G08740	unknown protein	-0.8811	0.4357	0.392	-0.2594	0.8115	0.4934	-0.6756	0.5433	0.3767	-0.05389	0.9603	0.4733	
255109_s_at	AT4G08750;AT4G08760	AT4G08750, transposable element gene];[AT4G08	0.2458	0.7792	0.5176	0.7131	0.4335	0.3569	-0.2875	0.7275	0.441	0.1797	0.8267	0.4362	
255110_at	AT4G08770	peroxidase, putative	0.9653	0.3268	0.3384	1.6762	0.1246	0.179	0.5323	0.2593	0.246	1.2431	0.0374	0.066	
255111_at	AT4G08780	peroxidase, putative	1.4945	0.2513	0.2942	0.2296	0.847	0.5036	0.4045	0.445	0.3361	-0.8604	0.1462	0.1523	
255112_at	AT4G08800	protein kinase, putative	0.7229	0.5536	0.4421	0.766	0.5313	0.3967	-1.8217	0.1789	0.1978	-1.7786	0.1872	0.1777	
255113_at	AT4G08820	transposable element gene	-2.5687	0.078	0.1609	-0.7897	0.5089	0.3882	-1.2117	0.3286	0.2827	0.5673	0.6303	0.3737	
255114_at	AT4G08830	transposable element gene	1.7402	0.2074	0.2668	-0.256	0.8359	0.5004	0.9206	0.2196	0.2234	-1.0755	0.1646	0.1641	
255115_at	AT4G08840	APUM11 (ARABIDOPSIS PUMILIO 11); RNA bindi	0.3638	0.7195	0.4992	-0.269	0.7897	0.486	0.007661	0.9939	0.5163	-0.6251	0.5439	0.3424	
255116_at	AT4G08850	leucine-rich repeat family protein / protein kinase fa	0.968	0.0106	0.0649	0.5754	0.0547	0.1161	0.05377	0.4273	0.3286	-0.3388	0.0051	0.0224	
255117_s_at	AT4G08700;AT5G41160	AT4G08700, ATPUP13 (Arabidopsis thaliana pure	0.3672	0.2187	0.2687	0.2074	0.4698	0.3721	-0.897	0.0261	0.0657	-1.0768	0.0144	0.0381	
255118_at	AT4G08790	nitrilase, putative	0.3037	0.1194	0.1997	0.4574	0.0409	0.1004	-0.05588	0.5253	0.3692	0.09783	0.2907	0.2339	
255119_at	AT4G08880	transposable element gene	-0.9903	0.2768	0.3099	1.7324	0.0926	0.1535	-0.6497	0.428	0.3288	2.0731	0.0482	0.0776	
255120_x_at	AT4G08840	transposable element gene	1.6256	0.1668	0.2389	-0.4481	0.666	0.447	-0.2068	0.6705	0.4212	0.9706	0.0979	0.1189	
255121_at	AT4G08480	MAPKKK9 (Mitogen-activated protein kinase kinase	0.1746	0.1388	0.2163	0.4583	0.0084	0.0507	-0.2969	0.0087	0.0375	-0.01318	0.8421	0.4407	
255122_at	AT4G08490	transposable element gene	-0.4917	0.6591	0.4789	-1.153	0.3271	0.307	0.2799	0.7924	0.4608	-0.3814	0.721	0.4043	
255123_at	AT4G08530	protease inhibitor/seed storage/lipid transfer protein	0.8771	0.3608	0.355	-0.1128	0.9009	0.5192	0.1184	0.896	0.4913	0.8827	0.358	0.2661	
255124_at	AT4G08560	APUM15 (ARABIOPSIS PUMILIO 15); RNA bindi	0.2141	0.7646	0.5128	-1.0248	0.1998	0.2327	0.7569	0.3205	0.2785	-0.482	0.5105	0.33	
255125_at	AT4G08250	scarecrow transcription factor family protein	0.6785	0.4778	0.4109	-0.3788	0.6849	0.4538	-0.2861	0.758	0.4507	-1.3434	0.1964	0.1828	
255126_at	AT4G08270	similar to DNA binding [Arabidopsis thaliana] (TAIR	-1.8168	0.0327	0.1049	-1.2882	0.0852	0.1469	0.6583	0.3096	0.2733	1.1858	0.1043	0.1236	
255127_at	AT4G08300	nodulin MtN21 family protein	-1.5949	0.0191	0.0821	-1.0057	0.0748	0.1371	-0.1468	0.5367	0.3739	0.4423	0.1118	0.1289	
255128_at	AT4G08310	similar to unknown protein [Arabidopsis thaliana] (T	0.3471	0.13	0.2085	0.8217	0.0108	0.0559	0.09368	0.6352	0.4095	0.5683	0.0358	0.0642	
255129_at	AT4G08280	nodulin MtN21 family protein	-0.06524	0.8837	0.5471	-0.2124	0.6385	0.4376	0.5235	0.1807	0.1992	0.3763	0.3091	0.243	
255130_at	AT4G08240	similar to unknown [Populus trichocarpa] (GB:ABK9	-0.1291	0.3138	0.3308	-0.281	0.6664	0.129	0.1862	0.1723	0.1934	0.03426	0.7753	0.4216	
255131_at	AT4G08280	similar to unnamed protein product [Vitis vinifera] (G	-0.1979	0.1414	0.2186	-0.3564	0.0301	0.0863	-0.3842	0.0106	0.0408	-0.5427	0.0031	0.018	
255132_at	AT4G08170	inositol 1,3,4-trisphosphate 5/6-kinase family protein	-0.1269	0.5739	0.4505	-0.3388	0.1779	0.2183	-0.1639	0.3859	0.3104	-0.3757	0.0897	0.1125	
255133_at	AT4G08320	tetratricopeptide repeat (TPR)-containing protein	0.5186	0.017	0.0782	0.09211	0.523	0.3933	0.1472	0.3263	0.2814	-0.2792	0.1014	0.1217	
255134_at	AT4G08330	Identical to Uncharacterized protein At4g08330, chl	-0.05705	0.7109	0.4965	-0.07734	0.618	0.4299	0.02506	0.7736	0.4555	0.004771	0.9561	0.4725	
255135_at	AT4G08340	glycosyl hydrolase family 10 protein / carbohydrate-	-1.7626	0.1085	0.1907	0.9314	0.3375	0.3123	-2.0152	0.0314	0.072	0.6789	0.335	0.2556	
255136_s_at	AT4G08360;AT4G08350	AT4G08360, KOW domain-containing protein];[AT4	0.523	0.0201	0.0837	0.5907	0.0135	0.0617	0.1549	0.3302	0.2834	0.2226	0.1868	0.1775	
255137_at	AT4G08370	proline-rich extensin-like family protein	0.5541	0.639	0.4726	0.814	0.498	0.3837	-0.5477	0.6143	0.4024	-0.2878	0.7886	0.4254	
255138_at	AT4G08380	proline-rich extensin-like family protein	-0.6982	0.3509	0.3501	0.4281	0.553	0.4058	-0.8952	0.2476	0.2397	0.2311	0.7445	0.4118	
255139_s_at	no_match	no_match	2.4007	0.1017	0.1843	-0.1278	0.9157	0.5229	0.6575	0.5158	0.3653	-1.8711	0.1127	0.1295	
255140_x_at	AT4G08410	proline-rich extensin-like family protein	-0.4213	0.4286	0.3885	-0.7651	0.1853	0.2233	1.0213	0.0218	0.0596	0.6775	0.0728	0.099	
255141_at	AT4G08420	transposable element gene	-0.421	0.6698	0.4825	0.6672	0.5069	0.3874	-0.8518	0.4053	0.3187	0.2365	0.809	0.4314	
255142_at	AT4G08390	SAPX; L-ascorbate peroxidase	-0.114	0.7635	0.5125	-0.6409	0.1443	0.1939	0.4157	0.0468	0.0907	-0.1113	0.4894	0.3217	
255143_at	AT4G08430	Ulp1 protease family protein	0.6487	0.6996	0.4923	0.817	0.629	0.434	-0.3691	0.7362	0.4437	-0.2008	0.8538	0.4438	
255144_at	no_match	no_match	1.4151	0.2802	0.3114	0.5876	0.6317	0.4352	0.401	0.7415	0.4452	-0.4264	0.726	0.4059	
255145_at	no_match	no_match	-0.7263	0.5122	0.4259	-2.6612	0.058	0.1197	0.5558	0.1146	0.1521	-1.3791	0.0075	0.027	
255146_at	AT4G08450	disease resistance protein (TIR-NBS-LRR class), p	1.6336	0.2956	0.3208	-1.1336	0.4511	0.3645	0.7243	0.3676	0.3018	-2.0429	0.0458	0.0752	
255147_at	AT4G08460	protein binding / zinc ion binding	0.4475	0.0786	0.1616	0.5918	0.036	0.0937	-0.3359	0.1404	0.1716	-0.1916	0.3543	0.2646	
255148_at	AT4G08470	MAPKKK10 (Mitogen-activated protein kinase kinas	1.6639	0.0075	0.0579	1.6891	0.0071	0.0476	-0.5315	0.0518	0.0964	-0.5063	0.0593	0.0879	
255149_at	AT4G08150	KNAT1 (BREVIPEDICELLUS 1); transcription factor	1.197	0.1022	0.1848	0.9398	0.1726	0.2146	-0.4229	0.3958	0.3146	-0.6801	0.2012	0.1858	
255150_at	AT4G08160	glycosyl hydrolase family 10 protein / carbohydrate-	0.007048	0.992	0.575	0.5992	0.4132	0.3475	0.1718	0.8066	0.4656	0.7639	0.3094	0.2431	
255151_at	AT4G08180	oxysterol-binding family protein	0.1844	0.2969	0.3214	0.2366	0.1988	0.2322	-0.1913	0.2808	0.2585	-0.139	0.4165	0.2911	
255152_at	AT4G08190	Ras-related GTP-binding protein, putative	-0.6251	0.6491	0.4762	1.127	0.426	0.3534	0.07545	0.9556	0.5067	1.8276	0.2244	0.1984	
255153_at	AT4G08210	pentatricopeptide (PPR) repeat-containing protein	0.2674	0.7707	0.5148	-0.8606	0.3723	0.3285	0.08638	0.9246	0.4991	-1.0416	0.2912	0.2342	
255154_at	AT4G08220	transposable element gene	0.4256	0.0708	0.1535	0.5774	0.0294	0.0852	-0.1241	0.149	0.1784	0.02775	0.7103	0.401	
255155_at	no_match	no_match	-0.3691	0.2245	0.2782	-0.2473	0.3906	0.337	0.3758	0.2125	0.2194	0.4975	0.1213	0.1359	
255156_at	AT4G07780	transposable element gene	0.9027	0.6949	0.4911	-1.4272	0.5415	0.4012	1.6844	0.4536	0.3403	-0.6454	0.7666	0.4188	
255157_at	AT4G07790	transposable element gene	-2.155	0.029	0.0986	0.8694	0.2496	0.2636	-1.7738	0.0172	0.0524	1.2506	0.0504	0.0797	
255158_s_at	AT3G13250;AT4G07800	AT3G13250, transposable element gene];[AT4G07	0.4393	0.6243	0.4679	0.4966	0.5815	0.4167	-0.7335	0.4264	0.3282	-0.6762	0.4606	0.3103	
255159_at	AT4G07810	transposable element gene	-0.04597	0.9547	0.5659	-0.3418	0.6763	0.4507	0.4566	0.5805	0.391	0.1608	0.8428	0.4408	
255160_at	AT4G07820	pathogenesis-related protein, putative	0.4727	0.0515	0.1304	-0.3112	0.1448	0.1943	0.7755	0.0108	0.0412	-0.00839	0.9635	0.4741	
255161_at	no_match	no_match	-1.8796	0.2626	0.3012	-0.3664	0.8121	0.4935	-2.4041	0.171	0.1926	-0.8909	0.5704	0.3528	
255162_at	AT4G07840	transposable element gene	-1.2018	0.3308	0.3404	-0.7822	0.5115	0.3892	2.1669	0.0803	0.124	2.5865	0.0498	0.0791	
255163_at	no_match	no_match	0.6594	0.522	0.4298	0.3475	0.7306	0.4687	0.5538	0.5617	0.3833	0.2419	0.7962	0.4276	
255164_at	no_match	no_match	2.9279	0.0183	0.0806	-0.7215	0.3967	0.3399	1.8734	0.0539	0.0988	-1.7761	0.0625	0.0907	
255165_at	AT4G07880	transposable element gene	0.2725	0.6468	0.4753	-0.224	0.7051	0.4607	1.2968	0.0781	0.1222	0.8004	0.2198	0.196	
255166_at	no_match	no_match	-1.3212	0.2318	0.283	-0.208	0.8353	0.5003	-1.1786	0.2325	0.2309	-0.06547	0.9415	0.4689	
255167_at	AT4G07920	transposable element gene	-0.5879	0.1644	0.2371	-1.1874	0.0265	0.0814	0.3438	0.3764	0.3059	-0.2556	0.5009	0.3263	
255168_at	AT4G07920	transposable element gene	0.9832	0.2995	0.3227	-1.353	0.1766	0.2174	1.0751	0.2628	0.248	-1.261	0.2014	0.1859	
255169_x_at	AT4G07940	similar to unknown protein [Arabidopsis thaliana] (T	-0.06451	0.965	0.5684	-0.4217	0.7752	0.4822	-0.1906	0.8968	0.4915	-0.5479	0.7117	0.4015	
255170_at	AT4G07970	transposable element gene	0.3231	0.8119	0.5274	1.8498	0.2194	0.2456	0.6427	0.6392	0.4108	2.1694	0.1626	0.1627	
255171_at	AT4G07940	DNAJ heat shock N-terminal domain-containing pro	0.3052	0.2047	0.2651	0.2012	0.3749	0.3299	0.3951	0.1014	0.1422	0.2911	0.1935	0.1811	
255172_x_at	AT4G08000	transposable element gene	-2.1409	0.1044	0.1866	-2.0459	0.116	0.1719	-0.3114	0.6379	0.4105	-0.2164	0.7417	0.411	
255173_at	AT4G08020	transposable element gene	0.5408	0.619	0.4662	-0.3247	0.7628	0.4782	1.0137	0.3702	0.303	0.1482	0.8899	0.4541	
255174_at	AT4G08030	transposable element gene	0.6853	0.6113	0.463	-1.7776	0.2266	0.2496	0.4329	0.7333	0.4427	-2.03	0.1618	0.1623	
255175_at	AT4G07960	ATCSLC12 (Cellulose synthase-like C12); transfera	0.1994	0.8763	0.5456	-1.2785	0.3474	0.3167	0.3031	0.8133	0.4676	-1.1748	0.3837	0.2775	
255176_s_at	AT4G07950;AT1G01210	AT4G07950, DNA-directed RNA polymerase III fan	0.3752	0.1227	0.203	0.1892	0.3807	0.3323	0.02463	0.8615	0.4816	-0.1614	0.29	0.2335	
255177_at	AT4G08040	ACS11 (1-Amino-cyclopropane-1-carboxylate synth	-0.5318	0.7626	0.5123	-0.5756	0.744	0.4728	-0.4867	0.6402	0.4111	-0.5305	0.6114	0.3672	
255178_at	AT4G08050	transposable element gene	-2.0689	0.1209	0.2012	0.142	0.8992	0.5187	-1.1842	0.3237	0.2801	1.0267	0.3847	0.2778	
255179_at	AT4G08090	transposable element gene	0.6109	0.6198	0.4665	-1.1347	0.3751	0.3299	1.2201	0.3388	0.2878	-0.5256	0.6644	0.3856	
255180_at	no_match	no_match	-0.5583	0.6846	0.4875	1.5232	0.299	0.291	-0.4825	0.6883	0.4272	1.5991	0.2258	0.1994	
255181_at	AT4G08110	transposable element gene	-0.2379	0.3229	0.336	0.000472	0.9983	0.5436	-1.1755	0.0051	0.03	-0.9371	0.0113	0.0334	
255182_at	AT4G08130	transposable element gene	-1.5975	0.2218	0.2762	-0.8988	0.4616	0.3686	0.04257	0.9711	0.5102	0.7412	0.5391	0.3409	
255183_at	AT4G08140	similar to AIRP1/ARP/N1A (26S proteasome regula	0.3939	0.7381	0.5052	1.3766	0.2785	0.2801	-2.5779	0.0788	0.1227	-1.5953	0.2201	0.1961	
255184_at	AT4G07730	transposable element gene	-1.2246	0.4272	0.3881	0.2907	0.8442	0.5028	-0.2934	0.7817	0.4579	1.2219	0.2846	0.2306	
255185_at	AT4G07740	similar to unknown protein [Arabidopsis thaliana] (T	-0.8403	0.214	0.2708	-0.2868	0.6409	0.4384	-0.7643	0.2506	0.2413	-0.2109	0.7299	0.4072	
255186_at	AT4G07750	transposable element gene	0.9388	0.3237	0.3365	0.974	0.1414	0.1917	0.3361	0.2302	0.2295	1.9089	0.0013	0.0133	
255187_s_at	AT4G07760;AT2G12390	AT4G07760, transposable element gene];[AT2G12	-0.7758	0.263	0.3015	-0.6279	0.3516	0.3189	0.3495	0.5892	0.3944	0.4973	0.4511	0.3064	
255188_at	no_match	no_match	-0.4585	0.7851	0.5193	-0.7252	0.6686	0.4479	-0.2596	0.8677	0.4835	-0.5263	0.7371	0.4094	
255189_at	AT4G07350	similar to unknown protein [Arabidopsis thaliana] (T	0.8157	0.4344	0.3912	-1.5732	0.1695	0.2122	0.4887	0.6306	0.4081	-1.9003	0.1133	0.13	
255190_x_at	AT4G07360	transposable element gene	-0.1849	0.8669	0.5427	-0.2671	0.8091	0.4927	-0.06628	0.952	0.506	-0.1485	0.8929	0.4551	
255191_at	AT4G07370	transposable element gene	1.2342	0.5332	0.4343	-0.4987	0.7968	0.4886	0.05136	0.9644	0.5086	-1.6816	0.1948	0.1818	
255192_at	AT4G07380	unknown protein	-0.8761	0.4407	0.394	0.00101	0.9993	0.5439	0.3099	0.7774	0.4565	1.187	0.3111	0.2439	
255193_at	AT4G07400	VFB3 (VIER F-BOX PROTEINE 3); ubiquitin-protei	-0.07553	0.7108	0.4965	-0.2669	0.2322	0.253	-0.1683	0.3864	0.3105	-0.3597	0.1065	0.125	
255194_at	AT4G07410	transducin family protein / WD-40 repeat family prot	0.2331	0.2525	0.2949	0.2416	0.2383	0.2567	-1.526	3.00E-04	0.0133	-1.5175	3.00E-04	0.0081	
255195_at	AT4G07425	transposable element gene	-0.3764	0.8225	0.5303	-1.449	0.4088	0.3454	1.0903	0.5186	0.3665	0.01765	0.9914	0.4805	
255196_x_at	AT4G07430	transposable element gene	-1.1266	0.3346	0.3427	0.4463	0.6865	0.4544	-0.3048	0.7816	0.4579	1.2681	0.2848	0.2307	
255197_x_at	AT4G07450	transposable element gene	0.4352	0.6746	0.4842	-0.4363	0.6738	0.4499	0.3056	0.7668	0.4532	-0.566	0.5881	0.3592	
255198_at	AT4G07460	transposable element gene	-0.3362	0.8005	0.5243	0.5216	0.6967	0.4578	-1.5362	0.2187	0.2229	-0.6783	0.5549	0.3469	
255199_at	AT4G07390	PQ-loop repeat family protein / transmembrane fam	0.5888	0.0179	0.0801	0.523	0.0262	0.081	0.03978	0.6454	0.4128	-0.02611	0.7607	0.4169	
255200_at	AT4G07480	transposable element gene	0.2419	0.1148	0.1963	-1.9075	0.1479	0.1966	1.7569	0.1746	0.1951	-2.2925	0.0978	0.1189	
255201_at	no_match	no_match	-0.4567	0.7961	0.5226	-1.56	0.3989	0.3409	2.4208	0.0736	0.1181	1.3175	0.2599	0.2177	
255202_at	AT4G07500	transposable element gene	0.3383	0.6226	0.4674	-1.0067	0.1882	0.2254	0.09444	0.889	0.4895	-1.2506	0.1204	0.1352	
255203_at	AT4G07510	transposable element gene	-0.7737	0.4908	0.4162	0.6891	0.5368	0.3992	0.2192	0.8406	0.4758	1.6818	0.1749	0.1702	
255204_at	AT4G07530	transposable element gene	-0.371	0.4578	0.4018	-0.9135	0.1133	0.1702	0.1885	0.698	0.4305	-0.354	0.4772	0.3165	
255205_at	AT4G07540	transposable element gene	-0.4141	0.7461	0.5078	0.03742	0.9765	0.5385	-2.4311	0.1113	0.1493	-1.9796	0.1725	0.1687	
255206_at	no_match	no_match	0.4069	0.508	0.4244	-0.837	0.2834	0.2827	-0.6069	0.4208	0.3257	-1.9338	0.0469	0.0753	
255207_at	AT4G07515	similar to unknown protein [Arabidopsis thaliana] (T	-2.0059	0.134	0.2124	0.7958	0.4982	0.3838	-1.2531	0.2538	0.2431	1.5486	0.1752	0.1703	
255208_at	AT4G07580	transposable element gene	-0.7767	0.508	0.4244	-0.0846	0.9408	0.5293	0.1512	0.8944	0.491	0.8433	0.4746	0.3155	
255209_at	AT4G07586	transposable element gene	1.2261	0.2898	0.3053	-0.6467	0.5387	0.3992	2.383	0.0677	0.1128	0.5102	0.6226	0.3711	
255210_at	AT4G07600	transposable element gene	0.3249	0.6618	0.48	0.7295	0.3493	0.3178	-1.7589	0.0497	0.0942	-1.3543	0.0988	0.1197	
255211_at	AT4G07600	transposable element gene	3.0227	0.0328	0.105	-1.9008	0.1143	0.1707	2.5152	0.0561	0.101	-2.4083	0.0632	0.0913	
255212_at	no_match	no_match	2.8886	0.0179	0.0802	-0.5456	0.505	0.3867	-0.4395	0.5874	0.3935	1.9035	0.0632	0.0912	
255213_at	AT4G07640	no_match	0.1637	0.9464	0.5637	-0.7651	0.7549	0.4767	-0.1029	0.9663	0.5091	-1.0317	0.6755	0.3892	
255214_at	no_match	no_match	1.6155	0.1116	0.1937	0.9348	0.3042	0.2938	-0.3212	0.6239	0.4069	-1.002	0.1733	0.1692	
255215_at	AT4G07660	transposable element gene	-0.7319	0.6536	0.4771	-1.6841	0.3277	0.3074	-0.4585	0.7768	0.4563	-1.4107	0.4036	0.2856	
255216_s_at	AT5G19740;AT4G07670	AT5G19740, peptidase M28 family protein];[AT4G0	-0.7385	0.2577	0.2982	0.7062	0.2759	0.2787	-1.8983	0.0275	0.0676	-0.4537	0.4634	0.3114	
255217_s_at	AT4G07680;AT3G30465;A	AT4G07680, transposable element gene];[AT3G30	-0.1626	0.7634	0.5125	-0.4181	0.4538	0.3655	-0.04263	0.9019	0.493	-0.2981	0.4107	0.2885	
255218_at	AT4G07700	transposable element gene	-0.5391	0.5708	0.4494	-0.1031	0.9118	0.5219	-0.7467	0.4411	0.3345	-0.3107	0.7402	0.4105	
255219_at	AT4G07720	pseudogene, hypothetical protein	0.4151	0.6385	0.4724	0.2325	0.7903	0.4861	-1.2439	0.0961	0.1378	-1.4265	0.0678	0.095	
255220_at	AT4G05320	UBQ10 (POLYUBIQUITIN 10); protein binding	-0.2463	0.4131	0.3816	-0.2751	0.3657	0.3256	-0.04443	0.6972	0.4302	-0.07326	0.5282	0.3372	
255221_at	AT4G05150	octicosappetide/Phox/Bem1p (PB1) domain-contain	0.9641	0.0037	0.046	0.7293	0.0101	0.0547	-0.5633	0.001	0.0175	-0.7981	3.00E-04	0.008	
255222_at	AT4G05340	ATP binding	-2.9072	0.0406	0.1161	0.1171	0.9101	0.5216	-1.488	0.2013	0.2125	1.5362	0.1899	0.1792	
255223_at	AT4G05370	similar to AAA-type ATPase family protein [Arabido	1.3065	0.1872	0.2536	0.7768	0.3983	0.3406	0.9637	0.2242	0.2262	0.434	0.5529	0.3461	
255224_at	AT4G05400	similar to unknown protein [Arabidopsis thaliana] (T	0.3754	0.0491	0.1274	0.3701	0.0511	0.1122	0.4511	0.0118	0.0432	0.4458	0.0123	0.0351	
255225_at	AT4G05410	transducin family protein / WD-40 repeat family prot	0.05155	0.5498	0.4411	0.1057	0.2521	0.2653	-0.2606	0.0039	0.0273	-0.2065	0.009	0.0295	
255226_at	AT4G05420	DDB1A (UV-damaged DNA-binding protein 1A); DN	0.2559	0.1536	0.2287	0.3426	0.0782	0.1402	-0.6021	0.0144	0.0479	-0.5155	0.024	0.0509	
255227_at	AT4G05440	EDA39 (embryo sac development arrest 39)	0.5342	0.012	0.0681	0.4018	0.0304	0.0865	0.1295	0.3497	0.2931	-0.00288	0.9823	0.4786	
255228_at	AT4G05470	F-box family protein (FBL21)	-0.807	0.3713	0.3602	-0.9273	0.312

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255290_at	AT4G04640	ATPC1 (ATP synthase gamma chain 1)	-0.4278	0.0304	0.1011	-0.6167	0.0091	0.0522	0.1196	0.0914	0.1337	-0.06921	0.2697	0.2226
255291_at	no_match	no_match	0.4444	0.291	0.3179	-0.1236	0.7524	0.4758	0.526	0.2236	0.2258	-0.04191	0.9143	0.461
255292_s_at	AT4G04710;AT4G04720	[AT4G04710, CPK22 (calcium-dependent protein k	0.4305	0.0756	0.1583	0.4901	0.0533	0.1145	-0.6117	0.0276	0.0676	-0.552	0.0377	0.0664
255293_at	AT4G04730	similar to unknown protein [Arabidopsis thaliana] (T	-1.3486	0.1567	0.2308	-1.5981	0.1081	0.1657	-0.3427	0.6811	0.4247	-0.5922	0.4872	0.3207
255294_at	AT4G04750	carbohydrate transmembrane transporter/ sugar:hy	-0.6775	0.0358	0.1093	-0.8202	0.0197	0.072	0.1272	0.4293	0.3293	-0.01561	0.9193	0.4625
255295_at	AT4G04760	sugar transporter family protein	0.49	0.5524	0.442	0.07252	0.9282	0.5263	-0.4775	0.5066	0.362	-0.895	0.2438	0.2092
255296_at	AT4G04790	similar to pentatricopeptide (PPR) repeat-containing	0.2009	0.3048	0.3255	0.3389	0.1183	0.1739	-0.05261	0.7735	0.4554	0.08539	0.6435	0.3784
255297_x_at	AT3G35025;AT4G04820	[AT3G35025, transposable element gene];[AT4G04	-1.9832	0.0944	0.1777	-0.4608	0.6387	0.4377	-0.6026	0.5434	0.3767	0.9198	0.3685	0.2706
255298_at	AT4G04840	methionine sulfoxide reductase domain-containing	-1.9771	0.0026	0.0425	-2.0457	0.0023	0.0334	0.9564	0.0024	0.0228	0.8877	0.0031	0.0182
255299_at	AT4G04880	adenosine/AMP deaminase family protein	0.1837	0.3415	0.346	0.05074	0.7806	0.4837	-0.1545	0.4157	0.3233	-0.2875	0.1667	0.1652
255300_at	AT4G04870	CLS (CARDIOLIPIN SYNTHASE); cardiolipin synth	-0.05741	0.7985	0.5235	-0.195	0.4066	0.3443	0.2196	0.1823	0.2004	0.08202	0.5796	0.3559
255301_at	AT4G04800	methionine sulfoxide reductase domain-containing	0.2957	0.1418	0.2189	0.3923	0.0725	0.1349	0.3243	0.1157	0.1529	0.4209	0.06	0.0886
255302_at	AT4G04830	methionine sulfoxide reductase domain-containing	-1.6748	0.0018	0.0391	-1.3467	0.004	0.0395	0.2593	0.2945	0.2658	0.5874	0.0524	0.0816
255303_at	AT4G04860	DER2.2 (DERLIN-2.2)	0.2887	0.0233	0.0894	0.3893	0.0085	0.051	-0.2011	0.0016	0.0204	-0.1005	0.0194	0.0447
255304_at	AT4G04850	KEA3 (K+ efflux antiporter 3); potassium:hydrogen	-0.3534	0.0147	0.0737	-0.2781	0.0319	0.0886	-1.137	2.00E-04	0.0126	-1.0617	2.00E-04	0.0079
255305_at	AT4G04770	ATABC1 (ARABIDOPSIS THALIANA NUCLEOSOM	-0.3255	0.0787	0.1616	-0.4582	0.0298	0.0858	-0.3679	0.0568	0.1018	-0.5006	0.0225	0.0488
255306_at	AT4G04740	CPK23 (calcium-dependent protein kinase 23); calr	-1.302	0.0807	0.1641	0.4318	0.4837	0.3775	-3.1081	0.0052	0.0301	-1.3743	0.2701	0.0971
255307_at	AT4G04900	RIC10 (ROP-INTERACTIVE CRIB MOTIF-CONTAI	-0.5905	0.5532	0.4421	-0.3231	0.7414	0.4718	-0.07454	0.877	0.4859	0.1929	0.6914	0.3945
255308_at	AT4G04910	NSF (N-ETHYLMALEIMIDE SENSITIVE FACTOR);	1.0599	5.00E-04	0.0325	1.4597	2.00E-04	0.0249	-0.09773	0.4027	0.3176	0.3022	0.0445	0.074
255309_at	AT4G04930	similar to hypothetical protein Cnl_03047 [Cryptos	0.6675	0.0232	0.0891	0.6537	0.0248	0.0789	-0.7281	0.0174	0.0528	-0.7418	0.0164	0.0408
255310_at	AT4G04955	ATALN (ARABIDOPSIS ALLANTOINASE); allantoir	-1.1694	0.0198	0.0832	-0.7138	0.0836	0.1453	-0.9439	0.0046	0.0289	-0.4883	0.0414	0.0706
255311_at	AT4G04560	transposable element gene	-1.7272	0.343	0.3463	0.9293	0.5941	0.421	-1.2223	0.4893	0.3552	1.4342	0.4226	0.2936
255312_at	AT4G04560	transposable element gene	0.2968	0.8029	0.525	-0.7832	0.5205	0.3924	1.3549	0.2904	0.2638	0.2748	0.8172	0.4335
255313_at	AT4G04590	transposable element gene	1.313	0.1909	0.256	-0.6655	0.47	0.3721	-0.1562	0.8567	0.4802	-2.1346	0.0581	0.0869
255314_at	AT4G04150	transposable element gene	-1.7508	0.2224	0.2766	0.6229	0.6346	0.4363	-0.1948	0.8802	0.4867	2.1789	0.1468	0.1527
255315_at	AT4G04165	transposable element gene	-0.6048	0.5405	0.437	-1.4958	0.1737	0.2153	0.6582	0.5073	0.3623	-0.2329	0.8096	0.4316
255316_at	AT4G04170	transposable element gene	0.3154	0.7525	0.5091	0.3311	0.7408	0.4715	-1.7101	0.0692	0.114	-1.6944	0.0709	0.0976
255317_at	AT4G04180	AAA-type ATPase family protein	1.3542	0.0476	0.1256	0.7281	0.2035	0.2351	-0.2212	0.6597	0.4178	-0.8474	0.1431	0.1502
255318_at	AT4G04190	similar to unknown protein [Vitis vinifera] (G	1.0284	0.012	0.0681	1.17	0.0077	0.0489	0.07222	0.7745	0.4557	0.2138	0.4154	0.2906
255319_at	AT4G04220	disease resistance family protein	1.4846	2.00E-04	0.0312	1.3911	3.00E-04	0.0249	-0.05093	0.6857	0.4263	-0.1444	0.2846	0.2306
255320_at	AT4G04230	transposable element gene	-0.4427	0.6028	0.4604	-0.8532	0.3381	0.3127	0.2135	0.5609	0.3829	-0.197	0.5903	0.3601
255321_at	no_match	no_match	-0.2544	0.7184	0.4989	-2.1357	0.0314	0.0881	0.4777	0.5077	0.3624	-1.4036	0.0996	0.1203
255322_at	AT4G04270	transposable element gene	0.4188	0.7008	0.4929	-0.8594	0.4445	0.3616	0.4962	0.6277	0.4071	-0.782	0.4549	0.3079
255323_at	AT4G04280	transposable element gene	1.3727	0.3574	0.4533	-0.1097	0.9378	0.5285	0.8646	0.5485	0.3786	-0.6178	0.6644	0.3856
255324_s_at	AT4G04290;AT2G07420	[AT4G04290, transposable element gene];[AT2G07	1.0761	0.5372	0.4358	0.1793	0.916	0.523	0.5767	0.7362	0.4437	-0.3201	0.8509	0.4429
255325_at	AT4G04210	PUX4 (PLANT UBX DOMAIN-CONTAINING PROT	-0.04587	0.8236	0.5306	0.0596	0.7725	0.4813	0.7292	1.00E-04	0.0105	0.8347	1.00E-04	0.0055
255326_at	AT4G04300	transposable element gene	2.9184	0.0346	0.1075	-1.7009	0.1404	0.1909	1.3428	0.221	0.2242	-3.2765	0.0241	0.051
255327_at	AT4G04320	malonyl-CoA decarboxylase family protein	0.5661	0.012	0.0681	0.3884	0.0402	0.0995	0.02935	0.8321	0.4733	0.1484	0.3166	0.2466
255328_at	AT4G04350	EMB2369 (EMBRYO DEFECTIVE 2369); ATP bind	-0.1173	0.3091	0.328	-0.3802	0.0195	0.0719	-0.4833	0.0087	0.0373	-0.7463	0.0018	0.0147
255329_at	AT4G04370	pentatricopeptide (PPR) repeat-containing protein	-0.7587	0.0088	0.1389	-0.1772	0.5736	0.4133	-1.1963	0.0082	0.0363	-0.6149	0.0663	0.0938
255330_s_at	AT3G45520;AT4G04380	[AT3G45520, transposable element gene];[AT4G04	0.5494	0.5801	0.4523	2.2122	0.0727	0.135	-0.5773	0.5619	0.3833	1.0855	0.3006	0.2389
255331_at	AT4G04330	similar to unnamed protein product [Vitis vinifera] (G	-0.1304	0.7365	0.5047	0.2301	0.5588	0.4079	0.2225	0.4181	0.3244	0.583	0.0774	0.1028
255332_at	AT4G04340	early-responsive to dehydration protein-related / ER	-2.4609	0.0123	0.0686	-0.4685	0.0015	0.0313	-0.123	0.1106	0.1488	-0.3305	0.0054	0.0229
255333_at	AT4G04410	transposable element gene	0.0678	0.8234	0.5306	0.6589	0.0816	0.1432	-5.1507	0	0.0092	-4.5596	0	0.0055
255334_at	AT4G04420	transposable element gene	-1.399	0.1708	0.2421	-0.1904	0.8316	0.4993	-0.8803	0.3534	0.2949	0.3283	0.7156	0.4027
255335_at	AT4G04430	transposable element gene	-0.3584	0.8443	0.5371	-0.1197	0.9476	0.5313	0.4552	0.8034	0.4645	0.6938	0.7059	0.3995
255336_at	AT4G04440	transposable element gene	1.1951	0.3537	0.3515	0.09314	0.9388	0.5287	2.4167	0.0159	0.0503	1.3148	0.094	0.116
255337_at	AT4G04450	WRKY42 (WRKY DNA-binding protein 42); transcri	-0.6321	0.4618	0.4037	-0.3803	0.6503	0.4419	0.6561	0.4017	0.3173	0.9079	0.2644	0.22
255338_at	AT4G04470	PMP22 (peroxisomal membrane protein 22)	0.3819	0.0786	0.1616	0.2404	0.2133	0.2415	0.8646	0.5485	0.3786	-0.6178	0.6644	0.3856
255339_at	AT4G04480	similar to F-box family protein [Arabidopsis thaliana	-0.9414	0.5528	0.4421	-0.3592	0.8171	0.495	-0.5233	0.7266	0.4407	0.05898	0.9683	0.475
255340_at	AT4G04490	protein kinase family protein	2.2331	0.0015	0.0381	2.0357	0.0022	0.0333	-0.2772	0.26	0.2464	-0.4746	0.0882	0.1114
255341_at	AT4G04500	protein kinase family protein	2.6939	4.00E-04	0.032	2.4424	5.00E-04	0.0263	0.1341	0.6084	0.4008	-0.1175	0.6523	0.3816
255342_at	AT4G04510	protein kinase family protein	1.2579	0.1056	0.1879	1.582	0.0588	0.1206	0.1805	0.7799	0.4573	0.5045	0.4505	0.3061
255343_at	AT4G04530	transposable element gene	-0.4727	0.5558	0.4431	-0.03988	0.9594	0.534	-0.3835	0.63	0.4079	0.04933	0.9498	0.4709
255344_s_at	AT4G04570;AT4G04540	[AT4G04570, protein kinase family protein];[AT4G0	0.7703	0.0325	0.1046	0.3603	0.2071	0.2377	-0.1712	0.5144	0.3647	-0.5812	0.0723	0.0987
255345_at	AT4G04460	aspartyl protease family protein	0.9598	0.084	0.1678	0.8301	0.1189	0.1744	-0.3291	0.4764	0.35	-0.4588	0.3353	0.2557
255346_at	AT4G03800	transposable element gene	0.05904	0.9649	0.5684	-2.5787	0.1101	0.1674	2.7795	0.092	0.1342	0.1417	0.9158	0.4616
255347_at	AT4G03810	transposable element gene	-0.7476	0.6552	0.4775	1.51	0.3857	0.3346	0.09317	0.955	0.5066	2.3506	0.2044	0.1876
255348_at	AT4G03820	similar to unknown protein [Arabidopsis thaliana] (T	0.5977	0.0416	0.1175	0.6119	0.0388	0.0977	-0.2194	0.3385	0.2877	-0.2052	0.3671	0.2701
255349_at	AT4G03830	myosin heavy chain-related	1.0636	0.1058	0.188	-1.7332	0.0275	0.0827	1.9549	0.0187	0.0548	-0.8419	0.1747	0.1701
255350_at	AT4G03840	transposable element gene	1.1793	0.414	0.3819	0.1205	0.9303	0.5267	0.8172	0.156	0.183	-0.2416	0.6332	0.3748
255351_x_at	AT4G03850	transposable element gene	1.3714	0.2469	0.2917	-0.4672	0.6683	0.4479	1.1793	0.3087	0.2728	-0.6593	0.5503	0.3452
255352_at	AT4G03860	transposable element gene	-3.5598	0.0073	0.0575	2.2806	0.0322	0.0889	-2.3584	0.003	0.0248	3.482	7.00E-04	0.0106
255353_at	AT4G03870	transposable element gene	0.7346	0.5477	0.4401	-0.4299	0.7206	0.4656	0.008705	0.9942	0.5163	-1.1558	0.3604	0.2672
255354_at	AT4G03880	transposable element gene	1.5773	0.1187	0.1992	1.5387	0.1255	0.1796	-1.969	0.0336	0.0749	-2.0076	0.0317	0.06
255355_at	AT4G03890	transposable element gene	-0.4618	0.3929	0.3715	0.1384	0.7885	0.4857	-0.6694	0.1259	0.1609	-0.06918	0.8517	0.4431
255356_x_at	AT2G10140;AT3G30680;A	[AT2G10140, transposable element gene];[AT3G30	-0.7679	0.4673	0.4062	-1.8966	0.1186	0.1742	0.8442	0.4276	0.3287	-0.2845	0.7811	0.4232
255357_at	AT4G03930	pectinesterase	-3.4137	0.012	0.0681	-1.3527	0.1584	0.2047	-1.2965	0.1124	0.1502	0.7645	0.2976	0.2374
255358_at	AT4G03940	unknown protein	-0.5496	0.6267	0.4686	0.6772	0.5522	0.4057	-0.03476	0.9648	0.5087	1.1921	0.1826	0.175
255359_at	AT4G03950	glucose-6-phosphate/phosphate translocator, putati	0.6557	0.4991	0.42	0.7568	0.4398	0.3595	-0.3391	0.7206	0.4388	-0.2379	0.8009	0.429
255360_at	AT4G03960	tyrosine specific protein phosphatase family protein	0.8417	0.0052	0.0513	0.8675	0.0046	0.0416	0.004143	0.9527	0.5062	0.02995	0.6718	0.388
255361_at	AT4G03990	transposable element gene	-0.4917	0.7321	0.503	0.5605	0.6971	0.4579	0.0296	0.9834	0.5135	1.0818	0.4645	0.3119
255362_at	AT4G04000	transposable element gene	0.1982	0.7703	0.5147	-0.1006	0.8817	0.5136	0.1099	0.8709	0.4844	-0.1889	0.7807	0.4232
255363_x_at	AT3G44500;AT2G06430;A	[AT3G44500, transposable element gene];[AT2G06	0.1322	0.7065	0.4949	-0.5907	0.1448	0.1943	0.1974	0.5782	0.39	-0.5254	0.183	0.1753
255364_s_at	AT4G22240;AT4G04020	[AT4G22240, plastid-lipid associated protein PAP_	-0.2835	0.3757	0.3622	-0.409	0.2241	0.248	-0.05477	0.6791	0.4242	-0.1803	0.2165	0.1943
255365_at	AT4G04030	MEE51 (maternal effect embryo arrest 51); diphosp	0.03769	0.7945	0.5223	0.0696	0.6343	0.4362	-0.349	0.0027	0.0237	-0.3171	0.0038	0.02
255366_x_at	AT4G04050	transposable element gene	-0.5094	0.1955	0.2595	-0.4468	0.245	0.261	-0.2432	0.4998	0.3596	-0.1805	0.6116	0.3673
255367_at	no_match	no_match	-0.5352	0.5805	0.4523	-2.0214	0.0859	0.1475	1.2439	0.0541	0.0989	-0.2423	0.6267	0.3726
255368_at	AT4G04070	transposable element gene	-0.3071	0.7979	0.5233	-0.532	0.6602	0.4451	-1.3631	0.2914	0.2643	-1.588	0.23	0.2015
255369_at	AT4G04080	ATISU3/ISU3 (IscU-like 3); structural molecule	-0.9512	0.3032	0.3249	-1.3998	0.1573	0.2039	-1.1867	0.2053	0.215	-1.6353	0.1057	0.1244
255370_at	AT4G04100	transposable element gene	0.4182	0.6466	0.4752	-1.6401	0.1242	0.1787	0.1876	0.8352	0.4742	-1.8706	0.0912	0.1138
255371_at	AT4G04110	Toll-interleukin-Resistance (TIR) domain-containing	1.784	0.2086	0.2672	-0.4284	0.7373	0.4704	0.7004	0.5882	0.3938	-1.512	0.2732	0.2245
255372_at	AT4G04120	transposable element gene	1.0077	0.3245	0.337	0.4903	0.614	0.4284	-0.8303	0.4074	0.3197	-1.3477	0.2077	0.1895
255373_s_at	AT4G04130;AT5G34810	[AT4G04130, transposable element gene];[AT5G34	1.0969	0.0298	0.1002	-0.3942	0.3005	0.2916	-0.7335	0.034	0.0754	-2.2245	7.00E-04	0.0105
255374_at	AT4G03770	transposable element gene	-1.0641	0.4163	0.383	-1.5813	0.2496	0.2636	-0.3137	0.8027	0.4644	-0.8309	0.5185	0.333
255375_at	AT4G03780	transposable element gene	-1.8154	0.0508	0.1296	2.2993	0.025	0.0791	-2.9388	0.0111	0.0417	1.1759	0.1482	0.1535
255376_x_at	AT4G03790	transposable element gene	-0.6432	0.2704	0.3056	-0.8604	0.1626	0.2078	0.3574	0.5169	0.3659	0.1403	0.7943	0.4273
255377_at	AT4G03500	ankyrin repeat family protein	0.01295	0.9417	0.5629	-0.08585	0.6331	0.4357	-0.04596	0.796	0.4622	-0.1448	0.4334	0.2982
255378_at	AT4G03550	ATGSL05 (GLUCAN SYNTHASE-LIKE 5); 1,3-beta	0.226	0.2771	0.3099	0.161	0.4209	0.3511	-0.5422	0.0059	0.032	-0.6071	0.0039	0.0202
255379_at	AT4G03520	ATHM2 (Arabidopsis thioredoxin M-type 2); thiol-di	-0.1271	0.0711	0.1537	-0.4653	9.00E-04	0.0284	0.4858	7.00E-04	0.016	0.1476	0.0471	0.0764
255380_at	AT4G03560	ATTPC1 (TWO-PORE CHANNEL 1); calcium chan	0.0047776	0.9733	0.5706	-0.09132	0.5327	0.3972	-0.2712	0.1128	0.1504	-0.3673	0.0517	0.081
255381_at	AT4G03510	RMA1 (Ring finger protein with Membrane Anchor 1	0.4516	0.4674	0.4062	0.9202	0.1775	0.2179	-0.2474	0.2429	0.2367	0.2213	0.288	0.2324
255382_at	AT4G03430	EMB2770/STA1 (STABILIZED1); RNA splicing fact	0.5027	0.0078	0.0583	0.4652	0.0102	0.0549	-0.5043	0.0077	0.0354	-0.5419	0.006	0.024
255383_at	AT4G03530	similar to unknown protein [Arabidopsis thaliana] (T	-1.1309	0.3555	0.3525	-0.2765	0.8112	0.4934	0.4621	0.6644	0.4193	1.3166	0.2536	0.2145
255384_at	AT4G03580	similar to cathepsin-related [Arabidopsis thaliana] (T	0.343	0.7741	0.5161	-0.7352	0.5465	0.4031	0.309	0.7825	0.4581	-0.7692	0.5031	0.327
255385_at	AT4G03610	phosphonate metabolism protein-related	0.4348	0.3595	0.3543	-0.4118	0.3828	0.3331	0.4742	0.2881	0.2626	-0.3725	0.3908	0.2803
255386_at	AT4G03620	myosin heavy chain-related	-0.7856	0.5096	0.4248	-0.6353	0.5901	0.4196	-0.3079	0.7909	0.4604	-0.1576	0.8917	0.4547
255387_at	AT4G03630	root nodule development protein-related	-0.1434	0.8795	0.5464	-0.7068	0.4707	0.3723	2.1665	0.0712	0.116	1.6031	0.1454	0.1518
255388_at	AT4G03640	transposable element gene	0.6066	0.614	0.4641	-0.6606	0.584	0.4178	1.2904	0.3099	0.2735	0.02314	0.9844	0.4791
255389_at	no_match	no_match	2.0078	0.2795	0.3111	-0.1521	0.9291	0.5265	1.0442	0.4477	0.3374	-1.1157	0.4197	0.2924
255390_at	AT4G03660	transposable element gene	2.0422	0.0433	0.1199	-0.47	0.5385	0.3999	-1.2454	0.0638	0.1088	-3.7576	0.0016	0.0139
255391_at	AT4G03670	transposable element gene	0.2257	0.8813	0.5465	-0.3237	0.8306	0.4991	0.04109	0.9512	0.5058	-0.5083	0.4657	0.3122
255392_at	AT4G03680	transposable element gene	-0.1417	0.8884	0.5479	-1.4983	0.189	0.2257	-0.275	0.7861	0.4591	-1.6316	0.1602	0.1613
255393_at	AT4G03690	transposable element gene	-1.0459	0.4684	0.4065	-1.5054	0.3135	0.2992	0.8431	0.3915	0.3127	0.3836	0.6849	0.3922
255394_at	AT4G03700	transposable element gene	-0.708	0.4813	0.4125	-2.6066	0.0461	0.1065	2.1233	0.054	0.0989	0.2247	0.7892	0.4255
255395_at	AT4G03710	transposable element gene	1.072	0.376	0.3623	-0.8248	0.4865	0.3789	1.9477	0.1449	0.1752	0.0509	0.9646	0.4744
255396_at	no_match	no_match	0.06847	0.9451	0.5635	0.4905	0.6276	0.4336	-0.7395	0.4733	0.349	-0.3175	0.7513	0.4142
255397_at	no_match	no_match	-0.446	0.465	0.4052	-0.7638	0.2392	0.2572	0.004068	0.9938	0.5163	-0.3137	0.5615	0.3495
255398_at	AT4G03740	similar to SLL3 ORF2 protein [Brassica oleracea] (G	-2.2115	0.081	0.1644	-1.8553	0.1232	0.1782	-0.4866	0.6363	0.41	-0.1305	0.8976	0.4666
255399_at	AT4G03750	transposable element gene	1.0222	0.2422	0.2889	-0.4073	0.6138	0.4284	1.6883	0.0719	0.1166	0.2588	0.7284	0.4066
255400_at	AT4G03760	transposable element gene	0.1227	0.9401	0.5625	-0.5809	0.7241	0.4667	-0.8073	0.3216	0.279	-1.5109	0.1019	0.122
255401_at	AT4G03600	similar to unknown protein [Arabidopsis thaliana] (T	0.8226	0.0752	0.1578	-0.2673	0.4808	0.3765	0.444	0.2667	0.2501	-0.646	0.1339	0.1443
255402_at	AT4G03205	HEMF2; coproporphyrinogen oxidase	-1.3275	0.065	0.1462	0.7028	0.2524	0.2654	-4.0242	0.0016	0.0202	-1.9939	0.0192	0.0444
255403_at	AT4G03400	DFL2 (DWARF IN LIGHT 2)	-0.8966	0.131	0.2093	-0.7463	0.1899	0.2264	-0.8814	0.047	0.091	-0.7311	0.0783	0.1034
255404_at	AT4G03153	kinase interacting family protein	-0.7856	0.5991	0.4594	-1.8759	0.245	0.261	0.7619	0.6097	0.4013	-0.3284	0.8233	0.4351
255405_s_at	AT4G03460;AT4G03440	[AT4G03460, ankyrin repeat family protein];[AT4G0	0.008028	0.9935	0.5754	-1.2083	0.2636	0.2719	1.799	0.1064	0.146	0.5828	0.5379	0.3406
255406_at	AT4G03490	ankyrin repeat family protein	1.1796	0.0329	0.1053	0.9084	0.1692	0.132	-0.08802	0.6708	0.4213	-0.3592	0.135	0.145
255407_at	AT4G03480	ankyrin repeat family protein	0.635	0.4894	0.4156	1.2486	0.2092	0.2391	-1.2106	0.1309	0.1645	-0.597	0.4028	0.2853
255408_at	AT4G03490	protein binding	0.9875	0.3283	0.3391	-0.372	0.6967	0.4578	-0.4999	0.5812	0.3912	-1.8594	0.0896	0.1125
255409_at	AT4G03090	similar to unnamed protein product [Vitis vinifera] (G	-0.2814	0.7301	0.5028	0.2952	0.7177	0.4645	-0.4063	0.6214	0.405	0.1703	0.8338	0.4383
255410_at	AT4G03100	rac GTPase activating protein, putative	-1.4126	0.1892	0.2548	-1.4348	0.1837	0.2224	0.3113	0.5003	0.3597	0.2891	0.5296	0.3378
255411_at	AT4G03110	RNA-binding protein, putative	-1.1977	0.02	0.0834	-1.1914	0.0203	0.0727	0.1417	0.4754	0.3497	0.148	0.4574	0.309
255412_at	AT4G03260	ABP1 (ENDOPLASMIC RETICULUM AUXIN BIND	0.2904	0.2741	0.308	0.1428	0.5672	0.4108	0.5343	0.0296	0.07	0.3867	0.0745	0.1004
255413_at	AT4G03140	oxidoreductase	-0.1533	0.5218	0.4297	0.2966	0.2463	0.2618	0.00854	0.934	0.5018	0.4584	0.0091	0.0297
255414_at	AT4G03156	small GTPase-related	2.1826	0.093	0.1766	0.5632	0.6011	0.424	-0.5007	0.5953	0.3966	-2.1202	0.0712	0.0978
255415_at	AT4G03160	similar to DNA binding [Arabidopsis thaliana] (TAIR	-0.9698	0.188	0.254	0.2671	0.6849	0.4538	-0.7574	0.2833	0.2599	0.4795	0.4769	0.3165
255416_at	AT4G03170	DNA binding	0.875	0.5222	0.4298	-1.7447	0.2349	0.2548	0.5896	0.6615	0.4184	-2.0301	0.1794	0.1729
255417_at	AT4G03190	GRH1 (GRR1-LIKE PROTEIN 1); ubiquitin-protein l	0.7534	0.0315	0.1029	0.8354	0.0228	0.0762	-0.253	0.1076	0.1469	-0.171	0.2349	0.2044
255418_at	AT4G03200	catalytic	0.5273	7.00E-04	0.0334	0.1058	0.1307	0.1833	-0.2954	0.004	0.0274	-0.7169	1.00E-04	0.0065
255419_at	AT4G03230	S-locus lectin protein kinase family protein	0.8903	0.0536	0.1446	0.03287	0.9297	0.5266	-0.7745	0.0912	0.1335	-1.632	0.0096	0.0304
255420_at	AT4G03240	ATFH/FH (FRATAXIN HOMOLOG)	-0.1706	0.3614	0.3552	-0.05302	0.765	0.4789	-0.1427	0.3779	0.3068	-0.02509	0.8701	0.4485
255421_at	AT4G03260	leucine-rich repeat family protein	-0.2336	0.2664	0.303	-0.4469	0.069	0.1318	-0.8096	0.0048	0.0294	-1.0229	0.002	0.0153
255422_at	AT4G03270	CYCD6;1 (CYCLIN D6;1); cyclin-dependent protein	0.454	0.4397	0.3936	0.3927	0.4996	0.3844	0.4093	0.3441	0.2903	0.348	0.4136	0.2898
255423_at	AT4G03290	calcium-binding protein, putative	0.7167	0.4389	0.3932	-0.5293	0.5604	0.4084	-1.3698	0.1761	0.196	-2.6159	0.035	0.0634
255424_at	AT4G03340	glycosyltransferase family 14 protein / core-2/i-bran	-0.3655	0.485	0.414	-0.2632	0.6095	0.4268	-0.4163	0.2487	0.2403	0.5186	0.1682	0.1661
255425_s_at	AT4G03360;AT4G02950	[AT4G03360, ubiquitin family protein];[AT4G02950,	0.08202	0.9232	0.5579	-0.1862	0.8272	0.4981	0.2634	0.7058	0.4333	-0.00481	0.9944	0.4813
255426_at	AT4G03370	ubiquitin family protein	-1.1821	0.0928	0.1764	-0.8539	0.1874	0.2247	-0.00281	0.9934	0.5162	0.3254	0.369	0.2708
255427_at	AT4G03380	similar to ATNAP-1/NAP-1 [Arabidopsis thaliana] (TA	0.08596	0.9203	0.5571	0.4669

255490_at	AT4G02660	WD-40 repeat family protein / beige-related	-0.02054	0.987	0.5736	1.1756	0.3784	0.3312	-1.4096	0.1282	0.1627	-0.2134	0.7864	0.4247
255491_at	AT4G02670	ATIDI2 (ARABIDOPSIS THALIANA INDETERMIN	-0.2274	0.7592	0.5115	-2.8019	0.0155	0.0652	2.2146	0.033	0.0742	-0.36	0.6308	0.3739
255492_at	AT4G02680	EOL1 (ETO1-LIKE 1); binding / protein binding	0.09745	0.5639	0.4463	-0.06945	0.6775	0.4511	0.198	0.1224	0.1582	0.03106	0.7745	0.4214
255493_at	AT4G02690	glutamate binding /	-0.2525	0.7128	0.4972	1.8628	0.0434	0.1034	-0.6687	0.3543	0.2954	1.4466	0.0863	0.11
255494_at	AT4G02710	kinase interacting family protein	0.9116	0.4943	0.4177	1.317	0.3389	0.3131	-0.5579	0.6696	0.4209	-0.1525	0.9061	0.459
255495_at	AT4G02720	similar to unnamed protein product [Vitis vinifera] (G	0.3129	0.0489	0.1271	0.4761	0.0131	0.0611	-0.5069	0.0091	0.0383	-0.3438	0.0327	0.0611
255496_at	AT4G02740	BZO2H1 (ARABIDOPSIS THALIANA BASIC LEUC	0.478	0.0178	0.0799	0.3217	0.0591	0.1209	0.5279	0.0127	0.0449	0.3716	0.0392	0.0681
255497_at	AT4G02750	UNE12 (unfertilized embryo sac 12); DNA binding	-0.0365	0.7001	0.4925	0.4012	0.0104	0.0552	0.0708	0.1757	0.1957	0.5084	3.00E-04	0.0083
255498_at	AT4G02620	(VACUOLAR ATPASE SUBUNIT F); hydrogen ion t	0.02539	0.8485	0.5379	0.2542	0.111	0.1681	0.4259	0.0061	0.0325	0.6547	0.0012	0.013
255499_at	AT4G02730	transducin family protein / WD-40 repeat family prot	0.6189	0.0236	0.0897	0.4361	0.0661	0.1287	0.2441	0.2012	0.2124	0.06126	0.7209	0.4043
255500_at	AT4G02390	APP (ARABIDOPSIS POLY(ADP-RIBOSE) POLYM	0.8899	0.0316	0.1031	1.4727	0.0058	0.0442	0.09439	0.7484	0.4476	0.6771	0.0692	0.0964
255501_at	AT4G02400	similar to U3 ribonucleoprotein (Utp) family protein [	0.3617	0.2231	0.2771	0.3488	0.2371	0.2561	0.1806	0.1514	0.1799	0.1677	0.1755	0.1704
255502_at	AT4G02410	lectin protein kinase family protein	0.1329	0.7195	0.4992	0.3515	0.3655	0.3255	-0.08364	0.5567	0.3816	0.135	0.3598	0.2669
255503_at	AT4G02420	lectin protein kinase, putative	-0.3111	0.335	0.3429	-0.4405	0.196	0.2301	0.2222	0.6998	0.1146	0.09285	0.3622	0.2679
255504_at	AT4G02200	drought-responsive family protein	-0.3402	0.144	0.2206	-0.3364	0.1474	0.1963	0.1432	0.1151	0.1525	0.1471	0.1082	0.1263
255505_at	AT4G02080	ASAR1 (Arabidopsis thaliana secretion-associated	0.02568	0.7071	0.4951	0.2681	0.0135	0.0617	-0.16	0.0163	0.051	0.08248	0.1091	0.127
255506_at	AT4G02130	GATL6/LGT10; polygalacturonate 4-alpha-galactur	0.1836	0.7098	0.4952	0.09867	0.8405	0.5016	-1.0084	0.039	0.0816	-1.0934	0.0306	0.0588
255507_at	AT4G02150	ATIMPALPHA3/MOS6 (IMPORTIN ALPHA 3); prot	0.6294	2.00E-04	0.0312	0.5794	3.00E-04	0.0249	-0.1469	0.0412	0.0842	-0.1969	0.0164	0.0409
255508_at	AT4G02220	zinc finger (MYND type) family protein / programme	1.2902	0.0013	0.0376	1.2666	0.0014	0.0313	-0.2523	0.1486	0.1782	-0.2759	0.1225	0.1368
255509_at	AT4G02230	similar to unknown protein [Arabidopsis thaliana] (T	-0.05536	0.8227	0.5304	0.4298	0.1368	0.1882	-0.5821	0.0288	0.069	-0.09691	0.6078	0.3659
255510_at	AT4G02020	EZA1 (SWINGER); transcription factor	0.1136	0.4857	0.414	0.1668	0.323	0.3048	-0.09737	0.5467	0.3781	-0.04421	0.7801	0.423
255511_at	AT4G02075	PHT1 (PITCHOUN 1); protein binding / zinc ion bind	0.04548	0.9284	0.5595	0.3639	0.4868	0.379	-0.1079	0.4715	0.3481	0.3015	0.0906	0.1134
255512_at	AT4G02195	SYP42 (SYNTAXIN OF PLANTS 41); SNAP receptor	0.5108	0.0528	0.1318	0.3892	0.1066	0.1648	0.3533	0.1328	0.1658	0.2316	0.2845	0.2306
255513_at	AT4G02060	PRL (PROLIFERA); ATP binding / DNA binding / DI	-0.00887	0.9665	0.5688	-0.2236	0.3231	0.3048	0.2693	0.0692	0.114	0.05456	0.6435	0.3784
255514_s_at	AT4G05330	AGL78; transcription factor	0.2438	0.2327	0.2834	-0.7332	0.6407	0.4384	1.5607	0.3437	0.2902	-1.2163	0.45	0.306
255515_at	AT4G02250	invertase/pectin methylesterase inhibitor family prot	0.9647	0.421	0.3854	-0.5106	0.6601	0.4451	1.2772	0.0249	0.064	-0.1982	0.6161	0.3688
255516_at	AT4G02270	pollen Ole e 1 allergen and extensin family protein	-0.9066	0.5192	0.4289	-1.2315	0.392	0.3377	1.119	0.4328	0.3309	0.7942	0.5699	0.3526
255517_at	AT4G02290	ATGH9B13 (ARABIDOPSIS THALIANA GLYCOSY	0.4822	0.5064	0.4235	0.2143	0.7622	0.4781	0.3053	0.3167	0.2766	0.03739	0.8954	0.4558
255518_at	AT4G02300	pectinesterase family protein	-1.8355	0.1428	0.2198	0.272	0.8007	0.4897	-0.7922	0.4759	0.3499	1.3153	0.262	0.2188
255519_at	AT4G02310	kelch repeat-containing F-box family protein	1.1357	0.2653	0.3023	1.8005	0.1095	0.167	-1.2431	0.2295	0.2292	-0.5783	0.5459	0.3433
255520_at	AT4G02270	60S ribosomal protein L19 (RPL19C)	0.3977	0.0024	0.0421	0.5221	9.00E-04	0.0284	-0.22	0.0198	0.0565	-0.0956	0.1776	0.1718
255521_at	AT4G02280	SUS3; UDP-glycosyltransferase/ sucrose synthase	0.8503	0.0295	0.0997	1.0318	0.0158	0.0655	-0.5581	0.0952	0.137	-0.3766	0.216	0.1941
255522_at	AT4G02260	RSH1 (RELA-SPOT HOMOLOG); catalytic	-0.03337	0.8638	0.542	-0.0151	0.938	0.5285	-0.841	0.0099	0.0398	-0.8228	0.0107	0.0324
255523_at	AT4G02330	pectinesterase family protein	-0.104	0.8755	0.5454	0.1311	0.8436	0.5027	-0.5091	0.4562	0.3413	-0.2741	0.6803	0.3905
255524_at	AT4G02340	ATPMEPCRB; pectinesterase	0.5617	0.4801	0.4119	0.4528	0.5647	0.41	0.1739	0.5546	0.3807	0.06501	0.8216	0.4346
255525_at	AT4G02340	epoxide hydrolase, putative	0.6355	0.0036	0.0457	0.5902	0.0047	0.0418	0.02789	0.8017	0.4641	-0.0174	0.8752	0.4499
255526_at	AT4G02350	exocyst complex subunit Sec15-like family protein	0.5655	0.0892	0.1722	0.5618	0.1599	0.1509	-0.6703	3.00E-04	0.0138	-0.6741	3.00E-04	0.0054
255527_at	AT4G02360	similar to unknown protein [Arabidopsis thaliana] (T	-0.3543	0.0736	0.1561	-0.1305	0.4249	0.3529	0.3862	0.0055	0.031	0.61	0.001	0.0121
255528_at	AT4G02090	similar to unnamed protein product [Vitis vinifera] (G	-0.2472	0.6369	0.472	0.1839	0.7237	0.4666	-0.4423	0.4131	0.3221	-0.01125	0.9826	0.4786
255529_at	AT4G02120	CTP synthase, putative / UTP--ammonia ligase	0.6626	0.0044	0.0482	-0.2236	0.0828	0.1446	-0.45	0.0091	0.0381	-1.2462	2.00E-04	0.0078
255530_at	AT4G02140	similar to unknown protein [Arabidopsis thaliana] (T	-0.09909	0.8684	0.5434	1.6295	0.044	0.1038	-0.2878	0.6351	0.4095	1.4407	0.0622	0.0905
255531_at	AT4G02160	similar to unknown protein [Arabidopsis thaliana] (T	1.399	0.3606	0.355	-0.3994	0.7831	0.4844	-0.164	0.9093	0.4951	-1.9624	0.2206	0.1963
255532_at	AT4G02170	similar to unknown protein [Arabidopsis thaliana] (T	-0.4328	0.6553	0.4776	-0.673	0.4957	0.3828	0.4312	0.6565	0.4167	0.1911	0.842	0.4407
255533_at	AT4G02180	DC1 domain-containing protein	1.1221	0.2756	0.309	1.8132	0.1111	0.1682	0.6716	0.3914	0.3126	1.3627	0.1232	0.1372
255534_at	AT4G02190	DC1 domain-containing protein	-0.5197	0.6658	0.4812	0.8056	0.5105	0.3889	-0.03875	0.974	0.511	1.2865	0.3134	0.2451
255535_at	AT4G01700	ribosomal protein L7Ae/L30e/S12e/Gadd45 family p	0.4983	0.1431	0.22	0.6771	0.0885	0.1317	0.242	0.1919	0.2067	0.4208	0.0526	0.0818
255536_at	AT4G01575	serine protease inhibitor, Kazal-type family protein	-0.2875	0.6072	0.4622	-0.2989	0.5936	0.4209	0.3161	0.4589	0.3426	0.3047	0.4741	0.3154
255537_at	AT4G01690	PPOX (PROTOPORPHYRINOGEN OXIDASE); pro	-0.1915	0.1319	0.2103	-0.7815	0.0015	0.0314	0.1889	0.1359	0.1683	-0.4011	0.0167	0.0413
255538_at	AT4G01680	MYB59; myb domain protein 59); DNA binding / tra	0.1652	0.6874	0.4884	-0.8444	0.0913	0.1524	0.1103	0.0131	0.0455	0.1013	0.7178	0.4033
255539_at	AT4G01710	CRK (CROOKED)	0.2448	0.1486	0.2243	0.6326	0.0099	0.0542	0.5271	0.0087	0.0373	0.915	0.0011	0.0126
255540_at	AT4G01800	preprotein translocase secA subunit, putative	-0.2621	0.2708	0.3058	-0.3225	0.1913	0.227	-0.9092	0.004	0.0274	-0.9695	0.0032	0.0183
255541_s_at	AT4G01630, AT4G01820	PGIP3 (POLYGALACTURONASE (ENDO-1,4-BETA-	-0.8625	0.4102	0.3801	-0.9304	0.3876	0.3357	0.06374	0.8846	0.4881	0.01586	0.9711	0.4758
255542_at	AT4G01860	transducin family protein / WD-40 repeat family prot	0.5242	0.1549	0.2297	0.5848	0.1225	0.1777	-1.2787	0.0129	0.0452	-1.2181	0.1052	0.0393
255543_at	AT4G01870	toIB protein-related	1.2986	0.0208	0.085	0.8377	0.0754	0.1377	0.4171	0.1937	0.2078	-0.04377	0.8779	0.4507
255544_at	AT4G01880	similar to unnamed protein product [Vitis vinifera] (G	0.5253	0.0453	0.1225	0.38	0.1061	0.1644	-0.263	0.2235	0.2257	-0.4082	0.0892	0.1121
255545_at	AT4G01890	glycoside hydrolase family 28 protein / polygalactur	0.01824	0.9802	0.5721	0.2066	0.7793	0.4834	0.3701	0.6121	0.4018	0.5585	0.4539	0.3075
255546_at	AT4G01910	DC1 domain-containing protein	0.7763	0.0431	0.1199	0.849	0.033	0.09	-0.3511	0.2568	0.2447	-0.2785	0.3537	0.2643
255547_at	AT4G01920	DC1 domain-containing protein	1.004	0.036	0.1096	1.2342	0.0188	0.0707	-0.08555	0.8043	0.4648	0.1447	0.6774	0.3899
255548_at	AT4G01930	DC1 domain-containing protein	-0.71	0.1808	0.2486	0.7483	0.1632	0.2081	-0.8569	0.1044	0.1445	0.6014	0.2157	0.194
255549_at	AT4G01950	ATGPAT3/GPAT3 (GLYCEROL-3-PHOSPHATE AC	-1.8966	0.0489	0.1271	-2.1148	0.0355	0.0929	0.168	0.6681	0.4206	-0.05018	0.8969	0.4564
255550_at	AT4G01970	ATSTI5 (ARABIDOPSIS THALIANA STACHYOSE S	-0.7198	0.0884	0.1724	-0.2196	0.5315	0.3967	0.06991	0.8382	0.4751	0.5701	0.1504	0.1549
255551_at	AT4G01840	KCO5 (Ca2+ activated outward rectifying K+ channe	-0.1847	0.4994	0.4201	-0.05338	0.8407	0.5016	-0.09515	0.7217	0.4391	0.03613	0.8916	0.4547
255552_at	AT4G01850	MAT2/SAM-2 (S-adenosylmethionine synthetase 2	0.04709	0.6496	0.4762	-0.07314	0.4888	0.3799	-0.4068	0.0021	0.0217	-0.527	8.00E-04	0.0109
255553_at	AT4G01960	similar to unknown protein [Arabidopsis thaliana] (T	0.5241	0.0309	0.1019	0.5799	0.0225	0.0757	0.3736	0.0804	0.124	0.4295	0.0054	0.0843
255554_at	AT4G01897	similar to unnamed protein product [Vitis vinifera] (G	-0.6474	0.0157	0.0755	0.2409	0.2077	0.2381	0.7185	0.0021	0.0217	1.125	4.00E-04	0.0089
255555_at	AT4G01810	protein transport protein-related	0.5107	0.0531	0.1323	0.1585	0.4465	0.3623	0.01998	0.9204	0.498	-0.3322	0.1519	0.1561
255556_at	AT4G01940	NFU1 (NFU domain protein 1)	0.05074	0.7237	0.5006	0.4884	0.0217	0.0748	-0.3811	0.0464	0.0904	0.1581	0.3027	0.24
255557_at	AT4G01990	pentatricopeptide (PPR) repeat-containing protein	0.4049	0.0975	0.1803	0.4766	0.0642	0.1265	-0.1222	0.551	0.3794	-0.0505	0.8014	0.429
255558_at	AT4G01900	GLB1 (glutamine synthetase B1)	-0.562	0.0393	0.1144	-0.5216	0.0488	0.1097	0.366	0.0399	0.0827	0.4064	0.029	0.057
255559_at	AT4G02010	protein kinase family protein	0.2565	0.3602	0.3547	0.1331	0.6206	0.4308	0.1193	0.5108	0.3635	-0.00411	0.9814	0.4783
255560_at	AT4G02030	similar to unknown protein [Arabidopsis thaliana] (T	0.7067	0.001	0.0356	0.5783	0.0022	0.0333	-0.2136	0.0312	0.0718	-0.342	0.0065	0.0249
255561_at	AT4G02050	sugar transporter, putative	1.2478	0.0018	0.0391	0.925	0.0055	0.0434	-0.1362	0.3567	0.2965	-0.4591	0.0247	0.0518
255562_at	AT4G02070	MSH6 (MUTS HOMOLOG 6-1)	0.6713	0.0919	0.1758	0.5786	0.1299	0.1828	-0.4887	0.0463	0.0902	-0.5815	0.0275	0.0552
255563_at	AT4G01740	DC1 domain-containing protein	1.5551	0.2114	0.2692	1.4551	0.2367	0.2558	0.8635	0.4556	0.3411	-2.1467	0.1095	0.1274
255564_s_at	AT4G01770,AT4G01750	[AT4G01770, RGXT1 (RHAMNOGALACTURONAN	0.4463	0.261	0.3002	0.8463	0.0682	0.1309	-0.8029	0.0366	0.0788	-0.4029	0.1961	0.1826
255565_at	AT4G01760	DC1 domain-containing protein	-0.02442	0.9983	0.5763	-0.6125	0.5866	0.4186	-0.8149	0.476	0.3499	-1.425	0.2414	0.2079
255566_s_at	AT4G01780,AT3G48670	[AT4G01780, XH/XS domain-containing protein]:[A	-0.2172	0.4579	0.4018	0.346	0.2612	0.2704	-0.5614	0.0571	0.1021	0.001866	0.9934	0.481
255567_at	AT4G01150	Identical to Uncharacterized protein At4g01150, chl	-0.8132	0.0011	0.036	-0.8491	9.00E-04	0.0285	-0.00466	0.9518	0.506	-0.04058	0.6054	0.3651
255568_at	AT4G01250	WRKY22 (WRKY DNA-binding protein 22); transcri	0.8836	0.0917	0.1757	-0.868	0.0958	0.1559	0.5248	0.1847	0.2019	0.5404	0.1747	0.1701
255569_at	AT4G01320	ATSTE24	0.5243	2.00E-04	0.0312	0.3232	0.0016	0.0316	-0.00802	0.7509	0.4485	-0.2091	9.00E-04	0.0116
255570_at	AT4G01100	mitochondrial substrate carrier family protein	0.1457	0.3923	0.3712	0.1781	0.3065	0.2954	-0.4947	0.0225	0.0606	-0.4623	0.0279	0.0558
255571_at	AT4G01220	similar to RGXT1 (RHAMNOGALACTURONAN XY	-0.1541	0.5865	0.4549	-0.1537	0.5873	0.4187	0.5873	0.122	0.6189	0.4042	0.1224	0.618
255572_at	AT4G01050	hydroxyproline-rich glycoprotein family protein	-0.3719	0.0424	0.1184	-0.5429	0.0127	0.0602	-0.7168	0.0042	0.0279	-0.8878	0.0019	0.015
255573_at	AT4G01400	pentatricopeptide (PPR) repeat-containing protein	0.4633	0.0055	0.052	0.6079	0.002	0.033	-0.4177	0.008	0.0358	-0.2731	0.0325	0.0608
255574_at	AT4G01420	CBL5 (CALCINEURIN B-LIKE PROTEIN 5)	0.7383	0.3127	0.3302	0.1334	0.845	0.503	-0.02512	0.9692	0.5097	-0.6301	0.3604	0.2672
255575_at	AT4G01430	nodulin MtN21 family protein	0.4947	0.1933	0.2578	0.6957	0.093	0.1538	0.06809	0.7581	0.4507	0.2691	0.2623	0.2189
255576_at	AT4G01440	nodulin MtN21 family protein	-0.1546	0.6575	0.4781	-0.3865	0.298	0.2906	-0.4719	0.2136	0.2201	-0.7038	0.0923	0.1146
255577_at	AT4G01410	harpin-induced family protein / HIN1 family protein /	-0.7712	0.0406	0.1162	-0.521	0.1141	0.1706	-0.00236	0.9895	0.5152	0.2479	0.2154	0.1939
255578_at	AT4G01450	nodulin MtN21 family protein	-0.5557	0.07	0.1524	-0.2877	0.2724	0.2768	-0.1227	0.5829	0.3917	0.1453	0.5186	0.333
255579_at	AT4G01460	basic helix-loop-helix (bHLH) family protein	-0.482	0.1232	0.2035	0.1919	0.4812	0.3767	-1.1347	0.0101	0.04	-0.4607	0.1361	0.1457
255580_at	AT4G01470	GAMMA-TIP3/TIP1;3 (tonoplast intrinsic protein 1;3	-0.2291	0.5778	0.4517	-0.6759	0.1489	0.1974	0.4481	0.2868	0.2617	0.001421	0.9971	0.4821
255581_at	AT4G01490	transposable element gene	0.7978	0.2396	0.2874	-0.4628	0.4681	0.3714	0.3973	0.5043	0.361	-0.8634	0.1865	0.1773
255582_at	AT4G01500	NGA4 (NGATHA4); transcription factor	-0.4447	0.2709	0.306	-0.02959	0.9364	0.5283	-0.3353	0.3904	0.3123	0.07979	0.8301	0.4372
255583_at	AT4G01510	ARV2	-0.0387	0.8148	0.5283	0.03288	0.8421	0.5021	0.002631	0.9824	0.5133	0.07421	0.545	0.3429
255584_at	AT4G01530	transposable element gene	0.1029	0.9446	0.5635	-1.9413	0.2353	0.255	0.6575	0.6611	0.4182	-1.3867	0.3752	0.2736
255585_at	AT4G01550	ANAC069 (Arabidopsis NAC domain containing pro	0.3664	0.1145	0.1961	0.2273	0.28	0.2809	0.02301	0.904	0.4934	-0.1161	0.5521	0.3459
255586_at	AT4G01560	MEE49 (maternal effect embryo arrest 49)	0.3659	0.1743	0.2444	0.3178	0.2251	0.2485	0.3277	0.1767	0.1963	0.2796	0.2346	0.2042
255587_at	AT4G01480	ATPPA5 (ARABIDOPSIS THALIANA PYROPHOSP	0.3002	0.2339	0.2839	0.2058	0.3913	0.3373	0.392	0.0701	0.1149	0.2975	0.1359	0.1456
255588_at	AT4G01570	pentatricopeptide (PPR) repeat-containing protein	-0.04799	0.8433	0.5367	0.265	0.3089	0.2968	-0.3162	0.1483	0.1779	-0.00321	0.9864	0.4793
255589_s_at	AT4G01590,AT4G35680	[AT4G01590, similar to unknown protein [Arabidops	0.1737	0.0835	0.1672	0.4179	0.0053	0.0429	0.111	0.2166	0.2216	0.3552	0.0094	0.0302
255590_at	AT4G01610	cathepsin B-like cysteine protease, putative	0.1856	0.005	0.0504	1.2833	0.0037	0.0387	-0.3653	0.107	0.1465	-0.2675	0.2038	0.1872
255591_at	AT4G01630	ATEXPA17 (ARABIDOPSIS THALIANA EXPANSIN	-0.2388	0.7408	0.5061	-1.743	0.0608	0.1225	1.5545	0.0823	0.1258	0.05027	0.9441	0.4694
255592_s_at	AT4G01640,AT2G34280	[AT4G01640, similar to S locus F-box-related / SLF	0.1449	0.8863	0.5474	-0.6445	0.5355	0.3987	-0.5381	0.6021	0.3989	-1.3275	0.2356	0.2048
255593_at	AT4G01650	similar to unknown protein [Arabidopsis thaliana] (T	0.01178	0.9495	0.5646	0.1772	0.368	0.3266	-0.2577	0.0195	0.0561	-0.09227	0.2477	0.2111
255594_at	AT4G01660	ABC1At (ARABIDOPSIS THALIANA ABC TRANSP	0.198	0.3246	0.337	-0.02566	0.8914	0.5162	0.3465	0.0299	0.0705	0.1228	0.3072	0.2421
255595_at	AT4G01700	chitinase, putative	0.1909	0.6045	0.461	0.4897	0.2233	0.2478	0.7494	0.0041	0.0275	1.0483	0.0012	0.0127
255596_at	AT4G01720	WRKY47 (WRKY DNA-binding protein 47); transcri	1.1224	0.0126	0.0694	0.9778	0.02	0.0724	0.5377	0.0105	0.0407	0.3932	0.0294	0.0575
255597_at	AT4G01730	zinc finger (DHHC type) family protein	0.24	0.5714	0.4495	0.07894	0.8494	0.5042	0.1311	0.7535	0.4492	-0.02993	0.9425	0.4691
255598_at	AT4G01800	RNA recognition motif (RRM)-containing protein	0.2764	0.1408	0.2182	0.6605	0.0119	0.0585	-0.312	0.1074	0.1467	0.07208	0.6576	0.3833
255599_at	AT4G01010	ATCNGC13 (cyclic nucleotide gated channel 13); c	1.3743	3.00E-04	0.0312	1.2224	4.00E-04	0.0251	-0.2111	0.1103	0.1486	-0.363	0.0245	0.0515
255600_s_at	AT4G01020,AT5G10370	[AT4G01020, helicase domain-containing protein /	0.4459	0.0466	0.1241	0.3368	0.098	0.1579	-0.7278	0.0097	0.0393	-0.8369	0.0059	0.0239
255601_at	AT4G01030	pentatricopeptide (PPR) repeat-containing protein	0.4334	0.2906	0.3177	0.2421	0.5341	0.3981	-0.3238	0.4149	0.323	-0.5152	0.2217	0.197
255602_at	AT4G01026	similar to unknown protein [Arabidopsis thaliana] (T	-0.04389	0.7221	0.5001	0.2206	0.1276	0.1812	-0.3558	0.0195	0.0561	-0.09134	0.3873	0.2789
255603_at	AT4G01040	glycosyl hydrolase family 18 protein	0.1038	0.2144	0.2711	-0.1323	0.2186	0.2449	-0.2663	0.0311	0.0717	-0.2944	0.0316	0.0598
255604_at	AT4G01080	similar to unknown protein [Arabidopsis thaliana] (T	-1.3744	0.0135	0.0715	-1.9976	0.0036	0.0377	0.2456	0.1987	0.211	-0.3776	0.0772	0.1026
255605_at	AT4G01090	extra-large G-protein-related	-0.4187	0.1784	0.2469	-0.2143	0.451	0.3644	0.1246	0.4147	0.3229	0.329	0.0743	0.1002
255606_at	AT4G01110	similar to unknown protein [Arabidopsis thaliana] (T	-0.8376	0.2633	0.3017	0.6833	0.3969	0.3399	0.3222	0.626	0.4066	1.9531	0.0363	0.0648
255607_at	AT4G01130	acetylesterase, putative	1.0192	0.0337	0.1062	0.2943	0.411	0.3465	0.08161	0.8118	0.4671	-0.6433	0.1155	0.1316
255608_at	AT4G01140	similar to unknown protein [Arabidopsis thaliana] (T	-0.5337	0.4382	0.3929	-2.3852	0.0184	0.0702	1.5133	0.0713	0.1161	-0.3383	0.6146	0.3682
255609_s_at	AT4G01180, AT4G35930	[AT4G01180, XH/XS domain-containing protein]:[A	0.1454	0.9179	0.5565	1.0335	0.4788	0.3757	-0.02678	0.9848	0.5138	0.9613	0.5509	0.3455
255610_at	AT4G01190	ATPIPK10 (ARABIDOPSIS PHOSPHATIDYLINOS	-0.3328	0.6371	0.4721	-1.6297	0.067	0.1296	1.0373	0.1786	0.1977	-0.2597	0.7043	0.3989
255611_at	AT4G01210	glycosyltransferase family protein 1	0.07786	0.559	0.4446	0.03306	0.8003	0.4897	-0.1863	0.0813	0.125	-0.2311	0.0452	0.0746
255612_at	AT4G01240	similar to unknown protein [Arabidopsis thaliana] (T	-0.4949	0.6447	0.4747	-0.3379	0.699	0.4586	-1.594	0.1215	0.1575	-1.5271	0.1336	0.1441
255613_at	AT4G01270	zinc finger (C3HC4-type RING finger) family protein	-0.937	0.0581	0.1382	-0.3334	0.4022	0.3422	-0.9832	0.0508	0.0955	-0.3796	0.3466	0.2609
255614_at	AT4G01280	myb family transcription factor	-0.09589	0.537	0.4358	-0.1412	0.3767	0.3305	-0.3048	0.0987	0.1398	-0.3502	0.0695	0.0965
255615_at	AT4G01290	similar to unnamed protein product [Vitis vinifera] (G	0.7048	0.025	0.0918	0.5771	0.0458	0.106	-0.1671	0.4538	0.3404	-0.2948	0.2176	0.1949
255616_at	AT4G01250	similar to unnamed protein product [Vitis vinifera] (G	0.01797	0.948	0.5642	0.2091	0.4644	0.3698	-1.9748	0.0016	0.0202	-1.7837	0.0023	0.0161
255617_at	AT4G01330	protein kinase family protein	-0.5314	0.1073	0.1895	-0.5573	0.0958	0.156	-0.2846	0.1014	0.1422	-0.3105	0.0818	0.1065
255618_at	AT4G01340	lectin protein kinase family protein	0.6748	0.0173	0.0748	0.03172	0.9714	0.537	0.9366	0.3237	0.2801	0.1827	0.8371	0.4393
255619_s_at	AT5G59920,AT4G01350	[AT5G59920, ULI3 (UV-B light insensitive 3)]:[AT4G	-0.955	0.1221	0.2024	-1.3701	0.0485	0.1094	0.2016	0.4401	0.3341	-0.2136	0.4156	0.2907
255620_at	AT4G01380	plastocyanin-like domain-containing protein	0.7786	0.2445	0.2903	-0.1289	0.8325	0.4996	-0.2524	0.6734	0.422	-1.1598	0.1053	0.1241
255621_at	AT4G01390	meprin and TRAF homology domain-containing pro	0.3764	0.4364	0.3921	0.02179	0.9625	0.5347	0.2868	0.4273	0.3286	-0.06779	0.8449

255690_at	AT4G00360	CYP89A2 (ABERRANT INDUCTION OF TYPE THI	-1.1957	0.0155	0.0752	-1.2032	0.0152	0.0647	-0.09855	0.4309	0.33	-0.106	0.3998	0.2841
255691_at	AT4G00370	ANTR2 (anion transporter 2); organic anion transpo	-0.2146	0.3331	0.3419	-0.7119	0.0218	0.0748	0.004417	0.9759	0.5116	-0.4929	0.0232	0.0496
255692_at	AT4G00400	GPAT8 (GLYCEROL-3-PHOSPHATE ACYLTRANS	-0.5186	0.1369	0.2149	-0.8156	0.0432	0.1032	0.1959	0.3151	0.2759	-0.1011	0.5853	0.3582
255693_s_at	AT5G01630;AT4G00020	[AT5G01630, BRCA2B (breast cancer 2 like 2B); pr	-0.5688	0.1149	0.1963	-0.1474	0.6301	0.4346	-1.189	0.0137	0.0466	-0.7676	0.0535	0.0826
255694_at	AT4G00050	UNE10 (unfertilized embryo sac 10); DNA binding	-0.9776	0.0078	0.0583	-1.2128	0.0036	0.0377	1.0039	0.0017	0.0205	0.7686	0.0046	0.0216
255695_at	AT4G00080	UNE11 (unfertilized embryo sac 11); pectinesterase	-1.0232	0.3472	0.3485	-1.9553	0.1117	0.1687	0.9134	0.3651	0.3005	-0.01867	0.9844	0.4791
255696_at	AT4G00110	GAE3 (UDP-D-GLUCURONATE 4-EPIMERASE 3);	0.2076	0.2217	0.2761	0.1835	0.2705	0.2758	-0.1016	0.5182	0.3663	-0.1258	0.4304	0.297
255697_at	AT4G00150	transcription regulator [Arabidopsis thaliar	-1.9326	0.139	0.2165	0.00765	0.9945	0.5428	-2.1861	0.0558	0.1008	-0.2458	0.779	0.4226
255698_at	AT4G00150	scarecrow-like transcription factor 6 (SCL6)	-0.1766	0.3875	0.3685	-0.7003	0.0184	0.0702	-0.1937	0.3478	0.292	-0.7174	0.017	0.0416
255699_at	AT4G00190	pectinesterase family protein	-0.118	0.7794	0.5177	-0.306	0.4808	0.3765	-0.5753	0.1738	0.1945	-0.7633	0.0934	0.1156
255700_at	AT4G00200	DNA binding	0.7697	0.043	0.1196	0.2872	0.3363	0.3116	-0.00304	0.9913	0.5155	-0.4855	0.1387	0.1474
255701_at	AT4G00220	JLO(LBD30 (JAGGED LATERAL ORGANS)	0.4027	0.4243	0.3869	0.00442	0.9927	0.5423	1.452	0.0327	0.0738	1.0537	0.0806	0.1056
255702_at	AT4G00230	XSP1 (XYLEM SERINE PEPTIDASE 1); subtilase	-0.3589	0.177	0.2461	-0.2648	0.2937	0.2885	-0.09864	0.4778	0.3506	-0.0045	0.9732	0.4764
255703_at	AT4G00040	chalcone and stilbene synthase family protein	2.0937	0.0754	0.158	0.1256	0.8931	0.5167	-2.8252	0.024	0.0628	-4.7933	0.0039	0.0201
255704_at	AT4G00170	vesicle-associated membrane family protein / VAM	0.1372	0.2572	0.2978	0.2478	0.0756	0.1379	0.1067	0.3626	0.2994	0.2173	0.1048	0.1239
255705_at	AT4G00160	F-box family protein	1.3353	0.3906	0.3702	-2.0799	0.2085	0.2386	1.3746	0.3324	0.2845	-2.0406	0.1773	0.1715
255706_at	AT4G00100	ATRPS13A (RIBOSOMAL PROTEIN S13A); structu	-1.0582	0.5141	0.4269	-1.8335	0.2985	0.2909	-0.156	0.8112	0.467	-0.8913	0.2187	0.1954
255707_at	AT4G00231	MEE50 (maternal effect embryo arrest 50); binding	-0.2333	0.2317	0.283	0.242	0.2178	0.2444	-0.6025	0.0047	0.0292	-0.1272	0.2964	0.2368
255708_at	AT4G00232	similar to unknown protein [Arabidopsis thaliana] (T	0.2759	0.7385	0.5053	-0.257	0.7556	0.4768	-0.6283	0.4609	0.3435	-1.1612	0.2065	0.1888
255709_at	AT4G00180	YAB3 (YABBY3); transcription factor	-0.1111	0.5353	0.4352	-0.3926	0.0749	0.1372	0.7627	0.0026	0.0235	0.4813	0.0135	0.0368
255710_at	AT4G00030	plastid-lipid associated protein PAP / fibrillin family p	0.2347	0.2529	0.2952	0.0087	0.9629	0.5347	-0.07208	0.7029	0.4322	-0.2981	0.1653	0.1644
255711_at	AT4G00060	transducin family protein / WD-40 repeat family prot	0.6838	0.0958	0.0532	0.5785	0.0105	0.0554	-0.6815	0.0059	0.032	-0.7867	0.0035	0.0193
255712_at	AT4G00280	similar to leucine-rich repeat protein kinase, putative	-0.2804	0.6316	0.4702	-0.5797	0.3444	0.3153	0.2059	0.7229	0.4396	-0.09329	0.8715	0.4489
255713_s_at	AT4G00290;AT4G00234	[AT4G00290, mechanosensitive ion channel domai	0.02366	0.8984	0.5508	0.08594	0.6474	0.4406	-1.2127	0.0018	0.0206	-1.1505	0.0022	0.0157
255714_at	AT4G00300	fringe-related protein	-0.5843	0.1306	0.209	-0.3367	0.3356	0.3112	0.1106	0.5105	0.3634	0.3582	0.0796	0.1046
255715_s_at	AT4G00320;AT5G41830	[AT4G00320, F-box family protein];[AT5G41830, F-	1.1255	0.1971	0.2606	2.0869	0.0457	0.1058	-0.1516	0.8452	0.4771	0.8098	0.3285	0.2526
255716_at	AT4G00330	CRCK2 (calmodulin-binding receptor-like cytoplasm	-0.225	0.4472	0.3968	0.09262	0.7464	0.4737	-0.3297	0.2453	0.2381	-0.01208	0.9626	0.4739
255717_at	AT4G00350	MATE efflux family protein	-0.02403	0.9794	0.572	1.1682	0.2518	0.2652	-1.4863	0.0462	0.0901	-0.2941	0.6025	0.3642
255718_at	AT1G32070	ATNSI (NUCLEAR SHUTTLE INTERACTING); N-a	0.0673	0.6525	0.4769	-0.1689	0.2897	0.2864	0.3135	0.012	0.0435	0.07728	0.3426	0.2591
255719_at	AT1G32080	membrane protein, putative	-1.2799	0.0016	0.0388	-1.3024	0.0015	0.0314	-0.3454	0.0713	0.1161	-0.3679	0.0603	0.0887
255720_at	AT1G32090	PRK (PHOSPHORIBULOKINASE); ATP binding / p	-0.6188	7.00E-04	0.0334	-0.9872	1.00E-04	0.0249	-0.1395	0.0982	0.1394	-0.5079	0.0014	0.0137
255721_at	AT1G31940	similar to unknown protein [Arabidopsis thaliana] (T	0.1562	0.3093	0.3281	0.07364	0.6126	0.4279	0.7552	0.0037	0.0267	0.6726	0.0056	0.0234
255722_at	AT3G29570	similar to surface antigen 2 (CA-2), putative [Trypar	0.945	0.286	0.3148	-0.6542	0.4424	0.3605	0.6701	0.255	0.2437	-0.929	0.1395	0.1478
255723_at	AT3G29575	similar to TMAC2 (TWO OR MORE ABRES-CONTA	0.8086	0.0137	0.0719	0.7018	0.0219	0.0749	0.2073	0.0302	0.0708	0.1004	0.1862	0.1771
255724_at	no_match	no_match	-0.8801	0.1365	0.2146	-1.2496	0.0575	0.1192	0.2103	0.6798	0.4243	-0.1593	0.7533	0.4146
255725_at	AT5G25540	PFT1 (PHYTOCHROME AND FLOWERING TIME	0.5744	0.0203	0.0839	0.3788	0.0697	0.1322	-0.4901	0.0086	0.0372	-0.6857	0.0025	0.0168
255726_at	AT5G25550	lysine and histidine specific transporter, putative	0.2767	0.6054	0.4615	0.8677	0.154	0.2011	-0.3940	0.4693	0.3473	0.1963	0.7114	0.4014
255727_at	AT5G25510	aspartyl protease family protein	-1.0982	0.5141	0.4269	-1.8335	0.2985	0.2909	-0.156	0.8112	0.467	-0.8913	0.2187	0.1954
255728_at	AT5G2500	choline transporter-related	0.7091	0.0062	0.0542	0.8264	0.0036	0.0377	-0.6945	0.0067	0.0335	-0.5772	0.0127	0.0357
255729_at	AT1G25472, CPJORF64	[AT1G25472, CPJORF64 (Conserved peptide upstr	0.1147	0.5245	0.431	0.5019	0.0382	0.0967	-0.2272	0.2389	0.2346	0.1593	0.3883	0.2792
255730_at	AT5G25460	oxidoreductase family protein	1.6428	0.2259	0.279	0.8752	0.4886	0.3798	0.1949	0.8735	0.4851	-0.5727	0.6443	0.3787
255731_at	AT5G25490	RCN1 (ROOTS CURL IN NPA); protein phosphatase	0.05415	0.7333	0.5033	-0.09183	0.569	0.4115	-0.5471	0.021	0.0583	-0.6931	0.0095	0.0303
255732_at	AT5G25450	very-long-chain fatty acid condensing enzyme, putat	-1.0975	0.1346	0.2131	-1.7145	0.0431	0.1031	-0.3976	0.0318	0.0726	-1.0146	0.0012	0.0127
255733_at	AT5G25400	similar to unknown protein [Arabidopsis thaliana] (T	-0.2702	0.6348	0.4711	0.5251	0.375	0.3299	0.06079	0.8308	0.473	0.8562	0.0326	0.0609
255734_at	AT5G25550	myb family transcription factor	0.2851	0.3866	0.3682	0.232	0.4737	0.3736	-0.1236	0.5434	0.3767	-0.1767	0.3965	0.2828
255735_at	AT5G25520	similar to unknown protein [Arabidopsis thaliana] (T	0.2178	0.2542	0.296	0.3378	0.1081	0.1657	-0.1328	0.4595	0.3428	-0.01274	0.9412	0.4688
255736_at	AT5G25380	mitochondrial substrate carrier family protein	0.6525	0.004	0.0468	0.4561	0.0142	0.0631	-0.02627	0.8228	0.4705	-0.2227	0.1126	0.1295
255737_at	AT5G25420	similar to unknown protein [Arabidopsis thaliana] (T	-0.08605	0.4858	0.414	-0.2614	0.0802	0.1421	0.108	0.3902	0.3122	-0.06735	0.5806	0.3563
255738_at	AT5G25570	leucine-rich repeat protein-related	0.02132	0.8658	0.5425	0.0412	0.7453	0.4733	-0.2644	0.0893	0.132	-0.2445	0.1078	0.126
255739_at	AT5G25580	ANAC008 (Arabidopsis NAC domain containing pro	0.7469	0.038	0.1123	0.4951	0.1133	0.1702	0.3072	0.1602	0.1857	0.0553	0.772	0.4206
255740_at	AT5G2590	protein kinase family protein	0.4013	0.0208	0.085	-0.1176	0.3393	0.3132	0.2305	0.1008	0.1417	-0.2884	0.0565	0.0853
255741_at	AT5G25410	ATIPT5 (Arabidopsis thaliana isopentenyltransferas	0.4333	0.8031	0.525	-1.0532	0.5527	0.4057	-0.2276	0.8955	0.4912	-0.8475	0.6299	0.3736
255742_at	AT5G25560	AP2 domain-containing transcription factor, putative	0.1833	0.5408	0.4371	0.7297	0.0565	0.1182	0.1823	0.0776	0.1217	0.7287	7.00E-04	0.0107
255743_at	AT5G2375	metallo-beta-lactamase family protein	0.4122	0.0188	0.0815	0.2437	0.087	0.1487	-0.0866	0.4676	0.3465	-0.2551	0.0775	0.1029
255744_at	AT5G25040	transposable element gene	0.861	0.0996	0.1787	1.9796	0.0075	0.0488	-1.843	0.0097	0.0392	-0.7245	0.1417	0.1493
255745_at	AT3G32030	DNA binding	-1.1679	0.2626	0.3012	-0.9323	0.3572	0.3215	-0.699	0.4057	0.3189	-0.4633	0.5715	0.3531
255746_at	AT3G32020	F-box family protein	-1.5622	0.1293	0.2079	-0.3056	0.7281	0.4683	-1.0798	0.258	0.2452	0.1768	0.8398	0.4399
255747_s_at	AT3G32010;AT5G38190	[AT3G32010, myosin heavy chain-related];[AT5G38	2.107	0.0244	0.0909	-1.2794	0.0994	0.159	0.9177	0.2	0.2118	-2.4686	0.0146	0.0384
255748_at	AT3G32000	similar to myosin heavy chain-related [Arabidopsis t	0.5081	0.1791	0.2475	-0.6044	0.55	0.4048	1.4314	0.0974	0.1389	-0.6811	0.363	0.2683
255749_at	AT3G31970	STRS1 (STRESS RESPONSE SUPPRESSOR 1);	0.02176	0.9248	0.5582	-0.01725	0.9403	0.5292	-0.3828	0.0684	0.1135	-0.4218	0.0525	0.0816
255750_at	AT3G31960	unknown protein	-0.09077	0.9451	0.5635	-0.3609	0.7852	0.4848	0.6136	0.6462	0.4131	0.3434	0.7952	0.4275
255751_at	AT3G31950	terpene synthase/cyclase family protein	1.2211	0.2474	0.292	-1.6951	0.1335	0.1856	1.4861	0.1749	0.1953	-1.4301	0.1882	0.1782
255752_at	AT3G32050	secretory carrier membrane protein (SCAMP) family	0.1894	0.1623	0.2357	0.2682	0.0726	0.1349	0.2977	0.0548	0.0996	0.3764	0.0273	0.0549
255753_at	AT1G18570	MYB51 (MYB DOMAIN PROTEIN 51); DNA binding	0.37	0.4004	0.3755	0.7633	0.1244	0.1789	0.2994	0.11	0.1485	0.6927	0.0091	0.0296
255754_at	AT1G43040	auxin-responsive protein, putative	1.7954	0.0895	0.1733	-2.3494	0.0432	0.1032	3.2452	0.0157	0.0499	-0.8996	0.3261	0.2513
255755_s_at	AT1G43110;AT1G43050;A	[AT1G43110, pseudogene, putative polygalacturon	-1.6675	0.2166	0.2729	-1.1335	0.3754	0.3301	1.7081	0.2076	0.2164	2.2421	0.12	0.135
255756_at	AT4G19840	ATGH9B5 (ARABIDOPSIS THALIANA GLYCOSYL	-1.0337	0.035	0.1082	-1.2276	0.0204	0.0729	0.3937	0.2879	0.2625	0.1998	0.568	0.352
255757_at	AT4G00460	ATROPGEF3/ROPGEF3 (KINASE PARTNER PRO	0.8845	0.6028	0.4604	-1.3113	0.45	0.3639	0.1213	0.9163	0.4968	-2.0746	0.1281	0.1403
255758_at	AT1G16800	tRNA-splicing endonuclease positive effector-relate	-0.4814	0.3278	0.3388	-0.4036	0.4034	0.3428	-0.4403	0.366	0.3008	-0.3625	0.4489	0.3056
255759_at	AT1G16790	ribosomal protein-related	0.1914	0.2134	0.2706	0.3932	0.0385	0.0972	0.4491	0.0049	0.0297	0.6909	0.0014	0.0133
255760_at	AT1G16780	vacuolar-type H+-translocating inorganic pyrophosp	-0.4736	0.0541	0.1334	-0.4989	0.0466	0.1071	-0.5762	0.0303	0.0709	-0.6015	0.0265	0.054
255761_at	AT1G16770	similar to unnamed protein product [Vitis vinifera] (G	1.1294	0.2161	0.2724	-0.06894	0.9329	0.5272	-0.5884	0.4871	0.3542	-1.7867	0.081	0.1058
255762_at	AT1G16710	HAC12 (HISTONE ACETYLTRANSFERASE OF TH	0.45622	0.7801	0.5179	0.03975	0.8058	0.4915	-0.6774	0.011	0.0416	-0.7624	0.0073	0.0266
255763_at	AT1G16730	similar to unknown [Picea sitchensis] (GB:ABK2120	-0.2726	0.1265	0.2058	-0.2665	0.1324	0.1847	-0.6469	0.0102	0.0401	-0.6414	0.0105	0.0321
255764_at	AT1G16720	HCF173 (HIGH CHLOROPHYLL FLUORESCENCE	-0.4704	0.0075	0.0579	-0.7642	0.0013	0.0305	-0.1127	0.0872	0.1304	-0.4065	0.0012	0.013
255765_at	AT1G16760	protein kinase family protein	0.7826	0.6118	0.4633	0.01306	0.9931	0.5425	0.04654	0.9755	0.5115	-0.723	0.6383	0.3766
255766_at	AT1G16750	similar to unknown protein [Arabidopsis thaliana] (T	-0.4953	0.1032	0.1855	-0.849	0.0226	0.076	0.05626	0.7943	0.4615	-0.2975	0.2147	0.1934
255767_at	AT1G16740	ribosomal protein L20 family protein	0.5649	0.0399	0.1151	0.5924	0.0346	0.0918	0.9883	0.0063	0.0328	1.0158	0.0057	0.0235
255768_at	AT1G16705	p300/CBP acetyltransferase-related protein-related	-2.248	0.0742	0.1566	0.5879	0.564	0.4097	-2.0716	0.0913	0.1336	0.7643	0.46	0.31
255769_at	AT1G18610	kelch repeat-containing protein	-0.04904	0.8717	0.5444	-0.03731	0.9021	0.5195	-0.0491	0.8715	0.4846	-0.03737	0.902	0.4579
255770_at	AT1G18560	hAT dimerisation domain-containing protein / BED z	0.5203	0.0394	0.1146	0.3281	0.1302	0.1829	-0.02234	0.9033	0.4932	-0.2145	0.282	0.2291
255771_at	AT1G18550	kinesin motor protein-related	1.1229	0.1828	0.2501	2.6975	0.018	0.0694	0.3724	0.4617	0.344	1.947	0.0131	0.0364
255772_at	AT1G18530	calmodulin, putative	-0.02293	0.9729	0.5705	-0.6837	0.3417	0.3143	-0.2121	0.7549	0.4496	-0.8729	0.2408	0.2076
255773_at	AT1G18590	sulfotransferase family protein	-0.4748	0.3177	0.3329	-0.4158	0.3745	0.3296	0.1312	0.3091	0.273	0.1903	0.1667	0.1652
255774_at	AT1G18620	similar to unknown protein [Arabidopsis thaliana] (T	0.07634	0.7412	0.5062	-0.08708	0.7034	0.4602	-0.4871	0.084	0.1274	-0.6495	0.038	0.0667
255775_at	AT1G18600	rhomboid family protein	0.129	0.3066	0.3264	0.3273	0.0411	0.1006	-0.1097	0.3758	0.3057	0.08865	0.466	0.3123
255776_at	AT1G18540	60S ribosomal protein L6 (RPL6A)	0.2665	0.0224	0.0876	0.4002	0.0056	0.0434	0.3884	8.00E-04	0.0162	0.5221	2.00E-04	0.0079
255777_at	AT1G18630	GR-RBP6 (glycine-rich RNA-binding protein 6); RN	0.3345	0.1157	0.1967	0.3105	0.1365	0.1881	0.7432	0.0013	0.0191	0.7192	0.0015	0.0137
255778_at	AT1G18640	PSP (3-PHOSPHOSERINE PHOSPHATASE)	0.3451	0.105	0.1872	0.3972	0.074	0.1365	0.3788	0.033	0.0742	0.431	0.022	0.0484
255779_at	AT1G18650	glycosyl hydrolase family protein 17	-0.7045	0.0234	0.0895	-0.6134	0.036	0.0937	0.272	0.0374	0.0798	0.3631	0.0149	0.0388
255780_at	AT1G18580	GAUT11 (Galacturonosyltransferase 11); polygalac	-0.4381	0.0266	0.0941	0.08749	0.5312	0.3966	-0.8938	0.0013	0.0188	-0.3682	0.0287	0.0567
255781_at	AT1G19880	regulator of chromosome condensation (RCC1) fam	0.3157	0.2862	0.3149	0.3186	0.2824	0.2823	-0.7954	0.0077	0.0354	-0.7925	0.0078	0.0275
255782_at	AT1G19850	MP (MONOPTEROS); transcription factor	0.6874	0.0438	0.1207	0.8113	0.0265	0.0815	0.004786	0.9829	0.5134	0.1288	0.5738	0.3538
255783_at	AT1G19870	IQD32 (IQ-domain 32); calmodulin binding	0.296	0.0435	0.1203	0.3748	0.021	0.074	-0.6356	0.0033	0.0256	-0.5568	0.0054	0.023
255784_at	AT1G19860	zinc finger (CCCH-type) family protein	0.2253	0.487	0.4145	0.3248	0.3322	0.3096	-0.3714	0.1624	0.1868	-0.272	0.2786	0.2274
255785_at	AT1G19920	APS2 (ATP SULFURYLASE PRECURSOR)	-0.2768	0.2785	0.3105	-0.5849	0.0571	0.1189	-0.1463	0.2285	0.2287	-0.4544	0.0116	0.0338
255786_at	AT1G19670	ATCLH1 (CORONATINE-INDUCED PROTEIN 1)	-0.8883	0.0202	0.0837	-0.8284	0.0252	0.0794	-0.06643	0.5134	0.3644	-0.0065	0.9475	0.4703
255787_at	AT3G23590	cinnamoyl-CoA reductase family	0.1591	0.347	0.3485	0.188	0.2769	0.2792	-0.09008	0.5792	0.3904	-0.06124	0.703	0.3984
255788_at	AT3G23310	IAA13 (indoleacetic acid-induced protein 13); transc	-0.05167	0.7127	0.4972	0.2267	0.1591	0.2052	0.3008	0.0051	0.03	0.5782	4.00E-04	0.0091
255789_at	AT3G23370	60S ribosomal protein L23 (RPL23B)	0.185	0.3839	0.3667	0.09555	0.6404	0.4384	0.1683	0.3523	0.2944	0.07884	0.648	0.3801
255790_at	AT3G23560	spindle checkpoint protein-related	-0.7854	0.5969	0.4586	-0.62	0.6741	0.4499	0.6288	0.6699	0.421	0.7942	0.593	0.3609
255791_at	AT3G23430	plastid developmental protein DAG, putative	0.006412	0.9499	0.5646	-0.1433	0.2093	0.2392	-0.1527	0.1663	0.1893	-0.3025	0.0287	0.0566
255792_at	AT3G23620	DNA-binding family protein / A.T-hook protein 1 (AH	0.3372	0.0421	0.1181	0.2184	0.129	0.1821	-0.2887	0.0617	0.1068	-0.4075	0.0221	0.0484
255793_at	AT3G23250	similar to unnamed protein product [Vitis vinifera] (G	-0.09078	0.6536	0.4771	-0.3353	0.1483	0.1969	-0.8585	0.0012	0.0187	-1.103	5.00E-04	0.0093
255794_at	AT3G23480	ANAC041 (Arabidopsis NAC domain containing pro	0.5173	0.1603	0.2337	0.5744	0.1286	0.1819	0.1707	0.6004	0.3984	0.2278	0.4908	0.3222
255795_at	AT3G23380	RD20 (RESPONSIVE TO DESICCATION 20); calci	-1.176	0.0091	0.0617	-1.0906	0.0119	0.0585	0.04412	0.6425	0.412	0.1295	0.2151	0.1937
255796_at	AT3G23290	SUVH2 (SU(VAR)3-9 HOMOLOG 2);	0.365	0.0683	0.1503	0.2976	0.1134	0.1702	-0.1337	0.3018	0.2695	-0.2011	0.1494	0.1542
255797_at	AT3G23630	3-beta hydroxysteroid dehydrogenase/isomerase fa	0.9296	0.004	0.0468	0.8504	0.0056	0.0434	-0.6297	0.0028	0.0241	-0.7089	0.0018	0.0147
255798_at	AT3G23255	hydrolase	-0.5641	0.019	0.0819	-0.5703	0.0183	0.07	0.08623	0.5742	0.3882	0.08001	0.601	0.3638
255799_at	AT4G10180	DET1 (DE-ETIOLATED 1); catalytic	0.2048	0.1112	0.1933	0.09866	0.3819	0.3328	-0.0886	0.1525	0.1806	-0.1948	0.0179	0.0428
255800_at	AT4G10200	hAT dimerisation domain-containing protein / transp	-2.2492	0.1181	0.1987	-0.0558	0.9631	0.5347	-2.1434	0.1314	0.165	0.05001	0.9669	0.4748
255801_at	AT4G10130	DNA/pantothenate N-terminal domain-containing pro	0.184	0.491	0.4163	0.4359	0.1472	0.1961	-0.2106	0.4348	0.3318	0.04132	0.8732	0.4494
255802_s_at	AT4G10150;AT4G10160	[AT4G10150, zinc finger (C3HC4-type RING finger)	-1.1109	0.056	0.1359	-0.9973	0.0748	0.1371	0.4694	0.2597	0.2463	0.5829	0.1785	0.1724
255803_at	AT4G10170	synaptobrevin-related family protein	-0.06322	0.7542	0.5097	-0.02548	0.899	0.5186	-0.1299	0.5287	0.3708	-0.09214	0.6506	0.361
255804_at	AT4G10220	similar to unknown protein [Arabidopsis thaliana] (T	0.06324	0.9259	0.5585	-1.8868	0.0418	0.1016	1.2569	0.1127	0.1504	-0.6932	0.3264	0.2515
255805_at	AT4G10240	zinc finger (B-box type) family protein	2.0645	0.1846	0.2514	0.3683	0.7893	0.4859	1.4742	0.2817	0.2591	-0.222	0.8606	0.446
255806_at	AT4G10260	pfkB-type carbohydrate kinase family protein	-1.0715	0.3618	0.3554	-0.8345	0.468	0.3713	-1.6283	0.175	0.1954	-1.3913	0.2322	0.2028
255807_at	AT4G10270	wound-responsive family protein	0.9856	0.0872	0.171	0.3821	0.4313	0.3559	0.8919	0.0965	0.1381	0.2885	0.5226	0.335
255808_at	AT4G10280	similar to unknown protein [Arabidopsis thaliana] (T	0.2223	0.3053	0.3257	0.2896	0.2007	0.2331	0.694	0.0214	0.059	0.7612	0.0158	0.0401
255809_at	AT4G10300	similar to unknown protein [Arabidopsis thaliana] (T	0.8132	4.00E-04	0.032	-0.6235	0.0011	0.0293	0.1717	8.00E-04	0.0148	0.9924	2.00E-04	0.0075
255810_at	AT4G10140	similar to unknown protein [Arabidopsis thaliana] (T	0.1609	0.2653	0.3023	0.07953	0.5573	0.4073	0.4604	0.0153	0.0493	0.379	0.0288	0.0567
255811_at	AT4G10250	ATHSP22.0 (Arabidopsis thaliana heat shock protei	0.2631	0.7056	0.4946	1.0477	0.1812	0.2205	-0.1851	0.7893	0.46	0.5995	0.4072	0.2871
255812_at	AT4G10310	HKT1 (HIGH-AFFINITY K+ TRANSPORTER 1); so	4.27	0.0073	0.0572	-3.221	0.019	0.071	0.2816	0.756	0.4501	1.3307	0.191	0.1798
255813_at	AT4G19930	kelch repeat-containing F-box family protein	0.9488	0.2395	0.2874	1.726	0.066	0.1284	-0.1627	0.8245	0.471	0.6145	0.4218	0.2932
255814_at	AT4G19900	glyoxal oxidase-related	0.5682	0.631	0.4701	0.174	0.8814	0.5135	1.5515	0.2292	0.2291	1.1573	0.3499	0.2626
255815_at	AT4G19890	ATMGH3/MGH3 (MALE-GAMETE-SPECIFIC HIST	1.1423	0.3474	0.3486	0.1862	0.8707	0.5101	0.5987	0.6061	0.4001	-0.3574	0.7554	0.4152
255816_at	AT2G33470	GLTP1 (GLYCOLIPID TRANSFER PROTEIN 1); gl	0.401	0.0104	0.0646	0.3221	0.0216	0.0747	0.1942	0.0232	0.0617	0.1153	0.1008	0.1212
255817_at	AT2G33330	33 kDa secretory protein-related	-1.245	0.0013	0.0376	-1.0277	0.0027	0.0349	-0.4313	0.0502	0.0949	-0.214	0.241	0.2077
255818_at	AT2G33570	similar to unknown protein [Arabidopsis thaliana] (T	-1.3197	0.0193	0.0823	-1.6168	0.0097	0.0537	0.1268	0.4179	0.3243	-0.1703	0.2923	0.2348
255819_s_at	AT2G40590;AT2G40510	[AT2G40590, 40S ribosomal protein S26 (RPS26B)]	0.04006	0.7701	0.5147	0.9991	0.0015	0.0313	-0.1772	0.2388	0.2346	0.7819	0.0036	0.0196
255820_at	AT2G40580	protein kinase family protein	-3.2076	0.0097	0.0631	-0.2887	0.6972	0.458	-1.2231	0.1511	0.1796	1.6958	0.0699	0.0968
255821_at	AT2G40570	relative RNA phosphoribosyl transferase family pro	0.4183	0.1477	0.2236	0.05513	0.8249	0.4974	-0.4938	0.1019	0.1426	-0.8569	0.0214	0.0475
255822_at	AT2G40610	ATEXP

255890_at	AT1G17850	similar to rhodanese-like domain-containing protein	-0.31	0.373	0.3609	-0.5074	0.1763	0.2173	-0.6363	0.1089	0.1476	-0.8337	0.0544	0.0834
255891_at	AT1G17870	ATEGY3	-0.02698	0.9364	0.5613	-0.468	0.2146	0.2424	-0.5818	0.1409	0.172	-1.0229	0.0323	0.0606
255892_at	AT1G17910	wall-associated kinase, putative	0.1035	0.8895	0.5483	1.2957	0.1376	0.1889	-0.4763	0.5333	0.3725	0.7159	0.3639	0.2686
255893_at	AT1G17940	threonyl-tRNA synthetase, putative / threonine--tRN	-0.9099	0.4747	0.4096	-1.4262	0.2843	0.2834	0.7213	0.5059	0.3617	0.2051	0.8458	0.4416
255894_at	AT1G17980	nucleotidyltransferase family protein	0.2576	0.1937	0.2581	0.1179	0.5145	0.3904	-0.00201	0.9907	0.5154	-0.1417	0.4311	0.2973
255895_at	AT1G18020;AT1G17990	[AT1G18020, 12-oxophytodienoate reductase, puta	-0.3283	0.3119	0.3297	-0.3165	0.3273	0.3072	-1.0056	0.0024	0.0228	-0.9938	0.0025	0.0165
255896_at	AT1G17800	plastocyanin-like domain-containing protein	1.4557	0.2846	0.314	-0.1483	0.906	0.5204	0.9227	0.4776	0.3505	-0.6813	0.5944	0.3614
255897_at	no_match	DNA-binding homodomain-containing protein	1.1029	0.4518	0.399	-0.1337	0.34	0.3134	0.02147	0.8704	0.4842	-0.2151	0.1566	0.159
255898_at	AT1G17930	similar to unknown protein [Arabidopsis thaliana] (T	0.2062	0.4602	0.4031	0.6655	0.0579	0.1196	-0.2875	0.1611	0.1862	0.1718	0.3628	0.2682
255899_at	AT1G17970	zinc finger (C3HC4-type RING finger) family protein	-0.161	0.5384	0.4362	-0.3537	0.214	0.2419	-0.1542	0.5548	0.3808	-0.347	0.2212	0.1967
255900_at	AT1G17930	similar to unknown protein [Arabidopsis thaliana] (T	0.4642	0.2095	0.2678	0.3639	0.3065	0.2954	-0.4594	0.1073	0.1467	-0.5597	0.0653	0.0931
255901_at	AT1G17890	GER2; catalytic	0.5956	0.0305	0.1012	0.4904	0.054	0.1152	0.153	0.0619	0.1069	0.04775	0.4672	0.3128
255902_at	AT1G17880	nascent polypeptide-associated complex (NAC) dor	-0.1743	0.0786	0.1616	-0.00619	0.9376	0.5284	0.2782	0.02	0.0567	0.4463	0.0039	0.0201
255903_at	AT1G17960	MYB52 (myb domain protein 52); DNA binding / tra	-0.09908	0.8977	0.5505	-0.2381	0.7585	0.4777	0.8739	0.2747	0.2551	0.7348	0.3476	0.2614
255904_at	AT1G17860	trypsin and protease inhibitor family protein / Kunitz	-0.4831	0.0723	0.155	-0.4575	0.0832	0.145	0.8164	0.0149	0.0486	0.842	0.0134	0.0367
255905_at	AT1G17810	BETA-TIP (BETA-TONOPLAST INTRINSIC PROTE	-0.8464	0.2492	0.2932	-0.6556	0.3557	0.3207	-0.5791	0.4088	0.3203	-0.3883	0.57	0.3526
255906_at	AT1G17790	DNA-binding homodomain-containing protein	1.1029	0.4518	0.399	-0.1337	0.34	0.3134	0.02147	0.8704	0.4842	-0.2151	0.1566	0.159
255907_at	AT1G17920	HDG12 (HOMEODOMAIN GLABROUS12); transcri	-0.1819	0.4557	0.4008	0.2281	0.3594	0.3226	-0.6976	0.0341	0.0755	-0.2876	0.2621	0.2189
255908_s_at	AT1G18010;AT1G18000	[AT1G18010, similar to unknown protein [Arabidops	0.2508	0.0711	0.1537	0.3095	0.0394	0.0984	-0.331	0.0062	0.0326	-0.2724	0.0122	0.0349
255909_at	AT1G18040	AT;CDKD;3;CAK2AT1;CDKD1;3 (CYCLIN-DEPEN	-0.3791	0.071	0.1537	-0.6928	0.0111	0.0566	0.2555	0.1751	0.1954	-0.05813	0.727	0.4062
255910_at	AT1G18030	protein phosphatase 2C, putative / PP2C, putative	0.1725	0.301	0.3235	0.14	0.3902	0.3369	-0.5706	0.0172	0.0524	-0.6032	0.0143	0.0379
255911_at	AT1G66590	serine/threonine protein kinase family protein	0.1564	0.9504	0.6644	-1.2152	0.3385	0.3129	-0.8484	0.4556	0.3411	-1.9867	0.1255	0.1385
255912_at	AT1G66960	lupeol synthase, putative / 2,3-oxidosqualene-thetra	2.8155	0.0251	0.0919	3.7767	0.0094	0.0531	-1.3402	0.1546	0.1821	-0.379	0.6462	0.3794
255913_at	AT1G66980	protein kinase family protein / glycerophosphoryl di	0.8163	0.0016	0.0383	0.5205	0.0081	0.0501	-0.6854	4.00E-04	0.0147	-0.9812	1.00E-04	0.0061
255914_at	AT1G22250	similar to metal ion binding [Arabidopsis thaliana] (T	0.4092	0.7551	0.5101	1.3272	0.3395	0.3132	-2.0538	0.1688	0.191	-1.1358	0.4062	0.2866
255915_at	AT1G28620	protein kinase C-related	-0.6139	0.6044	0.461	-0.0867	0.9406	0.5293	0.7075	0.2506	0.2413	1.2347	0.0792	0.1042
255916_at	AT1G28550	peptidase	-0.7612	0.3659	0.3573	-1.2296	0.1752	0.2164	-0.06067	0.9092	0.4951	-0.5291	0.3495	0.2623
255917_at	AT1G28560	unknown protein	0.5856	0.5474	0.4399	-1.032	0.3118	0.2883	0.5384	0.5722	0.3875	-1.0792	0.2856	0.2312
255918_at	AT1G28570	transposable element gene	-0.1185	0.9162	0.5559	-0.5287	0.6435	0.4394	1.1951	0.3217	0.279	0.7849	0.4993	0.3257
255919_at	no_match	no_match	0.5112	0.6034	0.4606	-0.2031	0.8339	0.4999	-1.1886	0.2096	0.2176	-1.9029	0.0751	0.1009
255920_at	AT1G28590	DNA-binding protein-related	0.1564	0.9504	0.6525	-0.8299	0.4134	0.3476	1.6808	0.1421	0.173	0.7145	0.4763	0.3162
255921_at	AT1G22240	APUM8 (ARABIDOPSIS PUMILIO 8); RNA binding	0.9881	0.0107	0.0649	-0.0353	0.8795	0.513	0.3389	0.196	0.2092	-0.6845	0.0352	0.0635
255922_at	AT1G22210	trehalose-6-phosphate phosphatase, putative	0.5975	0.7086	0.4958	1.3639	0.4114	0.3467	-0.8394	0.6029	0.3992	-0.07303	0.9632	0.4741
255923_at	AT1G22190	SEC14 cytosolic factor family protein / phosphoglyc	0.06255	0.8208	0.5298	0.9113	0.0759	0.138	-0.9293	0.0195	0.0561	-0.1106	0.6765	0.3896
255924_at	AT1G22170	phosphoglycerate/bisphosphoglycerate mutase fam	-0.3255	0.3895	0.3696	-0.2373	0.5208	0.3925	-0.1226	0.7349	0.4432	-0.03443	0.9237	0.4638
255925_at	AT1G22200	similar to unknown protein [Arabidopsis thaliana] (T	0.3947	0.0034	0.0448	0.3944	0.0034	0.0374	-0.4146	0.0029	0.0244	-0.4149	0.0029	0.0175
255926_at	AT1G22190	AP2 domain-containing transcription factor, putative	0.6451	0.1301	0.2086	-0.3472	0.364	0.3248	-1.0387	0.0058	0.0318	-0.7409	0.0185	0.0437
255927_at	AT1G12630	DNA binding / transcription activator/ transcription fa	1.1629	0.0983	0.181	-0.9543	0.1528	0.2003	1.1728	0.0963	0.1379	-0.9443	0.1561	0.1589
255928_at	AT1G12640	membrane bound O-acyl transferase (MBOAT) fam	0.1751	0.3743	0.3617	-0.09636	0.6117	0.4274	-0.3348	0.1286	0.163	-0.6063	0.0258	0.0533
255929_at	AT1G12650	similar to unnamed protein product [Vitis vinifera] (G	0.1982	0.3188	0.3337	0.6618	0.0191	0.0712	-0.4312	0.0685	0.1136	0.03237	0.8616	0.4463
255930_at	no_match	no_match	0.3771	0.7688	0.5143	-0.1113	0.9305	0.5267	1.0012	0.4233	0.3268	0.5128	0.6719	0.388
255931_at	AT1G12710	ATPP2-A12 (PHLOEM PROTEIN 2-A12); carbohyd	0.1597	0.7382	0.5052	-0.3652	0.4585	0.3674	-0.7651	0.1514	0.18	-1.2899	0.0406	0.0696
255932_at	AT1G12720	transposable element gene	0.2916	0.731	0.5027	0.06833	0.9353	0.5279	-0.04196	0.9452	0.5045	-0.2652	0.6679	0.3867
255933_at	AT1G12750	thioredoxin family protein	-0.1773	0.4778	0.4109	-0.7834	0.0259	0.0806	-1.0817	0.0088	0.0377	-1.6878	0.0017	0.0147
255934_at	AT1G12740	CYP87A2 (cytochrome P450, family 87, subfamily A	-0.603	0.5962	0.4584	-2.0388	0.1239	0.1785	-0.2957	0.6444	0.4124	-1.7315	0.0433	0.0727
255935_at	AT1G12760	helicase domain-containing protein / peroxisomal	-0.07054	0.8445	0.5371	-0.3267	0.3374	0.3356	-0.06929	0.8472	0.4778	-0.3255	0.389	0.2795
255936_at	AT1G12680	PEPKR2 (PHOSPHOENOLPYRUVATE CARBOXY	-0.1035	0.5922	0.4568	-0.04205	0.8249	0.4974	0.08575	0.0556	0.1005	0.1472	0.0101	0.0314
255937_at	AT1G12610	DDF1 (DWARF AND DELAYED FLOWERING 1); D	-3.6897	0.0024	0.0421	-2.3742	0.0115	0.058	-0.4824	0.3945	0.3139	0.8331	0.1751	0.1703
255938_at	AT1G12620	pentatricopeptide (PPR) repeat-containing protein	0.4852	0.1156	0.1967	0.2828	0.3078	0.2962	0.001715	0.9947	0.5164	-0.2007	0.4538	0.3075
255939_at	AT1G12730	cell division cycle protein-related	1.7235	0.1016	0.1843	0.3423	0.6956	0.4573	-0.8228	0.3691	0.3024	-2.2041	0.0536	0.0827
255940_at	AT1G20380	prolyl oligopeptidase, putative / prolyl endopeptidas	-0.5487	0.1916	0.2566	-0.1276	0.7337	0.4693	0.04585	0.86	0.4811	0.467	0.128	0.1402
255941_at	AT1G20390	ATTMR17-1 (Arabidopsis thaliana transducase inser	1.8615	0.0055	0.052	2.2905	0.0026	0.0341	0.3594	0.0913	0.1336	0.7883	0.0083	0.0283
255942_at	AT1G22360	ATUGT85A2 (UDP-GLUCOSYL TRANSFERASE 8	0.1283	0.4239	0.3868	0.2608	0.1448	0.1943	-0.00541	0.9477	0.505	0.1271	0.1769	0.1713
255943_at	AT1G22370	ATUGT85A5 (UDP-GLUCOSYL TRANSFERASE 8	0.8435	0.0067	0.0553	1.203	0.0018	0.0325	-0.5063	0.0364	0.0784	-0.1467	0.4203	0.2926
255944_at	AT1G28600	transposable element gene	0.7042	0.3621	0.3555	1.5451	0.1062	0.1645	-0.03992	0.9597	0.5076	0.741	0.3753	0.2736
255945_at	AT1G28610	similar to glycine-rich protein [Arabidopsis thaliana]	-0.9599	0.4774	0.4107	0.07726	0.9528	0.5325	-0.6037	0.5448	0.3773	0.4335	0.6598	0.3841
255946_at	AT1G22020	SHM6 (serine hydroxymethyltransferase 6); glycine	-0.00718	0.9813	0.5724	0.09288	0.7626	0.4782	-0.06089	0.8201	0.4698	0.03916	0.8835	0.4525
255947_at	AT1G22040	kelch repeat-containing F-box family protein	0.3289	0.1208	0.2011	0.3454	0.108	0.1656	-0.6149	0.0192	0.0556	-0.5984	0.021	0.047
255948_at	AT1G22060	similar to F-box family protein [Arabidopsis thaliana]	0.2417	0.0152	0.0746	0.1918	0.032	0.0887	-1.1161	0	0.0092	-1.1661	0	0.0053
255949_at	AT1G22080	similar to binding [Arabidopsis thaliana] (TAIR:AT3G	-0.4913	0.5935	0.4575	-0.7449	0.4294	0.355	0.6164	0.5076	0.3624	0.3628	0.6909	0.3943
255950_at	AT1G22110	structural constituent of ribosome	-0.8167	0.4781	0.411	2.0307	0.1238	0.1785	-1.1042	0.3502	0.2933	1.7432	0.1705	0.1675
255951_at	AT1G22050	MUB6 (MEMBRANE-ANCHORED UBIQUITIN-FOL	-0.4788	0.0141	0.0725	-0.2373	0.1079	0.1656	0.1558	0.247	0.2393	0.3972	0.0259	0.0534
255952_at	AT1G22130	AGL104; DNA binding / transcription factor	0.3083	0.7718	0.5152	-0.2391	0.8216	0.4962	-1.3894	0.2344	0.2319	-1.9368	0.123	0.137
255953_at	AT1G22070	TGA3 (TGA1a-related gene 3); DNA binding / calme	1.1453	3.00E-04	0.0312	1.0864	3.00E-04	0.0249	0.1941	0.0083	0.0366	0.1153	0.045	0.0744
255954_at	AT1G22090	EMB2204 (EMBRYO DEFECTIVE 2204)	0.09097	0.9105	0.5542	1.6557	0.095	0.1553	-1.3403	0.1527	0.1807	0.2245	0.7825	0.4236
255955_at	AT1G22030	similar to unknown protein [Arabidopsis thaliana] (T	0.03282	0.923	0.5579	0.4335	0.2458	0.2615	-0.2152	0.5369	0.374	0.1854	0.5923	0.3606
255956_at	AT1G22015	DD46; transferase, transferring hexosyl groups	-0.7152	0.2451	0.2906	0.09059	0.8715	0.5104	-0.2956	0.6037	0.3995	0.5101	0.3866	0.2785
255957_at	AT1G22160	senescence-associated protein related	0.4025	0.1267	0.2058	0.1989	0.3957	0.3393	-0.6876	0.0303	0.0709	-0.8912	0.0131	0.0362
255958_at	AT1G22150	SULTR1;3 (sulfate transporter); sulfate transmembr	0.07581	0.9396	0.5623	0.5954	0.561	0.4088	-0.5843	0.568	0.386	-0.06467	0.9485	0.4705
255959_at	AT1G21980	ATPIP5K1 (ARABIDOPSIS THALIANA 1-PHOSPH	-0.4256	0.092	0.1759	-0.1369	0.5171	0.3913	-0.05778	0.7467	0.4471	0.2309	0.2388	0.2064
255960_at	AT1G22140	similar to unnamed protein product [Vitis vinifera] (G	-0.3655	0.0789	0.1618	-0.00977	0.953	0.5325	0.5575	0.0099	0.0398	0.9132	0.0016	0.0143
255961_at	AT1G22340	ATUGT85A7 (UDP-GLUCOSYL TRANSFERASE 8	-0.3936	0.6139	0.4641	0.7385	0.3632	0.3244	0.6597	0.4117	0.3216	1.7918	0.0677	0.0949
255962_at	AT1G22330	RNA binding	-1.0606	0.0488	0.1271	-1.079	0.0465	0.1069	0.1991	0.3161	0.2763	0.1807	0.3575	0.2658
255963_at	AT1G22310	MBD8 (methyl-CpG-binding domain 8)	0.1776	0.4106	0.3802	0.06536	0.7525	0.4759	-0.4826	0.0496	0.0942	-0.5949	0.0265	0.0539
255964_at	AT1G22275	ZYP1b	-2.1251	0.004	0.0467	2.2211	0.0034	0.0373	-2.192	0.001	0.0175	2.1541	0.0011	0.0123
255965_at	AT1G22290	14-3-3 protein GF14, putative (GRF10)	-0.8731	0.1795	0.2476	-0.7062	0.2591	0.2695	-0.2768	0.6336	0.409	-0.11	0.8478	0.4422
255966_at	AT1G22300	GRF10 (GENERAL REGULATORY FACTOR 10); p	0.1389	0.1776	0.2464	0.3145	0.0209	0.0737	0.5898	1.00E-04	0.012	0.7654	1.00E-04	0.0055
255967_at	AT1G22280	protein phosphatase 2C, putative / PP2C, putative	0.1842	0.621	0.4668	0.5731	0.1713	0.2137	-0.389	0.008	0.0359	-0.00013	0.9988	0.4827
255968_at	AT1G22270	identical to TRM112-like protein At1g22270 (Arabid	0.7579	0.0093	0.0621	0.5637	0.0249	0.0791	0.6531	0.0154	0.0494	0.4589	0.0464	0.0758
255969_at	AT1G22330	RNA binding	-1.3594	0.0386	0.1132	-1.5469	0.026	0.0806	0.4853	0.1665	0.1894	0.2978	0.3586	0.2663
255970_s_at	AT3G31540;AT3G43000	[AT3G31540, transposable element gene];[AT3G43	-0.6129	0.6519	0.4766	0.8014	0.559	0.4079	-1.759	0.2349	0.2321	-0.3447	0.7978	0.4282
255971_at	AT3G29515	transposable element gene	0.8928	0.2611	0.3003	-1.6748	0.0702	0.1326	2.8367	0.0142	0.0475	0.2691	0.7136	0.4022
255972_at	AT5G25615;AT3G29510	[AT5G25615, transposable element gene];[AT3G29	-1.4363	0.1451	0.2213	-0.04179	0.9606	0.5343	-1.8798	0.0773	0.1214	-0.4852	0.5746	0.3541
255973_at	AT3G32400	formin homology 2 domain-containing protein / FH2	-0.02866	0.8888	0.5481	-0.1329	0.5278	0.3953	-0.1489	0.4822	0.352	-0.2531	0.2587	0.2173
255974_at	AT3G31023	transposable element gene	-0.3996	0.6579	0.4783	-1.3017	0.1948	0.2292	0.8267	0.3791	0.3073	-0.07538	0.9325	0.4664
255975_at	no_match	no_match	-0.4927	0.6589	0.4788	-1.8024	0.1566	0.2032	1.768	0.1628	0.187	0.4583	0.6808	0.3908
255976_at	AT1G22010	unknown protein	-0.1395	0.8937	0.5497	-0.6012	0.5727	0.4129	0.8605	0.3885	0.3115	0.3987	0.6775	0.3899
255977_at	AT1G34030	40S ribosomal protein S18 (RPS18B)	0.2082	0.1624	0.2357	0.3133	0.0618	0.1236	-0.03138	0.8094	0.4663	0.07365	0.5779	0.3552
255978_at	AT1G34010	similar to unknown protein [Arabidopsis thaliana] (T	-0.6361	0.0183	0.0804	-0.1497	0.4161	0.3488	-0.8176	5.00E-04	0.0155	-0.3311	0.0149	0.0388
255979_at	AT1G33980	ATUPF3/UPF3; nucleotide binding	0.09411	0.3243	0.3368	-0.00764	0.9317	0.5269	-0.2519	0.0082	0.0363	-0.3536	0.0024	0.0162
255980_at	AT1G33970	avirulence-responsive protein, putative / avirulence	1.4612	0.0205	0.0842	1.7641	0.0109	0.056	-0.01247	0.9322	0.5013	0.2904	0.1027	0.1224
255981_at	AT1G34020	transporter-related	0.205	0.0378	0.1121	0.1462	0.0949	0.1552	0.1258	0.0588	0.1039	0.06699	0.2354	0.2047
255982_at	AT1G34000	OHP2 (ONE-HELIX PROTEIN 2)	-0.6265	0.0044	0.0482	-0.8776	0.0013	0.0305	0.7187	5.00E-04	0.0148	0.4676	0.0024	0.0164
255983_at	AT1G33990	hydrolase, alpha/beta fold family protein	0.6364	0.0093	0.0622	0.8511	0.0033	0.0371	-0.3944	0.0343	0.0758	-0.1797	0.2239	0.1982
255984_at	AT1G34120	IP5PI (INOSITOL POLYPHOSPHATE 5-PHOSPHA	0.4399	0.078	0.161	0.1057	0.6015	0.4241	-0.02347	0.8778	0.4861	-0.3577	0.0671	0.0944
255985_at	AT1G34150	tRNA pseudouridine synthase family protein	0.2955	0.3247	0.3371	0.522	0.1185	0.1741	-0.3825	0.1698	0.1917	-0.1559	0.5329	0.339
255986_s_at	AT5G35010	transposable element gene	-0.7425	0.5518	0.4419	-1.9815	0.1584	0.2047	0.2611	0.8307	0.473	-0.9779	0.4409	0.3018
255987_s_at	AT5G35050	pseudogene, hypothetical protein, predicted protein	0.385	0.7061	0.4948	0.5524	0.5922	0.4204	0.8239	0.4349	0.3318	0.9913	0.3557	0.2651
255988_at	no_match	no_match	-0.3542	0.3919	0.371	0.3364	0.414	0.3478	-0.05624	0.8146	0.4681	0.6344	0.0476	0.077
255989_at	no_match	no_match	1.2311	0.1825	0.2501	-0.2845	0.7286	0.4683	1.0432	0.244	0.2374	-0.4724	0.5699	0.3526
255990_at	AT1G29870	tRNA synthetase class II (G, H, P and S) family pro	0.727	0.4748	0.4096	0.8821	0.3932	0.3383	-0.2567	0.7825	0.4581	-0.1016	0.9126	0.4607
255991_at	AT1G29820	similar to unknown protein [Arabidopsis thaliana] (T	-0.3429	0.1789	0.2473	-0.2123	0.3706	0.3278	0.421	0.1163	0.1534	0.5517	0.0589	0.0875
255992_at	AT1G29790	similar to [ARABIDOPSIS THALIANA RAS ASSOC	0.1958	0.0696	0.1521	0.3835	0.0085	0.0509	-0.5855	0.0018	0.0206	-0.3979	0.0075	0.027
255993_at	AT1G29770	NLI interacting factor (NIF) family protein	0.5208	0.7458	0.5077	0.1424	0.9289	0.5265	-0.4654	0.7042	0.4328	-0.8439	0.5005	0.3261
255994_at	AT1G29760	similar to unknown protein [Arabidopsis thaliana] (T	0.2491	0.0381	0.1124	0.2445	0.0403	0.0995	-0.2545	0.017	0.052	-0.2591	0.016	0.0494
255995_at	AT1G29750	RKF1 (RECEPTOR-LIKE KINASE IN FLOWERS 1	0.06193	0.7492	0.5085	0.03359	0.8617	0.5076	-0.1425	0.3848	0.31	-0.1709	0.3074	0.2422
255996_s_at	AT1G29740;AT1G29730	[AT1G29740, leucine-rich repeat family protein / pc	-0.3258	0.6975	0.4918	-1.6316	0.1045	0.1634	-0.6125	0.476	0.3499	-1.9183	0.0697	0.0967
255997_s_at	AT1G29910;AT1G29920;A	[AT1G29910, CAB3 (CHLOROPHYLL A/B BINDIN	-0.3804	0.1108	0.193	-0.4484	0.0738	0.1364	-0.1685	0.0656	0.1106	-0.2365	0.0242	0.051
255998_at	AT1G29780	NLI interacting factor (NIF) family protein	2.1323	0.0643	0.1453	2.4176	0.0453	0.1055	1.5904	0.1317	0.1651	-2.9595	0.0245	0.0515
255999_at	AT1G29860	WRKY71 (WRKY DNA-binding protein 71); transcri	1.9823	0.1663	0.2385	0.7007	0.5824	0.4172	0.4601	0.6984	0.4307	-0.8215	0.4983	0.3253
256000_at	AT1G29880	glycyl-tRNA synthetase / glycine--tRNA ligase	0.05144	0.8339	0.5336	-0.1367	0.5842	0.4178	0.1643	0.304	0.2707	-0.02383	0.8726	0.4492
256001_at	AT1G29850	double-stranded DNA-binding protein	-0.14	0.3577	0.3533	0.394	0.0431	0.1031	0.3944	0.0147	0.0483	0.9284	6.00E-04	0.0103
256002_at	AT1G29900	CARB (CARBAMOYL PHOSPHATE SYNTHETASE	0.4123	0.0784	0.1613	0.4373	0.0672	0.1298	-1.0249	0.0012	0.0187	-1	0.0013	0.0133
256003_at	AT3G31430	similar to unknown protein [Arabidopsis thaliana] (T	0.01598	0.9802	0.5721	-0.995	0.1755	0.2166	-0.6319	0.2144	0.2204	-1.6426	0.0185	0.0437
256004_at	AT3G31460	transposable element gene	-0.3933	0.8072	0.526	0.5613	0.7287	0.4683	-1.229	0.461	0.3436	-0.2745	0.8645	0.4469
256005_at	AT3G34080	transposable element gene	1.8447	0.114	0.1956	-1.0789	0.3036	0.2934	2.3406	0.0628	0.1077	-0.5831	0.5586	0.3483
256006_at	AT3G34070	similar to unknown protein [Arabidopsis thaliana] (T	0.8959	0.3617	0.3553	-0.3772	0.6872	0.4546	-1.7489	0.0518	0.0964	-1.2302	0.126	0.1389
256007_at	AT3G34065	SAMC2 (S-adenosylmethionine carrier 2); binding	-0.6523	0.0593	0.1393	-0.5676	0.0854	0.1471	-0.7645	0.0315	0.0721	-0.6799	0.0447	0.0741
256008_s_at	AT3G34040;AT1G34060	[AT1G34040, allinase family protein];[AT1G34060,	-0.7994	0.1352	0.2134	-0.9058	0.1017	0.1609	-0.1794	0.2174	0.2221	-0.2859	0.0802	0.1053
256009_at	AT3G34050	AP2 domain-containing transcription factor, putative	0.3895	0.0595	0.1395	1.1462	0.0927	0.1537	0.1875	0.4441	0.3399	0.4012	0.1437	0.1507
256010_at	AT1G19220	ARF19 (AUXIN RESPONSE FACTOR 11); transcri	0.2042	0.0898	0.1735	0.09767	0.3466	0.3163	-0.336	0.0215	0.059	-0.4425	0.0085	0.0286
256011_at	AT1G19230	respiratory burst oxidase protein E (RbohE) / NADP	0.07095	0.938	0.5618	-0.9866	0.3135	0.2992	1.2286	0.205	0.2148	0.1711	0.8435	0.441
256012_at	AT1G19250	FMO1 (FLAVIN-DEPENDENT MONOOXYGENASE	2.1177	0.0525	0.1315	4.2169	0.0056	0.0434	-0.1295	0.8756	0.4856	1.9698	0.0641	0.0921
256013_at	AT1G19270	ubiquitin interaction motif-containing protein / LIM s	0.7818	0.0138	0.0719	1.1228	0.0038	0.039	-0.4408	0.0772	0.1213	-0.09984	0.6205	0.3705
256014_at	AT1G19200	senescence-associated protein-related	-1.2302	0.212	0.2697	-0.5666	0.5319	0.3969	-0.9292	0.226	0.2271	-0.2656	0.7037	0.3986
256015_at	AT1G19190	LHCA4 (Photosystem I light harvesting complex ger	-1.209	1.00E-04	0.0312	-1.6152	0	0.0249	0.2564	0.0073	0.0344	-0.1108	0.1317	0.1428
256016_at	AT1G19240	similar to unnamed protein product [Vitis vinifera] (G	0.7668	0.0012	0.036	1.1423	3.00E-04	0.0249	-0.1651	0.1498	0.1788	0.2103	0.0861	0.1098
256017_at	AT1G19180	JAZ1/TIFY10A (JASMONATE-ZIM-DOMAIN PROT	-0.7937	0.0184	0.0806	-0.6263	0.0386	0.0973	0.203	0.3216	0.279	0.3704	0.1082	0.1263
256018_at	AT5G66300	HO4 (HEME OXYGENASE 4); heme oxygenase (de	0.7154	0.1477	0.2236	0.713	0.1487	0.1973	0.05949	0.8888	0.4894	0.05706	0.8933	0.4553
256019_at	no_match	no_match	0.3452	0.7262	0.5013	-0.2371	0.8091	0.4927	0.5806	0.5618	0.3833	-0.00174	0.9986	0.4826
256020_at	AT1G58290	HEMA1; glutamyl-tRNA reductase	-0.9292	0.0079	0.0585	-0.8489	0.0109	0.056	-1.1076	0.0042	0.0279	-1.0273	0.0055	0.0232
256021_at	AT1G58270	ZW9	-1.4406	0.014	0.0723	-1.3622	0.0169	0.0675	0.2237	0.4481	0.3377	0.3021	0.32	0.2483
256022_at	AT1G58360	AAP1 (AMINO ACID PERMEASE 1); amino acid tra	0.3308	0.0545	0.1341	-0.0226	0.863	0.5079	-0.08258	0.38	0.3078	-0.

256090_at	no_match	no_match	-0.7639	0.0488	0.1271	-0.4886	0.1478	0.1965	-0.06117	0.8265	0.4717	0.2142	0.4587	0.3095
256091_at	AT1G20693	HMGB2 (HIGH MOBILITY GROUP B 2); transcriptio	0.5191	0.1925	0.2572	0.6194	0.1351	0.1869	0.4649	0.115	0.1524	0.5652	0.0711	0.0977
256092_at	AT1G20696	HMGB3 (HIGH MOBILITY GROUP B 3); transcriptio	0.04358	0.8413	0.536	0.5107	0.0665	0.1291	0.6565	1.00E-04	0.0118	1.1236	0	0.0047
256093_at	AT1G20823	zinc finger (C3HC4-type RING finger) family protein	-1.9992	0.0028	0.0431	-2.0742	0.0025	0.0339	0.6595	0.0074	0.0348	0.5845	0.0113	0.0334
256094_at	AT1G20780	armadillo/beta-catenin repeat protein-related / U-bo	-0.6884	0.3903	0.37	-0.5368	0.4946	0.3824	-3.1885	0.0013	0.0191	-3.0369	0.0016	0.0139
256095_at	AT1G13630	pentatricopeptide (PPR) repeat-containing protein	-0.05259	0.9629	0.568	3.234	0.0382	0.0967	-2.8541	0.0105	0.0407	0.4324	0.5298	0.3379
256096_at	AT1G13650	similar to 18S pre-ribosomal assembly protein gar2	-3.2995	0.0013	0.0366	-3.3595	0.0012	0.0296	-0.59	0.0167	0.0515	-0.65	0.0121	0.0346
256097_at	AT1G13670	unknown protein	0.01668	0.9885	0.5741	0.3762	0.7466	0.4737	0.7901	0.336	0.2864	1.1496	0.1871	0.1777
256098_at	AT1G13700	glucosamine/galactosamine-6-phosphate isomerase	1.1262	0.0258	0.093	1.0443	0.0326	0.0894	0.01039	0.9508	0.5057	-0.07148	0.6751	0.389
256099_at	AT1G13710	CYP78A5 (cytochrome P450, family 78, subfamily A	0.3485	0.6885	0.4887	0.9386	0.3101	0.2974	0.08911	0.9175	0.4971	0.6792	0.448	0.3052
256100_at	AT1G13750	calcineurin-like phosphoesterase family protein	0.8642	0.0138	0.0719	0.735	0.0234	0.0771	0.3484	0.0927	0.1349	0.2192	0.2387	0.2064
256101_at	no_match	no_match	0.08611	0.9092	0.5538	-2.2008	0.0361	0.0939	0.1142	0.8799	0.4866	-2.1726	0.0376	0.0662
256102_at	AT1G13680	phospholipase C	-1.3154	0.1315	0.2099	-0.517	0.4984	0.3839	-0.8165	0.2408	0.2355	-0.018	0.9773	0.4775
256103_at	AT1G13540	similar to unknown protein [Arabidopsis thaliana] (T	-1.1062	0.1375	0.2154	-3.7224	0.0034	0.0371	1.778	0.0408	0.0839	-0.8382	0.233	0.2033
256104_at	AT1G16980	ATTPS2 (Arabidopsis thaliana trehalose-phosphata	-1.1427	0.4091	0.3795	0.03305	0.98	0.5393	-0.2449	0.8531	0.4793	0.9309	0.4947	0.3239
256105_at	AT1G16910	similar to unknown protein [Arabidopsis thaliana] (T	0.7453	0.2941	0.3198	0.1721	0.7944	0.4875	0.1652	0.8024	0.4643	-0.408	0.545	0.3429
256106_at	AT1G16870	mitochondrial 28S ribosomal protein S29-related	0.2485	0.123	0.2034	0.2507	0.1207	0.176	-0.3611	0.0063	0.0328	-0.3589	0.0064	0.0249
256107_at	AT1G16830	pentatricopeptide (PPR) repeat-containing protein	0.8743	0.1455	0.2217	0.09647	0.8519	0.505	-0.1895	0.4595	0.3428	-0.9673	0.014	0.0376
256108_at	AT1G16940	F-box family protein	0.4712	0.1912	0.2562	-0.0703	0.8262	0.4978	0.01169	0.9708	0.5102	-0.5298	0.152	0.1561
256109_at	AT1G16960	unknown protein	0.06241	0.9369	0.5614	0.2732	0.0488	0.1097	-1.3234	0.1203	0.1564	0.6874	0.3642	0.2687
256110_at	AT1G16900	sugar binding / transferase, transferring glycosyl gr	1.1028	1.00E-04	0.0312	1.037	1.00E-04	0.0249	-0.06681	0.3786	0.3071	-0.1326	0.1211	0.1358
256111_at	AT1G16610	vacuolar ATP synthase catalytic subunit-related / V	-0.2284	0.7806	0.618	-0.3063	0.7099	0.462	-1.0596	0.2391	0.2348	-1.1374	0.212	0.1919
256112_at	AT1G16920	RAB11 (ARABIDOPSIS RAB GTPASE HOMOLOG	-0.1496	0.683	0.4868	-0.2219	0.55	0.4048	-0.4716	0.0082	0.0362	-0.5439	0.0049	0.022
256113_at	AT1G16810	similar to CGI-144-like protein [Solanum lycopersico	0.139	0.2837	0.3137	0.4424	0.017	0.0677	0.6691	0.004	0.0274	0.9725	0.001	0.0121
256114_at	AT1G16860	unknown protein	-1.3183	0.0244	0.0909	-0.4235	0.3211	0.3036	0.2479	0.4965	0.3584	1.1427	0.0262	0.0536
256115_at	AT1G16880	uridylyltransferase-related	-0.6821	0.0015	0.038	-0.703	0.0013	0.0309	0.165	0.1326	0.1657	0.144	0.1753	0.1703
256116_at	AT1G16858,AT1G16860	[AT1G16858, CPuORF55 (Conserved peptide upstr	-0.8614	0.0308	0.1019	-0.697	0.0573	0.119	-0.2753	0.1176	0.1544	-0.111	0.4677	0.3129
256117_at	AT1G16840	similar to unknown protein [Arabidopsis thaliana] (T	0.2276	0.2451	0.2908	0.2268	0.2465	0.2618	0.3596	0.0153	0.0492	0.3586	0.0154	0.0395
256118_at	AT1G16970	ATKU70/KU70 (ARABIDOPSIS THALIANA KU70 H	0.2062	0.2912	0.318	0.2714	0.1851	0.2231	-0.1376	0.3895	0.3119	-0.07243	0.6384	0.3766
256119_at	AT1G18070	EF-1-alpha-related GTP-binding protein, putative	0.1203	0.2994	0.3226	0.1097	0.3386	0.313	-0.1312	0.0128	0.0449	-0.1419	0.0098	0.0309
256120_at	AT1G18110	tRNA synthetase-related / tRNA ligase-related	0.7418	0.6881	0.4886	-0.5112	0.7809	0.4838	1.1347	0.545	0.3774	-0.1183	0.9484	0.4705
256121_at	AT1G18160	protein kinase family protein	0.5337	0.0088	0.0609	0.5485	0.008	0.0499	-0.5781	0.0067	0.0335	-0.5633	0.0073	0.0266
256122_at	AT1G18180	oxidoreductase, acting on the CH-CH group of donc	-0.7238	0.2638	0.3018	-0.5416	0.3862	0.3348	-1.0313	0.1379	0.1695	-0.8491	0.2023	0.1865
256123_at	AT1G18190	GC2 (GOLGIN CANDIDATE 2)	-0.123	0.4531	0.3996	-0.3707	0.0666	0.1292	0.3092	0.0954	0.1371	0.06153	0.6876	0.393
256124_at	AT1G18220	ATPUP9 (Arabidopsis thaliana purine permease 9)	-0.8127	0.3752	0.362	-0.7354	0.4179	0.3497	-0.3919	0.6525	0.4155	-0.3147	0.7164	0.403
256125_at	AT1G18250	ATLP-1 (Arabidopsis thaumatin-like protein 1)	0.5753	0.2171	0.2733	0.05028	0.9044	0.5199	0.7389	0.053	0.0977	0.2139	0.4751	0.3157
256126_at	AT1G18050	SWAP (Suppressor-of-White-APricot)/surp domain-	0.5589	0.401	0.5758	-0.6121	0.362	0.3239	-0.2418	0.7055	0.4332	-1.4127	0.0766	0.1021
256127_at	no_match	no_match	-0.3896	0.6506	0.4765	0.4753	0.5832	0.4174	-0.9704	0.2904	0.2638	-0.1055	0.9011	0.4576
256128_at	AT1G18140	LAC1 (Laccase 1); copper ion binding / oxidoreduct	0.3694	0.7268	0.5015	-0.4558	0.6678	0.4477	-0.451	0.671	0.4214	-1.2762	0.2651	0.2203
256129_at	AT1G18080	calcium binding protein, putative	0.03464	0.8839	0.5471	0.3394	0.2063	0.2362	0.933	0.0046	0.0289	1.2375	0.0016	0.0142
256130_at	AT1G18170	immunophilin / FKBP-type peptidyl-prolyl cis-trans i	-0.9124	0.0087	0.0606	-0.9945	0.0064	0.0457	-0.00447	0.9718	0.5104	-0.08656	0.5069	0.3285
256131_at	AT1G13600	ATBZIP58 (ARABIDOPSIS THALIANA BASIC LEU	0.2644	0.7486	0.5084	1.8278	0.0765	0.1385	0.5131	0.4958	0.3581	2.0765	0.0388	0.0678
256132_at	AT1G13610	similar to unknown protein [Arabidopsis thaliana] (T	0.5786	0.5203	0.4291	-0.3564	0.6889	0.4545	-0.4755	0.5938	0.3961	-1.4106	0.1613	0.162
256133_at	AT1G13570	F-box family protein	0.5269	0.057	0.1369	0.3448	0.1579	0.2043	-0.364	0.0749	0.1192	-0.5461	0.0229	0.0494
256134_at	AT1G13560	AAPT1 (AMINOALCOHOLPHOSPHOTRANSFERA	-0.3544	0.0748	0.1572	-0.3132	0.1017	0.1609	-0.4988	0.028	0.0681	-0.4576	0.0365	0.065
256135_at	AT1G13530	GC2 (GOLGIN CANDIDATE 2)	1.2894	0.0182	0.0249	0.1736	0.8358	0.5004	0.02952	0.9718	0.5104	-1.0663	0.246	0.2101
256136_s_at	AT5G13205,AT1G58140,A	[AT5G13205, transposable element gene];[AT1G58	1.4668	0.4534	0.3997	0.3197	0.8653	0.5086	-0.172	0.9272	0.4999	-1.3191	0.4971	0.3247
256137_at	AT1G48690	auxin-responsive GH3 family protein	-0.4929	0.5795	0.4521	-0.1723	0.8436	0.5027	-0.4021	0.649	0.4142	-0.08149	0.9255	0.4643
256138_at	AT1G48670	auxin-responsive GH3 family protein	1.062	0.2838	0.3137	0.1675	0.8548	0.5059	1.3524	0.1826	0.2007	0.488	0.6001	0.3634
256139_at	AT1G48660	auxin-responsive GH3 family protein	0.8484	0.5402	0.4368	-1.3114	0.3595	0.3226	-0.4754	0.7268	0.4408	-2.6353	0.1063	0.1249
256140_at	AT1G48650	helicase domain-containing protein	-0.2107	0.5009	0.4209	-0.4011	0.2321	0.2529	-1.2167	0.0068	0.0337	-1.4072	0.004	0.0204
256141_at	AT1G48640	lysine and histidine specific transporter, putative	-1.2429	0.3598	0.3545	-0.5215	0.6869	0.4545	-0.474	0.7136	0.436	0.2473	0.8471	0.442
256142_at	AT1G48790	mov34 family protein	0.1461	0.3233	0.3362	0.2974	0.0837	0.1455	-0.1785	0.241	0.2356	-0.02718	0.8444	0.4412
256143_at	AT1G48830	40S ribosomal protein S7 (RPS7A)	0.1372	0.2211	0.2758	0.3023	0.0332	0.0903	0.3847	0.0153	0.0493	0.5497	0.0044	0.021
256144_at	AT1G48630	guanine nucleotide-binding family protein / activatec	-0.2545	0.5238	0.4306	-0.2672	0.5044	0.3864	-0.2063	0.204	0.2142	-0.2191	0.1826	0.175
256145_at	AT1G48750	protease inhibitor/seed storage/lipid transfer protein	0.2553	0.0812	0.1647	0.5602	0.007	0.0474	0.9408	0	0.0062	1.2457	0	0.0033
256146_at	AT1G48760	DELTA-ADR (DELTA-ADAPTIN); clathrin binding	0.5072	0.0103	0.0644	0.1206	0.3388	0.3131	-0.00754	0.9491	0.5053	-0.3941	0.0239	0.0507
256147_at	AT1G55080	similar to unknown protein [Arabidopsis thaliana] (T	0.5765	0.0029	0.0435	0.264	0.0415	0.1011	0.8732	6.00E-04	0.0158	0.5606	0.0033	0.0186
256148_at	AT1G55090	carbon-nitrogen hydrolase family protein	-0.1174	0.6654	0.4811	-0.04604	0.8638	0.5081	-1.0706	0.0103	0.0403	-0.9993	0.013	0.0362
256149_at	AT1G55110	ATIDD7 (ARABIDOPSIS THALIANA INDETERMIN	0.4578	0.1305	0.2089	0.3978	0.1743	0.2156	-0.2994	0.0847	0.1282	-0.3593	0.052	0.0813
256150_at	AT1G55120	ATFRUCT5 (BETA-FRUCTOFURANOSIDASE 5);	0.9938	0.003	0.0436	-0.3388	0.0933	0.1539	-0.3461	0.0885	0.1314	0.3089	0.1161	0.1321
256151_at	AT1G55130	endomembrane protein 70, putative	0.04352	0.6191	0.4662	-0.3669	0.0105	0.0554	-0.1431	0.1516	0.1801	-0.5535	0.0024	0.0162
256152_at	AT1G55150	DEAD box RNA helicase, putative (RH20)	0.4276	0.005	0.0504	0.457	0.0039	0.0391	0.01346	0.7409	0.445	0.04287	0.3221	0.2493
256153_at	AT1G55060	UBQ12 (UBIQUITIN 12)	-0.3277	0.6162	0.4649	0.2658	0.6825	0.453	-1.3695	0.0859	0.1292	-0.776	0.2681	0.2218
256154_at	AT3G08490	similar to unknown protein [Arabidopsis thaliana] (T	-0.9199	0.3364	0.3434	-2.157	0.0627	0.1244	0.3678	0.685	0.4261	-0.8693	0.3606	0.2672
256155_at	AT3G08500	MYB83 (myb domain protein 83); DNA binding / tra	0.6372	0.586	0.4547	0.9074	0.447	0.3625	0.5543	0.6107	0.4014	0.8245	0.4582	0.3093
256156_at	AT3G08510	ATPLC2 (PHOSPHOLIPASE C 2); phosphodiester d	0.1855	0.1158	0.1968	0.3752	0.0155	0.065	-0.1253	0.2477	0.2397	0.06449	0.5247	0.3357
256157_at	AT1G13580	LAG13 (LAG1 LONGEVITY ASSURANCE HOMOL	-0.5806	0.0917	0.1757	-0.9215	0.0247	0.0789	-0.3448	0.1386	0.1702	-0.6858	0.0214	0.0475
256158_at	AT1G13590	ATPSK1 (PHYTOSULFOKINE 1 PRECURSOR); gr	-0.00758	0.9868	0.5735	0.1098	0.8112	0.4934	-0.1334	0.668	0.4206	-0.01605	0.9583	0.4731
256159_at	AT1G30135	JAZ8/TIFY5A (JASMONATE-ZIM-DOMAIN PROTE	-1.7261	0.0065	0.0549	-1.0552	0.0335	0.0906	0.904	0.0528	0.0974	1.575	0.009	0.0296
256160_at	AT1G30120	PDH-E1 BETA (PYRUVATE DEHYDROGENASE E	-0.4532	0.0834	0.1671	-0.622	0.0345	0.0918	-0.08464	0.6902	0.4279	-0.2535	0.2685	0.222
256161_at	AT1G30090	kelch repeat-containing F-box family protein	0.352	0.0321	0.1037	0.3613	0.0296	0.0855	-0.06633	0.4623	0.3442	-0.05705	0.5233	0.3352
256162_at	AT1G55390	DC1 domain-containing protein	-0.4745	0.5604	0.445	-1.1108	0.2118	0.2408	0.986	0.2488	0.2403	0.3497	0.6575	0.3833
256163_at	AT1G48820	terpene synthase/cyclase family protein	2.1356	0.2025	0.264	0.8006	0.5987	0.4229	1.0727	0.487	0.3542	-0.2623	0.8607	0.4461
256164_at	AT1G48800	terpene synthase/cyclase family protein	0.3042	0.8425	0.5363	-0.8614	0.5806	0.4165	0.3679	0.8103	0.4667	-0.7976	0.6079	0.366
256165_at	AT1G48780	similar to unknown protein [Arabidopsis thaliana] (T	-0.9297	0.1452	0.2215	-0.1878	0.7337	0.4693	-1.3328	0.0373	0.0797	-0.591	0.2452	0.2098
256166_at	AT1G36920	similar to unknown protein [Arabidopsis thaliana] (T	0.09954	0.955	0.566	-0.6881	0.6993	0.4587	0.1215	0.9138	0.4961	-0.6662	0.5615	0.3495
256167_at	AT1G36830	transposable element gene	-0.3811	0.6025	0.4604	-1.789	0.057	0.1187	1.5184	0.0877	0.1307	0.1104	0.878	0.4508
256168_at	AT1G51805	leucine-rich repeat protein kinase, putative	-0.7512	0.0181	0.0804	-0.788	0.0155	0.065	0.01373	0.9294	0.5004	-0.02316	0.8813	0.4518
256169_at	AT1G51800	leucine-rich repeat protein kinase, putative	0.9187	0.0619	0.1429	1.1768	0.0301	0.0863	-0.1572	0.6672	0.4203	0.1009	0.781	0.4232
256170_at	AT1G51790	kinase	1.1381	0.0417	0.1176	0.7926	0.1085	0.1661	-0.04248	0.8896	0.4896	-0.388	0.2482	0.2115
256171_s_at	AT1G51750,AT3G14517	[AT1G51750, transposable element gene];[AT3G14	2.4394	0.0072	0.0571	-1.4104	0.0431	0.1031	3.115	0.003	0.0248	-0.7347	0.2024	0.1866
256172_at	no_match	no_match	-0.5414	0.0641	0.1449	-0.223	0.3547	0.3203	-0.2072	0.3864	0.3105	0.1112	0.6296	0.3736
256173_at	AT1G51730	RWD domain-containing protein	0.5176	0.0331	0.1054	0.8319	0.0068	0.0467	-0.4414	0.0032	0.0252	-0.1271	0.1432	0.1502
256174_at	AT1G51720	glutamate dehydrogenase, putative	0.0594	0.7674	0.5138	0.2509	0.2521	0.2653	-0.1294	0.4067	0.3193	0.06204	0.68	0.3905
256175_at	AT1G51670	similar to unknown protein [Arabidopsis thaliana] (T	-0.04734	0.9705	0.5701	0.8481	0.5192	0.3921	-2.0452	0.0927	0.1348	-1.1498	0.2839	0.2303
256176_at	AT1G51640	ATEXO70G2 (exocyst subunit EXO70 family protein	-0.126	0.9366	0.5614	0.8438	0.601	0.4239	0.3422	0.8294	0.4726	1.3119	0.4277	0.2958
256177_at	AT1G51620	protein kinase family protein	0.3205	0.6284	0.4691	0.7929	0.2651	0.2726	-0.4412	0.3453	0.2908	0.03124	0.9433	0.4692
256178_s_at	AT1G51760,AT1G51780	[AT1G51760, IAR3 (IAA-ALANINE RESISTANT 3);	-0.2961	0.623	0.4675	-1.4058	0.065	0.1274	1.6633	0.0012	0.0188	0.5536	0.0539	0.0829
256179_at	AT1G51710	UBP6 (UBIQUITIN-SPECIFIC PROTEASE 6); ubiq	0.6506	8.00E-04	0.0344	0.5605	0.0014	0.0313	-0.07126	0.3762	0.3058	-0.1614	0.0874	0.1108
256180_at	AT1G51810	kinase	-2.2783	0.0609	0.1415	-1.3335	0.2045	0.2358	0.3064	0.7149	0.4365	1.2511	0.1845	0.176
256181_at	AT1G51820	leucine-rich repeat protein kinase, putative	-0.6	0.4	0.3753	-0.6819	0.3451	0.3157	-0.162	0.7603	0.4513	-0.2439	0.6486	0.3803
256182_at	AT1G51740	SYP81 (SYNTAXIN 81); protein binding	0.07606	0.6645	0.4808	-0.1956	0.2955	0.2895	0.3432	0.0746	0.1189	0.07152	0.6436	0.3784
256183_at	AT1G51660	ATMKK4 (MITOGEN-ACTIVATED PROTEIN KINA	0.7726	0.0463	0.1237	0.7641	0.0478	0.1085	0.1626	0.4142	0.3227	0.1541	0.437	0.3001
256184_at	AT1G51650	ATP synthase epsilon chain, mitochondrial	0.01312	0.9327	0.5604	0.1076	0.5017	0.3853	0.5363	0.0213	0.0587	0.6308	0.0124	0.0352
256185_at	AT1G51700	ADOF1 (Arabidopsis dof zinc finger protein 1); DNA	-0.7769	0.0086	0.0605	-0.7084	0.0119	0.0586	0.422	0.0217	0.0594	0.4905	0.0132	0.0364
256186_at	AT1G51680	4CL1 (4-COUMARATE:COA LIGASE 1); 4-coumar	-0.489	0.2732	0.3073	-0.4697	0.2898	0.2864	-0.2433	0.2333	0.2313	-0.224	0.266	0.2208
256187_at	AT1G51690	ATB ALPHA (protein phosphatase 2A 55 kDa regul	0.1294	0.4245	0.387	-0.144	0.3787	0.3313	-0.2884	0.1187	0.1551	-0.5617	0.0182	0.0433
256188_at	AT1G30160	similar to unknown protein [Arabidopsis thaliana] (T	0.2142	0.0584	0.1386	0.171	0.104	0.1629	0.1503	0.1391	0.1705	0.1072	0.259	0.2173
256189_at	AT1G30140	similar to unknown protein [Arabidopsis thaliana] (T	-0.3228	0.8101	0.5268	0.4237	0.7532	0.4761	0.01697	0.9897	0.5152	0.7635	0.5712	0.353
256190_at	AT1G30100	NCED5 (NINE-CIS-EPOXYCAROTENOID DIOXYG	-0.5718	0.6946	0.4909	-2.0754	0.2001	0.2329	0.5315	0.7147	0.4364	-0.9721	0.5125	0.3307
256191_at	AT1G30130	similar to hypothetical protein [Brassica oleracea va	-0.2163	0.1705	0.2417	-0.2391	0.1387	0.1898	0.2221	0.0336	0.0749	0.1992	0.0464	0.0758
256192_at	AT1G30110	diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase,	-0.3638	0.6351	0.4713	0.4008	0.6022	0.4245	0.3299	0.601	0.3985	1.0945	0.1331	0.1438
256193_at	AT1G30200	F-box family protein	0.1019	0.663	0.4804	-0.00653	0.9774	0.5386	-0.4271	0.0247	0.0637	-0.5355	0.0117	0.0339
256194_at	AT1G36810	transposable element gene	0.4198	0.7419	0.5065	-1.2347	0.3578	0.3219	1.2493	0.2011	0.2123	-0.4062	0.646	0.3794
256195_at	no_match	no_match	0.1068	0.9297	0.5599	-0.3072	0.8005	0.4897	-1.933	0.1153	0.1527	-2.347	0.0716	0.098
256196_at	no_match	no_match	-0.3857	0.696	0.4914	0.9347	0.3663	0.3258	-0.3485	0.7236	0.4398	0.9719	0.3496	0.2623
256197_at	AT1G36910	transposable element gene	1.6065	0.1408	0.2183	0.05935	0.9493	0.5318	0.992	0.321	0.2787	-0.5552	0.5609	0.3492
256198_at	AT1G58220	myb family transcription factor	0.2793	0.3258	0.3378	0.3133	0.2777	0.2796	0.07896	0.7676	0.4534	0.1129	0.6744	0.3888
256199_at	AT1G58250	SAB (SABRE)	0.7112	0.0055	0.0521	0.3075	0.078	0.1399	-0.7332	5.00E-04	0.0148	-1.1369	1.00E-04	0.0058
256200_at	AT1G58210	EMB1674 (EMBRYO DEFECTIVE 1674)	0.2699	0.765	0.513	1.5924	0.1321	0.1845	-1.4195	0.121	0.157	-0.09702	0.8997	0.4571
256201_at	AT1G58230	WD-40 repeat family protein / beige-related	0.4968	0.0985	0.1811	0.3093	0.2526	0.2655	-1.1216	0.0051	0.0299	-1.3091	0.0029	0.0175
256202_s_at	AT1G48150,AT1G50780	[AT1G48150, MADS-box protein (AGL74)];[AT1G5	-0.2328	0.842	0.5362	0.1247	0.9148	0.5227	-0.5571	0.6376	0.4104	-0.1997	0.8642	0.4468
256203_at	AT1G50800	similar to unknown protein [Arabidopsis thaliana] (T	-1.0662	0.4395	0.3934	-0.447	0.7374	0.4704	-1.7962	0.2221	0.2247	-0.2831	0.8311	0.4375
256204_at	AT1G50840	POLGAMMA2 (polymerase gamma 2); DNA binding	-0.2987	0.1432	0.2202	-0.3312	0.114	0.1706	-0.9331	0.0047	0.0292	-0.9657	0.0042	0.0207
256205_at	AT1G50890	binding	-0.1161	0.6019	0.4602	-0.3137	0.2012	0.2334	-0.01183	0.9424	0.5038	-0.2094	0.2449	0.2096
256206_at	AT1G50910	similar to unnamed protein product [Vitis vinifera] (G	0.2355	0.1527	0.2279	0.226	0.1658	0.2096	0.06173	0.7183	0.4379	0.04231	0.7673	0.4191
256207_at	AT1G50920	GTP-binding protein-related	0.3321	0.1043	0.1866	0.1783	0.3237	0.3052	-0.025	0.5907	0.3949	-0.1788	0.014	0.0376
256208_at	AT1G50930	similar to unknown protein [Arabidopsis thaliana] (T	1.8985	0.2534	0.2955	-0.8172	0.5968	0.4221	1.1665	0.324	0.2803	-1.5491	0.2099	0.1909
256209_at	AT1G50940	ETFALPHA (ELECTRON TRANSFER FLAVOPRO	0.4355	0.0128	0.0697	0.4017	0.0167	0.0672	0.1167	0.5077	0.3624	0.256	0.1704	0.1675
256210_at	AT1G50950	thioredoxin-related	0.5148	0.0958	0.1788	0.3893	0.1761	0.2171	-0.07919	0.6817	0.4248	-0.2046	0.3176	0.2472
256211_at	AT1G50960	ATGA2OX7 (GIBBERELLIN 2-OXIDASE 7); gibber	-0.8359	0.4693	0.407	2.5632	0.0706	0.1328	-1.0933	0.2684	0.2512	2.3059	0.0536	0.0827
256212_at	AT1G50970	membrane trafficking VPS53 family protein	0.8272	0.1921	0.2569	0.454	0.4381	0.3589	-0.9901	0.0686	0.1136	-1.3633	0.0271	0.0547
256213_at	AT1G50990	protein kinase-related	-0.6371	0.6238	0.4678	-1.5114	0.2767	0.2791	0.8643	0.5115	0.3638	-0.00997	0.9938	0.4811
256214_x_at	AT1G51000	similar to unknown protein [Arabidopsis thaliana] (T	0.1214	0.9497	0.5646	-0.3272	0.8652	0.5086	1.6242	0.4198	0.3253	1.1756	0.551	0.3455
256215_at	AT1G50999	similar to hypothetical protein [Vitis vinifera] (GB:CA	-0.5644	0.03	0.1007	-0.6526	0.0189	0.071	0.0607	0.7299	0.4418	0.02747	0.875	0.4499
256216_at	AT1G56340	CRT1 (CALRETICULIN 1); calcium ion binding	0.7042	3.00E-04	0.0312	0.6852	3.00E-04	0.0249	0.6823	3.00E-04	0.0141	0.6633	4.00E-04	0.0089
256217_at	AT1G56320	similar to unknown protein [Arabidopsis thaliana] (T	0.263	0.7143	0.4974	1.2671	0.1312	0.1837	0.181	0.8001	0.4635	1.1852	0.1512	0.1555
256218_at	AT1G56270	unknown protein	0.6727	0.0571	0.137	-0.3233	0.272	0.2766	-0.01589	0.9531	0.5063	-1.0119	0.0163	0.0408
256219_at	AT1G56260	similar to hypothetical protein Osl_024078 [Oryza s	-0.2338	0.2825	0.3129	0.06316	0.7543	0.4765	0.3369	0.1483	0.1779	0.6338	0.0282	0.056
256220_at	AT1G56230	similar to unknown protein [Arabidopsis thaliana] (T	0.52	0.082	0.1657	0.4711	0.1045	0.1633	-0.209	0.3953	0.3144	-0.2579	0.3054	0.2412
256221_at	AT1G56300	DNAJ heat shock N-terminal domain-containing pro	1.2441	0.0516	0.1305	1.6062	0.0239	0.0778	-0.3517	0.4205	0.3256	0.01045	0.98	0.4782
256222_at	AT1G56210	copper chaperone (CCH)-related	-0.2403	0.2949	0.3203	-0.3066	0.1993	0.2324	0.1946	0.0885	0.1314	0.1283	0.2134	0.1927
256223_at	AT1G56200	EMB1303 (EMBR

256290_at	AT3G12203	SCPL17 (serine carboxypeptidase-like 17); serine c	-1.8875	0.0675	0.1492	-0.3719	0.6494	0.4415	0.6168	0.4615	0.3439	2.1324	0.0482	0.0775
256291_at	AT3G12200	ATNEK7 (NIMA-RELATED KINASE7); kinase	0.1387	0.2216	0.2761	0.2613	0.0527	0.1139	-0.2399	0.0667	0.1117	-0.1173	0.2884	0.2326
256292_at	AT1G69430	similar to unknown protein [Arabidopsis thaliana] (T	0.9485	0.1941	0.2583	0.09288	0.8861	0.5148	0.04202	0.9483	0.5052	-0.8136	0.2522	0.2137
256293_at	AT1G69440	AGO7 (ARGONAUTE7); nucleic acid binding	1.197	0.0981	0.1809	0.3135	0.6036	0.4247	-0.66	0.1806	0.1991	-1.5435	0.0193	0.0445
256294_at	AT1G69450	similar to HYP1 (HYPOTHETICAL PROTEIN 1) [Ar	0.08545	0.7411	0.5062	-0.2188	0.416	0.3488	-0.1382	0.0717	0.1164	-0.4424	0.0015	0.0137
256295_at	AT1G69470	unknown protein	-2.0226	0.1878	0.2539	0.5267	0.7007	0.4593	-0.5351	0.624	0.4059	2.0142	0.1167	0.1325
256296_at	AT1G69480	EXS family protein / ERD1/XPR1/SYG1 family prote	0.5901	0.0698	0.1522	0.2309	0.3906	337	-0.2863	0.2988	0.2682	-0.6456	0.0547	0.0836
256297_at	AT1G69500	oxygen binding	0.8845	0.6194	0.4663	1.4446	0.3199	0.3031	-1.284	0.201	0.2123	-0.5238	0.5665	0.3515
256298_at	no_match	no_match	-0.7812	0.2477	0.2923	-0.1868	0.7626	0.4782	-0.04923	0.9362	0.5023	0.5452	0.3987	0.2837
256299_at	AT1G69530	ATEXPA1 (ARABIDOPSIS THALIANA EXPANSIN	-0.5218	0.3123	0.33	-0.4884	0.3404	0.3137	0.1738	0.1934	0.2076	0.2072	0.1361	0.1457
256300_at	AT1G69490	NAP (NAC-LIKE, ACTIVATED BY AP3/PI); transcri	0.1063	0.8743	0.5451	0.08675	0.8972	0.518	0.7489	0.0136	0.0465	0.7294	0.0149	0.0388
256301_at	AT1G69510	similar to unknown protein [Arabidopsis thaliana] (T	0.1325	0.1696	0.2411	0.08375	0.35	0.318	-0.00709	0.933	0.5014	-0.05588	0.5194	0.3334
256302_at	AT1G69526	UbiE/COQ5 methyltransferase family protein	-0.1909	0.452	0.3992	-1.4829	0.0029	0.0355	-0.8686	0.0027	0.024	-2.1606	1.00E-04	0.0058
256303_at	AT1G69550	disease resistance protein (TIR-NBS class), putativ	-0.2814	0.4025	0.4041	-0.1102	0.7666	0.4793	-0.4788	0.0508	0.0954	-0.3075	0.1508	0.1552
256304_at	AT1G69523	UbiE/COQ5 methyltransferase family protein	-2.1144	0	0.0312	-2.3047	0	0.0249	-0.07491	0.5039	0.3609	-0.2652	0.0602	0.0887
256305_at	AT3G30400	ATMRP1 (Arabidopsis thaliana multidrug resistance	0.7269	0.0364	0.1099	0.393	0.1695	0.2122	-0.5963	0.021	0.0583	-0.9302	0.0045	0.0213
256306_at	AT1G30370	lipase class 3 family protein	0.8134	0.0437	0.1205	0.4317	0.1973	0.2312	0.5334	0.129	0.1633	0.1517	0.6161	0.3688
256307_at	AT1G30350	pectate lyase family protein	0.7155	0.5767	0.4512	-0.3412	0.7866	0.4851	-0.3435	0.7852	0.4588	-1.4002	0.3007	0.239
256308_s_at	AT1G30420;AT1G30410	AT1G30420; ATMRP12 (Arabidopsis thaliana multi	1.3626	3.00E-04	0.032	1.2025	5.00E-04	0.0264	-1.5229	2.00E-04	0.0129	-1.683	1.00E-04	0.0068
256309_at	AT1G30380	PSAK (PHOTOSYSTEM I SUBUNIT K)	-0.3235	0.1351	0.2134	-0.7314	0.0134	0.0617	0.2773	0.0697	0.1145	-0.1306	0.311	0.2438
256310_at	AT1G30360	ERD4 (EARLY-RESPONSIVE TO DEHYDRATION	-0.6777	0.1863	0.253	-0.6681	0.1913	0.227	-0.2464	0.1936	0.2077	-0.2368	0.208	0.1897
256311_at	AT1G30330	ARF6 (AUXIN RESPONSE FACTOR 6); transcripte	0.7431	0.0517	0.1306	0.8355	0.0368	0.0947	-0.1546	0.5988	0.3977	-0.06213	0.8298	0.4371
256312_x_at	AT1G30820	similar to unknown protein [Arabidopsis thaliana] (T	0.5906	0.3878	0.3686	-1.5919	0.0594	0.1212	1.4695	0.0677	0.1127	-0.713	0.294	0.2355
256313_s_at	AT1G35850;AT5G59280	[AT1G35850, APUM17 (ARABIDOPSIS PUMILIO 1	-0.7159	0.533	0.4342	1.138	0.3397	0.3133	-1.3126	0.2797	0.2579	0.5414	0.6336	0.3749
256314_at	AT1G35860	TOC75-I (TRANSLOCON OUTER MEMBRANE CC	-0.2798	0.7337	0.6035	0.2313	0.778	0.483	-0.4108	0.6205	0.4048	0.1002	0.9023	0.458
256315_at	AT1G35880	similar to TOC75-III (translocon outer membrane cc	-0.535	0.4599	0.403	-0.3376	0.6335	0.4358	0.1111	0.8736	0.4851	0.3085	0.6622	0.3849
256316_at	AT1G35890	DNA binding	0.7799	0.5351	0.4352	-0.2489	0.8393	0.5013	0.9705	0.4465	0.3368	-0.05823	0.9621	0.4737
256317_at	AT1G35900	unknown protein	-0.03699	0.9371	0.6615	-0.03336	0.9433	0.5302	-0.1051	0.8232	0.4706	-0.1015	0.8292	0.437
256318_s_at	AT2G14470;AT5G34960;A	[AT2G14470, transposable element gene];[AT5G34	-2.7089	0.1437	0.2204	-1.7723	0.3007	0.2917	-0.9652	0.553	0.3801	-0.02863	0.9856	0.4792
256319_at	AT1G35910	trehalose-6-phosphate phosphatase, putative	-0.00657	0.9947	0.5756	1.9726	0.0999	0.1593	0.1291	0.8502	0.4786	2.1083	0.0303	0.0585
256320_at	AT1G35720	DNAJ heat shock N-terminal domain-containing pro	-0.4198	0.1743	0.2202	-0.6833	0.0454	0.1056	0.2944	0.2642	0.2489	0.05095	0.8333	0.4381
256321_at	AT1G55020	LOX1 (Lipoxygenase 1); lipoxygenase	0.4372	0.0753	0.1579	0.64	0.025	0.0791	-0.3004	0.1761	0.1961	-0.09771	0.6218	0.3708
256322_at	AT1G54990	AXR4 (AUXIN RESISTANT 4)	-0.1454	0.4141	0.382	0.06244	0.7157	0.4639	-0.02072	0.8842	0.488	0.1871	0.234	0.2038
256323_at	AT1G54920	similar to hypothetical protein [Vitis vinifera] (GB:CA	-0.279	0.1743	0.2444	-0.1173	0.6259	0.3945	-1.3591	6.00E-04	0.0158	-1.1975	9.00E-04	0.0118
256324_at	AT1G66760	MATE efflux family protein	-0.7007	0.2695	0.3051	-0.3954	0.5098	0.3886	-1.1523	0.0042	0.0278	-0.847	0.0125	0.0353
256325_at	AT3G02330	pentatricopeptide (PPR) repeat-containing protein	1.3435	0.1025	0.185	-0.3351	0.6265	0.4334	-0.9582	0.2068	0.2159	-2.6369	0.0144	0.0381
256326_at	AT3G02360	zinc finger (C3HC4-type RING finger) family protein	0.00435	0.9806	0.6721	0.3978	0.6771	0.4392	-0.2739	0.1785	0.1927	0.4706	0.1282	0.4882	0.3212
256327_at	AT3G02350	GAUT9 (Galacturonosyltransferase 9); polygalacturo	-2.0563	0.1285	0.2071	-0.2109	0.1908	0.2268	-1.075582	0.602	0.3989	-0.03039	0.8318	0.4377
256328_at	AT3G02360	6-phosphogluconate dehydrogenase family protein	0.5168	0.02	0.0834	0.3284	0.0759	0.138	-0.1576	0.0624	0.1073	-0.346	0.0049	0.022
256329_at	AT1G76850	SEC5A, EXOCYST COMPLEX COMPONENT SEC	0.7476	0.0041	0.0468	0.4522	0.0234	0.077	-0.3167	0.0668	0.1117	-0.6121	0.0084	0.0286
256330_at	AT1G76870	similar to transcription factor [Arabidopsis thaliana]	0.266	0.444	0.3952	0.1751	0.6061	0.4256	-0.1538	0.6494	0.4144	-0.2446	0.4788	0.317
256331_at	AT1G76880	trihelix DNA-binding protein, putative	-0.00021	0.9986	0.5763	-0.00436	0.9722	0.5372	0.1328	0.1517	0.1802	0.1287	0.1618	0.1623
256332_at	AT1G76890	GT2; transcription factor	0.213	0.1163	0.1972	0.2119	0.1177	0.1734	0.1402	0.1084	0.1473	0.1391	0.1104	0.128
256333_at	AT1G76860	small nuclear ribonucleoprotein, putative / snRNP, p	0.6262	0.0293	0.0993	0.54	0.0457	0.1058	0.01333	0.947	0.5049	-0.07281	0.7189	0.4036
256334_at	AT1G72125	transporter	-0.07759	0.8746	0.5451	-0.3594	0.4793	0.3758	-0.2011	0.6691	0.4208	-0.4829	0.3308	0.2537
256335_at	AT1G72100	similar to unknown protein [Arabidopsis thaliana] (T	0.2311	0.8249	0.5331	-1.3653	0.2353	0.255	0.1253	0.9042	0.4935	-1.4711	0.2071	0.1891
256336_at	AT1G72030	GCN5-related N-acetyltransferase (GNAT) family pr	-0.01868	0.8943	0.5498	0.1422	0.3145	0.269	0.004	0.0274	-0.3925	0.001	0.012	
256337_at	AT1G72060	serine-type endopeptidase inhibitor	1.5093	0.0343	0.1071	1.9132	0.0161	0.066	-0.47	0.0858	0.1292	-0.06615	0.7654	0.4185
256338_at	AT1G72040	late embryogenesis abundant domain-containing pr	0.6381	0.5262	0.4316	-1.7725	0.1263	0.1803	2.9732	0.0062	0.0362	0.5626	0.4081	0.2874
256339_at	AT1G72080	contains InterPro domain HMG-I and HMG-Y, DNA-	-0.2185	0.7886	0.5201	-1.2653	0.1722	0.2143	-0.565	0.4996	0.3596	-1.6118	0.1019	0.122
256340_at	AT1G72070	DNAJ heat shock N-terminal domain-containing pro	0.1588	0.744	0.5071	1.0136	0.0893	0.1506	0.3815	0.4432	0.3355	1.2363	0.0511	0.0805
256341_at	AT1G72040	deoxyribonucleoside kinase family	0.4274	0.0204	0.0842	0.08654	0.493	0.3815	-0.1903	0.1729	0.1938	-0.5311	0.0098	0.0309
256342_at	AT1G72020	similar to unknown [Populus trichocarpa] (GB:ABK9	0.02391	0.849	0.5379	0.1508	0.2693	0.275	0.7336	0.0034	0.0257	0.8605	0.0019	0.0149
256343_at	AT1G72090	radical SAM domain-containing protein / TRAM dom	0.6817	0.0077	0.0582	0.608	0.0115	0.0579	-0.00489	0.9733	0.5108	-0.07861	0.5982	0.3629
256344_at	AT1G72050	zinc finger (C2H2 type) family protein	0.4174	0.184	0.251	0.6224	0.0747	0.1371	-0.4595	0.0308	0.0714	-0.2534	0.1455	0.1518
256345_at	AT1G55030	F-box family protein	-1.6465	0.0861	0.1702	-1.0673	0.2158	0.2433	-0.8786	0.2932	0.2653	-0.2994	0.7015	0.3978
256346_s_at	AT2G01029;AT2G15040;A	[AT2G01029, transposable element gene];[AT2G15	-1.0798	0.6511	0.4766	-0.8058	0.7342	0.4695	-2.3025	0.3569	0.2965	-2.0285	0.4112	0.2887
256347_at	AT1G56420	transposable element gene	-0.4405	0.8052	0.5255	0.8392	0.642	0.4389	-1.0306	0.5709	0.3869	0.2491	0.8888	0.4539
256348_at	AT1G54880	unknown protein	-0.2929	0.8186	0.5292	0.0603	0.9622	0.5346	1.3083	0.3354	0.2862	1.6615	0.2371	0.2057
256349_at	AT1G54890	late embryogenesis abundant protein-related / LEA	-0.2246	0.6974	0.4918	0.4206	0.4776	0.3753	-0.3947	0.5034	0.3606	0.2505	0.6653	0.3859
256350_at	AT1G54940	initiation PROTEIN 4); translation factor, transferring glyc	-0.3223	0.7412	0.5062	0.735	0.4647	0.3698	-0.5095	0.5812	0.3912	0.5478	0.5544	0.3467
256351_at	AT1G54960	ANP2 (Arabidopsis NPK1-related protein kinase 2);	-0.0881	0.6625	0.4802	-0.2311	0.2848	0.2837	0.08361	0.4159	0.3233	-0.05935	0.5549	0.3469
256352_at	AT1G54970	ATPPR1 (PROLINE-RICH PROTEIN 1); structural	-0.2869	0.5953	458	-0.4226	0.4438	0.3612	0.4961	0.3754	0.3055	0.3605	0.5091	0.3294
256353_at	AT1G55000	peptidoglycan-binding LysM domain-containing pro	0.2687	0.0938	0.1773	0.04203	0.7493	0.4747	-0.7248	9.00E-04	0.0169	-1.0356	2.00E-04	0.0078
256354_at	AT1G54870	oxidoreductase	0.5338	0.6548	0.4775	0.595	0.6193	0.4303	0.02014	0.9692	0.5097	0.08131	0.8763	0.4503
256355_at	AT1G55040	zinc finger (Ran-binding) family protein	-0.8381	0.2969	0.3214	1.6166	0.0819	0.1436	-2.1579	0.0155	0.0494	0.2968	0.6071	0.3657
256356_s_at	AT4G34620;AT1G66500	S-locus protein-related;[AT1G66500,	-1.0328	0.0157	0.0756	-0.5792	0.0886	0.1484	-0.7062	0.051	0.0956	-0.2526	0.3799	0.2757
256357_at	AT1G66490	F-box family protein	1.0253	0.4436	0.3951	0.06646	0.9587	0.534	1.6914	0.1241	0.1595	0.7326	0.4477	0.3051
256358_at	AT1G66470	basic helix-loop-helix (bHLH) family protein	-1.1693	0.2067	0.2662	-0.8687	0.326	0.3065	-0.5314	0.5315	0.3718	-0.2308	0.7812	0.4232
256359_at	AT1G66440	protein kinase family protein	-1.796	0.2208	0.2757	-3.3457	0.0541	0.1153	0.03209	0.9615	0.5081	-1.5177	0.072	0.0984
256360_at	AT1G66440	DC1 domain-containing protein	0.3562	0.5504	0.4413	-1.644	0.0397	0.0988	1.712	0.0352	0.0769	-0.2883	0.6261	0.3724
256361_at	AT1G66520	PDE194 (PIGMENT DEFECTIVE 194); formyltetrah	-0.2407	0.1767	0.2459	-0.2202	0.2084	0.2385	-0.1108	0.3889	0.3117	-0.09028	0.4756	0.316
256362_at	AT1G66450	DC1 domain-containing protein	-0.2665	0.8301	0.5325	-0.1833	0.8825	0.5138	0.9701	0.4513	0.3393	1.0533	0.4165	0.2911
256363_at	AT1G66510	AAR2 protein family	0.1574	0.4694	0.407	-0.2952	0.2086	0.2387	-0.2841	0.0985	0.1397	-0.7367	0.0051	0.0224
256364_at	AT1G66550	WRKY67 (WRKY DNA-binding protein 67); transcri	1.2226	0.2082	0.2671	0.6735	0.4552	0.3662	0.5237	0.3671	0.3015	-0.02538	0.9631	0.474
256365_at	AT1G66530	arginyl-tRNA synthetase, putative / arginine--tRNA	0.3145	0.0426	0.1188	0.2726	0.0637	0.1258	-0.2532	0.0774	0.1215	-0.2951	0.0511	0.0805
256366_at	AT1G66880	serine/threonine protein kinase family protein	1.8721	0.0011	0.036	1.8154	0.0013	0.0307	-0.2066	0.1839	0.2014	-0.2632	0.1105	0.128
256367_at	AT1G66810	zinc finger (CCCH-type) family protein	0.09132	0.8524	0.5389	-0.1088	0.8247	0.4974	0.09981	0.839	0.4753	-0.1004	0.8381	0.4395
256368_at	AT1G66800	cinnamyl-alcohol dehydrogenase family / CAD family	0.665	0.6208	0.4667	0.3786	0.7757	0.4824	1.3205	0.3477	0.292	1.0341	0.4519	0.3068
256369_at	AT1G66790;AT3G50674	[AT1G66790, similar to unknown protein [Arabidops	1.8367	0.1703	0.2416	-0.6534	0.5845	0.4179	-0.1572	0.8055	0.4651	-1.3405	0.0883	0.1115
256370_at	AT1G66780	MATE efflux family protein	0.6618	0.1571	0.231	-0.07951	0.8447	0.5029	-0.1223	0.7641	0.4524	-0.8636	0.0859	0.1096
256371_at	AT1G66770	nodulin MtN3 family protein	0.3802	0.7192	0.4992	-0.2721	0.7961	0.4884	0.5729	0.5862	0.3931	-0.07946	0.9386	0.468
256372_at	AT1G66750	AT;CDKD;2/CAK4AT/CDKD1;2/CDKD;2 (CYCLIN-D	0.2784	0.1434	0.2203	0.145	0.3976	0.3403	-0.03674	0.8224	0.4704	-0.1701	0.3292	0.253
256373_at	AT1G66740	AtSP7 (Anti- silencing function 1a)	0.1469	0.3583	0.3536	0.1093	0.4834	0.3774	0.06881	0.5955	0.3967	0.0312	0.8069	0.4307
256374_at	AT1G66730	ATP dependent DNA ligase family protein	0.6154	0.2568	0.2975	-0.189	0.7056	0.4608	-1.0995	0.0725	0.1171	-1.9038	0.0137	0.0372
256375_at	AT1G66720	S-adenosyl-L-methionine:carboxyl methyltransferas	-1.2152	0.2628	0.3013	-0.9772	0.3542	0.3201	-0.7021	0.4937	0.3571	-0.4641	0.6451	0.3791
256376_s_at	AT1G66690;AT1G66700	[AT1G66690, S-adenosyl-L-methionine:carboxyl me	2.2872	0.0032	0.0442	1.6291	0.0108	0.0559	0.6957	0.0698	0.1147	0.0376	0.9007	0.4575
256377_at	AT1G66650	seven in absentia (SINA) protein, putative	-1.0112	0.2394	0.2873	0.6081	0.4529	0.3653	-0.485	0.5439	0.3769	1.1342	0.1963	0.1827
256378_at	AT1G66830	leucine-rich repeat transmembrane protein kinase,	-0.7016	0.1163	0.1972	-0.3308	0.3994	0.341	-0.3432	0.1718	0.1932	0.02752	0.9004	0.4574
256379_at	AT1G66840	Identical to Protein PLASTID MOVEMENT IMPAIRE	-0.5999	0.1157	0.1967	-0.5338	0.1492	0.1976	-0.1506	0.5668	0.3855	-0.08455	0.744	0.4117
256380_at	AT1G66860	AR401	0.675	0.0091	0.0616	0.8084	0.0048	0.042	-0.7754	0.0047	0.0292	-0.642	0.0092	0.0299
256381_at	AT1G66850	protease inhibitor/seed storage/lipid transfer protein	1.4731	0.199	0.2619	1.554	0.1802	0.2196	-1.7399	0.1315	0.165	-1.659	0.1457	0.1519
256382_at	AT1G66860	hydrolase	1.1106	0.1288	0.2073	1.5518	0.0559	0.1175	0.09209	0.7405	0.4449	0.5333	0.109	0.1269
256383_at	AT1G66820	glycine-rich protein	-0.548	0.0938	0.1772	-0.1149	0.6702	0.4487	0.2846	0.0625	0.1074	0.7178	0.003	0.0177
256384_at	AT1G66660	seven in absentia (SINA) protein, putative	0.2097	0.4264	0.3878	0.5475	0.0821	0.1437	-0.2829	0.2986	0.2681	0.05487	0.8283	0.4367
256385_at	AT1G66580	60S ribosomal protein L10 (RPL10C)	0.1229	0.2663	0.3029	0.3087	0.0316	0.0884	0.07124	0.244	0.2374	0.257	0.0079	0.0277
256386_at	AT1G66540	cytochrome P450, putative	-0.8215	0.0735	0.1561	-1.0767	0.0342	0.0913	-0.1002	0.7833	0.4583	-0.3554	0.3559	0.2652
256387_at	AT3G06170	TMS membrane family protein / tumour differentiall	0.4449	0.0529	0.132	0.2226	0.245	0.261	0.2175	0.1721	0.1934	-0.0048	0.9725	0.4762
256388_at	AT3G06180	structural constituent of ribosome	0.2101	0.0436	0.1204	-0.2092	0.0441	0.1039	0.05513	0.1845	0.2017	-0.3642	5.00E-04	0.0093
256389_at	AT3G06220	DNA binding / transcription factor	0.2406	0.8069	0.5258	-0.2297	0.8154	0.4947	1.4387	0.1023	0.1428	0.9685	0.2282	0.2006
256390_at	AT3G06230	ATMKK8 (Arabidopsis thaliana MAP kinase kinase	-0.4693	0.7234	0.5006	-0.2408	0.855	0.5059	-0.3558	0.7778	0.4565	-0.1273	0.9192	0.4625
256391_at	AT3G06090	unknown protein	0.08234	0.8358	0.5341	-1.2107	0.0313	088	0.709	0.1296	0.1637	-0.5841	0.1918	0.1801
256392_at	AT3G06240	GATL4 (Galactonosyltransferase-like 4); polygala	-0.1331	0.8509	0.5384	-0.2103	0.7674	0.4797	-0.1211	0.8642	0.4826	-0.1983	0.7802	0.423
256393_at	AT3G06280	similar to F-box family protein [Arabidopsis thaliana	-0.4024	0.6279	0.4689	0.2103	0.7977	0.4888	-0.5733	0.4967	0.3585	0.03941	0.9615	0.4736
256394_at	AT3G06290	similar to SAC3/GANP family protein [Arabidopsis t	-0.1237	0.3087	0.3278	0.274	0.0613	0.1229	-0.8999	7.00E-04	0.0159	-0.5023	0.006	0.024
256395_at	AT3G06120	MUTE (MUTE); DNA binding / transcription factor	-0.6917	0.395	0.3726	0.8733	0.4317	0.356	-0.68	0.5337	0.3727	1.145	0.3159	0.2464
256396_at	AT3G06150	similar to unknown protein [Arabidopsis thaliana] (T	-0.7875	0.0197	0.0831	-0.6972	0.0291	0.0848	-0.4405	0.0018	0.0206	-0.3501	0.0043	0.0208
256397_at	AT3G06110	MKP2; protein tyrosine/serine/threonine phosphatas	0.5135	0.0028	0.0431	0.6658	0.0011	0.0293	0.03488	0.6802	0.4244	0.1871	0.0759	0.1015
256398_at	AT3G06100	NIP7;1/NLM6/NLM8 (NOP2/26-like intrinsic protein 7	-0.4177	0.321	0.335	-0.1061	0.7879	0.4856	-0.08715	0.8249	0.4712	0.2244	0.5761	0.3545
256399_at	AT3G06240	F-box family protein	0.3974	0.0263	0.0937	0.6103	0.0062	0.0451	-0.08086	0.5224	0.3679	0.132	0.3167	0.2467
256400_at	AT3G06140	zinc finger (C3HC4-type RING finger) family protein	-0.8394	0.0906	0.1744	-1.009	0.0559	0.1175	0.4345	0.3146	0.2757	0.2649	0.5222	0.3348
256401_at	AT3G06200	guanylate kinase, putative	0.03943	0.8524	0.5389	0.1171	0.5874	0.4187	-0.1123	0.4561	0.3413	-0.03458	0.8121	0.4323
256402_at	AT3G06130	heavy-metal-associated domain-containing protein	-0.3015	0.4335	0.391	-0.04915	0.8941	0.5169	-0.0823	0.569	0.3863	0.17	0.2696	0.2225
256403_at	AT3G06190	ATBPM2; protein binding	0.1213	0.5365	0.4356	0.2215	0.2851	0.2839	-0.3769	0.0708	0.1157	-0.2758	0.1474	0.153
256404_at	AT3G06250	FRS7 (FAR1-RELATED SEQUENCE 7); zinc ion bi	-0.06908	0.7703	0.5147	0.02503	0.9153	0.5228	-0.4933	0.0895	0.1322	-0.3992	0.1453	0.1518
256405_at	AT1G50700	CPK33 (calcium-dependent protein kinase 33); calc	0.3093	0.2924	0.3186	0.7135	0.0491	0.1097	-0.5955	0.08	0.1238	0.4274	0.1695	0.1669
256406_at	no_match	no_match	0.3772	0.1194	0.1997	-0.3161	0.1731	0.2149	0.01651	0.9014	0.4928	0.07758	0.8689	0.3523
256407_at	AT1G66570	ATSUC7 (SUCROSE-PROTON SYMPORTER 7);	1.2946	0.3023	0.3244	1.1147	0.366	0.3256	0.4985	0.6723	0.4218	0.3186	0.7854	0.4244
256408_at	AT1G66610	seven in absentia (SINA) protein, putative	-1.6962	0.117	0.1977	0.1855	0.8381	0.501	-1.8288	0.0716	0.1163	0.05284	0.9473	0.4703
256409_at	AT1G66620	seven in absentia (SINA) protein, putative	0.07521	0.8363	0.5343	0.0117	0.9581	0.5401	-0.3641	0.346	0.2912	1.0623	0.0357	0.0642
256410_at	AT1G66630	seven in absentia (SINA) protein, putative	-0.07632	0.946	0.5636	-0.4814	0.6732	0.4496	2.623	0.0685	0.1136	2.218	0.1045	0.1237
256411_at	AT1G66670	CLPP3 (Clp protease proteolytic subunit 3); endope	-0.1397	0.4648	0.4051	-0.2421	0.2346	0.2546	-0.1977	0.0576	0.1026	-0.3	0.0161	0.0405
256412_at	no_match	no_match	0.367	0.3377	0.3443	0.02533	0.9437	0.5302	-0.7115	0.1025	0.1429	-1.0531	0.0354	0.0638
256413_at	AT3G11100	transcription factor	0.4931	0.0617	0.1427	0.9452	0.0079	0.0494	-0.738	0.0183	0.0541	-0.2858	0.21	0.1909
256414_at	AT3G11200	PHD finger family protein	-0.03384	0.8769	0.5456	0.0837	0.704	0.4605	0.3089	0.1434	0.1741	0.4265	0.0662	0.0937
256415_at	AT3G11210	GDSL-motif lipase/hydrolase family protein	-0.3365	0.1956	0.2595	-0.4791	0.0917	0.1527	-0.7041	0.0204	0.0574	-0.8466	0.011	0.0328
256416_at	AT3G11050	ATFER2 (FERRITIN 2); ferric iron binding	1.3536	0.1063	0.1885	0.8122	0.2805	0.2811	-0.06101	0.9299	0.5006	-0.6024	0.4074	0.2871
256417_s_at	AT3G11170;AT5G05580	[AT3G11170, FAD7 (FATTY ACID DESATURASE	-0.8051	0.0057	0.0525	-0.9134	0.0036	0.0377	-0.3157	0.1015	0.1423	-0.4239	0.0466	0.076
256418_at	AT3G06160	transcriptional factor B3 family protein	0.1749	0.7676	0.5138	0.3216	0.592	0.4203	-0.3659	0.238	0.2342	-0.2192	0.4531	0.3073
256419_at	no_match	no_match	-1.3513	0.0397	0.115	0.2247	0.6435	0.4394	-2.899	0.0012	0.0187	-1.3229	0.0203	0.0459
256420_at	AT3G03475	Identical to Probable VAMP-like protein At1g33475	-0.1864	0.4294	0.3888	0.2503	0.3035	0.2933	-0.02444	0.8916	0.4901	0.4122	0.0707	0.0974
256421_at	AT3G03500	similar to kinase interacting family protein [Arabidop	-2.4162	0.1206	0.2008	0.2046	0.6758	0.5118	-0.04029	0.9754	0.5115	2.5806	0.1036	0.1231
256422_at	AT3G03520	MOS2 (MODIFIER OF SNC1, 2); RNA binding / nuc	-0.3332	0.1373	0.2153	0.4567	0.0638	0.126	-0.8037	0.0095	0.039	-0.01379	0.94	0.4685
256423_at	AT3G03540	SCPL18 (serine carboxypeptidase-like 18); serine c	-1.0382	0.4091	0.3795

256490_at	AT1G31460	similar to unknown protein [Arabidopsis thaliana] (T	0.3369	0.3872	0.3683	0.3735	0.3428	0.3147	-0.1852	0.6223	0.4055	-0.1485	0.6911	0.3944
256491_at	AT1G31500	endonuclease/exonuclease/phosphatase family pro	-0.03585	0.8206	0.5297	-0.4362	0.0422	0.1021	-0.02536	0.8724	0.4848	-0.4257	0.0453	0.0746
256492_at	AT1G31490	transferase family protein	-0.2096	0.4244	0.387	-0.00198	0.9937	0.5426	0.285	0.2936	0.2654	0.4927	0.105	0.124
256493_at	AT1G31600	oxidoreductase, 2OG-Fe(II) oxygenase family prote	-0.01372	0.9585	0.5668	0.03269	0.9013	0.5193	-1.3684	0.0024	0.0228	-1.322	0.0027	0.0171
256494_at	AT1G31520	unknown protein	0.4674	0.6259	0.4684	0.5444	0.5724	0.4129	1.1236	0.2738	0.2545	1.2006	0.2472	0.2109
256495_at	AT1G31530	endonuclease/exonuclease/phosphatase family pro	-0.9423	0.279	0.3107	0.4408	0.5897	0.4194	-1.7816	0.0772	0.1213	-0.3984	0.6247	0.3718
256496_at	AT1G31510	F-box family protein-related	0.2265	0.8252	0.531	-1.5885	0.1736	0.2153	0.7632	0.4714	0.3481	-1.0518	0.3351	0.2556
256497_at	AT1G31580	ECS1	-0.2039	0.404	0.3773	-0.4398	0.1147	0.1708	0.01922	0.847	0.4778	-0.2167	0.0812	0.106
256498_at	AT1G36670	transposable element gene	-0.11	0.9329	0.5605	0.7178	0.5899	0.4195	-2.7006	0.0926	0.1348	-1.8728	0.2017	0.1861
256499_at	AT1G36640	similar to unknown protein [Arabidopsis thaliana] (T	2.7274	0.0455	0.1226	1.8634	0.1215	0.1768	0.2642	0.7948	0.4618	-0.5999	0.5622	0.3497
256500_at	AT1G36620	transposable element gene	-0.4975	0.2413	0.2885	0.5439	0.1776	0.218	-0.4858	0.1883	0.2032	0.5155	0.1661	0.1649
256501_at	AT1G36756	similar to unknown protein [Arabidopsis thaliana] (T	-0.658	0.4531	0.3996	0.1531	0.8562	0.5062	-0.8264	0.168	0.1904	-0.01523	0.9768	0.4773
256502_at	AT1G36730;AT1G36732	initiation factor 5, putative / eIF-5, putative];[AT1G3	-0.2525	0.2159	0.2723	0.1036	0.5794	0.4159	-0.3292	0.1264	0.1612	0.02681	0.8829	0.4523
256503_at	AT1G75250	myb family transcription factor	-2.3489	0.0013	0.0376	-2.1731	0.0018	0.0323	1.1795	0.016	0.0505	1.3553	0.01	0.0312
256504_at	AT1G75210	5' nucleotidase family protein	-0.3954	0.0343	0.1071	-0.5413	0.0124	0.0597	-0.1972	0.1905	0.2059	-0.3431	0.0519	0.0812
256505_at	AT1G75200	flavodoxin family protein / radical SAM domain-cont	0.8393	0.019	0.0819	0.6705	0.0384	0.0971	-0.2765	0.1686	0.1908	-0.4453	0.0539	0.083
256506_at	AT1G75160	similar to unknown protein [Arabidopsis thaliana] (T	-2.0911	0.0778	0.1608	-1.5874	0.1479	0.1966	-0.5078	0.4304	0.3298	-0.00401	0.9948	0.4814
256507_at	AT1G75150	similar to unknown protein product [Vitis vinifera] (G	0.01292	0.9751	0.571	0.2655	0.5321	0.397	-0.5997	0.0723	0.1169	-0.3471	0.233	0.2033
256508_at	AT1G75140	Identical to Uncharacterized membrane protein At1	0.618	0.0027	0.0426	0.8367	8.00E-04	0.0284	0.06732	0.5096	0.3632	0.286	0.0372	0.0658
256509_at	AT1G75300	isoflavone reductase, putative	0.1258	0.7024	0.4934	-0.5878	0.1274	0.1811	0.4697	0.1999	0.2118	-0.2439	0.4704	0.3138
256510_at	AT1G33360	ATP-dependent Clp protease ATP-binding subunit (	0.2232	0.3734	0.3611	0.3046	0.2436	0.2603	-0.4153	0.0631	0.1081	-0.3339	0.1094	0.1273
256511_at	AT1G33390	helicase domain-containing protein	0.4143	0.2206	0.2756	0.8609	0.1119	0.1688	-0.6366	0.0898	0.1324	-0.4701	0.1752	0.1703
256512_at	AT1G33265	similar to unknown [Populus trichocarpa] (GB:ABK9	0.8306	0.0124	0.0687	0.7608	0.0166	0.0669	0.3129	0.1783	0.1975	0.2431	0.274	0.225
256513_at	AT1G31480	SGR2 (SHOOT GRAVITROPISM 2)	0.05215	0.7305	0.5027	-0.3401	0.0736	0.1362	0.09929	0.5206	0.3673	-0.293	0.1666	0.125
256514_at	AT1G66130	oxidoreductase N-terminal domain-containing prote	-0.4728	0.0013	0.0366	-0.4979	0.001	0.0293	-0.3033	0.0065	0.0332	-0.3284	0.0049	0.022
256515_at	AT1G66020	terpene synthase/cyclase family protein	-1.4905	0.1363	0.2144	0.2964	0.7301	0.4686	-0.8001	0.3744	0.3049	0.9868	0.2854	0.2311
256516_at	AT1G66150	TMK1 (TRANSMEMBRANE KINASE 1)	-0.3296	0.0966	0.1795	-0.4516	0.0414	0.1011	-0.148	0.0887	0.1315	-0.27	0.015	0.039
256517_at	AT1G66170	MMD1 (MALE MEIOCYTE DEATH 1); DNA binding	-0.3074	0.6642	0.4808	0.5593	0.4428	0.3606	-0.1468	0.8341	0.4738	0.7199	0.3347	0.2555
256518_at	AT1G66080	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.1106	0.7076	0.4952	0.09058	0.758	0.4774	0.4533	0.002	0.0211	0.4333	0.0024	0.0161
256519_at	AT1G66110	similar to unknown protein [Arabidopsis thaliana] (T	0.9296	0.6199	0.4665	-1.1444	0.5449	0.4025	0.9596	0.3817	0.3087	-1.1143	0.3178	0.2473
256520_at	AT1G66030	CYP98A14P (cytochrome P450, family 98, subfami	-0.398	0.6455	0.4748	-0.8076	0.3705	0.3278	0.6431	0.4588	0.3426	0.2334	0.7811	0.4232
256521_at	AT1G66120	acyl-activating enzyme 11 (AAE11)	-0.07936	0.9508	0.5648	0.5417	0.1014	-1.3892	0.2877	0.2624	2.2619	0.1168	0.1325	
256522_at	AT1G66160	U-box domain-containing protein	-0.7667	0.1685	0.2403	-0.4266	0.0431	0.3427	0.4435	0.0971	0.1386	0.7836	0.0189	0.044
256523_at	AT1G66070	initiation factor-related	-0.1167	0.8451	0.5474	-0.06899	0.9414	0.4089	0.4524	0.0145	0.048	0.4981	0.0103	0.0317
256524_at	AT1G66200	ATGSR2 (Arabidopsis thaliana glutamine synthase	-0.03869	0.7869	0.5198	-0.1658	0.2833	0.2827	-0.08873	0.1154	0.1527	-0.2158	0.0082	0.0281
256525_at	AT1G66180	aspartyl protease family protein	-0.2284	0.5261	0.4316	0.2486	0.4923	0.3813	0.1394	0.5583	0.3819	0.6164	0.0478	0.0772
256526_at	AT1G66090	disease resistance protein (TIR-NBS class), putative	0.3001	0.518	0.4285	-0.1503	0.7407	0.4715	-0.3981	0.2645	0.2491	-0.2484	0.1814	0.3116
256527_at	AT1G66100	thionin, putative	-1.2062	0.0273	0.0957	-1.593	0.0109	0.056	0.8451	3.00E-04	0.0141	0.4583	0.0034	0.019
256528_at	AT1G66140	ZFP4 (ZINC FINGER PROTEIN 4); nucleic acid bin	-0.1968	0.7247	0.501	-0.05433	0.9219	0.5245	0.7058	0.0574	0.1024	0.8482	0.0336	0.062
256529_at	AT1G33260	protein kinase family protein	0.2696	0.3727	0.3608	-0.3571	0.2647	0.2671	-0.4489	0.1703	0.192	-1.0756	0.0161	0.0405
256530_at	AT1G33290	sporulation protein-related	-0.5373	0.1014	0.1841	-0.418	0.1744	0.2156	-0.9573	0.0036	0.0263	-0.8381	0.0058	0.0236
256531_at	AT1G33320	cystathionine gamma-synthase, chloroplast, putative	-1.8705	0.2001	0.2622	1.5463	0.2741	0.2776	-0.8639	0.5086	0.3629	2.5519	0.0989	0.1198
256532_at	AT1G33330	pentatricopeptide (PPR) repeat-containing protein	0.4354	0.409	0.3795	-0.224	0.6602	0.4451	-0.03436	0.9455	0.5046	-0.6937	0.216	0.1941
256533_at	AT1G33250	fringe-related protein	0.5273	0.0585	0.1386	0.2101	0.3546	0.3203	-0.8731	4.00E-04	0.0146	-1.1902	1.00E-04	0.0062
256534_at	AT1G33270	patatin-related	0.12	0.336	0.3433	-0.3595	0.0307	0.087	-0.08262	0.4937	0.3571	-0.5621	0.0069	0.0259
256535_at	AT1G33280	ANAC015 (Arabidopsis NAC domain containing pro	-0.1417	0.858	0.5406	-1.4294	0.1268	0.1806	0.269	0.6796	0.4243	-1.0387	0.1372	0.1463
256536_at	AT1G33330	release factor, putative	-0.1507	0.1763	0.2457	-0.2677	0.0435	0.1034	-0.02355	0.7918	0.4606	-0.1406	0.1673	0.1656
256537_at	AT1G33340	epsin N-terminal homology (ENTH) domain-contain	-0.6204	0.0595	0.1396	-0.9701	0.0151	0.0646	0.2211	0.4051	0.3186	-0.1286	0.6173	0.3693
256538_x_at	AT1G33360	transposable element gene	0.4465	0.7519	0.5089	1.0462	0.3729	0.3729	-1.6142	0.2085	0.2169	-1.0145	0.3998	0.2941
256539_at	AT3G32910	transposable element gene	1.5167	0.0948	0.1779	-0.4648	0.5408	0.401	0.6695	0.3905	0.3124	-1.312	0.1325	0.1433
256540_at	AT3G32917	transposable element gene	-0.1569	0.8664	0.5425	-1.4378	0.1756	0.2166	-0.00515	0.9949	0.5164	-1.2861	0.1633	0.1633
256541_at	ATGLR3.3 (Arabidopsis thaliana glutamate receptor	0.3826	0.0553	0.135	0.2275	0.1863	0.2239	-0.6038	0.0134	0.046	-0.7589	0.006	0.0241	0.0116
256542_at	AT1G42550	PMI1 (PLASTID MOVEMENT IMPAIRED1)	-0.3941	0.0338	0.1063	-0.5375	0.0124	0.0597	-0.06988	0.604	0.3996	-0.2133	0.1613	0.1621
256543_at	AT1G42480	similar to unknown protein product [Vitis vinifera] (G	0.658	0.0221	0.0872	0.02018	0.9167	0.5231	0.4295	0.0399	0.0827	-0.2083	0.2193	0.1957
256544_at	AT1G42540	ATMLO6/MLO6 (MILDEW RESISTANCE LOCUS C	-0.4363	0.3715	0.3602	-0.7403	0.1631	0.2081	0.6816	0.0221	0.0601	0.3775	0.1146	0.131
256545_at	AT1G41800	transposable element gene	0.2061	0.1865	0.253	0.08547	0.5451	0.4026	-0.5422	0.0138	0.0469	-0.6629	0.0069	0.0258
256546_at	AT1G41820	carboxylesterase/ lipase	0.8377	0.4706	0.4076	-1.1243	0.3456	0.3158	1.3049	0.2828	0.2597	-0.6571	0.5663	0.3513
256547_at	AT1G41840	leucine-rich repeat family protein / protein kinase fa	0.6887	0.0311	0.1023	0.2146	0.3673	0.3263	-0.123	0.5917	0.3952	-0.5972	0.0475	0.0769
256548_at	AT1G41770	nodulin MtN3 family protein	-1.3299	0.0024	0.0421	-1.3641	0.0022	0.0333	-0.5	0.0619	0.1069	-0.5342	0.0515	0.0809
256549_at	AT3G31310	transposable element gene	-0.8922	0.2078	0.2669	-0.591	0.3765	0.3303	-0.5767	0.2976	0.2674	-0.2754	0.5983	0.3629
256550_at	no_match	no_match	0.4766	0.6509	0.4766	0.7161	0.5039	0.3862	-1.3095	0.2509	0.2414	-1.07	0.3346	0.2554
256551_at	AT3G31320	transposable element gene	-0.106	0.9341	0.5608	0.9334	0.4815	0.3768	0.963	0.4687	0.3469	2.0023	0.1717	0.1682
256552_at	no_match	no_match	-1.2867	0.2079	0.2669	1.827	0.1002	0.1595	-1.1969	0.2353	0.2323	1.9168	0.0891	0.1121
256553_at	AT3G31360	transposable element gene	-0.1186	0.7539	0.5222	0.07508	0.8682	0.5095	0.3906	0.4096	0.3206	0.5842	0.2408	0.2076
256554_at	AT3G31380	transposable element gene	0.06577	0.9648	0.5684	-0.4154	0.7813	0.4839	-0.2101	0.883	0.4876	-0.6913	0.6332	0.3748
256555_at	no_match	no_match	-0.5886	0.6239	0.4678	0.6362	0.5971	0.4222	0.4282	0.7193	0.4382	1.6529	0.2106	0.1912
256556_at	AT3G31403	transposable element gene	-0.4949	0.7071	0.4951	1.4066	0.3152	0.3004	0.5833	0.659	0.4177	2.4848	0.1126	0.1295
256557_at	AT3G31410	transposable element gene	0.7651	0.5864	0.4549	-0.3429	0.8042	0.4909	1.7976	0.2374	0.2337	0.6895	0.6226	0.3711
256558_at	AT3G31300	transposable element gene	-2.269	0.264	0.3019	0.6836	0.7156	0.4639	-3.1339	0.1474	0.1771	-0.1813	0.9224	0.4636
256559_at	AT3G31340	transposable element gene	0.7134	0.5141	0.4269	-0.3724	0.7279	0.4682	1.9441	0.1232	0.1588	0.8583	0.4382	0.3006
256560_s_at	AT3G31415;AT3G32030	[AT3G31415, terpene synthase/cyclase family prote	0.3393	0.6917	0.4899	-1.3777	0.1584	0.2047	-0.415	0.6294	0.4077	-2.1321	0.0552	0.0842
256561_s_at	AT3G31355;AT3G31330	[AT3G31355, transposable element gene];[AT3G31	1.5331	0.1301	0.2085	-0.359	0.6792	0.4516	2.7966	0.0256	0.065	0.9045	0.3248	0.2506
256562_at	AT3G29775	transposable element gene	-2.9484	0.0765	0.1592	0.08277	0.9501	0.5319	-0.8733	0.3942	0.3139	2.1578	0.0779	0.1032
256563_at	AT3G29780	RALFL27 (RALF-LIKE 27)	0.6877	0.6485	0.476	0.1399	0.9251	0.5254	0.01705	0.9909	0.5154	-0.5307	0.7235	0.4052
256564_at	AT3G29770	hydrolase, alpha/beta fold family protein	0.4753	0.2972	0.3215	1.1702	0.0421	0.1019	-0.3772	0.0509	0.0956	0.3176	0.0809	0.1057
256565_at	no_match	no_match	-1.727	0.1871	0.2534	0.1944	0.8667	0.5089	-3.8147	0.0246	0.0637	-1.8933	0.1563	0.159
256566_at	AT3G19530	unknown protein	-1.2942	0.3549	0.3523	0.9356	0.492	0.3812	-0.2335	0.8374	0.4749	1.9962	0.1345	0.1447
256567_at	AT3G19553	amino acid permease family protein	-0.1258	0.4659	0.4056	0.03367	0.8399	0.5014	-0.3173	0.0989	0.1401	-0.1578	0.3469	0.2611
256568_at	AT3G19520	similar to unknown protein [Arabidopsis thaliana] (T	0.7815	0.0018	0.0391	0.8778	0.0011	0.0294	-0.4055	0.0183	0.0541	-0.3092	0.0426	0.0719
256569_at	AT3G19550	similar to hypothetical protein [Vitis vinifera] (GB:CA	1.0018	0.2343	0.284	1.4448	0.1138	0.1704	1.0947	0.0335	0.0747	1.5377	0.0111	0.0329
256570_at	AT3G19540	similar to unknown protein [Arabidopsis thaliana] (T	0.4998	0.0313	0.1027	0.7647	0.0076	0.0489	-0.2827	0.1397	0.1709	-0.0178	0.9134	0.4607
256571_at	AT3G30730	contains domain HELICASE-RELATED (PTHR10	0.001788	0.9988	0.5763	-1.9505	0.1543	0.2014	-0.3242	0.7656	0.4529	-2.2765	0.0885	0.1116
256572_at	AT3G30740	40S ribosomal protein S25 (RPS25C), pseudogene	-0.03834	0.9747	0.571	-0.4796	0.6951	0.4571	-0.7517	0.545	0.3774	-1.1929	0.3536	0.2643
256573_at	AT3G14860	NHL repeat-containing protein	0.3087	0.0407	0.1163	0.3887	0.0199	0.0722	-0.1322	0.2708	0.2528	-0.05227	0.6403	0.3772
256574_at	AT3G14780	similar to ATGSL04 (GLUCAN SYNTHASE-LIKE 4);	-0.0114	0.9855	0.5733	0.8781	0.2118	0.2408	0.9947	0.1524	0.1806	1.8842	0.0288	0.0567
256575_at	AT3G14790	RHM3 (RHAMNOSE BIOSYNTHESIS 3); catalytic	-0.2607	0.2788	0.3107	-0.457	0.0933	0.1539	-0.4347	0.0157	0.05	-0.631	0.0043	0.0208
256576_at	AT3G28210	PMZ; zinc ion binding	1.7149	0.014	0.0724	2.2776	0.0052	0.0429	0.3926	0.2216	0.2245	0.9553	0.0244	0.0514
256577_at	AT3G28220	meprin and TRAF homology domain-containing pro	-0.4579	0.2032	0.2642	-0.3439	0.3174	0.3016	-0.2333	0.3171	0.2768	-0.1193	0.5905	0.3601
256578_at	AT3G28200	peroxidase, putative	-0.5175	0.1568	0.2309	-0.4317	0.2202	0.246	-0.1078	0.25	0.241	-0.02193	0.798	0.4282
256579_at	AT3G28720	similar to unknown protein [Arabidopsis thaliana] (T	0.2714	0.016	0.0764	0.2122	0.0349	0.0923	-0.3067	0.0105	0.0408	-0.3658	0.0057	0.0234
256580_s_at	AT3G28810;AT3G28820	[AT3G28810, similar to unknown protein [Arabidops	0.3022	0.7974	0.5231	-3.1642	0.0454	0.1055	2.1868	0.1181	0.1547	-0.6752	0.573	0.3535
256581_at	AT3G28830	similar to unknown protein [Arabidopsis thaliana] (T	0.01524	0.9809	0.5723	-0.1103	0.8625	0.5078	0.03042	0.9618	0.5081	-0.09508	0.8813	0.4518
256582_at	AT3G28840	similar to unknown protein [Arabidopsis thaliana] (T	-1.4942	0.0437	0.1206	-0.4399	0.44	0.3595	-0.3452	0.4216	0.326	0.7091	0.14	0.1481
256583_at	AT3G28850	glutaredoxin family protein	0.9578	0.1088	0.191	1.2526	0.0547	0.116	0.06631	0.854	0.4795	0.361	0.3457	0.2606
256584_at	AT3G28750	similar to unknown protein [Arabidopsis thaliana] (T	-1.3105	0.1409	0.2183	0.4114	0.596	0.4219	-1.6148	0.087	0.1301	0.1071	0.8882	0.4537
256585_at	AT3G28760	similar to unknown protein product [Vitis vinifera] (G	-1.0836	0.0224	0.0875	-1.2511	0.014	0.0627	0.1747	0.4755	0.3498	0.007094	0.976	0.4772
256586_at	AT3G28770	similar to unknown protein [Arabidopsis thaliana] (T	-1.7809	0.1385	0.2161	0.8911	0.4077	0.3448	-2.5862	0.0551	0.1	0.08579	0.9334	0.4665
256587_at	AT3G28780	similar to unknown protein [Arabidopsis thaliana] (T	-0.4745	0.6571	0.478	0.06781	0.9487	0.5316	0.3619	0.7335	0.4427	0.9042	0.4132	0.2897
256588_at	AT3G28790	similar to unknown protein [Arabidopsis thaliana] (T	0.2402	0.8538	0.5392	0.4154	0.7511	0.4753	-1.7715	0.0992	0.1403	-1.5963	0.1261	0.139
256589_at	AT3G28740	cytochrome P450 family protein	-1.349	0.0445	0.1217	-1.8802	0.0163	0.0664	0.7753	0.1294	0.1635	0.264	0.5517	0.3457
256590_at	AT3G28730	ATHMG (HIGH MOBILITY GROUP); transcription fa	0.1935	0.0167	0.0775	-0.2013	0.0146	0.0638	0.1208	0.0689	0.1137	-0.274	0.005	0.0221
256591_at	AT3G31910	similar to Ulp1 protease family protein [Arabidopsis	-0.3658	0.4877	0.4149	0.4225	0.4277	0.3543	0.1252	0.8067	0.4656	0.9135	0.1292	0.1409
256592_at	AT3G31915	transposable element gene	0.3179	0.7984	0.5235	-0.4937	0.6934	0.4567	-0.7945	0.4792	0.3511	-1.606	0.1902	0.1794
256593_at	AT3G28510	AAA-type ATPase family protein	2.5053	0.1348	0.2132	4.1955	0.0351	0.0926	-0.3392	0.7601	0.4512	1.3509	0.2629	0.2192
256594_at	AT3G28520	AAA-type ATPase family protein	-0.5864	0.5808	0.4525	0.215	0.8366	0.5007	-0.861	0.4281	0.3288	-0.05953	0.9544	0.4722
256595_x_at	AT3G28530;AT1G36770	[AT3G28530, UDP-glucose 4-epimerase];[AT1G36	-0.00871	0.9715	0.5702	0.04673	0.8482	0.5039	0.4946	0.0968	0.1383	0.55	0.0741	0.1
256596_at	AT3G28540	AAA-type ATPase family protein	2.165	0.0112	0.0662	2.3195	0.0088	0.0516	0.3532	0.1786	0.1977	0.5077	0.0792	0.1042
256597_at	AT3G28500	60S acidic ribosomal protein P2 (RPP2C)	0.9007	0.0378	0.1121	0.9788	0.0293	0.0851	0.5576	0.0254	0.0647	0.6368	0.0166	0.0411
256598_at	AT3G30180	BRI5OX2/CYP85A2 (BRASSINOSTEROID-6-OXID	0.01642	0.9495	0.5646	0.01128	0.9653	0.5353	-0.4884	0.0375	0.08	-0.4936	0.0364	0.0649
256599_at	AT3G14760	similar to unnamed protein product [Vitis vinifera] (G	-1.941	0.0059	0.0534	-1.0354	0.0463	0.1067	-1.0943	0.0394	0.0821	-0.1886	0.6308	0.3739
256600_at	AT3G14850	similar to unknown protein [Arabidopsis thaliana] (T	-1.0272	0.0356	0.1089	-0.9245	0.0484	0.1093	0.02129	0.8738	0.4851	0.124	0.3801	0.2758
256601_s_at	AT3G28290;AT3G28300	[AT3G28290, ATA4];[AT3G28300, ATA4]	-0.05275	0.8575	0.5406	0.2756	0.3738	0.3294	-0.6884	0.0153	0.0493	-0.3601	0.1007	0.1211
256602_at	AT3G28310	similar to ATA4 [Arabidopsis thaliana] (TAIR:AT3G	0.5939	0.6072	0.4622	0.7396	0.5261	0.3946	-1.2236	0.2682	0.2512	-1.0779	0.3209	0.2487
256603_at	AT3G28270	Identical to UPF0496 protein At3g28270 [Arabidops	0.1627	0.5708	0.4493	-0.04413	0.8887	0.5155	0.8997	0.2092	0.2173	-0.1869	0.4389	0.301
256604_at	AT3G28640	transposable element gene	-1.3666	0.242	0.2887	2.4894	0.0668	0.1294	-1.2961	0.2631	0.2482	2.5599	0.062	0.0903
256605_at	AT3G32940	RNA binding	0.7265	0.0106	0.0649	0.3493	0.0954	0.1557	-0.08652	0.4983	0.359	-0.4638	0.0163	0.0408
256606_at	AT3G32960	contains InterPro domain Region of unknown functi	0.096168	0.8963	0.5503	-0.8847	0.2709	0.2759	1.0255	0.071	0.1159	0.237	0.6025	0.3642
256607_at	AT3G32930	similar to unnamed protein product [Vitis vinifera] (G	-0.2167	0.1123	0.1941	-0.1076	0.3707	0.3278	0.09293	0.4332	0.331	0.202	0.1314	0.1425
256608_at	AT3G30840	unknown protein	-0.3547	0.7198	0.4993	0.533	0.5939	0.421	-1.8702	0.1122	0.15	-0.9825	0.3463	0.2608
256609_at	AT3G30843	transposable element gene	-0.1596	0.8184	0.5212	-0.1066	0.9324	0.5282	0.1917	0.7831	0.4583	-0.6654	0.3645	0.2689
256610_at	AT3G30845	unknown protein	-1.0976	0.4183	0.3841	-0.9836	0.4645	0.3698	-2.2538	0.1378	0.1695	-2.1398	0.1537	0.1573
256611_at	AT3G29270	ubiquitin-protein ligase	0.2126	0.3231	0.3361	0.2371	0.2774	0.2795	0.06844	0.5764	0.3891	0.09297	0.4557	0.3082
256612_at	AT3G29280	similar to unknown [Populus trichocarpa] (GB:ABK9	1.9229	6.00E-04	0.0033	1.6896	2.00E-04	0.0249	0.559	0.0021	0.0216	0.09224	0.3061	0.2415
256613_at	AT3G29290	EMB2076 (EMBRYO DEFECTIVE 2076)	-0.4412	0.0606	0.141	-0.4227	0.068	0.1307	-0.9363	0.0053	0.0306	-0.9179	0.0057	0.0235
256614_at	AT3G29300	unknown protein	0.7884	0.4811	0.4124	0.144	0.8941	0.5169	0.7494	0.5016	0.3601	0.105	0.9226	0.4636
256615_at	AT3G29260	UDP-glucuronosyl/UDP-glucosyl transferase family	-1.1516	0.2545	0.2962	0.1215	0.8952	0.5173	0.2106	0.8199	0.4698	1.4838	0.162	0.1624
256616_at	AT3G22250	OTU-like cysteine protease family protein	0.3157	0.3032	0.3249	0.6922	0.0608	0.1225	0.06524	0.6906	0.428	0.4417	0.0442	0.0737
256617_at	AT3G22240	unknown protein	-0.2566	0.4041	0.3773	-1.3969	0.0071	0.0477	1.4083	0.0069	0.0339	0.269	0.3838	0.2775
256618_at	AT3G29440	VRN5 (VERNALIS-LIKE 1)	0.09099	0.7532	0.5095	0.2183	0.4644	0.3698	-0.3471	0.0933	0.1354	-0.2198	0.2372	0.2057
256619_at	AT3G24460	TMS membrane family protein / tumour differentially	-0.8622	0.6087	0.4627	-2.0959	0.2489	0.2632	-1.3087	0.245	0.238	-2.5424	0.0573	0.0862
256620_at	AT3G24480	leucine-rich repeat family protein / extensin family p	-1.1619	0.1061	0.1884	-0.8685	0.1951	0.2294	-0.5751	0.3118	0.2744	-0.2817	0.6013	0.3638
256621_at	AT3G24450	copper-binding family protein	0.8739	0.4567	0.4012	2.1663	0.1109	0.1681	0.6068	0.5982	0.3975	1.8992	0.1481	0.1535
256622_at	AT3G28920	ATH634 (ARABIDOPSIS THALIANA HOMEOBOX	0.2103	0.1272	0.206	0.2627	0.0744	0.1368	0.5148	0.0093	0.0386	0.5672	0.0066	0.0253
256623_at	AT3G19960	ATATM (myosin 1); motor	0.5999	0.0462	0.1237	0.6566	0.0354	0.0929	-0.5005	0.0513	0.0961	-0.4438	0.0713	0.0978
256624_at	AT3G19990	binding	0.6962	0.0261	0.0934	0.5676	0.0483	0.1091	0.1211	0.5316	0.3718	-0.0075	0.9682	0.475
256625_at	AT3G20010	SNF2 domain-containing protein / helicase domain-	0.7612	0.0729	0.1555	-0.01757	0.9582	0.5338	-0.6548	0.0921	0.1343	-1.4335	0.0085	0.0286
256626_at	AT3G20015	pepsin A	-0.2017	0.6184	0.

256690_at	AT3G32160	similar to unknown protein [Arabidopsis thaliana] (T	-0.5262	0.2433	0.2895	-1.5871	0.0146	0.0637	0.6078	0.1363	0.1686	-0.4531	0.2377	0.206
256691_at	AT3G32140	transposable element gene	-0.5147	0.5668	0.4476	-1.8799	0.085	0.1468	0.9608	0.3092	0.273	-0.4045	0.6498	0.3808
256692_at	AT3G32050	similar to unknown protein [Arabidopsis thaliana] (T	-0.2821	0.7815	0.5181	0.9356	0.3809	0.3324	-0.775	0.4609	0.3436	0.4428	0.6658	0.3861
256693_at	AT3G32060	transposable element gene	0.04331	0.974	0.5708	-0.6373	0.637	0.4372	-0.1816	0.8243	0.471	-0.8623	0.3235	0.2499
256694_at	AT3G32080	transposable element gene	-0.00781	0.9921	0.575	0.03662	0.963	0.5347	-1.1922	0.183	0.2009	-1.1478	0.1964	0.1828
256695_at	AT3G32090	transcription factor-related	-0.7777	0.479	0.4115	0.5266	0.6254	0.433	-1.1139	0.3266	0.2816	0.1905	0.8578	0.4452
256696_at	AT3G32650	mRNA capping enzyme family protein	0.1839	0.2242	0.2779	0.2703	0.1022	0.1613	-0.3595	0.0224	0.0605	-0.273	0.0516	0.0809
256697_at	AT3G32060	similar to EDA30 (embryo sac development arrest 3	0.1926	0.4852	0.414	0.4982	0.1178	0.1735	-0.3843	0.1691	0.1912	-0.07883	0.7489	0.4134
256698_at	AT3G20680	similar to predicted protein [Physcomitrella patens s	0.0181	0.9094	0.5538	-0.1806	0.2933	0.2883	-0.1044	0.5231	0.3682	-0.3031	0.1124	0.1293
256699_at	AT3G20690	F-box protein-related	1.0504	0.245	0.2906	0.7622	0.3791	0.3314	-0.1655	0.8112	0.467	-0.4537	0.5229	0.335
256700_at	AT3G52260	pseudouridine synthase family protein	0.2363	0.1576	0.2313	0.2712	0.1171	0.173	-0.5311	0.0175	0.053	-0.4962	0.0219	0.0482
256701_at	AT3G52270	ATP binding / RNA polymerase II transcription facto	0.7447	0.5195	0.4289	-0.3375	0.7652	0.4789	0.5211	0.3667	0.3013	-0.5611	0.335	0.2556
256702_at	AT3G30380	similar to unknown protein [Arabidopsis thaliana] (T	-0.07541	0.7813	0.518	0.2174	0.4401	0.3596	-0.6631	0.0594	0.1045	-0.3702	0.2186	0.1954
256703_at	AT3G30260	MADS-box protein (AGL79)	0.7084	0.5061	0.4233	-1.9882	0.11	0.1674	1.665	0.1615	0.1864	-1.0316	0.3479	0.2615
256704_at	AT3G30280	transferase family protein	-0.5011	0.6368	0.4719	-0.4698	0.6573	0.4442	1.1577	0.2791	0.2575	1.1889	0.2682	0.2218
256705_at	AT3G30290	CYP702A8 (cytochrome P450, family 702, subfami	-0.1179	0.9019	0.5518	-1.6389	0.1422	0.1923	0.5934	0.429	0.3292	-0.9277	0.2413	0.2078
256706_at	AT3G30300	similar to EDA30 (embryo sac development arrest 3	0.2629	0.2246	0.2783	0.317	0.1587	0.205	-0.6453	0.0141	0.0473	-0.5912	0.0188	0.044
256707_at	AT3G30310	transposable element gene	0.3606	0.6896	0.489	-1.0025	0.2983	0.2907	1.2622	0.2071	0.2161	-0.1009	0.9101	0.4599
256708_at	AT3G30320	unknown protein	0.08307	0.9443	0.5635	-0.8887	0.4709	0.3725	0.6643	0.5027	0.3605	-0.3075	0.7505	0.414
256709_at	AT3G30330	transposable element gene	0.4957	0.6478	0.4757	1.2137	0.2938	0.2885	-0.5861	0.5911	0.3951	0.132	0.9019	0.4579
256710_at	AT3G30350	unknown protein	-0.06954	0.9131	0.5548	0.9249	0.197	0.231	-0.5564	0.1805	0.199	0.438	0.2711	0.2233
256711_at	AT3G30390	amino acid transporter family protein	0.09822	0.4619	0.4038	0.03866	0.765	0.4789	-0.4692	0.0178	0.0534	-0.5268	0.0119	0.0343
256712_at	AT3G34020	calcium ion binding	1.9541	0.2232	0.2771	0.07804	0.9569	0.5335	2.1259	0.1105	0.1488	0.2499	0.822	0.4348
256713_at	AT3G34060	peroxidase, putative	-1.1751	0.0033	0.0446	-1.095	0.0042	0.0403	-0.5086	0.0528	0.0975	-0.4285	0.0835	0.1078
256714_at	AT3G34080	cysteine proteinase, putative	-0.1403	0.8884	0.5479	0.01955	0.9844	0.5402	-1.8078	0.1264	0.1613	-1.6477	0.154	0.1575
256715_at	AT3G34090	MEE18 (maternal effect embryo arrest 18)	0.6902	0.0459	0.1232	0.93	0.0182	0.0697	0.161	0.5411	0.3757	0.4008	0.1719	0.1684
256716_at	AT3G34100	unknown protein	1.8374	0.0438	0.1207	-1.9344	0.0376	0.096	2.9116	0.01	0.0398	-0.8602	0.245	0.2097
256717_at	AT3G34110	similar to forkhead-associated domain-containing p	0.6624	0.5329	0.4341	-0.9768	0.3717	0.3282	0.7039	0.509	0.363	-0.9353	0.3903	0.2801
256718_at	AT3G34120	cytochrome-c oxidase	0.9491	0.3923	0.3712	-0.02235	0.9831	0.54	0.2461	0.816	0.4686	-0.7254	0.5047	0.3276
256719_at	no_match	no_match	-0.05544	0.9651	0.5684	-0.6675	0.6046	0.425	-0.5593	0.6627	0.4188	-1.1714	0.3804	0.276
256720_at	AT3G34140	Dof-type zinc finger domain-containing protein	1.3227	0.0064	0.0545	1.2581	0.0076	0.0488	1.1092	0.0016	0.0204	1.0447	0.0021	0.0154
256721_at	AT3G34150	WAVE1 (WASP (WISKOTT-ALDRICH SYNDROME	-0.1668	0.1427	0.2197	-0.204	0.0899	0.1511	-0.1056	0.1917	0.2065	-0.1428	0.1011	0.1214
256722_at	AT3G34050	similar to unknown protein product [Vitis vinifera] (G	0.4105	0.1487	0.2243	0.4208	0.1411	0.1916	0.6077	0.0417	0.0849	0.618	0.0396	0.0687
256723_at	AT3G34160	nuclear matrix protein	-0.06334	0.6736	0.4839	0.2229	0.6985	0.4396	0.7557	0.0063	0.0328	1.044	0.0019	0.0151
256724_at	AT3G34040	apoptosis inhibitory 5 (API5) family protein	0.6266	0.0118	0.0679	0.4143	0.0441	0.1039	-0.08904	0.3409	0.2887	-0.3014	0.0217	0.0479
256725_at	AT3G34070	similar to unknown protein [Arabidopsis thaliana] (T	0.5972	0.0771	0.1598	0.2709	0.3434	0.3149	-0.281	0.1421	0.173	-0.6073	0.0169	0.0415
256726_at	no_match	no_match	-0.2806	0.2735	0.3075	-0.4017	0.1436	0.1934	-0.4328	0.1221	0.1581	-0.5537	0.0666	0.094
256727_at	AT3G52240	similar to unnamed protein product [Vitis vinifera] (G	0.5779	0.0163	0.0771	0.7687	0.0061	0.0449	-0.3141	0.0939	0.1358	-0.1232	0.4391	0.301
256728_at	AT3G52660	glutamyl-tRNA(Gln) amidotransferase, putative	-0.3988	0.095	0.1781	-0.6824	0.0204	0.0729	-0.3647	0.1173	0.1541	-0.6483	0.024	0.0509
256729_at	AT3G52680	similar to unknown protein [Arabidopsis thaliana] (T	-0.4522	0.1078	0.1899	-0.05023	0.8298	0.4988	-1.3578	0.0028	0.0241	-0.9558	0.0098	0.0309
256730_at	no_match	no_match	-2.8924	0.0531	0.1323	3.0529	0.0455	0.1057	-0.1035	0.9272	0.4999	-0.264	0.8163	0.4333
256731_at	AT3G30340	nodulin MtN21 family protein	0.2694	0.7624	0.5123	-0.3724	0.6777	0.4511	2.1434	0.0616	0.1068	1.5016	0.1455	0.1518
256732_at	AT3G30360	transposable element gene	-2.0984	0.0478	0.1259	-1.6737	0.0877	0.1492	-1.1529	0.1923	0.2069	-0.7281	0.3785	0.2749
256733_at	AT3G30370	similar to SWAP (Suppressor-of-White-APricot)/sur	0.2098	0.9049	0.5526	0.1065	0.9516	0.5323	-0.5472	0.7566	0.4502	-0.6505	0.7132	0.4021
256734_at	AT3G29390	RIK (RS2-INTERACTING KH PROTEIN)	0.2425	0.3199	0.3343	-0.1827	0.4409	0.3599	-1.2123	0.0032	0.0251	-1.6375	0.001	0.0122
256735_at	AT3G29400	ATEXO70E1 (exocyst subunit EXO70 family protein	0.1473	0.3319	0.3411	0.1431	0.3443	0.3153	-0.1519	0.3119	0.2778	-0.1561	0.3074	0.2422
256736_at	AT3G29410	terpene synthase/cyclase family protein	-0.1174	0.886	0.5474	-0.5541	0.5109	0.389	-0.6056	0.4749	0.3495	-1.0423	0.2466	0.2105
256737_at	AT3G29420	geranylgeranyl pyrophosphate synthase-related / G	0.1675	0.8321	0.5331	-0.8594	0.3101	0.2974	-0.8781	0.3011	0.2693	-1.9049	0.0617	0.0901
256738_at	AT3G29430	geranylgeranyl pyrophosphate synthase, putative /	0.3676	0.8062	0.5257	1.2311	0.4296	0.3551	0.1298	0.9306	0.5009	0.9935	0.5178	0.3327
256739_s_at	AT3G29460.AT2G11180	[AT3G29460, transposable element gene];[AT2G11	-0.201	0.8747	0.5451	-1.4394	0.2953	0.2894	-0.9893	0.4548	0.3408	-2.2277	0.1361	0.1457
256740_at	AT3G29330	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.6771	0.1577	0.2315	0.4911	0.2766	0.279	0.2222	0.5303	0.3713	0.03619	0.9164	0.4617
256741_at	AT3G29375	KH domain-containing protein	-0.3781	0.4087	0.3795	-0.4017	0.199	0.2323	-0.1019	0.8042	0.4648	-0.3544	0.4093	0.2879
256742_at	AT3G29380	transcription factor IIB (TFIIB) family protein	0.07628	0.8724	0.5447	-0.6779	0.2028	0.2347	0.6021	0.1338	0.1665	-0.152	0.6603	0.3843
256743_at	AT3G29370	similar to unknown protein [Arabidopsis thaliana] (T	-0.8895	0.0847	0.1686	-0.3361	0.4374	0.3585	-0.06911	0.8272	0.4719	0.4843	0.1779	0.1719
256744_at	AT3G29360	AHP2 (HISTIDINE-CONTAINING PHOSPHOTRAN	-0.3251	0.1332	0.2117	-0.00646	0.972	0.5372	0.1376	0.1326	0.1657	0.4562	0.0033	0.0188
256745_at	AT3G29360	UDP-glucose 6-dehydrogenase, putative	-0.04918	0.7996	0.5239	-0.05436	0.7792	0.4833	-0.09984	0.5949	0.3964	-0.105	0.5767	0.3548
256746_at	AT3G29320	glucan phosphorylase, putative	0.8455	0.0244	0.0909	0.4931	0.1092	0.1668	-0.05788	0.8027	0.4644	-0.4103	0.1314	0.1425
256747_at	AT3G29180	similar to unknown protein [Arabidopsis thaliana] (T	0.6531	0.0048	0.0497	0.6364	0.0053	0.0429	-0.4116	0.0075	0.0351	-0.4283	0.0065	0.0251
256748_x_at	AT3G30396	transposable element gene	0.5581	0.4381	0.3929	1.4339	0.0916	0.1527	-1.0236	0.1375	0.1693	-0.1478	0.8022	0.4293
256749_at	AT3G30400	transposable element gene	-0.6623	0.5593	0.4447	-0.00286	0.9979	0.5435	1.4803	0.2282	0.2285	2.1398	0.1091	0.127
256750_at	AT3G27150	kelch repeat-containing F-box family protein	1.4916	0.1263	0.2057	-0.809	0.3549	0.3204	0.4076	0.6264	0.4067	-1.893	0.0708	0.0976
256751_at	AT3G27170	CLC-B (chloride channel protein B); anion channel/	-1.0142	0.0274	0.0958	-1.1138	0.0203	0.0727	-0.6008	0.067	0.112	-0.7004	0.0436	0.073
256752_at	no_match	no_match	-0.2526	0.2951	0.3205	-0.1219	0.5927	0.4205	-0.4591	0.0608	0.1059	-0.3283	0.1379	0.1468
256753_at	AT3G27160	GHS1 (GLUCOSE HYPERSENSITIVE 1); structura	-0.8487	8.00E-04	0.0339	-0.7193	0.0015	0.0313	0.05619	0.5001	0.3597	0.1856	0.0708	0.0976
256754_at	AT3G29590	CHUP1 (CHLOROPLAST UNUSUAL POSITIONIN	-0.2843	0.1636	0.2366	-0.3347	0.1154	0.1714	-0.1433	0.4389	0.3336	-0.1937	0.3103	0.2436
256755_at	AT3G25600	calmodulin, putative	0.5433	0.3436	0.3465	0.5902	0.3084	0.2966	1.0254	0.0014	0.0193	1.0724	0.0011	0.0126
256756_at	AT3G25610	haloacid dehalogenase-like hydrolase family protein	1.6391	0.0206	0.0845	1.5882	0.0228	0.0762	-0.4818	0.1282	0.1627	-0.5327	0.1018	0.122
256757_at	AT3G25620	ABC transporter family protein	-0.2956	0.3418	0.346	0.1397	0.6373	0.4372	-0.6443	0.0298	0.0704	-0.209	0.3443	0.26
256758_at	AT3G25630	transposable element gene	1.2299	0.3625	0.3557	-1.6269	0.2459	0.2615	1.8808	0.1886	0.2046	-0.976	0.4575	0.309
256759_at	AT3G25640	similar to unknown protein [Arabidopsis thaliana] (T	-0.283	0.7846	0.5191	1.3221	0.2438	0.2605	-0.06472	0.9499	0.5055	-1.5403	0.1868	0.1775
256760_at	AT3G25650	ASK15 (ARABIDOPSIS SKP1-LIKE 15); ubiquitin-p	-1.8961	0.0611	0.1418	-0.3604	0.6491	0.4414	1.6167	0.0261	0.0658	3.1524	0.0026	0.0168
256761_at	AT3G25670	leucine-rich repeat family protein	-1.1425	0.0105	0.0646	-1.0027	0.0163	0.0664	-0.1922	0.1051	0.145	-0.05237	0.5999	0.3634
256762_at	AT3G25655	unknown protein	0.08997	0.935	0.561	-0.4875	0.6624	0.4458	0.4789	0.6579	0.4206	-0.09859	0.9288	0.4653
256763_at	AT3G16860	COBL8 (COBRA-LIKE PROTEIN 8 PRECURSOR)	-0.58	0.1401	0.2176	-0.9525	0.0393	0.0982	0.4552	0.1424	0.1733	0.08264	0.7573	0.4159
256764_at	AT3G29310	calmodulin-binding protein-related	0.2012	0.1132	0.1949	0.3157	0.0338	0.0908	0.1469	0.0676	0.1127	0.2614	0.0114	0.0335
256765_at	AT3G22200	POP2 (POLLEN-PISTIL INCOMPATIBILITY 2); 4-a	0.1127	0.0338	0.1063	0.5744	0.0043	0.0408	-0.4616	0.0074	0.0348	-0.1999	0.0956	0.1173
256766_at	AT3G22231	PCC1 (PATHOGEN AND CIRCADIAN CONTROLL	-0.3046	0.1251	0.2047	-0.4829	0.0374	0.0956	0.6046	0.0032	0.0251	0.4262	0.0111	0.033
256767_at	AT3G13680	F-box family protein	-1.0439	0.3626	0.3557	1.1661	0.3154	0.3004	-0.2694	0.8042	0.4648	1.9406	0.129	0.1408
256768_at	AT3G13682	LDL2 (LSD1-LIKE2); amine oxidase	0.287	0.575	0.4508	-0.1037	0.8364	0.5006	-0.06089	0.9033	0.4932	-0.4517	0.3917	0.2807
256769_at	AT3G13690	protein kinase family protein	0.2039	0.2414	0.2885	0.2843	0.1278	0.1815	-0.5942	0.0161	0.0505	-0.5138	0.0258	0.0532
256770_at	AT3G13700.AT3G13710	[AT3G13700, RNA-binding protein, putative];[AT3G	-0.1781	0.416	0.3827	-0.399	0.1121	0.169	-0.4055	0.056	0.101	-0.6264	0.0146	0.0385
256771_at	AT3G13700.AT3G13710	[AT3G13700, RNA-binding protein, putative];[AT3G	-0.3704	0.3392	0.3449	-0.1651	0.6542	0.4432	0.3873	0.3202	0.2784	0.5926	0.1578	0.1598
256772_at	AT3G13750	BGAL1 (BETA GALACTOSIDASE 1); beta-galactos	-0.3853	0.1481	0.2238	-0.1347	0.5655	0.4102	-0.9276	0.0063	0.0328	-0.677	0.0187	0.0438
256773_at	AT3G13630	unknown protein	1.4535	0.0991	0.1816	-0.508	0.4961	0.3829	0.2117	0.7708	0.4544	-1.7498	0.0616	0.09
256774_at	AT3G13760	DC1 domain-containing protein	-0.1126	0.7691	0.5143	-0.2519	0.5209	0.3925	-0.00739	0.9845	0.5138	-0.1467	0.7032	0.3984
256775_at	AT3G13770	pentatricopeptide (PPR) repeat-containing protein	0.2596	0.6038	0.4608	0.2277	0.6476	0.4407	-0.3046	0.5454	0.3775	-0.3365	0.5064	0.3283
256776_at	AT3G13772	endomembrane protein 70, putative	0.7866	0.0072	0.0569	0.4985	0.0326	0.0895	0.1279	0.0603	0.1055	-0.1601	0.0314	0.0598
256777_at	AT3G13780	similar to SMAD/FHA [Medicago truncatula] (GB:AE	0.1522	0.7042	0.494	0.1253	0.7538	0.4763	0.5691	0.2017	0.2127	0.5423	0.2197	0.1959
256778_at	AT3G13782	NAP1;4 (NUCLEOSOME ASSEMBLY PROTEIN1;4	-0.6643	0.4073	0.379	2.1424	0.0406	0.0999	-1.3918	0.0835	0.1272	1.4148	0.0801	0.1052
256779_at	AT3G13784	ATCWINV5 (ARABIDOPSIS THALIANA CELL WAL	-0.4964	0.3017	0.324	-0.1745	0.6984	0.4584	-0.3897	0.3974	0.3154	-0.06789	0.877	0.4505
256780_at	AT3G13840	ATRLI1 (Arabidopsis thaliana RNase L inhibitor pro	0.2858	0.5846	0.4541	-0.1576	0.7597	0.4778	0.4234	0.4036	0.3181	-0.01996	0.967	0.4748
256781_at	AT3G13650	disease resistance response	0.0805	0.6345	0.471	-0.1796	0.3156	0.3005	0.9676	0.0023	0.0226	0.7075	0.0073	0.0266
256782_at	AT3G13660	disease resistance response	0.3916	0.602	0.4602	1.6774	0.0726	0.1349	-0.3877	0.6054	0.3999	0.8981	0.2645	0.22
256783_at	AT3G13670	protein kinase family protein	0.6054	0.0117	0.0677	0.3847	0.0492	0.1099	-0.06149	0.3609	0.2985	-0.2822	0.0091	0.0297
256784_at	AT3G13674	similar to unknown protein [Arabidopsis thaliana] (T	0.2244	0.4986	0.4199	0.02892	0.9283	0.5263	0.5984	0.104	0.1442	0.403	0.2308	0.2018
256785_at	AT3G13720	prenylated rab acceptor (PRA1) family protein	-0.7785	0.0101	0.064	-0.5221	0.0369	0.0949	0.5277	0.0017	0.0205	0.7841	4.00E-04	0.0089
256786_at	AT3G13740	URF 4-related	-0.2366	0.4926	0.417	-0.1153	0.7317	0.4688	-0.1046	0.6041	0.3996	0.01661	0.9332	0.4665
256787_at	AT3G13790	ATBFRUCT1/ATCWINV1 (ARABIDOPSIS THALIA	1.0859	0.0011	0.036	1.1813	8.00E-04	0.0277	0.1031	0.4583	0.3423	0.1985	0.1895	0.179
256788_at	AT3G13730	CYP90D1 (CYTOCHROME P450, FAMILY 90, SU	-1.1497	0.0508	0.1296	-0.9953	0.0751	0.1374	-0.2808	0.5105	0.3634	-0.1265	0.7615	0.4172
256789_at	AT3G13672	seven in absentia (SINA) family protein	1.6824	0.0056	0.0522	0.806	0.0156	0.0652	-0.1812	0.4151	0.3231	-0.4576	0.0835	0.1078
256790_at	AT3G16857	ARR1 (ARABIDOPSIS RESPONSE REGULATOR	0.3768	0.0737	0.1562	0.4343	0.0501	0.111	0.06884	0.6827	0.4251	0.1264	0.4647	0.3119
256791_at	no_match	no_match	-1.6693	0.2563	0.2972	1.3367	0.349	0.3177	-1.5028	0.2833	0.2599	1.5032	0.2832	0.2298
256792_at	AT3G22150	pentatricopeptide (PPR) repeat-containing protein	-0.4256	0.0033	0.0445	-0.4087	0.0038	0.0387	-1.4194	0	0.0092	-1.4026	0	0.0053
256793_at	AT3G22160	VQ motif-containing protein	0.6641	0.0793	0.1623	0.6192	0.0945	0.1548	0.4345	0.0921	0.1343	0.3896	0.1191	0.1341
256794_at	AT3G22230	60S ribosomal protein L27 (RPL27B)	0.15	0.5391	0.4366	0.5383	0.0738	0.1364	-0.207	0.3988	0.316	0.1813	0.455	0.3079
256795_at	AT3G22210	PAC1 (26S proteasome alpha subunit C1); peptida	0.2931	0.0059	0.0534	0.05033	0.4106	0.3463	-0.3849	7.00E-04	0.0159	0.1421	0.0241	0.051
256796_at	AT3G22210	unknown protein	-0.6847	0.0436	0.1204	-0.8419	0.0231	0.0768	0.4717	0.1153	0.1526	0.3145	0.252	0.2136
256797_at	AT3G18600	DEAD/DEAH box helicase, putative	0.5624	0.0701	0.1527	0.3396	0.2124	0.241	-0.1072	0.45	0.3386	-0.33	0.0617	0.0901
256798_at	AT3G18630	uracil DNA glycosylase family protein	-0.1774	0.8708	0.5442	-0.7598	0.4991	0.3841	0.7404	0.5095	0.3632	0.158	0.8848	0.4528
256799_at	AT3G18560	similar to unknown protein [Arabidopsis thaliana] (T	-0.84	0.0062	0.0542	-0.4817	0.0392	0.0982	0.5303	0.0293	0.0696	0.8886	0.0051	0.0224
256800_at	AT3G20900	unknown protein	-0.03202	0.9747	0.571	-0.00675	0.9947	0.5428	-0.2824	0.7806	0.4576	-0.2571	0.7996	0.4286
256801_at	no_match	no_match	0.07243	0.9274	0.5591	-0.2359	0.768	0.4799	-0.2122	0.57	0.3867	-0.5205	0.2041	0.1874
256802_at	AT3G20950	CYP705A32 (cytochrome P450, family 705, subfam	-0.09936	0.9237	0.558	0.07651	0.9412	0.5293	0.5257	0.4873	0.3543	0.7016	0.3654	0.2693
256803_at	AT3G20960	CYP705A33 (cytochrome P450, family 705, subfam	0.6601	9.00E-04	0.0347	1.2606	0.0024	0.0339	0.1063	0.5003	0.3597	-0.2626	0.2288	0.2009
256804_at	AT3G20920	translocation protein-related	0.647	0.0165	0.0771	0.3193	0.0811	0.1428	0.1231	0.4216	0.326	-0.1046	0.4895	0.3217
256805_at	AT3G20930	RNA recognition motif (RRM)-containing protein	-0.4713	0.0049	0.0502	-0.7203	0.001	0.0291	0.1269	0.1068	0.1464	-0.1221	0.1166	0.1324
256806_at	AT3G20910	CCAAT-binding transcription factor (CBF-B/NF-YA)	0.4412	0.0976	0.1804	0.138	0.5376	0.3995	0.3296	0.0202	0.0571	0.02654	0.7785	0.4225
256807_at	AT3G20970	NFU4 (NFU domain protein 4)	0.08773	0.3814	0.3652	-0.0143	0.8805	0.5133	0.05853	0.5478	0.3784	-0.04351	0.6515	0.3813
256808_at	AT3G21430	DNA binding	0.04224	0.8299	0.5325	-0.1073	0.5915	0.4201	-0.1537	0.2627	0.248	-0.3033	0.062	0.0904
256809_at	AT3G21430	DNA binding	-0.04997	0.9324	0.5604	0.08341	0.8875	0.5152	-0.03292	0.9554	0.5067	0.1005	0.8648	0.447
256810_at	no_match	no_match	0.3913	0.3701	0.3596	0.2279	0.5883	0.4188	-0.3299	0.443	0.3354	-0.4932	0.2724	0.2241
256811_at	AT3G21340	leucine-rich repeat protein kinase, putative	-1.5536	0.1144	0.196	-0.2709	0.7433	0.4725	-0.4744	0.572	0.3874	0.8083	0.3541	0.2645
256812_at	AT3G21360	RNA polymerase transcriptional regulation mediator	0.2603	0.1647	0.2373	-0.258	0.2176	0.2109	-0.4122	0.0193	0.0557	-0.9305	0.001	0.0122
256813_at	AT3G21360	oxidoreductase	-0.3108	0.0844	0.1682	-0.2137	0.1914	0.2271	0.2366	0.157	0.1837	0.3338	0.0703	0.0971
256814_at	AT3G21370	glycosyl hydrolase family 1 protein	-0.3805	0.6763	0.4847	0.2881	0.7507	0.4751	-0.2343	0.7688	0.4537	0.4343	0.5911	0.3603
256815_at	AT3G21380	similar to MBP1 (MYROSINASE-BINDING PROTE	0.2533	0.8422	0.5362	0.9563	0.4676	0.3711	-1.1449	0.3321	0.2843	-0.612	0.6349	0.3755
256816_at	AT3G21400	similar to unknown [Populus trichocarpa] (GB:ABK9	-0.09806	0.5408	0.4371	-0.3049	0.1065	0.1646	0.2358	0.1493	0.1785	0.02895	0.8375	0.4394
256817_at	AT3G21410	F-box family protein (FBW1)	0.2564	0.7264	0.5014	-0.08739	0.9044	0.5199	0.6533	0.3319	0.2842	0.3095	0.6289	0.3734
256818_at	AT3G21420	oxidoreductase, 2OG-Fe(II) oxygenase family pro	0.1289	0.4086	0.3795	-0.392	0.5485	0.1094	0.1574	0.3229	0.2796	-0.1057	0.4915	0.3225
256819_at	AT3G21390	mitochondrial substrate carrier family protein	-0.4751	0.0362	0.1097	-0.7039	0.0101	0.0545	-0.4854	0.0339	0.0752	-0.7143	0.0096	0.0304
256820_at	AT3G22170	FHY3 (FAR-RED ELONGATED HYPOCOTYLS 3);	0.4525	0.0674	0.1491	0.5062	0.0495	0.1103	-0.9009	0.0077	0.0354	-0.8472	0.0096	0.0304
256821_at	AT3G22180	zinc finger (DHHC type) family protein	1.2899	0.2196	0.2748	1.8982	0.0991	0.1588	-0.5803	0.5486	0.3796	0.02803	0.9763	0.4772
256822_at	AT3G22190	IQD5 (IQ-domain 5); calmodulin binding	-0.353	0.0452	0.1225	0.3422	0.0494	0.1102	-0.915	0.0017	0.0205	-0.2199	0.1476	0.1532
256823_at	AT3G22220	hAT dimerisation domain-containing protein	0.12	0.3948	0.3726	0.1014	0.4657	0.3702	-0.6882	0.0034	0.0256	-0.7067	0.003	0.0179
256824_at	AT3G22121	other RNA	0.2162	0.5199	0.429	-0.2989	0.588	0.4187	0.6476	0.2715	0.2531	0.7068	0.2367	0.2054
256825_at	AT3G22120	CWLP (CELL WALL-PLASMA MEMBRANE LINKE	-0.1152	0.6515	0.4766	-0.6202	0.0586	0.1203	0.6726	0.0101	0.0399	0.1677	0.3162	0.2465
256826_at	AT3G18540	unknown protein	-0.7497	0.3805	0.3647	-0.2271

256890_at	AT3G22930	GR-RBP4/CRP4 (GLYCINE-RICH RNA-BINDING P	0.1556	0.5045	0.4224	0.04296	0.8496	0.5043	0.1674	0.4749	0.3495	0.05471	0.8095	0.4315
256891_at	AT3G19030	similar to unknown protein [Arabidopsis thaliana] (T	-0.6619	0.0393	0.1144	-0.4344	0.1189	0.1744	0.3919	0.0204	0.0575	0.6194	0.0042	0.0207
256892_at	AT3G19000	oxidoreductase, 2OG-Fe(II) oxygenase family prote	-0.1868	0.2908	0.3178	-0.5387	0.0247	0.0789	0.1892	0.1581	0.1844	-0.1626	0.2106	0.1912
256893_x_at	AT3G30660	transposable element gene	0.1013	0.9513	0.565	-1.7607	0.3221	0.3043	-1.7901	0.3151	0.2759	-0.1307	0.9372	0.4676
256894_at	AT3G21870	CYCP2;1 (cyclin p2;1); cyclin-dependent protein kin	-0.5622	0.0896	0.1734	-0.7085	0.0483	0.1092	-0.2809	0.0033	0.0255	-0.4272	7.00E-04	0.0105
256895_at	AT3G24680	transposable element gene	0.7947	0.1153	0.1966	-0.06944	0.8694	0.5097	0.1533	0.4964	0.3584	-0.7108	0.0257	0.0531
256896_at	AT3G24630	similar to unnamed protein product [Vitis vinifera] (G	-0.7045	0.0299	0.1005	-0.7255	0.0273	0.0826	-0.4911	0.0828	0.1265	-0.5121	0.0744	0.1003
256897_at	AT3G24640	lysine	0.1223	0.8117	0.5273	-0.1842	0.7211	0.4658	0.4078	0.4147	0.3229	0.1013	0.8323	0.4379
256898_at	AT3G24650	ABI3 (ABA INSENSITIVE 3); DNA binding / transcri	-1.3878	0.259	0.2992	-1.5795	0.209	0.2389	-0.2154	0.8483	0.4782	-0.4071	0.7194	0.4038
256899_at	AT3G24660	TMKL1 (TRANSMEMBRANE KINASE-LIKE 1); ATI	1.0886	0.0206	0.0845	0.7855	0.0553	0.1168	0.2743	0.4025	0.3176	-0.02879	0.9265	0.4647
256900_at	AT3G24670	pectate lyase family protein	0.01187	0.967	0.569	-0.3661	0.2466	0.2619	-0.6735	0.0414	0.0845	-1.0514	0.0098	0.0309
256901_at	AT3G30800	transposable element gene	-1.8155	0.1471	0.2231	-0.3789	0.727	0.4678	0.784	0.2166	0.2216	2.2206	0.0142	0.0379
256902_s_at	AT3G23910;AT3G24255	[AT3G23910, similar to unknown protein [Arabidops	1.019	4.00E-04	0.032	0.7212	0.0015	0.0314	-0.3701	0.0167	0.0516	-0.6679	0.002	0.0153
256903_at	AT3G23960	F-box family protein	0.7246	0.5321	0.4337	-1.054	0.3768	0.3305	0.08699	0.9386	0.503	-1.6919	0.1861	0.177
256904_at	AT3G23980	similar to hypothetical protein Osl_004770 [Oryza s	-0.5237	0.0276	0.0963	0.3879	0.0661	0.1287	-1.0511	9.00E-04	0.0171	-0.1395	0.3077	0.2423
256905_at	AT3G23990	HSP60 (Heat shock protein 60); ATP binding / prote	0.4593	0.0885	0.1724	0.5048	0.0694	0.132	-0.8901	9.00E-04	0.0171	-0.8446	0.0011	0.0126
256906_at	AT3G24000	pentatricopeptide (PPR) repeat-containing protein	-0.03095	0.965	0.5684	1.0178	0.1991	0.2324	-2.0015	0.0391	0.0816	-0.9528	0.2236	0.198
256907_at	AT3G24030	hydroxyethylthiazole kinase family protein	-0.4171	0.0031	0.0441	-0.1402	0.0991	0.1588	0.1348	0.1088	0.1476	0.4117	0.0033	0.0186
256908_at	AT3G24040	glycosyltransferase family 14 protein / core-2/I-bran	0.06634	0.6317	0.4702	-0.02955	0.8288	0.4986	0.01096	0.9359	0.5023	-0.08493	0.5434	0.3422
256909_at	AT3G24060	self-incompatibility protein-related	-1.2781	0.3176	0.3329	-0.1627	0.8915	0.5162	-0.4788	0.6911	0.4282	0.6366	0.6002	0.3634
256910_at	AT3G24080	KRR1 family protein	0.4234	0.2749	0.3085	0.4719	0.2317	0.2527	0.05155	0.6913	0.4282	0.09999	0.4541	0.3076
256911_at	AT3G24090	transaminase	1.2738	0.0012	0.0362	0.3404	0.0941	0.1545	0.502	0.0322	0.073	-0.4313	0.0504	0.0797
256912_at	AT3G23850	unknown protein	0.3206	0.6808	0.4863	-0.4635	0.557	0.4072	0.5743	0.4721	0.3484	-0.2098	0.7865	0.4247
256913_at	AT3G23870	permease-related	0.2208	0.2026	0.264	0.008185	0.9577	0.5336	0.3112	0.0985	0.1397	0.09853	0.5342	0.3395
256914_at	AT3G23880	F-box family protein	-1.2706	0.048	0.1261	-1.0208	0.0884	0.1482	-0.8289	0.0032	0.0251	-0.5791	0.0114	0.0335
256915_at	AT3G23900	RNA recognition motif (RRM)-containing protein	-0.1875	0.5545	0.4426	0.3226	0.3297	0.3084	-1.3286	0.0016	0.0204	-0.8185	0.0096	0.0305
256916_at	AT3G24050	GATA transcription factor 1 (GATA-1)	-0.1414	0.3632	0.3559	-0.1224	0.4251	0.353	0.4285	0.036	0.078	0.4475	0.0315	0.0598
256917_at	AT3G18930	zinc finger (C3HC4-type RING finger) family protein	0.0707	0.7723	0.5153	0.3115	0.2442	0.2606	-0.3834	0.1684	0.1907	-0.1426	0.5661	0.3513
256918_at	AT3G18960;AT4G01580	[AT3G18960, transcriptional factor B3 family protein	-0.2501	0.5323	0.4338	0.1925	0.6271	0.4334	0.04799	0.8807	0.487	0.4906	0.1774	0.1716
256919_at	AT3G18970	pentatricopeptide (PPR) repeat-containing protein	-0.5914	0.0586	0.1386	0.2244	0.3759	0.3301	-0.5793	0.062	0.107	0.2366	0.3532	0.2641
256920_at	AT3G18980	F-box family protein	0.2637	0.2036	0.0897	0.2129	0.0453	0.1055	-0.2839	0.0186	0.0546	0.3346	0.0107	0.0324
256921_at	AT3G18940	dast3-related	0.8072	0.0018	0.0391	0.8356	0.0016	0.0317	0.08974	0.4597	0.3429	0.1182	0.3424	0.2591
256922_at	AT3G19010	oxidoreductase, 2OG-Fe(II) oxygenase family prote	0.3988	0.2101	0.2683	0.5607	0.104	0.1629	0.1778	0.2836	0.26	0.3397	0.0773	0.1027
256923_at	AT3G29635	transferase family protein	-0.05832	0.9419	0.563	-0.3489	0.6669	0.4474	-0.5327	0.5179	0.3662	-0.8232	0.3352	0.2557
256924_at	AT3G29590	AT5MAT; O-malonyltransferase/ transferase	-0.3537	0.4693	0.407	-0.1288	0.7857	0.4848	-0.6789	0.2002	0.2119	-0.4539	0.3634	0.2684
256925_at	AT3G29600	transposable element gene	-0.09136	0.9545	0.5659	1.2633	0.4487	0.3634	-1.2413	0.2652	0.2494	0.1134	0.9116	0.4604
256926_at	AT3G22540	similar to unknown protein [Arabidopsis thaliana] (T	-1.2578	0.0255	0.0924	-0.6613	0.1417	0.192	0.05343	0.8665	0.4831	0.6499	0.0947	0.1166
256927_at	AT3G22550	senescence-associated protein-related	0.8535	0.1108	0.193	0.4988	0.2988	0.2909	0.1637	0.407	0.3195	0.191	0.3409	0.2584
256928_at	AT3G22590	RNA pol II accessory factor Cdc73 family protein	0.02352	0.8784	0.5461	0.01727	0.9104	0.5216	0.114	0.4313	0.3301	0.1077	0.455	0.3079
256929_at	no_match	no_match	0.2408	0.7264	0.5014	1.7938	0.049	0.1097	-0.4687	0.5055	0.3615	1.0843	0.1682	0.1649
256930_at	AT3G22460	cysteine synthase, putative / O-acetylserine (thiol)-l	1.0113	0.1537	0.2287	1.2084	0.1037	0.1626	-1.3425	0.0424	0.0857	-1.1454	0.0661	0.0936
256931_at	AT3G22490	late embryogenesis abundant protein, putative / LE	-0.9009	0.3346	0.3427	0.1048	0.9047	0.52	-0.822	0.3739	0.3046	0.1838	0.8341	0.4383
256932_at	AT3G22520	similar to unknown protein [Arabidopsis thaliana] (T	-0.8444	0.5162	0.4276	-0.00839	0.947	0.5312	0.1851	0.1168	0.1537	0.2612	0.0481	0.0775
256933_at	AT3G22600	protease inhibitor/seed storage/lipid transfer protein	1.5477	0.0565	0.1362	1.7475	0.0399	0.0989	0.7383	0.0378	0.0804	0.9381	0.0178	0.0427
256934_at	AT3G22530	similar to unknown protein [Arabidopsis thaliana] (T	0.1523	0.3822	0.3657	-0.1045	0.5378	0.3996	0.2858	0.0097	0.0392	0.02887	0.663	0.3852
256935_at	AT3G22570	protease inhibitor/seed storage/lipid transfer protein	-0.8966	0.3576	0.3533	-0.5949	0.5286	0.3956	-0.434	0.6415	0.4116	-0.1323	0.8856	0.4531
256936_at	AT3G22480	prefoldin-related KE2 family protein	0.2029	0.3054	0.3257	-0.2765	0.1848	0.2231	0.5655	0.0239	0.0627	0.08614	0.6178	0.3695
256937_at	AT3G22620	protease inhibitor/seed storage/lipid transfer protein	0.9156	0.0085	0.0602	1.0978	0.0044	0.041	0.5292	0.033	0.0742	0.7113	0.0127	0.0356
256938_at	AT3G22500	ATECP31 (late embryogenesis abundant protein E6	0.1917	0.8748	0.5451	-0.1581	0.8965	0.5177	0.6563	0.3252	0.281	0.3067	0.6283	0.3731
256939_at	AT3G22630	PBD1 (PROTEASOME SUBUNIT PRGB); peptidas	0.5015	0.0041	0.0468	0.5781	0.0024	0.0339	0.2699	0.0332	0.0745	0.3465	0.0149	0.0388
256940_at	AT3G30720	unknown protein	-0.6875	0.0457	0.1229	-0.9764	0.0152	0.0648	-1.3748	0.001	0.0173	-1.6636	5.00E-04	0.0093
256941_at	AT3G30710	transposable element gene	1.8256	0.2374	0.2861	-0.5638	0.3969	0.3399	0.8264	0.2318	0.2304	-0.563	0.3917	0.2807
256942_at	AT3G23290	similar to unknown protein [Arabidopsis thaliana] (T	1.8111	3.00E-04	0.0312	1.8161	3.00E-04	0.0249	0.511	6.00E-04	0.0158	0.516	6.00E-04	0.01
256943_at	AT3G18910	F-box family protein	-0.01138	0.9238	0.558	0.767	0.0024	0.0338	-0.6853	0.0036	0.0265	0.0931	0.452	0.3068
256944_at	AT3G18990	VRN1 (REDUCED VERNALIZATION RESPONSE	0.409	0.0698	0.1522	0.3458	0.1062	0.1644	0.3361	0.0846	0.128	0.2729	0.1375	0.1465
256945_at	AT3G19020	leucine-rich repeat family protein / extensin family p	-0.1197	0.8962	0.5503	0.9661	0.325	0.3059	0.02624	0.9772	0.5119	1.1121	0.2665	0.221
256946_at	AT3G19040	HAF2/TAF1/TAF 1B (HISTONE ACETYLTRANSFE	-0.2712	0.4908	0.4162	0.1459	0.7044	0.4605	0.004768	0.99	0.5153	0.4218	0.3038	0.2406
256947_at	AT3G19050	POK2 (PHRAGMOPLAST ORIENTING KINESIN 2	0.1006	0.2951	0.2476	-0.00839	0.947	0.5312	0.1851	0.1168	0.183	-0.6722	0.4676	0.3129
256948_at	AT3G18930	zinc finger (C3HC4-type RING finger) family protein	0.5383	0.1264	0.2058	0.9169	0.0305	0.0866	-0.2356	0.4467	0.3369	0.1431	0.6355	0.3756
256949_at	AT3G19070	cell wall protein-related	-1.6565	0.1066	0.1888	0.7488	0.4013	0.3418	-0.7726	0.3735	0.3045	1.6326	0.1019	0.122
256950_at	AT3G19080	SWI8 complex BAF60b domain-containing protein	-0.4895	0.6599	0.4792	0.7875	0.4878	0.3795	-1.2977	0.2768	0.2562	-0.02067	0.985	0.4791
256951_at	AT3G19085	similar to F-box family protein [Arabidopsis thaliana	-0.5102	0.548	0.4402	-0.8599	0.3314	0.3091	1.2097	0.1204	0.1565	0.8601	0.2342	0.204
256952_at	AT3G21160	mannosyl-oligosaccharide 1,2-alpha-mannosidase,	0.2996	0.0928	0.1764	-0.08976	0.5461	0.403	0.4266	0.0352	0.0769	0.03717	0.7985	0.4283
256953_at	AT3G29630	glycosyltransferase family protein	1.9997	0.0982	0.181	0.5755	0.57	0.4119	-0.3358	0.7366	0.4438	-1.76	0.1317	0.1428
256954_at	AT3G13550	FUS9 (FUSCA 9); ubiquitin-protein ligase	0.4515	0.0716	0.1542	0.5288	0.0463	0.1067	-0.1998	0.2922	0.2648	-0.1225	0.4987	0.3254
256955_at	AT3G13390	SKS11 (SKU5 Similar 11); copper ion binding / oxid	-0.05264	0.8371	0.5344	-0.1565	0.5498	0.4048	0.2892	0.2847	0.2606	0.1853	0.4733	0.3151
256956_at	AT3G13410	similar to unknown protein [Arabidopsis thaliana] (T	0.06509	0.7604	0.5117	-0.0452	0.8317	0.4993	0.01381	0.9481	0.5052	-0.09648	0.6537	0.382
256957_at	AT3G13420	similar to unknown protein [Arabidopsis thaliana] (T	-0.6975	0.4067	0.3788	-0.6764	0.4198	0.3505	-1.1405	0.2045	0.2145	-1.1194	0.2113	0.1915
256958_at	AT3G13430	zinc finger (C3HC4-type RING finger) family protein	0.1308	0.4391	0.3932	0.717	0.0093	0.0527	-0.2338	0.087	0.1302	0.3524	0.0272	0.0549
256959_at	AT3G13440	similar to unnamed protein product [Vitis vinifera] (G	0.3814	0.1151	0.1963	0.4246	0.089	0.1504	-0.7721	0	0.0062	-0.7288	0	0.0043
256960_at	AT3G13510	similar to unknown protein [Arabidopsis thaliana] (T	-0.6421	0.0349	0.1078	-0.7188	0.0246	0.0787	0.2356	0.3135	0.2751	0.1589	0.4806	0.3178
256961_at	AT3G13445	TBP1 (TRANSCRIPTION FACTOR IID-1); DNA bin	0.6514	0.0016	0.0388	0.658	0.0016	0.0316	0.1764	0.0122	0.0439	0.183	0.0108	0.0325
256962_at	AT3G13560	glycosyl hydrolase family 17 protein	0.4086	0.0622	0.1432	0.3359	0.1024	0.1615	0.2814	0.1517	0.1802	0.2088	0.2598	0.2177
256963_at	AT3G13490	OVA5 (OVULE ABORTION 5); ATP binding / amino	0.0056578	0.9804	0.5721	0.09626	0.6803	0.4521	-0.5859	0.025	0.0641	-0.4953	0.0418	0.0711
256964_at	AT3G13520	AGP12 (ARABINOGALACTAN PROTEIN 12)	-0.8714	0.0407	0.1162	-1.2666	0.0123	0.0595	0.4942	0.0755	0.1197	0.099	0.6577	0.3833
256965_at	AT3G13450	GN4 (GARK INDUCIBLE 4); 3-methyl-2-oxobutanoa	0.9377	0.0212	0.0855	1.0838	0.0131	0.0611	-0.4926	0.017	0.062	-0.3465	0.6502	0.3796
256966_at	AT3G13400	SKS13 (SKU5 Similar 13); copper ion binding / oxid	-0.1442	0.7471	0.5081	-0.2167	0.631	0.4349	-0.5097	0.1937	0.2078	-0.5821	0.1493	0.1542
256967_at	AT3G21060	transducin family protein / WD-40 repeat family prot	0.01573	0.934	0.5608	-0.01648	0.9309	0.5268	-0.5603	0.035	0.0767	-0.5925	0.0295	0.0576
256968_at	AT3G21070	NADK1 (NAD kinase 1); NAD+ kinase/ NADH kinase	-1.5182	0.0773	0.16	-0.524	0.4603	0.368	-1.4038	0.061	0.1061	-0.4096	0.4928	0.323
256969_at	AT3G21080	ABC transporter-related	1.1999	0.3558	0.3525	0.743	0.5536	0.406	0.2014	0.8695	0.4841	-0.2556	0.835	0.4386
256970_at	AT3G21090	ABC transporter family protein	0.4428	0.6037	0.4608	0.7562	0.3911	0.3372	-0.6989	0.2657	0.2496	-0.3855	0.5151	0.3317
256971_at	AT3G21100	RNA recognition motif (RRM)-containing protein	-0.6775	0.6388	0.4725	-0.6457	0.6542	0.4432	-1.1204	0.4489	0.338	-1.0887	0.4609	0.3104
256972_at	AT3G21140	FMN binding	0.6973	0.0208	0.0849	0.8412	0.0111	0.0565	-0.2575	0.2432	0.2369	-0.1137	0.5785	0.3555
256973_at	AT3G20980	similar to unknown protein [Arabidopsis thaliana] (T	-0.9955	0.409	0.3795	-0.01478	0.9897	0.5416	-1.1184	0.3575	0.2968	-0.1376	0.9044	0.4586
256974_at	AT3G20990	transposable element gene	1.2442	0.2425	0.2891	0.3258	0.7379	0.4706	0.9715	0.125	0.16	0.05313	0.9208	0.463
256975_at	AT3G21000	similar to unknown protein [Arabidopsis thaliana] (T	-0.9547	0.269	0.3048	-1.9119	0.0621	0.1239	-0.6131	0.2346	0.2319	-1.5703	0.0231	0.0496
256976_at	AT3G21020	transposable element gene	0.001376	0.9963	0.5761	-0.1265	0.6704	0.4487	0.06297	0.8306	0.473	-0.06489	0.8256	0.4359
256977_at	AT3G21040	transposable element gene	-1.6382	0.0241	0.0905	-0.4922	0.3477	0.3169	0.2153	0.6458	0.4129	1.3613	0.0349	0.0632
256978_at	AT3G21110	PUR7 (PURIN 7); phosphoribosylaminoimidazolesu	-0.374	0.0948	0.1779	-0.3554	0.1072	0.1651	-0.3218	0.0835	0.1271	-0.3031	0.0967	0.118
256979_at	AT3G21055	PSBTN (photosystem II subunit T)	-0.5857	0.004	0.0467	-0.7349	0.0017	0.0321	0.3567	0.0029	0.0247	0.2076	0.0198	0.0451
256980_at	AT3G26932	DRB3 (DSRNA-BINDING PROTEIN 3); double-stra	-1.4812	0.0162	0.077	-0.9419	0.0641	0.1263	-1.0528	0.047	0.0909	-0.5135	0.2386	0.2064
256981_at	AT3G13380	BRL3 (BRI1-LIKE 3); protein binding / protein kinase	1.8731	2.00E-04	0.0312	2.0092	1.00E-04	0.0249	-0.4016	0.0258	0.0652	-0.2655	0.084	0.1082
256982_at	AT3G13460	ECT2; protein binding	0.4437	0.1372	0.2152	0.6181	0.0611	0.1227	-1.089	0.0029	0.0245	-0.9146	0.0055	0.0231
256983_at	AT3G13470	chaperonin, putative	1.0564	0.0106	0.0647	-1.1616	0.0076	0.0488	-0.3049	0.0798	0.1237	-0.4102	0.0348	0.0631
256984_at	AT3G13480	similar to unknown protein [Arabidopsis thaliana] (T	0.1646	0.5022	0.4215	-0.06485	0.7861	0.4849	-0.2909	0.2629	0.2481	-0.5204	0.0804	0.1054
256985_at	AT3G13540	ATMYB5 (MYB DOMAIN PROTEIN 5); DNA bindin	-0.2406	0.0755	0.1582	-0.2201	0.0945	0.1548	0.02995	0.7813	0.4578	0.05042	0.6434	0.3784
256986_at	AT3G28700	similar to Os01g0588800 [Oryza sativa (japonica cu	0.4937	0.0086	0.0605	0.4115	0.0161	0.066	0.04059	0.713	0.4359	-0.04163	0.7061	0.3995
256987_at	AT3G28560	similar to AAA-type ATPase family protein [Arabidop	-2.2439	0.1583	0.2321	-0.9024	0.5245	0.3939	-0.7798	0.5797	0.3906	0.5618	0.6869	0.3929
256988_s_at	AT3G28715;AT3G28710	[AT3G28715, H+-transporting two-sector ATPase, p	0.03586	0.8103	0.5268	0.1557	0.3279	0.3075	-0.1914	0.2429	0.2367	-0.07169	0.6357	0.3756
256989_at	AT3G28580	AAA-type ATPase family protein	1.8129	0.1523	0.2276	3.4081	0.0294	0.0852	-0.2191	0.6917	0.4283	1.3761	0.0553	0.0843
256990_at	AT3G28590	unknown protein	0.001409	0.9979	0.5763	0.03204	0.9513	0.5322	-0.23	0.6652	0.4196	-0.1994	0.7067	0.3997
256991_at	AT3G28600	ATP binding / ATPase	1.5568	0.1567	0.2309	2.5059	0.0487	0.1096	0.2903	0.6196	0.4045	1.2393	0.0835	0.1078
256992_at	AT3G28630	similar to unknown protein [Arabidopsis thaliana] (T	0.06687	0.6879	0.4885	-0.4503	0.0437	0.1035	0.165	0.3463	0.2914	-0.3522	0.6851	0.1091
256993_at	AT3G28670	oxidoreductase/ zinc ion binding	0.3512	0.1692	0.2407	0.03839	0.8636	0.5081	-0.07817	0.7281	0.4412	-0.3909	0.1356	0.1454
256994_s_at	AT3G25830;AT3G25820	[AT3G25830, ATTPS-CIN (TERPENE SYNTHASE-	-0.472	0.1897	0.2551	-0.3593	0.2959	0.2896	-0.3471	0.3103	0.2736	-0.2344	0.477	0.3165
256995_at	AT3G25850	protein kinase family protein	0.2536	0.1764	0.2457	0.01215	0.9411	0.5293	-0.6208	0.0064	0.033	-0.8622	0.0019	0.015
256996_at	AT3G25850	DC1 domain-containing protein	0.6099	0.5174	0.4282	-0.4041	0.6629	0.446	0.2356	0.7952	0.4619	-0.7784	0.4112	0.2887
256997_at	AT3G14067	subtilase family protein	-0.3614	0.0019	0.0391	-0.5635	3.00E-04	0.0249	-0.04844	0.383	0.3093	-0.2506	0.0072	0.0264
256998_at	AT3G14180	transcription factor	0.9446	0.0066	0.0549	1.3929	0.0016	0.0316	-0.4513	0.0228	0.061	-0.00327	0.9805	0.4782
256999_at	AT3G14200	DNAJ heat shock N-terminal domain-containing pro	0.294	0.6786	0.4855	0.1186	0.866	0.5088	-0.2896	0.371	0.3034	-0.4651	0.1813	0.1742
257000_at	AT3G14120	similar to hypothetical protein Osj_033267 [Oryza s	0.7604	0.0032	0.0443	1.2784	4.00E-04	0.0251	-0.7064	0.0042	0.0278	-0.1885	0.1923	0.1805
257001_at	AT3G14080	small nuclear ribonucleoprotein, putative / snRNP,	-0.07968	0.7072	0.4951	0.08741	0.6809	0.4523	0.1702	0.4374	0.333	0.3373	0.1628	0.163
257002_at	AT3G14100	oligouridylate-binding protein, putative	0.2785	0.1557	0.2302	0.1941	0.2905	0.2868	-0.2923	0.1324	0.1655	-0.3767	0.0719	0.0984
257003_at	AT3G14110	FLU (FLUORESCENT IN BLUE LIGHT); binding	0.07564	0.7597	0.5116	-0.2218	0.3912	0.3373	-0.02189	0.7255	0.4403	-0.1681	0.6445	0.074
257004_s_at	AT3G14130;AT3G14150	[AT3G14130, (S)-2-hydroxy-acid oxidase, peroxiso	0.7185	0.058	0.1381	0.9986	0.0216	0.0747	-0.6172	0.0381	0.0806	-0.3371	0.1712	0.168
257005_at	AT3G14190	similar to unknown protein [Arabidopsis thaliana] (T	0.07447	0.8355	0.534	-0.2496	0.4989	0.3841	0.688	0.1101	0.1485	0.3639	0.3399	0.258
257006_at	AT3G14075	lipase class 3 family protein	0.6036	0.008	0.0587	0.439	0.0234	0.077	-0.05442	0.6065	0.4002	-0.219	0.088	0.1113
257007_at	AT3G14205	phosphoinositide phosphatase family protein	-0.1906	0.1445	0.2209	-0.1954	0.137	0.1885	-0.4539	0.0125	0.0444	-0.4587	0.0121	0.0346
257008_at	AT3G14210	ESM1 (EPITHIOSPECIFIER MODIFIER 1); carboxy	-0.5531	0.0069	0.0558	-0.7748	0.002	0.033	0.05218	0.6539	0.4158	-0.1695	0.1913	0.1799
257009_at	AT3G14160	oxidoreductase, 2OG-Fe(II) oxygenase family prote	0.3337	0.233	0.2837	0.4849	0.1109	0.1681	-0.1067	0.596	0.3968	0.01451	0.9542	0.4722
257010_at	AT3G14090	ATEXO70D3 (exocyst subunit EXO70 family protei	0.4729	0.1233	0.2035	0.2125	0.4308	0.3557	0.007071	0.9575	0.5071	-0.2533	0.1119	0.129
257011_at	AT3G14070	CAX9 (CATION EXCHANGER 9); cation:cation anti	-0.1197	0.6978	0.4919	0.5847	0.111	0.1681	-0.3812	0.2543	0.2433	0.3232	0.3226	0.2495
257012_at	AT3G26120	TEL1 (TERMINAL EAR1-LIKE 1); RNA binding	-1.2781	0.2034	0.2643	-0.1387	0.6771	0.5123	0.8412	0.3474	0.3047	1.9807	0.0782	0.1034
257013_at	AT3G26920	F-box family protein	-0.08452	0.8226	0.5304	-0.7638	0.0966	0.1566	0.09428	0.8027	0.4644	-0.585	0.173	0.169
257014_at	AT3G26930	similar to F-box family protein [Arabidopsis thaliana	-0.01224	0.985	0.5733	0.08341	0.8984	0.5184	-0.00188	0.9977	0.5172	0.09377	0.8847	0.4528
257015_at	AT3G26860	prolylcarboxypeptidase-related	-0.454	0.5846	0.4541	0.2662	0.7191	0.465	0.5033	0.6463	0.3779	1.2525	0.1767	0.1712
257016_at	AT3G28690	protein kinase, putative	0.04257	0.4853	0.414	0.252	0.0104	0.0553	-0.6317	3.00E-04	0.0133	-0.4222	0.0012	0.0129
257017_at	AT3G19620	glycosyl hydrolase family 3 protein	-0.00321	0.9901	0.5745	-0.03289	0.8987	0.5185	0.5509	0.0754	0.1196	0.5212	0.0869	0.1104
257018_at	AT3G19630	radical SAM domain-containing protein	0.4335	0.1743	0.2444	0.1318	0.6423	0.4389	-0.3324	0.2006	0.2121	-0.6341	0.2432	0.0726
257019_at	AT3G19640	magnesium transporter CorA-like family protein (MF	0.6909	0.0018	0.0391	0.6845	0.0019	0.0329	0.2081	0.0905	0.133	0.2018	0.0976	0.1188
257020_at	AT3G19590	WD-40 repeat family protein / mitotic checkpoint pr	-0.6203	0.0595	0.1396	-0.4455	0.1343	0.1863	0.04485	0.7592	0.4511	0.2197	0.1832	0.1754
257021_at	AT3G19710	BCAT4 (BRANCHED-CHAIN AMINOTRANSFERA	-0.7501	0.1524	0.2277	-0.8958	0.1028	0.1617	0.6556	0.0177	0.0532	0.51	0.0389	0.0679
257022_at	AT3G19580	AZF2 (ARABIDOPSIS ZINC-FINGER PROTEIN 2);	-0.1723	0.6806	0.4862	-0.144	0.73	0.4686	0.451	0.0216	0.0593	0.4794	0.0177	0.0427
257023_at	AT3G19760	initiation factor 4A, putative / eIF-4A, putative / DEA	-0.126	0.2806	0.3116	0.

257090_at	AT3G20530	protein kinase family protein	0.0355	0.9715	0.5702	0.9397	0.3708	0.3278	-0.322	0.7474	0.4473	0.5822	0.5664	0.3514
257091_at	no_match	no_match	-0.6907	0.5436	0.4384	0.207	0.8522	0.5051	-0.9462	0.3452	0.2908	-0.04853	0.9589	0.4731
257092_at	AT3G20550	DDL (DAWDLE)	0.2063	0.1958	0.2596	-0.0826	0.5681	0.4112	-0.08095	0.3706	0.3032	-0.3698	0.01	0.0312
257093_at	AT3G20570	plastocyanin-like domain-containing protein	-0.8193	0.0109	0.0655	-0.4592	0.0655	0.128	0.8831	0.0053	0.0303	1.2432	0.0015	0.0137
257094_at	AT3G20480	tetraacyldisaccharide 4'-kinase family protein	0.03767	0.959	0.567	1.2066	0.1549	0.2019	-0.05618	0.9389	0.5031	1.1127	0.1817	0.1744
257095_at	AT3G20560	ATPDIL5-3 (PDI-LIKE 5-3); thiol-disulfide exchange	0.3154	0.1723	0.2429	0.04107	0.8394	0.5013	0.1266	0.486	0.3539	-0.1478	0.4213	0.2929
257096_at	AT3G20820	similar to unknown protein [Arabidopsis thaliana] (T	0.3946	0.7422	0.5065	-0.2088	0.1426	0.1926	1.3472	0.0976	0.139	-1.0862	0.1576	0.1598
257097_at	AT3G20830	transposable element gene	-0.0673	0.9205	0.5571	0.7627	0.2937	0.2885	-0.6182	0.3831	0.3093	0.2116	0.7544	0.415
257098_at	AT3G20810	transposable element gene	0.1987	0.8718	0.5444	0.3837	0.7565	0.477	-0.3738	0.2866	0.2616	-0.1888	0.5685	0.3522
257099_s_at	AT3G24982;AT3G25020	disease resistance family protein [similar to (AT3G24982, protein binding);[AT3G25020, disease	0.4288	0.2719	0.3065	2.3876	0.0021	0.0331	-2.4866	1.00E-04	0.012	-0.5279	0.0378	0.0665
257100_at	AT4G25910	disease resistance family protein	0.3172	3.00E-04	0.0312	3.1287	2.00E-04	0.0249	-0.05484	0.8183	0.4693	0.05665	0.8125	0.4324
257101_at	AT3G25020	disease resistance family protein	3.7788	0.0044	0.0482	3.1756	0.0082	0.0504	0.3046	0.4836	0.3527	-0.2986	0.4918	0.3227
257102_at	AT3G25050	XTH3 (XYLOGLUCAN ENDOTRANSGLUCOSYLA	1.0519	0.4415	0.3944	0.7007	0.6001	0.4236	-2.1026	0.115	0.1524	-2.4537	0.079	0.1041
257103_at	AT3G25060	pentatricopeptide (PPR) repeat-containing protein	1.2815	0.2039	0.2645	-0.2467	0.7847	0.4847	1.7913	0.0886	0.1314	0.263	0.7587	0.4162
257104_at	AT3G25040	ER lumen protein retaining receptor, putative / HDE	-0.03756	0.6541	0.4773	-0.1305	0.1684	0.2115	0.02355	0.7741	0.4555	-0.06938	0.4166	0.2911
257105_at	AT3G25030	VQ motif-containing protein	0.2419	0.3895	0.3696	0.5733	0.0843	0.1461	0.6019	0.0369	0.0792	0.9333	0.0088	0.0292
257106_at	AT3G25060	similar to EXS family protein / ERD1/XPR1/SYG1 fa	-1.1001	0.345	0.3474	0.8804	0.4402	0.3596	-1.5243	0.2124	0.2194	0.4562	0.6803	0.3905
257107_at	AT3G29070	protein transmembrane transporter	-1.1877	0.3968	0.3737	0.3321	0.8041	0.4909	-1.4197	0.3204	0.2785	0.1001	0.9402	0.4685
257108_x_at	AT3G30490	transposable element gene	-0.9508	0.3972	0.374	-1.331	0.2556	0.2676	0.8977	0.4218	0.3261	0.5175	0.6334	0.3749
257109_s_at	AT4G07690;AT2G24900;A	AT4G07690, transposable element gene];[AT2G24	-1.4071	0.2885	0.3164	-2.5507	0.0909	0.1521	-0.3861	0.7541	0.4494	-1.5297	0.2544	0.215
257110_x_at	AT3G30440	transposable element gene	0.3702	0.1457	0.2218	0.4825	0.0785	0.1404	-0.2524	0.2046	0.2145	-0.1401	0.448	0.3052
257111_x_at	AT3G30490	transposable element gene	-0.4437	0.6469	0.4753	-1.9876	0.0911	0.1522	3.1841	0.0238	0.0626	1.64	0.1415	0.1492
257112_at	AT3G20120	CYP705A21 (cytochrome P450, family 705, subfam	0.5075	0.0079	0.0583	0.3491	0.0274	0.0827	-0.4895	0.0089	0.0378	-0.6479	0.0032	0.0185
257113_at	AT3G20130	CYP705A22 (cytochrome P450, family 705, subfam	-0.3458	0.7922	0.5214	0.6673	0.6156	0.429	-0.7534	0.5726	0.3876	0.2598	0.8428	0.4408
257114_at	AT3G20140	CYP705A23 (cytochrome P450, family 705, subfam	0.4285	0.6857	0.4878	0.8955	0.4143	0.3479	1.7357	0.1525	0.1806	2.2028	0.0888	0.1118
257115_at	AT3G20150	kinesin motor family protein	0.7389	0.1056	0.1878	-0.07644	0.8399	0.5014	0.412	0.3099	0.2734	-0.4033	0.3189	0.2477
257116_at	AT3G20020	protein arginine N-methyltransferase family protein	0.04956	0.825	0.531	-0.08948	0.6919	0.4562	-0.3312	0.1898	0.2054	-0.4703	0.0886	0.1117
257117_at	AT3G20160	geranylgeranyl pyrophosphate synthase, putative /	0.7839	0.4486	0.3974	-0.1048	0.9161	0.523	1.8789	0.1467	0.1767	0.7902	0.4452	0.304
257118_at	AT3G20180	metal ion binding	1.8918	0.1119	0.194	-0.3681	0.7127	0.463	1.8751	0.0795	0.1233	-0.3848	0.6563	0.3829
257119_at	AT3G20190	leucine-rich repeat transmembrane protein kinase,	2.0579	0.1195	0.1997	-1.0543	0.3688	0.327	-0.2137	0.8475	0.4779	-3.3259	0.0331	0.0615
257120_at	AT3G20200	protein kinase family protein	1.5433	0.2971	0.3214	-1.62	0.277	0.2793	-0.3595	0.6481	0.4139	-2.4361	0.5823	0.357
257121_at	AT3G20220	auxin-responsive protein, putative	1.6337	0.0637	0.1446	-0.3647	0.6006	0.4238	-0.1926	0.7792	0.457	-2.191	0.027	0.0546
257122_at	AT3G20250	APUM5 (ARABIDOPSIS PUMILIO 5); RNA binding	0.9234	0.0241	0.0905	0.8769	0.0284	0.0836	-0.1476	0.3021	0.2696	-0.1942	0.1944	0.1816
257123_at	AT3G20030	F-box family protein	1.8602	0.2056	0.2658	-0.3653	0.7816	0.484	-2.6044	0.1021	0.1426	-1.1094	0.4188	0.292
257124_at	AT3G20040	ATHXK4; ATP binding / hexokinase	-0.07059	0.6709	0.4829	-0.6996	0.0105	0.0554	-0.1325	0.4386	0.3335	-0.7616	0.0078	0.0276
257125_at	AT3G20050	ATTCP-1 (Arabidopsis thaliana T-complex protein 1	0.2496	0.1192	0.1995	0.2199	0.1564	0.2031	0.08987	0.5158	0.3653	0.06022	0.6581	0.3835
257126_at	AT3G20060	UBC19 (UBIQUITIN-CONJUGATING ENZYME 19);	0.2119	0.2942	0.3198	0.01631	0.9935	0.5267	0.5776	0.0115	0.0423	0.382	0.0429	0.0723
257127_at	AT3G20070	TTN9 (TITAN9)	-0.1544	0.2966	0.3212	-0.5341	0.0143	0.0631	0.1206	0.402	0.3174	-0.2591	0.1144	0.1309
257128_at	AT3G20080	CYP705A15 (cytochrome P450, family 705, subfam	1.015	0.0476	0.1257	0.575	0.1849	0.2231	0.6664	0.0815	0.1252	0.2264	0.4754	0.3159
257129_at	AT3G20100	CYP705A19 (cytochrome P450, family 705, subfam	1.6404	3.00E-04	0.0312	0.9199	0.0026	0.0342	0.03369	0.822	0.4703	-0.6875	0.0075	0.027
257130_at	AT3G20210	DELTA-VPE (delta vacuolar processing enzyme); c	1.8089	0.286	0.3148	1.4957	0.1639	0.2085	0.4152	0.6491	0.4142	0.83	0.3819	0.2765
257131_at	AT3G20240	mitochondrial substrate carrier family protein	0.6201	0.0302	0.1009	0.3407	0.1449	0.1944	-0.1711	0.3627	0.2994	-0.4506	0.0539	0.083
257132_at	AT3G20230	50S ribosomal protein L18 family	-0.07247	0.6636	0.4806	-0.2814	0.1428	0.1928	-0.1297	0.3262	0.2814	-0.3386	0.0433	0.0727
257133_at	AT3G17190	unknown protein	1.6337	0.0637	0.1446	-0.3647	0.6006	0.4238	-0.1926	0.7792	0.457	-2.191	0.027	0.0546
257134_at	AT3G12870	similar to unknown protein [Arabidopsis thaliana] (T	-0.06971	0.8595	0.5409	-0.588	0.1867	0.2242	1.2672	0.0058	0.0318	0.749	0.0337	0.062
257135_at	AT3G12900	oxidoreductase, 2OG-Fe(II) oxygenase family prote	0.06432	0.9242	0.5581	-0.07861	0.9293	0.5265	0.2897	0.6194	0.4044	0.1268	0.8256	0.4359
257136_at	AT3G12890	ASML2 (ACTIVATOR OF SPOMIN::LUC2)	0.4411	0.4496	0.3979	1.3834	0.0585	0.1202	0.2698	0.6356	0.4097	1.2121	0.0829	0.1074
257137_at	AT3G28860	ATMDR1/ATPGP19/MDR1/MDR11/PGP19 (P-GL	-0.1416	0.3178	0.333	0.2797	0.0874	0.1489	-0.2023	0.1787	0.1977	0.219	0.1525	0.1565
257138_at	AT3G28870	similar to unknown protein [Arabidopsis thaliana] (T	0.06432	0.9242	0.5581	-0.07861	0.9293	0.5265	0.2897	0.6194	0.4044	0.1268	0.8256	0.4359
257139_at	AT3G28890	leucine-rich repeat family protein	1.4921	0.0029	0.0433	1.3358	0.0044	0.0409	-0.5906	0.062	0.107	-0.747	0.0314	0.0597
257140_at	AT3G28910	MYB30 (myb domain protein 30); DNA binding / tra	0.5884	0.0078	0.0583	0.7563	0.0032	0.0366	0.4407	0.0209	0.0582	0.6076	0.007	0.0261
257141_at	AT3G28900	60S ribosomal protein L34 (RPL34C)	-0.1457	0.4928	0.417	0.2312	0.2975	0.2904	0.02835	0.7509	0.4485	0.4053	0.0083	0.0283
257142_at	AT3G20090	CYP705A18 (cytochrome P450, family 705, subfam	-2.0979	0.0264	0.0939	-0.7705	0.2755	0.2784	-2.0492	0.0127	0.0449	-0.7217	0.2053	0.188
257143_at	AT3G20110	CYP705A20 (cytochrome P450, family 705, subfam	-1.1432	0.5228	0.4301	-0.2327	0.8936	0.5169	-0.9164	0.5763	0.3891	-0.00595	0.997	0.4821
257144_at	AT3G27300	GEPOD (GLUCOSE-6-PHOSPHATE DEHYDROGE	0.176	0.5794	0.4521	0.1964	0.5383	0.3997	0.02507	0.7885	0.4596	0.04547	0.6304	0.3737
257145_at	AT3G27320	hydrolase	0.2844	0.141	0.2183	0.1405	0.4168	0.3491	0.02963	0.784	0.4586	-0.3953	0.0174	0.0421
257146_at	AT3G27260	GTE8 (GLOBAL TRANSCRIPTION FACTOR GRO	0.2738	0.1118	0.194	0.246	0.1419	0.1922	-0.6478	0.0081	0.0362	-0.6757	0.007	0.0261
257147_at	AT3G27270	similar to DNA-binding storekeeper protein-related	0.3509	0.305	0.3256	-0.2476	0.4536	0.3655	0.2693	0.3758	0.3057	0.3727	0.2404	0.2073
257148_at	AT3G27240	cytochrome c1, putative	-0.04781	0.6971	0.4918	-0.1523	0.2534	0.2661	0.3645	0.0121	0.0437	0.26	0.036	0.0645
257149_at	AT3G27280	ATPHB4 (PROHIBITIN 4)	0.6671	0.0115	0.0671	0.408	0.054	0.1152	0.2509	0.0902	0.1328	-0.00826	0.9452	0.4697
257150_at	AT3G27230	similar to (ARABIDOPSIS THALIANA RAS ASSOC	0.5285	0.0091	0.1776	0.5303	0.0933	0.1539	-0.3047	0.0844	0.1279	-0.3029	0.0856	0.1095
257151_at	AT3G27200	plastocyanin-like domain-containing protein	0.7324	0.0499	0.1284	0.7015	0.0563	0.1179	0.8459	0.0326	0.0737	0.815	0.0365	0.065
257152_at	AT3G27310	PUX1 (PLANT UBX DOMAIN-CONTAINING PROT	0.4565	0.0392	0.1143	0.2952	0.1226	0.1777	0.3179	0.06	0.1051	0.1567	0.2691	0.2223
257153_at	AT3G27220	ketch repeat-containing protein	0.2438	0.3562	0.3527	0.3175	0.2464	0.2618	-0.4158	0.1502	0.179	-0.3422	0.2175	0.1949
257154_at	AT3G27210	Identical to Uncharacterized protein At3g27210 (Y-J	1.1203	0.0101	0.064	1.0574	0.0123	0.0594	0.5711	0.0791	0.1231	0.5082	0.1055	0.1242
257155_at	AT3G27290	F-box family protein	0.1301	0.9081	0.5535	-2.9088	0.0515	0.1126	2.593	0.0635	0.1086	-0.4459	0.6841	0.392
257156_at	AT3G24260	similar to unknown protein [Arabidopsis thaliana] (T	-0.5985	0.6112	0.463	0.7383	0.5343	0.3981	-0.8787	0.4642	0.3449	0.4581	0.6951	0.3959
257157_at	AT3G24350	SYP32 (syntaxin 32); SNAP receptor	0.3098	0.1493	0.225	0.3913	0.0876	0.149	0.1007	0.5731	0.3878	0.1822	0.3298	0.2532
257158_at	AT3G24360	enoyl-CoA hydratase/isomerase family protein	0.1994	0.8568	0.5404	0.5794	0.606	0.4256	0.7691	0.4994	0.3595	1.1491	0.3299	0.2532
257159_at	AT3G24400	pseudogene, protein kinase family, contains Pfam fi	0.05115	0.9725	0.5704	0.9123	0.5485	0.4042	-0.8434	0.5778	0.3898	0.01773	0.9905	0.4803
257160_at	no_match	no_match	-1.116	0.2545	0.2962	-1.2114	0.2225	0.2474	-0.03732	0.9667	0.5092	-0.1327	0.8821	0.4521
257161_at	AT3G24280	SMAP2 (SMALL ACIDIC PROTEIN 2)	1.0183	0.4426	0.3948	-0.438	0.7328	0.469	0.2732	0.7882	0.4595	-1.1831	0.2813	0.2288
257162_s_at	AT3G24290;AT3G24300	AT3G24290, ammonium transporter, putative];[AT3	-2.0597	0.1503	0.2258	-0.1225	0.9209	0.5242	-0.548	0.6611	0.4182	1.3892	0.2969	0.2371
257163_at	AT3G24310	MYB305 (myb domain protein 305); DNA binding / t	-0.1471	0.8812	0.5465	1.2522	0.2467	0.2619	-1.3869	0.1144	0.1519	0.01243	0.9865	0.4793
257164_at	AT3G24320	ATMSH1/CHM/CHM1/MSH1 (MUTL PROTEIN HO	0.1232	0.6993	0.4923	-0.1088	0.7326	0.4689	-0.2313	0.4794	0.3512	-0.4633	0.1936	0.1811
257165_at	AT3G24330	glycosyl hydrolase family 17 protein	0.9451	0.0993	0.1817	-0.5306	0.2962	0.2898	0.4389	0.3769	0.3062	-1.0368	0.0789	0.104
257166_at	AT3G24710	similar to flavodoxin family protein [Arabidopsis thal	0.7559	0.4582	0.402	-1.4306	0.1956	0.2298	1.3006	0.2311	0.23	-0.8859	0.3909	0.2803
257167_at	AT3G24340	CHR40 (chromatin remodeling 40); ATP binding / D	0.4808	0.6652	0.481	-0.2579	0.8148	0.4946	-1.2982	0.1081	0.1472	-2.0368	0.0318	0.06
257168_at	AT3G24430	HCF101 (HIGH-CHLOROPHYLL-FLUORESCENCE	0.4892	0.0038	0.0461	-0.6829	0.0011	0.0293	-0.0827	0.2624	0.2479	-0.2764	0.0121	0.0346
257169_at	AT3G24315	ATSEC20	-0.0585	0.6094	0.4628	0.2009	0.1301	0.1829	-0.5828	0.0053	0.0304	-0.3234	0.0377	0.0663
257170_at	AT3G23770	glycosyl hydrolase family 17 protein	-0.3477	0.7796	0.5178	-1.3648	0.3052	0.2944	0.2543	0.8374	0.4749	-0.7628	0.5472	0.3439
257171_at	AT3G23760	similar to transferase, transferring glycosyl groups [	-0.405	0.1027	0.1852	-0.5344	0.0497	0.1105	-0.0171	0.9023	0.4931	-0.1465	0.3256	0.251
257172_at	AT3G23700	S1 RNA-binding domain-containing protein	-0.4563	0.0182	0.0804	-0.6847	0.0044	0.041	0.2228	0.0749	0.1192	-0.00557	0.9552	0.4723
257173_at	AT3G23810	SAHH2 (S-ADENOSYL-L-HOMOCYSTEINE (SAH)	-1.5843	0.0185	0.081	-1.7972	0.0122	0.0591	-0.1348	0.6036	0.3995	-0.3477	0.2201	0.1961
257174_at	AT3G27190	uracil phosphoribosyltransferase, putative / UMP py	0.01379	0.9416	0.5629	0.001919	0.9919	0.5421	0.1087	0.3123	0.2746	0.0998	0.1616	0.2677
257175_s_at	AT3G23480;AT3G23470	[AT3G23480, cyclopropane fatty acid synthase-rela	0.154	0.4389	0.3932	0.3105	0.1583	0.2047	-2.0912	1.00E-04	0.0101	-1.9346	1.00E-04	0.0058
257176_s_at	AT3G23530;AT3G23510	[AT3G23530, cyclopropane fatty acid synthase, put	-1.078	0.0138	0.0719	-1.0199	0.0166	0.0668	-0.807	0.0141	0.0473	-0.749	0.018	0.0431
257177_at	AT3G23490	CYN (CYANASE); cyanate hydratase	-0.02039	0.8202	0.5296	0.2419	0.045	0.1052	-0.3277	0.0175	0.053	-0.06546	0.4794	0.3173
257178_at	AT3G13070	CBS domain-containing protein / transporter associ	-0.166	0.3588	0.3538	-0.1801	0.3238	0.3052	-0.5731	0.0208	0.058	-0.5873	0.0192	0.0444
257179_at	AT3G13170	ATSPO11-1; ATP binding / DNA binding / DNA topo	0.05569	0.966	0.5687	0.6284	0.636	0.4369	-1.1481	0.403	0.3178	-0.5754	0.664	0.3855
257180_at	AT3G13180	NOL1/NOP2/sun family protein / antitermination Nu	-0.0322	0.8905	0.5484	-0.2869	0.2363	0.2556	-0.3593	0.0833	0.127	-0.6159	0.017	0.0417
257181_at	AT3G13190	myosin heavy chain-related	0.04683	0.8778	0.5459	0.4031	0.2314	0.2524	-0.6927	0.0725	0.1171	-0.3365	0.3045	0.2408
257182_s_at	AT3G13210;AT5G45990	[AT3G13210, crooked neck protein, putative / cell c	0.3983	0.285	0.3142	-0.1305	0.7068	0.4612	0.4204	0.2628	0.2481	-0.1083	0.7542	0.4149
257183_at	AT3G13220	ABC transporter family protein	-0.8828	0.0451	0.1224	1.5341	0.2004	0.233	-3.4252	0.0268	0.0666	0.9917	0.3782	0.2749
257184_at	AT3G13090	ATMRP8 (Arabidopsis thaliana multidrug resistance	0.6466	0.0714	0.154	0.03552	0.9	0.5189	-0.03926	0.8856	0.4884	-0.6503	0.0641	0.0921
257185_at	AT3G13100	ATMRP7 (Arabidopsis thaliana multidrug resistance	3.6063	0.0101	0.064	1.1421	0.2197	0.2457	-0.6042	0.446	0.3367	-3.0684	0.0128	0.0358
257186_at	AT3G13130	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.593	0.5261	0.4316	-1.4613	0.1626	0.2078	0.72238	0.4449	0.3361	-1.3305	0.1947	0.1818
257187_at	AT3G13140	hydroxyproline-rich glycoprotein family protein	-0.905	0.4167	0.3832	0.3627	0.7352	0.4698	-0.8141	0.4613	0.3438	0.4535	0.6737	0.3886
257188_at	AT3G13150	pentatricopeptide (PPR) repeat-containing protein	0.6552	0.1759	0.2454	0.4863	0.2899	0.2865	0.5061	0.1891	0.205	0.3372	0.3517	0.2634
257189_at	AT3G13222	GIP1 (GBF-INTERACTING PROTEIN 1)	-0.2092	0.2546	0.3088	0.0977	0.1575	-0.2245	0.227	0.2277	-0.3541	0.0876	0.1109	
257190_at	AT3G13120	30S ribosomal protein S10, chloroplast, putative	-0.6323	0.0025	0.0424	-0.6596	0.0021	0.0333	0.226	0.0061	0.0325	0.1987	0.0096	0.0306
257191_at	AT3G13175	similar to unnamed protein product [Vitis vinifera] (G	1.3516	0.0016	0.0388	0.8902	0.0075	0.0488	-0.1735	0.3856	0.3103	-0.635	0.0236	0.0502
257192_at	AT3G13200	EMB2769 (EMBRYO DEFECTIVE 2769)	0.4332	0.0735	0.1561	0.5463	0.0384	0.0971	0.2373	0.2578	0.2451	0.3501	0.1233	0.1372
257193_at	AT3G13160	pentatricopeptide (PPR) repeat-containing protein	0.2584	0.2216	0.2761	0.5821	0.0311	0.0877	-0.01997	0.9144	0.4963	0.3038	0.1568	0.1591
257194_at	AT3G13110	AtSerat2;2 (SERINE ACETYLTRANSFERASE 1); s	-0.2779	0.118	0.1986	-0.2923	0.1049	0.1636	-0.1309	0.3565	0.2964	-0.1453	0.3121	0.2444
257195_at	AT3G23680	F-box family protein-related	-2.1267	0.0689	0.1485	-0.9944	0.3076	0.2961	0.4522	0.6234	0.4057	1.5845	0.1362	0.1457
257196_at	AT3G23790	AMP-binding protein, putative	0.4901	0.1484	0.2242	0.1377	0.642	0.4389	-0.6907	0.0289	0.069	-1.0432	0.0073	0.0266
257197_at	AT3G23800	selenium-binding family protein	0.2927	0.8053	0.5255	0.7073	0.5592	0.408	0.08052	0.9457	0.5046	0.4951	0.6791	0.3902
257198_at	AT3G23690	basic helix-loop-helix (bHLH) family protein	0.09029	0.5601	0.4449	0.2001	0.2324	0.2532	0.3401	0.0439	0.0874	0.4824	0.0184	0.0436
257199_at	AT3G23710	chloroplast inner membrane import protein Tic22, p	0.5547	0.0224	0.0875	0.4947	0.0321	0.0889	0.1463	0.3727	0.3042	0.08623	0.5862	0.3584
257200_at	AT3G23720	transposable element gene	5.3822	0.0408	0.1164	-3.7261	0.1082	0.1658	2.8317	0.1922	0.2069	-6.2766	0.0255	0.0528
257201_at	AT3G23740	similar to unknown protein [Arabidopsis thaliana] (T	-0.07593	0.8808	0.5465	-1.4951	0.0346	0.0919	0.8195	0.0204	0.0575	-0.5996	0.0527	0.0819
257202_at	AT3G23750	leucine-rich repeat family protein / protein kinase fa	-0.3549	0.2066	0.2662	-0.3308	0.2331	0.2535	0.02659	0.8758	0.4856	0.05068	0.7668	0.4189
257203_at	AT3G23730	xyloglucan xyloglucosyl transferase, putative / xylog	-0.7034	0.3377	0.3443	-1.0854	0.1684	0.2115	-0.4213	0.358	0.297	-0.6542	0.0672	0.0945
257204_at	AT3G23805	RALFL24 (RALF-LIKE 24)	-1.109	0.0192	0.0822	-0.8703	0.0408	0.1002	0.6914	0.0062	0.0328	0.93	0.0021	0.0155
257205_at	AT3G16520	UDP-glucuronosyl/UDP-glucosyl transferase family	-0.1594	0.1525	0.2277	-0.3365	0.0204	0.0729	0.1185	0.1361	0.1684	-0.05862	0.4092	0.2879
257206_at	AT3G16530	legume lectin family protein	-0.7551	0.0404	0.116	-0.8342	0.0299	0.0859	0.895	5.00E-04	0.0154	0.816	7.00E-04	0.0108
257207_at	AT3G14900	similar to unnamed protein product [Vitis vinifera] (G	0.4191	0.1963	0.2599	0.4267	0.1899	0.2264	-0.01083	0.9669	0.5093	-0.00327	0.99	0.4802
257208_at	AT3G14910	similar to unnamed protein product [Vitis vinifera] (G	0.3616	0.1044	0.1866	0.3461	0.1156	0.1716	-0.08226	0.6587	0.4175	-0.09776	0.6017	0.3638
257209_at	AT3G14930	similar to unknown protein [Arabidopsis thaliana] (T	0.3939	0.0414	0.1171	0.318	0.0749	0.1372	0.3065	0.0823	0.1269	0.2306	0.1576	0.1598
257210_at	AT3G14950	TTL2 (TETRATRICOPEPTIDE-REPEAT THIOREDO	0.7912	0.4273	0.3881	0.6856	0.487	0.3791	0.6388	0.4347	0.3318	-0.8381	0.3187	0.2477
257211_at	AT3G15080	exonuclease family protein	0.6577	0.02	0.0834	0.3548	0.1135	0.1702	0.1868	0.1227	0.1585	-0.1162	0.2916	0.2344
257212_at	AT3G15060	oxidoreductase, zinc-binding dehydrogenase family	0.1795	0.3859	0.3678	-0.09915	0.6197	0.4304	-0.1275	0.5276	0.3703	-0.0472	0.8108	0.4319
257213_at	AT3G15020	malate dehydrogenase (NAD), mitochondrial, putati	0.2591	0.1352	0.2134	-0.111	0.4683	0.3714	0.7513	0.0056	0.0311	0.3812	0.051	0.0804
257214_at	AT3G15040	similar to unknown protein [Arabidopsis thaliana] (T	0.3988	0.0878	0.1719	0.6667	0.0198	0.0721	-0.3472	0.122	0.1579	-0.0792	0.6784	0.39
257215_at	AT3G15070	zinc finger (C3HC4-type RING finger) family protein	0.00128	0.995	0.5758	0.3274	0.1644	0.2086	-0.06989	0.7351	0.4433	0.2588	0.2602	0.2126
257216_at	AT3G14990	4-methyl-5(b-hydroxyethyl)-thiazole monophosphat	0.5389	0.0118	0.0679	0.7827	0.0031	0.0363	0.2853	0.081	0.1247	0.529	0.0126	0.0355
257217_at	AT3G14940	ATPPC3 (PHOSPHOENOLPYRUVATE CARBOXY	-0.5956	0.1151	0.1963	-0.5087	0.1615	0.2069	-0.5871	0.0085	0.037	-0.5002	0.0148	0.0386
257218_at	AT3G15000	identical to Uncharacterized mitochondrial protein A	0.8189	0.0148	0.0737	0.5461	0.0522	0.1133	-0.02346	0.9122	0.4957	-0.2962	0.2121	0.1919
257219_at	AT3G14930	HEME1; uroporphyrinogen decarboxylase	-0.3759	0.1814	0.2492	-0.6386	0.0517	0.1128	-0.8812	0.0068	0.0338	-1.1438	0.0026	0.017
257220_at	AT3G27810	ATMYB21 (MYB DOMAIN PROTEIN 21); DNA bind	2.2043	0.122	0.2022	-0.01313	0.9913	0.542	1.3775	0.2885	0.2627	-0.84	0.4973	0.3248
257221_at	AT3G27920	GL1 (GLABRA 1); transcription factor	-0.4824	0.5218	0.4297	-0.2538	0.7308	0.4687	-0.2992	0.7255	0.4403	-0.03061	0.9666	0.4748
257222_at	AT3G27925	DEGP1 (DEGP PROTEASE 1); serine-type peptida	-0.1709	0.0637	0

257290_at	AT3G15560	similar to unnamed protein product [Vitis vinifera] (G	0.2112	0.7879	0.52	-1.3332	0.1436	0.1934	1.7693	0.0736	0.1181	0.2249	0.7746	0.4214
257291_at	AT3G15590	DNA-binding protein, putative	0.8828	7.00E-04	0.0334	0.7843	0.0011	0.0294	-0.525	0.0051	0.0301	-0.6234	0.0027	0.0172
257292_s_at	AT3G15600;AT2G07770	[AT3G15600, transposable element gene];[AT2G07	0.384	0.4504	0.3984	-0.2617	0.5995	0.4233	-0.4893	0.3471	0.2917	-1.135	0.069	0.0962
257293_at	AT3G15580	APG8H/ATG8I (AUTOPHAGY 8H); APG8 activating	0.2272	0.4678	0.4063	0.6006	0.1015	0.1608	0.3273	0.0456	0.0894	0.7008	0.0036	0.0194
257294_at	AT3G15570	phototropic-responsive NPH3 family protein	0.2095	0.3391	0.3449	0.02542	0.9016	0.5194	-0.2669	0.0666	0.1116	-0.5018	0.0093	0.0301
257295_at	AT3G17420	GPK1 (Glyoxysomal protein kinase 1); kinase	0.7888	0.0015	0.0383	1.1604	4.00E-04	0.0249	-0.3239	0.0345	0.076	0.04771	0.6666	0.3863
257296_at	no_match	no_match	-0.4522	0.5795	0.4521	-0.2601	0.7466	0.4737	-0.7076	0.3994	0.3164	-0.5155	0.5302	0.338
257297_at	AT3G28040	leucine-rich repeat transmembrane protein kinase,	-0.09156	0.6558	0.4778	-0.5019	0.0579	0.1196	0.003633	0.9803	0.5127	-0.4067	0.0427	0.0721
257298_at	AT3G28155	similar to MOR1 (MICROTUBULE ORGANIZATION	0.7896	0.2716	0.3065	0.02965	0.9641	0.535	0.9046	0.2181	0.2225	0.1447	0.8269	0.4362
257299_at	AT3G28050	nodulin MtN21 family protein	0.435	0.0736	0.1561	0.2447	0.2468	0.2619	-0.5338	0.0286	0.0687	-0.7241	0.0105	0.032
257300_at	AT3G28080	nodulin MtN21 family protein	0.2691	0.4071	0.379	0.129	0.6801	0.4519	-0.4882	0.0043	0.0282	-0.6282	0.0017	0.0145
257301_at	AT3G30190	transposable element gene	1.6968	0.227	0.2798	0.4536	0.7224	0.4661	-0.9002	0.4914	0.3563	-2.1434	0.146	0.1521
257302_at	AT3G30220	similar to unknown protein [Arabidopsis thaliana] (T	0.4146	0.7138	0.4972	-0.3987	0.7242	0.4667	1.5458	0.2159	0.2213	0.7325	0.5249	0.3358
257303_at	AT3G30230	myosin heavy chain-related	1.8835	0.189	0.2547	0.4695	0.7136	0.4632	0.6937	0.2998	0.2686	-1.6593	0.0465	0.0759
257304_at	AT3G30240	transposable element gene	-0.9408	0.207	0.2665	0.4508	0.5109	0.389	-0.275	0.6829	0.4252	1.1167	0.1487	0.1538
257305_at	AT3G30250	transposable element gene	-0.4925	0.7013	0.4929	0.7881	0.5456	0.4029	-1.5575	0.2414	0.2358	-0.2769	0.819	0.4338
257306_at	AT3G30200	fructose-6-phosphate 2-kinase-related / fructose-2,(	-0.297	0.6715	0.483	-0.4999	0.0823	0.1439	-0.526	0.4582	0.3423	-1.7289	0.0543	0.0834
257307_at	AT3G30210	MYB121 (myb domain protein 121); DNA binding / t	-0.0794	0.9356	0.5611	0.6437	0.5241	0.3938	-0.9437	0.3645	0.3003	-0.2206	0.8229	0.4351
257308_at	AT3G28120	unknown protein	2.6604	0.1227	0.203	0.5448	0.7098	0.462	1.943	0.2272	0.2278	-0.1726	0.9053	0.4589
257309_at	AT3G28180	similar to unknown protein [Arabidopsis thaliana] (T	-0.4591	0.3624	0.3556	0.4835	0.3403	0.3136	-0.2948	0.4768	0.3502	0.6478	0.16	0.1612
257310_at	AT3G26560	ATP-dependent RNA helicase, putative	0.4195	0.0111	0.0659	0.3398	0.0223	0.0755	-0.4453	0.009	0.0379	-0.5251	0.005	0.0222
257311_at	AT3G26570	PHT2;1 (phosphate transporter 2;1)	-0.9644	0.0453	0.1225	-0.8871	0.0107	0.0557	0.2713	0.1229	0.1586	-0.05142	0.7303	0.4073
257312_at	no_match	no_match	-0.1978	0.5802	0.4523	0.3526	0.3443	0.3153	-0.413	0.1666	0.1895	0.1375	0.604	0.3646
257313_at	AT3G26520	TIP2 (TONOPLAST INTRINSIC PROTEIN 2); wate	-0.3895	0.0059	0.0534	-0.408	0.005	0.0425	0.1292	0.0991	0.1402	0.1108	0.1405	0.1485
257314_at	AT3G26590	MATE efflux family protein	0.2042	0.3729	0.3609	0.26	0.2709	0.2759	-0.4416	0.0961	0.1378	-0.3857	0.1312	0.1424
257315_at	AT3G30775	ERD5 (EARLY RESPONSIVE TO DEHYDRATION	-1.3877	0.0233	0.0893	-0.8116	0.1048	0.1635	-0.08707	0.6924	0.4285	0.489	0.0752	0.1009
257316_at	AT3G30750	transposable element gene	0.9039	0.5532	0.4421	-2.2621	0.181	0.2203	0.8411	0.5011	0.36	-2.3249	0.1107	0.1282
257317_at	AT3G01060	hypothetical protein	0.06192	0.9238	0.558	-0.7379	0.2916	0.2876	-2.5327	0.0141	0.0474	-3.3325	0.0054	0.023
257318_at	ATMG01090;AT2G07777	[ATMG01090, hypothetical protein];[AT2G07777, Id	0.3002	0.6802	0.4861	-1.0002	0.2134	0.2416	-2.9279	0.0124	0.0442	-4.2282	0.0033	0.0188
257319_at	ATMG01100	hypothetical protein	0.9726	0.2182	0.274	-0.1502	0.8328	0.4996	-0.3937	0.5365	0.3739	-1.5165	0.06	0.0885
257320_at	AT2G07749;ATMG01110	[AT2G07749, Identical to Uncharacterized mitochor	0.667	0.297	0.3214	-0.6419	0.3707	0.4477	0.605	0.3998	0.3598	-2.0465	0.0625	0.0907
257321_at	ATMG01130	hypothetical protein	-0.5971	0.4023	0.3764	-0.3088	0.6536	0.443	-2.1239	0.0291	0.0693	-1.8357	0.0451	0.0745
257322_at	ATMG01180	hypothetical protein	0.3143	0.4536	0.3998	-0.4203	0.3297	0.3084	-1.1184	0.042	0.0852	-1.853	0.0081	0.028
257323_at	ATMG01200	hypothetical protein	0.04647	0.9682	0.5693	-0.7369	0.5379	0.3996	-2.1417	0.1221	0.1581	-2.9251	0.0557	0.0846
257324_at	ATMG01210	hypothetical protein	0.07975	0.9255	0.5584	-0.7745	0.3882	0.3359	-1.8962	0.077	0.1212	-2.7505	0.0264	0.0538
257325_at	ATMG01220	hypothetical protein	-0.9197	0.3817	0.3655	-0.4497	0.6562	0.444	-2.1081	0.0311	0.0717	-1.6382	0.0644	0.0922
257326_s_at	AT2G07697;AT2G07697	[ATMG01230, hypothetical protein];[AT2G07697, tr	1.5523	0.1346	0.2131	-1.4775	0.1495	0.1977	1.1892	0.1383	0.1698	-1.8406	0.0459	0.0753
257327_at	ATMG01240	hypothetical protein	1.6481	0.1043	0.1866	-1.6755	0.1003	0.1597	1.1279	0.2251	0.2265	-2.1957	0.0493	0.0786
257328_s_at	AT2G07697;AT2G07697	[ATMG01250, hypothetical protein];[AT2G07697, tr	1.5194	0.1736	0.244	0.5594	0.5756	0.414	-0.07879	0.849	0.4783	-1.0388	0.0554	0.0843
257329_at	ATMG01260	hypothetical protein	0.1431	0.8564	0.5403	0.8823	0.3	0.2913	-0.0159	0.9839	0.5137	0.7234	0.3846	0.2778
257330_at	ATMG01290	hypothetical protein	0.6872	0.4089	0.3795	-0.7844	0.3522	0.3192	-0.5673	0.4892	0.3552	-2.0389	0.0522	0.0814
257331_at	ATMG01330	hypothetical protein	-1.4738	0.1145	0.1961	-0.1857	0.8124	0.4937	-1.9076	0.0598	0.1049	-0.6195	0.4453	0.3041
257332_at	ATMG01350	hypothetical protein	-0.07091	0.9204	0.5571	-0.3328	0.6437	0.4394	-0.8641	0.0967	0.1383	-1.126	0.048	0.0774
257333_at	ATMG01360	cytochrome c oxidase subunit 1	0.2329	0.3697	0.3594	0.008257	0.9732	0.5374	-2.6368	3.00E-04	0.0141	-2.8614	2.00E-04	0.0079
257334_at	ATMG01370	hypothetical protein	0.3432	0.2638	0.3018	-0.6012	0.0852	0.1469	-2.7439	3.00E-04	0.0138	-3.6883	1.00E-04	0.006
257335_at	ATMG01400	hypothetical protein	-0.2564	0.7092	0.4959	-0.1682	0.8079	0.4923	-0.209	0.7017	0.4319	-0.1178	0.828	0.4366
257336_at	ATMG01410	Identical to Uncharacterized mitochondrial protein A	0.1609	0.5522	0.442	-0.8178	0.0301	0.0863	-0.1538	0.5691	0.3863	-1.1325	0.0103	0.0317
257337_at	ATMG00060	Mitochondrial NADH dehydrogenase subunit 5. The	-2.1556	0.115	0.1963	0.02561	0.9821	0.5397	-3.18	0.0414	0.0846	-0.9987	0.4048	0.286
257338_s_at	ATMG00513;AT2G07711	Mitochondrial NADH dehydrogenase	1.7734	0.0019	0.0391	-0.1568	0.5558	0.4068	-2.617	2.00E-04	0.0129	-4.5472	0	0.0052
257339_s_at	ATMG00040;AT2G07671;A	[ATMG00040, hypothetical protein];[AT2G07671, H	0.2461	0.4054	0.3781	-0.5224	0.1198	0.1752	-2.7465	4.00E-04	0.0147	-3.5149	2.00E-04	0.007
257340_at	AT2G10760	transposable element gene	-0.00354	0.9975	0.5763	-0.8453	0.4687	0.3714	0.92	0.4332	0.331	0.07825	0.9445	0.4695
257341_at	AT2G10400	transposable element gene	0.5548	0.2028	0.2731	-1.4056	0.4032	0.3427	2.091	0.1952	0.2089	0.1307	0.9273	0.4649
257342_at	AT3G42365	transposable element gene	-0.9313	0.2585	0.2988	-1.4474	0.1103	0.1676	0.899	0.2728	0.2539	0.3829	0.6172	0.3693
257343_s_at	AT1G34967;AT1G34904;A	[AT1G34967, transposable element gene];[AT1G34	-1.5578	0.2229	0.277	-1.1235	0.3572	0.3215	0.7556	0.214	0.2203	1.1899	0.0807	0.1056
257344_s_at	AT1G12150;AT2G16150;A	[AT1G12150, transposable element gene];[AT2G16	0.01811	0.9759	0.5712	-0.1746	0.7726	0.4813	-0.3435	0.5757	0.3887	-0.5362	0.396	0.2826
257345_s_at	AT1G41700;AT1G36540;A	[AT1G41700, transposable element gene];[AT1G36	-1.0151	0.226	0.279	-1.0977	0.1969	0.2309	-0.464	0.549	0.3787	-0.5466	0.4842	0.3193
257346_at	AT3G30846	transposable element gene	0.2843	0.6902	0.4893	-1.7316	0.0593	0.121	0.04118	0.9535	0.5064	-1.9746	0.0408	0.0699
257347_at	AT3G29792	transposable element gene	-1.6208	0.1188	0.1992	0.8459	0.5033	0.4394	-0.8641	0.0967	0.2342	0.6565	0.4676	0.3129
257348_at	AT2G42140	VQ motif-containing protein	1.6105	0.3435	0.3465	-1.0879	0.5085	0.388	2.0357	0.0379	0.0804	-0.6627	0.3764	0.274
257349_at	AT2G30630	similar to unknown protein [Arabidopsis thaliana] (T	-0.2631	0.8479	0.5378	0.5778	0.6764	0.4507	-1.447	0.3234	0.2799	-0.6061	0.662	0.3848
257350_x_at	no_match	no_match	1.1324	0.2964	0.3212	-0.1452	0.8852	0.5147	0.3181	0.753	0.4491	-0.9594	0.3669	0.2699
257351_at	AT3G33820	ATMBAC1; L-histidine transmembrane transporter/	-0.2754	0.1779	0.2466	-0.2498	0.2128	0.2413	-0.973	0.0045	0.0286	-0.9473	0.0049	0.0221
257352_at	AT3G34900	IMB1 (IMBIBITION-INDUCIBLE 1); DNA binding	0.2136	0.4116	0.381	0.8733	0.0201	0.0724	-0.9244	0.0166	0.0514	-0.2647	0.3199	0.2483
257353_at	AT3G23050	phototropic-responsive NPH3 family protein	-0.7096	0.3358	0.3432	-0.5325	0.4582	0.3674	0.4304	0.424	0.327	0.6075	0.2776	0.2269
257354_x_at	AT3G23480	transposable element gene	0.08463	0.9063	0.5528	0.6521	0.3886	0.3362	0.1587	0.8256	0.4714	0.7262	0.3425	0.2591
257355_at	AT3G38150	transferase; transferase, transferring glycosyl group	0.2967	0.7618	0.5121	2.3663	0.0608	0.1225	-1.4193	0.1955	0.209	0.6503	0.5161	0.3321
257356_s_at	AT2G32490;AT2G36110	[AT2G32490, pseudogene of 3'-5' exonuclease dom	-1.2279	0.2209	0.2757	-0.6608	0.479	0.3757	-1.0077	0.2933	0.2653	-0.4406	0.6251	0.372
257357_at	AT2G41050	PQ-loop repeat family protein / transmembrane fam	-1.5674	0.0677	0.1493	-1.7242	0.0521	0.1132	-0.6356	0.2145	0.2205	-0.7924	0.14	0.1481
257358_at	AT2G40990	zinc finger (DHHC type) family protein	-1.1811	0.1808	0.2486	0.6335	0.4342	0.3571	-1.0689	0.1974	0.2102	0.7458	0.3419	0.2589
257359_x_at	AT3G34290	protein kinase family protein	1.1789	0.051	0.1299	-0.1895	0.6806	0.4522	0.3437	0.4667	0.346	-1.0248	0.0747	0.1005
257360_at	AT3G39240	RNA polymerase I transcription factor	-1.0324	0.282	0.3126	0.3314	0.7104	0.4623	-1.9244	0.0815	0.1252	-0.5605	0.537	0.3403
257361_at	AT2G07740	transposable element gene	-0.495	0.473	0.4091	-0.8603	0.241	0.2585	0.9348	0.2094	0.2174	0.5695	0.4141	0.29
257362_at	AT2G45840	similar to unknown protein [Arabidopsis thaliana] (T	-0.6075	0.3581	0.3535	-0.7211	0.2856	0.2841	-0.3786	0.5531	0.3801	-0.4922	0.4479	0.3052
257363_at	no_match	no_match	0.1361	0.7764	0.5168	0.2248	0.6421	0.4389	0.1753	0.6901	0.4278	0.264	0.5535	0.3463
257364_at	AT2G45940	similar to unknown protein [Arabidopsis thaliana] (T	0.6706	0.5161	0.4276	-0.9981	0.3493	0.3178	0.3803	0.4701	0.3477	-1.2883	0.0541	0.0832
257365_x_at	AT2G26020	PDF1.2c (plant defensin 1.2b)	-1.9312	0.0689	0.151	-2.9167	0.0203	0.0727	1.8811	0.0295	0.0698	-0.8957	0.1895	0.179
257366_s_at	AT2G03290;AT2G03040	[AT2G03290, protein transmembrane transporter];[	0.2168	0.0122	0.0685	2.7046	0.0053	0.0429	0.1474	0.7785	0.4568	0.7252	0.2129	0.1923
257367_at	AT2G25780	similar to unknown protein [Arabidopsis thaliana] (T	1.0834	0.3733	0.361	0.7383	0.5324	0.397	0.8221	0.0939	0.1358	0.4771	0.273	0.2245
257368_at	AT2G29860	kelch repeat-containing F-box family protein	0.06613	0.8651	0.5423	-0.5596	0.2001	0.2329	0.3596	0.3804	0.308	-0.2661	0.5065	0.3283
257369_at	AT3G35550	ATBPC7/BBR/BPC7/BPC7 (BASIC PENTACYSTE	0.1638	0.5922	0.4568	0.245	0.4338	0.357	-0.1243	0.682	0.4249	-0.04316	0.8857	0.4531
257370_at	AT3G35080	ATP binding / aminoacyl-tRNA ligase/ nucleotide bi	0.2533	0.8243	0.5308	-0.4995	0.6645	0.4465	-0.7485	0.5223	0.3679	-1.5014	0.2328	0.2031
257371_at	AT2G47810	histone-like transcription factor (CBF/NF-Y) family p	-0.1289	0.8354	0.534	-0.2543	0.6845	0.4537	-0.5318	0.4123	0.3218	-0.6572	0.3216	0.2491
257372_at	AT3G43220	DC1 domain-containing protein	-0.501	0.6372	0.4721	-1.9745	0.1151	0.1712	1.8503	0.133	0.166	0.3768	0.7211	0.4043
257373_at	AT3G43140	DNA binding / transcription factor	0.4807	0.6674	0.4817	0.4198	0.7066	0.4611	0.124	0.9107	0.4955	0.06301	0.9545	0.4722
257374_at	AT3G43280	far-red impaired response family protein / FAR1 fa	-0.1176	0.598	0.4589	-0.08515	0.7001	0.4591	-0.09259	0.6759	0.423	-0.06013	0.7845	0.4242
257375_at	AT3G38640	similar to unknown protein [Arabidopsis thaliana] (T	0.1846	0.3477	0.3488	0.1306	0.4938	0.382	0.7265	0.0139	0.047	0.6725	0.018	0.043
257376_at	AT3G32350	similar to ubiquitin family protein [Arabidopsis thalia	-0.1656	0.8536	0.5392	-0.2058	0.8188	0.4955	-0.7611	0.4169	0.3238	-0.8014	0.3949	0.2822
257377_at	AT2G28890	PLL4 (POLTERGEIST LIKE 4); protein serine/threo	0.4102	0.1367	0.2147	0.3802	0.1601	0.206	0.08286	0.3359	0.2864	0.05286	0.5241	0.3355
257378_s_at	AT2G02290;AT5G23470	[AT2G02290, NLI interacting factor (NIF) family pro	0.6029	0.6562	0.4779	-1.2823	0.3649	0.3252	-0.5268	0.6964	0.4299	-2.4121	0.1271	0.1396
257379_x_at	AT2G12150;AT1G45070;A	[AT2G12150, transposable element gene];[AT1G45	0.3413	0.776	0.5167	1.2732	0.3195	0.3029	-0.7287	0.5512	0.3795	0.2032	0.865	0.447
257380_at	AT2G28090	heavy-metal-associated domain-containing protein	0.9083	0.2884	0.3164	-0.299	0.7249	0.4669	0.7188	0.4153	0.3231	-0.5485	0.5266	0.3365
257381_at	AT2G37950	zinc finger (C3HC4-type RING finger) family protein	-0.232	0.5491	0.4407	-0.1521	0.6904	0.4557	-0.1066	0.705	0.4331	-0.0267	0.9238	0.4638
257382_at	AT2G40750	WRKY54 (WRKY DNA-binding protein 54); transcri	0.762	0.0229	0.0885	0.1765	0.4518	0.3648	0.6333	0.0404	0.0834	0.0478	0.8326	0.438
257383_at	AT2G19830	F-box family protein	0.3473	0.8216	0.53	-0.1696	0.9121	0.522	0.8897	0.5708	0.3869	0.3727	0.8089	0.4314
257384_at	AT2G15110	pseudogene, hypothetical protein, contains Pfam pr	-1.1351	0.3863	0.3681	-0.9215	0.4744	0.374	-0.6991	0.4604	0.3434	-0.4856	0.6013	0.3638
257385_at	AT2G01800	COP1-interacting protein-related	1.4303	0.3438	0.3466	-1.4534	0.337	0.312	0.6173	0.6675	0.4203	-2.2664	0.1644	0.1639
257386_at	AT2G42440	LOB domain protein 17 / lateral organ boundaries d	0.314	0.5026	0.4216	0.1348	0.7679	0.4799	0.1062	0.8157	0.4685	-0.07306	0.8723	0.4491
257387_s_at	AT2G14510;AT2G14440	[AT2G14510, leucine-rich repeat protein kinase, pu	-0.2736	0.795	0.5224	1.68	0.1634	0.2082	-1.36	0.2396	0.235	0.5935	0.5794	0.3558
257388_at	no_match	no_match	0.4171	0.7494	0.5085	-1.5022	0.2853	0.284	2.3447	0.1268	0.1615	0.4254	0.7447	0.4119
257389_at	AT2G17970	oxidoreductase, 2OG-Fe(II) oxygenase family prote	0.4941	0.1502	0.2258	-0.07835	0.7921	0.4868	-0.2651	0.3945	0.3139	-0.8375	0.0395	0.0685
257390_x_at	AT2G06700	transposable element gene	-0.7905	0.5713	0.4495	-0.4912	0.7215	0.4659	0.4516	0.7357	0.4435	0.751	0.5797	0.3559
257391_at	AT2G32050	cell cycle control protein-related	0.03419	0.9674	0.5691	1.7015	0.0966	0.1566	-0.3698	0.6628	0.4189	1.2976	0.1744	0.1699
257392_at	AT2G24450	FLA3 (FASCICLIN-LIKE ARABINOGALACTAN PR	-0.08263	0.9186	0.5566	0.3266	0.6894	0.4555	-0.4288	0.4764	0.35	-0.01954	0.9732	0.4764
257393_at	no_match	no_match	0.9035	0.5129	0.4262	0.2448	0.8554	0.506	1.0265	0.4608	0.3435	0.3678	0.7848	0.4243
257394_at	no_match	no_match	-0.0613	0.9571	0.5665	0.3674	0.7491	0.4747	0.4897	0.6715	0.4215	0.9184	0.4399	0.3013
257395_at	AT2G19630	pentatricopeptide (PPR) repeat-containing protein	0.5667	0.3059	0.3261	0.1132	0.8262	0.4978	0.07592	0.8827	0.4875	-0.3775	0.4782	0.317
257396_at	AT2G20875	EPF1 (EPIDERMAL PATTERNING FACTOR 1)	-0.4473	0.1137	0.1954	-0.4844	0.0941	0.1545	-0.9459	0.013	0.0452	-0.983	0.0114	0.0335
257397_at	AT2G20430	RIC6 (ROP-INTERACTIVE CRIB MOTIF-CONTAIN	0.08225	0.7228	0.5003	-0.7003	0.0317	0.0884	0.5324	0.0694	0.1142	-0.2502	0.3114	0.244
257398_at	AT2G01990	similar to unknown protein [Arabidopsis thaliana] (T	-0.3253	0.1165	0.1973	-0.01954	0.9114	0.5219	-0.025	0.8598	0.481	0.2847	0.8985	0.1194
257399_at	AT1G23690	similar to unknown protein [Arabidopsis thaliana] (T	-1.451	0.2898	0.3171	0.03276	0.9794	0.5393	-0.701	0.5145	0.3648	0.7827	0.4698	0.3136
257400_s_at	AT1G24250;AT1G23810	[AT1G24250, paired amphipathic helix repeat-conta	0.312	0.8123	0.5275	1.4278	0.3104	0.2975	-0.7611	0.5696	0.3865	0.3547	0.7874	0.425
257401_at	AT1G23500	SIR2 (SIMILAR TO RCD ONE 2); NAD+ ADP-ribo	0.8031	0.041	0.1166	0.6254	0.0815	0.143	0.1929	0.3748	0.3052	0.01522	0.941	0.4688
257402_at	AT1G23570	similar to unknown protein [Arabidopsis thaliana] (T	0.618	0.4849	0.4139	1.2406	0.1976	0.2314	-1.4245	0.1511	0.1796	-0.8018	0.375	0.2735
257403_at	AT1G62520	similar to unknown protein [Arabidopsis thaliana] (T	0.3693	0.0392	0.1143	-0.3387	0.6883	0.4551	-3.1338	0.0162	0.0507	-1.1074	0.2311	0.202
257404_at	AT1G04050	F-box family protein	-0.9468	0.1157	0.1967	0.4288	0.4156	0.3487	-1.0598	0.0263	0.0659	0.3158	0.3634	0.2684
257405_at	AT2G24620	polcalcin, putative / calcium-binding pollen allergen,	-1.7204	0.1749	0.2448	-1.1358	0.3381	0.3127	-0.3458	0.739	0.4445	0.2387	0.8174	0.4336
257406_at	AT1G27060	regulator of chromosome condensation (RCC1) fam	0.07281	0.6828	0.4868	-0.4828	0.0434	0.1034	0.02481	0.8814	0.4871	-0.3852	0.6692	0.3964
257407_at	AT1G27100	similar to unknown protein [Arabidopsis thaliana] (T	-0.4666	0.0148	0.0737	-0.3647	0.0327	0.0896	0.1443	0.2731	0.2541	0.2462	0.0963	0.1177
257408_at	AT1G27310	SON1 (SUPPRESSOR OF NIM1-1 1)	-1.3927	0.1444	0.2209	-1.5052	0.122	0.1772	0.1176	0.8859	0.4884	0.005174	0.995	0.4814
257409_at	AT1G27470	similar to unknown protein [Arabidopsis thaliana] (T	-0.2262	0.9446	0.5635	0.6764	0.609	0.4287	-1.3974	0.0162	0.0161	0.2763	-0.8113	0.5428	0.3419
257410_at	AT1G24340	EMB2421 (EMBRYO DEFECTIVE 2421); monooxy	0.2603	0.077	0.1596	-0.1261	0.3152	0.3004	-0.6474	0.0042	0.0277	-1.0339	7.00E-04	0.0107
257411_s_at	AT1G61330;AT1G61320	[AT1G61330, F-box family protein];[AT1G61320, st	0.2453	0.7957	0.5226	-0.3028	0.7498	0.4748	-0.09011	0.9239	0.4989	-0.6382	0.5114	0.3302
257412_at	no_match	no_match	1.2679	0.2032	0.2642	-0.917	0.3334	0.3099	1.2877	0.0992	0.1403	-0.9171	0.1967	0.1829
257413_at	AT1G22910	RNA recognition motif (RRM)-containing protein	-0.4602	0.0351	0.1083	-0.3942	0.0551	0.1165	-0.5389	0.0113	0.0422	-0.473	0.0176	0.0425
257414_at	no_match	no_match	-1.2895	0.1163	0.1972	0.9266	0.2243	0.2481	-1.1498	0.1493	0.1785	1.0662	0.1738	0.1695
257415_at	AT1G70040	similar to unknown protein [Arabidopsis thaliana] (T	0.1281	0.0277	0.0966	-0.2069	0.7599	0.4778	1.1143	0.0314	0.072	0.3365	8.00E-04	0.0116
257416_at	AT2G17750	similar to unknown protein [Arabidopsis thaliana] (T	-0.5582	0.5821	0.4531	-0.2365	0.8125	0.4937	-0.08591	0.9233	0.4988	0.2357	0.7926	0.4268
257417_at	AT1G10110	F-box family protein	-0.1209	0.8265	0.5316	-1.4273	0.0507	0.1117	-0.3741	0.5092	0.363	-1.6804	0.0313	0.0596
257418_at	AT1G30850	similar to unknown protein [Arabidopsis thaliana] (T	0.1089	0.9337	0.5608	-0.00194	0.9988	0.5437	0.6706	0.6146	0.4025	0.7775	0.5616	0.3495
257419_at	AT1G30800	similar to unknown protein [Arabidopsis thaliana] (T	-1.6944	0.1443	0.2208	-2.1574	0.0823	0.1439	0.4969	0.6234	0.4057	0.03385	0.9729	0.4763
257420_at	AT1G77250	PHD finger family protein	-0.1804	0.51	0.4249	-0.297	0.3	0.2913	-0.134	0.5605	0.3828	-0.2506	0.3013	0.2393
257421_at	AT1G12200	similar to unknown protein [Arabidopsis thaliana] (T	-0.08333	0.9094	0.5538	1.23	0.1481	0.1967	-0.4799	0.2396	0.235	0.8335	0.0746	0.1004
257422_at	AT1G11940	similar to unknown protein [Arabidopsis thaliana] (T	0.5265	0.0752	0.1577	-0.1873	0.443	0.3608	0.4402	0.0792	0.1231	-0.2736	0.2191	0.1956
257423_at	AT1G62010	mitochondrial transcription termination factor-relat	0.3247	0.3215	0.3352	0.3761	0.2604	0.27	0.05277	0.6732	0.422	0.1043	0.4202	0.2926
257424_at	AT1G78940	F-box family protein	-0.1347	0.8895	0.5483	-0.04148	0.9658	0.5355	-0.248	0.7988	0.463	-0.1548	0.8732	0.4494

257490_x_at	AT1G01380	ETC1 (ENHANCER OF TRY AND CPC 1); DNA bir	-1.5502	0.0634	0.1442	-0.5546	0.4133	0.3476	-0.2253	0.6069	0.4003	0.7703	0.1293	0.1409
257491_at	AT1G06170	basic helix-loop-helix (bHLH) family protein	-2.0657	0.1434	0.2203	1.109	0.3846	0.334	-0.7067	0.5553	0.381	2.4681	0.0881	0.1114
257492_at	AT1G49190	ARR19 (ARABIDOPSIS RESPONSE REGULATOR	-0.3408	0.7967	0.5228	1.0974	0.4253	0.3531	-1.0986	0.4248	0.3275	0.3395	0.7974	0.428
257493_at	AT1G48180	similar to unknown protein [Arabidopsis thaliana] (T	-0.4001	0.6899	0.4892	-0.1638	0.869	0.5096	-1.3379	0.2246	0.2263	-1.1017	0.3028	0.24
257494_at	AT1G32375	F-box family protein	-0.4353	0.4489	0.3976	-0.2522	0.6525	0.4426	-0.5626	0.1868	0.2035	-0.3795	0.3436	0.2597
257495_at	AT1G07960	ATPDIL5-1 (PDI-LIKE 5-1); thiol-disulfide exchange	0.384	0.2033	0.2643	0.2552	0.3696	0.3274	0.1995	0.363	0.2996	0.07074	0.7345	0.4086
257496_s_at	AT2G43730;AT2G43740	similar to oxidoreductase, 2OG-Fe(II) oxygenase fa	-0.4147	0.4902	0.416	0.09654	0.8684	0.5095	-0.5528	0.3689	0.3023	-0.04161	0.943	0.4692
257497_at	AT1G51430	similar to unknown protein [Arabidopsis thaliana] (T	0.1456	0.5033	0.4219	0.05689	0.7883	0.4857	-1.002	0.0059	0.0321	1.0438	0.0067	0.0255
257498_at	AT1G69660	meprin and TRAF homology domain-containing pro	-2.8901	0.0207	0.0848	-0.4019	0.6336	0.4358	-1.968	0.007	0.0341	0.5203	0.2498	0.2124
257499_at	AT1G63850	PRLI-interacting factor-related	-0.361	0.2506	0.2939	-0.3834	0.2271	0.2498	-0.3714	0.2394	0.2349	-0.3939	0.2169	0.1946
257500_s_at	AT1G73300;AT5G36180	AT1G73300; SCPL2 (serine carboxypeptidase-like	-2.0379	0.0986	0.1812	-1.017	0.3448	0.3155	-0.8123	0.4408	0.3344	0.2086	0.837	0.4393
257501_at	AT1G35380	transposable element gene	-0.4172	0.6563	0.4779	-0.2555	0.7834	0.4844	0.6367	0.4883	0.3548	0.7984	0.3932	0.2813
257502_at	AT1G78110	similar to unknown protein [Arabidopsis thaliana] (T	-0.2075	0.4656	0.4054	0.5033	0.1224	0.1776	0.4893	0.1303	0.1641	1.2001	0.0096	0.0305
257503_at	AT1G72530	plastid developmental protein DAG, putative	0.02261	0.8992	0.5509	0.05192	0.7723	0.4812	-0.1147	0.5315	0.3718	-0.08542	0.6373	0.3762
257504_at	AT1G52250	dynein light chain type 1 family protein	-0.1995	0.7941	0.5223	0.6195	0.4353	0.3577	-0.2389	0.7552	0.4498	0.5802	0.4628	0.3112
257505_at	AT1G47940	similar to oxidoreductase, 2OG-Fe(II) oxygenase fa	1.2086	0.434	0.391	-0.06658	0.9641	0.535	1.6237	0.1785	0.1977	0.3485	0.7441	0.4117
257506_at	AT1G29440	auxin-responsive family protein	-1.4882	0.0018	0.0391	-1.5254	0.0017	0.032	1.081	0.0059	0.0321	1.0438	0.0067	0.0255
257507_at	AT1G29600	zinc finger (CCCH-type) family protein	-0.09417	0.8953	0.55	-1.6656	0.0682	0.1309	-1.2219	0.143	0.1738	-2.7934	0.0142	0.0377
257508_at	AT1G64320	myosin heavy chain-related	-0.2226	0.8862	0.5474	-0.6943	0.6593	0.4447	0.2781	0.5088	0.363	-0.1936	0.6405	0.3773
257509_at	AT1G63190	similar to unknown protein [Arabidopsis thaliana] (T	0.123	0.8792	0.5463	0.9643	0.2733	0.2772	-0.5877	0.4825	0.3521	0.2536	0.7554	0.4152
257510_at	AT1G55360	similar to unknown protein [Arabidopsis thaliana] (T	-0.9511	0.0018	0.0391	-0.9836	0.0016	0.0317	0.1115	0.4375	0.333	0.07891	0.5749	0.3541
257511_at	AT1G43000	zinc-binding family protein	0.1633	0.8487	0.5379	2.0749	0.0609	0.1226	-0.1549	0.8563	0.4802	1.7568	0.0937	0.1158
257512_at	AT1G35250	hoedansare family protein	-0.3199	0.6198	0.4665	-0.9155	0.1992	0.2324	-0.81	0.2456	0.2384	-1.4056	0.0777	0.103
257513_s_at	AT1G12390;AT1G12340	[AT1G12390, cornichon family protein];[AT1G12340	0.3275	0.1063	0.1886	0.05817	0.7308	0.4687	-0.4324	0.0184	0.0543	-0.7016	0.0034	0.0189
257514_at	AT1G43940	transposable element gene	0.00717	0.9957	0.576	-0.1592	0.9041	0.5199	0.21	0.8738	0.4851	0.04365	0.9736	0.4765
257515_at	AT1G13290	zinc finger (C2H2 type) family protein	-0.3092	0.8032	0.525	-0.9743	0.4487	0.3634	0.1327	0.9145	0.4963	-0.5324	0.6704	0.3875
257516_at	AT1G69040	ACR4 (ACT REPEAT 4); amino acid binding	-0.1575	0.704	0.4939	-0.1912	0.646	0.4402	-0.199	0.5214	0.3675	-0.2327	0.4578	0.3091
257517_at	AT1G16130	similar to unknown protein [Arabidopsis thaliana] (T	-2.1273	0.0938	0.1773	0.9738	0.3731	0.3291	2.0334	0.028	0.068	0.8799	0.2182	0.1952
257518_at	AT3G03880	similar to unknown protein [Arabidopsis thaliana] (T	-0.1056	0.4898	0.4158	0.2238	0.1827	0.2216	-0.207	0.1599	0.1857	0.1224	0.3657	0.2694
257519_at	AT3G01210	nucleic acid binding	-0.6156	0.0074	0.0577	-0.6868	0.005	0.0424	0.05059	0.7013	0.4317	-0.02054	0.8752	0.4499
257520_at	AT3G07710	similar to DNA-binding storekeeper protein-related (	0.1873	0.8846	0.5471	2.654	0.0935	0.154	-1.9405	0.1844	0.2017	0.5262	0.6863	0.3928
257521_at	AT3G09140	similar to unknown protein [Arabidopsis thaliana] (T	-2.273	0.0354	0.1085	1.4839	0.1109	0.1681	-1.0181	0.2342	0.2318	2.7388	0.0197	0.045
257522_at	AT3G08990	yippee family protein	0.5837	0.099	0.1816	0.6013	0.0921	0.1531	-0.1929	0.5184	0.3664	-0.1753	0.5553	0.3471
257523_at	AT3G01620	glycosyl transferase family 17 protein	1.2755	0.2087	0.2672	0.07165	0.937	0.5284	-0.06068	0.9375	0.5029	1.2644	0.1569	0.1592
257524_at	AT3G01330	DEL3 (DP-E2F-like 3); transcription factor	-0.1474	0.7532	0.5095	-0.6915	0.1894	0.226	-0.3075	0.5212	0.3675	-0.8515	0.1237	0.1375
257525_at	AT3G04900	heavy-metal-associated domain-containing protein	0.9452	0.3746	0.3618	0.4474	0.6612	0.4455	1.1135	0.3048	0.271	0.6157	0.551	0.3455
257526_s_at	AT3G09330;AT3G09340	AT3G09330; amino acid transporter family protein	1.9226	0.0413	0.1171	1.4412	0.0903	0.1516	2.0992	0.01	0.0398	0.3797	0.5896	0.3598
257527_at	AT3G01080	similar to unknown protein [Arabidopsis thaliana] (T	0.6264	0.3966	0.3735	-0.1779	0.801	0.4897	0.5482	0.3228	0.2796	-0.2562	0.6263	0.3724
257528_at	AT3G02125	similar to unknown protein [Arabidopsis thaliana] (T	0.752	0.4324	0.3906	-0.9368	0.3384	0.3129	1.0511	0.2899	0.2635	-0.6378	0.5006	0.3262
257529_at	AT3G03290	universal stress protein (USP) family protein	-0.569	0.5394	0.4366	0.795	0.402	0.3421	-1.5281	0.1462	0.1763	-0.1641	0.8561	0.4447
257530_at	AT3G03040	F-box family protein	0.1002	0.3523	0.3509	0.166	0.1565	0.2032	-0.8454	6.00E-04	0.0158	-0.7796	8.00E-04	0.0113
257531_at	AT3G07250	nuclear transport factor 2 (NTF2) family protein / RN	0.5157	0.3715	0.3602	-1.4775	0.045	0.1051	1.3631	0.0565	0.1015	-0.6301	0.2866	0.2316
257532_at	AT3G04700	similar to unknown protein [Arabidopsis thaliana] (T	0.32	0.5005	0.4208	-0.26	0.5802	0.4163	-0.688	0.1467	0.1767	-1.2679	0.0296	0.0577
257533_at	AT3G10840	hydrolase, alpha/beta fold family protein	-1.4804	0.0039	0.0463	-1.3995	0.0047	0.0418	0.09695	0.3309	0.2837	0.1779	0.1124	0.1293
257534_at	AT3G09670	PWWP domain-containing protein	0.01687	0.9354	0.5611	0.2175	0.3281	0.3076	-0.1709	0.4314	0.3302	0.02979	0.8862	0.4532
257535_at	AT3G09440	chloroplast lumen common family protein	1.0151	0.0373	0.1114	1.037	0.035	0.0923	0.03208	0.9091	0.4951	0.05403	0.8477	0.4422
257536_at	AT3G02800	phosphoprotein phosphatase	0.08605	0.704	0.4939	0.5202	0.0691	0.1318	0.2876	0.2441	0.2374	0.7218	0.0267	0.0542
257537_at	AT3G22350	F-box family protein	-0.1667	0.9008	0.5513	0.03377	0.9798	0.5393	-0.794	0.5615	0.3832	-0.5935	0.6611	0.3846
257538_at	AT3G16160	transcription factor	0.9474	0.0974	0.1802	-0.4481	0.3656	0.3256	0.3858	0.4299	0.3295	-1.0099	0.0832	0.1076
257539_at	no_match	no_match	-0.3253	0.5301	0.4331	-0.2292	0.6538	0.443	-1.2114	0.0123	0.0441	-1.1153	0.0163	0.0408
257540_at	AT3G21520	similar to unknown protein [Arabidopsis thaliana] (T	1.5705	0.0193	0.0823	1.0868	0.0587	0.1204	0.8983	0.0063	0.0328	0.4146	0.0724	0.0987
257541_at	AT3G25950	similar to DNA-binding storekeeper protein-related (	-0.3271	0.3216	0.3352	0.2206	0.4884	0.3798	-0.503	0.1573	0.1838	0.04474	0.8846	0.4528
257542_at	AT3G26050	similar to unknown protein [Arabidopsis thaliana] (T	-0.3711	0.7032	0.4936	0.1417	0.8834	0.514	-0.6474	0.5146	0.3649	-0.1346	0.8892	0.454
257543_at	AT3G28960	amino acid transporter family protein	-0.3823	0.3952	0.3728	-0.4007	0.375	0.3299	0.04728	0.6441	0.4123	0.0288	0.7763	0.4219
257544_at	AT3G26080	zinc finger (C2H2 type) protein (WIP4)	0.5397	0.4008	0.3758	0.06354	0.9302	0.5267	0.2428	0.6944	0.4292	-0.2433	0.6937	0.3953
257545_at	AT3G23200	identical to UPF0497 membrane protein At3g23200	0.08987	0.6571	0.478	0.1322	0.5201	0.3923	0.273	0.1149	0.1524	0.3153	0.0811	0.1059
257546_s_at	AT5G02700;AT3G28410	[AT5G02700, F-box family protein];[AT3G28410, F-	1.9522	0.0834	0.1671	-2.236	0.0583	0.1201	2.8717	0.0039	0.0273	-1.3165	0.0518	0.081
257547_at	AT3G13000	transcription factor	-0.795	0.0357	0.1091	-0.7434	0.0436	0.1035	-0.4165	0.0974	0.1389	-0.3649	0.1321	0.1431
257548_s_at	AT3G26660;AT3G26620	[AT3G26660, LBD24 (LOB DOMAIN-CONTAINING	-0.07228	0.9289	0.5597	0.7802	0.3634	0.3245	-0.2625	0.7476	0.4474	0.59	0.4817	0.3182
257549_at	AT3G18650	AGL103 (AGAMOUS-LIKE 103); transcription factor	-1.2066	0.3375	0.3441	-1.7629	0.1869	0.2242	-0.5114	0.6685	0.4207	-1.0677	0.3899	0.2799
257550_at	AT3G18460	similar to unknown protein [Arabidopsis thaliana] (T	-1.3415	0.1627	0.236	0.479	0.5748	0.4138	-0.6279	0.4522	0.3396	-1.1926	0.1892	0.1789
257551_at	AT3G13270	transposable element gene	-0.4283	0.609	0.4627	-1.4634	0.1313	0.1837	-1.4578	0.1324	0.1655	-2.4928	0.0321	0.0604
257552_at	AT3G26130	glycosyl hydrolase family 5 protein / cellulase family	-0.4549	0.694	0.4908	2.0453	0.1299	0.1828	-2.5697	0.0311	0.0718	-0.06949	0.934	0.4667
257553_at	AT3G16830	TPR2 (TOPLESS-RELATED 2)	0.415	0.0455	0.1226	0.1313	0.4153	0.3485	0.001839	0.9905	0.5154	-0.2819	0.123	0.137
257554_at	AT3G24890	ATVAMP728 (Arabidopsis thaliana vesicle-associat	0.116	0.6389	0.4725	0.5967	0.0596	0.1213	-0.657	0.0455	0.0893	-0.1764	0.484	0.3193
257555_at	AT3G24780	similar to unknown protein [Arabidopsis thaliana] (T	0.03791	0.9601	0.5674	-1.7358	0.0715	0.1338	1.1299	0.1879	0.2043	-0.6439	0.4172	0.2913
257556_at	no_match	no_match	0.1149	0.6461	0.4751	0.4423	0.129	0.1821	-0.7296	0.0346	0.0761	-0.4022	0.1577	0.1598
257557_at	AT3G14490	terpene synthase/cyclase family protein	-0.2949	0.3714	0.3602	-0.01153	0.9705	0.5368	-0.4194	0.2258	0.227	-0.136	0.6668	0.3864
257558_s_at	AT3G22000;AT4G20680	[AT3G22000, receptor-like protein kinase-related];[	-1.8439	0.1339	0.2124	-0.8473	0.4372	0.3585	-0.3588	0.609	0.401	0.6378	0.3804	0.276
257559_at	AT3G02050	receptor-like protein kinase-related	-0.4027	0.6703	0.4827	-0.194	0.8359	0.5004	1.3317	0.2039	0.2142	1.5404	0.1542	0.1575
257560_at	AT3G14960	galactosyltransferase family protein	0.2817	0.1123	0.1941	0.3841	0.0505	0.1115	-0.3911	0.0223	0.0604	-0.2888	0.0556	0.0844
257561_at	AT3G24270	APUM25 (ARABIDOPSIS PUMILIO 25); RNA bindi	-1.0277	0.3427	0.3463	0.1107	0.9134	0.5222	-0.01239	0.9894	0.5152	1.1259	0.2695	0.2225
257562_at	AT3G30480	transposable element gene	0.23	0.5463	0.4395	0.1926	0.6107	0.4271	0.01743	0.9626	0.5083	-0.01995	0.9572	0.4727
257563_at	AT3G19610	similar to unknown protein [Arabidopsis thaliana] (T	0.4862	0.3607	0.355	0.2122	0.676	0.4506	-0.2049	0.6862	0.4265	-0.479	0.3671	0.2701
257564_at	AT3G28610	ATP binding / ATPase	-1.2618	0.1382	0.2159	-0.2511	0.7316	0.4688	-0.8522	0.2799	0.258	0.1585	0.8277	0.4366
257565_at	AT3G28620	zinc finger (C3HC4-type RING finger) family protein	-0.5349	0.5037	0.4327	0.5532	0.7257	0.4673	-0.4391	0.78	0.4574	0.6491	0.6816	0.391
257566_x_at	AT3G29610	transposable element gene	-0.3613	0.7868	0.5197	-0.1954	0.8833	0.514	-0.5043	0.7071	0.4337	-0.3385	0.7999	0.4287
257567_at	AT3G23930	similar to unknown protein [Arabidopsis thaliana] (T	0.2924	0.7859	0.5196	0.9718	0.3889	0.3363	1.3004	0.2659	0.2497	1.9799	0.1205	0.1354
257568_s_at	AT3G23950;AT3G23970	[AT3G23950, F-box family protein];[AT3G23970, F-	-0.2213	0.7307	0.5027	0.07502	0.9605	0.5205	0.04067	0.9492	0.5053	0.337	0.6041	0.3646
257569_at	AT3G26350	similar to unknown protein [Arabidopsis thaliana] (T	-0.5733	0.3583	0.3536	0.6744	0.2896	0.2863	-0.7077	0.2698	0.2521	0.5401	0.384	0.2776
257570_at	AT3G13662	disease resistance-responsive protein-related / ding	-2.2921	0.0059	0.0534	0.5015	0.3076	0.2961	-2.248	0.0064	0.0329	0.5455	0.2727	0.2243
257571_at	AT3G16870	zinc finger (GATA type) family protein	0.03357	0.866	0.5425	0.1185	0.56	0.4084	-0.04375	0.7144	0.4363	0.04121	0.73	0.4072
257572_at	AT3G16880	F-box protein-related	0.03846	0.9578	0.5666	-1.4201	0.1062	0.1644	1.482	0.0952	0.137	0.02335	0.9743	0.4767
257573_at	AT2G33990	IQD9 (IQ-domain 9); calmodulin binding	-0.1508	0.3014	0.3238	-0.325	0.063	0.1249	0.2749	0.0721	0.1167	0.1008	0.4238	0.294
257574_at	AT3G20710	F-box protein-related	0.1782	0.8697	0.5438	0.7318	0.5123	0.3896	-0.3297	0.6889	0.4274	0.224	0.7844	0.4224
257575_at	AT3G29265	transposable element gene	-0.6765	0.6164	0.4651	-0.09424	0.9434	0.5302	0.144	0.9137	0.4961	0.7262	0.5917	0.3604
257576_at	AT3G28280	Identical to Putative F-box protein At3g28280 [Arab	-0.03859	0.9381	0.5618	-0.5474	0.3063	0.2953	-0.3356	0.4821	0.352	-0.8445	0.1233	0.1372
257577_at	AT3G30150	transposable element gene	0.7297	0.594	0.4575	1.8192	0.2228	0.2475	0.5498	0.6855	0.4263	1.6394	0.2637	0.2195
257578_x_at	AT3G30160	similar to unknown protein [Arabidopsis thaliana] (T	1.0265	0.2073	0.2667	0.9506	0.2364	0.2556	-0.06838	0.9251	0.4992	-0.1443	0.843	0.4408
257579_at	AT3G11000	similar to kelch repeat-containing protein [Arabidopsi	-0.01639	0.9855	0.5733	-0.6832	0.4656	0.3702	0.8704	0.3399	0.2883	0.2036	0.8126	0.4325
257580_at	AT3G06210	binding	0.815	0.0589	0.1389	0.4077	0.2605	0.27	-1.043	0.0013	0.0188	-1.4503	4.00E-04	0.0088
257581_s_at	AT1G51120;AT1G50680	[AT1G51120, AP2 domain-containing transcription f	1.7407	0.2004	0.2624	-1.8982	0.1702	0.2127	2.1569	0.1306	0.1643	-1.4821	0.2622	0.2189
257582_at	AT1G50720	stigma-specific Stig1 family protein	0.7721	0.53	0.4331	0.1102	0.9266	0.5258	0.9662	0.4387	0.3335	0.3043	0.8001	0.4288
257583_at	AT1G66480	PMI2 (plastid movement impaired 2)	0.1275	0.5864	0.4549	-0.2195	0.3667	0.326	0.6927	0.0121	0.0437	0.3457	0.0956	0.1173
257584_at	AT1G54955	transposable element gene	1.8722	0.1591	0.2328	-0.5971	0.611	0.4272	0.8362	0.4834	0.3526	-1.6331	0.2063	0.1887
257585_at	AT3G12420	pseudogene of 3'-5' exonuclease containing protein	-0.5655	0.5392	0.4366	0.4184	0.6458	0.4402	-0.4821	0.5982	0.3975	0.5018	0.5839	0.3576
257586_at	AT1G50760	similar to unknown protein [Arabidopsis thaliana] (T	-1.7689	0.0952	0.1782	-1.6881	0.1065	0.1646	-0.2613	0.6903	0.4279	-0.1805	0.782	0.4234
257587_at	AT1G56310	3'-5' exonuclease domain-containing protein	0.2358	0.3604	0.3548	0.07217	0.7679	0.4799	-0.3347	0.2169	0.2217	-0.4984	0.0947	0.1165
257588_x_at	AT1G30150	transposable element gene	0.1629	0.8387	0.535	-1.2187	0.1797	0.2194	1.0924	0.2192	0.2232	-0.2892	0.7196	0.4038
257589_at	AT1G55590	similar to unknown protein [Arabidopsis thaliana] (T	0.1159	0.1455	0.2217	0.2065	0.7325	0.4689	0.8136	0.0407	0.0836	0.004132	0.9886	0.4798
257590_s_at	AT3G24880;AT3G24870	[AT3G24880, DNA binding];[AT3G24870, DNA bind	0.2099	0.1195	0.1997	0.2061	0.1245	0.1789	-0.5544	0.0064	0.0331	-0.5582	0.0063	0.0246
257591_at	AT3G24900	disease resistance family protein / LRR family protei	3.0131	9.00E-04	0.0349	2.6913	0.0015	0.0313	-0.07993	0.6314	0.4084	-0.4017	0.0596	0.0882
257592_at	AT3G24982	protein binding	2.1172	0.0027	0.0426	2.2156	0.0023	0.0335	0.1152	0.7371	0.4439	0.2136	0.5411	0.3413
257593_at	AT3G24840	SEC14 cytosolic factor, putative / phosphoglyceride	0.6842	0.4929	0.4171	1.9971	0.0926	0.1536	-0.4055	0.6782	0.4238	0.9074	0.374	0.273
257594_at	AT3G24740	similar to zinc ion binding [Arabidopsis thaliana] (TA	0.1022	0.4491	0.3977	0.1604	0.2589	0.2695	-0.4759	0.012	0.0434	-0.4178	0.0185	0.0436
257595_at	AT3G24750	unknown protein	0.1951	0.7648	0.513	1.2155	0.1168	0.1727	-1.2682	0.0948	0.1366	-0.2479	0.692	0.3947
257596_at	AT3G24760	F-box family protein	0.5618	0.1264	0.2058	0.2299	0.4747	0.3741	0.1524	0.5985	0.3976	-0.1795	0.538	0.3406
257597_at	AT3G24790	kinase	-0.9906	0.3245	0.337	0.9603	0.3378	0.3125	-1.0004	0.3204	0.2785	0.9505	0.3422	0.259
257598_at	AT3G24800	PRT1 (PROTEOLYSIS 1); ubiquitin-protein ligase	0.1223	0.438	0.3929	-0.1542	0.3388	0.3131	-1.2351	0.1014	0.1422	-0.04138	0.728	0.4065
257599_at	AT3G24830	60S ribosomal protein L13A (RPL13aB)	0.1475	0.3353	0.343	0.2773	0.1088	0.1664	-0.3133	0.0154	0.0494	-0.1835	0.0764	0.1019
257600_at	AT3G24770	CLE41 (CLAVATA3/ESR-RELATED 41); receptor b	0.651	0.0993	0.1817	0.1884	0.5694	0.4116	0.7709	0.0645	0.1096	0.3083	0.3684	0.2706
257601_at	AT3G24820	BSD domain-containing protein	-0.2806	0.3483	0.3491	0.7104	0.0548	0.1162	-0.233	0.4279	0.3288	0.7581	0.0456	0.0749
257602_at	AT3G13800	metallo-beta-lactamase family protein	-0.06592	0.7452	0.5075	-0.4123	0.0949	0.1553	-0.4202	0.0646	0.1096	-0.7666	0.0099	0.0311
257603_at	AT3G13820	F-box family protein	-0.5397	0.6721	0.4833	-0.7742	0.5487	0.4043	0.8404	0.2178	0.2224	0.6119	0.3505	0.2628
257604_s_at	AT3G13830;AT1G11810	[AT3G13830, F-box family protein];[AT1G11810, F-	-2.8542	0.0394	0.1145	-0.4018	0.6932	0.4567	-1.7999	0.0262	0.0658	0.6525	0.2798	0.2281
257605_at	AT3G13840	scarecrow transcription factor family protein	0.04356	0.9452	0.5635	-0.6843	0.3143	0.2997	0.742	0.0946	0.1365	0.01418	0.9888	0.4752
257606_at	AT3G13870	RHD3 (ROOT HAIR DEFECTIVE 3)	0.03776	0.6815	0.4865	-0.1053	0.2853	0.284	-0.7975	7.00E-04	0.016	-0.9406	4.00E-04	0.0089
257607_at	AT3G13880	pentatricopeptide (PPR) repeat-containing protein	-0.9184	0.0867	0.1706	-0.07103	0.8698	0.5098	-0.4936	0.2914	0.2643	0.3538	0.4332	0.2982
257608_at	AT3G13860	chaperonin, putative	0.6819	0.0148	0.0737	0.6072	0.0217	0.0747	-0.02036	0.825	0.4712	-0.09502	0.3325	0.2546
257609_at	AT3G13845	unknown protein	0.1477	0.164	0.2368	0.2064	0.0761	0.1382	0.4222	0.006	0.0321	0.8162	7.00E-04	0.0107
257610_at	AT3G13810	ATIDD11 (ARABIDOPSIS THALIANA INDETERMI	0.6861	0.0208	0.085	0.6993	0.0196	0.0719	-0.03458	0.7609	0.4514	-0.02134	0.8504	0.4428
257611_at	AT3G26580	binding	0.2041	0.2071	0.2666	-0.2464	0.1438	0.1935	0.3673	0.0538	0.0987	-0.0832	0.5731	0.3536
257612_at	AT3G26660	armadillo/beta-catenin repeat family protein	0.9356	0.0039	0.0463	0.619	0.0164	0.0666	0.1148	0.2943	0.2658	-0.2017	0.1016	0.1218
257613_at	AT3G26610	polygalacturonase, putative / pectinase, putative	0.5186	0.643	0.4739	-1.0115	0.3842	0.3339	0.9484	0.2592	0.246	-0.5817	0.4656	0.3122
257614_at	AT3G26614	transposable element gene	0.4545	0.6727	0.4836	0.9665	0.388	0.3359	0.499	0.6436	0.4123	1.011	0.3687	0.2707
257615_at	AT3G26620	oxidosqualeptide/Pro/Bem 1p (PB1) domain-contair	0.5562	0.1337	0.2122	0.5724	0.1255	0.1796	-0.03976	0.7764	0.4562	-0.02359	0.8657	0.4472
257616_at	AT3G26540	pentatricopeptide (PPR) repeat-containing protein	-0.2731	0.7074	0.4951	-0.1678	0.8165	0.495	-0.1595	0.7422	0.4455	-0.05417	0.9105	0.46
257617_at	AT3G26550	DC1 domain-containing protein	0.13	0.9345	0.5609	-1.4597	0.3814	0.3327	-0.2055	0.8967	0.4915	-1.7952	0.2934	0.2353
257618_at	AT3G24715	ATP binding / protein kinase/ protein-tyrosine kinase	-0.2214	0.3031	0.3248	-0.4845	0.0611	0.1227	-0.1737	0.4043	0.3183	-0.4368	0.0792	0.1042
257619_at	AT3G24810	IOK3 (kip-related protein 5); cyclin-dependent prote	-0.238	0.1505	0.226	-0.1719	0.269	0.2749	0.2551	0.1298	0.1638	0.3212	0.0747	0.1005
257620_at	AT3G24850	DNA binding	-0.4579	0.5321	0.4337	1.1781	0.1538	0.201	-1.1011	0.1266	0.1614	0.5349	0.4027	0.2853
257621_at	AT3G24910	CPK9 (CALMODULIN-DOMAIN PROTEIN KINASE	0.4556	0.0373	0.1115	0.8692	0.0042	0.0404	-0.3629	0.0709	0.1158	0.05074	0.7497	0.4137
257622_at	AT3G20280	PHD finger family protein	0.0541	0.7712	0.515	0.08375	0.6552	0.4436	-0.07927	0.6721	0.4217	-0.04962	0.7895	0.4256
257623_at	AT3G26210	CYP71B23 (cytochrome P450, family 71, subfamily	1.2944	0.0218	0.0867	1.5262	0.0126	0.0601	-0.3753	0.0171	0.0524	-0.1435	0.2076	0.1895
257624_at	AT3G26220	CYP71B21 (cytochrome P450, family 71, subfamily	1.5421	0.0282	0.0973	1.7842	0.0177	0.0688	-0.1927	0.0978	0.1391	0

257690_at	AT3G12830	auxin-responsive family protein	0.8975	0.0236	0.0897	0.8929	0.024	0.078	0.2081	0.2823	0.2594	0.2035	0.2916	0.2344
257691_at	AT3G12660	FLA14 (FASCICLIN-LIKE ARABINOGALACTAN PR	0.1966	0.7644	0.5128	1.6001	0.0593	0.121	-0.02278	0.9596	0.5076	1.3807	0.0308	0.0591
257692_at	AT3G12840	unknown protein	0.1901	0.811	0.5271	0.3997	0.6197	0.4305	-1.2665	0.0913	0.1336	-1.057	0.1385	0.1472
257693_at	AT3G12850	COP9 signalosome complex-related / CSN complex	-0.8755	0.4036	0.3772	-0.8857	0.3986	0.3407	0.2133	0.8313	0.4731	0.2031	0.8392	0.4398
257694_at	AT3G12860	nucleolar protein Nop56, putative	0.1063	0.6861	0.4879	0.6513	0.0561	0.1177	-0.3591	0.144	0.1745	0.1859	0.4009	0.2846
257695_at	AT3G12680	HUA1 (ENHANCER OF AG-4 1)	0.2258	0.141	0.2183	0.02384	0.8561	0.5062	0.3974	0.0322	0.073	0.1955	0.1881	0.1782
257696_at	AT3G12690	protein kinase, putative	-0.4482	0.0104	0.0646	-0.2629	0.0558	0.1174	-0.7265	0.0018	0.0206	-0.5412	0.0053	0.0228
257697_at	AT3G12700	aspartyl protease family protein	-0.4558	0.6222	0.4674	-2.1975	0.062	0.1238	1.6237	0.0675	0.1126	-0.118	0.8653	0.4471
257698_at	AT3G12730	myb family transcription factor	0.3246	0.2702	0.3055	0.138	0.6157	0.429	1.0122	0.0091	0.0381	0.8256	0.0181	0.0432
257699_at	AT3G12780	PGK1 (PHOSPHOGLYCERATE KINASE 1); phosp	-0.328	0.0381	0.1123	-0.7448	0.0023	0.0335	-0.1568	0.2187	0.2229	-0.5737	0.006	0.0239
257700_at	AT3G12740	LEM3 (ligand-effect modulator 3) family protein / CD	0.5177	0.0188	0.0814	0.4325	0.0332	0.0903	0.2728	0.0554	0.1003	0.1876	0.1394	0.1478
257701_at	AT3G12710	methyladenine glycosylase family protein	-0.1948	0.3803	0.3646	-0.4204	0.1006	0.16	0.4405	0.082	0.1256	0.215	0.3225	0.2495
257702_at	AT3G12670	EMB2742 (EMBRYO DEFECTIVE 2742); CTP synt	0.09346	0.6699	0.4825	-0.06656	0.76	0.4778	-0.2662	0.2037	0.2141	-0.4262	0.072	0.0984
257703_at	AT3G12640	RNA binding / nucleic acid binding	0.3344	0.0078	0.0583	0.3739	0.0052	0.0429	-0.2234	0.0298	0.0704	-0.1839	0.0531	0.0823
257704_at	AT3G12720	AtMYB67/AtY53 (myb domain protein 67); DNA bin	0.368	0.2981	0.3222	-0.3876	0.2766	0.279	0.9103	0.0097	0.0392	0.1547	0.4736	0.3152
257705_at	AT3G12760	elongation factor EF1B, N-terminal (InterPro:IPR00	0.8932	0.0019	0.0391	0.7064	0.0045	0.0413	-0.05111	0.6981	0.4306	-0.238	0.1242	0.1378
257706_at	AT3G12685	similar to catalpol (Arabidopsis thaliana) (TAIR:AT1	-1.143	0.0222	0.041	-2.6126	0.0198	0.072	-2.3671	0.0873	0.1304	0.1633	0.3726	0.2724
257707_at	AT3G12650	similar to unnamed protein product [Vitis vinifera] (G	0.6169	0.0695	0.1521	0.6851	0.0522	0.1133	0.2474	0.3793	0.3075	0.3156	0.2763	0.2263
257708_at	AT3G13330	binding	1.4316	0.0014	0.038	1.2667	0.0022	0.0334	-0.7497	0.0084	0.0367	-0.9145	0.0041	0.0205
257709_at	AT3G12725	catalytic hydrolase, acting on ester bonds	0.2373	0.4676	0.4063	-0.1911	0.5536	0.406	-0.8381	0.0472	0.0912	-1.2664	0.0129	0.0359
257710_at	AT3G12350	similar to unknown protein [Arabidopsis thaliana] (T	-0.2814	0.4259	0.3875	-0.4407	0.2378	0.2565	0.1622	0.1313	0.1649	0.002904	0.9746	0.4767
257711_at	AT3G12430	PBB1 (20S proteasome beta subunit B 1); peptidas	0.4023	0.007	0.0562	0.2331	0.0417	0.1015	0.4995	0.0032	0.0251	0.3303	0.0138	0.0374
257712_at	AT3G12420	similar to unknown protein [Arabidopsis thaliana] (T	0.2011	0.0422	0.1182	-0.00347	0.9619	0.5345	0.05198	0.4888	0.355	-0.1525	0.0892	0.1121
257713_at	AT3G12380	SDH2-1 (succinate dehydrogenase 2-1)	0.4978	0.0085	0.0604	0.3478	0.0282	0.0835	0.4883	0.0091	0.0383	0.3383	0.0307	0.059
257714_at	AT3G12360	histone H3	-0.7743	0.0234	0.0895	-0.2319	0.3454	0.3157	0.7021	0.0318	0.0725	1.2446	0.0046	0.0214
257715_at	AT3G12750	ZIP1 (ZINC TRANSPORTER 1 PRECURSOR); zinc	-0.3148	0.1972	0.2606	-0.01365	0.9498	0.5319	-0.07652	0.6337	0.409	0.2246	0.2051	0.1879
257716_at	AT3G18300	similar to unknown protein [Arabidopsis thaliana] (T	0.5147	0.603	0.4605	-0.3173	0.7457	0.4734	0.5076	0.5219	0.3678	-0.3244	0.6774	0.3899
257717_at	AT3G18390	EMB1865 (EMBRYO DEFECTIVE 1865)	-0.1945	0.0737	0.1562	-0.06603	0.4596	0.3678	-0.5363	0.0027	0.0237	-0.4078	0.0072	0.0265
257718_at	AT3G18400	ANAC058 (Arabidopsis NAC domain containing pro	0.8657	0.5149	0.4272	1.1551	0.3949	0.3391	-0.2747	0.8319	0.4733	0.0147	0.9909	0.4804
257719_at	AT3G18440	ATALMT9 (ALUMINUM-ACTIVATED MALATE TRA	1.0476	0.0045	0.0484	0.9522	0.0063	0.0456	0.08559	0.6621	0.4186	-0.00981	0.9595	0.4732
257720_at	AT3G18450	similar to unknown protein [Arabidopsis thaliana] (T	0.3559	0.537	0.4358	0.04165	0.9409	0.5293	-0.02574	0.9634	0.5084	-0.34	0.5544	0.3467
257721_at	AT3G18310	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.05903	0.7811	0.518	0.3517	0.1512	0.1992	-0.05388	0.7752	0.4558	0.2388	0.2472	0.2109
257722_at	AT3G18490	aspartyl protease family protein	-0.1314	0.3596	0.3544	-0.3173	0.067	0.1296	0.323	0.015	0.0488	0.1371	0.1577	0.1598
257723_at	AT3G18500	similar to endonuclease/exonuclease/phosphatase	0.02405	0.9201	0.6571	-0.2527	0.3246	0.3057	-0.3623	0.0237	0.0624	-0.659	0.0036	0.0194
257724_at	AT3G18510	unknown protein	0.6121	0.0887	0.1727	0.8791	0.0324	0.0892	0.1333	0.4737	0.3492	0.4002	0.0766	0.1021
257725_at	AT3G18524	MSH2 (MUTS HOMOLOG 2); ATP binding / damag	0.1179	0.6477	0.4757	0.8918	0.0203	0.0727	-0.173	0.3735	0.3045	0.6009	0.0254	0.0527
257726_at	AT3G18360	VQ motif-containing protein	0.08047	0.9208	0.6571	-1.6761	0.1532	0.0923	0.715	0.25	0.241	1.0415	0.1218	0.1363
257727_at	AT3G18380	sequence-specific DNA binding / transcription factor	-0.2069	0.2782	0.3103	-0.03291	0.8517	0.505	-0.00863	0.9608	0.5079	0.1654	0.373	0.2726
257728_at	AT3G18295	similar to unknown protein [Arabidopsis thaliana] (T	-0.4641	0.1265	0.2058	0.14	0.5925	0.4205	-0.03371	0.8955	0.4912	0.5704	0.0771	0.1025
257729_at	AT3G18520	HDA15 (HISTONE DEACETYLASE 15); histone de	0.1417	0.5366	0.4356	0.2619	0.2803	0.281	-0.6805	0.0316	0.0723	-0.5604	0.0558	0.0947
257730_at	AT3G18420	tetratricopeptide repeat (TPR)-containing protein	0.01374	0.9527	0.5654	0.2071	0.3958	0.3394	-0.2989	0.2422	0.2363	-0.1055	0.6536	0.382
257731_at	AT3G18430	calcium-binding EF hand family protein	0.5934	0.037	0.111	0.2663	0.2394	0.2573	0.8271	0.0039	0.0273	0.5001	0.0223	0.0487
257732_at	AT3G18480	CCAAT-displacement protein-related / CDP-related	0.5487	0.0168	0.0777	0.3036	0.094	0.1545	0.5537	0.0163	0.051	0.3087	0.0903	0.1131
257733_at	AT3G18350	similar to unknown protein [Arabidopsis thaliana] (T	0.4541	0.1608	0.2341	0.1144	0.6873	0.4546	-0.3499	0.0719	0.1166	-0.6895	0.0087	0.029
257734_at	AT3G18370	ATSYTF/NTMC2T3/NTMC2TYPE3/SYTF	0.3861	0.1088	0.191	0.6739	0.0229	0.0764	-0.1692	0.2927	0.265	0.1186	0.444	0.3034
257735_at	AT3G18460	pectate lyase family protein	1.4843	0.001	0.0355	1.3134	0.0016	0.0317	0.2591	0.208	0.2166	0.1848	0.6366	0.3759
257736_at	AT3G27410	unknown protein	0.6582	0.6429	0.4739	0.4336	0.7581	0.4775	0.1981	0.8875	0.489	-0.8937	0.534	0.3394
257737_at	AT3G27440	uracil phosphoribosyltransferase, putative / UMP py	0.9701	0.2778	0.3101	-1.1133	0.2233	0.2478	1.6841	0.0949	0.1367	-0.3994	0.6327	0.3747
257738_at	no_match	no_match	-0.4983	0.5315	0.4334	-0.2424	0.756	0.4769	-0.7757	0.3469	0.2917	-0.5198	0.5149	0.3316
257739_at	AT3G27470	similar to unknown protein [Arabidopsis thaliana] (T	-0.3868	0.1924	0.2572	-0.4724	0.1284	0.1819	-0.148	0.498	0.3589	-0.2336	0.3053	0.2412
257740_at	AT3G27330	zinc finger (C3HC4-type RING finger) family protein	-0.5247	0.2771	0.3099	-2.6806	0.003	0.0358	2.4132	0.0044	0.0284	0.2573	0.5709	0.3529
257741_at	AT3G27340	similar to unnamed protein product [Vitis vinifera] (G	0.1477	0.6574	0.4781	0.2365	0.4864	0.3789	-1.1803	0.0161	0.0506	-1.0915	0.0208	0.0468
257742_at	AT3G27380	SDH2-1 (succinate dehydrogenase 2-1)	-1.7068	0.188	0.254	0.07262	0.9494	0.5318	-1.1674	0.2517	0.2416	0.612	0.5215	0.3345
257743_at	AT3G27390	Identical to Uncharacterized membrane protein Ati3	-0.1067	0.484	0.4136	0.03749	0.7999	0.4896	-0.3943	0.0068	0.0337	-0.2502	0.0311	0.0595
257744_at	AT3G29230	pentatricopeptide (PPR) repeat-containing protein	-0.6084	0.0067	0.0552	-0.4103	0.0253	0.0797	-0.1213	0.3616	0.299	0.0768	0.5503	0.3452
257745_at	AT3G29240	similar to unknown protein [Arabidopsis thaliana] (T	0.2004	0.1092	0.1913	0.3707	0.0191	0.0712	-0.1723	0.1381	0.1697	-0.00205	0.9835	0.4788
257746_at	AT3G29200	CM1 (chorismate mutase 1); chorismate mutase	-0.7666	0.0922	0.176	-0.9871	0.047	0.1076	0.00708	0.9474	0.505	-0.2133	0.1017	0.1219
257747_at	AT3G18700	similar to ACA1, (AUTOINHIBITED CA2+/ATPASE	0.2124	0.538	0.4294	0.3047	0.786	0.4849	-0.4413	0.5555	0.3811	-0.349	0.6381	0.3766
257748_at	AT3G18710	U-box domain-containing protein	-1.1417	0.0273	0.0957	-0.7746	0.0823	0.1439	0.2511	0.011	0.0416	0.6182	4.00E-04	0.0089
257749_at	AT3G18780	ACT2 (ACTIN 2); structural constituent of cytoskele	-0.4667	0.1211	0.2015	-0.4738	0.1171	0.1729	-0.9525	0.016	0.0505	-0.9596	0.0156	0.0399
257750_at	AT3G18800	similar to unnamed protein product [Vitis vinifera] (G	-0.5121	0.3277	0.3388	-1.2667	0.0511	0.1122	0.2219	0.6093	0.4011	-0.5327	0.2546	0.215
257751_at	AT3G18690	MKS1 (MAP KINASE SUBSTRATE 1)	-0.3332	0.203	0.2642	-0.1567	0.514	0.3903	0.5828	0.0071	0.0342	0.7593	0.0027	0.0172
257752_at	AT3G18720	F-box family protein	-0.9624	0.311	0.3292	-1.3295	0.1846	0.2229	1.4615	0.0999	0.1409	1.0945	0.1855	0.1766
257753_at	AT3G18740	60S ribosomal protein L30 (RPL30C)	0.04862	0.8016	0.5246	-0.1395	0.484	0.3776	0.4727	0.0594	0.1045	0.2846	0.1911	0.1798
257754_at	AT3G18820	ATRABG3/ATARb7B (Arabidopsis Rab GTPase hon	0.3912	0.0335	0.1059	0.5266	0.0128	0.0604	0.4446	0.0053	0.0306	0.5801	0.002	0.0152
257755_at	AT3G18760	ribosomal protein S6 family protein	0.2537	0.1753	0.2451	0.2369	0.1992	0.2324	0.5827	0.0049	0.0297	0.5659	0.0055	0.0231
257756_at	AT3G18680	aspartate/glutamate/uridylate kinase family protein	0.1373	0.5124	0.426	-0.1076	0.6036	0.4247	0.3817	0.0226	0.0608	0.1368	0.2657	0.2207
257757_at	AT3G18660	initiation PROTEIN 1); transferase, transferring glyc	-0.119	0.6316	0.4702	-0.2093	0.4135	0.3476	0.04375	0.8582	0.4805	-0.04656	0.8492	0.4426
257758_at	AT3G22980	elongation factor Tu family protein	0.2518	0.2787	0.3107	-0.05632	0.7932	0.4872	-0.153	0.4785	0.3508	-0.4611	0.0783	0.1034
257759_at	AT3G23070	similar to unknown protein [Arabidopsis thaliana] (T	-0.1153	0.5998	0.4597	-0.4281	0.1022	0.1613	-0.2422	0.216	0.2213	-0.555	0.0282	0.056
257760_s_at	AT1G59770;AT3G23085	[AT1G59770.1 transposable element gene];[AT3G23	0.3483	0.8049	0.5255	0.8271	0.5648	0.41	-2.3894	0.1444	0.1748	-1.9106	0.2212	0.1967
257761_at	AT3G23090	similar to WDL1 (WVD2-LIKE 1) [Arabidopsis thalia	-1.0995	0.0122	0.0684	-0.6879	0.0529	0.1141	0.7583	0.0399	0.0827	1.1699	0.0098	0.0309
257762_at	AT3G23100	XRCC4 (Arabidopsis thaliana homolog of human DI	0.00025	0.9993	0.5764	0.2919	0.3095	0.2972	-0.3991	0.0952	0.137	-0.1074	0.5895	0.3598
257763_s_at	AT3G23120;AT3G23110	[AT3G23120, leucine-rich repeat family protein];[AT	2.2603	3.00E-04	0.032	1.8216	8.00E-04	0.0276	-0.4232	0.0656	0.1107	-0.8619	0.0069	0.0258
257764_at	AT3G23010	disease resistance family protein / LRR family protei	0.8919	0.0736	0.1561	1.0237	0.0505	0.1115	-1.371	0.0207	0.0579	-1.2392	0.0286	0.0565
257765_at	AT3G23020	pentatricopeptide (PPR) repeat-containing protein	0.7226	0.059	0.139	0.4888	0.1451	0.1945	-0.2892	0.354	0.2952	0.513	0.1367	0.146
257766_at	AT3G23030	IAA2 (indoleacetic acid-induced protein 2); transcrip	-0.8374	0.003	0.0435	-0.2683	0.1076	0.1654	0.1789	0.1911	0.2062	0.748	0.0028	0.0173
257767_at	AT3G23040	unknown protein	-0.3503	0.7677	0.5138	0.4461	0.7079	0.4613	0.4583	0.6159	0.4031	1.2547	0.2113	0.1915
257768_at	AT3G23050	zinc finger (C3HC4-type RING finger) family protein	0.4266	0.5136	0.4266	1.165	0.1223	0.1775	-0.7002	0.3052	0.2713	0.03814	0.952	0.4715
257769_at	AT3G23060	IAA7 (AUXIN RESISTANT 2); transcription factor	-0.02355	0.8595	0.5409	0.01758	0.8948	0.5171	0.8698	0.0022	0.0222	0.9109	0.0019	0.0149
257770_at	AT3G22990	binding	-0.157	0.4758	0.4101	-0.1121	0.6047	0.425	-0.1976	0.1868	0.2035	-0.1526	0.2864	0.2315
257771_at	AT3G23000	CIPK7 (CBL-INTERACTING PROTEIN KINASE 7);	0.01272	0.9667	0.5689	-0.0624	0.8384	0.501	-0.5756	0.0689	0.1137	-0.6507	0.0491	0.0785
257772_at	AT3G23080	similar to unknown protein [Arabidopsis thaliana] (T	0.0462	0.7145	0.4974	-0.0541	0.6694	0.4484	-0.3617	0.0371	0.0794	-0.462	0.0171	0.0419
257773_at	AT3G29185	similar to hypothetical protein MrBDRAFT_AC14748	-0.4738	0.0105	0.0646	-0.5166	0.0078	0.049	-0.2321	0.0901	0.1327	-0.2749	0.0579	0.0866
257774_at	AT3G29250	oxidoreductase	2.7169	0.0136	0.0719	4.1517	0.003	0.0357	0.6251	0.3882	0.3113	2.0599	0.0333	0.0616
257775_at	AT3G29260	short-chain dehydrogenase/reductase (SDR) family	0.9842	0.2791	0.3108	-1.239	0.1904	0.2267	0.3987	0.639	0.4108	-1.8245	0.0812	0.106
257776_at	AT3G29190	lyase/ magnesium ion binding	0.1761	0.7895	0.5204	0.1872	0.7767	0.4826	-0.5067	0.4575	0.342	-0.4955	0.4667	0.3126
257777_x_at	AT3G29210	transposable element gene	0.2771	0.6375	0.4722	-0.1639	0.7783	0.4832	0.7056	0.1958	0.2092	0.2646	0.592	0.3605
257778_at	AT3G29220	transposable element gene	1.2422	0.4052	0.3779	-0.9821	0.5031	0.3859	-0.2876	0.725	0.4402	-2.5119	0.03	0.0582
257779_at	AT3G26940	CDG1 (CONSTITUTIVE DIFFERENTIAL GROWTH	-0.1522	0.7609	0.5119	-1.0532	0.0872	0.1488	0.7681	0.1754	0.1956	-0.1329	0.79	0.4258
257780_at	AT3G27100	similar to unknown [Picea sitchensis] (GB:ABK233	0.5298	0.0779	0.1608	0.7672	0.0269	0.0821	0.3804	0.1658	0.189	0.6178	0.0514	0.0808
257781_at	AT3G27120	ATPase	1.0992	0.0645	0.1453	0.09147	0.8434	0.5027	-0.6582	0.2039	0.2142	-1.666	0.0185	0.0436
257782_at	AT3G27120;AT3G27130	[AT3G27120, ATPase];[AT3G27130, similar to ATP	1.0573	0.3536	0.3515	-0.5833	0.594	0.421	0.8354	0.4541	0.3405	-0.8052	0.4694	0.3135
257783_at	AT3G26930	binding	-0.1932	0.248	0.2924	-0.2076	0.2201	0.246	-0.1706	0.1835	0.2011	-0.185	0.1564	0.159
257784_at	AT3G26980	MUB4 (MEMBRANE-ANCHORED UBIQUITIN-FOL	0.2922	0.3364	0.3434	0.3123	0.3081	0.2963	0.4051	0.0076	0.0353	0.4253	0.0064	0.0249
257785_at	AT3G26980	MUB4 (MEMBRANE-ANCHORED UBIQUITIN-FOL	0.03374	0.9176	0.5564	-0.1122	0.7325	0.4689	0.6722	0.0304	0.0709	0.5262	0.0619	0.0902
257786_at	AT3G26990	similar to unknown protein [Arabidopsis thaliana] (T	0.3275	0.1212	0.2016	-0.09203	0.6107	0.4271	0.1851	0.3296	0.2831	-0.2345	0.2328	0.2031
257787_at	AT3G27000	ARP2 (ACTIN RELATED PROTEIN 2); structural co	0.6954	0.0029	0.0431	0.9914	7.00E-04	0.0275	-0.04765	0.6782	0.4238	0.2484	0.0804	0.1054
257788_at	AT3G27010	AT-TCP20 (ARABIDOPSIS THALIANA TEOSINTE	0.0603	0.8808	0.5465	0.7018	0.1365	0.188	0.04181	0.8172	0.469	0.6833	0.0157	0.0399
257789_at	AT3G27020	YSL6 (YELLOW STRIPE LIKE 6); oligopeptide tran	-0.3028	0.1583	0.2321	-0.3642	0.1057	0.1642	-0.5439	0.0255	0.0649	-0.6052	0.0181	0.0432
257790_at	AT3G27080	similar to unknown protein [Arabidopsis thaliana] (T	-0.1076	0.462	0.4039	-0.2259	0.163	0.2081	-0.1641	0.2828	0.2597	-0.2824	0.0998	0.1204
257791_at	AT3G27110	peptidase M48 family protein	-0.07843	0.5728	0.45	-0.07133	0.6067	0.4259	-0.4174	5.00E-04	0.0148	-0.4103	5.00E-04	0.0095
257792_at	AT3G27080	TOM20-3 (TRANSLOCASE OF OUTER MEMBRAN	0.3745	0.0248	0.0914	0.5821	0.0055	0.0434	0.6765	0.0023	0.0226	0.8841	8.00E-04	0.0113
257793_at	AT3G26960	similar to unknown protein [Arabidopsis thaliana] (T	-2.5244	4.00E-04	0.032	-2.4852	4.00E-04	0.0251	1.1791	0.0062	0.0328	1.2184	0.0055	0.0232
257794_at	AT3G27050	similar to unnamed protein product [Vitis vinifera] (G	-0.8331	0.0138	0.072	-0.7181	0.0225	0.0758	0.04489	0.8325	0.4733	0.1599	0.4664	0.3125
257795_at	AT3G15910	unknown protein	0.3353	0.6057	0.4616	0.6585	0.3336	0.3101	0.2096	0.7442	0.4462	0.5328	0.4243	0.2942
257796_at	AT3G15930	pentatricopeptide (PPR) repeat-containing protein	-0.7467	0.434	0.391	-0.1593	0.862	0.5077	-1.2469	0.2204	0.2238	-0.6595	0.4856	0.3199
257797_at	AT3G15940	glycosyl transferase family 1 protein	0.2505	0.281	0.3119	0.1465	0.5067	0.3873	0.08386	0.6239	0.4059	-0.0201	0.905	0.4588
257798_at	AT3G15950	(TSA1-LIKE); protein binding	0.6378	0.005	0.0504	1.1051	0.0027	0.0348	0.2257	0.2481	0.24	0.3929	0.0784	0.1035
257799_at	AT3G15890	protein kinase family protein	0.1099	0.7285	0.502	0.163	0.6102	0.427	-0.6648	0.058	0.1031	-0.6117	0.0726	0.0988
257800_at	AT3G15900	similar to unknown [Populus trichocarpa] (GB:ABK9	-0.3095	0.0033	0.0446	-0.3219	0.0029	0.0355	0.0198	0.7097	0.4346	0.007417	0.8882	0.4537
257801_at	AT3G15760	WNK6 (Arabidopsis WNK kinase 6); kinase	-2.5679	0.0071	0.0568	-1.9553	0.0182	0.0696	-0.2649	0.3366	0.2866	0.3477	0.2254	0.1991
257802_at	AT3G18770	similar to unknown protein [Arabidopsis thaliana] (T	1.6373	0.1485	0.2242	0.266	0.786	0.4849	-0.2732	0.7787	0.4568	-1.6445	0.1447	0.1513
257803_at	AT3G18790	similar to hypothetical protein [Vitis vinifera] (GB:CA	-0.0511	0.8193	0.6294	0.01832	0.9345	0.5278	-2.0444	0.3012	0.2694	-0.179	0.4409	0.3018
257804_at	AT3G18810	protein kinase family protein	-0.1037	0.8094	0.5266	-0.1787	0.68	0.4519	0.04821	0.9104	0.4954	-0.02681	0.9501	0.4709
257805_at	AT3G18830	ATPLT5 (POLYOL TRANSPORTER 5); D-ribose to	0.6353	0.0251	0.0919	0.807	0.0114	0.0576	-0.4841	0.0077	0.0353	-0.3124	0.0327	0.0611
257806_at	AT3G18870	ankyrin repeat family protein	0.2851	0.4854	0.5589	0.4448	0.2879	0.0452	0.1053	0.4648	0.3569	0.2965	1.4696	0.3305	0.0588
257807_at	AT3G26650	GAPA (GLYCERALDEHYDE 3-PHOSPHATE DEH	-0.2656	0.0061	0.0539	-0.5331	0.0075	0.0487	-0.3654	0.0238	0.0625	-0.3329	0.0318	0.0601
257808_at	AT3G26935	zinc finger (DHHC type) family protein	-0.3176	0.1903	0.2556	-0.4324	0.0986	0.1582	-0.3773	0.1346	0.1673	-0.4921	0.0712	0.0978
257809_at	AT3G27060	TSO2 (TSO MEANING 'UGLY' IN CHINESE); ribon	0.4594	0.1445	0.2209	0.4514	0.1498	0.1979	-0.2036	0.2688	0.2515	-0.2116	0.2533	0.2143
257810_at	AT3G27070	TOM20-1 (TRANSLOCASE OUTER MEMBRANE 2	1.7774	0.0587	0.1388	0.121	0.8671	0.509	0.9692	0.2261	0.2271	-0.6872	0.3681	0.2705
257811_at	AT3G25280	proton-dependent oligopeptide transport (POT) fam	0.6844	0.2494	0.2932	0.4047	0.4704	0.3723	-0.1584	0.7709	0.4544	-0.438	0.4374	0.3002
257812_at	AT3G25560	F-box family protein-related	0.157	0.8943	0.6498	-2.3476	0.1018	0.1609	2.2822	0.1089	0.1476	-0.2226	0.8508	0.4429
257813_at	AT3G25100	CDC45 (CELL DIVISION CYCLE 45)	0.04983	0.921	0.5572	-0.571	0.293	0.2881	-0.3031	0.5558	0.3811	-0.9239	0.1219	0.1364
257814_at	AT3G25110	ATFATA (ARABIDOPSIS FATA ACYL-ACP THIOE	0.8802	0.0209	0.085	0.3836	0.1825	0.2215	0.3693	0.1959	0.2092	-0.1272	0.6216	0.3707
257815_at	AT3G25130	similar to unnamed protein product [Vitis vinifera] (G	1.8648	0.1054	0.1876	0.7341	0.4579	0.3672	0.8776	0.382	0.3087	-0.2532	0.7912	0.4263
257816_at	AT3G25140	GAUT8/QUA1 (GALACTURONOSYLTRANSFERA	-0.1251	0.3888	0.3692	-0.3987	0.037	0.0949	0.241	0.1362	0.1685	-0.03266	0.8133	0.4326
257817_at	AT3G25150	nuclear transport factor 2 (NTF2) family protein / RN	0.5029	0.0146	0.0732	0.4207	0.026	0.0808	-0.7407	7.00E-04	0.016	-0.823	5.00E-04	0.0095
257818_at	AT3G25120	mitochondrial import inner membrane translocase s	0.6506	0.0198	0.0832	0.6694	0.0181	0.0694	-0.3377	0.1229	0.1586	-0.3189	0.1393	0.1477
257819_at	AT3G25165	RALFL25 (RALF-LIKE 25)	2.9281	0.0344	0.1073	-0.5476	0.5871	0.4187	1.2389	0.2531	0.2426	-2.2367	0.0737	0.0997
257820_at	AT3G25220	FKBP15-1 (FK506-binding protein 15 kD-1); FK506	0.1003	0.6689	0.4822	0.3358	0.1977	0.2314	0.2093	0.3905	0.3124	0.4448	0.1104	0.128
257821_at	AT3G25170	RALFL26 (RALF-LIKE 26)	-1.0525	0.2612	0.3003	0.006882	0.9936	0.5426	-1.2614	0.1922	0.2069	-0.202	0.8142	0.4327
257822_at	AT3G25230

257890_s_at	AT3G42570,AT3G17070	[AT3G42570, peroxidase-related];[AT3G17070, per	-0.2812	0.4989	0.42	-0.3785	0.374	0.3294	-0.6097	0.1592	0.1852	-0.707	0.1158	0.1317
257891_at	AT3G17170	RFC3 (REGULATOR OF FATTY ACID COMPOSIT	-0.2741	0.303	0.3248	0.1875	0.4646	0.3698	-0.3159	0.1845	0.2017	0.1457	0.501	0.3263
257892_at	AT3G17020	universal stress protein (USP) family protein	0.6267	0.0572	0.1371	0.9023	0.0189	0.071	0.6322	0.0074	0.0347	0.9078	0.002	0.0151
257893_at	AT3G17000	UBC32 (UBIQUITIN-CONJUGATING ENZYME 32)	0.4289	0.0077	0.058	0.6476	0.0017	0.032	-0.1212	0.2332	0.2312	0.09747	0.3222	0.2493
257894_at	AT3G17100	transcription factor	0.3164	0.0705	0.1531	0.572	0.0114	0.0577	-0.08369	0.5202	0.367	0.1719	0.2217	0.197
257895_at	AT3G16950	LPD1 (LIPOAMIDE DEHYDROGENASE 1)	-0.6074	0.0799	0.163	-0.3235	0.2817	0.282	-0.7243	0.0085	0.0369	-0.4404	0.0425	0.0719
257896_at	AT3G16920	chitinase	-0.4591	0.2504	0.2937	0.3631	0.3481	0.317	-0.3966	0.3106	0.2737	0.4257	0.2811	0.2287
257897_at	AT3G16930	ATHAL3A (Arabidopsis thaliana Hal3-like protein A)	0.3592	0.0858	0.1699	0.2689	0.1646	0.2088	0.06728	0.6761	0.4231	-0.02303	0.8851	0.4529
257898_s_at	AT5G45082,AT1G40125,A	[AT5G45082, transposable element gene];[AT1G40	-0.9541	0.3385	0.3447	-0.4085	0.6661	0.4471	-0.08555	0.9271	0.4999	0.4601	0.6281	0.3731
257899_at	AT3G28345	ABC transporter family protein	-0.1286	0.9009	0.5514	-1.6333	0.1674	0.2108	-2.6641	0.0515	0.0962	-4.1687	0.0127	0.0356
257900_at	AT3G28420	contains domain PROKAR_LIPOPROTEIN (PS512	-1.6471	0.0952	0.1782	-1.2681	0.1692	0.212	-2.4857	0.3893	0.3119	0.8646	0.161	0.1618
257901_at	no_match	no_match	0.17	0.8495	0.538	-0.119	0.8942	0.517	-0.3712	0.5898	0.3947	-0.6602	0.3568	0.2655
257902_at	AT3G28450	leucine-rich repeat transmembrane protein kinase,	0.5573	0.0281	0.097	0.394	0.0759	0.138	-0.2427	0.2163	0.2215	-0.406	0.0702	0.0971
257903_at	AT3G28460	similar to hypothetical protein [Vitis vinifera] (GB:C	-0.1434	0.4676	0.4063	-0.3408	0.1294	0.1825	-0.2722	0.2026	0.2133	-0.4696	0.0584	0.0871
257904_at	AT3G28470	AtMYB35 (myb domain protein 35); DNA binding / tr	-0.2852	0.8517	0.5387	-1.3282	0.4057	0.3439	1.3924	0.3855	0.3102	0.3494	0.8191	0.4338
257905_at	no_match	no_match	-0.1951	0.7011	0.4929	1.0196	0.0974	0.1572	-0.7833	0.0142	0.0475	0.4314	0.084	0.1082
257906_at	AT3G29520	ATL5 (A. THALIANA RIBOSOMAL PROTEIN L5); s	0.2071	0.4435	0.3951	0.2331	0.3932	0.3383	-0.2514	0.0029	0.0245	-0.2254	0.0043	0.0209
257907_at	AT3G25470	bacterial hemolysin-related	0.3505	0.0391	0.1141	0.09141	0.4746	0.3741	0.02374	0.8164	0.4687	-0.2353	0.0699	0.0968
257908_at	AT3G25410	bile acid:sodium symporter family protein	-0.1205	0.303	0.3248	-0.6693	0.0028	0.0351	0.01326	0.9028	0.4931	-0.5355	0.0063	0.0246
257909_at	AT3G25480	rhodanese-like domain-containing protein	-0.6224	0.0094	0.0624	-0.8598	0.0029	0.0355	0.2295	0.1591	0.1852	-0.0078	0.956	0.4725
257910_at	AT3G25580	thioredoxin-related	-0.5466	0.0576	0.1375	-0.03955	0.8578	0.5066	0.5338	0.0157	0.0501	1.0409	0.0014	0.0136
257911_at	AT3G25530	ATGH6DH/GHBDH; 3-hydroxybutyrate dehydrogen	0.1756	0.1698	0.2412	-0.09522	0.4157	0.3487	0.394	0.0199	0.0566	0.1232	0.3057	0.2413
257912_at	AT3G25500	AFH1 (FORMIN HOMOLOGY 1); actin binding	-0.14	0.5203	0.4291	-0.5081	0.0629	0.1249	-0.08285	0.2107	0.2182	-0.451	0.0013	0.013
257913_at	AT3G25540	LAG1 (Longevity assurance gene 1)	0.2732	0.0863	0.1704	0.2712	0.088	0.1494	-0.6409	0.006	0.0324	-0.643	0.006	0.024
257914_at	AT3G25545	similar to unknown [Populus trichocarpa] (GB:ABK9	0.879	0.0035	0.0451	0.4901	0.0263	0.0811	0.2438	0.0471	0.0911	-0.145	0.1672	0.1655
257915_at	AT3G23130	SUP (SUPERMAN); DNA binding / nucleic acid bin	0.3235	0.7731	0.5158	1.0857	0.359	0.3224	-0.3294	0.7692	0.4539	0.4329	0.7009	0.3977
257916_at	AT3G23210	basic helix-loop-helix (bHLH) family protein	-0.3559	0.1419	0.2189	-0.5567	0.0461	0.1064	0.6489	0.0291	0.0693	0.4481	0.083	0.1075
257917_at	AT3G23220	DNA binding / transcription factor	0.0177	0.2847	0.2703	0.3141	0.442	0.3604	0.3852	0.5302	0.3713	0.07049	0.9061	0.459
257918_at	AT3G23230	ethylene-responsive factor, putative	-0.7388	0.1993	0.2619	-0.5371	0.3267	0.3069	0.6966	0.0067	0.0335	0.8983	0.0026	0.0169
257919_at	AT3G23250	AtMYB15/AtY19/MYB15 (myb domain protein 15); t	0.1407	0.7502	0.5086	0.6296	0.2015	0.2336	0.2429	0.5127	0.3642	0.7319	0.0967	0.118
257920_at	AT3G23260	F-box family protein	-0.7041	0.0967	0.1796	0.6305	0.4686	0.3714	-2.4075	0.0247	0.0637	-0.07284	0.9206	0.463
257921_at	AT3G23270	regulator of chromosome condensation (RCC1) fam	-0.9342	0.6252	0.4682	1.1123	0.5634	0.4096	-1.5365	0.4081	0.3199	0.5099	0.7746	0.4214
257922_at	AT3G23150	ETR2 (ETHYLENE RESPONSE 2); receptor	1.6966	0.1031	0.1855	0.852	0.3502	0.3181	-0.624	0.4821	0.352	-1.4687	0.1426	0.1498
257923_at	AT3G23160	similar to unknown protein [Arabidopsis thaliana] (T	0.1421	0.5684	0.4483	0.1963	0.4333	0.3569	-0.02107	0.9311	0.501	0.03609	0.8824	0.4521
257924_at	AT3G23190	lesion inducing protein-related	-0.1327	0.87	0.544	-1.2154	0.1855	0.2235	1.5192	0.1167	0.1536	0.4365	0.597	0.3624
257925_at	AT3G23170	similar to unknown protein [Arabidopsis thaliana] (T	0.09236	0.7075	0.4952	0.1226	0.621	0.4309	0.4895	0.0275	0.0675	0.5197	0.0227	0.049
257926_at	AT3G23280	zinc finger (C3HC4-type RING finger) family protein	1.416	0.0126	0.0692	1.5537	0.0091	0.0522	-0.1102	0.4999	0.3596	0.07234	0.8633	0.4467
257927_at	AT3G23240	ATERF-1/ERF1 (ETHYLENE RESPONSE FACTOR	0.2492	0.4605	0.4033	0.5769	0.132	0.1844	0.417	0.244	0.2374	0.7447	0.0714	0.0979
257928_at	AT3G16890	pentatricopeptide (PPR) repeat-containing protein	0.1506	0.9049	0.5526	0.9842	0.4524	0.365	-0.8094	0.5316	0.3718	0.0242	0.9847	0.4791
257929_at	AT3G16980	DNA-directed RNA polymerase II, putative	-1.5593	0.0216	0.0863	0.2918	0.3561	0.3966	-1.424	0.0152	0.0481	0.4261	0.29	0.2335
257930_at	AT3G17010	transcriptional factor B3 family protein	-0.8037	0.5376	0.4359	0.9472	0.4719	0.3729	-1.7672	0.1085	0.1474	-0.01636	0.9857	0.4792
257931_at	AT3G17030	similar to unknown protein product [Vitis vinifera] (G	0.2341	0.1447	0.221	-0.07292	0.6031	0.4247	0.02088	0.8796	0.4865	-0.2861	0.0915	0.114
257932_at	AT3G17040	HCF107 (HIGH CHLOROPHYLL FLUORESCENT	-0.2646	0.2096	0.0998	-0.5345	0.0026	0.0342	-0.4646	0.0043	0.0282	-0.7344	8.00E-04	0.0109
257933_at	AT3G25585	AAPT2 (AMINOALCOHOLPHOSPHOTRANSFER	-0.01131	0.9409	0.5628	-0.1815	0.2742	0.2776	-0.8772	0.0306	0.0265	-1.0474	0.0019	0.0149
257934_at	AT3G25420	SCPL21 (serine carboxypeptidase-like 21); serine c	-0.9778	0.0181	0.0804	-0.4183	0.1737	0.2153	-0.4046	0.1088	0.1476	0.1549	0.475	0.3157
257935_at	AT3G25440	similar to unknown protein [Arabidopsis thaliana] (T	-0.4698	0.3868	0.3682	0.7573	0.1929	0.2278	-1.9725	0.0152	0.0491	-0.7454	0.1985	0.164
257936_at	AT3G25450	transposable element gene	-0.1664	0.9037	0.5524	-0.5462	0.6942	0.4568	0.7086	0.6125	0.402	0.3288	0.8116	0.4322
257937_at	AT3G19810	similar to unknown protein product [Vitis vinifera] (G	-0.1439	0.3457	0.3477	0.2524	0.1342	0.1862	-0.4529	0.0179	0.0536	-0.05662	0.6534	0.3819
257938_at	AT3G19820	DWF1/DIM/BUL1/ IU1; catalytic	-0.6084	0.0947	0.1778	-0.6044	0.0962	0.1562	-0.9701	4.60E-04	0.0147	-0.9661	4.00E-04	0.0091
257939_at	AT3G19930	STP4 (SUGAR TRANSPORTER 4); carbohydrate t	0.7889	0.0074	0.0578	0.8315	0.0062	0.0451	-0.3074	0.0813	0.1249	-0.2649	0.1164	0.1323
257940_at	AT3G21790	UDP-glucuronosyl/UDP-glucosyl transferase family	0.3044	0.2344	0.284	0.348	0.185	0.2231	-0.7375	0.0218	0.0596	-0.6939	0.0265	0.0539
257941_at	AT3G21800	UDP-glucuronosyl/UDP-glucosyl transferase family	-0.4697	0.7446	0.5073	-0.6443	0.4441	0.5203	-0.1102	0.4999	0.3596	0.07234	0.8633	0.4467
257942_at	AT3G21830	ASK8 (ARABIDOPSIS SKP1-LIKE 8); ubiquitin-prot	0.9536	0.6028	0.4604	0.1713	0.9242	0.5252	-0.5135	0.7366	0.4437	-1.2959	0.4142	0.29
257943_at	AT3G21840	ASK7 (ARABIDOPSIS SKP1-LIKE 7); ubiquitin-prot	-0.6126	0.2449	0.2906	-0.7745	0.1602	0.2061	-0.4633	0.3447	0.2906	-0.6252	0.2221	0.1971
257944_at	AT3G21850	ASK9 (ARABIDOPSIS SKP1-LIKE 9); ubiquitin-prot	-1.1551	0.5508	0.4415	-0.1793	0.9244	0.5252	-0.9197	0.6318	0.4084	0.05617	0.9763	0.4772
257945_at	AT3G21860	ASK10 (ARABIDOPSIS SKP1-LIKE 10); ubiquitin-p	-1.8079	0.1375	0.2154	0.5607	0.5963	0.422	-0.974	0.2311	0.23	1.3946	0.1135	0.1302
257946_at	AT3G21710	unknown protein	0.1334	0.8092	0.5266	0.4424	0.4405	0.3596	0.1099	0.7978	0.4627	0.4189	0.3556	0.2651
257947_at	AT3G21720	isocitrate lyase, putative	-0.09738	0.8764	0.5456	-0.3078	0.6279	0.4337	0.01705	0.9782	0.5122	-0.1934	0.7585	0.4162
257948_at	AT3G21740	APO4 (ACCUMULATION OF PHOTOSYSTEM ONE	0.5469	0.099	0.1816	0.09713	0.7231	0.4664	0.3771	0.214	0.2203	-0.07271	0.7901	0.4258
257949_at	AT3G21750	UDP-glucuronosyl/UDP-glucosyl transferase family	0.4398	0.192	0.2568	0.2118	0.4923	0.3813	-0.00696	0.9784	0.5122	-0.235	0.3867	0.2786
257950_at	AT3G21760	UGT73B5 (UDP-GLUCOSYL TRANSFERASE 73B	2.4697	0.011	0.0656	1.2997	0.0778	0.1398	0.3059	0.4985	0.3591	-0.8641	0.1036	0.1232
257951_at	AT3G21700	GTP binding	-0.1821	0.4127	0.3815	0.01379	0.9482	0.5315	-0.2298	0.3135	0.2751	-0.03382	0.8736	0.4495
257952_at	AT3G21770	peroxidase 30 (PER30) (P30) (PRXR9)	1.6425	0.0053	0.0515	1.1612	0.0175	0.0686	-0.1045	0.6398	0.411	-0.5859	0.0472	0.0765
257953_at	AT3G21865	PEX22 (PEROXIN 22); protein binding	0.04119	0.7195	0.4992	0.006994	0.9509	0.5321	0.1027	0.3908	0.3124	0.06852	0.5562	0.3474
257954_at	AT3G21760	UDP-glucuronosyl/UDP-glucosyl transferase family	-0.3316	0.3988	0.3748	-0.5228	0.2111	0.2404	0.07024	0.7852	0.4588	-0.1209	0.6422	0.378
257955_at	AT3G21810	zinc finger (CCCH-type) family protein	0.381	0.1581	0.2319	0.289	0.259	0.2695	-0.3137	0.0994	0.1404	-0.4057	0.0506	0.0799
257956_at	AT3G25400	similar to unnamed protein product [Vitis vinifera] (G	0.102	0.7299	0.5025	0.7139	0.0606	0.1223	0.4241	0.0836	0.1272	1.036	0.005	0.0221
257957_at	AT3G25490	wall-associated kinase, putative	0.2264	0.804	0.5251	-1.0371	0.2913	0.2873	1.3453	0.1683	0.1906	0.08192	0.9234	0.4637
257958_at	AT3G25510	disease resistance protein (TIR-NBS-LRR class), p	-1.5152	0.3998	0.3752	-1.081	0.5386	0.3999	-0.7114	0.6814	0.4248	-0.2772	0.8716	0.4489
257959_at	AT3G25560	NIK2 (NSP-INTERACTING KINASE 2); protein kina	-0.3759	0.0759	0.1585	-0.4828	0.0377	0.0962	-0.01129	0.9464	0.5048	-0.1181	0.4959	0.3242
257960_at	AT3G25570,AT3G25572	[AT3G25570, adenosylmethionine decarboxylase fa	-0.4697	0.2985	0.3224	-0.2965	0.493	0.3815	-0.144	0.7328	0.4426	0.02918	0.9444	0.4695
257961_at	AT3G19780	similar to unknown protein [Arabidopsis thaliana] (T	-1.1137	0.6496	0.4762	-0.4858	0.8411	0.5017	-0.6681	0.7833	0.4583	-0.04026	0.9867	0.4794
257962_at	AT3G19790	unknown protein	0.1611	0.42	0.3849	-0.07194	0.7089	0.4616	0.2232	0.029	0.0691	0.3124	0.0096	0.0304
257963_at	AT3G19840	FF domain-containing protein / WW domain-contain	0.1071	0.575	0.4508	0.3236	0.1391	0.1899	-0.6444	0.0214	0.0589	-0.4279	0.0714	0.0979
257964_at	AT3G19850	phototropic-responsive NPH3 family protein	-0.4285	0.0526	0.1315	-0.06231	0.7119	0.4628	-0.6794	0.0022	0.0221	-0.3132	0.0322	0.0605
257965_at	AT3G19900	similar to unknown [Picea sitchensis] (GB:ABK2523	-0.1332	0.3564	0.3529	-0.184	0.2236	0.2479	0.004708	0.9724	0.5106	-0.04609	0.7368	0.4093
257966_at	AT3G19800	similar to unnamed protein product [Vitis vinifera] (G	-0.3749	0.0475	0.1254	-0.4952	0.0202	0.0727	0.03372	0.542	0.3762	-0.0866	0.1625	0.1627
257967_at	AT3G19910	zinc finger (C3HC4-type RING finger) family protein	0.6685	0.0032	0.0442	0.6349	0.0038	0.039	-0.1161	0.2295	0.2292	-0.1497	0.1418	0.1493
257968_at	AT3G27550	group II intron splicing factor CRS1-related	1.1161	0.297	0.3214	0.7497	0.3704	0.4661	-0.1918	0.5837	0.3921	-0.5582	0.1582	0.1601
257969_at	AT3G27520	similar to unnamed protein product [Vitis vinifera] (G	-0.3409	0.3155	0.3318	-0.2277	0.4865	0.3789	0.1735	0.578	0.3899	0.2868	0.3741	0.2731
257970_at	AT3G27570	similar to unknown protein [Arabidopsis thaliana] (T	0.3699	0.1021	0.1847	0.4418	0.0651	0.1275	0.116	0.5438	0.3769	0.1878	0.3436	0.2597
257971_at	AT3G27530	GC6 (GOLGIN CANDIDATE 6); binding / protein tra	0.2303	0.2197	0.2749	0.5065	0.033	0.09	-0.8035	0.0071	0.0341	-0.5273	0.0292	0.0572
257972_at	AT3G27560	ATN1; kinase/ protein serine/threonine/tyrosine kina	0.5878	0.0069	0.0562	0.6165	0.0059	0.0442	0.1314	0.1294	0.1635	0.1601	0.081	0.1058
257973_at	AT3G20720	similar to hypothetical protein Osl_016901 [Oryza s	0.4269	0.0213	0.0856	0.3693	0.0335	0.0906	-0.3979	0.0266	0.0663	-0.4555	0.0172	0.042
257974_at	AT3G20820	leucine-rich repeat family protein	-0.438	0.0792	0.1622	-0.5557	0.0411	0.1006	0.4206	0.012	0.0434	0.3029	0.0346	0.0629
257975_at	AT3G20830	protein kinase family protein	0.1191	0.5608	0.4451	0.3206	0.1633	0.2082	-0.2031	0.3408	0.2886	-0.00157	0.9937	0.4811
257976_at	AT3G20840	PLT1 (PLETHORA 1); transcription factor	0.2733	0.4641	0.4048	0.1361	0.7079	0.4613	0.1159	0.7489	0.4478	-0.02131	0.9528	0.4717
257977_at	AT3G20850	proline-rich family protein	0.2286	0.8335	0.5335	0.1563	0.8856	0.5147	1.2679	0.236	0.2328	1.1956	0.2592	0.2174
257978_at	AT3G20860	ATNEK5; kinase	-0.6534	0.0619	0.1429	0.05717	0.8331	0.4997	-0.8318	0.0307	0.0714	-0.1212	0.6582	0.3835
257979_at	AT3G20730	pentatricopeptide (PPR) repeat-containing protein	0.3316	0.812	0.5274	-0.1131	0.9351	0.5279	0.8971	0.5221	0.3678	0.4524	0.7417	0.411
257980_at	AT3G20760	similar to unknown protein [Arabidopsis thaliana] (T	0.06551	0.9542	0.5658	0.129	0.8956	0.5174	-0.05151	0.8681	0.4837	0.02102	0.9459	0.4698
257981_at	AT3G20770	EIN3 (ETHYLENE-INSENSITIVE3); transcription fa	0.3016	0.0894	0.1732	0.3877	0.0455	0.1057	-0.3156	0.0453	0.0891	-0.2295	0.1049	0.124
257982_at	AT3G20780	ATTOP6B (BRASSINOSTEROID INSENSITIVE 3,	-2.1175	0.0454	0.1226	-0.4805	0.5502	0.4049	-2.0741	0.0328	0.0738	-0.4371	0.5365	0.3401
257983_at	AT3G20790	sedoheptulose kinase, putative	-0.3435	0.0774	0.1602	-0.3023	0.1062	0.1644	-0.3875	0.0232	0.0616	-0.3463	0.033	0.0613
257984_at	AT3G20800	rcd1-like cell differentiation protein, putative	0.3817	0.0195	0.0826	0.4157	0.0147	0.064	-0.1827	0.1451	0.1753	-0.1488	0.2151	0.1937
257985_at	AT3G20810	transcription factor jumonji (jmjC) domain-containing	0.4521	0.1455	0.2217	-0.2858	0.3176	0.3017	0.1015	0.6262	0.4066	-0.6365	0.0298	0.058
257986_at	AT3G20865	AGP40 (ARABINOGALACTAN-PROTEIN 40)	-0.7182	0.326	0.3379	-1.8777	0.0431	0.1031	1.4454	0.0875	0.1306	0.2859	0.6791	0.3902
257987_at	AT3G20740	FIE (FERTILIZATION-INDEPENDENT ENDOSPER	0.3784	0.1558	0.2302	0.1279	0.5869	0.4187	-0.1039	0.4091	0.3205	-0.3544	0.0348	0.0631
257988_at	AT3G20870	metal transporter family protein	0.2123	0.054	0.1333	0.03829	0.6515	0.4422	0.01542	0.854	0.4795	-0.1585	0.1138	0.1304
257989_at	AT3G19770	ATVPS9A (ARABIDOPSIS THALIANA VACUOLAR	0.4461	0.0236	0.0897	0.5063	0.0156	0.0652	-0.2894	0.0822	0.1257	-0.2292	0.1415	0.1492
257990_at	AT3G19860	basic helix-loop-helix (bHLH) family protein	0.426	0.0396	0.1148	0.4446	0.0348	0.0921	-0.7597	0.0058	0.0319	-0.7411	0.0064	0.0247
257991_at	AT3G19870	binding	0.7176	0.0176	0.0794	0.4205	0.0845	0.1463	-0.3448	0.1345	0.1671	-0.6419	0.0252	0.0525
257992_at	AT3G19880	F-box family protein	1.0959	0.2371	0.2859	0.1959	0.8161	0.4949	0.7058	0.4215	0.326	-0.1942	0.8177	0.4336
257993_at	AT3G19890	F-box family protein	-0.9282	0.3273	0.3385	1.2751	0.2003	0.233	0.3144	0.7248	0.4402	2.5177	0.039	0.0679
257994_at	AT3G19920	similar to unknown protein [Arabidopsis thaliana] (T	-0.7591	0.5151	0.4272	0.9007	0.4451	0.3619	-2.3164	0.0144	0.0479	-0.6566	0.3062	0.2416
257995_at	AT3G19940	sugar transporter, putative	0.8578	0.2377	0.2861	-0.1164	0.8598	0.5071	0.7978	0.2665	0.2499	-0.1763	0.7897	0.4257
257996_at	AT3G19950	zinc finger (C3HC4-type RING finger) family protein	0.3561	0.0343	0.1071	0.1035	0.4109	0.3464	0.4774	0.0026	0.0234	0.2247	0.0344	0.0627
257997_at	no_match	no_match	-2.1562	0.0164	0.0771	-3.5448	0.0028	0.0352	-0.6972	0.2672	0.2505	-2.0858	0.0183	0.0434
257998_at	AT3G27510	protein binding / zinc ion binding	-0.2993	0.609	0.4627	-0.6164	0.3174	0.3016	-0.00862	0.9817	0.5132	-0.3257	0.4094	0.2879
257999_at	AT3G27540	glycosyl transferase family 17 protein	-0.6534	0.0538	0.1331	-0.7865	0.0312	0.0877	-0.7247	0.0215	0.059	-0.8578	0.0122	0.035
258000_at	AT3G28940	avirulence-responsive protein, putative / avirulence	-0.00122	0.9919	0.575	0.3302	0.0431	0.1032	0.4706	0.0112	0.0419	0.802	0.0016	0.0142
258001_at	AT3G28950	avirulence-responsive protein-related / avirulence r	0.7441	0.0889	0.1729	1.2769	0.0185	0.0702	0.3457	0.024	0.0628	0.8785	8.00E-04	0.0113
258002_at	AT3G28930	AIG2 (AVRRPT2-INDUCED GENE 2)	0.1309	0.641	0.4734	0.5151	0.1186	0.1742	0.7915	0.0271	0.0669	1.1757	0.0072	0.0264
258003_at	AT3G29030	ATEXPA6 (ARABIDOPSIS THALIANA EXPANSIN,	-1.8575	0.0087	0.0605	-2.4181	0.0037	0.0371	0.8231	0.0582	0.1033	0.2625	0.4489	0.3056
258004_at	AT3G29020	MYB110 (myb domain protein 110); DNA binding /	1.1964	0.2336	0.2839	1.0292	0.2943	0.2888	0.6352	0.2994	0.2684	0.468	0.4296	0.2966
258005_at	AT3G19390	cysteine proteinase, putative / thiol protease, putati	1.7205	0.1131	0.1948	1.5423	0.1439	0.1936	-0.08881	0.8839	0.4879	-0.2671	0.6641	0.3855
258006_at	AT3G19400	cysteine proteinase, putative	0.011117	0.9389	0.562	0.07407	0.6171	0.4295	0.7773	0.0047	0.0292	0.8625	0.0032	0.0185
258007_at	AT3G19420	phosphonic monoester hydrolase	0.1025	0.269	0.3048	0.08961	0.3248	0.3058	-0.3379	0.0134	0.046	-0.3507	0.0118	0.0341
258008_at	AT3G19430	late embryogenesis abundant protein-related / LEA	0.2062	0.6751	0.4845	0.3432	0.4942	0.3822	0.2639	0.5443	0.3771	0.4009	0.3716	0.2719
258009_at	AT3G19440	pseudouridine synthase family protein	0.2987	0.3731	0.3609	0.0843	0.7914	0.4865	0.0366	0.9082	0.4948	-0.1778	0.583	0.3573
258010_at	AT3G19300	protein kinase family protein	0.01423	0.9793	0.572	-0.5625	0.3363	0.3116	0.6859	0.1681	0.1905	0.1091	0.8023	0.4294
258011_at	AT3G19510	homeobox protein (HAT 3.1)	0.4148	0.1571	0.231	-0.05739	0.8217	0.4963	0.07887	0.7251	0.4402	-0.3933	0.1331	0.1438
258012_at	AT3G19310	phospholipase C	-0.01689	0.9755	0.5711	-1.3124	0.0641	0.1264	0.5848	0.3213	0.2788	-0.7107	0.2413	0.2079
258013_at	AT3G19320	leucine-rich repeat family protein	-0.8077	0.4406	0.394	-0.9235	0.3834	0.3334	0.2619	0.7952	0.4619	0.146	0.8846	0.4528
258014_at	AT3G19330	polyadenylate-binding protein-related / PABP-related	-0.5068	0.5041	0.4222	0.1792	0.8083	0.4924	-0.0321	0.9652	0.5088	0.6539	0.3977	0.2833
258015_at	AT3G19340	sodium:dicarboxylate symporter	-0.2739	0.0628	0.1437	-0.199	0.1367	0.1882	0.03024	0.7916	0.4606	0.1052	0.3817	0.2765
258016_at	AT3G19350	polyadenylate-binding protein-related / PABP-related	0.1221	0.7365	0.5047	-0.1719	0.6381	0.4375	-0.03767	0.894	0.4909	-0.3317	0.2795	0.2279
258017_at	AT3G19370	similar to transport protein-related [Arabidopsis thal	-0.4694	0.0055	0.052	-0.2869	0.029	0.0848	-0.2192	0.0161	0.0505	-0.03681	0.5382	0.3406
258018_at	AT3G19500	ethylene-responsive protein -related	0.006133	0.9792	0.572	-0.8704	0.0169	0.0675	0.1096	0.6453	0.4127	-0.7869	0.0255	0.0527
258019_at	AT3G19470	F-box family protein	-0.146	0.7181	0.4988	-0.1844	0.6503	0.4419	-0.0398	0.7656	0.4529	-0.07812	0.5651	0.3509
258020_at	AT3G19490	ATNHD1 (Arabidopsis thaliana Na/H antiporter 1); s	0.5629	0.0186	0.081	0.4729	0.0323	0.0889	-0.3715	0.0383	0.0808	-0.4615	0.0194	0.0447
258021_at	AT3G19380	U-box domain-containing protein	-0.8228	0.0784	0.1614	-0.8111	0.0813	0.1429	-0.05931	0.8251	0.4712	-0.04764	0.859	0.4455
258022_at	AT3G19460	reticulon family protein (RTNLB11)	-0.06175	0.6651	0.481	-0.01734	0.9021	0.5195	-0.2905	0.0932	0.1353	-0.2461	0.1365	0.1459
258023_at	AT3G19450	CAD4

258090_at	AT3G14600	60S ribosomal protein L18A (RPL18aC)	0.2393	0.2137	0.2707	0.3384	0.105	0.1636	-0.5795	0	0.0092	-0.4804	0	0.0053
258091_at	AT3G14560	unknown protein	-0.5205	0.0767	0.1594	-0.1927	0.4294	0.355	0.8874	0.0156	0.0497	1.2152	0.0052	0.0226
258092_at	AT3G14595	similar to unknown protein [Arabidopsis thaliana] (T	-0.1816	0.3985	0.3747	-0.3144	0.1774	0.2179	-0.4077	0.0607	0.1057	-0.5405	0.0264	0.0539
258093_at	AT3G14750	similar to unknown protein [Arabidopsis thaliana] (T	0.5245	0.025	0.0918	0.2445	0.1787	0.2187	-0.1357	0.3507	0.2937	-0.4157	0.0318	0.0601
258094_at	AT3G14690	CYP72A15 (cytochrome P450, family 72, subfamily	0.1007	0.6285	0.4691	0.1357	0.5196	0.3922	-0.3904	0.0101	0.0399	-0.3554	0.0139	0.0375
258095_at	AT3G23610	dual specificity protein phosphatase (DsPTP1)	-0.1025	0.6088	0.4627	-0.1441	0.4791	0.3757	0.604	0.0308	0.0715	0.5624	0.0383	0.0671
258096_at	AT3G23650	protein kinase-related	-0.1008	0.8938	0.5497	1.3759	0.1242	0.1787	-0.7591	0.3445	0.2905	0.7176	0.3685	0.2706
258097_at	AT3G23660	transport protein, putative	0.585	0.0115	0.0669	0.4701	0.0237	0.0773	-0.3007	0.0853	0.1287	-0.4156	0.0347	0.063
258098_at	AT3G23670	KINESIN-12B/PAKRP1L; microtubule motor/ plus-e	0.4328	0.6149	0.4645	0.5011	0.5625	0.4092	0.1366	0.8719	0.4847	0.2049	0.8092	0.4315
258099_at	AT3G23540	similar to unknown protein [Arabidopsis thaliana] (T	0.2114	0.3378	0.3444	0.1538	0.4728	0.3733	-0.2208	0.313	0.2749	-0.2784	0.2197	0.1959
258100_at	AT3G23550	MATE efflux family protein	-1.1136	0.011	0.0658	-0.6784	0.0527	0.1138	-0.2548	0.3637	0.2999	0.1803	0.5088	0.3293
258101_at	AT3G23590	RFR1 (REF4-RELATED 1)	-0.1166	0.6609	0.4796	-0.5056	0.1097	0.1672	-0.861	8.00E-04	0.0163	-1.25	2.00E-04	0.0076
258102_at	AT3G23600	dienelactone hydrolase family protein	0.5042	0.0055	0.0521	0.4516	0.0082	0.0504	0.2152	0.0807	0.1244	0.1628	0.1537	0.1573
258103_at	AT3G23630	ATPT7 (Arabidopsis thaliana isopentenyltransferas	3.746	0.0095	0.0627	2.0475	0.0632	0.1252	0.008256	0.9916	0.5156	-1.6902	0.0836	0.1078
258104_at	AT3G23620	brix domain-containing protein	0.6888	0.0768	0.1594	0.5834	0.1151	0.1712	0.3499	0.0101	0.0399	0.2445	0.0327	0.0611
258105_at	AT3G23605	UBX domain-containing protein	0.5105	0.0918	0.1757	0.6391	0.0506	0.1116	0.42	0.1384	0.17	0.5486	0.0733	0.0994
258106_at	AT3G23580	RNR2/RNR4/2A (RIBONUCLEOTIDE REDUCTASE	0.1984	0.0866	0.1705	0.06459	0.5025	0.3857	-0.08366	0.3944	0.3139	-0.2174	0.0684	0.0955
258107_at	AT3G23560	ALF5 (ABERRANT LATERAL ROOT FORMATION	0.6013	0.035	0.108	0.552	0.045	0.1052	-0.0114	0.9183	0.4973	-0.06074	0.5919	0.3605
258108_at	AT3G23570	dienelactone hydrolase family protein	0.09483	0.6272	0.4687	-0.03627	0.8506	0.5046	0.3434	0.0686	0.1137	0.2123	0.2008	0.1856
258109_at	AT3G23640	HGL1 (HETEROGLYCAN GLUCOSIDASE 1); hydr	0.5112	0.0356	0.1089	0.5158	0.0347	0.092	-0.4627	0.0477	0.0917	-0.4581	0.0491	0.0785
258110_at	AT3G14610	CYP72A7 (cytochrome P450, family 72, subfamily A	2.5627	0.0246	0.0911	1.7026	0.0799	0.1419	-0.275	0.4975	0.3587	-1.1351	0.0371	0.0656
258111_at	AT3G14630	CYP72A9 (cytochrome P450, family 72, subfamily A	0.4479	0.0479	0.1177	1.3024	0.0284	0.0836	-0.2052	0.2569	0.2447	-0.04751	0.7749	0.4215
258112_at	AT3G14640	CYP72A10 (cytochrome P450, family 72, subfamily	0.6199	0.0658	0.1471	-0.2367	0.3915	0.3374	0.3752	0.0268	0.0666	-0.4814	0.0118	0.0341
258113_at	AT3G14650	CYP72A11 (cytochrome P450, family 72, subfamily	0.007573	0.9694	0.5697	-0.3743	0.1141	0.1706	-0.02478	0.8496	0.4785	-0.4066	0.0294	0.0575
258114_at	AT3G14660	CYP72A13 (cytochrome P450, family 72, subfamily	1.2379	0.0012	0.036	0.489	0.0025	0.0339	-0.6821	2.00E-04	0.0129	-0.7911	1.00E-04	0.0096
258115_at	AT3G14670	unknown protein	1.0237	0.4922	0.4167	-2.2534	0.1718	0.214	1.4046	0.3587	0.2973	-1.8725	0.2394	0.2067
258116_at	AT3G14520	terpene synthase/cyclase family protein	-0.1713	0.8135	0.5278	-2.0282	0.0406	0.1	1.3412	0.1198	0.1561	-0.5157	0.4904	0.3221
258117_at	AT3G14700	similar to SART-1 family protein [Arabidopsis thalia	0.4506	0.3899	0.3699	0.3705	0.4726	0.3733	0.2259	0.4387	0.3335	0.1459	0.6087	0.3663
258118_at	AT3G14710	F-box family protein	-0.2238	0.8111	0.5271	0.04569	0.9609	0.5343	0.8098	0.408	0.3199	1.0794	0.2858	0.2312
258119_at	AT3G14720	ATMPK19 (Arabidopsis thaliana MAP kinase 19); M	-0.04918	0.8128	0.5275	-0.2061	0.349	0.3177	-0.21	0.2398	0.235	-0.3669	0.0735	0.0996
258120_at	AT3G14730	pentatricopeptide (PPR) repeat-containing protein	-0.01521	0.9624	0.5679	-0.8757	0.0446	0.1046	0.4441	0.2167	0.2021	0.4164	0.2415	0.208
258121_s_at	AT3G14530;AT3G14550	[AT3G14530, geranylgeranyl pyrophosphate synthe	-0.9324	0.4897	0.4158	1.1919	0.3865	0.3349	-1.8194	0.0489	0.0931	0.3048	0.6535	0.3853
258122_at	AT3G14570	ATGSL04 (GLUCAN SYNTHASE-LIKE 4); 1,3-beta	0.5868	0.1319	0.2103	0.8967	0.0447	0.1048	-0.4002	0.1015	0.1423	-0.09035	0.6574	0.3833
258123_at	AT3G14640	MPK9 (MAP KINASE 9); MAP kinase	0.09981	0.3852	0.3674	-0.05276	0.6338	0.4359	-0.5323	0.0065	0.0332	-0.4852	0.0091	0.0297
258124_at	AT3G18215	similar to unknown protein [Arabidopsis thaliana] (T	0.2462	0.2797	0.3111	-0.261	0.2559	0.2678	-0.4914	0.0763	0.1114	-0.9986	0.007	0.0261
258125_s_at	AT3G23530;AT3G23510	[AT3G23530, cyclopropane fatty acid synthase, put	-3.8215	0.0018	0.0391	-1.4994	0.0437	0.1035	-5.3028	1.00E-04	0.0101	-2.9807	7.00E-04	0.0108
258126_at	AT3G24490	transcription factor	0.2446	0.1624	0.2357	0.6531	0.0103	0.0551	-0.44	0.0371	0.0794	-0.0314	0.837	0.4393
258127_at	AT3G24570	peroxisomal membrane 22 kDa family protein	-0.1666	0.2348	0.2843	-0.05359	0.6763	0.4507	-0.2038	0.1625	0.1869	-0.09077	0.4888	0.3214
258128_at	AT3G24590	signal peptidase I family protein	-0.5467	0.0236	0.0897	-1.0837	0.0021	0.0332	0.783	0.007	0.034	0.246	0.1844	0.176
258129_at	AT3G24620	ATRDD5/FIB-ASSOCIATED KINASE PARTNER PRC	-0.8182	0.5504	0.4413	0.2844	0.832	0.4994	-1.0807	0.2396	0.2344	0.02193	0.9789	0.4779
258130_at	AT3G24510	Encodes a defensin-like (DEFL) family protein.	-1.0129	0.2526	0.295	0.1535	0.8494	0.5042	-0.2799	0.7307	0.442	0.8865	0.3074	0.2422
258131_at	AT3G24540	protein kinase family protein	-0.04558	0.9521	0.5652	0.3041	0.692	0.4562	-0.7218	0.2638	0.2487	-0.3721	0.5397	0.341
258132_at	AT3G24550	ATPEN1 (PROLINE EXTENSIN-LIKE RECEPTOR	0.108	0.4479	0.3971	0.1739	0.2474	0.2622	0.1617	0.1491	0.1784	0.2276	0.0661	0.0936
258133_at	AT3G24500	ATMBF1C/MBF1C (MULTIPROTEIN BRIDGING FA	1.2044	0.0463	0.1237	1.5927	0.0196	0.0719	0.7944	0.0094	0.0388	1.1827	0.0022	0.0158
258134_at	AT3G24530	AAA-type ATPase family protein / ankyrin repeat fa	-0.4005	0.2063	0.2661	-0.373	0.2331	0.2535	0.0396	0.7731	0.4553	0.06711	0.6287	0.3733
258135_at	AT3G24506	similar to unknown protein [Arabidopsis thaliana] (T	-0.08953	0.6157	0.4648	-0.4536	0.0512	0.1123	-0.1219	0.4043	0.3183	-0.486	0.0206	0.0465
258136_at	AT3G24560	RSY3 (RASPBERRY 3)	-1.0304	0.047	0.1248	-1.4145	0.0176	0.0687	-0.4563	0.2773	0.2565	-0.8404	0.0816	0.1063
258137_at	AT3G24515	UBC37 (UBIQUITIN-CONJUGATING ENZYME 37)	-0.03693	0.8746	0.5451	0.3286	0.2089	0.2389	-0.2738	0.2804	0.2584	0.09164	0.6979	0.3967
258139_at	AT3G24445	MSH7 (MUTS HOMOLOG 6-2); ATP binding / mismi	0.4523	0.1641	0.2369	0.07594	0.7894	0.4859	0.04091	0.8042	0.4648	-0.3355	0.0956	0.1173
258139_at	AT3G24520	AT-HSFC1 (Arabidopsis thaliana heat shock transc	-1.0751	0.0497	0.1282	-0.6897	0.1489	0.1974	0.1926	0.3118	0.2744	0.578	0.0256	0.0529
258140_at	AT3G24503	ALDH2C4 (REDUCED EPIDERMAL FLUORESCE	0.5989	0.0153	0.0748	0.3851	0.0593	0.121	0.1898	0.2674	0.2506	-0.02403	0.8784	0.4509
258141_at	AT3G18035	HON4; DNA binding	0.5536	0.0214	0.0859	0.786	0.0065	0.0458	0.0097	0.945	0.5045	0.2421	0.1433	0.1504
258142_at	AT3G18120	F-box family protein-related	-1.1895	0.4997	0.4203	-0.2687	0.8752	0.5116	-0.09714	0.9457	0.5046	0.8237	0.572	0.3532
258143_at	AT3G18170	similar to unknown protein [Arabidopsis thaliana] (T	-1.4914	0.0072	0.0572	-0.9953	0.0281	0.0835	-0.3457	0.307	0.272	0.1504	0.6375	0.3763
258144_at	AT3G18180	similar to unknown protein [Arabidopsis thaliana] (T	-1.0859	0.3138	0.3308	-1.1299	0.2971	0.2902	-0.1699	0.8316	0.4732	-0.2138	0.7893	0.4255
258145_at	AT3G18200	nodulin MtN21 family protein	-1.0384	0.2632	0.3016	1.2638	0.1886	0.2255	-1.586	0.1179	0.1546	0.7162	0.4204	0.2927
258146_at	AT3G18060	transducin family protein / WD-40 repeat family prot	0.3209	0.1212	0.2016	0.2684	0.1762	0.2171	-0.3376	0.1079	0.147	-0.3901	0.0755	0.1012
258147_at	AT3G18070	glycosyl hydrolase family 1 protein	0.2468	0.022	0.0871	-0.0469	0.0269	0.0821	-0.02047	0.9828	0.5134	0.1795	0.8504	0.4428
258148_s_at	AT3G18090;AT3G23780	[AT3G18090, NRPD2b (nuclear RNA polymerase D	0.1387	0.4622	0.404	0.2222	0.2632	0.2716	-0.688	0.0158	0.0501	-0.6046	0.024	0.0509
258149_at	AT3G18110	EMB1270 (EMBRYO DEFECTIVE 1270)	-0.2703	0.1453	0.2216	-0.3021	0.1136	0.1704	-0.2603	0.136	0.1684	-0.292	0.1049	0.124
258150_at	AT3G18160	PEX3-1 (PEROXIN 3-1)	-0.3866	0.086	0.17	-0.2186	0.2477	0.2624	0.04237	0.7056	0.4332	0.1904	0.1423	0.1496
258151_at	AT3G18080	glycosyl hydrolase family 1 protein	0.6552	0.0511	0.1299	0.6676	0.0484	0.1093	0.07286	0.6798	0.4243	0.08532	0.6303	0.3737
258152_at	AT3G18190	chaperonin, putative	0.2439	0.4358	0.392	0.2576	0.4126	0.3473	-0.6023	0.0235	0.0621	-0.5886	0.0253	0.0525
258153_at	AT3G18165	MOS4 (MODIFIER OF SNC1,4)	0.1713	0.2342	0.2839	0.4322	0.0242	0.0782	-0.06326	0.6326	0.4086	0.1977	0.1816	0.1744
258154_at	AT3G18210	oxidoreductase, 2OG-Fe(II) oxygenase family protei	-0.2071	0.1801	0.2481	0.1766	0.2389	0.2571	-0.4247	0.0292	0.0694	-0.04099	0.7643	0.4181
258155_at	AT3G18130	guanine nucleotide-binding family protein / activatec	-0.07867	0.788	0.52	-0.06305	0.8291	0.4986	-0.06842	0.613	0.4021	-0.0528	0.6942	0.3955
258156_at	AT3G18050	similar to unknown protein [Arabidopsis thaliana] (T	0.04641	0.7007	0.4929	-0.3096	0.0511	0.1122	-0.07012	0.5663	0.3853	-0.4261	0.0192	0.0444
258157_at	AT3G18100	MYB4R1 (myb domain protein 4R1); transcription fa	0.04132	0.8621	0.5416	0.1128	0.6396	0.4381	-0.3755	0.1675	0.1901	-0.304	0.2445	0.2096
258158_at	AT3G17790	ATACP5 (acid phosphatase 5); acid phosphatase/ p	2.1517	0.0132	0.0709	1.876	0.0209	0.0737	0.01579	0.9311	0.501	-0.2599	0.2042	0.1874
258159_at	AT3G17840	RLK902 (receptor-like kinase 902); ATP binding / ki	-0.5492	0.1054	0.1875	-0.848	0.0528	0.1139	-0.04355	0.8955	0.4912	-0.2423	0.4797	0.3174
258160_at	AT3G17820	ATGSK8 (Arabidopsis thaliana glutamine synthase	1.31	2.00E-04	0.0312	1.3133	2.00E-04	0.0249	0.506	0.0072	0.0342	0.5093	0.007	0.0261
258161_at	AT3G17930	similar to unknown [Populus trichocarpa] (GB:ABK9	-0.2981	0.0968	0.1798	-0.246	0.1492	0.1976	0.1448	0.2658	0.2497	0.1969	0.1537	0.1573
258162_at	AT3G17810	dihydroorotate dehydrogenase family protein / dihyc	0.3882	0.0172	0.0786	0.3321	0.0284	0.0837	0.04744	0.5399	0.3752	-0.00882	0.9091	0.4596
258163_at	AT3G17940	aldose 1-epimerase family protein	0.2201	0.2795	0.3111	0.4841	0.0514	0.1125	0.06733	0.6866	0.4266	0.3313	0.0995	0.1202
258164_at	AT3G17910	SURF1 (SURFEIT 1)	0.8899	0.0049	0.0502	0.6368	0.0158	0.0655	-0.1526	0.3897	0.312	-0.4057	0.0625	0.0907
258165_at	AT3G17900	similar to unnamed protein product [Vitis vinifera] (G	0.3223	0.0623	0.1433	0.5371	0.0129	0.0606	-0.2674	0.1004	0.1414	-0.05254	0.6974	0.3966
258166_at	AT3G21540	transducin family protein / WD-40 repeat family prot	0.5286	0.0058	0.053	0.3399	0.0259	0.0806	-0.3665	4.00E-04	0.0147	-0.5553	1.00E-04	0.0058
258167_at	AT3G21560	UGT84A2; UDP-glycosyltransferase/ sinapate 1-glu	-1.5804	0.0279	0.0968	-1.4598	0.0356	0.093	-0.1359	0.6068	0.4003	-0.01527	0.953	0.4717
258168_at	AT3G21570	unknown protein	0.6832	0.3077	0.3273	-0.04794	0.9573	0.5336	-0.4019	0.6253	0.4064	-1.4331	0.1328	0.1435
258169_at	AT3G21590	similar to senescence/dehydration-associated protei	1.0484	0.46	0.403	0.3088	0.8218	0.4963	0.417	0.7616	0.4516	-0.3227	0.814	0.4327
258170_at	AT3G21600	senescence/dehydration-associated protein-related	0.2707	0.0551	0.1348	0.1269	0.277	0.2793	0.08619	0.4412	0.3346	-0.05761	0.5987	0.3629
258171_at	AT3G21610	similar to unknown protein [Arabidopsis thaliana] (T	0.2416	0.1775	0.2464	0.06336	0.8902	0.4557	0.2967	0.1151	0.1525	0.1185	0.4675	0.3129
258172_at	AT3G21620	early-response to dehydration protein-related / ER	-1.2786	0.2548	0.2964	-2.0779	0.0971	0.157	-0.9994	0.3578	0.2969	-1.7986	0.1351	0.1451
258173_at	AT3G21630	CERK1 (CHITIN ELICITOR RECEPTOR KINASE 1	0.4471	0.0497	0.1281	0.2029	0.2753	0.2783	0.5762	0.023	0.0614	0.332	0.1077	0.1259
258174_at	AT3G21670	pentatricopeptide (PPR) repeat-containing protein	1.4508	0.1746	0.2445	0.5903	0.5391	0.4001	0.67	0.4889	0.355	-0.1905	0.8392	0.4398
258175_at	AT3G21640	TWD1 (TWISTED DWARF 1); FK506 binding / pept	0.6576	0.0037	0.0459	0.7022	0.0029	0.0355	0.2585	0.0186	0.0546	0.3031	0.0109	0.0326
258176_at	AT3G21650	serine/threonine protein phosphatase 2A (PP2A) re	0.1633	0.2095	0.2678	0.1016	0.4052	0.3436	-0.3305	0.039	0.0816	-0.3922	0.023	0.0494
258177_at	AT3G21660	UBX domain-containing protein	-0.9207	0.4901	0.4159	-1.4672	0.293	0.2881	-0.7531	0.5683	0.3861	-1.2996	0.3443	0.26
258178_at	AT3G21680	unknown protein	-0.04962	0.9744	0.5709	0.8591	0.5862	0.4185	0.747	0.6343	0.4092	1.6557	0.3181	0.2474
258179_at	AT3G21690	MATE efflux family protein	0.03938	0.8831	0.5471	-0.2767	0.3329	0.3097	-0.453	0.0284	0.0684	-0.769	0.0047	0.0217
258180_at	no_match	no_match	0.6899	0.0472	0.1251	0.373	0.2004	0.233	-0.4117	0.1663	0.1893	-0.7286	0.0403	0.0694
258181_at	AT3G21670	nitrate transporter (NTP3)	-1.1762	2.00E-04	0.0312	-1.1517	2.00E-04	0.0249	-0.6132	0.0028	0.0241	-0.5886	0.0032	0.0184
258182_at	AT3G21500	DXPS1; 1-deoxy-D-xylulose-5-phosphate synthase	0.5845	0.3353	0.343	-0.2261	0.6938	0.4567	-0.3097	0.5932	0.3959	-1.1203	0.104	0.1234
258183_at	AT3G21550	similar to unknown protein [Arabidopsis thaliana] (T	-0.4865	0.3747	0.3618	-0.2578	0.6249	0.4328	0.3019	0.549	0.3787	0.5306	0.3146	0.2458
258184_at	AT3G21510	AHP1 (HISTIDINE-CONTAINING PHOSPHOTRAN	-0.09252	0.7168	0.4983	-0.08769	0.7308	0.4687	0.5434	0.0238	0.0626	0.5482	0.0232	0.0496
258185_at	AT3G21580	cobalt ion transmembrane transporter	-0.5306	0.0659	0.1472	-1.161	0.0053	0.0431	0.6374	0.0378	0.0804	0.00701	0.9748	0.4768
258186_s_at	AT3G17850;AT1G48490	[AT3G17850, protein kinase, putative];[AT1G48490	0.1305	0.4366	0.3923	-0.1307	0.4361	0.358	-0.7212	0.0088	0.0377	-0.9824	0.0029	0.0175
258187_at	AT3G17880	ATTDX (TETRATRICOPEPTIDE DOMAIN-CONTAIN	0.3866	0.1256	0.2052	0.5055	0.0649	0.1273	-0.4788	0.075	0.1192	-0.3598	0.1466	0.1525
258188_at	AT3G17800	mRNA level of the MEB5.2 gene (At3g17800) rema	-0.4474	0.0201	0.0837	-0.5773	0.0085	0.0509	-0.05739	0.1077	0.1469	-0.1874	0.0025	0.0167
258189_at	AT3G17860	JAZ3/JAZ3/TIFY9B (JASMONATE-ZIM-DOMAIN PR	-0.5077	0.0605	0.1408	-0.4432	0.0803	0.1481	-0.1333	0.2013	0.2124	-0.06881	0.4744	0.3155
258190_at	AT3G29080	unknown protein	-0.8069	0.5549	0.4428	-0.5731	0.6713	0.449	-0.6314	0.641	0.4114	-0.3977	0.767	0.419
258191_at	AT3G29100	VTI13 (vesicle transport v-SNARE 13); SNARE bino	0.24	0.4627	0.4042	0.5293	0.1481	0.1967	-0.9432	0.0333	0.0745	-0.6539	0.0916	0.1141
258192_at	AT3G29110	terpene synthase/cyclase family protein	1.3938	0.335	0.3429	0.0978	0.9424	0.5299	0.256	0.8504	0.4786	-1.0399	0.4597	0.3099
258193_at	AT3G29090	pectinesterase family protein	0.2808	0.1339	0.2124	0.2154	0.2236	0.2479	0.06131	0.6964	0.4299	-0.00414	0.9787	0.4778
258194_at	AT3G29170	similar to unknown protein [Arabidopsis thaliana] (T	0.4576	0.1007	0.1834	0.4897	0.0853	0.1469	0.5322	0.0048	0.0293	0.5643	0.0039	0.0201
258195_at	AT3G13890	MYB26 (myb domain protein 26); DNA binding / trai	0.7563	0.2871	0.3156	-0.5156	0.4499	0.3639	-0.6356	0.3607	0.2985	-0.3949	0.5566	0.3475
258196_at	AT3G13980	similar to unknown protein [Arabidopsis thaliana] (T	-0.3946	0.0455	0.1226	-0.7369	0.0059	0.0442	0.6046	0.0117	0.0429	0.2623	0.1291	0.1409
258197_at	AT3G14000	ATBRXL2/BRX-LIKE2	-0.1776	0.5943	0.4576	0.1174	0.7219	0.4661	-0.01167	0.9689	0.5096	0.2834	0.3714	0.2718
258198_at	AT3G14020	CCAAT-binding transcription factor (CBF-B/NF-YA)	0.1295	0.5181	0.4285	0.02079	0.915	0.5227	-0.251	0.2422	0.2363	-0.3597	0.1208	0.1356
258199_at	AT3G14030	similar to F-box family protein [Arabidopsis thaliana	-0.783	0.0997	0.1823	-0.3914	0.3462	0.3161	-0.2733	0.4977	0.3588	0.1183	0.7632	0.4178
258200_at	AT3G13900	haloacid dehalogenase-like hydrolase family protein	-1.5111	0.1989	0.2619	-0.8922	0.4152	0.3485	0.1459	0.8586	0.4806	0.7647	0.3758	0.2738
258201_at	AT3G13910	similar to unknown protein [Arabidopsis thaliana] (T	0.8256	0.001	0.064	1.2749	0.0021	0.0331	0.0293	0.6653	0.4196	0.4785	0.0016	0.0141
258202_at	AT3G13940	DNA binding / DNA-directed RNA polymerase	0.7203	0.0658	0.1471	0.583	0.1116	0.1687	0.5326	0.0101	0.0399	0.3953	0.0271	0.0547
258203_at	AT3G13950	similar to unknown protein [Arabidopsis thaliana] (T	1.9098	0.0122	0.0685	2.2739	0.0066	0.0461	0.1608	0.7336	0.4428	0.5246	0.2989	0.2381
258204_at	AT3G13960	AGIF5 (GROWTH-REGULATING FACTOR 5)	-0.7629	0.5796	0.4521	-0.3356	0.8042	0.4909	-0.6527	0.6336	0.409	-0.2255	0.8674	0.4475
258205_at	AT3G13965	pseudogene, hypothetical protein	0.278	0.4378	0.3928	-0.3638	0.3228	0.3047	0.4957	0.1995	0.2116	-0.1461	0.6743	0.3888
258206_at	AT3G14010	CID4 (CTC-interacting Domain 4); protein binding	0.2894	0.1068	0.1888	0.5543	0.0165	0.0667	-0.7449	0.0059	0.032	-0.48	0.0262	0.0537
258207_at	AT3G14050	RSH2 (RELA-SPOT HOMOLOG); catalytic	0.1468	0.6064	0.4619	0.2835	0.3416	0.3143	-0.3751	0.0168	0.0517	-0.2384	0.0659	0.0935
258208_at	AT3G13930	dihydrolipoamide S-acetyltransferase, putative	0.1043	0.3761	0.3623	-0.3294	0.0348	0.0921	0.4304	0.0148	0.0485	-0.00329	0.9765	0.4773
258209_at	AT3G14060	similar to unknown protein [Arabidopsis thaliana] (T	1.2355	0.0309	0.102	2.0828	0.0053	0.0431	0.0953	0.461	0.3436	1.0414	0.012	0.0344
258210_at	AT3G13920	initiation factor 4A-1); ATP-dependent helicase	0.259	0.1592	0.2329	0.1459	0.3858	0.3346	-0.3985	0.0379	0.0804	-0.5117	0.0172	0.042
258211_at	AT3G17890	unknown protein	0.05377	0.653	0.4771	0.03241	0.7846	0.4847	0.02835	0.6609	0.4182	0.006992	0.9128	0.4607
258212_at	AT3G17920	protein binding	-0.1564	0.2744	0.3081	-0.087	0.6202	0.3923	-0.3286	0.0449	0.0885	-0.2992	0.0851	0.1091
258213_at	AT3G17950	Identical to Uncharacterized protein AtG17950 (Y-:	-0.08865	0.7205	0.4996	0.1243	0.619	0.4302	0.1852	0.4519	0.3395	0.3981	0.148	0.1534
258214_at	AT3G17970	ATTOC64-III (ARABIDOPSIS THALIANA TRANSLO	-0.06737	0.8053	0.5255	0.1485	0.5926	0.4205	-1.2396	1.00E-04	0.0118	-1.0237	2.00E-04	0.0078
258215_at	AT3G17970	ATTOC64-III (ARABIDOPSIS THALIANA TRANSLO	0.6209	0.0566	0.1363	0.1569	0.5389	0.4	0.007563	0.9505	0.5056	-0.4565	0.0163	0.0408
258216_at	AT3G17980	C2 domain-containing protein	1.9311	0.1383	0.216	0.2582	0.8169	0.495	-0.00286	0.9979	0.5173	-1.6757	0.184	0.1758
258217_at	AT3G17998;AT3G18000	[AT3G17998, CPuORF30 (Conserved peptide upst	0.166	0.1076	0.01788	0.9555	0.5332	-1.3544	0.0109	0.0414	-0.6415	0.1004	0.1209	
258218_at	AT3G17998;AT3G18000	[AT3G17998, CPuORF30 (Conserved peptide upst	0.7043	0.0507	0.1296	0.1247	0.6504	0.4419	-0.0722	0.5449	0.3778	-0.6528	0.0042	0.0207
258219_at	AT3G17880	ATTDX (TETRATRICOPEPTIDE DOMAIN-CONTAIN	0.4483	0.0348	0.1077	0.3706	0.0602	0.1219	0.3732	0.0393	0.082	0.2955	0.0753	0.101
258220_at	AT3G17830	DNAJ heat shock family protein	-0.2582	0.6202	0.4666	-0.5031	0.3551	0.3205	-0.1777	0.6694	0.4208	-0.4226	0.3354	0.2558
258221_at	**AT3G29160**	**AKIN11 (ARABIDOPSIS SNF1 KINASE HOMOLO**	**0.1

258290_at	AT3G23460	cyclopropane fatty acid synthase-related	-2.2221	0.0923	0.176	-0.5603	0.608	0.4264	-0.1888	0.6548	0.4161	1.473	0.0197	0.0451
258291_at	AT3G23310	protein kinase, putative	-0.6655	0.0032	0.0442	-0.7973	0.0016	0.0317	0.151	0.2242	0.2262	0.0193	0.8633	0.4467
258292_at	AT3G23330	pentatricopeptide (PPR) repeat-containing protein	0.01009	0.9801	0.5721	0.6998	0.1396	0.1905	-0.2154	0.5608	0.3829	0.4743	0.2355	0.2047
258293_at	AT3G23430	PHO1 (PHOSPHATE 1)	-0.6955	0.1491	0.2249	-0.5707	0.2172	0.2441	-0.1232	0.7679	0.4535	0.001611	0.9969	0.4821
258294_at	AT3G23350	similar to hypothetical protein [Vitis vinifera] (GB:CA	1.0097	0.3743	0.3617	-0.5071	0.6422	0.4389	0.7915	0.4773	0.3504	-0.7252	0.5127	0.3308
258295_at	AT3G23400	plastid-lipid associated protein PAP / fibrillin family p	-0.398	0.0089	0.0609	-0.5326	0.0031	0.0362	0.4793	0.0046	0.0288	0.3447	0.0145	0.0384
258296_at	AT3G23390	60S ribosomal protein L36a/L44 (RPL36aA)	-0.01715	0.9055	0.5526	0.1693	0.2798	0.2808	0.7883	0.0044	0.0282	0.9748	0.002	0.0152
258297_at	AT3G23325	splicing factor, putative	-0.3148	0.0891	0.173	-0.2851	0.1129	0.1699	0.4969	0.0244	0.0634	0.5256	0.0203	0.0459
258298_at	AT3G23300	dehydration-responsive protein-related	-0.3606	0.2026	0.2641	-0.4715	0.1174	0.1732	-0.1908	0.2683	0.2512	-0.3017	0.112	0.1291
258299_at	AT3G23410	alcohol oxidase-related	-0.6322	0.0337	0.1062	-1.4451	0.0019	0.033	0.5464	0.0496	0.0942	-0.2666	0.2458	0.2101
258300_at	AT3G23340	CKL10 (Casein Kinase I-like 10); casein kinase I/ ki	-0.4163	0.0045	0.0488	-0.133	0.1401	0.1906	-0.06627	0.4119	0.3216	0.217	0.0401	0.0691
258301_at	AT3G30510	transposable element gene	-1.2649	0.1237	0.2038	-0.3504	0.6186	0.4301	0.5921	0.4141	0.3226	1.5066	0.0814	0.1062
258302_at	AT3G30610	transposable element gene	-0.2321	0.8851	0.5471	-2.1662	0.2241	0.248	3.1822	0.1024	0.1429	1.248	0.4543	0.3077
258303_at	AT3G30620	transposable element gene	-0.3176	0.602	0.4602	-1.4164	0.0653	0.1278	1.6315	0.0124	0.0442	0.5327	0.2308	0.2018
258304_at	AT3G30640	transposable element gene	-1.0663	0.1017	0.1843	-0.4103	0.461	0.3684	-0.6751	0.2512	0.2415	-0.01918	0.9714	0.4759
258305_at	AT3G30650	transposable element gene	-0.9105	0.1776	0.2464	-1.7764	0.0333	0.0903	-0.1663	0.7501	0.4484	-1.0323	0.1016	0.1219
258306_at	AT3G30530	ATBZIP42 (ARABIDOPSIS THALIANA BASIC LEU	0.2053	0.8281	0.5318	1.3283	0.2082	0.2384	1.0079	0.3188	0.2777	2.1308	0.0739	0.0999
258307_x_at	AT3G30560	transposable element gene	0.4696	0.7063	0.4948	-0.6412	0.6098	0.4269	0.4154	0.7383	0.4443	-0.6954	0.5811	0.3565
258308_at	AT3G30570	transposable element gene	-1.3059	0.1131	0.1948	-0.8875	0.2412	0.2586	-0.8172	0.2742	0.2547	-0.3988	0.5701	0.3527
258309_at	AT3G30580	transposable element gene	-1.5343	0.1277	0.2065	0.6197	0.482	0.377	-2.0554	0.0621	0.1071	0.09855	0.9079	0.4594
258310_at	AT3G26744	ICE1 (INDUCER OF CBF EXPRESSION 1); DNA b	0.0184	0.9325	0.5604	-0.1755	0.4381	0.3589	-0.03862	0.859	0.4807	-0.2325	0.318	0.2473
258311_at	AT3G26810	AFB2 (AUXIN SIGNALING F-BOX 2); auxin binding	0.09328	0.8201	0.5296	-0.04563	0.9112	0.5219	-1.2322	0.0051	0.0301	-1.3711	0.0035	0.0192
258312_at	AT3G26170	acyl-activating enzyme 13 (AAE13)	-0.08166	0.8315	0.5329	0.2637	0.504	0.3863	0.07503	0.388	0.3112	0.4204	0.0056	0.0234
258313_at	AT3G15970	Ran-binding protein 1 domain-containing protein / R	0.3231	0.0578	0.1377	0.5772	0.0092	0.0526	0.02636	0.8159	0.4685	0.2805	0.0572	0.0861
258314_at	AT3G16100	transposable element gene	-0.2124	0.098	0.1808	-0.1477	0.2093	0.2392	0.07711	0.4788	0.351	0.1418	0.2246	0.1985
258315_at	AT3G16175	thioesterase family protein	-1.0712	0.0024	0.0421	-1.0358	0.0027	0.0349	0.5176	0.0055	0.0311	0.553	0.0044	0.0209
258316_at	AT3G22660	rRNA processing protein-related	1.163	0.0038	0.0463	1.4063	0.0019	0.0329	-0.05437	0.6197	0.4045	0.1889	0.1354	0.1453
258317_at	AT3G22670	pentatricopeptide (PPR) repeat-containing protein	0.07039	0.7571	0.5108	-0.2721	0.2696	0.2753	0.04772	0.8333	0.4736	-0.2947	0.2377	0.2059
258318_at	AT3G22680	Identical to Uncharacterized protein At3g22680 [Ara	0.5267	0.0314	0.1027	0.3158	0.1232	0.1782	0.426	0.0083	0.0366	0.2151	0.0704	0.0972
258319_at	AT3G22700	F-box family protein	1.7379	0.0944	0.1777	0.613	0.4841	0.3777	0.7432	0.4032	0.3179	-0.3817	0.6565	0.383
258320_at	AT3G22710	F-box family protein	-0.9731	0.2984	0.3224	1.0819	0.255	0.2673	-0.4983	0.5808	0.3911	1.5966	0.1048	0.1239
258321_at	AT3G22840	ELIP1 (EARLY LIGHT-INDUCABLE PROTEIN); chl	-0.7006	0.0797	0.1628	-0.6603	0.0925	0.1534	0.585	0.0022	0.0221	0.6253	0.0017	0.0147
258322_at	AT3G22740	HMT3 (Homocysteine S-methyltransferase 3); homo	-0.732	0.1876	0.2538	-0.2488	0.6181	0.4299	0.458	0.0449	0.0886	0.9412	0.0041	0.0205
258323_at	AT3G22750	protein kinase, putative	-0.9355	0.1574	0.2313	-0.1841	0.5827	0.4173	-0.5114	0.0457	0.0894	-0.16	0.4208	0.2928
258324_at	AT3G22780	TSO1 (CHINESE FOR 'UGLY'); transcription factor	-0.05089	0.7866	0.5197	-0.2434	0.2383	0.2567	0.3511	0.1165	0.1535	0.1585	0.4181	0.2918
258325_at	AT3G22830	AT-HSFA6B (Arabidopsis thaliana heat shock trans	0.7347	0.6608	0.4795	-0.8522	0.6123	0.4278	0.546	0.7429	0.4458	-1.0409	0.5394	0.3409
258326_at	AT3G22760	SOL1 (TSO1-Like); transcription factor	-0.3787	0.336	0.3433	-0.3121	0.4188	0.3502	-0.587	0.1657	0.1889	-0.5204	0.2077	0.1895
258327_at	AT3G22640	cupin family protein	0.7162	0.2585	0.2988	0.4619	0.4439	0.3612	0.4011	0.502	0.3603	0.1468	0.8007	0.4289
258328_at	AT3G16090	zinc finger (C3HC4-type RING finger) family protein	-0.2202	0.5387	0.4364	0.1568	0.6575	0.4443	-0.513	0.0696	0.1144	-0.136	0.5498	0.345
258329_at	AT3G16110	ATPDIL1-6 (PDI-LIKE 1-6); thiol-disulfide exchange	0.502	0.0054	0.0511	0.1042	0.3188	0.3024	0.1868	0.1084	0.1473	-0.209	0.0847	0.1087
258330_at	AT3G16130	ATROPGEF13/ROPGEF13 (KINASE PARTNER PR	-2.3153	0.0202	0.0837	-2.4615	0.0165	0.0667	0.5977	0.1883	0.2045	0.4516	0.2974	0.2373
258331_at	AT3G15980	coatomer protein complex, subunit beta 2 (beta prir	0.3943	0.0891	0.173	0.2235	0.2739	0.2775	-0.4369	0.0685	0.1135	-0.6078	0.0262	0.0536
258332_at	AT3G16180	late embryogenesis abundant domain-containing pr	-0.06586	0.8806	0.5465	-0.5047	0.2872	0.285	0.02008	0.956	0.5069	-0.4187	0.2884	0.2326
258333_at	AT3G16000	MFP1 (MAR BINDING FILAMENT-LIKE PROTEIN	-0.4278	0.0156	0.0754	-0.2943	0.0498	0.1106	-0.2715	0.0624	0.1074	-0.138	0.2624	0.219
258334_at	AT3G16010	pentatricopeptide (PPR) repeat-containing protein	-0.1366	0.5247	0.4311	-0.01008	0.9615	0.5343	-0.6886	0.0052	0.0301	-0.5621	0.0106	0.0322
258335_at	AT3G16020	phosphatidylserine-2	-0.4959	0.7894	0.5204	0.02635	0.9886	0.5413	-1.2823	0.5013	0.3601	-0.76	0.6843	0.392
258336_at	AT3G16050	A37 (PYRIDOXINE BIOSYNTHESIS 1.2); protein h	1.3317	0.0089	0.0609	1.5206	0.0055	0.0434	-0.1328	0.6592	0.4177	0.05608	0.8506	0.4429
258337_at	AT3G16040	similar to unknown protein [Arabidopsis thaliana] (T	-1.188	0.2033	0.2643	1.0351	0.2562	0.268	-0.7712	0.3799	0.3077	1.4519	0.1369	0.1461
258338_at	AT3G16150	L-asparaginase, putative / L-asparagine amidohydro	-1.5312	0.0246	0.0911	-0.9653	0.0912	0.1524	0.0432	0.4024	0.3175	0.2234	0.5747	0.3541
258339_at	AT3G16120	dynein light chain, putative	-1.7689	0.0629	0.1438	-1.3105	0.1312	0.1837	-0.6358	0.1677	0.1902	-0.1774	0.6631	0.3852
258340_at	AT3G22770	F-box family protein-related	0.7813	0.1169	0.1977	0.3824	0.3843	0.3339	0.1861	0.6596	0.4178	-0.2128	0.6159	0.3687
258341_at	AT3G22790	kinase interacting family protein	-0.00609	0.9623	0.5679	0.1318	0.3372	0.3121	-0.5327	0.0117	0.0429	-0.3942	0.0311	0.0595
258342_at	AT3G22800	leucine-rich repeat family protein / extensin family p	-1.3575	0.1728	0.2434	0.4486	0.6131	0.4281	-1.1149	0.0531	0.0978	0.6913	0.1672	0.1655
258343_at	AT3G22810	similar to unknown protein [Arabidopsis thaliana] (T	-0.7924	0.1248	0.2045	-0.3782	0.4076	0.3447	-0.182	0.6665	0.42	0.2322	0.5855	0.3582
258344_at	AT3G22650	F-box family protein	-0.3079	0.7418	0.5065	-0.4201	0.6551	0.4435	1.4164	0.1796	0.1983	1.3042	0.2091	0.1903
258345_at	AT3G22845	emp24/gp25L/p24 protein-related	0.3372	0.0098	0.0633	0.7232	6.00E-04	0.0266	0.2599	0.0233	0.0618	0.6459	9.00E-04	0.0116
258346_at	AT3G22690	pentatricopeptide (PPR) repeat-containing protein	0.2373	0.6885	0.4887	-1.1797	0.0986	0.1582	0.8798	0.0861	0.1294	-0.5372	0.2387	0.2064
258347_at	AT3G22740	late embryogenesis abundant domain-containing pr	0.3187	0.8154	0.5284	1.147	0.4203	0.3507	1.4588	0.2353	0.2323	2.2872	0.0939	0.1159
258348_at	AT3G17710	F-box family protein	0.1148	0.345	0.3474	0.7675	0.002	0.033	-0.0892	0.4278	0.3288	0.5635	0.0051	0.0224
258349_at	AT3G17609	HYH (HYS-HOMOLOG); DNA binding / transcriptior	-0.8242	0.0199	0.0834	-0.6329	0.045	0.1052	0.3205	0.0181	0.0539	0.5118	0.0035	0.0193
258350_at	AT3G17510	CIPK1 (CBL-INTERACTING PROTEIN KINASE 1);	-0.7249	0.0122	0.0685	-0.8876	0.006	0.0447	-0.7179	0.0059	0.032	-0.8805	0.0028	0.0174
258351_at	AT3G17700	CNB1 (CYCLIC NUCLEOTIDE-BINDING TRANSP	0.7775	0.0222	0.0874	0.9404	0.0118	0.0584	-0.1731	0.1647	0.1883	-0.0102	0.9251	0.4642
258352_at	AT3G17600	IAA31 (indoleacetic acid-induced protein 31); transc	-0.5382	0.7326	0.5031	-0.4101	0.7939	0.4874	1.2891	0.4297	0.3295	1.4172	0.3892	0.2796
258353_s_at	AT3G17650,AT5G45450	YSL8 (YELLOW STRIPE LIKE 5); oli	-0.06918	0.6465	0.4752	-0.1312	0.4009	0.3415	-0.7859	0.0049	0.0297	-0.848	0.0037	0.0198
258354_at	AT3G14320	zinc finger (C3HC4-type RING finger) family protein	-0.09058	0.9263	0.5586	-0.3845	0.6976	0.4581	0.5121	0.6076	0.4005	0.2183	0.8242	0.4354
258355_at	AT3G14330	pentatricopeptide (PPR) repeat-containing protein	-0.6909	0.0339	0.1063	-0.6912	0.0338	0.0909	-0.3277	0.207	0.216	-0.3281	0.2067	0.1888
258356_at	AT3G14340	unknown protein	-0.1976	0.574	0.4505	0.04276	0.9011	0.5192	0.5843	0.0289	0.0691	0.8246	0.0092	0.03
258357_at	AT3G14350	SRF7 (STRUBBELIG-RECEPTOR FAMILY 7); ATF	-0.3205	0.0979	0.1807	-0.4007	0.0547	0.1161	-0.00996	0.9421	0.5038	-0.09015	0.5227	0.335
258358_at	AT3G14380	integral membrane family protein	0.2143	0.4383	0.3929	0.07345	0.7828	0.4844	0.01344	0.9596	0.5076	-0.1274	0.6362	0.3758
258359_s_at	AT3G14415,AT3G14420	(S)-2-hydroxy-acid oxidase, peroxisor	-0.5553	0.0254	0.0924	-0.4218	0.0575	0.1192	-0.7165	0.0034	0.0258	-0.5829	0.0072	0.0264
258360_at	AT3G14250	protein binding / zinc ion binding	-0.142	0.894	0.5498	-0.8623	0.4372	0.3585	0.1095	0.9181	0.4972	-0.6108	0.5744	0.354
258361_at	AT3G14270	phosphatidylinositol-4-phosphate 5-kinase family pr	0.6059	0.0244	0.0908	0.5371	0.0354	0.0929	-0.3007	0.1143	0.1519	-0.3694	0.0687	0.0959
258362_at	AT3G14280	similar to hypothetical protein [Vitis vinifera] (GB:CA	1.7336	0.0778	0.1608	1.6161	0.0928	0.1538	0.8177	0.0247	0.0637	0.7003	0.0398	0.0689
258363_at	AT3G14300	ATPMEPCRC; pectinesterase	-0.1084	0.903	0.5521	-0.1284	0.8852	0.5147	-1.0485	0.1907	0.2059	-1.0685	0.1841	0.1758
258364_at	AT3G14225	GLIP4; carboxylesterase	0.363	0.4025	0.3765	-1.034	0.0561	0.1177	0.7729	0.1172	0.1541	-0.6241	0.183	0.1753
258365_s_at	AT3G11880,AT3G14390	6-diaminopimelate decarboxylase, puta	-0.07417	0.618	0.4657	-0.3568	0.0602	0.1219	0.01677	0.8959	0.4913	-0.2659	0.0917	0.1141
258366_at	AT3G14230	RAP2.2; DNA binding / transcription factor	0.4241	0.066	0.1473	0.6103	0.0225	0.0758	0.1606	0.0959	0.1376	0.3468	0.0094	0.0303
258367_at	AT3G14370	WAG2; kinase	0.26	0.7423	0.5065	0.0896	0.9092	0.5212	0.7867	0.3463	0.2914	0.6163	0.4504	0.3061
258368_at	AT3G14240	subtilase family protein	0.1438	0.5932	0.4573	0.1017	0.7028	0.46	-0.3733	0.0102	0.0401	-0.4154	0.007	0.0281
258369_at	AT3G14310	ATPME3 (Arabidopsis thaliana pectin methylestera	-0.3858	0.1086	0.1909	-0.2538	0.2471	0.2621	0.09001	0.5157	0.3653	0.222	0.1538	0.1574
258370_at	AT3G14395	unknown protein	0.3409	0.7711	0.515	0.1786	0.8784	0.5127	0.8954	0.0286	0.0686	0.7331	0.0518	0.081
258371_at	AT3G14440	transporter-related	0.6641	0.0659	0.1471	0.4187	0.1883	0.2254	-0.2965	0.281	0.2587	-0.5419	0.0852	0.1091
258372_at	AT3G14400	UBP25 (UBIQUITIN-SPECIFIC PROTEASE 25); ub	0.06122	0.8059	0.5257	0.2289	0.382	0.3328	-0.8592	0.0113	0.0421	-0.6915	0.0232	0.0498
258373_at	AT3G14290	PAE2 (20S proteasome alpha subunit E2); peptidas	0.5655	0.0028	0.0429	0.3695	0.0127	0.0602	0.1293	0.2073	0.2161	-0.06675	0.481	0.318
258374_at	AT3G14360	lipase class 3 family protein	1.0574	0.3233	0.3362	0.6321	0.0107	0.0557	-0.1344	0.391	0.3125	0.3404	0.0717	0.0981
258375_at	AT3G17470	RelA/SpoT domain-containing protein / calcium-bin	-0.1665	0.4901	0.4159	-0.2699	0.286	0.2843	-0.4119	0.1189	0.1553	-0.5153	0.0685	0.0957
258376_at	AT3G17680	similar to unknown protein [Arabidopsis thaliana] (T	0.2219	0.4615	0.4036	0.04408	0.8794	0.513	0.151	0.5472	0.3782	-0.02678	0.9129	0.4607
258377_at	AT3G17690	ATCNGC19 (cyclic nucleotide gated channel 19); c	3.3557	6.00E-04	0.0325	3.8358	3.00E-04	0.0249	0.2988	0.4225	0.3265	0.7789	0.0806	0.1055
258378_at	AT3G17490	F-box family protein	1.139	0.1679	0.2397	-0.9725	0.2244	0.2482	0.5131	0.4909	0.356	-1.5984	0.0777	0.103
258379_at	AT3G16700	fumarylacetoacetate hydrolase family protein	0.06186	0.8318	0.533	-0.1179	0.6879	0.4548	0.2375	0.4333	0.331	0.05766	0.843	0.4408
258380_at	AT3G16650	PP1/PP2A phosphatases pleiotropic regulator 2 (PF	0.2803	0.0623	0.1433	0.4777	0.012	0.0587	-0.1839	0.1678	0.1903	0.01349	0.9077	0.4593
258381_at	AT3G16630	ATKINESIN-13A/KINESIN-13A; microtubule motor	-0.2293	0.34	0.3453	-0.4236	0.1162	0.1722	0.2311	0.3368	0.2867	0.03681	0.8705	0.4485
258382_at	AT3G15355	PFU1/UBC25 (UBIQUITIN-CONJUGATING ENZY	0.3299	0.1181	0.1987	0.6694	0.0158	0.0653	-1.2209	0.0017	0.0205	-0.8813	0.0057	0.0234
258383_at	AT3G15440	similar to zinc finger (C3HC4-type RING finger) fam	-0.721	0.5399	0.4367	-0.6837	0.5601	0.4084	-1.8874	0.1546	0.1821	-1.8501	0.161	0.1618
258384_at	AT3G15490	similar to unknown protein [Arabidopsis thaliana] (T	0.8583	0.1763	0.2457	0.17	0.7616	0.478	1.0767	0.1088	0.1476	0.3883	0.4993	0.3257
258385_at	AT3G15510	ATNAC2 (Arabidopsis thaliana NAC domain contair	0.02589	0.9585	0.5668	0.09941	0.8422	0.5021	-0.2381	0.3376	0.2871	-0.1646	0.4937	0.3235
258386_at	AT3G15520	peptidyl-prolyl cis-trans isomerase TLP38, chloropla	-1.1599	0.0034	0.0447	-1.4077	0.0016	0.0319	-0.2515	0.0527	0.0974	-0.4993	0.0057	0.0234
258387_at	AT3G15550	similar to unnamed protein product [Vitis vinifera] (G	0.04991	0.9675	0.5691	-1.9896	0.1586	0.2049	0.7684	0.489	0.3551	-1.2711	0.2765	0.2264
258388_at	AT3G15370	ATEXPA12 (ARABIDOPSIS THALIANA EXPANSIN	-0.4144	0.3081	0.3275	-0.7524	0.1015	0.1608	-0.07837	0.8115	0.467	-0.4164	0.2474	0.211
258389_at	AT3G15380	SDE5 (SILENCING DEFECTIVE 5)	0.6196	0.274	0.308	0.854	0.1558	0.2026	0.07189	0.8253	0.4713	0.3063	0.3723	0.2723
258390_at	AT3G15410	leucine-rich repeat family protein	-0.3041	0.0917	0.1757	-0.1187	0.4372	0.3585	-0.2241	0.1787	0.1977	-0.03874	0.7923	0.4266
258391_at	AT3G15420	similar to unknown protein [Arabidopsis thaliana] (T	0.5164	0.0738	0.1562	0.6148	0.0456	0.1058	0.01036	0.9514	0.5058	0.1088	0.5331	0.339
258392_at	AT3G15400	ATA20 (Arabidopsis thaliana anther 20)	-0.3662	0.6042	0.4609	1.3722	0.103	0.162	-1.8184	0.0284	0.0684	-0.08007	0.8896	0.4541
258393_at	AT3G15480	similar to unknown protein [Arabidopsis thaliana] (T	-0.6577	0.0205	0.0843	-0.4274	0.0731	0.1355	-0.01223	0.8808	0.487	0.2181	0.0465	0.0758
258394_at	AT3G15530	methyltransferase	0.04269	0.8113	0.5272	0.1404	0.4487	0.3634	-0.2618	0.0381	0.0806	-0.1641	0.1287	0.1407
258395_at	AT3G15500	ATNAC3 (ARABIDOPSIS NAC DOMAIN CONTAIN	-0.2007	0.6921	0.4899	0.5706	0.2925	0.2879	-0.2558	0.3361	0.2864	0.5154	0.0926	0.1149
258396_at	AT3G15460	brix domain-containing protein	0.285	0.3495	0.3495	-0.03491	0.9031	0.5196	0.3774	0.0667	0.1117	0.05755	0.7224	0.4049
258397_at	AT3G15357	unknown protein	-0.4244	0.504	0.4222	0.7626	0.2477	0.2624	0.755	0.1786	0.1977	1.962	0.0133	0.0366
258398_at	AT3G15360	ATHM4 (Arabidopsis thioredoxin M-type 4); thiol-dis	-0.4536	0.0284	0.0975	-0.3271	0.0727	0.135	0.3494	0.03	0.0706	0.4759	0.0109	0.0327
258399_at	AT3G15540	IAA19 (indoleacetic acid-induced protein 19); transc	-0.3933	0.4235	0.3868	-0.6949	0.1908	0.2268	1.3893	0.0021	0.0218	1.0878	0.0052	0.0226
258400_at	AT3G15470	WD-40 repeat family protein	-0.4058	0.0438	0.1207	-0.5979	0.0128	0.0604	-0.3713	0.0204	0.0574	-0.5634	0.0048	0.0219
258401_at	AT3G15430	regulator of chromosome condensation (RCC1) fam	0.8919	0.0103	0.0644	0.7	0.0232	0.0768	0.2118	0.0056	0.0313	0.01986	0.6379	0.3765
258402_at	AT3G15450	similar to unknown protein [Arabidopsis thaliana] (T	-0.6286	0.0285	0.0977	-0.03379	0.8657	0.5087	-0.2584	0.1819	0.2001	0.3364	0.1036	0.1231
258403_at	AT3G15380	choline transporter-related	0.3258	0.0454	0.1226	-0.00488	0.9678	0.536	-0.4029	0.0238	0.0626	-0.7334	0.003	0.0176
258404_at	AT3G17465	RPL3P (ribosomal protein large subunit 3P); structu	0.2825	0.3113	0.3295	0.2811	0.3133	0.2991	-0.3177	0.1511	0.1796	-0.319	0.1498	0.1545
258405_at	AT3G17590	BSH (BUSHY GROWTH)	0.3848	0.047	0.1248	0.4987	0.0213	0.0742	-0.4332	0.0331	0.0743	-0.3193	0.0782	0.1034
258406_at	AT3G17611	rhomboid family protein / zinc finger protein-related	-0.1057	0.4072	0.379	0.04785	0.6988	0.4578	-0.06406	0.6049	0.3998	0.08949	0.4772	0.3165
258407_at	AT3G17620	F-box family protein	-0.1485	0.8939	0.5497	-1.1126	0.3472	0.3166	0.2485	0.8237	0.4707	-0.7155	0.5313	0.3385
258408_at	AT3G17630	ATCHX19 (CATION/H+ EXCHANGER 19); monova	-0.5834	0.5074	0.4241	0.2977	0.7294	0.4684	-1.784	0.0711	0.116	-0.9029	0.2843	0.2305
258409_at	AT3G17640	leucine-rich repeat family protein	-0.6809	0.3136	0.3307	-1.5985	0.0539	0.1152	0.6539	0.2408	0.2355	-0.5441	0.1154	0.1315
258410_at	AT3G16780	60S ribosomal protein L19 (RPL19B)	0.08318	0.6969	0.4918	0.2067	0.3569	0.3214	0.4223	0.0654	0.1104	0.5458	0.0312	0.0595
258411_at	AT3G17280	F-box family protein	-0.1333	0.8448	0.5371	1.1799	0.1382	0.1893	-0.3685	0.5947	0.3964	0.9447	0.213	0.1924
258412_at	AT3G17690	stable protein 1-related	-0.5393	9.00E-04	0.0349	-0.3441	0.0049	0.0422	0.1705	0.049	0.0933	0.3657	0.0039	0.0201
258413_at	AT3G17300	similar to unnamed protein product [Vitis vinifera] (G	0.4165	0.0505	0.1292	0.3914	0.06	0.1217	0.6434	0.0129	0.0452	0.6182	0.0148	0.0386
258414_at	AT3G17380	meprin and TRAF homology domain-containing pro	-0.06154	0.8089	0.5265	0.3263	0.2427	0.2596	0.3453	0.2208	0.224	0.7332	0.037	0.0655
258415_at	AT3G17390	MTO3 (S-adenosylmethionine synthase 3); methior	-0.6291	0.0563	0.136	-0.9832	0.0142	0.0629	0.4034	0.0333	0.0745	0.04932	0.7166	0.403
258416_at	AT3G17310	methyltransferase family protein	-0.00485	0.9753	0.5711	-0.1395	0.3969	0.3399	-0.1588	0.1525	0.1806	-0.2935	0.0311	0.0595
258417_at	AT3G17365	calsticlin	0.2794	0.153	0.2281	0.1365	0.441	0.3699	0.2581	0.179	0.1979	0.1143	0.5111	0.3302
258418_at	no_match	no_match	-0.2734	0.4121	0.3812	-0.7672	0.0622	0.1239	0.3383	0.3159	0.2762	-0.1556	0.6262	0.3724
258419_at	AT3G16670	similar to unknown protein [Arabidopsis thaliana] (T	-3.4276	2.00E-04	0.0312	-3.1048	3.00E-04	0.0249	0.5029	0.1332	0.1661	0.8257	0.0367	0.0652
258420_at	AT3G16680	DNA binding / DNA-directed RNA polymerase	-0.3092	0.6234	0.4676	-1.6683	0.0456	0.1058	0.27	0.4153	0.3231	-1.0891	0.0216	0.0478
258421_at	AT3G16690	nodulin MtN3 family protein	-1.0439	0.0223	0.0875	-1.2235	0.0132	0.0612	0.4873	0.0166	0.0514	0.3078	0.0663	0.0938
258422_at	AT3G16710	pentatricopeptide (PPR) repeat-containing protein	-0.4147	0.2018	0.2633	0.08093	0.7808	0.4838	-0.682	0.0662	0.1113	-0.1863	0.5308	0.3383
258423_at	AT3G16730	similar to unnamed protein product [Vitis vinifera] (G	-0.3554	0.196	0.2597	-0.2864	0.2797	0.2808	-0.00535	0.9825	0.5133	0.06368	0.795	0.4274
258424_at	AT3G16750	unknown protein	-0.3578

258490_at	AT3G02670	proline-rich family protein	-0.07434	0.9261	0.5585	1.1338	0.2064	0.2371	0.03209	0.968	0.5096	1.2402	0.1745	0.17
258491_at	AT3G02700	NC domain-containing protein	0.4151	0.0785	0.1615	0.4106	0.0808	0.1426	-0.5969	0.0278	0.0679	-0.6015	0.0272	0.0548
258492_at	no_match	no_match	1.3745	0.2533	0.2954	3.3275	0.032	0.0887	-2.2219	0.0974	0.1389	-0.2688	0.8071	0.4307
258493_at	AT3G02555	similar to unknown protein [Arabidopsis thaliana] (T	-0.1013	0.5909	0.4565	0.009435	0.9593	0.534	0.1064	0.5732	0.3878	0.2172	0.2793	0.2279
258494_at	AT3G02450	cell division protein ftsH, putative	-0.1627	0.1858	0.2526	-0.2482	0.0717	0.134	-0.3651	0.0117	0.0428	-0.4506	0.0056	0.0233
258495_at	AT3G02690	integral membrane family protein	-0.05118	0.7056	0.4946	-0.4508	0.0233	0.0769	-0.4632	0.0213	0.0587	-0.8628	0.0024	0.0162
258496_at	AT3G02460	plant adhesion molecule, putative	0.4761	0.0615	0.1423	0.53	0.0455	0.1057	-0.09526	0.4378	0.3331	-0.04132	0.7277	0.4065
258497_at	AT3G02380	COL2 (CONSTANS-LIKE 2); transcription factor/ zi	-1.1268	0.0144	0.0731	-0.1092	0.7088	0.4616	-1.1587	0.0131	0.0455	-0.1412	0.6315	0.3742
258498_at	AT3G02480	ABA-responsive protein-related	0.4277	0.5777	0.4517	2.1657	0.0375	0.0959	0.4864	0.5292	0.371	2.2244	0.0346	0.0629
258499_at	AT3G02540	RAD23-3 (PUTATIVE DNA REPAIR PROTEIN RAD	-0.394	0.1698	0.2412	-0.2886	0.2878	0.2853	-0.467	0.1061	0.1458	-0.3616	0.1827	0.1751
258500_at	[AT3G02468:AT3G02470	[AT3G02468: CPuORF9 (Conserved peptide upstr	-0.4673	0.0037	0.046	-0.5068	0.0028	0.0351	-0.3311	0.0127	0.0447	-0.3707	0.0086	0.0288
258501_at	AT3G06780	glycine-rich protein	-0.2109	0.4274	0.3881	-0.0965	0.707	0.4613	-0.03647	0.7673	0.4533	0.07792	0.5357	0.34
258502_at	AT3G02490	pentatricopeptide (PPR) repeat-containing protein	0.189	0.4201	0.3849	0.2203	0.3544	0.3202	-0.2781	0.2571	0.2448	-0.2467	0.3063	0.2416
258503_at	AT3G02500	similar to unknown protein [Arabidopsis thaliana] (T	-0.3433	0.5614	0.4454	0.3729	0.5298	0.3962	-0.00241	0.9943	0.5163	0.7139	0.0869	0.1104
258504_at	AT3G02590	delta 7-sterol-C5-desaturase, putative	-0.083	0.7862	0.5196	-0.4013	0.2334	0.2537	0.03312	0.9	0.4924	-0.2852	0.3132	0.245
258505_at	AT3G06530	BAP28-related	0.3332	0.2854	0.3146	0.3239	0.2972	0.2902	-1.0125	0.0185	0.0544	-1.0218	0.018	0.043
258506_at	AT3G06520	agenet domain-containing protein	-1.1268	0.0144	0.0731	-0.1092	0.7088	0.4616	-1.1587	0.0131	0.0455	-0.1412	0.6315	0.3742
258507_at	AT3G06500	beta-fructofuranosidase, putative / invertase, putati	-0.152	0.6805	0.4862	-0.1019	0.7811	0.4838	-0.7941	5.00E-04	0.0148	-0.744	6.00E-04	0.0101
258508_at	AT3G06640	protein kinase family protein	0.2686	0.7651	0.5131	-0.02108	0.9812	0.5395	0.8098	0.3895	0.3119	0.5201	0.5692	0.3523
258509_at	AT3G06620	protein kinase family protein	0.2098	0.6134	0.4639	0.7517	0.1215	0.1768	-0.549	0.2255	0.2267	-0.00712	0.9861	0.4792
258510_at	AT3G06600	unknown protein	0.04832	0.9572	0.5665	1.5043	0.1499	0.198	0.1747	0.8032	0.4645	1.6307	0.0678	0.0951
258511_at	AT3G06590	transcription factor	-0.172	0.4762	0.4102	-0.1209	0.6104	0.4271	0.8588	0.0011	0.0181	0.9097	9.00E-04	0.0114
258512_at	AT3G06510	SFR2 (SENSITIVE TO FREEZING 2); hydrolase, h	0.1419	0.1664	0.2386	-0.2581	0.0372	0.0953	-0.2548	0.0386	0.0812	-0.6548	0.0015	0.0137
258513_at	AT3G06630	protein kinase family protein	0.3723	0.756	0.5104	-1.0348	0.4073	0.3446	0.9414	0.4474	0.3373	-0.4657	0.6985	0.397
258514_at	AT3G06610	DNA-binding enhancer protein-related	-0.03687	0.8289	0.532	0.2079	0.2632	0.2716	0.3303	0.0542	0.099	0.5751	0.0093	0.0301
258515_at	AT3G06650	ACLB-1 (ATP-citrate lyase B-1)	-0.5863	0.0061	0.0539	-0.6452	0.0043	0.0408	-0.1581	0.0383	0.0809	-0.217	0.014	0.0376
258516_at	AT3G06490	MYB108 (MYB DOMAIN PROTEIN 108); DNA bind	-0.2102	0.5892	0.4559	-0.1044	0.7854	0.4848	0.7038	0.085	0.1284	0.8097	0.0588	0.0874
258517_at	AT3G06580	GAL1 (GALACTOSE KINASE 1); ATP binding / gal	0.5131	0.0209	0.085	0.2428	0.1551	0.2021	0.2507	0.1392	0.1705	-0.01453	0.9216	0.4633
258518_at	AT3G06570	kelch repeat-containing F-box family protein	0.1088	0.2357	0.2849	0.01309	0.875	0.5116	-0.4773	0.0306	0.0265	-0.573	0.0018	0.0148
258519_at	AT3G06760	Identical to Protein DEHYDRATION-INDUCED 19 h	-0.2619	0.2077	0.2669	-0.1904	0.3366	0.3118	0.01346	0.8734	0.4851	0.08504	0.3437	0.2597
258520_at	AT3G06710	similar to protein binding / zinc ion binding [Arabido	0.4246	0.75	0.5086	-0.3325	0.4903	0.816	0.5488	0.0378	0.3781	0.06084	0.9633	0.4741
258521_at	AT3G06680	60S ribosomal protein L29 (RPL29B)	-0.2669	0.3092	0.3281	-0.3395	0.2129	0.2414	1.1727	0.0069	0.0339	1.1001	0.0087	0.029
258522_at	AT3G06660	PAPA-1-like family protein / zinc finger (HIT type) fa	0.3578	0.0136	0.0719	0.2709	0.0333	0.0904	-0.08262	0.3181	0.2774	-0.1695	0.0795	0.1046
258523_at	AT3G06830	pectinesterase family protein	-0.09793	0.7471	0.5081	-0.4083	0.223	0.2476	-0.05256	0.813	0.4675	0.363	0.156	0.1589
258524_at	AT3G06810	IBR3 (IBA-RESPONSE 3); acyl-CoA dehydrogenas	0.8344	0.0051	0.0512	0.8159	0.0056	0.0434	-0.2706	0.0825	0.1261	-0.2891	0.0695	0.0965
258525_at	AT3G06810	IBR3 (IBA-RESPONSE 3); acyl-CoA dehydrogenas	-1.566	0.088	0.1719	0.6894	0.3786	0.3313	-2.9277	0.0095	0.039	-0.6723	0.344	0.2598
258526_at	AT3G06790	elastid development protein DAG, putative	0.3439	0.0209	0.085	0.2428	0.1551	0.2021	0.2507	0.1392	0.1705	-0.01453	0.9216	0.4633
258527_at	AT3G06850	DIN3/LTA1 (DARK INDUCIBLE 3); alpha-ketoacid c	0.5115	0.0246	0.0911	0.4908	0.028	0.0833	-0.02881	0.8386	0.4752	-0.04948	0.7279	0.4065
258528_at	AT3G06770	glycoside hydrolase family 28 protein / polygalactur	-0.5518	0.1271	0.206	-0.7956	0.0503	0.1112	-0.03328	0.8433	0.4767	-0.2771	0.1541	0.1575
258529_at	AT3G06740	zinc finger (GATA type) family protein	-0.4048	0.3561	0.3527	-0.6049	0.1943	0.2289	0.6	0.1274	0.162	0.3999	0.27	0.2227
258530_at	AT3G06840	similar to unknown protein [Arabidopsis thaliana] (T	-3.1593	0.0137	0.0719	-1.0889	0.2214	0.2468	-1.7313	0.013	0.0452	0.3391	0.4501	0.306
258531_at	AT3G06720	AT-IMP (Arabidopsis thaliana importin alpha); prote	0.3008	0.0949	0.178	0.3663	0.0573	0.119	-0.479	0.0256	0.065	-0.4145	0.0399	0.069
258532_at	AT3G06705	unknown protein	0.0098811	0.9582	0.5667	0.3961	0.6784	0.1489	0.8188	0.0096	0.0391	1.2051	0.0024	0.0162
258533_at	AT3G06670	60S ribosomal protein L29 (RPL29A)	-0.2669	0.3092	0.3281	-0.3395	0.2129	0.2414	1.1727	0.0069	0.0339	1.1001	0.0087	0.029
258534_at	AT3G06730	thioredoxin family protein	-0.1385	0.4898	0.4158	-0.378	0.1069	0.1649	0.7645	0.0096	0.039	0.525	0.0328	0.0611
258535_at	AT3G06830	hydroxyproline-rich glycoprotein family protein	-0.998	0.003	0.0436	-1.1249	0.0019	0.033	0.2275	0.2172	0.2219	0.1006	0.5527	0.3446
258536_at	AT3G06540	GDP dissociation inhibitor family protein / Rab GTP	0.4439	0.0147	0.0736	0.1623	0.2072	0.2377	-0.1462	0.2471	0.2394	-0.4278	0.0166	0.0412
258537_at	AT3G04210	disease resistance protein (TIR-NBS class), putative	0.01278	0.9749	0.571	0.1116	0.7848	0.4847	-0.137	0.3727	0.3042	-0.03821	0.7936	0.4271
258538_at	AT3G06950	tRNA pseudouridine synthase family protein	0.2642	0.0751	0.2281	0.0249	0.0791	0.1966	-0.2614	0.016	0.0505	-0.2975	0.0103	0.0317
258539_at	no_match	no_match	-1.0934	0.4988	0.4199	-0.8499	0.5946	0.4213	-0.5611	0.6659	0.4198	-0.3176	0.8053	0.4302
258540_at	AT3G06990	DC1 domain-containing protein	0.6235	0.1572	0.2311	-0.7595	0.1017	0.1609	0.5085	0.2293	0.2291	-0.8744	0.0714	0.0979
258541_at	AT3G07000	DC1 domain-containing protein	-0.1003	0.9193	0.5568	-1.3609	0.2175	0.2442	1.1482	0.1864	0.2032	0.222	0.8232	0.4351
258542_at	AT3G07030	pseudogene, similar to OSJNBa0042L16.13, blastp	0.8981	9.00E-04	0.0349	0.5882	0.0046	0.0416	0.2549	0.0683	0.1134	-0.05501	0.621	0.3706
258543_at	AT3G06870	proline-rich family protein	1.1688	0.0269	0.0949	-0.4334	0.2743	0.2776	0.3715	0.3183	0.2775	-1.2307	0.0195	0.0449
258544_at	AT3G06940	RPM1 (RESISTANCE TO P. SYRINGAE PV MACL	0.1064	0.6113	0.463	-0.1444	0.4964	0.383	-0.8567	1.00E-04	0.012	-0.8948	1.00E-04	0.0063
258545_at	AT3G07050	GTP-binding family protein	0.5147	0.1036	0.1859	0.6329	0.0611	0.1227	-0.1133	0.4153	0.3231	0.004924	0.9704	0.4756
258546_at	AT3G07060	EMB1974 (EMBRYO DEFECTIVE 1974)	-0.1094	0.6374	0.4722	0.4498	0.1044	0.1633	-0.7353	0.0267	0.0664	-0.1761	0.4584	0.3094
258547_at	AT3G06895	unknown protein	0.2182	0.8409	0.5358	-0.8319	0.4601	0.3679	2.25	0.0706	0.1155	1.2	0.2618	0.2187
258548_at	AT3G06910	Ulp1 protease family protein	0.0195	0.912	0.5546	0.1681	0.3677	0.3264	0.139	0.4486	0.3379	0.2876	0.1576	0.1598
258549_at	AT3G06930	protein arginine N-methyltransferase family protein	0.06373	0.7146	0.4974	0.04999	0.7734	0.4817	-0.2512	0.1966	0.2096	-0.2649	0.1779	0.1719
258550_at	AT3G06940	transposable element gene	0.1724	0.3245	0.337	0.499	0.0314	0.0881	-0.4056	0.0576	0.1026	-0.07904	0.634	0.3751
258551_at	AT3G06890	similar to unknown [Populus trichocarpa] (GB:ABK9	0.229	0.2923	0.3186	0.1173	0.5685	0.4113	0.7348	0.0177	0.0533	0.6231	0.03	0.0582
258552_at	AT3G07010	pectate lyase family protein	0.0299	0.8713	0.5443	0.2112	0.2897	0.2864	0.1846	0.3467	0.2916	0.3659	0.1022	0.1221
258553_at	AT3G06960	PDE320 (PIGMENT DEFECTIVE 320)	0.6204	0.0046	0.0488	0.6053	0.005	0.0424	-0.973	8.00E-04	0.0167	-0.9881	8.00E-04	0.011
258554_at	AT3G06980	DEAD/DEAH box helicase, putative	-0.2715	0.2439	0.2899	-0.5413	0.0528	0.114	-0.3699	0.0264	0.0661	-0.6397	0.004	0.0204
258555_at	AT3G06860	MFP2 (MULTIFUNCTIONAL PROTEIN); enoyl-CoA	0.7532	0.0124	0.0688	0.7327	0.0136	0.0618	-0.3737	0.0168	0.0517	-0.3943	0.014	0.0376
258556_at	AT3G07020	UDP-glucose:sterol glucosyltransferase (UGT80A2	-0.2461	0.261	0.3003	0.2232	0.3011	0.2919	-0.1051	0.6062	0.4001	-0.1279	0.5339	0.3394
258557_at	AT3G05990	leucine-rich repeat family protein	-0.09879	0.7016	0.493	-0.643	0.0552	0.1166	-0.3879	0.1377	0.1695	-0.9321	0.0113	0.0332
258558_at	AT3G06000	leucine-rich repeat family protein	-0.41	0.5532	0.4421	-1.8056	0.0466	0.107	-0.5101	0.4265	0.3282	-1.9057	0.0298	0.058
258559_at	AT3G06010	ATCHR12; ATP binding / DNA binding	-0.0548	0.6489	0.4761	0.007062	0.9524	0.5324	-0.5338	0.0087	0.0375	-0.4719	0.0134	0.0396
258560_at	AT3G06020	similar to unknown protein [Arabidopsis thaliana] (T	-0.4457	0.2944	0.32	-0.7111	0.1268	0.1806	1.0515	0.0467	0.0906	0.786	0.1006	0.1211
258561_at	AT3G05960	sugar transporter, putative	-0.3808	0.6721	0.4833	0.3814	0.6716	0.4491	0.3795	0.6731	0.422	1.1416	0.2434	0.209
258562_at	AT3G05980	similar to unknown protein [Arabidopsis thaliana] (T	-0.5086	0.3595	0.3544	-0.1578	0.7645	0.4787	-0.4717	0.3919	0.3129	-0.1208	0.8181	0.4337
258563_at	AT3G05970	LACS6 (LONG-CHAIN ACYL-COA SYNTHETASE	1.0291	4.00E-04	0.032	1.1615	2.00E-04	0.0249	-0.3832	0.0143	0.0477	-0.2508	0.0535	0.0826
258564_at	AT3G06560	polynucleotide adenylyltransferase/ protein binding	0.547	0.4858	0.414	-1.3493	0.1314	0.1839	0.8081	0.01	0.0398	-1.0882	0.0035	0.0191
258565_at	AT3G06950	similar to unknown protein [Arabidopsis thaliana] (T	0.06248	0.8073	0.526	0.3318	0.2386	0.2569	-1.4881	8.00E-04	0.016	-1.2188	0.0016	0.0142
258566_at	AT3G04110	GLR1 (GLUTAMATE RECEPTOR 1)	0.4949	0.0504	0.1292	0.4326	0.0728	0.1351	-0.1105	0.4635	0.3447	-0.1728	0.274	0.225
258567_at	AT3G04080	ATAPY1 (APYRASE 1); calmodulin binding	0.2131	0.2181	0.2739	0.3859	0.0574	0.1191	-0.2134	0.2176	0.2222	-0.04069	0.7943	0.4273
258568_at	AT3G04470	similar to ankyrin repeat family protein [Arabidopsis	0.5468	0.0111	0.066	0.3369	0.0513	0.1123	-0.3916	0.0174	0.0529	-0.6016	0.0039	0.0201
258569_at	AT3G04400	EMB2171 (EMBRYO DEFECTIVE 2171); structural	-0.1492	0.4155	0.3825	-0.06594	0.7089	0.4616	0.3097	0.1328	0.1658	0.3929	0.0752	0.1009
258570_at	AT3G04530	PPCK2 (PHOSPHOENOLPYRUVATE CARBOXYL	-1.2066	0.3568	0.353	-1.6041	0.2387	0.2569	0.0321	0.9792	0.5124	-0.3655	0.7683	0.4194
258571_at	AT3G04420	ANAC048 (Arabidopsis NAC domain containing pro	0.6276	0.4869	0.4145	-0.9201	0.3249	0.3058	1.0936	0.2534	0.2428	-0.4542	0.6094	0.3665
258572_at	AT3G04270	two-component response regulator	-0.4225	0.5726	0.45	0.08699	0.9056	0.5203	-0.1383	0.8506	0.4786	0.3712	0.6184	0.3698
258573_at	AT3G04260	PTAC3 (PLASTID TRANSCRIPTIONALLY ACTIVE	0.09843	0.5366	0.4356	0.002836	0.9854	0.5405	-0.3203	0.0264	0.066	-0.4159	0.0111	0.0331
258574_at	AT3G04250	F-box family protein-related	-0.1997	0.8077	0.5262	-0.4861	0.5612	0.4088	-0.1364	0.8633	0.4822	-0.4228	0.5999	0.3634
258575_at	AT3G04240	SEC (SECRET AGENT); transferase, transferring g	0.8827	0.0014	0.038	0.4209	0.0196	0.0719	-0.1911	0.1619	0.1866	-0.6529	0.0043	0.0208
258576_at	AT3G04230	40S ribosomal protein S16 (RPS16B)	0.5111	0.0092	0.0618	0.7467	0.0023	0.0336	0.5055	0.0096	0.039	0.741	0.0024	0.0162
258577_at	AT3G04220	disease resistance protein (TIR-NBS-LRR class), p	0.6453	0.078	0.1609	0.249	0.4146	0.348	0.005432	0.9792	0.5124	-0.3908	0.162	0.1321
258578_at	AT3G04200	germin-like protein, putative	0.6245	0.6138	0.4641	0.1331	0.9129	0.5221	0.1168	0.9235	0.4989	-0.3746	0.7595	0.4165
258579_s_at	AT3G04190;AT3G04180	[AT3G04190, germin-like protein, putative];[AT3G04	0.3142	0.8386	0.535	0.3605	0.8153	0.4947	-1.3404	0.4062	0.3191	-1.2941	0.4212	0.2929
258580_at	AT3G04170	germin-like protein, putative	-1.5969	0.1436	0.2204	0.8483	0.3894	0.3364	-0.9646	0.3256	0.2811	1.4605	0.1721	0.1685
258581_at	AT3G04160	similar to hypothetical protein [Vitis vinifera] (GB:CA	-0.7993	0.5006	0.4208	0.1728	0.8808	0.5134	-3.6862	0.027	0.0668	-2.7141	0.066	0.0936
258582_at	AT3G04150	germin-like protein, putative	0.216	0.7293	0.5023	-0.5852	0.3714	0.328	-0.08632	0.8892	0.4895	-0.8875	0.2018	0.1862
258583_at	AT3G04140	AGL57; DNA binding / transcription factor	-1.2926	0.3431	0.3464	-0.3255	0.8001	0.4897	-0.5959	0.6463	0.4131	0.3711	0.7731	0.4209
258584_at	AT3G04090	SIP1;1 (SMALL AND BASIC INTRINSIC PROTEIN	0.4815	0.0032	0.0445	0.223	0.0432	0.1032	0.2923	0.0165	0.0512	0.03378	0.67	0.3874
258585_at	AT3G04340	EMB2458 (EMBRYO DEFECTIVE 2458); ATPase	0.1951	0.1395	0.2171	-0.2482	0.0792	0.1411	-0.542	0.0069	0.0339	-0.9852	7.00E-04	0.0108
258586_s_at	AT3G04320;AT3G04330	[AT3G04320, endopeptidase inhibitor];[AT3G04330	0.713	0.6568	0.4779	-0.4675	0.769	0.4801	2.2199	0.1271	0.1618	1.0394	0.4192	0.2922
258587_at	AT3G04310	similar to unknown protein [Arabidopsis thaliana] (T	-0.02402	0.9431	0.5632	0.00706	0.9833	0.54	-0.1924	0.4156	0.3233	-0.1613	0.4892	0.3216
258588_s_at	AT3G04120	GAPC (GLYCERALDEHYDE-3-PHOSPHATE DEH	0.501	7.00E-04	0.0334	0.2249	0.0131	0.0611	0.05269	0.3754	0.3055	-0.2234	0.0134	0.0367
258589_at	AT3G04290	ATCHR12; LI-TCL1/LI-TCL1A/LI-TCL1B; ATPase; 1	-1.2569	0.1177	0.1983	-1.0333	0.1775	0.2179	0.2204	0.4228	0.3266	0.444	0.1468	0.1526
258590_at	AT3G04280	ARR22 (ARABIDOPSIS RESPONSE REGULATOR	-1.7488	0.1133	0.195	-0.7521	0.4337	0.3569	0.3176	0.7321	0.4424	1.3143	0.2033	0.187
258591_at	AT3G04360	C2 domain-containing protein	0.7734	0.4073	0.3791	-1.3434	0.1834	0.2221	0.2169	0.8039	0.4647	-1.8999	0.0808	0.1057
258592_at	AT3G04130	pentatricopeptide (PPR) repeat-containing protein	-0.3458	0.3001	0.3229	-0.1494	0.6346	0.4363	-0.6464	0.0619	0.1069	-0.4499	0.1479	0.1534
258593_at	AT3G04480	endoribonuclease	0.5644	0.1219	0.2022	0.5711	0.1187	0.1742	-0.9276	0.0264	0.066	-0.9209	0.027	0.0546
258594_at	no_match	no_match	0.7365	0.2379	0.2862	-0.7933	0.2096	0.2393	0.7925	0.1932	0.2074	-0.7373	0.2197	0.1959
258595_at	AT3G04500	RNA recognition motif (RRM)-containing protein	-0.4738	0.0152	0.0744	0.09409	0.4637	0.3697	0.2955	0.064	0.109	0.6751	0.0044	0.021
258596_at	AT3G04510	similar to LSH1 (LIGHT-DEPENDENT SHORT HYP	0.1915	0.5773	0.4515	0.5878	0.1365	0.188	0.4878	0.1737	0.1944	0.8841	0.0401	0.0691
258597_x_at	AT3G04390	xanthine dehydrogenase family protein	0.2986	0.7942	0.5223	-1.0358	0.3882	0.3359	0.6492	0.5623	0.3835	-0.6851	0.5419	0.3416
258598_at	AT3G04410	transcription factor	-0.1098	0.8476	0.5378	-1.9586	0.0216	0.0747	1.5253	0.0465	0.0904	-0.3235	0.5784	0.3535
258599_at	AT3G04520	THA2 (THREONINE ALDOLASE 2); threonine aldo	-0.1498	0.339	0.3449	0.0343	0.8161	0.4949	0.193	0.0642	0.1093	0.3771	0.0077	0.0274
258600_at	AT3G02810	protein kinase family protein	-1.7191	0.2111	0.269	-1.7527	0.204	0.2355	-0.4019	0.7456	0.4467	-0.4354	0.7255	0.4058
258601_at	AT3G02760	histidyl-tRNA synthetase, putative / histidine--tRNA	0.3238	0.2686	0.3031	0.3193	0.2724	0.2768	-0.3948	0.038	0.0806	-0.3993	0.0367	0.0652
258602_at	AT3G02750	phosphate transporter 2C family protein / PP2C fami	-0.5086	0.1413	0.2185	-0.2032	0.5054	0.3868	-1.1802	0.0096	0.0391	-0.8747	0.0261	0.0535
258603_at	AT3G02900	ATHSFA1E (Arabidopsis thaliana heat shock transc	0.2266	0.4017	0.3761	1.0147	0.0137	0.062	-0.3814	0.1897	0.2054	0.4067	0.1677	0.1658
258604_at	AT3G02980	GCN5-related N-acetyltransferase (GNAT) family pr	0.1596	0.7314	0.5028	0.5263	0.2914	0.2873	-0.00577	0.9895	0.5152	0.361	0.4289	0.2962
258605_at	AT3G02970	phosphate-responsive 1 family protein	-0.3989	0.7299	0.5025	2.0807	0.1296	0.1796	-1.2972	0.2948	0.266	1.1824	0.3339	0.2552
258606_at	AT3G02940	immediate-early fungal elicitor family protein	-0.6471	0.1767	0.2459	-0.8676	0.093	0.1539	0.6632	0.055	0.1	0.4427	0.1478	0.1533
258607_at	AT3G02730	ATF1/TRXF1 (THIOREDOXIN F-TYPE 1); thiol-dis	-0.6728	0.0297	0.1	-0.7697	0.0193	0.0716	0.4251	0.0107	0.041	0.3281	0.0252	0.0525
258608_at	AT3G03020	unknown protein	-0.117	0.553	0.4421	0.1696	0.4013	0.3418	-0.7322	0.0013	0.0192	-0.4456	0.0082	0.0281
258609_at	AT3G02910	Identical to UPI0131 protein At3g02910 [Arabidops	0.5486	0.139	0.2165	-0.1027	0.7473	0.474	0.9069	0.0013	0.0191	0.2555	0.0865	0.1101
258610_at	AT3G02875	ILR1 (IAA-LEUCINE RESISTANT 1); metallopeptidas	0.4824	0.0223	0.0875	0.4429	0.0293	0.085	0.04542	0.7503	0.4484	0.005912	0.9667	0.4748
258611_at	AT3G02860	zinc ion binding	0.5673	0.0378	0.1121	0.5477	0.0419	0.1018	0.09112	0.6491	0.4142	0.07143	0.7199	0.4039
258612_at	AT3G02800	replication protein-related	0.1656	0.1232	0.2035	-0.1611	0.1692	0.2099	0.2863	0.0397	0.0825	0.3109	0.031	0.0593
258613_at	AT3G02870	VTC4; 3'(2'),5'-bisphosphate nucleotidase/ L-galact	-0.6154	0.0272	0.0957	-0.7198	0.0164	0.0666	0.2638	0.1518	0.1802	0.1593	0.3456	0.2606
258614_at	AT3G02770	dimethylmenaquinone methyltransferase family pro	0.6151	0.0092	0.0618	1.0321	0.0014	0.0312	-0.081	0.4031	0.3178	0.3359	0.0179	0.0429
258615_at	AT3G02780	aspartyl protease family protein	0.8204	1.00E-04	0.0312	0.4542	8.00E-04	0.0277	-0.4748	7.00E-04	0.0159	-0.841	1.00E-04	0.0058
258616_at	AT3G02880	leucine-rich repeat transmembrane protein kinase,	-0.7859	0.0597	0.1398	-0.8212	0.0529	0.114	0.04645	0.8181	0.4693	0.01121	0.9556	0.4724
258617_at	AT3G03000	calmodulin, putative	0.007147	0.9813	0.5724	0.5677	0.1183	0.1739	0.5939	0.0387	0.0813	1.1545	0.0041	0.0207
258618_at	AT3G02885	GASA6 (GAST1 PROTEIN HOMOLOG 5)	1.0892	0.1839	0.251	0.6543	0.3897	0.3366	0.1684	0.8163	0.4686	-0.2665	0.7147	0.4024
258619_at	AT3G02780	IDI2/IPIAT1/IPP2 (ISOPENTENYL DIPHOSPHATE	0.1882	0.1074	0.1895	0.1809	0.1176	0.1734	0.5525	0.0035	0.0261	0.5453	0.0037	0.0197
258620_at	AT3G02940	MYB107 (myb domain protein 107); DNA binding / t	-1.0606	0.5126	0.4261	-0.7443	0.6409	0.4384	0.7855	0.6106	0.4014	1.1018	0.4822	0.3185
258621_at	AT3G02930	ZFN1 (ZINC FINGER PROTEIN 1); nucleic acid bin	-0.839	0.0027	0.0426	-0.9327	0.0018	0.0323	-0.2647	0.1044	0.1445	-0.3583	0.0471	0.0765
258622_at	AT3G02720	DJ-1 family protein / protease-related	-0.3009	0.0347	0.1076	-0.5085	0.006	0.0447	-0.3557	0.0205	0.0576	-0.5633	0.0042	0.0207
258623_at	AT3G02790	zinc finger (C2H2 type) family protein	0.2722	0.1363	0.2144	-0.1329

256690_at	AT3G07960	phosphatidylinositol-4-phosphate 5-kinase family pr	1.3116	0.3198	0.3343	-1.462	0.2746	0.2778	1.1055	0.3112	0.2741	-1.6681	0.1554	0.1585
258691_at	AT3G08630	similar to alphavirus core protein family [Arabidopsis	-0.3042	0.1267	0.2058	-0.1046	0.5444	0.4024	-0.3558	0.0876	0.1307	-0.1562	0.379	0.2753
258692_at	AT3G08640	alphavirus core protein family	0.3334	0.1664	0.2386	0.359	0.143	0.193	0.2935	0.0281	0.0681	0.3192	0.0215	0.0478
258693_at	AT3G08650	metal transporter family protein	0.5277	0.0228	0.0882	0.7273	0.0077	0.0489	-0.1543	0.3519	0.2942	0.04528	0.7728	0.4209
258694_at	AT3G08660	phototropic-responsive protein, putative	-0.222	0.6112	0.463	0.3817	0.3974	0.3402	0.1311	0.667	0.4203	0.7349	0.0602	0.0887
258695_at	AT3G09640	APX2 (ASCORBATE PEROXIDASE 2); L-ascorbat	-0.8904	0.2415	0.2886	1.3836	0.0997	0.1592	0.09026	0.896	0.4913	2.3643	0.0218	0.0481
258696_at	AT3G09650	HCF152 (HIGH CHLOROPHYLL FLUORESCENCE	-0.3247	0.2437	0.2898	-0.2842	0.2979	0.2906	-0.45	0.0116	0.0426	-0.4095	0.0159	0.0402
258697_at	AT3G09660	MCM8; ATP binding / DNA binding / DNA-dependen	0.4889	0.4948	0.418	-0.8328	0.2703	0.2756	0.3388	0.6305	0.4081	-0.9828	0.2059	0.1884
258698_at	AT3G09690	hydrolase, alpha/beta fold family protein	-0.4429	0.0492	0.1276	0.1103	0.525	0.3941	-0.3286	0.0214	0.0589	0.2247	0.0661	0.0936
258699_at	AT3G09470	Identical to UNC93-like protein [Arabidopsis Thalian	0.2366	0.4035	0.3771	-0.1984	0.4776	0.3753	0.4977	0.1211	0.1571	0.06272	0.8168	0.4334
258700_at	AT3G09710	IQD1 (IQ-DOMAIN 1); calmodulin binding	-0.7245	0.0107	0.0649	-0.5818	0.0222	0.0753	0.02913	0.8647	0.4826	0.1718	0.3442	0.26
258701_at	AT3G09720	DEAD/DEAH box helicase, putative	0.5683	0.1938	0.2582	-0.329	0.4176	0.3495	0.04421	0.8494	0.4784	-0.853	0.0174	0.0422
258702_at	AT3G09730	similar to unnamed protein product [Vitis vinifera] (G	0.2712	0.2247	0.2784	-0.1461	0.483	0.3773	0.09367	0.3967	0.315	-0.3236	0.0306	0.0589
258703_at	AT3G09750	unknown protein	-0.8224	0.1732	0.2437	-0.3746	0.4929	0.3815	-1.4115	0.9488	0.0907	-0.9636	0.1245	0.1379
258704_at	AT3G09780	protein kinase family protein	-0.307	0.4281	0.3884	-0.1328	0.7225	0.4662	0.06324	0.8535	0.4794	0.2374	0.5007	0.3262
258705_at	AT3G09470	Identical to UNC93-like protein [Arabidopsis Thalian	0.3249	0.134	0.2124	0.4637	0.0554	0.1169	-1.1744	0.0025	0.0232	-1.0356	0.0039	0.0202
258706_at	AT3G09550	similar to unknown protein [Arabidopsis thaliana] (T	0.3445	0.1501	0.2257	0.3818	0.1202	0.1755	-0.1217	0.5641	0.3844	-0.08443	0.6856	0.3925
258707_at	AT3G09480	histone H2B, putative	-0.07898	0.897	0.5504	1.4133	0.0692	0.1319	0.6772	0.1988	0.2111	2.1695	0.0079	0.0277
258708_at	AT3G09580	amine oxidase family protein	-0.7832	0.0022	0.0414	-0.704	0.0033	0.0371	-0.4047	0.0069	0.0338	-0.3255	0.0146	0.0385
258709_at	AT3G09500	60S ribosomal protein L35 (RPL35A)	-0.01833	0.8765	0.5456	0.2153	0.1236	0.1784	-0.2588	0.0274	0.0674	-0.02516	0.758	0.4161
258710_s_at	AT4G08520;AT3G09800	[AT4G08520, clathrin adaptor complex small chain	0.01995	0.8931	0.5495	0.4743	0.0272	0.0825	0.1468	0.3514	0.294	0.6011	0.0125	0.0353
258711_at	AT3G09790	UBQ8 (ubiquitin 8)	-0.5663	0.4742	0.4095	-0.1122	0.8833	0.514	-0.3595	0.4335	0.3311	0.09459	0.8302	0.4372
258712_s_at	AT3G09680;AT5G02960	[AT3G09680, 40S ribosomal protein S23 (RPS23A);	-0.222	0.1099	0.192	-0.03354	0.7724	0.4813	0.02823	0.7659	0.453	0.2167	0.0707	0.0975
258713_at	AT3G09735	DNA-binding S1FA family protein	0.5669	0.0546	0.1342	0.5227	0.0681	0.1309	0.3714	0.1528	0.1807	0.3272	0.1954	0.1821
258714_at	AT3G09770	zinc finger (C3HC4-type RING finger) family protein	0.0632	0.7239	0.5006	0.2975	0.1489	0.1974	-0.2299	0.0914	0.1337	0.004444	0.9679	0.475
258715_at	AT3G09630	60S ribosomal protein L4/L1 (RPL4A)	0.2406	0.2723	0.3067	0.1269	0.539	0.4	-0.0719	0.3694	0.3025	-0.1856	0.0595	0.0881
258716_at	AT3G09700	DNAJ heat shock N-terminal domain-containing pro	0.05741	0.7222	0.5001	0.6654	0.0115	0.0578	0.3982	0.0365	0.0785	1.0063	0.0014	0.0137
258717_at	AT3G09740	SYP71 (SYNTAXIN OF PLANTS 71)	0.1475	0.4356	0.392	0.1358	0.47	0.3722	-0.295	0.1476	0.1773	-0.3066	0.136	0.1457
258718_at	AT3G09760	zinc finger (C3HC4-type RING finger) family protein	0.04968	0.8362	0.5342	0.3226	0.2252	0.2485	-0.493	0.0937	0.1357	-0.2201	0.3836	0.2774
258719_at	AT3G09540	pectate lyase family protein	-1.0971	0.0025	0.0421	-1.3135	0.0012	0.0303	0.4044	0.0664	0.1115	0.188	0.309	0.2429
258720_at	AT3G09560	ankyrin repeat family protein	-0.8299	0.1846	0.2514	1.0679	0.1084	0.1659	-0.9457	0.1421	0.173	0.952	0.1401	0.1482
258721_at	AT3G09360	lipin family protein	-0.1504	0.4219	0.386	-0.2171	0.2664	0.2735	-0.4633	0.0291	0.0693	-0.53	0.019	0.0441
258722_at	AT3G09590	pathogenesis-related protein, putative	0.06821	0.9191	0.5567	0.8965	0.2116	0.2408	0.3921	0.5513	0.3795	1.2233	0.1126	0.1295
258723_at	AT3G09600	myb family transcription factor	-1.4403	0.0128	0.0698	-0.7597	0.0866	0.1484	-1.1938	0.0141	0.0474	-0.5132	0.1481	0.1535
258724_at	AT3G09600	myb family transcription factor	-1.1102	0.006	0.0538	-1.483	0.0021	0.0331	-0.2974	0.1819	0.2001	-0.6702	0.022	0.0484
258725_at	AT3G09620	DEAD/DEAH box helicase, putative	-0.1885	0.7592	0.5115	1.2066	0.1037	0.1626	0.8103	0.2202	0.2237	2.2043	0.0168	0.0414
258726_at	AT3G11745	unknown protein	-1.4403	0.4957	0.1176	0.1983	0.5362	0.1576	-0.03106	0.8929	0.4905	0.00889	0.9697	0.4754
258727_at	AT3G11930	universal stress protein (USP) family protein	-0.6838	0.0685	0.1505	-0.6336	0.0835	0.1452	1.4031	0.0012	0.0188	1.4533	0.0011	0.0124
258728_at	AT3G11800	similar to unknown protein [Arabidopsis thaliana] (T	0.3088	0.1074	0.1895	0.06416	0.6895	0.4555	0.5769	0.0112	0.0418	0.3323	0.0621	0.0904
258729_at	AT3G11900	ANT1 (ADENOSINE NUCLEOTIDE) AND NEUTRAL TRANSPORTE	-0.07285	0.5099	0.4249	-0.301	0.0405	0.0998	-0.5753	0.0047	0.0291	-0.8035	0.0013	0.0133
258730_at	AT3G11730	ATFP8 (Arabidopsis Rab GTPase homolog D1); GT	0.09878	0.5234	0.4304	0.1355	0.3924	0.338	0.1782	0.1039	0.1441	0.2149	0.0647	0.0925
258731_at	AT3G11880	similar to unknown protein [Arabidopsis thaliana] (T	0.7807	5.00E-04	0.032	0.5856	0.0014	0.0312	-0.02947	0.6581	0.4173	-0.2246	0.022	0.0484
258732_at	AT3G09820	beta-fructofuranosidase, putative / invertase, putativ	0.9567	0.3285	0.3392	-0.6321	0.5197	0.3922	-0.7645	0.4419	0.3349	-2.3933	0.0558	0.0847
258733_at	AT3G05850	transposable element gene	0.07901	0.7302	0.5026	-0.06332	0.7816	0.484	-0.1061	0.6455	0.4128	-0.2484	0.3095	0.2431
258734_at	AT3G05860	MADS-box protein (AGL45)	-0.3703	0.7315	0.5028	0.4012	0.7104	0.4622	-1.4856	0.2033	0.2138	-0.7141	0.5057	0.328
258735_at	AT3G05880	RC2/A (RARE-COLD-INDUCIBLE 2A)	-0.5979	0.1113	0.1934	-0.1338	0.6721	0.4492	0.4423	0.2055	0.2151	0.9064	0.0364	0.0949
258736_at	AT3G05900	neurofilament protein-related	-1.2191	0.0066	0.0549	-0.9753	0.0143	0.0632	-0.2649	0.1209	0.1569	-0.02113	0.8831	0.4523
258737_at	AT3G05940	similar to unknown protein [Arabidopsis thaliana] (T	0.2332	0.0302	0.1009	-0.2835	0.0161	0.066	0.05684	0.4063	0.3191	-0.4598	0.0017	0.0145
258738_at	AT3G05750	similar to unknown protein [Arabidopsis thaliana] (T	-0.2429	0.1891	0.2547	-0.1454	0.3978	0.3403	-0.3482	0.0862	0.1295	-0.2506	0.1783	0.1722
258739_s_at	AT3G05770;AT1G54300	[AT3G05770, catalytic/ cobalamin binding];[AT1G54	1.5314	0.2031	0.2642	2.6033	0.0611	0.1227	-1.5645	0.1599	0.1857	-0.4925	0.6163	0.3689
258740_at	AT3G05780	Lon protease, putative	0.061	0.9539	0.5657	-0.2847	0.7884	0.4857	2.011	0.1126	0.1504	1.6653	0.1686	0.1664
258741_at	AT3G05790	Lon protease, putative	1.2894	0.1795	0.2476	2.0155	0.064	0.1262	-0.82647	0.1838	0.2013	-0.1006	0.8547	0.4441
258742_at	AT3G05800	transcription factor	-0.9104	0.0277	0.0966	-0.3153	0.3065	0.2954	0.1338	0.6452	0.4127	0.7289	0.0537	0.0828
258743_s_at	AT5G26751;AT3G05840	[AT5G26751, ATSK11 (Arabidopsis thaliana SHAG	-0.1732	0.1124	0.1942	-0.1822	0.0998	0.1593	0.3212	0.0198	0.0565	0.3122	0.0217	0.0479
258744_at	AT3G05930	Encodes alpha-helical IF (intermediate filament)-like	0.3969	0.7475	0.5081	0.2069	0.8661	0.5088	-0.7509	0.5497	0.379	-0.9409	0.4595	0.3098
258745_at	AT3G11920	glutaredoxin-related	0.04874	0.9629	0.568	-1.603	0.1786	0.2187	-1.4517	0.2141	0.2204	-3.1034	0.0344	0.0627
258746_at	AT3G05950	germin-like protein, putative	-0.2648	0.7239	0.5006	-1.5647	0.0886	0.15	1.1953	0.1621	0.1868	-0.1046	0.8882	0.4537
258747_at	AT3G05810	similar to unknown protein [Arabidopsis thaliana] (T	0.485	0.0838	0.1675	0.5583	0.0577	0.1194	-0.04628	0.8377	0.4749	0.02708	0.9044	0.4586
258748_at	AT3G05930	GLP8 (GERMIN-LIKE PROTEIN 8); manganese ion	-0.6491	0.5716	0.4495	-0.1291	0.9085	0.5211	-1.7454	0.1734	0.1942	-1.2254	0.31	0.2434
258749_at	AT3G05760	nucleic acid binding / zinc ion binding	0.7905	0.007	0.0562	0.8328	0.0058	0.044	0.1414	0.4131	0.3221	0.1837	0.3014	0.2394
258750_at	AT3G05910	pectinacetylesterase, putative	-0.1819	0.2268	0.2797	-0.2173	0.1635	0.2083	0.2594	0.0228	0.061	0.224	0.0359	0.0644
258751_at	AT3G05890	RCI2B (RARE-COLD-INDUCIBLE 2B)	-1.494	0.007	0.0564	-0.8633	0.0422	0.1021	0.4643	0.0862	0.1295	1.095	0.0059	0.0239
258752_at	AT3G09520	ATEXO70H4 (exocyst subunit EXO70 family protein	0.4	0.536	0.4355	-0.3631	0.5726	0.4129	0.3059	0.6324	0.4086	-0.4572	0.4827	0.3188
258753_at	AT3G09530	ATEXO70H3 (exocyst subunit EXO70 family protein	0.3969	0.7475	0.5081	0.2069	0.8661	0.5088	-0.7509	0.5497	0.379	-0.9409	0.4595	0.3098
258754_at	AT3G11920	glutaredoxin-related	0.04874	0.9629	0.568	-1.603	0.1786	0.2187	-1.4517	0.2141	0.2204	-3.1034	0.0344	0.0627
258755_at	AT3G11945	ATHST; prenyltransferase	-0.6523	0.0493	0.1276	-1.1461	0.008	0.0499	0.3406	0.21	0.2178	-0.1532	0.539	0.3409
258756_at	AT3G11960	cleavage and polyadenylation specificity factor (CP	0.5937	0.0514	0.1302	0.5011	0.081	0.1428	-0.4377	0.1082	0.1472	-0.5303	0.0669	0.0942
258757_at	AT3G10912;AT3G10910	[AT3G10912, CPuORF63 (Conserved peptide upst	0.5363	0.2179	0.2737	0.2874	0.4776	0.3753	-0.00178	0.9962	0.5166	-0.2507	0.5163	0.3321
258758_at	AT3G10810	zinc finger (C3HC4-type RING finger) family protein	0.2098	0.3132	0.3304	-0.3047	0.1694	0.2121	0.6255	0.0105	0.0407	0.111	0.4657	0.3122
258759_at	AT3G10800	BZIP2B; DNA binding / transcription factor	0.8258	0.0085	0.0602	0.7341	0.0128	0.0603	0.1705	0.2309	0.2299	0.07882	0.5496	0.3449
258760_at	AT3G10780	emp24/gp25L/p24 family protein	0.5777	0.7347	0.5038	0.2774	0.8699	0.5098	0.3612	0.8126	0.4674	0.061	0.9679	0.475
258761_at	AT3G10760	myb family transcription factor	-0.157	0.4138	0.3819	-0.458	0.0565	0.1182	-0.1541	0.1866	0.2034	-0.4551	0.0093	0.0301
258762_at	AT3G10750	similar to F-box family protein [Arabidopsis thaliana	-0.4647	0.7429	0.5067	-1.2882	0.385	0.3341	-0.3817	0.7714	0.4546	-1.2052	0.3818	0.2765
258763_s_at	AT3G10900;AT3G30540	[AT3G10900, (1-4)-beta-mannan endohydrolase, p	-1.1063	0.4178	0.3838	-0.9565	0.4789	0.3757	-0.3039	0.8164	0.4687	-0.1541	0.9061	0.459
258764_at	AT3G10720	pectinesterase, putative	-0.6549	0.1776	0.2464	-0.941	0.0787	0.1406	0.4854	0.0037	0.0267	0.1993	0.0667	0.0941
258765_at	AT3G10710	pectinesterase family protein	-0.09041	0.7828	0.5185	-0.4238	0.2391	0.2572	-0.1349	0.6828	0.4251	-0.4683	0.2014	0.186
258766_at	AT3G10700	GHMP kinase family protein	-0.3841	0.3142	0.331	0.1757	0.6267	0.4334	-0.8182	0.0704	0.1153	-0.2584	0.4822	0.3185
258767_at	AT3G10890	(1-4)-beta-mannan endohydrolase, putative	0.09402	0.9244	0.5581	0.8776	0.3993	0.3409	-0.8433	0.0944	0.1363	-0.05974	0.8846	0.4528
258768_at	AT3G10880	similar to unknown protein [Arabidopsis thaliana] (T	-0.09526	0.879	0.5463	-0.544	0.4065	0.3443	0.7852	0.252	0.2419	0.3364	0.5973	0.3625
258769_at	AT3G10870	hydrolase, alpha/beta fold family protein	-0.3454	0.2134	0.2706	-0.4912	0.1034	0.1624	0.2419	0.1532	0.181	0.09618	0.5226	0.335
258770_at	AT3G10830	unknown protein	0.4365	0.5104	0.425	0.2047	0.7521	0.4756	0.3993	0.5452	0.3774	0.1675	0.7955	0.4275
258771_at	AT3G10770	nucleic acid binding	0.4626	0.0056	0.0521	0.7241	0.0011	0.0293	-0.5069	0.004	0.0274	-0.2454	0.045	0.0744
258772_at	AT3G10860	ubiquinol-cytochrome C reductase complex ubiquin	0.004317	0.981	0.5723	0.2511	0.2142	0.2421	0.7115	0.0139	0.0471	0.9584	0.0049	0.022
258773_at	AT3G10730	sad1/unc-84-like 2 family protein	0.1127	0.3418	0.346	0.3049	0.0434	0.1034	0.363	0.0256	0.0649	0.5552	0.0061	0.0241
258774_at	AT3G10740	ASD1 (ALPHA-L-ARABINOFURANOSIDASE); hyd	0.3292	0.009	0.0613	0.8925	0.007	0.0471	0.03891	0.8348	0.474	0.1022	0.5902	0.3601
258775_at	AT3G10850	GLX2-2 (GLYOXALASE 2-2); hydroxyacylglutathion	0.2682	0.0243	0.0908	0.3114	0.0149	0.0643	0.1006	0.074	0.1184	0.1438	0.0264	0.0538
258776_at	AT3G11830	chaperonin, putative	0.2964	0.1928	0.2574	0.3744	0.1193	0.1748	-0.4125	0.09	0.1326	-0.3345	0.1453	0.1518
258777_at	AT3G11850	similar to unknown protein [Arabidopsis thaliana] (T	0.2164	0.594	0.4575	0.2621	0.5222	0.393	0.109	0.7852	0.4588	0.1547	0.7004	0.3975
258778_s_at	AT3G11890;AT3G11860	[AT3G11890, similar to unknown protein [Arabidops	0.2225	0.5207	0.4293	0.2908	0.41	0.3459	-1.2735	0.0096	0.0392	-1.2051	0.0117	0.0339
258779_at	AT3G11870	protein kinase-related	-1.8795	0.054	0.1334	-0.7709	0.33	0.3085	-0.5384	0.4823	0.352	0.5702	0.4586	0.3094
258780_at	AT3G11910	ubiquitin-specific protease, putative	0.7829	5.00E-04	0.032	0.6709	8.00E-04	0.0284	-0.5791	0.0014	0.0197	-0.6911	7.00E-04	0.0108
258781_at	AT3G11740	similar to unknown protein [Arabidopsis thaliana] (T	0.4706	0.5525	0.442	0.4093	0.6034	0.4247	1.5431	0.101	0.1419	1.4818	0.1111	0.1285
258782_at	AT3G11750	dihydroneopterin aldolase, putative	-0.4543	0.0726	0.1553	0.002266	0.9909	0.5419	0.4528	0.0733	0.1178	0.9093	0.0084	0.0284
258783_at	AT3G11760	similar to unknown protein [Arabidopsis thaliana] (T	0.1688	0.4882	0.4151	0.2189	0.3786	0.3313	0.13	0.5886	0.394	0.1801	0.4615	0.3106
258784_at	AT3G11770	nucleic acid binding	0.5059	0.0272	0.0954	0.3782	0.0637	0.1258	-0.2905	0.1069	0.1464	-0.4183	0.0406	0.0696
258785_at	no_match	no_match	0.8787	0.5155	0.4275	1.4424	0.3071	0.2957	1.5553	0.2758	0.2556	2.1189	0.1609	0.1618
258786_at	AT3G11820	SYP121 (syntaxin 121); SNAP receptor	0.2445	0.561	0.4452	0.423	0.3349	0.3107	0.2314	0.2405	0.2355	0.4098	0.0712	0.0978
258787_at	AT3G11840	U-box domain-containing protein	0.4233	0.1737	0.244	0.7595	0.0413	0.101	0.219	0.1104	0.1487	0.5552	0.0066	0.0253
258788_at	AT3G11780	MD-2-related lipid recognition domain-containing pr	0.2017	0.3819	0.3655	0.1917	0.4035	0.3428	0.5448	0.0043	0.0279	0.5349	0.0046	0.0213
258789_at	AT3G04605	transposable element gene	-0.04071	0.7787	0.5175	-0.01601	0.9116	0.5219	-0.236	0.0979	0.1392	-0.2113	0.1265	0.1392
258790_at	AT3G04610	FLK (FLOWERING LOCUS KH DOMAIN); nucleic a	0.2593	0.0805	0.1638	0.1396	0.2784	0.2801	-0.06516	0.5901	0.3948	-0.1848	0.1725	0.1687
258791_at	AT3G04720	PR4 (PATHOGENESIS-RELATED 4)	0.6723	0.3696	0.3593	0.8867	0.2536	0.2662	0.498	0.1387	0.1703	0.7125	0.0576	0.0864
258792_at	AT3G04640	glycine-rich protein	-0.4224	0.526	0.4316	-0.3212	0.6257	0.4332	0.6757	0.1099	0.1484	0.5766	0.0679	0.0951
258793_at	AT3G04780	Encodes a protein with little sequence identity with	0.1612	0.1807	0.2486	0.4903	0.0079	0.0496	0.736	0.0018	0.0206	1.0651	4.00E-04	0.0091
258794_at	AT3G04710	ankyrin repeat family protein	0.5312	0.0056	0.0521	0.1732	0.1515	0.1994	0.2084	0.1003	0.1413	-0.1497	0.2008	0.1856
258795_at	AT3G04570	DNA-binding protein-related	-0.4455	0.5014	0.4212	0.437	0.509	0.3883	0.3207	0.6233	0.4057	1.2032	0.117	0.1326
258796_at	AT3G04630	WDL1 (WVD2-LIKE 1)	-0.7909	0.1066	0.1888	-0.4508	0.3024	0.2926	0.0676	0.5708	0.3869	0.4076	0.0205	0.0463
258797_at	AT3G04730	IAA16 (indoleacetic acid-induced protein 16); transc	-0.5078	0.0045	0.0482	-0.2374	0.0541	0.1153	0.08218	0.4028	0.3177	0.3526	0.016	0.0403
258798_at	AT3G04540	Encodes a defensin-like (DEFL) family protein.	0.2768	0.8096	0.5266	-0.1001	0.9303	0.5267	-1.2792	0.2084	0.2169	-1.6562	0.1244	0.1379
258799_at	AT3G04770	RPSAB (40S RIBOSOMAL PROTEIN SA B); struct	0.6384	0.0436	0.1204	-0.0455	0.8457	0.5032	0.4705	0.0984	0.1397	-0.2135	0.3853	0.2781
258800_at	AT3G04550	similar to unknown protein [Arabidopsis thaliana] (T	0.3975	0.1757	0.2452	0.05299	0.8373	0.5008	-0.1546	0.5137	0.3645	-0.4991	0.0819	0.1066
258801_at	AT3G04560	similar to unnamed protein product [Vitis vinifera] (G	0.4985	0.0975	0.1803	0.5676	0.0702	0.1325	-0.5935	0.0623	0.1073	-0.5243	0.0861	0.1098
258802_at	AT3G04650	oxidoreductase	-0.2826	0.0821	0.1658	-0.4333	0.024	0.078	-0.3796	0.0362	0.0782	-0.5303	0.0123	0.0351
258803_at	AT3G04670	WRKY39 (WRKY DNA-binding protein 39); transcrip	0.7323	0.0442	0.1213	0.8189	0.0317	0.0884	-0.399	0.0361	0.0782	-0.3124	0.072	0.0984
258804_at	AT3G04760	pentatricopeptide (PPR) repeat-containing protein	0.3278	0.2518	0.2944	0.17	0.5258	0.3944	-0.1947	0.3812	0.3084	-0.3525	0.1497	0.1544
258805_at	AT3G04040	glycosyl hydrolase family 17 protein	-0.5788	0.1696	0.2411	-0.02734	0.9408	0.5293	0.245	0.3518	0.2942	0.7965	0.0267	0.0542
258806_at	AT3G04020	similar to unnamed protein product [Vitis vinifera] (G	0.4288	0.407	0.3799	0.2479	0.6193	0.4303	0.06752	0.8746	0.4852	-0.1114	0.7951	0.4275
258807_at	AT3G04030	myb family transcription factor	-0.8766	0.0184	0.0807	-0.6085	0.056	0.1176	-0.2669	0.307	0.272	0.001194	0.9961	0.4818
258808_at	AT3G04050	pyruvate kinase, putative	0.513	0.5528	0.4421	0.8576	0.3401	0.3135	-0.2784	0.7431	0.4459	0.06622	0.9374	0.4677
258809_at	AT3G04070	ANAC047 (Arabidopsis NAC domain containing pro	0.1311	0.1531	0.2268	1.6565	0.0376	0.1193	-0.00095	0.994	0.5163	0.5635	0.009	0.0296
258810_at	AT3G03970	binding	0.1644	0.4655	0.4054	0.2276	0.3269	0.3069	0.1433	0.5212	0.3675	0.2065	0.3685	0.2706
258811_at	AT3G03990	esterase/lipase/thioesterase family protein	-0.06553	0.3274	0.3387	-0.00459	0.9415	0.5295	0.1467	0.0455	0.0893	0.2076	0.0153	0.0395
258812_at	AT3G03960	ECT1; protein binding	0.7039	0.0164	0.0771	0.8199	0.0098	0.0538	-0.2148	0.2916	0.2644	-0.09882	0.6063	0.3655
258813_at	AT3G04060	ANAC046 (Arabidopsis NAC domain containing pro	1.7597	0.0645	0.1453	1.0177	0.2168	0.2439	-0.04548	0.9302	0.5007	-0.7874	0.1816	0.1743
258814_at	AT3G03980	short-chain dehydrogenase/reductase (SDR) family	-0.04504	0.7881	0.52	-0.02896	0.8624	0.5078	0.328	0.0699	0.1147	0.3441	0.0615	0.0899
258815_at	AT3G04000	short-chain dehydrogenase/reductase (SDR) family	-0.1942	0.3963	0.3734	-0.1204	0.6878	0.4187	0.2192	0.1718	0.1932	0.293	0.0904	0.1132
258816_at	AT3G03960	chaperonin, putative	0.4167	0.1253	0.2049	0.322	0.2095	0.2393	0.2789	0.0511	0.0957	0.1842	0.143	0.1501
258817_at	AT3G04750	pentatricopeptide (PPR) repeat-containing protein	0.1312	0.6265	0.4685	-0.1089	0.6848	0.4538	-0.6648	0.056	0.101	-0.9049	0.0222	0.0485
258818_at	AT3G04690	ESN4 (ETHYLENE INSENSITIVE 4); receptor	0.2516	0.6167	0.4652	0.2408	0.3437	0.315	-0.1259	0.5111	0.3636	-0.03364	0.8817	0.4519
258819_at	AT3G04590	DNA-binding family protein	-0.2009	0.4402	0.3938	-0.2249	0.3922	0.3378	0.2126	0.4018	0.3173	0.1886	0.4526	0.3071
258820_at	AT3G04600	tRNA synthetase class I (W and Y) family protein	0.4064	0.1478	0.2236	0.5142	0.0861	0.1479	-0.08263	0.7297	0.4417	0.02513	0.9157	0.4616
258821_at	AT3G07230	stress-responsive protein-related	0.2336	0.297	0.3214	0.2786	0.2262	0.2494	0.9519	0.0081	0.0362	0.9969	0.0069	0.0259
258822_s_at	AT3G07220;AT3G07260	[AT3G07220, transcriptional activator, putative];[AT	0.4816	0.0634	0.1442	0.8187	0.0123	0.0595	-0.6632	0.0247	0.0637	-0.3262	0.1593	0.1608
258823_at	AT3G07200	zinc finger (C3HC4-type RING finger) family protein	-0.1531	0.2794	0.311	-0.2007	0.1767	0.2174	0.1086	0.4069	0.3194	0.061	0.6303	0.3737
258824_at	AT3G07190	similar to unknown protein [Arabidopsis thaliana] (T	0.1403	0.5715	0.4495	-0.05	0.8371	0.5008	0

258890_at	AT3G05690	ATHAP2B;HAP2B;UNE8 (HEME ACTIVATOR PRO	0.5748	0.1127	0.1945	0.7796	0.0515	0.1126	0.2692	0.2945	0.2658	0.4741	0.1011	0.1214
258891_at	no_match	no_match	-0.094	0.7703	0.5147	0.1442	0.6567	0.4441	-0.9696	0.0257	0.6651	-0.7314	0.0592	0.0878
258892_at	AT3G05670	PHD finger family protein	-0.1181	0.4233	0.3867	-0.1703	0.2683	0.2745	-0.02444	0.8627	0.482	-0.0766	0.5943	0.3614
258893_at	AT3G05660	kinase1 protein binding	0.5087	0.3476	0.3487	-0.1402	0.784	0.4847	0.07586	0.8711	0.4844	-0.5731	0.2613	0.2185
258894_at	AT3G05650	disease resistance family protein	1.0643	0.0362	0.1097	0.8575	0.0688	0.1294	-0.8071	0.0164	0.0511	-1.0139	0.0075	0.027
258895_at	AT3G05600	epoxide hydrolase, putative	-0.4019	0.7423	0.5065	0.6246	0.613	0.4281	0.1394	0.8701	0.4841	1.1659	0.2189	0.1955
258896_at	AT3G05710	SYP43 (syntaxin 43); SNAP receptor	0.09715	0.6301	0.4698	-0.05968	0.7651	0.4789	-0.1737	0.3512	0.2939	-0.3305	0.1152	0.1314
258897_at	AT3G05730	Encodes a defensin-like (DEFL) family protein.	-2.375	4.00E-04	0.032	-1.7723	0.0012	0.0296	1.0525	0.008	0.0359	1.6552	0.0015	0.0138
258898_at	AT3G05740	RECQI1 (Arabidopsis RecQ helicase I1); ATP-depe	0.1532	0.8684	0.5434	0.9835	0.3204	0.3034	0.3705	0.6914	0.4282	1.2008	0.2387	0.2064
258899_at	AT3G05675	protein binding	-0.05737	0.852	0.5389	0.37	0.2688	0.2749	-0.4489	0.1946	0.2085	-0.02146	0.9442	0.4694
258900_at	AT3G05590	RPL18 (RIBOSOMAL PROTEIN L18); structural co	-0.2539	0.0971	0.1799	-0.5521	0.0094	0.0528	0.3318	0.0045	0.0287	0.03353	0.5921	0.3605
258901_at	AT3G05640	protein phosphatase 2C, putative / PP2C, putative	-0.6604	0.0885	0.1724	-0.194	0.5462	0.403	-0.7193	0.0249	0.064	-0.2529	0.2861	0.2314
258902_at	AT3G06483	PDK (PYRUVATE DEHYDROGENASE KINASE); A	0.3723	0.0252	0.0921	0.215	0.1145	0.1708	-0.02181	0.7962	0.4622	-0.1792	0.0859	0.1097
258903_at	AT3G06410	nuclear cap binding	0.1328	0.0856	0.1696	-0.07201	0.2855	0.2841	0.6987	3.00E-04	0.0136	0.4939	0.0011	0.0123
258904_at	AT3G06400	CHR11 (CHROMATIN-REMODELING PROTEIN 1	0.5155	0.0052	0.0514	0.4088	0.0118	0.0585	0.009582	0.9231	0.4987	-0.09717	0.356	0.2652
258905_at	AT3G06390	integral membrane family protein	-0.08813	0.8911	0.5486	-0.7414	0.2872	0.285	-0.4674	0.4824	0.3521	-1.1207	0.1373	0.1464
258906_at	AT3G06380	ATTLP9 (TUBBY-LIKE PROTEIN 9); phosphoric de	0.5542	0.0094	0.0624	0.6048	0.0069	0.047	-0.3741	0.0152	0.0492	-0.3235	0.0245	0.0515
258907_at	AT3G06370	NHX4 (sodium proton exchanger 4); sodium:hydrog	-1.1987	0.1527	0.2278	-1.1053	0.1793	0.2191	-0.7407	0.3354	0.2862	-0.6474	0.3931	0.2813
258908_at	AT3G06350	EMB3004/MEE32 (EMBRYO DEFECTIVE 3004); 3	0.332	0.0119	0.0679	-0.0861	0.3196	0.3029	-0.06988	0.2108	0.2183	-0.488	5.00E-04	0.0094
258909_at	AT3G06340	DNAJ heat shock N-terminal domain-containing pro	0.4288	0.0834	0.1671	0.3764	0.1142	0.1707	-0.249	0.0522	0.0969	-0.3014	0.0297	0.0578
258910_at	AT3G06480	DEAD box RNA helicase, putative	0.1154	0.4864	0.4141	0.0794	0.626	0.4333	-0.2705	0.147	0.1769	-0.3065	0.1116	0.1288
258911_at	AT3G06460	GNS1/SUR4 membrane family protein	0.3139	0.2995	0.3227	-0.00769	0.9781	0.5388	-0.05803	0.8293	0.4726	-0.3796	0.2068	0.1889
258912_at	AT3G06460	GNS1/SUR4 membrane family protein	0.05629	0.9283	0.5594	-0.2064	0.7431	0.4725	0.01438	0.9775	0.5119	-0.2483	0.6312	0.374
258913_at	AT3G06450	anion exchange family protein	1.3711	4.00E-04	0.032	1.3176	4.00E-04	0.0251	-0.4916	0.0051	0.0301	-0.5451	0.0035	0.0193
258914_at	AT3G06360	AQP27 (ARABINOGALACTAN PROTEIN 27)	1.0293	0.2827	0.3012	0.3208	0.7056	0.4608	0.7454	0.2183	0.2227	0.03688	0.9459	0.4698
258915_at	AT3G10640	VPS60.1	0.4048	0.1998	0.2621	0.5202	0.12	0.1752	0.7822	0.0022	0.0221	0.8976	0.0013	0.0133
258916_at	AT3G10670	ATNAP7 (Arabidopsis thaliana non-intrinsic ABC pr	-0.2634	0.1792	0.2475	-0.379	0.0794	0.1412	-0.2441	0.1696	0.1916	-0.3597	0.0693	0.0965
258917_at	AT3G10630	glycosyl transferase family 1 protein	-0.01843	0.9434	0.5632	0.1504	0.5707	0.4121	-0.5694	0.0797	0.1235	-0.4006	0.1756	0.1706
258918_at	AT3G10560	CYP77A7/UNE9 (CYTOCHROME P450, FAMILY 7	-1.0951	0.183	0.2503	-0.04464	0.9509	0.5321	-0.7105	0.3027	0.2699	0.34	0.602	0.3639
258919_at	AT3G10525	similar to SIM (SIAMESE) [Arabidopsis thaliana] (T	-0.2496	0.3745	0.3617	-0.3729	0.21	0.2396	0.7414	0.0024	0.0229	0.6181	0.0047	0.0217
258920_at	AHB2	AHB2 (NON-SYMBIOTIC HAEMOGLOBIN 2)	-0.9349	0.0436	0.1188	-0.9544	0.0401	0.0993	0.5357	0.0106	0.0409	0.5162	0.012	0.0345
258921_at	AT3G10500	ANAC053 (Arabidopsis NAC domain containing pro	1.5721	0.0017	0.0391	1.5026	0.002	0.033	0.2146	0.2295	0.2292	0.1451	0.3925	0.281
258922_at	AT3G10610	40S ribosomal protein S17 (RPS17C)	-0.5927	0.0406	0.1162	-0.4322	0.0953	0.1555	0.5014	0.0057	0.0316	0.662	0.0021	0.0154
258923_at	AT3G10450	SCPL7; serine carboxypeptidase	1.0557	0.0081	0.059	1.1306	0.0064	0.0457	-0.1031	0.6581	0.4173	-0.0282	0.9025	0.458
258924_at	AT3G10620	diadenosine 5',5''-P1,P4-tetraphosphate hydrolase,	-0.2125	0.0537	0.1331	-0.1332	0.1648	0.2089	0.5262	0.0026	0.0234	0.6054	0.0015	0.0138
258925_at	AT3G10420	sporulation protein-related	-0.4442	0.0063	0.0544	-0.914	4.00E-04	0.0251	0.1868	0.0759	0.12	-0.2829	0.0226	0.0489
258926_s_at	AT3G10490;AT3G10480	ANAC051/ANAC052 (Arabidopsis NA	-0.2005	0.3478	0.3488	0.01905	0.9244	0.5262	-0.7539	0.0116	0.0425	-0.5383	0.035	0.0633
258927_at	AT3G10160	ATDFC (A. THALIANA DHFS-FPGS HOMOLOG C	0.3478	0.047	0.1248	-0.8039	0.0138	0.0621	-0.4535	0.0167	0.0516	-0.7133	0.0034	0.019
258928_at	AT3G10070	initiation factor	0.417	0.1142	0.1958	0.04036	0.8549	0.5059	0.428	0.1075	0.1468	0.05142	0.8161	0.4332
258929_at	AT3G10060	immunophilin, putative / FKBP-type peptidyl-prolyl c	-0.9655	4.00E-04	0.032	-0.991	4.00E-04	0.0251	0.167	0.1397	0.1709	0.1414	0.1943	0.1816
258930_at	AT3G10040	transcription factor	-0.0556	0.7898	0.5205	0.3027	0.1958	0.23	-0.6986	0.0232	0.0616	-0.3403	0.1561	0.1589
258931_at	AT3G10010	DML2 (DEMETER-LIKE 2); 4 iron, 4 sulfur cluster b	0.9718	0.0359	0.1093	1.0935	0.0249	0.0791	-0.6411	0.1095	0.148	-0.5194	0.1718	0.1683
258932_at	AT3G10150	calmodulin-related protein, putative	-0.7407	0.1384	0.216	-1.0943	0.0525	0.1136	-0.01244	0.967	0.5093	-0.396	0.2643	0.2199
258933_at	AT3G09980	similar to unknown protein [Arabidopsis thaliana] (T	-0.5712	0.1435	0.2203	-0.159	0.6398	0.4382	0.418	0.2143	0.2204	0.8302	0.0429	0.0723
258934_at	AT3G10140	RECA3 (RECA HOMOLOG 3); DNA binding / DNA-	0.1201	0.5138	0.4267	0.4851	0.0445	0.1046	-0.4945	0.0421	0.0855	-0.1295	0.4834	0.3191
258935_at	AT3G10120	similar to unknown protein [Arabidopsis thaliana] (T	-0.5678	0.2451	0.2906	-0.2353	0.6028	0.4246	0.8173	0.0525	0.0972	1.1498	0.0185	0.0436
258936_s_at	AT3G10100	transposable element gene	0.4172	0.6526	0.4769	-1.2128	0.2308	0.2521	-0.1949	0.8193	0.4696	-1.8249	0.0845	0.1086
258937_at	AT3G10090	40S ribosomal protein S28 (RPS28A)	0.01946	0.9045	0.5525	0.01964	0.9036	0.5198	0.6001	0.0015	0.0199	0.6002	0.0015	0.0138
258938_at	AT3G10080	germin-like protein, putative	-0.0274	0.8925	0.5492	0.1606	0.4403	0.3623	0.8052	0.0134	0.046	0.9932	0.0064	0.0249
258939_at	AT3G10020	similar to Os12g0147200 [Oryza sativa (japonica cu	0.4164	0.1614	0.2346	1.3375	0.0053	0.043	0.3212	0.1726	0.1936	1.2422	0.003	0.0179
258940_at	AT3G09930	GDSL-motif lipase/hydrolase family protein	0.953	0.4386	0.393	1.383	0.2804	0.2811	0.06512	0.9513	0.5058	0.4951	0.6472	0.3797
258941_at	AT3G09940	ATMDAR3/MDAR6 (MONODEHYDROASCORBAT	1.8907	0.0066	0.0549	1.6639	0.0104	0.0552	0.03102	0.8916	0.4901	-0.1957	0.4114	0.2888
258942_at	AT3G09960	calcineurin-like phosphoesterase family protein	1.1423	0.0359	0.1094	0.4333	0.3037	0.2934	0.6188	0.1026	0.143	-0.09028	0.7737	0.4211
258943_at	AT3G10400	RNA recognition motif (RRM)-containing protein	-0.226	0.3841	0.3667	0.553	0.0753	0.1376	0.217	0.4016	0.3173	0.996	0.0126	0.0355
258944_at	AT3G10390	FLD (FLOWERING LOCUS D); amine oxidase	0.4851	0.271	0.306	0.01742	0.9656	0.5355	-0.2047	0.5858	0.3929	-0.6723	0.1238	0.1375
258945_at	AT3G10660	CPK2 (CALMODULIN-DOMAIN PROTEIN KINASE	-0.2114	0.7659	0.5133	-1.9266	0.0439	0.1037	-0.04854	0.9452	0.5045	-1.7638	0.0565	0.0853
258946_at	AT3G10650	similar to nucleoporin-related [Arabidopsis thaliana]	0.2896	0.1662	0.2384	0.3212	0.134	0.1861	-0.2053	0.105	0.1449	-0.1737	0.1521	0.1562
258947_at	AT3G10830	calmodulin-related protein, putative	-0.7501	0.1054	0.1875	0.984	0.0521	0.1132	0.7918	0.0249	0.0639	1.0256	0.0105	0.0321
258948_at	AT3G01910	SOX (SULFITE OXIDASE); sulfite oxidase	0.1065	0.3065	0.3264	-0.00536	0.9558	0.5332	0.2153	0.0196	0.0562	0.1034	0.1442	0.1511
258949_at	AT3G01370	ATCFM2/CFM2 (CRM FAMILY MEMBER 2)	0.1541	0.2361	0.2852	-0.226	0.1107	0.1679	-0.09909	0.4211	0.3258	-0.4792	0.0123	0.0351
258950_at	AT3G01460	MBD9 (METHYL-CPG-BINDING DOMAIN 9); DNA	-0.07586	0.6807	0.4863	-0.7491	0.0119	0.0587	0.004084	0.9821	0.5133	-0.6691	0.0174	0.0422
258951_at	AT3G01380	phosphatidylinositolglycan class N (PIG-N) family p	0.3324	0.1698	0.2412	-0.07975	0.7088	0.4616	-0.6461	0.0314	0.072	-1.0583	0.006	0.024
258952_at	AT3G01410	RNase H domain-containing protein	0.238	0.5705	0.4492	0.1257	0.7608	0.478	0.966	0.0664	0.1115	0.8537	0.0912	0.1138
258953_at	AT3G01430	similar to NHL repeat-containing protein [Arabidops	0.2287	0.2806	0.3116	0.5166	0.048	0.1088	-0.5596	0.038	0.0806	-0.2717	0.2128	0.1923
258954_at	AT3G01400	armadillo/beta-catenin repeat family protein	0.1873	0.1464	0.2225	0.5196	0.0075	0.0488	0.6037	0.0022	0.0219	0.936	4.00E-04	0.0089
258955_s_at	AT3G18530;AT3G01450	[AT3G18530, binding];[AT3G01450, binding]	-0.153	0.5101	0.4249	0.3556	0.1686	0.2116	-0.7302	0.0261	0.0658	-0.2216	0.3546	0.2647
258956_at	AT3G01440	oxygen evolving enhancer 3 (PsbQ) family protein	-1.3008	0.0062	0.0542	-1.354	0.0054	0.0432	0.3369	0.0161	0.0506	0.2838	0.028	0.0558
258957_at	AT3G01420	ALPHA-DOX1 (ALPHA-DIOXYGENASE 1)	0.6193	0.3272	0.3385	0.7835	0.231	0.2522	-0.2992	0.2614	0.2473	-0.1349	0.5874	0.3588
258958_at	AT3G01390	VMA10 (VACUOLAR MEMBRANE ATPASE 10)	0.05716	0.6339	0.4709	0.3012	0.0534	0.1146	0.4936	0.0113	0.0421	0.7376	0.0027	0.017
258959_at	AT3G01600	CAT7 (CATIONIC AMINO ACID TRANSPORTER 7	-0.1768	0.7091	0.4959	-0.844	0.1283	0.1818	0.8081	0.141	0.172	0.1409	0.7655	0.4185
258960_at	AT3G01590	myb family transcription factor	1.0073	0.179	0.2473	2.0195	0.031	0.0875	-0.2146	0.7462	0.4469	0.7975	0.2671	0.2212
258961_at	AT3G01580	myb family transcription factor	0.9777	0.3017	0.324	-0.2676	0.7619	0.4781	0.4354	0.4783	0.3508	-0.8099	0.2198	0.196
258962_at	AT3G01670	CYP77A6 (cytochrome P450, family 77, subfamily A	-1.0463	0.1162	0.1971	-0.1685	0.7635	0.4784	-1.6107	0.0134	0.046	-0.7329	0.1265	0.1392
258963_at	AT3G01550	inositol or phosphatidylinositol phosphatase/ phospl	-0.1109	0.5903	0.4563	-0.3697	0.1232	0.1782	-0.396	0.0756	0.1197	-0.6547	0.0169	0.0416
258964_at	AT3G01540	3-phosphoinositide-dependent protein kinase, putat	-0.4651	0.0788	0.1617	-0.1691	0.4416	0.3602	-0.4492	0.0525	0.0972	-0.1532	0.4046	0.286
258965_at	AT3G01530	transducin family protein / WD-40 repeat family prot	0.7502	0.0298	0.1004	0.1738	0.4868	0.379	0.01292	0.943	0.504	-0.5635	0.0295	0.0576
258966_at	AT3G01690	DNA gyrase subunit A family protein	0.2943	0.1392	0.2166	0.4031	0.0651	0.1275	-0.541	0.0276	0.0676	-0.4322	0.0538	0.0828
258967_at	AT3G01470	zinc finger (C2H2 type) family protein	-0.7433	0.1667	0.2388	-0.2089	0.66	0.4451	-0.4005	0.4146	0.3229	0.134	0.7761	0.4218
258968_at	AT3G01460	self-incompatibility protein-related	2.3594	0.0289	0.0949	1.8148	0.0584	0.1201	-0.08998	0.9027	0.4931	-0.6346	0.4103	0.2883
258969_at	AT3G01680	heat shock protein-related	-0.1989	0.7555	0.5104	0.07783	0.9025	0.5195	0.9118	0.201	0.2123	1.1885	0.1171	0.1327
258970_at	AT3G01410	SCPL49 (serine carboxypeptidase-like 49); serine c	0.613	0.0661	0.1474	0.6879	0.048	0.1087	0.0493	0.7496	0.4481	0.1243	0.4374	0.3002
258971_at	AT3G01990	ACR6 (ACT Domain Repeat 6)	-0.8189	0.5214	0.4296	-1.9551	0.1691	0.2119	0.05994	0.9615	0.5081	-1.0763	0.4085	0.2876
258972_at	AT3G01920	yrdC family protein	-0.8225	0.0247	0.0914	-0.9069	0.018	0.0694	-0.4994	0.1003	0.1413	-0.5838	0.0675	0.0948
258973_at	AT3G01900	CYP94B2 (cytochrome P450, family 94, subfamily B	-0.6613	0.5037	0.422	-1.1706	0.2637	0.2719	-0.5879	0.5055	0.3615	-1.0971	0.2444	0.2095
258974_at	AT3G01890	SWIB complex BAF60b domain-containing protein	-0.4184	0.2775	0.3101	-0.7441	0.0893	0.1506	-0.2941	0.4273	0.3286	-0.6198	0.1364	0.1458
258975_at	AT3G01970	WRKY45 (WRKY DNA-binding protein 45); transcri	1.0264	0.2645	0.3021	1.1419	0.2226	0.2474	-0.06614	0.8823	0.4874	0.04933	0.912	0.4605
258976_at	AT3G01980	short-chain dehydrogenase/reductase (SDR) family	0.09485	0.5329	0.4341	0.241	0.1583	0.2047	0.1988	0.1928	0.2072	0.3449	0.0533	0.0825
258977_s_at	AT3G02020;AT5G14060	[AT3G02020, aspartate kinase, lysine-sensitive, put	-0.4534	0.0505	0.1293	-0.5696	0.0255	0.0799	-0.5473	0.0062	0.0327	-0.6634	0.0031	0.018
258978_at	AT3G09320	zinc finger (DHHC type) family protein	0.2405	0.1236	0.2038	0.05304	0.6901	0.4557	-0.7962	0.003	0.0248	-0.9837	0.0014	0.0133
258979_at	AT3G09440	heat shock cognate 70 kDa protein 3 (HSC70-3) (H	0.7554	0.1761	0.2455	0.1409	0.7748	0.4821	0.1577	0.5107	0.3635	-0.4568	0.105	0.124
258980_at	AT3G09800	RGP3 (REVERSIBLY GLYCOSYLATED POLYPEP	-0.1143	0.9128	0.5548	-0.3593	0.7327	0.469	-1.0943	0.3271	0.2819	-1.3393	0.2439	0.2092
258981_at	AT3G08880	similar to unknown protein [Arabidopsis thaliana] (T	-0.05768	0.9058	0.5527	0.02505	0.959	0.534	-0.5405	0.3032	0.2701	-0.4578	0.374	0.273
258982_at	AT3G08870	lectin protein kinase, putative	0.9095	0.0411	0.1168	0.6455	0.1026	0.1617	0.2295	0.2688	0.2515	-0.0345	0.8565	0.4448
258983_at	AT3G08860	alanine--glyoxylate aminotransferase, putative / bet	-0.173	0.7438	0.507	-0.4984	0.37	0.3275	-0.331	0.1689	0.191	-0.6564	0.0292	0.0572
258984_at	AT3G08970	DNAJ heat shock N-terminal domain-containing pro	1.215	0.1016	0.1843	2.235	0.0176	0.0687	-0.1368	0.8233	0.4706	0.8832	0.1986	0.184
258985_at	AT3G08960	protein transporter	-0.4155	0.0125	0.0691	0.3977	0.0144	0.0635	-1.8384	0	0.0092	-1.0252	4.00E-04	0.0091
258986_at	AT3G08910	DNAJ heat shock protein, putative	-0.2769	0.2832	0.3135	-0.6864	0.0373	0.0955	0.1841	0.343	0.2898	-0.2253	0.2588	0.2173
258987_at	AT3G08950	electron transport SCO1/SenC family protein	0.1747	0.3464	0.3481	0.1826	0.3277	0.3073	-0.2775	0.1656	0.1888	-0.2697	0.1752	0.1703
258988_at	AT3G08890	similar to unknown protein [Arabidopsis thaliana] (T	-0.466	0.009	0.0612	-0.4213	0.0127	0.0602	0.3915	0.0052	0.0302	0.4362	0.0035	0.0193
258989_at	AT3G08920	rhodanese-like domain-containing protein	-0.5083	0.0053	0.0517	-0.5915	0.003	0.0358	0.06899	0.4013	0.3172	0.01415	0.8568	0.4449
258990_at	AT3G08840	D-alanine--D-alanine ligase family	-0.06583	0.8191	0.5293	-0.3016	0.3258	0.3064	-1.0134	9.00E-04	0.0169	-1.2491	4.00E-04	0.0089
258991_at	AT3G08820	pentatricopeptide (PPR) repeat-containing protein	-0.2753	0.8236	0.5306	0.8164	0.5193	0.3921	-2.1386	0.1268	0.1615	-1.0469	0.3997	0.2841
258992_at	AT3G08930	similar to LMBR1 integral membrane family protein	0.01222	0.931	0.5601	-0.06436	0.6527	0.4426	-0.2424	0.0931	0.1352	-0.319	0.0446	0.0741
258993_at	AT3G08940	LHCB4.2 (LIGHT HARVESTING COMPLEX PSII);	-0.4306	0.0158	0.076	-0.619	0.0044	0.041	-0.06902	0.5542	0.3805	-0.2574	0.0739	0.0999
258994_at	AT3G08850	ATRAPTOR18/RAPTOR18 (RAPTOR1); nucleotide	0.08215	0.6031	0.4605	0.1888	0.2649	0.2726	-0.6074	0.0141	0.0473	-0.5007	0.0264	0.0538
258995_at	AT3G01790	ribosomal protein L13 family protein	0.2739	0.0131	0.0706	0.1186	0.1391	0.1899	0.2058	0.0136	0.0465	0.05055	0.3598	0.2669
258996_at	AT3G01800	ribosome recycling factor family protein / ribosome	0.04836	0.9001	0.5511	0.1815	0.6422	0.4389	-0.02109	0.8764	0.4857	0.112	0.4282	0.296
258997_at	AT3G01810	similar to nucleolar protein gar2-related [Arabidopsi	-0.4558	0.0029	0.0433	-0.744	4.00E-04	0.0251	-0.01087	0.8667	0.4832	-0.2991	0.0079	0.0277
258998_at	AT3G01820	adenylate kinase family protein	0.3758	0.323	0.336	0.2446	0.504	0.3863	-0.83	0.0435	0.087	-0.2096	0.5024	0.3267
258999_at	AT3G01850	ribulose-phosphate 3-epimerase, cytosolic, putative	0.6315	0.0567	0.1364	0.3711	0.1937	0.2284	-0.7515	0.0342	0.0756	-1.0119	0.0131	0.0363
259000_at	AT3G01860	similar to unknown protein [Arabidopsis thaliana] (T	0.2811	0.1624	0.2357	0.1801	0.3349	0.3107	1.0819	0.0028	0.0241	0.9808	0.004	0.0202
259001_at	unknown protein	unknown protein	-1.1758	0.0074	0.0577	-1.0276	0.0118	0.0585	0.8546	0.0088	0.0376	1.0028	0.005	0.0221
259002_at	AT3G02000	ROXY1; thiol-disulfide exchange intermediate	-1.0054	0.4132	0.3816	0.6152	0.6064	0.4257	0.01501	0.9898	0.5152	1.6356	0.2119	0.1918
259003_at	AT3G02010	pentatricopeptide (PPR) repeat-containing protein	1.6642	0.265	0.3022	0.003258	0.9981	0.5435	-1.0408	0.336	0.2864	-0.2767	0.0475	0.0768
259004_at	AT3G01840	protein kinase family protein	1.4527	0.1787	0.2472	1.0647	0.2986	0.2909	0.5949	0.5208	0.3673	0.2069	0.8188	0.4338
259005_at	AT3G01930	nodulin family protein	-0.03253	0.8485	0.5379	0.08953	0.605	0.4251	-0.08504	0.5466	0.378	0.03703	0.7888	0.4254
259006_at	AT3G09200	60S acidic ribosomal protein P0 (RPP0B)	0.4094	0.019	0.0819	0.08802	0.4593	0.3676	-0.3754	0.0051	0.03	-0.6868	5.00E-04	0.0095
259007_at	AT3G09370	MYB3R-3 (myb domain protein 3R-3); DNA binding;	-0.1843	0.4298	0.389	-0.00316	0.9887	0.5413	-0.2451	0.3081	0.2725	-0.06397	0.7759	0.4217
259008_at	AT3G09390	MT2A (METALLOTHIONEIN 2A)	0.1654	0.4223	0.3861	0.5569	0.0396	0.0986	0.3322	2.00E-04	0.0126	0.7238	0	0.0043
259009_at	AT3G09260	PYK10 (phosphate starvation-response 3.1); hydrol	0.5829	0.0012	0.036	0.2783	0.0022	0.0334	0.4062	0.1359	0.1683	0.00147	0.9949	0.4814
259010_at	AT3G07340	basic helix-loop-helix (bHLH) family protein	-0.6679	0.1684	0.2402	-0.7387	0.1368	0.1883	-0.07341	0.573	0.3878	-0.1441	0.2951	0.2361
259011_s_at	AT3G07380;AT3G60990;A	[AT3G07380, similar to unknown protein [Arabidops	-1.3783	0.2748	0.3085	0.8573	0.4756	0.3744	-0.5283	0.6533	0.4157	1.7073	0.1924	0.1805
259012_at	AT3G07360	armadillo/beta-catenin repeat family protein / U-box	-0.8935	0.1734	0.2438	-0.3171	0.4267	0.3537	-0.3956	0.0491	0.0934	-0.1191	0.4474	0.305
259013_at	AT3G07430	EMB1990 (EMBRYO DEFECTIVE 1990)	0.00039	0.9969	0.5763	-0.2211	0.0774	0.1394	0.1862	0.1173	0.1541	-0.03524	0.7255	0.4058
259014_at	AT3G07320	glycosyl hydrolase family 17 protein	-1.0912	0.0847	0.1685	-0.4849	0.3682	0.3267	0.07561	0.8649	0.4827	0.682	0.1771	0.1714
259015_at	AT3G07350	similar to unknown protein [Arabidopsis thaliana] (T	0.2403	0.6169	0.4652	0.347	0.4778	0.3754	0.1145	0.6249	0.4063	0.2213	0.3646	0.2689
259016_at	AT3G07480	electron carrier/ non-sulfur cluster binding	0.07239	0.4283	0.3884	0.09783	0.2998	0.2913	0.4284	7.00E-04	0.016	0.4538	6.00E-04	0.0101
259017_at	AT3G07310	similar to unknown protein [Arabidopsis thaliana] (T	-0.2869	0.1611	0.2343	-0.3986	0.0755	0.1378	0.01787	0.8098	0.4665	-0.09384	0.2485	0.2116
259018_at	AT3G07390	AIR12 (Auxin-Induced in Root cultures 12); extracel	-0.6183	0.0482	0.1265	-0.6126	0.0495	0.1103	0.6369	0.034	0.0754	0.6426	0.0331	0.0814
259019_at	AT3G07370	ATCHIP/CHIP (CARBOXYL TERMINUS OF HSC70	0.1406	0.3557	0.3525	0.117	0.4341	0.3571	0.02635	0.8208	0.47	0.002786	0.9808	0.4783
259020_at	AT3G07470	similar to unknown protein [Arabidopsis thaliana] (T	-0.5009	0.1921	0.2569	-0.2482	0.4807	0.3765	-0.4485	0.1077	0.1469	-0.1958	0.4181	0.2918
259021_at	AT3G07540	formin homology 2 domain-containing protein / FH2	1.1657	0.0019	0.0391	0.7028	0.0117	0.0583	0.2462	0.1984	0.2109	-0.2168	0.2466	0.2105
259022_at	AT3G07420

259090_at	AT3G04920	40S ribosomal protein S24 (RPS24A)	-0.1119	0.2921	0.3186	0.2893	0.035	0.0924	-0.3265	3.00E-04	0.0136	0.07463	0.0523	0.0814
259091_at	AT3G04890	similar to unknown protein [Arabidopsis thaliana] (T	-0.08529	0.6984	0.4921	0.2426	0.3018	0.2923	0.0137	0.9286	0.5002	-0.1436	0.3742	0.2731
259092_at	AT3G04870	ZDS (ZETA-CAROTENE DESATURASE); carotene	-0.2234	0.008	0.0587	-0.5241	3.00E-04	0.0249	-0.1179	0.0606	0.1057	-0.4186	8.00E-04	0.0109
259093_at	AT3G04860	similar to unknown protein [Arabidopsis thaliana] (T	-0.1587	0.3084	0.3277	-0.3241	0.076	0.138	-0.2564	0.1267	0.1615	-0.4217	0.034	0.0624
259094_at	AT3G04940	ATCYSD1 (Arabidopsis thaliana cysteine synthase	-0.03577	0.8181	0.5291	0.01697	0.9129	0.5221	0.02535	0.8703	0.4841	0.04414	0.777	0.422
259095_at	AT3G05020	ACP1 (ACYL CARRIER PROTEIN 1)	-0.4028	0.1061	0.1884	-0.1376	0.5167	0.3913	0.8565	3.00E-04	0.0141	1.1217	1.00E-04	0.0062
259096_at	AT3G04840	40S ribosomal protein S3A (RPS3aA)	-0.0023	0.9859	0.5734	-0.05391	0.6807	0.4522	0.357	0.0427	0.086	0.3054	0.0661	0.0936
259097_at	AT3G05430	binding	0.06952	0.5026	0.4216	0.1649	0.1558	0.2026	0.3814	0.0035	0.0261	0.4768	0.0015	0.0138
259098_at	AT3G04790	ribose 5-phosphate isomerase-related	-0.8133	0.0015	0.038	-1.1579	4.00E-04	0.0251	0.4904	9.00E-04	0.0173	0.1459	0.0602	0.0887
259099_at	AT3G05010	transmembrane protein, putative	-0.01982	0.8941	0.5498	0.3915	0.0488	0.1096	-0.2143	0.1343	0.167	0.1971	0.1599	0.1612
259100_at	AT3G04880	DRT102 (DNA-DAMAGE-REPAIR/TOLERATION 2	0.6643	0.0174	0.079	0.6724	0.0167	0.0671	-0.2907	0.1622	0.1868	-0.2826	0.1715	0.1681
259101_at	AT3G11640	unknown protein	-0.3542	0.7589	0.5114	1.0429	0.388	0.3359	-0.7901	0.5041	0.3609	0.607	0.6033	0.3644
259102_at	AT3G11660	NHL1 (NDR1/HIN1-like 1)	-0.06918	0.7159	0.498	-0.2498	0.2311	0.2522	0.5503	0.0033	0.0255	0.3697	0.0135	0.0368
259103_at	AT3G11690	similar to unknown protein [Arabidopsis thaliana] (T	-0.9425	6.00E-04	0.0332	-0.8258	0.001	0.0293	-0.2096	0.0964	0.138	-0.09285	0.3919	0.2807
259104_at	AT3G02170	LNG2 (LONGIFOLIA2)	0.3148	0.1517	0.2271	0.3779	0.101	0.1604	0.01224	0.9119	0.4957	0.07532	0.5085	0.3291
259105_at	AT3G05500	elongation factor (REF) family protein	0.7372	0.0256	0.0927	0.6175	0.0438	0.1037	0.6715	0.0085	0.037	0.5518	0.0166	0.0411
259106_at	AT3G05490	RALF-LIKE 22 (RALF-LIKE 22)	-1.2898	0.062	0.143	-0.856	0.1634	0.2082	0.4722	0.0432	0.0867	0.906	0.005	0.0221
259107_at	AT3G05460	sporozoite surface protein-related	-0.07657	0.9445	0.5635	0.4098	0.7117	0.4627	1.1451	0.3296	0.2831	1.6315	0.1893	0.1789
259108_at	AT3G05540	translationally controlled tumor family protein	-1.2987	0.0998	0.1823	0.7309	0.2961	0.2897	-0.5775	0.3964	0.3149	1.452	0.0755	0.1012
259109_at	AT3G05480	serine/threonine protein phosphatase, putative	-0.416	0.1866	0.2531	-0.3745	0.225	0.2485	-0.3631	0.1614	0.1864	-0.3216	0.2033	0.187
259110_at	AT3G05570	similar to unknown protein [Arabidopsis thaliana] (T	0.3331	0.2018	0.2632	0.4187	0.1276	0.1812	0.2881	0.1366	0.1687	0.3737	0.0734	0.0995
259111_at	AT3G05620	F-actin capping protein alpha subunit family protein	-0.2129	0.3186	0.3336	-0.178	0.3961	0.3391	0.3174	0.165	0.1885	0.3522	0.1328	0.1435
259112_at	AT3G05560	60S ribosomal protein L22-2 (RPL22B)	-0.1008	0.617	0.4652	-0.05862	0.7686	0.4801	0.2672	0.0703	0.1152	0.3094	0.0469	0.0762
259113_at	AT3G05510	phospholipid/glycerol acyltransferase family protein	-0.04945	0.7133	0.4972	0.3431	0.052	0.1132	-0.2663	0.0958	0.1375	0.1263	0.3616	0.2677
259114_at	AT3G05530	RPT5A (regulatory particle triple-A 5A); ATPase/ ca	0.4708	0.0048	0.0497	0.2942	0.024	0.078	-0.2379	0.0458	0.0896	-0.4145	0.0076	0.027
259115_at	AT3G01360	similar to unknown protein [Arabidopsis thaliana] (T	0.3058	0.0656	0.1468	0.4808	0.0167	0.0672	-0.09397	0.3619	0.2991	0.08102	0.4254	0.2947
259116_at	AT3G01350	proton-dependent oligopeptide transport (POT) fam	-0.4014	0.247	0.2917	-0.6578	0.0906	0.1518	0.1578	0.35	0.2933	-0.09867	0.5446	0.3427
259117_at	AT3G01320	similar to paired amphipathic helix repeat-containing	0.3817	0.0433	0.1199	0.2791	0.0596	0.1591	-0.9589	0.0018	0.0206	-1.0614	0.0013	0.013
259118_at	AT3G01310	acid phosphatase/ oxidoreductase/ transition metal	1.2096	0.0491	0.1274	1.0738	0.0682	0.1309	-1.1068	0.0017	0.0206	-1.2427	0.0011	0.0126
259119_at	AT3G01340	protein transport protein SEC13 family protein / WD	0.2157	0.0978	0.1805	0.4699	0.0094	0.053	-0.2719	0.0534	0.0982	-0.01768	0.8685	0.4479
259120_at	AT3G01240	similar to unknown protein [Arabidopsis thaliana] (T	0.789	0.4898	0.4157	0.6928	0.541	0.401	0.1699	0.7615	0.4516	0.07376	0.8947	0.4556
259121_at	AT3G02220	similar to hypothetical protein [Cleome spinosa] (GE	0.1596	0.5099	0.4249	0.3148	0.2273	0.2498	0.3549	0.0313	0.0719	0.5101	0.0095	0.0303
259122_at	AT3G02210	COBL1 (COBRA-LIKE PROTEIN 1 PRECURSOR)	0.7921	0.2638	0.3018	0.3273	0.6199	0.4305	-0.3368	0.6101	0.4013	-0.8016	0.259	0.2173
259123_at	AT3G02200	proteasome family protein	0.6099	0.0459	0.1983	0.3983	0.1332	0.1854	-0.9515	0.0016	0.0204	-1.1591	8.00E-04	0.0108
259124_at	AT3G02310	SEP2 (SEPALLATA2); DNA binding / transcription f	1.0117	0.1517	0.2271	0.9342	0.1778	0.2182	0.8647	0.0378	0.0804	0.7871	0.0497	0.079
259125_at	AT3G02300	regulator of chromosome condensation (RCC1) fam	-0.3942	0.1151	0.1963	-0.05393	0.7972	0.4887	-1.5998	0.0012	0.0188	-1.2594	0.003	0.0179
259126_at	AT3G02280	fibrodoin family protein	0.205	0.2869	0.3154	0.04855	0.787	0.4848	-0.4333	0.0604	0.1056	-0.5895	0.0242	0.0511
259127_at	AT3G02270	eIF4-gamma/eIF5/eIF2-epsilon domain-containing	-1.7987	0.2368	0.2856	-0.5779	0.6782	0.4512	0.3779	0.7585	0.4508	1.5987	0.2361	0.205
259128_at	AT3G02260	BIG (DARK OVER-EXPRESSION OF CAB 1); bind	0.6051	0.0245	0.0909	0.5414	0.0345	0.0918	-1.4109	0	0.0092	-1.4746	0	0.0053
259129_at	AT3G02150	PTF1 (PLASTID TRANSCRIPTION FACTOR 1); tra	0.06245	0.825	0.531	0.09276	0.7435	0.4726	0.07139	0.7573	0.4505	0.1017	0.6618	0.3948
259130_at	AT3G02190	60S ribosomal protein L39 (RPL39B)	1.0568	0.0091	0.0617	0.8762	0.0173	0.0681	1.4618	0.0028	0.0243	1.2813	0.0046	0.0214
259131_at	AT3G02180	SP1L3 (SPIRAL 1-LIKE3)	-0.3858	0.1007	0.1834	-0.1736	0.3931	0.3383	1.1167	4.00E-04	0.0147	1.329	2.00E-04	0.0078
259132_at	AT3G02250	similar to unknown protein [Arabidopsis thaliana] (T	-0.8743	0.0238	0.0899	-0.8881	0.0226	0.076	-0.3791	0.1172	0.1541	-0.3929	0.1079	0.1261
259133_at	AT3G05400	sugar transporter, putative	-1.2225	0.0644	0.1453	-0.7299	0.2049	0.236	-0.5825	0.2939	0.2655	-0.08993	0.8612	0.4462
259134_at	AT3G05390	similar to unknown protein [Arabidopsis thaliana] (T	-0.0555	0.932	0.5603	-0.8647	0.2299	0.2514	0.3509	0.5964	0.3969	-0.4583	0.4949	0.3239
259135_at	AT3G05480	cell cycle checkpoint control protein family	0.1988	0.8038	0.5251	-0.6929	0.3473	0.3446	0.03955	0.9604	0.5078	-0.4545	0.5767	0.3548
259136_at	AT3G05470	formin homology 2 domain-containing protein / FH2	-0.3189	0.3488	0.3492	-0.5086	0.1661	0.2099	0.02042	0.9491	0.5053	-0.1693	0.6036	0.3645
259137_at	AT3G10300	calcium-binding EF hand family protein	0.7211	0.0979	0.1806	0.6986	0.1055	0.1641	0.3324	0.1118	0.1497	0.3099	0.1309	0.1422
259138_s_at	AT3G04130,AT3G10270	[ATSDH4130, DNA topoisomerase, ATP-hydrolyzing	-0.1311	0.3695	0.3593	-0.2579	0.1177	0.1735	-0.5361	0.0102	0.04	-0.663	0.0048	0.0218
259139_at	AT3G10240	F-box protein-related	-2.1921	0.0306	0.1016	-0.8231	0.2861	0.2844	-0.04026	0.9549	0.5066	1.3287	0.1181	0.1334
259140_at	AT3G10230	LYC (LYCOPENE CYCLASE); lycopene beta cyclas	-0.4122	0.0377	0.112	-0.4025	0.0404	0.0997	-0.8102	0.0017	0.0205	-0.8005	0.0018	0.0147
259141_at	AT3G10220	tubulin folding cofactor B	0.2867	0.3221	0.3355	0.4003	0.1902	0.2265	-0.7177	0.0348	0.0765	-0.6041	0.0574	0.0862
259142_at	AT3G10200	dehydration-responsive protein-related	-1.2663	0.2419	0.2887	-0.00685	0.9944	0.5428	-1.2422	0.2266	0.2275	0.01732	0.9851	0.4791
259143_at	AT3G10190	calmodulin, putative	1.9319	0.0013	0.0369	1.8678	0.0015	0.0313	0.3238	0.1544	0.1819	0.2597	0.2324	0.2029
259144_at	AT3G10180	kinesin motor protein-related	1.968	0.0162	0.077	0.5582	0.3207	0.3035	-0.04893	0.9262	0.4996	-1.4584	0.0416	0.0708
259145_at	AT3G10180	kinesin motor protein-related	2.2353	0.0205	0.0842	1.8346	0.0379	0.0964	-0.4017	0.5151	0.3651	-0.8024	0.2274	0.2001
259146_at	AT3G10370	glycerol-3-phosphate dehydrogenase, putative	-0.09587	0.4592	0.4025	-0.1476	0.2762	0.2789	0.2669	0.085	0.1284	0.2152	0.1402	0.1483
259147_at	no_match	no_match	0.1444	0.3341	0.3424	-0.0745	0.6015	0.4241	-0.08668	0.5085	0.3628	-0.3056	0.0629	0.0911
259148_at	AT3G10350	anion-transporting ATPase family protein	-0.08446	0.34	0.3453	-0.3044	0.0175	0.0686	0.1055	0.2477	0.2397	-0.1144	0.2166	0.1945
259149_at	AT3G10340	phenylalanine ammonia-lyase, putative	-0.4177	0.2097	0.268	-0.06129	0.8373	0.5008	-0.4066	0.2197	0.2234	-0.05027	0.8661	0.4472
259150_at	AT3G10320	similar to unknown protein [Arabidopsis thaliana] (T	1.4401	0.1965	0.2602	2.0663	0.0905	0.1517	-0.3334	0.2883	0.2627	0.2928	0.343	0.2593
259151_at	AT3G10310	kinesin motor protein-related	-1.0899	0.8299	0.5325	-0.07259	0.8615	0.5076	0.01979	0.9547	0.5066	0.03668	0.9162	0.4617
259152_at	AT3G10210	similar to Rho-GTPase-activating protein-related (A	0.5996	0.0064	0.0547	0.313	0.0528	0.1139	0.2826	0.0697	0.1146	-0.00398	0.974	0.4766
259153_at	AT3G10250	similar to unknown protein [Arabidopsis thaliana] (T	0.5844	0.0439	0.1208	0.4066	0.1134	0.1702	0.4511	0.0257	0.0651	0.2734	0.1037	0.1232
259154_at	AT3G10260	reticulon family protein	-0.05801	0.8419	0.5362	0.1784	0.5486	0.4042	0.1421	0.4037	0.3181	0.3785	0.0679	0.0951
259155_at	AT3G10330	initiation factor IIB-2 / general transcription factor TF	0.1942	0.248	0.2924	0.09999	0.5249	0.3941	0.4269	0.0411	0.0842	0.3327	0.0816	0.1063
259156_at	AT3G10380	SEC8 (secretion 8)	0.7521	8.00E-04	0.0346	0.3606	0.0125	0.06	-0.5482	0.0028	0.0243	-0.9396	4.00E-04	0.0088
259157_at	AT3G05440	C2 domain-containing protein	-0.2892	0.8193	0.5294	0.9296	0.4768	0.375	-1.5705	0.2559	0.2442	-0.3517	0.7815	0.4233
259158_at	AT3G05430	PWWP domain-containing protein	-0.8094	0.0797	0.1628	-0.7142	0.1083	0.1658	-0.01834	0.947	0.5049	0.07688	0.7815	0.4233
259159_at	AT3G05420	ACBP4 (ACYL-COA BINDING PROTEIN 4); acyl-C	0.1058	0.4235	0.3868	0.01939	0.8782	0.5126	0.3102	0.0592	0.1044	0.2239	0.1324	0.1433
259160_at	AT3G05410	similar to hypothetical protein Osl_004967 [Oryza s	-0.1997	0.3558	0.3525	-0.4019	0.1038	0.1627	-0.5955	0.0211	0.0584	-0.7976	0.0078	0.0276
259161_at	AT3G01500	CA1 (CARBONIC ANHYDRASE 1); carbonate dehy	-0.8135	0.0085	0.0601	-1.0445	0.0034	0.0374	-0.02092	0.746	0.4468	-0.2519	0.0139	0.0375
259162_at	AT3G01640	GHMP kinase family protein	0.3646	0.3725	0.3607	0.1706	0.6632	0.446	0.1886	0.4745	0.3495	-0.00542	0.983	0.4787
259163_at	AT3G01490	protein kinase, putative	0.1248	0.604	0.4608	0.4592	0.1074	0.1653	0.07844	0.5267	0.3698	0.4128	0.0219	0.0482
259164_at	AT3G01770	ATBET10 (ARABIDOPSIS THALIANA BROMODOM	0.7817	0.0159	0.0762	0.7213	0.0207	0.0735	-1.0705	0.0053	0.0306	-1.1309	0.0044	0.0209
259165_at	AT3G01472,AT3G01470	AT3G01472 CPuORF33 (Conserved peptide upst	0.2159	0.364	0.3562	0.2044	0.3875	0.3356	0.2804	0.0044	0.0283	0.2689	0.0051	0.0224
259166_at	AT3G01670	similar to unknown protein [Arabidopsis thaliana] (T	-0.742	0.0585	0.1386	-0.4623	0.1773	0.2179	0.03379	0.8452	0.4771	0.3134	0.1254	0.1385
259167_at	AT3G01570	glycine-rich protein / oleosin	-0.5692	0.7284	0.502	1.1982	0.4768	0.375	-1.1372	0.3304	0.2835	0.6302	0.5728	0.3535
259168_at	AT3G03570	similar to signal transducer [Arabidopsis thaliana] (T	0.5986	0.014	0.0723	0.4013	0.0489	0.1097	0.0743	0.5234	0.3683	-0.123	0.3119	0.2443
259169_at	AT3G03520	phosphoesterase family protein	0.7381	0.0361	0.1097	0.7439	0.0353	0.0927	-0.08914	0.6968	0.4301	-0.08342	0.715	0.4025
259170_at	AT3G03510	phototropic-responsive NPH3 family protein	0.3407	0.7848	0.5192	-0.8868	0.4895	0.3802	1.559	0.2524	0.2422	0.3315	0.7904	0.4259
259171_at	AT3G03590	SWIB complex BAF60b domain-containing protein	-0.2205	0.4089	0.3795	0.2902	0.2919	0.2876	0.7	0.0238	0.0625	1.2107	0.0036	0.0194
259172_at	AT3G03630	CS26 (cysteine synthase 26); cysteine synthase	0.07385	0.7366	0.5047	0.121	0.5863	0.4185	-0.07127	0.7454	0.4466	-0.0241	0.912	0.4605
259173_at	AT3G03640	GLUC (Beta-glucosidase homolog); hydrolase, hydr	3.2081	2.00E-04	0.0312	2.9132	3.00E-04	0.0249	0.3595	0.1333	0.1662	0.0646	0.7525	0.4145
259174_at	AT3G03690	UNE7 (unfertilized embryo sac 7); acetylglucosamin	-0.2042	0.0384	-0.1662	0.0685	0.1313	0.1009	0.1659	0.1891	0.1388	0.0804	0.0804	0.1054
259175_at	AT3G01560	proline-rich family protein	0.5939	0.0036	0.0452	0.1332	0.2404	0.258	0.1003	0.2489	0.2404	-0.3604	0.0084	0.0285
259176_at	AT3G01610	CDC48C (EMBRYO DEFECTIVE 1354); ATPase	0.08044	0.7008	0.4929	0.4144	0.1004	0.1598	-0.4879	0.0664	0.1115	-0.1539	0.4737	0.3152
259177_at	AT3G01630	similar to NF24 (NUCLEAR FUSION DEFECTIVE 4	-1.8161	0.178	0.2467	0.1786	0.8803	0.5133	-2.4971	0.0883	0.1312	-0.5024	0.6751	0.389
259178_at	AT3G01650	RGLG1 (RING DOMAIN LIGASE1); protein binding	0.1153	0.514	0.4268	-0.3975	0.6693	0.132	0.2802	0.1533	0.1811	-0.2326	0.2178	0.195
259179_at	AT3G01660	methyltransferase	-0.1015	0.5944	0.4577	0.04044	0.8293	0.4986	0.1843	0.1746	0.1951	0.3263	0.0433	0.0727
259180_at	AT3G01680	similar to unknown protein [Arabidopsis thaliana] (T	-0.6545	0.0145	0.0731	-0.6684	0.0135	0.0617	0.1212	0.4205	0.3256	0.1073	0.4718	0.3144
259181_at	AT3G01690	similar to unknown protein [Arabidopsis thaliana] (T	0.2489	0.3134	0.3305	0.01141	0.9604	0.5343	-0.3879	0.0164	0.0511	-0.6254	0.003	0.0179
259182_at	AT3G01750	ankyrin repeat family protein	-0.00961	0.9614	0.5677	-0.01735	0.9305	0.5267	0.2982	0.1856	0.2026	0.2905	0.1949	0.1819
259183_at	AT3G01580	pentatricopeptide (PPR) repeat-containing protein	-0.2058	0.8562	0.5402	0.8552	0.4672	0.3709	0.4546	0.6807	0.4245	1.5155	0.2138	0.1928
259184_at	AT3G01520	universal stress protein (USP) family protein	0.1912	0.068	0.1498	0.2822	0.0215	0.0746	-0.3945	0.0069	0.0338	-0.3035	0.0169	0.0416
259185_at	AT3G01550	triose phosphate/phosphate translocator, putative	-1.4571	0.012	0.0681	-2.378	0.0021	0.0331	0.6455	0.0725	0.1171	-0.2754	0.3597	0.2669
259186_at	AT3G01590	adobe 1-epimerase family protein	0.1274	0.4856	0.414	0.5256	0.034	0.0911	-0.8186	6.00E-04	0.0158	-0.4204	0.0071	0.0264
259187_at	AT3G01530	AtMYB57 (myb domain protein 57); DNA binding / tr	0.08373	0.9447	0.5635	0.06416	0.9576	0.5336	1.0863	0.3925	0.3131	1.0668	0.4003	0.2843
259188_at	AT3G01510	5'-AMP-activated protein kinase beta-1 subunit-rela	-0.6143	0.12	0.2004	-0.4556	0.2176	0.2443	-0.9567	0.0288	0.0689	-0.798	0.0494	0.0787
259189_at	AT3G01700	AGP11 (ARABINOGALACTAN PROTEIN 11)	-1.0798	0.3081	0.3275	1.7929	0.1248	0.1791	-1.9345	0.0439	0.0875	0.9383	0.2317	0.2024
259190_at	AT3G01780	TPLATE; binding	0.7235	0.0066	0.0551	0.4458	0.0333	0.0903	-0.05143	0.2024	0.2132	-0.3291	6.00E-04	0.0103
259191_at	AT3G01720	similar to unknown protein [Arabidopsis thaliana] (T	0.5795	0.0187	0.0813	0.4574	0.0393	0.0982	0.1189	0.3934	0.3135	-0.00323	0.9806	0.4782
259192_at	AT3G01740	similar to unknown protein [Arabidopsis thaliana] (T	0.2183	0.1224	0.2027	0.2852	0.0631	0.1251	0.576	0.0067	0.0336	0.6429	0.0045	0.0213
259193_at	AT3G01480	CYP38 (CYCLOPHILIN 38); peptidyl-prolyl cis-trans	-0.626	0.0151	0.0743	-1.1143	0.0019	0.033	0.2753	0.0768	0.121	-0.2131	0.1405	0.1485
259194_at	AT3G01540	DRH1 (DEAD box RNA helicase 1)	0.4511	0.0998	0.1823	0.2918	0.2397	0.2575	-1.0572	0.0064	0.033	-1.2164	0.0039	0.0201
259195_at	AT3G01730	unknown protein	0.8491	0.5393	0.4366	0.2031	0.8804	0.5133	0.4972	0.7132	0.4359	-0.1487	0.9117	0.4604
259196_at	AT3G03600	RPS2 (RIBOSOMAL PROTEIN S2); structural cons	0.1184	0.5066	0.4236	-0.1134	0.5238	0.3936	0.4701	0.0102	0.0401	0.2383	0.0811	0.1059
259197_at	AT3G03670	peroxidase, putative	-0.6032	0.5426	0.438	-0.9718	0.3445	0.3154	-0.03695	0.9695	0.5098	-0.4056	0.678	0.3899
259198_at	AT3G03610	phagocytosis and cell motility protein ELMO1-relate	0.9416	7.00E-04	0.0334	0.9238	8.00E-04	0.0277	0.2501	0.0678	0.1128	0.2323	0.0821	0.1067
259199_at	AT3G08980	signal peptidase I family protein	-0.989	0.0194	0.0823	-0.9221	0.0243	0.0783	-0.3393	0.2486	0.2402	-0.2724	0.3396	0.2579
259200_at	AT3G09070	glycine-rich protein	1.9364	0.0546	0.1341	2.4624	0.0267	0.0817	-0.1407	0.8545	0.4796	0.3853	0.6207	0.3705
259201_at	AT3G09080	transducin family protein / WD-40 repeat family prot	-0.1134	0.8238	0.5307	-0.8884	0.136	0.1877	0.1245	0.575	0.3884	-0.6506	0.0333	0.0617
259202_at	AT3G09100	mRNA capping enzyme family protein	0.1533	0.6065	0.462	0.4149	0.2055	0.2364	-0.8288	0.0106	0.0409	-0.5673	0.0363	0.0648
259203_at	AT3G09130	similar to unknown protein [Arabidopsis thaliana] (T	0.5514	0.6073	0.4622	-0.1276	0.9037	0.5198	-0.2138	0.8396	0.4755	-0.8929	0.4182	0.2918
259204_s_at	AT3G09170,AT1G34610	[AT3G09170] transposable element gene];[AT1G34	0.1799	0.3247	0.337	-0.485	0.6408	0.4384	0.9668	0.0985	0.1397	-0.5981	0.2551	0.2152
259205_at	AT3G09030	potassium channel tetramerisation domain-containe	0.5353	0.0222	0.0874	0.7321	0.0077	0.0489	-0.3936	0.0559	0.1009	-0.1969	0.2529	0.214
259206_at	AT3G09040	pentatricopeptide (PPR) repeat-containing protein	1.2147	0.1184	0.1989	-0.5069	0.4545	0.3659	-0.5131	0.4462	0.3367	-2.2387	0.0217	0.0479
259207_at	AT3G09050	similar to unknown [Populus trichocarpa x Populus	-0.4169	0.0517	0.1306	-0.1303	0.4394	0.3594	-0.04296	0.7914	0.4606	0.2437	0.184	0.1758
259208_at	AT3G09060	pentatricopeptide (PPR) repeat-containing protein	-2.4936	0.0633	0.1442	-0.8848	0.4167	0.349	-2.3354	0.0753	0.1195	-0.7266	0.4987	0.3254
259209_at	AT3G09160	RNA recognition motif (RRM)-containing protein	-1.2453	0.0461	0.1235	-0.5879	0.2488	0.2631	-1.4517	0.019	0.0553	-0.7943	0.1055	0.1243
259210_at	AT3G09150	HY2 (ELONGATED HYPOCOTYL 2); phytochromo	-0.1118	0.3498	0.3496	0.03293	0.771	0.4807	-0.6667	0.0027	0.0237	-0.522	0.0065	0.0251
259211_at	AT3G09020	alpha 1,4-glycosyltransferase family protein / glyco	0.8239	0.2884	0.3164	1.1617	0.1597	0.2057	0.06073	0.6437	0.4123	0.3985	0.0306	0.0588
259212_at	AT3G09010	similar to unnamed protein product [Vitis vinifera] (G	0.3894	0.0212	0.0855	0.3985	0.0197	0.072	-0.02986	0.7918	0.4606	-0.02077	0.854	0.4439
259213_at	AT3G09010	protein kinase family protein	0.529	0.0656	0.1468	0.2709	0.267	0.2737	0.0829	0.615	0.4026	-0.1752	0.3138	0.2454
259214_at	AT3G09085	similar to unnamed protein product [Vitis vinifera] (G	0.677	0.0333	0.1057	0.9477	0.0112	0.0566	0.339	0.1857	0.2027	0.6097	0.0455	0.0748
259215_at	AT3G09120	DEX1 (DEFECTIVE IN EXINE FORMATION 1)	0.3772	0.0184	0.0807	0.1542	0.227	-0.09682	0.381	0.3083	-0.3195	0.0312	0.0595	
259216_at	AT3G09000	proline-rich family protein	0.3016	0.1378	0.2157	0.2521	0.1968	0.2308	0.1579	0.379	0.3073	0.1083	0.535	0.3398
259217_at	AT3G03620	MATE efflux family protein	-0.7888	0.4678	0.4063	0.6642	0.5373	0.3994	-0.4913	0.6443	0.4124	0.9627	0.3839	0.2776
259218_at	AT3G03580	pentatricopeptide (PPR) repeat-containing protein	0.822	0.1203	0.2006	0.1095	0.8267	0.4979	-0.00571	0.9909	0.5154	-0.8182	0.1555	0.1585
259219_at	AT3G03560	similar to unknown protein [Arabidopsis thaliana] (T	0.6441	0.0169	0.0778	0.607	0.0205	0.073	-0.5539	0.0106	0.0409	-0.591	0.0085	0.0287
259220_at	AT3G03550	zinc finger (C3HC4-type RING finger) family protein	0.0799	0.6001	0.4597	-0.00713	0.962	0.5345	0.3389	0.0178	0.0534	0.2519	0.0447	0.0742
259221_s_at	AT3G03530,AT3G03540	[AT3G03530, NPC4 (NONSPECIFIC PHOSPHOLIP	-1.4197	0.2472	0.2919	0.6348	0.5776	0.415	-1.6112	0.1746	0.1952	0.4433	0.6737	0.3886
259222_at	AT3G03680	C2 domain-containing protein	-0.4431	0.055	0.1346	-0.5961	0.0225	0.0758	-1.0109	0.0036	0.0265	-1.164	0.0021	0.0156
259223_at	AT3G03660	DNA binding / transcription factor

259290_at	AT3G11520	CYCB1;3 (CYCLIN B1;3); cyclin-dependent protein	0.05123	0.7902	0.5206	0.08944	0.6492	0.4414	-0.2381	0.2479	0.2399	-0.2009	0.3178	0.2473
259291_at	AT3G11550	integral membrane family protein	-0.5572	0.438	0.3929	0.4768	0.5024	0.3857	-0.6326	0.3643	0.3002	0.4014	0.5518	0.3457
259292_at	AT3G11560	similar to unknown protein [Arabidopsis thaliana] (T	-0.00522	0.9699	0.5698	-0.1182	0.4144	0.348	-0.6083	0.003	0.0248	-0.7212	0.0016	0.014
259293_at	AT3G11580	DNA-binding protein, putative	1.8662	0.0018	0.0391	1.5131	0.0038	0.039	0.3064	0.1077	0.1469	-0.04671	0.7686	0.4194
259294_at	no_match	no_match	-0.4488	0.6632	0.4804	0.5237	0.613	0.4281	0.2821	0.7827	0.4582	1.2546	0.2597	0.2176
259295_at	no_match	no_match	-0.4456	0.1175	0.1983	-0.5842	0.0595	0.1212	-1.0732	0.0087	0.0374	-1.2118	0.0057	0.0234
259296_at	AT3G05350	aminopeptidase	-0.3581	0.0984	0.181	-0.5606	0.0283	0.0836	-0.1793	0.1286	0.163	-0.3818	0.0152	0.0393
259297_at	AT3G05360	disease resistance family protein / LRR family protei	0.5047	0.0631	0.144	0.9812	0.0077	0.0489	0.04008	0.8492	0.4784	0.5166	0.0592	0.0878
259298_at	AT3G05370	disease resistance family protein	-0.3073	0.2662	0.3029	-0.1645	0.5274	0.3951	-1.3011	0.0054	0.0309	-1.1583	0.0082	0.0282
259299_at	AT3G05080	unknown protein	0.2011	0.7782	0.5174	0.8959	0.2507	0.2644	0.3268	0.65	0.4145	1.0216	0.2006	0.1855
259300_at	AT3G05100	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.04735	0.8666	0.5426	-0.1166	0.6819	0.4527	-0.4356	0.1748	0.1953	-0.5995	0.0859	0.1097
259301_at	AT3G05110	similar to unknown protein [Arabidopsis thaliana] (T	-0.3663	0.611	0.463	-0.2322	0.7445	0.4729	1.5377	0.0818	0.1254	1.6718	0.0657	0.0933
259302_at	AT3G05120	ATGID1A/GID1A (GA INSENSITIVE DWARF1A); h	0.4809	0.1368	0.2148	1.2541	0.0084	0.0507	-0.7894	0.0106	0.0409	-0.0163	0.9301	0.4657
259303_at	AT3G05130	similar to unknown protein [Arabidopsis thaliana] (T	0.8448	0.3167	0.3325	0.4479	0.577	0.4148	0.4445	0.4997	0.3596	0.04766	0.9405	0.4686
259304_at	AT3G05210	ERCC1 (UV REPAIR DEFICIENT 7)	0.4491	0.0411	0.1168	0.3611	0.0753	0.1377	-0.173	0.0668	0.1118	-0.261	0.0196	0.0449
259305_at	AT3G05070	similar to unnamed protein product [Vitis vinifera] (G	0.1123	0.3982	0.3745	0.2856	0.0742	0.1366	0.5164	0.0122	0.0439	0.6896	0.0044	0.021
259306_at	AT3G05060	mitochondrial substrate carrier family protein	0.2151	0.0799	0.1629	0.2715	0.0421	0.102	-0.3543	0.0073	0.0343	-0.2978	0.0132	0.0365
259307_at	AT3G05230	signal peptidase subunit family protein	0.5526	0.0223	0.0875	0.8298	0.0056	0.0434	0.5913	0.0179	0.0536	0.8685	0.0047	0.0217
259308_at	AT3G05180	GDSL-motif lipase/hydrolase family protein	-1.3815	6.00E-04	0.0332	-1.4344	5.00E-04	0.0263	-0.1049	0.5002	0.3597	-0.1578	0.3278	0.2523
259309_at	AT3G05090	protein kinase family protein	0.1485	0.3501	0.3497	0.338	0.0739	0.1365	-0.08098	0.5953	0.3966	0.1084	0.4833	0.319
259310_s_at	AT3G05160;AT3G05165	[AT3G05160; sugar transporter, putative];[AT3G05	-0.3688	0.0626	0.1436	-0.5433	0.0196	0.0719	-0.5264	0.002	0.0211	-0.701	7.00E-04	0.0105
259311_at	AT3G05960	SAR DNA-binding protein, putative	0.3344	0.1462	0.2222	0.198	0.3465	0.3162	-0.2988	0.1	0.141	-0.4352	0.0361	0.0646
259312_at	AT3G05200	ATL6 (Arabidopsis T?xicos en Levadura 6); protein	0.6712	0.0933	0.1771	0.6601	0.0972	0.1572	0.6964	7.00E-04	0.016	0.6853	8.00E-04	0.0109
259313_at	AT3G05090	transducin family protein / WD-40 repeat family prot	0.7659	0.003	0.0435	0.6814	0.0045	0.0415	-0.3731	0.0115	0.0424	-0.4576	0.0056	0.0234
259314_at	AT3G05260	short-chain dehydrogenase/reductase (SDR) family	-0.3868	0.6235	0.4676	-1.9622	0.0544	0.1158	2.5193	0.0258	0.0653	0.9439	0.2647	0.2202
259315_at	AT3G01200	similar to phosphoprotein phosphatase/ protein kina	0.348	0.0116	0.0672	0.3282	0.0141	0.0629	0.215	0.0167	0.0516	0.1952	0.023	0.0494
259316_at	AT3G01175	similar to structural constituent of ribosome [Arabid	0.1809	0.5628	0.4459	0.3171	0.3313	0.3091	-0.8716	0.0386	0.0811	-0.7354	0.0625	0.0908
259317_at	no_match	no_match	0.7908	0.303	0.3248	0.2441	0.7339	0.4695	-0.9005	0.1754	0.1956	-1.4473	0.0574	0.0862
259318_at	AT3G01100	HYP1 (HYPOTHETICAL PROTEIN 1)	0.44	0.0098	0.0633	-0.1029	0.3395	0.3132	0.09876	0.3569	0.2965	-0.4441	0.0095	0.0303
259319_at	**AT3G01090**	**AKIN10 (ARABIDOPSIS SNF1 KINASE HOMOLO**	**0.4879**	**0.0187**	**0.0813**	**0.112**	**0.4294**	**0.355**	**-0.08983**	**0.5064**	**0.3619**	**-0.4658**	**0.0194**	**0.0447**
259320_at	AT3G01980	WRKY58 (WRKY DNA-binding protein 58); transcri	1.4791	0.3164	0.3323	2.0503	0.1875	0.2251	0.09289	0.9462	0.5047	0.6641	0.6345	0.3753
259321_at	AT3G01040	GAUT13 (Galacturonosyltransferase 13); polygalac	-0.1616	0.3628	0.3558	0.2257	0.2251	0.2485	-0.9148	0.044	0.0283	-0.5274	0.0286	0.0565
259322_at	AT3G05270	similar to myosin heavy chain-related [Arabidopsis t	0.2831	0.3569	0.353	0.339	0.2808	0.2813	-0.2748	0.243	0.2368	-0.2189	0.3368	0.2564
259323_at	AT3G05280	integral membrane Yip1 family protein	0.5007	0.0062	0.0542	0.4403	0.0097	0.0537	0.07693	0.4648	0.3562	0.01614	0.8731	0.4494
259324_at	AT3G05310	GTP-binding protein-related	0.6698	0.49	0.4159	0.4633	0.6272	0.4334	1.092	0.2835	0.2599	0.8855	0.3723	0.2723
259325_at	AT3G05320	similar to unnamed protein product [Vitis vinifera] (G	-0.6139	0.2486	0.2928	-0.7511	0.1741	0.2155	0.1999	0.5089	0.363	0.06274	0.8313	0.4375
259326_at	AT3G16480	MPPA2 (MPA, mitochondrial processing peptidase a	0.1145	0.3123	0.3299	0.05655	0.6361	0.4369	-0.4873	0.0011	0.0181	-0.5511	7.00E-04	0.0105
259327_at	AT3G16460	jacalin lectin family protein	1.1616	0.0063	0.0543	1.3779	0.0034	0.0373	-0.203	0.2577	0.2451	0.01325	0.9355	0.4672
259328_at	AT3G16440	ATMLP-300B (MYROSINASE-BINDING PROTEIN-	0.4781	0.6447	0.4747	-0.7878	0.458	0.3673	-1.2642	0.2583	0.2455	-2.5301	0.0579	0.0866
259329_at	AT3G16360	AHP4 (HPT PHOSPHOTRANSMITTER 4); histidine	0.6283	0.0576	0.1375	1.7324	0.0484	0.1092	0.8076	0.2264	0.2267	0.9118	0.1813	0.1742
259330_at	AT3G16270	binding	0.1801	0.273	0.3073	0.2164	0.2019	0.2339	-0.3763	0.0569	0.1018	-0.34	0.1046	0.1005
259331_at	AT3G03840	auxin-responsive protein, putative	-1.1517	0.0048	0.0496	-0.8715	0.0127	0.0602	0.2071	0.3651	0.3005	0.4874	0.0742	0.1001
259332_at	AT3G03830	auxin-responsive protein, putative	-0.3901	0.2653	0.3023	-0.4103	0.2451	0.2611	0.7017	0.0482	0.0922	0.6815	0.0523	0.0815
259333_at	AT3G03810	EDA30 (embryo sac development arrest 30)	0.2759	0.263	0.3015	0.02093	0.9261	0.5256	-0.3854	0.1432	0.174	-0.6404	0.0391	0.0681
259334_at	AT3G03790	ankyrin repeat family protein / regulator of chromos	-0.2826	0.2115	0.2693	-0.425	0.0891	0.1504	-0.5131	0.0307	0.0714	-0.6555	0.0139	0.0375
259335_s_at	AT3G03930;AT3G03940	[AT3G03930; protein kinase-related];[AT3G03940,	0.4735	0.0079	0.0585	0.4836	0.0074	0.0484	-0.1773	0.1391	0.1705	-0.1672	0.1571	0.1594
259336_at	AT3G03750	SET domain-containing protein	0.2649	0.2617	0.3006	0.4686	0.0821	0.1437	-0.1157	0.5989	0.3977	0.08791	0.6872	0.3929
259337_at	AT3G03720	CAT4 (CATIONIC AMINO ACID TRANSPORTER 4	0.5474	0.0064	0.0547	0.3783	0.0226	0.076	-0.1253	0.2982	0.2678	-0.2944	0.0485	0.0778
259338_at	AT3G03800	SYP131 (syntaxin 131); SNAP receptor	0.1549	-0.1729	0.1549	0.2297	-0.114	0.8614	0.5076	-0.859	0.2145	0.2205	0.09989	0.8722
259339_at	AT3G03900	adenylylsulfate kinase, putative	-0.6398	0.0277	0.0966	-0.6265	0.0296	0.0855	0.2118	0.3256	0.2811	0.2251	0.3	0.2386
259340_at	AT3G03870	similar to unknown protein [Arabidopsis thaliana] (T	-0.282	0.2594	0.2993	0.2671	0.2815	0.2818	0.2796	0.1032	0.1435	0.8287	0.0034	0.0189
259341_at	AT3G03740	SYP121 (SYNTAXIN 121); ABA and MATH DOMAIN 4;	0.1987	0.089	0.1729	0.2558	0.0451	0.1052	-0.04104	0.6683	0.4207	0.01606	0.8653	0.4471
259342_at	AT3G03890	FMN binding	0.2165	0.0473	0.1252	0.1608	0.1035	0.1624	0.1519	0.0479	0.0919	0.09616	0.149	0.154
259343_s_at	AT5G17920;AT3G03780	[AT5G17920; ATCIMS (COBALAMIN-INDEPENDE	-0.5258	0.0444	0.1214	-0.6563	0.0225	0.0758	-0.5285	0.0149	0.0486	-0.659	0.0069	0.0259
259344_at	AT3G03710	RIF10 (RESISTANT TO INHIBITION WITH FSM 10	0.112	0.7446	0.5073	-0.2317	0.5102	0.3887	0.5632	0.0868	0.1299	-0.9069	0.0222	0.0484
259345_s_at	AT3G03700;AT3G04440	[AT3G03700, similar to unknown protein [Arabidopsis	1.4443	0.1246	0.2044	0.6291	0.4461	0.3622	0.3061	0.7023	0.432	-0.5091	0.5319	0.3387
259346_at	AT3G03910	glutamate dehydrogenase, putative	-1.6496	0.0021	0.0406	-1.6124	0.0023	0.0335	-0.0746	0.7648	0.4527	-0.03743	0.8801	0.4514
259347_at	AT3G03920	Sar1 RNA-binding region family protein	0.4208	0.0074	0.0576	0.5874	0.0022	0.0333	-0.342	0.0151	0.0489	-0.1754	0.1044	0.1237
259348_at	AT3G03770	leucine-rich repeat transmembrane protein kinase, p	-0.5792	0.0208	0.0849	-0.9328	0.004	0.0394	-0.09933	0.5599	0.3826	-0.4529	0.0443	0.0738
259349_at	AT3G03860	ATAPRL5 (APR-LIKE 5)	0.3036	0.0493	0.1276	0.06473	0.5839	0.4177	0.3193	0.0426	0.086	0.08041	0.5009	0.3263
259350_at	AT3G03850	RBK2 (ROP BINDING PROTEIN KINASES 2); kina	-1.0692	0.3135	0.3305	1.1322	0.2895	0.2863	-0.9389	0.3689	0.3023	1.2624	0.2453	0.2098
259351_at	AT3G05150	sugar transporter family protein	-0.5738	0.5732	0.4501	-0.3289	0.7431	0.4725	0.6268	0.3399	0.3752	0.8718	0.4046	0.286
259352_at	AT3G05170	phosphoglycerate/bisphosphoglycerate mutase fam	-0.03216	0.8778	0.5459	0.3454	0.1531	0.2004	-0.00615	0.9765	0.5117	0.3714	0.1313	0.1424
259353_at	AT3G05190	aminotransferase class IV family protein	-1.1522	0.0451	0.1224	-1.3693	0.0268	0.0818	0.1435	0.7382	0.4443	-0.07363	0.8246	0.4467
259354_at	AT3G05220	heavy-metal-associated domain-containing protein	-0.07362	0.7448	0.5074	-0.3109	0.2148	0.2426	0.573	0.0533	0.0981	0.3357	0.1869	0.1775
259355_at	AT3G05240	pentaticopeptide (PPR) repeat-containing protein	-0.8641	0.13	0.2085	0.185	0.7047	0.4606	-0.6055	0.2535	0.2429	0.4436	0.3843	0.2777
259356_at	AT3G05250	zinc finger (C3HC4-type RING finger) family protein	0.5309	0.1381	0.2159	0.6111	0.1003	0.1597	-0.5979	0.0018	0.0206	-0.5177	0.0031	0.0182
259357_at	AT1G13380	similar to unknown protein [Arabidopsis thaliana] (T	0.1467	0.3916	0.3709	-0.1599	0.3548	0.3203	-0.4253	0.0407	0.0836	-0.7318	0.0068	0.0257
259358_at	AT1G13250	GATL3 (Galacturonosyltransferase-like 3); polygala	-0.9578	0.0029	0.0434	-0.9299	0.0032	0.037	0.2619	0.0802	0.1239	0.2898	0.0614	0.0898
259359_at	AT1G13460	serine/threonine protein phosphatase 2A (PP2A) re	0.259	0.3668	0.3578	0.8154	0.0329	0.0898	-0.3342	0.2598	0.2463	0.2223	0.4322	0.2977
259360_at	AT1G13310	similar to unnamed protein product [Vitis vinifera] (G	-0.1605	0.8301	0.5325	1.7713	0.0648	0.1272	-0.967	0.2398	0.235	0.9648	0.2406	0.2075
259361_at	AT1G13440	GAPC-2; glyceraldehyde-3-phosphate dehydrogena	-0.05642	0.6513	0.4766	-0.2604	0.0876	0.149	-0.05661	0.5743	0.3883	-0.2606	0.0482	0.0776
259362_s_at	AT1G13350;AT3G53640	[AT1G13350; protein kinase family protein];[AT3G5	-0.3189	0.3119	0.3297	0.1348	0.6505	0.4419	-1.4568	5.00E-04	0.0155	-1.0031	0.0022	0.0157
259363_at	AT1G13270	MAP1C (METHIONINE AMINOPEPTIDASE 1B); m	0.526	0.1709	0.2421	0.5555	0.1532	0.2004	-0.1055	0.571	0.3869	-0.07602	0.6801	0.3905
259364_at	AT1G13260	RAV1 (Related to ABI3/VP1 1); DNA binding / trans	-0.1977	0.6668	0.4815	0.3729	0.431	0.3557	-0.02448	0.8817	0.4872	0.5462	0.0241	0.0509
259365_at	AT1G13300	myb family transcription factor	1.0217	0.3964	0.3735	0.07227	0.9497	0.5319	0.816	0.4907	0.3559	-0.1335	0.9073	0.4592
259366_at	AT1G13280	AOC4 (ALLENE OXIDE CYCLASE 4)	0.2337	0.1998	0.2621	0.1506	0.379	0.3314	0.4858	0.0333	0.0745	0.4027	0.0574	0.0862
259367_at	AT1G69070	binding	0.4017	0.1103	0.1924	0.1945	0.378	0.331	-0.5046	0.0236	0.0623	-0.7117	0.0074	0.0268
259368_at	AT1G69100	sepsin A	1.6019	0.2142	0.271	1.4155	0.2623	0.2711	-0.08417	0.9419	0.5038	-0.2706	0.8155	0.433
259369_s_at	AT3G43890;AT1G69150	[AT3G43890, DC1 domain-containing protein];[AT1	-1.8278	0.0634	0.1443	-0.7993	0.3276	0.3073	-1.8077	0.0107	0.0411	-0.7792	0.1236	0.1374
259370_at	AT1G69050	unknown protein	1.0044	0.2731	0.3073	1.2005	0.2038	0.2353	-0.8974	0.32	0.2783	-0.7014	0.4254	0.2947
259371_at	AT1G69080	universal stress protein (USP) family protein	-0.7058	0.3943	0.3723	-1.1322	0.2009	0.2331	0.945	0.1116	0.1496	0.5187	0.3267	0.2517
259372_at	AT1G69120	AP1 (APETALA1); DNA binding / transcription facto	0.05124	0.9641	0.5682	-0.0144	0.9899	0.5416	0.5883	0.2991	0.2682	0.5226	0.3492	0.2622
259373_at	AT1G69160	unknown protein	-1.1765	0.0164	0.0771	-1.2825	0.0122	0.0593	0.2164	0.2709	0.2528	0.1104	0.5505	0.3453
259374_at	AT1G69280	DNA binding / transcription factor	-0.9258	0.0796	0.1626	0.2872	0.5085	0.388	-0.4967	0.2781	0.257	0.7163	0.1448	0.1514
259375_at	AT3G16370	GDSL-motif lipase/hydrolase family protein	-0.7282	0.0167	0.0775	-0.9558	0.0065	0.046	0.6207	0.004	0.0274	0.3931	0.0197	0.045
259376_at	AT3G16320	binding	-0.2755	0.4565	0.4011	-0.547	0.1773	0.2179	0.06682	0.5328	0.3724	-0.2047	0.105	0.124
259377_at	AT3G16380	initiation factor	0.1635	0.6415	0.4735	-0.177	0.6151	0.4288	0.1821	0.6054	0.3999	-0.1584	0.6517	0.3814
259378_at	AT3G16310	mitotic phosphoprotein N' end (MPPN) family protein	0.2178	0.3376	0.3442	0.3895	0.1234	0.1782	-0.7167	0.008	0.0359	-0.545	0.0203	0.0459
259379_at	AT3G16350	myb family transcription factor	-0.8812	0.0105	0.0646	-0.7893	0.0152	0.0648	-0.09097	0.2443	0.2376	0.000985	0.9889	0.4799
259380_at	AT3G16340	ATPDR1;PDR1 (PLEIOTROPIC DRUG RESISTAN	-0.04044	0.8934	0.5495	-0.02025	0.9465	0.531	-0.8535	0.0022	0.0219	-0.8333	0.0024	0.0162
259381_s_at	AT3G16410;AT3G16390;A	[AT3G16410, jacalin lectin family protein];[AT3G16	1.3234	4.00E-04	0.032	1.217	5.00E-04	0.0263	0.5435	0.0106	0.0409	0.4372	0.0219	0.0483
259382_s_at	AT3G16430;AT3G16420	[AT3G16430, jacalin lectin family protein];[AT3G164	1.1925	0.0075	0.0579	1.6648	0.0022	0.0334	0.6838	0.015	0.0487	1.156	0.0023	0.016
259383_at	AT3G16470	JR1 (Jacalin lectin family protein)	0.2903	0.3489	0.3492	0.2256	0.4565	0.3666	-0.00852	0.9744	0.5111	-0.07327	0.784	0.4242
259384_at	AT3G16450	jacalin lectin family protein	1.0906	0.143	0.22	2.136	0.0235	0.0772	0.2764	0.6688	0.4208	1.3218	0.0922	0.1145
259385_at	AT1G13470	similar to unknown protein [Arabidopsis thaliana] (T	1.6222	0.0061	0.0539	1.9312	0.0032	0.0369	-0.3831	0.1271	0.1618	-0.07409	0.7291	0.4068
259386_at	AT1G13400	JGL/NUB (NUBBIN); nucleic acid binding / zinc ion	0.3902	0.5759	0.4511	0.01727	0.9798	0.5393	0.6555	0.248	0.24	0.2825	0.5915	0.3604
259387_at	AT1G13370	histone H3, putative	-1.0748	0.2382	0.2864	0.5147	0.5434	0.402	0.344	0.3577	0.2968	1.9335	0.0043	0.0208
259388_at	AT1G13420	sulfotransferase family protein	-0.105	0.9229	0.5579	0.3528	0.7467	0.4737	0.04365	0.9679	0.5096	0.5014	0.6486	0.3803
259389_at	AT1G06320	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.2348	0.8607	0.5412	-0.0614	0.9633	0.5348	-0.1591	0.8894	0.4895	-0.4553	0.6933	0.3952
259390_at	AT1G06340	agenet domain-containing protein	0.7989	0.5424	0.438	2.1063	0.1544	0.2015	-0.5565	0.6673	0.4203	0.7509	0.5658	0.3512
259391_s_at	AT1G06360;AT1G06350	[AT1G06360, fatty acid desaturase family protein];[	-2.2534	0.0227	0.0881	-1.634	0.0592	0.1209	-0.09624	0.7812	0.4578	0.5231	0.1817	0.1744
259392_at	AT1G06400	ribosomal protein-related	0.4159	0.012	0.0681	0.5448	0.0046	0.0416	0.1466	0.1982	0.2107	0.2755	0.0443	0.0738
259393_at	AT1G06410	ATTPS7 (Arabidopsis thaliana trehalose-phosphata	-0.00403	0.9891	0.5743	-0.0495	0.8671	0.509	-0.2459	0.1107	0.1489	-0.2914	0.0728	0.099
259394_at	AT1G06420	unknown protein	0.2942	0.8352	0.5339	-0.13	0.9265	0.5258	1.0717	0.4639	0.3448	0.6475	0.6506	0.381
259395_at	AT1G06400	ARA2 (Arabidopsis Rab GTPase homolog A1a); GT	0.07309	0.6534	0.4771	0.3434	0.0852	0.1469	-0.07018	0.382	0.3087	0.2001	0.0489	0.0783
259396_at	AT1G06390	GSK1 (GSK3/SHAGGY-LIKE PROTEIN KINASE 1)	0.009407	0.9425	0.5631	0.1122	0.4115	0.3468	-0.4057	0.0296	0.07	-0.3029	0.0688	0.096
259397_at	AT1G17680	transcription factor-related	0.5724	0.0185	0.081	0.681	0.0103	0.0551	-0.6482	0.0038	0.0271	-0.5397	0.0074	0.0268
259398_at	AT1G17700	prenylated rab acceptor (PRA1) family protein	-1.0669	0.0378	0.1121	-1.0529	0.0393	0.0982	0.7813	0.0015	0.0199	0.7953	0.0014	0.0134
259399_at	AT1G17710	phosphoric monoester hydrolase	0.4919	0.2982	0.3223	-0.3258	0.4731	0.3734	0.169	0.5803	0.3909	-0.6487	0.0823	0.1069
259400_at	AT1G17750	leucine-rich repeat transmembrane protein kinase,	-0.1762	0.5286	0.4327	-0.2466	0.3894	0.3364	-0.3673	0.1523	0.1805	-0.4377	0.1032	0.1229
259401_at	AT1G17760	ATCS1?/?CS1?7 (Cleavage stimulation factor 77	0.4834	0.0252	0.0921	0.5085	0.0215	0.0746	-0.1393	0.372	0.3039	-0.1143	0.4562	0.3085
259402_at	AT1G17730	VPS46.1	0.03382	0.8057	0.5257	0.06007	0.665	0.4466	1.0452	3.00E-04	0.0138	1.0715	3.00E-04	0.0081
259403_at	AT1G17745	PGDH (3-PHOSPHOGLYCERATE DEHYDROGEN	0.4467	0.0236	0.0897	0.8252	0.0028	0.0351	-0.5959	0.009	0.0378	-0.2174	0.1582	0.1601
259404_at	AT1G17760	ATB BETA (Arabidopsis thaliana serine/threonine p	0.2716	0.1314	0.2099	0.7411	0.0195	0.0719	-0.1659	0.4353	0.3321	0.2036	0.3477	0.2614
259405_at	AT1G17744	unknown protein	0.6092	0.679	0.4857	0.6786	0.6457	0.4401	-1.7262	0.2754	0.2554	-1.6567	0.2924	0.2348
259406_at	AT1G17690	similar to unnamed protein product [Vitis vinifera] (G	0.3473	0.1331	0.2116	-0.1652	0.4215	0.3513	-0.2011	0.2529	0.2425	-0.7136	0.0091	0.0297
259407_at	AT1G17620	PP2AA3/PR65 (PROTEIN PHOSPHATASE 2A SU	0.07814	0.3671	0.3579	0.07151	0.4051	0.3436	-0.3932	0.0069	0.0339	-0.3998	0.0065	0.0251
259408_at	AT3G25800	PDF1 (65 KDA REGULATORY SUBUNIT OF PRO	0.3316	0.0377	0.1121	0.1009	0.4048	0.3434	-0.3338	0.02	0.0567	-0.5645	0.0032	0.0183
259409_at	AT1G13330	similar to unnamed protein product [Vitis vinifera] (G	-0.104	0.8923	0.5491	1.6932	0.0788	0.1407	-0.5609	0.4395	0.3338	1.2313	0.1355	0.1454
259410_at	AT1G13340	similar to unknown protein [Arabidopsis thaliana] (T	2.1502	5.00E-04	0.032	2.6226	2.00E-04	0.0249	-0.1746	0.3321	0.2843	1.2978	0.1331	0.1438
259411_at	AT1G13410	binding	-0.7135	0.2323	0.2833	-0.2231	0.6828	0.4531	-0.8758	0.1594	0.1853	-0.3854	0.4898	0.3218
259412_at	AT1G13450	DNA binding protein GT-1	0.5693	0.032	0.1037	0.8547	0.0205	0.0733	-0.714	0.001	0.0175	-0.6286	0.0016	0.0142
259413_at	AT1G02320	unknown protein	0.03984	0.966	0.5687	2.6279	0.0404	0.0996	-2.6302	0.0403	0.0832	0.0375	0.968	0.475
259414_at	AT1G02420	pentaticopeptide (PPR) repeat-containing protein	0.7156	0.3548	0.3522	-0.1613	0.8253	0.4975	-1.0405	0.1923	0.2069	-1.9173	0.0447	0.0741
259415_at	AT1G02230	similar to unnamed protein product [Vitis vinifera] (G	0.2312	0.076	0.1585	0.6739	0.0023	0.0334	0.7509	0.0015	0.0199	1.1936	3.00E-04	0.0079
259416_at	AT1G02305	cathepsin B-like cysteine protease, putative	0.8432	0.0054	0.0519	0.5493	0.0234	0.0771	-0.1565	0.3124	0.2746	-0.4505	0.0293	0.0573
259417_at	AT1G02340	HFR1 (LONG HYPOCOTYL IN FAR-RED); DNA bi	-0.5979	0.4489	0.3976	-0.8702	0.2894	0.2862	0.1724	0.1874	0.2039	-0.09991	0.4094	0.2879
259418_at	AT1G02390	ATGPX2(GPX2) (GLYCEROL-3-PHOSPHATE AC	0.1369	0.673	0.4837	-0.1759	0.6879	0.4187	0.09017	0.7685	0.4537	0.01016	0.9522	0.4716
259419_at	AT1G06310	ACX6 (ACYL-COA OXIDASE 6); acyl-CoA oxidase	-0.04749	0.874	0.5451	-1.0433	0.0206	0.0732	0.5102	0.1436	0.1742	-0.4857	0.1589	0.1606
259420_at	AT1G13900	calcineurin-like phosphoesterase family protein	0.06446	0.6723	0.4834	-0.01876	0.9009	0.5192	0.2981	0.036	0.078	0.2149	0.0887	0.1117
259421_at	AT1G13910	leucine-rich repeat family protein	0.3287	0.0487	0.1271	-0.4245	0.0224	0.0756	0.2417	0.1094	0.1473	-0.5115	0.0121	0.0346
259422_at	AT1G13810	DNA binding / magnesium ion binding / nuclease	-0.07729	0.7168	0.4983	-0.04128	0.8454	0.5031	0.1396	0.5207	0.3673	0.1756	0.4263	0.2952

259490_at	no_match	no_match	0.1646	0.5253	0.4314	-0.00956	0.9697	0.5366	0.2144	0.4165	0.3236	0.04023	0.8733	0.4494
259491_at	AT1G15820	LHCB6 (LIGHT HARVESTING COMPLEX PSII); ch	-0.4448	0.0119	0.068	-0.5522	0.0056	0.0434	0.1125	0.234	0.2317	0.005041	0.953	0.4717
259492_at	AT1G15830	unknown protein	-1.1053	0.0794	0.1624	-0.5605	0.301	0.2919	-0.915	0.1248	0.1599	-0.3702	0.477	0.3165
259493_at	AT1G15840	unknown protein	-0.4755	0.2809	0.3118	0.2731	0.5139	0.3902	-0.1829	0.6381	0.4106	0.5658	0.1911	0.1798
259494_at	AT1G15850	transducin family protein / WD-40 repeat family prot	-0.2259	0.4337	0.391	0.01892	0.9455	0.5307	0.2101	0.4642	0.3449	0.4171	0.1838	0.1758
259495_at	AT1G15890	disease resistance protein (CC-NBS-LRR class), p	0.8594	0.0135	0.0715	0.7675	0.0196	0.0719	-0.578	0.0469	0.0907	-0.6699	0.0302	0.0584
259496_at	AT1G15900	similar to hypothetical protein OsJ_020585 [Oryza s	-0.4335	0.5097	0.4248	0.7208	0.2957	0.2895	0.1139	0.8586	0.4806	1.2682	0.1019	0.122
259497_at	AT1G15910	calcium ion binding	0.2867	0.0572	0.1371	0.3139	0.6442	0.1041	0.44	0.0125	0.0444	0.4672	0.0102	0.0316
259498_at	AT1G15880	GOS11 (GOLGI SNARE 11); SNARE binding	0.4707	0.0202	0.0838	0.6471	0.0068	0.0467	-0.4212	0.0288	0.0689	-0.2448	0.124	0.1377
259499_at	AT1G15730	PRLI-interacting factor L, putative	-0.05264	0.6978	0.4919	-0.5309	0.0136	0.0618	0.2251	0.1489	0.1783	-0.2532	0.1151	0.1313
259500_at	AT1G15740	leucine-rich repeat family protein	0.5664	0.026	0.0933	0.5627	0.0266	0.0816	-0.1935	0.0046	0.0289	-0.1972	0.0043	0.0208
259501_at	AT1G15750	TPL/WSIP1 (WUS-INTERACTING PROTEIN 1); pr	0.3532	0.222	0.2763	0.03996	0.8781	0.5125	-0.3269	0.2346	0.2319	-0.6401	0.052	0.0812
259502_at	AT1G15670	kelch repeat-containing F-box family protein	0.7874	0.0485	0.1269	0.9663	0.0262	0.081	-0.1006	0.438	0.3331	0.07829	0.5397	0.341
259503_at	AT1G15870	mitochondrial glycoprotein family protein / MAM33 f	0.4854	0.5792	0.4521	0.3118	0.7001	0.4591	0.3438	0.6718	0.4215	0.2016	0.8022	0.4293
259504_at	AT1G15690	AVP1 (vacuolar-type H+-pumping pyrophosphatase	-0.2371	0.2317	0.283	-0.5719	0.0273	0.0826	-0.256	0.0788	0.1227	-0.5908	0.0056	0.0234
259505_at	AT1G15810	ribosomal protein S15 family protein	0.5205	0.0191	0.082	0.368	0.0548	0.1162	0.387	0.0475	0.0914	0.2344	0.162	0.1624
259506_at	AT1G43390	protein phosphatase 2C, putative / PP2C, putative	-0.2408	0.1506	0.2261	-0.08247	0.5761	0.4143	0.04107	0.6372	0.4102	0.1994	0.0687	0.0959
259507_at	AT1G43910	AAA-type ATPase family protein	1.6279	0.0207	0.0848	2.0335	0.0098	0.0538	0.04579	0.922	0.4985	0.4514	0.3621	0.2679
259508_at	AT1G43920	transposable element gene	-0.1687	0.8484	0.5379	0.6506	0.4759	0.3745	0.2255	0.7988	0.463	1.0449	0.2755	0.2258
259509_at	AT1G43930	transposable element gene	0.3822	0.7658	0.5133	0.3661	0.7753	0.4822	1.1121	0.4061	0.319	1.096	0.4123	0.2892
259510_at	AT1G43970	unknown protein	-0.412	0.6387	0.4725	-1.9343	0.0759	0.138	0.4425	0.6149	0.4026	-1.0798	0.2545	0.215
259520_at	AT1G12360	CCS1 (copper chaperone for superoxide dismutase	2.0505	4.00E-04	0.032	2.0727	4.00E-04	0.0251	0.1517	0.3647	0.3003	0.1739	3.00E-04	0.2417
259512_at	AT1G12360	KEU (KEULE); protein transporter	0.7439	0.0026	0.0425	0.6164	0.0051	0.0427	-0.2869	0.0121	0.0437	-0.4145	0.0033	0.0186
259513_at	AT1G12430	PAK (PHOSPHATIDIC ACID KINASE); microtubule	0.03667	0.9001	0.5511	0.1042	0.7234	0.4665	-0.1932	0.3271	0.2819	-0.1257	0.5082	0.329
259514_at	AT1G12480	CDI3/OZS1/RCD3/SLAC1 (SLOW ANION CHANN	-0.8395	0.1575	0.2313	-1.0584	0.0938	0.1543	-1.0985	0.0856	0.129	-1.3173	0.0528	0.0819
259515_at	AT1G20430	similar to unknown [Populus trichocarpa] (GB:ABK	0.6564	0.0211	0.0854	0.7374	0.0144	0.0634	-0.4732	0.024	0.0628	-0.3922	0.0426	0.0719
259516_at	AT1G20450	ERD10/LTI45 (EARLY RESPONSIVE TO DEHYDR	-0.776	0.1753	0.2451	-0.7829	0.1723	0.2144	1.1783	0.0038	0.0271	1.1714	0.0039	0.0202
259517_at	AT1G20630	CAT1 (CATALASE 1); catalase	0.3517	0.2892	0.3049	0.3998	0.2188	0.2451	-0.3241	0.0784	0.1224	-0.276	0.1158	0.1317
259518_at	AT1G20510	OPCL1 (OPC-8:0 COA LIGASE1); 4-coumarate-Co	-0.1456	0.536	0.4355	-0.3357	0.1939	0.2287	0.004172	0.9731	0.5107	-0.186	0.1851	0.1764
259519_at	AT1G12270	stress-inducible protein, putative	0.3956	0.034	0.1066	0.6087	0.0082	0.0504	0.0344	0.7967	0.4624	0.2475	0.1187	0.1338
259520_at	AT1G12320	similar to unknown protein [Arabidopsis thaliana] (T	0.6252	0.041	0.1156	0.6625	0.037	0.0908	0.2606	0.1328	0.1658	0.2979	0.0977	0.1188
259521_at	AT1G12410	CLPR2 (Clp protease proteolytic subunit 2); endope	-0.1045	0.4358	0.392	-0.2881	0.0755	0.1378	0.0694	0.5963	0.3969	-0.1142	0.3978	0.2833
259522_at	AT1G12490	F-box family protein-related	1.0584	0.2842	0.3139	-2.8078	0.0306	0.0868	3.1712	0.0208	0.058	-0.695	0.4626	0.3111
259523_at	AT1G12500	phosphate translocator-related	-0.7891	0.0142	0.0728	-1.3762	0.0019	0.033	0.03817	0.7629	0.452	-0.5484	0.0102	0.0316
259524_at	AT1G12550	oxidoreductase family protein	-0.6814	0.0573	0.1372	-0.7152	0.05	0.1109	0.1618	0.564	0.3844	0.1281	0.6452	0.3791
259525_at	AT1G12560	ATEXPA7 (ARABIDOPSIS THALIANA EXPANSIN	-1.3467	0.1267	0.2058	0.208	0.7811	0.4838	-0.1619	0.7921	0.4608	1.3928	0.0725	0.0987
259526_at	AT1G12600	glucose-methanol-choline (GMC) oxidoreductase fa	0.2631	0.7201	0.4994	-0.2725	0.7107	0.4623	0.562	0.0927	0.1348	0.02644	0.9225	0.4636
259527_at	AT1G12600	similar to ATUTR2/UTR2 (UDP-GALACTOSE TRA	-0.7057	0.0902	0.174	0.6101	0.1269	0.1806	-0.6275	0.0751	0.1194	0.6884	0.0587	0.0873
259528_at	AT1G12330	similar to unknown protein [Arabidopsis thaliana] (T	-0.3898	0.2364	0.2854	-0.5308	0.131	0.1835	0.6163	0.0502	0.0949	0.4754	0.0993	0.1201
259529_at	AT1G12400	DNA binding	0.3257	0.2029	0.2642	0.1533	0.5136	0.39	0.7757	0.0223	0.0603	0.6034	0.0479	0.0773
259530_at	AT1G12450	similar to unknown protein [Arabidopsis thaliana] (T	-0.2981	0.4129	0.3816	-0.06943	0.842	0.5021	-0.00074	0.9921	0.5157	0.2279	0.0305	0.0588
259531_at	AT1G12460	leucine-rich repeat transmembrane protein kinase,	-0.7977	0.0941	0.1776	-0.6932	0.1303	0.183	-0.03547	0.8374	0.4749	0.06901	0.692	0.3947
259532_at	AT1G12470	Pex3/Vps18/deep orange family protein	0.4641	0.0945	0.1777	0.1928	0.4158	0.3487	-0.2296	0.1391	0.1705	-0.5009	0.0159	0.0401
259533_at	AT1G12530	similar to unknown protein [Arabidopsis thaliana] (T	0.1065	0.6418	0.4736	-0.00442	0.9844	0.5402	0.9555	0.0108	0.0412	0.8446	0.0163	0.0408
259534_at	AT1G12290	disease resistance protein (CC-NBS-LRR class), pu	1.3795	0.0218	0.0867	1.7619	0.0096	0.0535	-0.1737	0.6698	0.421	0.2087	0.6102	0.3669
259535_at	AT1G12520	disease resistance protein (CC-NBS-LRR class), pu	0.02639	0.9469	0.5639	0.3041	0.4803	0.368	-1.2911	0.0234	0.062	-1.0134	0.0488	0.0782
259536_s_at	AT1G12350,ATCOAB (4-PHOSPHO-PANTO-THE	0.3338	0.2346	0.2842	0.485	0.112	0.1689	-0.2453	0.3623	0.2992	-0.09403	0.7138	0.4022	
259537_at	AT1G12370	PHR1 (PHOTOLYASE 1)	-0.9378	0.1553	0.2299	-1.2996	0.0725	0.1349	-0.03824	0.9231	0.4987	-0.4001	0.3429	0.2593
259538_at	AT1G12310	calmodulin, putative	-0.1912	0.4555	0.4007	0.2949	0.272	0.2766	0.4028	0.0039	0.0273	0.889	2.00E-04	0.0076
259539_at	AT1G20550	similar to unknown protein [Arabidopsis thaliana] (T	-0.00506	0.9882	0.5741	0.3831	0.2996	0.2912	-0.1198	0.7285	0.4413	-0.4979	0.1967	0.1829
259540_at	AT1G20640	RWP-RK domain-containing protein	-0.06855	0.605	0.4613	-0.234	0.1282	0.1817	-0.1364	0.0576	0.1026	-0.3019	0.0043	0.0208
259560_at	AT1G20660	protein kinase	-0.5811	0.0074	0.0576	-0.3995	0.026	0.0807	-0.202	0.0443	0.088	-0.02046	0.7839	0.4242
259542_at	AT1G20575	dolichyl-phosphate beta-D-mannosyltransferase, pu	0.08826	0.2967	0.3213	0.3163	0.0127	0.0602	-0.01377	0.8607	0.4813	0.2143	0.0436	0.073
259543_at	AT1G20580	small nuclear ribonucleoprotein, putative / snRNP, p	-0.2596	0.1107	0.193	0.2682	0.1026	0.1616	-0.08333	0.409	0.3204	0.4444	0.008	0.0278
259544_at	AT1G20620	CAT3 (CATALASE 3); catalase	0.2919	0.2838	0.3137	0.0447	0.859	0.5069	0.05435	0.7	0.4313	-0.1928	0.2157	0.194
259545_at	AT1G20560	AMP-dependent synthetase and ligase family protei	0.2366	0.2562	0.2971	0.3459	0.125	0.1792	-0.2424	0.2465	0.239	-0.133	0.498	0.3252
259546_at	AT1G20570	similar to SHB1 (SHORT HYPOCOTYL UNDER BL	-0.1114	0.8224	0.5303	-0.3383	0.5071	0.3875	-0.3506	0.083	0.1267	-0.5776	0.0193	0.0445
259547_at	AT1G20590	transposable element gene	0.4522	0.4132	0.3816	-1.0997	0.1132	0.1682	1.1132	0.0537	0.0986	-0.4787	0.3092	0.243
259548_at	AT1G35260	MLP165 (MLP-LIKE PROTEIN 165)	1.201	0.3365	0.3434	1.1815	0.3435	0.315	0.5587	0.1305	0.1643	0.5391	0.1409	0.1488
259549_at	AT1G35290	thioesterase family protein	0.3766	0.6852	0.4877	-0.3235	0.7269	0.4678	0.4471	0.6319	0.4084	-0.2531	0.784	0.4242
259550_at	AT1G35230	AGP5 (ARABINOGALACTAN-PROTEIN 5)	0.2775	0.0113	0.0666	2.7295	0.0043	0.0407	0.7812	0.0016	0.0202	1.4332	1.00E-04	0.0069
259551_at	AT1G21190	small nuclear ribonucleoprotein, putative / snRNP, p	0.4658	0.0829	0.1666	0.9768	0.0085	0.0509	0.236	0.3085	0.2727	0.7471	0.021	0.0471
259552_at	AT1G21320	nucleic acid binding / nucleotide binding	-0.25	0.7297	0.5025	-1.0227	0.2041	0.2355	-0.7013	0.3572	0.2966	-1.474	0.0942	0.1161
259553_x_at	AT1G21310	ATEXT3 (EXTENSIN 3); structural constituent of ce	3.7016	0.0188	0.1814	3.2297	0.029	0.0848	0.3205	0.2297	0.2253	-0.1514	0.54	0.341
259554_at	AT1G21220	transposable element gene	0.9373	0.0145	0.0731	0.2818	0.2822	0.2822	0.111	0.5818	0.3914	-0.5445	0.0425	0.0719
259555_at	AT1G21290	transposable element gene	-0.4113	0.7028	0.4935	-0.4939	0.6482	0.441	0.007544	0.9944	0.5163	-0.07507	0.9439	0.4693
259556_at	AT1G21300	transposable element gene	0.9888	0.3955	0.373	-0.4623	0.6797	0.4518	1.1195	0.3423	0.2895	-0.3316	0.7658	0.4185
259557_at	AT1G21210	WAK4 (WALL ASSOCIATED KINASE 4); protein se	-0.1088	0.9211	0.5572	0.6023	0.5909	0.4198	-2.3192	0.0396	0.0823	-1.6082	0.1053	0.1241
259558_at	AT1G21230	WAK5 (WALL ASSOCIATED KINASE 5); kinase/ p	-0.2825	0.8642	0.5422	-1.5904	0.3627	0.3242	0.8044	0.631	0.4083	-0.5034	0.7615	0.4172
259559_at	AT1G21240	WAK3 (WALL ASSOCIATED KINASE 3); kinase/ pr	2.7246	0.003	0.0436	2.842	0.0026	0.0342	-0.0936	0.4666	0.346	0.02371	0.8486	0.4424
259560_at	AT1G21270	WAK2 (wall-associated kinase 2); protein serine/thr	0.9972	0.0105	0.0647	0.9487	0.0125	0.0599	0.00753	0.9547	0.5066	-0.04093	0.759	0.4163
259561_at	AT1G21250	WAK1 (CELL WALL-ASSOCIATED KINASE); kinas	1.4098	0.0032	0.0443	1.2232	0.0054	0.0432	0.02989	0.7646	0.4526	-0.1566	0.1683	0.1662
259562_at	AT1G21200	transcription factor	0.1262	0.3587	0.3538	0.7233	0.004	0.0395	-0.385	0.0342	0.0755	0.2121	0.1566	0.159
259563_s_at	AT1G20590,AT1G20610	[AT1G20590, cyclin, putative];[AT1G20610, CYCB2	-0.5654	0.6026	0.4604	1.1759	0.3055	0.2947	-0.8313	0.4532	0.3401	0.91	0.415	0.2904
259564_at	AT1G20540	transducin family protein / WD-40 repeat family prot	0.3566	0.0138	0.0719	0.0793	0.4037	0.3429	-0.6871	0.0012	0.0187	-0.9644	3.00E-04	0.0085
259565_at	AT1G20550	similar to unknown protein [Arabidopsis thaliana] (T	0.3062	0.8369	0.5344	-2.6826	0.1267	0.1806	1.7636	0.1398	0.171	-1.0252	0.3914	0.2806
259566_at	AT1G20520	similar to unknown protein [Arabidopsis thaliana] (T	1.6812	0.1233	0.2035	-0.4152	0.6557	0.4438	1.3204	0.2008	0.2122	-0.776	0.4195	0.2924
259567_at	no_match	no_match	0.4288	0.7161	0.4981	-0.7114	0.5524	0.4057	0.1427	0.8405	0.4758	-0.9975	0.2077	0.1895
259568_at	AT1G20490	AMP-dependent synthetase and ligase family protei	0.4339	0.3637	0.3562	0.249	0.5884	0.4188	-0.928	0.0937	0.1357	-1.1129	0.0584	0.0871
259569_at	AT1G20480	4-coumarate--CoA ligase family protein / 4-coumaric	-0.2683	0.7816	0.5181	-0.6662	0.5024	0.3857	-0.8537	0.3353	0.2862	-1.2515	0.184	0.1758
259570_at	AT1G20440	COR47 (cold regulated 47)	-0.8593	0.032	0.1036	-0.6167	0.0813	0.1429	0.7801	0.0015	0.0199	1.0227	5.00E-04	0.0096
259571_at	AT1G20410	similar to unnamed protein product [Vitis vinifera] (G	0.3561	0.218	0.2739	0.3165	0.2642	0.272	0.1367	0.605	0.3998	0.09709	0.7109	0.4013
259572_at	AT1G20400	myosin heavy chain-related	-1.0072	0.3164	0.3323	-1.4046	0.1858	0.2236	0.3546	0.7077	0.4339	-0.04289	0.9635	0.4741
259573_at	AT1G20390	transposable element gene	-0.6017	0.3836	0.3665	-0.3828	0.5676	0.411	-1.1231	0.1421	0.173	-0.9042	0.2157	0.194
259574_at	AT1G35310	MLP168 (MLP-LIKE PROTEIN 168)	0.6546	0.2752	0.3087	0.5224	0.3705	0.3277	0.9958	0.0588	0.1039	0.8636	0.0856	0.1094
259575_at	AT1G35320	similar to unknown protein [Arabidopsis thaliana] (T	-0.9629	0.3314	0.3408	1.0375	0.2999	0.2913	-0.6629	0.3858	0.3104	1.3376	0.1212	0.1359
259576_at	AT1G35330	zinc finger (C3HC4-type RING finger) family protein	1.4551	0.1198	0.2001	0.9531	0.2659	0.2732	-0.0442	0.9551	0.5066	-0.5462	0.5001	0.326
259577_at	AT1G35340	ATP-dependent protease La (LON) domain-contain	-0.2642	0.0975	0.1804	-0.5384	0.0118	0.0584	-0.0715	0.5636	0.3842	-0.3458	0.0384	0.0672
259578_at	AT1G27990	similar to unknown protein [Arabidopsis thaliana] (T	-0.8935	0.3267	0.3383	-0.5299	0.544	0.4022	-1.1561	0.222	0.2247	-0.7926	0.378	0.2748
259579_at	AT1G28010	PGP14 (P-GLYCOPROTEIN 14); ATPase, coupled	-0.497	0.347	0.3485	-0.5145	0.3323	0.3096	-0.5554	0.0678	0.1128	-0.5728	0.0624	0.0907
259580_at	AT1G28030	oxidoreductase, 2OG-Fe(II) oxygenase family prote	0.3589	0.6337	0.4708	0.1836	0.8052	0.4913	0.1408	0.8498	0.4785	-0.03451	0.9629	0.4739
259581_at	AT1G28040	protein binding / zinc ion binding	0.136	0.8738	0.5451	-0.178	0.8355	0.5003	-0.5461	0.5339	0.3727	-0.8601	0.3446	0.2601
259582_at	AT1G28060	small nuclear ribonucleoprotein family protein / snR	0.2776	0.2051	0.2654	0.1793	0.3841	0.3339	-0.02207	0.8819	0.4873	-0.1204	0.4367	0.2999
259583_at	AT1G28070	protein binding	0.9347	0.0027	0.0426	1.2655	7.00E-04	0.0275	-0.3033	0.063	0.1079	0.06749	0.6001	0.3634
259584_at	AT1G28080	similar to unknown protein [Arabidopsis thaliana] (T	1.4514	0.2077	0.2669	-0.8652	0.4214	0.3512	0.548	0.6011	0.3985	-1.7685	0.1413	0.149
259585_at	AT1G28090	polynucleotide adenylyltransferase family protein	-0.08599	0.7899	0.5205	0.2195	0.5074	0.3876	-0.6265	0.1051	0.145	-0.321	0.345	0.2603
259586_at	AT1G28100	similar to unnamed protein product [Vitis vinifera] (G	0.1681	0.4722	0.4085	-0.2016	0.3954	0.3392	-0.3238	0.2013	0.2125	-0.3573	0.1671	0.1655
259587_at	AT1G28120	Identical to Ubiquitin thioesterase otubain-like [Ara	0.6057	0.001	0.035	0.6043	0.001	0.0291	-0.2235	0.0232	0.0616	-0.225	0.0227	0.049
259588_at	AT1G27930	similar to unknown protein [Arabidopsis thaliana] (T	0.6209	0.0103	0.0644	0.4307	0.0341	0.0911	0.5048	0.0103	0.0403	0.3146	0.0466	0.076
259589_at	AT1G28135	unknown protein	0.5131	0.6668	0.4815	-1.1758	0.3476	0.3168	-0.4469	0.7068	0.4336	-2.1358	0.1256	0.1387
259590_at	AT1G28160	ethylene-responsive element-binding family protein	-0.568	0.2265	0.2795	0.5682	0.2263	0.2494	-0.3692	0.4058	0.3189	0.767	0.1261	0.139
259591_at	AT1G28150	Identical to UPF0426 protein At1g28150, chloroplas	-0.1008	0.6768	0.4848	-0.1588	0.5185	0.3919	0.102	0.5963	0.3969	0.04397	0.8165	0.4333
259592_at	AT1G27950	lipid transfer protein-related	0.7037	0.0716	0.1541	-0.9283	0.0325	0.0894	1.3938	2.00E-04	0.0126	1.1693	4.00E-04	0.0089
259593_at	AT1G27970	NTF2B (NUCLEAR TRANSPORT FACTOR 2B); Ra	0.04902	0.6644	0.4808	0.3508	0.0287	0.0842	0.327	0.017	0.052	0.6288	0.0016	0.0143
259594_at	AT1G28140	similar to unnamed protein product [Vitis vinifera] (G	0.1744	0.1845	0.2514	-0.03519	0.7628	0.4782	-0.3205	0.0423	0.0856	-0.5302	0.0082	0.0282
259595_at	AT1G28050	zinc finger (B-box type) family protein	0.08022	0.6309	0.47	0.4224	0.0522	0.1133	0.1326	0.3055	0.2715	0.4747	0.0137	0.0371
259596_at	AT1G28130	GH3.17; indole-3-acetic acid amido synthetase	0.8171	0.0011	0.036	1.5589	1.00E-04	0.0249	-0.2005	0.1098	0.1483	0.5412	0.0052	0.0226
259597_at	AT1G27900	RNA helicase, putative	0.5224	0.09	0.1737	0.5622	0.0747	0.1371	-0.09545	0.4538	0.3403	-0.05562	0.6543	0.3822
259598_at	AT1G27980	pyridoxal-dependent decarboxylase family protein	1.8606	2.00E-04	0.0312	1.7972	2.00E-04	0.0249	-0.3626	0.0248	0.0638	-0.426	0.0146	0.0385
259599_at	AT1G28110	SCPL45; serine carboxypeptidase	0.2706	0.4707	0.4076	0.5836	0.1612	0.2067	0.2205	0.1561	0.183	0.5335	0.0135	0.0368
259600_at	AT1G35220	similar to hypothetical protein Osl_001520 (Oryza s	0.347	0.2365	0.2855	0.3975	0.1862	0.2239	-0.4998	0.0889	0.1316	-0.4493	0.1146	0.131
259601_s_at	AT2G12210,AT2G11060,A	[AT2G12210, transposable element gene];[AT2G1	-1.3758	0.1498	0.2254	0.6536	0.4456	0.3621	-1.8761	0.0723	0.1169	0.1534	0.8525	0.4434
259602_at	AT1G56520	oxidoreductase, 2OG-Fe(II) oxygenase family prote	0.3174	0.7326	0.5031	0.1678	0.8558	0.5061	-1.484	0.1619	0.1866	-1.6336	0.1324	0.1433
259603_at	AT1G56510	haloacid dehalogenase-like hydrolase family protein	-0.848	0.0021	0.0406	-1.1285	7.00E-04	0.0275	0.1753	0.215	0.2208	-0.1052	0.4266	0.2953
259604_at	AT1G56450	PBG1 (20S proteasome beta subunit G1); peptidase	0.7781	0.0368	0.1105	0.6929	0.0516	0.1127	0.6376	0.0248	0.0639	0.5524	0.0386	0.0675
259605_at	AT1G27910	U-box domain-containing protein	-0.9144	0.0205	0.0842	-1.2338	0.0074	0.0485	0.09027	0.7246	0.4401	-0.2291	0.3916	0.2807
259606_at	AT1G27920	microtubule associated protein (MAP65/ASE1) fam	-0.4111	0.7133	0.4972	0.8642	0.4533	0.3653	-0.1679	0.8798	0.4866	1.1075	0.3475	0.2614
259607_at	AT1G27940	PGP13 (P-GLYCOPROTEIN 13); ATPase, coupled	-0.7572	0.3413	0.3459	-2.6192	0.0202	0.0727	1.0514	0.1207	0.1568	-0.8106	0.2042	0.1874
259608_at	AT1G27960	ECT9 (evolutionarily conserved C-terminal region 9)	-0.1827	0.4297	0.3889	-0.08855	0.6924	0.4563	0.1347	0.5526	0.38	0.2289	0.3332	0.2549
259609_at	AT1G27940	TSA1 (TSK-ASSOCIATING PROTEIN 1); calcium ic	0.9998	0.0046	0.0488	0.9009	0.0065	0.0461	-0.2747	0.1621	0.1868	-0.3737	0.0804	0.1054
259610_at	AT1G52320	similar to unknown protein [Arabidopsis thaliana] (T	0.5783	0.0356	0.1089	0.671	0.0224	0.0756	-0.5419	0.0431	0.0867	-0.4493	0.0726	0.0988
259611_at	AT1G52280	AtRABG3d (Arabidopsis Rab GTPase homolog G3d	-0.6217	0.0547	0.1342	-0.5386	0.0802	0.1421	0.4161	0.0293	0.0696	0.4992	0.0163	0.0408
259612_at	AT1G52300	60S ribosomal protein L37 (RPL37B)	0.087115	0.5688	0.4485	0.1344	0.3383	0.3383	0.3371	0.0745	0.1188	0.3844	0.0522	0.0814
259613_at	AT1G48010	invertase/pectin methylesterase inhibitor family prot	-0.3867	0.831	0.5327	-1.9641	0.3117	0.2983	1.5518	0.4124	0.3218	-0.02562	0.9887	0.4798
259614_at	AT1G47990	ATGA2OX4 (GIBBERELLIN 2-OXIDASE 4); gibber	-0.6106	0.2821	0.3127	-0.03589	0.9453	0.5307	-0.8649	0.0136	0.0464	-0.2902	0.2307	0.2018
259615_at	AT1G47980	similar to unknown protein [Arabidopsis thaliana] (T	1.5133	0.2217	0.2762	1.8421	0.1532	0.2004	-0.0129	0.9807	0.5128	0.3159	0.5629	0.3501
259616_at	AT1G47960	CVIF1 (CELL WALL / VACUOLAR INHIBITOR OF	0.4707	0.0982	0.181	0.6173	0.048	0.1087	0.779	0.0015	0.0199	0.9256	8.00E-04	0.0109
259617_at	AT1G47970	unknown protein	-0.03173	0.8565	0.5403	0.1153	0.5222	0.393	0.7962	0.0084	0.0368	0.9433	0.0046	0.0214
259618_at	AT1G48000	MYB112 (myb domain protein 112); DNA binding / t	0.7508	0.0769	0.1595	0.5529	0.1737	0.2153	0.1112	0.72	0.4386	-0.1285	0.6795	0.3903
259619_at	no_match	no_match	0.9817	0.189	0.2547	-0.06773	0.9184	0.5237	0.0343	0.957	0.5071	-1.0151	0.1645	0.164
259620_s_at	AT1G42705,AT4G12260	[AT1G42705, transposable element gene];[AT4G12	-0.2768	0.7449	0.5074	-1.1429	0.2233	0.2478	-0.00486	0.9954	0.5164	-0.871	0.3341	0.2552
259621_at	AT1G42710	similar to hAT dimerisation domain-containing prote	0.862	0.3026	0.3246	0.3633	0.6444	0.4397	0.1627	0.8343	0.4738	-0.3359	0.6689	0.387
259622_at	AT1G43010	pentatricopeptide (PPR) repeat-containing protein	-2.1729	0.1509	0.2264	0.07183	0.9561	0.5333	-0.8675	0.5181	0.3663	1.3773	0.324	0.2502
259623_at	AT1G42700

259690_at	AT1G63160	replication factor C 40 kDa, putative	0.3713	0.1332	0.2118	0.378	0.1281	0.1816	0.002149	0.9918	0.5156	0.008888	0.9563	0.4748
259691_at	AT1G63200	similar to unknown protein [Arabidopsis thaliana] (T	-0.4018	0.299	0.3224	-0.2741	0.4615	0.3686	0.8891	0.0576	0.1026	1.0168	0.0392	0.0682
259692_at	AT1G63080	pentatricopeptide (PPR) repeat-containing protein	-0.08287	0.7946	0.5223	0.4608	0.1966	0.2306	-0.8256	0.0502	0.0949	-0.2819	0.3973	0.2831
259693_at	AT1G63060	similar to unknown protein [Arabidopsis thaliana] (T	-0.3263	0.6632	0.4804	-0.4803	0.5277	0.3953	-0.03815	0.9359	0.5023	-0.1921	0.6887	0.3934
259694_at	AT1G63180	UGE3 (UDP-D-GLUCOSE/UDP-D-GALACTOSE 4-	0.3093	0.2971	0.3214	0.6977	0.054	0.1152	-0.1952	0.4898	0.3555	0.1932	0.4939	0.3236
259695_at	AT1G63170	zinc finger (C3HC4-type RING finger) family protein	-0.2622	0.1783	0.2469	-0.2785	0.1584	0.2047	-0.4858	0.0085	0.037	-0.5021	0.0076	0.0271
259696_at	AT1G63150	pentatricopeptide (PPR) repeat-containing protein	1.1969	0.0218	0.0868	0.8646	0.0579	0.1196	-0.4519	0.2406	0.2355	-0.7842	0.0752	0.1009
259697_at	AT1G68920	basic helix-loop-helix (bHLH) family protein	0.1787	0.4695	0.407	0.2491	0.3281	0.3076	0.1771	0.4731	0.3489	0.2475	0.3308	0.2537
259698_at	AT1G68930	pentatricopeptide (PPR) repeat-containing protein	0.5269	0.5189	0.4288	0.7433	0.3754	0.3301	-0.1104	0.8432	0.4766	0.106	0.8493	0.4426
259699_at	AT1G68940	armadillo/beta-catenin repeat protein-related / U-bo	-0.6025	0.563	0.446	-0.8216	0.4389	0.3591	0.1554	0.8788	0.4864	-0.06368	0.9501	0.4709
259700_at	AT1G68980	pentatricopeptide (PPR) repeat-containing protein	0.02787	0.885	0.5471	0.199	0.3329	0.3097	-0.3452	0.0109	0.0414	-0.1741	0.086	0.1098
259701_at	AT1G77770	protein binding / zinc ion binding	-0.05765	0.6822	0.4866	0.2374	0.1437	0.1935	-0.01362	0.9221	0.4985	0.2814	0.0978	0.1189
259702_at	AT1G77780	glycosyl hydrolase family 17 protein	-0.193	0.8525	0.5389	0.7109	0.5056	0.3869	-0.3949	0.6914	0.4282	0.5091	0.6113	0.3672
259703_at	AT1G77790	glycosyl hydrolase family 17 protein	-0.7644	0.5873	0.4553	0.03555	0.9794	0.5393	0.4401	0.7515	0.4486	1.2401	0.3932	0.2813
259704_at	AT1G77680	ribonuclease II family protein	-0.8998	0.0766	0.1594	-0.6999	0.1388	0.1898	-1.5024	0.0041	0.0276	-1.3025	0.0069	0.0258
259705_at	AT1G77450	ANAC032 (Arabidopsis NAC domain containing pro	-0.1281	0.6627	0.4803	-0.3451	0.2739	0.2775	1.0331	0.0162	0.0508	0.8161	0.0343	0.0627
259706_at	AT1G77540	Encodes a H3/H4 histone acetyltransferase. Belong	0.2539	0.2279	0.2806	0.7174	0.0159	0.0655	0.7534	0.0131	0.0455	1.217	0.0023	0.0161
259707_at	AT1G77490	TAPX; L-ascorbate peroxidase	-1.0513	0.0014	0.038	-1.4723	4.00E-04	0.0251	0.1676	0.1169	0.1538	-0.2533	0.0394	0.0684
259708_at	AT1G77420	hydrolase, alpha/beta fold family protein	0.2627	0.2514	0.2942	0.02239	0.9146	0.5226	-0.138	0.4873	0.3543	-0.3784	0.1043	0.1236
259709_at	AT1G77655	unknown protein	-0.2356	0.6342	0.4709	-0.6084	0.255	0.2673	2.3472	0.0069	0.0338	1.9744	0.0126	0.0354
259710_at	AT1G77670	aminotransferase class I and II family protein	-0.8713	0.0162	0.077	-0.9557	0.0119	0.0585	0.08137	0.4622	0.3442	-0.00305	0.9771	0.4774
259711_at	AT1G77570	DNA binding / transcription factor	0.389	0.7259	0.6013	0.5304	0.6266	0.4334	-0.4915	0.546	0.3778	-0.3402	0.672	0.3881
259712_at	AT1G77440	PBC2 (205 proteasome beta subunit C 2); peptidas	0.4178	0.0048	0.0496	0.5246	0.0021	0.0331	0.04864	0.545	0.3774	0.1554	0.1024	0.1222
259713_at	AT1G77610	glucose-6-phosphate/phosphate translocator-relate	0.2758	0.1732	0.2437	0.1341	0.4659	0.3703	-0.1963	0.3039	0.2707	-0.338	0.1124	0.1293
259714_at	AT1G60980	GTG2/GTG1 GTP-binding protein 2; cation transmem	0.2402	0.197	0.2606	-1.5392	0.3082	0.2965	2.9748	0.0712	0.116	-0.6045	0.794	0.1294
259715_at	AT1G60990	aminomethyltransferase	-0.1114	0.6874	0.4884	-0.2182	0.4441	0.3613	-0.2427	0.3989	0.3161	-0.3495	0.2459	0.2101
259716_at	AT1G60995	similar to S3 self-incompatibility locus-linked pollen	0.3414	0.1889	0.2547	0.1829	0.4446	0.3616	0.1553	0.4295	0.3294	-0.00323	0.9863	0.4793
259717_at	AT1G61010	CPSF73-I; protein binding	0.4649	0.0538	0.1331	0.169	0.5488	0.3341	-0.2657	0.1232	0.1588	-0.5657	0.0143	0.0379
259718_at	AT1G61040	VIP5 (VERNALIZATION INDEPENDENCE 5)	0.236	0.2135	0.2706	0.4556	0.0463	0.1066	-0.1864	0.2424	0.2364	0.03316	0.8194	0.4339
259719_at	AT1G61070	LCR68/PDF2.4 (Low-molecular-weight cysteine-rich	0.6475	0.5942	0.4576	0.8347	0.4976	0.3835	-0.5377	0.6563	0.4166	-0.3505	0.77	0.4199
259720_at	AT1G61080	proline-rich family protein	0.379	0.7259	0.6013	0.5304	0.6266	0.4334	-0.4915	0.546	0.3778	-0.3402	0.672	0.3881
259721_at	AT1G60890	phosphatidylinositol-4-phosphate 5-kinase family pr	0.8469	7.00E-04	0.0334	0.6058	0.0026	0.0342	-0.07305	0.3617	0.299	-0.3142	0.0115	0.0336
259722_at	AT1G60930	ATRECQ4B/RECQL4B (ARABIDOPSIS RECQ HE	-0.2143	0.5676	0.4479	-0.5761	0.1698	0.2124	-0.00208	0.9955	0.5164	-0.3638	0.3505	0.2628
259723_at	AT1G60960	WT3 (Iron regulated transporter 3); cation transmer	0.9392	0.0549	0.1344	0.6158	0.1529	0.2003	0.08332	0.8031	0.4645	-0.24	0.4856	0.3199
259724_at	AT1G60940	SNRK2-10/SNRK2.10/SRK2B (SNF1-RELATED PF	0.8441	0.0074	0.0577	1.0332	0.0036	0.0377	0.2441	0.1232	0.1588	0.4332	0.2259	0.0533
259725_at	AT1G61065	similar to unknown protein [Arabidopsis thaliana] (T	0.4076	0.0776	0.1604	0.7884	0.0103	0.0551	-0.4013	0.0808	0.1244	-0.02051	0.9112	0.4603
259726_at	AT1G60965	SCRL5 (SCR-Like 8)	0.2972	0.8035	0.5251	0.7309	0.5488	0.4043	0.8705	0.3193	0.2779	1.3043	0.1639	0.1636
259727_at	AT1G60950	FED A (FERREDOXIN 2); 2 iron, 2 sulfur cluster bir	-0.5461	0.0332	0.1056	-0.6842	0.0162	0.0663	0.2211	0.0082	0.0362	0.08311	0.1405	0.1485
259728_at	AT1G60970	clathrin adaptor complex small chain family protein	1.2556	0.1677	0.2396	-0.1691	0.8318	0.4993	0.09221	0.9076	0.4946	-1.3325	0.1487	0.1537
259729_at	AT1G77640	AP2 domain-containing transcription factor, putative	0.075001	0.9382	0.6618	-0.3239	0.7395	0.4711	0.8162	0.0878	0.1308	0.5673	0.1931	0.1809
259730_at	AT1G77660	MORN (Membrane Occupation and Recognition Ne	0.334	0.2568	0.2976	0.9786	0.018	0.0694	-0.4356	0.1599	0.1857	0.209	0.4547	0.3079
259731_at	AT1G77460	binding	0.4993	0.1246	0.2044	0.1825	0.5178	0.3916	-0.4463	0.09	0.1326	-0.7631	0.019	0.0441
259732_at	AT1G77470	replication factor C 36 kDA, putative	0.07465	0.6365	0.4718	-0.1062	0.5077	0.3877	-0.191	0.1356	0.1681	-0.3719	0.0221	0.0485
259733_at	AT1G77480	nucellin protein, putative	0.2806	0.0238	0.09	0.3938	0.0076	0.0488	-0.5376	0.0024	0.0231	-0.4244	0.0058	0.0237
259734_at	AT1G77500	similar to unknown protein [Arabidopsis thaliana] (T	0.2043	0.5732	0.4501	0.228	0.5316	0.3968	-0.3283	0.3806	0.308	-0.3045	0.4128	0.2895
259735_at	AT1G64405	2.06	0.0273	0.0957	1.047	0.1591	0.2052	1.8021	0.041	0.084	0.7891	2.6627	0.2192	0.0273
259736_at	AT1G64390	ATGH9C2 (ARABIDOPSIS THALIANA GLYCOSYL	-1.0939	0.017	0.0781	-1.1298	0.0152	0.0648	-0.738	0.031	0.0716	-0.7739	0.0267	0.0543
259737_at	AT1G64400	long-chain-fatty-acid--CoA ligase, putative / long-ch	-0.1372	0.7224	0.5002	-0.1095	0.776	0.4825	0.3089	0.044	0.0876	0.3366	0.0341	0.0624
259738_at	AT1G64355	similar to unnamed protein product [Vitis vinifera] (G	-0.4339	0.0144	0.0731	-0.1672	0.186	0.2237	-0.3117	0.041	0.084	-0.04497	0.6901	0.3939
259739_at	AT1G64350	SEH1H; nucleotide binding	1.2777	0.0038	0.0461	0.9831	0.0096	0.0536	0.1565	0.4867	0.3541	-0.1382	0.5362	0.3401
259740_at	AT1G64300	protein kinase family protein	1.3061	0.2079	0.2669	0.6794	0.4787	0.3757	0.4328	0.6451	0.4127	-0.1938	0.8347	0.4385
259741_at	AT1G77020	armadillo/beta-catenin repeat family protein / U-box	-0.7187	0.0071	0.0567	-0.4422	0.0354	0.0929	-0.4224	0.0312	0.0718	-0.1472	0.3211	0.2488
259742_at	AT1G71120	GLIP6 (GDSL-motif lipase/hydrolase 6); carboxyles	-0.8388	0.2176	0.2736	0.3458	0.5793	0.4159	-0.04827	0.82	0.4698	0.4447	0.0888	0.1118
259743_at	AT1G71140	MATE efflux family protein	0.4777	0.0193	0.0823	0.391	0.0361	0.0939	0.002716	0.9804	0.5127	-0.0839	0.4655	0.3122
259744_at	AT1G71160	beta-ketoacyl-CoA synthase family protein	0.3583	0.808	0.5263	1.5407	0.3269	0.3069	-1.9469	0.2312	0.2301	-0.7645	0.6092	0.3665
259745_at	AT1G71190	SAG18 (SENESCENCE ASSOCIATED GENE 18)	0.6507	0.0052	0.0514	0.7574	0.003	0.0356	0.0668	0.4822	0.352	0.1736	0.1147	0.1311
259746_at	AT1G71060	pentatricopeptide (PPR) repeat-containing protein	0.5644	0.5894	0.4559	-1.3938	0.2214	0.2468	1.186	0.2748	0.2551	-0.7722	0.4567	0.3087
259747_at	AT1G71170	6-phosphogluconate dehydrogenase NAD-binding c	0.2216	0.4141	0.382	1.0319	0.0133	0.0614	-0.4131	0.1279	0.1624	0.3971	0.1393	0.1477
259748_at	AT1G71180	6-phosphogluconate dehydrogenase NAD-binding c	0.063	0.7194	0.4992	0.244	0.2096	0.2393	-0.3264	0.1164	0.1535	-0.1454	0.4238	0.294
259749_at	AT1G71100	RSW10 (RADIAL SWELLING 10); ribose-5-phosph	0.506	0.0797	0.1628	0.4941	0.0847	0.1465	0.4233	0.0412	0.0843	0.4114	0.0448	0.0742
259750_at	AT1G71130	AP2 domain-containing transcription factor, putative	0.5888	0.0372	0.1113	0.6837	0.0235	0.0771	0.3587	0.1347	0.1673	0.4535	0.0772	0.1026
259751_at	AT1G71030	ATMYBL2 (Arabidopsis myb-like 2); DNA binding / t	-0.2928	0.6584	0.4786	-0.4304	0.5221	0.393	0.5445	0.0312	0.0719	0.4069	0.0718	0.0982
259752_at	AT1G71040	LPR2 (LOW PHOSPHATE ROOT2); copper ion bin	0.6017	4.00E-04	0.032	0.4624	0.001	0.0291	-0.06793	0.2714	0.253	-0.2073	0.0177	0.0426
259753_at	AT1G71050	heavy-metal-associated domain-containing protein	0.9213	0.0258	0.093	-0.763	0.0457	0.1059	0.6528	0.0693	0.114	-1.0315	0.0176	0.0425
259754_at	AT1G71090	auxin efflux carrier family protein	0.3318	0.0651	0.1463	0.06091	0.6673	0.4475	-0.04286	0.5068	0.362	-0.3138	0.006	0.0239
259755_at	AT1G71070	glycosyltransferase family 14 protein / core-2/I-bran	-0.3319	0.1255	0.2051	-0.3699	0.0976	0.1574	-0.309	0.1464	0.1764	-0.347	0.1134	0.1301
259756_at	AT1G71080	similar to unknown protein [Arabidopsis thaliana] (T	0.9061	0.0099	0.0638	1.0524	0.0059	0.0442	-0.4538	0.0821	0.1257	-0.3076	0.1925	0.1806
259757_at	AT1G77510	ATPDIL1-2 (PDI-LIKE 1-2); protein disulfide isomer	2.2744	5.00E-04	0.0323	2.3793	4.00E-04	0.0251	0.4727	0.0116	0.0427	0.5776	0.0058	0.0236
259758_s_at	AT1G77530;AT1G77520	[AT1G77530, O-methyltransferase family 2 protein];	-0.6655	0.6818	0.4865	1.2906	0.4404	0.3596	-0.4674	0.7585	0.4508	1.4887	0.3536	0.2643
259759_at	AT1G77550	protein binding / tubulin-tyrosine ligase	0.714	0.1146	0.1961	0.1355	0.7221	0.4661	-0.313	0.249	0.2404	-0.8915	0.0185	0.0436
259760_at	AT1G77580	myosin heavy chain-related	-0.403	0.4273	0.3881	-0.9307	0.1111	0.1682	-0.1603	0.5989	0.3977	-0.6879	0.0706	0.0973
259761_at	AT1G77590	LACS9 (LONG CHAIN ACYL-COA SYNTHETASE	-0.4706	0.0655	0.1467	-0.7599	0.0153	0.0649	-0.00098	0.9931	0.516	-0.2903	0.0529	0.082
259762_at	AT1G77600	binding	-0.2945	0.1793	0.2475	-0.2031	0.3249	0.3058	-0.6793	0.0199	0.0567	-0.5879	0.0315	0.0598
259763_at	AT1G77630	peptidoglycan-binding LysM domain-containing prot	-0.3483	0.2898	0.3172	-0.4104	0.2243	0.2481	0.1826	0.4666	0.346	0.1205	0.6239	0.3715
259764_at	AT1G64280	NPR1 (NONEXPRESSER OF PR GENES 1); protei	0.7037	0.0069	0.0562	0.5422	0.017	0.0677	0.1195	0.2043	0.2143	-0.04201	0.6225	0.3711
259765_at	AT1G64370	unknown protein	-0.1769	0.6119	0.4633	0.3434	0.3461	0.316	0.9702	0.002	0.0212	1.4905	4.00E-04	0.0089
259766_at	AT1G64360	unknown protein	-0.3644	0.4036	0.3772	0.1242	0.7664	0.4793	1.0833	0.0012	0.0188	1.5719	3.00E-04	0.0083
259767_s_at	AT1G29370;AT1G29350	[AT1G29370, kinase-related];[AT1G29350, similar t	0.6712	0.0025	0.0421	0.5536	0.005	0.0424	-0.504	0.005	0.0298	-0.6216	0.0023	0.016
259768_at	AT1G29390	CORI3/14-TM2 (cold regulated 314 thylakoid membr	-0.2695	0.1187	0.1992	-0.6985	0.0068	0.0467	0.5838	0.0127	0.0449	0.1549	0.3186	0.2477
259769_at	AT1G29400	AML5 (ARABIDOPSIS MEI2-LIKE PROTEIN 5); RN	-0.02934	0.8115	0.5273	-0.3115	0.0539	0.1152	-0.5217	0.0106	0.0408	-0.1809	0.1914	18
259770_s_at	AT1G07780.AT1G29410;A	[AT1G07780, PAI1 (PHOSPHORIBOSYLANTHRAN	-0.3343	0.1408	0.2183	-0.01494	0.9387	0.5287	0.06606	0.7356	0.4435	0.3854	0.1022	0.1221
259771_at	AT1G29470	dehydration-responsive protein-related	-0.1619	0.5819	0.2496	-0.311	0.0362	0.094	-0.2279	0.0044	0.0284	-0.377	7.00E-04	0.0105
259772_at	AT1G29480	unknown protein	0.3701	0.6598	0.4792	-0.9202	0.3034	0.2933	0.9179	0.1094	0.148	-0.3725	0.4518	0.3068
259773_at	AT1G29500	auxin-responsive protein, putative	-2.0863	0.002	0.04	-1.763	0.0038	0.0389	0.9545	0.0042	0.0279	1.2778	0.0014	0.0136
259774_at	AT1G29520	AWPM-19-like membrane family protein	-0.3793	0.189	0.2547	-0.1327	0.6095	0.4268	0.2883	0.2958	0.2666	0.5348	0.0897	0.1125
259775_at	AT1G29530	similar to unknown protein [Arabidopsis thaliana] (T	-1.2829	0.0041	0.0468	-1.4598	0.0026	0.0341	0.7914	0.022	0.0598	0.6145	0.0476	0.0769
259776_s_at	AT1G29590;AT1G29550	initiationinitiation factor 4E, putative / eIF-4E, putati	0.1962	0.2646	0.3021	0.3202	0.1018	0.1609	0.3877	0.0625	0.1074	0.5117	0.0278	0.0555
259777_at	AT1G29570	zinc finger protein-related	-1.5824	0.2093	0.2677	-1.4297	0.2482	0.2627	-0.693	0.2038	0.2141	-0.5402	0.3024	0.2399
259778_at	AT1G29610	similar to zinc finger protein related [Arabidopsis tha	0.6424	0.6343	0.4709	-1.2589	0.3708	0.3278	-1.0515	0.4475	0.3373	-2.9529	0.0774	0.1028
259779_s_at	AT1G32720.AT1G29620;A	[AT1G32720, cytochrome-c oxidase];[AT1G29620,	-0.3883	0.4858	0.414	-1.9881	0.0171	0.0679	0.7708	0.2025	0.2132	-0.8289	0.1768	0.1712
259780_at	AT1G29630	identical to Exonuclease 1 (EXO1) [Arabidopsis Th	-0.8865	0.4432	0.3951	-0.9838	0.2901	0.2866	-0.5631	0.4023	0.3175	-0.8604	0.2259	0.1994
259781_at	AT1G29650	transposable element gene	0.396	0.6502	0.4764	0.01922	0.9822	0.5397	0.4691	0.5435	0.3768	0.09232	0.9025	0.458
259782_at	AT1G29680	similar to unknown protein [Arabidopsis thaliana] (T	-0.4068	0.4089	0.3795	-0.00771	0.9869	0.5408	0.3868	0.4304	0.3298	0.7859	0.1496	0.1544
259783_at	AT1G29510	SAUR68 (SMALL AUXIN UPREGULATED 68)	-1.764	0.0236	0.0897	-1.3914	0.0483	0.1092	1.3685	0.0018	0.0206	1.7411	7.00E-04	0.0108
259784_at	AT1G29450	auxin-responsive protein, putative	-1.86	0.007	0.0563	-0.7028	0.1264	0.1803	-0.01066	0.9698	0.5099	1.1466	0.0123	0.0351
259785_at	AT1G29490	auxin-responsive family protein	-2.1937	0.1688	0.2404	0.7083	0.6169	0.4295	-0.8888	0.5025	0.3604	2.0132	0.1708	0.1676
259786_at	AT1G29660	GDSL-motif lipase/hydrolase family protein	-1.0018	0.0524	0.1314	-1.4991	0.015	0.0645	0.4932	0.0447	0.0885	-0.00411	0.982	0.4785
259787_at	AT1G29460	auxin-responsive protein, putative	-1.0707	0.0816	0.1652	-0.6007	0.2639	0.2719	0.424	0.3465	0.2915	0.894	0.0879	0.1112
259788_at	AT1G29670	GDSL-motif lipase/hydrolase family protein	-0.346	0.4909	0.4162	-0.4118	0.4182	0.3499	0.2938	0.0183	0.0541	0.228	0.0404	0.0695
259789_at	AT1G29395	COR414-TM1 (cold regulated 414 thylakoid membr	-0.8855	0.0037	0.046	-0.7717	0.0062	0.0451	0.2239	0.1504	0.1792	0.3378	0.0553	0.0843
259790_s_at	AT1G29430;AT5G27780	[AT1G29430, auxin-responsive family protein];[AT5	-1.317	0.0048	0.0498	-1.3264	0.0047	0.0418	0.8469	0.0221	0.06	0.8376	0.0229	0.0492
259791_at	AT1G29700	similar to unnamed protein product [Vitis vinifera] (G	-0.3738	0.0322	0.1041	-0.6382	0.0053	0.0431	-0.1188	0.0438	0.0874	-0.3832	7.00E-04	0.0108
259792_at	AT1G29690	CAD1 (CONSTITUTIVELY ACTIVATED CELL DEA	0.02541	0.9222	0.6576	0.3222	0.2576	0.2688	-0.2505	0.2904	0.2638	0.0463	0.833	0.438
259793_at	AT1G64380	AP2 domain-containing transcription factor, putative	-0.6283	0.3174	0.3328	-0.2154	0.7156	0.4639	0.08344	0.5284	0.3706	0.4964	0.0148	0.0387
259794_at	AT1G64330	myosin heavy chain-related	-0.3395	0.2495	0.2933	-0.3043	0.2942	0.2888	0.1314	0.4801	0.3514	0.1667	0.3797	0.2756
259795_at	AT1G64290	F-box protein-related	-1.6301	0.1233	0.2035	-0.1113	0.9006	0.5191	-0.1664	0.8522	0.4791	1.3524	0.1814	0.1743
259796_at	AT1G64270	transposable element gene	-0.5286	0.2551	0.2964	0.3166	0.4712	0.3726	-1.4531	0.0036	0.0265	-0.6079	0.0627	0.0908
259797_at	AT1G64410	transposable element gene	0.1797	0.746	0.5078	-0.3552	0.5304	0.3964	0.5061	0.3289	0.2828	-0.02886	0.9525	0.4717
259798_at	AT1G64310	pentatricopeptide (PPR) repeat-containing protein	0.9021	0.5871	0.4552	-0.3974	0.8079	0.4923	-0.00054	0.9997	0.5178	-1.3	0.4433	0.3023
259799_at	AT1G72290	trypsin and protease inhibitor family protein / Kunitz	-1.1504	0.2493	0.2932	-0.05214	0.9542	0.5329	-0.03702	0.9652	0.5088	1.0612	0.2535	0.2144
259800_at	AT1G72175	zinc finger (C3HC4-type RING finger) family protein	0.3018	0.2673	0.3036	0.3259	0.2368	0.2659	0.1902	0.2188	0.2229	0.2142	0.176	0.1708
259801_at	AT1G72230	plastocyanin-like domain-containing protein	-0.9299	0.0207	0.0848	-0.5803	0.0818	0.1435	0.35	0.2356	0.2325	0.6996	0.0494	0.0787
259802_at	AT1G72260	TH12.1 (THIONIN 2.1); toxin receptor binding	0.91	0.1775	0.2464	0.499	0.4208	0.351	0.4048	0.3014	0.2694	-0.00621	0.9864	0.4793
259803_at	AT1G72150	PATL1 (PATELLIN 1); transporter	-0.1965	0.343	0.3463	-0.1323	0.5095	0.3884	-0.08162	0.4022	0.3175	-0.01737	0.8518	0.4431
259804_at	AT1G72160	SEC14 cytosolic factor family protein / phosphoglyc	0.0678	0.8327	0.5332	0.6303	0.1042	0.1631	0.1869	0.4236	0.3269	0.7494	0.0234	0.05
259805_at	AT1G74890	disease resistance family protein	1.0893	0.1108	0.193	0.5935	0.3284	0.3078	-0.6922	0.2644	0.249	-1.1879	0.09	0.1128
259806_at	AT1G74900	similar to unknown protein [Arabidopsis thaliana] (T	-0.1453	0.4418	0.3945	-0.1615	0.397	0.34	-0.3324	0.1074	0.1184	-0.3486	0.0653	0.0931
259807_at	AT1G74920	syntaxin-related family protein	0.1643	0.9135	0.5549	1.2837	0.4172	0.3493	-0.6037	0.6927	0.4286	0.5156	0.735	0.4087
259808_at	AT1G49790	F-box family protein-related	-0.4154	0.3965	0.3735	0.718	0.1764	0.2173	-0.3273	0.4964	0.3584	0.8062	0.1394	0.1478
259809_at	AT1G49800	unknown protein	2.5112	0.0012	0.036	-0.0377	0.9074	0.5207	1.9977	0.0028	0.0242	-0.5511	0.1444	0.1511
259810_at	AT1G49810	ATNHD2 (Arabidopsis thaliana Na/H antiporter 2); s	0.6937	0.2227	0.2769	-1.8026	0.02	0.0724	1.6081	0.0093	0.0386	-0.8882	0.0603	0.0887
259811_at	AT1G49830	ethylene-responsive protein -related	-0.4335	0.1979	0.2613	0.2224	0.4731	0.3734	-0.8671	0.0219	0.0597	-0.2112	0.4248	0.2945
259812_at	AT1G49840	similar to unknown protein [Arabidopsis thaliana] (T	0.5209	0.0062	0.0542	0.5935	0.0039	0.0391	-0.2792	0.0065	0.0331	-0.2065	0.0182	0.0434
259813_at	AT1G49860	ATGSTF14 (Arabidopsis thaliana Glutathione S-tran	-1.6291	0.1918	0.2567	-1.3136	0.2746	0.2778	-0.5921	0.5991	0.3978	-0.2766	0.8032	0.4296
259814_at	AT1G49900	zinc finger (C2H2 type) family protein	2.3422	0.0248	0.0915	-0.6781	0.3679	0.3266	0.3404	0.6247	0.4062	-2.6798	0.0141	0.0377
259815_at	AT1G49870	similar to MBD10 (methyl-CpG-binding domain 10),	1.0534	0.3038	0.3252	-0.3548	0.7116	0.4627	0.42	0.6628	0.4189	-0.9882	0.3308	0.2537
259816_at	AT1G49850	zinc finger (C3HC4-type RING finger) family protein	0.363	0.0852	0.1691	0.603	0.0194	0.0717	-0.3437	0.0974	0.1389	-0.1036	0.5512	0.3455
259817_at	AT1G49880	Erv1/Alr family protein	0.2236	0.2256	0.2789	-0.2963	0.1318	0.1842	0.3528	0.0869	0.1301	-0.1662	0.3476	0.2614
259818_at	AT1G49890	similar to unknown protein [Arabidopsis thaliana] (T	-0.2431	0.2277	0.2803	-0.1923	0.3231	0.3048	-0.2154	0.0753	0.1195	-0.1647	0.1419	0.1494
259819_at	AT1G49820	ATMTK; S-methyl-5-thioribose kinase	0.9487	7.00E-04	0.0334	1.0912	4.00E-04	0.0251	-0.413	0.0153	0.0492	-0.2705	0.0562	0.0851
259820_at	AT1G66210	subtilase family protein	-0.1146	0.8643	0.5422	1.7986	0.046	0.1062	-0.2502	0.5786	0.3901	1.663	0.016	0.0403
259821_at	AT1G66220	subtilase family protein	0.1245	0.7204	0.4995	-0.6892	0.1005	0.1599	-0.2547	0.4757	0.3498	-1.0684	0.03	0.0582
259822_at	AT1G66230	MYB20 (myb domain protein 20); DNA binding / tra	-0.7937	0.0024	0.0421	-0.5768	0.0078	0.049	0.2133	0.0527	0.0974	0.4302

259890_at	AT1G72750	ATTIM23-2 (Arabidopsis thaliana translocase inner	0.2197	0.4471	0.3967	0.4251	0.1785	0.2186	-0.1836	0.1939	0.2079	0.02182	0.862	0.4464
259891_at	AT1G72730	initiation factor 4A, putative / eIF-4A, putative	-0.4604	0.2349	0.2843	-0.2643	0.4674	0.371	-0.2651	0.3687	0.3023	-0.06901	0.8052	0.4302
259892_at	AT1G72610	GLP1 (GERMIN-LIKE PROTEIN 1); manganese ion	-0.4201	0.0305	0.1012	-0.6368	0.0076	0.0489	0.1464	0.0077	0.0354	-0.07037	0.0758	0.1014
259893_at	AT1G71390	disease resistance family protein / LRR family prote	0.1753	0.7278	0.5018	0.6511	0.2377	0.2564	-0.4219	0.4196	0.3252	0.05394	0.9141	0.461
259894_at	AT1G71430	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.3734	0.0238	0.0899	0.5278	0.0074	0.0485	1.014	3.00E-04	0.014	1.1684	2.00E-04	0.0075
259895_at	AT1G71440	PFI (PRIFFERLING); protein binding	0.787	0.0144	0.0731	0.4197	0.092	0.1531	0.1828	0.2622	0.2478	-0.1845	0.2586	0.2172
259896_at	AT1G71500	Rieske (2Fe-2S) domain-containing protein	-0.4791	0.0033	0.0446	-0.4778	0.0034	0.0371	0.0726	0.3968	0.315	0.07386	0.3894	0.2797
259897_at	AT1G71380	ATCEL3/ATGH9B3 (ARABIDOPSIS THALIANA GL	-0.302	0.8167	0.5287	1.2415	0.3666	0.3259	-1.1226	0.4097	0.3206	0.4209	0.7476	0.4129
259898_at	AT1G71200	basic helix-loop-helix (bHLH) family protein	-1.6009	0.1811	0.2489	0.4669	0.6617	0.4457	-2.1004	0.1011	0.142	-0.03255	0.9753	0.4769
259899_at	AT1G71210	pentaticopeptide (PPR) repeat-containing protein	0.8369	0.0327	0.1049	1.3697	0.0063	0.0456	-1.0612	0.0153	0.0493	-0.5283	0.113	0.1298
259900_at	AT1G71230	AJH2/CSN5/CSN8B (COP9-SIGNALOSOME 8/J); p	-0.08933	0.7758	0.5167	-0.253	0.4368	0.3583	0.6725	0.0467	0.0906	0.5089	0.0978	0.1188
259901_at	AT1G74180	leucine-rich repeat family protein	-0.497	0.4003	0.3755	0.1318	0.8154	0.4947	-2.0734	0.0172	0.0524	-1.4446	0.0523	0.0815
259902_at	AT1G74170	protein binding	0.2152	0.6324	0.4704	0.3668	0.428	0.3544	-1.7945	0.0125	0.0444	-1.6429	0.0169	0.0415
259903_at	AT1G74160	similar to hypothetical protein [Arabidopsis thaliana] (T	-0.03545	0.8188	0.5293	-0.00819	0.9576	0.5336	-0.2051	0.169	0.1912	-0.1778	0.2198	0.196
259904_at	AT1G74150	similar to unknown protein [Arabidopsis thaliana] (T	-0.5285	0.3703	0.3597	-1.2076	0.0826	0.1443	0.5794	0.1998	0.2117	-0.09976	0.8047	0.4301
259905_s_at	AT1G74140;AT1G74130	[AT1G74140, similar to rhomboid family protein [Ara	0.7053	0.3129	0.3303	-0.6396	0.3546	0.3203	0.6027	0.3801	0.3078	-0.7422	0.2916	0.2344
259906_at	AT1G74120	mitochondrial transcription termination factor-relate	-0.00789	0.9787	0.5719	-0.1101	0.712	0.4628	-0.3005	0.34	0.2884	-0.4027	0.2205	0.1963
259907_at	AT1G60860	ARF GTPase-activating domain-containing protein	0.4687	0.0667	0.1483	0.3405	0.1434	0.1933	-0.9398	0.0074	0.0348	-1.068	0.0047	0.0217
259908_at	AT1G60850	ATRPAC42 (Arabidopsis thaliana RNA polymerase	0.675	0.0115	0.0671	0.2274	0.2106	0.2401	0.5822	0.0078	0.0354	0.1346	0.3162	0.2465
259909_at	AT1G60870	MEE9 (maternal effect embryo arrest 9)	0.06254	0.6412	0.4734	0.4836	0.0177	0.0688	-0.4302	0.0156	0.0497	-0.00913	0.9358	0.4673
259910_at	AT1G72700	haloacid dehalogenase-like hydrolase family protein	0.7549	0.0181	0.0804	0.6725	0.0262	0.081	-0.342	0.1549	0.1822	-0.4244	0.0955	0.1172
259911_at	AT1G72680	cinnamyl-alcohol dehydrogenase, putative	1.5585	0.0011	0.036	1.5477	0.0011	0.0293	0.3386	0.066	0.1112	0.3281	0.0723	0.0986
259912_at	AT1G72670	IQD8 (IQ-domain 8); calmodulin binding	-2.2313	0.0898	0.1735	-0.0295	0.9779	0.5388	-1.1713	0.3072	0.2721	1.0305	0.3617	0.2677
259913_at	AT1G72660	developmentally regulated GTP-binding protein, put	0.7556	0.2642	0.302	-0.06624	0.9149	0.5227	-0.2624	0.6756	0.4229	-1.0842	0.1361	0.1457
259914_at	no_match	no_match	-0.4606	0.1583	0.2321	-0.2374	0.4226	0.3518	-0.9379	0.0243	0.0632	-0.7146	0.0548	0.0838
259915_at	AT1G72790	hydroxyproline-rich glycoprotein family protein	0.5823	0.2067	0.2662	0.1953	0.6402	0.4384	0.4888	0.1022	0.1428	0.1018	0.6828	0.3915
259916_at	AT1G72600	hydroxyproline-rich glycoprotein family protein	1.4038	0.1216	0.202	1.1444	0.1854	0.2233	-0.8312	0.3104	0.2736	-1.0906	0.2025	0.1867
259917_at	AT1G72580	unknown protein	-1.4444	0.1297	0.2083	-0.8725	0.3142	0.2997	-0.6021	0.4718	0.3483	-0.03027	0.9701	0.4765
259918_at	AT1G72570	DNA binding / transcription factor	-0.3813	0.7615	0.512	-1.0621	0.4165	0.349	0.4457	0.7233	0.4397	-0.2351	0.8509	0.4429
259919_at	AT1G72560	PSD (PAUSED); tRNA binding	0.2539	0.279	0.3107	0.01919	0.9292	0.5265	-0.9347	0.01	0.0398	-1.1694	0.0045	0.0213
259920_at	AT1G72550	tRNA synthetase beta subunit family protein	0.3068	0.2034	0.2643	0.1926	0.6993	0.3388	0.04286	0.7486	0.4477	-0.07132	0.5984	0.3629
259921_at	AT1G72540	protein kinase, putative	1.1613	0.2404	0.2877	3.0746	0.0218	0.0748	-0.02436	0.9783	0.5122	1.889	0.0886	0.1116
259922_at	AT1G72770	HAB1 (HOMOLOGY TO ABI1); protein serine/threo	0.2168	0.4601	0.403	0.471	0.1508	0.1988	-0.6387	0.0458	0.0895	-0.3844	0.1599	0.1611
259923_at	AT1G72760	protein kinase family protein	0.8454	0.4788	0.4105	-0.01994	0.9861	0.5406	-0.1042	0.9277	0.5	-0.9695	0.4194	0.2923
259924_at	AT1G72740	DNA-binding family protein / histone H1/H5 family p	-0.3288	0.1141	0.1957	-0.02977	0.8641	0.5082	0.009895	0.9315	0.5011	0.3089	0.0461	0.0755
259925_at	AT1G75040	PR5 (PATHOGENESIS-RELATED GENE 5)	1.3437	0.0066	0.0549	1.5817	0.0036	0.0379	0.7031	0.0019	0.0207	0.9411	6.00E-04	0.0103
259926_at	AT1G75090	methyltransferase glycosyltransferase family protein	-0.04136	0.9324	0.5604	0.2199	0.6563	0.444	-0.3351	0.3517	0.2941	-0.07384	0.8279	0.4366
259927_at	AT1G75100	JAC1 (J-DOMAIN PROTEIN REQUIRED FOR CHL	-0.3982	0.0877	0.1717	-0.5697	0.0323	0.089	-0.1237	0.2562	0.2444	-0.2952	0.0342	0.0625
259928_at	AT1G74380	5'-3' exonuclease family protein	0.6019	0.0264	0.0939	0.6175	0.0244	0.0783	0.07281	0.6887	0.4273	0.08837	0.6285	0.3732
259929_at	no_match	no_match	-1.4063	0.0812	0.1647	-0.00821	0.9899	0.5416	-1.1065	0.1292	0.1634	0.2947	0.6382	0.3766
259930_at	AT1G74355	forkhead-associated domain-containing protein / FH	0.219	0.7721	0.5153	0.01222	0.987	0.5408	0.9856	0.2355	0.2324	0.7788	0.3322	0.2545
259931_at	AT1G74400	unknown protein	0.3783	0.6125	0.4635	0.08681	0.9059	0.5204	0.6728	0.0714	0.1161	0.3812	0.2393	0.2067
259932_at	AT1G74370	STOP1 (SENSITIVE TO PROTON RHIZOTOXICIT	0.2135	0.2497	0.2934	0.2691	0.1652	0.2091	-0.01251	0.941	0.5037	0.04308	0.7995	0.4286
259933_at	AT1G74350	similar to unnamed protein product [Vitis vinifera] (G	0.2305	0.2706	0.3057	0.2848	0.1897	0.2263	0.6237	0.0259	0.0654	0.678	0.0198	0.0452
259934_at	AT1G71340	glycerophosphoryl diester phosphodiesterase family	-0.02578	0.9131	0.5548	-0.8205	0.0209	0.0738	-1.0351	0.0096	0.039	-1.8298	0.0012	0.0127
259935_at	AT1G71250	SDS_motif lipase/hydrolase family protein	-0.2155	0.8633	0.5419	0.03934	0.9749	0.538	-0.9293	0.1971	0.2099	-0.6744	0.3248	0.2506
259936_at	no_match	no_match	1.3494	3.00E-04	0.0312	1.4149	2.00E-04	0.0249	-0.3482	0.0384	0.0809	-0.2827	0.0691	0.0963
259937_s_at	AT3G13080;AT1G71330	[AT3G13080, ATMRP3 (Arabidopsis thaliana multid	0.5533	0.2238	0.2777	1.0807	0.0484	0.1092	-2.2741	0.0025	0.0232	-1.7467	0.0065	0.025
259938_at	AT1G71310	similar to unknown protein [Arabidopsis thaliana] (T	0.1781	0.3474	0.3486	0.3482	0.1061	0.1644	0.3133	0.0898	0.1324	0.4832	0.0263	0.0538
259939_s_at	AT1G71270;AT1G71300	[AT1G71270, POK (POKY POLLEN TUBE)][AT1G	0.1917	0.242	0.2887	0.4865	0.0253	0.0796	-0.4671	0.0288	0.0689	-0.1724	0.285	0.2308
259940_at	AT1G71290	F-box family protein-related	0.8689	0.5761	0.4511	-0.5862	0.7028	0.46	1.1985	0.4252	0.3276	-0.2565	0.8587	0.4454
259941_s_at	AT1G71370;AT1G71280	[AT1G71370, DEAD/DEAH box helicase, putative];[	0.1788	0.2624	0.3011	-1.332	0.2148	0.2426	0.2603	0.5497	0.379	0.1071	0.8017	0.4291
259942_at	AT1G71260	ATWHY2 (A. THALIANA WHIRLY 2); DNA binding	0.625	0.0109	0.0655	0.8239	0.0041	0.0397	-0.3382	0.0578	0.1028	-0.1393	0.3386	0.2573
259943_at	AT1G71480	nuclear transport factor 2 (NTF2) family protein	-0.4582	0.074	0.1564	-0.717	0.0197	0.072	-0.08243	0.6876	0.4269	-0.3412	0.1479	0.1533
259944_at	AT1G71470	similar to unknown protein [Arabidopsis thaliana] (T	-0.2177	0.109	0.1912	-0.8808	0.4202	0.3507	-0.8391	0.4408	0.3344	0.2978	0.7767	0.422
259945_at	AT1G71460	pentaticopeptide (PPR) repeat-containing protein	0.2649	0.4613	0.4036	-0.4069	0.2793	0.2805	0.2763	0.4014	0.3172	-0.3955	0.2505	0.2128
259946_at	AT1G71450	AP2 domain-containing transcription factor, putative	0.5563	0.4634	0.4045	-0.9799	0.2268	0.2497	-0.09182	0.864	0.4825	-1.628	0.0317	0.06
259947_at	AT1G71530	protein kinase family protein	0.2317	0.8093	0.5266	-0.2763	0.7739	0.4817	-1.0003	0.3075	0.2722	-1.5583	0.158	0.16
259948_at	AT1G71350	initiation factor SUI1 family protein	0.2493	0.3303	0.3402	0.3306	0.216	0.2434	0.2557	0.0524	0.0971	0.337	0.0228	0.0491
259949_at	AT1G71420	pentaticopeptide (PPR) repeat-containing protein	0.1541	0.7348	0.5038	-0.3284	0.4821	0.377	-0.3072	0.3888	0.3116	-0.7898	0.068	0.0952
259950_at	AT1G71410	protein kinase family protein	0.4318	0.0084	0.0599	0.1169	0.2597	0.2697	-0.6865	1.00E-04	0.012	-1.0014	0	0.0053
259951_at	AT1G71490	pentaticopeptide (PPR) repeat-containing protein	0.3085	0.6462	0.4751	0.6078	0.3842	0.3339	-0.265	0.6922	0.4284	0.03433	0.9587	0.4731
259952_at	AT1G71400	disease resistance family protein / LRR family prote	-0.0244	0.9235	0.558	-0.8941	0.02	0.0724	-0.02354	0.9262	0.4996	-0.8932	0.0201	0.0457
259953_at	AT1G74810	BOR5; anion exchanger	-0.667	0.0207	0.0846	-0.8443	0.0093	0.0528	-0.6141	0.0269	0.0667	-0.7914	0.0117	0.0339
259954_at	AT1G75130	CYP721A1 (cytochrome P450, family 721, subfami	0.7712	0.0237	0.0898	1.1801	0.0056	0.0434	-0.751	0.0249	0.0639	-0.3422	0.1859	0.1769
259955_s_at	AT1G75080;AT1G19350	[AT1G75080, BZR1 (BRASSINAZOLE-RESISTANT	-0.2475	0.1389	0.2163	-0.5282	0.017	0.0677	0.03755	0.7453	0.4466	-0.2431	0.0873	0.1106
259956_at	AT1G75110	RRA2 (REDUCED RESIDUAL ARABINOSE 2)	0.64	0.6202	0.4656	-0.2414	0.8496	0.5043	-0.9096	0.4714	0.3481	-1.791	0.1928	0.1807
259957_at	AT1G67890	protein kinase family protein	-0.1509	0.265	0.3022	-0.2275	0.1225	0.1777	-0.5429	0.0096	0.039	-0.6196	0.006	0.024
259958_at	AT1G53730	SRF6 (STRUBBELIG-RECEPTOR FAMILY 6); ATP	-0.5456	0.1579	0.2316	-0.8417	0.0555	0.1169	-0.1332	0.5126	0.3641	-0.4294	0.0817	0.1064
259959_at	AT1G53720	ATCYP59;CYP59 (CYCLOPHILIN 59); RNA binding	0.3437	0.3402	0.3452	0.5287	0.1714	0.2138	-0.407	0.2694	0.2519	-0.222	0.5232	0.3351
259960_at	AT1G53710	protein serine/threonine phosphatase	0.4588	0.3224	0.3357	1.4166	0.0253	0.0796	-1.6328	0.016	0.0505	-0.675	0.1724	0.1686
259961_at	AT1G53700	WAG1; kinase	-0.5474	0.6087	0.4627	-1.6006	0.1801	0.2196	1.7454	0.1239	0.1593	0.6922	0.4838	0.3192
259962_at	AT1G53690	DNA-directed RNA polymerases I, II, and III 7 kDa s	-1.8929	0.1074	0.1895	-0.5152	0.6035	0.4247	-0.798	0.4324	0.3307	0.5797	0.5608	0.3492
259963_at	AT1G53660	phosphate translocator-related	0.6212	0.5434	0.4384	0.4755	0.6384	0.4376	0.008502	0.9882	0.5149	-0.1372	0.8119	0.4323
259964_at	AT1G53680	ATGSTU28 (Arabidopsis thaliana Glutathione S-tra	0.5902	0.3996	0.3751	-1.2178	0.1239	0.1785	1.2571	0.1153	0.1526	-0.5509	0.4289	0.2962
259965_at	AT1G53670	MSRB1 (METHIONINE SULFOXIDE REDUCTASE	-0.0941	0.8802	0.5464	-1.14	0.0097	0.0537	1.6393	0.0026	0.0235	0.5387	0.0931	0.1153
259966_at	AT1G76500	DNA-binding family protein	1.951	0.02	0.0834	0.4979	0.393	0.3383	-0.262	0.6412	0.4115	-1.7151	0.0301	0.0583
259967_at	AT1G76510	ARID/BRIGHT DNA-binding domain-containing prot	0.1888	0.0985	0.1811	0.3712	0.0135	0.0617	-0.05974	0.5346	0.373	0.1226	0.236	0.2049
259968_at	AT1G76530	auxin efflux carrier family protein	-0.3918	0.3648	0.3567	-0.7437	0.1245	0.1789	-0.1919	0.6431	0.4121	-0.5438	0.2292	0.2011
259969_at	AT1G76550	pyrophosphate--fructose-6-phosphate 1-phosphotra	-0.3521	0.1385	0.2161	-0.1021	0.6205	0.4308	-0.2228	0.3075	0.2722	0.0272	0.8935	0.4553
259970_at	AT1G76570	chlorophyll A-B binding family protein	-0.7664	0.0033	0.0446	-1.2187	6.00E-04	0.0265	0.1695	0.2377	0.2339	-0.2827	0.0817	0.1064
259971_at	AT1G76580	transcription factor	0.3418	0.2197	0.2749	0.2473	0.3522	0.3192	-0.7547	7.00E-04	0.0159	-0.8492	4.00E-04	0.009
259972_at	AT1G76420	CUC3 (CUP SHAPED COTYLEDON3); transcriptio	0.01475	0.9856	0.5733	0.1774	0.8285	0.4985	0.03398	0.9668	0.5093	0.1966	0.8104	0.4319
259973_at	AT1G76630	tetratricopeptide repeat (TPR)-containing protein	-0.1784	0.5897	0.456	0.2864	0.4005	0.3413	-1.8899	0.0034	0.0259	-1.4252	0.0095	0.0303
259974_at	AT1G76430	phosphate transporter family protein	-0.6417	0.5649	0.4469	1.1831	0.3123	0.2986	-0.2308	0.8327	0.4734	1.594	0.1946	0.1817
259975_at	AT1G76470	cinnamoyl-CoA reductase	1.181	0.0904	0.1741	-0.5539	0.3561	0.3209	0.2773	0.6294	0.4077	-1.4577	0.0518	0.081
259976_at	AT1G76560	CP12-3	0.1752	0.6503	0.4764	0.5077	0.2294	0.2511	0.0788	0.8203	0.4698	0.4112	0.2743	0.2252
259977_at	AT1G76590	zinc-binding family protein	0.6498	0.2047	0.2651	1.0735	0.0667	0.1293	-0.09643	0.7849	0.4588	0.3273	0.378	0.2748
259978_at	AT1G76540	CDKB2;1 (CYCLIN-DEPENDENT KINASE B2;1); k	-0.1677	0.6072	0.4622	0.04415	0.8905	0.5159	0.01161	0.97	0.5099	0.2234	0.4836	0.3192
259979_at	AT1G76600	similar to unknown protein [Arabidopsis thaliana] (T	-1.0894	0.0969	0.1798	-0.5507	0.3362	0.3116	0.02761	0.9291	0.5003	0.5663	0.1241	0.1377
259980_at	AT1G76520	auxin efflux carrier family protein	0.3105	0.0588	0.1388	0.0732	0.5702	0.4119	0.1352	0.3176	0.2771	-0.1022	0.4372	0.3001
259981_at	AT1G76450	oxygen-evolving complex-related	-0.9375	5.00E-04	0.0323	-0.7343	0.0013	0.0307	-0.6833	0.0017	0.0205	-0.4802	0.0062	0.0244
259982_at	AT1G76410	ATL8; protein binding / zinc ion binding	-0.01119	0.9754	0.5711	-0.1355	0.7111	0.4625	0.7605	0.0894	0.1321	0.6362	0.1352	0.1452
259983_at	AT1G76490	HMG1 (3-HYDROXY-3-METHYLGLUTARYL COA	-0.4516	0.1069	0.1892	-0.6988	0.0327	0.0896	-0.8525	0.0047	0.0292	-1.0997	0.0018	0.0148
259984_at	AT1G76460	RNA recognition motif (RRM)-containing protein	-0.1123	0.6059	0.4617	-0.2414	0.2956	0.2895	-0.5033	0.0663	0.1114	-0.6325	0.0345	0.0628
259985_at	AT1G76620	similar to unknown protein [Arabidopsis thaliana] (T	-0.2974	0.5092	0.4246	-0.7232	0.1532	0.2004	0.3587	0.0677	0.1128	-0.0671	0.6659	0.3861
259986_at	AT1G75050	similar to ATLP-3 (Arabidopsis thaliana thaumatin-like protei	-0.3027	0.729	0.5023	-0.8834	0.3392	0.3131	1.3597	0.005	0.0298	0.779	0.0325	0.0609
259987_at	AT1G75030	ATLP-3 (Arabidopsis thaumatin-like protein 3)	-1.7503	0.0129	0.0699	-1.5201	0.0206	0.0732	0.1576	0.2577	0.2451	0.3878	0.0315	0.0598
259988_at	AT1G41797	transposable element gene	-1.7392	0.4875	0.4148	0.5859	0.8096	0.4928	1.4875	0.5492	0.3788	3.8127	0.1693	0.1668
259989_at	AT1G41750	transposable element gene	1.1244	0.3506	0.3499	0.002784	0.998	0.5435	1.3352	0.2782	0.257	0.2136	0.8508	0.4429
259990_s_at	AT5G23410;AT1G68050;A	[AT5G23410, similar to FKF1 (FLAVIN-BINDING KE	0.5897	0.1722	0.2429	1.0026	0.0477	0.1084	-0.1035	0.7391	0.4445	0.3093	0.3463	0.2608
259991_at	AT1G68040	S-adenosyl-L-methionine:carboxyl methyltransferas	-1.6282	0.0759	0.1585	-0.04784	0.9476	0.5313	-1.2168	0.1498	0.1788	0.3636	0.6232	0.3713
259992_at	AT1G67970	AT-HSFA8 (Arabidopsis thaliana heat shock transc	1.9625	0.0019	0.0391	1.6749	0.0035	0.0374	0.4487	0.0424	0.0858	0.1611	0.3509	0.263
259993_at	AT1G67960	similar to unnamed protein product [Vitis vinifera] (G	0.694	0.0164	0.0771	0.3906	0.0886	0.15	-0.5762	0.0202	0.0572	-0.8795	0.0047	0.0217
259994_at	AT1G68130	ATIDD14 (ARABIDOPSIS THALIANA INDETERMI	0.09786	0.08	0.4615	0.4036	0.5602	0.0096	0.0536	0.06765	0.4176	0.3241	0.53	0.0021
259995_at	AT1G67930	transporter, complex protein-related	0.3447	0.08	0.1632	0.1113	0.4932	0.3816	-0.1694	0.3155	0.276	-0.4028	0.0527	0.0818
259996_at	AT1G67910	similar to unknown protein [Arabidopsis thaliana] (T	-0.6078	0.1633	0.2365	-0.4854	0.2449	0.261	0.9357	0.0131	0.0455	1.0581	0.0086	0.0288
259997_at	AT1G67880	glycosyl transferase family 17 protein	-0.2503	0.138	0.2159	-0.02709	0.8511	0.5048	-0.4073	0.0193	0.0557	-0.1841	0.162	0.1624
259998_at	AT1G67900	ATBPC3/BBR/BPC3 (BPC3 (BASIC PENTACYSTEI	1.2681	0.2232	0.2771	0.9537	0.3396	0.3133	-0.6081	0.3702	0.303	-0.9226	0.2007	0.1896
259999_at	AT1G68080	oxidoreductase, acting on paired donors, with incor	0.06092	0.8974	0.5505	0.07099	0.8806	0.5133	-0.3743	0.4462	0.3367	-0.3643	0.4576	0.3091
260000_at	AT1G68060	ATMAP70-1 (MICROTUBULE-ASSOCIATED PRO	-0.05973	0.7355	0.5041	0.156	0.3977	0.3403	0.4796	0.0437	0.0872	0.6954	0.0135	0.0368
260001_at	AT1G67990	caffeoyl-CoA 3-O-methyltransferase, putative	1.4363	0.146	0.2221	1.155	0.221	0.2466	-1.6254	0.0968	0.1384	-1.9067	0.0644	0.0922
260002_at	AT1G67940	ATNAP3 (Arabidopsis thaliana non-intrinsic ABC pr	0.4095	0.0676	0.1493	0.469	0.0464	0.1068	0.5383	0.0308	0.0715	0.5978	0.0221	0.0485
260003_at	AT1G68100	IAR1 (IAA-ALANINE RESISTANT 1); metal ion tran	0.735	0.0036	0.0456	0.6633	0.0052	0.0429	-0.1393	0.3111	0.2741	-0.2108	0.154	0.1575
260004_at	AT1G67860	similar to unknown protein [Arabidopsis thaliana] (T	-0.3474	0.2847	0.3141	-0.09949	0.7416	0.4718	1.2969	0.002	0.0212	1.5448	0.001	0.0122
260005_at	AT1G67920	similar to unknown protein [Arabidopsis thaliana] (T	1.2707	0.0944	0.1777	1.5759	0.0537	0.1149	0.3511	0.2995	0.2685	0.6563	0.09	0.1129
260006_at	AT1G68090	ATPIS1 (Arabidopsis thaliana phosphatidylinositol s	0.1527	0.395	0.3726	0.4449	0.2512	0.2647	-0.5157	0.0507	0.0954	-0.1255	0.5382	0.3406
260007_at	AT1G67870	glycine-rich protein	-0.9753	0.015	0.0741	-0.6685	0.0487	0.1095	0.9825	3.00E-04	0.0138	1.2893	1.00E-04	0.0061
260008_at	AT1G68070	zinc finger (C3HC4-type RING finger) family protein	0.4575	0.0109	0.0655	0.2969	0.0435	0.1034	-0.0677	0.5429	0.3765	-0.2283	0.0886	0.1117
260009_at	AT1G67850	RNA recognition motif (RRM)-containing protein	0.6376	0.0751	0.1576	-0.6072	0.0541	0.1153	0.6478	9.00E-04	0.0173	0.5882	0.0014	0.0137
260010_at	AT1G68020	ATTPS6 (Arabidopsis thaliana trehalose phosphata	-0.2797	0.3129	0.3303	0.2989	0.2852	0.2839	-1.6624	0.0017	0.0205	-1.0839	0.008	0.0279
260011_at	AT1G68110	epsin N-terminal homology (ENTH) domain-contain	1.0026	0.1872	0.2535	0.7045	0.3266	0.3068	-1.2241	0.1243	0.1596	-1.5222	0.0733	0.0994
260012_at	AT1G67865	unknown protein	0.7514	0.0909	0.1747	-0.8132	0.0744	0.1368	0.7583	0.0115	0.0425	0.6984	0.0154	0.0395
260013_at	AT1G68090	ANN5/ANNAT5 (ANNEXIN ARABIDOPSIS 5); calci	-1.3579	0.3086	0.3277	-2.8376	0.0716	0.1339	1.2316	0.3501	0.2933	-0.2481	0.8418	0.4406
260014_at	AT1G68010	HPR (HYDROXYPYRUVATE REDUCTASE); glyce	-0.4999	0.0153	0.0747	-0.699	0.0047	0.0418	-0.278	0.0559	0.1009	0.4771	0.0102	0.0316
260015_at	AT1G68060	CCoAMT (caffeoyl-CoA 3-O-methyltransferase); cat	0.2727	0.0257	0.0929	0.217	0.0717	0.0748	0.09291	0.6148	0.4025	0.2152	0.2754	0.2258
260016_at	AT1G41795	transposable element gene	-1.0562	0.5714	0.4495	-0.4326	0.8133	0.4941	-0.2942	0.8721	0.4847	0.3294	0.8571	0.445
260017_at	AT1G41810	transposable element gene	0.6859	0.4358	0.392	-1.137	0.2249	0.2484	1.2708	0.0881	0.131	-0.5521	0.3846	0.2778
260018_at	AT1G41820	unknown protein	0.4429	0.7474	0.5081	-0.8579	0.5404	0.4008	0.2547	0.8303	0.4728	-1.0461	0.4008	0.2946
260019_at	AT1G41825	transposable element gene	0.3096	0.6195	0.4663	-0.5656	0.3817	0.3328	0.5162	0.4208	0.3257	-0.3589	0.567	0.3516
260020_at	AT1G29990	prefoldin, putative	0.06777	0.477	0.4106	0.7818	8.00E-04	0.0284	0.3027	0.0087	0.0373	1.0168	1.00E-04	0.0058
260021_at	AT1G30010	intron maturase, type II family protein	-0.3356	0.2815	0.2122	-0.08623	0.7652	0.4789	-0.2862	0.2359	0.2328	-0.03688	0.8662	0.4472
260022_at	AT1G30020	similar to unknown protein [Arabidopsis thaliana] (T	1.1437	0.2769	0.3099	-0.6

260090_at	AT1G73310	SCPL4 (serine carboxypeptidase-like 4); serine carl	0.4334	0.0329	0.1051	-0.2577	0.1297	0.1827	-0.8261	0.0036	0.0266	-1.5171	4.00E-04	0.0088
260091_at	AT1G73290	SCPL5 (serine carboxypeptidase-like 5); serine carl	-1.1715	0.4425	0.3948	1.2283	0.4225	0.3518	-1.0206	0.4685	0.3468	1.3793	0.3405	0.2583
260092_at	AT1G73280	SCPL3 (serine carboxypeptidase-like 3); serine carl	-0.1996	0.9309	0.5601	0.3138	0.8916	0.5162	0.2	0.9125	0.4959	0.7134	0.6979	0.3967
260093_at	AT1G73270	SCPL6 (serine carboxypeptidase-like 6); serine carl	-2.8307	0.1189	0.1993	0.9101	0.5591	0.408	-2.6265	0.1094	0.1479	1.1142	0.433	0.2981
260094_at	AT1G73250	ATFXGER1 (GDP-4-KETO-6-DEOXYMANNOSE-3	0.01853	0.9427	0.5631	0.2918	0.2946	0.289	-0.5585	0.0557	0.1007	-0.2853	0.244	0.2093
260095_at	AT1G73230	nascent polypeptide-associated complex (NAC) dor	-0.01039	0.911	0.5543	-0.08839	0.3688	0.327	0.3211	0.006	0.0321	0.2431	0.0157	0.0399
260096_at	AT1G73240	similar to unnamed protein product [Vitis vinifera] (G	0.3295	0.141	0.2183	-0.3189	0.151	0.1989	0.2191	0.2902	0.2637	-0.4293	0.0755	0.1012
260097_at	AT1G73220	ATOCT1 (ARABIDOPSIS THALIANA ORGANIC CA	0.6075	0.4533	0.3997	0.4978	0.5339	0.3979	-0.3748	0.4486	0.3339	-0.4846	0.3389	0.2575
260098_at	AT1G73320	similar to Expressed protein [Arabidopsis thaliana] (	-0.2222	0.1953	0.2594	-0.1592	0.3281	0.3076	-0.3647	0.0634	0.1084	-0.3017	0.1026	0.1224
260099_at	AT1G73180	initiation factor-related	0.2447	0.3352	0.3429	0.3575	0.1849	0.2231	-0.95	7.00E-04	0.016	-0.8371	0.0012	0.0127
260100_at	AT1G73177	BNS (BONSAI)	-0.5028	4.00E-04	0.032	-0.3637	0.0015	0.0315	0.874	1.00E-04	0.0092	1.0131	0	0.0053
260101_at	AT1G73260	trypsin and protease inhibitor family protein / Kunitz	0.5399	0.4976	0.4195	0.6892	0.3954	0.3392	0.5908	0.0681	0.1132	0.7402	0.0359	0.0644
260102_at	AT1G35470	SPla/RYanodine receptor (SPRY) domain-containin	-0.1692	0.0695	0.152	-0.1574	0.0838	0.1455	-0.04378	0.5499	0.379	-0.03195	0.6589	0.3838
260103_at	AT1G35430	similar to unknown [Populus trichocarpa] (GB:ABK9	-0.239	0.3536	0.3515	-0.1258	0.6105	0.4271	-0.1954	0.4396	0.3339	-0.08219	0.7367	0.4093
260104_x_at	AT1G35410	similar to unknown protein [Arabidopsis thaliana] (T	0.001788	0.9975	0.5763	0.4061	0.4864	0.3789	-0.5664	0.2573	0.2448	-0.1621	0.7248	0.4056
260105_at	AT1G35480	transposable element gene	0.3981	0.757	0.5108	-2.2328	0.1366	0.1881	1.5683	0.2612	0.2472	-1.0626	0.4258	0.295
260106_at	AT1G35420	dienelactone hydrolase family protein	-0.1944	0.0941	0.1776	-0.269	0.039	0.0979	-0.09263	0.184	0.2015	-0.1672	0.0444	0.0739
260107_at	AT1G66430	pfkB-type carbohydrate kinase family protein	-0.5951	0.0219	0.0868	-0.3957	0.0724	0.1349	0.1832	0.3246	0.2806	0.3825	0.0791	0.1041
260108_at	AT1G63280	serpin-related / serine protease inhibitor-related	1.7084	0.1659	0.2381	0.1889	0.8607	0.5073	0.572	0.6013	0.3986	-0.9476	0.4011	0.2846
260109_at	AT1G63260	TET10 (TETRASPANIN10)	-0.4672	0.1745	0.2445	-0.568	0.1155	0.1715	-0.5286	0.1051	0.145	-0.6294	0.0678	0.095
260110_at	AT1G63350	disease resistance protein (CC-NBS-LRR class), p	0.7383	0.0214	0.0859	0.407	0.1132	0.1701	0.04576	0.8313	0.4731	-0.2856	0.2289	0.2009
260111_at	no_match	no_match	-0.7768	0.5278	0.4323	-0.7777	0.5274	0.3951	-0.00137	0.9991	0.5176	-0.00226	0.9985	0.4928
260112_at	AT1G63310	similar to oxidoreductase, acting on NADH or NADP	-0.6128	0.1194	0.1997	-0.212	0.5319	0.3969	1.3462	0.0123	0.044	1.747	0.0049	0.022
260113_at	AT1G63300	similar to unknown protein [Arabidopsis thaliana] (T	-0.5564	0.1583	0.2321	1.0155	0.0341	0.0912	-0.4743	0.1588	0.185	1.0976	0.0161	0.0405
260114_at	AT1G33880	avirulence-responsive family protein / avirulence inc	1.1364	0.2387	0.2889	-0.793	0.389	0.3363	1.1005	0.2514	0.2415	-0.8289	0.37	0.2713
260115_at	AT1G33870	avirulence-responsive protein, putative / avirulence	-0.3345	0.6708	0.4829	-1.9245	0.0579	0.1196	1.6471	0.0872	0.1304	0.05712	0.9414	0.4689
260116_at	AT1G33960	AIG1 (AVRRPT2-INDUCED GENE 1); GTP binding	1.6904	2.00E-04	0.0312	2.464	0	0.0249	0.02849	0.8277	0.472	0.8021	0.0028	0.0174
260117_at	AT1G33950	avirulence-responsive family protein / avirulence inc	1.4375	0.1064	0.1887	0.854	0.2848	0.2837	0.9181	0.2428	0.2365	0.3346	0.6438	0.3785
260118_s_at	AB518700;AT1G33940	AB518700; EMB3013 (EMBRYO DEFECTIVE 30	-0.4764	0.008	0.0586	-1.0498	4.00E-04	0.0251	-0.5659	0.0043	0.028	-1.1394	3.00E-04	0.0083
260119_at	AT1G33930	avirulence-responsive family protein / avirulence inc	-1.4567	0.1841	0.2511	-1.2748	0.2332	0.2535	-1.6713	0.1379	0.1695	-1.4895	0.1744	0.1699
260120_at	AT1G33920	ATPP2-A4 (Phloem protein 2-A4); carbohydrate bin	0.1121	0.8977	0.5505	-1.2367	0.2055	0.2364	1.4468	0.1521	0.1804	0.3221	0.7141	0.4023
260121_at	AT1G33910	avirulence-responsive family protein / avirulence inc	-0.8008	0.4062	0.3784	-1.48	0.1617	0.2069	0.2219	0.8099	0.4665	-0.4573	0.6244	0.3717
260122_at	AT1G33900	avirulence-responsive protein, putative / avirulence	-1.6308	0.1505	0.2261	-0.7986	0.4337	0.3569	-0.1739	0.8179	0.4692	0.6583	0.4048	0.286
260123_at	AT1G33890	avirulence-responsive protein, putative / avirulence	0.7279	0.5208	0.4293	0.6686	0.4263	0.3	0.4497	0.6572	0.4169	0.3984	0.6991	0.3971
260124_at	AT1G36340	UBC31 (UBIQUITIN-CONJUGATING ENZYME 31)	0.9291	0.4826	0.4131	2.2031	0.1407	0.1911	-0.5178	0.5887	0.4274	0.7562	0.5633	0.3502
260125_at	AT1G36390	co-chaperone grpE family protein	-0.2659	0.2248	0.2784	-0.6674	0.0228	0.0761	1.0006	0.0057	0.0315	0.5991	0.0319	0.0602
260126_at	AT1G36370	SHM7 (serine hydroxymethyltransferase 7); glycine	-1.7748	0.0016	0.0383	-2.0312	9.00E-04	0.0288	0.2568	0.1416	0.1726	0.000163	0.9991	0.4828
260127_at	AT1G36320	similar to unknown protein [Arabidopsis thaliana] (	0.2282	0.0645	0.1453	-0.1095	0.2911	0.2872	-0.4573	0.0071	0.0341	-0.7949	9.00E-04	0.0117
260128_at	AT1G36310	methyltransferase	0.0646	0.7068	0.495	-0.07173	0.6768	0.4508	-0.09677	0.4902	0.3557	-0.2331	0.1416	0.1492
260129_at	AT1G36380	electron carrier/ ubiquinol-cytochrome-c reductase	-0.1762	0.3251	0.3374	-0.02539	0.8795	0.513	0.4355	0.0166	0.0514	0.5863	0.0059	0.0239
260130_s_at	AT1G66280;AT1G66270	[AT1G66280, glycosyl hydrolase family 1 protein];[A	1.4884	0.222	0.2764	0.7207	0.5227	0.3932	-0.8367	0.4623	0.3442	-1.6044	0.1944	0.1816
260131_at	AT1G66310	F-box family protein	2.5621	0.0188	0.0814	0.5739	0.4403	0.3596	1.5063	0.088	0.1309	-0.4819	0.5121	0.3306
260132_s_at	AT1G66340;AT1G66320	[AT1G66340, similar to F-box family protein (Arabid	0.3141	0.6122	0.4635	0.641	0.3253	0.3061	-0.4655	0.4615	0.3439	-0.1386	0.8205	0.4343
260133_at	AT1G66340	ETR1 (ETHYLENE RESPONSE 1); two-component	0.3693	0.1556	0.2302	-0.2193	0.3543	0.3202	-0.3122	0.2105	0.2181	-0.8974	0.0128	0.0358
260134_at	AT1G66370	MYB113 (myb domain protein 113); DNA binding / t	-0.05888	0.871	0.5443	-0.3064	0.4187	0.3501	0.3344	0.2072	0.2161	0.08691	0.7159	0.4028
260135_at	AT1G66400	calmodulin-related protein, putative	-1.8148	0.0101	0.064	-0.6464	0.1778	0.2182	-0.1581	0.58	0.3907	1.0103	0.0184	0.0436
260136_at	AT1G66360	C2 domain-containing protein	0.5637	0.4562	0.401	1.47	0.0981	0.1579	0.2857	0.6977	0.4304	1.192	0.1563	0.159
260137_at	AT1G66330	senescence-associated family protein	-0.2558	0.1548	0.2297	-0.2652	0.1437	0.1935	-0.188	0.164	0.1878	-0.1973	0.1486	0.1537
260138_at	AT1G66410	CAM4 (CALMODULIN 4); copper ion binding	0.3699	0.2358	0.2849	0.8434	0.0336	0.0906	0.6987	0.0318	0.0726	1.1722	0.0056	0.0234
260139_at	AT1G66380	MYB114 (myb domain protein 114); DNA binding / t	0.7094	0.523	0.4303	0.5404	0.6532	0.4428	0.3697	0.7507	0.4485	0.1307	0.91	0.4599
260140_at	AT1G66390	PAP2 (PRODUCTION OF ANTHOCYANIN PIGME	0.4727	0.5035	0.422	2.5673	0.0163	0.0664	-0.7049	0.3351	0.286	1.3897	0.097	0.1183
260141_at	AT1G66350	RGL1 (RGA-LIKE 1); transcription factor	-0.248	0.2418	0.2887	-0.3942	0.0945	0.1549	0.0792	0.4925	0.3566	-0.06701	0.9579	0.3481
260142_at	AT1G71900	similar to permease-related [Arabidopsis thaliana] (	-0.0283	0.8786	0.5462	-0.221	0.2725	0.2768	-0.6432	0.0208	0.058	-0.8359	0.0086	0.0288
260143_at	AT1G71880	SUC1 (SUCROSE-PROTON SYMPORTER 1); car	0.4783	0.1182	0.1987	0.2524	0.3541	0.3201	0.2745	0.3184	0.2775	0.04849	0.8503	0.4428
260144_at	AT1G71960	ABC transporter family protein	0.2448	0.0784	0.1613	0.3363	0.032	0.0887	0.2632	0.0648	0.1098	0.3547	0.0221	0.0547
260145_at	AT1G52920	GCR2/GPCR (G PROTEIN COUPLED RECEPTOR	-0.301	0.3756	0.3622	-0.06848	0.8318	0.4993	0.1659	0.4545	0.3407	0.3984	0.1179	0.1333
260146_at	AT1G52770	phototropic-responsive NPH3 family protein	0.8505	0.1272	0.206	1.7337	0.0173	0.0681	-0.5899	0.028	0.068	0.2934	0.1687	0.1664
260147_at	AT1G52790	oxidoreductase, 2OG-Fe(II) oxygenase family prote	0.1118	0.9275	0.5591	0.6706	0.5926	0.4205	-1.7035	0.157	0.1837	-0.9211	0.4003	0.2843
260148_at	AT1G52800	oxidoreductase, 2OG-Fe(II) oxygenase family prote	1.0579	0.0923	0.176	1.0169	0.1016	0.1608	0.4003	0.1606	0.186	0.3593	0.1976	0.1835
260149_at	AT1G52810	2-oxoglutarate-dependent dioxygenase-related	1.1014	0.0489	0.1271	0.7683	0.1226	0.1777	-0.5466	0.2371	0.2335	-0.8798	0.089	0.112
260150_at	AT1G52820	2-oxoglutarate-dependent dioxygenase, putative	-1.0068	0.3413	0.3459	-0.7005	0.4946	0.3824	0.01558	0.9875	0.5146	0.3218	0.7476	0.4129
260151_at	AT1G52910	similar to unknown protein [Arabidopsis thaliana] (	-1.0264	0.0367	0.1104	-1.1399	0.0266	0.0816	-0.1706	0.5487	0.3786	-0.2841	0.3373	0.2566
260152_at	AT1G52830	IAA6 (indoleacetic acid-induced protein 6); transcrip	-1.1834	0.0756	0.1583	-0.5976	0.2949	0.2892	0.8014	0.02	0.0567	1.3872	0.0029	0.0176
260153_at	AT1G52760	esterase/lipase/thioesterase family protein	0.7471	0.1542	0.1336	0.6833	0.0691	0.1319	-0.1897	0.1637	0.1877	-0.2535	0.0851	0.1091
260154_at	AT1G52740	HTA9; DNA binding	0.1016	0.6089	0.4627	0.2903	0.1885	0.2255	-0.2883	0.0965	0.1381	-0.09955	0.4965	0.3245
260155_at	AT1G52870	peroxisomal membrane protein-related	-0.3773	0.0031	0.0437	-0.684	3.00E-04	0.0249	-0.3647	0.0027	0.0241	-0.6714	3.00E-04	0.0081
260156_at	AT1G52880	NAM (Arabidopsis NAC domain containing protein 1	0.3557	0.4336	0.391	0.5944	0.2198	0.2458	0.4944	0.0317	0.0725	0.7331	0.0086	0.0289
260157_at	AT1G52930	brix domain-containing protein	0.6599	0.0013	0.0376	0.738	9.00E-04	0.0284	-0.4963	7.00E-04	0.016	-0.4182	0.0014	0.0136
260158_at	AT1G79910	similar to unknown protein [Arabidopsis thaliana] (T	-0.3415	0.6488	0.4761	-1.3081	0.1329	0.1852	0.7161	0.361	0.2986	-0.2504	0.7368	0.4093
260159_at	AT1G79890	helicase-related	0.8656	0.4346	0.3913	-0.6406	0.5558	0.4068	0.5556	0.6073	0.4004	-0.9506	0.3947	0.2821
260160_at	AT1G79880	La domain-containing protein	0.4826	0.0161	0.0768	0.6735	0.005	0.0425	-0.6297	0.0064	0.033	-0.4388	0.022	0.0484
260161_at	AT1G79860	ATROPGEF12/MEE64/ROPGEF12 (MATERNAL E	0.2469	0.746	0.5078	-0.2189	0.7736	0.4817	-0.9474	0.2537	0.243	-1.4133	0.1179	0.1333
260162_at	AT1G79830	GC5 (GOLGIN CANDIDATE 5)	0.6022	0.0025	0.0425	0.3293	0.0213	0.0742	-0.6111	0.0024	0.023	-0.884	6.00E-04	0.0101
260163_at	AT1G79900	ATMBAC2/BAC2 (Arabidopsis mitochondrial basic (	1.2709	0.104	0.1864	0.614	0.3684	0.3268	-0.08956	0.8897	0.4896	-0.7464	0.2856	0.2312
260164_at	AT1G79870	oxidoreductase family protein	0.5749	0.0077	0.058	0.2142	0.1378	0.1891	0.521	0.0108	0.0413	0.1603	0.2381	0.2061
260165_at	AT1G79850	RPS17 (ribosomal protein S17); structural constitue	-0.7314	0.0022	0.0411	-0.6965	0.0027	0.0345	0.9114	1.00E-04	0.0119	0.9463	1.00E-04	0.0061
260166_at	AT1G79840	GL2 (GLABRA 2); DNA binding / transcription factor	-1.2976	0.1891	0.2547	-2.0261	0.0691	0.1318	0.5385	0.5477	0.3784	-0.19	0.8283	0.4367
260167_at	AT1G71970	similar to unknown protein [Arabidopsis thaliana] (T	-0.4029	0.0654	0.1467	-0.2782	0.157	0.2036	0.5149	5.00E-04	0.0148	0.6396	2.00E-04	0.0078
260168_at	AT1G71980	protease-associated zinc finger (C3HC4-type RING	0.3387	0.1349	0.2133	0.2904	0.1534	0.2006	-0.01967	0.8874	0.489	-0.03795	0.7856	0.4245
260169_at	AT1G71990	FUT13 (fucosyltransferase 13); fucosyltransferase/	-0.5732	0.1427	0.2198	-1.3387	0.0131	0.0611	0.2323	0.5014	0.3601	-0.5332	0.1655	0.1645
260170_at	AT1G71890	ATSUC5/SUC5 (SUCROSE-PROTON SYMPORTE	-0.4653	0.5028	0.4217	0.1471	0.8276	0.4982	-0.7047	0.3277	0.2822	-0.09232	0.891	0.4545
260171_at	AT1G71910	unknown protein	0.7265	0.0375	0.1118	0.1482	0.5659	0.4103	0.5799	0.0708	0.1157	0.001656	0.9948	0.4814
260172_s_at	AT5G10330;AT1G71920	[AT5G10330, EMB2196/HIS1N6/AHP41 (EMBRYO	-0.19	0.2394	0.2873	-0.03989	0.7862	0.485	-0.2264	0.0367	0.0788	-0.07633	0.3567	0.2655
260173_at	AT1G71930	VND7 (VASCULAR RELATED NAC-DOMAIN PRO	-0.07567	0.8587	0.5407	-1.0941	0.0517	0.1128	1.0549	0.0328	0.074	0.03653	0.917	0.4619
260174_at	AT1G71940	similar to unknown protein [Arabidopsis thaliana] (T	0.2834	0.0692	0.1515	0.4325	0.0197	0.072	-0.206	0.1475	0.1772	-0.05693	0.6463	0.3795
260175_at	AT1G72000	beta-fructofuranosidase, putative / invertase, putati	0.8859	0.2116	0.2693	0.09771	0.8778	0.5124	-0.1732	0.7649	0.4527	-0.9615	0.1503	0.1548
260176_at	AT1G71950	identical protein binding / sublitase	-0.1307	0.6252	0.4682	0.1718	0.5255	0.3943	0.8429	0.0022	0.0219	1.1454	7.00E-04	0.0105
260177_at	AT1G70650	zinc finger (Ran-binding) family protein	-2.067	0.0602	0.1404	-1.5761	0.1188	0.1742	-2.1706	0.0526	0.0973	-1.6796	0.1024	0.1223
260178_at	AT1G70720	invertase/pectin methylesterase inhibitor family prot	0.5695	0.5796	0.4521	-0.04683	0.9629	0.5347	-0.1958	0.8461	0.4775	-0.8121	0.439	0.301
260179_at	AT1G70690	kinase-related	0.4882	0.1143	0.196	0.9956	0.0148	0.0641	0.4067	0.1688	0.191	0.9141	0.0196	0.0449
260180_at	AT1G70660	MMZ2/UEV1B (MMS ZWEI HOMOLOGE 2); protein	0.3388	0.071	0.1537	0.2482	0.1479	0.1966	0.2993	0.097	0.1386	0.2088	0.2065	0.1888
260181_at	AT1G70710	AtGH9B1 (ARABIDOPSIS THALIANA GLYCOSYL	0.9627	0.0193	0.0823	0.8576	0.028	0.0833	-0.2749	0.3103	0.2736	-0.3799	0.1839	0.1758
260182_at	AT1G70750	similar to unknown protein [Arabidopsis thaliana] (T	-0.2971	0.3894	0.3696	-0.263	0.4413	0.36	-0.5801	0.0894	0.1321	-0.546	0.1035	0.1231
260183_at	AT1G35970	transposable element gene	-2.3274	0.0381	0.1123	-0.5807	0.4893	0.3801	-1.8099	0.0768	0.121	-0.06316	0.938	0.4678
260184_s_at	AT1G35950;AT2G05084;A	[AT1G35950, transposable element gene];[AT2G05	0.2108	0.8806	0.5465	-1.848	0.2331	0.2535	1.2983	0.3187	0.2777	-0.7605	0.5415	0.3415
260185_at	AT1G36030	F-box family protein	0.822	0.6836	0.487	-0.1503	0.9399	0.5291	1.2089	0.554	0.3804	0.2367	0.9056	0.459
260186_at	AT1G36020	similar to DEAD/DEAH box helicase, putative [Arab	0.7155	0.5928	0.4571	-2.0364	0.1739	0.2154	0.4973	0.7073	0.4337	-2.2545	0.1414	0.1491
260187_at	AT1G36000	LBD5 (LOB DOMAIN-CONTAINING PROTEIN 5)	-0.6338	0.422	0.386	0.8401	0.3018	0.2923	-1.7535	0.0688	0.1137	-0.2795	0.7136	0.4022
260188_at	AT1G35995	transposable element gene	0.4256	0.7307	0.5027	-0.6836	0.5852	0.4182	-0.3112	0.773	0.4553	-1.4205	0.2316	0.2024
260189_at	AT1G67500	URE (UREASE); urease	0.7494	0.0147	0.0736	0.8026	0.0116	0.0581	-0.5607	0.037	0.0793	-0.5075	0.0495	0.0788
260190_at	AT1G67560	lipoxygenase family protein	0.2357	0.1224	0.2027	0.2953	0.0706	0.1329	-0.0521	0.551	0.3794	0.007476	0.9301	0.4657
260191_at	AT1G67580	protein kinase family protein	0.2014	0.3422	0.3461	0.1107	0.5858	0.4183	-0.6898	0.0034	0.0257	-0.7805	0.0021	0.0156
260192_at	AT1G67630	POLA2: alpha DNA polymerase	-0.8393	0.1387	0.2162	-0.1326	0.7851	0.4848	-0.2906	0.5461	0.3779	0.4161	0.3991	0.2838
260193_at	AT1G67640	lysine and histidine specific transporter, putative	1.4517	0.1149	0.1963	1.0757	0.2108	0.2402	-0.2555	0.504	0.3609	-0.6315	0.1441	0.151
260194_at	AT1G67530	armadillo/beta-catenin repeat family protein / U-box	0.09403	0.1911	0.2562	-0.019	0.7667	0.4794	-0.3294	0.0053	0.0305	-0.4424	0.0018	0.0147
260195_at	AT1G67540	similar to hypothetical protein [Vitis vinifera] (GB:CA	-1.5041	0.3537	0.3515	1.224	0.4417	0.3602	-1.4338	0.3743	0.3048	1.2944	0.418	0.2917
260196_at	AT1G67570	similar to unknown protein [Arabidopsis thaliana] (T	-0.104	0.7373	0.5049	-0.1225	0.6935	0.4567	-0.3556	0.2495	0.2407	-0.3741	0.2297	0.2013
260197_at	AT1G67623	F-box family protein	0.2256	0.8679	0.5432	0.181	0.8938	0.5169	-0.5412	0.5105	0.3634	-0.5858	0.4784	0.317
260198_at	AT1G67635	similar to phosphatidylinositol 3- and 4-kinase famil	0.8704	0.467	0.406	1.4582	0.2506	0.2643	0.8399	0.4817	0.3519	1.4247	0.259	0.2173
260199_at	AT1G67590	remorin family protein	-0.1967	0.6315	0.4702	0.3254	0.4395	0.3594	-0.2951	0.3155	0.276	0.2271	0.4274	0.2957
260200_at	AT1G67620	similar to hypothetical protein [Vitis vinifera] (GB:CA	-0.01419	0.9557	0.5663	0.3659	0.202	0.2339	0.5026	0.029	0.0691	0.8828	0.0042	0.0208
260201_at	AT1G67600	similar to catalytic [Arabidopsis thaliana] (TAIR:AT1	-0.7684	0.1816	0.2493	0.8633	0.1438	0.1935	-0.9837	0.1075	0.1468	0.648	0.2448	0.2096
260202_at	AT1G52840	transposable element gene	1.3926	0.3143	0.331	0.2829	0.8268	0.498	2.2551	0.1361	0.1685	1.1454	0.3979	0.2833
260203_at	AT1G52890	ANAC019 (Arabidopsis NAC domain containing pro	0.4447	0.0677	0.1494	1.1329	0.0032	0.0366	0.0432	0.8141	0.4679	0.7314	0.0131	0.0364
260204_at	AT1G52900	disease resistance protein (TIR class), putative	0.2239	0.8198	0.5295	1.7676	0.1272	0.181	0.2932	0.5034	0.3606	1.8369	0.01	0.0312
260205_at	AT1G70700	JAZ9/TIFY7 (JASMONATE-ZIM-DOMAIN PROTEIN	-0.6073	0.0212	0.0855	-0.7045	0.013	0.0609	0.221	0.177	0.1965	0.1239	0.4107	0.2885
260206_at	AT1G70740	protein kinase family protein	-0.1887	0.4759	0.4101	-0.1879	0.4778	0.3754	0.2479	0.2758	0.2556	0.2485	0.2743	0.2262
260207_at	AT1G70730	phosphoglucomutase, cytoplasmic, putative / glucos	-0.00344	0.9751	0.571	-0.4462	0.0125	0.0599	0.1115	0.327	0.2819	-0.3313	0.0295	0.0576
260208_s_at	AT1G70670;AT1G70680	[AT1G70670, calcesin-related family protein];[AT1G	0.1348	0.5202	0.4291	0.8944	0.0099	0.0541	0.4171	0.0723	0.1169	1.1666	0.0025	0.0164
260209_at	AT1G68050;AT1G68850	[AT1G68050, CPuORF53 (Conserved peptide upst	0.006612	0.9837	0.573	0.1103	0.7649	0.4697	-0.309	0.0457	0.0895	-0.2053	0.1298	0.1413
260210_at	AT1G74420	FUT3 (fucosyltransferase 3); fucosyltransferase/ tra	-1.0307	0.0712	0.1538	-0.8764	0.1067	0.1648	-0.8226	0.1233	0.1589	-0.6683	0.1888	0.1787
260211_at	AT1G74440	similar to unknown protein [Arabidopsis thaliana] (T	0.7666	0.0706	0.1533	0.5661	0.145	0.1945	-0.1124	0.5507	0.3794	-0.3129	0.1443	0.1511
260212_at	AT1G74480	RWP-RK domain-containing protein	0.2037	0.9053	0.5526	0.2647	0.6772	0.5123	0.4761	0.7819	0.458	0.5371	0.7552	0.4162
260213_at	AT1G74490	protein kinase, putative	0.394	0.7258	0.5013	1.0877	0.3575	0.3217	-0.25	0.8222	0.4703	0.4437	0.6922	0.3947
260214_at	AT1G74510	kelch repeat-containing F-box family protein	-0.05008	0.6592	0.479	0.3063	0.0438	0.1036	-0.5209	0.0078	0.0355	-0.1645	0.1933	0.1809
260215_at	AT1G74530	similar to unnamed protein product [Vitis vinifera] (G	0.01356	0.9374	0.5616	-0.2781	0.1616	0.2069	-0.4447	0.0518	0.0965	0.153	0.3991	0.2838
260216_at	AT1G74580	pentatricopeptide (PPR) repeat-containing protein	-0.5595	0.5255	0.4314	0.1021	0.9053	0.5202	-1.4783	0.1077	0.1469	-0.8168	0.3173	0.2471
260217_at	AT1G74600	pentatricopeptide (PPR) repeat-containing protein	0.5436	0.157	231	0.8212	0.0584	0.1201	-0.4337	0.2376	0.2338	-0.1561	0.6436	0.3784
260218_at	AT1G74620	zinc finger (C3HC4-type RING finger) family protein	0.3079	0.0442	0.1212	-0.8357	0.3531	0.3197	-0.7009	0.3801	0.3078	0.7713	0.3391	0.2675
260219_at	AT1G74630	pentatricopeptide (PPR) repeat-containing protein	-0.03333	0.9005	0.5512	-0.4013	0.1841	0.2225	0.6164	0.0241	0.0629	0.2485	0.2274	0.2001
260220_at	AT1G74650	AtMYB31/AtY13 (myb domain protein 31); DNA bin	-0.02992	0.9761	0.5712	-0.7492	0.4693	0.3718	0.5548	0.0694	0.1142	-0.1644	0.5058	0.3281
260221_at	AT1G74670	glyoxalase I family protein	-0.8293	0.1071	0.1893	-0.5474	0.2433	0.2601	0.5842	0.0735	0.118	0.8661	0.0233	0.0498
260222_at	AT

260290_at	AT1G80510	amino acid transporter family protein	0.4906	0.0164	0.0771	0.1322	0.3438	0.3151	-0.2963	0.0739	0.1184	-0.6548	0.006	0.0241
260291_at	AT1G63700	YDA (YODA); kinase	0.03276	0.8893	0.5483	-0.1593	0.5106	0.3889	-0.3488	0.0684	0.1135	-0.5408	0.0184	0.0436
260292_at	AT1G63680	ATMURE/PDE316 (PIGMENT DEFECTIVE EMBRY	-0.3164	0.1654	0.2378	-0.2605	0.2355	0.255	-0.8014	4.00E-04	0.0147	-0.7455	5.00E-04	0.0096
260293_at	AT1G63670	similar to unknown protein [Arabidopsis thaliana] (T	0.446	0.0758	0.1584	0.3254	0.1571	0.2037	0.3225	0.1601	0.1857	0.2019	0.3414	0.2587
260294_at	AT1G63660	GMP synthase (glutamine-hydrolyzing), putative / g	0.5339	0.012	0.0681	0.1351	0.3311	0.3089	-0.4605	0.0101	0.0399	-0.8592	0.001	0.0122
260295_at	AT1G63770	peptidase M1 family protein	0.586	0.0099	0.0637	0.2561	0.1135	0.1702	-0.4306	0.0057	0.0314	-0.7605	7.00E-04	0.0105
260296_at	AT1G63750	ATP binding / nucleoside-triphosphatase/ nucleotide	0.3321	0.2481	0.2924	0.2984	0.2915	0.2874	-0.1607	0.549	0.3787	-0.1944	0.4733	0.3151
260297_at	AT1G80280	hydrolase, alpha/beta fold family protein	-0.1879	0.5974	0.4586	-0.1024	0.7704	0.4805	-0.1819	0.5592	0.3823	-0.09647	0.7528	0.4145
260298_at	AT1G80320	oxidoreductase, 2OG-Fe(II) oxygenase family prote	0.7512	0.4088	0.3795	0.5143	0.5623	0.4091	-0.9368	0.3144	0.2756	-1.1737	0.2233	0.1979
260299_at	AT1G80330	ATGA3OX4 (GIBBERELLIN 3-OXIDASE 4); gibber	-0.7792	0.2996	0.3227	0.1929	0.7828	0.4844	0.000808	0.9991	0.5176	0.9729	0.2113	0.1915
260300_at	AT1G80340	GA4H (gibberellin 3 beta-hydroxylase); gibberellin 3	-2.2078	0.0505	0.1292	-1.7006	0.1001	0.1594	-0.6924	0.3863	0.3105	-0.1852	0.8078	0.431
260301_at	AT1G80290	glycosyltransferase family protein 47	0.2964	0.2147	0.2714	0.5235	0.0599	0.1215	-0.3379	0.1647	0.1883	-0.1107	0.6075	0.3659
260302_at	AT1G80310	sulfate transmembrane transporter	0.5806	0.0088	0.0607	0.3639	0.0402	0.0994	0.02838	0.7842	0.4586	-0.1883	0.124	0.1377
260303_at	AT1G70520	protein kinase family protein	0.3053	0.2227	0.2769	0.473	0.0892	0.1505	-0.1027	0.1651	0.1885	0.06495	0.344	0.2598
260304_at	AT1G70480	similar to unknown protein [Arabidopsis thaliana] (T	-0.0876	0.6313	0.4702	0.2136	0.2745	0.2778	-0.3183	0.0234	0.0619	-0.01702	0.8579	0.4452
260305_at	AT1G70490	ATARFA1D; GTP binding / phospholipase activator	0.129	0.3656	0.3571	0.037	0.7845	0.4847	0.1916	0.2046	0.2145	0.09957	0.4754	0.3159
260306_at	AT1G70540	EDA24 (embryo sac development arrest 24); peptidy	-0.3344	0.4344	0.3912	-0.8873	0.0826	0.1444	0.1084	0.7924	0.4608	-0.4445	0.3128	0.2448
260307_at	AT1G70620	cyclin-related	0.4415	0.2104	0.2685	-0.1777	0.5809	0.4165	-1.3881	0.006	0.0322	-2.0073	0.0015	0.0139
260308_at	AT1G70610	ATTAP1 (Arabidopsis thaliana transporter associate	-1.1861	0.0065	0.0549	-1.4181	0.0034	0.0374	-0.9993	0.0119	0.0433	-1.2313	0.0057	0.0235
260309_at	AT1G80340	AOAT2 (GLUTAMATE:GLYOXYLATE AMINOTRAN	-0.206	0.1687	0.2404	-0.4397	0.0232	0.0768	-0.2769	0.0872	0.1304	-0.5105	0.0142	0.0378
260310_at	AT1G70590	F-box family protein	0.3421	0.0714	0.154	0.4181	0.0408	0.1001	-0.2458	0.1548	0.1822	-0.1698	0.2928	0.235
260311_at	AT1G70570	anthranilate phosphoribosyltransferase, putative	0.2405	0.2048	0.2651	0.04408	0.7953	0.488	-0.3372	0.1012	0.142	-0.5336	0.0284	0.0562
260312_at	AT1G63880	disease resistance protein (TIR-NBS-LRR class), p	0.4649	0.0043	0.0474	0.324	0.0152	0.0646	-0.974	3.00E-04	0.0133	-1.1149	1.00E-04	0.0069
260313_at	AT1G63870	disease resistance protein (TIR-NBS-LRR class), p	0.8699	0.2111	0.269	-1.0222	0.1554	0.2023	1.5736	0.0546	0.0995	-0.3186	0.6149	0.3684
260314_at	AT1G63830	proline-rich family protein	0.5204	0.1309	0.2092	0.6542	0.0757	0.1379	0.2085	0.2346	0.2319	0.3422	0.0834	0.1077
260315_at	AT1G63820	similar to unknown protein [Arabidopsis thaliana] (T	-0.9232	0.0639	0.1448	-1.1994	0.0299	0.0859	-0.2352	0.3969	0.3151	-0.5113	0.1083	0.1264
260316_at	AT1G63810	similar to unknown protein product [Vitis vinifera] (G	0.4139	0.0895	0.1733	-0.04561	0.8179	0.4953	-0.4793	0.0611	0.1062	-0.9388	0.0072	0.0264
260317_at	AT1G63800	UBC5 (UBIQUITIN-CONJUGATING ENZYME 5); ut	0.02	0.9568	0.6664	0.2555	0.5006	0.3848	0.3811	0.1497	0.1788	0.6166	0.045	0.0744
260318_at	AT1G63960	contains domain PTHR22814 (PTHR22814); contai	-1.5866	0.197	0.2606	0.875	0.4419	0.3603	-0.77	0.4948	0.3576	1.6917	0.1746	0.17
260319_at	AT1G63950	heavy-metal-associated domain-containing protein	-1.7323	0.2426	0.2891	-2.5375	0.1152	0.1713	0.3063	0.8205	0.4699	-0.4988	0.7134	0.4021
260320_at	AT1G63930	similar to unknown protein [Arabidopsis thaliana] (T	-0.3756	0.5169	0.428	-0.6455	0.2894	0.2862	-0.03422	0.9501	0.5056	-0.3041	0.5899	0.3583
260321_at	AT1G63900	zinc finger (C3HC4-type RING finger) family protein	0.3178	0.0205	0.0843	0.04941	0.5942	0.4211	0.2581	0.0392	0.0818	-0.01028	0.9101	0.4599
260322_at	AT1G63900	zinc finger (C3HC4-type RING finger) family protein	0.114	0.6231	0.4675	0.175	0.4602	0.3679	-0.1479	0.5282	0.3706	-0.0869	0.706	0.3995
260323_at	AT1G63790	IMP4	0.4956	0.059	0.1391	0.5614	0.0415	0.1011	-0.4718	4.00E-04	0.0147	-0.4059	8.00E-04	0.011
260324_at	AT1G63970	ISPF (Homolog of E. coli ispF (isoprenoid F)); 2-C	-0.2178	0.0725	0.1552	-0.3278	0.0218	0.0748	0.6005	0.0026	0.0235	0.4905	0.0055	0.0231
260325_at	AT1G63940	monodehydroascorbate reductase, putative	-0.3532	0.2047	0.2651	-0.5561	0.0758	0.1379	-0.2736	0.1187	0.1551	-0.4764	0.0261	0.0535
260326_at	AT1G63910	ATMYB103 (MYB DOMAIN PROTEIN 103); DNA bi	0.6834	0.4331	0.3908	0.3691	0.6111	0.4272	-0.9606	0.2249	0.2264	-0.00837	0.9906	0.4803
260327_at	AT1G63840	zinc finger (C3HC4-type RING finger) family protein	0.8433	0.0264	0.0939	0.5772	0.0784	0.1404	0.6564	0.0309	0.0716	0.3903	0.1242	0.1378
260328_at	AT1G80360	aminotransferase class I and II family protein	0.178	0.1178	0.1985	0.02904	0.762	0.4781	0.2701	0.0393	0.082	0.1212	0.2474	0.211
260329_at	AT1G80370	CYCA2;4 (CYCLIN A2;4); cyclin-dependent protein	1.1142	0.4019	0.3762	-0.3184	0.8022	0.4902	-0.128	0.9187	0.4974	-1.5606	0.2556	0.2155
260330_at	AT1G80400	zinc finger (C3HC4-type RING finger) family protein	0.1489	0.4395	0.3934	0.3167	0.1421	0.1923	-0.346	0.117	0.1539	-0.1781	0.3628	0.2682
260331_at	AT1G80270	DNA-binding protein, putative	0.4628	0.0957	0.1787	0.07095	0.756	0.4769	0.4496	0.1006	0.1415	0.05771	0.7983	0.4283
260332_at	AT1G70470	similar to unknown protein [Arabidopsis thaliana] (T	0.4681	0.1315	0.2099	1.2218	0.1905	0.2267	0.1988	0.8104	0.4667	-0.04741	0.9542	0.4722
260333_at	AT1G70500	polygalacturonase, putative / pectinase, putative	0.9316	0.437	0.3925	2.0901	0.125	0.1792	0.1561	0.892	0.4902	1.3147	0.2903	0.2337
260334_at	AT1G70510	KNAT2 (KNOTTED-LIKE FROM ARABIDOPSIS TH	0.879	0.0709	0.1536	0.7506	0.1052	0.1638	-0.5879	0.1774	0.1968	-0.7163	0.1172	0.1328
260335_at	AT1G74000	SS3 (STRICTOSIDINE SYNTHASE 3)	1.3428	0.1743	0.2444	0.2199	0.8004	0.4897	0.02915	0.9731	0.5107	-1.0938	0.2501	0.2126
260336_at	AT1G73990	SPPA (signal peptide peptidase); protease IV seris	-0.1595	0.1792	0.2475	-0.3891	0.0166	0.0668	-0.5247	0.0059	0.032	-0.7543	0.0015	0.0139
260337_at	AT1G69310	WRKY57 (WRKY DNA-binding protein 57); transcri	0.2696	0.5726	0.45	0.03724	0.9365	0.5283	0.4086	0.1367	0.1689	0.1763	0.4678	0.3129
260338_at	AT1G69320	nuclear transport factor 2 (NTF2) family protein / R	0.4599	0.1979	0.2613	0.4024	0.2486	0.263	0.05551	0.8214	0.4702	-0.00201	0.9934	0.481
260339_at	AT1G69220	SIK1 (ERINE/THREONINE KINASE 1); kinase	0.5867	0.021	0.0851	0.3219	0.1127	0.1697	-0.3965	0.0279	0.068	-0.6613	0.0049	0.022
260340_at	AT1G69190	2-amino-4-hydroxy-6-hydroxymethyldihydropteridin	-0.6369	0.5685	0.4484	-0.6887	0.539	0.4	-0.4058	0.7128	0.4359	-0.4577	0.6787	0.3902
260341_at	AT1G69170	squamosa promoter-binding protein-like 6 (SPL6)	1.851	0.1146	0.1961	0.2138	0.8277	0.4983	-0.2452	0.788	0.4595	-1.8824	0.0919	0.1143
260342_at	no_match	no_match	0.2047	0.7477	0.5082	0.5656	0.3949	0.3391	-0.7581	0.2709	0.2528	-0.3972	0.5403	0.3411
260343_at	AT1G69200	kinase	0.005023	0.9725	0.5704	-0.1407	0.3624	0.324	-0.2212	0.1816	0.1999	-0.3669	0.0553	0.0843
260344_at	AT1G69240	hydrolase, alpha/beta fold family protein	-0.7854	0.2701	0.3055	-2.8018	0.0103	0.0551	2.0819	0.0126	0.0447	0.06553	0.8989	0.4568
260345_at	AT1G69270	RPK1 (RECEPTOR-LIKE PROTEIN KINASE 1); kir	0.8125	0.0013	0.0375	0.7975	0.0014	0.0312	-0.3885	0.0184	0.0543	-0.4035	0.0163	0.0408
260346_at	no_match	no_match	0.3284	0.5263	0.4317	0.8751	0.1384	0.1895	-0.5304	0.3255	0.2811	0.0163	0.9742	0.4766
260347_at	AT1G69420	zinc finger (DHHC type) family protein	-0.7763	0.0018	0.0391	-0.6602	0.0033	0.0371	-0.3423	0.018	0.0538	-0.2262	0.063	0.0911
260348_at	AT1G69350	pentatricopeptide (PPR) repeat-containing protein	-0.1175	0.769	0.5143	0.1506	0.7075	0.4613	-0.5685	0.2028	0.2134	-0.3004	0.4665	0.3125
260349_at	AT1G69400	transducin family protein / WD-40 repeat family prot	0.06121	0.9024	0.5519	-0.06232	0.9006	0.5191	0.2097	0.6777	0.4237	0.08614	0.8631	0.4467
260350_at	AT1G69410	initiation factor 5A, putative / eIF-5A, putative	0.1117	0.6342	0.4709	0.6947	0.0329	0.0899	0.3754	0.0021	0.0216	0.9584	1.00E-04	0.0056
260351_at	AT1G69380	similar to unknown protein [Arabidopsis thaliana] (T	0.5519	0.0409	0.1164	0.05208	0.7927	0.487	0.2045	0.3318	0.2842	-0.2952	0.1865	0.1772
260352_at	AT1G69295	beta-1,3-glucanase-related	-0.05586	0.8262	0.5314	-0.2146	0.4186	0.3501	0.3905	0.1204	0.1565	0.2317	0.3077	0.2423
260353_at	AT1G69230	SPL12	-0.09256	0.7715	0.515	-0.4441	0.2102	0.2397	-0.3943	0.1971	0.2099	-0.7459	0.0431	0.0725
260354_at	AT1G69330	zinc finger (C3HC4-type RING finger) family protein	0.1095	0.7105	0.4964	0.2589	0.3992	0.3409	-0.1329	0.6537	0.4158	0.01648	0.955	0.4723
260355_at	AT1G69180	CRC (CRABS CLAW); transcription factor	-0.4137	0.7346	0.5037	-0.7285	0.5568	0.4072	-0.7422	0.5498	0.379	-1.057	0.4055	0.2863
260356_at	AT1G69390	ATMINE1 (ARABIDOPSIS HOMOLOGUE OF BAC	0.1034	0.38	0.3645	-0.2067	0.12	0.1752	0.5206	0.0015	0.0199	0.2105	0.0354	0.0638
260357_at	AT1G69260	similar to unknown protein [Arabidopsis thaliana] (T	0.7895	0.0624	0.1434	0.8703	0.0475	0.1082	0.3301	0.0317	0.0723	0.4109	0.0157	0.0399
260358_at	AT1G69340	appr-1-p processing enzyme family protein	0.3317	0.0888	0.1728	0.2989	0.1139	0.1704	0.0816	0.6112	0.4016	0.04881	0.7584	0.4162
260359_at	AT1G69210	similar to unknown protein [Arabidopsis thaliana] (T	-0.2846	0.2725	0.307	0.475	0.1011	0.1604	-0.9529	0.0053	0.0304	-0.1933	0.3257	0.251
260360_at	AT1G69370	CM3 (CHORISMATE MUTASE 3); chorismate muta	-0.2684	0.1493	0.225	-0.00479	0.9762	0.5384	-0.4359	0.0032	0.0253	-0.1723	0.0673	0.0946
260361_at	AT1G69360	similar to unknown protein [Arabidopsis thaliana] (T	0.6907	0.1271	0.206	0.6628	0.139	0.1899	-0.9465	0.0018	0.0206	-0.9743	0.0016	0.0142
260362_at	AT1G70530	protein kinase family protein	0.6749	0.0187	0.0813	1.0628	0.0038	0.039	-0.233	0.2076	0.2163	0.155	0.3743	0.2732
260363_at	AT1G70550	similar to unknown protein [Arabidopsis thaliana] (T	-0.9562	0.058	0.138	-1.2994	0.0232	0.0768	0.3979	0.2863	0.2614	0.05464	0.8741	0.4496
260364_at	AT1G70560	allinase C-terminal domain-containing protein	-0.2835	0.5297	0.4331	-0.3062	0.4991	0.3841	0.366	0.3294	0.2831	0.3432	0.3569	0.2655
260365_at	AT1G70630	similar to unknown protein [Arabidopsis thaliana] (T	0.4203	0.5264	0.4317	-0.254	0.6968	0.4578	-0.6447	0.3476	0.292	-1.3191	0.0952	0.117
260366_at	AT1G70460	protein kinase, putative	-0.455	0.7116	0.4968	-0.9172	0.4684	0.3714	0.2275	0.8523	0.4792	-0.2347	0.8477	0.4422
260367_at	AT1G69760	similar to unknown protein [Arabidopsis thaliana] (T	-0.9087	0.0109	0.0655	-0.7584	0.02	0.0724	0.01142	0.9577	0.5071	0.1617	0.469	0.3134
260368_at	AT1G69700	ATHVA22C (Arabidopsis thaliana HVA22 homologu	-0.2193	0.3054	0.3257	-0.1507	0.465	0.37	-0.105	0.6041	0.3996	-0.03631	0.8553	0.4444
260369_at	AT1G69620	RPL34 (RIBOSOMAL PROTEIN L34); structural co	0.158	0.1866	0.2531	0.1517	0.2013	0.2335	0.4143	0.014	0.0472	0.408	0.0147	0.0386
260370_at	AT1G69740	HEMB1; porphobilinogen synthase	-0.1088	0.4006	0.3757	-0.04896	0.694	0.4568	-0.03116	0.7775	0.4565	0.02865	0.7949	0.4274
260371_at	AT1G69690	TCP family transcription factor, putative	0.09831	0.6118	0.4633	0.2331	0.2623	0.2711	-0.04726	0.8046	0.4649	0.08757	0.65	0.3808
260372_at	AT1G73980	phosphoribulokinase/uridine kinase family protein	1.3401	0.0308	0.1018	0.3304	0.4655	0.3701	0.09811	0.7775	0.4565	-0.9117	0.0484	0.0777
260373_at	AT1G73970	similar to unnamed protein product [Vitis vinifera] (G	0.3948	0.1717	0.2427	0.662	0.0494	0.1102	-0.6209	0.019	0.0553	-0.3537	0.0961	0.1175
260374_at	AT1G73960	TAF2 (TBP-ASSOCIATED FACTOR 2); metallopep	0.6056	0.0087	0.0606	-0.00793	0.953	0.5325	0.1041	0.3015	0.2694	-0.5094	0.0044	0.021
260375_at	AT1G73950	zinc finger (C3HC4-type RING finger) family protein	-0.4223	0.0927	0.1764	0.104	0.6168	0.4295	-1.0048	0.0035	0.0262	-0.4786	0.0429	0.0723
260376_at	AT1G74110	CYP78A10 (cytochrome P450, family 78, subfamily	-0.7174	0.1794	0.2475	-0.1846	0.6973	0.458	-0.3381	0.4864	0.354	0.1948	0.6819	0.3912
260377_at	AT1G73930	similar to unnamed protein product [Vitis vinifera] (G	-0.07515	0.6897	0.4891	-0.0941	0.6193	0.4303	-0.2698	0.1981	0.2106	-0.2887	0.1744	0.1699
260378_at	AT1G73910	ATARP4A (ACTIN-RELATED PROTEINS 4A); stru	-1.9671	0.1132	0.1949	1.0926	0.3242	0.3055	-2.3991	0.0692	0.114	0.6607	0.5343	0.3396
260379_at	no_match	no_match	-0.1426	0.4074	0.3791	-0.03987	0.8087	0.4926	-0.2465	0.1852	0.2022	-0.1437	0.404	0.2858
260380_at	AT1G73870	zinc finger (B-box type) family protein	-0.6781	0.0593	0.1394	-0.8197	0.0343	0.0914	-0.7183	0.0068	0.0338	-0.8599	0.0036	0.0194
260381_at	AT1G73860	microtubule motor	1.4924	0.2983	0.3224	1.6262	0.263	0.2715	-0.407	0.761	0.4514	-0.2732	0.8377	0.4394
260382_at	AT1G73850	structural constituent of ribosome	0.03776	0.9683	0.5694	2.7723	0.0362	0.094	-0.2252	0.7755	0.4559	2.5094	0.0273	0.0549
260383_s_at	AT1G74060, AT1G74050	60S ribosomal protein L6 (RPL6B)[A	0.07215	0.5742	0.4505	0.3697	0.0352	0.0926	-0.1379	0.2294	0.2233	0.1596	0.1676	0.1658
260384_at	AT1G74040	IMS1; 2-isopropylmalate synthase	-0.00465	0.9816	0.5725	-0.393	0.1067	0.1648	-0.6562	0.0143	0.0477	-1.0446	0.0027	0.0172
260385_at	AT1G74090	sulfotransferase family protein	-0.788	0.0056	0.0523	-0.8142	0.005	0.0424	0.4184	0.0037	0.0268	0.3921	0.0047	0.0217
260386_at	AT1G74010	strictosidine synthase family protein	0.05906	0.8942	0.5498	-0.1029	0.8171	0.495	0.2797	0.494	0.3572	0.1177	0.7675	0.4191
260387_at	AT1G74100	sulfotransferase family protein	-0.1616	0.2923	0.3186	-0.2013	0.2058	0.2366	0.5138	0.015	0.0487	0.4741	0.0195	0.0448
260388_at	AT1G74070	peptidyl-prolyl cis-trans isomerase cyclophilin-type f	-0.975	0.0022	0.041	-0.9034	0.0029	0.0355	-0.1372	0.38	0.3078	-0.0657	0.6615	0.3847
260389_at	AT1G74055	unknown protein	0.6933	0.0155	0.0751	0.6011	0.0246	0.0788	0.7531	0.0117	0.0428	0.6609	0.0181	0.0432
260390_at	AT1G73940	similar to unknown protein [Arabidopsis thaliana] (T	0.631	0.0026	0.0426	0.4544	0.0087	0.0512	0.07328	0.267	0.2503	-0.1033	0.1434	0.1505
260391_at	AT1G74020	SS2 (STRICTOSIDINE SYNTHASE 2); strictosidine	0.2473	0.3537	0.3515	0.08847	0.7267	0.4677	0.3834	0.1483	0.1779	0.2246	0.3541	0.2645
260392_at	AT1G74050	enolase, putative	-0.2988	0.3868	0.3682	-0.2308	0.4951	0.3826	-0.09158	0.781	0.4577	-0.02358	0.9426	0.4691
260393_at	AT1G73920	lipase family protein	-0.09054	0.7434	0.5068	-0.4895	0.1307	0.1833	-0.5751	0.0097	0.0393	-0.9741	0.0014	0.0135
260394_at	AT1G74080	MYB122 (myb domain protein 122); DNA binding / s	-0.8913	0.476	0.4101	0.7992	0.5201	0.3923	-0.8828	0.2545	0.2434	0.8077	0.2908	0.234
260395_at	AT1G74090	ATHB33; DNA binding / transcription factor	0.6444	0.0163	0.0771	0.8091	0.0074	0.0486	0.1511	0.4026	0.3176	0.3159	0.1222	0.1366
260396_at	AT1G69720	HO3 (HEME OXYGENASE 3); heme oxygenase (d	1.3851	0.0262	0.0937	1.1356	0.0477	0.1084	0.1248	0.4547	0.3407	-0.1246	0.4555	0.3082
260397_at	AT1G69680	similar to unknown [Populus trichocarpa] (GB:ABK9	-0.0425	0.8546	0.5394	-0.05811	0.8025	0.4903	0.1818	0.3913	0.3126	0.1662	0.4296	0.2966
260398_at	AT1G69670	APUM23 (ARABIDOPSIS PUMILIO 23); RNA bindi	0.599	0.079	0.1619	0.3081	0.2944	0.2888	-0.5243	0.0191	0.0555	-0.8152	0.0041	0.0206
260399_at	AT1G72520	lipoxygenase, putative	-0.6517	0.1777	0.2465	-0.8851	0.0908	0.152	-0.02512	0.8981	0.4918	-0.2586	0.2331	0.2033
260400_at	AT1G69860	proton-dependent oligopeptide transport (POT) fam	1.4006	0.3265	0.3382	0.01356	0.9919	0.5421	0.9554	0.4885	0.3549	-0.4316	0.748	0.413
260401_at	AT1G69840	band 7 family protein	0.5902	0.0724	0.155	0.7043	0.1444	0.1044	0.08215	0.2407	0.2355	0.1962	0.0303	0.0585
260402_at	AT1G69820	GGT3/GGT4 (GAMMA-GLUTAMYL TRANSPEPTI	-0.1438	0.7097	0.4962	-0.4671	0.2638	0.2719	0.3089	0.2345	0.2319	-0.01442	0.9511	0.4712
260403_at	AT1G69810	WRKY36 (WRKY DNA-binding protein 36); transcri	0.557	0.4503	0.4003	0.6741	0.1366	0.2222	0.5906	0.1165	0.1535	0.7577	0.4504	0.1297	0.1409
260404_at	AT1G69950	transposable element gene	0.0685	0.6452	0.4748	0.02168	0.8826	0.5138	-0.08594	0.5666	0.3854	-0.1328	0.3898	0.2799
260405_at	AT1G69930	ATGSTU11 (Arabidopsis thaliana Glutathione S-tra	1.5329	0.1016	0.1843	2.4083	0.0292	0.0849	-0.03604	0.9497	0.5055	0.8394	0.1927	0.1806
260406_at	AT1G69940	ATGSTU12 (Arabidopsis thaliana Glutathione S-tra	0.9922	0.1638	0.2367	1.7629	0.0498	0.1106	1.1598	0.0447	0.1752	1.8505	0.0448	0.0742
260407_at	AT1G69910	ATHB9 (thioredoxin H-type 8); thiol-disulfide exchang	0.2808	0.3227	0.3359	0.1896	0.4889	0.3799	0.5027	0.0047	0.0292	0.4116	0.0096	0.0306
260408_at	AT1G69880	ATH8 (thioredoxin H-type 8); thiol-disulfide exchang	-0.4825	0.3731	0.3609	0.1075	0.8343	0.5	0.4016	0.4513	0.3392	0.9916	0.1086	0.1266
260409_at	AT1G69835	similar to unknown protein [Arabidopsis thaliana] (T	0.3836	0.0162	0.0769	0.0464	0.854	0.4431	0.2248	0.0644	0.1094	0.5698	0.0034	0.0191
260410_at	AT1G69870	proton-dependent oligopeptide transport (POT) fam	-0.1791	0.5363	0.4355	-0.1604	0.5778	0.4151	0.04677	0.6477	0.4136	0.06548	0.5278	0.337
260411_at	AT1G69890	similar to unknown protein [Arabidopsis thaliana] (T	-0.7277	0.0189	0.0818	-0.01713	0.9328	0.5272	0.1289	0.5368	0.374	0.8394	0.0117	0.034
260412_at	AT1G69930	AMY3/ATAMY3 (ALPHA-AMYLASE-LIKE 3); alpha-	0.1302	0.3224	0.3357	0.08128	0.52	0.3923	-0.6987	5.00E-04	0.0148	-0.9102	2.00E-04	0.0073
260413_at	AT1G69800	CBS domain-containing protein	0.08054	0.6666	0.4815	0.1186	0.5316	0.3968	-0.2002	0.2179	0.2224	-0.1621	0.3024	0.2399
260414_at	AT1G69850	ATNRT1:2 (NITRATE TRANSPORTER 1:2); calciu	0.5547	1.00E-04	0.0312	0.4571	1.00E-04	0.0249	-0.1737	0.0026	0.0236	-0.2714	5.00E-04	0.0094
260415_at	AT1G69790	protein kinase, putative	0.4366	0.1441	0.2206	0.1244	0.6327	0.4355	-0.2773	0.1414	0.1724	-0.03489	0.8293	0.437
260416_at	AT1G69670	ATCUL3B/CUL3B (Cullin 3B); protein binding / ubiq	0.5248	5.00E-04	0.032	0.4321	0.001	0.0291	-0.2097	0.0032	0.0251	-0.3025	8.00E-04	0.011
260417_at	AT1G69770	CMT3 (CHROMOMETHYLASE 3)	0.07057	0.7576	0.511	-0.7054	0.0298	0.0859	-0.05044	0.7702	0.4543	-0.8264	0.0069	0.0258
260418_s_at	AT1G69750, AT1G66590	[AT1G69750, cox19 family protein]:[AT1G66590, cc	0.6676	0.0057	0.0625	0.9442	0.0092	0.0526	-0.4524	0.0652	0.1101	-0.5753	0.0326	0.061
260419_at	AT1G69730	protein kinase family protein	0.3817	0.0065	0.0547	-0.262	0.0232	0.0768	0.3087	0.0135	0.0463	-0.335	0.0102	0.0316
260420_at	AT1G69610	structural constituent of ribosome	0.2451	0.1345	0.2131	0.5027	0.0185	0.0702	-0.2522	0.0218	0.0596	0.005433	0.9411	0.4688
260421_at	AT1G69640	acid phosphatase, putative	0.0414	0.845	0.5372	0.2853	0.2239	0.248	-0.0964	0.6526	0.4155	0.1475	0.4986	0.3254
260422_at	AT1G69630	F-box family protein	1.146	0.4744	0.4096

260490_at	AT1G51500	CER5 (ECERIFERUM 5); ATPase, coupled to trans	-0.1238	0.395	0.3726	-0.2277	0.155	0.202	-0.1965	0.2054	0.2151	-0.3003	0.0821	0.1068
260491_at	AT1G51440	lipase class 3 family protein	-0.6748	0.117	0.1977	-1.3094	0.018	0.0694	0.675	0.0252	0.0644	0.04039	0.8449	0.4413
260492_at	AT2G41850	PGAZAT (POLYGALACTURONASE ABSCISSION	1.5933	0.1267	0.2058	0.5741	0.5263	0.3946	0.06201	0.9051	0.4938	-0.9572	0.1215	0.1361
260493_at	AT2G41830	cyclin-related	0.2069	0.4205	0.3851	-0.2452	0.3479	0.3169	0.09521	0.701	0.4316	-0.3568	0.1968	0.183
260494_at	AT2G41820	leucine-rich repeat transmembrane protein kinase,	0.02271	0.9303	0.56	0.2804	0.3141	0.2996	-0.04427	0.8069	0.4656	0.2135	0.2765	0.2264
260495_at	AT2G41810	similar to unknown protein [Arabidopsis thaliana] (T	-1.0602	0.1659	0.2381	-0.7928	0.2745	0.2778	-0.1615	0.8093	0.4663	0.1059	0.8739	0.4495
260496_at	AT1G47200	ATPase, coupled to transmembrane movement of s	0.8556	0.0046	0.0491	0.5517	0.021	0.074	-0.6375	0.013	0.0453	-0.9414	0.0033	0.0185
260497_at	AT1G47210	40S ribosomal protein S2 (RPS2C)	0.283	0.2276	0.2803	0.2403	0.2932	0.2882	-0.1688	0.4009	0.3171	-0.2114	0.3047	0.2409
260498_at	AT1G47710	ovule development protein, putative	0.3252	0.2746	0.3084	0.4614	0.1472	0.1961	-0.1819	0.4221	0.3263	-0.04569	0.8334	0.4381
260499_at	AT1G47760	similar to unnamed protein product [Vitis vinifera] (G	0.4393	0.0202	0.0839	-0.3774	0.0327	0.0896	0.355	0.0393	0.082	-0.4616	0.0172	0.042
260500_at	AT1G47705	camphor resistance CrcB family protein	0.6583	0.0437	0.1206	0.5212	0.0826	0.1443	-0.562	0.0529	0.0976	-0.6991	0.0276	0.0554
260501_at	AT1G41770	similar to unknown protein [Arabidopsis thaliana] (T	-0.302	0.0068	0.0555	-0.259	0.0116	0.058	-0.05709	0.3685	0.3022	-0.01408	0.8151	0.4329
260502_at	AT1G47270	AITLP6 (TUBBY LIKE PROTEIN 6); phosphoric die	0.4205	0.0303	0.1009	0.2485	0.1241	0.1787	-0.7516	0.0042	0.0278	-0.9236	0.002	0.0151
260503_at	AT1G47250	PAF2 (20S proteasome alpha subunit F2); peptidas	0.4514	0.0193	0.0823	0.5478	0.0101	0.0545	0.3865	0.0316	0.0723	0.4828	0.0155	0.0397
260504_at	AT1G47220	CYCA3;3 (CYCLIN A3;3); cyclin-dependent protein	0.09458	0.9181	0.5566	0.2836	0.7592	0.4778	-1.7448	0.0621	0.1071	-1.5557	0.0839	0.1081
260505_at	AT1G47230	CYCA3;4; cyclin-dependent protein kinase regulator	-0.4081	0.1504	0.226	-0.2162	0.4001	0.3412	0.08474	0.731	0.4421	0.2766	0.2951	0.2361
260506_at	AT1G47210	CYCA3;2; cyclin-dependent protein kinase	0.4811	0.4476	0.397	-0.05993	0.9216	0.5244	-1.0242	0.039	0.0816	-1.5653	0.0099	0.031
260507_at	AT1G47200	WPP2 (WPP domain protein 2)	-0.2162	0.0894	0.1732	0.1739	0.1469	0.196	0.8816	8.00E-04	0.0162	1.2718	2.00E-04	0.0076
260508_at	AT1G47260	APR1; carbonate dehydratase	-0.05564	0.4047	0.3777	-0.2078	0.0254	0.0798	0.1935	0.0133	0.046	0.04133	0.4171	0.2913
260509_at	AT1G47240	NRAMP2 (NRAMP metal ion transporter 2); metal i	0.00282	0.9892	0.5743	0.08805	0.6758	0.4505	-0.1338	0.5314	0.3718	-0.04292	0.837	0.4393
260510_at	AT1G51580	KH domain-containing protein	0.1631	0.1282	0.2069	-0.1072	0.277	0.2792	0.3916	0.0101	0.0399	0.1212	0.2281	0.2006
260511_at	AT1G51590	C2 domain-containing protein	-0.323	0.2419	0.2887	-0.2819	0.2972	0.2902	0.0477	0.7884	0.4596	0.08883	0.6215	0.3707
260512_at	AT1G51520	nucleic acid binding / nucleotide binding	-0.7337	0.3307	0.3403	-0.4964	0.4958	0.3828	-0.6	0.4168	0.3238	-0.3627	0.6136	0.3679
260513_at	AT1G51490	glycosyl hydrolase family 1 protein	0.08634	0.8995	0.551	-0.7903	0.2856	0.2841	-0.5631	0.4042	0.3183	-1.4397	0.0758	0.1014
260514_at	AT1G51480	disease resistance protein (CC-NBS-LRR class), pu	0.7885	0.5503	0.4412	-0.1939	0.8805	0.5133	1.862	0.1988	0.2111	0.8796	0.5077	0.3288
260515_at	AT1G51460	ABC transporter family protein	1.3792	0.1227	0.203	0.601	0.4429	0.3608	-0.2078	0.7308	0.442	-0.986	0.1549	0.158
260516_at	AT1G51450	SPla/RYanodine receptor (SPRY) domain-containin	-0.08495	0.6972	0.4918	-0.1635	0.4659	0.3703	-0.4693	0.0787	0.1227	-0.5479	0.0519	0.0811
260517_at	AT1G51510	sucrose-phosphatase, putative	-1.1789	0.036	0.1096	-0.8384	0.0917	0.1527	-0.06878	0.865	0.4827	0.2716	0.5136	0.3311
260518_at	AT1G51410	cinnamyl-alcohol dehydrogenase, putative (CAD)	1.3193	0.2768	0.3099	-0.02829	0.9798	0.5393	1.3663	0.2626	0.248	0.01872	0.9866	0.4794
260519_at	AT1G51540	similar to kelch repeat-containing protein [Arabidop	0.1115	0.3502	0.3497	0.09617	0.4135	0.3476	0.3911	0.0033	0.0255	0.3758	0.0038	0.02
260520_at	AT1G51590	mannosyl-oligosaccharide 1,2-alpha-mannosidase,	0.3915	0.0174	0.079	0.895	9.00E-04	0.0284	-0.2326	0.0807	0.1244	0.2709	0.0537	0.0828
260521_at	AT1G41740	VLN2 (VILLIN 2); actin binding	-0.07358	0.6837	0.487	-0.05159	0.7739	0.4817	-0.2417	0.2231	0.2255	-0.2198	0.2605	0.2181
260522_x_at	AT1G41730	similar to unknown protein [Arabidopsis thaliana] (T	0.5943	0.1462	0.2222	1.0075	0.0379	0.0965	0.5644	0.0437	0.0872	0.9776	0.0073	0.0266
260523_at	AT1G47720	EMB2261 (EMBRYO DEFECTIVE 2654)	0.0898	0.1194	0.1997	-0.2937	0.003	0.0355	-0.2254	0.0071	0.0341	-0.6089	2.00E-04	0.0071
260524_at	AT1G47230	agenet domain-containing protein	-0.01165	0.9689	0.5695	-0.582	0.107	0.165	0.05089	0.865	0.4827	-0.5195	0.1381	0.147
260525_at	AT1G47250	RNA helicase, putative	0.4365	0.0034	0.0448	0.2742	0.0176	0.0688	-0.6995	6.00E-04	0.0158	-0.8618	3.00E-04	0.008
260526_at	AT1G47410	nucleotide binding	0.13	0.5789	0.4521	-0.09761	0.674	0.4499	-0.7689	0.0234	0.0619	-0.9965	0.0098	0.0309
260527_at	AT1G47270	transcription factor/ transcription regulator	-0.4787	0.6226	0.4674	-0.2757	0.7744	0.4819	2.2978	0.0564	0.1015	2.5008	0.0444	0.0739
260528_at	AT1G47260	WRKY23 (WRKY DNA-binding protein 23); transcri	1.0301	6.00E-04	0.0329	-0.2272	0.0962	0.1563	-0.03977	0.7238	0.4399	-1.2971	2.00E-04	0.0079
260529_at	AT1G47240	CP12-1 (CP12 domain-containing protein 1)	-0.3707	0.0342	0.1069	-0.05942	0.6391	0.4379	-0.4473	0.0188	0.055	-0.1366	0.3088	0.2429
260530_at	AT1G47320	peptidyl-prolyl cis-trans isomerase cyclophilin-type f	0.2477	0.0613	0.1421	0.3104	0.0319	0.0886	0.1283	0.2523	0.2421	0.191	0.1175	0.133
260531_at	AT1G47240	long-chain-fatty-acid--CoA ligase family protein / lor	-0.1163	0.8375	0.5346	0.2524	0.6597	0.4449	-0.3781	0.0794	0.1232	-0.00938	0.9565	0.4725
260532_at	AT1G47330	DEAD/DEAH box helicase, putative	0.4364	0.0119	0.0679	0.3455	0.0257	0.0801	0.4101	0.0048	0.0292	0.3191	0.0115	0.0337
260533_at	no_match	no_match	0.6361	0.0227	0.0882	0.5756	0.0311	0.0876	-0.4496	0.0636	0.1086	-0.5101	0.0447	0.0741
260534_at	no_match	no_match	-0.2345	0.8034	0.525	-1.2017	0.2445	0.2607	0.5802	0.1743	0.195	-0.387	0.3329	0.2548
260535_at	AT2G43390	unknown protein	-0.8878	0.4735	0.4094	0.7573	0.3571	0.3993	-0.9984	0.4243	0.3272	0.6466	0.5957	0.3619
260536_at	AT3G43400	ETFQO (ELECTRON-TRANSFER FLAVOPROTEI	0.08072	0.7321	0.503	-0.02622	0.9108	0.5218	-0.7871	0.0232	0.0616	-0.7326	0.0291	0.0571
260537_at	AT3G43450	unknown protein	-0.02875	0.9639	0.5682	0.2672	0.6772	0.451	-0.247	0.6074	0.4005	0.04902	0.9173	0.462
260538_at	AT3G43460	60S ribosomal protein L38 (RPL38A)	-0.1534	0.4736	0.4094	-0.09817	0.6397	0.4382	0.1851	0.3944	0.3139	0.2404	0.2834	0.23
260539_at	AT3G43480	peroxidase, putative	-0.3711	0.7136	0.4972	-1.3615	0.2218	0.247	1.1571	0.2865	0.2616	0.1668	0.868	0.4477
260540_at	AT3G43500	RWP-RK domain-containing protein	-0.1974	0.5972	0.4586	0.6136	0.1493	0.1976	-0.8121	0.0778	0.1219	-0.00115	0.9975	0.4822
260541_at	AT3G43530	trypsin inhibitor, putative	0.09716	0.7468	0.5077	0.3576	0.2701	0.2755	0.6535	0.0525	0.0972	0.9139	0.0188	0.044
260542_at	AT3G43560	immunophilin / FKBP-type peptidyl-prolyl cis-trans i	-0.6606	0.0015	0.038	-0.794	7.00E-04	0.0275	0.412	5.00E-04	0.0155	0.2785	0.0023	0.0161
260543_at	AT3G43330	ATINT1 (INOSITOL TRANSPORTER 1); carbohydr	-0.4016	0.1268	0.2058	-0.4048	0.1246	0.179	-0.5408	0.001	0.0175	-0.5441	0.001	0.012
260544_at	AT3G43540	similar to hypothetical protein [Vitis vinifera] (GB:CA	1.2638	0.0059	0.0534	1.0882	0.01	0.0543	-0.1881	0.2412	0.2356	-0.3636	0.0565	0.0854
260545_at	AT3G43350	ATGPX3 (GLUTATHIONE PEROXIDASE 3); glutat	0.5679	0.0327	0.1049	0.3059	0.1592	0.2053	-0.00519	0.9758	0.5115	-0.2671	0.1715	0.1682
260546_at	AT3G43520	ATTI2 (ARABIDOPSIS THALIANA TRYPSIN INHIB	-0.5989	0.0012	0.036	-0.402	0.0053	0.0429	0.4598	0.0032	0.0252	0.6566	8.00E-04	0.0113
260547_at	AT3G43550	trypsin inhibitor, putative	-1.3094	0.0015	0.038	-1.1136	0.0028	0.0351	0.5111	0.0392	0.0818	0.707	0.0139	0.0375
260548_at	AT3G43360	BIO2 (BIOTIN AUXOTROPH 2); biotin synthase	-0.2382	0.2262	0.2793	-0.3469	0.106	0.1643	0.2975	0.1489	0.1783	0.1888	0.3206	0.2486
260549_at	AT3G43535	trypsin inhibitor, putative	-0.2662	0.4282	0.3884	-0.6199	0.1096	0.1671	1.0432	0.026	0.0656	0.6895	0.0847	0.1087
260550_at	AT3G43420	3-beta hydroxysteroid dehydrogenase/isomerase fa	0.7832	0.0159	0.0763	0.4711	0.0732	0.1356	0.2537	0.2632	0.2483	-0.05836	0.7797	0.4229
260551_at	AT3G43510	ATTI1 (ARABIDOPSIS THALIANA TRYPSIN INHIB	1.1877	0.0998	0.1823	1.3689	0.0698	0.1322	1.0521	0.0092	0.0385	1.2334	0.0052	0.0226
260552_at	AT3G43430	GLX2-1 (GLYOXALASE 2-1); hydroxyacylglutathior	-0.00501	0.9663	0.5688	0.2066	0.1381	0.1892	-0.392	0.0033	0.0256	-0.1804	0.0452	0.0745
260553_at	AT3G41800	similar to unknown protein [Arabidopsis thaliana] (T	0.7248	0.0925	0.1762	1.0642	0.0319	0.0886	-0.07389	0.8334	0.4736	0.2656	0.4652	0.3121
260554_at	AT2G41790	peptidase M16 family protein / insulinase family pro	0.9523	6.00E-04	0.0325	0.7014	0.0018	0.0325	-0.5052	0.0061	0.0325	-0.756	0.0014	0.0133
260555_at	AT2G41780	unknown protein	1.8556	0.0637	0.1446	1.8218	0.067	0.1296	-0.05118	0.9474	0.505	-0.08498	0.9129	0.4607
260556_at	AT2G41820	chitinase, putative	1.5272	0.0027	0.0426	1.7295	0.0017	0.0321	0.6123	0.0259	0.0653	0.8145	0.01	0.0312
260557_at	AT3G43610	glycoside hydrolase family 19 protein	-0.4282	0.34	0.3453	0.09742	0.8176	0.4952	0.4165	0.3518	0.2942	0.942	0.0759	0.1015
260558_at	AT3G43600	glycoside hydrolase family 19 protein	0.2119	0.8447	0.5371	-0.8305	0.459	0.3676	-0.1241	0.9086	0.4949	-1.1665	0.3143	0.2456
260559_at	AT3G43860	polygalacturonase, putative / pectinase, putative	0.4967	0.6077	0.4623	1.403	0.1912	0.227	-0.6353	0.4417	0.3348	0.271	0.7343	0.4086
260560_at	AT3G43590	chitinase, putative	0.1105	0.7769	0.517	1.0031	0.0513	0.1124	0.1243	0.6644	0.4193	1.0169	0.0187	0.0438
260561_at	AT3G43580	chitinase, putative	-0.07145	0.9455	0.5635	1.1955	0.2901	0.2866	1.519	0.1965	0.2096	2.786	0.0469	0.0762
260562_at	AT3G43850	ankyrin protein kinase, putative (APK1)	0.5638	0.0936	0.1772	1.0894	0.0133	0.0615	-0.4338	0.007	0.034	0.09181	0.3413	0.2586
260563_at	AT3G43840	UDP-glucuronosyl/UDP-glucosyl transferase family	1.4025	0.1433	0.2202	-0.7758	0.3716	0.3281	1.6045	0.1061	0.1458	-0.5737	0.4984	0.3253
260564_at	AT3G43810	small nuclear ribonucleoprotein F, putative / U6 snR	-0.06408	0.5202	0.4291	0.2468	0.0535	0.1147	-0.3424	0.0197	0.0565	-0.03152	0.7465	0.4125
260565_at	AT3G43800	formin homology 2 domain-containing protein / FH2	-0.01299	0.9731	0.5705	-0.04931	0.8983	0.5184	0.4109	0.1009	0.1418	0.3746	0.1249	0.1382
260566_at	AT3G43750	OASB (O-ACETYLSERINE (THIOL) LYASE B); cys	-0.6285	0.0161	0.0767	-0.7777	0.0077	0.049	-0.2874	0.0074	0.0348	-0.4366	0.0016	0.0141
260567_at	AT3G43820	GT/UGT74F2 (UDP-GLUCOSYLTRANSFERASE 7	0.3936	0.1576	0.2313	0.3057	0.2489	0.2632	-0.5959	0.0293	0.0696	-0.6839	0.0189	0.0441
260568_at	AT3G43570	chitinase, putative	2.3061	0.0102	0.0641	2.7281	0.0056	0.0434	0.5625	0.0177	0.0533	0.9845	0.0024	0.0164
260569_at	AT3G43640	signal recognition particle 14 kDa family protein / SI	0.1843	0.195	0.2591	0.4484	0.0194	0.0717	0.4788	0.0078	0.0354	0.7429	0.0015	0.0139
260570_at	AT3G43710	SSI2 (fatty acid biosynthesis 2); acyl-[acyl-carrier-pr	-0.6948	0.0043	0.0474	-0.9173	0.0015	0.0314	-0.6004	0.005	0.0297	-0.8229	0.0015	0.0139
260571_at	AT3G43790	ATMPK6 (MAP KINASE 6); MAP kinase/ kinase	0.5574	0.0342	0.1071	0.4749	0.0546	0.116	-0.3879	0.0598	0.1049	-0.4703	0.0343	0.0626
260572_at	AT3G43760	molybdopterin biosynthesis MoaE family protein	0.1141	0.2305	0.2823	0.1682	0.1058	0.1642	0.2001	0.0684	0.1135	0.2542	0.0346	0.0629
260573_at	AT2G47280	pectinesterase	-0.1642	0.8893	0.5483	1.0242	0.4075	0.3447	-0.4414	0.7062	0.4334	0.747	0.5306	0.3383
260574_at	AT2G47300	ribonuclease P	-0.5594	0.5368	0.4357	0.5545	0.5402	0.4007	-1.0641	0.2686	0.2513	0.04976	0.955	0.4723
260575_at	AT2G47300	ribonuclease P	0.7726	0.3831	0.3663	0.3169	0.7086	0.4616	-0.7157	0.2698	0.2521	-1.1714	0.1043	0.1236
260576_at	AT2G47310	flowering time control protein-related / FCA gamma	0.05215	0.8551	0.5397	0.7443	0.0498	0.1106	-0.848	0.011	0.0416	-0.1558	0.4573	0.3089
260577_at	AT2G47340	invertase/pectin methylesterase inhibitor family prot	-1.7091	0.0724	0.155	0.3355	0.6589	0.4446	-1.4505	0.1088	0.1476	0.5941	0.4468	0.3048
260578_at	AT2G47350	PAPA-1-like family protein / zinc finger (HIT type) fa	-0.1092	0.701	0.4929	0.0395	0.8886	0.5155	0.09689	0.7328	0.4426	0.2456	0.4059	0.2865
260579_at	AT2G47380	cytochrome c oxidase subunit Vc family protein / CO	0.1878	0.1935	0.2579	0.3458	0.0453	0.1055	0.3575	0.0411	0.0841	0.5155	0.0128	0.0358
260580_at	AT2G47390	serine-type endopeptidase / serine-type peptidase	0.3059	0.2751	0.3087	0.2079	0.439	0.3892	-0.5662	0.0215	0.059	-0.6642	0.0127	0.0356
260581_at	AT2G47190	MYB2 (myb domain protein 2); DNA binding / transc	0.6784	0.1187	0.1991	1.1636	0.0273	0.0826	-0.4351	0.0457	0.0894	0.0501	0.758	0.4161
260582_at	AT2G47200	unknown protein	1.1458	0.4841	0.4136	-0.8629	0.593	0.4206	0.07109	0.9642	0.5085	-1.9376	0.2627	0.2191
260583_s_at	AT2G47220	3'-exoribonuclease family domain 1 protein-related	0.2075	0.8891	0.5482	0.9426	0.5367	0.3992	-2.3233	0.1596	0.1855	-1.5882	0.3037	0.2405
260584_at	AT2G43660	glycosyl hydrolase family protein 17	1.7434	0.276	0.3093	-0.1256	0.932	0.527	0.5411	0.7155	0.4367	-1.3279	0.3913	0.2806
260585_at	AT2G43650	EMB2777 (EMBRYO DEFECTIVE 2777)	0.3635	0.326	0.3379	0.2681	0.4557	0.3663	-0.3178	0.1207	0.1568	-0.4132	0.0629	0.091
260586_at	AT2G43630	similar to glycine-rich protein [Arabidopsis thaliana]	0.1497	0.3421	0.3461	-0.2321	0.1702	0.2127	0.05445	0.7152	0.4366	-0.02799	0.8502	0.4428
260587_at	AT1G53210	sodium/calcium exchanger family protein / calcium-i	-0.03241	0.8708	0.5442	-0.3365	0.1463	0.1955	0.122	0.5263	0.3696	-0.1821	0.359	0.2666
260588_at	AT1G53320	AITLP7 (TUBBY LIKE PROTEIN 7); phosphoric die	0.2655	0.1959	0.2597	0.1214	0.5174	0.3915	0.1142	0.4403	0.3342	-0.02997	0.8332	0.4381
260589_at	AT1G53400	similar to unknown protein [Arabidopsis thaliana] (T	0.2887	0.0517	0.1306	0.373	0.0239	0.0778	0.4516	0.0127	0.0448	0.5358	0.007	0.0261
260590_at	AT1G53310	ATPPC1 (PHOSPHOENOLPYRUVATE CARBOXY	0.8401	0.0011	0.036	0.7565	0.0016	0.0317	-0.4646	0.0012	0.0186	-0.5482	6.00E-04	0.0103
260591_at	AT1G53325	F-box family protein-related	0.11	0.9234	0.558	-2.185	0.1118	0.1688	0.2738	0.8115	0.467	-2.0211	0.1332	0.1438
260592_at	AT5G05850	ATCSLE1 (Cellulose synthase-like E1); cellulose sy	0.594	0.0846	0.1684	0.5053	0.1242	0.1787	-0.6894	0.0227	0.0609	-0.7781	0.0153	0.0394
260593_at	AT1G55870	AHG2/ATPARN; ribonuclease	0.1637	0.5813	0.4527	0.2025	0.4997	0.3844	-0.4308	0.19	0.2055	-0.392	0.2247	0.1986
260594_at	AT1G55880	pyridoxal-5'-phosphate-dependent enzyme, beta fat	1.1994	0.0448	0.1221	1.0251	0.0694	0.132	-1.4014	0.0281	0.0681	-1.5758	0.0193	0.0445
260595_at	AT1G55890	pentatricopeptide (PPR) repeat-containing protein	0.3266	0.1955	0.2595	-0.07498	0.7396	0.4711	-0.4301	0.0793	0.1232	-0.8317	0.0106	0.0322
260596_at	AT1G55900	TIM50 (EMBRYO DEFECTIVE 1860)	0.1929	0.0475	0.1254	0.03244	0.6593	0.4447	-0.1214	0.1498	0.1788	-0.2818	0.0145	0.0383
260597_at	AT1G55915	zinc ion binding	-0.7427	0.2047	0.2651	-0.6722	0.2426	0.2595	-0.7109	0.0302	0.0708	-0.6404	0.0414	0.0706
260598_at	AT1G55930	CBS domain-containing protein / transporter associ	0.2029	0.487	0.4145	-0.3058	0.3133	0.2991	-0.4638	0.0742	0.1186	-0.9725	0.0073	0.0266
260599_at	AT1G55940	CYP708A1 (cytochrome P450, family 708, subfami	0.8568	0.5183	0.4286	-0.7225	0.5829	0.4174	1.2083	0.3242	0.2805	-0.371	0.7476	0.4129
260600_at	AT1G55950	similar to DNA-binding storekeeper protein-related [	0.1317	0.8034	0.525	0.974	0.1206	0.1759	0.04892	0.9261	0.4996	0.8912	0.1463	0.1523
260601_at	AT1G55910	ZIP11 (ZINC TRANSPORTER 11 PRECURSOR);	0.3494	0.2076	0.2669	-0.05736	0.8174	0.4951	0.2409	0.3534	0.2949	-0.1659	0.5101	0.3298
260602_at	AT1G55920	AtSerat2;1 (SERINE ACETYLTRANSFERASE 1)	-0.3329	0.4082	0.3793	-0.682	0.1315	0.1839	0.2126	0.178	0.1972	-0.1365	0.3537	0.2643
260603_at	AT1G55960	similar to unknown protein [Arabidopsis thaliana] (T	-1.3436	0.0124	0.0687	-1.6254	0.0064	0.0456	-0.1088	0.3331	0.2849	-0.3904	0.0168	0.0414
260604_at	AT1G55840	SEC14 cytosolic factor (SEC14) / phosphoglyceride	0.3454	0.0381	0.1124	0.331	0.0432	0.1032	-0.11	0.3869	0.3108	-0.1244	0.3342	0.2552
260605_at	AT1G53780	similar to hypothetical protein Osl_037823 [Oryza s	0.7456	0.0539	0.1332	0.6947	0.0654	0.1279	0.7994	0.0369	0.0792	0.7485	0.0449	0.0742
260606_at	AT1G53730	transducin family protein / WD-40 repeat family pro	0.324	0.0863	0.1704	0.2722	0.1299	0.1828	0.3289	0.0114	0.0423	-0.3704	0.0067	0.0256
260607_at	AT1G53700	lectin protein kinase family protein	1.5705	0.1771	0.2462	1.1851	0.2845	0.2835	0.1082	0.7918	0.4606	-0.2772	0.5097	0.3296
260608_at	AT1G53870	polygalacturonase, putative / pectinase, putative	-0.6279	0.551	0.4416	0.207	0.8408	0.5016	1.1912	0.2677	0.2508	2.0261	0.0939	0.1159
260609_at	AT1G53680	lectin protein kinase, putative	0.2094	0.5615	0.4454	0.4995	0.206	0.2368	0.1001	0.7776	0.4565	0.3992	0.304	0.2407
260610_at	AT2G43680	IQD14; calmodulin binding	0.266	0.2465	0.2915	-0.1508	0.4848	0.378	-0.6302	0.0325	0.0735	-1.047	0.0059	0.0239
260611_at	AT2G43670	glycosyl hydrolase family protein 17	0.9929	0.5718	0.4495	0.06655	0.9691	0.5365	0.5084	0.7686	0.4537	-0.418	0.8085	0.4313
260612_at	AT1G53350	F-box family protein-related	-1.1978	0.0527	0.1316	0.724	0.1747	0.2159	-0.3227	0.491	0.356	1.5889	0.0224	0.0487
260613_at	AT1G53380	similar to unknown protein [Arabidopsis thaliana] (T	-0.4687	0.1577	0.2314	-0.3567	0.2571	0.2684	-0.2603	0.1887	0.2047	-0.1483	0.4183	0.2918
260614_at	AT1G53390	ATPase, coupled to transmembrane movement of s	0.3918	0.1184	0.1989	0.05084	0.8096	0.4928	-0.1829	0.275	0.2552	-0.5239	0.0224	0.0487
260615_at	AT1G53240	malate dehydrogenase (NAD), mitochondrial	0.1978	0.2645	0.3021	-0.6369	0.014	0.0627	0.5368	0.0063	0.0366	0.09772	0.4289	0.2954
260616_at	AT1G53280	DJ-1 family protein	0.2556	0.165	0.2374	-0.00172	0.9914	0.542	-0.00114	0.9896	0.5152	-0.2584	0.034	0.0623
260617_at	AT1G53345	similar to unknown protein [Arabidopsis thaliana] (T	-1.5924	0.1032	0.1855	0.05802	0.9426	0.5299	-0.8867	0.3064	0.2718	0.7638	0.37	0.2713
260618_at	AT1G53230	TCP3 (TCP-DOMAIN PROTEIN 3); CYCLOPHILIN	0.2136	0.3421	0.3461	0.0707	0.7385	0.4711	-0.4493	0.0613	0.1065	-0.5922	0.0273	0.0549
260619_at	AT1G08110	lactoylglutathione lyase, putative / glyoxalase I, puta	-0.2275	0.1913	0.2562	-0.07004	0.6539	0.443	-0.696	0.0086	0.0372	-0.5386	0.0205	0.0463
260620_at	AT1G08070	pentatricopeptide (PPR) repeat-containing protein	0.177	0.7321	0.503	0.1815	0.7257	0.4673	-0.1742	0.736	0.4436	-0.1697	0.7425	0.4113
260621_at	AT1G08065	carbonate dehydratase/ zinc ion binding	-0.9408	0.0845	0.1683	-2.0479	0.0077	0.0489	1.2598	0.0378	0.0804	0.1526	0.73	0.4072
260622_at	AT1G07980	histone-like transcription factor (CBF/NF-Y) family p	-0.1491	0.6022	0.4603	0.3208	0.2909	0.287	0.4488	0.1115	0.1495	0.9187	0.0141	0.0376
260623_at	AT1G08090	ATNRT2:1 (Arab

260690_at	AT1G32340	NHL8 (NDR1/HIN1-like 8); protein binding / zinc ion	0.9312	0.0018	0.0391	1.0748	0.0011	0.0293	-0.3716	0.0427	0.0861	-0.228	0.1464	0.1523
260691_s_at	AT2G23880,AT1G32390	similar to unknown protein [Arabidopsis thaliana] (T	-0.3681	0.7494	0.5085	-0.761	0.5183	0.3918	0.5872	0.6142	0.4024	0.1943	0.8655	0.4472
260692_at	AT1G32430	F-box family protein	-0.4823	0.3273	0.3385	-0.2482	0.5969	0.4221	-0.1869	0.669	0.4208	0.04729	0.9128	0.4607
260693_at	AT1G32450	proton-dependent oligopeptide transport (POT) fam	0.198	0.6185	0.4658	0.5211	0.229	0.251	-0.4949	0.0379	0.0805	-0.1718	0.3491	0.2621
260694_at	AT1G32480	oxidoreductase	0.8354	0.2581	0.2985	-0.2493	0.7143	0.4634	0.8508	0.2508	0.2414	-0.2338	0.7311	0.4075
260695_at	AT1G32490	EMB2733/ESP3 (EMBRYO DEFECTIVE 2733); AT	0.3498	0.0298	0.1003	0.2264	0.0992	0.1588	-0.4867	0.01	0.0398	-0.61	0.0045	0.0213
260696_at	AT1G32520	similar to unnamed protein product [Vitis vinifera] (G	-0.8924	0.0037	0.0459	-0.8371	0.0047	0.0418	-0.2235	0.0576	0.1026	-0.1683	0.1177	0.1332
260697_at	AT1G32530	zinc finger (C3HC4-type RING finger) family protein	0.5552	0.0254	0.0924	0.3485	0.0945	0.1548	-0.2105	0.2579	0.2452	-0.4171	0.0593	0.0879
260698_at	AT1G32300	FAD-binding domain-containing protein	0.09204	0.9498	0.5646	-1.7934	0.2618	0.2708	1.8415	0.217	0.2218	-0.04397	0.9738	0.4765
260699_at	AT1G32320	ATMKK10 (Arabidopsis thaliana MAP kinase kinase	-0.4716	0.628	0.4689	-2.5334	0.0481	0.1088	2.7973	0.0207	0.0579	0.7355	0.385	0.2779
260700_at	AT1G32260	similar to unknown protein [Arabidopsis thaliana] (T	0.4767	0.0087	0.0605	0.7098	0.002	0.033	-0.1032	0.358	0.297	0.13	0.2611	0.2184
260701_at	AT1G32330	ATHSFA1D (Arabidopsis thaliana heat shock transc	0.3735	0.1995	0.262	0.3078	0.2745	0.2778	-0.08887	0.7334	0.4427	-0.1546	0.5598	0.3487
260702_at	AT1G32250	calmodulin, putative	-0.04936	0.9546	0.5659	1.0566	0.2644	0.2722	-1.0941	0.2504	0.2413	0.01186	0.9891	0.4799
260703_at	AT1G32270	ATSYP24 (syntaxin 24); protein binding	-0.7435	0.4398	0.3936	-0.1867	0.8402	0.5015	-1.3224	0.2022	0.213	-0.7656	0.4275	0.2957
260704_at	AT1G32470	glycine cleavage system H protein, mitochondrial, p	-0.9135	5.00E-04	0.032	-0.7837	8.00E-04	0.0284	0.1871	0.0258	0.0652	0.3169	0.0042	0.0208
260705_at	AT1G32400	TOM2A (TOBAMOVIRUS MULTIPLICATION 2A)	-0.1345	0.3935	0.3719	-0.09704	0.5286	0.3956	-0.1313	0.4038	0.3181	-0.09385	0.5415	0.3415
260706_at	AT1G32350	AOX1D (ALTERNATIVE OXIDASE 1D); alternative	0.5969	0.0361	0.1097	2.3518	0.0217	0.0748	0.2183	0.4807	0.3517	0.5731	0.111	0.1285
260707_s_at	AT1G32410	vacuolar protein sorting 55 family protein / VPS55 fa	-0.2905	0.0969	0.1798	-0.276	0.1095	0.167	0.559	0.0142	0.0475	0.5736	0.013	0.0362
260708_at	AT1G32310	similar to unknown protein [Oryza sativa] (GB:AAL6	0.2184	0.368	0.3584	-0.1099	0.6367	0.4371	0.1058	0.5645	0.3845	-0.2226	0.2574	0.2165
260709_at	AT1G32500	ATNAP6 (NON-INTRINSIC ABC PROTEIN 6); prot	-0.1315	0.1166	0.1973	-0.2393	0.0221	0.0751	0.04021	0.5745	0.3883	-0.06766	0.3623	0.268
260710_at	AT1G17545	protein phosphatase 2C-related / PP2C-related	-0.5277	0.1793	0.2475	-0.6531	0.1145	0.1708	-0.4603	0.2292	0.2291	-0.5856	0.1455	0.1516
260711_at	AT1G32560	MYA1 (ARABIDOPSIS MYOSIN); motor/ protein bir	0.6256	0.0049	0.05	0.0282	0.812	0.4935	-0.726	4.00E-04	0.0147	-1.3234	0	0.0054
260712_at	AT1G17550	HAB2 (Homology to ABI2); protein serine/threonine	-0.1621	0.1346	0.2131	0.1067	0.2852	0.2839	-0.0271	0.77	0.4543	0.2417	0.0493	0.0786
260713_at	AT1G17615	disease resistance protein (TIR-NBS class), putative	-0.2081	0.7867	0.5197	0.02682	0.972	0.5372	-0.8137	0.3213	0.2788	-0.5787	0.4663	0.3125
260714_at	AT1G14980	CPN10 (CHAPERONIN 10)	0.06435	0.9347	0.4225	0.378	0.0126	0.0601	0.8912	1.00E-04	0.0101	1.2048	0	0.0047
260715_at	AT1G48200	similar to unnamed protein product [Vitis vinifera] (G	0.6734	0.0857	0.1698	0.2928	0.3794	0.3316	0.4531	0.2014	0.2125	0.07251	0.8189	0.4338
260716_at	AT1G48130	ATPER1 (Arabidopsis thaliana 1-cysteine peroxired	-1.0767	0.3168	0.3325	-1.6458	0.1555	0.2025	0.001583	0.9985	0.5174	-0.5675	0.509	0.3294
260717_at	AT1G48120	calcineurin-like phosphoesterase family protein	-0.3303	0.3267	0.3383	-0.4133	0.2348	0.2547	-0.4047	0.2431	0.2368	-0.4877	0.1745	0.17
260718_at	AT1G48110	ECT7 (evolutionarily conserved C-terminal region 7	-0.1039	0.379	0.3639	-0.1763	0.169	0.2119	0.2106	0.0407	0.0837	0.1382	0.122	0.1364
260719_at	AT1G48090	C2 domain-containing protein	0.5028	0.0453	0.1225	0.1251	0.5141	0.3903	-1.1018	0.0016	0.0202	-1.4795	5.00E-04	0.0095
260720_at	AT1G48095	similar to unknown protein [Arabidopsis thaliana] (T	0.6504	0.6381	0.4724	-1.1929	0.4041	0.3431	0.7194	0.1041	0.3996	0.1768	0.8968	0.4564
260721_at	AT1G48060	F-box family protein	-1.1443	0.331	0.3406	1.3462	0.2634	0.2717	-2.1719	0.1039	0.1441	0.3186	0.7736	0.4211
260722_at	AT1G48040	protein serine/threonine phosphatase	0.3183	0.4614	0.4036	-0.2756	0.5199	0.3923	-0.2079	0.6232	0.4057	-0.8019	0.1097	0.1275
260723_at	AT1G48070	contains InterPro domain Protein kinase family (InterP	1.2942	0.0596	0.1396	-1.0012	0.1138	0.1704	1.7987	0.0223	0.0603	-0.4968	0.3734	0.2728
260724_at	AT1G48140	dolichol-phosphate mannosyltransferase-related	0.6835	9.00E-04	0.0349	0.6103	0.0014	0.0312	0.5892	0.0016	0.0204	0.516	0.0026	0.017
260725_at	AT1G48170	similar to expressed protein [Oryza sativa (japonica	0.2597	0.125	0.2046	0.4598	0.0266	0.0816	-0.2292	0.1627	0.187	-0.02905	0.8392	0.4398
260726_at	AT1G48160	signal recognition particle 54 kDa protein, putative /	0.4527	0.0192	0.0823	0.5744	0.0086	0.051	0.576	0.0065	0.037	0.6977	0.0043	0.0208
260727_at	AT1G48100	glycoside hydrolase family 28 protein / polygalactur	-1.7827	0.0106	0.0647	-1.2375	0.0346	0.0919	-0.5053	0.1968	0.1383	0.03988	0.8729	0.4493
260728_at	AT1G48210	serine/threonine protein kinase, putative	1.105	0.096	0.1789	1.3499	0.057	0.1188	-0.07552	0.7903	0.4603	0.1694	0.5584	0.3483
260729_at	AT1G48050	ATKUP6/UBC (Arabidopsis thaliana Ku80 homolog	0.3935	0.1997	0.2621	0.09872	0.7199	0.4654	0.2126	0.4253	0.3277	-0.08217	0.749	0.4134
260730_at	AT1G48030	dihydrolipoamide dehydrogenase 1, mitochondrial /	0.08228	0.3931	0.3716	-0.2791	0.0316	0.0883	-0.02676	0.7713	0.4546	-0.3882	0.0107	0.0324
260731_at	AT1G17500	ATPase, coupled to transmembrane movement of v	0.4348	0.0691	0.1513	0.2754	0.193	0.2278	-0.6189	0.0246	0.0636	-0.7784	0.0115	0.0337
260732_at	AT1G17520	DNA-binding protein, putative	-0.0917	0.7213	0.4998	0.504	0.1032	0.1621	-0.5151	0.0979	0.1392	0.08056	0.7535	0.4147
260733_at	AT1G17640	RNA recognition motif (RRM)-containing protein	0.3736	0.2109	0.2689	0.4141	0.1744	0.2156	0.3751	0.2094	0.2174	0.4156	0.1731	0.1691
260734_at	AT1G17600	disease resistance protein (TIR-NBS-LRR class), p	1.1947	0.0491	0.1274	0.5666	0.2557	0.2677	-0.03244	0.9355	0.5022	-0.6606	0.1543	0.1576
260735_at	AT1G17610	disease resistance protein (TIR-NBS class)	0.6489	0.0613	0.1421	0.6295	0.0665	0.1291	-0.2023	0.3612	0.2987	-0.2217	0.3221	0.2493
260736_at	AT1G17630	pentatricopeptide (PPR) repeat-containing protein	-0.2765	0.5789	0.4521	0.04833	0.9211	0.5243	-0.4327	0.3987	0.316	-0.1078	0.8256	0.4359
260737_at	AT1G17540	kinase	0.3009	0.6917	0.4899	0.4246	0.5798	0.416	-0.2203	0.7705	0.4544	-0.09658	0.8977	0.4566
260738_at	AT1G48460	similar to hypothetical protein [Oryza sativa (japonic	0.3962	0.001	0.064	0.2154	0.0671	0.1296	0.9686	4.00E-04	0.0145	0.7877	8.00E-04	0.011
260739_at	AT1G15000	SCPL50 (serine carboxypeptidase-like 50); serine c	-0.8159	0.0492	0.1276	-0.9618	0.0302	0.0863	-0.4846	0.0409	0.084	-0.6306	0.018	0.043
260740_at	AT1G15020	ATGSOX1/GSO2 (QUIESCIN-SULFHYDRYL OXID	0.609	0.0325	0.1046	0.417	0.0926	0.1536	-0.7271	0.0185	0.0545	-0.9191	0.0083	0.0284
260741_at	AT1G15040	glutamine amidotransferase-related	1.2084	0.3449	0.3474	2.3133	0.1099	0.1674	1.1002	0.0967	0.1382	0.00464	0.9932	0.481
260742_at	AT1G15050	IAA34 (indoleacetic acid-induced protein 34); transc	0.0397	0.9293	0.5598	-0.2092	0.6449	0.4399	0.3405	0.4635	0.3447	0.09157	0.8383	0.4396
260743_at	no_match	no_match	1.0329	0.3428	0.3463	-1.7246	0.147	0.1961	2.8742	0.0221	0.0601	0.1167	0.8899	0.4541
260744_at	AT1G15010	similar to unknown protein [Arabidopsis thaliana] (T	-1.601	0.016	0.0764	-1.209	0.0398	0.0977	1.0302	0.0175	0.053	1.4222	0.0057	0.0236
260745_at	AT1G78370	ATGSTU20 (Arabidopsis thaliana Glutathione S-tra	-1.1549	0.0238	0.0899	-1.5292	0.0093	0.0528	1.0095	0.0052	0.0302	0.6352	0.0251	0.0524
260746_at	AT1G78380	ATGSTU19 (GLUTATHIONE TRANSFERASE 8); g	-0.1415	0.335	0.3429	0.03656	0.7912	0.4865	0.2987	0.0818	0.1254	0.4767	0.021	0.047
260747_at	AT1G78420	protein binding / zinc ion binding	0.2834	0.0495	0.1278	0.3856	0.0193	0.0715	-0.1934	0.1301	0.164	-0.09116	0.4209	0.2928
260748_at	AT1G49210	zinc finger (C3HC4-type RING finger) family protein	0.2974	0.5915	0.4566	0.6522	0.2706	0.2758	0.2273	0.6793	0.4242	0.582	0.318	0.2473
260749_at	no_match	no_match	-0.5119	0.3797	0.3643	0.5441	0.3535	0.3199	-1.113	0.0985	0.1397	-0.05699	0.9178	0.4621
260750_at	AT1G49100	leucine-rich repeat protein kinase, putative	0.7165	0.19	0.2554	-1.0778	0.0766	0.1387	0.2167	0.6273	0.407	-1.5776	0.0187	0.0439
260751_at	AT1G49040	SCD1 (STOMATAL CYTOKINESIS-DEFECTIVE 1)	0.7724	0.0021	0.0406	0.151	0.2377	0.2564	0.128	0.305	0.2712	-0.4934	0.0106	0.0322
260752_at	AT1G49030	similar to unknown protein [Arabidopsis thaliana] (T	-0.2943	0.6264	0.4685	-1.1558	0.1075	0.1653	1.365	0.0711	0.1159	0.5035	0.4187	0.292
260753_at	AT1G49230	zinc finger (C3HC4-type RING finger) family protein	-0.4758	0.4379	0.3929	0.3214	0.5922	0.4204	0.6211	0.241	0.2356	1.4182	0.0348	0.0631
260754_at	AT1G49000	similar to unknown protein [Arabidopsis thaliana] (T	0.1522	0.7313	0.5028	1.0196	0.0692	0.1319	0.802	0.0442	0.0879	1.6693	0.0038	0.02
260755_at	AT1G48980	similar to oxidoreductase, 2OG-Fe(II) oxygenase fa	-0.587	0.2178	0.2737	-0.05969	0.8891	0.5155	-0.4849	0.1671	0.1898	0.04237	0.89	0.4541
260756_at	AT1G48970	initiation factor	0.743	0.0102	0.064	0.474	0.0432	0.1032	-0.3565	0.0931	0.1352	-0.6255	0.0182	0.0434
260757_at	AT1G48940	plastocyanin-like domain-containing protein	0.2161	0.8478	0.5378	0.3491	0.7575	0.4774	0.4451	0.695	0.4294	0.5781	0.6131	0.3677
260758_at	AT1G48930	ATGH9C1 (ARABIDOPSIS THALIANA GLYCOSYL	0.2343	0.8576	0.5406	-1.0732	0.4304	0.3554	0.8039	0.5297	0.3712	-0.5035	0.689	0.3935
260759_at	AT1G49160	protein kinase family protein	0.1626	0.4878	0.4149	0.05497	0.8091	0.4927	-0.505	0.0077	0.0353	-0.6126	0.0038	0.02
260760_at	AT1G49170	similar to unknown protein [Arabidopsis thaliana] (T	0.5686	0.0409	0.1164	1.3644	0.002	0.033	-0.9605	1.00E-04	0.0115	-0.1647	0.0585	0.0872
260761_at	AT1G49150	unknown protein	1.48	0.2684	0.3044	2.4117	0.1045	0.1633	0.05374	0.951	0.5057	0.9855	0.2963	0.2368
260762_at	AT1G49015	initiation factor-related	-0.2049	0.8494	0.538	-1.4506	0.2249	0.2485	1.8914	0.1349	0.1674	0.6457	0.5581	0.3482
260763_at	AT1G49220	zinc finger (C3HC4-type RING finger) family protein	-0.6701	0.5523	0.442	-0.09297	0.9327	0.5272	0.5195	0.6418	0.4117	1.0966	0.3487	0.2619
260764_at	AT1G48950	zinc ion binding	0.1597	0.2439	0.29	0.2727	0.0801	0.142	-0.5734	0.008	0.0359	-0.4604	0.017	0.0417
260765_at	AT1G49240	ACT8 (ACTIN 8); structural constituent of cytoskele	0.1316	0.5181	0.4285	0.171	0.4097	0.3458	-1.251	0	0.0062	-1.2115	0	0.0043
260766_at	AT1G48960	universal stress protein (USP) family protein	-0.1511	0.3975	0.3741	-0.4416	0.0505	0.1115	-0.2009	0.2766	0.2561	-0.4914	0.037	0.0655
260767_s_at	AT1G49140,AT3G18410	[AT1G49140, NADH-ubiquinone oxidoreductase-re	-0.2235	0.1593	0.2329	-0.2093	0.1812	0.2204	0.6401	0.0018	0.0206	0.6543	0.0017	0.0145
260768_at	AT1G49245	contains InterPro domain Prefoldin (InterPro:IPR00	0.7505	0.0756	0.1583	0.9338	0.0413	0.1009	-0.3248	0.3605	0.2983	-0.1414	0.6765	0.3895
260769_at	AT1G49010	myb family transcription factor	-0.3089	0.3225	0.3358	-0.6569	0.0745	0.1369	0.3135	0.0124	0.0443	-0.03442	0.6598	0.3841
260770_at	AT1G49200	zinc finger (C3HC4-type RING finger) family protein	-0.7358	0.0116	0.0672	-0.3421	0.1094	0.167	-0.817	0.0025	0.0233	-0.4233	0.0251	0.0523
260771_at	AT1G49160	WNK7 (Arabidopsis WNK kinase 7); kinase	0.3273	0.0323	0.1041	0.2563	0.0652	0.1277	-0.2361	0.0422	0.0856	-0.3071	0.0187	0.0438
260772_at	AT1G49050	aspartyl protease family protein	1.0826	0.0057	0.0528	0.8957	0.0112	0.0568	-0.3769	0.0884	0.1313	-0.5637	0.0285	0.0563
260773_at	AT1G78440	ATGA2OX1 (GIBBERELLIN 2-OXIDASE 1); gibber	-2.9835	0.0251	0.0919	-1.8091	0.1017	0.1609	-1.2044	0.0775	0.1216	-0.03004	0.9559	0.4725
260774_at	AT1G78290	serine/threonine protein kinase, putative	1.2581	0.033	0.1054	1.368	0.0255	0.0799	-0.3685	0.0068	0.0337	-0.2586	0.0227	0.049
260775_at	AT1G78300	GRF2 (GENERAL REGULATORY FACTOR 2); pro	0.2092	0.2573	0.2978	0.3546	0.0889	0.1504	0.01081	0.9471	0.5049	0.1562	0.3656	0.2694
260776_at	AT1G14580	zinc finger (C2H2 type) family protein	0.03734	0.8557	0.54	-0.3107	0.1821	0.2213	0.001574	0.9918	0.5156	-0.3464	0.0735	0.0996
260777_at	AT1G14560	mitochondrial substrate carrier family protein	0.2832	0.0913	0.1753	-0.1549	0.2927	0.288	-0.2505	0.0738	0.1183	-0.6886	0.0027	0.0171
260778_at	AT1G14640	SWAP (Suppressor-of-White-APricot)/surp domain-	0.8143	0.2191	0.2746	0.1508	0.8009	0.4897	-0.9846	0.1532	0.181	-1.6482	0.0421	0.0715
260779_at	AT1G14650	SWAP (Suppressor-of-White-APricot)/surp domain-	0.5084	0.1543	0.2293	0.6092	0.1035	0.1624	0.085	0.6881	0.4272	0.1858	0.3987	0.2837
260780_at	AT1G14610	TWN2 (TWIN 2); ATP binding / aminoacyl-tRNA lig	0.2323	0.1566	0.2308	-0.3201	0.0744	0.1368	0.03344	0.6813	0.4248	-0.5189	0.0024	0.0161
260781_at	AT1G14620	DECOY (endoxyloglucan transferase A2)	0.6158	0.0033	0.0446	0.7317	0.0017	0.0321	-0.3969	0.0063	0.0328	-0.2809	0.0204	0.0462
260782_at	AT1G14570	UBX domain-containing protein	0.2317	0.0721	0.1548	0.2443	0.0626	0.1242	-0.2684	0.0479	0.0919	-0.2557	0.0549	0.0838
260783_at	AT1G06160	ethylene-responsive factor, putative	-0.5414	0.0343	0.1071	0.2552	0.211	0.2404	0.07277	0.5397	0.3752	0.8693	0.0013	0.0133
260784_at	AT1G06180	ATMYB13 (myb domain protein 13); DNA binding /	0.5787	0.1647	0.2373	0.4642	0.2448	0.2609	0.3234	0.3964	0.3149	0.209	0.5729	0.3535
260785_at	AT1G06200	serine-type peptidase/ signal peptidase	0.2747	0.0237	0.0898	0.1857	0.0741	0.1366	-0.04071	0.5814	0.3913	-0.1297	0.129	0.1409
260786_s_at	AT1G06220,AT5G25230	elongation factor/elongation factor Tu family protein	0.2963	0.0093	0.1771	-0.0166	0.9081	0.521	-0.3534	0.0262	0.0658	-0.6664	0.0029	0.0175
260787_at	AT1G06230	GTE4 (GLOBAL TRANSCRIPTION FACTOR GRO	0.1736	0.3516	0.3505	0.4202	0.0633	0.1253	-0.06787	0.7015	0.4318	0.1787	0.339	0.2575
260788_at	AT1G06260	cysteine proteinase, putative	1.3194	0.118	0.1987	1.9406	0.0432	0.1032	-0.8684	0.2613	0.2472	-0.2472	0.7287	0.4067
260789_s_at	AT3G06690,AT1G06290	[AT3G06690, acyl-CoA oxidase family];[AT1G0629	0.5442	0.0033	0.0446	0.5895	0.0025	0.0339	-0.1833	0.1024	0.1428	-0.138	0.1872	0.1777
260790_at	AT1G06240	oxidoreductase/ transition metal ion binding	-0.3721	0.1265	0.2058	-0.6619	0.0267	0.0816	-0.2554	0.0503	0.095	-0.5452	0.0041	0.0205
260791_at	AT1G06250	lipase class 3 family protein	-0.3492	0.2862	0.3149	-0.1899	0.5403	0.4008	-0.2598	0.3901	0.3122	-0.1005	0.7285	0.4067
260792_at	AT1G06270	pentatricopeptide (PPR) repeat-containing protein	-0.3227	0.4189	0.3844	-0.1132	0.768	0.4799	-0.03505	0.8974	0.4917	0.1745	0.5318	0.3386
260793_at	AT1G06190	ATP binding / ATPase, coupled to transmembrane	-0.6269	0.0334	0.1057	-0.7018	0.0234	0.0771	-0.1472	0.4552	0.3409	-0.2222	0.2806	0.2284
260794_at	AT1G06210	VHS domain-containing protein / GAT domain-conta	0.1774	0.3242	0.3368	0.4637	0.0426	0.1026	-0.02602	0.8519	0.4791	0.2603	0.1173	0.1328
260795_at	AT1G06225	CLE3 (CLAVATA3/ESR-RELATED 3); receptor bin	-1.329	0.3325	0.3416	-0.3654	0.7771	0.4827	-0.0874	0.8529	0.4792	0.8761	0.1186	0.1337
260796_at	AT1G78360	ATGSTU21 (Arabidopsis thaliana Glutathione S-tra	-1.5888	0.227	0.2798	0.8492	0.4884	0.3798	-1.1284	0.3685	0.3022	1.3096	0.305	0.241
260797_at	AT1G78390	NCED9 (NINE-CIS-EPOXYCAROTENOID DIOXYG	1.0974	0.3023	0.3244	0.05182	0.9581	0.5338	2.3394	0.0471	0.091	1.2938	0.1919	0.1802
260798_at	AT1G78280	transcription factor jumonji (jmjC) domain-containing	0.1414	0.4084	0.3794	0.09514	0.5685	0.4113	-0.3353	0.046	0.0898	-0.3816	0.0313	0.0596
260799_at	AT1G78270	ATUGT85A4 (UDP-GLUCOSYL TRANSFERASE 8	0.2107	0.4666	0.4058	0.3333	0.2723	0.2768	-0.4188	0.1418	0.1728	-0.2961	0.2662	0.2209
260800_at	AT1G78240	TSD2 (TUMOROUS SHOOT DEVELOPMENT 2); r	0.1102	0.5594	0.4447	0.001412	0.9939	0.5427	-0.1402	0.3094	0.2731	-0.249	0.1078	0.126
260801_at	AT1G78430	Identical to Uncharacterized protein At1g78430 [Ara	-1.327	0.2928	0.3188	0.4815	0.6833	0.4532	-0.773	0.5197	0.3669	1.0355	0.3985	0.2836
260802_at	AT1G78400	glycoside hydrolase family 28 protein / polygalactur	-0.6782	0.5312	0.4334	1.0149	0.3635	0.3245	-1.7067	0.16	0.1857	-0.01354	0.9897	0.4801
260803_at	AT1G78340	ATGSTU22 (Arabidopsis thaliana Glutathione S-tra	-0.03654	0.9405	0.5627	0.412	0.4213	0.3512	0.2055	0.6104	0.4014	0.654	0.1538	0.1574
260804_at	AT1G78410	VQ motif-containing protein	1.089	0.1038	0.1862	1.4436	0.0497	0.1105	1.4461	9.00E-04	0.0167	1.8007	4.00E-04	0.0088
260805_at	AT1G78320	ATGSTU23 (Arabidopsis thaliana Glutathione S-tra	-1.1107	0.008	0.0587	-0.8176	0.0226	0.0759	0.5339	0.0518	0.0964	0.8269	0.0132	0.0364
260806_at	AT1G78260	RNA recognition motif (RRM)-containing protein	-0.5651	0.3459	0.3478	-0.6057	0.3164	0.301	-0.2469	0.6652	0.4196	-0.2875	0.6159	0.3687
260807_at	AT1G78310	VQ motif-containing protein	0.9411	0.0096	0.0628	0.7428	0.0213	0.0742	0.4375	0.078	0.1222	0.2392	0.2672	0.2213
260808_at	AT1G43715	transposable element gene	1.2356	0.3358	0.3432	1.3187	0.3083	0.2965	0.4461	0.7133	0.4359	0.5292	0.6641	0.3855
260809_at	AT1G43730	similar to unknown protein [Arabidopsis thaliana] (T	0.2643	0.7993	0.5238	-1.1746	0.2937	0.2885	0.3357	0.7333	0.4427	-1.0835	0.3277	0.2523
260810_s_at	AT1G43755,AT1G43745	[AT1G43755, transposable element gene];[AT1G43	1.2207	0.4241	0.3868	0.3488	0.8119	0.4935	-0.4816	0.6318	0.4084	-1.3535	0.2192	0.1957
260811_s_at	AT1G43740,AT1G43750	[AT1G43740, transposable element gene];[AT1G43	-0.6076	0.6129	0.4636	-0.7328	0.5449	0.4025	-0.9518	0.4391	0.3337	-1.0771	0.3865	0.2785
260812_at	AT1G43650	integral membrane family protein / nodulin MtN21-re	-0.6857	0.0234	0.0895	-0.9525	0.0077	0.049	0.7063	0.0213	0.0587	0.4398	0.0842	0.1083
260813_at	AT1G43700	VIP1 (VIRE2-INTERACTING PROTEIN 1); transcri	0.6026	0.0128	0.0698	0.5701	0.0155	0.065	0.3235	0.0832	0.1268	0.291	0.1076	0.1259
260814_at	AT1G43710	EMB1075 (EMBRYO DEFECTIVE 1075); carboxy-l	0.02216	0.8149	0.5263	-0.1869	0.1026	0.1616	-0.3186	0.0228	0.0611	-0.5276	0.004	0.0203
260815_at	AT1G43690	ATTIC110/TIC110 (TRANSLOCON AT THE INNER	0.484	0.0512	0.13	0.1572	0.4215	0.3513	-0.2775	0.0755	0.1197	-0.7043	0.0112	0.0332
260816_at	AT1G06930	unknown protein	-0.08743	0.5119	0.4257	-0.3863	0.0336	0.0907	0.516	0.0132	0.0458	0.2171	0.1488	0.1538
260817_at	AT1G06900	metalloendopeptidase	0.08185	0.6734	0.4838	0.2992	0.1724	0.2145	-1.1898	8.00E-04	0.0161	-0.9725	0.0016	0.0143
260818_at	AT1G06890	transposable element gene	0.4615	0.0947	0.1778	0.3888	0.1401	0.1906	-0.2553	0.2563	0.2444	-0.328	0.1643	0.1639
260819_at	AT1G06850	ATBZIP52 (ARABIDOPSIS THALIANA BASIC LEU	-0.2588	0.107	0.1893	-0.5406	0.0124	0.0596	0.5412	0.0087	0.0375	0.2593	0.0836	0.1079
260820_at	AT1G06840	leucine-rich repeat transmembrane protein kinase,	0.2403	0.2652	0.3023	0.2299	0.2834	0.2827	-0.3594	0.0479	0.0918	-0.3699	0.0441	0.0736
260821_at	AT1G06820	CRTISO (CAROTENOID ISOMERASE); carotenoid	0.1228	0.4001	-0.08781	0.538	0.3996	-0.3738	0.

260890_at	AT1G29090	peptidase C1A papain family protein	1.8485	0.1982	0.2615	-0.5751	0.6567	0.4441	1.9092	0.0735	0.118	-0.5144	0.5513	0.3456
260891_at	AT1G29080	peptidase C1A papain family protein	0.264	0.6808	0.4863	-0.1546	0.8083	0.4924	-0.2682	0.6762	0.4231	-0.6868	0.3136	0.2452
260892_at	AT1G29110	cysteine proteinase, putative	-0.6191	0.6164	0.4651	0.8923	0.4781	0.3755	-0.6901	0.5781	0.39	0.8213	0.5117	0.3304
260893_at	AT1G29180	DC1 domain-containing protein	-1.5556	0.1643	0.237	-0.1425	0.8837	0.5142	-1.875	0.1098	0.1483	-0.4619	0.6402	0.3772
260894_at	AT1G29220	transcriptional regulator family protein	0.2033	0.0249	0.0915	0.2829	0.0082	0.0504	0.6047	5.00E-04	0.0148	0.6843	3.00E-04	0.0083
260895_at	AT1G29250	nucleic acid binding	-0.01783	0.8843	0.5471	0.252	0.0935	0.154	0.7473	0.0029	0.0245	1.0172	9.00E-04	0.0116
260896_at	AT1G29310	protein transport protein sec61, putative	0.8519	0.0039	0.0463	0.7851	0.0052	0.0429	-0.1448	0.3649	0.3004	-0.2117	0.2098	0.1908
260897_at	AT1G29330	ER22 (ER lumen protein retaining receptor 2); rece	0.105	0.7572	0.5109	0.2175	0.5305	0.3965	-0.2096	0.4716	0.3482	-0.09714	0.7316	0.4076
260898_at	AT1G29070	ribosomal protein L34 family protein	-0.555	0.0112	0.0661	-0.6809	0.0054	0.0433	-0.1445	0.0151	0.0489	-0.2704	0.0016	0.014
260899_at	AT1G21370	similar to unnamed protein product [Vitis vinifera] (G	0.7244	0.0052	0.0514	0.8477	0.003	0.0355	-0.06441	0.5423	0.3763	0.0589	0.5758	0.3544
260900_s_at	AT1G21400,AT5G34780	[AT1G21400, 2-oxoisovalerate dehydrogenase, put	1.4203	0.008	0.0587	1.7033	0.0042	0.04	-0.4588	0.1881	0.2043	-0.1757	0.5765	0.3547
260901_at	AT1G21430	YUC11; monooxygenase	2.1011	0.1575	0.2313	0.9672	0.4689	0.3715	2.0208	0.1701	0.1919	0.887	0.504	0.3273
260902_at	AT1G21440	mutase family protein	-0.8293	0.0347	0.1076	-1.0398	0.0169	0.0676	0.3145	0.1014	0.1422	0.1039	0.5222	0.3348
260903_at	AT1G02460	glycoside hydrolase family 28 protein / polygalactur	-0.2705	0.2523	0.2948	-0.4443	0.0931	0.1539	0.4151	0.1053	0.1451	0.2413	0.292	0.2346
260904_at	AT1G02450	NIMIN-1/NIMIN1; protein binding	0.5535	0.1454	0.2216	0.9447	0.0369	0.0949	0.8809	0.0453	0.0891	1.2721	0.0143	0.0379
260905_at	AT1G02710	glycine-rich protein	-0.3156	0.6015	0.4601	0.4031	0.5095	0.3885	0.4877	0.4216	0.326	1.2064	0.0913	0.1139
260906_at	AT1G02540	unknown protein	-1.8107	0.0532	0.1323	0.6413	0.3906	0.337	-0.4114	0.5706	0.3869	2.0407	0.0376	0.0663
260907_at	AT1G02570	similar to unknown protein [Arabidopsis thaliana] (T	-0.736	0.3502	0.3497	-1.1882	0.1631	0.2081	0.3758	0.618	0.4039	-0.07643	0.9179	0.4621
260908_at	AT1G02580	MEA (MEDEA); transcription factor	-0.09856	0.9327	0.5604	0.8704	0.4715	0.3727	-0.6194	0.6021	0.3989	0.3496	0.7657	0.4185
260909_at	AT1G02670	DNA methyltransferase, putative	-1.3192	0.1265	0.2058	-0.3227	0.6622	0.4458	-1.2818	0.1072	0.1466	-0.2853	0.6589	0.387
260910_at	AT1G02690	importin alpha-2 subunit, putative	0.4211	0.0937	0.1772	0.4966	0.0612	0.1228	-0.2504	0.2248	0.2264	-0.1749	0.3731	0.2727
260911_at	AT1G02490	unknown protein	1.029	0.3555	0.3525	0.8854	0.4198	0.3505	0.4505	0.6713	0.4215	0.307	0.771	0.4203
260912_at	AT1G02560	CLPP5 (NUCLEAR ENCODED CLP PROTEASE 1	-0.08339	0.404	0.3773	-0.1032	0.3128	0.2989	-0.03004	0.7539	0.4493	-0.04989	0.6068	0.3656
260913_at	AT1G02500	SAM1 (S-adenosylmethionine synthetase 1); methi	0.1992	0.4129	0.3816	0.1829	0.449	0.3636	-0.6507	0.0025	0.0231	-0.667	0.0022	0.0158
260914_at	AT1G02640	BXL2 (BETA-XYLOSIDASE 2); hydrolase, hydrolyz	0.8564	0.1057	0.1879	-0.2229	0.6165	0.4294	-0.4504	0.2587	0.2457	0.1831	0.6211	0.3706
260915_at	AT1G02660	lipase class 3 family protein	-0.1918	0.6444	0.4747	0.2409	0.5654	0.4101	-0.6554	0.0078	0.0355	-0.2227	0.1683	0.1662
260916_at	AT1G02475	similar to unknown protein [Arabidopsis thaliana] (T	-0.04721	0.7944	0.5223	-0.1057	0.5668	0.4107	0.4503	1.00E-04	0.0118	0.3919	2.00E-04	0.0076
260917_at	AT1G02700	similar to unknown protein [Arabidopsis thaliana] (T	-0.7934	0.1815	0.2492	-0.9197	0.1344	0.1863	0.7851	0.1756	0.1957	0.6587	0.24	0.2071
260918_at	AT1G21510	similar to unknown [Populus trichocarpa] (GB:ABK9	-0.5974	0.6276	0.4689	-1.6318	0.2252	0.2485	0.3633	0.7657	0.4529	-0.6711	0.5874	0.3588
260919_at	no_match	no_match	3.3686	4.00E-04	0.032	4.0995	2.00E-04	0.0249	0.9824	0.0054	0.0306	1.7133	7.00E-04	0.0105
260920_at	no_match	no_match	1.3135	0.2323	0.2833	1.3892	0.2111	0.2404	0.07301	0.9321	0.5013	0.1487	0.8626	0.4465
260921_at	AT1G21540	AMP-binding protein, putative	0.5192	0.6189	0.4661	0.03004	0.9766	0.5385	-1.859	0.1261	0.161	-2.3481	0.0716	0.0981
260922_at	AT1G21560	similar to unknown protein [Arabidopsis thaliana] (T	0.2035	0.3242	0.3368	-0.2107	0.3095	0.2971	0.09728	0.6198	0.4045	-0.3169	0.1551	0.1582
260923_at	AT1G21570	zinc finger (CCCH-type) family protein	0.06046	0.7275	0.5017	0.243	0.2074	0.2378	-1.0364	2.00E-04	0.0126	-0.8539	4.00E-04	0.0089
260924_at	AT1G21590	protein kinase family protein	0.2364	0.3255	0.3375	0.3532	0.1696	0.2123	-0.7724	0.0038	0.0269	-0.6557	0.0068	0.0257
260925_at	AT1G21340	Dof-type zinc finger domain-containing protein	0.5259	0.576	0.4511	1.1098	0.2688	0.2749	-1.0376	0.1184	0.155	-0.4537	0.4348	0.299
260926_at	AT1G21360	GLYP2 (GLYCOLYPID TRANSFER PROTEIN 2); gl	-0.69	0.4803	0.4119	-0.1143	0.6937	0.5198	-0.9485	0.3453	0.2908	-0.3728	0.696	0.3961
260927_at	AT1G05940	CAT9 (CATIONIC AMINO ACID TRANSPORTER 9	0.4296	0.0828	0.1665	0.2071	0.3294	0.3083	-0.2379	0.2714	0.253	-0.4604	0.0692	0.0964
260928_at	AT1G02720	GATL5; polygalacturonate 4-alpha-galactu	-0.64	0.3766	0.3626	0.2994	0.6662	0.4471	-1.1081	0.1605	0.1859	-0.1687	0.8063	0.4306
260929_at	AT1G02730	TAF15 (TBP-ASSOCIATED FACTOR 15); RNA pol	0.1189	0.6302	0.4698	0.4974	0.095	0.1554	0.07466	0.7602	0.4512	0.4531	0.1183	0.1336
260930_at	AT1G02620	GTP-binding protein (SAR1A)	-0.9378	0.1374	0.2154	0.5438	0.3429	0.3148	-1.0557	0.1052	0.1451	0.4258	0.4473	0.305
260931_at	AT1G02550	invertase/pectin methylesterase inhibitor family prot	-0.6781	0.4991	0.42	0.1687	0.8625	0.5078	-0.05419	0.9555	0.5067	0.7926	0.4345	0.2988
260932_s_at	AT1G02530,AT1G02520	[AT1G02530, PGP12 (P-GLYCOPROTEIN 12); AT1	1.9801	0.1943	0.2586	2.267	0.1491	0.1976	-1.1307	0.1581	0.1844	-0.8438	0.2655	0.2206
260933_at	AT1G02470	similar to unknown protein [Arabidopsis thaliana] (T	0.2355	0.5637	0.4463	0.155	0.7004	0.4592	-0.1043	0.3611	0.2987	-0.1849	0.1418	0.1494
260934_at	AT1G45100	polyadenylate-binding protein, putative / PABP, puta	-0.6261	0.455	0.4005	-1.2101	0.1855	0.2234	0.758	0.3737	0.3045	0.1741	0.8296	0.437
260935_at	AT1G45110	tetrapyrrole methylase family protein	0.015	0.9759	0.5712	0.3376	0.5086	0.388	-1.0774	0.0817	0.1253	-0.7549	0.1803	0.1735
260936_at	AT1G45150	similar to predicted protein [Physcomitrella patens s	0.439	0.1383	0.216	0.1318	0.6087	0.4266	-0.2252	0.2119	0.2191	-0.5324	0.0247	0.0517
260937_at	AT1G45160	kinase	0.2216	0.2035	0.2643	0.1605	0.3332	0.3098	-0.4731	0.0125	0.0443	-0.5343	0.0082	0.0281
260938_at	AT1G45170	similar to unknown protein [Arabidopsis thaliana] (T	0.04276	0.8387	0.535	0.08054	0.7035	0.4603	-0.503	0.0367	0.0789	-0.4672	0.0461	0.0755
260939_at	AT1G45180	zinc finger (C3HC4-type RING finger) family protein	-0.1612	0.5109	0.4252	0.497	0.0903	0.1516	-0.4835	0.0066	0.1382	0.1746	0.4784	0.317
260940_at	AT1G45000	26S proteasome regulatory complex subunit p42D,	0.4212	0.0056	0.0521	0.2776	0.0232	0.0768	0.3944	0.0071	0.0341	0.2508	0.0319	0.0601
260941_at	AT1G44970	peroxidase, putative	-0.3388	0.7882	0.5201	-0.3435	0.7854	0.4848	-0.9468	0.394	0.3139	-0.9515	0.3918	0.2807
260942_s_at	AT1G45190,AT3G11990	[AT1G45190, similar to unknown protein [Arabidops	0.1213	0.8702	0.5441	0.06594	0.9291	0.5265	-0.8592	0.2848	0.2606	-0.9145	0.2594	0.2175
260943_at	AT1G45145	ATTRX5 (thioredoxin H-type 5); thiol-disulfide exch	0.5888	0.1281	0.2068	1.0138	0.03	0.0862	0.8219	0.0075	0.0351	1.2468	0.0016	0.0143
260944_at	AT1G45130	SGALS (beta-galactosidase 5); beta-galactosidase	-0.3969	0.1703	0.2416	-0.4387	0.1388	0.1898	0.02647	0.8451	0.4771	-0.01529	0.91	0.4599
260945_at	AT1G05950	similar to unnamed protein product [Vitis vinifera] (G	0.07996	0.9286	0.5596	-0.8357	0.3755	0.3301	0.7968	0.3057	0.2716	-0.1189	0.8695	0.4482
260946_at	AT1G06010	unknown protein	0.2342	0.394	0.3722	0.4382	0.1487	0.1973	-0.1625	0.5441	0.377	0.04156	0.8737	0.4495
260947_at	AT1G06020	dnaB-type carbohydrate kinase family protein	2.307	0.2003	0.2624	0.7688	0.6366	0.437	0.7063	0.6555	0.4163	-0.8319	0.6011	0.3638
260948_at	AT1G06100	fatty acid desaturase family protein	-0.6769	0.1185	0.1989	-1.3846	0.0154	0.0649	0.09256	0.7824	0.4581	-0.6152	0.1211	0.1358
260949_at	AT1G06110	SKIP16 (SKP1/ASK-INTERACTING PROTEIN 16);	0.3461	0.0191	0.082	0.3891	0.0129	0.0607	-0.4565	0.0074	0.0348	-0.4134	0.0105	0.0321
260950_s_at	AT1G06120,AT1G06090	[AT1G06120, fatty acid desaturase family protein][A	0.4725	0.6176	0.4656	1.7661	0.1135	0.1702	0.2983	0.7502	0.4484	1.5918	0.1428	0.1499
260951_at	AT1G06145	EMB1444 (EMBRYO DEFECTIVE 1444)	0.9539	0.4169	0.3833	0.007005	0.995	0.5429	-0.7269	0.4157	0.3233	-1.6738	0.105	0.124
260952_at	AT1G06140	pentatricopeptide (PPR) repeat-containing protein	0.0989	0.9096	0.5538	2.1708	0.0567	0.1184	-1.3145	0.1833	0.2011	0.7575	0.4068	0.2869
260953_at	AT1G06070	bZIP transcription factor, putative (bZIP69)	0.0445	0.765	0.513	0.06633	0.6582	0.4444	-0.3238	0.0723	0.1169	0.3456	0.6607	0.3891
260954_at	AT1G06130	GLX2-4 (GLYOXALASE 2-4); hydroxyacylglutathion	-0.02704	0.8036	0.5251	0.327	0.0325	0.0893	-0.1802	0.1501	0.179	0.1738	0.1616	0.1623
260955_at	AT1G06000	UDP-glucuronosyl/UDP-glucosyl transferase family	-1.4878	0.0577	0.1376	-1.7555	0.0358	0.0932	0.4559	0.076	0.1202	0.1883	0.3815	0.2764
260956_at	AT1G06040	STO (SALT TOLERANCE); transcription factor/ zinc	-0.3363	0.0459	0.1232	-0.5192	0.0116	0.058	0.4301	0.0113	0.0421	0.2472	0.0631	0.0912
260957_at	AT1G06080	ADS1 (DELTA 9 DESATURASE 1); oxidoreductase	-1.7706	0.0228	0.0882	-1.0179	0.1073	0.1653	-0.01697	0.9301	0.5006	0.7357	0.0155	0.0397
260958_at	AT1G06060	RanBPM-related	-0.3754	0.0984	0.181	-0.2013	0.3139	0.2994	-0.06801	0.7172	0.4374	0.1061	0.5769	0.3548
260959_at	AT1G06050	similar to unknown protein [Arabidopsis thaliana] (T	0.09625	0.5092	0.4246	0.09223	0.5261	0.3946	-0.2063	0.1545	0.1819	-0.2103	0.1484	0.1536
260960_at	AT1G05990	calcium-binding protein, putative	0.9243	0.3728	0.3608	-1.1567	0.2779	0.2797	0.3375	0.7296	0.4417	-1.7435	0.128	0.1402
260961_at	AT1G05960	binding	-0.08199	0.7441	0.5071	0.0477	0.8487	0.504	-0.938	0.0147	0.0483	-0.8083	0.0239	0.0507
260962_at	AT1G44980	pectinesterase family protein	0.134	0.8988	0.5508	-0.7384	0.4972	0.3832	0.749	0.4914	0.3562	-0.1234	0.9068	0.4591
260963_at	AT1G44990	unknown protein	0.4302	0.6104	0.463	0.9179	0.3043	0.2938	0.2986	0.7212	0.439	1.6467	0.1022	0.1221
260964_at	AT1G45050	ATUBC2-1 (ARABIDOPSIS THALIANA UBIQUITIN	0.197	0.3768	0.3626	0.462	0.0803	0.1421	-0.2464	0.2819	0.2592	0.0186	0.9298	0.4656
260965_s_at	AT1G45090,AT2G12100	[AT1G45090, transposable element gene][AT2G12	-1.1139	0.5008	0.4209	-0.7849	0.6299	0.4345	0.04543	0.9774	0.5119	0.3744	0.816	0.4332
260966_at	AT1G12220	RPS5 (RESISTANT TO P. SYRINGAE 5)	0.02951	0.8798	0.5464	0.1175	0.5559	0.4068	-0.7921	0.0124	0.0442	-0.6451	0.0244	0.0514
260967_at	AT1G12230	transaldolase, putative	-0.2185	0.2726	0.307	0.05686	0.7574	0.4774	-0.254	0.1936	0.2077	0.02137	0.9018	0.4579
260968_at	AT1G12250	thylakoid lumenal protein-related	-0.7219	0.0173	0.0787	-0.8416	0.0103	0.0551	0.224	0.1416	0.1726	0.1043	0.4427	0.3027
260969_at	AT1G12240	ATBETAFRUCT4/VAC-INV (VACUOLAR INVERTA	0.05025	0.627	0.4687	-0.2275	0.0761	0.1381	0.001219	0.99	0.5153	-0.176	0.1252	0.1384
260970_at	AT1G53640	unknown protein	0.1614	0.556	0.4432	-0.1667	0.5438	0.4022	0.3769	0.0983	0.1395	0.04883	0.7946	0.4274
260971_at	no_match	no_match	0.1816	0.8478	0.5378	0.6942	0.4775	0.3753	0.02236	0.9673	0.5095	0.535	0.356	0.2652
260972_at	AT1G53530	signal peptidase I family protein	0.264	0.1329	0.2115	0.291	0.1066	0.1647	-0.4344	0.0363	0.0784	-0.4074	0.0439	0.0733
260973_at	AT1G53490	DNA binding	-0.1556	0.7996	0.5239	-1.1328	0.1196	0.1749	-0.2155	0.6986	0.4308	-1.1927	0.0826	0.1071
260974_at	AT1G53440	leucine-rich repeat family protein / protein kinase fa	0.7165	0.0416	0.1175	0.2101	0.4346	0.3574	-0.4395	0.0635	0.1086	-0.9459	0.0054	0.023
260975_at	AT1G53430	leucine-rich repeat family protein / protein kinase fa	0.1894	0.5743	0.4506	-0.1539	0.6456	0.4401	-0.1014	0.6126	0.402	-0.4447	0.074	0.0999
260976_at	AT1G53650	CID8; RNA binding / protein binding	-0.02052	0.9157	0.5557	0.1509	0.4537	0.3655	0.06329	0.7456	0.4467	0.2347	0.2668	0.2211
260977_at	AT1G53420	serine/threonine protein kinase-related	-0.7315	0.4931	0.4172	0.2685	0.7958	0.4882	1.2444	0.2692	0.2517	2.2443	0.0819	0.1065
260978_at	AT1G53540	17.6 kDa class I small heat shock protein (HSP17.6	1.1917	0.0248	0.0915	3.8593	3.00E-04	0.0249	-0.2829	0.4524	0.3397	2.3847	0.0022	0.0157
260979_at	AT1G53510	ATMPK18 (ARABIDOPSIS THALIANA MAP KINAS	0.2052	0.3716	0.3602	-0.07395	0.7354	0.4698	-0.743	0.0059	0.032	-1.0221	0.0018	0.0148
260980_at	AT1G53600	pentatricopeptide (PPR) repeat-containing protein	-1.031	0.4401	0.3937	0.05342	0.9667	0.5357	-1.3906	0.3124	0.2746	-0.3062	0.8118	0.4323
260981_at	AT1G53460	structural molecule	0.04369	0.6281	0.4689	0.3957	0.009	0.052	-0.1708	0.1099	0.1484	0.1811	0.0956	0.1173
260982_at	AT1G53520	chalcone-flavanone isomerase-related	-1.3643	0.0287	0.0983	-1.6808	0.0146	0.0638	0.1647	0.2091	0.2173	-0.1518	0.2402	0.2072
260983_at	AT1G53560	similar to unknown protein [Arabidopsis thaliana] (T	-0.6515	0.031	0.102	-0.5592	0.0487	0.1096	0.1653	0.3072	0.2721	0.2576	0.1425	0.1498
260984_at	AT1G53645	hydroxyproline-rich glycoprotein family protein	0.6387	0.0172	0.0786	0.5775	0.0238	0.0777	0.3771	0.0422	0.0856	0.3159	0.0693	0.0964
260985_at	AT1G53500	MUM4 (MUCILAGE-MODIFIED 4); catalytic	-0.3893	0.232	0.2831	-0.6686	0.073	0.1353	-0.05445	0.8286	0.4723	-0.3338	0.2296	0.2013
260986_at	AT1G53580	ETHE1/GLX2-3/GLY3 (GLYOXALASE 2-3); hydrox	0.3588	0.0894	0.1732	0.579	0.0221	0.0751	0.3969	0.0196	0.0562	0.6201	0.0041	0.0207
260987_at	AT1G53590	NTMC2T6.1/NTMC2TYPE6.1	0.3488	0.2637	0.3018	0.6635	0.0688	0.1317	-0.5694	0.0759	0.12	-0.2547	0.3468	0.2611
260988_at	AT1G53570	MAP3KA (Mitogen-activated protein kinase kinase k	-0.09185	0.5983	0.459	0.1788	0.3284	0.3078	-0.469	0.0433	0.0869	-0.1984	0.2847	0.2307
260989_at	AT1G53450	similar to unknown protein [Arabidopsis thaliana] (T	-0.1318	0.5376	0.4359	-0.3831	0.1219	0.1772	-0.167	0.4417	0.3348	-0.4182	0.0994	0.1202
260990_at	AT1G12180	similar to heat shock protein-related [Arabidopsis th	0.3303	0.726	0.5013	-1.0525	0.2971	0.2902	0.7887	0.4201	0.3254	-0.5941	0.536	0.34
260991_at	AT1G12160	flavin-containing monooxygenase family protein / FI	1.1266	0.0876	0.1715	1.35	0.0543	0.1156	-0.5118	0.1244	0.1597	-0.2883	0.336	0.2561
260992_at	AT1G12150	similar to myosin heavy chain-related [Arabidopsis t	-1.3151	0.2057	0.2659	-1.7521	0.1147	0.1708	-1.1002	0.2424	0.2364	-1.5373	0.128	0.1402
260993_at	AT1G12140	flavin-containing monooxygenase family protein / FI	0.353	0.0227	0.0882	0.2954	0.0394	0.0983	0.1851	0.132	0.1653	0.1276	0.2629	0.2192
260994_at	AT1G12130	flavin-containing monooxygenase family protein / FI	1.0281	0.3476	0.3487	1.0807	0.3263	0.3066	-0.4574	0.6609	0.4182	-0.4048	0.697	0.3965
260995_at	AT1G12120	similar to unknown protein [Arabidopsis thaliana] (T	0.1512	0.5711	0.4494	0.3863	0.1906	0.2268	-1.0621	0.0081	0.0361	-0.5246	0.0731	0.0992
260996_at	AT1G12210	RFL1 (RPS5-LIKE 1); ATP binding / protein binding	1.8365	0.0226	0.0879	1.1288	0.0909	0.1521	0.2578	0.4095	0.3206	-0.4499	0.1835	0.1756
260997_at	AT1G26610	zinc finger (C2H2 type) family protein	0.5422	0.2618	0.3006	-0.4471	0.3423	0.3145	0.4183	0.319	0.2778	-0.571	0.1955	0.1822
260998_at	AT1G26590	zinc finger (C2H2 type) family protein	0.026504	0.9572	0.5665	-0.1009	0.8356	0.5003	-0.4446	0.3844	0.3098	-0.5715	0.278	0.2271
260999_at	AT1G26580	similar to myb family transcription factor / ELM2 dor	0.8739	0.0194	0.0824	1.058	0.0102	0.0549	-2.0469	9.00E-04	0.0169	-1.8628	0.0013	0.0132
261000_at	AT1G26540	agenet domain-containing protein	1.3231	0.2873	0.3157	-0.811	0.4941	0.3822	0.9945	0.408	0.3199	-1.1396	0.3496	0.2623
261001_at	AT1G26530	similar to unknown protein [Arabidopsis thaliana] (T	-0.04448	0.9624	0.5679	-0.132	0.8888	0.5155	-2.0632	0.0803	0.124	-2.1507	0.0722	0.0985
261002_at	AT1G26520	similar to PRL1-interacting factor L, putative [Arabid	0.4814	0.117	0.1977	0.1623	0.5383	0.3997	-0.4852	0.1149	0.1524	-0.8042	0.0291	0.0571
261003_at	AT1G26500	pentatricopeptide (PPR) repeat-containing protein	1.2074	0.1334	0.212	-0.5084	0.4731	0.3734	0.6963	0.3394	0.2882	-1.0194	0.1678	0.178
261004_at	AT1G26450	beta-1,3-glucanase-related	1.5282	0.1046	0.1868	1.677	0.0833	0.1451	0.445	0.5753	0.3886	0.5938	0.4619	0.3108
261005_at	AT1G26420	FAD-binding domain-containing protein	1.3381	0.2742	0.308	2.9381	0.0498	0.1106	-0.08999	0.9122	0.4957	1.51	0.12	0.135
261006_at	AT1G26410	FAD-binding domain-containing protein	1.6455	0.2213	0.276	1.7544	0.1976	0.2314	0.2913	0.7316	0.4422	0.4002	0.6398	0.3771
261007_at	AT1G26400	FAD-binding domain-containing protein	0.6674	0.5631	0.446	0.4471	0.6949	0.4571	1.1075	0.3551	0.2957	0.8872	0.4498	0.306
261008_at	AT1G26370	RNA helicase, putative	-0.09814	0.7989	0.5236	0.1437	0.7105	0.4623	-0.254	0.3331	0.2849	-0.01224	0.9603	0.4733
261009_at	no_match	no_match	-0.4166	0.2928	0.3188	-0.2212	0.5546	0.4065	0.02701	0.9401	0.5034	0.2214	0.5477	0.3441
261010_at	AT1G26350	unknown protein	-1.0747	0.2306	0.2823	0.9677	0.2722	0.2767	-1.3443	0.1519	0.1802	0.6981	0.4107	0.2885
261011_at	AT1G26340	B5 #6 (cytochrome b5 family protein #6); heme bind	0.1286	0.6261	0.4684	0.1453	0.5836	0.4176	0.9223	0.0133	0.0458	0.939	0.0125	0.0353
261012_at	AT1G26450	CLE9 (CLAVATA3/ESR-RELATED 9); receptor bind	-0.2471	0.332	0.3411	-0.579	0.0611	0.1227	-0.5452	0.0385	0.0811	-0.8771	0.0081	0.028
261013_at	AT1G26440	ATUPS5 (ARABIDOPSIS THALIANA URIDINE PER	0.9585	0.0099	0.0638	1.1588	0.0051	0.0425	-0.9436	0.0047	0.0292	-0.7433	0.011	0.0328
261014_at	AT1G26460	pentatricopeptide (PPR) repeat-containing protein	0.3411	0.1236	0.2038	0.4142	0.0775	0.1395	-0.3648	0.1059	0.1456	-0.2918	0.1714	0.1681
261015_at	AT1G26480	GRF12 (GENERAL REGULATORY FACTOR 12); p	-1.9975	0.3496	0.3456	-0.9682	0.4955	0.3828	0.9321	0.5109	0.3636	1.3614	0.3618	0.2634
261016_at	AT1G26560	glycosyl hydrolase family 1 protein	-0.1592	0.1575	0.2313	-0.6101	0.0027	0.0344	0.007203	0.9412	0.5037	-0.4437	0.0084	0.0285
261017_at	AT1G26570	ATUGD1/UGD1 (UDP-glucose dehydrogenase 1);	-0.2868	0.333	0.3418	-0.6343	0.0717	0.134	0.2514	0.146	0.1761	-0.09615	0.5287	0.3374
261018_at	AT1G26550	peptidyl-prolyl cis-trans isomerase FPPC-type family	0.3429	0.1073	0.1895	0.5533	0.0289	0.0847	0.7811	0.0068	0.0338	0.9915	0.0029	0.0175
261019_at	AT1G26470	similar to Os05g0512500 [Oryza sativa (japonica cu	0.3164	0.0488	0.1271	0.6362	0.0049	0.0422	0.2589	0.0837	0.1272	0.5788	0.0069	0.0258
261020_at	AT1G26390	FAD-binding domain-containing protein	1.0806	0.3227	0.3359	1.7375	0.1442	0.1939	-0.07395	0.7567	0.4502	0.583	0.0591	0.0878
261021_at	AT1G26380	FAD-binding domain-containing protein	1.6503	0.0819	0.1656	1.8765	0.0583	0.1201	0.3998	0.3122	0.2746	0.586	0.133	0.1437
261022_at	AT1G12260	VND4 (VASCULAR RELATED NAC-DOMAIN PRO	-0.1187	0.8995	0.551	0.3542	0.7087	0.4616	0.1789	0.8492	0.4784	0.6518	0.5011	0.3263
261023_at	AT1G12200	flavin-containing monooxygenase family protein / FI	0.5643	0.0227	0.0882	0.5102	0.0312	0.0877	0.3645	0.0449	0.0887	0.3105	0

261090_at	AT1G07560	leucine-rich repeat protein kinase, putative	0.159	0.7101	0.4962	0.2717	0.5558	0.4068	0.4715	0.3276	0.2822	0.5743	0.2463	0.2104
261091_at	AT1G07550	leucine-rich repeat protein kinase, putative	0.8927	0.1356	0.2139	-1.6747	0.0249	0.0791	1.5869	0.0094	0.0388	-0.9804	0.0443	0.0737
261092_at	no_match	no_match	-0.6899	0.0853	0.1692	-0.3267	0.342	0.3144	-0.4397	0.2207	0.224	-0.07652	0.8132	0.4326
261093_at	AT1G62890	transposable element gene	-0.1643	0.8853	0.5472	-1.2481	0.3077	0.2961	0.1259	0.9119	0.4957	-0.9579	0.4207	0.2928
261094_at	AT1G62920	similar to proteasome maturation factor UMP1 famil	0.09537	0.8738	0.5451	-0.7311	0.264	0.272	0.1089	0.8561	0.4801	-0.7176	0.2716	0.2236
261095_at	AT1G62930	binding	1.36	0.0146	0.0734	0.1378	0.6979	0.4582	0.7224	0.094	0.1359	-0.4998	0.2048	0.1878
261096_at	AT1G62940	4-coumarate--CoA ligase family protein / 4-coumaro	-0.6977	0.4677	0.4063	-0.7529	0.4358	0.3579	-0.2314	0.7983	0.4628	-0.2866	0.7522	0.4144
261097_at	AT1G62950	KNAT7 (Knotted-like Arabidopsis thaliana); DNA bir	-0.4546	0.3617	0.3553	-0.4487	0.3673	0.3263	-0.27	0.5742	0.3882	-0.2641	0.5822	0.357
261098_at	AT1G62970	DNAJ heat shock N-terminal domain-containing pro	0.03572	0.9088	0.5536	-0.2319	0.4726	0.3733	-0.4812	0.1756	0.1957	-0.7488	0.0628	0.091
261099_at	AT1G62980	ATEXPA18 (ARABIDOPSIS THALIANA EXPANSIN	1.1889	0.2558	0.2969	-0.06935	0.9421	0.5298	2.0281	0.0788	0.1227	0.7699	0.4233	0.2939
261100_at	AT1G63020	NRPD1a (NUCLEAR RNA POLYMERASE D 1A); D	-0.4018	0.1944	0.2586	0.7943	0.037	0.095	-1.3441	0.0065	0.0331	-0.148	0.597	0.3624
261101_at	AT1G63030	DDF2 (DWARF AND DELAYED FLOWERING 2); D	-1.4144	0.0946	0.1778	-2.3101	0.0235	0.0772	-0.3882	0.5817	0.3913	-1.2839	0.1188	0.1339
261102_at	AT1G62880	comichon family protein	0.03653	0.8808	0.5465	0.3379	0.2134	0.2416	-0.2653	0.3103	0.2736	0.03606	0.8823	0.4521
261103_s_at	AT1G63140,AT1G62900	[AT1G63140, O-methyltransferase, putative];[AT1G	0.5444	0.6791	0.4857	0.2075	0.8734	0.511	-0.3091	0.8128	0.4675	-0.646	0.6251	0.372
261104_at	AT1G62910	pentatricopeptide (PPR) repeat-containing protein	-0.4393	0.6655	0.4811	0.3692	0.7153	0.4638	-3.2193	0.0269	0.0667	-2.4108	0.0628	0.091
261105_at	AT1G63000	NRS/ER (NUCLEOTIDE-RHAMNOSE SYNTHASE/	-0.1796	0.3264	0.3382	-0.06529	0.7053	0.4607	-0.2082	0.2648	0.2492	-0.09393	0.5902	0.3601
261106_at	AT1G62990	KNAT7 (Knotted-like Arabidopsis thaliana); DNA bir	-0.5317	0.1979	0.2613	-0.05022	0.8913	0.5161	-0.3732	0.2711	0.2529	0.1082	0.7302	0.4072
261107_at	AT1G63010	SPX (SYG1/Pho81/XPR1) domain-containing protei	0.2937	0.0478	0.1259	0.2319	0.09	0.1512	0.1825	0.0336	0.0748	0.1207	0.1035	0.1231
261108_at	AT1G62960	ACS10 (ACC SYNTHASE 10); 1-aminocyclopropan	-0.3051	0.2113	0.2691	-0.5265	0.0623	0.124	-0.4929	0.0742	0.1186	-0.7144	0.0253	0.0526
261109_at	AT1G75450	CKX5 (CYTOKININ OXIDASE 5); cytokinin oxidase/	-0.5495	0.0918	0.1757	-1.0356	0.0141	0.0629	-0.1554	0.2713	0.253	-0.6414	0.0062	0.0245
261110_at	AT1G75440	UBC16 (UBIQUITIN-CONJUGATING ENZYME 16)	0.1699	0.4947	0.418	0.1849	0.46	0.3679	0.5067	0.0099	0.0396	0.5217	0.0089	0.0295
261111_at	AT1G75410	transcription factor	0.7195	0.6161	0.4649	-0.1856	0.8954	0.5173	-0.2009	0.8683	0.4837	-1.1059	0.3857	0.2782
261112_at	AT1G75420	glycosyl transferase family 1 protein	0.1436	0.3754	0.3621	0.2719	0.1323	0.1847	-0.4267	0.0165	0.0512	-0.2984	0.0499	0.0792
261113_at	AT1G75400	protein binding / zinc ion binding	-0.0734	0.5126	0.4636	0.2418	0.1451	0.1946	-0.01125	0.9371	0.5027	0.304	0.0856	0.1095
261114_at	AT1G75390,AT1G75388	[AT1G75390, ATBZIP44 (ARABIDOPSIS THALIAN	0.3407	0.2	0.2622	0.7043	0.0339	0.091	0.02648	0.9109	0.4955	0.39	0.1541	0.1575
261115_at	AT1G75360	unknown protein	-0.4413	0.6077	0.4623	1.0584	0.2531	0.2658	-1.7186	0.0962	0.1379	-0.2189	0.7963	0.4276
261116_at	AT1G75370	SEC14 cytosolic factor, putative / phosphatidylinosi	-0.00095	0.9969	0.5763	-0.05816	0.8157	0.4948	-0.3753	0.1835	0.2011	-0.4326	0.1378	0.1468
261117_at	AT1G75310	AUL1 (auxin-like 1 protein); heat shock protein bind	0.4523	0.0453	0.1733	0.5835	0.7884	0.4857	-0.517	0.0122	0.044	-0.6254	0.0063	0.0246
261118_at	AT1G75460	ATP-dependent protease La (LON) domain-contain	-0.5849	0.0464	0.1238	-0.7493	0.0217	0.0748	0.3994	0.052	0.0966	0.235	0.1824	0.1749
261119_at	AT1G75350	EMB2184 (EMBRYO DEFECTIVE 2184); structural	-0.8735	0.0025	0.0424	-0.8491	0.0028	0.0352	-0.0197	0.8355	0.4743	0.004703	0.9604	0.4733
261120_at	AT1G75410	BLH3; DNA binding / transcription factor	0.08929	0.5744	0.4506	0.06523	0.6786	0.4514	-0.4406	0.0045	0.0286	-0.4646	0.0037	0.0197
261121_at	AT1G75340	zinc finger (CCCH-type) family protein	0.2419	0.1979	0.2613	-0.5192	0.0297	0.0856	0.3612	0.0203	0.0573	-0.3999	0.0145	0.0384
261122_at	AT1G75330	OTC (ORNITHINE CARBAMOYLTRANSFERASE);	0.07541	0.5783	0.4519	-0.06698	0.6199	0.4305	-0.2953	0.0371	0.0795	-0.4377	0.0104	0.0318
261123_at	AT1G62860	pseudogene of pentatricopeptide (PPR) repeat-con	1.2983	0.1133	0.195	-0.1473	0.8299	0.4988	-1.1102	0.1589	0.1851	-2.5558	0.0164	0.0409
261124_at	AT1G04900	similar to hypothetical protein Os_004408 [Oryza s	0.7466	0.0291	0.0989	0.8415	0.0199	0.0722	-0.644	0.0454	0.0892	-0.5492	0.0705	0.0973
261125_at	AT1G04990	zinc finger (CCCH-type) family protein	1.0237	0.0064	0.0547	1.4221	0.0019	0.033	-0.1359	0.317	0.2768	0.2625	0.0921	0.1144
261126_at	AT1G04950	initiation factor	0.001117	0.9929	0.5752	0.07013	0.5837	0.4177	-0.7465	3.00E-04	0.0138	-0.6775	4.00E-04	0.0091
261127_at	AT1G04790	zinc finger (C3HC4-type RING finger) family protein	0.1847	0.1006	0.1833	0.3431	0.0168	0.0673	-0.2203	0.0642	0.1093	-0.06183	0.5158	0.332
261128_at	AT1G04860	UBP2 (UBIQUITIN-SPECIFIC PROTEASE 2); ubiq	0.2511	0.0516	0.1306	0.03115	0.7506	0.4751	-0.1276	0.2051	0.2148	-0.3475	0.0146	0.0385
261129_at	AT1G04820	TUA4 (tubulin alpha-4 chain)	-0.3444	0.2352	0.2845	-0.2896	0.3095	0.2947	-0.1967	0.1069	0.1464	-0.1418	0.2092	0.1904
261130_at	AT1G04870	protein arginine N-methyltransferase family protein	0.5219	0.0528	0.1318	0.7445	0.0177	0.0689	-1.0279	0.0034	0.0259	-0.8053	0.0083	0.0282
261131_at	AT1G19835	similar to unknown protein [Arabidopsis thaliana] (T	0.1197	0.5432	0.4382	-0.138	0.4868	0.379	0.1877	0.1498	0.1788	-0.07	0.5432	0.3422
261132_at	AT1G19880	TGD1 (TRIGALACTOSYLDIACYLGLYCEROL 1)	-0.3439	0.0287	0.0982	-0.4304	0.0183	0.0623	-0.08703	0.4449	0.3361	-0.1735	0.1667	0.1652
261133_at	AT1G19715	jacalin lectin family protein	-0.6463	0.014	0.0723	-0.4932	0.0333	0.0904	-0.9849	9.00E-04	0.0172	-0.8318	0.0018	0.0147
261134_at	AT1G19630	CYP722A1 (cytochrome P450, family 722, subfami	-0.2546	0.6972	0.4918	-0.4046	0.5425	0.4017	0.1931	0.6913	0.4282	0.04309	0.9286	0.4653
261135_at	AT1G19610	LCR78/PDF1.4 (low-molecular-weight cysteine-rich	1.2983	0.1133	0.1934	1.6833	0.0667	0.1292	0.5579	0.1332	0.1661	0.872	0.0424	0.0718
261136_at	AT1G19600	pfkB-type carbohydrate kinase family protein	0.4106	0.0929	0.1765	0.7393	0.0167	0.0672	-1.176	0.001	0.0179	-0.8473	0.0036	0.0194
261137_at	AT1G19830	auxin-responsive protein, putative	1.2138	0.346	0.3478	0.4587	0.7074	0.4613	-0.4394	0.7189	0.4382	-1.1945	0.3529	0.264
261138_at	AT1G19710	glycosyl transferase family 1 protein	-0.2941	0.0862	0.1703	-0.059	0.6731	0.4496	-0.1918	0.214	0.2203	0.04343	0.7548	0.4151
261139_at	AT1G19700	BEL10/BLH10A (BEL1-LIKE HOMEODOMAIN 10);	-0.2155	0.4215	0.3858	-0.5197	0.097	0.157	-0.3551	0.0284	0.0684	-0.6594	0.0034	0.019
261140_at	AT1G19680	protein binding / zinc ion binding	0.4984	0.1718	0.2427	0.2073	0.5273	0.3951	-0.9337	0.0029	0.0245	-1.2247	0.001	0.0123
261141_at	AT1G19670	ATP-dependent protease La (LON) domain-contain	-0.1228	0.3366	0.2435	-0.4072	0.0224	0.0756	0.09999	0.389	0.3117	-0.1844	0.1496	0.1543
261142_at	AT1G19780	ATCNGC6 (CYCLIC NUCLEOTIDE GATED CHAN	-2.8666	0.0066	0.0551	-1.1381	0.1093	0.1669	0.7128	0.2679	0.251	2.4414	0.0117	0.0338
261143_at	AT1G19770	ATPUP14 (Arabidopsis thaliana purine permease 1	-0.7719	0.023	0.0887	-0.5895	0.0519	0.1131	-0.04718	0.6689	0.4208	0.1352	0.2572	0.2164
261144_s_at	AT1G19660,AT1G75380	AUL1 (auxin-like 1 protein); heat shock protein bind	0.3638	0.2495	0.2933	0.377	0.2355	0.255	-0.1694	0.1435	0.1742	-0.1562	0.1693	0.1668
261145_at	AT1G19730	ATTRX4 (thioredoxin H-type 4); thiol-disulfide exch	0.08623	0.7508	0.5087	0.4829	0.1294	0.1825	0.6603	0.0521	0.0967	1.0569	0.0119	0.0342
261146_at	AT1G19620	unknown protein	-0.7312	0.1522	0.2276	-0.7269	0.154	0.2012	-1.0267	0.059	0.104	-1.0224	0.0596	0.0882
261147_at	AT1G19690	binding / catalytic/ coenzyme binding	-0.3811	0.0995	0.182	-0.1305	0.5049	0.3867	-0.7385	0.0051	0.0301	-0.4879	0.0214	0.0476
261148_at	AT1G19580	GAMMA CA1 (GAMMA CARBONIC ANHYDRASE	-0.3804	0.0563	0.136	-0.2243	0.1917	0.2272	-0.1237	0.3163	0.2764	0.03245	0.7791	0.4226
261149_s_at	AT1G19570,AT1G19550	[AT1G19570, DHAR1 (DEHYDROASCORBATE RE	-0.4927	0.115	0.1963	-0.5494	0.0886	0.15	0.5402	0.0132	0.0457	0.4834	0.0191	0.0443
261150_at	AT1G19640	JMT (JASMONIC ACID CARBOXYL METHYLTRAN	-0.2123	0.002	0.04	-1.9571	0.0023	0.0334	-0.3993	0.1256	0.1605	-0.4545	0.0928	0.115
261151_at	AT1G19650	SEC14 cytosolic factor, putative / phosphoglyceride	-0.1773	0.5104	0.425	-0.4667	0.1302	0.1829	-0.5639	0.0822	0.1257	-0.8534	0.025	0.0522
261152_at	AT1G04930	hydroxyproline-rich glycoprotein family protein	0.121	0.5813	0.4527	-0.3295	0.178	0.2183	0.1383	0.3962	0.3149	-0.3121	0.0988	0.1197
261153_at	AT1G04850	ubiquitin-associated (UBA)/TS-N domain-containing	0.3941	0.0106	0.0649	0.4898	0.0049	0.0423	0.1835	0.1029	0.1432	0.2792	0.0327	0.0611
261154_at	AT1G04970	lipid-binding serum glycoprotein family protein	0.5648	0.0284	0.0975	0.4457	0.057	0.1188	-0.2218	0.0173	0.0525	-0.3409	0.0038	0.02
261155_at	AT1G04960	similar to bZIP family transcription factor [Arabidops	0.2137	0.191	0.2562	-0.2202	0.1805	0.2199	0.3151	0.0813	0.125	-0.1188	0.4314	0.2975
261156_s_at	AT1G04520,AT1G34490	[AT1G04520, long-chain-alcohol O-fatty-acyltransfe	-2.4295	0.1246	0.2044	-0.5789	0.6681	0.4478	-0.4089	0.7606	0.4513	-2.5995	0.1067	0.1251
261157_at	AT1G34510	peroxidase, putative	-0.3148	0.8079	0.5262	0.0245	0.9848	0.5404	0.8433	0.3798	0.3077	1.1825	0.2388	0.2064
261158_at	AT1G34500	membrane bound O-acyl transferase (MBOAT) fam	2.4189	0.0213	0.0858	-0.6398	0.3863	0.3349	1.4666	0.0745	0.1189	-1.5922	0.0598	0.0884
261159_s_at	AT1G34460,AT5G06150	[AT1G34460, CYCB1;4 (CYCLIN 3); cyclin-dependi	1.1859	0.096	0.179	0.7984	2.2181	0.2447	-2.5158	0.01	0.0398	-2.9033	0.0061	0.0241
261160_at	AT1G34480	DC1 domain-containing protein	-1.6545	0.3086	0.3277	-0.6098	0.6896	0.4555	0.4091	0.7866	0.4592	1.4538	0.3618	0.2678
261161_at	AT1G34420	leucine-rich repeat family protein / protein kinase fa	1.1941	0.0018	0.0391	0.7093	0.012	0.0587	0.3236	0.0534	0.0982	-0.1612	0.248	0.2114
261162_at	AT1G34440	similar to unknown protein [Arabidopsis thaliana] (T	0.3132	0.4578	0.4018	-0.1459	0.7216	0.4659	-0.02872	0.9436	0.5042	-0.4879	0.2701	0.2228
261163_x_at	AT1G34410	ARF21 (AUXIN RESPONSE FACTOR 21); transcri	-1.3417	0.226	0.279	0.673	0.5129	0.3899	-1.5659	0.1705	0.1922	0.4487	0.6574	0.3833
261164_at	AT1G34470	permease-related	-0.2602	0.1655	0.2378	0.02928	0.8581	0.5067	-0.9106	0.0041	0.0274	-0.6212	0.0155	0.0398
261165_at	AT1G34430	EMB3003 (EMBRYO DEFECTIVE 3003); dihydrolip	-0.1907	0.4015	0.376	-0.7232	0.0237	0.0773	0.201	0.2623	0.2479	-0.3315	0.0979	0.1189
261166_s_at	AT3G15750,AT1G34570	[AT3G15750, similar to unknown protein [Arabidops	-0.3525	0.0767	0.1594	0.0501	0.753	0.4761	-0.5368	0.0225	0.0606	-0.1343	0.4173	0.2914
261167_at	AT1G04980	ATPDIL2-2 (PDI-LIKE 2-2); thiol-disulfide exchange	1.614	4.00E-04	0.032	1.5073	6.00E-04	0.0266	0.1556	0.363	0.2996	0.04881	0.7637	0.4179
261168_at	AT1G04945	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.5723	0.004	0.0466	0.6426	0.0026	0.0342	-0.4264	0.0113	0.0422	-0.3562	0.0207	0.0466
261169_at	AT1G04920	ATSPS3F (sucrose phosphate synthase 3F); sucro	0.8838	0.0404	0.1159	-0.9507	0.0324	0.0892	0.1835	0.3297	0.2831	-1.651	6.00E-04	0.01
261170_at	AT1G04910	Identical to DUF246 domain-containing protein At1g	0.4466	0.0091	0.0615	0.2129	0.0869	0.1485	-0.3326	0.0131	0.0455	-0.5662	0.0019	0.0151
261171_at	AT1G04880	high mobility group (HMG1/2) family protein / ARID	-0.4018	0.7334	0.5034	0.2464	0.8338	0.4999	0.07368	0.9461	0.5047	0.7218	0.52	0.3337
261172_at	AT1G04840	pentatricopeptide (PPR) repeat-containing protein	-0.6002	0.5915	0.4566	0.4825	0.664	0.4462	1.0188	0.2206	0.2239	2.1014	0.0403	0.0694
261173_at	AT1G04830	RabGAP/TBC domain-containing protein	0.3213	0.0353	0.1085	0.1189	0.3117	0.2983	-0.6869	0.0026	0.0235	-0.8893	0.001	0.0121
261174_at	AT1G04810	26S proteasome regulatory subunit, putative	0.8588	1.00E-04	0.0312	0.4005	0.0011	0.0294	-0.3983	0.0012	0.0187	-0.8566	1.00E-04	0.0056
261175_at	AT1G04800	glycine-rich protein	-0.5368	0.216	0.2723	-1.1519	0.0345	0.0918	-1.0917	0.0405	0.0835	-1.7068	0.0095	0.0304
261176_at	AT1G04780	ankyrin repeat family protein	0.4201	0.1044	0.1866	0.2151	0.3439	0.3151	-0.2051	0.3643	0.3002	-0.4101	0.1104	0.128
261177_at	AT1G04770	male sterility MS5 family protein	-0.6016	0.4738	0.4094	-0.8111	0.3469	0.3165	0.1194	0.1986	0.211	-0.09015	0.3097	0.2432
261178_at	AT1G04760	ATVAMP726 (VESICLE-ASSOCIATED MEMBRAN	1.8051	0.1893	0.2548	-1.2087	0.3497	0.3179	1.1738	0.3623	0.2992	-1.8401	0.1826	0.175
261179_at	AT1G04985	similar to unnamed protein product [Vitis vinifera] (G	0.2397	0.1908	0.256	-0.1567	0.362	0.3239	-0.2644	0.1552	0.1824	-0.6607	0.012	0.0344
261180_at	AT1G34590	transposable element gene	0.1133	0.8451	0.5372	0.3361	0.5701	0.4119	-0.7041	0.2651	0.2493	-0.4813	0.4261	0.2951
261181_at	AT1G34580	monosaccharide transporter, putative	-0.4384	0.3581	0.3535	-0.02688	0.9523	0.5324	0.04124	0.9245	0.4991	0.4528	0.33	0.2533
261182_at	AT1G34575	FAD-binding domain-containing protein	-0.328	0.7464	0.5078	-1.2285	0.2641	0.272	1.2114	0.0687	0.1137	0.3109	0.56	0.3488
261183_at	AT1G34560	EMB2756 (EMBRYO DEFECTIVE 2756)	0.02387	0.889	0.5462	-0.3074	0.1281	0.1816	0.1488	0.4066	0.3193	-0.1825	0.3192	0.2479
261184_at	AT1G34545	transposable element gene	-1.2352	0.2695	0.3051	-0.8659	0.42	0.3506	0.7212	0.4961	0.3583	1.0904	0.3214	0.249
261185_at	AT1G34540	CYP94D1 (cytochrome P450, family 94, subfamily D	0.9057	0.4976	0.4195	0.2713	0.8343	0.5	1.4559	0.2971	0.2672	0.8215	0.5362	0.3401
261186_at	AT1G34530	transposable element gene	-0.7529	0.5231	0.4303	0.2107	0.8544	0.5059	0.2279	0.8428	0.4766	1.1915	0.3308	0.2537
261187_at	AT1G32860	glycosyl hydrolase family 17 protein	-0.5126	0.3036	0.325	-1.0013	0.0826	0.1443	0.2623	0.3325	0.2845	-0.2265	0.3955	0.2825
261188_at	AT1G33000	transposable element gene	0.6532	0.367	0.3579	0.2295	0.7391	0.471	-0.667	0.358	0.297	-1.0907	0.165	0.1643
261189_at	AT1G33040	NACAS (NASCENT POLYPEPTIDE-ASSOCIATED	-0.3449	0.0084	0.06	-0.2525	0.0239	0.0779	1.0981	1.00E-04	0.0101	1.1905	1.00E-04	0.0055
261190_at	AT1G32990	PRPL11 (PLASTID RIBOSOMAL PROTEIN L11); s	-0.6596	0.0055	0.052	-0.8403	0.0023	0.0334	0.3559	0.0422	0.0856	0.1752	0.2209	0.1965
261191_at	AT1G32900	starch synthase, putative	-1.0429	0.1351	0.2134	-1.386	0.068	0.1307	-0.2592	0.1696	0.1916	-0.6023	0.0177	0.0426
261192_at	AT1G32870	ANAC013 (Arabidopsis NAC domain containing pro	0.7595	0.0267	0.0944	0.6916	0.0356	0.093	-0.00087	0.997	0.517	-0.06877	0.772	0.4206
261193_at	AT1G32920	similar to unknown protein [Arabidopsis thaliana] (T	-0.6319	0.3392	0.3449	0.09054	0.8841	0.5143	0.4011	0.1637	0.1877	1.1235	0.0088	0.0293
261194_at	AT1G12775	binding	0.06346	0.8256	0.5311	0.1236	0.6707	0.4488	0.1296	0.6561	0.4165	0.1897	0.5207	0.3341
261195_at	AT1G12820	AFB3 (AUXIN SIGNALING F-BOX 3); auxin binding	0.02003	0.9488	0.5645	-0.1808	0.5708	0.4122	-0.3624	0.0015	0.0199	-0.5632	3.00E-04	0.0082
261196_at	AT1G12860	basic helix-loop-helix (bHLH) family protein / F-box	-0.7877	0.0065	0.0548	-1.2444	0.0012	0.0298	0.06089	0.7077	0.4339	-0.3957	0.0589	0.0876
261197_at	AT1G12900	GAPA-2; glyceraldehyde-3-phosphate dehydrogena	-0.7576	0.002	0.0398	-1.0075	7.00E-04	0.027	0.06916	0.1797	0.1983	-0.1808	0.0132	0.0364
261198_at	AT1G12940	ATNRT2.5 (NITRATE TRANSPORTER2.5); nitrate	-0.2302	0.6772	0.4849	0.1881	0.753	0.4761	0.4178	0.2552	0.2438	0.3557	0.3217	0.2491
261199_at	AT1G12950	MATE efflux family protein	0.7635	0.5612	0.4454	0.3926	0.7612	0.478	0.895	0.4994	0.3595	0.5242	0.6864	0.3928
261200_at	AT1G12960	60S ribosomal protein L27A (RPL27aA)	-0.8125	0.459	0.4024	-2.083	0.1038	0.1627	0.338	0.7506	0.4485	-0.9325	0.4007	0.2845
261201_at	AT1G12850	phosphoglycerate/bisphosphoglycerate mutase fam	0.001968	0.9877	0.5738	-0.1021	0.4419	0.3603	-0.1467	0.2876	0.2624	-0.2508	0.1043	0.1236
261202_at	AT1G12910	ATAN11 (ANTHOCYANIN11); nucleotide binding	1.0113	2.00E-04	0.0312	0.6288	0.0014	0.0313	-0.00244	0.9599	0.5076	-0.385	0.0011	0.0123
261203_at	AT1G12845	similar to hypothetical protein MtDRAFT_AC14913	0.8517	0.1192	0.1995	0.7122	0.1735	0.2153	-0.6533	0.0104	0.0404	-0.7927	0.0052	0.0228
261204_s_at	AT1G12920,AT3G26618	release factor/release factor/release fac	0.1458	0.5346	0.435	0.4067	0.1312	0.1837	-1.0681	0.0076	0.0353	-0.8072	0.0198	0.0452
261205_at	AT1G12790	similar to unnamed protein product [Vitis vinifera] (G	-0.8727	0.0896	0.1734	-0.5454	0.2359	0.2553	-1.2081	0.0367	0.0789	-0.8808	0.0876	0.1109
261206_at	AT1G12800	S1 RNA-binding domain-containing protein	-0.7215	0.0012	0.0365	-0.6543	0.0019	0.0323	-0.2782	0.0349	0.0767	-0.211	0.076	0.1016
261207_at	AT1G12830	unknown protein	0.3918	0.0489	0.1271	0.6771	0.0084	0.0507	0.3861	0.0029	0.0244	0.6714	3.00E-04	0.0087
261208_at	AT1G12930	importin-related	0.3594	0.1192	0.1995	0.335	0.1391	0.1899	-0.9702	0.0017	0.0205	-0.9946	0.0016	0.014
261209_at	AT1G12810	proline-rich family protein	0.2814	0.198	0.2001	0.8828	0.0035	0.0374	0.2484	0.1	0.141	0.8498	0.0019	0.0149
261210_at	AT1G12840	DET3 (DE-ETIOLATED 3)	0.2163	0.1195	0.1998	0.274	0.0666	0.1292	-0.436	0.0164	0.0511	-0.3782	0.026	0.0534
261211_at	AT1G12780	UGE1 (UDP-D-GLUCOSE/UDP-D-GALACTOSE 4-	1.2364	0.0081	0.0591	1.337	0.0062	0.0451	-0.2562	0.0831	0.1268	-0.1556	0.2352	0.2045
261212_at	AT1G12880	ATNUDT12 (Arabidopsis thaliana Nudix hydrolase 1	0.3104	0.3638	0.3562	0.5539	0.1417	0.1921	-1.1396	0.0191	0.0555	-0.8961	0.0404	0.0695
261213_at	AT1G12970	leucine-rich repeat family protein	0.6869	0.049	0.1273	0.4287	0.1559	0.2027	0.0438	0.8391	0.4754	-0.2145	0.3487	0.2619
261214_at	no_match	no_match	-0.873	0.4125	0.3814	-2.6348	0.051	0.112	0.1223	0.8974	0.4916	-1.6395	0.1393	0.1477
261215_at	AT1G32970	subtilase family protein	1.3952	0.2453	0.2908	0.3939	0.7205	0.4656	-0.4183	0.6351	0.4095	-1.4196	0.1568	0.1591
261216_at	AT1G33030	O-methyltransferase family 2 protein	0.9367	0.0325	0.1046	1.4202	0.0082	0.0504	-0.07878	0.7173	0.4374	0.4047	0.1165	0.1323
261217_at	AT1G32850	ubiquitin carboxyl-terminal hydrolase family protein	-0.4047	0.7846	0.5191	-0.4584	0.7572	0.4773	0.4584	0.631	0.4083	0.4047	0.6705	0.3875
261218_at	AT1G20020	ATLFNR2 (LEAF FNR 2); NADPH dehydrogenase/	-0.5365	0.0627	0.1436	-0.5958	0.0473	0.108	-0.3428	0.0045	0.0286	-0.4	0.0025	0.0167
261219_at	AT1G19980	cytomatrix protein-related	-0.1201	0.3296	0.3398	0.313	0.0446	0.1046	-0.2315	0.0994	0.1405	0.2017	0.136	0.1457
261220_at	AT1G19970	ER lumen protein retaining receptor family protein	-0.5041	0.2113	0.2691	-0.7441	0.0932	0.1539	0.3801	0.1886	0.2047	0.14	0.5911	0.3603
261221_at	AT1G19960	similar to transmembrane receptor [Arabidopsis tha	-0.08979	0.7722	0.5153	0.05029	0.8707	0.5101	0.6057	0.0069	0.0338

261290_at	AT1G36990	similar to unknown protein [Arabidopsis thaliana] (T	0.04266	0.7464	0.5078	-0.2599	0.1034	0.1624	-0.2816	0.0851	0.1284	-0.5844	0.0091	0.0298
261291_at	AT1G36970	similar to unknown protein [Arabidopsis thaliana] (T	0.6968	0.4839	0.4136	-0.3699	0.7035	0.4602	1.0973	0.2917	0.2644	0.03059	0.9746	0.4767
261292_at	AT1G36940	unknown protein	0.2246	0.6412	0.4734	0.8205	0.1398	0.1905	0.4483	0.3297	0.2831	1.0441	0.0612	0.0896
261293_at	AT1G36980	similar to unnamed protein product [Vitis vinifera] (G	0.3932	0.1337	0.2122	0.3418	0.1781	0.2183	0.204	0.3852	0.3102	0.1526	0.5067	0.3284
261294_at	AT1G48430	dihydroxyacetone kinase family protein	0.7063	0.0319	0.1035	0.6231	0.0483	0.1067	-0.4223	0.0734	0.1179	-0.5055	0.0447	0.0741
261295_at	AT1G48450	similar to unknown protein [Arabidopsis thaliana] (T	-0.1881	0.2358	0.2849	-0.316	0.0793	0.1411	-0.7225	0.0059	0.032	-0.8504	0.0032	0.0185
261296_at	AT1G48460	similar to unknown protein [Arabidopsis thaliana] (T	0.05372	0.6881	0.4885	0.1725	0.2377	0.2564	-0.3202	0.0617	0.1068	-0.2014	0.1807	0.1737
261297_at	no_match	no_match	-1.5797	0.2084	0.2672	0.06019	0.9572	0.5335	-1.5785	0.2087	0.217	0.06138	0.9564	0.4725
261298_at	AT1G48510	cytochrome c oxidase assembly protein surfeit-relat	1.4864	0.1213	0.2016	-1.2711	0.1687	0.2116	1.1528	0.2027	0.2134	-1.6048	0.1015	0.1218
261299_at	AT1G48550	vacuolar protein sorting-associated protein 26 famil	0.672	0.0171	0.0785	0.579	0.0277	0.083	-0.7204	0.0068	0.0337	-0.8134	0.0044	0.021
261300_at	AT1G48560	unknown protein	0.392	0.1339	0.2124	0.9037	0.0124	0.0597	-0.4216	0.1138	0.1514	0.09016	0.6883	0.3933
261301_at	AT1G48570	zinc finger (Ran-binding) family protein	0.4183	0.0325	0.1046	0.2793	0.0985	0.1581	-0.09583	0.5024	0.3604	-0.2348	0.1455	0.1518
261302_at	AT1G48580	similar to unnamed protein product [Vitis vinifera] (G	0.9836	0.0326	0.1048	0.2157	0.5204	0.3924	0.3008	0.1664	0.1894	-0.4672	0.0586	0.0873
261303_at	AT1G48620	HON5 (HIGH MOBILITY GROUP FAMILY A 5); DN	-0.04413	0.8442	0.5371	0.008821	0.9686	0.5363	0.01368	0.9403	0.5035	0.06663	0.7178	0.4033
261304_at	AT1G48440	similar to unknown protein [Arabidopsis thaliana] (T	0.3768	0.0432	0.1199	0.453	0.0246	0.0788	0.2051	0.0278	0.0679	0.2813	0.0098	0.0309
261305_at	AT1G48470	GLN1;5 (GLUTAMINE SYNTHETASE 1;5); glutama	0.653	0.1559	0.2302	-0.6434	0.1606	0.2063	0.4627	0.0329	0.074	-0.8338	0.0045	0.0212
261306_at	AT1G48610	AT hook motif-containing protein	-0.8421	0.0485	0.1269	0.2672	0.06019	0.9572	0.5335	-1.5785	0.2087	0.217	0.06138	0.9564
261307_at	AT1G48520	GATB (GLU-ADT SUBUNIT B); glutaminyl-tRNA sy	-0.3339	0.1804	0.2484	-0.1318	0.557	0.4072	-0.5776	0.003	0.0248	-0.3755	0.0139	0.0374
261308_at	AT1G48480	RKL1 (Receptor-like kinase 1); ATP binding / kinase	-1.3478	0.0057	0.0525	-1.4974	0.0039	0.0391	0.1576	0.1926	0.2071	0.007977	0.9407	0.4687
261309_at	AT1G48598,AT1G48600	[AT1G48598, CPuORF31 (Conserved peptide upst	-0.7325	0.0019	0.0391	-0.9378	7.00E-04	0.0275	0.1578	0.1929	0.2073	-0.04749	0.6625	0.385
261310_at	GO5750	PDE247 (PIGMENT DEFECTIVE 247)	-0.03032	0.9132	0.5548	-0.05409	0.8461	0.5033	-0.7638	0.0021	0.0218	-0.7876	0.0019	0.015
261311_at	GO5770	jacalin lectin family protein	-2.8809	0.0233	0.0893	-0.6952	0.4371	0.3584	0.6531	0.4633	0.3446	2.8387	0.0244	0.0514
261312_at	GO5790	lipase class 3 family protein	0.6574	0.009	0.0614	0.4066	0.0427	0.1027	-1.0315	6.00E-04	0.0158	-1.2822	2.00E-04	0.0079
261313_at	GO5270	similar to unknown protein [Arabidopsis thaliana] (T	1.5331	0.1758	0.2453	0.4055	0.6864	0.4544	0.2848	0.6441	0.4123	-0.8428	0.214	0.193
261314_at	GO5280	GTP-binding family protein	0.5712	0.1317	0.2101	0.5819	0.1264	0.1804	-0.6515	0.005	0.0298	-0.6407	0.0053	0.0227
261315_at	GO3170	ATERF-9/ATERF8 (ETHYLENE RESPONSE ELEM	-0.6403	0.0047	0.0494	-0.6738	0.0039	0.0391	0.8887	9.00E-04	0.0169	0.8551	0.001	0.0122
261316_at	GO3165	kinase	0.5895	0.0111	0.066	0.459	0.0255	0.0798	-0.1995	0.2054	0.2151	-0.33	0.0669	0.0942
261317_at	GO5300	cytochrome c oxidase copper chaperone family prot	1.3849	0.0334	0.1057	0.9006	0.1071	0.165	-0.1399	0.7638	0.4523	-0.6242	0.2245	0.1985
261318_at	GO3035	similar to unknown protein [Arabidopsis thaliana] (T	-0.1582	0.654	0.4773	-0.3117	0.3946	0.3389	0.494	0.2056	0.2152	0.3404	0.3568	0.2655
261319_at	GO3090	SPA4 (SPA1-RELATED 4); signal transducer	-0.1577	0.6056	0.4616	-0.4762	0.1663	0.2099	-0.08504	0.4351	0.3319	-0.4035	0.0147	0.0386
261320_at	GO3120	RNA-binding S4 domain-containing protein	-0.1914	0.0379	0.1122	-0.6043	6.00E-04	0.027	-0.498	0.0014	0.0193	-0.9108	1.00E-04	0.0065
261321_at	GO4740	unknown protein	-0.3932	0.69	0.4892	1.0679	0.3087	0.2967	-1.3471	0.2156	0.2212	0.1141	0.907	0.4591
261322_at	GO4750	ATPUP11 (Arabidopsis thaliana purine permease 1	0.1978	0.0725	0.1552	0.2697	0.0299	0.0859	-0.17	0.0619	0.1069	-0.09812	0.2119	0.1918
261323_at	GO4760	universal stress protein (USP) family protein	0.2996	0.2824	0.3129	0.1666	0.5281	0.3954	0.03516	0.8912	0.4901	-0.09797	0.7099	0.3995
261324_at	GO4770	similar to unknown protein [Arabidopsis thaliana] (T	0.3877	0.2	0.2622	0.3828	0.2046	0.2358	0.3235	0.0149	0.0486	0.3185	0.0157	0.0399
261325_at	GO4780	similar to unknown protein [Arabidopsis thaliana] (T	0.3541	0.3994	0.375	0.2393	0.5589	0.4079	0.3706	0.3798	0.3077	0.2558	0.5334	0.3391
261326_s_at	AT1G44180,AT1G44820	[AT1G44180, aminoacylase, putative / N-acyl-L-am	0.04887	0.8246	0.5309	0.1418	0.9301	0.3964	-0.3907	0.0964	0.138	-0.2	0.33	0.2533
261327_at	AT1G44830	AP2 domain-containing transcription factor TINY,	-0.2295	0.4586	0.4023	-0.1546	0.6103	0.427	0.2893	0.3599	0.298	0.3641	0.2633	0.2194
261328_at	AT1G44835	YbaK/prolyl-tRNA synthetase family protein	-0.08355	0.6979	0.4919	0.1224	0.574	0.4135	0.4845	0.0728	0.1173	0.6905	0.0261	0.0535
261329_at	no_match	no_match	-1.5573	0.1684	0.2402	1.7546	0.1315	0.1839	0.8495	0.2467	0.2391	1.0467	0.1701	0.1674
261330_at	AT1G44900	ATP binding / DNA binding / DNA-dependent ATPa	0.04212	0.766	0.5133	-0.5157	0.0175	0.0686	0.02563	0.767	0.4533	-0.448	0.0052	0.0225
261331_at	AT1G44935	transposable element gene	-1.051	0.3103	0.3287	-0.5867	0.5523	0.4057	-0.05184	0.9566	0.507	0.4125	0.6691	0.387
261332_s_at	AT1G45232,AT4G03981	[AT1G45232, transposable element gene];[AT4G03	0.8643	0.5519	0.4419	0.3335	0.8147	0.4946	-0.6526	0.6499	0.4145	-1.1834	0.4247	0.2944
261333_at	AT1G44910	protein binding	0.6116	0.0232	0.0892	0.8769	0.0068	0.0467	-0.3034	0.1506	0.1792	-0.03811	0.8345	0.4385
261334_at	AT1G44960	similar to unknown protein [Arabidopsis thaliana] (T	0.3119	0.0984	0.181	0.3772	0.0603	0.1219	0.3691	0.0609	0.1059	0.4344	0.0382	0.067
261335_at	AT1G44800	nodulin MtN21 family protein	0.07714	0.6978	0.4919	0.678	0.0214	0.0745	0.2216	0.3074	0.2722	0.8169	0.0115	0.0337
261336_at	AT1G44790	ChaC-like family protein	-0.3722	0.0083	0.0599	-0.2474	0.0322	0.0889	0.05578	0.5076	0.3624	0.1806	0.0782	0.1034
261337_at	AT1G44810	transcription regulator	0.2004	0.24	0.2875	0.8365	0.0045	0.0414	-0.2089	0.224	0.2261	0.4273	0.0424	0.0718
261338_at	AT1G44920	similar to unnamed protein product [Vitis vinifera] (G	-0.7205	0.0011	0.036	-0.8632	6.00E-04	0.0265	0.1282	0.1652	0.1885	-0.01445	0.8577	0.4452
261339_at	AT1G35710	leucine-rich repeat transmembrane protein kinase,	1.4719	8.00E-04	0.0345	0.9697	0.004	0.0394	-1.7375	1.00E-04	0.0119	-2.2397	0	0.0055
261340_at	AT1G35730	APUM9 (ARABIDOPSIS PUMILIO 9); RNA binding	-0.2548	0.7204	0.4995	-0.2822	0.6923	0.4563	1.0312	0.1593	0.1853	1.0038	0.1681	0.1661
261341_s_at	AT1G52940,AT1G52950	[AT1G52940, ATPAP5/PAP5 (purple acid phosphat	0.4489	0.7075	0.4952	1.495	0.2506	0.2643	0.1147	0.9229	0.4987	1.1608	0.3561	0.2652
261342_at	AT1G52950	replication protein-related	-0.2726	0.1108	0.193	-1.9462	0.1277	0.1814	-0.05863	0.9567	0.507	0.06786	0.9499	0.4709
261343_s_at	AT1G52960,AT3G43350	[AT1G52960, transposable element gene];[AT3G43	-0.4511	0.7655	0.5132	-0.1839	0.9027	0.5196	-0.2884	0.8285	0.4723	-0.02122	0.9872	0.4795
261344_at	AT1G79600	integral membrane transporter family protein	-0.1147	0.5098	0.4249	-0.06713	0.694	0.4568	-0.01607	0.9242	0.499	0.0315	0.8524	0.4434
261345_at	AT1G79760	DTA4 (DOWNSTREAM TARGET OF AGL15-4)	0.5438	0.5644	0.4466	-1.105	0.2713	0.2762	1.5667	0.1449	0.1752	-0.08207	0.9291	0.4654
261346_at	AT1G79720	aspartyl protease family protein	-0.5314	0.0739	0.1563	-0.9213	0.014	0.0627	-0.08161	0.4943	0.3574	-0.4715	0.0123	0.035
261347_at	AT1G79730	ELF7 (EARLY FLOWERING 7)	0.1051	0.3691	0.3591	0.2162	0.1059	0.1642	-0.1881	0.0747	0.119	-0.07694	0.3824	0.2768
261348_at	AT1G79810	TED3 (REVERSAL OF THE DET PHENOTYPE); p	0.1257	0.237	0.2858	-0.4064	0.0109	0.056	0.08654	0.3144	0.2756	-0.4455	0.0041	0.0205
261349_at	no_match	no_match	1.2696	0.3313	0.3407	0.8291	0.5106	0.3889	0.1031	0.6965	0.4299	-0.3375	0.2416	0.208
261350_at	AT1G79770	similar to unknown protein [Arabidopsis thaliana] (T	-1.2355	0.0729	0.1555	-0.6618	0.2648	0.2725	-0.1124	0.6108	0.4015	0.4612	0.0865	0.1101
261351_at	AT1G79790	haloacid dehalogenase-like hydrolase family protein	-0.1885	0.0211	0.0855	-0.1571	0.0372	0.0954	-0.2175	0.0131	0.0456	-0.1862	0.022	0.0483
261352_at	AT1G79650	RAD23; damaged DNA binding	0.03017	0.8609	0.5413	-0.04623	0.7889	0.4858	-0.2453	0.2035	0.2139	-0.3217	0.1172	0.1328
261353_at	AT1G79600	ABC1 family protein	-0.7077	0.0042	0.0468	-0.9006	0.0017	0.0321	-0.5265	0.006	0.0322	-0.7193	0.0019	0.015
261354_at	AT1G79690	ATNUDT3 (Arabidopsis thaliana Nudix hydrolase ho	0.4923	0.0069	0.0559	0.4047	0.0136	0.0618	0.08966	0.307	0.272	0.002014	0.9803	0.4782
261355_at	AT1G79750	ATNADP-ME4 (NADP-MALIC ENZYME 4); malate	-0.3874	0.124	0.2039	-0.4503	0.0869	0.1486	-0.8283	0.01	0.0398	-0.8912	0.0078	0.0275
261356_at	AT1G79660	similar to unknown protein [Arabidopsis thaliana] (T	-0.167	0.4254	0.4074	-0.1502	0.4699	0.3721	0.5177	0.0099	0.0396	0.5345	0.0088	0.0293
261357_at	AT1G41860	transposable element gene	-0.3132	0.7945	0.5223	-1.9857	0.1522	0.1998	1.6097	0.0566	0.1016	-0.06285	0.9224	0.4636
261358_s_at	AT2G06541,AT3G29450	[AT2G06541, pseudogene of hAT dimerisation dom	-1.8324	0.0251	0.0919	1.0567	0.1143	0.1707	-1.8261	0.0253	0.0646	1.0629	0.1128	0.1296
261359_at	AT1G41900	transposable element gene	-0.5699	0.6025	0.4604	-0.0353	0.9738	0.5376	1.4643	0.1382	0.1698	1.9989	0.0651	0.0929
261360_at	AT1G41870	transposable element gene	-0.101	0.9096	0.5538	-0.2412	0.7871	0.4852	-0.7587	0.3668	0.3013	-0.8988	0.2948	0.236
261361_at	no_match	no_match	0.09698	0.9479	0.5642	-0.4881	0.7442	0.4728	-0.9405	0.5373	0.3742	-1.5256	0.3358	0.256
261362_s_at	AT3G55750,AT1G41880	[AT3G55750, 60S ribosomal protein L35a (RPL35a	-0.3315	0.0297	0.1	-0.1746	0.1563	0.2031	0.576	0.0045	0.0287	0.7329	0.0019	0.0149
261363_at	AT1G41830	SKS6 (SKU5 Similar 6); pectinesterase	-1.2095	0.0052	0.0513	-1.3678	0.0033	0.0371	0.4063	0.0698	0.1146	0.248	0.2078	0.1896
261364_at	AT1G53140	dynamin family protein	1.8301	0.0078	0.0583	-0.1285	0.7464	0.4737	0.8172	0.0922	0.1343	-1.1414	0.037	0.0655
261365_at	AT1G53160	chorismate mutase	0.4402	0.2012	0.2629	0.9986	0.0257	0.0801	-0.74	0.0492	0.0935	-0.1816	0.5309	0.3384
261366_at	AT1G53100	acetylglucosaminyltransferase	2.1373	0.0848	0.1687	0.7365	0.4761	0.3746	-0.2963	0.7678	0.4535	-1.6971	0.1445	0.1512
261367_at	AT1G53080	legume lectin family protein	1.2455	0.1993	0.2619	0.5976	0.502	0.3855	0.6183	0.3214	0.2788	-0.0295	0.9596	0.4732
261368_at	AT1G53070	legume lectin family protein	0.2446	0.4895	0.4157	0.02673	0.9378	0.5285	0.8143	0.0337	0.075	0.5965	0.0807	0.1056
261369_at	AT1G53060	legume lectin family protein	-0.05599	0.8874	0.5477	-0.3415	0.4099	0.3459	-0.09319	0.8142	0.4679	-0.3786	0.3655	0.2694
261370_at	AT1G53050	protein kinase family protein	0.2161	0.0424	0.1185	0.1807	0.0698	0.1322	-0.08068	0.334	0.2854	-0.116	0.1896	0.179
261371_at	AT1G53020	PFU3/UBC26 (UBIQUITIN-CONJUGATING ENZYM	0.4258	0.736	0.5044	1.8078	0.1996	0.2327	-0.5923	0.6415	0.4116	0.7897	0.5393	0.3409
261372_at	AT1G53010	zinc finger (C3HC4-type RING finger) family protein	-1.1262	0.3534	0.3515	0.1246	0.9132	0.5222	-0.08517	0.9104	0.4954	1.1657	0.1763	0.1709
261373_at	AT1G53000	cytidylyltransferase family	0.2225	0.3656	0.3571	0.467	0.0991	0.1588	-0.6665	0.0088	0.0376	-0.4219	0.0391	0.068
261374_at	AT1G52990	thioredoxin family protein	-0.558	0.2443	0.2902	-0.1614	0.7133	0.4632	-0.143	0.7443	0.4463	0.2536	0.5689	0.3523
261375_at	AT1G53160	SPL4 (SQUAMOSA PROMOTER BINDING PROTE	0.44	0.3149	0.3313	0.8312	0.0959	0.156	0.6527	0.0146	0.0483	1.0438	0.0028	0.0172
261376_at	AT1G18660	zinc finger (C3HC4-type RING finger) family protein	-0.446	0.059	0.1391	-0.2653	0.1947	0.2292	-0.8632	0.0072	0.0342	-0.6825	0.0161	0.0405
261377_at	AT1G18850	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.8005	0.0132	0.0707	0.8526	0.0106	0.0556	-0.1937	0.1379	0.1695	-0.1415	0.2476	0.2111
261378_at	AT1G18890	ATCDPK1; calmodulin-dependent protein kinase/ ki	0.2651	0.3333	0.3419	0.8119	0.0281	0.0835	-0.3815	0.0406	0.0836	0.1653	0.2658	0.2207
261379_at	AT1G18720	similar to unknown protein [Arabidopsis thaliana] (T	0.3255	0.0515	0.1304	0.3179	0.0551	0.1165	0.3379	0.0014	0.0197	0.3303	0.0016	0.0139
261380_at	AT1G05400	similar to unknown protein [Arabidopsis thaliana] (T	0.6833	0.4092	0.3795	0.9928	0.2518	0.2652	-0.5474	0.5015	0.3601	-0.2379	0.7645	0.4181
261381_at	AT1G05460	SDE3 (SILENCING DEFECTIVE)	-0.5078	0.2417	0.2887	-0.3918	0.3491	0.3177	0.3802	0.166	0.1891	0.4961	0.0919	0.1143
261382_at	AT1G05470	endonuclease/exonuclease/phosphatase family pro	-0.7891	0.1607	0.234	-0.7847	0.1625	0.2077	-0.1433	0.7686	0.4537	-0.1389	0.7755	0.4216
261383_at	AT1G05380	DNA binding	0.4268	0.0035	0.0451	0.3494	0.0073	0.0481	-1.1044	0	0.0092	-1.1818	0	0.0053
261384_at	AT1G05440	similar to unnamed protein product [Vitis vinifera] (G	-0.8627	0.4216	0.3859	0.03257	0.9747	0.538	0.5484	0.4224	0.3265	1.4436	0.0785	0.1036
261385_at	AT1G05450	protease inhibitor/seed storage/lipid transfer protein	-0.3459	0.2663	0.3029	-0.6823	0.0635	0.1257	0.4262	0.1869	0.2036	0.08976	0.7545	0.415
261386_at	AT1G05430	similar to unnamed protein product [Vitis vinifera] (G	0.05473	0.3282	0.339	0.01477	0.779	0.4833	-0.1068	0.0956	0.1374	-0.1468	0.0406	0.0696
261387_at	AT1G05410	similar to unknown protein [Arabidopsis thaliana] (T	0.09223	0.6282	0.469	0.3422	0.124	0.1786	-0.5996	0.0272	0.067	-0.3496	0.1181	0.1335
261388_at	GO5385	photosystem II 11 kDa protein-related	-0.2654	0.3105	0.3289	0.01992	0.9348	0.5278	-0.5281	0.0338	0.0752	-0.2428	0.2185	0.1954
261389_s_at	AT1G41835,AT1G35735	[AT1G41835, transposable element gene];[AT1G35	-0.6995	0.4252	0.3874	1.4994	0.2175	0.2443	-0.01955	0.9847	0.5138	2.3893	0.0676	0.0949
261390_at	AT1G35040	similar to unknown protein [Arabidopsis thaliana] (T	-0.06015	0.8975	0.5505	-0.4335	0.0051	0.0429	0.02193	0.9625	0.5083	-2.3514	0.0058	0.0237
261391_at	AT1G35030	similar to unknown protein [Arabidopsis thaliana] (T	-1.1137	0.4599	0.403	1.3355	0.3829	0.3331	-1.8893	0.1838	0.2013	0.5599	0.6591	0.3838
261392_at	AT1G79780	Identical to UPF0497 membrane protein At1g79780	0.215	0.8062	0.5257	-0.4482	0.6139	0.4284	0.4335	0.6252	0.4064	-0.2298	0.7933	0.427
261393_at	AT1G79580	ANAC033; transcription factor	0.5289	0.371	0.36	-0.3548	0.5364	0.3991	-0.3723	0.5176	0.3661	-1.256	0.0751	0.1008
261394_at	AT1G79680	wall-associated kinase, putative	1.8135	0.0105	0.0646	1.8983	0.0089	0.0518	0.1118	0.6291	0.4077	0.1965	0.4104	0.2884
261395_at	AT1G79700	ovule development protein, putative	0.03143	0.9013	0.5515	0.08614	0.7356	0.4698	-0.2921	0.1324	0.1656	-0.2374	0.2002	0.1852
261396_at	AT1G79800	plastocyanin-like domain-containing protein	-1.3814	0.2942	0.3198	-0.82	0.5135	0.39	-0.05606	0.9633	0.5084	0.5053	0.6818	0.3911
261397_at	AT1G79820	SGB1; carbohydrate transmembrane transporter/ s	0.1574	0.5349	0.4351	-0.188	0.4635	0.3695	-0.1877	0.3585	0.2972	-0.5331	0.0422	0.0716
261398_at	AT1G79610	sodium proton exchanger, putative (NHX6)	0.9052	0.0016	0.0388	0.4629	0.018	0.0694	0.0864	0.5099	0.3633	-0.3559	0.0409	0.07
261399_at	AT1G79620	leucine-rich repeat transmembrane protein kinase,	0.04768	0.9052	0.5526	0.3266	0.4338	0.3569	0.01934	0.9483	0.5052	0.2983	0.3469	0.2611
261400_at	AT1G79630	protein phosphatase 2C family protein / PP2C family	-0.264	0.3233	0.3362	0.4809	0.1097	0.1672	-0.5482	0.0796	0.1235	0.1966	0.449	0.3056
261401_at	AT1G79640	kinase	0.1755	0.6915	0.4898	-0.6859	0.1708	0.2132	-0.3007	0.4578	0.3421	-1.1621	0.0338	0.0621
261402_at	AT1G79670	RFO1 (RESISTANCE TO FUSARIUM OXYSPORU	0.2239	0.4139	0.3819	0.7334	0.0406	0.0999	-0.6626	0.047	0.0909	-0.1531	0.5478	0.3442
261403_at	AT1G79590	SYP52 (SYNTAXIN OF PLANTS 52)	0.3069	0.2765	0.2796	0.4669	0.0955	0.1557	0.1793	0.4308	0.33	0.3393	0.1729	0.169
261404_at	AT1G68690	transferase/ transferase, transferring glycosyl group	0.7668	0.0983	0.181	0.6609	0.1379	0.1891	-0.4907	0.1059	0.1456	-0.5966	0.0647	0.0925
261405_at	AT1G68740	similar to unknown protein [Arabidopsis thaliana] (T	-0.7673	0.0572	0.1371	-0.4099	0.2303	0.2517	0.003416	0.9829	0.5134	0.3608	0.0741	0.1
261406_at	AT1G68800	NRP2 (NAP1-RELATED PROTEIN 2); DNA binding	-0.1375	0.3766	0.3626	-0.05502	0.7112	0.4626	0.3921	0.0302	0.0708	0.1996	0.1692	0.1667
261407_at	AT1G68810	phytochrome kinase substrate-related	-1.0749	0.014	0.0724	-0.9025	0.0249	0.0791	0.649	0.0052	0.0303	0.8214	0.0022	0.0157
261408_at	AT1G07660,AT1G07820	[AT1G07660, histone H4];[AT1G07820, histone H4/	-0.1831	0.3836	0.3665	0.3585	0.1281	0.1816	0.4374	0.0797	0.1236	0.9789	0.0064	0.0248
261409_at	AT1G07640	OBP2 (OBF BINDING PROTEIN 2); DNA binding /	0.5471	0.0284	0.0976	-0.1986	0.2901	0.2866	0.06377	0.7157	0.4368	0.4122	0.0648	0.0926
261410_at	AT1G07610	MTIC (metallothionein 1C)	-0.5201	0.2272	0.2799	-0.2285	0.5653	0.4101	0.93	0.0316	0.0723	1.2217	0.0131	0.0362
261411_at	AT1G07790	HTB1; DNA binding	-0.7309	8.00E-04	0.0336	-0.5407	0.0024	0.0339	0.8557	4.00E-04	0.0147	1.046	2.00E-04	0.0076
261412_at	AT1G07890	APX1/ASCORBATE PEROXIDASE 1); L-ascorbate	0.1313	0.3488	0.3492	0.2912	0.1504	0.2873	-0.4507	0.0012	0.0188	0.4699	0.001	0.0123
261413_at	AT1G07630	PLL5 (POL-like 5); protein serine/threonine phosph	0.2523	0.2173	0.2734	0.4069	0.0777	0.1397	-0.1295	0.1565	0.1833	0.02511	0.7525	0.4145
261414_at	AT1G07795	similar to unknown protein [Arabidopsis thaliana] (T	-0.7574	0.409	0.3795	-0.5196	0.5617	0.409	-0.2383	0.7305	0.4419	-0.00045	0.9995	0.4829
261415_at	AT1G07750	nuplin family protein	1.0535	0.0022	0.041	1.0551	0.0022	0.0333	0.6738	0.0109	0.0414	0.6754	0.0108	0.0326
261416_at	AT1G07770	RPS15A (RIBOSOMAL PROTEIN S15A); structural	0.4345	0.0054	0.0519	0.3033	0.0188	0.0707	-0.2918	9.00E-04	0.0171	-0.423	2.00E-04	0.0078
261417_at	GO7700	thioredoxin family protein	0.001372	0.9927	0.5752	-0.3709	0.0591	0.1209	0.2677	0.0862	0.1295	-0.1045	0.4265	0.2953
261418_at	GO7830	ribosomal protein L29 family protein	0.4894	0.0984	0.181	0.3485	0.2012	0.2334	0.05249	0.7844	0.4586	0.08944	0.6479	0.38
261419_at	GO7840	leucine zipper factor-related	0.03955	0.8648	0.5423	0.3655	0.1688	0.2117	-0.2178	0.3743	0.3048	0.1082	0.6455	0.3792
261420_at	GO7720	beta-ketoacyl-CoA synthase family protein	-0.9335	0.1052	0.1875	-0.891	0.1172	0.1731	0.08146	0.7867	0.4592	0.124	0.6825	0.3914
261421_at	GO7840	IQD30; calmodulin binding	-0.3842	0.0119	0.0679	-0.3304	0.0197	0.072	0.2886	0.0302	0.0708	0.3424	0.0175	0.0423
261422_at	AT1G18730	similar to unknown [Populus trichocarpa] (GB:ABK9	-0.819	0.0079	0.0584	-0.6752	0.0153	0.0649	0.4777	0.0452	0.0891	0.6216	0.0201	0.0457
261423_at	AT1G18750	AGL65; DNA binding / transcription factor	-0.3289	0.0602	0.1404	-0.1547	0.2888	0.286	-0.3854	0.0383	0.0808	-0.2112	0.1707	0.1676
261424_at	AT1G18700	DNAJ heat shock N-terminal domain-containing pro

261490_at	AT1G14320	60S ribosomal protein L10 (RPL10A) / Wlm's tumor	0.004463	0.9723	0.5704	-0.06937	0.5967	0.4221	0.3202	0.0527	0.0974	0.2464	0.104	0.1234
261491_at	AT1G14350	FLP (FOUR LIPS); DNA binding / transcription factor	-0.7378	0.1191	0.1995	-0.3137	0.4477	0.3629	0.3628	0.1889	0.2036	0.7869	0.0261	0.0535
261492_at	AT1G14290	acid phosphatase, putative	-0.46	0.1149	0.1963	-0.5935	0.0605	0.1223	-0.2321	0.1515	0.18	-0.3656	0.0494	0.0787
261493_at	AT1G14410	ATWHY1/PTAC1 (A. THALIANA WHIRLY 1); DNA	-0.01726	0.9099	0.554	0.1911	0.2531	0.2658	-0.202	0.2314	0.2302	0.006428	0.9664	0.4748
261494_at	AT1G28420	HB-1 (homeobox-1); transcription factor	0.8088	4.00E-04	0.032	0.4653	0.0032	0.0364	-0.572	0.0014	0.0197	-0.9154	2.00E-04	0.0078
261495_at	AT1G28410	similar to myosin heavy chain-related [Arabidopsis t	0.1143	0.6023	0.4604	-0.157	0.4813	0.3767	-0.6061	0.0199	0.0566	-0.8774	0.0056	0.0233
261496_at	AT1G28360	ATERF12/ERF12 (ERF domain protein 12); DNA bi	-0.1435	0.844	0.5369	0.1782	0.8072	0.492	1.1527	0.1567	0.1835	1.4744	0.0899	0.1128
261497_x_at	AT1G28460	AGL59; DNA binding / transcription factor	2.103	0.0926	0.1763	1.0132	0.3489	0.3176	-0.5392	0.6028	0.3992	-1.629	0.1635	0.1634
261498_at	AT1G28440	HSL1 (HAESA-LIKE 1); ATP binding / kinase/ protei	0.2536	0.2421	0.2888	-0.1158	0.565	0.41	0.2519	0.0936	0.1356	-0.1175	0.3647	0.2689
261499_at	AT1G28430	CYP705A24 (cytochrome P450, family 705, subfam	1.7419	0.3304	0.3402	-0.2816	0.8667	0.5089	1.1415	0.4227	0.3266	-0.882	0.5285	0.3373
261500_at	AT1G28400	similar to unknown protein [Arabidopsis thaliana] (T	1.0528	0.0016	0.0388	1.2927	7.00E-04	0.0275	0.9712	6.00E-04	0.0158	1.2111	3.00E-04	0.008
261501_at	AT1G28390	protein kinase family protein	-0.00644	0.9901	0.5745	-0.5227	0.3454	0.3157	-0.03824	0.9414	0.5037	-0.5545	0.3202	0.2484
261502_at	AT1G14440	ATHB31 (ARABIDOPSIS THALIANA HOMEOBOX	-0.2166	0.4453	0.3958	-0.5163	0.114	0.1706	0.2115	0.2751	0.2553	-0.08825	0.6259	0.3724
261503_at	AT1G71691	GDSL-motif lipase/hydrolase family protein	-0.1349	0.7306	0.5027	-0.3634	0.3761	0.3302	0.3324	0.3759	0.3057	0.1039	0.7713	0.4203
261504_at	AT1G71692	AGL12 (AGAMOUS-LIKE 12); transcription factor	-0.2137	0.7793	0.5177	-0.6306	0.4265	0.3536	0.4936	0.4189	0.3248	0.07677	0.8954	0.4558
261505_at	AT1G71696	SOL1 (suppressor of LLP 1); carboxypeptidase A	0.5197	0.5234	0.4304	-0.513	0.5284	0.3956	-0.7416	0.3753	0.3055	-1.7743	0.0756	0.1013
261506_at	AT1G71697	ATCK1 (CHOLINE KINASE)	-0.4467	0.3285	0.3392	-0.1861	0.6673	0.4475	0.104	0.6671	0.1122	0.3646	9.00E-04	0.0119
261507_at	AT1G71720	S1 RNA-binding domain-containing protein	-0.3499	0.012	0.0681	-0.6179	0.0015	0.0314	-0.3012	0.0198	0.0565	-0.5691	0.0021	0.0154
261508_at	AT1G71730	similar to unknown [Brassica rapa] (GB:ABL97948;	-0.05791	0.7582	0.5112	0.1581	0.419	0.3502	-0.5203	0.0056	0.0313	-0.3043	0.0338	0.0621
261509_at	AT1G71740	similar to unknown protein [Arabidopsis thaliana] (T	0.05379	0.8348	0.5339	-0.1032	0.6912	0.4559	0.05416	0.8308	0.473	-0.1029	0.6872	0.3929
261510_at	AT1G71760	similar to unknown protein product [Vitis vinifera] (G	0.02021	0.9849	0.5733	-0.116	0.9134	0.5222	0.2327	0.7147	0.4364	0.09649	0.8786	0.4509
261511_at	AT1G71770	PAB5 (POLY(A)-BINDING PROTEIN); RNA binding	0.1605	0.6313	0.4702	-0.3027	0.3834	0.3334	0.2278	0.5024	0.3604	-0.2354	0.4893	0.3216
261512_at	AT1G71790	F-actin capping protein beta subunit family protein	-0.5357	0.1281	0.2068	-0.4098	0.2169	0.2439	-0.6087	0.0025	0.0232	-0.4828	0.0059	0.0238
261513_at	AT1G71840	transducin family protein / WD-40 repeat family prot	0.3593	0.061	0.1417	0.3785	0.0528	0.1139	0.4013	0.0064	0.0331	0.4206	0.0055	0.0231
261514_at	AT1G71870	MATE efflux family protein	-0.04857	0.9556	0.5662	-0.9114	0.3285	0.3078	0.965	0.3044	0.2709	0.1022	0.9068	0.4591
261515_at	AT1G71800	cleavage stimulation factor, putative	0.129	0.6328	0.4706	0.4876	0.1227	0.1777	-0.3224	0.2602	0.2465	0.03622	0.8901	0.4541
261516_at	AT1G71750	phosphoribosyltransferase family protein	-0.4583	0.0536	0.133	-0.3453	0.1109	0.1681	-0.2489	0.1113	0.1493	-0.1359	0.3284	0.2525
261517_at	AT1G71780	similar to unnamed protein product [Vitis vinifera] (G	0.08954	0.5436	0.4384	-0.06897	0.6364	0.437	0.8162	0.0012	0.0187	0.6577	0.0027	0.0171
261518_at	AT1G71695	peroxidase 12 (PER12) (P12) (PRXR6)	-0.03492	0.7193	0.4992	-0.1615	0.149	0.1974	0.3834	0.0133	0.0459	-0.2569	0.047	0.0763
261519_at	AT1G71810	ABC1 family protein	-0.4289	0.0368	0.1105	-0.8167	0.0042	0.0402	-0.2232	0.0686	0.1137	-0.611	0.0025	0.0165
261520_at	AT1G71820	similar to hypothetical protein Osl_008770 [Oryza s	0.4759	0.0213	0.0857	0.3821	0.042	0.1018	-0.4452	0.0207	0.0579	-0.5389	0.0109	0.0327
261521_at	AT1G71830	SERK1 (SOMATIC EMBRYOGENESIS RECEPTO	0.09573	0.6906	0.4894	0.318	0.228	0.2502	0.2898	0.2646	0.2491	0.512	0.0838	0.1081
261522_at	AT1G71710	inositol polyphosphate 5-phosphatase, putative	-0.4016	0.0673	0.1489	-0.5163	0.0327	0.0897	-0.144	0.2971	0.2672	-0.2587	0.0978	0.1188
261523_at	AT1G71860	PTP1 (PROTEIN TYROSINE PHOSPHATASE 1)	0.2149	0.0203	0.084	0.1567	0.0531	0.1142	0.1291	0.0887	0.1315	0.07087	0.2861	0.2314
261524_at	AT1G14300	binding	0.8408	0.0097	0.0632	0.3735	0.108	0.1657	-0.3112	0.004	0.0273	-0.7785	1.00E-04	0.0062
261525_at	AT1G14330	kelch repeat-containing F-box family protein	-0.1516	0.7258	0.5013	0.2655	0.5459	0.4029	-0.4188	0.3572	0.2967	-0.00177	0.9967	0.4821
261526_at	AT1G14370	APK2A (PROTEIN KINASE 2A); kinase	1.0029	0.0599	0.14	0.7179	0.1361	0.1877	0.01233	0.9141	0.4962	-0.2727	0.0641	0.0921
261527_at	AT1G14390	leucine-rich repeat transmembrane protein kinase,	-2.2607	0.0734	0.1561	-1.5291	0.1782	0.2184	-0.2717	0.4062	0.3191	0.4599	0.1916	0.1801
261528_at	AT1G14420	AT59 (Arabidopsis homolog of tomato LAT59); lyase	1.8121	0.1013	0.1841	0.2478	0.7863	0.485	1.2156	0.228	0.2284	-0.3487	0.7042	0.3988
261529_at	AT1G14430	glycoal oxidase-related	-1.2048	0.1488	0.2245	-1.1518	0.2081	0.2681	0.06041	0.933	0.5014	0.1134	0.8748	0.4498
261530_at	AT1G63460	glutathione peroxidase, putative	0.4738	0.112	0.194	0.6501	0.0494	0.1102	0.4098	0.1537	0.1814	0.5861	0.0658	0.0934
261531_at	AT1G63490	transcription factor jumonji (jmjC) domain-containing	0.4403	0.2719	0.3065	0.1681	0.6524	0.4426	-0.458	0.256	0.2442	-0.7302	0.1023	0.1222
261532_at	AT1G71680	amino acid transmembrane transporter	1.4241	0.1882	0.2541	0.04841	0.9586	0.5341	-0.8051	0.4019	0.3174	0.6675	0.4808	0.3178
261533_at	AT1G71690	similar to unknown protein [Arabidopsis thaliana] (T	-1.3852	0.1462	0.2222	-1.4467	0.1332	0.1854	1.2363	0.1833	0.2011	1.1748	0.2015	0.186
261534_at	AT1G01820	PEX11C	0.5446	0.0278	0.0966	0.7335	0.0104	0.0552	-0.3046	0.1316	0.1651	-0.1157	0.5123	0.3306
261535_at	AT1G01725	similar to unnamed protein product [Vitis vinifera] (G	0.0085005	0.9779	0.5717	0.3425	0.2093	0.2921	0.0045912	0.9772	0.5119	0.3386	0.0849	0.1089
261536_at	AT1G01790	KEA1 (K EFFLUX ANTIPORTER 1); potassium/hyc	-0.9635	8.00E-04	0.0336	-1.3667	2.00E-04	0.0249	-0.4667	0.0111	0.0417	-0.8699	0.0011	0.0126
261537_at	AT1G01800	short-chain dehydrogenase/reductase (SDR) family	0.3872	0.0039	0.0464	0.2833	0.0119	0.0587	0.1093	0.1326	0.1657	0.005407	0.9302	0.4657
261538_at	AT1G01830	armadillo/beta-catenin repeat family protein	0.3641	0.2333	0.2838	0.5434	0.1044	0.1633	-0.02614	0.8698	0.4841	0.1531	0.364	0.2686
261539_at	AT1G01840	similar to hypothetical protein MtrDRAFT_AC15588	-0.6388	0.0303	0.1009	-0.2472	0.2725	0.2768	0.2486	0.2654	0.2494	0.6403	0.029	0.0571
261540_at	AT1G63610	similar to unknown protein [Arabidopsis thaliana] (T	-0.1845	0.04	0.1156	-0.2079	0.0278	0.0831	0.07056	0.0922	0.1343	0.04709	0.2151	0.1937
261541_at	AT1G63600	protein kinase-related	1.6102	0.1109	0.193	-0.8477	0.3432	0.3149	2.0165	0.0629	0.1079	-0.4415	0.6057	0.3653
261542_at	AT1G63560	Identical to Cysteine-rich repeat secretory protein 8	-2.7434	0.0299	0.1005	-1.4275	0.1611	0.2066	-0.2678	0.7635	0.4523	1.0481	0.2759	0.226
261543_at	AT1G63550	ATP binding / nucleoside diphosphate kinase	0.1328	0.7298	0.5025	0.3704	0.3597	0.3226	-0.1387	0.7184	0.438	0.09892	0.7962	0.4276
261544_at	AT1G63540	hydroxyproline-rich glycoprotein family protein	0.4188	0.4828	0.4132	-0.9813	0.1444	0.1941	0.3905	0.511	0.3636	-1.0096	0.136	0.1456
261545_at	AT1G63535	similar to hydroxyproline-rich glycoprotein family pr	1.3635	0.0083	0.0598	1.2724	0.0106	0.0555	0.6088	0.0959	0.1376	0.5178	0.1389	0.1475
261546_at	AT1G63520	similar to unknown protein [Arabidopsis thaliana] (T	-1.0022	0.3761	0.3623	-0.8224	0.4601	0.3679	0.713	0.131	0.1646	0.8928	0.0766	0.1021
261547_at	AT1G63500	protein kinase-related	-0.5615	0.1357	0.2139	-0.5485	0.1426	0.1926	-0.7393	0.0081	0.036	-0.7263	0.0086	0.0288
261548_at	AT1G63480	DNA-binding family protein	0.66	0.2359	0.285	-0.1622	0.7492	0.4747	0.4078	0.3386	0.2877	-0.4145	0.3316	0.2542
261549_at	AT1G63470	DNA-binding family protein	-0.00917	0.9569	0.5665	0.3832	0.0741	0.1366	-0.3246	0.0169	0.0519	0.06786	0.4557	0.3083
261550_at	AT1G63450	catalytic	-0.747	0.4431	0.3951	1.1944	0.2456	0.2614	-0.06347	0.9356	0.5022	1.878	0.0638	0.0918
261551_at	AT1G63440	HMA5 (HEAVY METAL ATPASE 5); ATPase, coup	1.7539	0.2054	0.2657	1.6367	0.2315	0.2525	0.3392	0.7847	0.4587	0.2219	0.8577	0.4452
261552_at	AT1G63430	leucine-rich repeat transmembrane protein kinase,	-0.4291	0.1031	0.1855	-0.05312	0.8073	0.4921	-0.2682	0.1121	0.15	0.1079	0.4599	0.31
261553_at	AT1G63420	similar to unknown protein [Arabidopsis thaliana] (T	-0.6682	0.0581	0.1382	-0.685	0.0543	0.1156	0.1232	0.5691	0.3863	0.1064	0.6209	0.3705
261554_at	AT1G63400	pentatricopeptide (PPR) repeat-containing protein	-1.5492	0.1278	0.2066	-0.3981	0.6482	0.441	-1.318	0.0545	0.0993	-0.1669	0.7502	0.4139
261555_s_at	AT1G63630;AT1G63230	AT1G63630, pentatricopeptide (PPR) repeat-conta	-0.8088	0.5156	0.4275	1.0033	0.4268	0.3538	-1.2447	0.3345	0.2857	0.5673	0.6436	0.3784
261556_s_at	AT1G63390;AT1G62600	AT1G63390, flavin-containing monooxygenase-rela	-1.2936	0.0444	0.1214	-1.07674	0.872	0.5105	-2.8423	0.0031	0.0251	-1.6255	0.022	0.0484
261557_at	AT1G63640	kinesin motor protein-related	-0.2091	0.355	0.3523	-0.1509	0.4926	0.3814	-0.1072	0.6206	0.4048	-0.04901	0.8185	0.4338
261558_at	AT1G01770	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.005489	0.9795	0.572	0.3487	0.1574	0.2039	-1.7955	9.00E-04	0.0169	-1.4523	0.0019	0.0151
261559_at	AT1G01780	LIM domain-containing protein	0.04562	0.7571	0.5108	-0.1044	0.4907	0.3806	-0.8009	0.0044	0.0282	-0.9509	0.0023	0.016
261560_at	AT1G01710	acyl-CoA thioesterase family protein	-0.2035	0.1807	0.2486	-0.2758	0.0933	0.1539	-0.2031	0.1813	0.1996	-0.2754	0.0935	0.1156
261561_at	AT1G01730	similar to unnamed protein product [Vitis vinifera] (G	0.6079	0.0182	0.0804	0.8326	0.0061	0.0451	0.14	0.1901	0.2056	0.3647	0.0148	0.0387
261562_at	AT1G01750	actin-depolymerizing factor, putative	-1.2774	0.4068	0.3789	0.9702	0.5206	0.3925	-1.5976	0.3112	0.2741	0.65	0.662	0.3849
261563_at	AT1G01630	SEC14 cytosolic factor, putative / phosphoglyceride	-0.2659	0.0183	0.0805	-0.2411	0.0251	0.0793	0.5977	2.00E-04	0.0126	0.6225	1.00E-04	0.0068
261564_at	AT1G01720	ATAF1 (Arabidopsis NAC domain containing protei	-0.4096	0.035	0.1081	-0.0526	0.7077	0.4613	0.0266	0.6535	0.4157	0.3836	0.0022	0.0157
261565_at	AT1G63220	beta-1,3-glucanase, putative	0.04761	0.9371	0.5615	0.577	0.366	0.3256	-0.00114	0.9984	0.5174	0.5282	0.3892	0.2796
261566_at	AT1G63230	similar to unknown protein [Arabidopsis thaliana] (T	-0.2122	0.3287	0.3392	0.1842	0.3893	0.3364	-0.2443	0.1373	0.1692	0.1522	0.3123	0.2445
261567_at	AT1G63055	unknown protein	1.2584	0.2191	0.2745	1.4743	0.1632	0.2081	0.2445	0.6012	0.3986	0.4604	0.346	0.2608
261568_at	AT1G01030	NGA3 (NGATHA3); transcription factor	-0.6925	0.0715	0.1541	-1.1532	0.0154	0.0649	0.4756	0.1696	0.1916	0.0149	0.9607	0.4734
261569_at	AT1G01060	LHY (LATE ELONGATED HYPOCOTYL); DNA bin	-0.6164	0.0871	0.1709	-0.9503	0.0254	0.0797	0.1278	0.6643	0.4193	-0.2061	0.4928	0.323
261570_at	AT1G01120	KCS1 (3-KETOACYL-COA SYNTHASE 1); acyltran	-1.4615	0.0629	0.1438	-1.7434	0.0381	0.0966	0.2148	0.309	0.2729	-0.06713	0.7343	0.4086
261571_at	AT1G01050	DNA binding / zinc ion binding	-1.7704	0.2541	0.296	0.2111	0.8816	0.5136	-0.6874	0.6327	0.4086	1.2942	0.3858	0.2782
261572_at	AT1G01170	ozone-responsive stress-related protein, putative	0.1849	0.1816	0.2493	0.2637	0.0826	0.1443	0.3709	0.0066	0.0335	0.4498	0.0033	0.0187
261573_at	AT1G01180	similar to nucleic acid binding [Arabidopsis thaliana]	0.05216	0.9586	0.5669	-0.9886	0.3541	0.3201	-0.0116	0.9908	0.5154	-1.0524	0.3275	0.2522
261574_at	AT1G01190	CYP78A8 (cytochrome P450, family 78, subfamily a	-2.8801	0.0374	0.1115	-4.0462	0.0125	0.06	0.9178	0.3304	0.2835	-0.2483	0.7795	0.4228
261575_at	AT1G01130	similar to unknown protein [Arabidopsis thaliana] (T	-0.8175	0.4542	0.4	-0.8554	0.4351	0.3576	1.5721	0.1624	0.1868	1.5342	0.1705	0.1675
261576_at	AT1G01070	nodulin MtN21 family protein	0.7305	0.1632	0.2365	0.9227	0.0975	0.1573	0.6525	0.0026	0.0235	0.8447	0.001	0.0121
261577_at	AT1G01080	33 kDa ribonucleoprotein, chloroplast, putative / RN	-0.3626	0.0417	0.1176	-0.6136	0.0075	0.0487	0.1378	0.0565	0.1015	-0.1132	0.0942	0.1162
261578_at	AT1G01100	60S acidic ribosomal protein P1 (RPP1A)	-0.01149	0.9221	0.5576	0.2443	0.0911	0.1523	0.04532	0.6874	0.4268	0.3011	0.0452	0.0745
261579_at	AT1G01050	ATPPA1 (ARABIDOPSIS THALIANA PYROPHOSF	-0.07641	0.565	0.4469	-0.2173	0.1494	0.1977	0.07102	0.5916	0.3952	-0.06989	0.5973	0.3625
261580_at	AT1G01110	IQD18 (IQ-domain 18)	-3.3694	0.0072	0.0572	-0.1479	0.8355	0.5003	-1.5598	0.0797	0.1235	1.6617	0.0676	0.0948
261581_at	AT1G01140	CIPK9 (CBL-INTERACTING PROTEIN KINASE 9);	0.4689	0.0464	0.1239	0.4137	0.0658	0.1283	-0.1587	0.0651	0.1101	-0.214	0.0273	0.0549
261582_at	AT1G01160	GIF2 (GRF1-INTERACTING FACTOR 2)	0.483	0.0509	0.1298	0.2769	0.1889	0.2257	-0.04075	0.8274	0.472	-0.2468	0.2314	0.2023
261583_at	AT1G01090	PDH-E1 ALPHA (PYRUVATE DEHYDROGENASE	-0.3931	0.0758	0.1584	-0.5404	0.0307	0.0869	-0.3177	0.0683	0.1134	-0.465	0.0222	0.0485
261584_at	AT1G01040	DCL1 (DICER-LIKE1); ATP-dependent helicase/ rib	0.8368	0.008	0.0587	0.391	0.0836	0.1453	-1.4632	8.00E-04	0.0161	-1.909	3.00E-04	0.0081
261585_at	AT1G01010	ANAC001 (Arabidopsis NAC domain containing pro	0.553	0.1954	0.2595	1.1116	0.0355	0.0929	-0.4232	0.3004	0.2689	0.1353	0.7232	0.4051
261586_at	AT1G01640	spectle-type POZ protein-related	1.4661	0.002	0.04	0.8308	0.0154	0.0649	0.5359	0.059	0.1041	-0.09945	0.6528	0.3817
261587_at	AT1G01660	U-box domain-containing protein	0.1829	0.7635	0.5125	0.8228	0.2209	0.2465	-1.3734	0.0518	0.0964	-0.7335	0.2168	0.1945
261588_at	AT1G01670	U-box domain-containing protein	0.3777	0.3545	0.352	0.61	0.1664	0.21	-0.4003	0.1303	0.1641	-0.168	0.4698	0.3136
261589_at	no_match	no_match	-1.2108	0.3529	0.3513	-1.0168	0.4277	0.3543	-0.1778	0.811	0.467	0.01626	0.9825	0.4786
261590_at	AT1G01700	ATROPGEF2/ROPGEF2 (KINASE PARTNER PRO	0.7446	0.5752	0.4508	0.2315	0.8589	0.5069	0.6711	0.5968	0.3969	0.158	0.8991	0.4568
261591_at	AT1G01740	protein kinase family protein	-0.3202	0.1877	0.2538	-0.4066	0.1141	0.1706	-0.6754	0.0049	0.0297	-0.7619	0.0032	0.0183
261592_at	AT1G01760	RNA binding / adenosine deaminase	0.6233	0.3613	0.3552	0.1272	0.8439	0.5027	-0.142	0.723	0.4396	-0.6381	0.1625	0.1627
261593_at	AT1G33170	dehydration-responsive family protein	-0.6913	0.0152	0.0745	-0.4029	0.0765	0.1386	-0.4387	0.044	0.0876	-0.1504	0.3759	0.2738
261594_at	AT1G33240	AT-GTL1 (Arabidopsis thaliana GT2-like 1); transcr	-0.4517	0.0067	0.0553	-0.4424	0.0072	0.048	-0.4499	0.0068	0.0337	-0.4406	0.0073	0.0267
261595_at	AT1G33070	sequence-specific DNA binding / transcription factor	-2.541	0.0899	0.1736	1.0051	0.4282	0.3544	-1.7042	0.2096	0.2176	1.8419	0.1818	0.1744
261596_at	AT1G33080	MATE efflux family protein	-0.4014	0.0404	0.1159	-0.5202	0.0179	0.0693	-0.4168	0.0361	0.0781	-0.5355	0.0163	0.0408
261597_at	AT1G49780	U-box domain-containing protein	-0.5918	0.0243	0.0908	-0.7079	0.0135	0.0617	0.3056	0.0561	0.101	0.1895	0.1737	0.1695
261598_at	AT1G49790	leucine-rich repeat family protein	0.00412	0.972	0.5704	-0.3892	0.0243	0.0783	0.2708	0.0275	0.0675	-0.1226	0.1996	0.1848
261599_at	AT1G49700	similar to unknown protein [Arabidopsis thaliana] (T	0.6208	0.0695	0.152	0.6128	0.0719	0.1343	-0.262	0.3575	0.2968	-0.2699	0.3446	0.2601
261600_x_at	AT4G28870;AT1G49680	[AT4G28870, similar to unknown protein [Arabidops	0.349	0.6391	0.4726	-1.6166	0.0788	0.1407	0.9696	0.2321	0.2306	-0.996	0.2218	0.197
261601_at	AT1G49810	ARP protein (REF)	0.4197	0.0454	0.1226	0.3595	0.0697	0.1322	0.4997	0.0413	0.0844	-0.4727	0.0273	0.0549
261602_at	AT1G49630	ATPREP2; metalloendopeptidase	-0.2292	0.1769	0.246	-0.2779	0.1181	0.1738	-0.5394	0.0183	0.0541	-0.5881	0.0137	0.0371
261603_at	AT1G49600	ATRBP47A (ARABIDOPSIS THALIANA RNA-BIND	0.3049	0.5408	0.4371	0.2595	0.6002	0.4236	-0.7363	0.007	0.034	-0.7819	0.0056	0.0234
261604_at	AT1G49590	formin-binding protein-related	0.05658	0.8018	0.5246	0.2989	0.2293	0.2511	0.05918	0.3985	0.316	0.3015	0.0086	0.0288
261605_at	AT1G49580	calcium-dependent protein kinase, putative / CDPK	-0.6984	0.0054	0.0519	-1.0639	0.0011	0.0294	-0.3151	0.0165	0.0512	-0.6806	0.001	0.0122
261606_at	AT1G49570	peroxidase, putative	-0.5349	0.2267	0.2796	0.1543	0.7017	0.4597	0.02387	0.9523	0.5061	0.713	0.1299	0.1414
261607_at	AT1G49660	ATCKX5 (ARABIDOPSIS THALIANA CARBOXYES	-0.7584	0.0023	0.0417	-0.339	0.0368	0.0947	-0.1132	0.1729	0.1938	0.3062	0.011	0.0328
261608_at	AT1G49650	cell death associated protein-related	0.05495	0.8632	0.5418	-0.11	0.7316	0.4688	-0.2955	0.1187	0.1551	-0.4605	0.0367	0.0652
261609_at	AT1G49640	phospholipase C	-0.2841	0.1782	0.2468	-0.3979	0.0844	0.1461	0.2404	0.2397	0.235	0.1266	0.5077	0.3288
261610_at	AT1G49560	myb family transcription factor	0.2344	0.4685	0.4065	1.1114	0.0192	0.0714	-0.2146	0.5045	0.361	0.6624	0.0866	0.1102
261611_at	AT1G49730	protein kinase family protein	-0.3092	0.4213	0.3856	-0.02315	0.9498	0.5319	-1.3813	0.0016	0.0204	-1.0953	0.0039	0.0201
261612_at	AT1G49720	FUT12 (fucosyltransferase 12); fucosyltransferase/	0.5675	0.0146	0.0732	0.6338	0.01	0.0543	-0.3668	0.0061	0.0326	-0.2805	0.0126	0.0355
261613_at	AT1G49720	ABF1 (ABSCISIC ACID RESPONSIVE ELEMENT-I	1.6882	0.0092	0.0618	1.5601	0.0121	0.0589	-0.4162	0.1703	0.192	-0.5443	0.0943	0.1162
261614_at	AT1G49760	initiation factor	0.1052	0.7255	0.5012	0.1741	0.5666	0.4106	-1.0051	0.003	0.0248	-0.9361	0.0039	0.0202
261615_at	AT1G33060	similar to unknown protein [Arabidopsis thaliana] (T	0.4882	0.0499	0.1284	0.5692	0.0317	0.0885	-1.1533	0.0028	0.0242	-1.0723	0.0037	0.0196
261616_at	AT1G33060	ANAC014; transcription factor	-0.05091	0.7878	0.52	0.4403	0.0675	0.1302	-0.5665	0.0328	0.0739	-0.07529	0.6923	0.3947
261617_s_at	AT1G33090;AT1G33100	[AT1G33090, MATE efflux family protein];[AT1G33	1.4831	0.3422	0.3461	0.05616	0.9694	0.5365	0.2332	0.8738	0.4851	-1.1937	0.435	0.299
261618_at	AT1G33110	MATE efflux family protein	-0.4681	0.0648	0.1458	-0.7256	0.0173	0.0681	-1.1959	0.001	0.0175	-1.4536	5.00E-04	0.0093
261619_x_at	AT1G33130	transposable element gene	0.3174	0.4789	0.4115	-0.2048	0.6411	0.4385	0.1308	0.7639	0.4523	-0.3914	0.3905	0.2802
261620_s_at	AT1G33140;AT1G33120	[AT1G33140, 60S ribosomal protein L9 (RPL90A/C	0.06932	0.6462	0.4751	0.3742	0.0555	0.117	-0.5663	0.0124	0.0442	-0.2613	0.1165	0.1323
261621_at	AT1G01960	EDA10 (embryo sac development arrest 10); guany	0.7961	0.0088	0.0606	0.2001	0.2955	0.2895	-0.6031	0.0223	0.0603	-1.1991	0.002	0.0151
261622_at	AT1G01970	pentatricopeptide (PPR) repeat-containing protein	-0.2321	0.4656	0.4054	-0.6014	0.1051	0.1637	-0.1052	0.6498	0.4144	-0.4745	0.

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261690_at	AT1G50090	aminotransferase class IV family protein	0.04828	0.9621	0.5679	-1.9461	0.111	0.1681	0.3417	0.7383	0.4443	-1.6527	0.1582	0.1601
261691_at	AT1G50060	pathogenesis-related protein, putative	-0.7281	0.6331	0.4706	-0.1161	0.9384	0.5286	0.6921	0.6495	0.4144	1.3041	0.4077	0.2872
261692_at	AT1G08450	CRT3 (CALRETICULIN 3); calcium ion binding	1.9283	0.001	0.0356	2.1021	7.00E-04	0.0275	-0.0672	0.4725	0.3486	0.1066	0.2771	0.2267
261693_at	AT1G08370	DCP1 (DECAPPING 1); m7G(5')ppp(5')N diphosphatas	0.5323	0.006	0.0536	0.2183	0.0943	0.1547	0.3015	0.0393	0.082	-0.01242	0.9071	0.4591
261694_at	AT1G08360	60S ribosomal protein L10A (RPL10aA)	0.1942	0.13	0.2085	0.2044	0.1159	0.1719	-0.1236	0.2929	0.2651	-0.1134	0.3292	0.253
261695_at	AT1G08520	CHLD/PDE166 (PIGMENT DEFECTIVE 166); magn	-0.2686	0.0937	0.1772	-0.3789	0.0366	0.0945	-0.2276	0.0298	0.0703	-0.3378	0.008	0.0278
261696_at	AT1G08470	strictosidine synthase family protein	-0.5245	0.0919	0.1758	-0.7564	0.0334	0.0905	0.2282	0.3512	0.2939	-0.0037	0.9872	0.4795
261697_at	AT1G32610	hydroxyproline-rich glycoprotein family protein	-0.1161	0.5867	0.455	-0.3131	0.1866	0.2241	0.3588	0.1421	0.173	0.1618	0.4568	0.3088
261698_at	AT1G32630	unknown protein	-0.1053	0.6299	0.4698	0.6024	0.0408	0.1001	-0.2469	0.1615	0.1864	0.4608	0.0329	0.0612
261699_at	AT1G32660	F-box family protein	0.4958	0.6603	0.4794	0.3248	0.7717	0.481	-0.1457	0.7975	0.4627	-0.3166	0.5834	0.3574
261700_at	AT1G32690	similar to unknown protein [Arabidopsis thaliana] (T	0.4519	0.0509	0.1298	0.6722	0.0148	0.0642	0.2091	0.271	0.2528	0.4294	0.0588	0.0874
261701_at	AT1G32750	HAF01 (HISTONE ACETYLTRANSFERASE OF TH	0.5177	0.0332	0.1056	0.3635	0.0885	0.15	-0.448	0.0508	0.0955	-0.6022	0.0206	0.0465
261702_at	AT1G32760	glutaredoxin family protein	-1.2882	0.2928	0.3188	-1.3912	0.2612	0.2704	-1.0576	0.1602	0.1857	-1.1606	0.1318	0.1428
261703_at	AT1G32770	ANAC012/NST3/SND1 (ARABIDOPSIS NAC DOM	-0.8387	0.4908	0.4162	0.9706	0.4301	0.3953	-0.8658	0.4778	0.3506	0.9435	0.442	0.3023
261704_at	AT1G32600	F-box family protein-related	-0.5621	0.6194	0.4663	1.7221	0.1749	0.2161	-0.1705	0.8784	0.4862	2.1136	0.1133	0.13
261705_at	AT1G32670	unknown protein	0.4265	0.7538	0.5097	-0.7168	0.6025	0.4246	1.7239	0.0688	0.1137	0.5806	0.452	0.3068
261706_at	AT1G32680	transposable element gene	0.3509	0.7534	0.5095	-0.7754	0.4984	0.3839	1.1311	0.277	0.2563	0.1848	0.8679	0.4477
261707_at	AT1G32650	unknown protein	1.2779	0.2993	0.3226	-1.2782	0.2992	0.291	1.1735	0.3353	0.2862	-1.3826	0.2668	0.2211
261708_at	AT1G32740	protein binding / zinc ion binding	0.4669	0.0655	0.1468	0.3367	0.1435	0.1934	0.0724	0.7158	0.4368	-0.05773	0.7711	0.4203
261709_at	AT1G32790	CID11: RNA binding / protein binding	0.5667	0.0055	0.0521	0.6412	0.0035	0.0374	-0.01062	0.9163	0.4968	0.06392	0.5377	0.3405
261710_at	AT1G32730	electron carrier/ iron-sulfur cluster binding	-0.9985	0.244	0.29	-0.2701	0.7307	0.4687	0.04703	0.9193	0.4976	0.7754	0.1499	0.1545
261711_at	AT1G32780	zinc-binding family protein	0.3356	0.2215	0.2761	0.8164	0.0245	0.0786	-0.00189	0.9921	0.5157	0.4789	0.0565	0.0854
261712_at	AT1G32780	alcohol dehydrogenase, putative	-1.7412	0.1309	0.2092	-3.8666	0.0136	0.0618	2.76	0.0398	0.0825	0.6346	0.5276	0.337
261713_at	AT1G32640	ATMYC2 (JASMONATE INSENSITIVE 1); DNA bin	-0.8195	0.0018	0.0391	-0.5609	0.0074	0.0485	-0.1082	0.3666	0.3013	0.1504	0.2303	0.2017
261714_at	AT1G18510	TET16 (TETRASPANIN16)	-0.9512	0.3554	0.3525	-0.2768	0.7764	0.4826	0.9756	0.2263	0.2273	1.6499	0.0731	0.0992
261715_at	AT1G18485	pentatricopeptide (PPR) repeat-containing protein	-0.4085	0.157	0.231	-0.4118	0.1545	0.2015	-0.09375	0.7102	0.4349	-0.097	0.7008	0.3977
261716_at	AT1G18410	kinesin motor protein-related	-0.1633	0.7485	0.5084	-1.0519	0.0914	0.1524	0.1918	0.6293	0.4077	-0.6967	0.1309	0.1422
261717_at	AT1G18400	BEE1 (BR ENHANCED EXPRESSION 1); transcrip	-0.9533	0.0046	0.0488	-1.7799	4.00E-04	0.0251	1.0435	0.0033	0.0254	2.1459	0.2616	0.2186
261718_at	AT1G18390	protein kinase family protein	0.5276	0.0946	0.1778	0.9145	0.0194	0.0717	0.06594	0.6712	0.4214	0.4528	0.0348	0.0632
261719_at	AT1G18380	Identical to Uncharacterized protein At1g18380 pre	0.09455	0.819	0.5293	0.6316	0.178	0.2183	-0.8357	0.0014	0.0194	-0.2986	0.0475	0.0768
261720_at	AT1G08460	HDA08 (histone deacetylase 8); histone deacetylase	1.3506	0.001	0.0355	1.102	0.0022	0.0333	-0.3284	0.1044	0.1475	-0.577	0.0212	0.0474
261721_at	AT1G08480	similar to unknown [Populus trichocarpa] (GB:ABK(	0.06263	0.6756	0.4846	0.2238	0.1827	0.2216	0.714	0.0014	0.0197	0.8751	7.00E-04	0.0105
261722_at	AT1G08510	FATB (FATTY ACYL-ACP THIOESTERASES B); a	-0.6749	0.019	0.0819	-0.6474	0.0218	0.0748	0.01683	0.929	0.5003	0.04432	0.815	0.4329
261723_at	AT1G76200	similar to unknown [Populus trichocarpa x Populus	-0.2047	0.1125	0.1942	0.0181	0.8664	0.5088	0.6445	3.00E-04	0.0138	0.8673	1.00E-04	0.006
261724_at	AT1G76185	similar to unknown protein [Arabidopsis thaliana] (T	0.4229	0.2134	0.2706	0.6028	0.1028	0.1617	-0.523	0.0862	0.1295	-0.343	0.2116	0.1916
261725_at	AT1G76300	SMD3 (SNRNP CORE PROTEIN SMD3)	0.3774	0.0533	0.1325	0.5903	0.0132	0.0613	0.3266	0.0725	0.1171	0.5395	0.0161	0.0405
261726_at	AT1G76270	similar to unknown protein [Arabidopsis thaliana] (T	0.02675	0.9193	0.6568	0.4454	0.6727	0.2209	-0.1881	0.4758	0.3499	0.2276	0.3956	0.2826
261727_at	AT1G76090	SMT3 (S-adenosyl-methionine-sterol-C-methyltrans	-0.3511	0.5846	0.4541	-0.08954	0.8869	0.515	-0.7163	0.0161	0.0506	-0.4548	0.0639	0.092
261728_at	AT1G76160	SKS5 (SKU5 Similar 5); copper ion binding / oxidor	-0.4296	0.3432	0.3464	-0.5079	0.2729	0.277	-0.07577	0.6084	0.4008	-0.1541	0.322	0.2492
261729_s_at	AT1G47880,AT1G47840	[AT1G47880, transposable element gene];[AT1G47	0.5085	0.0252	0.1007	0.3873	0.6374	0.3285	0.3078	-0.2643	0.6687	0.4208	-0.1354	0.8249	0.4357
261730_s_at	AT1G47816,AT4G04520	[AT1G47816, transposable element gene];[AT4G04	0.3945	0.7786	0.5175	-1.0294	0.4766	0.3748	1.7525	0.2526	0.2423	0.3286	0.8146	0.4328
261731_s_at	AT1G47780,AT1G47786	[AT1G47780, acyl-protein thioesterase-related];[AT	-0.1303	0.9127	0.5547	1.7657	0.1889	0.2257	0.2281	0.8481	0.4781	2.1241	0.1298	0.1414
261732_at	AT1G47770	beta-galactosidase	-0.2673	0.8491	0.5379	-1.5869	0.2947	0.2891	0.4958	0.641	0.4114	-0.824	0.4496	0.3099
261733_at	AT1G47830	dathrin coat assembly protein, putative	0.05285	0.7422	0.5065	0.2034	0.2464	0.2618	0.6187	0.0145	0.0481	0.7693	0.0068	0.0257
261734_at	AT1G47790	F-box family protein	1.213	0.2685	0.3045	1.2846	0.2455	0.2613	-1.3326	0.2312	0.23	-1.261	0.2528	0.2139
261735_at	AT1G47765	F-box family protein	1.0021	0.4164	0.383	-0.7908	0.5143	0.3904	0.8035	0.4354	0.3321	-0.9895	0.3464	0.2609
261736_at	AT1G47810	F-box family protein	-0.5852	0.4949	0.418	-0.6266	0.4669	0.3707	0.2699	0.7468	0.4472	0.2285	0.7842	0.4242
261737_at	AT1G47885	leucine-rich repeat family protein	-0.9245	0.2617	0.3006	0.3541	0.6432	0.4393	-1.1549	0.0773	0.1214	0.1237	0.8126	0.4325
261738_s_at	AT1G47813,AT1G47820	[AT1G47813, similar to unknown protein [Arabidops	0.3405	0.1315	0.2099	0.1301	0.5098	0.3886	0.7617	0.0013	0.0192	0.5513	0.0044	0.0211
261739_at	AT1G47750	PEX11A	0.2756	0.0941	0.1776	0.6388	0.0071	0.0478	0.3777	0.0212	0.0586	0.7409	0.002	0.0151
261740_at	AT1G47740	similar to unknown protein [Arabidopsis thaliana] (T	-0.3951	0.0152	0.0745	-0.4867	0.0074	0.0485	-0.1066	0.3337	0.2853	-0.1982	0.1107	0.1282
261741_at	AT1G47710	ATEXPA12/EXP12/EXPC8 (ARABIDOPSIS HOMOLO	0.3328	0.2012	0.2629	-0.02346	0.9194	0.5239	0.2494	0.3159	0.2762	-0.1068	0.6496	0.3807
261742_at	AT1G08390	nucleic acid binding	-0.1211	0.6918	0.4899	-0.1544	0.6156	0.429	-0.3237	0.0374	0.0798	-0.357	0.0277	0.0555
261743_s_at	AT2G27210,AT1G08420	[AT2G27210, kelch repeat-containing serine/threon	0.1757	0.5635	0.4462	0.5237	0.1341	0.1861	-0.2237	0.3954	0.3145	0.1243	0.6252	0.372
261744_at	AT1G08490	ATCPNIF3/ATNFS2/ATSUFSCPNIF3/SUFS (CHL	-0.2452	0.3545	0.352	-0.4973	0.1011	0.1604	-0.5363	0.084	0.1274	-0.7884	0.0282	0.056
261745_at	AT1G08500	plastocyanin-like domain-containing protein	-0.6225	0.2117	0.2694	1.1219	0.0554	0.1169	-0.2052	0.4156	0.3233	1.5392	0.0024	0.0164
261746_at	AT1G08380	PSAO (photosystem I subunit O)	-0.4501	0.0521	0.131	-0.6159	0.0201	0.0724	0.2261	0.0309	0.0715	0.06022	0.4332	0.2982
261747_at	AT1G08360	endomembrane protein 70 family protein	0.844	0.0122	0.0685	0.6421	0.0298	0.0858	-0.3986	0.1095	0.148	-0.6005	0.0365	0.065
261748_at	AT1G76070	Identical to Uncharacterized protein At1g76070 [Ara	-0.3817	0.1836	0.2508	-0.2871	0.2936	0.2885	0.4925	0.0237	0.0624	0.5871	0.0133	0.0365
261749_at	AT1G76180	ERD14 (EARLY RESPONSE TO DEHYDRATION	-0.2338	0.2606	0.3	0.1252	0.5218	0.3929	0.541	2.00E-04	0.0126	0.9001	0	0.0048
261750_at	AT1G76120	tRNA pseudouridine synthase family protein	0.2456	0.144	0.2206	-0.2125	0.1918	0.2272	-0.1323	0.3135	0.2751	-0.5904	0.0068	0.0256
261751_at	AT1G76080	ATCDSP32/CDSP32 (CHLOROPLASTIC DROUGH	-0.5921	0.0066	0.0549	-0.7716	0.0025	0.034	0.4903	0.003	0.0248	0.3107	0.0153	0.0395
261752_at	AT1G76290	AMP-dependent synthetase and ligase family protei	-1.1451	0.1283	0.2069	0.1392	0.8275	0.4982	-1.5889	0.0567	0.1017	-0.3046	0.6376	0.3764
261753_at	AT1G76340	integral membrane family protein	-0.07185	0.7073	0.4951	-0.5035	0.0475	0.1082	0.167	0.3997	0.3165	-0.2647	0.21	0.1909
261754_at	AT1G76130	AMY2/ATAMY2 (ALPHA-AMYLASE-LIKE 2); alpha	-0.03627	0.8476	0.5378	-0.2212	0.2793	0.2805	0.145	0.3021	0.2696	-0.03997	0.7606	0.4169
261755_at	AT1G08170	histone H2B family protein	-1.8361	0.0087	0.0605	-1.4813	0.018	0.0694	-0.3514	0.4105	0.321	0.003402	0.9933	0.481
261756_at	AT1G08315	armadillo/beta-catenin repeat family protein	0.2014	0.2329	0.2836	0.2899	0.1133	0.1702	0.3119	0.0953	0.1371	0.4003	0.0492	0.0786
261757_at	AT1G08210	aspartyl protease family protein	0.1784	0.2054	0.2657	0.1723	0.2182	0.2447	-0.523	0.0082	0.0363	-0.5291	0.0079	0.0277
261758_at	AT1G08250	ADT6 (AROGENATE DEHYDRATASE 6); arogenat	-0.2726	0.4795	0.4117	-0.2701	0.4832	0.3774	0.2248	0.3453	0.2908	0.2273	0.3406	0.2584
261759_at	AT1G76590	similar to zinc finger (C3HC4-type RING finger) fam	0.4049	0.7692	0.5143	0.2709	0.8438	0.5027	0.1795	0.1587	0.1849	-0.9455	0.2043	0.1875
261760_at	AT1G15600	similar to unknown protein [Arabidopsis thaliana] (T	0.06788	0.7472	0.5081	-0.2358	0.2964	0.2899	0.2384	0.2919	0.2645	-0.0653	0.7564	0.4156
261761_at	AT1G15660	similar to CENP-C [Arabidopsis arenosa] (GB:AAU(	0.01114	0.9515	0.5651	-0.4438	0.0613	0.123	0.1928	0.3251	0.281	-0.2621	0.2022	0.1864
261762_at	AT1G15510	pentatricopeptide (PPR) repeat-containing protein	0.5086	0.0659	0.1472	0.6843	0.0278	0.0831	-0.4655	0.083	0.1267	-0.2898	0.2257	0.1992
261763_at	AT1G15620	ATPDR12/PDR12 (PLEIOTROPIC DRUG RESISTA	0.6056	0.1186	0.199	0.7836	0.0623	0.124	-0.4372	0.1722	0.1934	-0.2591	0.3807	0.2761
261764_at	AT1G15530	receptor lectin kinase, putative	1.3826	0.1712	0.2424	-0.02284	0.9794	0.5393	-1.0725	0.2661	0.2498	-2.4779	0.0406	0.0696
261765_at	AT1G15570	CYCA2;3 (CYCLIN A2;3); cyclin-dependent protein	-1.073	0.1111	0.1933	-0.4579	0.4334	0.3569	-0.373	0.5092	0.363	0.2421	0.663	0.3852
261766_at	AT1G15580	IAA5 (indoleacetic acid-induced protein 5); transcrip	-1.1512	0.0563	0.136	-0.3829	0.426	0.3534	0.1909	0.601	0.3985	0.9592	0.0465	0.0758
261767_s_at	AT1G15500,AT1G80300	[AT1G15500, ATNIT2; ATP-ADP antiporter];[AT1G	-0.3253	0.2683	0.3043	-0.01028	0.9696	0.5365	-1.1374	1.00E-04	0.0101	-0.8224	2.00E-04	0.0079
261768_at	AT1G15550	GA4 (GA REQUIRING 4); gibberellin 3-beta-dioxyge	-0.02059	0.9406	0.5627	-0.471	0.1438	0.1935	0.273	0.1188	0.1552	-0.1774	0.2675	0.2214
261769_at	AT1G76100	plastocyanin	-0.5156	0.0069	0.056	-0.6098	0.0038	0.0387	0.5668	0.0026	0.0236	0.4726	0.0052	0.0225
261770_at	AT1G76140	prolyl oligopeptidase	0.4784	0.0627	0.1436	0.1098	0.5884	0.4188	-0.09842	0.4623	0.3442	-0.4669	0.0183	0.0434
261771_at	AT1G76160	mauC-like dehydratase domain-containing protein	0.3639	0.0964	0.1795	0.5104	0.0386	0.0973	-0.1054	0.5648	0.3846	0.04112	0.8188	0.4338
261772_at	AT1G76240	similar to unknown protein [Arabidopsis thaliana] (T	-1.3896	0.0251	0.0919	-2.0056	0.0073	0.0482	0.7115	0.1485	0.178	0.09558	0.8221	0.4348
261773_at	AT1G76250	similar to unknown protein product [Vitis vinifera] (G	-0.127	0.8989	0.5508	0.4395	0.6639	0.4462	-0.2942	0.7696	0.4541	0.2723	0.7861	0.4246
261774_at	AT1G76260	transducin family protein / WD-40 repeat family prot	0.09263	0.5196	0.4289	0.2578	0.1213	0.1766	0.1632	0.2821	0.2593	0.3283	0.0668	0.0942
261775_at	AT1G76280	pentatricopeptide (PPR) repeat-containing protein	0.09305	0.8838	0.5471	0.7547	0.2751	0.2782	-3.1503	0.0062	0.0327	-2.4887	0.0141	0.0376
261776_at	AT1G76190	auxin-responsive protein family	-0.7701	0.0212	0.0855	-0.6962	0.0293	0.0851	0.3641	0.1028	0.1431	0.439	0.0639	0.092
261777_at	AT1G76210	similar to unknown protein [Arabidopsis thaliana] (T	-0.797	0.3871	0.3683	0.1694	0.8468	0.5035	-0.8611	0.3539	0.2952	0.1053	0.9042	0.4586
261778_at	AT1G76220	similar to unmanned protein product [Vitis vinifera] (G	-0.4296	0.5938	0.4575	-2.0251	0.0526	0.1137	2.2299	0.0362	0.0783	0.6344	0.4275	0.2957
261779_at	AT1G76230	similar to unknown protein [Arabidopsis thaliana] (T	-0.7384	0.4913	0.4163	1.9855	0.1116	0.1687	-0.9527	0.3842	0.3098	1.7713	0.1437	0.1507
261780_at	AT1G76310	CYGB2-4 (CYCLIN B2;4); cyclin-dependent protein	-0.1738	0.5557	0.4431	-0.3782	0.2349	0.2547	0.5571	0.1087	0.1475	0.3528	0.2624	0.219
261781_at	AT1G76320	FRS4 (FAR1-RELATED SEQUENCE 4); zinc ion bi	0.0247	0.9239	0.558	0.2872	0.3023	0.2926	-0.1858	0.4868	0.3541	0.07674	0.7678	0.4192
261782_at	AT1G76110	high mobility group (HMG1/2) family protein / ARID	-0.6788	0.0117	0.0676	-0.5204	0.028	0.0833	-0.9909	0.003	0.0248	-0.8325	0.0057	0.0235
261783_at	AT1G08190	vacuolar assembly protein, putative (VPS41)	-0.3373	0.0276	0.0964	-0.441	0.0115	0.0577	-0.2718	0.0525	0.0972	-0.3755	0.0196	0.0449
261784_at	AT1G08220	similar to unmanned protein product [Vitis vinifera] (G	0.1627	0.6953	0.4912	0.08813	0.8307	0.4991	0.5649	0.2175	0.2221	0.4903	0.2732	0.2245
261785_at	AT1G08230	amino acid transporter family protein	-0.348	0.2999	0.3229	-0.6791	0.081	0.1427	-0.5258	0.0916	0.1339	-0.8569	0.0227	0.0491
261786_at	AT1G15990	ATCNGC7 (CYCLIC NUCLEOTIDE-GATED CHAN	0.3334	0.7854	0.5195	-1.4722	0.268	0.2744	0.2473	0.8396	0.4755	-1.5583	0.2452	0.2098
261787_at	AT1G16020	similar to unknown protein [Arabidopsis thaliana] (T	-0.163	0.4312	0.3898	-0.4349	0.0799	0.1419	0.1388	0.3689	0.3023	-0.1331	0.3869	0.2787
261788_at	AT1G15980	similar to unmanned protein product [Vitis vinifera] (G	-0.6404	0.0078	0.0583	-0.9994	0.0015	0.0314	0.3402	0.0023	0.0223	-0.01878	0.7212	0.4044
261789_at	AT1G15930	40S ribosomal protein S12 (RPS12A)	0.3912	0.0475	0.1254	0.3789	0.052	0.1132	-0.1979	0.2259	0.227	-0.2102	0.2033	0.187
261790_at	AT1G16000	similar to unknown protein [Arabidopsis thaliana] (T	-0.063	0.7127	0.4972	0.3862	0.0724	0.1349	0.6095	0.0187	0.0548	1.0586	0.0027	0.017
261791_at	AT1G16170	similar to unknown protein [Arabidopsis thaliana] (T	-0.2383	0.3501	0.3497	-0.4464	0.1188	0.1742	0.4098	0.1052	0.1451	0.2017	0.3625	0.2681
261792_at	AT1G15950	CCR1 (CINNAMOYL COA REDUCTASE 1)	-0.05591	0.8635	0.5419	-0.5545	0.1434	0.1933	0.146	0.4715	0.3481	-0.3526	0.1276	0.1399
261793_at	AT1G16080	similar to unknown [Populus trichocarpa] (GB:ABK(	-1.5512	0.0018	0.0391	-1.9626	7.00E-04	0.0275	0.273	0.2466	0.2391	-0.1384	0.5296	0.3378
261794_at	AT1G16060	ovule development protein, putative	-0.5687	0.0667	0.1482	-0.4402	0.1249	0.1792	-0.5096	0.0885	0.1314	-0.381	0.1691	0.1667
261795_at	AT1G16010	magnesium transporter CorA-like family protein (MF	0.5465	0.0152	0.0744	0.6092	0.0105	0.0554	-0.5342	0.0164	0.051	-0.4714	0.0246	0.0515
261796_at	AT1G30440	phototropic-responsive NPH3 family protein	-0.5024	0.1245	0.2043	-0.5231	0.1136	0.1703	-0.1481	0.1601	0.1857	-0.1688	0.1212	0.1359
261797_at	AT1G30455	initiation factor/ zinc ion binding	-1.4187	0.0212	0.0855	-0.2959	0.4856	0.3784	-1.0591	0.0515	0.0962	0.06379	0.8766	0.4503
261798_at	AT1G30460	ATCPSF30/CPSF30; RNA binding / calmodulin bin	0.1167	0.1497	0.2253	1.1612	0.0448	0.105	-0.5967	0.2125	0.2194	-0.1523	0.7245	0.4055
261799_at	AT1G30473	metal ion binding	2.9764	0.0337	0.1062	-1.6887	0.1461	0.1954	2.3729	0.0646	0.1096	-2.2922	0.0709	0.0976
261800_at	AT1G30490	PHV (PHAVOLUTA); DNA binding / transcription fac	0.9692	0.0093	0.0621	0.4132	0.1156	0.1716	-0.3342	0.1341	0.1668	-0.8902	0.0075	0.027
261801_at	AT1G30520	AAE14 (ACYL-ACTIVATING ENZYME 14); AMP bi	-0.9522	0.0085	0.0602	-0.6168	0.0354	0.0929	-1.2643	2.00E-04	0.0126	-0.9288	7.00E-04	0.0105
261802_at	AT1G30550	similar to WW domain-containing protein [Arabidop	0.01283	0.9722	0.5704	0.1216	0.7428	0.4724	-0.1729	0.6252	0.4064	-0.06404	0.8544	0.444
261803_at	AT1G30600	CCAAT-binding transcription factor (CBF-B/NF-YA)	0.2467	0.2228	0.2769	0.2116	0.2838	0.2831	0.1677	0.3825	0.309	0.1326	0.4816	0.3182
261804_at	AT1G30530	UDP-glucono(xylo)UDP-glucosyl transferase family	-0.8572	0.0222	0.0875	-0.6327	0.0554	0.1169	-0.2032	0.0787	0.1227	0.02131	0.8176	0.4336
261805_at	AT1G30540	ATPase, BadF/BadG/BcrA/BcrD-type family	-0.1047	0.3458	0.3478	-0.03822	0.7165	0.4641	0.01272	0.903	0.4932	0.07918	0.4646	0.3119
261806_at	AT1G30510	ATRFNR2 (ROOT FNR 2); oxidoreductase	0.05143	0.8149	0.5283	0.393	0.5283	0.1819	0.07556	0.6043	0.3996	0.4172	0.0362	0.0647
261807_at	AT1G30515	unknown protein	-0.3499	0.6805	0.4862	0.09257	0.9123	0.522	0.404	0.6357	0.4097	0.8464	0.3439	0.2598
261808_at	AT1G30480	DRT111 (DNA-damage-repair/toleration protein 111	0.4279	0.0632	0.1441	0.3493	0.1056	0.1641	0.07273	0.6169	0.4035	-0.00581	0.9676	0.475
261809_at	AT1G30340	rac GTPase activating protein, putative	-0.7171	0.0411	0.1168	-0.203	0.6477	0.3629	0.2241	0.2836	0.26	0.7382	0.0151	0.0392
261810_at	AT1G08130	ATLIG1 (ARABIDOPSIS THALIANA DNA LIGASE	-0.1295	0.4879	0.4149	-0.27	0.1867	0.2242	-0.1049	0.5696	0.3865	-0.2455	0.2215	0.1968
261811_at	AT1G08260	EMB2284/EMB529/POL2A/TIL1 (EMBRYO DEFEC	0.05154	0.92	0.557	0.9569	0.118	0.1737	-0.348	0.5102	0.3634	0.5574	0.3118	0.2442
261812_at	AT1G08270	similar to SKD1/VPS4, ATP binding [Arabidopsis th	1.7133	0.0704	0.1529	1.8687	0.1157	0.1771	-0.7992	0.3167	0.2766	-2.0428	0.0492	0.2879
261813_at	AT1G08280	glycosyl transferase family 29 protein / sialyltranste	-0.5403	0.0523	0.1312	-0.132	0.5408	0.401	-0.4294	0.0956	0.1373	-0.02109	0.9202	0.4628
261814_at	AT1G08310	esterase/lipase/thioesterase family protein	0.3209	0.4948	0.418	-1.1185	0.0591	0.1209	1.4288	0.0288	0.0689	-0.01059	0.9814	0.4783
261815_at	AT1G08330	bZIP family transcription factor	0.9692	0.4685	0.4065	0.06569	0.9594	0.534	-0.9855	0.4616	0.3439	0.04945	0.9694	0.4754
261816_at	AT1G08135	ATCHX6B/CHX6B (CATION/H+ EXCHANGER 6B);	-0.538	0.5538	0.4423	0.03525	0.9683	0.5362	-0.9881	0.3015	0.2694	-0.4149	0.6449	0.379
261817_at	AT1G08180	similar to unknown protein [Arabidopsis thaliana] (T	0.1462	0.6152	0.4645	0.2786	0.3583	0.3221	0.497	0.0715	0.1162	0.6294	0.0368	0.0653
261818_at	AT1G11390	ABC1 family protein	-0.4481	0.1183	0.1989	-0.02771	0.9083	0.521	-1.1394	0.0073	0.0344	-0.7191	0.0334	0.0617
261819_at	AT1G11410	S-locus protein kinase, putative	-0.4587	0.039	0.114	-0.4441	0.0429	0.1029	0.3904	0.005	0.0299	0.405	0.0044	0.021
261820_at	AT1G11420	agenet domain-containing protein	0.5213	0.1519	0.2273	-0.2088	0.5181	0.3917	0.2276	0.4147	0.3229	-0.5025	0.1152	0.1313
261821_at	AT1G11530	ATCXC2 (C-TERMINAL CYSTEINE RESIDUE IS	-0.3527	0.2125	0.2699	0.3029	0.272	0.2766	0.5873	0.0691	0.1139	1.243	0.0064	0.0248

261890_at	AT1G80970	XH domain-containing protein	0.8203	0.238	0.2863	-1.4483	0.0706	0.1329	0.5218	0.4277	0.3288	-1.7468	0.0419	0.0712
261891_at	AT1G80790	XH/XS domain-containing protein / XS zinc finger d	0.1392	0.2566	0.2974	-0.05636	0.6208	0.4309	-0.09351	0.4246	0.3274	-0.2891	0.0516	0.0809
261892_at	AT1G80840	WRKY40 (WRKY DNA-binding protein 40); transcri	-0.9366	0.0747	0.157	-0.8293	0.1012	0.1605	0.3865	0.1646	0.1882	0.4938	0.0958	0.1174
261893_at	AT1G80690	similar to unknown protein [Arabidopsis thaliana] (T	-0.6766	0.1187	0.1991	-0.5008	0.2164	0.2437	0.235	0.4908	0.356	0.4108	0.2559	0.2157
261894_at	AT1G80900	magnesium transporter CorA-like family protein (MG	0.3701	0.129	0.2076	0.1799	0.4063	0.3442	-0.1374	0.5178	0.3662	-0.3277	0.1664	0.1651
261895_at	AT1G80830	NRAMP1 (NRAMP metal ion transporter 1); manga	0.2675	0.1719	0.2427	0.4689	0.0435	0.1034	-0.8027	0.0033	0.0256	-0.6013	0.0094	0.0303
261896_at	AT1G80670	transducin family protein / WD-40 repeat family prot	0.5218	0.0235	0.0896	0.1656	0.321	0.3036	0.156	0.3001	0.2688	-0.2002	0.2015	0.186
261897_at	AT1G80950	phosphatidylglycerol acyltransferase family protein	0.4357	0.0864	0.1704	0.08117	0.695	0.4571	0.4066	0.025	0.0641	0.05108	0.6826	0.3914
261898_at	AT1G80720	mitochondrial glycoprotein family protein / MAM33 f	0.5353	0.0728	0.1554	0.1888	0.4414	0.3601	-0.107	0.497	0.3585	-0.4535	0.0341	0.0624
261899_at	AT1G80820	CCR2 (CINNAMOYL COA REDUCTASE)	0.7226	0.029	0.0986	1.1512	0.006	0.0447	0.07532	0.6733	0.422	0.5039	0.0385	0.0674
261900_at	AT1G80940	similar to predicted protein [Populus alba x Populus	0.07127	0.7963	0.5227	0.02504	0.9274	0.526	0.09025	0.6953	0.4295	0.04403	0.8473	0.4421
261901_at	AT1G80920	J8; heat shock protein binding / unfolded protein bir	-0.2496	0.5857	0.4546	0.1817	0.6887	0.4552	0.2215	0.1388	0.1703	0.6528	0.0056	0.0233
261902_at	AT1G80860	N-methyltransferase	0.2476	0.0281	0.097	0.3953	0.0058	0.044	-0.1909	0.0328	0.0739	-0.04323	0.5084	0.3291
261903_at	AT1G80740	CMT1 (CHROMOMETHYLASE 1); DNA binding	0.4815	0.6544	0.4775	0.5422	0.6155	0.429	0.7734	0.4813	0.3517	0.8341	0.4499	0.306
261904_at	no_match	no_match	0.2459	0.2104	0.2685	0.2465	0.2094	0.2393	-0.08762	0.6235	0.4058	-0.08702	0.6258	0.3723
261905_at	AT1G65070	DNA mismatch repair MutS family protein	0.1109	0.4963	0.4188	-0.3648	0.0697	0.1322	-0.4803	0.0172	0.0525	-0.9559	0.0015	0.0137
261906_at	AT1G65080	OXA1 family protein	0.5626	0.141	0.2183	0.5302	0.1595	0.2055	0.2163	0.4082	0.3199	-0.8764	0.0201	0.0457
261907_at	AT1G65060	4CL3 (4-coumarate:CoA ligase 3); 4-coumarate-Co	-3.3925	0.0108	0.0654	-3.5918	0.0089	0.0517	-0.2756	0.2764	0.256	-0.475	0.0958	0.1174
261908_at	AT1G65050	stigma-specific Stig1 family protein	-0.00243	0.9983	0.5763	-0.8388	0.4756	0.3744	0.7725	0.509	0.363	-0.06392	0.9551	0.4723
261909_at	AT1G80940	MOS3/PRE/SAR3 (SUPPRESSOR OF ALLIN RES	0.4614	0.0024	0.0421	0.5341	0.0014	0.0312	-0.5799	7.00E-04	0.0159	-0.5072	0.0011	0.0124
261910_at	AT1G80730	ZFP1 (ARABIDOPSIS THALIANA ZINC-FINGER P	-2.0027	0.1438	0.2205	-0.0703	0.9523	0.5324	-0.8887	0.4658	0.3456	1.0437	0.3979	0.2833
261911_at	AT1G80750	60S ribosomal protein L7 (RPL7A)	0.634	0.0508	0.1297	0.4223	0.1398	0.1905	0.2013	0.0797	0.1235	-0.01038	0.9099	0.4599
261912_s_at	AT1G66060;AT1G66000	[AT1G66060, binding];[AT1G66000, similar to unkn	0.7684	0.5846	0.4541	-1.5406	0.2997	0.2912	1.5482	0.2977	0.2674	-0.7608	0.5882	0.3592
261913_at	AT1G65860	flavin-containing monooxygenase family protein / FM	-1.0655	0.047	0.1248	-0.825	0.093	0.1538	0.3692	0.0736	0.1181	0.6097	0.0164	0.0409
261914_at	AT1G65870	disease resistance-responsive family protein	-1.153	0.0325	0.1046	-1.0731	0.0403	0.0995	0.458	0.2708	0.2528	0.538	0.2082	0.1898
261915_at	AT1G65880	BZO1; benzoate-CoA ligase	-2.3239	0.0546	0.1342	1.2556	0.2197	0.2457	-2.4446	0.0473	0.0913	1.135	0.2591	0.2173
261916_at	AT1G65910	ANAC028 (Arabidopsis NAC domain containing pro	-0.05801	0.8457	0.5373	0.1965	0.5208	0.3925	0.02747	0.9092	0.4951	0.282	0.2807	0.2285
261917_at	AT1G65930	regulator of chromosome condensation (RCC1) fam	-0.9442	0.0498	0.1282	1.0347	0.0381	0.0966	-1.1097	0.0308	0.0715	0.8691	0.0626	0.0908
261918_at	AT1G65940	pseudogene, similar to Dof zinc finger protein, blast	-0.5014	0.8142	0.5281	-2.2749	0.3184	0.3021	1.2501	0.5654	0.3849	-0.5233	0.8063	0.4306
261919_at	AT1G65980	TPX1 (THIOREDOXIN-DEPENDENT PEROXIDAS	0.2608	0.2231	0.2771	0.2742	0.2043	0.2357	0.3579	0.0038	0.027	0.3713	0.0033	0.0187
261920_at	AT1G65930	isocitrate dehydrogenase, putative / NADP+ isocitra	0.3686	0.0952	0.1762	0.2744	0.1787	0.2187	0.007626	0.9574	0.5071	0.08461	0.8624	0.4348
261921_at	AT1G65900	similar to unnamed protein product [Vitis vinifera] (G	0.4437	0.2064	0.2661	0.09003	0.7751	0.4822	-0.0759	0.8093	0.4663	-0.4296	0.2184	0.1953
261922_at	AT1G65890	acyl-activating enzyme 12 (AAE12)	-0.426	0.7247	0.501	2.0663	0.1409	0.1914	-1.1387	0.2951	0.2661	1.3525	0.226	0.1994
261923_at	AT1G65940	ATUGT85A3 (UDP-GLUCOSYL TRANSFERASE 8	0.1632	0.5295	0.4521	-0.05302	0.8545	0.6059	-0.3709	0.2431	0.2368	-0.2607	0.3907	0.2803
261924_at	AT1G22550	proton-dependent oligopeptide transport (POT) fam	-0.4185	0.2224	0.2767	-0.139	0.6567	0.4441	-0.1367	0.5974	0.3972	0.1429	0.5814	0.3566
261925_at	AT1G22540	proton-dependent oligopeptide transport (POT) fam	0.568	0.1172	0.1979	0.3625	0.2726	0.2768	-0.09407	0.7581	0.4507	-0.2996	0.3528	0.264
261926_at	AT1G22530	PATL2 transporter	-0.6489	0.2946	0.3201	-0.7087	0.2585	0.2692	-0.1353	0.3407	0.2886	-0.195	0.1942	0.1816
261927_at	AT1G22500	zinc finger (C3HC4-type RING finger) family protein	1.1633	0.122	0.2022	2.1179	0.0235	0.0772	0.9372	0.1129	0.1505	0.01738	0.9718	0.4759
261928_at	AT1G22480	plastocyanin-like domain-containing protein	3.594	0.0086	0.0604	2.3983	0.0325	0.0894	0.031	0.9582	0.5072	-1.1647	0.104	0.1234
261929_at	AT1G22460	similar to unknown protein [Arabidopsis thaliana] (T	0.9767	0.1285	0.2071	-1.058	0.1071	0.1651	0.6483	0.2744	0.2548	-1.3881	0.0531	0.0823
261930_at	AT1G22440	alcohol dehydrogenase, putative	1.9046	0.1702	0.2416	-0.4181	0.7325	0.4689	1.3949	0.2884	0.2627	-0.9278	0.4616	0.3107
261931_at	AT1G22430	alcohol dehydrogenase, putative	-0.6234	0.0167	0.0776	-0.9198	0.0043	0.0407	-0.7691	0.0039	0.0271	-1.0655	0.0011	0.0126
261932_at	AT1G22420	hydroxyproline-rich glycoprotein family protein	-0.4696	0.6733	0.4838	0.3311	0.7649	0.4789	-1.1013	0.3469	0.2917	-0.3006	0.7858	0.4245
261933_at	AT1G22410	2-dehydro-3-deoxyphosphoheptonate aldolase, puta	0.3328	0.2079	0.2669	0.1216	0.6128	0.428	0.3081	0.0339	0.0752	0.09689	0.3755	0.2737
261934_at	AT1G22400	ATUGT85A1/UGT85A1 (UDP-GLUCOSYL TRANSF	0.2554	0.4636	0.4046	0.5128	0.1794	0.2191	-0.3232	0.0334	0.0747	-0.06582	0.5522	0.3459
261935_at	AT1G22360	C2 domain-containing protein	0.4714	0.0399	0.1152	0.3711	0.0774	0.1394	0.1089	0.5262	0.3696	0.008685	0.9586	0.4731
261936_at	AT1G22600	similar to late embryogenesis abundant domain-cor	-0.6198	0.2028	0.2642	-0.7944	0.123	0.1779	0.4945	0.2916	0.2644	0.3199	0.4763	0.3162
261937_at	AT1G22570	proton-dependent oligopeptide transport (POT) fam	0.9775	0.0027	0.0428	1.0658	0.002	0.033	-0.5518	0.0015	0.0199	-0.4634	0.0029	0.0175
261938_at	AT1G22510	zinc finger (C3HC4-type RING finger) family protein	0.5275	0.1104	0.1926	0.7718	0.0403	0.0995	0.2443	0.0421	0.0855	0.4886	0.0041	0.0207
261939_at	AT1G22450	COX6B (CYTOCHROME C OXIDASE 6B); cytochro	0.1651	0.2952	0.3205	0.3301	0.0739	0.1364	0.2616	0.086	0.1294	0.4266	0.2009	0.0469
261940_at	AT1G22520	similar to unknown protein [Arabidopsis thaliana] (T	-0.02758	0.8816	0.5466	0.2907	0.1698	0.2124	0.3872	0.0176	0.053	0.7055	0.0021	0.0154
261941_at	AT1G22490	basic helix-loop-helix (bHLH) family protein	-0.08422	0.7486	0.5086	-0.1399	0.6004	0.4237	0.4013	0.1765	0.1977	0.3457	0.2331	0.2033
261942_at	AT1G22590	AGL87; transcription factor	-1.8925	0	0.0312	-1.6726	0	0.0249	0.06332	0.2683	0.2512	0.2832	0.0045	0.0213
261943_at	AT1G80660	AHA9 (Arabidopsis H(+)-ATPase 9); hydrogen-expo	0.8545	0.4763	0.4102	-0.124	0.9148	0.5227	-0.2305	0.8426	0.4765	-1.209	0.3289	0.2529
261944_at	AT1G64550	similar to unknown protein [Arabidopsis thaliana] (T	-0.023	0.8488	0.5379	-0.4133	0.0217	0.0748	0.3068	0.0534	0.0983	-0.08348	0.5015	0.3264
261945_at	AT1G64530	RWP-RK domain-containing protein	0.9046	0.1702	0.2416	-0.4181	0.7325	0.4689	1.3949	0.2884	0.2627	-0.9278	0.4616	0.3107
261946_at	AT1G64560	pseudogene of S-adenosylmethionine-dependent m	0.1566	0.8971	0.5504	-0.8639	0.4894	0.3802	-0.7278	0.5567	0.3816	-1.7483	0.1987	0.1842
261947_at	AT1G64470	ubiquitin family protein	-1.9797	0.0237	0.0898	0.1546	0.7952	0.4879	-3.2073	0.0045	0.027	-1.0729	0.1265	0.1392
261948_at	AT1G64680	similar to unknown protein [Arabidopsis thaliana] (T	-0.8927	0.003	0.0436	-0.8883	0.003	0.0358	-0.1507	0.2617	0.2474	-0.1462	0.2737	0.2249
261949_at	AT1G64670	BDG1 (BODYGUARD1); hydrolase	-0.7598	0.0831	0.1668	-1.0357	0.0351	0.0925	0.5315	0.0133	0.0458	0.2557	0.111	0.1285
261950_at	AT1G64620	Dof-type zinc finger domain-containing protein	0.05028	0.8616	0.5415	0.09188	0.7513	0.4754	-0.1028	0.7232	0.4397	-0.245	0.4164	0.2911
261951_at	AT1G64490	similar to unknown protein [Arabidopsis thaliana] (T	0.1806	0.5081	0.4244	1.1058	0.0113	0.0572	-0.05811	0.8267	0.4718	0.8671	0.0252	0.0525
261952_at	AT1G64430	similar to unnamed protein product [Vitis vinifera] (G	-0.3281	0.0356	0.109	-0.5869	0.0051	0.0425	-0.3285	0.0355	0.0773	-0.5874	0.0051	0.0223
261953_at	AT1G64440	RHD1 (ROOT HAIR DEFECTIVE 1); UDP-glucose	-0.6236	0.0439	0.1208	0.3791	0.1522	0.1998	-1.4433	7.00E-04	0.016	-0.4407	0.0466	0.076
261954_at	AT1G64510	ribosomal protein S6 family protein	-0.7166	6.00E-04	0.0329	-0.7867	4.00E-04	0.0251	0.4175	0.0016	0.0204	0.3473	0.0033	0.0186
261955_at	AT1G64520	RPN12A (REGULATORY PARTICLE NON-ATPAS	0.716	0.0062	0.0542	0.7724	0.0047	0.0418	0.08697	0.4003	0.3167	0.1434	0.1959	0.1825
261956_at	AT1G64590	short-chain dehydrogenase/reductase (SDR) family	-1.0963	0.0336	0.1061	-0.5405	0.1922	0.2275	-0.4987	0.1312	0.1648	0.05711	0.8389	0.4398
261957_at	AT1G64660	ATMGL; catalytic/ methionine gamma-lyase	0.4865	0.2639	0.3018	0.6003	0.1844	0.2228	0.01203	0.9533	0.5063	0.1258	0.5498	0.345
261958_at	AT1G64500	glutaredoxin family protein	-0.4424	0.3845	0.367	-0.8123	0.1477	0.1965	0.1607	0.4359	0.3322	-0.2092	0.3231	0.2497
261959_s_at	AT1G31970;AT1G36590	[AT1G31970, transposable element gene];[AT1G36	-0.2351	0.7788	0.5175	0.7974	0.3658	0.3256	-0.4672	0.5825	0.3917	0.5652	0.51	0.3298
261960_at	AT1G36550	transposable element gene	0.4137	0.7015	0.493	-1.3143	0.2607	0.2701	0.9774	0.3855	0.3102	-0.7506	0.4964	0.3244
261961_at	AT1G36510	similar to unknown protein [Arabidopsis thaliana] (T	1.0879	0.241	0.2883	0.3236	0.7034	0.4602	1.1995	0.0926	0.1348	0.4353	0.4693	0.3135
261962_s_at	AT1G15560;AT1G36485	[AT1G15560, transposable element gene];[AT1G36	0.5875	0.6423	0.4737	0.5628	0.6559	0.4439	-1.3311	0.1047	0.1447	-1.3568	0.1002	0.1208
261963_at	AT1G36430	transposable element gene	-2.3889	0.045	0.1223	-0.5361	0.5532	0.4059	-1.9663	0.0437	0.0872	-0.1135	0.8748	0.4498
261964_at	AT1G36600	transposable element gene	-1.5952	0.1793	0.2475	-3.0708	0.0352	0.0926	0.9513	0.3872	0.3109	-0.5244	0.6214	0.3706
261965_at	no_match	no_match	-0.04608	0.9735	0.5707	0.08783	0.9495	0.5318	-1.2624	0.224	0.2261	-1.1284	0.2682	0.2218
261966_x_at	AT2G10630;AT2G12260;A	[AT2G10630, transposable element gene];[AT2G12	-0.706	0.2757	0.309	-2.1935	0.0173	0.0681	1.5805	0.0476	0.0916	0.09301	0.8761	0.4502
261967_at	AT1G36440	transposable element gene	-1.1063	0.3597	0.3544	0.1912	0.8669	0.509	-2.4898	0.0806	0.1243	-1.1923	0.3278	0.2523
261968_at	AT1G65850	disease resistance protein (TIR-NBS-LRR class), pu	-0.04932	0.9206	0.5571	0.3867	0.4524	0.365	-0.7909	0.1642	0.1879	-0.3549	0.4878	0.321
261969_at	AT1G65950	ABC1 family protein	0.03133	0.8952	0.55	-0.6017	0.0545	0.1158	-0.9764	0.0109	0.0414	-1.6094	0.0018	0.0147
261970_at	AT1G65960	GAD2 (GLUTAMATE DECARBOXYLASE 2); calmo	-0.3143	0.0033	0.0446	-0.2195	0.0119	0.0585	-0.1853	0.0208	0.058	-0.0905	0.1451	0.1516
261971_at	AT1G65990	type 2 peroxiredoxin-related / thiol specific antioxida	-0.6057	0.3176	0.3329	-0.9876	0.1364	0.188	-0.6062	0.3173	0.2769	-0.9881	0.1362	0.1457
261972_at	AT1G64600	copper ion binding	0.552	0.0827	0.1664	0.2515	0.3534	0.3198	-0.01232	0.9613	0.5081	-0.3128	0.2601	0.2178
261973_at	AT1G64610	WD-40 repeat family protein	0.4213	0.0463	0.1237	0.5255	0.0236	0.0773	-0.4369	0.0404	0.0834	-0.3327	0.0853	0.1092
261974_at	AT1G64630;AT1G64628	[AT1G64630, protein kinase family protein];[AT1G6	0.179	0.4571	0.4015	0.1427	0.5477	0.4038	-0.6571	0.0377	0.0802	-0.6933	0.032	0.0603
261975_at	AT1G64640	plastocyanin-like domain-containing protein	-0.8428	0.0455	0.1226	-0.8357	0.0466	0.107	0.7226	0.0696	0.1145	0.7297	0.0678	0.0951
261976_at	no_match	no_match	0.8974	0.6404	0.4733	0.1919	0.9193	0.5239	0.3051	0.8722	0.4847	-0.4004	0.8329	0.438
261977_at	AT1G37057	transposable element gene	2.3108	0.0596	0.1355	0.364	0.6799	0.4519	1.6252	0.0678	0.1128	-0.3016	0.6685	0.3869
261978_at	AT1G37060	transposable element gene	-1.5697	0.4791	0.4116	0.7785	0.7187	0.4648	-1.9697	0.2624	0.2479	0.3785	0.8145	0.4328
261979_at	AT1G37130	NIA2 (NITRATE REDUCTASE 2)	-1.1201	0.0292	0.099	-0.9803	0.0436	0.1035	-0.5167	0.054	0.0989	-0.3769	0.1201	0.135
261980_at	AT1G33820	unknown protein	-0.501	0.6528	0.477	1.0244	0.3771	0.3306	1.6332	0.1887	0.2047	3.1586	0.0377	0.0663
261981_at	AT1G33811	GDSL-motif lipase/hydrolase family protein	-0.7749	0.0521	0.131	-1.5313	0.0057	0.0435	-1.2668	0.0063	0.0328	-2.0232	0.0011	0.0124
261982_at	AT1G33780	similar to unknown protein [Arabidopsis thaliana] (T	0.3173	0.1507	0.2261	0.2572	0.2236	0.2479	-0.1886	0.1147	0.1521	-0.2486	0.0569	0.0858
261983_at	AT1G33770	protein kinase family protein	-1.0944	0.0711	0.1538	-1.0456	0.0801	0.142	-0.641	0.0582	0.1032	-0.5923	0.072	0.0984
261984_at	AT1G33760	AP2 domain-containing transcription factor, putative	-1.4724	0.2056	0.2658	-2.6798	0.0515	0.1126	1.6172	0.0407	0.0836	0.4097	0.492	0.3228
261985_at	AT1G33750	terpene synthase/cyclase family protein	-0.7625	0.3145	0.3311	0.3518	0.624	0.4324	-0.3301	0.5223	0.3679	0.7843	0.1714	0.1681
261986_s_at	AT1G33730;AT1G33720	[AT1G33730, CYP76C5 (cytochrome P450, family :	1.4072	0.0185	0.0809	1.6534	0.0108	0.0958	-1.0256	0.0042	0.0277	-0.7794	0.011	0.0328
261987_at	AT1G33710	similar to unknown protein [Arabidopsis thaliana] (T	-0.6107	0.3414	0.3459	-0.8192	0.2214	0.2468	0.7609	0.2501	0.241	0.5524	0.3844	0.2778
261988_at	AT1G33680	nucleic acid binding	-0.1864	0.5845	0.4541	-0.1929	0.572	0.4127	-1.5464	0.0079	0.0357	-1.553	0.0078	0.0275
261989_at	AT1G33670	leucine-rich repeat family protein	-0.272	0.831	0.5327	-1.2501	0.3543	0.3202	0.724	0.5771	0.3895	-0.254	0.842	0.4406
261990_at	AT1G33660	peroxidase family protein	0.1528	0.6037	0.4608	-0.2395	0.4277	0.3543	0.4971	0.1412	0.1723	0.1047	0.7194	0.4038
261991_at	AT1G33700	catalytic	-0.09408	0.8021	0.5247	-0.3696	0.3522	0.3192	-0.3778	0.3428	0.2898	-0.6533	0.1365	0.1459
261992_at	AT1G33680	nucleic acid binding	0.08929	0.5458	0.4393	-0.2983	0.0924	0.1534	-0.5229	0.0181	0.0539	-0.9105	0.0026	0.0168
261993_at	AT1G33860	unknown protein	-1.1196	0.4491	0.3977	-0.6692	0.6427	0.4391	-0.726	0.6156	0.4029	-0.2756	0.8466	0.4418
261994_at	AT1G33640	unknown protein	0.2369	0.7353	0.5041	-1.5162	0.0812	0.1428	0.7679	0.2938	0.2655	-0.9853	0.1963	0.1827
261995_at	no_match	no_match	-1.956	0.1119	0.194	0.01023	0.992	0.5421	-1.0203	0.2078	0.2165	0.9459	0.2365	0.2053
261996_at	AT1G33830	avirulence-responsive family protein / avirulence in	0.4469	0.7383	0.5052	-1.4186	0.319	0.3025	0.5625	0.6032	0.3993	-1.303	0.2618	0.2187
261997_at	AT1G33817	transposable element gene	-1.158	0.1885	0.2543	-0.7749	0.3491	0.3177	-0.8817	0.2944	0.2658	-0.4986	0.5329	0.339
261998_at	AT1G33813	transposable element gene	-0.2208	0.7997	0.5239	0.3967	0.6515	0.4422	-0.6003	0.5017	0.3601	0.01709	0.9843	0.4791
261999_at	AT1G33800	similar to unknown protein [Arabidopsis thaliana] (T	-0.2346	0.4759	0.4101	0.3132	0.3533	0.3197	-0.03449	0.91	0.4952	0.5132	0.1479	0.1533
262000_at	AT1G33810	similar to unknown [Populus trichocarpa] (GB:ABK9	-0.06401	0.731	0.5027	0.03318	0.8577	0.5066	0.6828	0.017	0.0522	0.78	0.0109	0.0326
262001_at	AT1G33790	jacalin-lectin family protein	0.06195	0.9236	0.558	0.2116	0.745	0.4732	0.5261	0.3573	0.2967	0.6757	0.2528	0.2139
262002_at	AT1G64450	proline-rich family protein	0.1007	0.8489	0.5379	0.4833	0.3846	0.334	0.1873	0.6441	0.4123	0.5699	0.2036	0.1871
262003_at	AT1G64460	phosphatidylinositol 3- and 4-kinase family protein	0.151	0.4834	0.4133	0.686	0.0249	0.0789	0.7497	0.0186	0.0546	-0.2147	0.334	0.2552
262004_at	AT1G64480	CBL8 (CALCINEURIN B-LIKE PROTEIN 8);	-1.2601	0.1931	0.2577	0.00233	0.9978	0.5435	0.06439	0.9402	0.5035	-1.3268	0.1752	0.1703
262005_at	AT1G64550	ATGCN3 (Arabidopsis thaliana general control non-	0.503	0.0261	0.0933	0.09586	0.5469	0.4032	-0.1729	0.2468	0.2391	-0.5801	0.0104	0.032
262006_at	AT1G64570	DNA binding	-0.6663	0.0049	0.0502	-0.266	0.0883	0.1498	-0.8935	0.0017	0.0205	-0.4832	0.0141	0.0377
262007_at	AT1G64580	pentatricopeptide (PPR) repeat-containing protein	0.5692	0.3925	0.3713	-0.00543	0.9932	0.5425	-0.3256	0.5497	0.379	-0.9002	0.1456	0.1519
262008_s_at	AT1G30680;AT4G03900;A	[AT1G30680, transposable element gene];[AT4G03	-0.4649	0.7264	0.5014	0.8049	0.5512	0.4054	-0.6887	0.6078	0.4006	0.5812	0.6634	0.3853
262009_at	AT1G30690	DC1 domain-containing protein	-0.1246	0.7563	0.5106	-0.5854	0.1936	0.2283	-0.199	0.6238	0.4069	-0.6597	0.1534	0.1571
262010_at	AT1G35612	transposable element gene	0.4216	0.1358	0.2139	0.2016	0.4232	0.3521	-1.5268	0.001	0.0178	-1.7468	6.00E-04	0.0103
262011_at	AT1G35614	similar to unknown protein [Arabidopsis thaliana] (T	-0.1238	0.8826	0.547	0.3884	0.6476	0.4407	-0.8931	0.32	0.2783	-0.3809	0.6538	0.382
262012_s_at	AT1G35630;AT1G35630	[AT1G35625, protease-associated zinc finger (C3H	0.4057	0.4175	0.3836	-0.3479	0.4819	0.377	-0.4523	0.3104	0.2736	-0.3016	0.4821	0.3184
262013_s_at	AT5G44875;AT2G29230;A	[AT5G44875, transposable element gene];[AT2G29	2.1089	0.09	0.1737	0.7294	0.4843	0.3778	0.4042	0.3852	0.3102	-0.9753	0.0785	0.1036
262014_at	AT1G35660	binding	0.6014	0.0651	0.1463	0.3938	0.1738	0.2153	-0.5893	0.0687	0.1137	-0.7969	0.0287	0.0567
262015_at	AT1G35663	transposable element gene	1.8709	0.2235	0.2768	0.08244	0.9524	0.5324	-1.1361	0.4304	0.3298	0.6524	0.8413	0.3777
262016_at	AT1G35513	pseudogene of isochorismate synthase-related / isc	-0.941	0.1267	0.2058	0.1029	0.8437	0.5027	-1.1508	0.0783	0.1223	-0.1069	0.8377	0.4394
262017_at	AT1G35550	elongation factor Tu C-terminal domain-containing p	0.2147	0.3068	0.3266	0.3492	0.1296	0.1826	0.172	0.2365	0.2331	0.3065	0.0682	0.0954
262018_at	AT1G35617	expressed protein	0.2132	0.868	0.482	0.9518	0.1081	0.1657	0.03988	0.9416	0.5037	0.7746	0.1684	0.1663
262019_s_at	AT5G44890;AT3G26530;A	[AT5G44890, transposable element gene];[AT3G26	-1.0258	0.4367	0.3923	-0.0971	0.9388	0.5287	-0.8948	0.4934	0.3569	0.03391	0.9786	0.4778
262020_at	AT1G35647	transposable element gene	1.5613	0.3086	0.3277	-2.1885	0.1777	0.218	1.8883	0.2092	0.2173	-1.8615	0.2145	0.1933
262021_at	AT1G35545	other RNA	-0.745	0.221	0.2758	-0.6595	0.269	0.2749	0.3034	0.587	0.3934	0.3889	0.4917	0.3226
262022_at	AT1G35490	bZIP family transcription factor	0.17	0.9105	0.5541	-0.2131	0.8879	0.5153	1.1303	0.4704	0.3478	0.7473	0.6264	0.3725
262023_at	AT1G35500	similar to unknown protein [Arabidopsis thaliana] (T	1.2854	0.1762	0.2456	-1.5364	0.1214	0.1767	1.686	0.0977	0.1391	-1.1358	0.2207	0.1964
262024_at	AT1G35520	ATPDIL5-2 (PDI-LIKE 5-2); thiol-disulfide exchange	0.5254	0.0035	0.0448	0.5292	0.0034	0.0371	0.5355	0.0032

262090_at	AT1G55970	ATHPCAT2/HAC4 (HISTONE ACETYLTRANSFER	-0.489	0.1811	0.2489	0.01464	0.9637	0.5349	-1.0621	0.0246	0.0636	-0.5585	0.1385	0.1472
262091_at	AT1G56160	AMYB72/MYB72 (myb domain protein 72); DNA bi	-0.9311	0.2539	0.2958	-1.2808	0.141	0.1914	0.1134	0.8791	0.4864	-0.2363	0.7524	0.4145
262092_at	AT1G56150	auxin-responsive family protein	1.3743	4.00E-04	0.032	1.5957	2.00E-04	0.0249	0.9289	5.00E-04	0.0155	1.1503	2.00E-04	0.0078
262093_at	AT1G56145	leucine-rich repeat family protein / protein kinase fa	1.4091	0.006	0.0538	1.0695	0.0157	0.0653	-0.3542	0.0256	0.0649	-0.6939	0.0024	0.0164
262094_at	AT1G56110	NOP56 (ARABIDOPSIS HOMOLOG OF NUCLEOL	0.6193	0.0522	0.1312	0.3616	0.1857	0.2235	-0.208	0.3709	0.3034	-0.4656	0.0872	0.1106
262095_at	AT1G56090	tetratricopeptide repeat (TPR)-containing protein	0.4277	0.0253	0.0923	0.5547	0.0107	0.0558	-0.3234	0.0581	0.1032	-0.1964	0.1853	0.1765
262096_at	AT1G56010	NAC1 (Arabidopsis NAC domain containing protein	0.4685	0.3786	0.3637	0.2812	0.5847	0.418	-0.1215	0.6658	0.4198	-0.3088	0.3021	0.2397
262097_at	AT1G55990	glycine-rich protein	1.3032	0.3562	0.3527	-0.7899	0.5619	0.409	1.4244	0.3183	0.2775	-0.6687	0.6212	0.3706
262098_at	AT1G56170	HAP5B (Heme activator protein (yeast) homolog 5B	0.5073	0.1032	0.1855	0.2608	0.3403	0.3137	0.4635	0.106	0.1457	0.2169	0.3854	0.2781
262099_s_at	AT4G37390;AT1G59500	(AT4G37390, YDK1 (YADOKARI 1); indole-3-acetic	1.8603	0.1746	0.2445	2.6337	0.0796	0.1415	-0.5851	0.2793	0.2576	0.192	0.7025	0.3982
262100_s_at	AT4G14250, AT1G59550	(AT4G14250, LBX domain-containing protein); [AT1	-0.5497	0.6986	0.4921	0.4442	0.7535	0.4763	0.4646	0.7428	0.4458	0.5701	0.6883	0.3933
262101_at	AT1G59535	unknown protein	-1.2111	0.2037	0.2645	0.8559	0.3439	0.3151	-0.143	0.8665	0.4831	1.924	0.0735	0.0996
262102_at	AT1G02980	CUL2 (cullin 2); ubiquitin protein ligase binding	1.3717	0.2971	0.3214	-1.7668	0.1977	0.2314	2.507	0.0938	0.1358	-0.6316	0.6106	0.367
262103_at	AT1G02940	ATGSTF5 (Arabidopsis thaliana Glutathione S-trans	-0.2212	0.7307	0.5027	0.1124	0.8603	0.5072	0.4675	0.4789	0.351	0.8011	0.2522	0.2137
262104_at	AT1G02910	LPA1 (LOW PSII ACCUMULATION1); binding	-0.2898	0.0421	0.1181	-0.2703	0.0515	0.1126	-0.4096	0.0141	0.0474	-0.3901	0.0166	0.0411
262105_at	AT1G02810	pectinesterase family protein	0.1778	0.8424	0.5363	-1.6033	0.1285	0.1819	0.9551	0.2453	0.2382	-0.8261	0.3046	0.2409
262106_at	AT1G02970	WEE1 (ARABIDOPSIS WEE1 KINASE HOMOLOG	-0.3098	0.42	0.3849	-0.2459	0.5155	0.3908	-0.3111	0.4182	0.3244	-0.2472	0.5134	0.331
262107_at	AT1G02750	zinc ion binding	0.6481	0.0088	0.0607	0.6872	0.0071	0.0478	0.09412	0.0142	0.0476	0.1333	0.0042	0.0207
262108_at	AT1G02740	chromatin binding	0.6939	0.0383	0.1128	0.7302	0.0329	0.0898	0.1143	0.6274	0.4071	0.1506	0.5274	0.337
262109_at	AT1G02730	ATCSLD5 (CELLULOSE SYNTHASE-LIKE D5); 1,4	-0.2694	0.4677	0.4063	-0.3366	0.3732	0.3291	-0.2737	0.3505	0.2983	-0.341	0.2681	0.2218
262110_at	AT1G02840	SR1 (splicing factor 2); RNA binding	0.1278	0.6832	0.4869	0.3605	0.283	0.2826	-0.6389	0.0297	0.0702	-0.4062	0.1034	0.123
262120_at	AT1G02750	similar to unknown protein [Arabidopsis thaliana] (T	-0.1004	0.4512	0.3987	0.2077	0.1598	0.2057	-0.6547	0.0056	0.0311	-0.3466	0.0451	0.0744
262112_at	AT1G02870	similar to unnamed protein product [Vitis vinifera] (G	0.5078	0.041	0.1166	0.8472	0.0077	0.0489	-0.158	0.1819	0.2001	0.1814	0.1377	0.1468
262113_at	AT1G02820	late embryogenesis abundant 3 family protein / LEA	-2.3306	5.00E-04	0.0325	-2.6058	3.00E-04	0.0249	0.3322	0.0287	0.0688	0.05703	0.5965	0.3623
262114_at	AT1G02860	NLA (NITROGEN LIMITATION ADAPTATION); pro	0.005672	0.9842	0.6731	0.2029	0.4931	0.3815	0.0454	0.9542	0.5065	0.2118	0.4234	0.2939
262115_at	AT1G02813	ATGSTF5 (Arabidopsis thaliana Glutathione S-trans	-0.2262	0.8327	0.5332	0.5023	0.6429	0.4392	0.2063	0.8126	0.4674	0.9348	0.3151	0.246
262116_at	AT1G02816	similar to unknown protein [Arabidopsis thaliana] (T	-0.3388	0.2516	0.2942	-0.2483	0.3819	0.3328	0.4733	0.0064	0.033	0.5638	0.0034	0.019
262117_at	AT1G02860	EMB2207 (EMBRYO DEFECTIVE 2366); structural	0.07191	0.3876	0.3685	0.1873	0.0836	0.1453	0.175	0.0739	0.1184	0.4415	0.0037	0.0198
262118_at	AT1G02850	glycosyl hydrolase family 1 protein	1.9331	0.0042	0.0471	1.6656	0.0072	0.0479	-0.4082	0.1263	0.1611	-0.6757	0.0332	0.0616
262119_s_at	AT1G02930;AT1G02920	[AT1G02930, ATGSTF6 (EARLY RESPONSIVE TO	0.4803	0.3906	0.3702	0.8965	0.147	0.1961	0.2355	0.0749	0.1192	0.6517	0.0027	0.0171
262120_at	AT1G02930	ATGSTF4 (GLUTATHIONE S-TRANSFERASE 31)	0.6065	0.1252	0.2048	-0.7652	0.0432	0.1032	0.924	0.0019	0.0009	0.6653	0.0065	0.025
262121_at	AT1G02800	ATCEL2 (Arabidopsis thaliana Cellulase 2); hydrola	-1.6935	0.1762	0.2456	-0.212	0.8473	0.5037	-0.06978	0.9451	0.5045	1.4117	0.2123	0.192
262122_at	AT1G02790	PGA4 (POLYGALACTURONASE 4); polygalacturo	1.1306	0.3188	0.3337	-1.6909	0.164	0.2085	0.4995	0.5809	0.3911	-2.322	0.0494	0.0787
262123_at	AT1G59630	F-box family protein-related	-1.5413	0.1335	0.2121	0.7001	0.4416	0.3602	-0.7183	0.412	0.3217	1.5232	0.1243	0.1379
262124_at	AT1G59660	nucleoporin family protein	1.8013	0.1796	0.2476	2.5618	0.082	0.1437	0.1644	0.7363	0.4437	0.9249	0.1121	0.1291
262125_at	AT1G59680	EDA1 (embryo sac development arrest 1)	0.8149	0.1622	0.2355	-0.5726	0.2954	0.2894	1.3074	0.0516	0.0962	-0.08013	0.8745	0.4497
262126_at	AT1G59620	CWS; ATP binding	0.9741	0.0265	0.0941	0.6039	0.1001	0.1594	-1.2477	0.0095	0.0389	-1.6159	0.0037	0.0199
262127_at	AT1G02550	similar to unknown protein [Arabidopsis thaliana] (T	-0.5102	0.1559	0.2302	-0.5454	0.1356	0.1873	0.4857	0.172	0.1934	0.4505	0.1982	0.1838
262128_at	AT1G02690	late embryogenesis abundant protein, putative / LEA	0.8076	0.2762	0.3094	2.3276	0.0221	0.0752	0.3144	0.4481	0.3377	1.8344	0.008	0.0279
262129_at	AT1G02500	ATPPI2 (ATPPIase 2); NIMA-1/ATNIMH-2/FPG-1/F	-0.233	0.4998	0.4204	0.6858	0.0946	0.155	-0.5359	0.1636	0.1876	0.383	0.2902	0.2336
262130_at	AT1G02890	AAA-type ATPase family protein	-0.0427	0.8215	0.53	0.2805	0.1887	0.2256	-0.623	0.0062	0.0327	-0.2997	0.0641	0.0921
262131_at	AT1G02900	RALFL1 (RALF-LIKE 1)	-1.4118	0.0196	0.0828	-0.7434	0.1181	0.1738	-0.2105	0.583	0.3918	0.4579	0.2643	0.2199
262132_at	AT1G02830	60S ribosomal protein L22 (RPL22A)	-1.3519	0.1992	0.2619	2.6114	0.0412	0.1009	-1.7631	0.1146	0.1521	2.2002	0.066	0.0936
262133_at	AT1G78000	SULTR1;2 (SULFATE TRANSPORTER 1;2); sulfat	0.802	0.0686	0.1506	1.7391	0.0058	0.0442	-0.1598	0.6369	0.4101	0.7772	0.0682	0.0954
262134_at	AT1G77990	AST56 (sulphate transporter 2.2); sulfate transmem	0.1003	0.6972	0.4918	-0.1089	0.6733	0.4496	0.1885	0.2705	0.2526	-0.02062	0.8956	0.4559
262135_at	AT1G78080	RAP2.4 (related to AP2 4); DNA binding / transcript	-0.2381	0.144	0.2206	0.6354	0.0084	0.0507	-2.1359	0	0.0092	-1.2624	2.00E-04	0.0078
262136_at	AT1G77850	ARF17 (AUXIN RESPONSE FACTOR 17); transcri	0.6304	0.0177	0.0798	-0.2611	0.1826	0.2216	0.1649	0.3668	0.3013	-0.7267	0.011	0.0328
262137_at	AT1G77920	bZIP family transcription factor	0.6601	0.2322	0.2833	0.8784	0.1345	0.1864	0.1039	0.6317	0.4084	0.3222	0.1834	0.1755
262138_at	AT1G78020	disease resistance protein, putative	1.6293	0.1243	0.2042	0.5257	0.5652	0.41	0.1391	0.8764	0.4857	-0.9644	0.3147	0.2459
262139_at	AT1G52610	transposable element gene	-0.9592	0.4693	0.407	-0.7916	0.546	0.4029	0.4496	0.6625	0.4188	0.6172	0.5535	0.3463
262140_at	AT1G52470	similar to unknown protein [Arabidopsis thaliana] (T	-0.4203	0.7044	0.4941	1.3489	0.2609	0.2703	-1.0481	0.3669	0.3014	0.7211	0.5229	0.335
262141_s_at	AT1G52440;AT1G52440	[AT1G52440, similar to unknown protein [Arabidop	0.2218	0.8505	0.5383	-0.08909	0.9395	0.5289	1.4471	0.2598	0.2463	1.1362	0.3612	0.2675
262142_at	AT1G52640	pentatricopeptide (PPR) repeat-containing protein	-0.4891	0.4842	0.4136	-0.5022	0.4733	0.3734	-0.08455	0.877	0.4859	-0.09766	0.8582	0.4453
262143_at	AT1G52630	similar to unknown protein [Arabidopsis thaliana] (T	-0.1822	0.4894	0.4156	0.04645	0.8557	0.5061	-0.2539	0.349	0.2927	-0.02528	0.9211	0.4631
262144_at	AT1G52620	pentatricopeptide (PPR) repeat-containing protein	0.1586	0.5446	0.4389	-0.3338	0.2365	0.2557	-0.09425	0.7144	0.4363	-0.5866	0.0708	0.0976
262145_at	AT1G52730	transducin family protein / WD-40 repeat family prot	0.2137	0.3702	0.3597	0.2631	0.2823	0.2823	0.1098	0.5227	0.368	0.1592	0.368	0.2705
262146_at	AT1G52580	rhomboid family protein	0.8144	0.1899	0.2553	0.9521	0.139	0.1899	0.05531	0.9199	0.4977	0.193	0.7276	0.4064
262147_at	AT1G52570	PLDALPHA2 (PHOSPHOLIPASE D ALPHA 2); phos	0.044405	0.8492	0.538	-0.03482	0.8804	0.5133	-0.1555	0.5138	0.3645	-0.2343	0.3415	0.2587
262148_at	AT1G52560	26.5 kDa class I small heat shock protein-like (HSP	0.4342	0.5033	0.4219	2.2085	0.0202	0.0726	-0.163	0.7445	0.4464	1.6113	0.026	0.0534
262149_at	AT1G52530	similar to hypothetical protein [Vitis vinifera] (GB:CA	-0.11	0.6789	0.4857	-0.5081	0.1086	0.1662	0.1789	0.4714	0.3481	-0.2192	0.3854	0.2781
262150_at	AT1G52540	RSE (FAR1-related sequence 5); zinc ion binding	-0.3058	0.2384	0.2866	-0.2203	0.3751	0.3299	-0.4576	0.0934	0.1355	-0.3721	0.1492	0.1541
262151_at	AT1G52510	hydrolase, alpha/beta fold family protein	-1.0902	0.0042	0.0472	-1.1112	0.004	0.0394	-0.1427	0.388	0.3112	-0.1637	0.3292	0.253
262152_s_at	AT1G52430;AT1G52450	[AT1G52430, ubiquitin carboxyl-terminal hydrolase-	-2.0681	0.0528	0.1319	-0.1724	0.8316	0.4993	-2.2401	0.042	0.0853	-0.3444	0.6737	0.3886
262153_at	no_match	no_match	-0.3893	0.4435	0.3951	-0.2023	0.6818	0.4527	-0.8141	0.1503	0.1791	-0.6271	0.243	0.2087
262154_at	AT1G52700	phospholipase/carboxylesterase family protein	1.1814	0.2395	0.2874	-0.3374	0.7135	0.4632	0.3479	0.7051	0.4331	-1.1709	0.243	0.2087
262155_at	AT1G52420	glycosyl transferase family 1 protein	0.8675	0.0011	0.036	0.9658	7.00E-04	0.0275	-0.3052	0.042	0.0852	-0.207	0.116	0.132
262156_at	AT1G52680	late embryogenesis abundant protein-related / LEA	-0.6253	0.3281	0.339	0.02666	0.9644	0.5351	-1.1547	0.109	0.1478	-0.5028	0.4214	0.293
262157_at	AT1G52670	biotin/lipoyl attachment domain-containing protein	-0.2082	0.4223	0.3861	-0.5874	0.0654	0.1278	0.03403	0.8698	0.4841	-0.3452	0.151	0.1554
262158_at	AT1G52540	protein kinase, putative	-0.1321	0.6302	0.4698	0.01934	0.9429	0.53	-0.3542	0.2297	0.2293	-0.2028	0.4629	0.3112
262159_at	AT1G52720	similar to unknown protein [Arabidopsis thaliana] (T	-0.5461	0.2663	0.3029	-0.2216	0.6281	0.4337	0.9805	0.0274	0.0674	1.3051	0.0107	0.0324
262160_at	AT1G52590	Identical to DCC family protein At1g52590, chlorop	-0.2388	0.4166	0.3832	-0.2684	0.3666	0.3259	0.2152	0.4395	0.3338	0.1856	0.5005	0.3261
262161_at	AT1G52600	signal peptidase, putative	0.6702	0.0018	0.0391	0.6919	0.0016	0.0317	0.3096	0.006	0.0322	0.3312	0.0047	0.0217
262162_at	AT1G78020	senescence-associated protein-related	-0.6857	0.0326	0.1048	-0.4775	0.0892	0.1505	-0.2783	0.0731	0.1177	-0.0701	0.5758	0.3544
262163_at	AT1G77940	60S ribosomal protein L30 (RPL30B)	-0.1235	0.4951	0.4181	0.0779	0.6609	0.4454	0.1873	0.3189	0.2778	0.3887	0.0777	0.103
262164_at	AT1G78070	WD-40 repeat family protein	-1.1448	0.0198	0.0832	-1.1068	0.0221	0.0751	-1.3636	0.01	0.0398	-1.3256	0.011	0.0328
262165_at	AT1G75020	LPAT4; acyltransferase	0.6197	0.0276	0.0963	0.5249	0.0455	0.1057	0.177	0.0182	0.0541	0.08215	0.148	0.1534
262166_at	AT1G74840	myb family transcription factor	-0.1756	0.3247	0.337	-0.1374	0.4296	0.3551	-0.01718	0.8942	0.4909	0.02103	0.8707	0.4486
262167_at	AT1G74990	zinc finger (C3HC4-type RING finger) family protein	-0.0753	0.923	0.5579	-0.2727	0.7283	0.4683	-0.5239	0.5134	0.3644	-0.7213	0.3799	0.2757
262168_at	AT1G74730	similar to unknown [Populus trichocarpa x Populus	-0.5747	0.006	0.0538	-0.8473	0.0014	0.0313	0.7813	0.001	0.0173	0.5087	0.0048	0.0218
262169_at	AT1G74860	similar to unknown protein [Arabidopsis thaliana] (T	-0.1063	0.5471	0.4398	-0.1731	0.345	0.3156	0.006051	0.972	0.5105	-0.06077	0.7264	0.4061
262170_at	AT1G74940	senescence-associated protein-related	0.672	0.2186	0.2742	0.7556	0.1765	0.2173	0.04207	0.7591	0.451	0.1257	0.3821	0.2767
262171_at	AT1G74950	JAZ2/TIFY10B (JASMONATE-ZIM-DOMAIN PROT	-0.4374	0.2233	0.2772	-0.373	0.2868	0.2848	0.2986	0.1058	0.1456	0.3629	0.0646	0.0925
262172_at	AT1G74970	RPS9 (RIBOSOMAL PROTEIN S9); structural cons	-0.8903	0.0142	0.0727	-0.7674	0.0231	0.0768	-0.312	0.0905	0.133	-0.1891	0.2495	0.2122
262173_at	AT1G74920	ALDH10A8 (Aldehyde dehydrogenase 10A8); 3-chl	0.3002	0.2104	0.2685	0.3726	0.138	0.1891	-0.8137	4.00E-04	0.0147	-0.7412	6.00E-04	0.0103
262174_at	AT1G74910	ADP-glucose pyrophosphorylase family protein	0.3028	0.0449	0.1221	0.176	0.169	0.2119	-0.1177	0.1592	0.1852	-0.2444	0.023	0.0494
262175_at	AT1G74880	NDH-O (NAD(P)H-PLASTOQUINONE DEHYDROG	-0.913	0.0046	0.049	-0.9955	0.0033	0.0371	-0.267	0.0769	0.1211	-0.3495	0.0362	0.0647
262176_at	AT1G74960	FAB1 (FATTY ACID BIOSYNTHESIS 1); fatty-acid	-0.5876	0.0365	0.1102	-0.6475	0.0271	0.0824	-0.6775	0.0089	0.0378	-0.7373	0.0066	0.0252
262177_at	AT1G74710	ICS1 (ISOCHORISMATE SYNTHASE1); isochorism	1.2522	0.0049	0.0502	0.9285	0.014	0.0627	-0.116	0.4883	0.354	-0.4396	0.0439	0.0733
262178_at	AT1G77860	KOM (KOMPEITO)	-0.02644	0.9537	0.5657	-1.3353	0.0355	0.0929	0.7413	0.1583	0.1845	-0.5675	0.2555	0.2154
262179_at	AT1G77980	AGL66; transcription factor	-1.2802	0.1469	0.2229	-0.2627	0.7311	0.4688	-0.5945	0.3228	0.2796	0.4229	0.4677	0.3129
262180_at	AT1G78050	phosphoglycerate/bisphosphoglycerate mutase fam	-0.01995	0.9525	0.5653	0.218	0.5269	0.3949	0.4296	0.0312	0.0719	0.6676	0.0072	0.0264
262181_at	AT1G78060	glycosyl hydrolase family 3 protein	0.2867	0.1456	0.2218	0.01908	0.9103	0.5216	0.1347	0.2729	0.2539	-0.133	0.2782	0.2272
262182_at	no_match	no_match	-1.0138	0.2537	0.2957	-0.476	0.5656	0.4102	-0.5836	0.4054	0.3188	-0.04581	0.9454	0.4697
262183_at	AT1G77890	similar to unknown protein [Arabidopsis thaliana] (T	-0.02459	0.9081	0.5535	0.09532	0.6588	0.4446	-0.6212	0.0361	0.0781	-0.5013	0.0664	0.0939
262184_at	AT1G77910	unknown protein	1.0277	0.6093	0.4628	-0.1186	0.9521	0.5324	0.8152	0.6832	0.4253	-0.3311	0.8671	0.4474
262185_at	AT1G77950	AGL67; transcription factor	0.1546	0.8623	0.5416	0.493	0.5871	0.4187	-0.9895	0.3021	0.2696	-0.6511	0.4796	0.3174
262186_at	no_match	no_match	-0.8457	0.2651	0.3022	-1.5224	0.0802	0.142	-0.3067	0.6544	0.416	-0.9835	0.1964	0.1828
262187_at	no_match	no_match	1.0226	0.1402	0.2178	-0.531	0.3943	0.3388	0.5721	0.3623	0.2992	-0.9815	0.1528	0.1567
262188_at	AT1G77810	galactosyltransferase family protein	0.8634	0.0364	0.1099	0.9113	0.0309	0.0873	-0.06781	0.7266	0.4407	-0.01989	0.9177	0.462
262189_at	AT1G78010	RNA modification GTPase, putative	0.2055	0.212	0.2697	0.08583	0.569	0.4115	-0.2304	0.1716	0.1931	-0.35	0.0648	0.0927
262190_at	AT1G78030	similar to glycine-rich protein [Arabidopsis thaliana]	-0.7782	0.0311	0.1023	-0.8477	0.0238	0.0776	-0.75	0.0117	0.0428	-0.8195	0.0086	0.0288
262191_at	AT1G77820	transposable element gene	0.4217	0.7415	0.5064	0.281	0.8253	0.4975	0.1988	0.8674	0.4834	0.05822	0.9609	0.4734
262192_at	AT1G77830	zinc finger (C3HC4-type RING finger) family protein	1.3388	0.3192	0.334	-0.09875	0.932	0.5284	-0.6772	0.5962	0.3969	-2.1147	0.1471	0.1528
262193_at	AT1G77840	initiation factor 5, putative / eIF-5, putative	0.3616	0.1251	0.2047	0.3798	0.1119	0.1689	0.5143	0.013	0.0452	0.5326	0.0115	0.0337
262194_at	AT1G77930	DNAJ heat shock N-terminal domain-containing pro	-0.1418	0.117	0.1977	-0.3782	0.006	0.0447	0.08339	0.3062	0.2717	-0.1529	0.098	0.119
262195_at	AT1G78040	pollen Ole e 1 allergen and extensin family protein	-0.3973	0.0353	0.1085	-0.6347	0.0075	0.0487	0.2355	0.0052	0.0302	-0.0019	0.9666	0.4748
262196_at	AT1G77870	MUB5 (MEMBRANE-ANCHORED UBIQUITIN-FOL	-0.3747	0.3276	0.3387	-0.6283	0.135	0.1869	0.7074	0.1032	0.1435	0.4538	0.2484	0.2115
262197_at	AT1G53910	RAP2.12; DNA binding / transcription factor	0.401	0.0513	0.1301	0.6719	0.0099	0.0543	0.113	0.4812	0.3517	0.384	0.0579	0.0866
262198_at	AT1G53830	ATPMEPCRA (Arabidopsis thaliana pectin methylestera	0.2336	0.0131	0.0706	2.2361	0.0423	0.1022	-0.09008	0.908	0.4947	-1.0875	0.2114	0.1916
262199_at	AT1G53800	endonuclease	-0.1785	0.6233	0.4676	-0.7938	0.0774	0.1394	-0.6736	0.0401	0.083	-1.2889	0.0046	0.0214
262200_at	AT2G01070	similar to unknown protein [Arabidopsis thaliana] (T	-0.7521	0.0421	0.1181	-0.04638	0.8647	0.5085	-1.017	0.0163	0.051	-0.3112	0.2898	0.2334
262201_at	AT2G01120	ATORC4 (ORC4 ORIGIN RECOGNITION COMPLE	0.1097	0.7489	0.5084	0.3453	0.3411	0.314	-0.3157	0.3795	0.3075	-0.08008	0.8146	0.4328
262202_at	AT2G01110	APG2 (ALBINO AND PALE GREEN 2)	-0.5675	0.0359	0.1093	-0.3844	0.1028	0.1618	-0.53	0.0311	0.0717	-0.3469	0.0997	0.1204
262203_at	AT2G01060	myb family transcription factor	0.1722	5.00E-04	0.032	0.7404	4.00E-04	0.0251	-0.3125	0.0022	0.0222	-0.2843	0.0032	0.0183
262204_at	AT2G01100	similar to Os01g0120700 [Oryza sativa (japonica cu	0.7458	0.0201	0.0837	0.7505	0.0197	0.072	-0.9159	3.00E-04	0.014	-0.9113	3.00E-04	0.0085
262205_at	AT2G01080	similar to unknown protein [Arabidopsis thaliana] (T	0.754	0.0279	0.0968	0.5044	0.0868	0.1485	-0.495	0.0034	0.0259	-0.7446	7.00E-04	0.0108
262206_at	AT2G01090	ubiquinol-cytochrome C reductase complex 7.8 kDa	-0.6103	0.0315	0.1028	-0.1554	0.0154	0.0649	0.5586	0.0308	0.0714	0.416	0.0747	0.1006
262207_at	AT1G74850	PTAC2 (PLASTID TRANSCRIPTIONALLY ACTIVE	-0.1115	0.701	0.4929	-0.3461	0.2697	0.2753	-0.4357	0.1175	0.1543	-0.6702	0.0376	0.0663
262208_at	AT1G74800	galactosyltransferase family protein	0.02734	0.9084	0.5535	0.02564	0.914	0.5225	0.1011	0.6741	0.4223	0.09936	0.6792	0.3902
262209_at	AT1G74720	C2 domain-containing protein	-0.1587	0.2183	0.274	-0.2844	0.0592	0.1209	-0.3766	0.0258	0.0652	-0.5022	0.0099	0.0311
262210_at	AT1G74690	IQD31 (IQ-domain 31); calmodulin binding	-0.346	0.0895	0.1733	-0.1249	0.4659	0.3703	0.2232	0.2236	0.2258	0.4443	0.0457	0.0751
262211_at	AT1G74930	ORA47; DNA binding / transcription factor	-2.2289	0.022	0.0871	-1.6276	0.0566	0.1184	-0.03682	0.8346	0.4739	0.5645	0.0269	0.0545
262212_at	AT1G74890	ARR15 (RESPONSE REGULATOR 15); transcripti	-2.2777	0.0224	0.0875	-1.8768	0.0407	0.1	-0.4234	0.3001	0.2688	0.02246	0.9527	0.4717
262213_at	AT1G74870	protein binding / zinc ion binding	-2.1731	0.1405	0.2181	0.07228	0.9543	0.5329	-0.06327	0.96	0.5076	2.1821	0.1393	0.1477
262214_at	AT1G74820	cupin family protein	1.0653	0.236	0.285	1.4502	0.1307	0.1833	0.2512	0.6162	0.4032	0.6361	0.2414	0.2079
262215_at	AT1G74760	carboxyl-	-0.05389	0.7277	0.5017	-0.2634	0.1419	0.1923	0.2963	0.0619	0.1069	0.08678	0.4932	0.3232
262216_at	AT1G74780	nodulin family protein	-0.4478	0.0387	0.1134	-0.2168	0.216	0.2433	-0.7714	1.00E-04	0.0101	-0.5404	3.00E-04	0.0083
262217_at	AT1G74770	protein binding / zinc ion binding	-1.0473	0.3209	0.3349	0.9481	0.3634	0.3245	-1.5426	0.1708	0.1925	0.4527	0.6502	0.3809
262218_at	AT1G74770	protein binding / zinc ion binding	1.0618	0.0386	0.1132	0.2176	0.6677	0.411	-0.02223	0.9524	0.5061	-0.8665	0.0685	0.0957
262219_at	AT1G74750	pentatricopeptide (PPR) repeat-containing protein	0.3636	0.2004	0.2624	0.2601	0.3348	0.3107	-0.6689	0.0368	0.0791	-0.7724	0.0236	0.0502
262220_at	AT1G74740	CPK30 (calcium-dependent protein kinase 30); calr	-0.3737	0.1955	0.2595	0.03627	0.8875	0.5152	-0.1423	0.5709	0.3869	0.2677	0.3105	0.2436
262221_at	AT1G75010	GTP binding / GTPase	-0.07605	0.7952	0.5224	-0.1609	0.5888	0.419	-0.1769	0.5538	0.3804	-0.2618	0.3937	0.2816
262222_at	AT1G74700	NUZ	0.3867	0.1202	0.2006	0.3498	0.1494	0.1977	0.1246	0.5602	0.3827	0.08767	0.6783	0.39
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262290_at	AT1G70985	hydroxyproline-rich glycoprotein family protein	-2.6108	0.0968	0.1798	-2.7567	0.0847	0.1465	0.1024	0.7636	0.4523	-0.04347	0.8979	0.4566
262291_at	AT1G70790	C2 domain-containing protein	0.06705	0.7842	0.519	0.09092	0.7115	0.4627	-0.3619	0.1068	0.1464	-0.3381	0.1249	0.1382
262292_at	AT1G27595	similar to ESP4 (ENHANCED SILENCING PHENO	0.3907	0.0696	0.1521	-0.2745	0.1589	0.2051	-0.4242	0.0228	0.061	-1.0894	8.00E-04	0.0108
262293_at	AT1G27640	unknown protein	-0.01932	0.9831	0.5728	0.2316	0.7999	0.4896	-0.8427	0.3801	0.3078	-0.5918	0.5269	0.3367
262294_at	AT1G27610	unknown protein	-0.2806	0.8038	0.5251	0.6869	0.5645	0.4099	-0.1738	0.8816	0.4871	0.8037	0.5036	0.3272
262295_at	AT1G27650	ATU2AF35A; RNA binding	0.3331	0.2286	0.2811	0.5735	0.0708	0.1331	-0.65	0.0291	0.0692	-0.4096	0.1037	0.1233
262296_at	AT1G27630	CYCT1;3; cyclin-dependent protein kinase	0.5413	0.0965	0.1795	0.8406	0.0283	0.0836	-1.0501	0.0026	0.0234	-0.7508	0.0087	0.029
262297_at	AT1G27600	glycosyl transferase family 43 protein	-0.05214	0.8187	0.5292	0.3062	0.2241	0.248	-0.6267	0.016	0.0505	-0.2684	0.1611	0.1618
262298_at	AT1G27530	similar to unknown [Populus trichocarpa] (GB:ABK9	0.3961	0.0741	0.1564	0.2169	0.2585	0.2692	0.4016	0.0425	0.0858	0.2223	0.1791	0.1728
262299_at	AT1G27520	glycoside hydrolase family 47 protein	0.5539	0.0315	0.1029	0.1792	0.3532	0.3197	-1.8665	2.00E-04	0.0125	-2.2412	1.00E-04	0.0058
262300_at	AT1G70870	major latex protein-related / MLP-related	0.2637	0.7799	0.6178	-1.8343	0.1061	0.1644	2.1585	0.0707	0.1156	0.0605	0.9486	0.4705
262301_at	AT1G70880	Bet v I allergen family protein	0.07531	0.9342	0.5608	-2.0356	0.0764	0.1385	2.138	0.0672	0.1123	0.02716	0.9762	0.4772
262302_at	AT1G70910	zinc finger (C3HC4-type RING finger) family protein	-0.9728	0.3893	0.3695	-0.2202	0.8378	0.5009	-1.6995	0.1671	0.1898	-0.947	0.4008	0.2845
262303_at	AT1G70920	homeobox-leucine zipper protein, putative / HD-ZIP	0.1648	0.766	0.5133	-0.879	0.1646	0.2088	0.5078	0.3819	0.3087	-0.5369	0.3588	0.2665
262304_at	AT1G70890	MLP43 (MLP-LIKE PROTEIN 43)	-0.4547	0.1031	0.1855	-0.386	0.1486	0.1972	1.1349	2.00E-04	0.0131	1.2036	2.00E-04	0.0076
262305_at	AT1G70950	similar to unknown protein [Arabidopsis thaliana] (T	0.3727	0.7237	0.5006	-0.8852	0.4186	0.3501	-0.5493	0.606	0.4001	-1.8072	0.1397	0.148
262306_s_at	AT5G56680,AT1G70980	glycosyl transferase family 43 protein	0.2529	0.3111	0.3294	0.7125	0.031	0.0874	-0.7518	0.0099	0.0397	-0.2921	0.1473	0.1529
262307_at	AT1G71000	DNAJ heat shock N-terminal domain-containing pro	-0.3678	0.694	0.4908	-1.2987	0.2095	0.2393	-0.1039	0.8307	0.473	-1.0348	0.0855	0.1094
262308_at	AT1G71010	phosphatidylinositol-4-phosphate 5-kinase family pr	-0.06099	0.7309	0.5027	-0.09331	0.6026	0.4246	-0.5613	0.0109	0.0414	-0.5936	0.0089	0.0295
262309_at	AT1G70820	phosphoglucomutase, putative / glucose phosphom	0.2793	0.6489	0.4761	0.04287	0.9435	0.5302	-0.3014	0.0456	0.0893	-0.5379	0.0069	0.0259
262310_at	AT1G70840	MLP31 (MLP-LIKE PROTEIN 31)	0.4589	0.573	0.4501	-0.5699	0.4889	0.3799	1.1212	0.2086	0.2169	0.09234	0.9078	0.4593
262311_at	no_match	no_match	-1.6023	0.0698	0.1522	-1.2136	0.1179	0.1736	1.2463	0.111	0.1491	1.535	0.0659	0.0935
262312_at	AT1G70830	MLP28 (MLP-LIKE PROTEIN 28)	-1.3066	0.02	0.0834	-1.0306	0.0417	0.1015	-0.1925	0.2038	0.2141	0.08353	0.5463	0.3435
262313_at	AT1G70900	similar to unknown protein [Arabidopsis thaliana] (T	0.2567	0.1303	0.2088	0.199	0.2147	0.2425	-0.884	0.0013	0.0189	-0.9416	0.001	0.0121
262314_at	AT1G70810	C2 domain-containing protein	1.1117	0.0721	0.1548	1.2807	0.0489	0.1097	0.9227	0.0083	0.0366	1.0917	0.0045	0.0213
262315_at	AT1G70990	proline-rich family protein	-0.7492	0.4412	0.3943	-1.6237	0.1379	0.1891	1.306	0.2108	0.2183	0.4316	0.6485	0.3803
262316_at	AT2G48120	PAC (PALE CRESS)	-0.9598	0.0018	0.0391	-0.8467	0.0029	0.0355	0.04501	0.7482	0.4476	0.1581	0.2935	0.2354
262317_at	AT2G48140	EDA4 (embryo sac development arrest 4); lipid bind	0.5036	0.1016	0.1843	0.9775	0.4548	0.3659	0.2305	0.8254	0.4713	-1.2907	0.2664	0.221
262318_at	AT2G72620	transferase family protein	1.4566	0.174	0.2442	0.2751	0.707	0.4806	0.7848	0.1261	0.161	-0.3967	0.385	0.2779
262319_s_at	AT2G27580,AT1G27540	[AT1G27580, F-box family protein];[AT1G27540, F-	0.2483	0.0254	0.0923	0.4473	0.0033	0.0371	0.1037	0.2198	0.2235	0.3027	0.0132	0.0365
262320_at	AT2G27580	F-box family protein	0.6976	0.2771	0.31	1.8937	0.0959	0.156	-1.6318	0.0082	0.0363	1.3595	0.0154	0.0395
262321_at	AT1G27570	phosphatidylinositol 3- and 4-kinase family protein	0.8512	0.441	0.3942	1.2189	0.2883	0.2856	-0.6179	0.5687	0.3863	-0.2503	0.814	0.4327
262322_at	AT1G27590	similar to phosphatidylinositol 3- and 4-kinase famil	-1.316	0.0698	0.1523	-0.2882	0.619	0.4302	-1.9548	0.0218	0.0595	-0.9269	0.1585	0.1603
262323_at	AT1G64190	6-phosphogluconate dehydrogenase family protein	0.3517	0.0105	0.0647	0.3461	0.0111	0.0566	-0.104	0.7762	0.1961	-0.1097	0.6824	0.1604
262324_at	AT1G64170	ATCHX16 (CATION/H+ EXCHANGER 16); monova	1.5663	0.0346	0.1075	1.1124	0.0891	0.1504	-0.1512	0.7614	0.4515	-0.6051	0.2631	0.2193
262325_at	AT1G64160	disease resistance-responsive family protein / dirige	0.007116	0.9889	0.5743	-0.9002	0.1334	0.1855	3.0607	0.002	0.0211	2.1534	0.0072	0.0264
262326_at	AT1G64140,AT1G64142	[AT1G64140, similar to loricin-related [Arabidopsis	0.1291	0.2949	0.3203	0.0634	0.586	0.4184	-0.3384	0.0343	0.0757	-0.1459	0.245	0.2097
262327_at	AT1G64130	contains domain Bet v1-like (SSF55961)	0.01635	0.9864	0.5735	1.4192	0.1898	0.2264	0.337	0.7269	0.4408	1.7399	0.1252	0.1384
262328_at	AT1G64100	pentaticopeptide (PPR) repeat-containing protein	-0.8252	0.3573	0.3533	2.0632	0.0601	0.1218	-1.6426	0.1073	0.1467	1.2458	0.1917	0.1801
262329_at	AT1G64090	reticulon family protein (RTN3)	0.2748	0.1499	0.2254	0.125	0.4639	0.3697	-0.2557	0.1131	0.1507	-0.4055	0.0326	0.061
262330_at	AT1G64070	RLM1 (RESISTANCE TO LEPTOSPHAERIA MACU	0.5205	0.4269	0.3881	-0.1149	0.8549	0.5059	0.2294	0.7096	0.4346	-0.406	0.5181	0.3328
262331_at	AT1G64050	similar to unnamed protein product [Vitis vinifera] (G	-0.1343	0.4534	0.3997	-0.06713	0.6997	0.459	-0.178	0.3333	0.285	-0.1108	0.5312	0.3385
262332_at	AT1G64030	serpin family protein / serine protease inhibitor fami	0.1741	-1.6138	0.2443	0.2568	0.7933	0.4872	-1.3687	0.1115	0.1495	0.4018	0.5823	0.357
262333_at	AT1G64020	serpin-related / serine protease inhibitor-related	-0.3677	0.4391	0.3932	-1.43	0.0289	0.0847	0.2248	0.5219	0.3678	-0.8376	0.0593	0.0879
262334_at	AT1G64010	serpin, putative / serine protease inhibitor, putative	-0.04258	0.9709	0.5702	-0.1189	0.9189	0.5238	-0.4112	0.7267	0.4408	-0.4875	0.6797	0.3903
262335_at	AT1G63960	DNA topoisomerase VIA, putative (SPO11-2)	0.2646	0.8081	0.5263	0.5553	0.615	0.4288	1.072	0.3068	0.272	1.3628	0.211	0.1913
262336_at	AT1G64220	TOM7-2 (TRANSLOCASE OF OUTER MEMBRANE	0.4075	0.3382	0.3446	1.1899	0.0337	0.0908	1.1956	0.0332	0.0745	1.9781	0.0062	0.0244
262337_at	AT1G64260	zinc finger protein-related	0.4098	0.34	0.3453	-0.0511	0.8992	0.5187	0.4134	0.3363	0.2865	-0.04746	0.9063	0.4591
262338_at	AT1G64185	lactoylglutathione lyase family protein / glyoxalase I	0.2943	0.3384	0.3447	0.7764	0.0456	0.1058	-0.3573	0.2576	0.2451	0.1249	0.6686	0.3869
262339_at	AT1G64000	WRKY56 (WRKY DNA-binding protein 56); transcri	-1.9461	0.2763	0.3095	1.2795	0.4542	0.3657	-1.8136	0.2734	0.2543	1.412	0.3793	0.2754
262340_at	AT1G64100,AT1G64105	[AT1G64100, pentaticopeptide (PPR) repeat-conta	0.05364	0.7282	0.502	0.5247	0.0218	0.0748	0.5372	0.0202	0.0572	1.0083	0.0022	0.0157
262341_at	AT1G64230	UBC28 (ubiquitin-protein ligase	0.3353	0.0175	0.0793	0.2021	0.0784	0.1404	-0.5991	2.00E-04	0.013	-0.7323	1.00E-04	0.0061
262342_at	AT1G64150	similar to unknown protein [Arabidopsis thaliana] (T	-0.4915	0.0074	0.0576	-0.7296	0.0017	0.0321	-0.168	0.0252	0.0644	-0.406	0.0011	0.0124
262343_at	AT1G64040	TOPP3 (Type one serine/threonine protein phospha	0.31	0.0116	0.0674	0.2918	0.0143	0.0632	-0.3115	0.0114	0.0423	-0.3298	0.0094	0.0301
262344_at	AT1G64060	ATRBOH F (RESPIRATORY BURST OXIDASE PR	0.7122	0.0199	0.0833	-0.1407	0.4994	0.3842	-0.01661	0.9344	0.5019	-0.8695	0.0101	0.0315
262345_at	AT1G64180	intracellular protein transport protein USO1-related	-0.3663	0.126	0.2055	-0.02132	0.916	0.523	-0.1679	0.3731	0.3043	0.177	0.3504	0.2628
262346_at	AT1G63980	D111/G-patch domain-containing protein	0.2073	0.1507	0.2261	0.5805	0.0077	0.0489	-1.1233	3.00E-04	0.014	-0.75	0.0015	0.0138
262347_at	AT1G64110	AAA-type ATPase family protein	0.8894	0.1873	0.2536	1.083	0.1251	0.1793	-0.0772	0.8268	0.4718	0.1165	0.7423	0.4112
262348_at	AT1G64160	PWWP domain-containing protein	-0.03288	0.6779	0.4852	0.1402	0.1293	0.1824	-0.7783	5.00E-04	0.0148	-0.6052	0.0012	0.0128
262349_at	AT1G64130	protease inhibitor/seed storage/lipid transfer protein	-0.05894	0.8712	0.5443	-0.06473	0.8588	0.5068	0.1199	0.743	0.4458	0.1141	0.7548	0.4151
262350_at	AT1G64150	ATGPX4 (GLUTATHIONE PEROXIDASE 4); glutat	0.5108	0.6995	0.4923	1.1037	0.4206	0.3509	-0.2459	0.8514	0.4789	0.347	0.792	0.4285
262351_at	AT1G72990	BGAL17 (BETA-GALACTOSIDASE 17); beta-galac	-0.1669	0.4761	0.4101	-0.1592	0.4953	0.3826	-0.4051	0.1293	0.1634	-0.3975	0.1348	0.1449
262352_at	AT1G64250	transposable element gene	-1.0973	0.4202	0.385	-0.5009	0.703	0.4601	-0.245	0.851	0.4788	0.3515	0.788	0.4252
262353_at	AT1G64210	leucine-rich repeat transmembrane protein kinase,	0.3076	0.6249	0.4682	-0.1253	0.8399	0.5014	0.07624	0.8995	0.4922	-0.3548	0.5749	0.3541
262354_at	AT1G64200	VHA-E3 (VACUOLAR H+-ATPASE SUBUNIT E IS	-0.8927	0.0679	0.1496	-0.6039	0.1681	0.2113	0.4094	0.008	0.036	0.6983	0.0011	0.0126
262355_at	AT1G72820	mitochondrial substrate carrier family protein	-0.1075	0.1408	0.2183	-0.05294	0.4178	0.3496	-0.4307	0.0018	0.0206	-0.3762	0.003	0.0179
262356_at	AT1G73000	similar to Bet v I allergen family protein [Arabidopsis	-0.7487	0.3869	0.3682	1.037	0.2502	0.2641	0.09151	0.9113	0.4956	1.8772	0.0718	0.0983
262357_at	AT1G73040	jacalin lectin family protein	1.6727	0.0038	0.0462	1.8097	0.0029	0.0354	1.0079	0.0094	0.0388	1.1448	0.006	0.024
262358_at	AT1G73050	(R)-mandelonitrile lyase, putative / (R)-oxynitrilase,	1.137	0.3145	0.3311	0.4469	0.6749	0.4501	-0.27	0.7984	0.4629	-0.9602	0.3867	0.2786
262359_at	AT1G73066	protein binding	0.5628	0.6116	0.4632	-0.417	0.7045	0.4606	0.4843	0.6214	0.405	-0.4955	0.6137	0.3679
262360_at	AT1G73080	PEPR1 (PEP1 RECEPTOR 1); ATP binding / kinase	-0.9058	0.0401	0.1156	-0.6115	0.1132	0.1701	-0.1647	0.2192	0.2232	0.1296	0.316	0.2464
262361_at	AT1G73150	DNA-binding bromodomain-containing protein	0.2238	0.2779	0.3101	0.1739	0.3847	0.334	-0.1104	0.5696	0.3865	-0.1602	0.4197	0.2924
262362_at	AT1G73240	ATP binding / protein binding / transmembrane rece	1.106	0.2447	0.2904	-0.3095	0.7224	0.4661	-0.3135	0.719	0.4382	-1.729	0.1002	0.1207
262363_at	AT1G72840	disease resistance protein (TIR-NBS class), putative	-0.744	0.1135	0.1952	-0.02542	0.9483	0.5315	-0.3019	0.4584	0.3424	0.4166	0.3213	0.2489
262364_at	AT1G72860	disease resistance protein (TIR-NBS-LRR class), p	-2.6695	0.0711	0.1538	-1.4423	0.2576	0.2688	-1.3814	0.2751	0.2553	-0.1542	0.8947	0.4556
262365_at	AT1G72870	disease resistance protein (TIR-NBS class), putative	0.1845	0.1437	0.2204	-0.669	0.2849	0.2838	0.6292	0.3105	0.2737	-1.0243	0.1319	0.1429
262366_at	AT1G72890	disease resistance protein (TIR-NBS class), putative	0.271	0.4621	0.4039	0.32	0.3916	0.3375	-0.5091	0.0339	0.0752	-0.4601	0.0457	0.0751
262367_at	AT1G73030	VPS46.2	0.321	0.2034	0.2643	0.4832	0.0842	0.146	0.7441	8.00E-04	0.0162	0.9063	4.00E-04	0.0088
262368_at	AT1G73060	similar to unknown protein [Arabidopsis thaliana] (T	-0.6805	0.0057	0.0525	-0.7554	0.0039	0.0391	-0.2187	0.157	0.1837	-0.2937	0.0798	0.1049
262369_at	AT1G73010	phosphoric monoester hydrolase	0.3529	0.2522	0.2947	0.08716	0.7578	0.4774	0.3061	0.2443	0.2376	0.04038	0.866	0.4472
262370_at	AT1G73090	similar to unnamed protein product [Vitis vinifera] (G	-0.5254	0.039	0.1139	-0.7106	0.015	0.0644	-0.08688	0.638	0.4105	-0.2721	0.1865	0.1773
262371_at	AT1G73160	glycosyl transferase family 1 protein	0.1426	0.8901	0.5483	-1.258	0.2639	0.2719	0.821	0.4444	0.336	-0.5796	0.5819	0.3568
262372_at	AT1G73130	similar to unknown protein [Arabidopsis thaliana] (T	1.2661	0.0873	0.1711	0.9798	0.156	0.2028	-0.2582	0.6696	0.4209	-0.5445	0.3873	0.2789
262373_at	AT1G73120	similar to hypothetical protein [Vitis vinifera] (GB:CA	-1.3412	0.2319	0.2831	0.08119	0.9362	0.5282	0.2977	0.7703	0.4543	1.72	0.1453	0.1518
262374_s_at	AT1G72910,AT1G72930	[AT1G72910, disease resistance protein (TIR-NBS	-0.01529	0.9284	-0.2368	0.2127	0.2412	0.6011	0.006	0.0322	0.3796	0.0283	0.0562	
262375_at	AT1G73100	SUVH3 (SU(VAR)3-9 HOMOLOG 3)	0.1688	0.246	0.2912	-0.1739	0.2343	0.2545	-0.205	0.1743	0.195	-0.5477	0.0116	0.0338
262376_at	AT1G72970	HTH (HOTHEAD); aldehyde-lyase	-1.6314	0.0235	0.0896	-1.6614	0.0221	0.0752	0.1935	0.5534	0.3802	0.1635	0.6142	0.3681
262377_at	AT1G73110	ribulose bisphosphate carboxylase/oxygenase activ	-0.8537	0.0192	0.0822	-1.2227	0.0056	0.0434	0.0191	0.8505	0.4786	-0.3499	0.0212	0.0473
262378_at	AT1G72830	HAP2C (Heme activator protein (yeast) homolog 2C	1.3971	0.0054	0.0519	0.7834	0.0374	0.0957	0.4886	0.0192	0.0555	-0.1252	0.386	0.2782
262379_at	AT1G73020	similar to unnamed protein product [Vitis vinifera] (G	-0.3825	0.2351	0.2844	-0.3804	0.2372	0.2562	-0.1626	0.5318	0.3719	-0.1605	0.5368	0.3402
262380_at	AT1G72810	threonine synthase, putative	0.0047	0.9833	0.5729	-0.1905	0.4189	0.3502	0.351	0.063	0.1079	0.1557	0.3203	0.2485
262381_at	AT1G72900	disease resistance protein (TIR-NBS class), putative	0.1106	0.8016	0.5246	0.4738	0.314	0.2995	-0.4419	0.0236	0.0623	-0.07866	0.5607	0.3492
262382_at	AT1G72920	disease resistance protein (TIR-NBS class), putative	0.1303	0.8628	0.5417	0.04354	0.9539	0.5328	0.5172	0.1614	0.1864	0.4305	0.2266	0.1997
262383_at	AT1G72940	disease resistance protein (TIR-NBS class), putative	-0.00871	0.9834	0.5729	0.116	0.783	0.4844	-1.1359	0	0.0083	-1.0111	0	0.0047
262384_at	AT1G72950	disease resistance protein (TIR-NBS class), putative	-0.00278	0.9933	0.5753	0.6473	0.1059	0.1642	-0.3926	0.2753	0.2554	0.2574	0.4543	0.3077
262385_at	AT1G72960	root hair defective 3 GTP-binding (RHD3) family pro	-0.4206	0.7119	0.497	0.2374	0.8338	0.4999	-0.05019	0.9645	0.5086	0.6078	0.5973	0.3625
262386_at	AT1G49370	pseudogene, similar to OSJNBa0037F16.8, blastp e	0.0408	0.8775	0.5459	-0.8113	0.0309	0.0873	0.1974	0.4711	0.3481	-0.6546	0.0578	0.0866
262387_s_at	AT1G49340,AT1G51040	[AT1G49340, ATPI4K ALPHA (Arabidopsis thaliana	0.641	0.0283	0.0974	0.4963	0.06	0.1216	-0.628	0.0254	0.0646	-0.7727	0.0128	0.0359
262388_at	AT1G49320	BURP domain-containing protein	0.8561	0.0207	0.0848	0.8406	0.022	0.075	0.6336	0.0518	0.0964	0.618	0.0555	0.0844
262389_at	AT1G49270	protein kinase family protein	-0.1746	0.8801	0.5464	-1.9755	0.143	0.193	0.954	0.4293	0.3293	-0.8469	0.479	0.3171
262390_at	AT1G49260	similar to unknown protein [Arabidopsis thaliana] (T	-0.5395	0.3426	0.3463	0.1221	0.8196	0.4958	0.05355	0.9201	0.4978	0.7152	0.227	0.1999
262391_at	AT1G49530	GGPS6 (GERANYLGERANYL PYROPHOSPHATE	-1.118	0.1993	0.2619	-1.6678	0.0837	0.1454	-1.1842	0.179	0.1979	-1.734	0.0758	0.1014
262392_at	AT1G49520	SWI3 complex BAF60b domain-containing protein	-0.8854	0.0438	0.1207	-0.5077	0.1709	0.2133	-0.3174	0.3151	0.2759	0.06032	0.838	0.4395
262393_at	AT1G49490	leucine-rich repeat family protein / extensin family p	-0.428	0.6915	0.4898	-1.7063	0.1641	0.2085	-0.5994	0.3581	0.297	-1.8776	0.0314	0.0597
262394_at	AT1G49510	EMB1273 (EMBRYO DEFECTIVE 1273)	-0.2408	0.1673	0.2393	-0.2986	0.105	0.1637	-0.2499	0.1554	0.1825	-0.3077	0.0977	0.1188
262396_at	AT1G49540	nucleotide binding	2.9051	2.00E-04	0.0312	0.6333	0.0471	0.1078	-0.3639	0.0786	0.1227	-2.6357	1.00E-04	0.0058
262396_at	AT1G49470	similar to unknown protein [Arabidopsis thaliana] (T	0.2382	0.4052	0.3779	-0.06866	0.802	0.4902	1.2578	0.0012	0.0188	0.9509	0.0035	0.0193
262397_at	AT1G49380	cytochrome c biogenesis protein family	-0.7933	0.0029	0.0435	-0.8235	0.0025	0.034	-0.4805	0.0172	0.0524	-0.5108	0.014	0.0376
262398_at	AT1G49500	pfkB-type carbohydrate kinase family protein	0.5743	0.0044	0.0482	0.6948	0.0022	0.0333	-0.3706	0.0123	0.0441	-0.2501	0.043	0.0724
262399_at	AT1G49500	similar to unknown protein [Arabidopsis thaliana] (T	-0.4258	0.1535	0.2286	-0.3498	0.2221	0.2471	0.3414	0.0844	0.1279	0.4174	0.0492	0.0785
262400_at	AT1G49480	RTV1 (REALTED TO VERNALIZATION 1); DNA b	0.02971	0.8493	0.538	0.2255	0.1988	0.2322	0.4133	0.0263	0.066	0.6092	0.0071	0.0264
262401_at	AT1G49300	ATRAN2; GTP binding	0.2306	0.2282	0.2808	0.07961	0.6493	0.4414	0.6269	0.0153	0.0493	0.4759	0.0368	0.0653
262402_at	AT1G49410	TOM6 (TRANSLOCASE OF THE OUTER MITOCH	0.03324	0.8648	0.5423	0.4047	0.0916	0.1527	0.3417	0.0832	0.1269	0.7132	0.0087	0.029
262403_s_at	AT2G14772,AT3G42730,A	[AT2G14772, transposable element gene];[AT3G42	0.4425	0.529	0.4328	0.9513	0.2129	0.2414	-2.2234	0.0258	0.0653	-1.7145	0.0559	0.0848
262404_at	AT1G49460	transposable element gene	0.08095	0.947	0.5639	2.0591	0.1462	0.1955	0.1923	0.8315	0.4732	2.1704	0.0624	0.0907
262405_at	AT1G49650	HDG10 (HOMEODOMAIN GLABROUS10); DNA bi	-0.7918	0.4241	0.3868	-0.3722	0.6974	0.4581	-0.04372	0.9422	0.5038	0.3759	0.5432	0.3422
262406_at	AT1G49670	AtMYB93 (myb domain protein 93); DNA binding / t	0.7024	0.5058	0.4231	-0.9563	0.3764	0.3303	-0.1118	0.8979	0.4917	-0.3658	0.6781	0.3899
262407_at	AT1G49630	similar to unknown protein [Arabidopsis thaliana] (T	0.1986	0.3529	0.3513	-0.2153	0.3184	0.3022	-0.4207	0.0902	0.1328	-0.8347	0.0116	0.0337
262408_at	AT1G49750	protein phosphatase 2C, putative / PP2C, putative	0.9167	0.0098	0.0636	1.0922	0.0053	0.0429	-0.2987	0.2062	0.2156	-0.1232	0.5677	0.3518
262409_at	AT1G49842	transposable element gene	0.1539	0.8527	0.5389	0.4492	0.5944	0.4212	0.6382	0.402	0.3174	0.9335	0.2426	0.2085
262410_at	AT1G34770	MAGE-B antigen-related	0.1861	0.3117	0.3297	-0.2593	0.1824	0.2215	0.4409	0.0519	0.0965	-0.00449	0.9791	0.4779
262411_at	AT1G34640	similar to Os07g0622900 [Oryza sativa (japonica cu	-0.1741	0.3116	0.3296	0.03133	0.8452	0.5031	0.9895	0.0028	0.0241	1.1949	0.0014	0.0133
262412_at	AT1G34660	GRF1-1 (general regulatory factor 11); amino acid b	0.6003	0.0182	0.0804	-0.6471	0.0075	0.0488	0.0678	0.595	0.3964	-0.08202	0.5057	0.328
262413_at	AT1G34780	ATAPRL4 (APR-LIKE 4)	0.08436	0.7264	0.5014	0.02298	0.9235	0.525	-1.0603	0.0092	0.0384	-1.1216	0.0075	0.027
262414_at	AT1G49430	LACS2 (LONG-CHAIN ACYL-COA SYNTHETASE	-0.9127	0.0777	0.1605	-0.805	0.1058	0.1642	0.3547	0.3481	0.2922	0.4623	0.2384	0.2062
262415_at	AT1G49400	EMB1210 (EMBRYO DEFECTIVE 1129); structural	-0.8681	0.5975	0.4587	0.07383	0.9583	0.4112	0.5683	0.6408	0.4015	0.0199	0.7927	7.00E-04	0.0106
262416_at	AT1G49390	oxidoreductase, 2OG-Fe(II) oxygenase family protein	-0.4446	0.6112	0.463	-0.07474	0.9307	0.5267	1.3065	0.106	0.1457	1.6763	0.0559	0.0847
262417_at	AT1G50170	ATSIRB; sirohydrochlorin ferrochelatase	-0.1176	0.1753	0.2451	-0.285	0.0163	0.0664	0.3616	0.0072	0.0343	0.1942	0.0532	0.0824
262418_at	AT1G50320	ATHX (THORESOXIN X); thiol-disulfide exchange	-0.3925	0.0156	0.0754	-0.4436	0.0103	0.0551	-0.1084	0.2827	0.2596	-0.1596	0.142	0.1495
262419_at	AT1G50380	prolyl oligopeptidase family protein	0.3935	0.2373	0.286	0.2491	0.4289	0.3549	-0.6211	0.0127	0.0447	-0.7654	0.0061	0.0242
262420_at	AT1G50300	TAF15 (TBP-ASSOCIATED FACTOR 15); RNA bin	0.2251	0.0752	0.1578	0.413	0.0118	0.0585	-0.1856	0.1202	0.1564	0.002338	0.9814	0.4783
262421_at	AT1G50290	unknown protein	-0.6767	0.087	0.1708	-0.533	0.1501	0.1981	-1.0377	0.004	0.0274	-0.894	0.0069	0.0259
262422_at	no_match	no_match	0.3458	0.0608	0.1415	0.4168	0.0356	0.093	0.3022

262490_at	AT1G21840	UREF (UREASE ACCESSORY PROTEIN F); nicke	0.2173	0.4421	0.3946	0.2886	0.321	0.3036	-0.7513	0.0421	0.0855	-0.68	0.056	0.0848
262491_at	AT1G21650	ATP binding	0.5095	0.4138	0.3819	0.6931	0.2829	0.2826	-1.2523	0.0171	0.0524	-1.0686	0.0285	0.0564
262492_at	AT1G21630	calcium-binding EF hand family protein	0.2892	0.0243	0.0908	0.1461	0.1495	0.1977	-0.05512	0.5385	0.3747	-0.1982	0.0731	0.0992
262493_at	AT1G21660	heat shock protein binding	-0.5677	0.0333	0.1056	-0.7858	0.0116	0.058	0.02362	0.8846	0.4881	-0.1945	0.272	0.2239
262494_at	AT1G21810	similar to myosin heavy chain-related [Arabidopsis t	0.1701	0.5794	0.4521	0.4217	0.2097	0.2393	0.7562	0.0525	0.0972	1.0077	0.022	0.0484
262495_at	AT1G21780	BTB/POZ domain-containing protein	0.5549	0.0227	0.0881	0.1471	0.3935	0.3384	-0.6764	0.0118	0.0429	-1.0842	0.0021	0.0156
262496_at	AT1G21790	similar to unnamed protein product [Vitis vinifera] (G	-0.9517	0.0553	0.1351	-0.927	0.0595	0.1212	-0.1419	0.4511	0.3391	-0.1172	0.5287	0.3374
262497_at	AT1G21720	PBC1 (20S proteasome beta subunit C1); peptidase	0.8264	5.00E-04	0.0325	0.7972	6.00E-04	0.0266	0.0996	0.2109	0.2183	0.07039	0.3521	0.2636
262498_at	AT1G21710	OGG1 (8-oxoguanine-DNA glycosylase 1)	0.1966	0.3278	0.3388	-0.04038	0.8303	0.4989	-0.638	0.0063	0.0328	-0.8749	0.002	0.0151
262499_at	AT1G21770	similar to unknown protein [Arabidopsis thaliana] (T	0.4675	0.0335	0.1059	0.7627	0.0066	0.0461	0.02297	0.8226	0.4704	0.3182	0.0295	0.0576
262500_at	AT1G21760	F-box family protein	0.02925	0.6587	0.4788	-0.00533	0.935	0.5278	0.005898	0.9281	0.5	-0.02868	0.6648	0.3857
262501_at	AT1G21690	EMB1968 (EMBRYO DEFECTIVE 1968); ATPase	-0.1958	0.1817	0.2494	0.07976	0.5467	0.4032	0.07721	0.559	0.3822	0.3528	0.0437	0.0731
262502_at	AT1G21620	PTAC6 (PLASTID TRANSCRIPTIONALLY ACTIVE	-0.2232	0.3987	0.3747	0.05308	0.8334	0.4998	-0.9398	0.0038	0.0269	-0.6635	0.0129	0.0361
262503_at	AT1G21670	similar to myosin protein [Arabidopsis thaliana] (T	0.06493	0.752	0.509	0.2533	0.2571	0.2684	-0.01904	0.9257	0.4994	0.1694	0.4272	0.2996
262504_at	AT1G21750	ATPDIL1-1 (PDI-LIKE 1-1); protein disulfide isomer	1.7094	0.0021	0.0406	1.6836	0.0022	0.0334	0.0188	0.8879	0.4891	-0.00696	0.9583	0.4731
262505_at	AT1G21680	similar to unknown protein [Arabidopsis thaliana] (T	0.3262	0.1544	0.2293	0.4199	0.087	0.1486	-0.4214	0.0862	0.1295	-0.3278	0.1529	0.1567
262506_at	AT1G21640	NADK2 (NAD KINASE 2); NAD+ kinase/ calmodulir	0.2313	0.1762	0.2456	0.5666	0.0159	0.0655	-0.1553	0.1248	0.1599	-0.9532	3.00E-04	0.0083
262507_at	AT1G21330	S-locus lectin protein kinase family protein	0.7753	0.0441	0.1212	0.6594	0.0692	0.1319	0.1046	0.666	0.4198	-0.01122	0.9626	0.4739
262508_at	AT1G21300	carbohydrate binding / kinase	0.7249	0.061	0.1417	0.6365	0.0857	0.1474	-0.08163	0.4633	0.3446	-0.17	0.1669	0.1654
262509_at	AT1G21290	pentatricopeptide (PPR) repeat-containing protein	-0.4375	0.0432	0.1199	-0.4167	0.0497	0.1105	-0.9393	0.0013	0.0191	-0.9185	0.0014	0.0135
262510_at	AT1G21270	F-box family protein	2.0746	0.0729	0.1555	1.9886	0.0813	0.1429	-0.675	0.4276	0.3287	-0.761	0.3764	0.274
262511_at	AT1G21250	SYP125 (syntaxin 125); SNAP receptor	0.2704	0.7964	0.6227	-0.09628	0.9265	0.6288	1.0476	0.2796	0.2578	0.6809	0.4623	0.311
262512_at	AT1G17145	protein binding / zinc ion binding	0.247	0.1091	0.1912	0.3169	0.0578	0.1195	-0.8873	0.0018	0.0206	-0.8174	0.0024	0.0164
262513_at	AT1G17170	exostosin family protein	0.4224	0.0932	0.1769	0.1661	0.4369	0.3583	0.332	0.1042	0.1443	0.07562	0.658	0.3835
262514_at	AT1G17180	ANAC017 (Arabidopsis NAC domain containing pro	0.5089	0.0158	0.0758	0.4315	0.0269	0.0821	0.006976	0.9523	0.5061	-0.07042	0.5554	0.3471
262515_at	AT1G17190	oxidoreductase family protein	0.06042	0.7193	0.4992	0.2004	0.27	0.2754	-0.1273	0.4359	0.3322	0.01261	0.9359	0.4673
262516_at	AT1G17200	ATGSTU26 (Arabidopsis thaliana Glutathione S-tra	-1.5181	0.019	0.0819	-0.6841	0.1616	0.2069	0.1184	0.6377	0.4104	0.9523	0.0149	0.0388
262517_at	AT1G17180	ATGSTU25 (Arabidopsis thaliana Glutathione S-tra	1.4258	0.3171	0.3327	0.01632	0.9902	0.5417	1.0294	0.4559	0.3412	-0.38	0.776	0.4217
262518_at	AT1G17170	ATGSTU24 (ARABIDOPSIS THALIANA GLUTATH	0.7482	0.4542	0.4	1.9138	0.1016	0.1608	1.3011	0.2233	0.2256	2.4666	0.0525	0.0816
262519_at	AT1G17160	pfkB-type carbohydrate kinase family protein	0.6764	0.0328	0.105	0.3629	0.1608	0.2064	0.4096	0.0309	0.0715	0.0961	0.4861	0.3201
262520_at	AT1G17150	glycoside hydrolase family 28 protein / polygalactur	0.915	0.401	0.3537	-1.3388	0.2785	0.2801	0.9921	0.4101	0.3207	1.2717	0.2998	0.2386
262521_at	AT1G17130	cell cycle control protein-related	-0.1383	0.2285	0.281	0.06611	0.5344	0.3981	0.4911	0.0073	0.0344	0.6955	0.002	0.0153
262522_at	AT1G17120	CAT8 (CATIONIC AMINO ACID TRANSPORTER 8	0.2214	0.3338	0.3422	0.1008	0.6433	0.4393	-0.6417	0.0334	0.0747	-0.7623	0.0194	0.0447
262523_at	AT1G17110	UBP15 (UBIQUITIN-SPECIFIC PROTEASE 15); ub	0.2109	0.1694	0.241	0.1579	0.2784	0.2801	0.01217	0.928	0.5	-0.04092	0.7616	0.4172
262524_at	AT1G17070	D111/G-patch domain-containing protein	0.4774	0.032	0.1037	0.088	0.5837	0.4177	0.04978	0.7151	0.4366	-0.3396	0.0556	0.0845
262525_at	AT1G17060	CYP72C1 (cytochrome P450, family 72, subfamily	0.277	0.7616	0.512	0.1066	0.9066	0.5206	0.1872	0.6691	0.4208	0.01676	0.9691	0.4753
262526_at	AT1G17050	SPS2 (SOLANESYL DIPHOSPHATE SYNTHASE 2	-0.8399	0.0156	0.0754	-1.1758	0.0048	0.0421	0.07735	0.6497	0.4144	-0.2585	0.1767	0.1712
262527_at	AT1G17010	oxidoreductase, 2OG-Fe(II) oxygenase family protei	-0.387	0.7629	0.5124	-0.2356	0.8537	0.5057	-0.7229	0.4559	0.3412	-0.5716	0.55	0.3451
262528_at	AT1G17260	AHA10 (AUTOINHIBITED H(+)-ATPASE ISOFORM	0.02243	0.9656	0.5686	-0.0148	0.9773	0.5386	-0.3557	0.5074	0.3624	-0.3929	0.4669	0.3126
262529_at	AT1G17250	leucine-rich repeat family protein	0.7906	0.0519	0.1307	0.2658	0.4091	0.3455	0.07333	0.7769	0.4563	-0.4515	0.1353	0.1452
262530_at	AT1G17240	leucine-rich repeat family protein	0.6535	0.1143	0.1959	1.0046	0.0364	0.0942	-0.02659	0.9386	0.503	0.3245	0.3739	0.273
262531_at	AT1G17230	protein binding / protein kinase	-0.3283	0.457	0.4015	0.000878	0.9984	0.5436	-0.3553	0.1306	0.1643	-0.02603	0.8961	0.4561
262532_at	AT1G17210	zinc ion binding	0.06639	0.5018	0.4213	-0.008542	0.929	0.5265	-0.06617	0.5031	0.3606	-0.124	0.2404	0.2073
262533_at	AT1G17090	unknown protein	0.419	0.3817	0.3655	0.7379	0.1588	0.2051	-0.07638	0.8653	0.4827	0.2425	0.5967	0.3624
262534_at	AT1G17040	transcription factor-related	0.0326	0.8842	0.5471	-0.1191	0.6012	0.424	-0.315	0.2082	0.2167	-0.4667	0.0905	0.1132
262535_at	AT1G17000	similar to Arabidopsis thaliana trehalose-phosphata	0.8921	0.633	0.4706	-1.0337	0.162	0.4169	-0.2579	0.8701	0.4841	-2.1833	0.2137	0.1928
262536_at	AT1G17100	SOUL heme-binding family protein	-0.5094	0.169	0.2406	-0.8525	0.0485	0.1094	0.1385	0.4084	0.3201	-0.2047	0.2444	0.2095
262537_s_at	AT1G17280;AT5G50430	[AT1G17280, UBC34 (UBIQUITIN-CONJUGATING	0.007418	0.9421	0.563	0.1787	0.1359	0.1876	0.01195	0.9069	0.4943	0.1832	0.1287	0.1407
262538_at	AT1G17220	tropomyosin-related	0.3383	0.0836	0.1673	0.3136	0.1007	0.16	0.3923	0.0565	0.1015	0.3675	0.0674	0.0947
262539_at	AT1G17200	integral membrane family protein	-0.5722	0.0044	0.0482	-0.4142	0.0138	0.0621	0.0542	0.6124	0.4019	0.2122	0.0982	0.1192
262540_at	AT1G34260	phosphatidylinositol-4-phosphate 5-kinase family pr	0.196	0.2824	0.3129	0.04418	0.7935	0.4872	-0.5295	0.0075	0.0351	-0.6813	0.003	0.0179
262541_at	AT1G34240	transposable element gene	1.1403	0.2252	0.2787	0.6415	0.4654	0.3701	-0.4913	0.4813	0.3517	-0.9901	0.1931	0.1809
262542_at	AT1G34180	ANAC016 (Arabidopsis NAC domain containing pro	2.963	8.00E-04	0.0346	2.9249	9.00E-04	0.0285	0.06088	0.6181	0.4039	0.02274	0.8501	0.4428
262543_at	AT1G34245	similar to EPF1 (EPIDERMAL PATTERNING FACT	-1.2015	0.0558	0.1356	-0.7234	0.1831	0.2219	-0.912	0.1049	0.1448	-0.4339	0.3765	0.274
262544_at	AT1G19420	similar to unnamed protein product [Vitis vinifera] (G	0.6974	0.0276	0.0964	0.1516	0.5025	0.3857	0.02379	0.8423	0.4754	-0.522	0.0096	0.0305
262545_at	no_match	no_match	-0.6874	0.3327	0.3417	-0.5464	0.4309	0.3557	-0.4121	0.3003	0.2689	-0.2711	0.4779	0.3169
262546_at	AT1G31260	ZIP10 (ZINC TRANSPORTER 10 PRECURSOR);	-0.225	0.6482	0.4759	-0.8935	0.1223	0.1775	-0.3442	0.4933	0.3569	-1.0127	0.091	0.1136
262547_at	AT1G31270	unknown protein	-0.3049	0.76	0.5117	1.528	0.1765	0.2173	-1.0461	0.3246	0.2806	0.7868	0.4462	0.3045
262548_at	AT1G31280	AGO2 (ARGONAUTE 2); nucleic acid binding	1.5961	0.0011	0.036	2.0479	4.00E-04	0.0251	-0.7403	0.0178	0.0534	-0.2884	0.2051	0.1879
262549_at	AT1G31290	PAZ domain-containing protein / piwi domain-conta	1.3787	0.0144	0.0731	1.4272	0.0128	0.0604	-0.6173	0.0793	0.1232	-0.5688	0.0973	0.1185
262550_at	AT1G31310	hydroxyproline-rich glycoprotein family protein	-0.1912	0.6759	0.4846	-0.4302	0.3684	0.3268	-0.3154	0.4295	0.3294	-0.5543	0.1976	0.1835
262551_at	no_match	no_match	-0.8302	0.0224	0.0875	0.2207	0.3905	0.337	0.5845	0.0552	0.1001	1.6353	0.0017	0.0145
262552_at	AT1G31350	F-box family protein	-0.2616	0.3509	0.3501	0.2468	0.3758	0.3301	-0.3064	0.0716	0.1163	0.202	0.1839	0.1758
262553_at	AT1G31360	RECQ2 (Arabidopsis RecQ helicase l2); ATP-depe	0.9805	0.0263	0.0937	0.4904	0.1603	0.2061	-0.3125	0.2511	0.2415	-0.8026	0.0262	0.0536
262554_at	AT1G31380	similar to meprin and TRAF homology domain-cont	0.007314	0.9944	0.5756	1.0417	0.3484	0.3173	0.8786	0.0942	0.1361	1.9129	0.0089	0.0295
262555_at	AT1G31400	meprin and TRAF homology domain-containing pro	-1.294	0.2938	0.3197	1.2014	0.3251	0.306	-0.5564	0.4794	0.3512	1.9389	0.0533	0.0825
262556_at	AT1G31370	similar to meprin and TRAF homology domain-cont	-1.9137	0.1761	0.2455	0.6093	0.6289	0.434	-1.8057	0.1964	0.2095	0.7172	0.5717	0.3531
262557_at	AT1G31330	PSAF (photosystem I subunit F)	-0.3487	0.0897	0.1735	-0.6232	0.0164	0.0665	0.2238	0.0562	0.1011	-0.05064	0.5793	0.3558
262558_at	AT1G31335	unknown protein	-0.5554	0.0189	0.0817	-0.5943	0.0151	0.0646	0.6942	0.0016	0.0204	0.6553	0.002	0.0153
262559_at	AT1G31340	similar to unknown protein [Arabidopsis thaliana] (T	-0.1668	0.193	0.2576	-0.3991	0.0201	0.0725	0.3113	0.0434	0.087	0.07896	0.5005	0.3261
262560_at	AT1G34280	unknown protein	0.5851	0.5402	0.4368	-1.2834	0.2162	0.2435	1.262	0.2226	0.2251	-0.6065	0.5262	0.3364
262561_at	AT1G34340	esterase/lipase/thioesterase family protein	0.2147	0.2642	0.302	0.1034	0.566	0.4104	-1.1636	0.0018	0.0206	-1.2749	0.0013	0.013
262562_at	AT1G34220	similar to unknown protein [Arabidopsis thaliana] (T	0.8664	0.0113	0.0665	0.5051	0.0606	0.1223	-0.1004	0.5282	0.3706	-0.4617	0.0338	0.0621
262563_at	AT1G34210	SERK2 (SOMATIC EMBRYOGENESIS RECEPTOI	0.1795	0.4977	0.4195	0.07632	0.7673	0.4796	-0.8307	0.0014	0.0197	-0.9339	9.00E-04	0.0118
262564_at	AT1G34330	pseudogene, putative peroxidase, similar to anionic	0.4602	0.3752	0.362	-0.4675	0.3685	0.3268	0.9622	0.0293	0.0695	0.03447	0.911	0.4602
262565_at	AT1G34320	similar to unknown protein [Arabidopsis thaliana] (T	0.1959	0.1516	0.2271	0.1146	0.3592	0.3225	-0.4117	0.007	0.034	-0.493	0.0036	0.0196
262566_at	AT1G34310	ARF12 (AUXIN RESPONSE FACTOR 12); transcri	-0.8533	0.067	0.1487	-1.5462	0.0106	0.0556	-0.2324	0.4611	0.3436	-0.9253	0.0316	0.0599
262567_at	AT1G34300	lectin protein kinase family protein	0.4272	0.0387	0.1134	0.6636	0.0092	0.0526	-0.5289	0.0099	0.0398	-0.2924	0.0633	0.0914
262568_at	AT1G34290	leucine-rich repeat family protein	-0.6346	0.5658	0.4472	-0.3286	0.7624	0.4782	0.2416	0.8236	0.4707	0.5476	0.6182	0.3697
262569_at	AT1G15180	MATE efflux family protein	-0.221	0.5234	0.4304	-0.3751	0.3016	0.2923	-1.0345	0.0121	0.0437	-1.1885	0.0075	0.0269
262570_at	AT1G15200	protein-protein interaction regulator family protein	0.2777	0.3086	0.3277	0.3293	0.2392	0.2572	-0.6589	0.0339	0.0752	-0.6074	0.0432	0.0726
262571_at	AT1G15430	similar to zinc ion binding [Arabidopsis thaliana] (TA	0.4599	0.1414	0.2186	0.5124	0.1113	0.1684	0.2083	0.2446	0.2378	0.2608	0.1632	0.1632
262572_at	AT1G15140	oxidoreductase NAD-binding domain-containing pro	-0.6538	0.0138	0.0719	-0.9406	0.0038	0.0389	0.4287	0.006	0.0321	0.142	0.1525	0.1565
262573_at	AT1G15390	PDF1A (PEPTIDE DEFORMYLASE 1A); peptide de	0.07739	0.6671	0.4817	0.05582	0.7549	0.4767	-0.4765	0.0462	0.0901	-0.4981	0.0406	0.0697
262574_at	AT1G15230	similar to unnamed protein product [Vitis vinifera] (G	0.6004	0.0253	0.0921	0.5005	0.0439	0.1037	0.3254	0.1233	0.1589	0.2255	0.2484	0.2115
262575_at	AT1G15210	ATPDR7/PDR7 (PLEIOTROPIC DRUG RESISTAN	0.05309	0.8768	0.5456	-0.1417	0.6822	0.4528	-0.03664	0.8581	0.4805	-0.2314	0.2951	0.2361
262576_at	AT1G15280	glycine-rich protein	-0.2138	0.3678	0.3583	0.205	0.3858	0.3346	-0.5034	0.0419	0.0852	-0.08459	0.646	0.3794
262577_at	AT1G15290	binding	-0.1411	0.3683	0.3586	-0.3025	0.0956	0.1558	-0.7473	0.0033	0.0255	-0.9087	0.0016	0.014
262578_at	AT1G15300	transposable element gene	0.7932	0.2673	0.3036	1.0804	0.1543	0.2014	-0.7543	0.0982	0.1395	-0.4671	0.2543	0.2148
262579_at	AT1G15320	similar to unnamed protein product [Vitis vinifera] (G	0.792	0.4588	0.4023	0.723	0.4962	0.3829	1.1601	0.2965	0.2669	1.0911	0.3223	0.2494
262580_at	AT1G15330	CBS domain-containing protein	-0.1449	0.7196	0.4992	0.02775	0.9447	0.5306	0.2842	0.4919	0.3564	0.4568	0.2912	0.2342
262581_at	AT1G15370	similar to unknown protein [Arabidopsis thaliana] (T	0.3479	3.00E-04	0.0312	0.4558	1.00E-04	0.0249	0.4902	1.00E-04	0.0101	0.5981	0	0.0053
262582_at	AT1G15410	aspartate-glutamate racemase family	-1.2211	0.0023	0.0414	-1.5492	9.00E-04	0.0286	0.06027	0.6045	0.3996	-0.2678	0.0672	0.0945
262583_at	AT1G15510	phosphatidyl serine synthase family protein	0.9732	0.0287	0.0981	0.7134	0.0702	0.1325	-0.2533	0.3714	0.3036	-0.5131	0.1113	0.1286
262584_at	AT1G15440	transducin family protein / WD-40 repeat family prot	0.596	0.0129	0.0699	0.4454	0.0331	0.09	-0.00307	0.9787	0.5123	-0.1537	0.228	0.2005
262585_at	AT1G15460	ATBOR4/BOR4; anion exchanger	-0.1754	0.8501	0.5382	-0.04308	0.9629	0.5347	-0.8301	0.3267	0.2817	-0.6979	0.401	0.2846
262586_at	AT1G15480	DNA binding	0.3451	0.4755	0.41	1.373	0.0352	0.0926	-0.2573	0.5891	0.3943	0.7706	0.1539	0.1574
262587_at	AT1G15490	hydrolase, alpha/beta fold family protein	-0.8927	0.0095	0.0626	-0.7362	0.0183	0.0698	-0.7506	0.0103	0.0403	-0.5941	0.0225	0.0487
262588_at	AT1G15130	hydroxyproline-rich glycoprotein family protein	1.0982	7.00E-04	0.0334	0.6833	0.0044	0.0409	0.4775	0.0046	0.0288	0.06253	0.4941	0.3237
262589_s_at	AT1G15150;AT1G15160	[AT1G15150, MATE efflux family protein];[AT1G151	0.4268	0.6882	0.4886	0.8947	0.4166	0.349	-1.1746	0.3005	0.269	-0.7067	0.5142	0.3313
262590_at	AT1G15100	RHA2A (RING-H2 finger A2A); protein binding / zin	-0.0198	0.9339	0.5608	0.08131	0.7351	0.4698	0.1801	0.4667	0.346	0.2812	0.2779	0.227
262591_at	AT1G15220	ATCCMH; oxidoreductase	-0.4173	0.2234	0.2772	-0.03165	0.9183	0.5237	-0.5203	0.0188	0.055	-0.1351	0.3781	0.2748
262592_at	AT1G15400	similar to unknown protein [Arabidopsis thaliana] (T	0.1107	0.5446	0.4389	0.0916	0.0919	0.153	-0.01609	0.8688	0.4839	0.2428	0.0565	0.0854
262593_at	AT1G15120	ubiquinol-cytochrome C reductase complex 7.8 kDa	0.3278	0.0653	0.1465	0.5926	0.0104	0.0552	0.5799	0.0112	0.0418	0.8446	0.0029	0.0175
262594_at	AT1G15250	60S ribosomal protein L37 (RPL37A)	0.5777	0.067	0.1487	0.4605	0.1174	0.1732	0.6299	0.0028	0.0244	0.5126	0.006	0.024
262595_at	AT1G15360	SHN1/WIN1 (SHINE1); DNA binding / transcription	0.6413	0.3154	0.3318	-0.5684	0.3669	0.3261	1.4642	0.0589	0.104	0.2546	0.6726	0.3883
262596_at	AT1G15080	ATPAP2 (PHOSPHATIDIC ACID PHOSPHATASE	0.9322	0.0875	0.1713	-0.5891	0.2278	0.2501	0.3783	0.4125	0.3218	-1.143	0.0508	0.0801
262597_at	AT1G15470	transducin family protein / WD-40 repeat family prot	0.09587	0.5167	0.428	0.2139	0.1882	0.2254	0.08328	0.5706	0.3869	0.2013	0.2101	0.1909
262598_at	AT1G15260	similar to unknown protein [Arabidopsis thaliana] (T	-0.1945	0.6472	0.4754	-0.4779	0.2698	0.2754	1.0658	0.0015	0.0199	0.7724	0.0049	0.0221
262599_at	AT1G15350	similar to unknown protein [Arabidopsis thaliana] (T	0.2344	0.1878	0.2539	0.09102	0.5712	0.4124	-0.4689	0.0171	0.0523	-0.6123	0.0068	0.0257
262600_at	AT1G15340	MBD10 (methyl-CpG-binding domain 10); DNA bin	-0.2691	0.2044	0.265	0.02617	0.89	0.5157	0.3798	0.0993	0.1404	0.675	0.0191	0.0443
262601_at	AT1G15240	ATHSP40A (Arabidopsis thaliana signal recognition	-0.2781	0.0993	0.1817	-0.3927	0.0392	0.0981	0.3518	0.0539	0.0987	0.2372	0.1423	0.1496
262602_at	AT1G15270	similar to unknown protein [Arabidopsis thaliana] (T	-0.2208	0.3763	0.3624	0.1308	0.5874	0.4187	0.6635	0.0404	0.0834	1.0151	0.0102	0.0316
262603_at	AT1G15380	lactoylglutathione lyase family protein / glyoxalase I	1.1185	0.1803	0.2483	0.9723	0.2315	0.2525	0.467	0.0321	0.073	0.3208	0.091	0.1136
262604_at	AT1G15060	similar to unknown protein [Arabidopsis thaliana] (T	-0.3889	0.2913	0.318	-0.6605	0.1081	0.1657	-0.6516	0.0771	0.1213	-0.9231	0.0285	0.0564
262605_at	AT1G15170	MATE efflux family protein	0.2365	0.4811	0.4125	-0.1113	0.7335	0.4693	-0.5308	0.1596	0.1834	-0.8786	0.0449	0.0743
262606_at	AT1G15190	Identical to Fasciclin-like arabinogalactan protein 15	0.2855	0.6637	0.4806	-0.0543	0.9333	0.5274	-0.02085	0.9743	0.5111	-0.3607	0.5856	0.3582
262607_at	AT1G13990	similar to unnamed protein product [Vitis vinifera] (G	1.7816	0.0161	0.0768	1.3822	0.0361	0.0938	0.5652	0.0336	0.0749	0.1659	0.4039	0.2857
262608_at	AT1G14120	2-oxoglutarate-dependent dioxygenase, putative	1.1843	0.3089	0.3279	0.4943	0.6523	0.4426	-0.1429	0.8951	0.4912	-0.8328	0.4588	0.3095
262609_at	AT1G19030	similar to nodulin-related [Arabidopsis thaliana] (TA	1.8016	0.024	0.0904	-0.4755	0.0284	0.0838	1.0088	0.0021	0.0214	1.0349	0.0019	0.0149
262610_at	AT1G14140	mitochondrial substrate carrier family protein	0.1926	0.1767	0.2459	0.09399	0.4689	0.3715	-0.5874	0.0066	0.0333	-0.6861	0.0037	0.0198
262611_at	AT1G14060	similar to unknown protein [Arabidopsis thaliana] (T	0.2432	0.1106	0.1928	0.5432	0.0103	0.0551	0.1952	0.0794	0.1232	0.4952	0.004	0.0204
262612_at	AT1G14150	oxygen evolving enhancer 3 (PsbQ) family protein	3.299	2.00E-04	0.0312	3.5254	1.00E-04	0.0249	0.6138	0.0043	0.0282	0.4183	0.0166	0.0411
262613_at	AT1G13960	WRKY4 (WRKY DNA-binding protein 4); transcripti	-0.02099	0.8584	0.5406	0.3665	0.0294	0.0852	-0.0701	0.5599	0.3826	0.3174	0.0452	0.0746
262614_at	AT1G13980	GN (GNOM)	0.9247	1.00E-04	0.0312	0.5908	8.00E-04	0.0277	-0.6444	3.00E-04	0.0141	-0.9783	1.00E-04	0.0058
262615_at	AT1G13870	initiation/elation factor	0.3074	0.4241	0.3868	0.2677	0.482	0.377	0.08384	0.5746	0.3883	0.04408	0.7643	0.4181
262616_at	AT1G06620	2-oxoglutarate-dependent dioxygenase, putative	0.8956	0.0153	0.0748	0.7531	0.0269	0.0819	0.2902	0.0362	0.0782	0.1477	0.1896	0.179
262617_at	AT1G06590	binding	1.5616	0.107	0.1893	-0.03614	0.9641	0.535	-1.0611	0.179	0.1978	-2.6588	0.0151	0.0391
262618_at	AT1G06560	NOL1/NOP2/sun family protein	0.3223	0.1153	0.1965	0.1203	0.2285	0.1676	-0.1403	0.0214	0.059	-0.4416	0.0224	0.0487
262619_at	AT1G06550	enoyl-CoA hydratase/isomerase family protein	-1.3858	0.0556	0.1354	-0.9857	0.1299	0.1828	-0.6967	0.004	0.0273	-0.2966	0.064	0.092
262620_at	AT1G06540	similar to unknown protein [Arabidopsis thaliana] (T	-0.5882	0.6678	0.4819	-0.9511	0.4962	0.3829	-0.2434	0.7545	0.4495	-0.6063	0.4511	0.3064
262621_at	AT1G06530	myosin heavy chain-related	0.3936	0.0283	0.0974	0.648	0.0052	0.0429	0.2279	0.1056	0.1454	0.4823	0.0116	0.0338
262622_at	AT1G06510	similar to unnamed protein product [Vitis vinifera] (G	0.2191	0.2295	0.2818	0.28	0.1446	0.1942	-0.1854	0.2968	0.2671	-0.1246	0.4657	0.3122
262623_at	AT1G06470	phosphate translocator-related	-0.1594	0.3177	0.3329

262690_at	AT1G62720	binding	0.3075	0.7168	0.4983	-0.07403	0.9298	0.5266	-0.07919	0.9249	0.4992	-0.4607	0.5909	0.3602
262691_at	AT1G62740	stress-inducible protein, putative	0.4973	0.0166	0.0775	0.3491	0.0496	0.1103	0.6204	0.0078	0.0354	0.4721	0.0197	0.045
262692_at	no_match	no_match	0.2979	0.7782	0.5174	-0.9905	0.3731	0.3291	0.6213	0.5638	0.3843	-0.6671	0.5368	0.3402
262693_at	AT1G62780	similar to hypothetical protein [Vitis vinifera] (GB:CA	-0.9848	0.0018	0.0391	-0.9851	0.0018	0.0327	0.112	0.3549	0.2957	0.1117	0.3559	0.2652
262694_at	AT1G62790	protease inhibitor/seed storage/lipid transfer protein	0.9204	0.0245	0.0911	1.1711	0.011	0.0563	0.5593	0.0334	0.0747	0.8101	0.01	0.0311
262695_at	AT1G75850	binding	0.5994	0.0033	0.0446	0.1796	0.1343	0.1862	-0.6924	0.0019	0.021	-1.1122	3.00E-04	0.0084
262696_at	AT1G75870	unknown protein	-0.7415	0.513	0.4263	0.8755	0.445	0.3618	-2.074	0.0317	0.0723	-0.4569	0.5147	0.3315
262697_at	AT1G75940	ATA27 (Arabidopsis thaliana anther 27); hydrolase,	1.5307	0.2245	0.2782	1.7308	0.1789	0.2189	-2.8973	0.0532	0.098	-2.6921	0.0651	0.0929
262698_at	AT1G75960	AMP-binding protein, putative	-0.8993	0.0233	0.0894	-0.507	0.1142	0.1707	-0.4438	0.0963	0.138	-0.05157	0.8137	0.4327
262699_at	AT1G75980	similar to unnamed protein product [Vitis vinifera] (G	0.3938	0.0441	0.1211	0.7516	0.0052	0.0429	0.2589	0.1241	0.1595	0.6167	0.0098	0.0309
262700_at	AT1G76020	similar to unknown protein [Arabidopsis thaliana] (T	-0.4217	0.0155	0.0751	-0.5039	0.0084	0.0507	-0.01893	0.8177	0.4692	-0.1011	0.259	0.2173
262701_at	AT1G76480	pseudogene of pentatricopeptide (PPR) repeat-cont	1.34	0.2118	0.2695	0.4548	0.6408	0.4384	-0.2859	0.7673	0.4533	-1.1712	0.2642	0.2199
262702_at	AT1G76520	protein phosphatase 2C family protein / PP2C famil	-1.0949	0.2774	0.3101	1.199	0.241	0.2585	-0.5943	0.5133	0.3644	1.6995	0.1098	0.1276
262703_at	AT1G76510	auxin-responsive family protein	1.9397	9.00E-04	0.0348	1.409	0.0029	0.0355	0.9911	0.0095	0.039	0.4604	0.096	0.1175
262704_at	AT1G76530	ASL9/LBD3 (LOB DOMAIN-CONTAINING PROTEI	0.8303	0.0246	0.0911	0.7574	0.0327	0.0896	0.49	0.0357	0.0776	0.4172	0.0569	0.0858
262705_at	AT1G76600	protein kinase family protein	0.5889	0.002	0.0399	0.4483	0.0055	0.0434	-0.2456	0.0286	0.0687	-0.3862	0.0062	0.0245
262706_at	AT1G76280	DEAD/DEAH box helicase, putative	0.3518	0.0259	0.0931	0.04448	0.6848	0.4538	-0.03517	0.4941	0.3448	-0.3425	0.0014	0.0135
262707_at	AT1G76290	similar to predicted protein [Physcomitrella patens s	0.6706	0.1845	0.2514	0.2936	0.5218	0.3929	-0.2074	0.6463	0.4131	-0.5844	0.2353	0.2046
262708_at	AT1G76190	DNA repair protein RAD23, putative	0.06732	0.7602	0.5117	-0.4581	0.0902	0.1515	-0.06221	0.7777	0.4565	-0.5876	0.0463	0.0757
262709_at	AT1G76240	SYP51 (SYNTAXIN OF PLANTS 51)	0.1858	0.3079	0.3274	0.07939	0.6441	0.4396	0.4215	0.0571	0.102	0.3151	0.1189	0.1339
262710_at	AT1G76210	similar to unknown [Picea sitchensis] (GB:ABK2252	0.6576	0.0319	0.1035	0.5383	0.0573	0.119	0.8037	0.0084	0.0368	0.6844	0.0146	0.0384
262711_at	AT1G76500	similar to unknown protein [Arabidopsis thaliana] (T	0.7242	0.0821	0.1657	0.4202	0.2513	0.2648	0.434	0.1496	0.1787	0.13	0.6221	0.3709
262712_at	AT1G76460	ATRDH2 (ARABIDOPSIS THALIANA RHODANESE	0.1522	0.2945	0.3201	0.1108	0.4298	0.3552	-0.2725	0.0744	0.1188	-0.3139	0.0507	0.0799
262713_at	AT1G76520	similar to unknown protein [Arabidopsis thaliana] (T	0.3668	0.1353	0.2135	-0.05827	0.7815	0.484	0.3808	0.1246	0.1598	-0.04427	0.8327	0.438
262714_s_at	AT1G07950/AT1G16430	[AT1G07950, surfeit locus protein 5 family protein /	0.1641	0.5262	0.4316	0.2938	0.2823	0.2822	0.6643	0.0485	0.0925	0.794	0.0284	0.0563
262715_at	AT1G76490	AMYB58 (myb domain protein 58); DNA binding / tr	-0.4846	0.4313	0.3898	-0.3119	0.6036	0.4247	-0.306	0.3805	0.308	-0.1333	0.69	0.3939
262716_at	AT1G76470	PAB1 (PROTEASOME SUBUNIT PAB1); peptidase	0.8683	0.0035	0.0451	0.8308	0.0041	0.0399	0.4125	0.0099	0.0396	0.3749	0.0137	0.0371
262717_s_at	AT1G16410/AT1G76400	[AT1G16410, CYP79F1 (SUPERSHOOT 1)];[AT1G	1.5092	0.008	0.0587	1.2619	0.0149	0.0643	0.4716	0.0848	0.1282	0.719	0.0255	0.0527
262718_at	AT1G43570	transposable element gene	0.2243	0.8522	0.5389	0.45	0.7106	0.4623	0.5534	0.343	0.2898	0.7791	0.2048	0.1878
262719_at	AT1G43590	transposable element gene	-0.08411	0.674	0.484	-0.03749	0.8498	0.5043	-0.0814	0.6837	0.4255	-0.03477	0.8605	0.446
262720_s_at	AT1G43610/AT1G43610	[AT1G43600, NLI interacting factor (NIF) family prot	0.2054	0.1449	0.2213	0.02813	0.9684	0.5362	0.8017	0.2956	0.2664	2.0353	0.0379	0.0667
262721_at	AT1G43560	ATY2 (Arabidopsis thioredoxin y2); thiol-disulfide ex	-0.58	0.0442	0.1212	-1.0401	0.0065	0.046	0.6319	0.0343	0.0757	0.1718	0.4389	0.301
262722_at	AT1G43620	UDP-glucose:sterol glucosyltransferase, putative /	0.4199	0.2579	0.2983	0.353	0.3301	0.3085	-0.1076	0.7526	0.449	-0.1746	0.6129	0.3677
262723_at	AT1G43630	similar to unknown protein [Arabidopsis thaliana] (T	0.5642	0.3497	0.4492	-0.9624	0.1447	0.1943	0.9971	0.1293	0.1635	-0.5295	0.3687	0.2707
262724_s_at	AT4G00540/AT1G43330	[AT4G00540, ATMYB3R2/MYB3R-2/PC-MYB2 (MY	-0.2512	0.6466	0.4752	0.01369	0.9798	0.5393	-0.413	0.0744	0.1188	-0.1481	0.4379	0.3005
262725_at	AT1G43580	similar to unnamed protein product [Vitis vinifera] (G	0.2072	0.2306	0.2823	0.144	0.3818	0.3328	-0.2839	0.0466	0.0905	-0.3471	0.0254	0.0526
262726_at	AT1G43640	ANTLER (RUBBER LIKE PROTEIN 5); phosphoric die	0.5867	0.0263	0.0937	0.08206	0.918	0.5236	-1.9299	0.0622	0.1072	0.7392	0.3812	0.2763
262727_at	AT1G75800	pathogenesis-related thaumatin family protein	-0.1352	0.7025	0.4934	0.00576	0.9869	0.5408	-1.0647	2.00E-04	0.0126	-0.9237	3.00E-04	0.0086
262728_at	AT1G75820	CLV1 (CLAVATA 1); ATP binding / kinase/ protein k	-0.4726	0.0351	0.1083	-0.8265	0.0054	0.0432	-0.02221	0.8761	0.4856	-0.3761	0.0482	0.0775
262729_at	ATGPI7RCP4	(RHO-GTP BINDING PROT	-0.3989	0.213	0.2703	-0.05156	0.8576	0.5066	-0.07782	0.6528	0.4155	0.2695	0.1681	0.1661
262730_at	AT1G76390	ATOCT3 (ARABIDOPSIS THALIANA ORGANIC CA	0.2583	0.0034	0.0447	-3.0045	0.0017	0.0321	1.3557	0.0021	0.0218	0.8595	0.0111	0.0329
262731_at	AT1G76420	ATMC8 (METACASPASE 8); caspase	0.9323	0.094	0.1775	0.9377	0.0927	0.1537	0.2606	0.5075	0.3624	0.2659	0.4994	0.3257
262732_at	AT1G76440	protein kinase, putative	0.037715	0.9601	0.5674	-1.2801	0.1404	0.1909	-0.8188	0.3057	0.2715	-2.1361	0.0376	0.0663
262733_s_at	AT1G28660/AT1G28670	[AT1G28660, lipase, putative];[AT1G28670, ARAB	0.369	0.0603	0.1405	-0.06049	0.6923	0.4563	0.505	0.0147	0.0484	0.07553	0.5721	0.3532
262734_at	AT1G28640	GDSL-motif lipase, putative	-1.2089	0.1877	0.2539	2.2621	0.0412	0.1008	-1.6697	0.0935	0.1356	1.8013	0.0773	0.1027
262735_at	AT1G28630	similar to unknown protein [Arabidopsis thaliana] (T	-0.5177	0.6889	0.4887	1.4706	0.2882	0.2856	-1.3286	0.0247	0.0637	-0.6597	0.1566	0.159
262736_at	AT1G28570	GDSL-motif lipase, putative	-0.1311	0.3895	0.3696	-0.325	0.0751	0.1374	0.3542	0.0597	0.1049	0.1603	0.3037	0.2405
262737_at	AT1G28560	SRD2 (SHOOT REDIFFERENTIATION DEFECTIV	-0.9551	0.1293	0.2079	-0.8549	0.1631	0.2081	-0.624	0.0166	0.0514	-0.5239	0.0291	0.0571
262738_at	AT1G28530	similar to unknown protein [Arabidopsis thaliana] (T	0.01908	0.8366	0.5343	0.2011	0.0811	0.1428	-0.1102	0.2725	0.2538	0.07184	0.4538	0.3075
262739_at	AT1G28650	lipase, putative	-1.4768	0.1655	0.2378	-1.7992	0.1079	0.1656	0.02142	0.9816	0.5132	-0.3011	0.7471	0.4128
262740_at	AT1G28590	lipase, putative	0.6026	0.4527	0.3994	0.2239	0.7729	0.4815	1.787	0.0694	0.1141	1.4083	0.1241	0.1377
262741_at	AT1G28760	similar to unknown protein [Arabidopsis thaliana] (T	0.184	0.2335	0.2839	0.07133	0.6157	0.429	0.1281	0.3843	0.3098	0.0154	0.9123	0.4606
262742_at	AT1G28550	ATRABA1i (Arabidopsis Rab GTPase homolog A1i);	0.4236	0.7356	0.5042	-0.3124	0.8026	0.4903	1.5709	0.1519	0.1802	0.8349	0.4007	0.2845
262743_at	AT1G29020	calcium-binding EF hand family protein	-0.6627	0.5486	0.4405	-1.5308	0.2052	0.2362	1.1547	0.2352	0.2323	0.2866	0.7465	0.4125
262744_at	AT1G28680	transferase family protein	0.1809	0.2591	0.2992	-0.05444	0.7127	0.463	0.09836	0.5144	0.3647	-0.137	0.3761	0.2739
262745_at	AT1G28600	lipase, putative	-0.2714	0.4378	0.3928	-0.5484	0.1568	0.2034	0.2913	0.122	0.1579	0.01428	0.9282	0.4651
262746_at	AT1G28960	ATNUDT15 (ARABIDOPSIS THALIANA NUDIX HY	0.2644	0.0395	0.1147	0.1867	0.1007	0.16	-0.4396	0.0075	0.0349	-0.5174	0.0042	0.0207
262747_at	AT1G28540	similar to Os06g0624500 [Oryza sativa (japonica cu	0.2764	0.2682	0.3043	0.5837	0.0533	0.1146	0.8242	0.0075	0.0349	1.1315	0.0024	0.0161
262748_at	AT1G28610	GDSL-motif lipase, putative	-0.6947	0.0784	0.1613	-0.7892	0.0557	0.1173	-0.7639	0.0352	0.0769	-0.8583	0.0245	0.0515
262749_at	AT1G28580	GDSL-motif lipase, putative	1.0194	0.0016	0.0383	0.8927	0.0026	0.0341	-0.5844	0.0072	0.0343	-0.7112	0.0036	0.0194
262750_at	AT1G28710	similar to unknown protein [Arabidopsis thaliana] (T	-0.8849	0.3035	0.325	-0.3741	0.6442	0.4396	-1.1248	0.2081	0.2167	-0.6139	0.4591	0.3096
262751_at	AT1G16310	cation efflux family protein	-0.8356	0.0568	0.1366	-1.013	0.0324	0.0891	0.7161	0.0853	0.1287	0.5387	0.1623	0.1626
262752_at	AT1G16330	CYCB3;1 (CYCLIN B3;1); cyclin-dependent protein	-0.1665	0.589	0.4559	-0.00042	0.9989	0.5437	-0.4398	0.1763	0.1961	-0.2737	0.3651	0.2691
262753_at	AT1G16340	ATKDSA2/ATKDSA; 3-deoxy-8-phosphooctulonate	0.2268	0.2855	0.3146	-0.132	0.5132	0.3899	-0.03522	0.8318	0.4732	-0.394	0.0643	0.0922
262754_at	AT1G16350	inosine-5'-monophosphate dehydrogenase, putative	0.2871	0.019	0.0819	-0.05746	0.4889	0.3799	0.1387	0.14	0.1712	-0.2059	0.0526	0.0818
262755_at	AT1G16360	LEM3 (ligand-effect modulator 3) family protein / CD	1.8724	0.0335	0.1059	-2.6471	0.0108	0.056	2.0829	0.024	0.0629	-2.4366	0.0144	0.0381
262756_at	AT1G16370	ATOCT6; carbohydrate transmembrane transporter	-1.4832	0.0387	0.1134	-1.5245	0.0356	0.0931	0.3319	0.0783	0.1223	0.2905	0.1086	0.1266
262757_at	AT1G16380	ATCHX1 (CATION/H+ EXCHANGER 1); monovalen	-0.769	0.4434	0.3951	-0.1611	0.8674	0.5092	-1.6752	0.1378	0.1695	-1.0673	0.3036	0.2405
262758_at	AT1G16780	F-box family protein	-0.6118	0.2769	0.3099	0.1384	0.7901	0.4861	-1.28	0.0231	0.0615	-0.5298	0.2123	0.192
262759_at	AT1G16800	similar to hypothetical protein MtDRAFT_AC160515	0.06766	0.8971	0.5504	0.3104	0.5618	0.409	0.6538	0.254	0.2432	0.8965	0.142	0.1495
262760_at	AT1G10770	invertase/pectin methylesterase inhibitor family prot	-2.1444	0.1469	0.2229	-0.9201	0.4839	0.3776	-1.8147	0.2031	0.2137	-0.5904	0.6468	0.3797
262761_at	AT1G10720	BSD domain-containing protein	0.1622	0.3356	0.3431	0.07371	0.6453	0.4401	0.2735	0.139	0.1705	0.185	0.2803	0.2284
262762_at	AT1G10700	ribose-phosphate pyrophosphokinase 3 / phosphori	-0.029	0.833	0.5333	0.4981	0.0181	0.0694	-0.4748	0.0211	0.0584	0.0523	0.7057	0.3995
262763_at	AT1G28690	pentatricopeptide (PPR) repeat-containing protein	-2.4465	0.0378	0.1121	-1.3595	0.1648	0.2089	-1.4471	0.0356	0.0775	-0.3601	0.4813	0.3181
262764_at	AT1G13140	CYP86C3 (cytochrome P450, family 86, subfamily C	-0.8915	0.1144	0.196	0.5731	0.2653	0.2728	-0.7297	0.0888	0.1315	0.735	0.0872	0.1106
262765_at	AT1G13150	CYP86C4 (cytochrome P450, family 86, subfamily C	-1.5815	0.2398	0.2875	-0.6025	0.627	0.4334	-0.3603	0.623	0.4057	0.6187	0.4128	0.2895
262766_at	AT1G13160	SDA1 family protein	0.4145	0.1245	0.2043	0.3899	0.1422	0.1923	-0.4723	0.0565	0.1016	-0.4968	0.049	0.0784
262767_at	AT1G13170	oxysterol-binding family protein	-0.3122	0.2911	0.3179	-0.3384	0.2581	0.269	-0.1796	0.5229	0.3681	-0.2059	0.4678	0.3129
262768_at	AT1G12990	glycosyl transferase family 17 protein	0.1338	0.6395	0.4728	0.3323	0.2773	0.2794	-0.7472	0.0027	0.0238	-0.5487	0.0083	0.0282
262769_at	AT1G13180	DIS1 (DISTORTED TRICHOMES 1); structural com	0.7588	0.0766	0.1593	0.686	0.0985	0.1582	-0.1199	0.1919	0.2067	-0.1927	0.0654	0.0931
262770_at	AT1G13190	RNA recognition motif (RRM)-containing protein	0.4041	0.0474	0.1253	0.6719	0.0093	0.0527	-0.6682	0.0079	0.0358	-0.4003	0.042	0.0713
262771_at	AT1G13200	F-box family protein	-0.3331	0.6822	0.4866	-0.7537	0.375	0.3299	1.738	0.0756	0.1197	1.3174	0.145	0.1516
262772_at	AT1G13210	ACA1, (AUTOINHIBITED CA2+/ATPASE II); ATPas	0.7104	0.0258	0.093	0.637	0.0361	0.0939	-0.5058	0.028	0.0681	-0.5791	0.0181	0.0432
262773_at	AT1G13220	LINC2 (LITTLE NUCLEI2); protein binding	0.3182	0.6103	0.463	0.2572	0.6785	0.4514	-1.2575	0.0946	0.1365	-1.3185	0.0841	0.1083
262774_at	AT1G13230	leucine-rich repeat family protein	1.1384	0.2826	0.313	1.1465	0.2797	0.2808	0.2597	0.7912	0.4606	0.2677	0.785	0.4243
262775_at	AT1G13000	similar to unknown protein [Arabidopsis thaliana] (T	0.4161	0.0642	0.1452	0.3803	0.0813	0.1429	-0.183	0.2299	0.2294	-0.2187	0.1659	0.1648
262776_at	AT1G13020	initiation factor, putative (EIF4B5)	-0.2233	0.3602	0.3547	-0.5695	0.058	0.1197	0.4901	0.0861	0.1294	0.144	0.5421	0.3417
262777_at	AT1G13030	sphere organelles protein-related	0.2824	0.2903	0.3175	0.1186	0.636	0.4369	-0.2481	0.204	0.2142	-0.4118	0.0655	0.0932
262778_at	AT1G13050	similar to unknown protein [Arabidopsis thaliana] (T	0.06741	0.8703	0.5441	-0.1139	0.7834	0.4844	-0.2002	0.3566	0.2964	-0.3815	0.1182	0.1336
262779_at	AT1G13070	putative cytochrome P450	0.4513	0.5972	0.4586	-0.6369	0.4639	0.3697	0.4049	0.592	0.3953	-0.6833	0.3818	0.2765
262780_at	AT1G13090	CYP71B28 (cytochrome P450, family 71, subfamily	0.8985	0.002	0.04	0.5617	0.0111	0.0566	-0.07407	0.3253	0.281	-0.4109	0.0034	0.019
262781_s_at	AT3G26340/AT1G13060	[AT3G26340, 20S proteasome beta subunit E, puta	0.7052	7.00E-04	0.0334	0.7141	7.00E-04	0.0271	0.3735	0.0077	0.0354	0.3823	0.0071	0.0263
262782_at	AT1G13195	zinc finger (C3HC4-type RING finger) family protein	0.3428	0.007	0.0564	0.5273	0.0014	0.0313	0.06371	0.3975	0.3154	0.2482	0.0211	0.0471
262783_at	AT1G10850	ATP binding / protein serine/threonine kinase	-0.6798	0.0852	0.1691	-1.0201	0.0269	0.0821	-0.2246	0.494	0.3572	-0.5648	0.1316	0.1427
262784_at	AT1G10760	SEX1 (STARCH EXCESS 1)	0.1316	0.4748	0.4096	0.07133	0.6912	0.4559	-1.1311	0.0019	0.0207	-1.1913	0.0015	0.0139
262785_at	AT1G10750	similar to unknown protein [Arabidopsis thaliana] (T	-0.4527	0.6204	0.4666	-1.7785	0.103	0.1619	1.6902	0.0904	0.1329	0.3644	0.6568	0.3831
262786_at	AT1G10740	similar to unknown protein [Arabidopsis thaliana] (T	-0.6383	0.0157	0.0755	-0.8181	0.0066	0.0461	-0.3398	0.075	0.1193	-0.5196	0.0216	0.0479
262787_at	AT1G10730	clathrin adaptor complexes medium subunit family p	0.4767	0.1853	0.2522	0.428	0.2246	0.2483	-0.05996	0.8338	0.4737	-0.1086	0.7058	0.3995
262788_at	AT1G10690	similar to unknown protein [Arabidopsis thaliana] (T	1.0089	0.0434	0.12	0.9635	0.0495	0.1103	0.07325	0.5073	0.3623	0.02787	0.7957	0.4275
262789_at	AT1G10810	aldo/keto reductase family protein	0.1966	0.8662	0.5425	1.0957	0.3735	0.3292	0.9924	0.3677	0.3018	1.8916	0.1252	0.1384
262790_at	AT1G10840	initiationinitiation factor	0.256	0.3128	0.3302	0.2943	0.2553	0.2675	-0.3488	0.0732	0.1178	-0.3105	0.0981	0.1191
262791_at	AT1G10830	sodium symporter-related	-0.2341	0.1525	0.2277	-0.1891	0.2274	0.2498	-0.00606	0.9658	0.5089	0.03899	0.7836	0.424
262792_at	AT1G10710	similar to unknown protein [Arabidopsis thaliana] (T	0.4627	0.634	0.4709	0.528	0.5886	0.4189	-0.0996	0.9171	0.497	-0.03435	0.9714	0.4759
262793_at	AT1G13110	CYP71B7 (cytochrome P450, family 71, subfamily B	-0.1766	0.401	0.3758	-0.3108	0.1739	0.2154	0.3344	0.043	0.0865	0.2002	0.1547	0.1579
262794_at	AT1G13120	EMB1745 (EMBRYO DEFECTIVE 1745)	0.5591	0.0014	0.038	0.2868	0.0159	0.0655	-0.08958	0.2326	0.2309	-0.3619	0.0047	0.0217
262795_at	AT1G13130	glycosyl hydrolase family 9 (cellulase family); cellulase family	-0.802	0.587	0.4552	-1.3062	0.3911	0.3372	0.1063	0.9414	0.5037	-0.3979	0.7844	0.4242
262796_at	AT1G20850	XCP2 (XYLEM CYSTEINE PEPTIDASE 2); cysteine	-0.2805	0.385	0.3673	-0.4157	0.2222	0.2471	0.3271	0.1564	0.1833	0.192	0.3644	0.2688
262797_at	AT1G20840	TMT1 (TONOPLAST MONOSACCHARIDE TRANS	0.5347	0.1641	0.2369	0.376	0.2976	0.2904	-0.1239	0.2137	0.2202	-0.2826	0.0281	0.056
262798_at	AT1G20980	SPL14 (SQUAMOSA PROMOTER BINDING PROT	0.4333	0.0052	0.0513	0.5832	0.0017	0.0321	-0.277	0.024	0.0628	-0.1271	0.1795	0.173
262799_at	no_match	no_match	-0.8005	0.4492	0.3977	-0.4641	0.6525	0.4426	0.694	0.4467	0.3369	1.0304	0.2789	0.2276
262800_at	AT1G20960	EMB1507 (EMBRYO DEFECTIVE 1507); ATP-dep	0.522	0.0354	0.1085	0.2361	0.2304	0.2517	-0.7359	7.00E-04	0.0159	-1.0218	2.00E-04	0.0075
262801_at	AT1G21010	similar to unknown protein [Arabidopsis thaliana] (T	-0.5254	0.0728	0.1554	-0.00798	0.9724	0.5372	0.0533	0.5755	0.3886	0.5707	0.0029	0.0175
262802_at	AT1G20930	CDKB2;2 (CYCLIN-DEPENDENT KINASE B2;2); k	0.7633	0.0718	0.1545	0.5249	0.1698	0.2124	-0.4064	0.0858	0.1292	-0.6448	0.0228	0.0491
262803_at	AT1G21000	zinc-binding family protein	-0.05622	0.8282	0.5319	0.06626	0.7984	0.4891	0.0283	0.0789	0.1228	0.4078	0.0285	0.0564
262804_at	AT1G20880	RNA recognition motif (RRM)-containing protein	0.185	0.3337	0.3422	0.3793	0.0875	0.1489	-0.2867	0.164	0.1878	-0.09233	0.6128	0.3677
262805_at	AT1G20900	ESC (ESCAROLA)	-1.6637	0.016	0.0765	-0.5353	0.2667	0.2736	-0.9089	0.0938	0.1358	0.2195	0.6249	0.3719
262806_at	AT1G20960	pyrophosphate--fructose-6-phosphate 1-phosphotra	-0.6095	0.0524	0.1313	-0.8141	0.0218	0.0748	-0.1723	0.2664	0.2499	-0.3779	0.0482	0.0775
262807_at	AT1G11740	ankyrin repeat family protein	-1.0086	0.114	0.1956	-0.02264	0.9661	0.5355	0.87	0.157	0.1837	1.8559	0.0207	0.0465
262808_at	AT1G11730	galactosyltransferase family protein	1.813	0.0664	0.148	0.6565	0.4157	0.3487	-0.05182	0.9433	0.5041	-1.2083	0.1525	0.1565
262809_at	AT1G11720	ATS53 (STARCH SYNTHASE 3); starch synthase/	-0.05209	0.798	0.5233	-0.4029	0.1019	0.161	-0.9611	0.0035	0.026	-1.3419	0.0011	0.0123
262810_at	AT1G11710	pentatricopeptide (PPR) repeat-containing protein	-0.4091	0.5446	0.4389	0.54	0.432	0.3562	-1.8646	0.0394	0.0821	-0.9156	0.2129	0.1923
262811_at	AT1G11700	similar to unknown protein [Arabidopsis thaliana] (T	-0.6001	0.0772	0.1598	-0.7033	0.0502	0.1111	0.4971	0.0201	0.0571	0.3938	0.0414	0.0706
262812_at	AT1G11690	similar to unknown protein [Arabidopsis thaliana] (T	-0.05681	0.9709	0.5702	-0.08745	0.9552	0.5331	-0.6832	0.6646	0.4193	-0.7138	0.6509	0.3811
262813_at	AT1G11670	MATE efflux family protein	-0.8995	0.0822	0.1658	-1.1927	0.0376	0.096	0.489	0.0345	0.076	0.1958	0.2756	0.2259
262814_at	AT1G11660	heat shock protein, putative	0.5389	0.0443	0.1214	0.6331	0.0272	0.0825	-0.2393	0.268	0.251	-0.145	0.4794	0.3173
262815_at	AT1G11610	CYP71A1 (cytochrome P450, family 71, subfamily	0.2682	0.0145	0.0731	-0.712	0.2822	0.2823	2.2221	0.0079	0.0358	-0.2581	0.676	0.3894
262816_at	AT1G11780	oxidoreductase, 2OG-Fe(II) oxygenase family prote	0.1159	0.4553	0.4006	-0.2732	0.1233	0.1782	-0.06452	0.6037	0.3995	-0.4537	0.0167	0.0413
262817_at	AT1G11770	electron carrier	0.2516	0.8541	0.5392	0.3962	0.7734	0.4817	0.1807	0.8507	0.4787	0.3242	0.7368	0.4093
262818_at	AT1G11755	transferase	0.4046	0.0224	0.0875	0.3922	0.0249	0.079	-0.4858	0.0122	0.044	-0.4982	0.0112	0.0332
262819_at	AT1G11600	CYP77B1 (cytochrome P450, family 77, subfamily E	-0.2738	0.6447	0.4747	0.7511	0.2438	0.2605	-0.1658	0.778	0.4566	0.859	0.1933	0.181
262820_at	AT1G11680	CYP51G1 (CYTOCHROME P450 51); oxygen bind	0.1354	0.3536	0.3515	-0.09527	0.5015	0.3853	0.2595	0.6673	0.1123	0.02888	0.7952	0.4275
262821_at	AT1G11800	endonuclease/exonuclease/phosphatase family pro	-0.6369	0.0452	0.1225	-0.2477	0.2673	0.274	-0.11	0.6443	0.3771	0.188	0.3213	0.2489
262822_at	AT1G11630	pentatricopeptide (PPR) repeat-containing protein	-0.1956	0.2848	0.3141	0.2784	0.1539	0

262890_at	AT1G14850	NUP155 (Nucleoporin 155).	0.5838	0.0899	0.1736	0.07887	0.7785	0.4832	0.003412	0.9886	0.515	-0.5015	0.0886	0.1117
262891_at	AT1G79460	GA2 (GA REQUIRING 2); ent-kaurene synthase	0.5358	0.1003	0.1829	0.6807	0.5538	0.1152	-0.6503	0.0611	0.1062	-0.5054	0.115	0.1313
262892_at	AT1G79440	ALDH5F1 (SUCCINIC SEMIALDEHYDE DEHYDR	-0.05256	0.9323	0.5604	0.4489	0.4829	0.3773	-0.6241	0.1325	0.1657	-0.1226	0.73	0.4072
262893_at	AT1G59790	cullin-related	-0.7302	0.187	0.2534	-0.7139	0.195	0.2294	0.2554	0.6077	0.4006	0.2717	0.5858	0.3583
262894_at	AT1G59780	disease resistance protein (CC-NBS-LRR class), pu	0.5089	0.5768	0.4513	-0.07346	0.9344	0.5278	-0.4732	0.6027	0.3992	-1.0556	0.2766	0.2264
262895_at	AT1G59800	cullin-related	-1.1698	0.2256	0.2789	-0.8387	0.3628	0.3242	-0.2339	0.2888	0.263	0.09714	0.6386	0.3767
262896_at	AT1G59820	haloacid dehalogenase-like hydrolase family protein	0.3226	0.0815	0.1651	0.3745	0.0547	0.1161	-0.7347	0.0062	0.0327	-0.6827	0.008	0.0279
262897_at	AT1G59840	similar to unnamed protein product [Vitis vinifera] (G	-1.0572	0.0028	0.0431	-0.6049	0.0198	0.0721	-0.4812	0.0404	0.0834	-0.02892	0.8662	0.4472
262898_at	AT1G59850	binding	-0.3958	0.7696	0.5144	-2.1483	0.1641	0.2085	0.6039	0.6574	0.417	-1.1485	0.4145	0.2901
262899_at	AT1G59870	PDR8/PEN3 (PLEIOTROPIC DRUG RESISTANCE	0.4702	0.134	0.2124	0.4447	0.1508	0.1988	-0.4106	0.0517	0.0963	-0.4361	0.0435	0.0729
262900_at	AT1G59890	paired amphipathic helix repeat-containing protein	0.573	0.0121	0.0684	0.1074	0.4605	0.3681	-0.2755	0.1046	0.1446	-0.7411	0.0049	0.022
262901_at	AT1G59910	formin homology 2 domain-containing protein / FH2	-0.3664	0.2674	0.3037	-0.475	0.1705	0.2129	-0.00695	0.9577	0.5071	-0.1156	0.4013	0.2847
262902_x_at	AT1G59930	similar to unknown protein [Arabidopsis thaliana] (T	-0.9323	0.0414	0.1172	-0.8314	0.0574	0.1191	1.099	6.00E-04	0.0156	1.1999	4.00E-04	0.0089
262903_at	AT1G59950	aldo/keto reductase, putative	-0.7595	0.6203	0.4666	-0.6672	0.6623	0.4458	-0.2296	0.8791	0.4864	-0.1373	0.9275	0.4649
262904_at	AT1G59725	DNAJ heat shock protein, putative	-1.6977	0.1244	0.2043	-1.0957	0.2788	0.2803	-1.252	0.1801	0.1987	-0.65	0.4471	0.3049
262905_at	AT1G59730	ATH7 (thioredoxin H-type 7); thiol-disulfide exchang	1.9471	0.0121	0.0683	0.3407	0.4886	0.3799	0.6523	0.0528	0.0974	-0.954	0.0164	0.0408
262906_at	AT1G59760	ATP-dependent RNA helicase, putative	0.3109	0.3525	0.3511	0.5	0.1663	0.2099	-0.5368	0.0641	0.1092	-0.3477	0.1754	0.1704
262907_at	AT1G59720	pentatricopeptide (PPR) repeat-containing protein	-0.2742	0.4511	0.3986	-0.2852	0.4345	0.3573	-0.8236	0.0664	0.1115	-0.8346	0.0641	0.0921
262908_at	AT1G59900	AT-E1 ALPHA (pyruvate dehydrogenase complex E	0.5829	0.0065	0.0547	0.2798	0.0665	0.1291	-0.131	0.3062	0.2718	-0.4341	0.0178	0.0427
262909_at	AT1G59830	PP2A-1 protein phosphatase 2A-2); protein serine/	0.3511	0.1086	0.1909	0.16	0.4011	0.3417	-0.02908	0.8729	0.4849	-0.2201	0.2664	0.2221
262910_at	AT1G59710	similar to unknown protein [Arabidopsis thaliana] (T	0.197	0.5467	0.4396	0.024	0.94	0.5291	0.401	0.0627	0.1076	0.228	0.2192	0.1957
262911_s_at	AT1G59860 /// AT1G07400	[AT1G59860, 17.6 kDa class I heat shock protein (h	0.3208	0.6756	0.4846	2.1225	0.0407	0.1	0.1131	0.87	0.4841	1.9148	0.0418	0.0711
262912_at	AT1G59740	proton-dependent oligopeptide transport (POT) fam	-0.2915	0.1757	0.2452	-0.1136	0.5568	0.4071	-0.09113	0.6345	0.4093	0.08677	0.6504	0.3809
262913_at	AT1G59960	aldo/keto reductase, putative	-0.06205	0.6565	0.4779	0.2193	0.1653	0.2091	-0.6326	0.0081	0.0362	-0.3512	0.0533	0.0825
262914_at	AT1G59750	ARF1 (AUXIN RESPONSE FACTOR 1); transcription	0.2188	0.0385	0.1131	-0.2572	0.0234	0.077	-0.3716	0.0067	0.0336	-0.8477	3.00E-04	0.0083
262915_at	AT1G59940	ARR3 (RESPONSE REGULATOR 3); transcription	0.1099	0.9203	0.5571	-1.0051	0.3851	0.3342	-0.7813	0.4911	0.3561	-1.8962	0.1399	0.1481
262916_at	AT1G59700	ATGSTU16 (Arabidopsis thaliana Glutathione S-tra	-0.2974	0.2466	0.2916	-0.2487	0.3203	0.3033	0.09626	0.414	0.3226	0.145	0.2421	0.2083
262917_at	AT1G64880	unknown protein	0.1665	0.8278	0.5318	1.463	0.1109	0.1681	-0.2787	0.7173	0.4374	1.0178	0.2288	0.2009
262918_at	AT1G65000	similar to unknown protein [Arabidopsis thaliana] (T	-0.213	0.5323	0.4338	0.6365	0.1109	0.1681	0.5848	0.0605	0.1056	1.4342	0.0031	0.0182
262919_at	AT1G79380	copine-related	0.5118	0.0335	0.1059	0.08113	0.6408	0.4384	-0.1972	0.0262	0.0658	-0.6279	4.00E-04	0.0089
262920_at	AT1G79520	Arb3a1 (Arabidopsis thaliana KDO-8-phosphate sy	0.702	0.0204	0.0842	-0.6979	0.0208	0.0737	-0.04295	0.7924	0.4608	-0.03888	0.8115	0.4322
262921_at	AT1G79430	APL (ALTERED PHLOEM DEVELOPMENT); transc	-0.4043	0.1062	0.1885	-0.00901	0.9653	0.5353	0.1288	0.5441	0.377	0.2665	0.2425	0.2085
262922_at	AT1G79420	similar to unknown protein [Arabidopsis thaliana] (T	0.3395	0.4587	0.4023	0.2096	0.6397	0.4382	0.3354	0.4638	0.3448	0.2055	0.6461	0.3794
262923_at	AT1G79660	XRN3 (5'-3' exoribonuclease 3); 5'-3' exoribonuclea	0.1398	0.2859	0.2188	0.3986	0.0251	0.0793	-0.9579	0.0011	0.0181	-0.7008	0.0035	0.0193
262924_s_at	AT1G19910/ AVA-P2 (vacuolar-H+-pumping ATPa	[AT1G19910, AVA-P2 (vacuolar-H+-pumping ATPa	0.01222	0.9433	0.5632	-0.03904	0.8208	0.4961	-0.5574	0.0032	0.0253	-0.6086	0.0023	0.0161
262925_at	AT1G65730	YSL7 (YELLOW STRIPE LIKE 7); oligopeptide tran	0.5247	0.5002	0.4206	-0.1382	0.8549	0.5059	0.509	0.4752	0.3496	-0.1539	0.8236	0.4352
262926_s_at	AT1G65800, ARG2 (Arabidopsis Receptor Kinase	[AT1G65800, ARG2 (Arabidopsis Receptor Kinase	0.1135	0.0086	0.0549	1.2232	0.0064	0.0457	-0.5023	0.0019	0.0207	-0.4928	0.002	0.0152
262927_at	AT1G65810	RNA-splicing endonuclease positive effector-relate	0.06534	0.9388	0.562	0.9486	0.3014	0.2921	-0.8113	0.3679	0.3019	0.07199	0.9326	0.4664
262928_at	AT1G65760	F-box family protein	1.2008	0.2319	0.2831	-0.4877	0.5981	0.4226	0.2501	0.7441	0.4462	-1.4383	0.1146	0.1311
262929_at	AT1G65720	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.08593	0.2554	0.2966	-0.07179	0.33	0.3085	-0.2482	0.0033	0.0254	-0.4059	5.00E-04	0.0096
262930_at	AT1G65690	harpin-induced protein-related / HIN1-related / harp	1.3837	0.0063	0.0545	2.0458	0.0015	0.0314	0.1735	0.097	0.1385	0.8357	5.00E-04	0.0094
262931_at	AT1G65700	small nuclear ribonucleoprotein, putative / snRNP, p	0.3177	0.1011	0.184	0.1675	0.3259	0.3065	0.9769	0.0029	0.0244	0.8267	0.0053	0.0226
262932_at	AT1G65660	microsomal glutathione s-transferase, putative	0.6589	0.0194	0.0824	0.8152	0.01	0.0543	0.7345	0.0072	0.0343	0.8807	0.0038	0.0199
262933_at	AT1G65840	ATPAO4 (POLYAMINE OXIDASE 4); amine oxidase	-0.266	0.4542	0.4	-0.2887	0.4198	0.3505	-0.00944	0.9758	0.5115	-0.03205	0.918	0.4621
262934_s_at	AT1G16270/ AT1G79570	[AT1G16270, protein kinase family protein]/[AT1G7	0.5821	0.0503	0.129	0.485	0.0821	0.1438	-0.2963	0.2313	0.2301	-0.3933	0.1345	0.1447
262935_at	AT1G79410	ATOCT5 (ARABIDOPSIS THALIANA ORGANIC CA	-0.5048	0.087	0.1708	-0.768	0.0265	0.0813	0.3509	0.1492	0.1784	0.08773	0.6789	0.3902
262936_at	AT1G79400	ATCHX2 (CATION/H+ EXCHANGER 2); monovalen	1.3463	0.2183	0.274	-0.2669	0.7867	0.4851	-0.6638	0.4277	0.3288	-2.2769	0.039	0.0679
262937_at	AT1G79560	EMB1047/FTSH12 (EMBRYO DEFECTIVE 1047);	0.3103	0.1756	0.2452	0.01444	0.9427	0.5299	-0.1462	0.0744	0.1188	-0.4421	0.0019	0.015
262938_at	AT1G79540	pentatricopeptide (PPR) repeat-containing protein	1.7788	0.0706	0.1532	0.7978	0.3338	0.3102	-0.9174	0.2753	0.2554	-1.8984	0.0592	0.0878
262939_s_at	AT1G79530/ AT1G16300	[AT1G79530, GAPCP-1; glyceraldehyde-3-phospha	0.4365	0.1997	0.2621	0.86	0.0391	0.098	-0.586	0.1085	0.1474	-0.1625	0.5984	0.3629
262940_at	AT1G79520	cation efflux family protein	0.3691	0.253	0.2953	0.1278	0.6681	0.4478	-0.5267	0.051	0.0956	-0.768	0.0159	0.0401
262941_at	AT1G79500	EMB2217 (EMBRYO DEFECTIVE 2217)	0.4679	0.1725	0.2443	0.5876	0.1056	0.1641	-0.4999	0.0802	0.1239	-0.3802	0.1509	0.1553
262942_at	AT1G79450	LEM3 (ligand-effect modulator 3) family protein / C2	2.1219	0.1851	0.2519	2.8087	0.1017	0.1609	0.4711	0.5448	0.3773	1.1579	0.1796	0.173
262943_at	AT1G79470	inosine-5'-monophosphate dehydrogenase	0.7598	4.00E-04	0.032	0.9492	1.00E-04	0.0249	-0.2778	0.0147	0.0484	-0.08833	0.2613	0.2185
262944_at	AT1G79550	PGK (PHOSPHOGLYCERATE KINASE);	0.3438	0.0576	0.1375	0.3661	0.0482	0.109	0.3943	0.0292	0.0694	0.4067	0.0245	0.0514
262945_at	AT1G79510	similar to unknown protein [Arabidopsis thaliana] (T	-0.7027	0.0059	0.0534	0.8938	0.0024	0.0339	0.3695	0.0483	0.0924	0.1784	0.2465	0.2105
262946_at	AT1G79390	similar to unknown [Populus trichocarpa] (GB:ABK9	0.08251	0.4661	0.4056	0.3086	0.0396	0.0985	0.1655	0.0784	0.1224	0.3916	0.0051	0.0224
262947_at	AT1G79750	GASA1 (GAST1 PROTEIN HOMOLOG 1)	-0.2392	0.3929	0.3716	0.01297	0.9611	0.5343	0.4805	0.0031	0.0251	0.7327	6.00E-04	0.0103
262948_at	AT1G75560	zinc knuckle (CCHC-type) family protein	0.02117	0.8505	0.5383	0.1907	0.1445	0.1942	-0.1007	0.3932	0.3134	0.06881	0.5492	0.3448
262949_at	AT1G75790	SKS18 (SKU5 Similar 18); copper ion binding / pect	-0.3365	0.7694	0.5144	-0.5178	0.6545	0.4432	0.2487	0.8097	0.4665	0.06736	0.9478	0.4703
262950_at	AT1G75510	initiation factor IIF beta subunit (TFIIF-beta) family p	0.7354	0.0079	0.0585	0.9522	0.0031	0.0362	0.04056	0.7858	0.459	0.2574	0.1389	0.1475
262951_at	AT1G75500	nodulin MtN21 family protein	0.2629	0.2385	0.2866	-0.0437	0.8293	0.4986	-0.0454	0.8228	0.4705	-0.352	0.1374	0.1465
262952_at	AT1G75770	unknown protein	0.02872	0.9176	0.5564	0.2424	0.4051	0.3436	-0.8975	9.00E-04	0.0169	-0.6838	0.0025	0.0165
262953_at	AT1G75670	DNA-directed RNA polymerase/ RNA binding	0.924	0.0112	0.0663	0.8414	0.0154	0.0649	0.1389	0.3414	0.2889	0.05631	0.6844	0.3921
262954_at	AT1G54500	rubredoxin family protein	-0.2223	0.0512	0.1301	-0.5502	0.0024	0.0339	0.1618	0.0662	0.1113	-0.1661	0.0617	09
262955_at	AT1G54520	similar to unknown [Populus trichocarpa x Populus	-0.01741	0.9295	0.5598	-0.1576	0.4416	0.3602	0.08041	0.6255	0.4064	-0.05981	0.7146	0.4024
262956_at	AT1G54270	initiation factor 4A-2); ATP-dependent helicase	0.2795	0.2784	0.3104	-0.00855	0.9713	0.537	-0.1011	0.3454	0.2909	-0.3892	0.0147	0.0386
262957_s_at	AT1G54250, AT3G59600	[AT1G54250, ATPRABC16.5 (ARABIDOPSIS THA	0.3003	0.2185	0.2741	0.4627	0.0879	0.1494	0.9414	0.0063	0.0328	1.1038	0.0035	0.0193
262958_at	AT1G54410	dehydrin family protein	-0.4328	0.1121	0.194	0.2069	0.3864	0.3349	0.7837	0.0212	0.0587	1.4234	0.0026	0.0169
262959_at	AT1G54290	initiation factor SUI1, putative	-0.3961	0.1138	0.1955	-0.2869	0.2177	0.2443	0.781	0.0048	0.0292	0.8901	0.0029	0.0176
262960_at	AT1G54320	LEM3 (ligand-effect modulator 3) family protein / C2	0.5682	0.0032	0.0442	0.3918	0.012	0.0588	0.4389	0.0023	0.0224	0.2625	0.0143	0.038
262961_at	AT1G54490	AIN1 (ACC INSENSITIVE 1); 5'-3' exonuclease/ nu	-0.04645	0.8087	0.5264	0.2093	0.3087	0.2967	-0.2547	0.2089	0.2171	0.001084	0.9952	0.4815
262962_at	AT1G54340	ICDH; isocitrate dehydrogenase (NADP+)	0.3861	0.0928	0.1765	0.4876	0.05	0.1109	-0.1385	0.3604	0.2983	-0.03707	0.7961	0.4276
262963_at	AT1G54220	dihydrolipoamide S-acetyltransferase, putative	-0.1598	0.3986	0.3747	-0.5085	0.0398	0.0989	0.1763	0.1071	0.1465	-0.1723	0.113	0.1298
262964_at	AT1G54380	spliceosome protein-related	0.07749	0.7227	0.5003	0.04256	0.8445	0.5028	-0.3245	0.007	0.0339	-0.3594	0.0048	0.0219
262965_at	AT1G54310	RNA binding	-0.3687	0.2923	0.3186	-0.6527	0.0985	0.1582	-0.9797	0.0126	0.0446	-1.2638	0.0051	0.0225
262966_at	AT1G75760	ER lumen protein retaining receptor family protein	0.4426	0.0706	0.1532	0.279	0.1976	0.2314	0.07143	0.6928	0.4286	-0.09216	0.6127	0.3677
262967_at	AT1G75730	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.3882	0.1086	0.1909	0.3432	0.1429	0.1929	-0.03155	0.8753	0.4854	-0.07653	0.7056	0.3995
262968_at	AT1G75720	similar to unknown protein [Arabidopsis thaliana] (T	0.09092	0.8212	0.53	-0.478	0.2735	0.2773	1.039	0.0128	0.0451	0.47	0.1249	0.1382
262969_at	AT1G75710	zinc finger (C2H2 type) family protein	0.06708	0.8126	0.5275	-0.1378	0.6304	0.4346	0.3886	0.1077	0.1469	0.1837	0.384	0.2776
262970_at	AT1G75690	chaperone protein dnaJ-related	-0.9112	1.00E-04	0.0312	-1.2506	0	0.0249	0.6152	7.00E-04	0.0159	0.2758	0.0127	0.0356
262971_at	AT1G75640	F-box family protein	0.5768	0.2509	0.3237	-0.3257	0.491	0.3807	0.5578	0.2443	0.2489	-0.3447	0.4678	0.3129
262972_at	AT1G75620	glyoxal oxidase-related	0.02473	0.9767	0.5714	-0.9582	0.2951	0.2893	1.2392	0.1526	0.1806	0.2563	0.7338	0.4083
262973_at	AT1G75600	histone H3.2, putative	0.7412	0.6567	0.4779	-1.3455	0.4332	0.3569	-0.5724	0.73	0.4418	-2.6591	0.1606	0.1616
262974_at	AT1G75550	glycine-rich protein	-0.9565	0.2896	0.317	-0.04185	0.96	0.5341	-0.9714	0.2831	0.2599	-0.05682	0.9457	0.4698
262975_at	AT1G75540	STH2 (SALT TOLERANCE HOMOLOG2); transcrip	0.232	0.2981	0.3222	0.09204	0.6602	0.4451	0.3976	0.11	0.1484	0.2576	0.2553	0.2153
262976_at	AT1G75520	SRS5 (SHI-RELATED SEQUENCE 5)	-0.4899	0.6224	0.4674	-1.1672	0.2731	0.2771	-0.1972	0.8086	0.4662	-0.8745	0.3151	0.246
262977_at	AT1G75490	DNA binding / transcription factor	-0.05745	0.8021	0.5247	-0.1067	0.6449	0.4399	-0.1889	0.2167	0.2216	-0.2382	0.1384	0.1472
262978_at	AT1G75780	TUB1 (tubulin beta-1 chain); structural molecule	-0.06878	0.8584	0.5406	-0.06228	0.8716	0.5104	0.1334	0.592	0.3953	0.1399	0.5748	0.3541
262979_s_at	AT1G13370,AT1G75600/A	[AT1G13370, histone H3, putative]/[AT1G75600, hi	-1.9829	0.2325	0.2833	2.3462	0.1716	0.2139	-1	0.4927	0.3567	3.3291	0.066	0.0936
262980_at	AT1G75680	ATGH9B7 (ARABIDOPSIS THALIANA GLYCOSYL	0.09055	0.0111	0.066	-0.776	0.0187	0.0706	0.1808	0.3161	0.2763	0.3103	0.1208	0.1356
262981_at	AT1G75590	auxin-responsive family protein	-0.6477	0.4299	0.389	3.0266	0.0149	0.0643	-1.3642	0.1384	0.17	2.3101	0.0352	0.0635
262982_at	AT1G54390	PHD finger protein-related	0.1601	0.3214	0.3352	-0.2732	0.1258	0.1799	0.1155	0.4063	0.3191	-0.3177	0.0633	0.0914
262983_at	AT1G54550	F-box family protein	0.5494	0.6465	0.4752	-1.1653	0.353	0.3196	0.7522	0.5351	0.3733	-0.9625	0.4347	0.2989
262984_at	AT1G54460	similar to WD1 (WVD2-LIKE 1) [Arabidopsis thalia	0.01614	0.8963	0.5503	0.3823	0.0303	0.0864	0.4224	0.0221	0.06	0.7886	0.0025	0.0164
262985_s_at	AT1G23290	RPL27A (RIBOSOMAL PROTEIN L27A); structural	-0.1752	0.0837	0.1674	0.09003	0.3042	0.2938	0.2381	0.028	0.0681	0.5033	0.0021	0.0154
262986_at	AT1G23390	kelch repeat-containing F-box family protein	-0.1814	0.4246	0.387	0.07237	0.741	0.4716	-0.1135	0.153	0.1808	0.1403	0.0949	0.1167
262987_at	AT1G23240	calcesin-related family protein	0.1093	0.825	0.531	0.2061	0.6794	0.4517	-0.53	0.3164	0.2764	-0.4332	0.4026	0.2853
262988_at	AT1G23310	GGT1 (ALANINE-2-OXOGLUTARATE AMINOTRA	-0.1488	0.1799	0.2479	-0.3447	0.0198	0.072	-0.3774	0.0032	0.0251	-0.5733	6.00E-04	0.0105
262989_at	AT1G23420	IMD (INNER NO OUTER); transcription factor	1.1858	0.1345	0.213	-1.4272	0.0696	0.1322	1.8907	0.0311	0.0717	-0.6223	0.3437	0.2597
262990_at	AT1G23260	MMZ1/UEV1A (MMS ZWEI HOMOLOGE 1); protein	0.1439	0.1818	0.2495	0.2293	0.6618	0.1236	0.8514	7.00E-04	0.0159	0.9368	5.00E-04	0.0093
262991_at	no_match	no_match	1.1048	0.3307	0.3403	-0.02148	0.9823	0.5397	0.4705	0.6318	0.4084	-0.5558	0.5736	0.3537
262992_at	AT1G54210	ATG12 (AUTOPHAGY 12); protein binding	0.2862	0.0616	0.1425	0.4284	0.0192	0.0697	0.1787	0.183	0.2009	0.3208	0.0447	0.0741
262993_at	AT1G54230	DNA binding	-0.07531	0.9166	0.556	-0.377	0.6064	0.4257	0.3379	0.643	0.4121	0.03623	0.9598	0.4733
262994_at	AT1G54420	unknown protein	2.5772	0.0281	0.097	0.006562	0.9936	0.5426	1.0227	0.2522	0.2421	-1.5479	0.113	0.1298
262995_s_at	AT3G50420, AT1G54430	[AT3G50420, transposable element gene]:[AT1G54	-0.1325	0.9253	0.5584	-1.7965	0.2473	0.2622	1.6907	0.4568	0.3417	-0.5718	0.6888	0.3934
262996_at	AT1G54440	3'-5' exonuclease/ nucleic acid binding	1.0274	0.0066	0.0549	0.7655	0.0181	0.0694	-0.4461	0.0874	0.1305	-0.7081	0.0233	0.0498
262997_at	AT1G54470	RPP27 (RESISTANCE TO PERONOSPORA PARA	-0.5429	0.3633	0.356	-0.8539	0.1822	0.2214	0.4895	0.3635	0.2998	0.1786	0.7276	0.4064
262998_at	AT1G54280	haloacid dehalogenase-like hydrolase family protein	0.7697	0.5512	0.4417	-0.7836	0.5444	0.4024	0.622	0.4172	0.3239	-0.9314	0.2473	0.211
262999_at	AT1G54330	ANAC020 (Arabidopsis NAC domain containing pro	1.8238	0.0983	0.181	-0.6316	0.4984	0.3839	0.4354	0.5152	0.3651	-2.0199	0.0297	0.0579
263000_at	AT1G54350	ABC transporter family protein	-0.8177	0.0019	0.0391	-1.0616	7.00E-04	0.027	-0.5071	0.0066	0.0333	-0.751	0.0015	0.0139
263001_at	AT1G54360	initiation factor	0.6826	0.002	0.0399	0.3479	0.0217	0.0746	-0.2882	0.039	0.0816	-0.6228	0.0028	0.0174
263002_at	AT1G54200	similar to unknown protein [Arabidopsis thaliana] (T	-0.02579	0.8718	0.5444	-0.2564	0.1625	0.2077	0.4022	0.0286	0.0687	0.1715	0.2264	0.1996
263003_at	AT1G54450	calcium-binding EF-hand family protein	0.5845	0.2408	0.2881	-0.722	0.1643	0.2086	0.08385	0.8531	0.4793	-1.2226	0.0451	0.0744
263004_at	AT1G54510	ATNEK1; kinase	1.0792	0.1231	0.2034	1.0996	0.118	0.1736	-1.1446	0.1075	0.1468	-1.1242	0.1121	0.1291
263005_at	AT1G54540	similar to harpin-induced protein-related / HIN1-rela	0.875	0.2507	0.2939	-0.7887	0.2929	0.2881	1.5056	0.0821	0.1257	-0.1581	0.8203	0.4342
263006_at	AT1G54240	DNA binding	0.9074	0.0333	0.1056	-0.01521	0.9599	0.5341	-0.1631	0.5871	0.3934	-1.0905	0.0186	0.0438
263007_at	AT1G54260	histone H1/H5 family protein	-0.04837	0.8527	0.5389	0.4487	0.14	0.1906	-0.8886	0.022	0.0598	-0.3916	0.1841	0.1758
263008_at	AT1G54470	RPP27 (RESISTANCE TO PERONOSPORA PARA	-0.4841	0.7802	0.5179	-1.0961	0.5362	0.399	0.6276	0.696	0.4298	0.01567	0.9921	0.4806
263009_at	AT1G54370	ATNHX5/NHX5 (NA+/H+ ANTIPORTER 5); sodium	0.6746	0.0271	0.0866	0.0414	0.1011	0.0963	0.004	0.0274	1.0842	0.0029	0.0116	
263010_at	AT1G23330	similar to unknown protein [Arabidopsis thaliana] (T	-0.07832	0.4152	0.3824	-0.1282	0.2113	0.2406	-0.1195	0.1385	0.17	-0.1694	0.0589	0.0876
263011_at	AT1G23250	calcesin-related	-2.8859	0.0027	0.0426	-0.1433	0.7591	0.4778	-3.0923	2.00E-04	0.0126	-0.3498	0.211	0.1913
263012_at	no_match	no_match	1.8346	0.1633	0.2365	1.9895	0.138	0.1892	0.1268	0.9073	0.4945	0.2817	0.7965	0.4278
263013_at	AT1G23380	KNAT6 (Knotted-like Arabidopsis thaliana 6); DNA	2.7507	0.0343	0.1071	-0.1584	0.8646	0.5085	0.3	0.748	0.4476	-2.6091	0.0402	0.0692
263014_at	AT1G23400	ATCAF2/CAF2 (ARABIDOPSIS THALIANA HOMOL	-0.3511	0.0517	0.1306	-0.511	0.0162	0.0663	0.03856	0.7778	0.4565	-0.1213	0.3962	0.2827
263015_at	AT1G23440	pyrrolidone-carboxylate peptidase family protein	0.4516	0.0948	0.1778	1.043	0.0073	0.0482	-0.00703	0.9475	0.505	0.5843	0.0043	0.0209
263016_at	AT1G23410	ubiquitin extension protein, putative / 40S ribosoma	-0.3571	0.247	0.2917	-0.5451	0.1075	0.1653	0.217	0.4566	0.3416	0.029	0.9177	0.462
263017_at	AT1G71620	CYCB2;1 (CYCLIN B2;1); cyclin-dependent protein	0.1483	0.8677	0.5432	0.4669	0.6059	0.4255	-0.04822	0.9567	0.507	0.2704	0.7623	0.4175
263018_at	AT1G71610	transposable element gene	0.4873	0.6648	0.4809	-1.6011	0.1997	0.2327	0.9921	0.3955	0.3146	-0.1217	0.9128	0.4607
263019_at	AT1G23870	ATTPS9 (Arabidopsis thaliana trehalose-phosphata	-0.1634	0.5492	0.4407	0.3194	0.2706	0.2758	-0.35	0.1615	0.1864	0.1327	0.5512	0.3455
263020_at	AT1G23880	NHL repeat-containing protein	-0.4555	0.1232	0.2035	-0.7362	0.0346	0.0918	0.306	0.2607	0.247	0.02526	0.9192	0.4625
263021_at	AT1G23910	similar to Bet v I allergen family protein [Arabidopsis	0.3735	0.8252	0.531	-1.3226	0.4508	0

263090_at	AT2G16190	similar to hydroxyproline-rich glycoprotein family pro	2.3424	0.0313	0.1027	0.608	0.4461	0.3622	1.7178	0.0756	0.1197	-0.01656	0.9828	0.4787
263091_at	AT2G16200	protein binding / protein transporter/ structural mole	0.6127	0.6547	0.4775	-2.8759	0.0863	0.148	0.868	0.4748	0.3495	-2.6206	0.0761	0.1016
263092_at	AT2G16210	transcriptional factor B3 family protein	-0.1193	0.9338	0.5608	0.7498	0.6077	0.4262	-0.7876	0.5905	0.3949	0.08157	0.9547	0.4722
263093_at	AT2G16010	transposable element gene	0.08596	0.9378	0.5617	-0.3923	0.7239	0.4667	-0.7299	0.5195	0.3668	-1.2081	0.3078	0.2423
263094_at	AT2G16020	unknown protein	-1.3461	0.2388	0.287	-0.9059	0.4047	0.3434	-0.2009	0.8466	0.4776	0.2393	0.8179	0.4337
263095_at	AT2G16040	hAT dimerisation domain-containing protein / transp	0.3368	0.6002	0.4598	-0.8185	0.2394	0.2573	0.4355	0.2649	0.2492	-0.7199	0.0989	0.1198
263096_at	AT2G16060	AHB1 (ARABIDOPSIS HEMOGLOBIN 1)	1.5718	0.0069	0.056	1.4002	0.0104	0.0552	0.8966	0.0084	0.0367	0.725	0.0173	0.0421
263097_at	AT2G16070	PDV2 (PLASTID DIVISION2)	0.06381	0.6238	0.4678	0.1162	0.3888	0.3363	0.3199	0.0303	0.0708	0.3723	0.0187	0.0438
263098_at	AT2G16005	MD-2-related lipid recognition domain-containing pr	0.5572	0.7052	0.4944	-0.9897	0.5102	0.3887	0.1766	0.9037	0.4933	-1.3702	0.374	0.273
263099_at	AT2G05200	transposable element gene	0.636	0.1411	0.2183	-0.199	0.5974	0.4223	0.1173	0.7526	0.449	-0.7177	0.1077	0.1259
263100_at	AT2G05210	ATPOT1A (PROTECTION OF TELOMERES 1A); te	-0.00621	0.9843	0.5731	-0.2423	0.4583	0.3674	-1.0204	0.0117	0.0429	-1.2565	0.0056	0.0234
263101_s_at	AT2G05250;AT2G05230	[AT2G05250, DNAJ heat shock N-terminal domain-	0.313	0.0795	0.1626	0.3569	0.056	0.1176	-0.3716	0.0213	0.0587	-0.3276	0.0317	0.06
263102_at	AT2G05270	unknown protein	0.238	0.8396	0.5353	2.174	0.1197	0.1751	-0.7615	0.5275	0.3702	1.1745	0.3465	0.2609
263103_at	AT2G05290	transposable element gene	-0.8349	0.186	0.2528	-0.4381	0.4497	0.3638	0.4528	0.4358	0.3322	0.8495	0.18	0.1733
263104_at	AT2G05120	transporter	0.5584	0.0056	0.0521	0.585	0.0047	0.0418	-0.3046	0.0322	0.073	-0.2779	0.0423	0.0717
263105_at	AT2G05320	beta-1,2-N-acetylglucosaminyltransferase II	0.7881	0.0373	0.1114	1.0178	0.0166	0.0669	-0.5344	0.1058	0.1455	-0.3047	0.3008	0.239
263106_at	AT2G05100	zinc finger (CCCH-type) family protein / RNA recogn	-0.7796	0.1603	0.2337	-0.8155	0.1461	0.1955	-1.0056	0.0582	0.1032	-1.0415	0.0528	0.0819
263107_at	AT2G05180	CYP705A6 (cytochrome P450, family 705, subfami	-0.3757	0.3657	0.3572	-0.6418	0.1566	0.2032	0.3016	0.4591	0.3427	0.03548	0.9279	0.465
263108_at	AT2G65240	aspartyl protease family protein	0.1021	0.7309	0.5027	-0.1185	0.6907	0.4558	0.09104	0.7588	0.4509	-0.1296	0.6641	0.3855
263109_at	AT2G65260	DC1 domain-containing protein	0.4525	0.713	0.4972	-0.0224	0.8868	0.5407	1.0722	0.313	0.2749	0.5995	0.5542	0.3466
263110_at	AT2G65220	eIF4-gamma/eIF5/eIF2-epsilon domain-containing p	0.08078	0.18	0.248	0.234	0.0093	0.0528	0.143	0.0453	0.0891	0.2962	0.004	0.0203
263111_s_at	AT1G65190;AT1G65250	[AT1G65190, protein kinase family protein];[AT1G6	0.4382	0.0845	0.1454	-0.4473	0.061	0.1227	-0.2552	0.0211	0.0584	-0.2643	0.0188	0.044
263112_at	AT1G03080	kinase interacting family protein	-0.152	0.5094	0.4246	0.2268	0.341	0.314	-0.9074	0.0085	0.037	-0.5287	0.0485	0.0778
263113_at	AT1G03150	GCN5-related N-acetyltransferase (GNAT) family pr	0.4069	0.0532	0.1323	0.2289	0.2013	0.2335	0.07141	0.6585	0.4174	-0.1066	0.516	0.332
263114_at	AT1G03130	PSAD-2 (photosystem I subunit D-2)	0.5183	0.0301	0.1007	-0.5508	0.0249	0.0791	0.1869	0.0039	0.0273	0.1544	0.0078	0.0276
263115_at	AT1G03055	similar to unknown protein [Arabidopsis thaliana] (T	-1.1748	0.002	0.0399	-1.0679	0.0029	0.0354	0.03372	0.8469	0.4777	0.1406	0.4388	0.3009
263116_s_at	AT1G54590;AT1G03140	[AT1G54590, splicing factor Prp18 family protein];[A	0.6631	0.048	0.1261	0.8408	0.0234	0.077	0.06164	0.8035	0.4646	0.2393	0.3604	0.2672
263117_at	AT1G03040	basic helix-loop-helix (bHLH) family protein	0.3139	0.1636	0.2366	0.4541	0.0693	0.132	-0.05041	0.5858	0.3929	0.08974	0.3516	0.2633
263118_at	AT1G03090	MCCA (3-methylcrotonyl-CoA carboxylase 1)	0.04309	0.8794	0.5463	0.3067	0.3139	0.2994	-0.7802	0.0298	0.0704	-0.5166	0.094	0.116
263119_at	AT1G03110	transducin family protein / WD-40 repeat family prot	-0.1636	0.6772	0.4849	-0.4026	0.3319	0.3094	0.04499	0.7875	0.4594	-0.194	0.2817	0.229
263120_at	AT1G78540	CYP708A3 (cytochrome P450, family 708, subfami	0.4508	0.0889	0.1707	0.2574	0.2688	0.2736	0.405	0.0353	0.0771	0.2117	0.1777	0.1718
263121_at	AT1G78530	protein kinase family protein	-0.2281	0.7819	0.5183	0.2565	0.756	0.4769	-0.5982	0.481	0.3517	-0.1136	0.8899	0.4541
263122_at	AT1G78510	SPS1 (SOLANESYL DIPHOSPHATE SYNTHASE	0.01985	0.949	0.5645	-0.2347	0.4657	0.3702	-0.1262	0.2381	0.2342	-0.3808	0.0139	0.0375
263123_at	AT1G78500	pentacyclic triterpene synthase, putative	0.4604	0.0514	0.1466	-1.5599	0.174	0.2154	1.007	0.3464	0.2915	1.0132	0.3438	0.2597
263124_at	AT1G78480	prenyltransferase/squalene oxidase repeat-contain	-0.4229	0.288	0.3162	0.3527	0.365	0.3252	-0.7822	0.0863	0.1295	-0.00661	0.9856	0.4792
263125_at	AT1G78470	similar to F-box family protein [Arabidopsis thaliana	-0.8335	0.5569	0.4437	-0.9666	0.4991	0.3841	-0.2006	0.734	0.4429	-0.3337	0.5771	0.3549
263126_at	AT1G78460	SOUL heme-binding family protein	0.333	0.2389	0.287	0.5718	0.1385	0.1742	-0.63084	0.0101	0.0398	-0.392	0.0461	0.0755
263127_at	AT1G78610	mechanosensitive ion channel domain-containing p	-0.00746	0.9582	0.5667	-0.06628	0.6462	0.4402	-0.2192	0.1766	0.1963	-0.278	0.1062	0.1248
263128_at	AT1G78600	zinc finger (B-box type) family protein	0.6927	0.1741	0.2442	0.9265	0.0918	0.1528	0.2926	0.1708	0.1925	0.5265	0.04	0.0691
263129_at	AT1G78620	integral membrane family protein	0.02694	0.8893	0.5483	-0.03776	0.8455	0.5032	0.2437	0.2508	0.2414	0.179	0.3802	0.2759
263130_at	AT1G78650	POLD3	-0.1146	0.6673	0.4817	-0.05739	0.8279	0.4983	-0.1963	0.4443	0.3359	-0.1391	0.5804	0.3562
263131_at	AT1G78630	EMB1473 (EMBRYO DEFECTIVE 1473); structural	-0.624	0.0165	0.0774	-0.8155	0.0066	0.0461	0.1835	0.0597	0.1049	-0.00794	0.9156	0.4616
263132_at	AT1G78580	bile acid:sodium symporter family protein	-0.04697	0.8238	0.5307	-0.3522	0.1493	0.1976	-0.3473	0.0275	0.0675	-0.6527	0.0031	0.0181
263133_at	AT1G78450	SOUL heme-binding family protein	-2.0049	0.0201	0.0837	-1.6972	0.034	0.0911	-1.2165	0.0056	0.0311	-0.9087	0.0154	0.0395
263134_at	AT1G78570	RHM1/ROL1 (RHAMNOSE BIOSYNTHESIS1); UD	-0.8558	0.1083	0.1906	-1.0176	0.0704	0.1327	-0.1092	0.4252	0.3276	-0.271	0.0926	0.1148
263135_at	AT1G78550	oxidoreductase, 2OG-Fe(II) oxygenase family prote	0.4826	0.0107	0.0649	0.9217	0.0092	0.0524	-0.1575	0.3293	0.283	0.1184	0.451	0.3064
263136_at	AT1G78580	ATTPS1 (TREHALOSE-6-PHOSPHATE SYNTHAS	-0.4869	0.0368	0.1105	-0.8195	0.0066	0.0461	0.2061	0.0771	0.1213	-0.1265	0.2199	0.196
263137_at	AT1G78660	ATGGH1; gamma-glutamyl hydrolase	-0.1288	0.4461	0.3962	0.2104	0.2398	0.2576	0.08304	0.6053	0.3999	0.4222	0.0465	0.0759
263138_at	AT1G65090	similar to unknown protein [Arabidopsis thaliana] (T	0.4961	0.4586	0.4023	0.6865	0.3202	0.3033	0.1422	0.826	0.4715	0.3325	0.6122	0.3675
263139_at	AT1G65110	ubiquitin carboxyl-terminal hydrolase-related	-0.2402	0.8389	0.535	-0.8715	0.4753	0.3744	-0.9476	0.4014	0.3172	-1.5788	0.1931	0.1809
263140_at	no_match	no_match	-1.9729	0.1218	0.2022	-0.7826	0.4807	0.3765	-2.0455	0.1122	0.15	-0.8551	0.4438	0.3033
263141_at	AT1G65210	similar to lysase [Arabidopsis thaliana] (TAIR:AT4G3	0.76	0.5698	0.4489	-1.4744	0.2965	0.2899	1.8112	0.2146	0.2205	-0.4232	0.7479	0.413
263142_at	AT1G65230	similar to hypothetical protein [Vitis vinifera] (GB:CA	-0.9018	0.004	0.0466	-1.1738	0.0015	0.0314	0.4172	0.051	0.0956	0.1452	0.3915	0.2806
263143_at	AT1G03100	pentatricopeptide (PPR) repeat-containing protein	-0.2912	0.3695	0.3593	-0.3169	0.3333	0.3099	-0.128	0.6605	0.4181	-0.1537	0.6001	0.3634
263144_at	AT1G54070	dormancy/auxin associated protein-related	-1.5426	0.1094	0.1915	-0.8444	0.3241	0.3055	-1.9995	0.0596	0.1048	-1.2613	0.1686	0.1664
263145_at	AT1G54090	ATEXO70D2 (exocyst subunit EXO70 family protein	0.05762	0.7742	0.5161	0.03583	0.8579	0.5066	-0.3115	0.0694	0.1142	-0.3333	0.5578	0.3866
263146_at	AT1G53940	GLIP2 (GDSL-motif lipase 2); carboxylesterase	-0.5133	0.7235	0.5006	-1.1776	0.4329	0.3567	-0.226	0.8754	0.4854	-0.8903	0.5462	0.3435
263147_at	AT1G53980	polyubiquitin-related	0.69	0.6013	0.46	1.2529	0.3618	0.3238	0.6611	0.6161	0.4031	1.2241	0.3717	0.272
263148_at	AT1G53950	ubiquitin family protein	0.2454	0.0321	0.1039	-2.2097	0.043	0.103	2.8435	0.0197	0.0564	-1.8016	0.0755	0.1012
263149_at	AT1G53970	unknown protein	-0.197	0.8783	0.5461	0.012	0.9925	0.5423	0.1648	0.8981	0.4918	0.3738	0.7724	0.4207
263150_at	AT1G54050	17.4 kDa class III heat shock protein (HSP17.4-CIII	-0.7462	0.0038	0.0461	-0.3257	0.0574	0.1191	0.5791	0.0093	0.0387	0.9996	0.0013	0.013
263151_at	AT1G54120	similar to unknown protein [Arabidopsis thaliana] (T	0.007588	0.976	0.5712	0.2989	0.2766	0.279	0.4595	0.1251	0.1601	0.7508	0.0341	0.0624
263152_at	AT1G54060	transcription factor	-0.00834	0.9351	0.561	0.3265	0.0274	0.0827	-0.2066	0.0983	0.1396	0.1283	0.2533	0.2143
263153_s_at	AT1G54000;AT1G54010	[AT1G54000, myosin-like protein];[AT1G54010, putati	-0.2419	0.4932	0.4172	0.2609	0.4622	0.3689	-0.06687	0.8452	0.4771	0.4359	0.2462	0.2103
263154_at	AT1G54110	cation exchanger, putative (CAX10)	0.6181	0.0475	0.1254	0.3477	0.187	0.2244	0.157	0.4459	0.3366	-0.1134	0.5748	0.3541
263155_at	AT1G54140	initiation factor	0.2371	0.0423	0.1183	0.47	0.0043	0.0407	0.4741	0.0022	0.0219	0.707	5.00E-04	0.0093
263156_at	AT1G54160	GDSL-motif lipase, putative	0.6132	0.0073	0.0574	0.6278	0.0067	0.0464	0.1861	0.2014	0.2125	0.2007	0.1749	0.1702
263157_at	AT1G54100	ALDH7B4 (ALDEHYDE DEHYDROGENASE 7B4);	0.7625	0.015	0.0741	0.7308	0.0173	0.0681	-0.2349	0.214	0.2203	-0.2666	0.1692	0.1667
263158_at	AT1G54160	CCAAT-binding transcription factor (CBF-B/NF-YA)	0.6911	0.0032	0.0442	0.2605	0.0757	0.1379	0.7609	0.0022	0.0222	0.3303	0.0391	0.0681
263159_at	AT1G54150	RSH3 (RELASPOT HOMOLOG 3); catalytic	0.2835	0.1451	0.2213	0.1288	0.4577	0.3672	-0.0317	0.8367	0.4747	-0.1863	0.2657	0.2207
263160_at	AT1G54080	UBP1A; mRNA 3'-UTR binding	0.3744	0.1522	0.2276	0.01151	0.9593	0.534	-0.1715	0.464	0.3448	-0.5344	0.0653	0.0931
263161_at	AT1G54020	myrosinase-associated protein, putative	2.0607	0.0051	0.0509	2.2164	0.0039	0.0391	0.06348	0.8548	0.4797	0.2192	0.5373	0.3403
263162_at	AT1G54150	zinc finger (C3HC4-type RING finger) family protein	0.6617	0.0196	0.0828	0.3969	0.0887	0.1484	-0.00147	0.9937	0.5162	-0.2663	0.204	0.1873
263163_at	AT1G03160	FZL (FZO-LIKE); GTP binding / GTPase/ thiamin-pl	-0.4869	0.1252	0.2048	-0.4372	0.1574	0.2039	-1.4041	0.0051	0.0299	-1.3544	0.0058	0.0236
263164_at	AT1G03070	glutamate binding /	-0.3755	0.2851	0.3143	-0.4922	0.1814	0.2207	0.3713	0.2897	0.2635	0.2547	0.4501	0.306
263165_at	AT1G03060	WD-40 repeat family protein / beige-related	-0.4282	0.0965	0.1795	0.4842	0.0707	0.1329	-1.4848	0.001	0.0176	-1.4288	0.0012	0.0127
263166_at	AT1G03050	epsin N-terminal homology (ENTH) domain-contain	-0.6325	0.5006	0.4208	0.5792	0.5353	0.3987	-1.1964	0.2341	0.2318	0.01531	0.9866	0.4794
263167_at	AT1G03030	phosphoribulokinase/uridine kinase family protein	0.5011	0.0644	0.1453	0.1241	0.5643	0.4099	-0.2454	0.0165	0.0512	-0.6224	5.00E-04	0.0098
263168_at	AT1G03020	glutaredoxin family protein	-0.3403	0.4057	0.3782	0.1966	0.6201	0.4306	0.9743	0.0128	0.0451	1.5111	0.0027	0.017
263169_at	AT1G03010	phototropic-responsive NPH3 family protein	3.2343	0.0474	0.1254	2.783	0.0717	0.134	-0.9158	0.4681	0.3466	-1.3671	0.2979	0.2375
263170_at	AT1G03000	PEX8 (PEROXIN8); ATPase	0.4163	0.001	0.0349	0.2457	0.0068	0.0465	-0.3304	0.0023	0.0224	-0.5011	5.00E-04	0.0093
263171_at	AT1G54115	cation exchanger, putative	0.6414	0.0066	0.055	0.4737	0.0187	0.0706	-0.6562	0.0061	0.0325	-0.8239	0.0027	0.017
263172_at	AT1G54170	CID3 (CTC-Interacting Domain 3)	0.4184	0.0923	0.176	0.2474	0.2625	0.2712	-0.2516	0.1471	0.177	-0.4225	0.0394	0.0684
263173_at	AT1G54180	ATBRXL3/BRX-LIKE3 (BREVIS RADIX-LIKE 3)	-1.0382	0.1929	0.2575	1.9613	0.0418	0.1016	-1.4917	0.0879	0.1309	1.5078	0.0856	0.1094
263174_at	AT1G54040	ESP (EPITHIOSPECIFIER PROTEIN)	-0.5864	0.0679	0.1496	-0.5043	0.0995	0.1591	0.3019	0.2247	0.2264	0.384	0.1421	0.1495
263175_at	AT1G05510	similar to unknown protein [Arabidopsis thaliana] (T	-0.1768	0.7641	0.5127	-0.7822	0.2281	0.2502	1.2597	0.0839	0.1273	0.6542	0.3001	0.2387
263176_at	AT1G05530	UGT2/UGT75B2 (UDP-glucosyl transferase 75B2);	-0.00221	0.9987	0.5763	0.7639	0.5872	0.4187	0.5609	0.6874	0.4268	1.327	0.3637	0.2685
263177_at	AT1G05540	similar to unknown protein [Arabidopsis thaliana] (T	-1.4162	0.0078	0.0583	-1.6419	0.0046	0.0416	0.1135	0.7053	0.4332	-0.1123	0.7081	0.4003
263178_at	AT1G05550	similar to unknown protein [Arabidopsis thaliana] (T	-1.7058	0.0414	0.1171	0.2614	0.6732	0.4496	-1.0919	0.1306	0.1643	0.8753	0.2028	0.1868
263179_at	AT1G05710	ethylene-responsive protein, putative	1.4226	7.00E-04	0.0334	1.4043	8.00E-04	0.0277	0.01307	0.936	0.5023	-0.00518	0.9746	0.4767
263180_at	AT1G05620	inosine-uridine preferring nucleoside hydrolase fam	0.8227	0.0353	0.1085	0.6581	0.0687	0.1293	0.2651	0.2838	0.2601	0.1005	0.6636	0.3854
263181_at	AT1G05720	selenoprotein family protein	0.6376	0.0268	0.0947	0.8188	0.0118	0.0584	0.1874	0.1345	0.1671	0.3686	0.0211	0.0472
263182_at	AT1G05575	unknown protein	-0.5109	0.387	0.3682	0.01013	0.9856	0.5405	1.1418	0.021	0.0582	1.6629	0.0058	0.0236
263183_at	AT1G05570	CALS1 (CALLOSE SYNTHASE 1); transferase, trar	1.666	0.0025	0.0424	1.3808	0.005	0.0425	-0.4364	0.0125	0.0443	-0.7217	0.002	0.0153
263184_at	AT1G05560	UGT1 (UDP-glucosyl transferase 75B1); UDP-glyco	-1.1724	0.0012	0.036	-1.068	0.0017	0.032	-0.295	0.0377	0.0802	-0.1906	0.1192	0.1342
263185_at	AT1G05520	transport protein, putative	0.8887	1.00E-04	0.0312	0.3293	0.0029	0.0355	-0.1623	0.0326	0.0736	-0.7217	1.00E-04	0.0067
263186_at	AT1G05530	transposable element gene	0.5256	0.6314	0.4702	-1.6143	0.1865	0.224	1.9645	0.1246	0.1598	-0.1755	0.871	0.4486
263187_at	no_match	no_match	-0.1331	0.9103	0.5541	-1.3416	0.2935	0.2884	0.7783	0.3481	0.2922	-0.4302	0.5887	0.3595
263188_at	AT1G36095	electron carrier/ heme binding / iron ion binding	-0.6797	0.4476	0.397	-0.7736	0.3926	0.3381	0.121	0.8401	0.4757	0.02713	0.9638	0.4742
263189_at	AT1G36100	myosin heavy chain-related	-0.6194	0.6151	0.4645	-1.2598	0.3303	0.3085	1.004	0.3998	0.3165	0.3636	0.7503	0.4139
263190_at	AT1G36105	transposable element gene	-0.6024	0.4584	0.4022	-2.3759	0.0319	0.0886	-0.4763	0.5253	0.3692	-2.2497	0.0304	0.0587
263191_at	no_match	no_match	-1.119	0.1531	0.2282	-2.7719	0.012	0.0589	0.5258	0.4311	0.3301	-1.1271	0.134	0.1444
263192_at	AT1G36160	ACC1 (ACETYL-COENZYME A CARBOXYLASE 1	-0.2747	0.4032	0.3769	-0.3587	0.2895	0.2863	-0.8839	0.0033	0.0255	-0.968	0.0024	0.0161
263193_at	AT1G36050	similar to unknown protein [Arabidopsis thaliana] (T	0.5958	0.0039	0.0463	0.5425	0.0055	0.0434	-0.2567	0.0014	0.0193	-0.31	7.00E-04	0.0105
263194_at	AT1G36060	AP2 domain-containing transcription factor, putative	0.3193	0.7559	0.5104	2.1401	0.0894	0.1507	-2.0252	0.1022	0.1428	-0.2044	0.8416	0.4406
263195_at	AT1G36150	protease inhibitor/seed storage/lipid transfer protein	0.1501	0.8365	0.5343	0.9106	0.2525	0.2655	1.2951	0.0305	0.0711	0.2345	0.5847	0.358
263196_at	AT1G36070	WD-40 repeat family protein	0.4273	0.0431	0.1198	0.5905	0.0156	0.0652	-0.3552	0.0719	0.1166	-0.192	0.2592	0.2174
263197_at	AT1G35930	ubiquitin family protein	-1.3458	0.1759	0.2454	-0.2448	0.78	0.4836	-0.4509	0.6115	0.4017	0.6501	0.472	0.3145
263198_at	AT1G35990	GLIP3 (GDSL-motif lipase 3); carboxylesterase/ lipa	0.2265	0.856	0.5401	0.9249	0.4736	0.3735	-0.1272	0.8793	0.4865	0.5712	0.5075	0.3288
263199_at	AT1G05590	ATHEX3/HEXO2 (BETA-HEXOSAMINIDASE 2); be	-0.2589	0.0116	0.0674	0.2585	0.0117	0.0582	-0.5712	6.00E-04	0.0158	-0.05385	0.4112	0.2887
263200_at	AT1G05600	pentatricopeptide (PPR) repeat-containing protein	0.4372	0.0088	0.0606	0.1014	0.3293	0.3083	-0.1399	0.1607	0.186	-0.4757	0.0043	0.0208
263201_at	AT1G05610	APS2 (ADP-GLUCOSE PYROPHOSPHORYLASE S	0.232	0.7618	0.5121	-0.5158	0.5105	0.3889	-0.9718	0.2456	0.2384	-1.7195	0.0739	0.0999
263202_at	AT1G05630	5PTASE13/ATI5PTASE13; inositol or phosphatidylin	-0.1365	0.7734	0.5159	-0.3771	0.4428	0.3608	-0.3828	0.2699	0.2522	-0.6234	0.1056	0.1243
263203_at	AT1G05640	CHR31 (chromatin remodeling 31); ATP binding / D	-1.0638	0.1098	0.192	-1.4967	0.0449	0.105	0.8305	0.1813	0.1996	0.4064	0.4775	0.3167
263204_at	AT1G05490	CHR31 (chromatin remodeling 31); ATP binding / D	-0.1104	0.916	0.5559	0.3361	0.7497	0.4748	-1.7799	0.0244	0.0633	-1.3333	0.0577	0.0865
263205_at	AT1G05500	ATSYTE/NTMC2T2.1/NTMC2TYPE2.1/SYTE	-0.05859	0.4909	0.4163	-0.0531	0.53	0.3964	-0.2464	0.0172	0.0524	-0.2409	0.0185	0.0436
263206_at	AT1G05580	DNA-binding protein-related	0.5936	0.0168	0.0777	0.7639	0.007	0.0474	0.04919	0.7597	0.4512	0.2195	0.2176	0.1949
263207_at	AT1G10550	XTH33 (xyloglucan:xyloglucosyl transferase 33); hy	-0.4072	0.7453	0.5075	-1.4229	0.2907	0.287	0.1124	0.9141	0.4962	-0.9033	0.408	0.2874
263208_at	AT1G10480	ZFP5 (ZINC FINGER PROTEIN 5); nucleic acid bin	0.5882	0.4991	0.42	-0.3298	0.6985	0.4585	-0.212	0.7975	0.4627	-1.13	0.2176	0.1949
263209_at	AT1G10522	similar to unknown protein [Arabidopsis thaliana] (T	-0.1111	0.4588	0.4023	-0.05992	0.6836	0.4534	-0.00278	0.8857	0.4884	0.03085	0.8313	0.4375
263210_at	AT1G10585	transcription factor	-0.00744	0.9866	0.5735	0.4666	0.3265	0.3067	0.7093	0.1647	0.1883	1.1833	0.0472	0.0765
263211_at	AT1G10460	GLP7 (GERMIN-LIKE PROTEIN 7); manganese ion	0.3747	0.6821	0.4866	1.1884	0.2346	0.2546	0.1128	0.9009	0.4926	0.9265	0.337	0.2565
263212_at	AT1G10410	EMB2004 (EMBRYO DEFECTIVE 2004); protein bi	0.3872	0.1766	0.2458	-0.1874	0.4721	0.373	-0.3202	0.1439	0.1745	-0.1204	0.5326	0.3389
263213_at	AT1G30560	transporter, putative	-0.8905	0.3024	0.3244	-1.0668	0.2295	0.2511	1.7761	0.0736	0.1181	1.5998	0.0958	0.1174
263214_at	AT1G30600	toprim domain-containing protein	-0.6268	0.1839	0.251	0.5195	0.2544	0.2668	-0.4196	0.3136	0.2751	0.7267	0.1168	0.1325
263215_at	AT1G30710	ketoacyl-CoA synthase domain-containing protein	0.2479	0.8564	0.5403	-1.5321	0.2991	0.291	0.4355	0.7517	0.4487	-1.3445	0.3545	0.2646
263216_s_at	AT1G30720;AT1G30730	[AT1G30720, FAD-binding domain-containing prote	0.6133	0.4032	0.3769	0.9737	0.2123	0.241	-0.3251	0.1808	0.1993	0.03525	0.8692	0.4481
263217_at	AT1G30740	FAD-binding domain-containing protein	-0.8518	0.459	0.4024	-1.4905	0.2253	0.2486	0.9821	0.3987	0.316	0.3434	0.758	0.4161
263218_at	AT1G30570	protein kinase family protein	-0.2079	0.4835	0.4134	-0.04531	0.8746	0.5115	-0.4641	0.1366	0.1687	-0.3385	0.2775	0.2269
263219_at	AT1G30600	subtilase family protein	-0.2813	0.3961	0.3734	0.4055	0.2428	0.2597	-0.00561	0.9858	0.5141	0.6812	0.083	0.1075
263220_at	AT1G30610	EMB2279 (EMBRYO DEFECTIVE 2279)	0.2298	0.2029	0.2642	-0.08502	0.6037	0.4247	-0.2098	0.2373	0.2336	-0.5247	0.0255	0.0529
263221_at	AT1G30620	HSR8/MUR4/UXE1 (MURUS 4); UDP-arabinose 4-	0.3884	0.0189	0.0817	0.475	0.0096	0.0535	-0.1762	0.1588	0.1849	-0.08959	0.4289	0.2962
263222_at	AT1G30640	protein kinase, putative	0.424	0.2193	0.2747	0.5182	0.1499	0.198	0.2247	0.1874	0.2039	0.3189	0.0872	0.1106
263223_at	AT1G30630	coatomer protein epsilon subunit family protein / CO	0.4924	0.0105	0.0646	0.7011	0.0029

263290_at	AT2G10930	similar to unknown protein [Arabidopsis thaliana] (T	-0.2829	0.6602	0.4794	-0.07201	0.903	0.5196	0.2084	0.7261	0.4405	0.3993	0.5114	0.3302
263291_at	AT2G10920	unknown protein	-0.8785	0.3219	0.3354	1.5598	0.1155	0.1715	-1.1648	0.1256	0.1605	1.2734	0.1023	0.1222
263292_at	AT2G10900	transposable element gene	-0.4798	0.59	0.4561	-1.6321	0.1175	0.1733	0.4511	0.6116	0.4017	-0.7011	0.4409	0.3018
263293_x_at	AT2G10880	transposable element gene	-0.07658	0.9363	0.5613	-0.2007	0.8345	0.5	0.277	0.7737	0.4555	0.1528	0.8735	0.4494
263294_at	AT2G10870	transposable element gene	-1.3466	0.3695	0.3593	1.0408	0.4785	0.3756	-1.2438	0.4035	0.3181	1.1436	0.4393	0.301
263295_at	AT2G14210	ANR1; DNA binding / transcription factor	0.6188	0.6568	0.4779	0.05678	0.967	0.5358	-1.3268	0.3493	0.2928	-1.8888	0.2061	0.1886
263296_at	AT2G38800	calmodulin-binding protein-related	0.2567	0.1689	0.2405	0.6472	0.0134	0.0616	-0.2052	0.2513	0.2415	0.1854	0.2927	0.2349
263297_at	AT2G15310	ATARFB1A (ADP-ribosylation factor B1A); GTP bin	0.2587	0.5704	0.4492	0.6918	0.174	0.2154	0.7555	0.021	0.0584	1.1887	0.0044	0.021
263298_at	AT2G15290	ATTIC21/CIA5/PIC1/TIC21 (CHLOROPLAST IMPC	-0.3809	0.0307	0.1016	-0.6857	0.0041	0.04	0.8383	0.002	0.021	0.5335	0.0101	0.0315
263299_s_at	AT2G11570;AT2G11600	[AT2G11570, 3'-5'-exoribonuclease/ RNA binding];[	-0.5053	0.4988	0.4199	0.376	0.6099	0.4269	-0.5859	0.3774	0.3065	0.2954	0.6433	0.3784
263300_at	no_match	no_match	1.2337	0.2795	0.3111	-0.6882	0.524	0.3938	1.3625	0.2396	0.235	-0.5595	0.6011	0.3638
263301_x_at	AT2G04970;AT2G06440;A	[AT2G04970, transposable element gene];[AT2G06	-0.4943	0.5453	0.439	-0.576	0.4847	0.378	-0.7743	0.3015	0.2694	-0.856	0.2603	0.2179
263302_at	no_match	no_match	1.9205	0.1249	0.2045	-1.9587	0.1195	0.1749	0.7633	0.4844	0.3532	-3.1159	0.0348	0.0631
263303_at	AT2G15240	UNC-50 family protein	0.6262	0.0062	0.0542	0.6759	0.0047	0.0418	-0.8646	0.0019	0.0207	-0.8149	0.0024	0.0161
263304_at	AT2G01920	epsin N-terminal homology (ENTH) domain-contain	0.1526	0.7953	0.5225	-0.5537	0.3714	0.328	3.1054	0.0049	0.0295	2.3992	0.0121	0.0346
263305_at	AT2G01930	ATBPC1/BBR/BPC1/BPC1 (BASIC PENTACYSTEI	-0.4031	0.123	0.2033	0.3141	0.2032	0.2349	-1.0141	0.008	0.0359	-0.2969	0.2243	0.1984
263306_at	AT2G12480	SCPL43; serine carboxypeptidase	0.2453	0.6517	0.4766	-0.4351	0.4365	0.3582	-0.00738	0.9872	0.5145	-0.6878	0.1862	0.1771
263307_at	AT2G12520	transposable element gene	-0.5177	0.1557	0.2302	-1.136	0.0186	0.0704	0.3366	0.3196	0.2781	-0.2816	0.396	0.2826
263308_at	AT2G10380	transposable element gene	-0.7726	0.5534	0.4421	1.2237	0.364	0.3248	-1.7438	0.2185	0.2228	0.2524	0.8431	0.4408
263309_at	AT2G10370	transposable element gene	-1.1854	0.4329	0.3907	-1.2749	0.4019	0.3421	0.4735	0.7454	0.4466	0.3839	0.7919	0.4265
263310_s_at	AT2G10350;AT4G03970	[AT2G10350, transposable element gene];[AT4G03	0.6845	0.4552	0.4006	2.3706	0.0459	0.1061	-0.8534	0.3613	0.2987	0.8327	0.3718	0.272
263311_at	AT2G10360	unknown protein	-0.6067	0.4992	0.42	0.438	0.6205	0.4308	-0.7677	0.4009	0.3171	0.2771	0.7517	0.4143
263312_at	AT2G10460	transposable element gene	-0.253	0.8021	0.5247	0.8851	0.4018	0.3421	-1.0919	0.2844	0.2604	0.04609	0.9609	0.4734
263313_at	AT2G10450	14-3-3 protein, putative / gf15, putative	1.43	0.1181	0.1987	1.7696	0.07	0.1324	-0.9329	0.1385	0.1701	-0.5933	0.3054	0.2412
263314_at	AT2G05760	xanthine/uracil permease family protein	0.4241	0.23	0.2821	0.1291	0.6889	0.4553	0.272	0.4154	0.3231	-0.02298	0.9426	0.4691
263315_at	AT2G05755	integral membrane family protein	-0.1228	0.3321	0.3413	-0.3374	0.0388	0.0977	0.3031	0.0529	0.0976	0.08851	0.4712	0.3141
263316_s_at	AT2G24710;AT2G24720	[AT2G24710, ATGLR2.3 (Arabidopsis thaliana glut	-0.7455	0.5133	0.4264	0.02652	0.9809	0.5394	-1.3732	0.2574	0.2449	-0.6012	0.5944	0.3614
263317_s_at	AT2G24740;AT1G17770	[AT2G24740, SDG21 (SET DOMAIN GROUP 21)];[	0.6657	0.3474	0.3486	0.9821	0.1916	0.2271	-0.0288	0.9655	0.5089	0.2877	0.6696	0.3873
263318_at	AT2G24762	ATGDU4 (ARABIDOPSIS THALIANA GLUTAMINE	0.1078	0.7892	0.5203	0.8764	0.0807	0.1426	0.7155	0.1306	0.1643	1.4841	0.017	0.0416
263319_at	AT2G47160	BOR1 (REQUIRES HIGH BORON 1); anion exchar	-0.2247	0.4506	0.3984	-0.6625	0.0695	0.1321	-0.2114	0.1998	0.2117	-0.6492	0.0092	0.03
263320_at	AT2G47180	ATGALS1 (ARABIDOPSIS THALIANA GALACTINO	-1.0927	0.0066	0.0549	-0.7545	0.0231	0.0768	-0.2966	0.1428	0.1737	0.04166	0.8108	0.4319
263321_at	AT2G47170	ARF1A1c (ADP-RIBOSYLATION FACTOR 1); GTP	0.1227	0.2376	0.2861	0.1485	0.1685	0.2115	0.1348	0.1681	0.1905	0.1606	0.1158	0.1317
263322_at	AT2G04270	glycoside hydrolase starch-binding domain-contain	-0.02981	0.8902	0.5483	-0.01849	0.9317	0.5269	-1.2529	0.0035	0.026	-1.2416	0.0036	0.0195
263323_at	AT2G04300	leucine-rich repeat protein kinase, putative	0.4227	0.732	0.503	0.4535	0.7136	0.4632	0.9417	0.4391	0.3337	0.9725	0.4255	0.2947
263324_at	AT2G04220	similar to unknown protein [Arabidopsis thaliana] (T	0.3598	0.701	0.4929	0.05113	0.956	0.5333	0.8635	0.378	0.3068	0.5548	0.5591	0.3485
263325_at	AT2G04240	XERICO; protein binding / zinc ion binding	0.09821	0.6915	0.4898	0.2376	0.3601	0.3228	0.4316	0.0476	0.0916	0.571	0.0202	0.0458
263326_at	AT2G04280	similar to unknown protein [Arabidopsis thaliana] (T	-0.3456	0.0513	0.1301	-0.5094	0.0154	0.0649	0.1324	0.2255	0.2267	-0.03139	0.7513	0.4142
263327_at	AT2G15300	leucine-rich repeat transmembrane protein kinase,	0.009711	0.9864	0.5735	0.2248	0.6959	0.4574	-0.05905	0.0274	0.4971	0.156	0.785	0.4243
263328_at	AT2G15280	reticulon family protein (RTNLB10)	0.02877	0.8903	0.5484	-0.3942	0.1143	0.1707	-0.4145	0.0807	0.1244	-0.8375	0.0093	0.0301
263329_at	AT2G15260	zinc finger (C3HC4-type RING finger) family protei	-0.6909	0.4636	0.4046	0.25	0.7842	0.4847	0.01993	0.9825	0.5133	0.9606	0.3232	0.2498
263330_at	AT2G15320	leucine-rich repeat family protein	-0.06764	0.7374	0.5049	-0.1403	0.4973	0.3833	0.5159	0.0518	0.0964	0.4433	0.078	0.1032
263331_at	AT2G15270	similar to unnamed protein product [Vitis vinifera] (G	0.1323	0.24	0.2875	0.343	0.0233	0.0769	0.3761	0.012	0.0435	0.5868	0.0024	0.0164
263332_at	AT2G04870	small nuclear ribonucleoprotein, putative / snRNP, p	0.07979	0.4661	0.4056	0.2563	0.061	0.1227	0.988	6.00E-04	0.0158	1.1646	3.00E-04	0.0063
263333_at	AT2G03890	phosphatidylinositol 3- and 4-kinase family protein	0.5427	0.0417	0.1176	0.9628	0.0063	0.0456	-0.5682	0.0085	0.037	-0.1481	0.2772	0.2267
263334_at	AT2G03820	nonsense-mediated mRNA decay NMD3 family pro	0.523	0.0028	0.0429	0.4453	0.005	0.0424	-0.3839	0.0039	0.0273	-0.4616	0.002	0.0152
263335_x_at	AT2G04970;AT2G06440	[AT2G04970, transposable element gene];[AT2G06	0.8798	0.141	0.2183	-0.2282	0.835	0.5002	-1.9096	0.1363	0.1686	-0.2581	0.8139	0.4327
263336_x_at	no_match	no_match	-0.4426	0.2056	0.2658	-0.2763	0.3993	0.3409	-0.3798	0.2647	0.2491	-0.2135	0.5067	0.3284
263337_at	AT2G04990	transposable element gene	-0.4891	0.715	0.4977	-1.4562	0.3079	0.2962	1.1255	0.418	0.3243	0.1584	0.9051	0.4588
263338_at	AT2G05000	transposable element gene	-2.1878	0.1653	0.2377	0.9319	0.5102	0.3887	-0.8031	0.3191	0.2778	2.3166	0.0305	0.0588
263339_at	AT2G05010	transposable element gene	-0.34	0.7485	0.5084	-1.0899	0.3327	0.3097	1.1342	0.3158	0.2762	0.3843	0.7176	0.4033
263340_at	AT2G05020	transposable element gene	-1.6559	0.0278	0.0966	0.02686	0.9589	0.534	-1.8775	0.0112	0.0418	-0.1948	0.6676	0.3866
263341_at	AT2G05030	transposable element gene	-1.4853	0.2998	0.3229	0.6616	0.6241	0.4324	-0.9559	0.2267	0.1909	0.33	1.1911	0.3368
263342_at	AT2G05080	transposable element gene	1.7013	0.3358	0.3432	-1.4469	0.4052	0.3436	0.9945	0.5576	0.3819	-2.1536	0.2387	0.2064
263343_at	AT2G05090	transposable element gene	-1.0259	0.53	0.4331	0.06417	0.9678	0.536	-0.8807	0.5602	0.3827	0.2093	0.8874	0.4536
263344_at	AT2G22040	scramblase-related	0.0080014	0.942	0.563	0.416	0.0158	0.0655	-0.3482	0.026	0.0656	0.05977	0.5855	0.3582
263345_s_at	AT2G05070;AT2G05100	[AT2G05070, LHCB2.2 (Photosystem II light harves	-0.3126	0.2376	0.2861	-0.5332	0.0771	0.1392	0.05235	0.6918	0.4283	-0.1682	0.2425	0.2085
263346_at	AT2G05660	transposable element gene	-0.7614	0.5882	0.4558	-2.3115	0.1489	0.1974	0.7084	0.6135	0.4022	-0.8416	0.5512	0.3455
263347_at	AT2G05720	transducin family protein / WD-40 repeat family prot	-0.07205	0.8838	0.5471	0.02629	0.9576	0.5336	-0.3686	0.2753	0.2564	-0.27	0.4074	0.2871
263348_at	AT2G05710	aconitate hydratase, cytoplasmic, putative / citrate h	0.4309	0.1346	0.2131	0.2146	0.4041	0.3431	-0.1711	0.1035	0.1439	-0.3875	0.0089	0.0295
263349_at	AT2G13370	CHR5 (chromatin remodeling 5); ATP binding / DNA	0.1299	0.2701	0.3055	0.1299	0.27	0.2754	-1.2153	2.00E-04	0.0125	-1.2152	2.00E-04	0.0071
263350_at	AT2G13360	AGT (ALANINE:GLYOXYLATE AMINOTRANSFER	-0.4011	0.0059	0.0534	-0.4786	0.0031	0.0363	-0.07739	0.3106	0.2737	-0.1549	0.081	0.1059
263351_at	AT2G22120	protein binding / zinc ion binding	0.3051	0.1349	0.2133	0.5234	0.0327	0.0896	-0.3962	0.0722	0.1168	-0.1779	0.3369	0.2564
263352_at	AT2G22080	unknown protein	-0.5909	0.2415	0.2886	0.2304	0.6206	0.4308	-0.255	0.0996	0.1406	0.5663	0.009	0.0296
263353_at	AT2G22070	pentatricopeptide (PPR) repeat-containing protein	-0.1571	0.8745	0.5451	-0.2303	0.8173	0.4951	-0.1831	0.8541	0.4795	-0.2562	0.7973	0.428
263354_at	AT2G22060	similar to F-box family protein [Arabidopsis thaliana	1.6367	0.1928	0.2575	0.1536	0.8904	0.5159	-0.08597	0.9385	0.503	-1.569	0.2081	0.1897
263355_at	AT2G22100	RNA recognition motif (RRM)-containing protein	0.8449	0.1712	0.2424	-0.05405	0.9203	0.5241	0.8354	0.175	0.1954	-0.06348	0.9065	0.4591
263356_at	AT2G22090	UBA1A; AU-rich element binding / RNA binding	0.1217	0.358	0.3535	0.01146	0.9289	0.5259	0.3864	0.0301	0.0706	0.2762	0.0781	0.1033
263357_s_at	AT2G07250;AT5G34890;A	[AT2G07250, transposable element gene];[AT5G34	0.01596	0.9902	0.5745	-0.4141	0.7511	0.4753	-0.2456	0.8501	0.4785	-0.6756	0.6089	0.3663
263358_x_at	AT3G44500;AT3G47260	[AT3G44500, transposable element gene];[AT3G47	-0.6724	0.1375	0.2154	0.26	0.5133	0.3899	-1.2632	0.0253	0.0646	-0.3309	0.4134	0.2898
263359_at	AT2G15230	ATLIP1 (ARABIDOPSIS THALIANA LIPASE 1); gal	0.8382	0.0084	0.06	0.6776	0.0173	0.0681	0.1043	0.3364	0.2866	-0.05628	0.5877	0.3591
263360_at	AT2G03830	unknown protein	1.0491	0.2096	0.2678	-0.8609	0.2875	0.2852	2.2115	0.0346	0.0761	0.3015	0.6898	0.3939
263361_at	AT2G03840	TET13 (TETRASPANIN13)	0.6629	0.3467	0.3482	-0.1551	0.8154	0.4947	-0.04834	0.9313	0.5011	-0.8664	0.1756	0.1705
263362_at	AT2G03880	pentatricopeptide (PPR) repeat-containing protein	1.0014	0.2859	0.3148	0.9239	0.3196	0.3029	0.6354	0.4785	0.3508	0.5579	0.5306	0.3383
263363_at	AT2G03850	late embryogenesis abundant domain-containing pr	0.04985	0.9552	0.5661	2.2066	0.057	0.1188	-1.3685	0.0691	0.1139	0.7882	0.2282	0.2006
263364_at	AT2G20540	pentatricopeptide (PPR) repeat-containing protein	-1.3079	0.287	0.3155	-1.8138	0.164	0.2085	-1.4118	0.2285	0.2287	-1.9178	0.1259	0.1388
263365_at	AT2G20550	DNAJ chaperone C-terminal domain-containing prot	-0.09069	0.71	0.4962	-0.01396	0.9482	0.5315	0.354	0.0544	0.0993	0.4207	0.0328	0.0611
263366_at	no_match	no_match	-0.03772	0.9339	0.5608	-0.4018	0.4006	0.3414	0.3852	0.3745	0.305	0.02118	0.9588	0.4731
263367_at	AT2G20460	transposable element gene	-0.2838	0.8223	0.5303	-0.25	0.843	0.5026	1.0465	0.3598	0.298	1.0803	0.3462	0.2608
263368_at	no_match	no_match	-1.006	0.2143	0.271	-0.4776	0.5224	0.393	0.0236	0.9741	0.511	0.552	0.4638	0.3115
263369_at	AT2G20480	similar to unknown [Populus trichocarpa] (GB:ABK9	-0.8112	0.5963	0.4584	1.239	0.4296	0.3551	-0.5228	0.7299	0.4418	1.5274	0.3401	0.2581
263370_at	AT2G20500	unknown protein	-0.3641	0.3476	0.3487	-0.04267	0.9069	0.5207	0.603	0.0296	0.07	0.9244	0.0071	0.0263
263371_at	AT2G20490	EDA27/NOP10 (embryo sac development arrest 27	0.5503	0.0077	0.0582	0.5851	0.0062	0.0451	0.1813	0.0173	0.0525	0.2161	0.0095	0.0304
263372_at	AT2G20450	60S ribosomal protein L14 (RPL14A)	-0.105	0.6611	0.4796	0.1659	0.4965	0.383	0.1298	0.2189	0.223	0.4007	0.0108	0.0326
263373_at	AT2G20515	similar to unnamed protein product [Vitis vinifera] (G	-1.0705	0.0927	0.1764	0.1414	0.7858	0.4849	-0.2902	0.5831	0.3918	0.9217	0.1312	0.1424
263374_at	AT2G20560	DNAJ heat shock family protein	1.1567	0.0965	0.1795	1.5975	0.0404	0.0996	0.9013	7.00E-04	0.016	1.3421	1.00E-04	0.0069
263375_s_at	AT2G20530;AT4G28510	[AT2G20530, ATPHB6 (PROHIBITIN 6)];[AT4G285	0.3966	0.0182	0.0804	0.3975	0.0181	0.0694	0.2269	0.092	0.1342	0.2279	0.0911	0.1136
263376_at	AT2G20520	FLA6	-0.657	0.5534	0.4421	-0.4644	0.6716	0.4491	0.5369	0.6144	0.4025	0.7295	0.4998	0.3258
263377_at	AT2G40220	ABI4 (ABA INSENSITIVE 4); DNA binding / transcri	0.05115	0.971	0.5702	-0.4757	0.737	0.4703	0.56	0.6252	0.4064	0.03311	0.9766	0.4773
263378_at	AT2G40180	ATHPP2C5; protein serine/threonine phosphatase	-0.8502	0.4965	0.4189	0.08727	0.9425	0.5299	-0.8039	0.4994	0.3595	0.1336	0.9079	0.4594
263379_at	AT2G40140	CZF1/ZFAR1; transcription factor	0.03666	0.8679	0.5432	0.2312	0.3261	0.3065	0.08822	0.5904	0.3948	0.2827	0.1345	0.1447
263380_at	AT2G40200	basic helix-loop-helix (bHLH) family protein	0.00708	0.9719	0.5704	-0.07882	0.6978	0.4582	0.1392	0.0484	0.0924	0.05327	0.3428	0.2593
263381_at	AT2G40210	AGL48; transcription factor	0.05513	0.9422	0.563	-0.7804	0.336	0.3114	-0.2753	0.5948	0.3964	-1.1109	0.0804	0.1054
263382_at	AT2G40230	transferase family protein	-1.1422	0.0482	0.1265	-1.0303	0.0642	0.1265	0.08557	0.492	0.3564	0.1974	0.1562	0.159
263383_at	AT2G40120	protein kinase family protein	0.2673	0.6887	0.4822	0.5226	0.4184	0.3499	-0.336	0.322	0.2791	-0.08071	0.7996	0.4286
263384_at	AT2G40130	heat shock protein-related	-1.1829	0.2813	0.3121	-0.7482	0.4752	0.3744	-2.3459	0.0691	0.1139	-1.9112	0.1147	0.1311
263385_at	AT2G40170	ATEMB/GEA6 (ARABIDOPSIS EARLY METHIONIN	0.2286	0.8087	0.5264	0.5105	0.5947	0.4213	-1.1499	0.2456	0.2384	-0.868	0.3628	0.2682
263386_at	AT2G40150	similar to unknown protein [Arabidopsis thaliana] (T	-1.2388	0.0195	0.0753	-1.6851	0.0053	0.0431	0.2615	0.2969	0.2671	-0.1848	0.8448	0.3039
263387_at	AT2G40160	similar to unknown protein [Arabidopsis thaliana] (T	-0.1741	0.6803	0.4861	-0.1462	0.7284	0.4683	-0.5766	0.175	0.1954	-0.5487	0.1922	0.1804
263388_at	AT2G11690	transposable element gene	-0.2902	0.6908	0.4895	0.9778	0.2229	0.2475	-0.8917	0.2202	0.2237	0.3763	0.5732	0.3536
263389_at	AT2G11680	transposable element gene	0.08658	0.9337	0.5608	0.3786	0.7183	0.4648	0.6376	0.5433	0.3767	0.9297	0.3881	0.2792
263390_at	AT2G11830	transposable element gene	1.0258	0.4802	0.4119	-1.9364	0.216	0.2433	0.8021	0.299	0.2682	-2.1601	0.0325	0.0609
263391_at	AT2G11810	MGDC (monogalactosyldiacylglycerol synthase type	0.3102	0.6082	0.4625	-0.5677	0.3669	0.3261	0.4064	0.222	0.2247	-0.4715	0.169	0.1666
263392_at	AT2G10490	transposable element gene	-1.9424	0.1578	0.2315	-2.9921	0.0557	0.1172	1.1448	0.3269	0.2818	0.09506	0.9306	0.4658
263393_at	AT2G10500	transposable element gene	0.6793	0.6144	0.4643	-1.4964	0.2958	0.2896	-0.2341	0.8601	0.4811	-2.4098	0.1251	0.1384
263394_at	AT2G10465	transposable element gene	-2.1445	0.2952	0.3205	1.5152	0.4431	0.3608	-2.2643	0.2727	0.2538	1.3954	0.4774	0.3166
263395_at	AT2G20510	ATTIM44-1 (Arabidopsis thaliana translocase inner	0.8178	0.31	0.3285	2.4712	0.0247	0.0788	0.8446	0.1591	0.1852	2.498	0.0069	0.0259
263396_at	AT2G13710	similar to unknown protein [Arabidopsis thaliana] (T	0.07722	0.6317	0.4702	0.08941	0.5809	0.4165	0.5185	0.0254	0.0646	0.5307	0.0236	0.0502
263397_s_at	AT2G31540;AT2G31550	[AT2G31540, GDSL-motif lipase/hydrolase family p	-0.4552	0.2301	0.2821	-0.2748	0.4411	0.3599	0.1054	0.5439	0.3769	0.2858	0.1471	0.1528
263398_at	AtRABA5d	AtRABA5d (Arabidopsis Rab GTPase homolog A5d	0.1203	0.4333	0.3909	-0.2217	0.184	0.2225	0.3794	0.0517	0.0963	0.03737	0.8003	0.4289
263399_at	AT3G14190	similar to unknown [Populus trichocarpa] (GB:ABK9	-0.1482	0.5629	0.4459	-0.02499	0.9205	0.5241	0.5956	0.0645	0.1096	0.7188	0.0378	0.0665
263400_s_at	AT3G53870;AT2G31610	[AT3G53870, 40S ribosomal protein S3 (RPS3B)];[	0.07176	0.7541	0.5097	0.1509	0.5194	0.3922	0.2218	0.3584	0.2971	0.3009	0.2322	0.2028
263401_at	AT2G40470	transporter	1.0306	0.0732	0.1558	1.0027	0.0786	0.1405	-0.07528	0.854	0.4795	-0.1032	0.8013	0.429
263402_at	AT2G40450	MATE efflux family protein	3.2395	0.0152	0.0745	3.1528	0.0166	0.0669	-0.5654	0.0728	0.1173	-0.652	0.0493	0.0786
263403_at	AT2G40440	ATDTX1; antiporter/ multidrug efflux pump/ multidru	0.7867	0.2412	0.2885	0.005678	0.9926	0.5423	0.04918	0.9182	0.4973	-0.7318	0.179	0.1727
263404_s_at	AT2G04090;AT2G04100	[AT2G04090, MATE efflux family protein];[AT2G04	1.629	8.00E-04	0.0342	1.8115	5.00E-04	0.0263	0.3633	0.1115	0.1495	0.5458	0.0377	0.0664
263405_s_at	AT2G04080;AT2G04066	[AT2G04080, MATE efflux family protein];[AT2G04	0.09475	0.6259	0.4684	0.3321	0.1383	0.1893	-0.1338	0.4562	0.3413	0.1035	0.5585	0.3483
263406_at	AT2G04160	AIR3 (Auxin-Induced in Root cultures 3); subtilase	-0.02025	0.8711	0.5443	-0.2689	0.4164	0.3489	0.1452	0.0834	0.0143	0.0477	-0.5547	0.0017
263407_at	AT2G04038	ATBZIP48 (ARABIDOPSIS THALIANA BASIC LEU	0.7368	0.5293	0.4329	-0.9699	0.4164	0.3489	1.3364	0.0835	0.1271	-0.3703	0.5595	0.3486
263408_at	AT2G04060	beta-galactosidase, putative / lactase, putative	2.4489	0.0196	0.0828	-0.2653	0.704	0.4605	1.053	0.0929	0.1351	-1.6612	0.0257	0.0531
263409_at	AT2G04063	glycine-rich protein	0.3144	0.8032	0.525	0.5045	0.6911	0.4559	-1.9044	0.182	0.2002	-1.7143	0.2202	0.1961
263410_at	AT2G04039	similar to unnamed protein product [Vitis vinifera] (G	-1.0306	0.005	0.0504	-1.1704	0.0031	0.0363	0.256	0.0454	0.0892	0.1162	0.2624	0.219
263411_at	AT2G28710	zinc finger (C2H2 type) family protein	0.1745	0.5377	0.4359	0.4967	0.1279	0.1815	0.3345	0.1968	0.2098	0.6567	0.0385	0.0674
263412_at	AT2G28720	histone H2B, putative	0.2135	0.6853	0.4877	0.7355	0.2074	0.2378	0.2705	0.0152	0.0491	1.2529	0.0022	0.0157
263413_at	AT2G21240	ATBPC4/BBR/BPC4/BPC4 (BASIC PENTACYSTEI	0.4483	0.064	0.1448	0.5716	0.0317	0.0885	0.1637	0.4062	0.3191	0.287	0.1793	0.1729
263414_at	AT2G21230	bZIP family transcription factor	0.1997	0.1238	0.2039	0.1006	0.3828	0.3331	0.5192	0.0072	0.0343	0.4201	0.015	0.0389
263415_at	AT2G17250	EMB2742 (EMBRYO DEFECTIVE 2762)	0.6011	0.0277	0.0996	0.3179	0.1481	0.1967	-0.319	0.0998	0.1408	-0.6022	0.0158	0.04
263416_at	AT2G17170	protein kinase family protein	-1.3681	0.0648	0.1459	0.09586	0.8681	0.5094	-1.0843	0.0379	0.0805	0.3797	0.3452	0.2604
263417_at	AT2G17180	zinc finger (C2H2 type) family protein	-0.236	0.6872	0.4883	-1.0422	0.1283	0.1819	0.05836	0.8428	0.4766	-0.7478	0.0535	0.0827
263418_at	AT2G17210	pentatricopeptide (PPR) repeat-containing protein	0.1617	0.7353	0.5041	0.18	0.7071	0.4613	-0.2121	0.6592	0.4177	-0.1937	0.6864	0.3928
263419_at	AT2G17220	protein kinase, putative	0.151	0.3942	0.3723	-0.08981	0.6008	0.4239	0.322	0.1116	0.1496	0.08126	0.6348	0.3754
263420_at	AT2G17240	similar to unknown protein [Arabidopsis thaliana] (T	-0.1695	0.3902	0.37	-0.2408	0.2431	0.2599	0.05904	0.7542	0.4494	-0.01232	0.9476	0.4703
263421_at	AT2G17230	phosphoglycerate kinase 1 family protein	-0.152	0.866	0.5425	-0.5425	0.5559	0.4068	0.2583	0.1378	0.1695	-0.1321	0.3973	0.2831
263422_s_at	AT2G17190;AT2G17200	[AT2G17190, ubiquitin family protein];[AT2G17200,	0.4873	0.015	0.0741	0.5534	0.0097	0.0537	0.01467	0.9079	0.4947	0.08075	0.5349	0.3398
263423_at	AT2G31700	unknown protein	-1.5814	0.0455	0.1226	0.2561	0.6662	0.4471	-0.7974	0.1076	0.1469	1.0402	0.0543	0.0833
263424_at	AT2G31710	IBR domain-containing protein / ARIADNE-like prot	0.2165	0.0623	0.1433	0.4042	0.0087

263490_at	AT2G42620	MAX2 (MORE AXILLARY BRANCHES 2); ubiquitin	0.1684	0.364	0.3562	0.03201	0.8553	0.506	-0.04337	0.5607	0.3829	-0.1798	0.0584	0.0871
263491_at	AT2G42600	ATPPC2 (PHOSPHOENOLPYRUVATE CARBOXY	-0.1525	0.3069	0.3267	-0.4747	0.0219	0.075	-0.2736	0.1038	0.144	-0.5958	0.0103	0.0317
263492_at	AT2G42560	late embryogenesis abundant domain-containing pr	0.1859	0.6919	0.4899	2.125	0.0082	0.0504	-2.3523	0.0039	0.0273	-0.4133	0.3515	0.2633
263493_at	AT2G42520	DEAD box RNA helicase, putative	0.8868	0.0254	0.0923	0.5727	0.088	0.1494	-0.1586	0.3007	0.269	-0.4728	0.024	0.0509
263494_at	AT2G42590	GRF9 (GENERAL REGULATORY FACTOR 9); pro	-0.1123	0.1925	0.2572	-0.2205	0.0371	0.0952	0.3974	0.0052	0.0302	0.2892	0.0157	0.0399
263495_at	AT2G42530	COR15B	-1.2278	0.0291	0.0988	-0.9748	0.0573	0.119	0.6516	0.1188	0.1552	0.9047	0.0514	0.0808
263496_at	AT2G42570	similar to unknown protein [Arabidopsis thaliana] (T	1.1415	0.0045	0.0482	0.9884	0.0075	0.0487	-0.04598	0.7054	0.4332	-0.199	0.1535	0.1572
263497_at	AT2G42540	COR15A (COLD-REGULATED 15A)	-1.7358	0.0154	0.0751	-1.5011	0.0248	0.079	0.4459	0.0551	0.1	0.6806	0.0149	0.0388
263498_at	AT2G42610	similar to unknown protein [Arabidopsis thaliana] (T	0.7022	0.0231	0.089	0.8449	0.0125	0.06	-0.09035	0.6688	0.4208	0.05234	0.8027	0.4295
263499_at	AT2G42580	TTL3 (TETRATRICOPEPTIDE-REPEAT THIOREDO	-0.4432	0.4609	0.4034	-0.3314	0.5752	0.4139	-0.7328	0.0089	0.0378	-0.6209	0.0157	0.0399
263500_s_at	ATMG00750; ATMG01050	[ATG0076?2, Identical to Uncharacterized mitochon	-0.353	0.7422	0.5065	0.8644	0.4367	0.3583	-0.763	0.4885	0.3549	0.4544	0.6735	0.3886
263501_s_at	AT2G07673; ATMG0103	[AT2G07673, Identical to Uncharacterized mitochor	-0.8892	0.3571	0.3531	0.334	0.7159	0.464	-1.2699	0.2117	0.219	-0.04662	0.9591	0.4731
263502_s_at	ATMG00980; ATG07675	[ATMG00980, ribosomal protein L2];[AT2G07675, r	1.6216	0.1553	0.2299	-0.7719	0.452	0.3649	-1.5597	0.1655	0.1887	-3.9533	0.0127	0.0357
263503_s_at	ATG07676;ATMG00970	[AT2G07676, Identical to Uncharacterized mitochon	-0.4049	0.6364	0.4718	-1.1506	0.2202	0.246	-0.8607	0.3385	0.2877	-1.6064	0.1126	0.1295
263504_s_at	ATMG00940; ATG07677	[ATMG00940, hypothetical protein];[AT2G07677, a	-0.2687	0.7846	0.5191	1.5799	0.1608	0.2064	-1.3036	0.1288	0.1631	0.545	0.4694	0.3135
263505_s_at	ATMG00920; ATG07678	[ATMG00920, hypothetical protein];[AT2G07678, id	-1.5159	0.1517	0.2271	0.07961	0.9305	0.5267	-2.8969	0.0278	0.0679	-1.3014	0.2035	0.1871
263506_s_at	ATG07683;ATMG00810	[AT2G07683, transposable element gene];[ATMG0	0.07989	0.8648	0.5423	-0.3511	0.4696	0.372	0.2985	0.5347	0.3731	-0.1325	0.1783	0.4224
263507_s_at	AT2G07685;ATMG00770	[AT2G07685, transposable element gene];[ATMG0	-1.7567	0.0433	0.1199	-0.8212	0.2442	0.2606	-1.8209	0.039	0.0816	-0.8854	0.2153	0.1938
263508_s_at	ATMG00760; ATG07685	[ATMG00760, hypothetical protein];[AT2G07685, tr	-0.4364	0.5911	0.4565	0.1315	0.8691	0.5096	-1.3623	0.1147	0.1521	-0.7944	0.306	0.2414
263509_s_at	ATMG00730;AT2G07687	[ATMG00730, Encodes cytochrome c oxidase subu	0.3322	0.2734	0.3074	0.3201	0.2888	0.286	-1.299	0.0077	0.0354	-1.3112	0.0075	0.0269
263510_s_at	ATMG00900; AT2G07681	[ATMG00900, cytochrome c biogenesis orf256];[AT	-0.3093	0.6875	0.4884	-1.2174	0.1637	0.2084	-1.405	0.1207	0.1568	-2.3132	0.0318	0.06
263511_at	AT2G12420	transposable element gene	1.413	0.0767	0.1594	-0.4088	0.5304	0.3964	0.3891	0.5132	0.3644	-1.4327	0.0577	0.0865
263512_at	no_match	no_match	-0.1933	0.8258	0.5313	-1.1725	0.2273	0.2498	0.4262	0.6174	0.4037	-0.553	0.5216	0.3345
263513_at	AT2G12400	similar to unknown protein [Arabidopsis thaliana] (T	-0.1092	0.5339	0.4346	0.1444	0.4194	0.3504	0.07259	0.6361	0.4099	0.3262	0.0832	0.1076
263514_at	AT2G31860	pseudogene, poly (ADP-ribose) glycohydrolase, put	0.04902	0.8991	0.5808	0.1286	0.7411	0.4716	-0.6229	0.1612	0.1863	-0.4454	0.2871	0.2318
263515_at	AT2G12640	similar to unknown protein [Arabidopsis thaliana] (T	0.7473	0.0289	0.0985	1.0607	0.009	0.0521	0.9439	0.0135	0.0463	1.2573	0.0049	0.0221
263516_at	AT2G12600	ATRER1B (Arabidopsis thaliana endoplasmatic reti	0.1499	0.1994	0.2619	-0.1125	0.3132	0.2991	0.4376	0.0109	0.0415	0.1753	0.1469	0.1527
263517_at	AT2G12620	RD2 (RESPONSIVE TO DESSICATION 2)	0.5339	0.0191	0.082	0.8702	0.0034	0.0374	0.3986	0.0204	0.0575	0.735	0.0024	0.0161
263518_at	AT2G12655	similar to unknown protein [Arabidopsis thaliana] (T	1.9121	0.0897	0.1734	-0.8233	0.3915	0.3374	1.1728	0.2433	0.2369	-1.5626	0.1426	0.1498
263519_at	AT2G12580	40S ribosomal protein S25 (RPS25B)	0.01646	0.953	0.5655	0.2722	0.3579	0.3219	0.2577	0.2778	0.2568	0.5134	0.0667	0.0941
263520_at	AT2G42640	ATP binding / protein kinase/ protein serine/threonin	1.985	0.0139	0.0722	0.3763	0.4734	0.3735	-1.6027	0.0277	0.0637	-3.2169	0.0025	0.0165
263521_at	AT2G42960	DNA binding	0.3136	0.2062	0.2661	0.2355	0.3209	0.3036	-0.3647	0.0788	0.1227	-0.4427	0.0464	0.0758
263522_at	AT2G42950	similar to unknown protein [Arabidopsis thaliana] (T	-1.6183	0.234	0.2839	1.1812	0.3645	0.325	-1.7198	0.2109	0.2183	1.0798	0.403	0.2854
263523_at	AT2G42930	transposable element gene	3.5753	0.0513	0.1301	-1.0005	0.4842	0.3777	2.725	0.1039	0.1441	-1.8509	0.2274	0.2001
263524_x_at	AT2G42920	transposable element gene	-0.5946	0.6383	0.4724	-0.04413	0.9717	0.5371	0.5736	0.6294	0.4077	1.124	0.3644	0.2688
263525_at	AT2G42840	AGL61; DNA binding / transcription factor	-0.4502	0.6203	0.4666	0.649	0.4828	0.3773	-0.4645	0.3736	0.3045	0.6347	0.2433	0.2089
263526_at	AT2G42830	zinc finger (CCCH-type) family protein / D111/G-pat	0.4076	0.0285	0.0977	0.7565	0.0028	0.0352	-0.5693	0.0094	0.0388	-0.1814	0.21	0.1909
263527_at	AT2G42810	pathogenesis-related thaumatin family protein	0.4588	0.5894	0.4559	-0.7907	0.3698	0.3275	0.2601	0.6515	0.4151	-0.9895	0.1373	0.1464
263528_at	AT2G42800	peroxidase, putative	-1.9999	0.0519	0.1307	-1.151	0.1899	0.2264	-1.2605	0.119	0.1555	-0.4116	0.5535	0.3463
263529_at	AT2G42765	ADP-ribosyl-1/ATARL1 (ADP-RIBOSYLATION FACT	0.1276	0.2601	0.2997	0.25	0.062	0.1238	-0.3045	0.0392	0.0769	-0.1821	0.1347	0.1448
263530_at	no_match	no_match	0.4128	0.4819	0.4127	-0.7902	0.2124	0.241	1.6916	0.0042	0.0278	0.4886	0.1653	0.1644
263531_s_at	AT3G31900;AT2G25020	[AT3G31900, similar to unknown protein [Arabidops	-0.0724	0.9461	0.5636	-1.321	0.2594	0.2696	2.5844	0.062	0.107	1.3358	0.2549	0.2151
263532_s_at	AT3G37350;AT2G24990	[AT3G37350, RIC1 family protein];[AT2G24990, RI	0.9017	0.0024	0.0421	0.9497	0.002	0.033	-0.1715	0.2627	0.248	-0.1235	0.4014	0.2847
263533_at	AT2G42820	TIC55 (TRANSLOCON AT THE INNER ENVELOPE	-0.2901	0.0697	0.1522	-0.4857	0.0146	0.0638	0.2098	0.1499	0.1788	0.01418	0.9101	0.4599
263534_at	AT2G42945;AT2G42940	[AT2G42945, similar to unknown protein [Arabidops	-0.2506	0.1274	0.2063	0.1709	0.2606	0.2701	0.5956	0.0103	0.0403	1.0171	0.0015	0.0137
263535_at	AT2G42930	similar to unknown protein [Vitis vinifera] (E	-0.6499	0.1411	0.2183	-0.5324	0.2081	0.2383	0.4793	0.1189	0.1554	0.5969	0.0694	0.0965
263536_at	AT2G25000	WRKY60 (WRKY DNA-BINDING PROTEIN 60); tra	1.3036	0.0019	0.0391	1.2572	0.0021	0.0332	0.3977	0.0865	0.1296	0.3513	0.1163	0.1322
263537_at	AT2G24790	COL3 (CONSTANS-LIKE 3); protein binding / trans	-0.4014	0.0903	0.174	-0.08019	0.6799	0.4519	-0.5044	0.0073	0.0344	-0.1832	0.1412	0.1489
263538_at	AT2G25010	similar to unknown protein [Arabidopsis thaliana] (T	0.5507	0.0632	0.1441	0.2861	0.2556	0.2676	0.000049	0.9686	0.5096	-0.2556	0.3019	0.2396
263539_at	AT2G42850	TAT3 (TYROSINE AMINOTRANSFERASE 3); tran	1.8502	0.0087	0.0606	1.467	0.0191	0.0713	0.1041	0.5878	0.3937	-0.2791	0.1898	0.1791
263540_at	AT2G42780	unknown protein	0.929	0.5825	0.4533	-1.2667	0.4611	0.3684	-0.5611	0.7366	0.4437	-2.7567	0.151	0.1554
263541_at	AT2G42860	chaperone protein dnaJ-related	-0.105	0.3241	0.3368	-0.02199	0.8256	0.4975	0.4399	0.0093	0.0386	0.5229	0.005	0.0222
263542_at	AT2G21630	transport protein, putative	0.03216	0.8921	0.5491	0.03134	0.8949	0.5171	-0.2978	0.056	0.101	-0.2986	0.0556	0.0844
263543_at	AT2G21610	pectinesterase family protein	1.6511	0.0483	0.1266	-0.00649	0.9917	0.542	1.7171	0.0418	0.085	0.05951	0.9234	0.4637
263544_at	AT2G21590	APL4 (Apse subunit of AGP 4); glucose-1-phosphat	0.4001	0.0885	0.1724	0.05153	0.7871	0.4852	-1.0126	0.0032	0.0251	-1.3611	0.001	0.0123
263545_at	AT2G21560	similar to unknown protein [Arabidopsis thaliana] (T	0.826	0.0819	0.1656	1.3109	0.0214	0.0745	0.3839	0.3116	0.2743	0.8688	0.0589	0.0875
263546_at	AT2G21550	bifunctional dihydrofolate reductase-thymidylate syr	1.8548	0.1826	0.2501	0.7146	0.5685	0.4113	0.0387	0.9585	0.5073	-1.1015	0.1898	0.1791
263547_at	AT2G21680	kelch repeat-containing F-box family protein	0.781	0.403	0.3769	-1.2242	0.2169	0.2439	0.4918	0.588	0.3937	-1.5134	0.1445	0.1512
263548_at	AT2G21660	ATGRP7 (COLD, CIRCADIAN RHYTHM, AND RNA	0.6711	0.5648	0.4469	1.0657	0.3759	0.3301	-0.6373	0.1072	0.1466	-0.2427	0.4745	0.3155
263549_at	AT2G21650	MEE3 (maternal effect embryo arrest 3); DNA bind	-2.8323	3.00E-04	0.0312	-2.1895	8.00E-04	0.0278	0.5551	0.0817	0.1253	1.1979	0.0075	0.027
263550_at	AT2G17033	pentatricopeptide (PPR) repeat-containing protein	-0.04675	0.7515	0.5088	-0.09135	0.5437	0.4022	-0.7407	0.0058	0.0318	-0.7853	0.0047	0.0217
263551_at	AT2G17110	similar to unknown protein [Arabidopsis thaliana] (T	-0.02652	0.9288	0.5596	0.6573	0.0779	0.1398	-0.8871	0.0055	0.0311	-0.2033	0.2804	0.2284
263552_x_at	AT2G24980	proline-rich extensin-like family protein	-1.851	0.132	0.2104	-0.368	0.7264	0.4677	-0.7245	0.5009	0.3599	0.7585	0.4823	0.3185
263553_at	AT2G16430	ATPAP10/PAP10; protein serine/threonine phospha	0.1704	0.2323	0.2833	0.06979	0.5955	0.4217	0.1489	0.2484	0.2401	0.04831	0.6841	0.392
263554_at	AT2G16410	transposable element gene	0.6583	0.5466	0.4396	0.9813	0.3823	0.333	-0.7953	0.4713	0.3481	-0.4723	0.6616	0.3847
263555_at	AT2G16460	similar to unknown protein [Arabidopsis thaliana] (T	-0.1085	0.5431	0.4382	-0.2381	0.219	0.2452	0.3979	0.0549	0.0997	0.2684	0.1443	0.1511
263556_at	AT2G16365	F-box family protein	-0.1546	0.6485	0.476	0.1216	0.7186	0.4648	-0.4276	0.0229	0.0612	-0.1514	0.2723	0.2241
263557_at	AT2G16400	BLH7 (BELL1-LIKE HOMEODOMAIN 7); DNA bind	0.05672	0.6232	0.4675	-0.08092	0.4905	0.3805	-0.1302	0.2452	0.2381	-0.2678	0.0489	0.0782
263558_at	AT2G16380	SEC14 cytosolic factor family protein / phosphoglyc	-0.6363	0.0525	0.1315	-0.2603	0.3269	0.3069	-0.02299	0.907	0.4943	0.353	0.1287	0.1407
263559_at	AT2G16380	transposable element gene	0.8801	0.5598	0.4448	-1.825	0.1634	0.2083	1.3389	0.2162	0.2214	-1.1662	0.2703	0.2229
263560_s_at	AT2G15370;AT2G15350	[AT2G15370, FUT5 (Fucosyltransferase 5); fucosyl	0.3396	0.6968	0.4918	-0.2762	0.7504	0.4751	-0.1594	0.8537	0.4795	-0.7752	0.3931	0.2813
263561_at	AT2G15360	galactoside 2-alpha-L-fucosyltransferase	-0.5588	0.5897	0.456	0.5069	0.6235	0.4322	0.1565	0.5968	0.3969	1.2222	0.011	0.0328
263562_at	AT2G15420	myosin heavy chain-related	-1.7134	0.0639	0.1448	-1.5315	0.0856	0.1473	0.003754	0.9958	0.5165	0.1857	0.7938	0.4271
263563_at	AT2G15410	transposable element gene	-1.292	0.0034	0.0447	0.06423	0.7722	0.4812	-0.63	0.0286	0.0686	0.7262	0.0181	0.0432
263564_s_at	AT2G15400;AT2G15430	[AT2G15400, RBP36B (RNA polymerase II 36 kDa	0.5048	0.1627	0.236	0.7116	0.0736	0.1362	-0.2099	0.3395	0.2882	-0.0031	0.988	0.4797
263565_at	AT2G15360	FUT4 (fucosyltransferase 4); fucosyltransferase/ tra	0.7128	0.1998	0.2621	0.9711	0.1048	0.1636	-0.08693	0.4097	0.3206	0.1714	0.1439	0.1509
263566_at	AT2G15340	glycine-rich protein	-0.4165	0.5398	0.4367	0.2925	0.6627	0.4459	0.5218	0.4099	0.3207	1.2307	0.096	0.1175
263567_at	AT2G15440	similar to unknown protein [Arabidopsis thaliana] (T	-0.2255	0.6015	0.4601	-0.1467	0.7313	0.4688	0.1243	0.7706	0.4544	0.2031	0.6369	0.376
263568_at	no_match	no_match	1.8043	0.1267	0.2058	-0.2742	0.7845	0.4847	-0.9355	0.369	0.3023	-3.014	0.0311	0.0595
263569_at	AT2G27170	TTN7 (TITAN7); ATP binding	-0.1503	0.5506	0.4414	0.1159	0.6421	0.4389	-1.3236	2.00E-04	0.0126	-1.0574	4.00E-04	0.0091
263570_at	AT2G27150	AAO3 (ABSCISIC ALDEHYDE OXIDASE 3)	0.9595	0.0025	0.0424	0.5771	0.0154	0.0649	-0.6882	0.0084	0.0369	-1.0706	0.0017	0.0144
263571_at	AT2G17050	disease resistance protein (TIR-NBS-LRR class), p	-0.2874	0.7494	0.5085	-0.01869	0.9833	0.54	1.1365	0.2454	0.2382	1.4052	0.1679	0.166
263572_at	AT2G17060	disease resistance protein (TIR-NBS-LRR class), p	-0.02769	0.9845	0.5732	-0.2704	0.8501	0.5044	0.8338	0.2476	0.2397	0.5911	0.392	0.2807
263573_at	AT2G17150	RWP-RK domain-containing protein	-0.1834	0.389	0.3694	-0.3025	0.1867	0.2241	-0.2682	0.2166	0.2216	-0.3872	0.1018	0.1219
263574_at	AT2G16990	tetracycline transporter	-0.7516	0.0388	0.1135	-0.4004	0.1819	0.2211	-0.5348	7.00E-04	0.0159	-0.1835	0.0306	0.0589
263575_at	AT2G17070	similar to unknown protein [Arabidopsis thaliana] (T	-0.4924	0.5664	0.4474	0.1526	0.856	0.5062	-0.9891	0.1669	0.1896	-0.344	0.5888	0.3595
263576_at	AT2G17080	similar to unknown protein [Arabidopsis thaliana] (T	-1.9553	0.3414	0.3459	1.8612	0.3625	0.3241	-2.3035	0.2726	0.2538	1.513	0.4508	0.3063
263577_at	AT2G17090	SSP (SHORT SUSPENSOR); kinase	0.5275	0.5765	0.4512	0.6278	0.5099	0.3886	1.0397	0.1884	0.2046	1.1399	0.1575	0.1597
263578_at	AT2G17020	F-box family protein (FBL10)	0.2246	0.2665	0.3031	0.04663	0.8021	0.4902	-0.9545	0.0025	0.0232	-1.1325	0.0013	0.0133
263579_at	AT2G17030	F-box family protein	0.1816	0.242	0.2887	-0.00879	0.9502	0.532	0.073	0.5698	0.3866	-0.1174	0.3764	0.274
263580_at	AT2G17140	binding	-1.862	0.2768	0.3099	1.6765	0.3206	0.3035	-2.3196	0.1865	0.2033	1.2188	0.4499	0.306
263581_at	AT2G17160	protein kinase-related	0.607	0.5691	0.4486	-2.2417	0.0841	0.1458	2.0544	0.1038	0.144	-0.7943	0.4626	0.3111
263582_at	AT2G17120	LYM2 (LYSM DOMAIN GPI-ANCHORED PROTEIN	0.8542	0.006	0.0536	0.5931	0.0209	0.0738	0.7256	5.00E-04	0.0148	0.4645	0.0025	0.0165
263583_at	AT2G17130	IDH2 (ISOCITRATE DEHYDROGENASE SUBUNI	0.6503	0.0164	0.0771	0.9251	0.0048	0.042	-0.107	0.4907	0.3559	0.1677	0.3004	0.2388
263584_at	AT2G17040	ANAC036 (Arabidopsis NAC domain containing pro	1.3008	0.0653	0.1466	1.5121	0.0428	0.1028	0.3021	0.0796	0.1235	0.5135	0.0165	0.041
263585_at	AT2G25210	60S ribosomal protein L39 (RPL39A)	0.2668	0.3134	0.3305	0.5609	0.0725	0.1349	0.2154	0.2103	0.218	0.5095	0.0243	0.0512
263586_at	AT2G25350	phox (PX) domain-containing protein	0.5362	0.0137	0.0719	0.5	0.0173	0.0681	-0.01095	0.9358	0.5023	-0.04712	0.7308	0.4074
263587_at	AT2G25340	ATVAMP712 (Arabidopsis thaliana vesicle-associat	-1.1556	0.022	0.0871	-0.4913	0.1968	0.2308	-0.6274	0.1194	0.1558	0.03696	0.913	0.4607
263588_s_at	AT2G25330;AT2G25320	[AT2G25330, meprin and TRAF homology domain-	0.1239	0.7959	0.5226	-0.04587	0.9234	0.525	-0.2157	0.6367	0.41	-0.3854	0.4134	0.2898
263589_at	AT2G25280	similar to unknown [Populus trichocarpa] (GB:ABK9	0.3016	0.0602	0.1404	0.4569	0.017	0.0677	0.1614	0.2369	0.2334	0.3167	0.0526	0.0818
263590_at	AT2G21820	leucine-rich repeat protein kinase, putative	-0.191	0.361	0.3551	-0.3179	0.1615	0.2069	-0.1574	0.3408	0.2886	-0.2843	0.1228	0.1369
263591_at	AT2G01910	ATMAP65-6; microtubule binding	-0.3578	0.4701	0.4073	-0.353	0.4757	0.3744	0.2391	0.4584	0.3424	0.2439	0.4501	0.306
263592_at	AT2G01940	transposable element gene	-0.2348	0.794	0.5222	-0.8887	0.3503	0.3181	1.2488	0.2118	0.2191	0.5949	0.5185	0.333
263593_at	AT2G01860	EMB975 (EMBRYO DEFECTIVE 975)	-0.4208	0.0394	0.1145	-0.6551	0.0094	0.0529	-0.1677	0.1559	0.1829	-0.402	0.0139	0.0375
263594_at	AT2G01880	ATPAP17/PAP7 (purple acid phosphatase 7); acid p	-0.2076	0.872	0.5445	-0.7675	0.5599	0.4083	0.3738	0.7725	0.4551	-0.1861	0.8851	0.4529
263595_at	AT2G01890	PAP9 (PURPLE ACID PHOSPHATASE PRECURS	0.6193	2.00E-04	0.0312	-1.4981	3.00E-04	0.0249	-0.1487	0.2971	0.2672	-0.02747	0.8366	0.4388
263596_at	AT2G01900	endonuclease/exonuclease/phosphatase family pro	0.6016	0.5572	0.4438	-2.5861	0.0514	0.1125	1.4509	0.1977	0.2104	-1.7367	0.1385	0.1472
263597_at	AT2G01870	similar to unknown protein product [Vitis vinifera] (G	-0.438	0.1381	0.2159	-0.2974	0.2776	0.2796	0.5473	0.0188	0.055	0.6879	0.0087	0.0289
263598_at	AT2G01850	EXGT-A3 (endo-xyloglucan transferase A3); hydrol	-0.3078	0.2599	0.2996	-0.3675	0.1924	0.2276	-0.1874	0.0655	0.1104	-0.2471	0.5293	0.3574
263599_at	AT2G01830	WOL (WOODEN LEG)	-0.08483	0.8197	0.5295	0.2924	0.4489	0.3635	-0.4807	0.0086	0.0372	-0.1034	0.3599	0.267
263600_at	AT2G16390	DRD1 (DEFECTIVE IN RNA-DIRECTED DNA MET	-0.1809	0.7357	0.5042	-0.1901	0.723	0.4664	-1.9419	0.0178	0.0533	-1.951	0.0175	0.0423
263601_s_at	AT4G34570; AT2G16370	[AT4G34570, THY-2 (THYMIDYLATE SYNTHASE 2	0.01814	0.939	0.562	0.3171	0.2276	0.2499	-0.9419	0.0071	0.0341	-0.6429	0.0257	0.0531
263602_at	AT2G16360	40S ribosomal protein S25 (RPS25A)	0.6148	0.2333	0.2838	0.04543	0.9224	0.5247	0.1567	0.7361	0.4437	-0.4127	0.3952	0.2824
263603_at	AT2G16340	unknown protein	0.2359	0.838	0.5348	-1.5897	0.2155	0.2431	1.3169	0.2903	0.2638	-0.03692	0.9744	0.4767
263604_s_at	AT2G06690;AT2G12140	[AT2G06690, transposable element gene];[AT2G12	-0.9859	0.1864	0.253	-0.4666	0.4929	0.3815	-0.05228	0.9014	0.4928	0.4671	0.3036	0.2405
263605_at	AT2G16480	SWIB complex BAF60b domain-containing protein	0.8089	0.0013	0.0376	0.7263	0.002	0.033	-0.688	1.00E-04	0.0119	-0.7706	1.00E-04	0.0058
263606_at	AT2G16280	very-long-chain fatty acid condensing enzyme, putat	0.7641	0.023	0.0886	-1.0609	0.0076	0.0488	0.3435	0.0236	0.0622	0.04855	0.6429	0.3782
263607_at	AT2G16270	similar to unknown protein [Arabidopsis thaliana] (T	-0.4468	0.2923	0.3186	-0.503	0.2443	0.2606	0.0501	0.8701	0.4841	-0.00601	0.9843	0.4791
263608_at	AT2G16260	pseudogene of glycine-rich RNA-binding protein	0.1932	0.4436	0.3951	0.8932	0.0172	0.0679	-0.604	0.0567	0.1017	0.09598	0.6948	0.3958
263609_at	AT2G16250	leucine-rich repeat transmembrane protein kinase,	1.1697	0.3736	0.3612	0.1288	0.9175	0.5235	-0.8239	0.2348	0.2321	-1.8648	0.0341	0.0624
263610_at	AT2G16230	glycosyl hydrolase family 17 protein	-0.00206	0.9983	0.5763	-0.07725	0.9369	0.5284	-0.6368	0.5253	0.3692	0.712	0.4805	0.3177
263611_at	AT2G16450	F-box family protein	1.191	0.2563	0.2972	2.7719	0.0369	0.0949	-0.6401	0.4521	0.3396	0.9408	0.2884	0.2326
263612_at	AT2G16440	DNA replication licensing factor, putative	0.03702	0.9208	0.5571	0.05845	0.875	0.5116	-0.6184	0.1375	0.1693	-0.5969	0.1481	0.1535
263613_at	AT2G25250	similar to unknown protein [Arabidopsis thaliana] (T	-0.6373	0.0197	0.0831	-0.6489	0.0186	0.0704	0.2215	0.1564	0.1833	0.2099	0.1742	0.1698
263614_at	AT2G25240	serine-type endopeptidase inhibitor	0.04012	0.9564	0.5664	-1.8179	0.0579	0.1196	2.1134	0.0375	0.08	0.2553	0.73	0.4072
263615_at	AT2G25230	MYB108 (myb domain protein 108); DNA binding / t	1.196	0.3624	0.3556	-2.4839	0.0999	0.1593	2.186	0.1337	0.1665	1.4939	0.2688	0.2221
263616_at	AT2G04680	DC1 domain-containing protein	0.643	0.6205	0.4666	-0.7013	0.5903	0.4196	0.01393	0.9913	0.5155	-1.3304	0.3298	0.2532
263617_at	AT2G04670	transposable element gene	0.1026	0.9462	0.5636	-0.0746	0.9608	0.5343	-0.6782	0.6595	0.4178	-0.8554	0.5814	0.3566
263618_at	AT2G04660	APC2 (anaphase-promoting complex/cyclosome 2);	0.631	0.0261	0.0934	0.5799	0.0197	0.072	-0.354	0.0831	0.1268	-0.3051	0.1187	0.1338
263619_at	AT2G04650	ADP-glucose pyrophosphorylase family protein	-0.1825	0.6698	0.4825	-0.181	0.6722	0.4492	0.01211	0.9765	0.5117	0.01357	0.9737	0.4765
263620_at	no_match	no_match	-1.0484	0.4274	0.3881	-0.09356	0.941	0.5293	-0.9788	0.4564	0.3414	-0.02392	0.9849	0.4791
263621_at	AT2G04630	DNA-directed RNA polymerase II, putative	0.07909	0.7471	0.5081	0.42216	0.1356	0.1873	0.3643	0

263690_at	AT1G26960	ATHB23 (ARABIDOPSIS THALIANA HOMEOBOX	0.2486	0.3832	0.3663	0.5777	0.0853	0.147	0.1145	0.4653	0.3454	0.4436	0.0354	0.0637
263691_at	AT1G26880	60S ribosomal protein L34 (RPL34A)	-0.1693	0.0801	0.1633	0.2488	0.0266	0.0816	0.4663	0.003	0.0248	0.8843	3.00E-04	0.008
263692_at	AT1G26850	dehydration-responsive family protein	-0.1128	0.2076	0.2669	-0.1838	0.0707	0.1329	0.06455	0.1091	0.1478	-0.00643	0.8478	0.4422
263693_at	AT1G31200	ATPP2-A9 (Phloem protein 2-A9); carbohydrate bin	0.05813	0.8945	0.5498	0.02136	0.9611	0.5343	0.8819	0.0094	0.0388	0.8452	0.0109	0.0326
263694_at	AT3G60565,AT1G31210	[AT3G60565, transposable element gene];[AT1G3	-1.8804	0.0711	0.1537	-1.431	0.1367	0.1882	-0.8946	0.2541	0.2432	-0.4452	0.5441	0.3425
263695_at	AT1G31220	phosphoribosylglycinamide formyltransferase	0.0477	0.7836	0.5189	-0.2559	0.1903	0.2266	0.362	0.0428	0.0862	0.05834	0.6614	0.3847
263696_at	AT1G31230	AK-HSDH/AK-HSDH I (ASPARTATE KINASE-HOM	-0.5954	0.1001	0.1826	-0.4736	0.1653	0.2091	-0.157	0.3992	0.3163	-0.03523	0.8428	0.4408
263697_at	AT1G31080	F-box family protein	1.2346	0.5303	0.4331	-2.2095	0.2807	0.2848	1.4389	0.4291	0.3293	-2.0043	0.2883	0.2326
263698_at	AT1G31100	transposable element gene	0.02394	0.9737	0.5707	-1.5785	0.0816	0.1432	1.4525	0.1003	0.1413	-0.15	0.8367	0.4392
263699_at	AT1G31120	KUP10 (K+ transporter 10); potassium ion transmer	0.6084	0.2091	0.2675	0.9062	0.0898	0.1511	-0.4402	0.33	0.2833	-0.1424	0.7381	0.4097
263700_at	AT1G31150	similar to unknown protein [Arabidopsis thaliana] (T	-0.2126	0.3242	0.3368	-0.1146	0.5775	0.415	0.1686	0.2645	0.2491	0.2646	0.1085	0.1266
263701_at	AT1G31160	zinc-binding protein, putative / protein kinase C inhi	-0.5436	0.0466	0.1241	-0.5683	0.0409	0.1004	-0.01811	0.9223	0.4986	-0.04284	0.818	0.4337
263702_at	AT1G31240	DNA binding	-0.1182	0.7929	0.5217	0.5969	0.2295	0.2511	-0.03148	0.944	0.5042	0.6837	0.18	0.1733
263703_at	AT1G31170	ATSRX/SRX (SULFIREDOXIN); DNA binding / oxid	-0.3845	0.151	0.2265	-0.03798	0.8695	0.5098	0.6808	0.0053	0.0303	1.0273	0.0011	0.0126
263704_at	AT1G31130	similar to unknown protein [Arabidopsis thaliana] (T	0.5222	0.0815	0.1651	0.3519	0.1936	0.2284	-0.2829	0.2779	0.2569	-0.4532	0.1148	0.1311
263705_at	AT1G31190	inositol monophosphatase family protein	-0.5788	0.0094	0.0624	-0.7759	0.0033	0.0371	-0.2851	0.0821	0.1257	-0.4822	0.0174	0.0422
263706_s_at	AT1G31180,AT5G14200	F-box family protein	1.2346	0.5303	0.4331	-2.2095	0.2807	0.2848	1.4389	0.4291	0.3293	-2.0043	0.2883	0.2326
263707_at	AT1G09300	metallopeptidase M24 family protein	0.9299	0.0419	0.1177	1.3762	0.012	0.0587	-0.3326	0.3505	0.2935	0.1137	0.7363	0.4092
263708_at	AT1G09320	agenet domain-containing protein	0.3836	0.0284	0.0976	0.4662	0.0151	0.0646	-0.02954	0.8088	0.4662	0.05309	0.6665	0.3863
263709_at	AT1G09310	similar to unknown protein [Arabidopsis thaliana] (T	-0.6196	0.0093	0.0621	0.9312	0.0021	0.0331	0.7482	2.00E-04	0.0126	0.4366	0.0014	0.0133
263710_at	AT1G09330	Identical to Uncharacterized FAM18-like protein At1	0.3748	0.0521	0.131	0.3443	0.0658	0.1283	0.4861	0.0102	0.0401	0.4556	0.0128	0.0358
263711_at	AT2G03630	protein phosphatase 2C, putative / PP2C, putative	-0.1466	0.4336	0.391	-0.07498	0.6796	0.4518	0.506	0.009	0.0378	0.5776	0.0056	0.0234
263712_at	AT2G20585	NFD6 (NUCLEAR FUSION DEFECTIVE 6)	0.1155	0.3642	0.3564	-0.2291	0.1125	0.1694	1.3966	2.00E-04	0.0133	1.0519	7.00E-04	0.0108
263713_at	AT2G20595	similar to unknown protein [Arabidopsis thaliana] (T	0.5469	0.7138	0.4972	-0.7177	0.6325	0.4355	0.4833	0.7453	0.4466	-0.7812	0.6038	0.3645
263714_at	AT2G20610	SUR1 (SUPERROOT 1); transaminase	-0.3655	0.141	0.2183	-0.3695	0.1297	0.1827	0.1544	0.0399	0.0827	0.1404	0.0526	0.0818
263715_at	AT2G20570	GPR1 (GOLDEN2-LIKE 1); transcription factor	-0.1798	0.5635	0.4462	-0.5614	0.121	0.1763	0.2925	0.033	0.0742	-0.0891	0.3854	0.2781
263716_at	AT2G20580	AtRPN1a/RPN1A (26S proteasome regulatory subu	0.655	0.0154	0.0751	0.5882	0.022	0.075	-0.2487	0.1987	0.211	-0.3155	0.1227	0.1369
263717_at	AT2G20560	malate oxidoreductase, putative	0.641	0.0041	0.0468	0.3654	0.0283	0.0836	0.2815	0.0598	0.1049	0.005853	0.9594	0.4732
263718_at	AT2G13570	CCAAT-box binding transcription factor, putative	-1.8896	0.1433	0.2202	-1.5832	0.2025	0.2344	-1.2884	0.0279	0.068	-0.982	0.0618	0.0901
263719_at	AT2G13600	pentatricopeptide (PPR) repeat-containing protein	0.3958	0.4159	0.3827	-0.06381	0.8909	0.516	0.7354	0.1674	0.1901	0.2757	0.562	0.3497
263720_at	AT2G13630	ATCHX15 (cation/hydrogen exchanger 15); monove	0.1341	0.3273	0.3385	-0.8666	0.3593	0.3226	2.0489	0.0708	0.1586	0.2482	0.7817	0.4233
263721_at	AT2G13630	F-box family protein-related	0.084	0.9491	0.5645	0.9023	0.5063	0.3872	0.7762	0.5645	0.3845	1.5944	0.267	0.2212
263722_at	AT2G13650	GONST1 (GOLGI NUCLEOTIDE SUGAR TRANSP	0.5628	0.0128	0.0698	0.3138	0.0753	0.1376	0.1171	0.423	0.3267	-0.1318	0.3724	0.2723
263723_at	AT2G13500	similar to nucleic acid binding / zinc ion binding [Ara	0.7288	0.4655	0.4054	-0.3424	0.7242	0.4667	0.07773	0.9396	0.5022	-0.9934	0.3337	0.2551
263724_at	AT2G13510	similar to unknown protein [Arabidopsis thaliana] (T	0.0805	0.8059	0.5257	-0.5695	0.1368	0.1883	0.2872	0.3951	0.3143	-0.3627	0.2956	0.2364
263725_at	AT2G13550	unknown protein	-0.7425	0.4653	0.4053	2.0711	0.0878	0.1492	-1.3369	0.2202	0.2237	1.4766	0.1841	0.1758
263726_at	AT2G13610	ABC transporter family protein	-1.0747	0.0725	0.1551	-1.0556	0.0759	0.138	-0.4405	0.0284	0.0684	-0.4215	0.0325	0.0609
263727_at	AT2G13540	ABH1 (ABA HYPERSENSITIVE 1)	0.5124	0.0023	0.0414	0.148	0.1154	0.1714	-0.3721	0.0073	0.0344	-0.7365	6.00E-04	0.01
263728_at	AT1G60070	clathrin binding	0.2565	0.1315	0.2099	-0.01765	0.9027	0.5196	-0.1377	0.3672	0.3016	-0.4119	0.0385	0.0674
263729_at	AT1G60080	3' exoribonuclease family domain 1-containing prote	0.1283	0.0035	0.0448	0.6388	0.0184	0.0701	0.03167	0.7942	0.4615	-0.3578	0.0345	0.0628
263730_at	AT1G60090	glycosyl hydrolase family 1 protein	0.1239	0.762	0.5121	0.4525	0.3018	0.2923	-0.257	0.538	0.3744	0.0716	0.8605	0.446
263731_at	AT1G59970	matrixin family protein	-0.4741	0.0632	0.1441	-0.7478	0.0158	0.0654	0.574	0.0066	0.0333	0.3003	0.0534	0.0826
263732_at	AT1G59980	ARL2/ATSUMO-ACTIVATING ENZYME 2)	0.1943	0.1904	0.2572	-0.3357	0.7245	0.4668	+1.6898	0.1297	0.1637	-0.6352	0.5139	0.3312
263733_at	AT1G60020	transposable element gene	1.3008	0.203	0.2642	-1.1946	0.235	0.2548	1.5106	0.1522	0.1804	-0.9848	0.3137	0.2453
263734_at	AT1G60030	xanthine/uracil permease family protein	1.4316	9.00E-04	0.0349	1.201	0.0017	0.0321	0.239	0.2124	0.2194	0.00845	0.9607	0.4734
263735_s_at	AT1G60040,AT1G59810	[AT1G60040, AGL49; transcription factor];[AT1G59	0.1239	0.8425	0.5363	0.6593	0.3223	0.3044	-0.8687	0.2113	0.2187	-0.3332	0.599	0.3631
263736_at	AT1G60000	29 kDa ribonucleoprotein, chloroplast, putative / RN	-0.1815	0.4797	0.4117	-0.2181	0.4024	0.3424	-0.1407	0.3533	0.2949	-0.1773	0.2567	0.2162
263737_at	AT1G60010	similar to unknown protein [Arabidopsis thaliana] (T	-0.1426	0.4326	0.3907	0.02657	0.8789	0.5128	-0.317	0.0277	0.0678	-0.1478	0.1898	0.1791
263738_at	AT1G60060	similar to unknown protein [Arabidopsis thaliana] (T	0.3394	0.0721	0.1548	0.1522	0.74	0.4713	0.3075	0.5006	0.3597	-0.5799	0.2351	0.2945
263739_at	AT2G21320	zinc finger (B-box type) family protein	-0.7792	0.2598	0.2996	-0.7164	0.2942	0.2888	-0.2662	0.0916	0.1338	-0.2035	0.1663	0.165
263740_at	AT2G20660	RALFL14 (RALF-LIKE 14)	0.9108	0.1539	0.2289	0.4128	0.4706	0.3723	0.03321	0.952	0.506	-0.4648	0.4207	0.2928
263741_at	AT2G20620	similar to unknown protein [Arabidopsis thaliana] (T	-0.07643	0.9481	0.5841	-0.1537	0.3546	0.3203	0.3793	0.7378	0.4442	-0.698	0.545	0.3429
263742_at	AT2G20625	similar to unknown protein [Arabidopsis thaliana] (T	-1.4282	0.143	0.22	-0.5999	0.4874	0.3793	-1.2968	0.1691	0.1912	-0.4685	0.5776	0.3551
263743_at	AT2G21390	coatomer protein complex, subunit alpha, putative	0.5526	0.0019	0.0391	0.2984	0.0171	0.0678	-0.4266	0.0049	0.0297	-0.6808	9.00E-04	0.0114
263744_at	AT2G21420	zinc finger protein-related	-0.1867	0.7969	0.5229	0.6723	0.3779	0.3309	-0.3273	0.6548	0.4161	0.5317	0.4771	0.3165
263745_at	AT2G21450	CHR34 (chromatin remodeling 34); ATP binding / D	-0.2479	0.7686	0.5142	-1.1983	0.2027	0.2346	0.6758	0.4391	0.3337	-0.2746	0.7449	0.4119
263746_at	AT2G21460	transposable element gene	-0.03005	0.9806	0.5721	-1.1345	0.3831	0.3332	1.6419	0.2296	0.2292	0.5375	0.667	0.3864
263747_at	AT2G21470	SAE2 (SUMO-ACTIVATING ENZYME 2)	0.283	0.2548	0.2964	-0.03848	0.8655	0.5086	0.272	0.2563	0.2444	-0.04942	0.8218	0.4347
263748_at	AT2G21480	protein kinase family protein	0.2467	0.6683	0.4821	-0.337	0.5625	0.4092	0.09701	0.8648	0.4827	-0.4867	0.4139	0.29
263749_at	AT2G21520	transporter	0.5739	0.0478	0.1259	0.5585	0.0517	0.1128	-0.2221	0.2923	0.2648	-0.2375	0.2647	0.2202
263750_at	no_match	no_match	-0.2244	0.5403	0.4368	-0.2154	0.5558	0.4068	-0.1514	0.6087	0.4009	-0.1424	0.6294	0.3735
263751_at	AT2G21300	kinesin motor family protein	-0.3314	0.4743	0.4095	-0.5869	0.2348	0.2547	-1.0016	0.0756	0.1197	-1.2571	0.0402	0.0693
263752_at	AT2G21310	transposable element gene	-0.984	0.3156	0.3319	-0.2851	0.7565	0.477	-1.4646	0.1632	0.1873	-0.7658	0.4228	0.2937
263753_at	AT2G21490	LEA (DEHYDRIN LEA)	0.09419	0.9063	0.5528	1.2857	0.1622	0.2075	-0.5319	0.518	0.3662	0.6596	0.4296	0.2966
263754_at	AT2G21510	DNAJ heat shock N-terminal domain-containing pro	0.98	0.3506	0.3499	-0.1179	0.905	0.5201	1.3765	0.2122	0.2193	0.2786	0.779	0.4226
263755_at	AT2G21340	enhanced disease susceptibility protein, putative / s	0.06269	0.7565	0.5106	-0.1872	0.3775	0.3308	-0.5779	0.0272	0.0671	-0.8277	0.0082	0.0281
263756_at	AT2G21270	ubiquitin fusion degradation UFD1 family protein	0.6507	0.001	0.0358	0.529	0.0023	0.0334	0.5839	0.0016	0.0202	0.4622	0.0037	0.0198
263757_at	AT2G21430	cysteine proteinase A494, putative / thiol protease,	0.2884	0.4467	0.3966	0.6086	0.1499	0.198	-0.0685	0.7958	0.4621	0.2517	0.367	0.27
263758_s_at	AT2G21260,AT2G21250	[AT2G21260, mannose 6-phosphate reductase (NA	0.7951	0.0019	0.0391	0.7444	0.0024	0.0339	-0.2113	0.028	0.068	-0.262	0.0139	0.0375
263759_at	AT2G21580	identical to 30S ribosomal protein S31, mitochondri	0.1752	0.1596	0.2332	0.05343	0.6267	0.4334	0.7	0.0023	0.0226	0.5782	0.0047	0.0217
263760_at	AT2G21280	GC1 (GIANT CHLOROPLAST 1); binding / catalytic	-0.473	0.0167	0.0775	-0.6185	0.0066	0.0461	-0.286	0.0748	0.1191	-0.4315	0.0225	0.0488
263761_at	AT2G21330	fructose-bisphosphate aldolase, putative	-0.645	0.0023	0.0415	-0.6312	0.0025	0.0339	-0.3157	0.0275	0.0675	-0.3019	0.0316	0.0599
263762_at	AT2G21380	kinesin motor protein-related	0.09273	0.7013	0.4929	0.03146	0.8955	0.5174	-0.4195	0.1207	0.1568	-0.4807	0.0873	0.1107
263763_at	AT2G21385	similar to Os09g0531100 [Oryza sativa (japonica cu	-0.4618	0.0168	0.0777	-0.6552	0.005	0.0424	-0.2377	0.1118	0.1497	-0.431	0.0211	0.0471
263764_at	AT2G21410	VHA-A2 (VACUOLAR PROTON ATPASE A2); ATP	0.3634	0.0212	0.0855	0.1681	0.1639	0.2085	-0.1329	0.2495	0.2407	-0.3282	0.0293	0.0573
263765_at	AT2G21450	SEC14 cytosolic factor, putative / phosphoglyceride	-1.457	0.0169	0.0778	-1.8196	0.0079	0.0494	0.2857	0.1074	0.1467	-0.07691	0.6073	0.3658
263766_at	AT2G21440	RNA recognition motif (RRM)-containing protein	0.0381	0.8526	0.5389	0.1367	0.5164	0.3912	-0.1971	0.3632	0.2996	-0.09853	0.6354	0.3755
263767_at	AT2G06310	transposable element gene	-1.3512	0.4884	0.4152	-1.1996	0.5357	0.3988	-0.9259	0.2769	0.2563	-0.7744	0.3522	0.2636
263768_x_at	AT2G06330	transposable element gene	2.3066	0.1166	0.1973	-0.00679	0.9956	0.5431	1.336	0.3119	0.2744	-0.9774	0.4452	0.304
263769_at	AT2G06390	transposable element gene	0.531	0.669	0.4823	-2.355	0.1106	0.1679	0.7561	0.441	0.3345	-2.1299	0.0738	0.0998
263770_at	AT2G06410	transposable element gene	0.8119	0.3098	0.3285	-1.2188	0.156	0.2028	0.7149	0.3641	0.3001	-1.3158	0.1328	0.1435
263771_at	AT2G06260	transposable element gene	-0.8397	0.4028	0.3767	0.1195	0.9006	0.5191	-0.6784	0.4921	0.3564	0.2807	0.7702	0.42
263772_at	AT2G06255	ELF4-L3 (ELF4-LIKE 3)	0.6802	0.0313	0.1026	0.9784	0.0094	0.0532	-0.03095	0.8633	0.4822	0.2673	0.1881	0.1782
263773_at	AT2G21370	xylulose kinase, putative	-0.5855	0.0343	0.1071	-0.8692	0.0094	0.053	-0.2729	0.1931	0.2074	-0.5566	0.0333	0.0616
263774_at	AT2G06280	dehydration-responsive family protein	-0.03305	0.8758	0.5454	-0.4884	0.0696	0.1321	0.2143	0.341	0.2887	-0.2411	0.291	0.2341
263775_at	AT2G46410	CPC (CAPRICE); DNA binding / transcription factor	-0.8632	0.2777	0.3101	-2.3659	0.0263	0.0811	1.8473	0.0548	0.0997	0.3446	0.6426	0.3781
263776_s_at	AT2G46430,AT2G46440	[AT2G46430, ATCNGC3 (CYCLIC NUCLEOTIDE (	0.9896	0.0014	0.038	0.5996	0.0087	0.0512	-0.5415	0	0.0092	-0.9315	0	0.0043
263777_at	AT2G46450	ATCNGC12 (cyclic nucleotide gated channel 12); c	0.1179	0.6069	0.4621	-0.3517	0.1717	0.2139	-0.5866	0.0116	0.0428	-1.0683	0.0014	0.0136
263778_at	AT2G46470	OXA1L (INNER MEMBRANE PROTEIN OXA1-LIK	0.6755	0.0689	0.151	0.2367	0.4355	0.3577	-0.4163	0.0179	0.0535	-0.8552	0.0013	0.0133
263779_at	AT2G46340	SPA1 (SUPPRESSOR OF PHYA-105 1); signal tra	-0.5166	0.0304	0.1012	-0.6838	0.0122	0.0592	-0.5304	0.028	0.0681	-0.6976	0.0114	0.0335
263780_at	AT2G46340	SPA1 (SUPPRESSOR OF PHYA-105 1); signal tra	-0.868	0.0717	0.1543	-0.8685	0.0715	0.1339	-1.9392	0.0055	0.0311	-1.9397	0.0055	0.0232
263781_at	AT2G46360	unknown protein	-0.7569	0.3902	0.37	-0.493	0.5647	0.41	0.3479	0.681	0.4247	0.6118	0.4799	0.3175
263782_at	AT2G46380	similar to unknown protein [Arabidopsis thaliana] (T	-0.88	0.0153	0.0748	-0.425	0.1213	0.1767	-0.06787	0.6863	0.4265	0.3872	0.0683	0.0955
263783_at	**AT2G46400**	**WRKY46 (WRKY DNA-binding protein 46); trans**	1.6572	0.0126	0.0692	1.7342	0.0108	0.0559	0.6879	0.1449	0.1752	0.7649	61.148	0.1311
263784_at	AT2G46375	similar to unknown protein [Arabidopsis thaliana] (T	0.2543	0.6989	0.4922	-0.6195	0.3684	0.3268	0.1991	0.7611	0.4515	-0.6746	0.3319	0.2543
263785_at	AT2G46390	unknown protein	0.09232	0.5715	0.4495	0.5227	0.0252	0.0794	0.4374	0.0434	0.087	0.8678	0.0044	0.0211
263786_at	AT2G46370	JAR1 (JASMONATE RESISTANT 1)	-1.0036	0.1865	0.253	-1.1676	0.1375	0.1889	0.1422	0.5091	0.363	-0.02176	0.9171	0.4619
263787_at	AT2G46420	similar to unknown protein [Arabidopsis thaliana] (T	0.3049	0.1671	0.2391	0.00085	0.9965	0.5432	0.08599	0.6293	0.4077	-0.218	0.2563	0.2159
263788_at	AT2G46580	sarcosine oxidase family protein	-0.8542	0.0395	0.1147	-0.5425	0.1284	0.1819	-0.2662	0.4012	0.3172	0.04552	0.8803	0.4515
263789_at	AT2G46560	carboxylesterase	-0.2333	0.7811	0.518	-0.8188	0.3558	0.3207	1.1974	0.0993	0.1403	0.6119	0.3359	0.256
263790_at	AT2G42530	similar to unknown protein [Arabidopsis thaliana] (T	-0.4647	0.0449	0.1221	-0.1117	0.5264	0.3947	-0.6208	0.0183	0.0541	-0.2678	0.172	0.1684
263791_at	AT2G42520	AHA5 (ARABIDOPSIS H(+)-ATPASE 5); ATPase	-1.00E-04	0.9994	0.5764	-0.1342	0.3676	0.3263	-0.7312	0.0052	0.0303	-0.8653	0.0028	0.0174
263792_at	AT2G42660	transposable element gene	-0.2005	0.7283	0.502	-1.1744	0.0944	0.1548	1.0633	0.0617	0.1068	0.08929	0.8394	0.4398
263793_at	AT2G42630	ATCSLC08 (Cellulose synthase-like C8); transferase	-0.8098	0.0224	0.0875	-0.4807	0.0983	0.158	-0.6596	0.0421	0.0855	-0.3305	0.2139	0.1929
263794_at	AT2G42620	S-locus glycoprotein family protein	0.2147	0.7557	0.5104	-0.86	0.2529	0.2657	-0.1064	0.8625	0.4819	-1.1812	0.1099	0.1277
263795_at	AT2G42610	ATCNGC14 (cyclic nucleotide gated channel 14); c	0.01288	0.9791	0.5752	0.2261	0.6505	0.4419	-0.09489	0.8474	0.4778	0.1183	0.8106	0.4319
263796_at	AT2G42540	AFR (ATTENUATED FAR-RED RESPONSE)	-1.7509	0.0026	0.0426	-1.9012	0.0019	0.033	-0.1608	0.2616	0.2474	-0.3111	0.0649	0.0927
263797_at	AT2G42570	WRKY17 (WRKY DNA-binding protein 17); transcri	-0.07789	0.7864	0.5197	0.0483	0.8662	0.5088	0.4663	0.1531	0.181	0.5925	0.0889	0.1119
263798_at	AT2G42640	ubiquitin carboxyl-terminal hydrolase family protein	-0.4001	0.1165	0.1973	0.09409	0.6631	0.446	-0.7927	0.0088	0.0377	-0.2985	0.1469	0.1527
263799_at	AT2G42550	similar to unknown protein [Arabidopsis thaliana] (T	-0.3036	0.291	0.3179	0.0729	0.7849	0.4847	-0.1412	0.2488	0.2403	0.2353	0.088	0.1113
263800_at	AT2G42600	ankyrin repeat family protein	-0.253	0.5548	0.4427	-0.6524	0.1723	0.2144	-0.1849	0.4004	0.3168	-0.5843	0.0411	0.0703
263801_at	AT2G06310	transposable element gene	1.1867	0.4062	0.3784	-0.8251	0.5541	0.4062	1.7167	0.242	0.2362	-0.2952	0.8251	0.4357
263802_at	AT2G40430	Identical to Uncharacterized protein At2g40430 [Ara	0.3863	0.0587	0.1388	0.47	0.0332	0.0903	-0.1675	0.3192	0.2778	-0.08378	0.6001	0.3634
263803_at	AT2G40440	BTB/POZ domain-containing protein	-0.9846	0.2138	0.2707	0.9446	0.2295	0.2511	0.08601	0.8918	0.4901	2.0152	0.0274	0.0551
263804_at	AT2G40270	protein kinase family protein	0.224	0.2836	0.3136	0.08876	0.8496	0.4415	-0.08435	0.1647	0.1883	-0.2196	0.0115	0.0337
263805_at	AT2G40400	similar to unknown protein [Arabidopsis thaliana] (T	-0.6338	0.0327	0.1049	-0.6806	0.0262	0.081	-0.4314	0.0945	0.1364	-0.4782	0.0728	0.099
263806_at	AT2G40305	magnesium transporter CorA-like protein-related	-0.1026	0.6042	0.4609	-0.154	0.4466	0.3623	-0.5066	0.0113	0.0421	-0.5579	0.0081	0.028
263807_at	AT2G40400	indole-3-glycerol phosphate synthase (IGPS)	0.2159	0.3611	0.3551	0.1862	0.4245	0.3527	0.198	0.3832	0.3093	0.1683	0.4524	0.3027
263808_at	AT2G40340	similar to unknown [Picea sitchensis] (GB:ABK2274	0.1742	0.4481	0.3972	0.1422	0.5307	0.3965	0.3101	0.2092	0.2173	0.278	0.2511	0.2132
263809_at	AT2G40570	GDSL-motif lipase/hydrolase family protein	-0.7183	0.1687	0.2404	-0.7937	0.1374	0.1888	-0.2212	0.6135	0.4022	-0.2986	0.5049	0.3277
263810_at	AT2G40520	initiation factor 1A, putative / eIF-1A, putative / eIF-	0.05912	0.7619	0.5121	0.495	0.0532	0.1144	0.896	0.0079	0.0358	1.3318	0.0019	0.0149
263811_at	AT2G40350	long-chain-fatty-acid--CoA ligase family protein / lor	0.2673	0.1881	0.254	0.1439	0.4416	0.3602	0.03298	0.7988	0.463	-0.09045	0.4966	0.3245
263812_at	no_match	no_match	-0.5343	0.7144	0.4974	0.8395	0.5705	0.4121	-1.4667	0.3445	0.2905	-0.08284	0.9544	0.4722
263813_s_at	AT2G10000,AT1G41910	[AT2G10000, transposable element gene];[AT1G41	-1.5954	0.0736	0.1561	-0.7925	0.2974	0.2903	-0.2097	0.7673	0.4533	0.5933	0.4208	0.2928
263814_at	AT2G10010	transposable element gene	-1.4824	0.2603	0.2997	-2.4836	0.0931	0.1539	1.5824	0.2345	0.2319	0.5811	0.6346	0.3753
263815_at	AT2G10020	unknown protein	-0.7838	0.4496	0.394	-0.7656	0.4504	0.3641	1.3661	0.2103	0.218	1.3943	0.2054	0.188
263816_at	AT2G10050	transposable element gene	-0.3951	0.5728	0.45	0.7706	0.2976	0.2904	-0.9059	0.0877	0.1307	0.2598	0.5539	0.3465
263817_at	AT2G10070	transposable element gene	0.05509	0.8492	0.538	-0.564	0.1065	0.1647	0.3811	0.2334	0.2314	-0.238	0.4306	0.2971
263818_at	AT2G10090	transposable element gene	-0.227	0.7638	0.5126	-0.06765	0.9282	0.5263	-0.7066	0.3733	0.3044	-0.5472	0.4813	0.3181
263819_x_at	AT2G10140	transposable element gene	-1.5638	0.2253	0.2787	-0.3739	0.7492	0.4747	-0.1376	0.9058	0.4939	1.0523	0.3897	0.2799
263820_at	AT2G09910	transposable element gene	0.9179	0.3722	0.3606	1.882	0.1086	0.1662	-0.6362	0.5249	0.3691	0.3279	0.7379	0.4097
263821_s_at	AT1G18380,AT2G09990	[AT1G18380, 40S ribosomal protein S16 (RPS16C]	-0.00393	0.9629	0.668	0.2247	0.0474	0.1081	-0.1492	0.1337	0.1665	0.07946	0.3739	0.273
263822_at	AT2G40240	pentatricopeptide (PPR) repeat-containing protein	-0.6984	0.113	0.1947	-0.1459	0.6942	0.4568	-0.7148	0.1071	0.1465	-0.1622	0.6628	0.3852
263823_s_at	AT2G40340,AT2G40350	[AT2G40340, AP2 domain-containing transcription	0.763	0.4414	0.3944	-0.022	0.9815	0.5396	0.6932	0.4813	0.3517	-0.09174	0.9232	0.4636
263824_at	AT2G40360	transducin family protein / WD-40 repeat family prot

263890_at	AT2G37030	auxin-responsive family protein	-1.1278	0.2342	0.2839	-2.0375	0.0648	0.1271	0.4401	0.614	0.4023	-0.4696	0.5913	0.3603
263891_at	AT2G36850	ATGSL08 (GLUCAN SYNTHASE-LIKE 8); 1,3-beta	0.601	0.0151	0.0744	0.5356	0.0221	0.0751	-0.8325	0.0048	0.0295	-0.898	0.0037	0.0197
263892_at	AT2G36890	ATMYB38/MYB38/RAX2 (myb domain protein 38);	0.9481	0.3486	0.3492	1.461	0.1775	0.2179	0.6537	0.4847	0.3533	1.1666	0.2418	0.2081
263893_at	no_match	no_match	0.4608	0.5393	0.4366	2.1569	0.0349	0.0923	0.4899	0.5154	0.3652	2.186	0.0335	0.0619
263894_at	AT2G21910	CYP86A5 (cytochrome P450, family 86, subfamily A	0.005565	0.9963	0.5761	0.6905	0.5716	0.4126	0.122	0.8656	0.4828	0.8069	0.2987	0.238
263895_at	AT2G21920	similar to unknown protein [Arabidopsis thaliana] (T	0.8249	0.358	0.3535	-0.00349	0.9967	0.5432	0.757	0.3948	0.3142	-0.07133	0.9328	0.4664
263896_at	AT2G21930	F-box family protein	0.136	0.8597	0.541	1.3683	0.1309	0.1835	-0.1534	0.8321	0.4733	1.0789	0.1868	0.1775
263897_at	AT2G21940	shikimate kinase, putative	0.248	0.3978	0.3743	0.2412	0.4096	0.3458	0.2543	0.1902	0.2057	0.2475	0.1998	0.1849
263898_at	AT2G21950	SKIP6 (SKP1 INTERACTING PARTNER 6); ubiquit	0.3609	0.0295	0.0997	0.7028	0.003	0.0355	-0.7076	0.0029	0.0245	-0.3658	0.0283	0.0562
263899_at	AT2G21710	EMB2219 (EMBRYO DEFECTIVE 2219)	-0.1948	0.8091	0.5266	0.3529	0.6645	0.4465	-0.8237	0.3086	0.2727	-0.276	0.7161	0.4029
263900_at	AT2G36290	hydrolase, alpha/beta fold family protein	-0.3435	0.1356	0.2138	-0.1944	0.3506	0.3182	-0.07042	0.7216	0.4391	0.07862	0.6914	0.3945
263901_at	AT2G36320	zinc finger (AN1-like) family protein	-0.1632	0.5809	0.4525	0.08867	0.7609	0.478	0.394	0.0276	0.0676	0.6459	0.0052	0.0225
263902_at	AT2G36230	APG10 (ALBINO AND PALE GREEN 10); 1-(5-pho	-0.04748	0.8111	0.5271	-0.3516	0.1317	0.1841	0.43	0.0608	0.1059	0.1259	0.4907	0.3222
263903_at	AT2G36180	calmodulin-related protein, putative	0.1607	0.3865	0.3681	-0.0403	0.1351	0.1869	2.2834	0.1048	0.1447	-0.8176	0.4957	0.3241
263904_at	AT2G36380	ATPDR6/PDR6 (PLEIOTROPIC DRUG RESISTAN	0.06175	0.7888	0.5202	-0.1132	0.6272	0.4334	-0.4119	0.0473	0.0913	-0.5869	0.0157	0.0399
263905_at	AT2G36190	ATCWINV4 (ARABIDOPSIS THALIANA CELL WAL	-0.4667	0.4841	0.4136	-3.0998	0.0069	0.0469	0.9498	0.192	0.2068	-1.6832	0.0499	0.0792
263906_at	AT2G36250	FTSZ2-1 (FtsZ homolog 2-1); structural molecule	-0.2862	0.1639	0.2368	-0.4143	0.0694	0.132	-0.1727	0.0952	0.137	-0.3008	0.0193	0.0445
263907_at	AT2G36270	ABI5 (ABA INSENSITIVE 5); DNA binding / transcri	-1.9046	0.1138	0.1955	0.5222	0.6096	0.4268	-1.1196	0.3013	0.2694	1.3072	0.2384	0.2062
263908_at	AT2G36480	zinc finger (C2H2-type) family protein	0.2929	0.2479	0.2923	0.353	0.1787	0.2187	-0.1254	0.5335	0.3726	-0.06528	0.7409	0.4108
263909_at	AT2G36490	DML1/RDR1 (REPRESSOR OF SILENCING1); DN	-0.2322	0.1379	0.2158	-0.2131	0.1646	0.2088	-0.4903	2.00E-04	0.0126	-0.4713	2.00E-04	0.0078
263910_at	AT2G36550	similar to NLI interacting factor (NIF) family protein (	-1.2576	0.1776	0.2464	-0.1338	0.8704	0.51	-1.0784	0.2338	0.2316	0.04531	0.9559	0.4725
263911_at	AT2G36560	DNA-binding protein-related	-0.2908	0.5819	0.453	-0.8676	0.1488	0.1973	-0.2208	0.3799	0.3077	-0.7976	0.0235	0.0502
263912_at	AT2G36390	SBE2.1 (STARCH BRANCHING ENZYME 2.1); 1,4	0.272	0.339	0.3449	0.3243	0.2655	0.2729	-0.6197	0.0119	0.0433	-0.5674	0.016	0.0403
263913_at	AT2G36570	leucine-rich repeat transmembrane protein kinase,	-0.5537	0.1773	0.2463	-0.358	0.35	0.318	-0.2075	0.1054	0.1452	-0.01167	0.9123	0.4606
263914_at	AT2G36460	AtGRF3 (GROWTH-REGULATING FACTOR 3)	-0.7749	3.00E-04	0.0312	1.3735	7.00E-04	0.0274	-0.2209	0.2039	0.2142	-0.5964	0.0149	0.0388
263915_at	AT2G36430	similar to unknown protein [Arabidopsis thaliana] (	-0.02901	0.8763	0.5456	-0.3488	0.1169	0.1727	-0.03667	0.8207	0.47	-0.3564	0.0784	0.1035
263916_at	AT2G36440	unknown protein	0.5867	0.6364	0.4718	-1.1484	0.374	0.3294	1.068	0.4051	0.3186	-0.6671	0.5925	0.3607
263917_at	AT2G36450	HRD (HARDY); DNA binding / transcription activato	-1.5199	0.2504	0.2937	-1.1609	0.3629	0.3243	-0.4852	0.0202	0.0571	-1.0263	0.3856	0.2782
263918_at	AT2G36590	ProT3 (PROLINE TRANSPORTER 3); amino acid t	-1.0546	0.0401	0.1156	-1.4419	0.0149	0.0643	0.3209	0.1391	0.1705	-0.06634	0.7226	0.405
263919_at	AT2G36470	similar to unknown protein [Arabidopsis thaliana] (T	0.6415	0.0823	0.1659	0.5597	0.1145	0.1708	-0.4616	0.1722	0.1934	-0.5434	0.1224	0.1367
263920_at	AT2G36410	similar to unknown protein [Arabidopsis thaliana] (T	0.2799	0.395	0.3726	0.1852	0.563	0.4094	0.2668	0.0382	0.0807	0.7338	0.0011	0.0126
263921_at	AT2G36460	fructose-bisphosphate aldolase, putative	1.1706	7.00E-04	0.0334	0.7453	0.0039	0.0391	0.2277	0.1104	0.1487	0.1976	0.1507	0.1552
263922_s_at	AT2G36580;AT3G52990	[AT2G36580, pyruvate kinase, putative];[AT3G5299	0.4214	0.1024	0.1849	0.2764	0.2384	0.2568	-0.3582	0.0463	0.0902	-0.5032	0.016	0.0404
263923_at	AT2G36485	similar to pre-mRNA cleavage complex-related [Ara	-0.2269	0.3825	0.3659	0.1224	0.6251	0.4329	0.2755	0.3005	0.269	0.6244	0.0543	0.0833
263924_at	AT2G36530	LOS2 (Low expression of osmotically responsive ge	0.471	0.0071	0.0567	0.3316	0.0233	0.077	0.08751	0.1683	0.1907	-0.05197	0.375	0.2735
263925_at	AT2G21690	RNA-binding protein, putative	1.8478	0.1307	0.2091	-0.8911	0.412	0.347	0.4813	0.6471	0.4135	-2.2575	0.0813	0.106
263926_at	AT2G21800	similar to unknown protein [Arabidopsis thaliana] (T	0.05064	0.8181	0.5291	-0.3678	0.1492	0.1976	-0.07397	0.738	0.4443	-0.3911	0.1309	0.1422
263927_s_at	AT2G21890;AT2G21730	[AT2G21890, mannitol dehydrogenase, putative];[A	0.1597	0.6643	0.4808	0.1789	0.6279	0.4337	0.2424	0.0996	0.1406	0.2617	0.0825	0.107
263928_at	AT2G36330	Identical to UPF0497 membrane protein At2g36330	0.5832	0.0168	0.0777	0.5995	0.0153	0.0649	0.5676	0.008	0.0359	0.5838	0.0072	0.0264
263929_at	AT2G36310	inosine-uridine preferring nucleoside hydrolase fam	0.1901	0.2554	0.2966	-0.2876	0.1152	0.1713	0.4115	0.0035	0.0262	0.3139	0.0094	0.0301
263930_at	AT2G36300	integral membrane Yip1 family protein	0.2673	0.1477	0.2236	0.4222	0.0474	0.108	0.2646	0.1509	0.1795	0.4195	0.0483	0.0776
263931_at	AT2G36220	similar to unknown protein [Arabidopsis thaliana] (T	-0.1308	0.7607	0.5119	0.579	0.2223	0.2472	0.3389	0.0722	0.1168	1.0487	0.0017	0.0145
263932_at	AT2G35990	similar to carboxy-lyase [Arabidopsis thaliana] (TAI	-0.3103	0.6959	0.4914	-0.7352	0.3758	0.3301	0.6245	0.3996	0.3164	0.1997	0.7783	0.4224
263933_s_at	AT2G35970;AT4G09590	[AT2G35970, harpin-induced family protein / HIN1 f	0.397	0.6058	0.4616	0.5203	0.5043	0.3864	-0.9914	0.1753	0.1955	-0.8681	0.2231	0.1978
263934_at	AT2G35950	EDA12 (embryo sac development arrest 12)	0.8811	0.0487	0.1271	0.1625	0.6327	0.4355	0.6746	0.0769	0.1211	-0.04407	0.8845	0.4528
263935_at	AT2G35930	U-box domain-containing protein	0.2269	0.3825	0.3659	0.1224	0.6251	0.4329	0.2755	0.3005	0.269	0.6244	0.0543	0.0833
263936_at	AT2G35920	helicase domain-containing protein	0.256	0.1586	0.2323	0.2364	0.1854	0.2233	-1.0857	0.0018	0.0206	-1.1053	0.0017	0.0146
263937_at	AT2G35910	zinc finger (C3HC4-type RING finger) family protein	-0.3643	0.516	0.4276	-0.736	0.2239	0.248	0.07929	0.8712	0.4845	-0.2925	0.5587	0.3483
263938_at	AT2G35900	similar to Mal d 1-associated protein [Malus x dome	0.6293	0.0172	0.0786	0.7892	0.0079	0.0496	0.0079	0.3133	0.0872	0.1304	0.473	0.0221
263939_at	AT2G36070	ATTIM44-2 (Arabidopsis thaliana translocase inner	0.3811	0.0767	0.1594	0.2891	0.1465	0.1957	-0.1452	0.4081	0.3199	-0.2372	0.2059	0.1884
263940_at	AT2G35890	CPK25 (calcium-dependent protein kinase 25); calr	1.4395	0.2232	0.2771	1.0501	0.3527	0.3194	-0.03855	0.9578	0.5071	-0.4279	0.5657	0.3512
263941_at	no_match	no_match	0.8064	0.3155	0.3318	-0.4875	0.5264	0.3947	1.1484	0.1779	0.1971	1.4673	0.1053	0.1241
263942_at	AT2G35860	FLA16 (FASCICLIN-LIKE ARABINOGALACTAN PR	-1.5042	0.0028	0.0429	-1.9752	0.001	0.0291	1.5338	9.00E-04	0.0169	1.0628	0.0035	0.0194
263943_at	AT2G35800	mitochondrial substrate carrier family protein	-0.09669	0.6768	0.4848	-0.6257	0.0439	0.1037	-0.4202	0.1162	0.1533	-0.9493	0.0107	0.0324
263944_at	AT2G36040	transposable element gene	0.244	0.8686	0.5434	-1.0713	0.4819	0.377	1.7407	0.2422	0.2363	0.4255	0.7543	0.415
263945_at	AT2G36030	unknown protein	-0.2567	0.4438	0.3952	0.6632	0.0934	0.154	-0.66	0.0946	0.1364	0.2599	0.4386	0.3008
263946_at	AT2G36000	mitochondrial transcription termination factor-relate	0.1123	0.1372	0.2151	-0.1689	0.0492	0.1099	-0.6348	5.00E-04	0.0148	-0.916	1.00E-04	0.0062
263947_at	AT2G35820	similar to unknown protein [Arabidopsis thaliana] (T	-0.1234	0.7144	0.4974	-0.04688	0.8885	0.5155	-0.2252	0.4425	0.3352	-0.1487	0.6041	0.3646
263948_at	AT2G35980	YLS9 (YELLOW-LEAF-SPECIFIC GENE 9)	1.3784	0.1179	0.1986	1.806	0.0599	0.1215	0.471	0.2233	0.2256	0.8986	0.0515	0.0809
263949_at	AT2G36060	MMZ3/UEV1C (MMS ZWEI HOMOLOGE 3); protei	0.3883	0.0333	0.1057	0.4718	0.018	0.0694	0.3403	0.0236	0.0623	0.4238	0.0114	0.0335
263950_at	AT2G36020	HVA22 (HVA22-LIKE PROTEIN J)	0.5201	0.6822	0.4866	0.4165	0.742	0.472	0.7934	0.5383	0.3746	0.6898	0.5903	0.3601
263951_at	AT2G35960	NHL12 (NDR1/HIN1-like 12)	-1.6616	2.00E-04	0.0312	-1.9316	1.00E-04	0.0249	0.6062	0.0095	0.0389	0.3362	0.0605	0.089
263952_s_at	AT2G35830;AT2G35810	[AT2G35830, similar to unknown protein [Arabidops	-0.08884	0.4707	0.4076	-0.2084	0.1353	0.187	0.2237	0.1156	0.1528	0.1042	0.4036	0.2856
263953_at	AT2G35850	ATOPT15/OPT15 (Arabidopsis thaliana ovate famil	0.006566	0.991	0.6748	0.2277	0.6995	0.4589	-0.1304	0.769	0.4538	0.09066	0.8377	0.4394
263954_at	AT2G35840	sucrose-phosphatase 1 (SPP1)	-0.5371	0.0086	0.0605	-0.8837	0.0014	0.0312	0.2172	0.1243	0.1596	-0.1294	0.3119	0.2443
263955_at	AT2G36010	E2F3 (E2F TRANSCRIPTION FACTOR-3); transcri	0.234	0.6681	0.482	0.5388	0.3473	0.3167	0.02379	0.9633	0.5084	0.3286	0.5356	0.34
263956_at	AT2G35940	BLH1 (embryo sac development arrest 29); DNA bi	0.3997	0.1081	0.1904	0.139	0.513	0.3899	-0.2077	0.3441	0.2903	-0.4685	0.073	0.0991
263957_at	AT2G35880	similar to unknown protein [Arabidopsis thaliana] (T	-0.5962	0.1236	0.2038	-0.6089	0.1179	0.1736	1.0189	4.00E-04	0.0147	1.0062	4.00E-04	0.009
263958_at	AT2G36240	binding	0.3115	0.3717	0.3604	0.3713	0.2971	0.2902	-0.2772	0.0293	0.0696	-0.2175	0.0597	0.0883
263959_at	AT2G36210	auxin-responsive family protein	-0.7551	0.5274	0.4321	1.6008	0.2166	0.2438	-2.0209	0.043	0.0865	0.3351	0.653	0.3818
263960_at	AT2G36200	kinesin motor protein-related	-0.2648	0.7723	0.5153	-0.4791	0.6052	0.4252	-0.07168	0.9347	0.502	-0.286	0.7453	0.4121
263961_at	AT2G36370	ubiquitin-protein ligase	-0.08889	0.7082	0.4955	0.06283	0.7903	0.4861	-1.0038	0.0105	0.0406	-0.8521	0.0182	0.0434
263962_at	AT2G36350	protein kinase, putative	0.7227	9.00E-04	0.0349	1.2183	1.00E-04	0.0249	-0.2002	0.0714	0.1161	0.2954	0.0228	0.0492
263963_at	AT2G36080	DNA-binding protein, putative	2.6004	0.0224	0.0875	3.0363	0.0134	0.0616	-0.629	0.4002	0.3167	-0.1932	0.787	0.4249
263964_at	AT2G21880	zinc knuckle (CCHC-type) family protein	-0.07843	0.9538	0.5657	-1.5453	0.2913	0.2873	-0.1705	0.8772	0.4859	-1.6374	0.1892	0.1789
263965_at	AT2G21870	transposable element gene	-0.5863	0.6095	0.4628	-0.5261	0.6456	0.4401	-0.2539	0.8224	0.4704	-0.1937	0.8638	0.4488
263966_s_at	AT1G36270;AT1G42510;A	[AT1G36270, transposable element gene];[AT1G42	-1.8952	0.1854	0.2522	0.7789	0.5473	0.4035	-0.8456	0.5154	0.3652	1.8285	0.1981	0.1838
263967_at	AT2G21990	transposable element gene	-0.00354	0.9984	0.5763	-0.3486	0.8441	0.5028	0.3372	0.8207	0.47	-0.00788	0.9958	0.4817
263968_s_at	AT5G19015;AT1G42500;A	[AT5G19015, transposable element gene];[AT1G42	-1.7494	0.3333	0.3419	-0.9372	0.5875	0.4187	-0.06754	0.9553	0.5067	0.7447	0.5468	0.3437
263969_at	no_match	no_match	-3.2274	0.0099	0.0638	-0.8872	0.2733	0.2772	-0.2911	0.6345	0.4093	2.0491	0.0224	0.0487
263970_at	AT2G42850	CYP718 (cytochrome P450, family 718); oxygen bir	-0.3697	0.5303	0.4331	0.3314	0.5717	0.4126	-0.3027	0.6042	0.3996	0.3984	0.5006	0.3262
263971_at	AT2G42800	leucine-rich repeat family protein	0.2383	0.6365	0.4718	-0.1098	0.8256	0.4975	0.09702	0.7882	0.4595	-0.251	0.4986	0.3254
263972_at	AT2G42760	similar to unknown protein [Vitis vinifera] (G	-0.5124	0.0947	0.1778	-0.4703	0.116	0.1719	0.858	0.0218	0.0595	0.9002	0.0186	0.0438
263973_at	AT2G42740	RPL16A (ribosomal protein large subunit 16A); stru	0.4328	0.1836	0.2508	0.342	0.2733	0.2772	0.4548	0.0283	0.0684	0.364	0.0547	0.0837
263974_at	AT2G42720	F-box family protein	-0.507	0.194	0.2583	0.6352	0.3456	0.3158	-0.5567	0.4022	0.3175	1.0054	0.1661	0.1649
263975_at	AT2G42710	ribosomal protein L1 family protein	-0.03653	0.9112	0.5543	0.3331	0.3398	0.3133	-0.1541	0.5067	0.362	0.2155	0.3661	0.2696
263976_at	AT2G42700	similar to hypothetical protein Osl_034052 [Oryza s	1.3045	0.0036	0.0457	0.5025	0.0783	0.1404	0.1427	0.4833	0.3526	-0.6593	0.0235	0.0501
263977_at	AT2G42660	myb family transcription factor	-0.22	0.656	0.4778	-1.2925	0.0477	0.1084	-0.2525	0.6106	0.4014	-1.3251	0.0444	0.0739
263978_at	AT2G42680	ATMBF1A/MBF1A (MULTIPROTEIN BRIDGING FA	0.1113	0.4669	0.4059	0.603	0.0121	0.0591	0.7151	0.0013	0.0189	1.2068	2.00E-04	0.0072
263979_at	AT2G42840	PDF1 (PROTODERMAL FACTOR 1)	-1.2192	0.1301	0.2085	-0.7981	0.2813	0.2816	-0.02873	0.896	0.4913	0.3924	0.13	0.1415
263980_at	AT2G42770	peroxisomal membrane 22 kDa family protein	-0.752	0.0017	0.0391	-0.6347	0.0032	0.0369	0.1944	0.1538	0.1538	0.3117	0.033	0.0613
263981_at	AT2G42870	HLH1/PAR1 (PHY RAPIDLY REGULATED 1); trans	-0.5865	0.1378	0.2157	0.437	0.24	0.2577	0.08352	0.6725	0.4218	1.107	0.0038	0.02
263982_at	AT2G42860	unknown protein	0.5974	0.6272	0.4687	0.3129	0.7969	0.4886	-0.7513	0.4921	0.3564	-1.0358	0.3564	0.2654
263983_at	AT2G42780	similar to unknown [Populus trichocarpa] (GB:ABK9	0.2681	0.0084	0.06	0.5605	0.0088	0.0516	-0.1883	0.1505	0.1792	-0.1959	0.1385	0.1472
263984_at	AT2G42670	similar to unknown protein [Arabidopsis thaliana] (T	0.2559	0.2283	0.2808	-0.2139	0.3004	0.2915	0.04407	0.7687	0.4537	-0.4257	0.0384	0.0672
263985_at	AT2G42750	DNAJ heat shock N-terminal domain-containing pro	-0.1892	0.3399	0.3452	-0.3297	0.1323	0.1846	0.258	0.0094	0.0388	0.1175	0.0996	0.1203
263986_at	AT2G42790	CSY3 (CITRATE SYNTHASE 3); citrate (Si)-syntha	1.5248	0.0024	0.0421	1.3553	0.0037	0.0386	-0.07011	0.4775	0.3505	-0.2396	0.0555	0.0844
263987_at	AT2G42690	lipase, putative	-0.2685	0.0371	0.111	-0.4736	0.0056	0.0434	-0.4741	0.0056	0.0311	-0.6792	0.0015	0.0137
263988_at	AT2G42830	SHP2 (SHATTERPROOF 2); transcription factor	-2.034	0.0933	0.1771	0.9612	0.3585	0.3222	-1.7671	0.092	0.1341	1.2281	0.1999	0.185
263989_at	AT2G42880	ATMPK20 (Arabidopsis thaliana MAP kinase 20); M	-0.2922	0.1793	0.2475	-0.4033	0.0882	0.1497	-0.03239	0.8381	0.4751	-0.1435	0.3889	0.2795
263990_at	AT2G42810	PAPP5/PP5 (PROTEIN PHOSPHATASE 5); phosp	0.1942	0.4572	0.4016	0.2354	0.3756	0.3301	-0.691	0.0266	0.0663	-0.6498	0.0321	0.0605
263991_at	AT2G13020	transposable element gene	-0.8061	0.4867	0.4143	0.02347	0.9833	0.54	-0.4368	0.6996	0.4312	0.3927	0.7281	0.4066
263992_at	AT2G13290	transposable element gene	0.1894	0.8489	0.5379	0.3473	0.7284	0.4683	0.6433	0.5191	0.3666	0.8012	0.4289	0.2962
263993_at	no_match	no_match	-1.4101	0.1005	0.1832	-1.4565	0.0929	0.1538	-0.5351	0.4648	0.3452	-0.5815	0.4299	0.2967
263994_at	AT2G12900	DNA binding / transcription factor	-1.0957	0.2295	0.2818	-0.5337	0.5281	0.3954	0.3548	0.6257	0.4065	0.9168	0.2445	0.2095
263995_at	no_match	no_match	0.002349	0.9915	0.5749	0.2284	0.3348	0.3107	-0.2499	0.0026	0.0234	-0.02387	0.5557	0.3472
263996_at	AT2G22530	transferase	-0.06626	0.769	0.5143	0.3034	0.2236	0.2479	-1.207	0.0046	0.0289	-0.8373	0.0165	0.0411
263997_at	AT2G22520	unknown protein	1.7356	0.124	0.2039	0.224	0.8144	0.4945	2.0767	0.0187	0.0549	0.565	0.3571	0.2656
263998_at	AT2G22510	hydroxyproline-rich glycoprotein family protein	1.7452	0.1895	0.255	0.7101	0.5555	0.4068	1.8809	0.164	0.1878	0.8458	0.4868	0.3205
263999_at	AT2G22370	similar to unknown protein [Vitis vinifera] (G	0.06158	0.661	0.4796	0.4382	0.0282	0.0835	-0.2954	0.0859	0.1292	0.08121	0.5668	0.3515
264000_at	AT2G22500	mitochondrial substrate carrier family protein	-0.1152	0.8507	0.5383	0.1332	0.8278	0.4983	0.06826	0.7392	0.4446	0.3166	0.1732	0.1692
264001_at	AT2G22410	peroxidase 17 (PER17) (P17)	0.2778	0.4778	0.4109	-0.2737	0.4839	0.3776	0.2524	0.4552	0.3409	-0.2991	0.3832	0.2772
264002_at	AT2G22360	DNAJ heat shock family protein	0.0162	0.9639	0.5682	-0.2811	0.4503	0.3641	-0.3677	0.1705	0.1923	-0.6649	0.0393	0.0682
264003_at	AT2G22475	GEM	0.5511	0.0027	0.0426	0.5715	0.0023	0.0337	0.5025	0.0032	0.0252	0.523	0.0028	0.0173
264004_at	AT2G22425	signal peptidase	0.5327	0.0251	0.0919	0.58	0.0191	0.0711	0.3515	0.0825	0.1262	0.3988	0.0591	0.0878
264005_at	AT2G22470	AGP2 (ARABINOGALACTAN-PROTEIN 2)	-0.3312	0.1934	0.2579	0.3605	0.1644	0.2087	0.7931	0.0201	0.0571	1.4848	0.0022	0.0157
264006_at	AT2G22430	ATHB6 (ARABIDOPSIS THALIANA HOMEOBOX P	0.2342	0.061	0.1417	0.4675	0.0087	0.0463	-0.06361	0.2804	0.2584	0.1697	0.0292	0.0572
264007_at	AT2G21140	ATPRP2 (PROLINE-RICH PROTEIN 2)	-1.2198	0.0348	0.1077	-1.7712	0.0103	0.0551	-0.6272	0.1106	0.1488	-1.1785	0.0185	-0.0436
264008_at	AT2G21120	similar to unknown protein [Arabidopsis thaliana] (T	0.01381	0.9189	0.5567	-0.4111	0.032	0.0887	-0.1819	0.1664	0.1894	-0.6068	0.0049	0.022
264009_at	AT2G21110	disease resistance-responsive family protein	-1.883	0.2335	0.2839	1.0711	0.4698	0.3721	-0.9539	0.51	0.3633	1.9838	0.2137	0.1928
264010_at	AT2G21100	disease resistance-responsive protein-related / disc	0.07307	0.95	0.5646	-1.4071	0.2682	0.2745	-0.8402	0.3815	0.3085	-2.3203	0.0534	0.0825
264011_at	AT2G21090	pentatricopeptide (PPR) repeat-containing protein	-1.0399	0.262	0.3008	0.2468	0.7723	0.4812	-1.7992	0.087	0.1301	-0.5125	0.5553	0.3471
264012_at	AT2G21080	similar to extracellular ligand-gated ion channel [Ara	-0.2998	0.3155	0.3318	-0.973	0.0205	0.073	-0.1267	0.1977	0.1977	-1.0992	0.0137	0.0371
264013_at	AT2G21070	FIO1 (FIONA1)	0.2364	0.4495	0.3978	0.04463	0.882	0.5137	-0.3877	0.1602	0.1857	-0.5795	0.0617	0.0901
264014_at	AT2G21210	auxin-responsive protein, putative	-1.1188	0.0083	0.0599	-1.5613	0.0025	0.0339	0.7693	9.00E-04	0.0172	0.3268	0.0202	0.0459
264015_at	no_match	no_match	0.06382	0.8488	0.5379	-0.08265	0.8053	0.4913	0.06203	0.9459	0.5047	-0.1238	0.7134	0.4021
264016_at	AT2G21220	auxin-responsive protein, putative	0.07235	0.9452	0.5635	1.7083	0.1589	0.2051	-0.0149	0.9887	0.515	1.6211	0.1763	0.1709
264017_s_at	AT2G21190;AT4G38790	[AT2G21190, ER lumen protein retaining receptor fa	0.07173	0.6974	0.4918	0.6666	0.0179	0.0692	-0.7319	0.0029	0.0246	-0.138	0.2889	0.2328
264018_at	AT2G21170	TIM (TRIOSEPHOSPHATE ISOMERASE); triose-p	-0.4075	0.0723	0.155	-0.7623	0.0105	0.0554	-0.1118	0.5421	0.3762	-0.4666	0.0499	0.0792
264019_at	AT2G21130	peptidyl-prolyl cis-trans isomerase / cyclophilin (CY	0.2499	0.5168	0.428	0.3455	0.3818	0.3328	0.1085	0.7732	0.4554	0.2041	0.593	0.3609
264020_at	AT2G21160	translocon-associated protein alpha (TRAP alpha) f	0.3273	0.0323	0.1041	0.2543	0.0666	0.1292	0.1791	0.1528	0.1807	0.1061	0.3553	0.265
264021_at	AT2G21200	auxin-responsive protein, putative	-0.3618	0.2524	0.2949	-0.2394	0.4492	0.3637	0.0348	0.8402	0.4757	0.1772	0.3348	0.2555
264022_at	AT2G21185	unknown protein	-0.04512	0.902	0.5518	0.1181	0.7489	0.4747	0.2379	0.2308	0.2299	0.401	0.0759	0.1015
264023_at	AT2G21195	similar to unknown protein [Vitis vinifera] (G	0.09124	0.4915	0.4164	0

264090_at	AT1G79370	CYP79C1 (cytochrome P450, family 79, subfamily C	-0.28	0.7208	0.4996	-1.0417	0.2266	0.2496	0.7845	0.3429	0.2898	0.02276	0.9766	0.4773
264091_at	AT1G79110	protein binding / zinc ion binding	1.3683	0.0146	0.0732	0.8756	0.0576	0.1193	0.3264	0.2123	0.2193	-0.1663	0.4921	0.3228
264092_at	AT1G79040	PSBR (photosystem II subunit R)	-0.3372	0.0427	0.1189	-0.5487	0.0088	0.0516	0.1221	0.0059	0.032	-0.08944	0.0172	0.0419
264093_at	AT1G79220	mitochondrial transcription termination factor family	0.4626	0.2379	0.2862	-0.4701	0.2317	0.2526	-0.34	0.3659	0.3008	-1.2727	0.0189	0.044
264094_at	AT1G79200	similar to unnamed protein product [Vitis vinifera] (G	0.5343	0.0546	0.1342	0.8284	0.014	0.0627	0.6594	0.0293	0.0696	0.9536	0.0086	0.0289
264095_at	AT1G79230	ST1 (MERCAPTOPYRUVATE SULFURTRANSFER	0.09649	0.5625	0.4458	-0.3199	0.1047	0.1635	0.1402	0.047	0.091	-0.2762	0.005	0.0222
264096_at	AT1G78995	similar to unnamed protein product [Vitis vinifera] (G	-0.2341	0.6401	0.4731	-0.5024	0.3395	0.3132	-0.01627	0.8544	0.4796	-0.2845	0.0268	0.0543
264097_s_at	AT1G16700,AT1G79010	[AT1G16700, ATML1\4 (ARABIDOPSIS THALIANA	0.04963	0.7124	0.4971	0.2059	0.1757	0.2167	0.2185	0.1476	0.1773	0.3748	0.0372	0.0657
264098_at	AT1G79260	Identical to Uncharacterized protein At1g79260 [Ara	-0.9104	0.0182	0.0804	-0.6284	0.0563	0.118	-0.4577	0.1036	0.1439	-0.1756	0.4654	0.3121
264099_at	AT1G79050	DNA repair protein recA	0.5279	0.1523	0.2276	0.0317	0.9207	0.5242	0.39	0.0689	0.1137	-0.1062	0.538	0.3406
264100_at	AT1G78970	LUH (LUPEOL SYNTHASE 1); lupeol synthase	-0.2371	0.4883	0.4151	-0.9398	0.0391	0.098	0.6243	0.406	-0.5446	0.1419	0.1494	
264101_at	AT1G79000	HAC1 (P300/CBP ACETYLTRANSFERASE-RELA	0.1998	0.2665	0.3031	0.1435	0.4066	0.3443	-1.0436	0.0025	0.0233	-1.0999	0.0021	0.0154
264102_at	AT1G79270	ECT8 (evolutionarily conserved C-terminal region 8)	-0.3621	0.1205	0.2008	-0.4657	0.0646	0.127	-0.2573	0.2347	0.2319	-0.3609	0.1214	0.136
264103_at	AT1G79360	unknown protein	0.1235	0.8576	0.5406	-0.3549	0.6116	0.4274	-0.3637	0.6127	0.402	-0.8321	0.2668	0.2211
264104_at	AT1G79350	transposable element gene	-1.3957	0.3472	0.3485	-0.7814	0.5834	0.4175	-0.9044	0.364	0.3	-0.29	0.7592	0.4164
264105_x_at	AT1G79360	similar to unknown protein [Arabidopsis thaliana] (T	0.0597	0.9603	0.5674	-2.8968	0.0619	0.1237	1.7868	0.188	0.2043	-1.1697	0.3578	0.266
264106_at	no_match	no_match	-0.2289	0.7066	0.4949	0.9987	0.1524	0.2	-0.3	0.6241	0.4059	0.9277	0.1765	0.1711
264107_s_at	AT2G13790,AT2G13800	[AT2G13790, ATSERK4 (SOMATIC EMBRYOGEN	1.0909	0.0293	0.0992	0.7495	0.0844	0.1461	-0.2583	0.0675	0.1126	-0.5997	0.0045	0.0212
264108_at	AT2G13680	CALS5 (CALLOSE SYNTHASE 5); 1,3-beta-glucan	0.001459	0.9988	0.5763	-2.1465	0.0859	0.1475	1.4472	0.2009	0.2122	-0.7007	0.5001	0.326
264109_at	AT2G13720	ATP binding / DNA binding / DNA topoisomerase (A	-1.4682	0.1776	0.2464	-0.9214	0.3631	0.3243	1.1674	0.1223	0.1582	1.7141	0.0455	0.0748
264110_at	AT2G13730	transposable element gene	0.9517	0.3816	0.3654	-0.9052	0.403	0.3427	3.1504	0.0313	0.072	1.2934	0.2528	0.2139
264111_at	AT2G13690	PRLI-interacting factor, putative	0.01694	0.9059	0.5527	0.2393	0.15	0.198	-0.4004	0.0409	0.084	-0.1781	0.2562	0.2158
264112_at	AT2G13680	CALS8 (CALLOSE SYNTHASE 5); 1,3-beta-glucan	-1.16	0.1688	0.2404	-0.5757	0.452	0.3649	-1.7245	0.0672	0.1123	-1.1401	0.1746	0.17
264113_at	AT2G13260	APG9 (AUTOPHAGY 9)	0.005316	0.9626	0.568	0.5309	0.0076	0.0488	-0.5752	0.0057	0.0314	-0.04964	0.6655	0.3859
264114_at	AT2G13270	ATCDT1A/CDT1/CDT1A (ARABIDOPSIS HOMOLO	-0.4453	0.3215	0.3352	-0.1461	0.7296	0.4685	-0.04897	0.8723	0.4848	0.2503	0.4307	0.2971
264115_at	AT2G13290	similar to unknown protein [Arabidopsis thaliana] (T	-0.4942	0.1308	0.2092	0.3602	0.2392	0.2572	-0.6613	0.0522	0.0969	0.1931	0.4694	0.3135
264116_at	AT2G13320	poly (ADP-ribose) polymerase, putative / NAD(+) A	0.212	0.4382	0.3929	0.1942	0.4748	0.3742	-0.311	0.1912	0.2063	-0.3289	0.172	0.1684
264117_at	AT2G13210	basic helix-loop-helix (bHLH) family protein	-0.6276	0.6551	0.4775	0.07454	0.9571	0.5335	-1.1211	0.4378	0.3331	-0.4191	0.7637	0.4179
264118_at	AT1G79150	binding	0.7127	0.0697	0.1522	0.1782	0.5719	0.4126	0.05303	0.8194	0.4696	-0.4815	0.0914	0.1139
264119_at	AT1G79180	AtMYB63 (myb domain protein 63); DNA binding / tr	0.7784	0.2387	0.2868	-0.7869	0.2345	0.2546	0.5958	0.3493	0.2928	-0.9695	0.1599	0.1612
264120_at	AT1G79340	ATMCA2 (METACASPASE 4); caspase/ cysteine typ	0.3526	0.0063	0.0545	0.1259	0.1345	0.1864	0.2567	0.0017	0.0206	0.02993	0.435	0.299
264121_at	AT1G02280	TOC33 (PLASTID PROTEIN IMPORT 1); GTP bind	0.09336	0.6773	0.485	-0.1607	0.4835	0.3774	-0.5846	3.00E-04	0.014	-0.8387	1.00E-04	0.0058
264122_at	AT1G02130	ATRAB1B (Arabidopsis thaliana responsive to abac	0.1442	0.1913	0.2562	0.04338	0.6611	0.4455	0.4132	0.0104	0.0406	0.3124	0.0264	0.0538
264123_at	AT1G02270	endonuclease/exonuclease/phosphatase family pro	-0.0026	0.9836	0.5729	0.05981	0.641	0.4384	0.09913	0.4465	0.3369	0.1615	0.2414	0.2079
264124_at	AT1G79360	ATOCT2 (ARABIDOPSIS THALIANA ORGANIC CA	0.4086	0.2661	0.3028	-0.1355	0.6906	0.4558	-0.1135	0.6863	0.4265	-0.6575	0.0655	0.0932
264125_at	AT1G79350	EMB1135 (EMBRYO DEFECTIVE 1135); DNA bind	0.5475	0.0468	0.1246	0.0727	0.7252	0.4671	-0.2296	0.2952	0.2662	-0.7044	0.021	0.047
264126_at	AT1G79280	NUA (NUCLEAR PORE ANCHOR)	0.4854	0.0944	0.1777	0.1576	0.5175	0.3915	-0.4362	0.0055	0.0311	-0.764	7.00E-04	0.0105
264127_at	AT1G79250	protein kinase, putative	0.1475	0.8528	0.5389	2.4425	0.0306	0.0869	-1.1352	0.2025	0.2133	1.1597	0.1948	0.1818
264128_at	AT1G79190	binding	0.3854	0.1641	0.2368	-0.2038	0.4191	0.3503	-0.5395	0.0285	0.0685	-1.1286	0.0022	0.0157
264129_at	AT1G79190	unknown protein	0.4991	0.2282	0.2808	-0.7348	0.1633	0.1633	0.9143	0.0598	0.1048	0.3196	0.4141	0.29
264130_at	AT1G79160	similar to unknown protein [Arabidopsis thaliana] (T	-0.5553	0.0104	0.0646	-0.5115	0.0138	0.0621	0.4899	0.0108	0.0412	0.5338	0.008	0.0278
264131_at	AT1G79150	binding	0.289	0.1949	0.2591	-0.05436	0.7845	0.4847	-0.218	0.245	0.238	-0.5614	0.0248	0.0518
264132_at	AT1G79150	arginine/serine-rich protein-related	0.8058	0.5196	0.4289	1.4935	0.2613	0.2705	-2.1336	0.1353	0.1678	-1.4459	0.2745	0.2252
264133_at	AT1G79080	pentatricopeptide (PPR) repeat-containing protein	-0.3344	0.3387	0.3448	-0.2261	0.5036	0.3861	0.1345	0.6848	0.426	0.2428	0.4746	0.3155
264134_at	AT1G79070	SNARE-associated protein-related	0.4331	0.2399	0.2875	-0.07732	0.8176	0.4952	-0.1153	0.7319	0.4423	-0.6257	0.117	0.1327
264135_at	AT1G79030	DNaJ heat shock N-terminal domain-containing pro	-0.09989	0.7239	0.5006	0.05148	0.8546	0.5059	-0.4222	0.1835	0.2011	-0.2719	0.3605	0.2672
264136_at	AT1G78980	SRF5 (STRUBBELIG-RECEPTOR FAMILY 5); ATP	-0.5848	0.5109	0.4252	0.2637	0.7615	0.478	-0.136	0.8294	0.4726	0.7125	0.2946	0.2359
264137_at	AT1G78960	ATLUP2 (Arabidopsis thaliana lupeol synthase 2); l	0.2416	0.4382	0.3929	-0.1763	0.5643	0.4099	-0.5446	0.1246	0.1598	-0.9626	0.0266	0.0541
264138_at	AT1G78950	beta-amylin synthase, putative	-0.3597	0.464	0.4048	-0.8769	0.12	0.1752	-0.1329	0.78	0.4574	-0.65	0.2177	0.1949
264139_at	AT1G78940	protein kinase family protein	0.4888	0.587	0.4552	-0.7264	0.4299	0.3552	-1.7691	0.0995	0.1405	-2.0071	0.0725	0.0988
264140_at	AT1G79210	20S proteasome alpha subunit B, putative	0.818	0.0168	0.0777	0.7043	0.0272	0.0825	0.0779	0.1645	0.1882	-0.03584	0.4781	0.3169
264141_at	AT1G79090	similar to unknown protein [Arabidopsis thaliana] (T	0.2085	0.3084	0.3277	0.4217	0.0778	0.1398	-0.5393	0.019	0.0553	-0.3266	0.0826	0.1071
264142_at	AT1G78930	mitochondrial transcription termination factor-relate	0.2438	0.378	0.3634	-0.03584	0.8913	0.5161	-0.1941	0.4744	0.3495	-0.4738	0.1266	0.1393
264143_at	AT1G79330	AMC6/ATMC5/ATMCP2B (TYPE-II METACASPAS	0.1077	0.8707	0.5442	0.3144	0.6393	0.438	-0.1206	0.7915	0.4606	0.08615	0.8498	0.4427
264144_at	AT1G79320	ATMC6 (METACASPASE 6); caspase	0.6064	0.6986	0.4921	-0.2815	0.8562	0.5062	+1.1312	0.4598	0.343	-2.0191	0.2185	0.1954
264145_at	AT1G79310	ATMC7 (METACASPASE 7); caspase	1.4614	0.1071	0.1894	0.8438	0.2979	0.2906	1.4848	0.0856	0.129	0.8671	0.2553	0.2153
264146_at	AT1G02205	CER1 (ECERIFERUM 1)	0.9578	0.1437	0.2204	0.3697	0.5221	0.393	0.1945	0.2532	0.2427	-0.3935	0.0542	0.0833
264147_at	AT1G02205	CER1 (ECERIFERUM 1)	0.542	0.4662	0.401	0.4816	0.5046	0.3865	-1.6495	0.0083	0.0366	-1.7099	0.0073	0.0267
264148_at	AT1G02220	ANAC003 (Arabidopsis NAC domain containing pro	0.4824	0.1194	0.1997	1.1679	0.0088	0.0515	-0.3815	0.0234	0.0619	0.3041	0.0466	0.076
264149_at	AT1G02250	ANAC005 (Arabidopsis NAC domain containing pro	-1.7949	0.087	0.1708	1.5657	0.1204	0.1757	-1.9326	0.072	0.1167	1.428	0.1471	0.1528
264150_at	AT1G02050	FUS5 (FUSCA 5); MAP kinase kinase	1.0534\6	0.7504	0.5086	0.2919	0.1363	0.1679	-0.2373	0.2049	0.2147	0.001104	0.9947	0.4814
264151_at	AT1G02070	similar to zinc ion binding [Arabidopsis thaliana] (TA	1.9969	0.1304	0.2089	0.1182	0.9159	0.523	0.6039	0.5965	0.3969	-1.2748	0.2921	0.2347
264152_at	AT1G02140	HAP1/MAGO/MEE63 (MATERNAL EFFECT EMBR	-0.1733	0.0627	0.1436	0.2177	0.0325	0.0893	0.2264	0.0287	0.0689	0.6174	8.00E-04	0.0111
264153_at	AT1G02205	ATPPDK; carbohydrate binding	-3.5549	0.0574	0.1374	-3.0198	0.0882	0.1497	-0.282	0.433	0.3309	0.2531	0.4781	0.3169
264154_at	AT1G65430	zinc finger protein-related	-0.02122	0.8984	0.5508	0.05745	0.7313	0.4688	0.04312	0.7469	0.4472	0.1218	0.384	0.2776
264155_at	AT1G65440	GTB1 (GLOBAL TRANSCRIPTION FACTOR GRO	0.5332	0.1318	0.2101	0.423	0.2082	0.2384	-0.4977	0.1525	0.1806	-0.6078	0.0975	0.1187
264156_at	AT1G65280	heat shock protein binding	0.3324	0.1275	0.2063	0.3528	0.1114	0.1685	-0.7673	0.0038	0.027	-0.7669	0.0042	0.0207
264157_at	AT1G65310	ATXTH17 (XYLOGLUCAN ENDOTRANSGLUCOS	-0.4697	0.6579	0.4783	-0.8488	0.4368	0.3583	0.208	0.7767	0.4563	-0.171	0.8153	0.433
264158_at	AT1G65260	PTAC4 (PLASTID TRANSCRIPTIONALLY ACTIVE	-0.4795	0.0139	0.0722	-0.6184	0.0057	0.0438	-0.3021	0.0561	0.101	-0.441	0.0177	0.0426
264159_at	AT1G65270	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.2365	0.0587	0.1388	0.2793	0.0364	0.0942	0.7225	0.0013	0.0192	0.7652	0.0011	0.0123
264160_at	AT1G65450	transferase family protein	-0.6205	0.2597	0.2996	-1.047	0.0912	0.1524	0.3409	0.3433	0.29	-0.08552	0.8009	0.429
264161_at	AT1G65420	identical to Ycf20-like protein [Arabidopsis Thaliana	0.004568	0.9692	0.5696	-0.7158	0.003	0.0356	0.4121	0.0207	0.0579	-0.3082	0.0502	0.0795
264162_at	AT1G65290	MTACP2 (MITOCHONDRIAL ACYL CARRIER PRO	0.06967	0.5165	0.4278	0.2231	0.0851	0.1469	0.1278	0.2624	0.2479	0.2812	0.0455	0.0748
264163_at	AT1G65445	transferase-related	-3.3	0.0225	0.0876	-0.9131	0.3738	0.3294	-2.6007	0.0044	0.0283	-0.2138	0.6582	0.3835
264164_at	AT1G65295	similar to unknown protein [Arabidopsis thaliana] (T	-0.621	0.024	0.0904	-0.4379	0.0671	0.1296	0.5492	0.0352	0.0769	0.7322	0.014	0.0376
264165_at	AT1G65410	ATNAP11 (ARABIDOPSIS THALIANA NON-INTRI	-0.2142	0.1417	0.2189	0.01142	0.9271	0.526	-0.5225	0.0111	0.0418	-0.2669	0.0643	0.0922
264166_at	AT1G65370	meprin and TRAF homology domain-containing pro	0.7535	0.0538	0.1331	0.3552	0.2712	0.2761	-1.6641	8.00E-04	0.0164	-2.0624	4.00E-04	0.0088
264167_at	AT1G02060	pentatricopeptide (PPR) repeat-containing protein	-0.06496	0.9339	0.5608	1.0069	0.2429	0.2597	-2.4138	0.0265	0.0662	-1.3419	0.1291	0.1409
264168_at	AT1G02080	transcriptional regulator-related	0.5767	0.0078	0.0583	0.07878	0.536	0.3989	-0.6032	0.0066	0.0334	-1.1011	7.00E-04	0.0106
264169_at	AT1G02020	nitroreductase family protein	0.1771	0.2331	0.2837	-0.1186	0.4003	0.3413	-0.1569	0.2815	0.259	-0.4527	0.023	0.0494
264170_at	AT1G02260	transmembrane protein, putative	0.6767	0.0075	0.0579	0.2351	0.1579	0.2043	-0.5556	0.0058	0.032	-0.9972	7.00E-04	0.0105
264171_at	AT1G02100	leucine carboxyl methyltransferase family protein	0.127	0.4642	0.4049	0.4516	0.0453	0.1055	-0.5262	0.0041	0.0277	-0.6016	0.0186	0.0438
264172_at	AT1G02120	VAD1 (VASCULAR ASSOCIATED DEATH1)	0.6286	0.0201	0.0836	0.4835	0.0451	0.1053	-0.4443	0.0525	0.0972	-0.5894	0.0223	0.0487
264173_at	AT1G02160	similar to unnamed protein product [Vitis vinifera] (G	0.339	0.0209	0.085	0.593	0.003	0.0355	0.3543	0.0181	0.0539	0.6083	0.0027	0.0171
264174_s_at	AT1G47910,AT1G02228	pentatricopeptide (PPR) repeat-containing protein;[AT1G02	-0.7936	0.1523	0.2276	-1.0425	0.0813	0.1429	-0.05337	0.9112	0.4955	-0.3023	0.5362	0.3406
264175_at	AT1G02050	chalcone and stilbene synthase family protein	0.2275	0.8036	0.5251	0.6686	0.4786	0.3756	-2.1922	0.0626	0.1076	-1.7511	0.1103	0.1279
264176_at	AT1G02110	proline-rich family protein	-0.1651	0.513	0.4263	-0.4946	0.0981	0.1579	0.0489	0.8417	0.4762	-0.2806	0.2886	0.2327
264177_at	AT1G02150	pentatricopeptide (PPR) repeat-containing protein	-0.06971	0.6576	0.4782	-0.1668	0.3165	0.301	-0.8264	0.0023	0.0224	-0.9235	0.0015	0.0138
264178_at	AT1G02170	LOL3 (LSD ONE LIKE 3); caspase/ cysteine-type e	0.5486	0.026	0.0933	0.06398	0.7077	0.4613	0.7072	8.00E-04	0.0163	0.2227	0.0452	0.0745
264179_at	AT1G02180	ferredoxin-related	-0.3645	0.4739	0.4094	-0.6246	0.2474	0.2622	0.2912	0.4666	0.346	0.03109	0.9357	0.4673
264180_at	AT1G02190	CER1 protein, putative	1.4238	0.3632	0.3559	1.3232	0.3946	0.3389	-0.378	0.7989	0.463	-0.4786	0.7477	0.4129
264181_at	AT1G65350	UBQ13 (ubiquitin 13)	0.458	0.2098	0.2681	-0.5866	0.1285	0.1819	1.0198	0.014	0.0471	-0.02482	0.9239	0.4638
264182_at	AT1G65360	AGL23; DNA binding / transcription factor	0.717	0.4256	0.3874	-0.1886	0.8271	0.4981	-0.08027	0.918	0.4972	-0.9859	0.2496	0.2124
264183_at	AT1G65380	CLV2 (CLAVATA 2); protein binding	0.386	0.3171	0.3327	0.197	0.5912	0.42	0.5523	0.1775	0.1968	0.3633	0.3428	0.2593
264184_at	AT1G54790	GDSL-motif lipase/hydrolase family protein	-0.08419	0.857	0.5405	-0.1638	0.7275	0.468	0.1228	0.7932	0.4612	0.04316	0.9263	0.4646
264185_at	AT1G54780	thylakoid lumen 18.3 kDa protein	-0.382	0.0638	0.1447	-0.6852	0.0103	0.0551	0.3379	0.0109	0.0414	0.03469	0.6685	0.3869
264186_at	AT1G54570	esterase/lipase/thioesterase family protein	0.3583	0.3664	0.3575	-0.1418	0.7078	0.4613	-0.04189	0.8809	0.487	-0.542	0.1078	0.126
264187_at	AT1G54860	similar to unknown protein [Arabidopsis thaliana] (T	-0.2866	0.7759	0.5167	0.2458	0.8069	0.4919	-2.2687	0.0735	0.118	-1.7363	0.1388	0.1474
264188_at	AT1G54690	G-H2AX/GAMMA-H2AX/H2AX/HTA3; DNA bindin	-0.05621	0.6981	0.492	-0.1435	0.3472	0.3166	1.1495	0.001	0.0175	1.0622	0.0013	0.0133
264189_s_at	AT1G54580,AT1G54630	[AT1G54580, ACP2 (ACYL CARRIER PROTEIN 2);	0.002942	0.9713	0.5702	0.5293	0.0023	0.0336	0.6478	4.00E-04	0.0147	1.1742	0	0.0054
264190_at	AT1G54830	CCAAT-box binding transcription factor HapSa, puta	0.8844	0.0046	0.0488	0.5946	0.0182	0.0696	0.3959	0.0436	0.0871	0.1061	0.4786	0.317
264191_at	AT1G54730	sugar transporter, putative	-0.5584	0.1131	0.1949	0.1652	0.5817	0.4168	-1.4211	0.003	0.0248	-0.6974	0.0344	0.0628
264192_at	AT1G54710	AIAT2/1B9 (Arabidopsis thaliana homolog of yeast a	0.203	0.3393	0.345	-0.1056	0.6031	0.4247	-0.4533	0.0545	0.0994	-0.7619	0.0106	0.0323
264193_at	AT1G54610	protein kinase family protein	-0.09507	0.4883	0.4151	-0.1491	0.2979	0.2906	0.07889	0.5613	0.3831	0.0249	0.8515	0.4431
264194_at	AT1G22720	wall-associated kinase, putative	0.4702	0.1198	0.2001	-0.00499	0.9843	0.5402	0.3588	0.2067	0.2159	-0.1164	0.6509	0.3811
264195_at	AT1G22690	gibberellin-responsive protein, putative	-1.5222	9.00E-04	0.0347	-1.6418	6.00E-04	0.027	0.04388	0.8089	0.4662	-0.07574	0.6787	0.3902
264196_at	AT1G22670	protease-associated zinc finger (C3HC4-type RING	-0.1116	0.8449	0.5372	0.4904	0.411	0.3465	-0.06761	0.8485	0.4782	0.5344	0.1825	0.175
264197_at	AT1G22620	ATSAC1 (SUPPRESSOR OF ACTIN 1); phosphoin	0.7458	0.0337	0.1062	1.0279	0.0119	0.0587	-0.3309	0.2317	0.2304	-0.04896	0.8451	0.4414
264198_at	AT1G22800	methyltransferase	-0.0868	0.4912	0.4163	0.03927	0.7785	0.4832	-0.3642	0.0341	0.0755	-0.2261	0.121	0.1358
264199_at	AT1G22700	tetratricopeptide repeat (TPR)-containing protein	-0.1522	0.1796	0.2476	-0.1337	0.2266	0.2496	-0.2631	0.0484	0.0924	-0.2447	0.0593	0.0879
264200_at	AT1G22650	beta-fructofuranosidase, putative / invertase, putativ	0.06503	0.877	0.5456	0.005803	0.989	0.5413	-0.4518	0.161	0.1862	-0.511	0.124	0.1377
264201_at	AT1G22630	heat shock protein binding / unfolded protein binding	-0.6607	0.1289	0.2074	-0.3986	0.3136	0.2992	-0.01037	0.9224	0.4986	0.2517	0.0657	0.0933
264202_at	AT1G22810	AP2 domain-containing transcription factor, putative	-2.5199	0.0231	0.089	-1.1722	0.171	0.2134	0.1203	0.8725	0.4848	1.468	0.1053	0.1241
264203_at	AT1G22780	PFL (POINTED FIRST LEAVES); structural constitu	0.03206	0.8383	0.535	0.2124	0.2227	0.2475	-0.0133	0.9023	0.4931	0.1665	0.1895	0.179
264204_at	AT1G22710	SUC2 (SUCROSE-PROTON SYMPORTER 2); car	-0.6393	0.0087	0.0605	-0.8068	0.0038	0.0387	0.1881	0.1106	0.1488	0.02048	0.8349	0.4386
264205_at	AT1G22790	similar to unknown protein [Arabidopsis thaliana] (T	-0.232	0.405	0.3778	-0.03946	0.882	0.5137	-0.111	0.6794	0.4242	0.08154	0.7601	0.4167
264206_at	AT1G22730	MA3 domain-containing protein	0.2213	0.1764	0.2457	0.5742	0.0131	0.0611	0.6993	0.0039	0.0273	-0.3535	0.0404	0.0695
264207_at	AT1G22750	similar to unnamed protein product [Vitis vinifera] (G	0.1089	0.4739	0.4094	-0.1661	0.295	0.2892	0.1083	0.4693	0.3472	-0.1667	0.2865	0.2315
264208_at	AT1G22760	PAB3 (POLY(A) BINDING PROTEIN 3); RNA bindi	-0.5627	0.1724	0.243	-1.2093	0.0235	0.0771	0.7495	0.0916	0.1339	0.103	0.7765	0.4219
264209_at	AT1G22740	RAB7 (Ras-related protein 7); GTP binding	0.3222	0.1309	0.209	-0.1354	0.4697	0.3721	0.2967	0.0489	0.0932	0.4831	0.0103	0.0317
264210_at	AT1G22640	MYB3 (myb domain protein 3); DNA binding / transc	-0.1471	0.6739	0.4839	0.14	0.6885	0.4551	-0.06753	0.5394	0.3751	0.2196	0.0948	0.1166
264211_at	AT1G22770	GI (GIGANTEA); binding	0.2431	0.6163	0.465	0.2521	0.6039	0.4247	-0.4809	0.1086	0.1475	-0.472	0.1134	0.1301
264212_at	AT1G22660	tRNA-nucleotidyltransferase, putative / tRNA adeny	0.6149	0.0224	0.0875	-0.1515	0.4232	0.3521	0.1746	0.3626	0.2984	-0.5918	0.0253	0.0526
264213_at	AT1G65390	ATPP2-A5; carbohydrate binding	-2.2769	0.0054	0.0519	-2.0114	0.0084	0.0507	0.215	0.1724	0.1934	0.4805	0.0207	0.0466
264214_s_at	AT1G65330,AT1G65300	[AT1G65330, PHE1 (PHERES1); DNA binding / tra	0.2194	0.7452	0.5075	2.0473	0.0314	0.088	0.5778	0.4108	0.3211	2.4058	0.0188	0.044
264215_at	AT1G65340	CYP86A1 (cytochrome P450, family 86, subfamily A	2.2684	0.4284	0.3884	1.3002	0.4145	0.348	-0.04409	0.9567	0.507	2.9146	0.0301	0.0583
264216_at	AT1G60180	pseudogene of F-box family protein	-0.2638	0.7835	0.5188	1.5076	0.1685	0.2115	0.8584	0.3932	0.3134	2.6298	0.0429	0.0723
264217_at	AT1G60190	armadillo/beta-catenin repeat family protein / U-box	-0.7478	0.03	0.1007	-0.4525	0.1169	0.1727	-0.2353	0.1594	0.1853	0.05995	0.6829	0.3915
264218_at	AT1G60200	splicing factor PWI domain-containing protein / RNA	0.3463	0.0191	0.082	0.1515	0.1716	0.2139	-0.6841	0	0.0092	-0.8789	0	0.0047
264219_at	AT1G60420	DC1 domain-containing protein	1.0057	7.00E-04	0.0334	1.0119	7.00E-04	0.027	-0.2236	0.1007	0.1417	-0.2174	0.1077	0.1259
264220_at	AT1G60430	ARPC3 (actin-related protein C3); structural molecu	-0.09724	0.509	0.4245	-0.1089	0.4627	0.3692	-0.1683	0.1406	0.1718	-0.18	0.1214	0.136
264221_s_at	AT1G60610,AT1G60170	[AT3G60610, pseudogene, putative pre-mRNA proc	0.1987	0.1876	0.2538	0.3473	0.0501	0.1111	0.1221	0.3847	0.31	0.2706	0.0967	0.118
264222_at	AT1G60230	radical SAM domain-containing protein	-0

264290_at	AT1G76810	similar to hypothetical protein [Vitis vinifera] (GB:CA	-0.4785	0.049	0.1274	-0.02725	0.8812	0.5134	-0.3481	0.1068	0.1463	0.1032	0.5721	0.3532
264291_at	AT1G76800	glycosyl transferase family 1 protein	0.2254	0.219	0.2745	0.1511	0.3844	0.3339	-0.423	0.0191	0.0554	-0.4974	0.0111	0.0329
264292_at	AT1G78790	similar to unknown [Populus trichocarpa] (GB:ABK9	-0.7617	0.0395	0.1147	-0.5797	0.0838	0.1455	0.5272	0.0112	0.0418	0.7092	0.0039	0.0201
264293_at	AT1G78770	cell division cycle family protein	0.3988	0.3597	0.3544	-0.04741	0.9081	0.521	0.0396	0.9232	0.4987	-0.4066	0.3514	0.2633
264294_at	AT1G78750	F-box family protein	-0.2717	0.7221	0.5001	-0.9701	0.2446	0.2606	0.5202	0.5054	0.3615	-0.1781	0.8147	0.4328
264295_at	no_match	no_match	-0.06323	0.9532	0.5656	-2.5026	0.0688	0.1317	1.5406	0.2028	0.2134	-0.8988	0.4249	0.2945
264296_at	AT1G78720	protein transport protein sec61, putative	0.3907	0.273	0.3073	-0.4723	0.1996	0.2327	0.2731	0.3141	0.2755	-0.59	0.0678	0.0951
264297_at	AT1G78710	similar to unknown protein [Arabidopsis thaliana] (T	-0.6134	0.5658	0.4472	-1.9143	0.1228	0.1778	0.6764	0.5285	0.3706	-0.6245	0.5591	0.3485
264298_at	AT1G78690	phospholipid/glycerol acyltransferase family protein	-0.4716	0.0199	0.0833	-0.09938	0.4734	0.3735	-0.4804	0.0186	0.0546	-0.1081	0.4368	0.3
264299_s_at	AT1G78850,AT1G78860	cupin family protein	-0.315	0.6507	0.4765	-0.2212	0.7487	0.4747	0.5683	0.1165	0.1535	0.6621	0.0806	0.1055
264300_at	AT1G78670	ATGGH3 (GAMMA-GLUTAMYL HYDROLASE 3); g	0.3647	0.2988	0.3224	0.3616	0.3023	0.2926	-0.4054	0.0488	0.0931	-0.4085	0.0478	0.0771
264301_at	AT1G78780	pathogenesis-related family protein	1.4266	0.0844	0.1682	1.4025	0.0881	0.1496	1.1339	0.0189	0.0551	1.1098	0.0202	0.0459
264302_at	AT1G78900	VHA-A; ATP binding / hydrogen ion transporting AT	0.05147	0.6766	0.4848	-0.1476	0.2673	0.274	-0.2956	0.0613	0.1065	-0.4947	0.0125	0.0353
264303_s_at	AT1G16890,AT1G78870	[AT1G16890, UBC13B;UBC36 (UBIQUITIN-CONJ	0.372	0.1845	0.2514	0.2687	0.3117	0.2983	0.6816	0.0098	0.0396	0.5783	0.0172	0.0419
264304_at	AT1G78895	similar to pentatricopeptide (PPR) repeat-containing	0.1747	0.372	0.3605	0.3472	0.1166	0.1725	-0.214	0.1585	0.1847	-0.04147	0.7541	0.4149
264305_at	AT1G78815	similar to unknown protein [Arabidopsis thaliana] (T	-0.2929	0.7945	0.5223	3.4842	0.0296	0.0855	-1.8334	0.1564	0.1833	1.9437	0.1384	0.1472
264306_at	AT1G78890	similar to unknown protein [Arabidopsis thaliana] (T	0.4252	0.1261	0.2055	0.5475	0.068	0.1307	0.533	0.0203	0.0573	0.6533	0.0101	0.0314
264307_at	AT1G61900	Identical to Uncharacterized GPI-anchored protein /	-0.6549	0.0234	0.0895	-0.5689	0.0362	0.094	-0.119	0.0957	0.1375	-0.03287	0.581	0.3565
264308_at	AT1G61990	mitochondrial transcription termination factor-relate	0.6088	0.0379	0.1122	0.2722	0.2441	0.2606	0.0277	0.8963	0.4913	-0.3089	0.1963	0.1828
264309_at	AT1G62200	coatomer protein complex, subunit alpha, putative	0.5092	0.0098	0.0633	0.4331	0.0169	0.0676	-0.324	0.003	0.0248	-0.4002	0.0014	0.0133
264310_at	AT1G62030	DC1 domain-containing protein	-0.2	0.5034	0.4219	-0.265	0.3855	0.3345	0.03634	0.3155	0.276	-0.02867	0.4168	0.2912
264311_at	AT1G78400	similar to EMB1220 (EMBRYO DEFECTIVE 1220) (	0.6958	0.4743	0.4096	0.09873	0.9163	0.5231	0.6291	0.5151	0.3651	1.4236	0.1818	0.1744
264312_at	AT1G70450	protein kinase family protein	-0.6675	0.6733	0.4838	1.5752	0.3442	0.3152	-2.0923	0.2017	0.2127	0.1504	0.9179	0.4621
264313_at	AT1G70410	carbonic anhydrase, putative / carbonate dehydrata	-0.8191	7.00E-04	0.0334	-1.2594	1.00E-04	0.0249	0.3717	0.0132	0.0458	-0.0687	0.4767	0.3164
264314_at	AT1G70420	similar to unknown protein [Arabidopsis thaliana] (T	0.1375	0.8084	0.5263	0.6035	0.3191	0.3026	0.005922	0.9783	0.5122	0.4719	0.0823	0.1069
264315_at	AT1G70370	BURP domain-containing protein / polygalacturonas	-0.6823	0.0014	0.038	-0.5884	0.0024	0.0339	0.484	0.005	0.0298	0.5779	0.0026	0.0169
264316_at	AT1G70330	ENT1,AT (EQUILIBRATIVE NUCLEOTIDE TRANS	-0.1518	0.3651	0.3569	-0.3617	0.0718	0.1341	0.3992	0.0517	0.0963	0.1892	0.2632	0.2193
264317_at	AT1G70310	SPDS2 (SPERMIDINE SYNTHASE 2)	-0.06425	0.7809	0.518	0.02743	0.9051	0.5201	-0.704	0.0172	0.0524	-0.6124	0.027	0.0546
264318_at	AT1G04220	beta-ketoacyl-CoA synthase, putative	-0.5022	0.376	0.3623	-0.03259	0.9516	0.5323	-0.4202	0.3087	0.2728	0.04936	0.8977	0.4566
264319_at	GA04110	SDD1 (STOMATAL DENSITY AND DISTRIBUTION	-1.2321	0.2594	0.2994	-0.7583	0.4643	0.3698	-3.4582	0.0065	0.0331	-2.9845	0.0109	0.0326
264320_at	GA04090	similar to unknown protein [Arabidopsis thaliana] (T	0.891	0.3713	0.3602	0.9431	0.347	0.3165	0.5473	0.5701	0.3867	0.5994	0.5357	0.34
264321_at	GA04200	similar to hypothetical protein OsJ_003532 [Oryza s	0.4862	0.0821	0.1657	0.2024	0.3908	0.3371	0.1088	0.6325	0.4086	0.3926	0.1356	0.1454
264322_at	GA04190	tetratricopeptide repeat (TPR)-containing protein	0.2744	0.2781	0.3103	0.3018	0.24	0.2577	0.5381	0.0281	0.0681	0.5654	0.024	0.0509
264323_at	GA04180	flavin-containing monooxygenase family protein / FI	0.539	0.2516	0.2942	-0.01592	0.9703	0.5368	-0.981	0.0714	0.1152	-1.5359	0.0188	0.044
264324_at	GA04160	XIB (lysosin-like protein XIB)	-0.722	0.3114	0.3295	-2.0021	0.0326	0.0895	0.3079	0.6474	0.4136	-0.9722	0.194	0.1815
264325_at	GA04150	C2 domain-containing protein	-0.3934	0.2091	0.2675	-0.231	0.4294	0.355	-0.2117	0.382	0.3087	-0.04932	0.8304	0.4372
264326_at	GA04230	similar to unknown protein [Arabidopsis thaliana] (T	0.355	0.0032	0.0445	0.5173	8.00E-04	0.0227	0.03237	0.6964	0.3969	0.1947	0.026	0.0534
264327_at	GA04170	initiation factor 2 gamma subunit); translation factor	0.1988	0.4739	0.4094	0.1787	0.5171	0.3913	-0.2611	0.3503	0.0711	0.2812	0.2241	0.051
264328_at	GA04100	IAA10 (indoleacetic acid-induced protein 10); transc	-0.1678	0.4239	0.3868	-0.6473	0.0265	0.0815	0.3956	0.104	0.1441	-0.08385	0.6797	0.3903
264329_at	GA04140	transducin family protein / WD-40 repeat family prot	0.4097	0.012	0.0681	-0.1355	0.2218	0.247	-0.2452	0.0591	0.1042	-0.7904	0.0011	0.0124
264330_at	GA04120	ATMRP5 (Arabidopsis thaliana multidrug resistance	0.05439	0.8606	0.5412	0.1538	0.6247	0.4328	-0.3547	0.0911	0.1335	-0.2553	0.186	0.177
264331_at	GA04130	tetratricopeptide repeat (TPR)-containing protein	0.6132	0.2549	0.2964	0.2036	0.682	0.4528	0.3284	0.5162	0.3656	-0.08123	0.8689	0.448
264332_at	GA04160	unknown protein	-0.6555	0.1301	0.2085	0.02176	0.9527	0.5325	-0.2552	0.5002	0.3597	0.422	0.2882	0.2325
264333_at	AT1G61940	AtTLP4 (TUBBY LIKE PROTEIN 4); transcription fa	1.9618	0.0656	0.1468	0.1159	0.889	0.5155	0.4664	0.5819	0.3914	-1.3796	0.1515	0.1557
264334_at	GI61950	CPK19 (calcium-dependent protein kinase 19); calm	-0.8722	0.3533	0.3515	-2.2745	0.0521	0.1132	1.4258	0.1615	0.1864	0.02351	0.9788	0.4778
264335_s_at	AT1G55560,UPL1	(UBIQUITIN-PROTEIN LIGASE	0.1364	0.0116	0.0674	0.3623	0.1982	0.2318	-0.7324	0.0109	0.0414	-1.4065	0.001	0.0121
264336_at	AT1G70360	F-box protein-related	0.4689	0.0711	0.1538	0.4122	0.0985	0.1581	-0.5202	0.0536	0.0985	-0.577	0.0398	0.0689
264337_at	GI70350	unknown protein	0.3539	0.139	0.2165	0.3497	0.1425	0.1926	0.2234	0.0065	0.0332	0.2192	0.007	0.0261
264338_at	GI70300	KUP6 (K+ uptake permease 6); potassium ion trans	0.4083	0.0379	0.1121	0.5239	0.0173	0.0681	0.1174	0.4293	0.3293	0.233	0.1563	0.159
264339_at	AT1G70290	ATTPS8 (Arabidopsis thaliana trehalose phosphata	0.2134	0.372	0.3605	0.3684	0.1579	0.2043	-0.5474	0.0056	0.0313	-0.3924	0.0178	0.0427
264340_at	GI70280	NHL repeat-containing protein	0.1587	0.2601	0.2997	0.015	0.9074	0.5207	-0.101	0.0661	0.1113	-0.2447	0.0037	0.0197
264341_at	GI70270	unknown protein	-2.305	0.0482	0.1276	-2.9143	0.0243	0.0782	1.0264	0.2818	0.2591	0.4172	0.64	0.3772
264342_at	GI12080	contains domain PTHR22683 (PTHR22683)	-1.794	0.0019	0.0391	-1.0333	0.0138	0.0623	0.815	0.0299	0.0704	1.5757	0.0031	0.018
264343_at	GI11850	unknown protein	-2.1155	3.00E-04	0.0312	-1.7323	7.00E-04	0.027	-0.1042	0.5935	0.3959	0.279	0.1958	0.1825
264344_at	GI11910	aspartyl protease family protein	0.3596	0.0411	0.1168	0.1191	0.3809	0.3323	-0.08609	0.3961	0.3148	-0.3265	0.0227	0.049
264345_at	GI11915	similar to unknown protein [Arabidopsis thaliana] (T	-0.2384	0.8162	0.5286	0.4148	0.6881	0.455	1.3893	0.2216	0.2245	2.0424	0.1006	0.1211
264346_at	GI12010	1-aminocyclopropane-1-carboxylate oxidase, putati	-0.5806	0.1273	0.2061	-0.1766	0.5906	0.4197	-0.4541	0.2076	0.2164	-0.05011	0.8764	0.4503
264347_at	GI12040	LRX1 (LEUCINE-RICH REPEAT/EXTENSIN 1); pro	0.4219	0.3008	0.3234	-1.2459	0.3509	0.3184	1.067	0.4173	0.324	-1.5808	0.2517	0.2135
264348_at	GI12110	NRT1.1 (NITRATE TRANSPORTER 1.1); transport	-0.9267	0.0463	0.1237	-1.2373	0.019	0.071	-0.6264	0.07	0.1147	-0.937	0.0213	0.0474
264349_at	GI11930	alanine racemase family protein	0.1188	0.1124	0.1942	0.384	0.0028	0.0351	-0.3811	0.0029	0.0245	-0.116	0.1188	0.1338
264350_at	GI11870	AtSRS (OVULE ABORTION 7); serine-tRNA ligase	-0.2491	0.0402	0.1157	-0.5146	0.0035	0.0374	-0.2095	5.00E-04	0.0152	-0.475	0	0.0047
264351_at	GI03370	C2 domain-containing protein / GRAM domain-cont	0.2004	0.6053	0.4615	0.2886	0.4651	0.37	-0.8942	0.0024	0.023	-0.806	0.0036	0.0194
264352_at	GI03270	similar to unknown protein [Arabidopsis thaliana] (T	-0.4754	0.1329	0.2115	-0.5632	0.0895	0.1508	-0.3257	0.1414	0.1724	-0.4135	0.0809	0.1058
264353_at	GI03260	similar to unknown protein [Arabidopsis thaliana] (T	-0.1643	0.4296	0.3888	0.1449	0.4821	0.377	-0.3276	0.1408	0.1719	-0.01841	0.9229	0.4636
264354_s_at	AT1G03200,AT1G03240	[AT1G03200, similar to unknown protein [Arabidops	0.08801	0.947	0.5639	0.7636	0.5726	0.4129	-3.3291	0.0555	0.1004	-2.6536	0.0999	0.1205
264355_at	GI03210	phenazine biosynthesis PhzC/PhzF family protein	1.1414	2.00E-04	0.0312	0.9587	5.00E-04	0.0257	-0.02851	0.7732	0.4554	-0.2112	0.0844	0.1085
264356_at	GI03190	ATXPD/UVH6 (ULTRAVIOLET HYPERSENSITIVE	0.3678	0.1547	0.2296	0.8148	0.0178	0.0691	-0.5841	0.0497	0.0943	-0.1372	0.5493	0.3448
264357_at	GI03360	ATRRP4; exonuclease	0.1355	0.636	0.4716	0.2325	0.4298	0.3552	-0.1525	0.0903	0.1328	-0.05551	0.4637	0.3115
264358_at	GI03180	similar to unnamed protein product [Vitis vinifera] (G	-0.1929	0.414	0.3819	0.01764	0.9376	0.5284	-0.07891	0.7284	0.4413	0.1316	0.568	0.352
264359_at	GI03320	unknown protein	0.1562	0.8924	0.5492	0.4422	0.7044	0.4605	-0.4919	0.644	0.4123	-0.206	0.8447	0.4413
264360_at	GI03310	ATISA2/BE2/DBE1/ISA2 (DEBRANCHING ENZYM	0.3495	0.0464	0.1238	0.04614	0.7258	0.4673	0.2037	0.129	0.1633	-0.0997	0.4031	0.2854
264361_at	GI03300	agenet domain-containing protein	0.0337	0.9124	0.5547	-0.1233	0.6903	0.4557	0.07789	0.7967	0.4624	-0.07914	0.7936	0.4271
264362_at	GI03290	similar to unknown protein [Arabidopsis thaliana] (T	0.1177	0.003	0.0436	1.1409	0.0028	0.0351	0.09764	0.0742	0.1186	0.1209	0.041	0.0701
264363_at	GI03170	similar to unknown protein [Arabidopsis thaliana] (T	0.6519	0.4326	0.3907	1.5342	0.1095	0.1671	-0.7386	0.3793	0.3075	0.1437	0.857	0.445
264364_at	GI03330	small nuclear ribonucleoprotein D, putative / snRNP	0.1499	0.2331	0.2837	0.3318	0.036	0.0937	0.3814	0.0233	0.0618	0.5633	0.0062	0.0244
264365_s_at	AT1G03220,AT1G03230	[AT1G03220, extracellular dihydrogyceptein, put	-0.1583	0.5913	0.4565	0.2388	0.4291	0.3549	-0.4039	0.0055	0.031	0.8011	4.00E-04	0.009
264366_at	GI03250	similar to unknown [Populus trichocarpa] (GB:ABK9	-0.1896	0.234	0.2839	0.1749	0.2658	0.2731	0.1555	0.0203	0.0573	0.52	2.00E-04	0.0078
264367_at	GI03350	BSD domain-containing protein	0.2553	0.2282	0.2808	0.07568	0.6952	0.4571	0.4906	0.035	0.0767	0.3109	0.1178	0.1332
264368_at	GI03280	initiation factor IIE (TFIIE) alpha subunit family prot	0.2658	0.0981	0.1809	0.3605	0.0435	0.1034	-0.00762	0.9538	0.5065	0.08705	0.5204	0.3339
264369_at	GI70430	protein kinase family protein	-0.9482	0.4216	0.3858	-1.4537	0.2421	0.2592	-2.1104	0.1173	0.1541	-2.6159	0.0691	0.0963
264370_at	GI12100	lipid binding	0.1379	0.813	0.5277	-0.7681	0.2322	0.2531	0.2223	0.7047	0.433	-0.6837	0.2787	0.2275
264371_at	GI12090	ELP (EXTENSIN-LIKE PROTEIN); lipid binding	-0.5563	0.0069	0.0558	-0.7123	0.0028	0.0351	0.3154	0.0047	0.0292	0.1594	0.0454	0.0747
264372_at	AT1G11840	ATGLX1 (GLYOXALASE I HOMOLOG); lactoylglut	-0.1585	0.244	0.29	-0.04277	0.7313	0.4688	0.274	0.0776	0.1218	0.3897	0.0284	0.0563
264373_at	GI11890	SEC22 (secretion 22); transporter	-0.0874	0.4309	0.3896	0.05011	0.6422	0.4389	0.3316	0.0293	0.0696	0.4692	0.0093	0.0301
264374_at	AT2G25180	ARR12 (ARABIDOPSIS RESPONSE REGULATOR	-0.03397	0.5883	0.4558	-0.5685	6.00E-04	0.027	0.08725	0.2056	0.2152	-0.4473	0.0015	0.0138
264375_at	AT2G25090	CIPK16 (SNF1-RELATED PROTEIN KINASE 3.18)	1.2561	0.2509	0.2939	1.4429	0.1982	0.2318	0.02821	0.973	0.5107	0.2151	0.7975	0.4281
264376_at	AT2G25070	protein phosphatase 2C, putative / PP2C, putative	0.3646	0.094	0.1775	0.4563	0.0521	0.1132	-0.01413	0.9286	0.5002	0.07758	0.6281	0.3731
264377_at	AT2G25060	plastocyanin-like domain-containing protein	-1.2153	0.0463	0.1237	0.3179	0.4972	0.3832	0.03278	0.9424	0.5038	1.5659	0.0213	0.0474
264378_at	AT2G25220	protein kinase family protein	-0.9194	0.1013	0.1841	-1.3185	0.0383	0.097	0.3468	0.0356	0.0774	-0.05241	0.6619	0.3848
264379_at	AT2G25200	similar to unknown protein [Arabidopsis thaliana] (T	0.1199	0.7333	0.5033	0.3447	0.3526	0.3194	-0.05729	0.7417	0.4453	0.1675	0.3599	0.267
264380_at	AT2G25190	similar to unknown protein [Arabidopsis thaliana] (T	0.2229	0.1057	0.1879	0.4943	0.0099	0.0541	-0.4001	0.0029	0.0245	-0.1287	0.1047	0.1239
264381_at	AT2G25100	ribonuclease HII family protein	-0.06833	0.6344	0.4709	-0.2327	0.155	0.202	0.1481	0.1654	0.1887	-0.01626	0.8614	0.4462
264382_at	AT2G25110	SDF2 (STROMAL CELL-DERIVED FACTOR 2-LIK	1.1832	0.0019	0.0391	1.0584	0.0029	0.0355	0.6154	0.0134	0.0461	0.4907	0.0281	0.056
264383_at	AT2G25080	ATGPX1 (GLUTATHIONE PEROXIDASE 1); glutat	-0.6734	0.0085	0.0602	-0.5554	0.0165	0.0666	-0.02337	0.8739	0.4851	0.09467	0.5309	0.3384
264384_at	AT2G25170	PKL (PICKLE)	0.7727	0.0047	0.0492	0.1792	0.2562	0.268	-0.3081	0.0852	0.1285	-0.9016	0.0026	0.017
264385_at	GI12020	similar to unknown protein [Arabidopsis thaliana] (T	-0.2731	0.1015	0.1842	-0.2138	0.1724	0.2145	0.1571	0.2899	0.2635	0.2163	0.1685	0.1664
264386_at	GI12000	pyrophosphate--fructose-6-phosphate 1-phosphotra	0.2436	0.2313	0.2829	0.1165	0.537	0.3993	0.07336	0.6487	0.4142	-0.05372	0.737	0.4094
264387_at	GI11990	similar to unknown protein [Arabidopsis thaliana] (T	-1.2165	0.2062	0.2661	-3.3252	0.0146	0.0638	1.1342	0.2327	0.2309	-0.9746	0.2937	0.2354
264388_at	GI11970	contains InterPro domain Ubiquitin; (InterPro:IPR00	0.2696	0.8668	0.5427	-1.1403	0.4915	0.381	-0.06932	0.955	0.5066	-1.4792	0.2691	0.2223
264389_at	GI11960	early-responsive to dehydration protein-related / ER	-0.6174	0.3157	0.3319	-0.5724	0.3479	0.317	-0.2496	0.395	0.3143	-0.2046	0.4789	0.3171
264390_at	GI11950	transcription factor	0.396	0.2863	0.315	1.182	0.0214	0.0745	-0.695	0.013	0.0454	0.091	0.6065	0.3656
264391_at	GI11920	pectate lyase family protein	1.3483	0.1921	0.2569	-1.0122	0.3046	0.294	1.9287	0.0884	0.1313	-0.4318	0.6421	0.378
264392_at	GI11900	pentatricopeptide (PPR) repeat-containing protein	-0.1375	0.3931	0.3716	0.5067	0.0244	0.0783	-0.5405	0.0198	0.0565	0.1036	0.511	0.3302
264393_at	GI11880	similar to unnamed protein product [Vitis vinifera] (G	-0.8717	0.2259	279	0.04482	0.9449	0.5306	-1.1647	0.087	0.1302	-0.2482	0.6558	0.3828
264394_at	GI11860	aminomethyltransferase, putative	-1.0329	3.00E-04	0.0312	-0.8858	5.00E-04	0.0253	-0.3819	0.0108	0.0412	-0.2348	0.0503	0.0796
264395_at	GI12070	Rho GDP-dissociation inhibitor family protein	-0.7893	0.5599	0.4431	0.2674	0.8385	0.501	-0.6583	0.4861	0.3539	0.3984	0.6668	0.3864
264396_at	GI12050	fumarylacetoacetase, putative	0.414	0.1269	0.206	0.4348	0.1137	0.1704	-0.5467	0.0507	0.0954	-0.5259	0.0565	0.0854
264397_at	no_match	no_match	-0.4285	0.1521	0.2276	-0.4845	0.1165	0.1724	-0.1235	0.4771	0.3503	-0.1795	0.3182	0.2474
264398_at	AT1G61730	DNA-binding storekeeper protein-related	0.6912	0.0173	0.0787	0.922	0.0064	0.0457	0.5724	0.0315	0.0722	0.8032	0.0104	0.0319
264399_at	AT1G61780	postsynaptic protein-related	0.08715	0.4884	0.4152	0.4574	0.0161	0.066	0.8465	0.0018	0.0206	1.2167	4.00E-04	0.0091
264400_at	AT1G61800	GPT2 (glucose-6-phosphate/phosphate translocato	0.8691	0.2331	0.2837	1.1143	0.1463	0.1955	-0.5197	0.3858	0.3104	-0.2745	0.6345	0.3753
264401_at	AT1G61720	BAN (BANQUYULS)	0.7118	0.1206	0.2008	-0.7861	0.0956	0.1558	1.3688	0.0187	0.0548	-0.131	0.7325	0.4079
264402_at	AT2G25140	CLPB-M/CLPB4/HSP98.7 (HEAT SHOCK PROTEI	0.2328	0.419	0.3844	0.6799	0.0582	0.12	-0.5444	0.048	0.092	-0.0973	0.6412	0.3777
264403_at	AT2G25150	transferase family protein	0.1574	0.6626	0.4802	-0.5539	0.1732	0.215	-0.2629	0.5348	0.3731	-0.6234	0.1359	0.1456
264404_at	AT2G25160	ATCPR1 (CYTOCHROME P450, family 82, subfamily F	0.01667	0.9819	0.5725	1.1859	0.1606	0.2063	-0.4477	0.5516	0.3796	0.7215	0.3545	0.2646
264405_at	AT1G10210	ATMPK1 (MITOGEN-ACTIVATED PROTEIN KINA	0.6969	0.012	0.0681	1.136	0.0021	0.0331	-0.3814	0.0754	0.1196	0.05775	0.7361	0.4091
264406_at	GI10290	ADL6 (DYNAMIN-LIKE PROTEIN 6)	0.502	0.0174	0.0792	0.5798	0.0107	0.0558	-0.1094	0.4427	0.3353	-0.03151	0.8194	0.4338
264407_at	GI10180	similar to unknown protein [Arabidopsis thaliana] (T	0.2192	0.0768	0.1594	0.1774	0.1275	0.1812	0.1651	0.0435	0.087	0.1233	0.0952	0.117
264408_at	GI10240	FRS11 (FAR1-RELATED SEQUENCE 11); zinc ion	0.2228	0.2938	0.3196	-0.3423	0.1372	0.1886	0.712	0.0182	0.054	0.1469	0.4705	0.3139
264409_at	no_match	no_match	0.1131	0.4209	0.3854	-1.7246	0.2374	0.2562	-0.2219	0.8568	0.4802	-0.8506	0.5312	0.3384
264410_at	AT4G34205,AT4G07523,A	[AT4G34205, transposable element gene];[AT4G07	-1.1328	0.4896	0.4157	-0.2258	0.8869	0.515	-0.5906	0.7122	0.4357	0.3164	0.8423	0.4407
264411_at	no_match	no_match	0.737	0.4928	0.417	0.264	0.8004	0.4897	0.8282	0.4445	0.336	0.3552	0.7347	0.4086
264412_at	GI34280	similar to protein dimerization [Arabidopsis thaliana]	0.9216	0.4479	0.3971	2.0247	0.841	0.5017	-1.1247	0.363	0.2995	-1.8116	0.1738	0.1696
264413_s_at	AT4G34290,AT4G34450	[AT4G34290, transposable element gene];[AT3G42	0.2565	0.858	0.5406	0.5087	0.7243	0.4667	-1.0143	0.4925	0.3566	-0.7621	0.601	0.3638
264414_s_at	AT4G34300,AT4G34460	[AT4G34300, transposable element gene];[AT3G42	-0.05037	0.9611	0.5676	-0.4139	0.6914	0.4559	0.6036	0.4479	0.3376	0.2401	0.7549	0.4151
264415_at	GI34310	RAP2.4 (related to AP2 6); DNA binding / transcript	-1.0561	0.4421	0.3946	-0.3027	0.819	0.4955	1.0459	0.1603	0.1858	1.7992	0.0415	0.0707
264416_at	GI34140	pseudogene, cullin family, low similarity to Hs-CUL	0.2064	0.8862	0.5474	1.6386	0.2926	0.288	-0.5569	0.7018	0.4319	0.8753	0.553	0.3461
264417_at	no_match	no_match	1.3193	0.0582	0.1382	-0.3235	0.5541	0.4062	0.1938	0.7188	0.4381	-1.4489	0.0446	0.0741
264418_at	GI34190	polypeptidase trict-binding protein, putative / heter	0.1664	0.2493	0.2932	-0.09856	0.4638	0.3697	0.01132	0.9119	0.4957	-0.2513	0.6592	0.3878
264419_s_at	AT4G33310,AT5G33320	[AT4G33310, triose phosphate/phosphate translocc	-0.798	0.0142	0.0727	-0.9018	0.0093	0.0528	-0.3998	0.1057	0.1454	-0.5036	0.0585	0.0873
264420_at	GI34320	unknown protein	0.3505	0.7676	0.5138	0.6275	0.6015	0.4241	-1.5415	0.2367	0.2333	-1.2644	0.3176	0.2472
264421_at	GI34170	ARP1 (ARABIDOPSIS RIBOSOMAL PROTEIN 1);	0.04591	0.7316	0.5028	0.02241	0.8662	0.5088	-0.332	0.0564	0.1014	-0.3555	0.0465	0.0758
264422_at	GI34130	LCV2 (LIKE COV 2)	0.8794	0.0218	0.0867	0.8274	0.0264	0.0813	0.1176	0.5113	0.3637	0.06559	0.7085	0.4004
264423_at	GI61690	zinc ion binding	0.416	0.0633	0.1442	0.5337	0.0307	0.087	-0.4924	0.0392	0.0819	-0.3748	0.0832

264490_at	AT1G27390	TOM20-2 (TRANSLOCASE OUTER MEMBRANE 2	-0.03254	0.806	0.5257	0.2319	0.135	0.1868	0.2143	0.0682	0.1133	0.4787	0.0052	0.0225
264491_at	AT1G27410	DNA cross-link repair protein-related	0.4367	0.0924	0.1761	0.06934	0.7442	0.4728	-0.2266	0.3169	0.2767	-0.5939	0.0401	0.0692
264492_at	AT1G27430	GYF domain-containing protein	0.4333	0.3388	0.3448	-0.1628	0.7044	0.4605	-0.3393	0.1971	0.2099	-0.9353	0.013	0.0362
264493_at	AT1G27440	GUT2; catalytic	0.1477	0.3236	0.3364	0.2834	0.0972	0.1571	-0.1668	0.273	0.254	-0.03113	0.8243	0.4355
264494_at	AT1G27461	similar to unnamed protein product [Vitis vinifera] (G	0.5521	0.6213	0.4569	0.8844	0.4402	0.3596	-0.7017	0.5342	0.3729	-0.3694	0.7387	0.41
264495_at	AT1G27380	RIC2 (ROP-INTERACTIVE CRIB MOTIF-CONTAIN	0.7108	0.1225	0.2029	0.7202	0.119	0.1744	0.2469	0.3844	0.3098	0.2564	0.3683	0.2706
264496_at	AT1G27285	transposable element gene	-0.5678	0.6125	0.4635	-0.198	0.8576	0.5066	-1.0034	0.3872	0.3109	-0.6336	0.5735	0.3537
264497_at	AT1G30840	ATPUP4 (Arabidopsis thaliana purine permease 4);	0.648	0.1534	0.2286	-0.6664	0.1448	0.1943	0.6218	0.1688	0.1895	0.6034	0.1768	0.1712
264498_at	AT1G30825	ARPC2A/DIS2 (DISTORTED TRICHOMES 2); stru	0.1243	0.5702	0.4492	-0.5622	0.0491	0.1098	0.4488	0.0286	0.0687	-0.2377	0.1508	0.1553
264499_at	AT1G30795	hydroxyproline-rich glycoprotein family protein	0.8849	0.4907	0.4162	-1.9756	0.1659	0.2097	2.2019	0.1324	0.1655	-0.6586	0.6028	0.3642
264500_at	AT1G09370	enzyme inhibitor/ pectinesterase	-0.2847	-1.9604	0.2714	0.3064	1.3327	0.4351	0.3576	-2.0631	0.1661	0.1892	1.24	0.3649	0.269
264501_at	AT1G09390	GDSL-motif lipase/hydrolase family protein	0.469	0.0823	0.1659	-0.1144	0.6038	0.4247	0.5939	0.0069	0.0338	0.01049	0.9322	0.4662
264502_at	AT1G09400	12-oxophytodienoate reductase, putative	0.06482	0.9578	0.5666	0.6766	0.5883	0.4188	0.14	0.909	0.4951	0.7518	0.5493	0.3448
264503_at	AT1G09410	pentatricopeptide (PPR) repeat-containing protein	-0.3854	0.6347	0.4711	0.3138	0.6763	0.4507	-1.8099	0.0145	0.0481	-1.1378	0.0604	0.0888
264504_at	AT1G09430	ACLA-3 (ATP-citrate lyase A-3)	0.5808	0.0034	0.0447	0.6984	0.0017	0.0321	-0.2257	0.0729	0.1174	-0.1081	0.3111	0.2439
264505_at	AT1G09380	integral membrane family protein / nodulin MIN21-r	0.2391	0.5262	0.4316	0.139	0.7074	0.4613	0.08023	0.8222	0.4703	-0.01986	0.9555	0.4724
264506_at	AT1G09500	GLP5 (GERMIN-LIKE PROTEIN 5); manganese ion	0.4332	0.0219	0.087	0.3185	0.0554	0.1169	0.7741	0.0029	0.0245	0.6593	0.0052	0.0225
264507_at	AT1G09415	NIMIN-3 (NIM1-INTERACTING 3)	0.796	0.0395	0.1147	0.9672	0.0216	0.0747	-0.1126	0.6332	0.4088	0.05864	0.8015	0.4291
264508_at	AT1G09570	PHYA (PHYTOCHROME A); G-protein coupled pho	0.4507	0.0258	0.093	0.6386	0.008	0.0499	-0.619	0.0089	0.0378	-0.4311	0.0296	0.0578
264509_at	AT1G09520	similar to PHD finger family protein [Arabidopsis tha	0.2847	0.0665	0.1481	0.3031	0.0561	0.1177	-0.1265	0.1883	0.2032	-0.1082	0.2448	0.2096
264510_at	AT1G09530	PAP3/PIF3/POC1 (PHYTOCHROME INTERACTIN	0.1803	0.4436	0.3951	0.5154	0.0722	0.1346	-0.3364	0.0889	0.1316	-0.00136	0.9932	0.481
264511_at	AT1G09350	ATGDL53 (ARABIDOPSIS THALIANA GALACTINE	0.9747	0.015	0.0743	-0.7948	0.0291	0.0848	0.08247	0.7348	0.4432	0.2624	0.3122	0.2445
264512_at	AT1G09575	similar to unknown protein [Arabidopsis thaliana] (T	-0.3328	0.2768	0.3099	-0.6147	0.0808	0.1426	0.3958	0.2089	0.2171	0.1138	0.6891	0.3935
264513_at	AT1G09420	G6PD4 (GLUCOSE-6-PHOSPHATE DEHYDROGE	-0.09576	0.8612	0.5415	0.2922	0.6	0.4235	-0.664	0.1719	0.1933	-0.276	0.5277	0.337
264514_at	AT1G09500	cinnamyl-alcohol dehydrogenase family / CAD family	0.02851	0.962	0.5678	1.052	0.1006	0.16	-0.5953	0.005	0.0298	0.4818	0.0106	0.0322
264515_at	AT1G10090	similar to RXW8 [Arabidopsis thaliana] (TAIR:AT1G	-0.3171	0.0709	0.1536	-0.00295	0.983	0.5399	-0.6336	0.0026	0.0234	-0.3194	0.0277	0.0555
264516_at	AT1G10090	similar to RXW8 [Arabidopsis thaliana] (TAIR:AT1G	-0.5148	0.1161	0.1971	-0.4853	0.1324	0.1847	-1.1216	0.0041	0.0276	-1.0921	0.0045	0.0213
264517_at	AT1G10120	DNA binding / transcription factor	1.5997	1.00E-04	0.0018	1.3445	3.00E-04	0.0249	0.2008	0.0973	0.1388	-0.05426	0.5917	0.3604
264518_at	AT1G09980	similar to ZW18 [Arabidopsis thaliana] (TAIR:AT1G	1.1098	0.5106	0.425	1.5908	0.3595	0.3226	-2.2084	0.2245	0.2263	-1.7275	0.3243	0.2504
264519_at	AT1G10000	nucleic acid binding / ribonuclease H	-0.2567	0.3091	0.328	-0.105	0.6589	0.4446	-0.3085	0.2344	0.2319	-0.1567	0.5166	0.3322
264520_at	AT1G09010	AAP8 (amino acid permease 8); amino acid transme	1.3002	0.2188	0.2744	1.0565	0.3019	0.2924	0.8747	0.2139	0.2203	0.6281	0.3474	0.2613
264521_at	AT1G10020	similar to unknown protein [Arabidopsis thaliana] (T	-1.039	0.1632	0.2365	-1.1664	0.128	0.1815	-0.346	0.3591	0.2976	-0.4734	0.2296	0.2013
264522_at	AT1G10050	glycosyl hydrolase family 10 protein / carbohydrate-	0.8116	0.1094	0.1914	0.5437	0.2411	0.2586	-1.0374	0.0281	0.0681	-1.3054	0.0133	0.0365
264523_at	AT1G09030	ERG28 (ARABIDOPSIS HOMOLOG OF YEAST ER	0.4377	0.0732	0.1558	-0.7104	0.0173	0.0681	-0.1339	0.1432	0.174	-0.4066	0.0053	0.0226
264524_at	AT1G10070	ATBCAT-2; branched-chain-amino-acid transamina	0.7359	0.3925	0.3713	1.1165	0.2199	0.2458	-0.3755	0.4227	0.3266	0.005041	0.991	0.4804
264525_at	AT1G10060	ATBCAT-1; branched-chain-amino-acid transamina	-0.4598	0.0173	0.0787	-0.8577	0.0019	0.0329	-0.4291	0.0216	0.0593	-0.827	0.0021	0.0156
264526_at	AT1G10130	ECA3 (ENDOPLASMIC RETICULUM-TYPE CALC	1.1088	0.0034	0.0448	0.6316	0.024	0.078	-0.199	0.3361	0.2864	-0.6722	0.0197	0.045
264527_at	AT1G30760	FAD-binding domain-containing protein	0.6111	0.6384	0.4724	0.1346	0.9164	0.5231	-1.0225	0.4435	0.3356	-1.499	0.281	0.2287
264528_at	AT1G30810	transcription factor jumonji (jmj) family protein / zinc	0.3569	0.2112	0.269	0.4733	0.1199	0.1752	-0.5102	0.0594	0.1045	-0.3939	0.1141	0.1306
264529_at	AT1G30820	CTP synthase, putative / UTP--ammonia ligase, put	-0.41	0.1492	-0.7255	0.0344	0.0915	0.09435	0.8381	0.4106	-0.2211	0.2995	0.2383	
264530_at	no_match	no_match	1.1843	0.2709	0.306	0.3604	0.7175	0.4645	0.2956	0.766	0.453	-0.5283	0.5996	0.3633
264531_at	AT1G30790	F-box family protein	0.7717	0.3937	0.372	-0.3005	0.7289	0.4683	1.3934	0.1597	0.1856	0.3213	0.7113	0.4014
264532_at	AT1G55740	ATSIP1 (ARABIDOPSIS THALIANA SEED IMBIBIT	-2.0244	0.0089	0.061	-1.7601	0.0144	0.0634	-0.4087	0.229	0.229	-0.1444	0.6426	0.3781
264533_s_at	AT1G55730;AT1G55720	[AT1G55730, ATCAX5 (calcium exchanger 5); catic	0.6637	0.0789	0.1618	0.5562	0.1207	0.176	-0.1597	0.5942	0.3961	-0.2672	0.3881	0.2792
264534_at	AT1G55700	DC1 domain-containing protein	0.9476	0.4248	0.3871	0.3498	0.7595	0.4778	0.7982	0.4961	0.3583	0.2004	0.8602	0.4459
264623_at	AT1G55690	SEC14-cytosolic factor family protein / phosphoglyc	0.5558	0.0885	0.1724	-0.6947	0.0487	0.1096	-0.6783	0.0163	0.051	-0.8173	0.0086	0.0289
264536_at	AT1G55640	prenylated rab acceptor (PRA1) family protein	-0.5517	0.5383	0.4362	-2.4002	0.043	0.1031	2.2279	0.0469	0.0908	0.3795	0.654	0.3821
264537_at	AT1G55610	BRL1 (BRI 1-LIKE); kinase	0.7874	0.51	0.4249	2.3217	0.1002	0.1595	-0.2452	0.833	0.4735	1.2891	0.3024	0.2399
264538_at	AT1G55600	WRKY10 (MINISEED3); transcription factor	-1.216	0.2269	0.2797	-0.00298	0.9574	0.5434	-0.5028	0.587	0.3934	0.7102	0.4516	0.3067
264539_at	AT1G55590	F-box family protein	0.3296	0.1641	0.2369	0.08853	0.6714	0.449	-0.3027	0.0418	0.085	-0.5438	0.0061	0.0241
264540_at	AT1G55630	pentatricopeptide (PPR) repeat-containing protein	0.4698	0.2782	0.3103	0.3121	0.4518	0.3648	-0.4367	0.153	0.1808	-0.5944	0.0746	0.1004
264541_at	AT1G55660	F-box family protein	-0.8109	0.5299	0.4331	0.2361	0.8512	0.5048	-0.02816	0.9821	0.5133	1.0189	0.4367	0.2999
264542_at	AT1G55830	similar to unnamed protein product [Vitis vinifera] (G	0.3451	0.0822	0.1658	0.2999	0.1154	0.1714	-0.09741	0.5503	0.3792	-0.1426	0.3943	0.2819
264543_at	AT1G55780	heavy-metal-associated domain-containing protein	1.1054	0.1013	0.1841	1.0136	0.1238	0.1785	0.3733	0.5136	0.3645	0.2814	0.618	0.3696
264544_s_at	AT1G55880;AT1G55790	[AT1G55880, similar to ATP binding / nucleotide bir	0.06505	0.9237	0.558	-0.1391	0.8381	0.501	-0.01838	0.9491	0.5053	-0.2225	0.4572	0.3089
264545_at	AT1G55670	PSAG	-0.4724	0.014	0.0723	-0.6388	0.0049	0.0422	0.1785	0.1048	0.1448	0.01218	0.8935	0.4553
264546_at	AT1G55805	BolA-like family protein	0.004473	0.9823	0.5725	0.04593	0.8208	0.4961	0.2595	0.2437	0.2373	0.3009	0.1883	0.1783
264547_at	AT1G55620	CLC-F (CHLORIDE CHANNEL F); voltage-gated ch	0.1604	0.4461	0.3962	0.3198	0.1677	0.2109	-0.2133	0.3245	0.2806	-0.05392	0.7907	0.426
264548_at	AT1G55680	WD-40 repeat family protein	0.2286	0.1114	0.1935	0.1425	0.2731	0.2771	-0.5711	0.007	0.0341	-0.6572	0.0042	0.0208
264549_at	AT1G09440	protein kinase family protein	-0.2097	0.2794	0.311	-0.3014	0.1469	0.196	-0.05276	0.7628	0.452	-0.1444	0.4265	0.2953
264550_at	AT1G09450	haspin-related	-0.6657	0.3071	0.3269	-0.1053	0.8622	0.5078	-0.3888	0.3912	0.3126	0.1715	0.6935	0.3953
264551_at	AT1G09460	glucan endo-1,3-beta-glucosidase-related	1.0271	0.0112	0.0663	0.7345	0.0334	0.0905	0.127	0.6111	0.4016	-0.1655	0.5127	0.3308
264552_at	no_match	no_match	0.1397	0.781	0.518	0.4519	0.3906	0.337	-0.2809	0.5822	0.3915	0.03139	0.9499	0.4709
264553_s_at	AT1G09480;AT1G09490	[AT1G09480, cinnamyl-alcohol dehydrogenase fam	0.3121	0.0403	0.1158	-0.3637	0.0252	0.0794	-0.2864	0.0516	0.0962	-0.338	0.0317	0.06
264554_at	AT1G09510	cinnamyl-alcohol dehydrogenase family / CAD family	0.2577	0.7875	0.52	0.7587	0.4439	0.3612	-0.0676	0.9434	0.5041	0.4335	0.6532	0.3819
264555_at	AT1G09360	invertase/pectin methylesterase inhibitor family prot	-0.2532	0.738	0.5052	0.2976	0.6951	0.4571	0.4582	0.5518	0.3796	1.009	0.2262	0.1996
264556_at	no_match	no_match	1.5218	0.066	0.1473	0.0447	0.9448	0.5306	0.4392	0.5058	0.3617	-1.0379	0.1596	0.161
264557_at	AT1G09550	pectinacetylesterase, putative	-0.2036	0.8045	0.5253	-0.7026	0.413	0.3474	-0.321	0.6981	0.4306	-0.82	0.3468	0.2611
264558_at	AT1G09600	protein kinase family protein	-0.9162	0.2017	0.2632	0.7822	0.2626	0.2712	-1.4366	0.075	0.1192	0.2618	0.6853	0.3924
264559_at	AT1G09610	similar to unknown protein [Arabidopsis thaliana] (T	0.7694	0.0735	0.1561	-0.6418	0.1146	0.1708	-0.1766	0.6095	0.4012	-1.5878	0.0076	0.0271
264560_at	AT1G55820	similar to GIP1 (GBF-INTERACTING PROTEIN 1) [	0.3916	0.2106	0.2687	-0.08991	0.7496	0.4748	0.04633	0.8414	0.4761	-0.4352	0.1155	0.1315
264561_at	AT1G55810	uracil phosphoribosyltransferase, putative / UMP py	-0.1459	0.6377	0.4722	-0.06465	0.8327	0.4996	-0.6872	0.0091	0.0382	-0.606	0.014	0.0376
264562_at	AT1G55760	BTB/POZ domain-containing protein	0.1943	0.5173	0.4282	0.4877	0.1495	0.1977	-0.3968	0.2103	0.218	-0.1033	0.7177	0.4033
264563_s_at	AT1G55750;AT3G61420	[AT1G55750, transcription factor-related];[AT3G614	-0.2893	0.2004	0.2624	0.5459	0.0446	0.1046	-1.4552	0.0015	0.02	-0.6199	0.0304	0.0587
264564_at	AT1G05290	transcription factor	0.2289	0.8753	0.5453	0.7626	0.6073	0.4261	-0.9448	0.5282	0.3706	-0.4112	0.7789	0.4226
264565_at	AT1G05260	fringe-related protein	1.5306	0.173	0.2435	1.0621	0.3145	0.2999	-0.2104	0.831	0.473	-0.679	0.5033	0.3271
264566_at	AT1G05270	TraB family protein	-0.04015	0.8776	0.5459	0.7566	0.0365	0.0943	-1.3597	0.0051	0.0301	-0.5629	0.0829	0.1074
264567_s_at	AT1G05250;AT1G05240	[AT1G05250, peroxidase, putative];[AT1G05240, pe	0.4632	0.4351	0.3916	-1.4134	0.0573	0.119	1.2904	0.0732	0.1178	-0.5862	0.3344	0.2553
264568_at	AT1G05150	calcium-binding EF hand family protein	-0.2232	0.1795	0.2476	0.08868	0.5623	0.4091	-0.2893	0.1011	0.142	0.02056	0.8975	0.4536
264569_at	no_match	no_match	-0.8166	0.1161	0.1971	0.4591	0.3237	0.3052	-0.5936	0.2019	0.2128	0.6821	0.1546	0.1578
264570_at	AT1G05350	thiF family protein	-0.0377	0.8293	0.5322	0.03376	0.8469	0.5036	-0.1119	0.5324	0.3722	-0.0404	0.8174	0.4336
264571_at	AT1G05330	unknown protein	0.4964	0.7542	0.5097	0.8401	0.5704	0.412	1.211	0.3358	0.2863	1.5948	0.2234	0.1979
264572_at	no_match	no_match	0.3428	0.454	0.4	0.1754	0.6935	0.4567	-0.04095	0.8389	0.4753	-0.2084	0.3317	0.2542
264573_at	AT1G05310	pectinesterase family protein	-0.4126	0.1668	0.2389	-0.692	0.0474	0.108	0.4388	0.1472	0.177	0.1594	0.5502	0.3452
264574_at	AT1G05300	ZIP5 (ZINC TRANSPORTER 5 PRECURSOR); cati	1.422	0.1309	0.2092	1.7677	0.0779	0.1399	0.148	0.7406	0.4449	-0.4937	0.3021	0.2397
264575_at	AT1G05190	EMB2394 (EMBRYO DEFECTIVE 2394); structural	-0.6271	5.00E-04	0.0325	-0.5498	9.00E-04	0.0285	-0.1262	0.1114	0.1494	-0.04886	0.4745	0.3155
264576_at	AT1G05360	similar to unknown protein [Arabidopsis thaliana] (T	-0.2158	0.4621	0.4039	-0.1167	0.6831	0.4532	-0.4142	0.1939	0.2079	-0.3151	0.3012	0.2392
264577_at	AT1G05260	RIC3 (RARE COLD INDUCIBLE GENE 3); peroxida	0.4951	0.5891	0.4559	-0.1393	0.8745	0.5115	-0.1055	0.9047	0.4937	-0.7298	0.4275	0.2957
264578_at	AT1G05370	similar to unknown protein [Arabidopsis thaliana] (T	-1.4987	0.0545	0.1341	0.7405	0.2543	0.2667	-0.8816	0.1885	0.2046	1.3575	0.0713	0.0979
264579_at	AT1G05205	similar to hypothetical protein Os_t_021517 (Oryza s	-0.2327	0.3811	0.3651	0.2173	0.4105	0.3463	1.2376	0.0035	0.026	1.6876	0.0011	0.0123
264580_at	AT1G05340	similar to unknown protein [Arabidopsis thaliana] (T	0.3711	0.438	0.3929	1.1661	0.0539	0.1152	0.997	0.0107	0.0412	1.792	0.0013	0.013
264581_at	AT1G05210	similar to unknown protein [Arabidopsis thaliana] (T	0.1413	0.8335	0.5335	0.1643	0.8071	0.492	0.477	0.1176	0.1543	0.4999	0.1054	0.1242
264582_at	AT1G05230	homeobox-leucine zipper family protein / lipid-bindir	-0.4643	0.0123	0.0685	-0.2566	0.0746	0.137	-0.3427	0.0272	0.067	-0.135	0.251	0.2131
264583_at	AT1G05170	galactosyltransferase family protein	-0.529	0.2224	0.2767	-0.00826	0.9831	0.54	-0.04813	0.8956	0.4912	0.4726	0.2418	0.2081
264584_at	AT1G05140	membrane-associated zinc metalloprotease, putativ	0.01676	0.9447	0.5635	-0.2532	0.327	0.307	0.09482	0.5704	0.3869	-0.1751	0.3177	0.2473
264585_at	AT1G05180	AXR1 (AUXIN RESISTANT 1); small protein activat	0.8065	0.0014	0.038	0.9278	8.00E-04	0.0281	-0.1033	0.3685	0.3022	0.01797	0.8688	0.4479
264586_at	AT1G05160	CYP89A3 (ENT-KAURENOIC ACID HYDROXYLA	0.2625	0.2368	0.2856	0.1621	0.4389	0.3591	-0.7386	0.0096	0.039	-0.8389	0.0061	0.0242
264587_at	AT1G05200	ATGLR3.4 (Arabidopsis thaliana glutamate receptor	0.01397	0.9577	0.5666	-0.4862	0.121	0.1763	-0.7145	0.0043	0.028	-1.2147	6.00E-04	0.01
264588_at	AT1G27730	zinc finger (C3HC4-type RING finger) family protein	1.0347	0.0166	0.0775	0.7731	0.0415	0.1011	0.5226	0.039	0.0816	0.2611	0.2056	0.1882
264589_at	AT1G27650	AMP-dependent synthetase and ligase family protei	-0.4444	0.0258	0.093	-0.5059	0.017	0.0677	-0.4112	0.0328	0.074	-0.4727	0.0212	0.0473
264590_at	AT1G27710	similar to unnamed protein product [Vitis vinifera] (G	0.1441	0.6531	0.4771	0.4836	0.179	0.2189	0.4547	0.0462	0.0902	0.7942	0.0076	0.0271
264591_at	AT1G27670	pentatricopeptide (PPR) repeat-containing protein	0.8488	0.1289	0.2074	0.3808	0.44	0.3595	-0.09643	0.6447	0.4125	-0.5644	0.0435	0.0729
264592_at	AT1G27720	oxidoreductase, 2OG-Fe(II) oxygenase family prote	0.8611	0.0108	0.0654	0.7957	0.0141	0.0629	0.02988	0.8135	0.4677	-0.03544	0.7799	0.423
264593_at	AT1G27800	ARAC1/ATGP2/ATRAC1/AROP3/RAC1/ROP3 (RH	-0.3655	0.0374	0.1115	-0.3456	0.0441	0.1039	0.001719	0.9878	0.5147	0.02157	0.8484	0.4424
264594_at	AT1G27640	AtSerat3;1 (SERINE ACETYLTRANSFERASE-106	0.4112	0.141	0.2183	0.3708	0.1739	0.2154	-0.05907	0.7482	0.4476	-0.05946	0.5935	0.3611
264595_at	AT1G04750	VAMP79 (VESICLE-ASSOCIATED MEMBRANE P	0.4772	0.0518	0.1307	0.896	0.0068	0.0465	0.1828	0.2203	0.2238	0.6017	0.0088	0.0292
264596_at	AT1G04625	pseudogene, similar to Unknown protein, blastp ma	-0.4355	0.7346	0.5037	-0.2897	0.8208	0.4961	-1.1029	0.4093	0.3205	-0.9571	0.4691	0.3134
264597_at	AT1G04620	coenzyme F420 hydrogenase family / dehydrogena	-1.7378	0.0027	0.0426	-1.5498	0.0041	0.0399	-0.9943	0.0193	0.0557	-0.8063	0.0372	0.0658
264598_at	AT1G04610	flavin-containing monooxygenase / FMO YUCCA2	-1.2248	0.2129	0.2703	0.5258	0.5597	0.4082	-0.5812	0.4743	0.3494	1.1694	0.1876	0.1779
264599_at	AT1G04600	XIA (Myosin-like protein XIA); motor/ protein binding	0.2187	0.7059	0.4947	2.2309	0.0144	0.0635	-0.8429	0.1931	0.2074	1.1693	0.096	0.1175
264600_at	AT1G04730	AAA-type ATPase family protein	0.3375	0.3752	0.362	-0.5768	0.1636	0.2083	0.2293	0.2267	0.2275	-0.685	0.013	0.0362
264601_at	AT1G04640	C2 domain-containing protein	0.1324	0.9148	0.5554	-0.2375	0.8481	0.5039	0.2586	0.5322	0.4085	-0.1113	0.8347	0.4385
264602_at	AT1G04700	protein kinase family protein	0.4449	0.463	0.4044	1.112	0.1127	0.1697	0.1293	0.8253	0.4713	0.7965	0.2203	0.1962
264603_at	AT1G04670	similar to pollen-preferential protein [Brassica rapa	-0.4042	0.7685	0.5142	1.5293	0.2992	0.291	-2.109	0.0208	0.058	-0.1755	0.7735	0.4211
264604_at	AT1G04650	similar to unnamed protein product [Vitis vinifera] (G	1.7618	0.1045	0.1866	0.08356	0.9257	0.5255	-0.03454	0.9692	0.5097	-1.7128	0.1116	0.1288
264605_at	AT1G04550	IAA12 (AUXIN-INDUCED PROTEIN 12); transcripti	-0.4726	0.006	0.0537	-0.2218	0.067	0.1296	0.201	0.0733	0.1178	0.4518	0.0056	0.0234
264606_at	AT1G04660	glycine-rich protein	-0.7067	0.0743	0.1567	-0.3531	0.6455	0.4401	-0.2103	0.7815	0.4579	1.1427	0.1833	0.1755
264607_at	AT1G04690	KAB1 (POTASSIUM CHANNEL BETA SUBUNIT);	0.4377	0.0292	0.099	0.4754	0.0225	0.0758	-0.06172	0.6634	0.419	-0.02404	0.8639	0.4468
264608_at	AT1G04710	acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-	-0.7242	0.0061	0.0539	-0.708	0.0066	0.0461	0.06381	0.6456	0.4128	0.07996	0.5675	0.3518
264609_at	AT1G04730	binding	-0.3847	7.00E-04	0.0234	-0.5917	1.00E-04	0.0249	0.3707	8.00E-04	0.0161	0.1637	0.2152	0.1892
264610_at	AT1G04645	self-incompatibility protein-related	1.1404	0.4288	0.3885	0.1439	0.917	0.5233	1.913	0.2142	0.2204	0.9165	0.5187	0.333
264611_at	AT1G04680	pectate lyase family protein	-0.8421	0.0283	0.0974	-0.8026	0.0328	0.0897	0.3228	0.1812	0.1996	0.3623	0.1437	0.1507
264612_at	AT1G04640	ANP1/ HIK like membrane family protein	1.2122	0.3381	0.3446	-0.4367	0.7153	0.4638	1.9998	0.1473	0.1771	0.3509	0.7687	0.4194
264613_at	AT1G04640	LIP2 (LIPOYLTRANSFERASE 2)	-0.1393	0.2817	0.3124	-0.03327	0.7812	0.4839	-0.6202	0.0052	0.0302	-0.5142	0.0101	0.0314
264614_s_at	AT1G02590;AT1G04580	[AT1G02590, aldehyde oxidase, putative];[AT1G04	-1.1779	0.3567	0.353	0.02285	0.9849	0.5404	-1.0977	0.3869	0.3108	0.103	0.9318	0.4662
264615_at	AT1G27540	similar to EMB1417 (EMBRYO DEFECTIVE 1417)	0.0717	0.7177	0.4984	-0.2454	0.2538	0.2664	0.3456	0.0483	0.0924	0.02644	0.8285	0.4367
264616_at	AT2G17740	DC1 domain-containing protein	0.5763	0.369	0.3591	0.4659	0.4595	0.3677	0.6414	0.0856	0.1291	0.531	0.1333	0.1439
264617_at	AT2G17660	nitrate-responsive NOI protein, putative	-0.6172	0.2464	0.2915	-0.1818	0.7098	0.462	1.0133	0.0899	0.1326	1.4486	0.0334	0.0617
264618_at	AT2G17680	similar to unknown protein [Arabidopsis thaliana] (T	0.05065	0.9335	0.5607	0.2997	0.6268	0.4334	0.4026	0.4964	0.3584	0.6751	0.3018	0.2396
264619_at	AT2G17750	aspartyl protease family protein	0.656	0.0064	0.0547	0.5284	0.0136	0.0618	0.3912	0.0041	0.0276	0.2637	0.0164	0.0409
264620_at	AT2G17770	ATBZIP27/FDP (FD PARALOG); transcription factc	-1.496	0.2355	0.2848	1.0098	0.3998	0.3411	-1.4392	0.2507	0.2414	1.0665	0.3763	0.274
264621_at	AT2G17700	protein kinase family protein	0.2755	0.1218	0.2022	0.1118	0.4715	0.3727	-0.26	0.0503	0.095	-0.4237	0.0107	0.0324
264622_at	AT2G17790	similar to unknown protein [Arabidopsis thaliana] (T	0.5899	0.0083	0.0599	0.6407	0.0062	0.0451	-0.1516

264690_at	AT1G70060	putative amphipathic helix repeat-containing protein	0.1658	0.553	0.4421	0.1706	0.5422	0.4015	-0.7535	0.0424	0.0858	-0.7488	0.0432	0.0726
264691_s_at	AT4G03530;AT1G70010	transposable element gene;[AT1G70	-0.3392	0.8204	0.5296	-0.4217	0.7781	0.4831	0.06686	0.9642	0.5085	-0.01562	0.9916	0.4805
264692_at	AT1G70000	DNA-binding family protein	-0.5147	0.0154	0.0751	-0.6092	0.0086	0.0512	0.2459	0.1247	0.1598	0.1514	0.2988	0.2381
264693_at	AT1G69970	CLE26 (CLAVATA3/ESR-RELATED 26); receptor b	-0.9103	0.0487	0.1271	-0.4028	0.2827	0.2824	0.2544	0.3601	0.2981	0.7619	0.0365	0.065
264694_at	AT1G70250	receptor serine/threonine kinase, putative	0.5403	0.0758	0.1584	0.2254	0.3766	0.3304	-0.3057	0.2491	0.2404	-0.6205	0.0521	0.0814
264695_at	no_match	no_match	0.6954	0.5999	0.4597	1.7186	0.2325	0.2532	-1.3239	0.3398	0.2883	-0.3007	0.8178	0.4337
264696_at	AT1G70230	similar to unknown protein [Arabidopsis thaliana] (T	-0.6897	0.0248	0.0914	-0.5804	0.042	0.1018	-0.1008	0.6354	0.4095	0.00851	0.9676	0.475
264697_at	AT1G70210	CYCD1;1 (CYCLIN D1;1); cyclin-dependent	-1.5733	0.0135	0.0716	-1.5781	0.0134	0.0615	-0.3871	0.358	0.297	-0.3919	0.3526	0.2639
264698_at	AT1G70200	RNA recognition motif (RRM)-containing protein	-0.08114	0.7145	0.4974	-0.2439	0.303	0.2931	-0.02332	0.9155	0.4965	-0.1861	0.4185	0.2919
264699_at	AT1G69980	similar to unnamed protein product [Vitis vinifera] (G	0.4265	0.0587	0.1388	0.5266	0.0318	0.0885	0.2373	0.2186	0.2228	0.3374	0.1069	0.1253
264700_at	AT1G70100	similar to unknown protein [Arabidopsis thaliana] (T	-0.3073	0.1103	0.1924	-0.1668	0.3292	0.3082	-0.4066	0.0285	0.0685	-0.2661	0.0933	0.1154
264701_at	AT1G70160	similar to unknown protein [Arabidopsis thaliana] (T	0.7054	0.0071	0.0567	0.7926	0.0047	0.0417	-0.2621	0.0937	0.1357	-0.1749	0.2177	0.1949
264702_at	AT1G70190	ribosomal protein L12 family protein	0.5097	0.0282	0.0973	0.681	0.0109	0.056	-0.1574	0.347	0.2917	0.01384	0.9299	0.4656
264703_at	AT1G69960	PP2A (SERINE/THREONINE PROTEIN PHOSPHA	0.4424	0.0043	0.0479	0.3425	0.0108	0.0559	0.3807	0.0074	0.0349	0.2809	0.0209	0.0469
264704_at	AT1G70090	GATL9/LGT8 (Galacturonosyltransferase-like 9); pc	-1.0714	0.1139	0.1955	-0.4089	0.4844	0.3778	-0.4584	0.3761	0.3058	0.2041	0.6807	0.3907
264705_at	AT1G69620	ATP binding / aminoacyl-tRNA ligase	0.4466	0.0884	0.1724	0.3838	0.1262	0.1803	-0.6443	0.0011	0.0183	-0.7071	8.00E-04	0.0109
264706_at	AT1G69720	kinase interacting family protein	0.4022	0.6107	0.463	-2.0768	0.0465	0.107	1.7701	0.0723	0.1169	-0.7088	0.3882	0.2783
264707_at	AT1G09730	Ulp1 protease family protein	0.4941	0.0128	0.0697	0.2742	0.0761	0.1381	-0.6048	0.0063	0.0328	-0.8247	0.002	0.0153
264708_at	AT1G09740	ethylene-responsive protein, putative	0.2693	0.2986	0.3224	0.2314	0.363	0.3243	0.1354	0.3308	0.2837	0.0975	0.4704	0.3138
264709_at	AT1G09770	ATCDC5 (ARABIDOPSIS THALIANA HOMOLOG (	0.8896	1.008	0.0587	0.9683	0.0097	0.0513	-0.224	0.3296	0.2831	-0.2452	0.2914	0.2343
264710_at	AT1G09790	COBL6 (COBRA-LIKE PROTEIN 6 PRECURSOR)	-0.2956	0.4893	0.4156	-0.125	0.7638	0.4785	0.08687	0.799	0.4631	0.2574	0.4653	0.3121
264711_at	AT1G09800	tRNA pseudouridine synthase family protein	-0.4775	0.2651	0.3022	-0.4526	0.2871	0.285	-0.00745	0.9849	0.5138	0.0175	0.9644	0.4744
264712_at	AT1G09810	ECT11 (evolutionarily conserved C-terminal region	-0.146	0.5692	0.4486	0.4379	0.1369	0.1883	-0.5078	0.0203	0.0573	0.07611	0.6058	0.3653
264713_at	AT1G09820	pentatricopeptide (PPR) repeat-containing protein	-0.4661	0.0697	0.1522	-0.7146	0.0196	0.0719	0.08803	0.6489	0.4142	-0.1604	0.4211	0.2929
264714_at	AT1G69990	leucine-rich repeat transmembrane protein kinase,	-0.2247	0.5641	0.4465	-0.6042	0.1666	0.2102	0.3381	0.3982	0.3158	-0.04141	0.9134	0.4607
264715_at	AT1G70180	sterile alpha motif (SAM) domain-containing protein	0.2611	0.1993	0.2619	0.3755	0.0917	0.1528	-0.6895	0.0154	0.0494	-0.5752	0.0277	0.0555
264716_at	AT1G70170	MMP (MATRIX METALLOPROTEINASE); metallod	-0.183	0.7418	0.5065	1.0038	0.1248	0.1792	-0.3654	0.4864	0.354	0.8214	0.1602	0.1613
264717_at	AT1G70140	ATFH8 (FORMIN 8); actin binding / actin filament b	0.4517	0.3846	0.3671	0.1997	0.6885	0.4551	-0.08993	0.8303	0.4728	-0.3419	0.4337	0.2984
264718_at	AT1G70130	lectin protein kinase, putative	0.2861	0.6912	0.4897	-0.04351	0.9513	0.5322	0.144	0.7318	0.4423	-0.1855	0.6605	0.3844
264719_at	AT1G70110	lectin protein kinase family protein	-0.2779	0.8319	0.5331	0.6719	0.6131	0.4281	0.04745	0.971	0.5102	0.9973	0.462	0.3109
264720_at	AT1G69930	terpene synthase/cyclase family protein	1.644	0.249	0.293	0.63	0.6327	0.4355	-0.798	0.5487	0.3786	1.476	0.2929	0.235
264721_at	AT1G23000	heavy-metal-associated domain-containing protein	0.08453	0.9312	0.5601	-1.2331	0.2508	0.2645	1.1614	0.275	0.2552	-0.1562	0.8733	0.4494
264722_at	AT1G22970	protein binding	0.2866	0.1959	0.2597	0.3512	0.1302	0.1829	-0.3287	0.0879	0.1308	-0.264	0.1453	0.1518
264723_at	AT1G22960	pentatricopeptide (PPR) repeat-containing protein	-0.6942	0.375	0.3619	0.6001	0.3708	0.3278	-1.8692	0.0248	0.0639	-0.6749	0.2746	0.2253
264724_at	AT1G22920	AUH1/CSN5A/JAB1 (COP9 SIGNALOSOME 5A)	0.5936	0.0222	0.0875	0.3991	0.0714	0.1337	0.2196	0.1288	0.1631	0.02511	0.8378	0.4394
264725_at	AT1G22885	unknown protein	-0.6869	0.0347	0.1076	-0.1002	0.6701	0.4486	0.6124	0.0284	0.0684	1.1991	0.0028	0.0173
264726_at	AT1G22865	AP2 domain-containing transcription factor, putative	0.3116	0.3048	0.2255	0.8764	0.0297	0.0856	0.4068	0.198	0.2105	0.9733	0.0213	0.0474
264727_at	AT1G22840	ATCYTC-A/CYTC-1 (CYTOCHROME C-1); electror	0.1178	0.4975	0.4194	0.337	0.0999	0.1593	0.6222	0.017	0.052	0.8414	0.006	0.024
264728_at	AT1G22850	similar to unknown protein [Arabidopsis thaliana] (T	-0.5276	0.0048	0.0497	-0.8018	0.001	0.0291	-0.3166	0.0185	0.0544	-0.5908	0.002	0.0153
264729_at	AT1G22990	heavy-metal-associated domain-containing protein	0.2486	0.148	0.2238	1.1899	0.3573	0.3215	1.1774	0.1746	0.1952	0.3187	0.6785	0.3901
264730_at	AT1G62085	mitochondrial transcription termination factor family	0.1328	0.4435	0.3951	-0.05739	0.7322	0.4689	-0.1829	0.1359	0.1683	-0.3731	0.0191	0.0443
264731_at	AT1G62150	mitochondrial transcription termination factor-relatec	0.04099	0.9053	0.5526	-0.2864	0.4258	0.3534	-0.1246	0.6284	0.4074	-0.452	0.1305	0.1419
264732_at	AT1G62160	pseudogene, serpin (serine protease inhibitor), putat	0.2505	0.8323	0.5331	0.8767	0.4731	0.3734	1.2494	0.3226	0.2795	1.8756	0.1658	0.1648
264733_at	AT1G62170	serpin family protein / serine protease inhibitor family	0.01588	0.9798	0.572	-3.1213	0.0061	0.0449	2.323	0.0168	0.0518	-0.8142	0.2386	0.2064
264734_at	AT1G62280	SLAH1 (SLAC1 HOMOLOGUE 1); transporter	2.1714	0.0906	0.1744	-0.462	0.6614	0.4455	1.1715	0.1255	0.1605	-1.4619	0.0735	0.0996
264735_s_at	AT1G62080;AT1G62000;A	MA-like protein; similar to unknown protein [Arabidop	-0.2612	0.1278	0.2066	-1.051	0.3817	0.3328	-0.1282	0.9104	0.4954	0.872	0.4609	0.3104
264736_at	AT1G62200	proton-dependent oligopeptide transport (POT) fam	0.5709	0.6832	0.4869	0.02233	0.9055	0.5203	-0.08158	0.5094	0.3631	0.01835	0.8786	0.4509
264737_at	AT1G62210	unknown protein	-1.3459	0.2358	0.2849	-0.9906	0.3629	0.3243	0.2812	0.7854	0.4589	0.6364	0.5459	0.3433
264738_at	AT1G62250	similar to unnamed protein product [Vitis vinifera] (G	-1.0844	1.00E-04	0.0312	-1.3871	0	0.0249	0.4034	0.0033	0.0255	0.1007	0.1926	0.1806
264739_at	AT1G62260	pentatricopeptide (PPR) repeat-containing protein	0.6803	0.446	0.3962	1.2843	0.1862	0.2238	0.3668	0.493	0.3567	0.9708	0.1168	0.1325
264740_at	AT1G62070	unknown protein	-1.0086	0.3728	0.3608	-0.5342	0.6235	0.4322	1.1178	0.0763	0.1205	1.5922	0.0277	0.0554
264741_at	AT1G62290	peptidase M50 domain family protein	-0.04759	0.8658	0.5425	-0.05663	0.8407	0.5016	-0.5839	0.0916	0.1338	-0.593	0.0882	0.1114
264742_at	AT1G62130	AAA-type ATPase family protein	-0.2861	0.5519	0.4419	0.2683	0.5757	0.4141	-1.5933	0.0225	0.0606	-1.0389	0.078	0.1033
264743_at	AT1G62090	pseudogene, protein kinase family, similar to light re	0.01454	0.979	0.572	0.4741	0.4126	0.3473	-0.7271	0.2181	0.2225	-0.2675	0.6196	0.3702
264744_at	AT1G62050	similar to ankyrin repeat family protein [Arabidopsis	-0.2156	0.6322	0.4704	-0.5241	0.2771	0.2793	0.149	0.5059	0.3617	-0.1594	0.4786	0.317
264745_at	AT1G62180	APR2 (5'ADENYLYLPHOSPHOSULFATE REDUC	-1.3871	9.00E-04	0.0349	-1.5252	6.00E-04	0.027	0.1328	0.2221	0.2248	-0.00535	0.9564	0.4725
264746_at	AT1G62300	WRKY6 (WRKY DNA-binding protein 6); transcriptic	1.1464	0.1102	0.1923	1.2241	0.0942	0.1546	-0.06048	0.8817	0.4872	0.01723	0.9661	0.4748
264747_at	no_match	no_match	0.7649	0.0068	0.0558	0.4833	0.0316	0.0883	-0.846	0.0048	0.0282	-1.1275	0.0016	0.0143
264748_at	AT1G70070	EMB25 (EMBRYO DEFECTIVE 25); ATP-dependen	0.3451	0.0355	0.1088	0.1427	0.2666	0.2736	-0.8147	7.00E-04	0.016	-1.0172	3.00E-04	0.0083
264749_at	AT1G22830	pentatricopeptide (PPR) repeat-containing protein	0.3248	0.7075	0.4952	-0.831	0.3608	0.3232	-0.2121	0.7847	0.4587	-1.3679	0.1326	0.1434
264750_at	AT1G22870	protein kinase family protein	0.7505	0.0096	0.0627	0.2577	0.1846	0.2229	-0.7853	0.0081	0.0362	-1.2781	0.0014	0.0133
264751_at	AT1G23020	ATFRO3/FRO3 (FERRIC REDUCTION OXIDASE :	0.9661	0.0642	0.1452	0.8459	0.0905	0.1518	-0.2547	0.1711	0.1927	-0.375	0.0703	0.0972
264752_at	AT1G23010	LPR1 (LOW PHOSPHATE ROOT1); copper ion bin	0.3169	0.5605	0.445	2.0396	0.0151	0.0646	-0.0152	0.9772	0.5119	1.7075	0.0269	0.0545
264753_at	AT1G61490	S-locus protein kinase, putative	0.5773	0.4539	0.4	1.75	0.0659	0.1284	-0.4939	0.5175	0.366	0.6787	0.3851	0.278
264754_at	AT1G61400	S-locus protein kinase, putative	0.3196	0.5741	0.4505	0.09948	0.8584	0.5067	-0.3106	0.5845	0.3925	-0.5307	0.3675	0.2703
264755_at	AT1G61390	S-locus protein kinase, putative	0.8825	0.489	0.4155	-1.4282	0.2855	0.2841	1.1193	0.389	0.3117	-1.1914	0.3622	0.2679
264756_at	AT1G61370	S-locus lectin protein kinase family protein	1.4076	0.0241	0.0906	0.8848	0.0904	0.1517	-0.6514	0.1741	0.1948	-1.1742	0.0409	0.07
264757_at	AT1G61360	S-locus lectin protein kinase family protein	-0.3123	0.5198	0.429	-0.08103	0.8638	0.5081	0.2071	0.1559	0.1829	0.4384	0.0209	0.0469
264758_at	AT1G61340	F-box family protein	-0.7454	0.4328	0.3907	-0.3508	0.7028	0.46	0.2439	0.6317	0.4084	0.6384	0.2465	0.2105
264759_at	AT1G61480	S-locus protein kinase, putative	0.07969	0.7778	0.5173	0.7296	0.0488	0.1097	-0.52	0.1151	0.1525	0.131	0.6398	0.3771
264760_at	AT1G61290	SYP124 (syntaxin 124); SNAP receptor	0.4395	0.5356	0.4353	0.4133	0.559	0.4079	-0.00028	0.9997	0.5178	-0.02646	0.9694	0.4754
264761_at	AT1G61280	identical to Probable phosphatidylinositol N-acetylgl	-0.7807	0.4145	0.382	0.2043	0.8236	0.4971	0.324	0.725	0.4402	1.309	0.2019	0.1862
264762_at	AT1G61460	S-locus protein kinase, putative	0.1114	0.9258	0.5585	2.7803	0.0686	0.1315	-0.8834	0.4758	0.3498	1.7855	0.1873	0.1777
264763_at	AT1G61450	similar to unknown protein [Arabidopsis thaliana] (T	0.5354	0.5872	0.4552	-0.02346	0.9806	0.5394	0.4526	0.6444	0.4124	-0.1063	0.9125	0.4607
264764_at	AT1G61440	S-locus protein kinase, putative	-0.01362	0.9887	0.5742	1.1187	0.283	0.2826	-0.7281	0.4651	0.3454	0.4042	0.6775	0.3899
264765_at	AT1G61430	S-locus protein kinase, putative	0.2766	0.7597	0.5116	1.0729	0.2728	0.277	-1.3289	0.1907	0.2059	-0.5325	0.5625	0.3499
264766_at	AT1G61420	S-locus lectin protein kinase family protein	1.0858	0.0043	0.0474	1.0806	0.0044	0.0409	-0.5054	0.053	0.0977	-0.5106	0.0515	0.0809
264767_at	AT1G61380	S-locus protein kinase, putative	0.4336	0.0426	0.1188	0.983	0.0027	0.0344	-0.2261	0.1898	0.2054	0.3233	0.0971	0.1105
264768_at	AT1G61410	tolA protein-related	1.2366	0.0339	0.1065	-0.4699	0.2952	0.2893	2.0129	0.0067	0.0336	0.3064	0.4765	0.3163
264769_at	AT1G61350	armadillo/beta-catenin repeat family protein	-0.05702	0.4802	0.4119	-0.2238	0.0379	0.0965	-0.03576	0.6512	0.415	-0.2026	0.0507	0.0799
264770_at	AT1G23030	armadillo/beta-catenin repeat family protein / U-box	-0.2854	0.6153	0.4645	-0.3049	0.5922	0.4204	-0.4468	0.0618	0.1068	-0.4663	0.0549	0.0838
264771_at	AT1G22940	THI1 (THIAMINE REQUIRING 1); catalytic/ phospho	0.6237	0.7935	0.522	-0.2214	0.3767	0.3305	-0.2315	0.3514	0.294	-0.5152	0.0789	0.104
264772_at	AT1G22930	T-complex protein 11	0.965	0.0047	0.0493	0.8598	0.0071	0.0475	-0.6968	6.00E-04	0.0158	-0.802	4.00E-04	0.0088
264773_at	AT1G22900	similar to disease resistance-responsive family prot	-0.03713	0.9364	0.5613	0.6108	0.2352	0.2549	0.8262	0.0938	0.1358	1.4741	0.0175	0.0422
264774_at	AT1G22890	unknown protein	-0.1416	0.3119	0.3297	0.3151	0.0618	0.1236	-0.05505	0.6764	0.4231	0.4017	0.0305	0.0588
264775_at	AT1G22880	ATCEL5/ATGH9B4 (ARABIDOPSIS THALIANA GL	1.479	0.1725	0.243	-0.3413	0.7214	0.4658	-0.1095	0.9081	0.4948	-1.9298	0.0964	0.1178
264776_at	AT1G22860	TGF beta receptor associated protein-related	0.2398	0.2985	0.3224	0.07285	0.7351	0.4698	-0.6777	0.0175	0.053	-0.8446	0.0083	0.0283
264777_at	AT1G08630	THA1 (THRECNINE ALDOLASE 1); aldehyde-lyase	0.564	0.6241	0.4678	1.7782	0.164	0.2085	0.146	0.8916	0.4901	1.3703	0.2448	0.2096
264778_at	AT1G08780	ABI3 (ABI3-INTERACTING PROTEIN 3); unfolded	-0.2706	0.1332	0.2118	-0.08115	0.6029	0.4247	0.7882	0.0054	0.0308	0.9777	0.0025	0.0164
264779_at	AT1G08570	thioredoxin family protein	-0.02428	0.9538	0.5657	0.07369	0.8606	0.5073	-0.1807	0.1508	0.1794	-0.08277	0.4622	0.311
264780_at	AT1G08720	EDR1 (ENHANCED DISEASE RESISTANCE 1); ki	1.016	7.00E-04	0.0334	0.8014	0.0018	0.0323	-0.437	0.0156	0.0497	-0.6516	0.0038	02
264781_at	AT1G08540	SIGB (SIGMA FACTOR B); DNA binding / DNA-dire	-0.3145	0.0672	0.1489	-0.4686	0.0206	0.0732	0.3363	0.056	0.101	0.1823	0.2219	0.197
264782_at	AT1G08810	MYB60 (myb domain protein 60); DNA binding / tra	-1.0119	0.017	0.0781	-1.1059	0.0126	06	-0.36	0.2338	0.2316	-0.454	0.152	0.1561
264783_at	AT1G08650	PPCK1 (PHOSPHOENOLPYRUVATE CARBOXYL	0.2024	0.6504	0.4765	0.2407	0.5921	0.4204	-0.05555	0.8544	0.4796	-0.01726	0.9544	0.4722
264784_s_at	AT1G70830;AT5G42460	AT2G17830, F-box family protein];[AT5G42460, F-	0.258	0.3805	0.3647	0.418	0.1858	0.2236	0.1911	0.3244	0.2805	0.3511	0.1081	0.1262
264785_at	AT1G71910	transposable element gene	0.5584	0.5753	0.4509	-0.8702	0.3962	0.3396	0.7737	0.3327	0.2846	-0.6549	0.4041	0.2858
264786_at	AT1G71920	nucleic acid binding / zinc ion binding	-2.001	0.151	0.2264	-1.307	0.3113	0.2982	-0.3062	0.4967	0.3585	0.3878	0.3978	0.2833
264787_at	AT1G71840	ERD7 (EARLY-RESPONSIVE TO DEHYDRATION	-1.1179	0.1826	0.2501	-0.8019	0.3124	0.2986	0.3541	0.0222	0.0603	0.6701	0.0024	0.0161
264788_at	AT1G71880	DNA/J heat shock protein, putative	-1.6532	0.0125	0.0692	-1.391	0.0222	0.0753	0.7901	0.1084	0.1473	1.0524	0.0517	0.081
264789_at	AT1G71870	cold-shock DNA-binding family protein	0.3665	0.0327	0.1049	-0.03023	0.8044	0.491	0.8029	0.0011	0.0181	0.4062	0.0128	0.0359
264790_at	AT1G71820	ATHK1 (HISTIDINE KINASE 1)	0.5391	0.0622	0.1432	0.4709	0.0885	0.1499	-0.1125	0.4332	0.331	-0.1808	0.2346	0.2042
264791_at	AT1G71845	short-chain dehydrogenase/reductase (SDR) family	1.3386	0.2032	0.2642	1.516	0.1604	0.2061	0.4019	0.6719	0.4216	0.5792	0.5468	0.3437
264792_at	AT1G08620	transcription factor jumonji (jmj) family protein / zinc	0.3834	0.0905	0.1743	0.2285	0.2563	0.268	-0.5229	0.0114	0.0423	-0.6779	0.0046	0.0214
264793_at	AT1G08660	glycosyl transferase family 29 protein / sialyltranste	0.238	0.1809	0.2487	0.157	0.3458	0.3159	-0.5388	0.0215	0.059	-0.6198	0.0135	0.0369
264794_at	AT1G08670	epsin N-terminal homology (ENTH) domain-contain	0.7549	0.6093	0.4628	-0.2773	0.8487	504	1.4014	0.3621	0.2992	0.3691	0.8	0.4287
264795_at	AT1G08680	ZIGA4 (ARF GAP-LIKE ZINC FINGER-CONTAININ	-0.1532	0.6039	0.4608	-0.1099	0.7074	0.4613	-1.9521	0.001	0.0174	-1.9088	0.0011	0.0123
264796_at	AT1G08680	ZIGA4 (ARF GAP-LIKE ZINC FINGER-CONTAININ	0.002355	0.9818	0.5725	0.1535	0.1892	0.2259	0.03895	0.7089	0.4343	0.1901	0.122	0.1364
264797_at	AT1G08710	F-box family protein	0.7861	0.2548	0.2964	-0.1819	0.7739	0.4817	-0.5177	0.4311	0.3301	-1.4857	0.066	0.0936
264798_at	AT1G08730	XIC (Myrosin-like protein XIC); motor/ protein binding	0.059591	0.9876	0.5738	-0.3935	0.3091	0.2969	-0.04165	0.9079	0.4947	-0.4407	0.2622	0.2189
264799_at	AT1G08550	NPQ1 (NON-PHOTOCHEMICAL QUENCHING 1)	-0.3569	0.174	0.2442	-0.4944	0.0841	0.1458	-0.7001	9.00E-04	0.0169	-0.8375	4.00E-04	0.0091
264800_at	AT1G08800	similar to unknown protein [Arabidopsis thaliana] (T	-0.1822	0.4439	0.3952	-0.2931	0.244	0.2606	-0.08777	0.7037	0.4326	-0.1987	0.4072	0.2871
264801_at	AT1G08840	EMB2431 (EMBRYO DEFECTIVE 2411); ATP-depe	-0.3519	0.1007	0.1834	-0.8125	0.008	0.0498	0.008152	0.9631	0.5084	-0.4524	0.0523	0.0815
264802_at	AT1G08560	SYP111 (syntaxin 111); SNAP receptor	-0.2286	0.5981	0.4589	0.4345	0.3381	0.3127	0.2349	0.5136	0.3645	0.8979	0.0521	0.0813
264803_at	AT1G08580	similar to Pm52 [Prunus mume] (GB:BAE48663.1)	0.1787	0.4043	0.3774	0.6023	0.0349	0.0923	0.7363	0.0185	0.0544	1.1599	0.0038	0.0199
264804_at	AT1G08590	CLAVATA1 receptor kinase (CLV1)	-0.3309	0.3774	0.363	-0.4752	0.2275	0.2499	-0.03737	0.9103	0.4954	-0.1817	0.5912	0.3603
264805_at	AT1G08600	ATRX/CHR20; ATP binding / DNA binding / helicase	0.795	0.0061	0.0539	0.5338	0.0236	0.0773	-0.1964	0.1233	0.1589	-0.4576	0.0105	0.0321
264806_at	AT1G08610	pentatricopeptide (PPR) repeat-containing protein	0.5238	0.1792	0.2476	0.3229	0.3728	0.3289	-0.3481	0.3531	0.2948	-0.539	0.1696	0.1669
264807_at	AT1G08700	presenilin family protein	0.6915	0.0016	0.0383	0.4568	0.0072	0.048	-0.1087	0.2961	0.2667	-0.3434	0.0192	0.0444
264808_at	AT1G08770	prenylated rab acceptor (PRA1) family protein	-0.04862	0.8115	0.5273	0.2613	0.2427	0.2596	-0.1083	0.6006	0.3984	0.2016	0.3503	0.2628
264809_at	AT1G08830	CSD1 (COPPER/ZINC SUPEROXIDE DISMUTASE	0.1643	6.00E-04	0.0225	1.5149	1.00E-04	0.0249	0.4905	0.0099	0.0397	0.9412	8.00E-04	0.0116
264810_at	AT1G08750	GPI-anchor transamidase, putative	0.2267	0.1287	0.2073	-0.02394	0.85	0.5044	-0.01043	0.9342	0.5019	-0.2611	0.0927	0.1149
264811_at	AT1G08640	heat shock protein binding	-0.2074	0.0854	0.1694	-0.3843	0.0136	0.0618	0.2938	0.0323	0.0732	0.117	0.2692	0.2223
264812_at	AT1G27860	pathogenesis-related thaumatin family protein	0.8326	0.4351	0.3916	-0.3476	0.7358	0.4699	0.8165	0.3569	0.3816	-0.5651	0.588	0.3592
264813_at	AT1G27890	CPK16 (calcium-dependent protein kinase 16); calm	-0.9468	0.4861	0.4141	-0.1944	0.8826	0.5138	-0.7434	0.3053	0.2714	0.009038	0.9893	0.48
264814_at	AT1G27900	SDG37 (SET DOMAIN GROUP 37); zinc ion bindin	-0.2545	0.3295	0.3398	-0.289	0.2763	0.2789	-0.4613	0.1147	0.1522	-0.4958	0.0968	0.118
264815_at	AT1G03620	phagocytosis and cell motility protein ELMO1-relate	0.5384	0.2974	0.3217	0.08586	0.8579	0.5066	-0.2927	0.5507	0.3794	-0.7453	0.1729	0.169
264816_at	AT1G03560	pentatricopeptide (PPR) repeat-containing protein	-0.2832	0.4135	0.3817	0.4169	0.2507	0.2644	-0.312	0.372	0.3039	0.3881	0.2796	0.228
264817_at	AT1G03540	pentatricopeptide (PPR) repeat-containing protein	0.2286	0.8501	0.5382	-0.2425	0.8411	0.5017	0.8779	0.4821	0.352	0.4068	0.738	0.4097
264818_at	AT1G03530	ATNAP4/NAP1	0.5711	0.0937	0.1772	0.7384	0.0473	0.108	0.05108	0.8334	0.4736	0.2183	0.3916	0.2807
264819_at	AT1G03510	pentatricopeptide (PPR) repeat-containing protein	2.1875	0.0463	0.1237	0.08176	0.9202	0.5241	0.4729	0.284	0.2602	-1.6329	0.013	0.0361
264820_at	AT1G03475	initiation 2); coproporphyrinogen oxidase	0.08115	0.7157	0.498	-0.05917	0.7897	0.486	-0.3395	0.0935	0.1356	-0.4798	0.0363	0.0648
264821_at	AT1G03470	kinase interacting family protein	0.02061	0.9318	0.5603	0.6357	0.113	0.1699	-0.2441	0.4805	0.3516	0.4202	0.252	0.2136
264822_at	AT1G03457	RNA-binding protein, putative	0.07595	0.8748	0.5451	-0.9104	0.1145	0.1708	0.3118	0.4748	0.3495	-0.6745	0.1635	0.1634
264823_at	AT1G03445	BSU1

264890_at	AT1G23180	armadillo/beta-catenin repeat family protein	0.1935	0.1899	0.2553	-0.1119	0.4134	0.3476	-0.09136	0.4979	0.3589	-0.3968	0.0319	0.0601
264891_at	AT1G23200	pectinesterase family protein	-0.3189	0.3442	0.347	-0.6937	0.0802	0.142	-0.02769	0.8835	0.4877	-0.4025	0.0859	0.1096
264892_at	AT1G23160	auxin-responsive GH3 family protein	-1.2986	0.2692	0.3049	1.1108	0.3344	0.3105	0.8198	0.3349	0.286	3.2292	0.0125	0.0353
264893_at	AT1G23140	C2 domain-containing protein	0.9517	0.4467	0.1243	0.9884	0.0418	0.1016	0.7296	0.0037	0.0266	0.7663	0.003	0.0179
264894_at	AT1G23040	hydroxyproline-rich glycoprotein family protein	0.4578	0.0668	0.1484	0.1803	0.3806	0.3323	0.7069	0.0037	0.0267	0.4295	0.0208	0.0468
264895_at	AT1G23100	10 kDa chaperonin, putative	0.3648	0.4029	0.3768	0.5005	0.269	0.2749	0.8116	0.1061	0.1458	0.9473	0.0722	0.0986
264896_at	AT1G23210	ATGH9B6 (ARABIDOPSIS THALIANA GLYCOSYL	0.3421	0.7804	0.518	1.6876	0.2153	0.243	-0.408	0.6403	0.4112	0.9375	0.3107	0.2437
264897_at	AT1G23220	dynein light chain type 1 family protein	-0.05017	0.7737	0.5159	-0.1745	0.3447	0.3154	0.5593	0.0265	0.4662	0.4349	0.056	0.0848
264898_at	AT1G23205	invertase/pectin methylesterase inhibitor family prot	-1.2846	0.0749	0.1573	-1.9031	0.0239	0.0778	0.5239	0.2191	0.2231	-0.0945	0.8058	0.4304
264899_at	AT1G23130	Bet v I allergen family protein	-0.4811	0.0552	0.135	-0.129	0.512	0.3895	0.4455	0.0058	0.0318	0.7976	7.00E-04	0.0105
264900_at	AT1G23080	PIN7 (PIN-FORMED 7); auxin:hydrogen symporter/	0.2258	0.5491	0.4407	-0.00271	0.9941	0.5427	-0.313	0.1621	0.1868	-0.5415	0.0415	0.0707
264901_at	AT1G23090	AST91 (SULFATE TRANSPORTER 91); sulfate tra	-0.04795	0.8282	0.5319	-0.2936	0.2292	0.2511	0.03091	0.7993	0.4631	-0.2148	0.1322	0.1431
264902_at	AT1G23060	similar to unknown protein [Arabidopsis thaliana] (T	0.2224	0.4067	0.3788	-0.3066	0.2708	0.2759	0.5879	0.0604	0.1055	0.05894	0.8076	0.431
264903_at	AT1G23190	phosphoglucomutase, cytoplasmic, putative / gluco	0.4168	9.00E-04	0.0348	0.2781	0.004	0.0394	-0.05175	0.3294	0.2831	-0.1905	0.015	0.039
264904_s_at	AT4G35460;AT2G17420	[AT4G35460, NTR1 (NADPH-dependent thioredoxi	0.07518	0.6267	0.4686	0.1617	0.321	0.3036	-0.258	0.0816	0.1252	-0.1715	0.1988	0.1842
264905_at	AT2G17430	ATMLO7/MLO7 (MILDEW RESISTANCE LOCUS O	1.8961	0.0569	0.1369	1.3049	0.1422	0.1923	-0.5534	0.4823	0.3521	-1.1446	0.1848	0.1762
264906_at	AT2G17270	mitochondrial substrate carrier family protein	0.02857	0.9082	0.5535	0.2799	0.2655	0.2729	-0.2263	0.3565	0.2964	0.02799	0.9033	0.4582
264907_at	AT2G17280	phosphoglycerate/bisphosphoglycerate mutase fam	-0.2363	0.5953	0.458	-0.8896	0.0958	0.156	0.6936	0.1091	0.1478	0.04025	0.9108	0.4602
264908_at	AT2G17440	leucine-rich repeat family protein	0.813	0.0102	0.064	0.5889	0.0294	0.0852	-0.8158	0.0027	0.0241	-1.0399	0.0011	0.0124
264909_at	AT2G17390	similar to unknown protein [Arabidopsis thaliana] (T	-1.8647	0.0073	0.0572	-1.3693	0.0208	0.0736	0.1754	0.4929	0.3567	0.6708	0.0449	0.0743
264910_at	AT1G61100	disease resistance protein (TIR class), putative	-0.2767	0.6563	0.4779	-0.3859	0.5399	0.4007	-0.8356	6.00E-04	0.0158	-0.9448	4.00E-04	0.0089
264911_at	AT1G60560	aldo/keto reductase family protein	0.6279	0.0062	0.0565	-0.7859	0.0027	0.0349	0.1632	0.2428	0.2366	0.005125	0.9678	0.475
264912_at	AT1G60750	pseudogene, aldo/keto reductase family, contains P	0.4241	0.5357	0.4353	0.6872	0.3345	0.3105	-0.3977	0.5603	0.3827	-0.1346	0.8405	0.4402
264913_at	AT1G60770	pentatricopeptide (PPR) repeat-containing protein	0.3344	0.3842	0.3668	0.6815	0.1175	0.1733	-0.4911	0.0584	0.1034	-0.144	0.4842	0.3193
264914_at	AT1G60780	clathrin adaptor complexes medium subunit family p	0.01705	0.8793	0.5463	0.1014	0.3907	0.337	0.0363	0.7479	0.4475	0.1206	0.3163	0.2465
264915_at	no_match	no_match	-1.5389	0.1267	0.2058	-1.4341	0.1475	0.1963	-0.3915	0.5744	0.3883	-0.2868	0.6778	0.3899
264916_at	AT1G60810	ACLA-2 (ATP-citrate lyase A-2)	-0.1187	0.6768	0.4848	0.1269	0.6564	0.444	0.2061	0.2755	0.2555	0.4517	0.0506	0.0799
264917_at	AT1G60830	dynamin family protein	-0.00147	0.9988	0.6763	-0.4654	0.5932	0.4207	-0.003	0.9972	0.517	-0.4669	0.592	0.3605
264918_at	AT1G60530	dynamin family protein	0.2753	0.8192	0.5294	-1.1674	0.3592	0.3225	1.1451	0.3675	0.3018	-0.2976	0.805	0.4302
264919_at	AT1G60540	pseudogene of the dynamin family	-0.5828	0.4192	0.3845	-1.2737	0.1207	0.176	2.0442	0.0227	0.0609	1.3532	0.0757	0.1013
264920_at	AT1G60550	naphthoate synthase, putative / dihydroxynaphthoic	0.8592	0.0057	0.0525	-0.6375	0.016	0.0658	-0.6044	0.019	0.0553	-0.3826	0.0736	0.0997
264921_at	AT1G60650	glycine-rich RNA-binding protein, putative	1.0033	0.0048	0.0497	0.5862	0.0297	0.0856	0.4803	0.0535	0.0983	0.06331	0.7389	0.41
264922_s_at	AT1G60830;AT1G60900	[AT1G60830, U2 snRNP auxiliary factor large subu	0.4763	0.0275	0.0961	0.7007	0.0075	0.0488	-0.7187	0.0069	0.0339	-0.4942	0.0245	0.0514
264923_s_at	AT1G60970;AT1G60740	[AT1G60970, TPX2 (TARGET PROTEIN FOR XKLP2	0.5628	0.1596	0.2332	2.6555	0.0472	0.108	-0.9589	0.0208	0.058	0.04384	0.8738	0.4495
264924_at	AT1G60620	ATRPAC43 (Arabidopsis thaliana RNA polymerase	0.6018	0.073	0.1556	0.2848	0.3165	0.301	-0.00849	0.9619	0.5081	-0.3255	0.1229	0.137
264925_at	AT1G60670	similar to unknown protein [Arabidopsis thaliana] (T	-0.2418	0.1957	0.2595	-0.137	0.4288	0.3549	-0.1585	0.3666	0.3013	-0.05371	0.7477	0.4129
264926_at	AT1G60720	8S 45 (cytochrome b5 family, putative)	0.07119	0.6979	0.4919	-0.0346	0.9492	0.5042	0.3634	0.0271	0.067	0.2777	0.0693	0.0964
264927_at	AT1G60490	ATVPS34 (Arabidopsis thaliana vacuolar protein so	0.693	0.0068	0.0556	0.4176	0.0363	0.0941	0.05868	0.5261	0.3695	-0.2167	0.0625	0.0907
264928_at	AT1G60710	ATB2; oxidoreductase	0.02293	0.9069	0.553	-0.1149	0.5665	0.4106	0.1374	0.0465	0.0905	-0.00046	0.9928	0.4809
264929_at	AT1G60730	aldo/keto reductase family protein	-0.2297	0.4765	0.4103	0.1078	0.7434	0.4688	-0.3724	0.1885	0.2046	-0.03593	0.8863	0.4532
264930_at	AT1G60800	NIK3 (NSP-INTERACTING KINASE 3); kinase	-0.4534	0.1427	0.2198	-0.3975	0.1856	0.2235	0.02036	0.8866	0.4887	0.0763	0.5997	0.3633
264931_at	AT1G60590	polygalacturonase, putative / pectinase, putative	-1.9907	0.0057	0.0525	-1.9794	0.0058	0.0442	-0.5463	7.00E-04	0.016	-0.535	8.00E-04	0.0111
264932_at	AT1G61240	similar to unknown protein [Arabidopsis thaliana] (T	0.3241	0.2318	0.283	0.5279	0.0835	0.1452	-0.5263	0.0072	0.0343	-0.3225	0.0364	0.0649
264933_at	AT1G61160	contains InterPro domain Retrotransposon gag prot	0.4561	0.7067	0.4949	-0.7158	0.5603	0.4084	0.05441	0.9639	0.5085	-1.1175	0.3781	0.2748
264934_at	no_match	no_match	-0.2517	0.6949	0.491	-0.5193	0.4333	0.3569	-0.3888	0.5502	0.3792	-0.6564	0.3331	0.2549
264935_at	AT1G61150	similar to unknown protein [Arabidopsis thaliana] (T	0.1778	0.1083	0.1906	0.7442	0.0153	0.0649	0.07881	0.6894	0.4276	0.4452	0.0721	0.0984
264936_at	AT1G61140	EDA16 (embryo sac development arrest 16); ATP b	0.8742	9.00E-04	0.0349	0.5116	0.0069	0.0468	-0.1325	0.0573	0.1023	-0.4951	6.00E-04	0.0101
264937_at	AT1G61130	SCPL32; serine carboxypeptidase	0.2461	0.7227	0.5003	-0.282	0.6852	0.4539	-0.00758	0.9911	0.5155	-0.5357	0.4482	0.3053
264938_at	AT1G60610	protein binding / zinc ion binding	-0.3667	0.2141	0.2709	0.2253	0.416	0.3488	-0.9325	0.0199	0.0567	-0.3404	0.2427	0.2085
264939_at	AT1G60630	leucine-rich repeat family protein	0.673	0.1962	0.2598	-0.5665	0.2621	0.271	0.07096	0.8781	0.4862	-1.1685	0.0546	0.0836
264940_at	AT1G60470	ATGOLS4 (ARABIDOPSIS THALIANA GALACTINO	0.7375	0.3721	0.3605	0.8353	0.3189	0.3025	0.1449	0.7979	0.4627	0.2427	0.6705	0.3875
264941_at	AT1G60680	AGD2 (ARF-GAP DOMAIN 2); aldo-keto reductase	-0.1017	0.9066	0.6529	-1.0343	0.273	0.2771	-1.3159	0.1806	0.1991	-2.2519	0.0506	0.0799
264942_at	AT1G67340	zinc finger (MYND type) family protein / F-box famil	-0.2264	0.1823	0.25	-0.1358	0.3882	0.3359	-0.236	0.0389	0.0816	-0.1454	0.1356	0.1454
264943_at	AT1G67910	unknown protein	0.8211	0.2226	0.2768	2.6443	0.0097	0.0537	-0.1706	0.7228	0.4396	1.6526	0.0211	0.0471
264944_at	AT1G67120	RNA recognition motif (RRM)-containing protein	0.2254	0.2482	0.2925	0.2325	0.2362	0.2555	-0.1287	0.183	0.2009	-0.1217	0.2029	0.1868
264945_at	AT1G67080	MAF1 (MADS AFFECTING FLOWERING 1); transc	-0.849	0.0063	0.0545	-0.1885	0.3092	0.2969	-0.3192	0.1182	0.1548	0.3413	0.1011	0.1214
264946_at	AT1G67010	pentatricopeptide (PPR) repeat-containing protein	-0.6673	0.1768	0.246	0.7316	0.147	0.1961	-0.9983	0.0704	0.1153	0.4005	0.3812	0.2763
264947_at	AT1G67030	DNAJ heat shock N-terminal domain-containing pro	0.3101	0.2389	0.2834	0.02173	0.9374	0.5284	0.1146	0.682	0.4249	-0.1737	0.5407	0.3412
264948_at	AT1G67750	DEAD/DEAH box helicase, putative	1.1032	0.1359	0.214	0.7793	0.2585	0.2692	-1.0923	0.1013	0.1422	-1.4162	0.0515	0.0808
264949_at	AT1G67080	MAF1 (MADS AFFECTING FLOWERING 1); transc	-0.01616	0.96	0.5674	0.3426	0.3209	0.3036	-0.6231	0.0678	0.1128	-0.2644	0.351	0.2631
264950_at	no_match	no_match	-0.8653	0.124	0.2039	0.1257	0.7917	0.4866	0.008766	0.9852	0.5139	0.9998	0.0682	0.1114
264951_at	AT1G67690	VHS domain-containing protein / GAT domain-conta	0.9674	0.0361	0.1097	1.3354	0.0128	0.0604	-0.09728	0.5566	0.3815	0.2707	0.1491	0.1541
264952_at	AT1G67900	AITLP1 (TUBBY LIKE PROTEIN 1); phosphoric die	0.595	0.0074	0.0577	0.2853	0.074	0.1365	0.1108	0.4032	0.3179	-0.1989	0.1689	0.1666
264953_at	AT1G67120	ADH1 (ALCOHOL DEHYDROGENASE 1)	0.5576	0.0853	0.1693	0.5827	0.0763	0.1384	0.1374	0.6052	0.3999	0.1625	0.5438	0.3424
264954_at	AT1G67060	mutase family protein	-0.7298	0.0139	0.0722	-0.798	0.0102	0.0549	0.2412	0.2289	0.2289	0.173	0.3664	0.2698
264955_at	AT1G67620	F-box family protein (FBX3)	0.1478	0.3244	0.3369	0.1661	0.2755	0.2784	-0.6401	5.00E-04	0.0155	-0.6218	6.00E-04	0.0101
264956_at	AT1G67690	ACR3 (ACT Domain Repeat 3)	-0.4694	0.0499	0.1232	-0.5737	0.025	0.0791	-0.4474	0.0134	0.046	-0.5516	0.0065	0.025
264957_at	AT1G67000	ATSKP2;2/SKP2B (ARABIDOPSIS HOMOLOG OF	0.9119	0.0495	0.1278	0.7775	0.0764	0.1384	-0.07521	0.3161	0.2763	-0.2097	0.0332	0.0615
264958_at	AT1G67960	unknown protein	1.9993	0.0486	0.1271	2.1332	0.0403	0.0995	0.4746	0.0149	0.0486	0.6085	0.0063	0.0246
264959_at	AT1G67700	thylakoid lumenal 29.8 kDa protein	-1.0765	1.00E-04	0.0312	-1.235	1.00E-04	0.0249	0.2148	0.0333	0.0746	0.05635	0.4504	0.3061
264960_at	AT1G67930	ATEXT4 (EXTENSIN 4)	0.8523	0.1774	0.2464	0.6095	0.3071	0.2957	0.986	0.0434	0.087	0.7433	0.0928	0.115
264961_at	AT1G67950	PRAF1; Ran GTPase binding / chromatin binding /	-0.04815	0.8736	0.5451	-0.0728	0.8103	0.4931	-0.2291	0.0572	0.1022	-0.2537	0.0428	0.0722
264962_at	AT1G67710	PIN6 (PIN-FORMED 6); auxin:hydrogen symporter/	0.5622	0.2565	0.2973	0.3057	0.5118	0.3894	-0.1454	0.68	0.4243	-0.4019	0.2869	0.2317
264963_at	AT1G60600	ABC4 (ABERRANT CHLOROPLAST DEVELOPME	-0.1437	0.3335	0.3421	-0.4353	0.0291	0.0849	-0.3237	0.0685	0.1136	-0.6153	0.0093	0.03
264964_at	AT1G60460	similar to hypothetical protein Osl_023542 [Oryza s	-0.6353	0.5147	0.4271	-0.9824	0.3316	0.3092	-0.203	0.7811	0.4578	-0.5501	0.4659	0.3123
264965_at	AT1G60560	SWIM zinc finger family protein	-0.08337	0.6059	0.4616	-0.09312	0.5661	0.4104	-0.346	0.0412	0.0843	-0.3558	0.0379	0.0667
264966_at	AT1G60570	kelch repeat-containing F-box family protein	-1.0529	0.0765	0.1592	-0.4641	0.3544	0.3202	-0.8915	0.0754	0.1196	-0.3027	0.4631	0.3113
264967_at	AT1G67250	proteasome maturation factor UMP1 family protein	0.5229	0.0359	0.1093	0.775	0.01	0.0543	0.867	8.00E-04	0.0163	1.1192	3.00E-04	0.0083
264968_at	AT1G67360	elongation factor (REF) family protein	0.4688	0.058	0.138	0.4209	0.0774	0.1394	0.3497	0.065	0.11	0.3018	0.0948	0.1167
264969_at	AT1G67320	DNA primase, large subunit family	0.1505	0.2701	0.3055	0.6153	0.0064	0.0457	-0.412	0.0249	0.0639	0.0528	0.6769	0.3897
264970_at	AT1G67280	lactoylglutathione lyase, putative / glyoxalase I, puta	-0.2017	0.1717	0.2427	-0.2329	0.1273	0.1811	-0.1927	0.1615	0.1864	-0.2239	0.1171	0.1327
264971_at	AT1G67210	proline-rich spliceosome-associated (PSP) family pr	-0.5837	0.1735	0.2439	0.321	0.4145	0.348	0.2867	0.4622	0.3442	1.1914	0.0279	0.0557
264972_at	AT1G67370	ASY1 (ASYNAPTIC 1); DNA binding	0.967	0.4419	0.3945	-1.7395	0.1999	0.2327	1.7289	0.2021	0.213	-0.9776	0.4373	0.3001
264973_at	AT1G67040	nitrate transporter, putative	-0.1005	0.8844	0.5471	1.3713	0.1021	0.1613	-1.6438	0.0645	0.1095	-0.172	0.804	0.4299
264974_at	AT1G67050	ATHB54 (ARABIDOPSIS THALIANA HOMEOBOX	0.2845	0.3558	0.3525	0.5184	0.1302	0.1829	0.7519	0.051	0.0957	0.9858	0.0225	0.0487
264975_at	AT1G67070	5'-AMP-activated protein kinase-related	-0.2592	0.2367	0.2856	-0.07589	0.7048	0.4606	-0.5509	0.0418	0.085	-0.3675	0.1199	0.135
264976_at	AT1G67080	transporter	-0.1159	0.6301	0.4698	0.37	0.1719	0.214	-0.7888	0.0239	0.0628	-0.3029	0.2453	0.2098
264977_at	AT1G67090	glycine-rich protein	0.02211	0.9165	0.556	0.294	0.212	0.2409	-0.7343	0.0207	0.0579	-0.4624	0.0799	0.1049
264978_at	AT1G67120	galactosyltransferase family protein	-1.3759	0.0057	0.0525	-1.346	0.0061	0.0451	-0.4553	0.0561	0.101	-0.4253	0.0675	0.0948
264979_s_at	AT1G67170;AT1G27180	[AT1G27170, ATP binding / protein binding / transm	0.186	0.5156	0.4275	-0.02913	0.9166	0.5231	-0.5908	0.0864	0.1296	-0.8059	0.0367	0.0652
264980_at	AT1G67190	leucine-rich repeat transmembrane protein kinase,	0.1404	0.4912	0.4163	0.0213	0.9141	0.5225	-0.6862	0.0011	0.018	-0.8053	6.00E-04	0.01
264981_at	AT1G67160	valyl-tRNA synthetase / valine--tRNA ligase-related	1.4981	0.1063	0.1886	2.4404	0.0277	0.083	-0.01417	0.9853	0.5139	0.9281	0.2675	0.2214
264982_at	AT1G67220	paired amphipathic helix repeat-containing protein	0.7713	0.5549	0.4428	-0.2256	0.8599	0.5071	0.6187	0.5582	0.3819	-0.3782	0.7164	0.403
264983_at	AT1G67240	paired amphipathic helix repeat-containing protein	0.05858	0.8727	0.5448	-0.00721	0.9842	0.5402	-0.00031	0.9993	0.5177	-0.06611	0.8566	0.4449
264984_at	AT1G67000	bZIP family transcription factor	0.1502	0.074	0.1564	0.1632	0.0592	0.1209	0.1327	0.0979	0.1392	0.1457	0.0775	0.1028
264985_at	AT1G67150	binding	0.04083	0.832	0.5331	0.3729	0.1076	0.1654	-0.5381	0.0406	0.0836	-0.206	0.3171	0.247
264986_at	AT1G67130	ATGSTU13 (GLUTATHIONE S-TRANSFERASE 12	-0.8393	0.0611	0.1418	-0.6547	0.1141	0.1706	0.6695	0.0074	0.0347	0.854	0.003	0.0179
264987_at	AT1G67030	similar to unknown protein [Arabidopsis thaliana] (T	-0.9798	7.00E-04	0.0334	-0.61	0.0044	0.041	-0.1596	0.1614	0.1864	0.2103	0.0866	0.1102
264988_at	AT1G67140	ATGSTU14 (GLUTATHIONE S-TRANSFERASE 13	-1.2394	0.2525	0.2949	0.3078	0.7568	0.4772	-0.5914	0.5585	0.382	0.9558	0.3611	0.2675
264989_at	AT1G67200	similar to unknown protein [Arabidopsis thaliana] (T	-0.9644	0.0076	0.0579	-0.5326	0.0514	0.1125	-0.8217	0.0041	0.0276	-0.3898	0.0488	0.0781
264990_at	AT1G67210	binding	0.1017	0.681	0.4863	0.1163	0.6392	0.438	-0.7717	0.0057	0.0317	-0.757	0.0062	0.0243
264991_s_at	AT1G67400;AT3G43400	[AT1G67400, similar to phagocytosis and cell motili	0.244	0.5076	0.4241	-0.4811	0.2251	0.2485	-0.2886	0.1652	0.1886	-1.0137	0.004	0.0203
264992_at	no_match	hexose transporter, putative	0.7059	0.0102	0.0641	0.6304	0.015	0.0645	-0.8098	0.0023	0.0226	-0.8853	0.0017	0.0144
264993_at	AT1G67290	glyoxal oxidase-related	-0.2211	0.5555	0.443	-0.6798	0.1194	0.1748	0.7077	0.0547	0.0996	0.249	0.3976	0.2832
264994_at	AT1G67270	similar to unknown protein [Arabidopsis thaliana] (T	1.0737	0.3481	0.349	-2.3834	0.0779	0.1398	1.5037	0.1688	0.191	-1.9534	0.0949	0.1167
264995_at	AT1G67240	transposable element gene	1.8513	0.2509	0.2939	-2.4104	0.1557	0.2025	0.38	0.7967	0.4624	-3.8816	0.0482	0.0775
264996_at	AT1G67230	LINC1 (LITTLE NUCLEI1)	-0.22	0.0863	0.1704	-0.2865	0.042	0.1019	-0.4086	0.0136	0.0465	-0.4751	0.0081	0.028
264997_at	AT1G67220	ATHPCAT1/HAC2 (HISTONE ACETYLTRANSFER	-0.1665	0.827	0.5316	0.2321	0.7613	0.478	0.4901	0.5301	0.3713	0.8887	0.2811	0.2287
264998_at	AT1G67330	similar to unknown protein [Arabidopsis thaliana] (T	1.0534?	0.841	0.5359	-0.3049	0.2893	0.2862	1.1225	0.005	0.0298	0.7641	0.019	0.0441
264999_at	AT1G67310	calmodulin binding / transcription regulator	-0.06297	0.7584	0.5113	0.6618	0.0258	0.0803	-0.5558	0.0076	0.0352	0.169	0.2049	0.1878
265000_at	AT1G67410	exostosin family protein	-0.2757	0.1697	0.2412	-0.4379	0.0566	0.1182	0.02435	0.8897	0.4896	-0.1379	0.4499	0.306
265001_at	AT1G67350	unknown protein	-0.04677	0.589	0.4559	0.1072	0.2499	0.2638	0.6365	0	0.0092	0.7905	0	0.0047
265002_at	AT1G24400	LHT2 (LYSINE HISTIDINE TRANSPORTER 2); am	0.4904	0.2003	0.2624	-0.03103	0.9274	0.526	-0.4634	0.1233	0.1589	-0.9849	0.0144	0.0381
265003_at	AT1G26970	protein kinase, putative	-0.7983	0.5222	0.4298	1.1082	0.3859	0.3347	-0.5267	0.6686	0.4207	-0.2158	0.859	0.4455
265004_at	AT1G26990	transposable element gene	-0.2204	0.831	0.5327	0.292	0.7778	0.483	1.1642	0.2951	0.2661	1.6766	0.1581	0.16
265005_at	AT1G61667	similar to unknown protein [Arabidopsis thaliana] (T	0.2109	0.6183	0.4658	0.2876	0.5029	0.3858	0.4859	0.1122	0.15	0.5625	0.0785	0.1036
265006_at	AT1G61610	TIM13; P-P-bond-hydrolysis-driven protein transme	0.3574	0.2216	0.2761	0.8769	0.0519	0.1131	0.8503	0.0263	0.0659	1.1697	0.0091	0.0297
265007_s_at	AT1G61563;AT1G61566	[AT1G61563, RALFL8 (RALF-LIKE 8)];[AT1G61566	1.6021	0.0824	0.166	-0.2882	0.6995	0.4589	-1.3144	0.1314	0.165	-3.2048	0.0099	0.0311
265008_at	AT1G61560	MLO6 (MILDEW RESISTANCE LOCUS O 6); calm	0.4894	0.1878	0.2539	0.4463	0.2215	0.2468	-0.4994	0.1808	0.1993	-0.5424	0.1535	0.1572
265009_at	AT1G24650	leucine-rich repeat family protein / protein kinase fa	0.1686	0.1308	0.2092	-0.2187	0.7407	0.4715	-1.211	0.1209	0.1569	-0.281	0.6937	0.3953
265010_at	AT1G24510	T-complex protein 1 epsilon subunit, putative / TCP-	0.6256	0.0367	0.1105	0.2505	0.2841	0.2833	0.09504	0.6635	0.4191	-0.2801	0.2392	0.2067
265011_at	AT1G24490	ALB4 (ALBINA 4)	0.1125	0.4508	0.3985	-0.2704	0.1152	0.1713	-0.3526	0.059	0.1041	-0.7355	0.0055	0.0231
265012_at	AT1G24470	short-chain dehydrogenase/reductase (SDR) family	0.0343	0.944	0.5997	0.1209	0.5375	0.1666	0.2102	0.2962	0.1435	0.1742	-0.09162	0.603	0.3642
265013_at	AT1G24460	myosin-related	0.06045	0.4683	0.4065	0.2339	0.0363	0.0941	-0.9818	2.00E-04	0.0126	-0.8083	4.00E-04	0.0091
265014_at	AT1G24430	transferase family protein	-0.9646	0.5122	0.4259	-1.7597	0.2602	0.2699	0.7942	0.583	0.3918	-0.00085	0.9995	0.4829
265015_at	AT1G24440	transposable element gene	-0.07528	0.8719	0.5445	0.00823	0.9855	0.5405	0.1172	0.8023	0.4643	0.2007	0.6706	0.3876
265016_at	AT1G24420	transferase family protein	-0.7788	0.4368	0.3924	0.8497	0.3997	0.3411	-1.5269	0.1659	0.1891	0.1016	0.9158	0.4616
265017_at	AT1G24390	unknown protein	0.03009	0.9675	0.5691	1.6582	0.0752	0.1376	-1.1437	0.065	0.11	0.4844	0.345	0.2603
265018_s_at	AT2G13770;AT1G24370	[AT2G13770, similar to ribosomal protein-like [Oryz	0.2657	0.7825	0.5184	-0.2511	0.794	0.4874	1.2867	0.2259	0.227	0.7699	0.4404	0.3015
265019_at	no_match	no_match	0.2045	0.3605	0.3549	0.3433	0.1583	0.2047	-0.3142	0.188	0.2043	-0.1754	0.4261	0.2951
265020_at	AT1G24540	CYP86C1 (cytochrome P450, family 86, subfamily C	1.201	0.1355	0.2137	-1.6287	0.0646	0.127	0.717	0.2371	0.2335	-2.1127	0.0149	0.0388
265021_at	AT1G24610	SET-domain-containing protein	-0.4089	0.0767	0.1594	-0.1825	0.3496	0.3178	-0.2018	0.1082	0.1472	0.02464	0.8136	0.4326
265022_at	AT1G24520	BCP1 (Brassica campestris pollen protein 1)	-0.05596	0.8585	0.5406	-0.4089	0.2371	0.2561	-0.8707	0.0416	0.0849	-1.2236	0.0142	0.0378
265023_at	AT1G24440	protein binding / zinc ion binding	0.7533	0.0526	0.1316	0.8669	0.0349	0.0923	-0.358	0.0787	0.1227	-0.2444	0.1842	0.1759
265024_at	AT1G24600

265090_at	AT1G03960	calcium-binding EF hand family protein	-0.2994	0.496	0.4186	-0.5212	0.2628	0.2714	-1.0871	0.0337	0.075	-0.2665	0.48	0.3175
265091_s_at	AT1G03940,AT1G03495	[AT1G03940, transferase family protein];[AT1G034	-0.1155	0.7502	0.5086	-0.5416	0.185	0.2231	0.3561	0.1002	0.1412	-0.06999	0.6969	0.3965
265092_at	AT1G03910	similar to unnamed protein product [Vitis vinifera] (G	0.3578	0.052	0.1309	0.3763	0.045	0.1052	-0.6014	0.0044	0.0284	-0.583	0.0049	0.0221
265093_at	AT1G03905	ABC transporter family protein	0.3746	0.3744	0.3617	0.1093	0.7853	0.4848	-0.04885	0.9027	0.4931	-0.3142	0.4494	0.3058
265094_at	AT1G03890	cupin family protein	-2.0773	0.0459	0.1232	0.1733	0.8231	0.4969	-0.8118	0.3261	0.2814	1.4388	0.1186	0.1337
265095_at	AT1G03880	CRU2 (CRUCIFERIN 2); nutrient reservoir	0.3762	0.7719	0.5152	-2.1581	0.1498	0.1979	0.7299	0.3827	0.3091	-1.8045	0.0726	0.0988
265096_at	AT1G04030	similar to unknown protein [Arabidopsis thaliana] (T	3.1373	0.0176	0.0794	0.2188	0.7991	0.4894	0.3821	0.6597	0.4178	-2.5364	0.0344	0.0628
265097_at	AT1G04020	ATBARD1/BARD1 (BREAST CANCER ASSOCIAT	-0.437	0.2301	0.2822	-0.3595	0.3093	0.297	-0.2306	0.3388	0.2878	-0.1531	0.511	0.3302
265098_at	AT1G04010	phosphatidylcholine-sterol O-acyltransferase	-0.4811	0.1817	0.2494	-0.734	0.0694	0.132	-0.5487	0.1394	0.1706	-0.8016	0.0546	0.0836
265099_at	AT1G03990	alcohol oxidase-related	-0.3335	0.3006	0.3233	0.1389	0.6468	0.4404	0.003085	0.9915	0.5156	0.4754	0.1566	0.159
265100_at	AT1G31010	OSB4 (ORGANELLAR SINGLE-STRANDED DNA	0.1117	0.0459	0.1232	0.6763	0.1284	0.1819	0.3285	0.4056	0.3188	-0.00687	0.9854	0.4791
265101_at	AT1G30880	unknown protein	0.8647	2.00E-04	0.0312	0.8144	3.00E-04	0.0249	-0.6697	1.00E-04	0.0109	-0.72	1.00E-04	0.0058
265102_at	AT1G30870	cationic peroxidase, putative	0.9987	0.0589	0.1389	0.02426	0.9523	0.5324	0.8127	0.0834	0.1271	-0.1617	0.6715	0.3879
265103_at	AT1G31070	UDP-N-acetylglucosamine pyrophosphorylase-relat	-1.2192	0.0628	0.1436	-0.4507	0.3978	0.3403	-1.9097	0.0026	0.0234	-1.1413	0.0161	0.0405
265104_at	AT1G31020	ATO2 (Arabidopsis thioredoxin o2); thiol-disulfide e	0.1668	0.3372	0.3439	0.4141	0.0539	0.1152	0.08396	0.6127	0.402	0.3313	0.0965	0.1179
265105_s_at	AT1G63340,AT1G62580	[AT1G63340, flavin-containing monooxygenase-rela	0.5056	0.6888	0.4887	-0.5368	0.6711	0.449	-0.7648	0.4314	0.3302	-1.8072	0.1078	0.126
265106_s_at	AT1G62590,AT1G63330	[AT1G62590, pentatricopeptide (PPR) repeat-contai	0.05675	0.8356	0.534	0.1098	0.6904	0.4557	-0.6735	0.0594	0.1034	-0.6204	0.0728	0.099
265107_s_at	AT1G63380,AT1G62610	[AT1G63380, short-chain dehydrogenase/reductase	0.2622	0.3435	0.3465	0.5846	0.0749	0.1372	-0.7001	0.039	0.0816	-0.3777	0.1781	0.172
265108_s_at	AT1G62620,AT1G63370	[AT1G62620, flavin-containing monooxygenase fam	0.1288	0.624	0.4678	0.398	0.1766	0.2174	-0.4049	0.1708	0.1925	-0.1356	0.6063	0.3655
265109_s_at	AT1G63360,AT1G62630	[AT1G63360, disease resistance protein (CC-NBS-	0.07074	0.6887	0.4822	0.3595	0.0791	0.141	-0.7564	8.00E-04	0.0165	-0.4677	0.005	0.0221
265110_at	AT1G62490	mitochondrial transcription termination factor-relate	-0.4958	0.6763	0.4847	-1.6582	0.2071	0.2377	-1.1121	0.3703	0.303	-2.2744	0.1081	0.1262
265120_at	AT1G62540	protease inhibitor/seed storage/lipid transfer protein	-1.1732	0.0138	0.0719	-0.9975	0.0235	0.0771	0.5526	0.1106	0.1488	0.7283	0.0545	0.0835
265112_at	AT1G62530	similar to unknown protein [Arabidopsis thaliana] (T	-0.9662	0.3541	0.3518	-1.7774	0.1263	0.1803	1.1727	0.2497	0.2409	0.3615	0.6996	0.3973
265113_at	AT4G09455,AT1G62460	[AT4G09455, transposable element gene];[AT1G62	-0.2075	0.6297	0.4697	-0.7138	0.1475	0.1963	0.5708	0.225	0.2264	0.06453	0.8791	0.4511
265114_at	AT1G62440	LRX2 (LEUCINE-RICH REPEAT/EXTENSIN 2); pro	0.667	0.6412	0.4734	-0.8797	0.5432	0.402	0.6981	0.6262	0.4066	-0.8486	0.5568	0.3476
265115_at	AT1G62450	Rho GDP-dissociation inhibitor family protein	-0.4868	0.7212	0.4998	1.1375	0.4215	0.3513	0.9021	0.5171	0.3659	2.5264	0.1178	0.1333
265116_at	AT1G62480	vacuolar calcium-binding protein-related	-0.6454	0.0188	0.0814	-0.00548	0.9757	0.5383	0.5933	0.0247	0.0637	1.2332	0.0019	0.0149
265117_at	AT1G62500	protease inhibitor/seed storage/lipid transfer protein	-0.7487	0.2147	0.2714	-0.9224	0.1438	0.1935	-0.3492	0.3063	0.2718	-0.5228	0.1542	0.1575
265118_at	AT1G62660	beta-fructosidase (BFRUCT3) / beta-fructofuranosio	-0.3019	0.0747	0.157	-0.2005	0.1868	0.2242	-0.2542	0.8403	0.0832	-0.1528	0.1465	0.1524
265119_at	AT1G62570	flavin-containing monooxygenase family protein / FI	-0.5369	0.0037	0.0459	-0.7646	0.0077	0.0489	0.2612	0.1651	0.1885	0.4335	0.048	0.0774
265120_at	AT1G62640	KAS III (3-KETOACYL-ACYL CARRIER PROTEIN	0.2371	0.1951	0.2592	-0.1054	0.5275	0.3953	-0.3657	0.0139	0.047	-0.2339	0.0554	0.0843
265121_at	AT1G62560	flavin-containing monooxygenase family protein / FI	-1.1999	0.0363	0.1098	-1.028	0.0567	0.1184	0.2539	0.0101	0.0398	0.4258	0.0015	0.0138
265122_at	AT1G62540	flavin-containing monooxygenase family protein / FI	-0.2015	0.5389	0.4365	-0.03709	0.9076	0.5208	-0.1117	0.5394	0.3751	0.05274	0.7674	0.4191
265123_at	AT1G55440	DC1 domain-containing protein	-0.1791	0.8184	0.5292	0.4851	0.543	0.402	0.1389	0.7979	0.4627	0.8032	0.1888	0.1787
265124_at	AT1G55430	DC1 domain-containing protein	0.4087	0.7454	0.5075	-0.4394	0.7273	0.4679	-1.178	0.3726	0.3042	-2.0261	0.1595	0.1609
265125_at	AT1G55410	pseudogene, CHP-rich zinc finger protein, putative,	-0.3402	0.733	0.5032	0.01438	0.9884	0.5413	-2.2203	0.0741	0.1185	-1.8657	0.1136	0.1302
265126_s_at	AT1G55360,AT1G55420	[AT1G55360, DC1 domain-containing protein];[AT1	0.6963	0.5339	0.4346	-0.3189	0.4696	0.3004	-1.4533	0.1999	0.8309	0.473	0.4772	0.6153	0.3685
265127_at	AT1G55560	SKS14 (SKU5 Similar 14); copper ion binding / oxid	-1.3354	0.0934	0.1771	-0.02338	0.9712	0.537	-2.5171	0.0145	0.0479	-1.2051	0.119	0.134
265128_at	AT1G30860	protein binding / zinc ion binding	-0.195	0.7115	0.4968	-0.02232	0.9659	0.5355	0.2728	0.6081	0.4007	0.4456	0.4156	0.2906
265129_at	AT1G30970	SUF4 (SUPPRESSOR OF FRIGIDA4); DNA bindi	0.3401	0.0226	0.0879	-0.1295	0.2413	0.2587	0.01635	0.8551	0.4798	-0.4513	0.0087	0.0291
265130_at	AT1G30890	integral membrane HRF1 family protein	0.7335	0.0118	0.0679	0.7916	0.0091	0.0522	0.2342	0.2079	0.2166	0.2922	0.1345	0.1447
265131_at	AT1G23760	JR630; polygalactoronase	1.2187	0.2456	0.2908	-0.3086	0.748	0.4744	0.2643	0.7561	0.4501	-1.263	0.1872	0.1777
265132_at	AT1G23830	similar to unknown protein [Arabidopsis thaliana] (T	0.2069	0.5691	0.4486	0.3641	0.337	0.312	0.1342	0.3345	0.2857	0.2913	0.076	0.1015
265133_s_at	AT1G51240,AT1G51250	[AT1G51240, similar to unknown protein [Arabidops	-0.7399	0.4937	0.4174	-1.1819	0.2958	0.2895	-0.2841	0.787	0.4593	-0.7261	0.5013	0.3264
265134_at	AT1G51260	LPAT3 (Lysophosphatidyl acyltransferase 3); 1-acy	-0.4475	0.5256	0.4315	0.4585	0.516	0.391	0.4754	0.4246	0.3274	1.3814	0.0613	0.0897
265135_at	AT1G51270	structural molecule	0.2347	0.1679	0.2397	0.09964	0.5147	0.3904	-1.4533	4.00E-04	0.0145	-1.5883	3.00E-04	0.0081
265136_at	AT1G51270	structural molecule	-0.06051	0.8654	0.5424	0.5268	0.1908	0.2268	-2.511	0.0013	0.0189	-1.9236	0.0034	0.0191
265137_at	AT1G51290	F-box family protein (FBX10)	1.3444	0.3301	0.34	-0.3083	0.812	0.4935	0.7445	0.5727	0.3877	-0.9082	0.4958	0.3242
265138_at	AT1G51300	acyl-protein thioesterase-related	-0.723	0.0059	0.0534	-0.7361	0.0056	0.0434	0.675	0.0076	0.0352	0.6619	0.0081	0.028
265139_at	AT1G51310	tRNA (5-methylaminomethyl-2-thiouridylate)-methyl	-0.02207	0.9217	0.5575	-0.2432	0.3134	0.2992	-0.077	0.636	0.4099	-0.2981	0.1188	0.1339
265140_at	AT1G51320	F-box family protein (FBX11)	-0.6078	0.6181	0.4658	-0.5762	0.6359	0.4369	-1.1292	0.2934	0.2654	-1.0976	0.3053	0.2412
265141_at	AT1G51350	armadillo/beta-catenin repeat family protein	0.01072	0.9672	0.5691	-0.04638	0.859	0.5069	-0.2659	0.289	0.2631	-0.323	0.2121	0.1919
265142_at	AT1G51360	similar to unknown protein [Arabidopsis thaliana] (T	0.2098	0.3903	0.37	0.3396	0.1942	0.2289	-0.5832	0.0157	0.0499	-0.4534	0.035	0.0633
265143_at	no_match	no_match	0.2172	0.3496	0.3495	0.1191	0.5927	0.4205	-0.07011	0.6605	0.4181	-0.1682	0.3195	0.2481
265144_at	AT1G51170	protein kinase family protein	-0.31	0.5757	0.451	0.07521	0.8898	0.5157	0.2649	0.5058	0.3616	0.6501	0.1476	0.1532
265145_at	AT1G51190	PLT2 (PLETHORA 2); transcription factor	-0.3184	0.7859	0.5196	-0.3369	0.7739	0.4817	1.0334	0.3991	0.3163	1.0149	0.4069	0.2869
265146_at	AT1G51210	UDP-glucuronosyl/UDP-glucosyl transferase family	0.1375	0.6866	0.4881	-0.06715	0.8425	0.5022	-0.01538	0.9636	0.5084	-0.22	0.5255	0.3361
265147_at	AT1G51380	initiation factor 4A, putative / eIF-4A, putative	0.6306	0.0421	0.118	0.7887	0.0211	0.074	-0.4217	0.1199	0.1562	-0.2635	0.2853	0.2231
265148_at	AT1G51160	synbindin, putative	0.3932	0.0419	0.1177	0.4912	0.0211	0.074	0.1217	0.4127	0.3219	0.2196	0.1745	0.17
265149_at	AT1G51400	photosystem II 5 kD protein	-0.5875	0.0094	0.0624	-0.6146	0.0081	0.05	0.3364	0.0082	0.0362	0.3093	0.0109	0.0327
265150_at	AT1G51200	zinc finger (AN1-like) family protein	-0.06294	0.6655	0.4811	-0.4064	0.0396	0.0986	-0.6843	0.0027	0.0236	-1.0278	6.00E-04	0.01
265151_at	AT1G51340	MATE efflux family protein	-0.1897	0.5421	0.4378	-0.2525	0.4259	0.3534	-0.2112	0.4999	0.3596	-0.2739	0.391	0.2804
265152_s_at	AT1G30940,AT1G30935	[AT1G30940, pseudogene, F-box protein -related,(	0.4554	0.5943	0.4576	1.3214	0.1688	0.2117	0.2876	0.7149	0.4365	1.1536	0.1907	0.1796
265153_at	AT1G30910	UFO (UNUSUAL FLORAL ORGANS); ubiquitin-pro	-0.2867	0.822	0.5301	0.5433	0.6726	0.4493	0.3071	0.6524	0.4154	1.1371	0.1463	0.1523
265154_at	AT1G30960	GTP-binding protein (ERG)	0.6412	0.0843	0.168	0.8907	0.0337	0.0908	-0.3629	0.2434	0.2369	-0.1134	0.6912	0.3944
265155_at	AT1G30990	major latex protein-related / MLP-related	2.1841	0.0225	0.0878	-0.06766	0.9163	0.5231	1.7962	0.0412	0.0842	-0.4555	0.4933	0.3233
265156_at	AT1G31000	F-box family protein	-0.2579	0.8127	0.5275	-0.8103	0.4712	0.3726	0.6156	0.5033	0.3606	0.06316	0.9435	0.4693
265157_at	AT1G31030	transposable element gene	0.5503	0.6409	0.4734	-0.5	0.6709	0.4489	1.5807	0.2214	0.2244	0.5305	0.6526	0.3817
265158_at	AT1G31040	zinc ion binding	-0.57	0.5691	0.4486	2.2876	0.0677	0.1304	-0.6764	0.4944	0.3574	2.1812	0.0726	0.0989
265159_at	AT1G31060	unknown protein	-0.6014	0.519	0.4289	-1.0941	0.2682	0.2745	0.7246	0.019	0.0553	0.2319	0.2904	0.2337
265160_at	AT1G31050	transcription factor	-0.02456	0.9614	0.5676	1.6583	0.0254	0.0797	-0.7793	0.0994	0.1405	0.9035	0.0684	0.0956
265161_at	AT1G30900	vacuolar sorting receptor, putative	1.5414	2.00E-04	0.0312	1.5765	2.00E-04	0.0249	0.1305	0.1624	0.1868	0.1656	0.0958	0.1174
265162_at	AT1G30910	molybdenum cofactor sulfurase family protein	0.04975	0.4046	0.3777	0.04393	0.4573	0.3671	0.0861	0.1704	0.1922	0.08028	0.1946	0.1817
265163_at	AT1G23580	similar to unknown protein [Arabidopsis thaliana] (T	0.4026	0.5097	0.4248	-0.7046	0.2744	0.2777	0.6106	0.3344	0.2857	-0.4966	0.4229	0.2937
265164_at	AT1G23600	similar to unknown protein [Arabidopsis thaliana] (T	0.4021	0.3852	0.3674	-0.3628	0.4291	0.3549	0.3511	0.4429	0.3354	-0.4138	0.3729	0.2726
265165_at	AT1G23610	similar to unknown protein [Arabidopsis thaliana] (T	0.6141	0.2842	0.3139	-0.375	0.4925	0.3814	0.6016	0.0949	0.1367	-0.3874	0.2333	0.2033
265166_at	AT1G23640	pseudogene, hypothetical protein, contains Pfam pr	-0.7483	0.656	0.4778	-0.2639	0.8737	0.5112	0.2436	0.8833	0.4876	0.7281	0.6645	0.3856
265167_at	AT1G23680	contains InterPro domain Protein of unknown functi	-0.7946	0.2897	0.3171	-0.9643	0.2131	0.2415	0.002934	0.9963	0.5167	-0.1667	0.7954	0.4275
265168_at	AT1G23700	protein kinase family protein	-0.8687	0.1107	0.193	-0.7404	0.1568	0.2034	0.1916	0.6758	0.423	0.3199	0.494	0.3236
265169_x_at	AT1G23720	proline-rich extensin-like family protein	-0.07972	0.8769	0.5456	0.4804	0.3763	0.3303	0.5051	0.3548	0.2957	0.1044	0.8395	0.4398
265170_at	AT1G23730	carbonic anhydrase, putative / carbonate dehydrata	0.1177	0.6927	0.4902	0.2452	0.4262	0.3535	0.1091	0.7139	0.4362	0.2365	0.4414	0.302
265171_at	AT1G23790	similar to unknown protein [Arabidopsis thaliana] (T	-0.04889	0.9571	0.5665	-0.2094	0.8183	0.4953	0.7757	0.4122	0.3218	0.6152	0.5084	0.3291
265172_at	AT1G23820	SPDS1 (SPERMIDINE SYNTHASE 1)	0.4384	0.0074	0.0578	0.4211	0.0086	0.051	-0.2143	0.0511	0.0958	-0.2316	0.0409	0.07
265173_at	AT1G23530	similar to unknown protein [Arabidopsis thaliana] (T	-0.5163	0.1724	0.243	-0.1036	0.7559	0.4769	0.6005	0.1256	0.1605	1.0132	0.0311	0.0595
265174_s_at	AT1G23470,AT1G23460	[AT1G23470, pseudogene, polygalacturonase (pec	-0.3598	0.2894	0.317	-0.237	0.4666	0.3707	-0.4343	0.1758	0.1958	-0.3114	0.3041	0.2407
265175_at	AT1G23480	ATCSLA03 (Cellulose synthase-like A3); transferase	-0.7921	0.0513	0.1301	-1.0794	0.02	0.0723	-0.1427	0.5167	0.3658	-0.4301	0.099	0.1199
265176_at	AT1G23520	similar to unknown protein [Arabidopsis thaliana] (T	0.2189	0.679	0.4857	-0.3961	0.4652	0.3701	-0.1092	0.7833	0.4583	-0.7241	0.1228	0.1369
265177_at	AT1G23630	similar to unknown protein [Arabidopsis thaliana] (T	-2.5785	0.0956	0.1787	1.1951	0.3711	0.3278	-2.8306	0.0757	0.1198	0.943	0.4715	0.3143
265178_at	AT1G23540	protein kinase family protein	-0.9942	0.0742	0.1566	-0.1443	0.7448	0.4731	0.5113	0.2411	0.2356	1.3611	0.0216	0.0478
265179_at	AT1G23650	unknown protein	-0.8634	0.5544	0.4425	-1.3889	0.3584	0.3222	0.1914	0.893	0.4905	-0.3341	0.8148	0.4328
265180_at	AT1G23590	similar to unknown protein [Arabidopsis thaliana] (T	-1.2293	0.2521	0.2946	-0.04818	0.9721	0.5372	-0.4393	0.6791	0.4242	1.2418	0.2765	0.2264
265181_at	AT1G23510	similar to unknown protein [Arabidopsis thaliana] (T	0.1769	0.9111	0.5543	-2.4229	0.1787	0.2187	1.6552	0.2121	0.2192	-0.9446	0.4449	0.3039
265182_at	AT1G23740	oxidoreductase, zinc-binding dehydrogenase family	-0.7125	0.0357	0.109	-0.8782	0.0184	0.0702	-0.00636	0.873	0.485	-0.1721	0.01	0.0312
265183_at	AT1G23760	DNA-binding protein-related	-1.0428	0.0022	0.041	-0.6842	0.01	0.0544	0.1462	0.2969	0.2671	0.5047	0.0144	0.0381
265184_at	AT1G23710	similar to unknown protein [Arabidopsis thaliana] (T	-0.4699	0.2819	0.3126	0.4305	0.3186	0.3022	0.1841	0.1322	0.1654	1.0846	4.00E-04	0.0089
265185_at	AT1G23670	similar to unknown protein [Arabidopsis thaliana] (T	-0.6916	0.6323	0.4704	-0.1431	0.9199	0.5241	-1.3798	0.2924	0.2648	-0.8314	0.5059	0.3281
265186_at	AT1G23560	similar to unknown protein [Arabidopsis thaliana] (T	0.3453	0.3696	0.3593	0.5869	0.5647	0.41	-0.4918	0.5559	0.3812	-0.8503	0.3294	0.253
265187_at	AT1G23490	ATARF1/ATARF1/ATARFA1A (ADP-RIBOSYLATIO	-0.0164	0.9036	0.5523	-0.1166	0.404	0.3431	0.465	0.0036	0.0265	0.3645	0.0087	0.029
265188_at	AT1G23800	ALDH2B7 (Aldehyde dehydrogenase 2B7); 3-chloro	0.4187	0.1948	0.259	0.3088	0.3151	0.3004	-0.3641	0.2475	0.2396	-0.4739	0.153	0.1568
265189_at	AT1G23840	similar to unknown protein [Arabidopsis thaliana] (T	1.5614	0.0043	0.0479	1.8742	0.0022	0.0334	-0.283	0.3363	0.2865	0.02981	0.914	0.461
265190_at	AT1G23780	F-box family protein	0.3723	0.0246	0.0911	0.5716	0.0057	0.0437	0.1826	0.1356	0.1681	0.3819	0.0175	0.0423
265191_at	AT1G05120	SNF2 domain-containing protein / helicase domain-	0.4922	0.0732	0.1558	0.8285	0.0153	0.0649	-0.5127	0.033	0.0742	-0.1764	0.333	0.2549
265192_at	AT1G05060	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.1836	0.4385	0.393	0.1561	0.5053	0.3868	0.3682	0.1129	0.1505	0.3407	0.1342	0.1445
265193_at	AT1G05070	similar to unknown protein [Arabidopsis thaliana] (T	-0.2523	0.0494	0.1276	-0.4812	0.006	0.0447	0.01364	0.882	0.4873	-0.2152	0.0671	0.0944
265194_at	AT1G05010	EFE (ETHYLENE FORMING ENZYME)	-0.1033	0.5728	0.45	0.151	0.4206	0.3509	0.1781	0.1489	0.1783	0.4324	0.0123	0.0351
265195_at	AT1G26730	pentatricopeptide (PPR) repeat-containing protein	0.489	0.1415	0.2187	0.1119	0.6973	0.458	-0.2947	0.3325	0.2845	-0.6718	0.0659	0.0935
265196_at	AT2G36740	ATSWC2/SWC2; DNA binding	-0.06116	0.7672	0.5138	0.2614	0.2471	0.2621	-0.04483	0.8278	0.472	0.2778	0.2236	0.198
265197_at	AT2G36750	UGT72C1 (UDP-GLUCOSYL TRANSFERASE 72C	-1.2359	0.3387	0.3448	0.08346	0.9451	0.5306	-1.1199	0.1804	0.199	0.1994	0.7873	0.4249
265198_at	AT2G36760	UGT73C2 (UDP-GLUCOSYL TRANSFERASE 73C	0.0524	0.9409	0.5628	1.6884	0.0639	0.1262	-0.1825	0.7973	0.4626	1.4535	0.094	0.116
265199_s_at	AT2G36780,AT2G36770	[AT2G36780, UDP-glucuronosyl/UDP-glucosyl trans	0.9075	0.0972	0.1801	1.2271	0.0434	0.1033	-0.1206	0.6795	0.4243	0.199	0.5038	0.3273
265200_s_at	AT2G36800,AT2G36790	[AT2G36800, DOGT1 (DON-GLUCOSYLTRANSFE	-0.3926	0.52	0.429	-0.1345	0.8211	0.4962	-0.5543	0.1524	0.1806	-0.2963	0.399	0.2838
265201_at	AT2G36810	binding	0.3141	0.1689	0.2405	0.08136	0.6865	0.4544	-0.8389	0.011	0.0416	-1.2344	0.0027	0.0172
265202_at	AT2G36820	similar to unnamed protein product [Vitis vinifera] (G	-0.9594	0.5304	0.4331	-0.2171	0.8841	0.5143	-0.1987	0.8737	0.4851	0.5437	0.667	0.3864
265203_at	AT2G36630	similar to unknown protein [Arabidopsis thaliana] (T	0.1217	0.7387	0.5053	-0.3214	0.3983	0.3406	-0.6573	0.0337	0.075	-0.857	0.0144	0.0381
265204_at	AT2G36650	similar to unknown protein [Arabidopsis thaliana] (T	-0.2418	0.8038	0.5251	-3.09	0.0275	0.0827	2.6097	0.0457	0.0894	-2.2385	0.8063	0.4306
265205_at	AT2G36660	initiation factor	0.4334	0.4982	0.4197	0.1013	0.8703	0.51	0.378	0.5517	0.3796	0.046	0.9408	0.4687
265206_at	AT2G36670	aspartyl protease family protein	0.4153	0.1699	0.2413	0.3499	0.2319	0.2528	-0.166	0.5407	0.3755	-0.2314	0.4044	0.286
265207_at	AT2G36680	similar to unknown protein [Arabidopsis thaliana] (T	0.7834	0.0056	0.0521	0.4794	0.0293	0.085	0.1201	0.4519	0.3395	-0.1839	0.2713	0.2234
265208_at	AT2G36690	oxidoreductase, 2OG-Fe(II) oxygenase family protei	-0.4956	0.1394	0.2169	-0.3605	0.2515	0.2649	0.07842	0.7214	0.439	0.2135	0.3562	0.2653
265209_at	no_match	no_match	0.5775	0.3672	0.3579	-1.6734	0.3419	0.3144	2.3177	0.2099	0.2178	-0.9333	0.5803	0.3562
265210_at	AT2G36620	RPL24A (RIBOSOMAL PROTEIN L24); structural c	-0.1885	0.2542	0.296	0.000883	0.9953	0.543	0.4381	0.0083	0.0366	0.6275	0.0022	0.0158
265211_at	AT2G36640	ATECP63 (EMBRYONIC CELL PROTEIN 63)	0.574	0.5759	0.4511	0.7521	0.4701	0.3722	0.4565	0.6539	0.4158	0.6347	0.5381	0.3406
265212_at	AT2G36530	hexose transporter, putative	0.1263	0.5313	0.4334	-0.03543	0.8571	0.5085	-0.4073	0.0919	0.1341	-0.3165	0.1616	0.1623
265213_at	AT1G05020	epsin N-terminal homology (ENTH) domain-contain	0.6025	0.3184	0.3334	0.5965	0.3226	0.3046	0.09445	0.5029	0.3605	0.08847	0.5288	0.3374
265214_at	AT1G05000	tyrosine specific protein phosphatase family protein	0.3092	0.2648	0.3021	0.107	0.6771	0.4509	0.3202	0.2509	0.2414	0.118	0.647	0.3797
265215_at	AT1G05040	contains InterPro domain UBA-like (InterPro:IPR00	0.07805	0.9277	0.5592	-1.2519	0.1962	0.2303	1.2364	0.2007	0.2122	-0.00382	0.9133	0.4607
265216_at	AT1G05100	MAPKKK18 (Mitogen-activated protein kinase kinas	-0.0539	0.8422	0.5362	0.3698	0.2188	0.2451	0.1828	0.4791	0.3511	0.6065	0.0609	0.0893
265217_s_at	AT4G20720,AT1G05090	[AT4G20720, dentin sialophosphoprotein-related];[A	0.4502	0.0879	0.1719	0.5369	0.0552	0.1166	-0.139	0.5258	0.3694	-0.05234	0.8068	0.4307
265218_at	AT1G05055	ATGT16/ATGT2/GT2/HGT2 (GENERAL TRANSCRIPTION	-0.05561	0.6934	0.4904	0.3047	0.6809	0.4426	0.6809	0.05284	0.6001	0.3982	0.4132	0.0114	0.0334
265219_at	AT2G02050	NADH-ubiquinone oxidoreductase B18 subunit, puta	-0.1104	0.3587	0.3538	0.07967	0.4962	0.3829	0.7902	0.0018	0.0206	0.9803	8.00E-04	0.0109
265220_at	AT2G02040	ATPTR2-B (NITRATE TRANSPORTER 1); transpo	0.2394	0.2012	0.2629	0.02185	0.8958	0.5174	-0.01687	0.9139	0.4962	-0.2344	0.185	0.1763
265221_s_at	AT2G02000,AT2G02010	[AT2G02000, GAD3 (GLUTAMATE DECARBOXYL	1.2471	0.0618	0.1427	2.6595	0.0054	0.0432	0.4653

265290_at	AT2G22590	glycosyltransferase family protein	0.5528	0.6742	0.484	-0.3022	0.8167	0.495	-0.6221	0.6322	0.4085	-1.4771	0.2865	0.2316
265291_at	AT2G22720	similar to unknown protein [Arabidopsis thaliana] (T	0.000256	0.9972	0.5763	0.05561	0.469	0.3716	-0.2804	0.0158	0.0501	-0.225	0.0319	0.0601
265292_s_at	AT3G26260,AT2G14010	[AT3G26260, transposable element gene];[AT2G14	1.0534	0.5766	0.4512	0.6378	0.7319	0.4688	-1.2313	0.5172	0.3659	-1.647	0.3964	0.2827
265293_at	AT2G14020	transposable element gene	-1.2772	0.1869	0.2533	-0.4935	0.572	0.4127	-0.8636	0.3427	0.2897	-0.07991	0.9255	0.4643
265294_at	AT2G14030	transposable element gene	-0.7584	0.5581	0.4442	1.5486	0.2626	0.2712	-2.6615	0.0887	0.1315	-0.3545	0.7804	0.4231
265295_at	no_match	no_match	-0.2292	0.3236	0.3364	-0.705	0.0258	0.0804	0.2672	0.26	0.2464	-0.2086	0.3639	0.2686
265296_at	AT2G14060	S-adenosyl-L-methionine:carboxyl methyltransferas	-0.2302	0.8065	0.5257	-0.9322	0.349	0.3177	0.5828	0.5438	0.3769	-0.1191	0.8988	0.4568
265297_at	AT2G14080	disease resistance protein (TIR-NBS-LRR class), p	0.4535	0.3148	0.3313	0.3379	0.4403	0.3596	-1.2848	8.00E-04	0.0163	-1.4003	6.00E-04	0.01
265298_s_at	AT3G27327,AT2G13930	[AT3G27327, transposable element gene];[AT2G13	0.214	0.9033	0.5523	-2.2334	0.2485	0.263	0.8521	0.5362	0.3738	-1.5953	0.2745	0.2252
265299_at	AT2G13940	transposable element gene	-0.03425	0.9456	0.5636	-0.04761	0.9244	0.5252	-0.04242	0.9326	0.5014	-0.05578	0.9115	0.4604
265300_at	AT2G13950	DC1 domain-containing protein	-0.659	0.1917	0.2566	0.5341	0.2724	0.2768	-0.783	0.0324	0.0735	0.4101	0.1675	0.1658
265301_s_at	AT5G02320,AT2G13960	[AT5G02320, MYB3R-5 (myb domain protein 3R-5);	0.1415	0.72	0.4994	-0.1921	0.6289	0.434	0.5086	0.2387	0.2345	0.175	0.6588	0.3838
265302_at	AT2G13970	transposable element gene	-0.3831	0.1586	0.2323	0.183	0.4548	0.3659	-0.8528	0.0183	0.0541	-0.2867	0.265	0.2203
265303_at	AT2G14040	transposable element gene	-0.1375	0.8838	0.5471	-0.8343	0.398	0.3404	1.4553	0.1489	0.1783	0.7585	0.4051	0.2862
265304_at	AT2G20350	AP2 domain-containing transcription factor, putative	1.0792	0.184	0.251	-1.3095	0.1235	0.1784	-0.7649	0.3191	0.2778	-3.1537	0.0094	0.0302
265305_at	AT2G20340	tyrosine decarboxylase, putative	-0.687	0.0591	0.1391	-0.8652	0.0301	0.0863	-0.31	0.0861	0.1294	-0.4881	0.0234	0.05
265306_at	AT2G20320	DENN (AEX-3) domain-containing protein	0.6838	0.0555	0.1353	0.1225	0.6568	0.4441	-0.07708	0.7191	0.4382	-0.6383	0.033	0.0613
265307_at	AT2G20310	RIN13 (RPM1 INTERACTING PROTEIN 13)	-0.05145	0.5793	0.4521	-0.2002	0.079	0.1409	0.2288	0.0552	0.1002	0.08009	0.4014	0.2847
265308_at	AT2G20300	ALE2 (ABNORMAL LEAF SHAPE 2); kinase	-0.3386	0.0813	0.1649	0.0925	0.5611	0.4088	-0.1134	0.4809	0.3517	0.3177	0.0953	0.1171
265309_at	AT2G20290	XI3 (Myosin-like protein XI3); motor protein binding	0.004556	0.9866	0.5735	-0.1614	0.5611	0.4088	-0.4276	0.0024	0.0228	-0.5935	7.00E-04	0.0105
265310_at	AT2G20280	zinc finger (CCCH-type) family protein	0.2354	0.4351	0.3916	0.2988	0.3332	0.3098	-0.2076	0.0727	0.1173	-0.1442	0.168	0.166
265311_at	AT2G20260	unknown protein	0.3488	0.2932	0.3192	-0.7734	0.0552	0.1166	-0.2868	0.3768	0.3061	-1.4088	0.0081	0.028
265312_at	AT2G20240	similar to unknown protein [Arabidopsis thaliana] (T	-0.9839	0.0239	0.09	-0.385	0.2375	0.2562	-0.3349	0.2938	0.2655	0.264	0.3952	0.2824
265313_at	AT2G20210	leucine-rich repeat family protein	-0.1974	0.5596	0.4448	0.09169	0.7825	0.4843	-0.9255	0.0407	0.0837	-0.6365	0.1097	0.1275
265314_at	AT2G20210	leucine-rich repeat family protein	0.2267	0.3611	0.3551	0.1668	0.4906	0.3806	-1.0412	0.0091	0.0382	-1.1011	0.0075	0.0269
265315_at	AT2G20190	ATCLASPCLASP; binding	-2.0833	0.1196	0.1999	-1.9892	0.1325	0.1848	-0.9441	0.4216	0.326	-0.85	0.4657	0.3122
265316_at	AT2G20400	myb family transcription factor	-0.4181	0.0385	0.1131	-0.0026	0.9858	0.5405	-0.1185	0.4266	0.3283	0.297	0.0911	0.1136
265317_at	no_match	no_match	-0.1854	0.3417	0.346	0.1672	0.386	0.3347	0.2488	0.2214	0.2245	0.6013	0.025	0.0521
265318_at	AT2G22650	FAD-dependent oxidoreductase family protein	-0.03493	0.8445	0.5371	0.1457	0.4321	0.3562	-1.21	0.0019	0.0209	-1.0294	0.0035	0.0193
265319_at	AT2G22670	IAA8 (indoleacetic acid-induced protein 8); transcrip	-0.4985	0.0052	0.0514	-0.6278	0.0022	0.0334	0.5152	0.0046	0.029	0.3859	0.0129	0.0359
265320_at	AT2G18320	similar to F-box family protein [Arabidopsis thaliana	0.5234	0.0949	0.2489	0.07565	0.918	0.5236	-0.4369	0.468	0.3466	-1.1601	0.1022	0.1221
265321_at	AT2G18280	AITLP2 (TUBBY LIKE PROTEIN 2); phosphoric die	0.4899	0.0145	0.0731	0.4573	0.0183	0.0698	-1.1577	0	0.0092	-1.1903	0	0.0047
265322_at	AT2G18270	unknown protein	1.3252	0.2863	0.315	0.2267	0.8437	0.5027	-0.1105	0.8731	0.485	-1.2091	0.1362	0.1457
265323_at	AT2G18260	SYP131 (syntaxin 112); SNAP receptor	0.2406	0.7762	0.5168	0.7515	0.3955	0.3394	0.5188	0.5478	0.3784	1.0296	0.263	0.2192
265324_at	AT2G18250	ATCOAD (4-PHOSPHOPANTETHEINE ADENYLY	0.2128	0.2133	0.2706	0.4311	0.0401	0.0994	0.1406	0.3839	0.3096	0.3589	0.0672	0.0945
265325_at	AT2G18240	RER1 protein, putative	0.3725	0.2011	0.2628	0.1175	0.6549	0.4435	0.05195	0.7942	0.4615	-0.2031	0.3369	0.2564
265326_at	AT2G18220	identical to Nucleolar complex protein 2 homolog (#	0.3574	0.2419	0.2887	0.1891	0.508	0.3877	-0.1837	0.4894	0.3553	-0.352	0.2188	0.1955
265327_at	AT2G18210	similar to unknown protein [Arabidopsis thaliana] (T	-1.4169	0.0689	0.151	-0.9959	0.1574	0.2039	0.7817	0.134	0.1667	1.2027	0.0448	0.0742
265328_at	AT2G18200	similar to unknown protein [Arabidopsis thaliana] (T	-0.4393	0.5144	0.427	-1.7273	0.0483	0.1092	0.9729	0.1887	0.2047	-0.315	0.6354	0.3755
265329_at	AT2G18450	SDH1-2 (Succinate dehydrogenase 1-2)	0.2476	0.434	0.391	-0.7019	0.548	0.4409	1.5857	0.328	0.2824	-0.3538	0.8161	0.4332
265330_at	AT2G18440	GUT15 (GENE WITH UNSTABLE TRANSCRIPT 1	0.6352	0.097	0.1799	0.8536	0.0441	0.1039	-2.341	0.0012	0.0187	-2.1226	0.0018	0.0147
265331_at	AT2G18420	Encodes a Gibberellin-regulated GASA/GAST/Snal	-0.2162	0.7159	0.498	0.6754	0.2892	0.2862	-1.267	0.0838	0.1273	-0.3755	0.5346	0.3396
265332_at	AT2G18410	similar to unknown [Populus trichocarpa] (GB:ABK9	0.08898	0.6205	0.4666	0.5333	0.0447	0.1048	-0.6186	0.0284	0.0684	-0.1843	0.3737	0.2729
265333_at	AT2G18350	ATH824 (ARABIDOPSIS THALIANA HOMEOBOX	-0.04189	0.8814	0.5465	0.3741	0.2287	0.2508	0.2722	0.36	0.2981	0.6883	0.0593	0.0879
265334_at	AT2G18370	protease inhibitor/seed storage/lipid transfer protein	1.1813	0.0767	0.1594	1.0454	0.1038	0.1626	-0.1461	0.7839	0.4586	-0.282	0.6015	0.3638
265335_at	AT2G18245	similar to unknown protein [Arabidopsis thaliana] (T	0.4189	0.2035	0.2762	0.06602	0.849	0.5041	-0.02121	0.9424	0.5038	-0.3841	0.2362	0.205
265336_at	AT2G18290	anaphase-promoting complex, subunit 10 family / A	0.3367	0.3454	0.3475	0.497	0.1898	0.2264	0.2869	0.227	0.2277	0.4471	0.0904	0.1131
265337_at	AT2G18390	TTN5 (TITAN 5); GTP binding	0.5067	0.0898	0.1735	0.566	0.0675	0.1302	-0.3329	0.0319	0.0726	-0.2736	0.0566	0.0854
265338_at	AT2G18400	ribosomal protein L6 family protein	-0.07315	0.5737	0.4504	0.1876	0.1916	0.2271	0.6221	0.0056	0.0313	0.8829	0.0015	0.0139
265339_at	AT2G18230	ATPPA2 (ARABIDOPSIS THALIANA PYROPHOSP	-0.3367	0.0472	0.1251	0.8879	0.0017	0.0321	0.7301	0.0036	0.0263	0.1789	0.2068	0.1889
265340_at	AT2G18330	AAA-type ATPase family protein	0.5635	0.0426	0.1188	0.2841	0.213	0.2415	-0.00983	0.9563	0.507	-0.2893	0.161	0.1618
265341_at	AT2G18360	hydrolase, alpha/beta fold family protein	-0.6151	0.4579	0.4018	1.9514	0.0598	0.1214	-0.8397	0.2338	0.2316	1.7269	0.045	0.0743
265342_at	AT2G18300	basic helix-loop-helix (bHLH) family protein	-0.2842	0.0899	0.1735	-0.2086	0.1773	0.2179	0.2137	0.1162	0.1533	0.2893	0.0537	0.0828
265343_at	AT2G22570	ATNIC1;NIC1;NIC2 (A. THALIANA NICOTINAMIDA	0.9016	0.0076	0.0579	0.8617	0.0089	0.0518	0.3419	0.0738	0.1182	0.302	0.1007	0.1211
265344_at	AT2G22660	similar to glycine-rich protein [Arabidopsis thaliana]	1.5732	0.003	0.0436	1.2215	0.0076	0.0488	-0.2008	0.2541	0.2432	-0.5525	0.0216	0.0478
265345_at	AT2G22680	zinc finger (C3HC4-type RING finger) family protein	0.3908	0.0151	0.0743	0.4194	0.0119	0.0585	0.3442	0.0228	0.0611	0.3728	0.0176	0.0425
265346_at	no_match	no_match	-0.1416	0.8614	0.5415	-0.5138	0.5364	0.3991	1.7609	0.0816	0.1252	1.3887	0.1419	0.1494
265347_at	AT2G22740	SUVH6 (SU(VAR)3-9 HOMOLOG 6)	0.03169	0.8408	0.5358	-0.1799	0.2907	0.287	0.008233	0.9188	0.4975	-0.2033	0.0552	0.0842
265348_at	AT2G22600	KH domain-containing protein	2.533	0.1075	0.1896	-1.7356	0.2295	0.2511	1.7099	0.2352	0.2323	-2.5587	0.105	0.124
265349_at	AT2G22610	kinesin motor protein-related	-0.2705	0.6688	0.4822	-0.28	0.6581	0.4444	0.8041	0.2325	0.2309	0.7945	0.2372	0.2057
265350_at	AT2G22620	vesse	0.4828	0.7509	0.5087	-0.3573	0.8137	0.4942	0.5422	0.7219	0.4392	-0.2979	0.844	0.4412
265351_at	AT2G22630	AGL17 (AGAMOUS-LIKE 17); transcription factor	0.4205	0.476	0.4101	0.438	0.459	0.3676	0.4547	0.4433	0.3355	0.4723	0.4273	0.2957
265352_at	AT2G16600	ROC3 (rotamase CyP 3); peptidyl-prolyl cis-trans is	0.6263	0.0379	0.1122	1.036	0.0072	0.048	0.2229	0.0486	0.0928	0.6326	0.0014	0.0133
265353_at	AT2G16800	high-affinity nickel-transport family protein	0.3887	0.0056	0.0522	0.2827	0.0169	0.0675	0.03266	0.6721	0.4217	-0.1387	0.1249	0.1382
265354_at	AT2G16700	ADF5 (ACTIN DEPOLYMERIZING FACTOR 5); act	1.3101	0.0028	0.0431	1.8349	8.00E-04	0.0277	0.5474	0.0397	0.0825	1.0722	0.0042	0.0207
265355_at	AT2G16760	similar to unknown protein [Arabidopsis thaliana] (T	0.5651	0.54	0.4368	-2.3173	0.0517	0.1128	3.1507	0.0203	0.0573	0.2683	0.7666	0.4188
265356_at	AT2G16595	similar to translocon-associated protein alpha (TRA	1.0493	0.007	0.0565	1.0912	0.0061	0.045	0.3421	0.1723	0.1934	0.384	0.1359	0.1456
265357_at	AT2G16740	UBC29 (UBIQUITIN-CONJUGATING ENZYME 29)	0.00249	0.9938	0.5754	0.06489	0.8405	0.5016	0.9128	0.0072	0.0342	0.9752	0.0057	0.0234
265358_at	AT2G16710	hesB-like domain-containing protein	1.1824	0.0035	0.0448	1.5476	0.0013	0.0305	0.3455	0.0362	0.0783	0.7107	0.0031	0.0181
265359_at	AT2G16720	MYB7 (myb domain protein 7); DNA binding / transc	0.7886	0.0572	0.1371	0.9086	0.0381	0.0966	-0.1529	0.5708	0.3869	-0.03283	0.901	0.4576
265360_s_at	AT2G13260,AT2G13250	[AT2G13260, transposable element gene];[AT2G13	-0.07627	0.938	0.5618	0.722	0.4769	0.375	-1.278	0.2375	0.2338	-0.4798	0.6299	0.3736
265361_at	AT2G13230	transposable element gene	0.03671	0.9748	0.571	-0.2903	0.8034	0.4907	0.5832	0.5874	0.3935	0.2562	0.8086	0.4313
265362_at	AT2G13230	transposable element gene	0.4244	0.7014	0.4929	-1.4895	0.2216	0.2469	0.1791	0.8703	0.4841	-1.7347	0.1674	0.1656
265363_at	AT2G13335	transposable element gene	-0.69	0.5008	0.4209	2.4507	0.0585	0.1202	-0.1379	0.8859	0.4884	3.0027	0.0291	0.0571
265364_at	AT2G13330	transposable element gene	-0.3516	0.7093	0.496	0.3058	0.7452	0.4732	-0.5545	0.5509	0.3794	0.1029	0.9097	0.4599
265365_at	AT2G13310	transposable element gene	-0.2325	0.903	0.5521	0.4828	0.801	0.4897	-0.4702	0.806	0.4654	0.2452	0.8978	0.4566
265366_at	AT2G13290	glycosyl transferase family 17 protein	0.2974	0.2435	0.2897	0.5015	0.0826	0.1443	0.2177	0.1882	0.2045	0.4218	0.0373	0.0659
265367_at	AT2G13270	transposable element gene	0.8403	0.2399	0.2875	0.4352	0.5145	0.3904	0.7868	0.2661	0.2498	0.3817	0.5649	0.3508
265368_at	AT2G13350	C2 domain-containing protein	0.3483	0.5025	0.4216	0.7237	0.2009	0.2332	0.00372	0.9469	0.5049	0.4061	0.4018	0.2849
265369_s_at	AT2G06470,AT4G16910,A	[AT2G06470, transposable element gene];[AT4G16	0.4164	0.5889	0.4559	-0.5743	0.4637	0.3697	-0.4198	0.5403	0.3753	-1.4105	0.088	0.1112
265370_s_at	AT2G01029,AT2G06460,A	[AT2G01029, transposable element gene];[AT2G06	0.7708	0.5344	0.4349	-2.4901	0.0933	0.1539	1.3298	0.3065	0.2719	-1.9312	0.1642	0.1638
265371_at	AT2G06490	transposable element gene	1.7511	0.2855	0.3146	1.5245	0.344	0.3151	0.7809	0.3325	0.2845	0.5542	0.478	0.3169
265372_at	AT2G06500	hAT dimerisation domain-containing protein / transp	-0.6733	0.6519	0.4766	-1.068	0.4832	0.3773	0.9948	0.5118	0.3638	0.6001	0.6868	0.3929
265373_at	AT2G06510	replication protein, putative	0.8298	0.0064	0.0547	1.1579	0.0019	0.0329	-0.3302	0.0662	0.1113	-0.00214	0.9878	0.4797
265374_at	AT2G06520	PSBX (photosystem II subunit X)	-0.4375	0.0572	0.1371	-0.6331	0.0186	0.0705	0.2241	0.136	0.1684	0.02849	0.8245	0.4355
265375_at	AT2G06530	VPS2.1	0.2962	0.2119	0.2695	0.5457	0.0522	0.1133	0.8161	0.0013	0.0192	1.0656	5.00E-04	0.0094
265376_at	AT2G05810	armadillo/beta-catenin repeat family protein	-0.2192	0.4702	0.4074	0.2674	0.3861	0.3347	0.3633	0.2571	0.2448	0.8498	0.0366	0.0651
265377_at	AT2G05790	glycosyl hydrolase family 17 protein	-0.2042	0.3383	0.3447	-0.1736	0.4079	0.3448	0.04978	0.5884	0.3939	0.08036	0.3966	0.2828
265378_at	AT2G18380	transcription factor	-0.6998	0.1472	0.2231	-0.09572	0.8182	0.4953	0.4496	0.2345	0.2319	1.0537	0.0306	0.0588
265379_at	AT2G18340	late embryogenesis abundant domain-containing pr	-0.8672	0.3042	0.3253	-0.8342	0.3205	0.3034	-0.04407	0.9551	0.5066	-0.01105	0.9887	0.4798
265380_at	AT2G16670	transposable element gene	1.0322	0.3353	0.343	-0.744	0.4744	0.374	0.7799	0.4489	0.338	-0.9964	0.3443	0.26
265381_at	AT2G16680	transposable element gene	0.1673	0.7843	0.519	-0.2494	0.685	0.4538	0.3049	0.2544	0.2433	-0.1117	0.6515	0.3813
265382_at	AT2G16790	shikimate kinase family protein	0.7109	0.2289	0.2813	0.9398	0.1339	0.186	-0.1023	0.7314	0.4422	0.1266	0.6721	0.3881
265383_at	AT2G16780	MSI2 (NUCLEOSOME/CHROMATIN ASSEMBLY F	0.4597	0.2024	0.2639	0.3759	0.2809	0.2813	-0.202	0.5399	0.3752	-0.2857	0.3974	0.2831
265384_at	AT2G20760	protein binding / protein transporter/ structural mole	0.1313	0.3742	0.3617	0.4373	0.0292	0.0849	0.3132	0.0101	0.0399	0.6192	8.00E-04	0.0112
265385_at	AT2G20900	diacylglycerol kinase, putative	0.2349	0.3273	0.3385	0.3546	0.1676	0.2109	-0.3465	0.1753	0.1955	-0.2268	0.3422	0.259
265386_at	AT2G20930	similar to unknown [Populus trichocarpa] (GB:ABK9	0.6146	0.0034	0.0448	0.4003	0.0156	0.0652	0.6538	0.0018	0.0206	0.4395	0.0076	0.0271
265387_at	AT2G20670	similar to unknown protein [Arabidopsis thaliana] (T	-0.09166	0.7517	0.5089	0.5228	0.1253	0.1795	-0.7167	0.0022	0.0219	-0.1023	0.3734	0.2728
265388_s_at	AT2G21010,AT2G20990	[AT2G21010, C2 domain-containing protein];[AT2G	-0.3263	0.0928	0.1764	-0.09752	0.547	0.4033	-0.5816	0.0173	0.0525	-0.3528	0.0762	0.1018
265389_at	AT2G20980	lumazine-binding family protein	-0.02068	0.9001	0.5511	0.1376	0.5809	0.4165	-0.163	0.5165	0.3658	0.005264	0.9828	0.4787
265390_at	AT2G20820	similar to hypothetical protein [Capsicum chinense]	0.01856	0.819	0.5293	0.2865	0.0196	0.0719	0.4991	0.0022	0.0222	0.7671	4.00E-04	0.0091
265391_at	AT2G20810	GAUT10/LGT4 (Galacturonosyltransferase 10); pol	-0.3369	0.0825	0.1662	-0.08888	0.576	0.4142	-0.3738	0.0045	0.0286	-0.1258	0.1242	0.1378
265392_at	AT2G20870	LIP1 (LIPOIC ACID SYNTHASE 1); lipoic-acid synt	0.06005	0.8178	0.5291	-0.4378	0.1474	0.1963	0.4631	0.1307	0.1644	-0.03475	0.8937	0.4554
265393_at	AT2G20830	folic acid binding / transferase	-0.3273	0.2204	0.2754	-0.3728	0.1737	0.2153	-0.5296	0.0068	0.0337	-0.5751	0.005	0.0222
265394_at	AT2G20725	CAAX amino terminal protease family protein	0.3008	0.0801	0.1633	-0.3407	0.0576	0.1193	-0.8103	0.0011	0.0181	-1.4517	1.00E-04	0.0062
265395_at	AT2G20850	SRF1 (STRUBBELIG-RECEPTOR FAMILY 1); kina	1.3313	3.00E-04	0.032	1.2567	4.00E-04	0.0251	-0.647	0.005	0.0297	-0.7216	0.0033	0.0188
265396_at	AT2G21040	C2 domain-containing protein	-0.1035	0.9006	0.5513	-1.678	0.0971	0.1571	0.4372	0.604	0.3996	-1.1374	0.2174	0.1948
265397_at	AT2G21090	transposable element gene	0.3652	0.7952	0.5224	-2.001	0.2031	0.2348	1.6602	0.1639	0.1878	-0.706	0.5091	0.3294
265398_at	AT2G21000	ATMAK10 (Arabidopsis thaliana MAK10 homologue	0.2857	0.1013	0.1841	0.03573	0.804	0.4909	0.1003	0.2958	0.2666	-0.1496	0.1477	0.1532
265399_at	AT2G21010	similar to myosin heavy chain-related [Arabidopsis t	-0.1979	0.8463	0.5374	0.2443	0.8112	0.4934	0.3134	0.7599	0.4512	0.7555	0.4742	0.3154
265400_at	AT2G21040	protease inhibitor/seed storage/lipid transfer protein	-1.4589	0.0036	0.0456	-2.3231	6.00E-04	0.027	0.6813	0.015	0.0488	-0.1819	0.3366	0.2563
265401_at	AT2G21070	invertase/pectin methylesterase inhibitor family prot	-0.4011	0.6608	0.4795	1.8692	0.0921	0.1531	-2.6267	0.0363	0.0784	-0.3565	0.6957	0.3961
265402_at	AT2G21050	BSD domain-containing protein	0.2269	0.1151	0.1963	0.02681	0.8234	0.497	0.5087	0.0087	0.0373	0.3096	0.0433	0.0726
265403_at	AT2G16690	transposable element gene	-0.2119	0.8933	0.5495	-0.4182	0.3162	0.3009	-0.2639	0.349	0.2927	-0.6339	0.0662	0.0937
265404_at	AT2G16730	BGAL13 (beta-galactosidase 13); beta-galactosidas	-1.3693	0.3728	0.3608	-0.8033	0.588	0.4187	-0.9472	0.5261	0.3695	-0.3812	0.794	0.4272
265405_at	AT2G16750	protein kinase family protein	-1.1162	0.1367	0.2147	-1.0267	0.1626	0.2078	-0.4715	0.4764	0.35	-0.382	0.5594	0.3486
265406_at	AT2G16610	transposable element gene	0.09818	0.9458	0.5636	1.62	0.2986	0.2909	-0.2742	0.8499	0.4785	1.2477	0.4102	0.2883
265407_at	AT2G16810	F-box family protein (FBX8)	-0.5077	0.3563	0.3529	0.08203	0.8745	0.5115	-0.9467	0.124	0.1594	-0.357	0.5044	0.3275
265408_at	AT2G16820	transposable element gene	-2.4592	0.0568	0.1367	0.8518	0.4102	0.346	-2.561	0.0507	0.0954	0.7499	0.4639	0.3116
265409_at	no_match	no_match	0.8645	0.2319	0.2831	-0.2011	0.4778	0.3599	0.6206	0.4048	0.2923	0.1814	0.1814	0.1742
265410_at	AT2G16620	protein kinase-related	0.5513	0.767	0.5137	-0.5271	0.7768	0.4826	-0.2284	0.9018	0.493	-1.3068	0.494	0.3236
265411_at	AT2G16630	proline-rich family protein	0.04197	0.8649	0.5423	-0.4046	0.1552	0.2022	0.01498	0.8917	0.4901	-0.4316	0.0139	0.0375
265412_at	AT2G16640	ATG12/ATC12 (AUTOPHAGY 12); CHIMERIC TRANSLOCON	0.3851	0.0744	0.1688	0.3531	0.3197	-0.151	0.4	0.3166	-0.3676	0.0838	0.108	
265413_s_at	AT5G60430,AT2G16650	[AT5G60430, antiporter/ drug transporter];[AT2G16	0.6934	0.0171	0.0783	0.3655	0.1069	0.1649	-0.8703	0.0028	0.0244	-1.1982	8.00E-04	0.0113
265414_at	AT2G16660	nodulin family protein	0.3744	0.4609	0.4035	0.08474	0.8627	0.5078	-0.3697	0.157	0.1837	-0.6594	0.0362	0.0647
265415_at	AT2G20880	PSS2/3 (PHYLLOID FORMATION1)	0.5993	0.0061	0.0539	-0.8347	0.0018	0.0323	0.3689	0.0142	0.0475	0.1314	0.2109	0.1913
265416_at	AT2G37120	DNA-binding S1FA family protein	-0.09215	0.3061	0.3262	0.1633	0.1063	0.1645	0.3529	0.0109	0.0414	0.6084	0.0015	0.0138
265417_at	AT2G20920	similar to unnamed protein product [Vitis vinifera] (G	-0.03832	0.787	0.5198	-0.3866	0.0434	0.1034	0.4148	0.0013	0.0192	0.06651	0.2685	0.222
265418_at	AT2G20880	AP2 domain-containing transcription factor, putative	0.09694	0.914	0.5551	0.06607	0.9407	0.5293	0.3557	0.1854	0.2024	0.5177	0.0807	0.1056
265419_at	AT2G20840	secretory carrier membrane protein (SCAMP) family	-0.3696	0.06	0.14	-0.7568	0.006	0.0446	0.1161	0.2527	0.2423	-0.271	0.0356	0.064
265420_s_at	AT1G31880,AT2G21030	[AT1G31880, BRX-NIP3;1/NLM9 (BREVIS RADIX);	0.1182	0.8959	0.5502	0.8751	0.3604	0.3229	0.5413	0.558	0.3819	1.2981	0.2005	0.1854
265421_s_at	AT4G26815,AT2G20616	[AT4G26815, similar to unknown protein [Arabidops	0.6449	0.5717	0.4495	-2.779	0.0569	0.1187	-0.2633	0.8142	0.4679	-3.687	0.2045	0.0515
265422_at	AT2G20800	NDB4 (NAD(P)H DEHYDROGENASE B4); NADH c	-0.02178	0.9814	0.5724	1.7343	0.1191	0.1745	-1.4563	0.0278	0.0679	0.2998	0.525	0.3359
265423_at	AT2G20790	protein binding / protein transporter	0.5015	0.0174	0.079	0.2755	0.0982	0.1579	-0.1164	0.3099	0.2734	-0.3425	0.0268	0.0544
265424_at	AT2G20780	mannitol transporter, putative	-0.7645	0.1339	0.2124	0.7097	0.1565	0.2032	-0.9501	0.0506	0.0954	-1.0049	0.0431	0.0725
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265490_s_at	AT2G15450:AT2G15470:A	[AT2G15450, glycoside hydrolase family 28 protein	0.3046	0.8618	0.5416	1.2211	0.4982	0.3838	-0.6408	0.7162	0.4369	0.2757	0.8748	0.4498
265491_s_at	AT2G15650:AT1G50810	[AT2G15650, transposable element gene];[AT1G5	-2.4001	0.0892	0.1731	-2.5065	0.08	0.1419	0.1888	0.8691	0.484	0.08233	0.9426	0.4691
265492_at	AT2G15660	AGL95; transcription factor	-1.7198	0.1856	0.2525	0.8771	0.4613	0.3685	-0.6228	0.5942	0.3961	1.9741	0.1408	0.1487
265493_at	AT2G15670	similar to SEC14 cytosolic factor family protein / pho	-0.1063	0.9057	0.5527	-0.1416	0.8746	0.5115	-0.249	0.7822	0.4581	-0.2844	0.7526	0.4145
265494_at	AT2G15680	calmodulin-related protein, putative	-1.0426	0.0042	0.0471	-0.3234	0.1429	0.193	0.3953	0.0902	0.1328	1.1145	0.0033	0.0187
265495_at	AT2G15695	similar to unknown protein [Arabidopsis thaliana] (T	-0.3878	0.1151	0.1963	-0.4172	0.0969	0.1569	-0.3842	0.094	0.1359	-0.4136	0.0781	0.1034
265496_at	AT2G15700	transposable element gene	1.1495	0.4392	0.3932	-0.9755	0.5068	0.3873	2.1045	0.1912	0.2063	-0.02052	0.9885	0.4798
265497_at	AT2G15720	transposable element gene	-0.3018	0.5999	0.4597	2.1784	0.0148	0.0641	-0.1977	0.7283	0.4413	2.2824	0.0126	0.0355
265498_at	AT2G15740	zinc finger (C2H2 type) family protein	-0.7628	0.4996	0.4203	-0.07362	0.9464	0.531	-1.3922	0.2474	0.2396	-0.703	0.5319	0.3387
265499_at	AT2G15480	UGT73B5 (UDP-GLUCOSYL TRANSFERASE 73B	0.8709	0.0893	0.1732	1.008	0.061	0.1227	-0.4555	0.3078	0.2724	-0.3183	0.4603	0.3101
265500_at	AT2G15750	transposable element gene	-0.4838	0.6778	0.4852	-1.087	0.3717	0.3282	-0.3795	0.737	0.4439	-0.9827	0.4039	0.2857
265501_at	AT2G15490	UGT73B4; UDP-glycosyltransferase/ transferase, tr	-1.5412	0.1485	0.2242	-0.6913	0.4678	0.3712	-1.0673	0.2837	0.26	-0.2173	0.8135	0.4326
265502_at	AT2G15500	similar to PAB2 (POLY(A) BINDING PROTEIN 2), F	1.333	0.1048	0.1869	-0.1166	0.8638	0.5081	-0.153	0.8222	0.4703	-1.6026	0.0658	0.0934
265503_at	AT2G15510	transposable element gene	0.1454	0.7805	0.518	-1.0545	0.0967	0.1566	0.9874	0.0927	0.1349	-0.2124	0.6608	0.3844
265504_at	AT2G15520	transposable element gene	0.3476	0.646	0.475	-1.1216	0.1848	0.2231	0.4194	0.5818	0.3914	-1.0497	0.2086	0.19
265505_at	AT2G15530	zinc finger (C3HC4-type RING finger) family protein	-0.2453	0.1079	0.1901	-0.239	0.1146	0.1708	0.2461	0.0434	0.087	0.2524	0.0403	0.0694
265506_at	AT2G15540	transposable element gene	-0.3355	0.7379	0.5092	0.1937	0.8461	0.5033	0.6885	0.5143	0.3647	1.1977	0.2696	0.2225
265507_s_at	AT2G15940:AT1G42110	[AT2G15940, transposable element gene];[AT1G42	2.0868	0.1271	0.206	0.8221	0.4913	0.3809	1.1625	0.3448	0.2907	-0.1022	0.9296	0.4655
265508_at	AT2G15930	unknown protein	-0.03905	0.9574	0.5665	0.7464	0.3382	0.3128	-1.9447	0.0354	0.0771	-1.1592	0.1361	0.1457
265509_at	AT2G15920	transposable element gene	-0.3246	0.7891	0.5203	-0.872	0.4852	0.3782	0.5599	0.5732	0.3878	0.01249	0.9898	0.4801
265510_at	AT2G15630	ATG8D (autophagy gene 8-related); microtubule bir	0.9546	0.0364	0.1099	1.2981	0.0136	0.0618	0.5816	0.037	0.0794	0.925	0.0081	0.028
265511_at	AT2G15540	glycine-rich protein	-0.1224	0.9451	0.5924	-0.9064	0.4117	0.3687	0.1614	0.5939	0.3961	0.5374	0.1263	0.1391
265512_at	AT2G15590	similar to unknown protein [Arabidopsis thaliana] (T	-0.01247	0.9497	0.5646	0.182	0.3827	0.3331	-0.8126	0.0065	0.0331	-0.6182	0.0167	0.0413
265513_at	AT2G16140	transposable element gene	-0.2567	0.8303	0.5325	1.8922	0.167	0.2105	-2.3748	0.0603	0.1055	-0.226	0.8171	0.4335
265514_s_at	AT2G15602:AT2G06130:A	[AT3G15602, transposable element gene];[AT2G06	0.8709	0.5249	0.4311	0.7372	0.4872	0.3791	-0.228	0.8262	0.4716	1.1821	0.2876	0.2321
265515_at	AT2G06120	transposable element gene	-0.3037	0.7758	0.5167	-1.5896	0.1859	0.2236	-0.8722	0.4309	0.33	-2.1581	0.0963	0.1177
265516_at	AT2G06110	transposable element gene	-0.8885	0.303	0.3248	-0.8627	0.3153	0.3004	0.1967	0.8066	0.4656	0.2224	0.7822	0.4235
265517_at	AT2G06090	self-incompatibility protein-related	-0.4892	0.6522	0.4768	-0.7604	0.4919	0.3811	2.0898	0.1064	0.146	1.8185	0.145	0.1516
265518_at	AT2G06040	similar to unknown protein [Arabidopsis thaliana] (T	2.3946	0.0208	0.085	1.0678	0.1744	0.2156	-1.1326	0.1551	0.1823	-2.4594	0.0191	0.0443
265519_at	AT2G06040	similar to unknown protein [Arabidopsis thaliana] (T	0.2973	0.2979	0.3221	0.0303	0.9089	0.5212	-0.6168	0.0069	0.0339	-0.8838	0.0019	0.0149
265520_at	AT2G06050	myb family transcription factor	-0.3698	0.7797	0.5178	-0.8914	0.4997	0.3844	-0.02683	0.9833	0.5135	-0.5585	0.6665	0.3863
265521_at	AT2G06010	ORG4 (OBP3-RESPONSIVE GENE 4)	-0.1572	0.2218	0.2762	0.3504	0.0323	0.0889	-1.1022	5.00E-04	0.0155	-0.5947	0.0054	0.0231
265522_at	AT2G06210	ELF8 (EARLY FLOWERING 8); binding	0.1625	0.4865	0.4142	0.3566	0.169	0.2119	-0.4593	0.0296	0.07	-0.2662	0.1274	0.1399
265523_at	AT2G06190	transposable element gene	1.003	0.0684	0.1504	-0.1112	0.7971	0.4887	-0.2412	0.165	0.1885	-1.3554	7.00E-04	0.0105
265524_at	AT2G06180	transposable element gene	-1.5258	0.0391	0.1141	-0.1226	0.8202	0.496	-0.9226	0.1417	0.1727	0.4807	0.3951	0.2823
265525_at	AT2G06170	transposable element gene	0.4721	0.6925	0.4901	-0.9957	0.4205	0.3509	-0.4466	0.7079	0.4339	-1.9143	0.1595	0.1609
265526_s_at	AT2G06160	transposable element gene	0.2754	0.744	0.5071	3.9312	0.0075	0.0487	-0.675	0.4343	0.3316	2.9828	0.0183	0.0435
265527_at	AT2G06150	transposable element gene	1.1202	0.3411	0.3458	-0.4252	0.703	0.4601	-0.07295	0.9473	0.505	-1.6183	0.1939	0.1813
265528_at	AT2G06220	transposable element gene	-2.3038	0.0348	0.1077	-1.3007	0.1507	0.1988	0.5607	0.391	0.3125	1.5638	0.0552	0.0842
265529_at	AT2G06230	transposable element gene	-0.6742	0.5043	0.4223	-0.9694	0.3515	0.3188	1.5498	0.1674	0.1901	1.2543	0.2445	0.2095
265530_at	AT2G06050	OPR3 (OPDA-REDUCTASE 3); 12-oxophytodienoc	-1.0542	0.1787	0.2472	0.9488	0.2166	0.2438	-0.1235	0.4503	0.3386	-0.01815	0.9082	0.4594
265531_at	AT2G06200	AtGRF6 (GROWTH-REGULATING FACTOR 6)	-0.6681	0.3841	0.3667	0.1176	0.8719	0.5105	0.7978	0.3084	0.2727	1.5835	0.0816	0.1063
265532_at	AT2G11370	transposable element gene	-1.2069	0.2774	0.3101	-1.1591	0.2941	0.2887	-1.1458	0.1278	0.1624	-1.098	0.1402	0.1483
265533_at	AT2G11360	transposable element gene	2.699	0.0458	0.1232	-0.1875	0.8521	0.5051	1.3279	0.2318	0.2304	-1.5586	0.1737	0.1695
265534_at	AT2G11390	transposable element gene	-0.3334	0.6085	0.4627	-0.2864	0.6584	0.4445	0.6763	0.3232	0.2798	0.7232	0.295	0.2361
265535_at	AT2G15690	phox (PX) domain-containing protein	0.1749	0.292	0.3185	0.246	0.1633	0.2082	-0.7732	0.0015	0.0198	-0.7021	0.0021	0.0155
265536_at	AT2G15880	leucine-rich repeat family protein / extensin family p	-0.3638	0.8345	0.5339	-0.1201	0.9449	0.5306	-1.7929	0.1955	0.209	-1.5491	0.2509	0.2131
265537_at	AT2G15870	transposable element gene	0.5293	0.5965	0.4585	-0.151	0.8778	0.5124	-0.627	0.3402	0.2885	-1.3072	0.0871	0.1105
265538_at	AT2G15860	similar to unnamed protein product [Vitis vinifera] (G	0.8067	0.0023	0.0418	0.4417	0.0197	0.072	0.3815	0.0314	0.072	0.01599	0.8982	0.4566
265539_at	AT2G15830	similar to unknown protein [Arabidopsis thaliana] (T	-0.4675	0.4735	0.4094	-0.5314	0.4197	0.3505	-0.3465	0.5819	0.3914	-0.4104	0.5177	0.3327
265540_at	AT2G15810	transposable element gene	-0.2593	0.7877	0.52	-1.3454	0.2096	0.2393	0.2312	0.782	0.458	-0.8549	0.3353	0.2557
265541_at	AT2G15800	transposable element gene	-0.8331	0.5499	0.4394	-2.9555	0.0795	0.1414	0.3973	0.7551	0.4497	-1.7252	0.2205	0.1963
265542_at	AT2G28290	SYD (SPLAYED)	0.2736	0.1725	0.243	0.3953	0.0746	0.137	-0.8648	5.00E-04	0.0148	-0.7431	8.00E-04	0.0112
265543_at	AT2G28270	DC1 domain-containing protein	0.7955	0.4079	0.3792	1.7644	0.1098	0.1672	-0.5476	0.5594	0.3824	0.4213	0.6502	0.3809
265544_at	AT2G28260	ATCNGC15 (cyclic nucleotide gated channel 15); c	-0.7917	0.0289	0.0985	-0.7425	0.0352	0.0926	-0.328	0.2389	0.2346	-0.2787	0.305	0.241
265545_at	AT2G28250	protein kinase family protein. Binds AtRop4.	0.4305	0.5791	0.4521	1.1288	0.1891	0.2258	0.3419	0.6571	0.4169	1.0402	0.219	0.1956
265546_at	AT2G28240	hydroxyproline-rich glycoprotein family protein	0.03954	0.8712	0.5443	-0.2459	0.343	0.3148	0.3117	0.2142	0.2204	0.02626	0.9071	0.4591
265547_at	AT2G28305	similar to unknown protein [Arabidopsis thaliana] (T	-0.7177	0.0053	0.0519	-0.6674	0.0069	0.047	0.5187	0.0102	0.0401	0.569	0.0074	0.0267
265548_s_at	AT3G31980:AT2G07620	[AT3G31980, transposable element gene];[AT2G07	-1.9228	0.1677	0.2396	1.8156	0.1872	0.2246	-1.1846	0.3584	0.2971	2.5537	0.0891	0.112
265549_at	AT2G07520	transposable element gene	1.3682	0.4195	0.3847	-2.0854	0.2425	0.2595	1.8851	0.2612	0.2472	-1.5685	0.3379	0.2569
265550_at	AT2G07510	transposable element gene	-0.129	0.8739	0.5451	-0.07769	0.9238	0.5251	-0.9382	0.0704	0.1153	-0.8869	0.0815	0.1062
265551_at	AT2G07630	transposable element gene	-0.09253	0.8478	0.5378	-1.0095	0.0893	0.1506	1.1956	0.0573	0.1024	0.2786	0.5712	0.353
265552_at	AT2G07560	AHA6 (ARABIDOPSIS H(+)-ATPASE 6); ATPase	-0.3883	0.7023	0.4934	-1.0818	0.3163	0.3009	-0.9868	0.3555	0.2959	-1.6803	0.1501	0.1547
265553_at	AT2G07550	transposable element gene	-0.6802	0.4272	0.3881	-0.9258	0.2958	0.2896	0.6539	0.4439	0.3358	0.4083	0.6243	0.3717
265554_at	AT2G07505	similar to unknown protein [Arabidopsis thaliana] (T	2.3495	0.0805	0.1637	-0.3331	0.758	0.4774	1.2744	0.2753	0.2554	-1.4081	0.2355	0.2047
265555_at	AT2G07500	transposable element gene	1.0494	0.2145	0.2712	0.7614	0.3452	0.3157	-0.7332	0.2253	0.2267	-1.0212	0.1168	0.1325
265556_at	AT2G07490	transposable element gene	-0.8753	0.4636	0.4046	0.2687	0.816	0.4949	-1.5396	0.2276	0.2281	-0.3956	0.733	0.408
265557_at	AT2G05640	transposable element gene	1.1378	6.00E-04	0.0325	-0.1087	0.3936	0.3385	0.1501	0.1561	0.183	-1.0964	2.00E-04	0.0078
265558_at	AT2G05550	transposable element gene	-1.6404	0.1687	0.2404	1.3518	0.239	0.2571	-2.8492	0.0221	0.06	0.143	0.8642	0.4468
265559_at	AT2G05530	glycine-rich protein	-0.9203	0.2638	0.3018	-0.6059	0.4407	0.3597	0.000782	0.9992	0.5177	0.3152	0.6795	0.3903
265560_at	AT2G05520	GRP-3 (GLYCINE-RICH PROTEIN 3)	0.1507	0.5545	0.4426	0.1812	0.4818	0.377	0.3976	0.1644	0.1881	0.4281	0.1412	0.1489
265561_s_at	AT2G05440:AT2G05510	[AT2G05440, glycine-rich protein];[AT2G05510, gly	1.4319	0.1104	0.1926	1.2576	0.1471	0.1961	0.8694	0.1498	0.1788	0.6951	0.228	0.2005
265562_at	AT2G05500	unknown protein	1.1558	0.2958	0.3208	-1.3711	0.2271	0.2498	-0.1348	0.8953	0.4912	-2.6617	0.0505	0.0798
265563_s_at	AT2G12120:AT5G28482:A	[AT2G12120, transposable element gene];[AT5G28	0.5805	0.596	0.4583	1.3329	0.257	0.2683	0.7646	0.3987	0.316	1.5171	0.1344	0.1447
265564_s_at	AT2G16170:AT5G28480:A	[AT2G16170, transposable element gene];[AT5G28	-0.07363	0.9106	0.5542	-0.4213	0.5314	0.3967	0.4604	0.1143	0.1519	0.1127	0.6478	0.38
265565_at	AT2G05610	transposable element gene	0.1231	0.8858	0.5474	-0.2307	0.7884	0.4857	-0.6103	0.4901	0.3556	-0.9641	0.2967	0.2369
265566_at	AT2G05600	similar to F-box family protein [Arabidopsis thaliana	-0.7179	0.4417	0.3945	-0.4742	0.6033	0.4247	-0.2058	0.8188	0.4695	0.03797	0.9662	0.4748
265567_at	AT2G05580	pseudogene, glycine-rich protein	-0.0058	0.9933	0.5753	0.06938	0.9205	0.5241	0.05514	0.9367	0.5026	0.1303	0.8515	0.4431
265568_s_at	AT1G34720:AT2G28000:A	[AT1G34720, transposable element gene];[AT1G27	0.2894	0.2416	0.2886	0.1882	0.9075	0.5208	-2.0952	0.2405	0.2355	0.1824	0.9104	0.46
265569_at	AT2G05620	PGR5 (PROTON GRADIENT REGULATION 5)	-0.6691	0.0094	0.0624	-0.5901	0.0145	0.0635	0.04852	0.7511	0.4485	0.1276	0.4221	0.2934
265570_at	AT2G28310	similar to unknown protein [Arabidopsis thaliana] (T	-0.1511	0.6161	0.4649	-0.1446	0.631	0.4349	-0.5045	0.1442	0.1747	-0.498	0.1482	0.1535
265571_s_at	AT2G28020:AT2G28230	[AT2G28020, similar to unknown protein [Arabidops	0.1444	0.5517	0.4419	0.3034	0.2444	0.2607	0.6084	0.0522	0.0969	0.7674	0.0261	0.0535
265572_at	no_match	no_match	-1.223	0.0089	0.0611	-1.4919	0.0044	0.0409	-0.06489	0.7923	0.4608	-0.3339	0.221	0.1965
265573_at	AT2G28200	nucleic acid binding / transcription factor/ zinc ion bi	-0.9128	0.0785	0.1615	-1.253	0.0321	0.0888	0.3082	0.2994	0.2684	-0.03202	0.9075	0.4592
265574_at	no_match	no_match	-0.2214	0.8361	0.5342	-0.5665	0.6024	0.4246	-0.5968	0.5839	0.3921	-0.9419	0.4009	0.2846
265575_at	AT2G14260	PIP (proline iminopeptidase); prolyl aminopeptidase	0.2178	0.1376	0.2155	0.1507	0.269	0.2749	-0.1853	0.1675	0.1901	-0.2523	0.0836	0.1078
265576_at	AT2G20190	ATCLASP/CLASP; binding	0.00831	0.9668	0.5689	-0.2386	0.2721	0.2766	-0.2915	0.1949	0.2087	-0.5385	0.0454	0.0747
265577_at	AT2G20100	ethylene-responsive family protein	-0.305	0.3651	0.3569	-0.01061	0.9734	0.5374	0.6824	0.0844	0.1279	0.9767	0.0308	0.0591
265578_at	AT2G20100	ethylene-responsive family protein	-0.4341	0.3744	0.3617	-0.1486	0.7496	0.4748	-0.1384	0.7661	0.453	0.1471	0.7521	0.4144
265579_at	AT2G20070	similar to LCR81 (Low-molecular-weight cysteine-ri	-2.0198	0.1551	0.2299	-1.0701	0.4065	0.3443	-0.5179	0.5458	0.3778	0.4319	0.6118	0.3674
265580_at	no_match	no_match	0.1416	0.685	0.4876	-0.4094	0.2753	0.2783	-1.4185	0.0065	0.0331	-1.9695	0.0019	0.0151
265581_at	AT2G20050	protein serine/threonine phosphatase	-0.04174	0.8231	0.5306	-0.2911	0.1713	0.2137	-0.3322	0.1303	0.1641	-0.5816	0.0292	0.0572
265582_at	AT2G20030	zinc finger (C3HC4-type RING finger) family protein	-0.5896	0.4865	0.4142	0.0299	0.9709	0.5369	0.1597	0.8455	0.4772	0.7791	0.3679	0.2704
265583_at	AT2G20010	similar to unknown protein [Arabidopsis thaliana] (T	0.3189	0.0393	0.1144	0.2719	0.0618	0.1236	-0.3589	0.0161	0.0506	-0.406	0.0106	0.0322
265584_at	AT2G20180	PIL5 (PHYTOCHROME INTERACTING FACTOR 3	-0.09122	0.6097	0.4629	0.01411	0.936	0.5281	-0.2901	0.0462	0.0901	-0.1848	0.1431	0.1502
265585_at	AT2G20000	HBT (HOBBIT); binding	-0.2661	0.2442	0.2902	-0.4824	0.0687	0.1315	-0.6966	0.0234	0.0618	-0.9129	0.0095	0.0303
265586_at	AT2G19990	PR-1-LIKE (PATHOGENESIS-RELATED PROTEIN	1.0022	0.2315	0.283	1.5986	0.0878	0.1492	0.6891	0.3874	0.311	1.2855	0.1449	0.1515
265587_at	AT2G19980	allergen V5/Tpx-1-related family protein	-0.00402	0.9963	0.5761	-1.9159	0.0806	0.1424	0.6477	0.4756	0.3498	-1.2642	0.1996	0.1848
265588_at	AT2G19970	pathogenesis-related protein, putative	-0.06027	0.8991	0.5508	1.7504	0.0172	0.068	-0.1911	0.6905	0.428	1.6195	0.0222	0.0485
265589_at	AT2G20170	similar to unknown protein [Arabidopsis thaliana] (T	0.09143	0.9355	0.5611	0.8785	0.4545	0.3659	-1.3527	0.2717	0.2532	-0.5656	0.6225	0.3711
265590_at	AT2G20160	MEO (MEIDOS); ubiquitin-protein ligase	-1.6269	0.1296	0.2082	0.3565	0.6979	0.4582	-2.0791	0.0717	0.1164	-0.09578	0.9161	0.4617
265591_at	AT2G20150	unknown protein	0.9371	0.242	0.2887	1.1079	0.1801	0.2196	0.5749	0.2169	0.2218	0.7457	0.1303	0.1417
265592_at	AT2G20110	tesmin/TSO1-like CXC domain-containing protein	0.2023	0.6438	0.4744	0.1428	0.7423	0.4721	-0.1801	0.5389	0.3749	-0.2396	0.4224	0.2935
265593_s_at	AT2G20130:AT2G20120	[AT2G20130, LCV1 (LIKE COV 1)];[AT2G20120, C	0.1829	0.343	0.3463	0.1868	0.334	0.3103	-0.1423	0.45	0.3386	-0.1384	0.4616	0.3107
265594_at	AT2G20060	ribosomal protein L4 family protein	0.1894	0.0557	0.1355	0.1282	0.1448	0.1943	0.173	0.0711	0.116	0.1118	0.19	0.1792
265595_at	AT2G20140	26S protease regulatory complex subunit 4, putative	0.4835	0.0256	0.0927	0.3047	0.094	0.1545	0.2115	0.2014	0.2125	0.03267	0.825	0.4357
265596_at	AT2G20020	identical to CRS2-associated factor 1, chloroplast p	0.059	0.6973	0.4918	-0.2131	0.2054	0.2363	-0.4803	0.0184	0.0543	-0.7524	0.0038	0.02
265597_at	AT2G20142	transmembrane receptor	1.6551	0.0108	0.0655	1.1115	0.0392	0.0981	-0.0403	0.8999	0.4897	-0.5839	0.0995	0.1202
265598_at	AT2G14270	pseudogene, protein phosphatase 2C, blastp match	-1.9436	0.201	0.2628	-0.4581	0.7368	0.4703	-0.93	0.505	0.3613	0.5554	0.6847	0.3922
265599_at	no_match	no_match	-1.1769	0.153	0.2281	-0.5741	0.4387	0.359	-4.384	0.0028	0.0242	-3.7813	0.0048	0.0219
265600_at	AT2G14230	transposable element gene	0.06895	0.919	0.5567	-0.8146	0.27	0.2754	1.4402	0.0745	0.1188	0.5567	0.4063	0.2867
265601_at	AT2G14390	unknown protein	-1.1679	0.4341	0.3911	-1.3331	0.3776	0.3308	0.8188	0.5755	0.3886	0.6536	0.6524	0.3816
265602_at	AT2G14380	transposable element gene	0.7388	0.3751	0.3619	0.03825	0.9613	0.5343	0.9458	0.1938	0.2078	0.2452	0.7066	0.3996
265603_at	no_match	no_match	-1.814	0.0702	0.1527	1.0918	0.2138	0.2418	-1.3597	0.0875	0.1306	1.5462	0.0626	0.0908
265604_s_at	AT3G35707:AT3G33225:A	AT3G35707, transposable element gene];[AT3G33	-0.1221	0.6766	0.4848	-0.04432	0.8785	0.5127	0.5087	0.1146	0.1521	0.5865	0.0812	0.106
265605_at	AT2G25540	CESA10 (CELLULOSE SYNTHASE 10); transferase	0.4399	0.2342	0.2839	-1.1124	0.024	0.078	1.3629	0.0123	0.0441	-0.1894	0.5793	0.3558
265606_s_at	AT2G19910:AT2G31520:A	[AT3G09510, nucleic acid binding];[AT2G31520, tra	-0.53	0.675	0.4844	-1.3285	0.3209	0.3036	-0.3466	0.7826	0.4582	-1.1449	0.3845	0.2778
265607_at	AT2G25370	zinc finger protein-related	0.4	0.4494	0.3978	-0.07313	0.8857	0.5147	-0.475	0.3762	0.3058	-0.9482	0.1181	0.1334
265608_at	AT2G25380	pseudogene of zinc finger protein-related	0.4643	0.4383	0.3929	-0.6249	0.3115	0.2982	0.7788	0.1016	0.1424	-0.3104	0.4462	0.3045
265609_at	AT2G25420	similar to TPR4/WSP2 (TOPLESS-RELATED 4) [A	0.8012	0.2184	0.274	-0.1428	0.8076	0.4922	0.09953	0.865	0.4827	-1.0435	0.1302	0.1417
265610_at	AT2G25430	epsin N-terminal homology (ENTH) domain-contain	-0.03123	0.8787	0.5462	-0.2078	0.3402	0.3136	-0.1493	0.1769	0.1965	-0.3259	0.0233	0.0498
265611_at	AT2G25510	unknown protein	-0.09915	0.5696	0.4488	-0.2892	0.1453	0.1948	0.17	0.0788	0.1227	-0.02003	0.7959	0.4276
265612_at	no_match	no_match	0.2644	0.8315	0.5329	-0.5424	0.6656	0.4469	1.0505	0.418	0.3244	0.2437	0.8445	0.4412
265613_at	AT2G25560	DNAJ heat shock N-terminal domain-containing pro	0.375	0.122	0.2022	0.3674	0.1277	0.1813	-0.1242	0.5523	0.3799	-0.1318	0.5295	0.3378
265614_at	AT2G25355	exonuclease-related	0.5595	0.0171	0.0783	0.4363	0.0377	0.0961	0.5089	0.0232	0.0617	0.3848	0.0539	0.083
265615_at	AT2G25450	2-oxoglutarate-dependent dioxygenase, putative	-0.2805	0.5377	0.4359	-0.3243	0.4799	0.3761	0.2448	0.1852	0.2022	0.201	0.2596	0.2176
265616_at	AT2G25500	similar to Maf family protein [Arabidopsis thaliana] (	-1.738	0.1564	0.2306	-0.8679	0.4333	0.3569	-1.1597	0.1317	0.1651	-0.2896	0.6615	0.3847
265617_at	AT2G25520	phosphate translocator-related	0.6994	0.0262	0.0935	0.7179	0.0241	0.0781	-0.8079	0.0108	0.0413	-0.7894	0.0117	0.0339
265618_at	AT2G25460	similar to unknown protein [Arabidopsis thaliana] (T	0.2723	0.7486	0.5084	-0.8532	0.3425	0.3145	0.3219	0.7055	0.4332	-0.8036	0.3682	0.2705
265619_at	AT2G27320	similar to unknown protein [Arabidopsis thaliana] (T	-0.3287	0.4255	0.3874	0.7085	0.1286	0.1819	-0.3508	0.3977	0.3155	0.6864	0.1378	0.1468
265620_at	AT2G27310	F-box family protein	-0.3974	0.2691	0.3049	0.02381	0.9425	0.5299	-0.1792	0.5942	0.3961	0.242	0.4787	0.317
265621_at	AT2G27300	ANAC029/NTL8 (ARABIDOPSIS NAC DOMAIN CO	0.61	0.5312	0.4334	1.3712	0.1986	0.232	0.1856	0.7635	0.4523	0.9468	0.1757	0.1706
265622_at	AT2G27280	similar to unknown protein [Arabidopsis thaliana] (T	-0.07938	0.9559	0.5663	0.5531	0.7025	0.46	0.1082	0.9172	0.497	0.7407	0.4908	0.3222
265623_at	AT2G27270	similar to hairpin-responsive protein, putative (HIN1	0.794	0.2362	0.2852	-0.09141	0.8804	0.5133	-0.2648	0.6665	0.42	-1.1502	0.1139	0.1304
265624_at	AT2G27250	CLV3 (CLAVATA3); kinase activator/ receptor/ bindi	-1.6941	0.2151	0.2716	-0.5594	0.6525	0.4426	0.5371	0.6651	0.4196	1.6717	0.2201	0.1961
265625_at	AT2G27240	similar to unknown protein [Arabidopsis thaliana] (T	-0.2131	0.854	0.5392	-0.7044	0.5519	0.4056	-0.4468	0.7018	0.4319	-0.9381	0.4364	0.2998
265626_at	AT2G27260	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.2279	0.

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265690_at	AT2G24320	similar to unknown protein [Arabidopsis thaliana] (T	0.9543	0.1953	0.2594	-0.4668	0.4897	0.3802	-0.5502	0.4096	0.3206	-1.9712	0.03	0.0582
265691_at	AT2G24330	Identical to Uncharacterized protein At2g24330 [Ara	-0.2217	0.4071	0.379	-0.2147	0.4208	0.351	0.1497	0.1111	0.1492	0.1567	0.0997	0.1204
265692_at	AT2G24340	transcription factor	-0.5447	0.5554	0.443	-0.7096	0.4495	0.3637	0.6657	0.2945	0.2658	0.5008	0.4159	0.2908
265693_at	no_match	no_match	0.7847	0.4443	0.3953	1.1719	0.2742	0.2776	-1.1611	0.278	0.2569	-0.7739	0.4501	0.306
265694_at	AT2G24440	selenium binding	-0.7558	0.0343	0.1071	0.2118	0.4265	0.3536	-0.00925	0.971	0.5102	0.9583	0.0161	0.0405
265695_at	AT2G24490	ATRPA2/ROR1/RPA2 (REPLICON PROTEIN A); p	-0.1842	0.4439	0.3952	0.04297	0.8528	0.5054	0.1868	0.438	0.3331	0.4141	0.1292	0.1409
265696_at	no_match	no_match	-0.4482	0.6259	0.4684	0.4436	0.6294	0.4343	-0.6279	0.3474	0.2919	0.2639	0.6779	0.3899
265697_at	AT2G32170	similar to unknown protein [Arabidopsis thaliana] (T	-0.03877	0.7186	0.4989	-0.02047	0.8482	0.5039	-0.2462	0.0699	0.1147	-0.2279	0.0853	0.1092
265698_at	AT2G32160	similar to unknown protein [Arabidopsis thaliana] (T	0.6066	0.143	0.22	0.3282	0.3808	0.3323	-0.3009	0.0057	0.0314	-0.5793	5.00E-04	0.0094
265699_at	AT2G32550	hydrolase	-0.4603	0.028	0.097	-0.1934	0.2297	0.2512	-0.6577	0.0051	0.03	-0.3908	0.0297	0.0578
265700_at	AT2G33470	myb family transcription factor / ELM2 domain-conta	0.7526	0.0051	0.0511	0.953	0.0021	0.0333	0.5011	0.0208	0.058	-0.3006	0.0904	0.1132
265701_at	AT2G33460	similar to kelch repeat-containing F-box family prote	-0.09965	0.9265	0.5587	-1.1895	0.3061	0.2951	0.162	0.8809	0.487	-0.9278	0.4122	0.2892
265702_at	AT2G33450	ATPAP9/PAP9 (purple acid phosphatase 9); acid pl	0.4597	0.0274	0.0958	0.5958	0.0117	0.0581	0.0381	0.7923	0.4608	0.1742	0.2675	0.2214
265703_at	AT2G33430	ankyrin repeat family protein	0.5479	0.0254	0.0923	0.9163	0.0043	0.0408	0.1622	0.245	0.238	0.5307	0.0112	0.0332
265704_at	AT2G33420	similar to expressed protein [Oryza sativa (japonica	-0.1556	0.2504	0.2937	-0.2994	0.0611	0.1227	0.6671	0.0041	0.0276	0.5234	0.0097	0.0308
265705_at	AT2G33410	Mo25 family protein	0.9613	0.2617	0.3006	2.4199	0.0303	0.0864	-1.2827	0.1511	0.1796	0.1759	0.82	0.4342
265706_at	AT2G33390	uvrB/uvrC motif-containing protein	-0.2837	0.1193	0.1997	-0.3238	0.0949	0.1552	-0.7806	0.0063	0.0328	-0.8107	0.0055	0.0231
265707_at	AT2G33390	uvrB/uvrC motif-containing protein	-0.05546	0.6454	0.4748	-0.05453	0.6508	0.442	-0.1121	0.1676	0.1901	-0.1112	0.1704	0.1675
265708_at	AT2G33380	pentatricopeptide (PPR) repeat-containing protein	-0.5833	0.1889	0.2547	-0.6307	0.1624	0.2077	-0.5715	0.1962	0.2094	-0.6189	0.1686	0.1664
265709_at	AT2G33540	transposable element gene	0.1161	0.9272	0.559	1.3251	0.329	0.3081	-2.181	0.1416	0.1726	-0.9719	0.4611	0.3105
265710_at	AT2G33370	serine carboxypeptidase	-2.231	0.0978	0.1805	-1.5334	0.2132	0.2415	-0.0555	0.9599	0.5076	0.6421	0.5692	0.3523
265711_at	AT2G33360	similar to serine carboxypeptidase [Arabidopsis that	0.9677	0.3754	0.3621	0.7274	0.4954	0.3827	1.0158	0.3245	0.2806	0.7755	0.4398	0.3013
265712_s_at	AT3G11810,AT2G03330	[AT3G11810, similar to unknown protein [Arabidops	0.5078	0.0905	0.1742	0.129	0.6028	0.4246	-0.1324	0.514	0.3646	-0.5112	0.0508	0.0801
265713_at	AT2G33530	UPS2 (UREIDE PERMEASE 2)	0.3892	0.3993	0.375	0.3267	0.4731	0.3734	-0.4997	0.1121	0.15	-0.5622	0.0843	0.1084
265714_at	AT2G33520	ATUPS4 (ARABIDOPSIS THALIANA UREIDE PER	-0.7873	0.5417	0.4375	-1.0161	0.4383	0.3589	1.1632	0.1696	0.1916	0.9343	0.2502	0.2126
265715_s_at	AT1G13860,AT2G03480	[AT1G13860, dehydration-responsive protein-relate	-0.1929	0.1836	0.2508	-0.1321	0.3331	0.3098	0.06587	0.6126	0.402	0.1267	0.3512	0.2632
265716_at	AT2G33350	similar to unknown protein [Arabidopsis thaliana] (T	-0.3172	0.0938	0.1772	-0.5527	0.0189	0.0708	0.01938	0.9	0.4924	-0.2161	0.21	0.1909
265717_at	AT2G33510	band 7 family protein	0.8773	0.0087	0.0606	0.8517	0.0097	0.0537	0.6364	0.0071	0.0341	0.6109	0.0082	0.0282
265718_at	AT2G33340	WRKY3 (WRKY DNA-binding protein 3); transcriptio	0.525	0.1593	0.2329	0.6739	0.091	0.1522	0.3598	0.1328	0.1658	0.5087	0.0562	0.0851
265719_at	AT2G33500	myb family transcription factor	-0.04941	0.863	0.5418	-0.6048	0.0875	0.1489	0.204	0.4899	0.3555	-0.3514	0.2609	0.2183
265720_at	AT2G40110	yippee family protein	0.5194	0.0771	0.1598	0.8092	0.0211	0.074	0.1338	0.5484	0.3786	0.4237	0.1069	0.1253
265721_at	AT2G40090	ATATH9 (ABC2 homolog 9)	0.03112	0.8799	0.5464	-0.1145	0.5855	0.4183	-0.4234	0.0251	0.0643	-0.5691	0.0094	0.0302
265722_at	AT2G40100	LHCB4.3 (LIGHT HARVESTING COMPLEX PSII);	-1.0821	5.00E-04	0.0325	-1.5226	1.00E-04	0.0249	0.6048	0.0044	0.0284	0.1644	0.1905	0.1796
265723_at	AT2G40140	transmembrane receptor	1.3446	0.1689	0.2405	1.4162	0.1521	0.1998	-0.6613	0.2382	0.2342	-0.5897	0.2843	0.2305
265724_at	AT2G32100	ATOFP16/OFP16 (Arabidopsis thaliana ovate famil	-1.0333	0.0052	0.0513	-1.3496	0.0019	0.033	0.2426	0.0676	0.1127	-0.07371	0.4918	0.3227
265725_at	AT2G32030	GCN5-related N-acetyltransferase (GNAT) family pr	0.4527	0.4625	0.4041	0.8984	0.1825	0.2215	0.6615	0.2336	0.2315	1.1073	0.0788	0.104
265726_at	AT2G32010	endonuclease/exonuclease/phosphatase family pro	0.1051	0.7506	0.4887	0.105	0.7509	0.4752	-0.5682	0.01	0.0398	-0.3581	0.0441	0.0736
265727_at	AT2G32000	DNA topoisomerase family protein	0.2053	0.2322	0.2833	0.2878	0.1199	0.1752	-1.0504	0.002	0.0211	-0.968	0.0027	0.0171
265728_at	AT2G31990	exostosin family protein	0.9648	0.0427	0.1188	0.9834	0.0403	0.0995	-0.185	0.1454	0.1756	-0.1664	0.18	0.1733
265729_at	AT2G31960	ATGSL08 (GLUCAN SYNTHASE-LIKE 3); 1,3-beta	0.008152	0.9483	0.5644	0.1227	0.358	0.3219	-0.9573	7.00E-04	0.0159	-0.8428	0.0011	0.0124
265730_at	AT2G32220	60S ribosomal protein L27 (RPL27A)	-0.1496	0.6551	0.4775	0.1036	0.7553	0.4768	0.5898	0.0125	0.0444	0.843	0.0035	0.0194
265731_at	AT2G31130	ATP binding / helicase/ nucleic acid binding	-1.3967	0.14	0.2176	-0.2472	0.7613	0.478	-2.4277	0.0331	0.0742	-1.2781	0.1679	0.166
265732_s_at	AT2G06570,AT2G06645	similar to unknown protein [Arabidopsis thaliana] (T	0.196	0.7857	0.5196	-1.1002	0.178	0.2183	1.7099	0.038	0.0805	0.4137	0.5012	0.3264
265733_at	AT2G31190	ocliosaxapeptide/Phox/Bem1p (PB1) domain-contain	0.9229	0.0125	0.0691	0.4612	0.0972	0.1572	0.08292	0.718	0.4377	-0.3788	0.1512	0.1555
265734_at	AT2G31260	similar to unknown protein [Arabidopsis thaliana] (T	-0.7285	0.0224	0.0875	-0.6955	0.026	0.0807	-0.3775	0.0516	0.0962	-0.3445	0.0663	0.0938
265735_at	AT2G31240	fructose-bisphosphate aldolase, putative	0.6972	0.0296	0.0998	0.8619	0.0149	0.0643	-0.1024	0.6277	0.4071	0.06228	0.7657	0.4185
265736_at	AT2G31250	60S ribosomal protein L7 (RPL7B)	-0.05073	0.4985	0.4199	0.2654	0.0177	0.0689	-0.08972	0.2589	0.2458	0.2264	0.0294	0.0576
265737_at	AT2G31180	ATPAP1 (PHOSPHATIDIC ACID PHOSPHATASE	0.03872	0.9008	0.5513	-0.5708	0.1219	0.1772	0.6925	0.0325	0.0735	0.083	0.7197	0.4039
265738_at	AT2G31350	QPT (QUINOLINATE PHOSPHORIBOSYL TRANSFE	0.301	0.3526	0.3318	0.2751	0.0675	0.1302	-0.6613	0.2181	0.2225	-0.1872	0.1655	0.1545
265739_at	AT2G31270	ATQSOX2 (QUIESCIN-SULFHYDRYL OXIDASE 2	0.5437	0.0238	0.0898	0.5258	0.0264	0.0813	-0.7611	0.0032	0.0252	-0.779	0.0029	0.0176
265740_at	AT2G31150	RHA2B (RING-H2 FINGER PROTEIN 2B); protein	0.2911	0.0691	0.1513	0.01707	0.8919	0.5163	0.6878	1.00E-04	0.0101	0.4138	5.00E-04	0.0095
265741_at	AT2G31320	ABC transporter family protein	0.3258	0.1298	0.2058	0.104	0.5725	0.4129	-0.848	0.0046	0.0289	1.0678	0.0019	0.0151
265742_at	AT2G31290	ribose-5-phosphate isomerase	-0.2496	0.381	0.365	-0.6658	0.0586	0.1203	0.05987	0.5903	0.3948	-0.3563	0.0254	0.0526
265743_s_at	AT1G39110,AT3G42720,A	[AT1G39110, transposable element gene];[AT3G42	1.2885	0.0638	0.1447	1.6381	0.0319	0.0886	0.1413	0.6123	0.4019	0.4909	0.1293	0.1409
265744_at	AT2G06600	transposable element gene	-0.736	0.3871	0.3682	0.9439	0.0625	0.1242	-1.6702	0.082	0.1257	1.0097	0.2351	0.2045
265745_at	AT2G06640	transposable element gene	-1.7291	0.2771	0.3099	-0.7365	0.6207	0.4308	0.1694	0.8929	0.4905	1.162	0.3809	0.2761
265746_at	AT2G06630	transposable element gene	-1.2643	0.547	0.4398	-2.5378	0.2576	0.2688	1.0719	0.4952	0.3579	-0.2015	0.8948	0.4556
265747_s_at	AT2G06570, similar to unknown protein [Arabidopsis	0.196	0.7857	0.5196	-1.1002	0.178	0.2183	1.7099	0.038	0.0805	0.4137	0.5012	0.3264	0.2183
265748_at	AT2G10620	transposable element gene	-1.2687	0.0223	0.0875	-1.2371	0.0242	0.0782	-0.1497	0.6911	0.4282	-0.1181	0.753	0.4146
265749_at	AT2G10610	transposable element gene	-0.5877	0.5454	0.4391	-0.6148	0.528	0.3954	0.2365	0.8037	0.4646	0.2095	0.8256	0.4359
265750_x_at	AT2G10740	transposable element gene	0.3325	0.3966	0.3735	0.00214	0.9954	0.543	0.1648	0.6627	0.4188	-0.1698	0.6534	0.3819
265751_at	AT2G10690	transposable element gene	1.0033	0.4062	0.3784	-0.8771	0.463	0.3693	0.2485	0.8296	0.4726	-1.6319	0.2059	0.1884
265752_at	AT2G10660	transposable element gene	-1.1835	0.3544	0.352	0.7133	0.5625	0.4092	-1.8046	0.1437	0.1743	0.09227	0.9305	0.4658
265753_at	AT2G10650	transposable element gene	-1.467	0.1613	0.2346	1.5551	0.143	0.193	-1.4627	0.1622	0.1868	1.5594	0.1422	0.1496
265754_x_at	AT2G10640	transposable element gene	-0.536	0.4289	0.3885	0.4947	0.4625	0.3691	-0.3539	0.5926	0.3956	0.6768	0.3291	0.253
265755_at	AT2G10630	transposable element gene	1.1485	0.5846	0.4541	-0.8314	0.6895	0.4555	1.8721	0.3879	0.3112	-0.1079	0.9582	0.473
265756_at	AT2G13150	transcription factor	-1.3954	0.3296	0.3398	-0.9439	0.4948	0.3825	-0.5644	0.6769	0.4234	-0.113	0.9328	0.4664
265757_x_at	AT4G02314,AT2G13160,A	[AT4G02314, transposable element gene];[AT2G13	-0.8415	0.4237	0.3868	-0.7399	0.4776	0.3753	0.7459	0.4743	0.3494	0.8475	0.4207	0.2928
265758_at	AT2G13070	transposable element gene	0.009971	0.9936	0.5754	0.6645	0.6025	0.4246	-0.2396	0.8486	0.4783	0.4149	0.7422	0.4112
265759_at	AT2G13100	glycerol-3-phosphate transporter, putative / glycerol	0.2954	0.1575	0.2313	0.3535	0.1063	0.1645	-0.8891	0.0064	0.033	-0.8311	0.0081	0.028
265760_at	AT2G01220	nucleotidyltransferase	0.3246	0.0944	0.1777	0.4272	0.0453	0.1055	-0.7565	0.0012	0.0187	-0.6539	0.0021	0.0154
265761_at	AT2G01330	transducin family protein / WD-40 repeat family prot	0.0141	0.9479	0.5642	-0.3784	0.1353	0.187	-0.1417	0.1576	0.1841	-0.5343	0.0028	0.0174
265762_at	AT2G01240	reticulon family protein (RTNLB15)	-0.2934	0.5356	0.4353	0.09056	0.8447	0.5029	-0.4991	0.2154	0.2211	-0.1151	0.7516	0.4143
265763_at	AT2G48040	similar to unnamed protein product [Vitis vinifera] (G	0.5663	0.2255	0.2788	0.3197	0.4644	0.3698	-1.1669	0.0039	0.0271	-1.4135	0.0019	0.015
265764_at	AT2G48050	similar to hypothetical protein MsDRAFT_AC17210	0.4251	0.3254	0.3375	-0.4616	0.2908	0.287	-1.4291	0.0197	0.0564	-2.3158	0.0037	0.0196
265765_at	AT2G48060	oxidoreductase	0.26	0.7825	0.5184	-1.5545	0.1522	0.1998	0.2611	0.7816	0.4579	-1.5533	0.1524	0.1564
265766_at	AT2G48080	oxidoreductase, 2OG-Fe(II) oxygenase family protei	-0.9586	0.3948	0.3726	0.568	0.6027	0.4246	-0.5086	0.6253	0.4064	1.018	0.35	0.2626
265767_at	AT2G48110	REF4	-0.2438	0.5204	0.4291	0.1141	0.7584	0.4776	-0.6719	0.1244	0.1597	-0.314	0.4159	0.2908
265768_at	AT2G48020	sugar transporter, putative	-0.3555	0.1802	0.2482	-0.6048	0.0509	0.112	-0.4129	0.0554	0.1003	-0.6622	0.0127	0.0357
265769_at	AT2G48090	unknown protein	0.3279	0.6447	0.4747	0.6877	0.3554	0.3206	-0.04824	0.9451	0.5045	0.3115	0.6609	0.3845
265770_at	AT2G48100	exonuclease family protein	0.3222	0.1331	0.2117	0.3691	0.0974	0.1573	-0.5514	0.0064	0.033	-0.5045	0.0087	0.0291
265771_at	AT2G48030	endonuclease/exonuclease/phosphatase family pro	0.9051	0.068	0.1498	0.7031	0.126	0.18	0.5793	0.0623	0.1073	0.3774	0.1701	0.1673
265772_at	AT2G48010	RKF3 (RECEPTOR-LIKE KINASE IN IN FLOWERS	0.1816	0.4094	0.3796	0.06449	0.7601	0.4778	0.3279	0.1718	0.1932	0.2108	0.3454	0.2605
265773_at	AT2G48070	similar to unnamed protein product [Vitis vinifera] (G	-0.4599	0.0828	0.1666	-0.5671	0.047	0.1076	-0.3826	0.1016	0.1424	-0.4899	0.0535	0.0826
265774_at	AT2G07240	cysteine-type peptidase	0.5927	0.589	0.4559	0.01953	0.9855	0.5405	-0.04302	0.9681	0.5096	-0.6162	0.5749	0.3541
265775_at	AT2G07330	transposable element gene	-0.786	0.4423	0.3946	-0.751	0.4613	0.3685	0.2185	0.6131	0.4021	0.2536	0.5598	0.3487
265776_at	AT2G07340	prefoldin-related KE2 family protein	0.02984	0.7884	0.5201	0.4944	0.0089	0.0518	0.147	0.2302	0.2295	0.6116	0.0042	0.0207
265777_at	AT2G07340	prefoldin-related KE2 family protein	-0.07813	0.6378	0.4723	0.3208	0.1051	0.1637	0.3277	0.0939	0.1358	0.726	0.0083	0.0283
265778_at	AT2G07360	SH3 domain-containing protein	0.3511	0.0519	0.1307	0.2487	0.1242	0.1787	-0.4165	0.0314	0.072	-0.5189	0.0155	0.0397
265779_at	AT2G07360	SH3 domain-containing protein	-0.1184	0.7064	0.4948	0.03567	0.9088	0.5212	-2.2655	0.0015	0.0199	-2.1114	0.0019	0.0151
265780_at	AT2G07380	transposable element gene	-1.9711	0.2487	0.2928	-1.3486	0.4083	0.3451	-0.3482	0.8234	0.4706	0.2743	0.8603	0.4459
265781_at	AT2G07430	transposable element gene	-0.3825	0.6857	0.4878	-2.5602	0.0434	0.1034	1.3034	0.2119	0.2191	-0.8744	0.3758	0.2738
265782_at	AT2G07440	two-component responsive regulator-related / respo	-0.7039	0.5312	0.4334	-1.0177	0.3783	0.3312	0.06688	0.9122	0.4957	-0.2469	0.687	0.3929
265783_at	AT2G07455	transposable element gene	0.6223	0.5853	0.4545	0.9581	0.4132	0.3475	0.5948	0.396	0.3148	0.9306	0.2115	0.1916
265784_at	AT2G07280	unknown protein	-0.07684	0.9597	0.5673	0.1568	0.9178	0.5236	-0.7598	0.6229	0.4057	-0.5261	0.7313	0.4075
265785_at	AT2G07290	unknown protein	-0.5129	0.6753	0.4845	0.1555	0.8978	0.5182	-1.5362	0.248	0.24	-0.8678	0.4879	0.321
265786_at	AT2G07300	transposable element gene	-0.681	0.3379	0.3445	-1.8587	0.0412	0.1008	0.9398	0.2078	0.2165	-0.2379	0.7233	0.4051
265787_at	AT2G07320	transposable element gene	0.3118	0.5758	0.4511	-0.8688	0.1653	0.2091	1.2006	0.0792	0.1231	0.01996	0.9708	0.4757
265788_at	no_match	no_match	-2.5697	0.059	0.139	1.1919	0.2916	0.2874	-2.5252	0.0619	0.1069	1.2363	0.2765	0.2264
265789_at	AT2G01210	leucine-rich repeat transmembrane protein kinase,	0.7395	0.3409	0.3457	0.9478	0.2385	0.2568	-0.4895	0.5142	0.3647	-0.2812	0.7023	0.3981
265790_at	AT2G01170	amino acid permease family protein	0.4955	0.0919	0.1758	0.4302	0.1278	0.1814	-0.2574	0.0727	0.1173	-0.3226	0.0386	0.0675
265791_at	AT2G01280	MEE65 (maternal effect embryo arrest 65); RNA po	-0.14967	0.3417	0.346	-0.8771	0.5619	0.409	0.961	0.5269	0.3699	1.5807	0.3185	0.2476
265792_at	AT2G01390	pentatricopeptide (PPR) repeat-containing protein	0.07278	0.9442	0.5635	-3.4807	0.0236	0.0773	2.3003	0.0783	0.1223	-1.2532	0.2692	0.2223
265793_at	AT2G01220	nucleotidyltransferase	0.1733	0.3999	0.3752	0.0666	0.7359	0.4699	-1.3769	0.0013	0.0192	-1.4836	0.001	0.0121
265794_at	AT2G01310	contains domain PTHR10177 (PTHR10177); contai	0.232	0.8706	0.5442	-0.9434	0.5192	0.3921	-0.3389	0.8063	0.4655	-1.5143	0.3068	0.2419
265795_at	AT2G35780	SCPL26 (serine carboxypeptidase-like 26); serine c	0.1962	0.1773	0.1981	0.00855	0.935	0.5278	0.4828	0.008	0.036	0.2781	0.0477	0.0771
265796_at	AT2G35730	heavy-metal-associated domain-containing protein	-0.5774	0.3397	0.3452	0.8208	0.1985	0.232	-0.811	0.2029	0.2135	0.5872	0.3326	0.2546
265797_at	AT2G35710	glycogenin glucosyltransferase (glycogenin)-related	-1.3169	0.3055	0.3258	-0.02013	0.9865	0.5407	-1.7211	0.0597	0.1049	-0.4243	0.5557	0.3472
265798_at	AT2G35790	similar to unnamed protein product [Vitis vinifera] (G	0.4595	0.099	0.1816	0.3404	0.188	0.2252	0.3911	0.1425	0.1733	0.272	0.2739	0.2249
265799_at	AT2G35680	dual specificity protein phosphatase family protein	0.08703	0.6128	0.4636	-0.1705	0.3433	0.3149	0.4227	0.0198	0.0565	0.1651	0.2159	0.1941
265800_at	AT2G35630	MOR1 (MICROTUBULE ORGANIZATION 1)	0.397	0.0017	0.0391	0.2554	0.0084	0.0507	-0.6216	3.00E-04	0.0138	-0.7631	1.00E-04	0.0065
265801_at	AT2G35670	FIS2 (FERTILIZATION INDEPENDENT SEED 2); t	-0.6591	0.4477	0.397	-1.7938	0.084	0.1458	0.8408	0.3437	0.2902	-0.2938	0.7267	0.4061
265802_at	AT2G35533	unknown protein	0.02683	0.9652	0.5685	0.7014	0.2914	0.2873	-0.1534	0.7362	0.4437	0.5212	0.2869	0.2317
265803_at	AT2G35618	pseudogene, glycine-rich protein, predicted proteins	0.8728	0.3633	0.356	-1.6557	0.1237	0.1785	0.3963	0.6658	0.4198	-2.132	0.0665	0.0939
265804_at	AT2G18030	peptide methionine sulfoxide reductase family prote	-0.03955	0.8463	0.5374	0.4705	0.0698	0.1322	-0.5505	0.0229	0.0611	-0.04046	0.8047	0.4301
265805_s_at	AT4G36130,AT2G18020	[AT4G36130, 60S ribosomal protein L8 (RPL8C)];[A	-0.04765	0.5346	0.435	0.0007 18	0.9923	0.5422	0.1328	0.081	0.1247	0.1811	0.034	0.0623
265806_at	AT2G18010	auxin-responsive family protein	0.07656	0.9552	0.5661	-3.1852	0.0675	0.1302	3.0624	0.0624	0.1074	-0.02826	0.9824	0.4786
265807_at	AT2G17990	similar to kinectin-related [Arabidopsis thaliana] (TA	0.6749	0.0429	0.1193	0.8257	0.0231	0.0768	-0.1806	0.2969	0.2671	-0.02988	0.8526	0.4434
265808_at	AT2G17960	unknown protein	-0.5534	0.4739	0.4094	-0.09853	0.895	0.5172	-0.2003	0.7892	0.4599	0.2545	0.7348	0.4087
265809_at	AT2G18100	similar to unknown protein [Arabidopsis thaliana] (T	-0.2869	0.5112	0.4253	-0.1888	0.6592	0.4447	-0.07273	0.857	0.4803	-0.5474	0.2218	0.197
265810_at	AT2G18090	PHD finger family protein / SWIB complex BAF60b-	0.2025	0.0367	0.1105	0.1489	0.0859	0.1475	-0.2946	0.0109	0.0414	-0.3483	0.0061	0.0241
265811_at	AT2G18080	EDA2 (embryo sac development arrest 2); serine-ty	-0.576	0.2656	0.3025	-0.2363	0.624	0.4324	-0.0595	0.8859	0.4884	0.2803	0.5113	0.3302
265812_at	AT2G18070	contains domain PTHR13426 (PTHR13426); contai	0.001716	0.9765	0.5763	-0.607	0.553	0.4058	0.8661	0.368	0.302	0.2575	0.7782	0.4224
265813_at	AT2G18060	VND1 (VASCULAR RELATED NAC-DOMAIN PRO	-0.06844	0.8619	0.5416	0.02999	0.9391	0.5287	0.5797	0.1101	0.1485	0.6782	0.0748	0.1006
265814_at	AT2G17930	FAT domain-containing protein / phosphatidylinositc	0.6669	0.0522	0.1312	0.5869	0.0739	0.1364	-1.3576	0.0051	0.03	-1.4377	0.0041	0.0207
265815_at	AT2G17975	zinc finger (Ran-binding) family protein	0.6029	0.0125	0.0691	0.5175	0.0207	0.0735	-1.4708	5.00E-04	0.0153	-1.1562	0.0007	5.00E-04
265816_s_at	AT1G30230,AT2G18110	elongation factor/elongation factor 1-beta, putative /	0.4722	0.0182	0.0804	0.4026	0.0302	0.0863	-0.7904	0.002	0.0213	-0.8599	0.0015	0.0089
265817_at	AT2G18050	HIS1-3 (HISTONE H1-3); DNA binding	0.3241	0.5246	0.431	0.7172	0.1981	0.2317	0.5065	0.0437	0.0872	0.8996	0.0067	0.0253
265818_at	AT2G18040	PIN1AT (parvulin 1A)	0.235	0.1742	0.2444	0.4649	0.0309	0.0873	0.8165	0.0046	0.0289	1.0461	0.0018	0.0148
265819_at	AT2G17972	similar to unnamed protein product [Vitis vinifera] (G	-0.3705	0.062	0.1429	-0.184	0.271	0.2759	0.552	0.0186	0.0547	0.7385	0.0069	0.0258
265820_at	AT2G17940	similar to unnamed protein product [Vitis vinifera] (G	-0.5949	0.6009	0.4796	0.7333	0.5912	0.42	-0.714	0.6006	0.3984	0.6142	0.6509	0.3811
265821_at	AT2G17950	WUS (WUSCHEL); DNA binding / transcription facto	2.0566	0.1353	0.2135	1.455	0.2568	0.2683	0.5053	0.6132	0.4021	0.09534	0.9227	0.4636
265822_at	AT2G17980	ATSLY1; protein transporter	0.8	0.0018	0.0391	0.7844	0.002	0.033	-0.1959	0.1325	0.1657	-0.2116	0.1115	0.1288
265823_at	AT2G35760	integral membrane family protein	-1.7501	0.0038	0.0462	-1.553	0.0059	0.0442	0.4813	0.0475	0.0914	0.6784	0.0163	0.0408
265824_at	AT2G35650	ATCSLA09 (CELLULOSE SYNTHASE LIKE); trans	-0.3923	0.2559	0.297	-0.6408	0.0965	0.1565	-0.9784	0.0266	0.0663	-1.2268	0.0127	0.0356
265825_at	AT2G35635	UBQ7 (RELATED TO UBIQUITIN 2)	-0.1693	0.5079	0.4243	0.489	0.104	0.1628	0.4963	0.0735	0.118	1.1547	0

265890_s_at	AT4G08070:AT1G40107:A	[AT4G08070, transposable element gene];[AT1G40	-1.1771	0.2057	0.2658	0.03426	0.9671	0.5358	-0.5716	0.5042	0.3609	0.6398	0.458	0.3092
265891_at	AT2G15010	thionin, putative	0.4481	0.6835	0.487	0.1041	0.9237	0.5251	-0.9308	0.4136	0.3224	-1.2747	0.28	0.2282
265892_at	AT2G15020	similar to unknown protein [Arabidopsis thaliana] (T	-2.6591	0.0249	0.0915	-2.3671	0.0357	0.0931	-1.0307	0.0249	0.064	-0.7386	0.0663	0.0938
265893_at	AT2G15040	pseudogene, disease resistance protein-related, lo	0.6762	0.2232	0.2771	0.6741	0.2243	0.2481	-3.2364	9.00E-04	0.0169	-3.2385	9.00E-04	0.0116
265894_at	AT2G15050	LTP; lipid binding	-0.3624	0.1985	0.2617	-0.6045	0.0621	0.1239	0.3266	0.1177	0.1545	0.08448	0.6343	0.3752
265895_at	AT2G15000	similar to unknown protein [Arabidopsis thaliana] (T	-0.03061	0.8485	0.5379	0.02641	0.869	0.5096	1.0935	0.0019	0.0207	1.1505	0.0016	0.0139
265896_at	AT2G25660	EMB2410 (EMBRYO DEFECTIVE 2410)	-0.2396	0.3631	0.3559	-0.1687	0.5101	0.3887	-1.0099	0.0077	0.0354	-0.939	0.01	0.0312
265897_at	AT2G25565	similar to zinc finger (C3HC4-type RING finger) fam	-1.8706	0.1872	0.2535	0.0859	0.9453	0.5307	-0.693	0.5877	0.3936	1.2636	0.3435	0.2596
265907_at	AT2G25650	DNA-binding storekeeper protein-related	0.4464	0.657	0.478	2.0637	0.0912	0.1524	0.3897	0.6817	0.4248	2.007	0.0854	0.1093
265908_at	AT4G00270	DNA-binding storekeeper protein-related	-0.4245	0.1888	0.2546	0.7254	0.0539	0.1152	-0.5798	0.0968	0.1383	0.57	0.1008	0.1212
265909_at	AT2G25720	similar to hypothetical protein SDM1_56000007 [Sol	0.09639	0.6158	0.4648	0.6217	0.0248	0.079	1.1171	0.0033	0.0254	1.6425	8.00E-04	0.0108
265910_at	AT2G25610	H+-transporting two-sector ATPase, C subunit famil	-0.09204	0.3075	0.3271	0.008042	0.9236	0.5251	0.3046	0.018	0.0538	0.4047	0.0068	0.0257
265911_at	AT2G25670	similar to unknown protein [Arabidopsis thaliana] (T	0.4433	0.124	0.2039	0.6127	0.0549	0.1164	0.579	0.0488	0.0931	0.7484	0.0224	0.0487
265912_at	AT2G25570	binding	0.07406	0.5847	0.4541	-0.1748	0.2338	0.2541	0.2582	0.1072	0.1466	0.009399	0.9438	0.4693
265913_at	AT2G25625	similar to unnamed protein product [Vitis vinifera] (G	0.7343	0.1472	0.2231	0.153	0.7274	0.468	0.773	0.0031	0.025	0.1916	0.189	0.1788
265914_at	AT2G25060	transposable element gene	0.4311	0.5634	0.4462	-1.9656	0.0456	0.1057	0.8918	0.1665	0.1894	-1.505	0.0464	0.0758
265915_at	AT2G15070	transposable element gene	-0.9353	0.4101	0.38	0.7006	0.5291	0.3959	-0.4468	0.6834	0.4253	1.1891	0.3075	0.2422
265916_at	AT3G31920	transposable element gene	-0.09324	0.845	0.5372	-1.2982	0.044	0.1037	0.9128	0.0609	0.106	-0.2922	0.4543	0.3077
265917_at	AT2G15080	disease resistance family protein	-0.08564	0.8769	0.5456	-0.03201	0.9538	0.5328	-1.8829	0	0.0092	-1.8293	1.00E-04	0.0056
265918_at	AT2G15090	fatty acid elongase, putative	-0.4308	0.4731	0.4091	-0.117	0.8404	0.5016	0.2022	0.5582	0.3819	0.5161	0.1788	0.1726
265919_at	AT2G15100	transposable element gene	-1.6487	0.1884	0.2542	-0.03173	0.9771	0.5386	-0.4796	0.669	0.4208	1.1374	0.3359	0.2561
265920_s_at	AT2G15120	[AT2G15120, pseudogene, disease-resistance fami	0.01299	0.9823	0.5725	0.6662	0.2928	0.288	-0.08546	0.808	0.466	0.5678	0.1596	0.1609
265921_at	AT2G18490	zinc finger (C2H2 type) family protein	-1.1036	0.2102	0.2684	-1.9155	0.0608	0.1225	-1.1324	0.1316	0.165	-1.9442	0.0315	0.0598
265922_at	AT2G18480	mannitol transporter, putative	-0.6136	0.5835	0.4537	0.5765	0.6055	0.4253	-1.2998	0.2756	0.2555	-0.1097	0.9203	0.4629
265923_at	AT2G18470	protein kinase family protein	1.155	0.3306	0.3403	-1.8723	0.1473	0.1962	1.793	0.161	0.1862	1.2342	0.3025	0.2399
265924_at	AT2G18620	geranylgeranyl pyrophosphate synthase, putative /	0.848	0.3803	0.3646	0.5751	0.5406	0.4009	-0.7679	0.4227	0.3266	-1.0409	0.2931	0.2352
265925_at	AT2G18610	unknown protein	-0.911	0.2254	0.2788	2.3068	0.0222	0.0753	-0.2311	0.7348	0.4432	2.9867	0.0093	0.0301
265926_at	AT2G18600	RUB1-conjugating enzyme, putative	0.614	0.1745	0.2445	0.3297	0.7354	0.3534	0.7668	0.0127	0.0448	0.4626	0.054	0.083
265927_at	AT2G18590	transporter-related	-0.552	0.4748	0.4097	1.1556	0.1744	0.2156	-1.0293	0.2157	0.2212	0.6782	0.3878	0.279
265928_at	AT2G18580	transposable element gene	0.0124	0.9937	0.5754	1.0608	0.5139	0.3902	-1.0646	0.5124	0.3641	-0.01622	0.9918	0.4805
265929_s_at	AT2G18560	[AT2G18560, UDP-glucoronosyl/UDP-glucosyl tran	-0.3458	0.3763	0.3624	-0.2499	0.512	0.3895	-0.0805	0.9213	0.2788	0.01537	0.9896	0.4398
265930_at	AT2G18510	EMB2444 (EMBRYO DEFECTIVE 2444); RNA bind	-0.08167	0.5283	0.4326	0.3153	0.5062	0.1179	0.2829	0.0226	0.0608	0.04931	0.5638	0.3503
265931_at	AT2G18520	pentatricopeptide (PPR) repeat-containing protein	0.4447	0.3326	0.3416	1.5377	0.019	0.071	0.1271	0.7554	0.4498	1.2201	0.0328	0.0611
265932_at	AT2G18510	LBD8 (LOB DOMAIN-CONTAINING PROTEIN 8)	0.7152	0.3479	0.3489	-0.7897	0.3059	0.2949	0.877	0.0555	0.1005	-0.6279	0.1279	0.1402
265933_at	AT2G19550	esterase/lipase/thioesterase family protein	2.8097	0.025	0.0916	-0.6476	0.4654	0.3701	1.6511	0.109	0.1478	-1.8061	0.0878	0.1111
265934_at	AT2G19560	proteasome protein-related	-0.1181	0.3302	0.3401	0.2889	0.0536	0.1148	-0.8639	7.00E-04	0.016	-0.4569	0.0076	0.027
265935_at	AT2G19580	TET2 (TETRASPANIN2)	-0.4914	0.0211	0.0853	0.3865	0.0441	0.1039	-0.03234	0.8202	0.4698	-0.1373	0.3611	0.2675
265936_at	AT2G18620	ATKEA4 (Arabidopsis thaliana K+ efflux antiporter 4	0.848	0.3803	0.3646	0.5751	0.5406	0.4009	-0.7679	0.4227	0.3266	-1.0409	0.2931	0.2352
265937_at	AT2G19610	zinc finger (C3HC4-type RING finger) family protein	0.6279	0.5529	0.4421	0.4813	0.646	0.4402	0.4802	0.6148	0.4025	0.3337	0.7242	0.4054
265938_at	AT2G19590	Ndr family protein	-0.887	0.0537	0.1331	-0.5551	0.1655	0.2093	-0.2281	0.3299	0.3162	0.1038	0.69	0.3939
265939_at	AT2G19650	DC1 domain-containing protein	-0.7814	0.0505	0.1292	-1.1643	0.0146	0.0637	-0.0782	0.7199	0.4385	-0.4611	0.0858	0.1096
265940_at	AT2G19480	NAP1;2/NAP2 (NUCLEOSOME ASSEMBLY PROT	0.3436	0.0599	0.14	0.5726	0.0123	0.0595	-0.308	0.0801	0.1239	-0.07902	0.5819	0.3568
265941_s_at	AT2G19490	recA family protein [ATG32920, rec	0.06745	0.8661	0.5425	0.3282	0.4313	0.3559	-0.3471	0.3941	0.3139	-0.08637	0.824	0.4354
265942_at	AT2G19470	CKL5 (Casein Kinase I-like 5); casein kinase I/ kina	0.6356	0.0199	0.0833	0.7438	0.0118	0.0584	-0.2506	0.117	0.1539	-0.1425	0.3205	0.2485
265943_at	AT2G19570	CDA1 (CYTIDINE DEAMINASE 1)	0.9355	0.0042	0.0468	0.8804	0.0052	0.0429	0.4296	0.0476	0.0916	0.3745	0.0696	0.0966
265944_at	AT2G19580	ASHR2 (ASH1-RELATED PROTEIN 2)	0.998	0.1746	0.2446	0.873	0.2228	0.2475	0.2561	0.5226	0.368	0.1312	0.7382	0.4097
265945_at	AT2G19500	CKX2 (CYTOKININ OXIDASE 2); cytokinin dehydro	0.4031	0.3308	0.3404	-0.05809	0.8811	0.5134	-0.1343	0.7313	0.4422	-0.5954	0.1777	0.1718
265946_s_at	AT2G19520:AT4G29730	[AT2G19520, FVE];[AT4G29730, NFC5 (NUCLEOS	0.3136	0.1066	0.1888	0.5123	0.0275	0.0829	0.05011	0.7569	0.4503	0.2488	0.1751	0.1703
265947_at	AT2G19510	transducin family protein / WD-40 repeat family pro	0.7152	0.3479	0.3489	-0.7897	0.3059	0.2949	0.877	0.0555	0.1005	-0.6279	0.1279	0.1402
265948_at	AT2G19590	ACO1 (ACC OXIDASE 1); 1-aminocyclopropane-1-	-0.3742	0.7178	0.4987	-0.4771	0.6468	0.4404	0.9752	0.3692	0.3024	0.8724	0.4169	0.2912
265949_at	AT2G18540	cupin family protein	-0.4614	0.7131	0.4972	-1.0498	0.4197	0.3505	-0.548	0.6635	0.4191	-1.1364	0.3858	0.2782
265950_s_at	AT2G18530:AT3G46160	[AT2G18530, protein kinase family protein];[AT3G4	0.3581	0.3781	0.3635	0.3543	0.3827	0.3331	0.4218	0.1713	0.1929	0.418	0.1743	0.1699
265951_at	AT2G18500	ATOFP7/OFP7 (Arabidopsis thaliana ovate family p	-0.00301	0.9942	0.5755	0.9474	0.071	0.1333	0.04553	0.9061	0.494	0.9959	0.0515	0.0809
265952_at	AT2G37480:AT2G37478	[AT2G37480, similar to unknown protein [Arabidops	0.1048	0.5084	0.4244	0.09043	0.5655	0.4102	-0.4186	0.0443	0.088	-0.433	0.0401	0.0692
265953_at	AT2G37480:AT2G37478	[AT2G37480, similar to unknown protein [Arabidops	0.2342	0.0128	0.0698	0.4485	0.0012	0.0299	0.07815	0.2261	0.2271	0.2924	0.0059	0.0238
265954_at	AT2G37260	TTG2 (TRANSPARENT TESTA GLABRA 2); transc	-1.2242	0.0142	0.0727	-1.2683	0.0126	0.06	-0.3035	0.2978	0.2675	-0.3475	0.2428	0.2086
265955_at	AT3G37280	ATPDR5/PDR5 (PLEIOTROPIC DRUG RESISTAN	0.06846	0.7899	0.5205	-0.1757	0.5052	0.3867	-0.09732	0.7062	0.4334	-0.3415	0.2283	0.2006
265956_at	no_match	no_match	1.3696	0.4337	0.391	-0.358	0.8314	0.4993	1.4607	0.4063	0.3191	-0.2669	0.8737	0.4495
265957_at	AT2G37300	unknown protein	-0.385	0.4494	0.3978	-0.862	0.134	0.1861	-0.04943	0.9195	0.4977	-0.5264	0.316	0.2464
265958_at	AT2G37250	ADK/ATPADK1 (ADENOSINE KINASE); adenylate	0.2753	0.1588	0.2325	0.1889	0.3012	0.292	-0.5365	0.028	0.0681	-0.623	0.0174	0.0421
265959_at	AT2G37240	antioxidant/ oxidoreductase	-0.8532	0.0031	0.044	-1.1649	0.001	0.0291	0.384	0.0445	0.0883	0.07226	0.6154	0.3685
265960_at	AT2G37470	histone H2B, putative	-0.7322	0.0122	0.0685	0.2458	0.2187	0.245	0.2325	0.24	0.2352	1.2105	0.002	0.0152
265961_at	AT2G37400	chloroplast lumen common family protein	0.05491	0.5063	0.4235	0.1861	0.0689	0.1317	0.3625	0.0086	0.0371	0.4937	0.0028	0.0174
265962_at	AT2G37340	nodulin MtN21 family protein	-0.5912	0.1081	0.1904	-0.6039	0.1029	0.1618	0.4483	0.0977	0.139	0.4356	0.1046	0.1238
265963_s_at	AT3G11940:ATGP3720	[AT3G11940, ATRPS5A (RIBOSOMAL PROTEIN S	0.1569	0.4636	0.4046	0.1587	0.4587	0.3675	0.1698	0.3755	0.3055	0.1717	0.3708	0.2716
265964_at	AT2G37510	RNA-binding protein, putative	0.1242	0.7689	0.5143	0.5267	0.2534	0.2661	0.2516	0.5589	0.3822	0.6541	0.1732	0.1692
265965_at	AT2G37500	arginine biosynthesis protein ArgJ family	-0.05464	0.7864	0.5197	-0.29	0.2002	0.2329	-0.3656	0.1034	0.1438	-0.6008	0.026	0.0534
265966_at	AT2G37220	29 kDa ribonucleoprotein, chloroplast, putative / RN	-0.2854	0.2038	0.2645	-0.4181	0.0903	0.1516	-0.3883	0.0039	0.0273	-0.521	0.0013	0.0133
265967_at	AT2G37450	nodulin MtN21 family protein	-0.7781	0.0101	0.064	-0.7902	0.0096	0.0535	-0.8331	0.008	0.0359	-0.8452	0.0076	0.0271
265968_at	AT2G37410	ATTMT1/T2 (Arabidopsis thaliana translocase inner	0.4411	0.0498	0.1282	0.4528	0.0462	0.1066	-0.6481	0.0017	0.0205	-0.6364	0.0018	0.0148
265969_at	AT2G11110	transposable element gene	2.3012	0.0561	0.1359	-0.1267	0.8905	0.5159	1.5194	0.1533	0.181	-0.9084	0.3521	0.2636
265970_at	AT2G11210	transposable element gene	-0.0596	0.8624	0.5416	0.708	0.0932	0.1539	-0.05958	0.8624	0.4819	0.708	0.0932	0.1153
265971_at	AT2G11220	transposable element gene	-0.3517	0.7087	0.4958	-1.4401	0.1757	0.2167	-2.1054	0.0742	0.1186	-3.1938	0.0219	0.0482
265972_at	AT2G11235	transposable element gene	1.4205	0.2955	0.3208	-1.0913	0.4079	0.3448	-0.5125	0.6868	0.4266	-3.0243	0.0626	0.0908
265973_at	AT2G11240	transposable element gene	-2.3237	0.0482	0.1265	0.8825	0.3456	0.3158	-0.8807	0.3465	0.2915	2.3255	0.0481	0.0774
265974_at	no_match	no_match	0.4697	0.0158	0.0758	-0.153	0.2597	0.2697	-3.4439	0	0.0049	-4.0667	0	0.003
265975_at	AT2G11270	citrate synthase-related	-0.08322	0.9637	0.5682	-0.3622	0.8435	0.5027	0.5445	0.7675	0.4533	0.2655	0.8848	0.4529
265976_at	AT2G11120	transposable element gene	-0.01796	0.9842	0.5731	-0.1569	0.8628	0.5079	-0.973	0.2904	0.2638	-1.112	0.2365	0.2053
265977_at	no_match	no_match	2.8733	0.0219	0.087	-0.4589	0.592	0.4204	2.6834	0.0273	0.0671	-0.6488	0.4571	0.3089
265978_at	AT2G11140	transposable element gene	0.2454	0.5434	0.4384	0.5523	0.2097	0.2394	-0.3	0.4629	0.3444	0.00692	0.986	0.4792
265979_at	AT2G11150	transposable element gene	-0.7427	0.3672	0.3579	0.4683	0.5567	0.4071	-1.7528	0.0746	0.1189	-0.5418	0.4999	0.3259
265980_at	AT2G11165	transposable element gene	-0.5262	0.4245	0.387	0.6598	0.3277	0.3073	-0.9295	0.1916	0.2065	0.2565	0.6873	0.393
265981_s_at	AT4G19280:AT2G11166:A	[AT4G19280, transposable element gene];[AT2G11	-0.5695	0.5954	0.4581	0.4815	0.6517	0.4423	-0.4106	0.6992	0.4311	0.6404	0.5524	0.3459
265982_at	AT2G11190	transposable element gene	0.05321	0.9603	0.5674	-1.1512	0.3156	0.3005	-0.1495	0.8889	0.4894	-1.3539	0.2489	0.2119
265983_at	AT2G18550	ATHB21/HB-2 (homeobox-2); DNA binding / transc	1.305	0.0072	0.0572	0.8694	0.0282	0.0835	0.1006	0.7019	0.4319	-0.335	0.2426	0.2085
265984_at	AT2G24210	TPS10 (TERPENE SYNTHASE 10); myrcene/(E)-b	-1.8639	0.0517	0.1306	-1.6198	0.0756	0.1378	-0.5792	0.383	0.3093	-0.3351	0.6014	0.3638
265985_at	AT2G24220	ATPUP5 (Arabidopsis thaliana purine permease 5);	-0.7299	0.0047	0.0496	-0.5936	0.0098	0.0539	-0.1254	0.3839	0.3096	0.01086	0.9366	0.4674
265986_at	AT2G24230	leucine-rich repeat transmembrane protein kinase,	-0.06664	0.7253	0.5012	-0.2526	0.3803	0.3321	0.2264	0.4268	0.3284	0.07047	0.7969	0.4279
265987_at	AT2G24240	potassium channel tetramerisation domain-containi	1.0642	0.1022	0.1848	1.2277	0.0714	0.1338	-0.1479	0.5319	0.3719	0.01562	0.9459	0.4698
265988_at	AT2G24255	similar to F-box family protein [Arabidopsis thaliana	-0.8598	0.0284	0.0976	0.212	0.4545	0.3659	-0.2358	0.3969	0.3151	0.836	0.0283	0.0562
265989_at	AT2G24260	basic helix-loop-helix (bHLH) family protein	0.5147	0.2583	0.3018	0.7429	0.1301	0.1829	0.5504	0.0918	0.134	0.7786	0.0354	0.0637
265990_at	AT2G24280	serine carboxypeptidase S28 family protein	-0.1866	0.4756	0.41	-0.07919	0.7553	0.4768	-0.428	0.1198	0.1561	-0.3206	0.2136	0.1928
265991_at	AT2G24120	PDE319/SCA3 (SCABRA 3); DNA binding / DNA-di	-0.1935	0.5439	0.4385	-0.0801	0.7974	0.4887	-1.3706	0.0094	0.0388	-1.2572	0.0126	0.0355
265992_at	AT2G24130	leucine-rich repeat transmembrane protein kinase,	0.3474	0.4364	0.3922	-0.3003	0.4968	0.3831	-0.3624	0.4171	0.3239	-1.0101	0.0654	0.0931
265993_at	AT2G24160	pseudogene, leucine rich repeat protein family, con	0.8174	0.0259	0.093	0.8762	0.0207	0.0735	-1.9529	6.00E-04	0.0158	-1.8942	7.00E-04	0.0107
265994_at	AT2G24170	endomembrane protein 70, putative	-0.2448	0.5227	0.4301	-0.4394	0.2775	0.2795	-0.05493	0.8828	0.4875	-0.2495	0.5151	0.3317
265995_at	AT2G24140	similar to unknown protein [Arabidopsis thaliana] (T	-0.2134	0.8181	0.5291	1.2357	0.2279	0.2502	-0.05368	0.9385	0.503	1.3954	0.0999	0.1205
265996_at	AT2G24200	cytosol aminopeptidase	0.2909	0.085	0.1688	0.4635	0.0222	0.0753	-0.1646	0.2669	0.2502	0.007935	0.9534	0.4719
265997_at	AT2G24250	F-box family protein	0.3795	0.5854	0.4545	1.0482	0.177	0.2177	-0.4203	0.5475	0.3783	0.2485	0.7178	0.4033
265998_at	AT2G24270	ALDH11A3 (Aldehyde dehydrogenase 11A3); 3-chl	0.1472	0.2424	0.289	-0.3156	0.0425	0.1024	-0.1354	0.2761	0.2558	-0.3038	0.0475	0.0768
265999_at	AT2G24100	similar to unknown protein [Arabidopsis thaliana] (T	-0.07166	0.7948	0.5223	0.08536	0.7572	0.4773	0.1853	0.5119	0.3639	0.3423	0.2549	0.2151
266000_at	AT2G24180	CYP71B6 (CYTOCHROME P450 71B6); oxygen bi	0.9428	0.033	0.1053	0.7057	0.075	0.1373	0.08592	0.4705	0.3478	-0.1512	0.2338	0.2037
266001_at	AT2G24150	HIP3 (histidine-containing phosphotransfer protein	0.06602	0.6767	0.4848	-0.1164	0.4729	0.3733	-0.4072	0.0433	0.0868	-0.5896	0.0134	0.0367
266002_at	AT2G37310	pentatricopeptide (PPR) repeat-containing protein	0.3832	0.6469	0.4753	0.3637	0.6632	0.446	-0.179	0.8287	0.4723	-0.1984	0.8106	0.4319
266003_at	AT2G37320	pentatricopeptide (PPR) repeat-containing protein	0.9192	0.2506	0.2939	-0.2468	0.7368	0.4703	-0.2752	0.7083	0.434	-1.4412	0.1031	0.1228
266004_at	AT2G37330	ALS3 (ALUMINUM SENSITIVE 3)	-0.0235	0.8757	0.5454	0.006799	0.9639	0.535	-0.1811	0.2683	0.2512	-0.1508	0.3451	0.2603
266005_at	AT2G37340	RSZ33 (ARGININE/SERINE-RICH ZINC KNUCKLE	0.2912	0.0561	0.1359	0.4507	0.0145	0.0637	-0.5727	0.0063	0.0328	-0.4131	0.0194	0.0447
266006_at	AT2G37360	ABC transporter family protein	1.4108	0.3707	0.3599	-0.4938	0.7422	0.4721	1.5225	0.3381	0.2874	-0.3821	0.7985	0.4283
266007_at	AT2G37380	similar to unknown protein [Arabidopsis thaliana] (T	-0.8171	0.0705	0.153	-0.7269	0.0948	0.1552	0.443	0.2039	0.2142	-0.5332	0.1419	0.1494
266008_at	AT2G37390	heavy-metal-associated domain-containing protein	-0.658	0.4962	0.4188	0.73	0.4535	0.3655	0.497	0.6024	0.399	1.885	0.0989	0.1197
266009_at	AT2G37400	kinesin motor protein-related	1.3164	0.1762	0.2456	1.2689	0.1889	0.2257	0.3222	0.6694	0.4208	0.2747	0.7149	0.4025
266010_at	AT2G37430	zinc finger (C2H2 type) family protein (ZAT11)	-1.7235	0.048	0.1262	-3.125	0.007	0.0471	2.8228	0.0099	0.0398	1.4213	0.081	0.1058
266011_at	AT2G37440	endonuclease/exonuclease/phosphatase family pro	-0.783	0.1809	0.2487	2.8819	0.004	0.0394	-3.0701	0.0032	0.0251	0.5948	0.2862	0.2314
266012_s_at	ATMG00410:AT2G07741:A	[ATMG00410, ATP-ase subunit 6];[AT2G07741, AT	0.01385	0.9378	0.5816	-0.2884	0.1589	0.2051	-2.1217	0	0.0092	-2.4239	0	0.0047
266013_s_at	ATMG00440:AT2G07702:A	[ATMG00440, hypothetical protein];[AT2G07702, id	-0.846	0.3033	0.325	-2.2953	0.0328	0.0898	1.1824	0.1295	0.1635	-0.2669	0.6893	0.3936
266014_s_at	AT2G07722:ATMG00620:A	[AT2G07722, Identical to Uncharacterized mitochor	-1.5664	0.156	0.2302	-0.3241	0.7363	0.4701	-2.5226	0.0483	0.0924	-1.2804	0.227	0.1999
266015_at	AT2G24190	short-chain dehydrogenase/reductase (SDR) family	-0.3726	0.2337	0.2839	-0.6475	0.0716	0.1339	0.2401	0.4177	0.3242	-0.03476	0.9023	0.458
266016_at	AT2G18670	zinc finger (C3HC4-type RING finger) family protein	0.5586	0.0633	0.1442	0.4696	0.0986	0.1582	-0.1475	0.0955	0.1372	-0.2365	0.0252	0.0525
266017_at	AT2G18690	similar to unknown protein [Arabidopsis thaliana] (T	1.1156	0.0017	0.0391	1.5782	4.00E-04	0.0251	0.02135	0.8552	0.4798	0.481	0.0119	0.0342
266018_at	AT2G18710	SCY1 (SCY1-LIKE KINASE 1); P-P-bond-hydrolysis-d	-0.02459	0.8618	0.5416	-0.3512	0.0569	0.1186	-0.3644	0.0018	0.0206	-0.691	2.00E-04	
266019_at	AT2G18750	calmodulin-binding protein	-0.2602	0.2137	0.2707	0.6297	0.0233	0.0769	-2.0667	3.00E-04	0.0138	-1.1768	0.0026	0.0169
266020_at	AT2G05900	SET domain-containing protein / YDG/SRA domain	0.3569	0.7551	0.5101	-0.1862	0.8701	0.5099	0.5901	0.6058	0.4	0.04698	0.9666	0.4748
266021_at	AT2G05910	similar to unknown protein [Arabidopsis thaliana] (T	-0.1757	0.8117	0.5273	0.7051	0.3649	0.3252	0.188	0.6326	0.4086	1.0688	0.2425	0.0719
266022_at	AT2G05920	subtilase family protein	-0.326	0.1833	0.2505	-0.5398	0.0563	0.1179	0.02928	0.8745	0.4852	-0.1846	0.3485	0.2617
266023_at	AT2G05930	transposable element gene	0.3375	0.6409	0.4734	0.06514	0.9272	0.526	-0.1934	0.7872	0.4593	-0.4658	0.5252	0.336
266024_at	AT2G05940	transposable element gene	0.3812	0.6929	0.4902	1.1709	0.2621	0.271	-2.6624	0.0413	0.0844	-1.8726	0.1053	0.1241
266025_at	AT2G05960	transposable element gene	-0.1142	0.9422	0.563	-2.1935	0.2123	0.241	0.5478	0.7203	0.4387	-1.5316	0.3431	0.2593
266026_at	AT2G05980	transposable element gene	-1.1328	0.2477	0.2923	0.6589	0.4756	0.3744	-1.9423	0.0813	0.125	-0.1506	0.8661	0.4472
266027_at	AT2G05980	transposable element gene	-0.6919	0.2602	0.2997	0.1133	0.8405	0.5016	-1.4619	0.0504	0.095	-0.6566	0.2815	0.2288
266028_at	AT2G06000	pentatricopeptide (PPR) repeat-containing protein	0.2686	0.3567	0.353	-0.364	0.2312	0.2523	-0.1711	0.5437	0.3769	-0.8036	0.0357	0.0641
266029_at	AT2G05850	SCPL38 (serine carboxypeptidase-like 38); serine c	0.3995	0.7625	0.5123	0.4066	0.7584	0.4776	-0.2162	0.8695	0.4841	-0.209	0.8738	0.4495
266030_x_at	AT2G05870	transposable element gene	0.6408	0.4477	0.397	-0.6797	0.4228	0.3519	0.3188	0.6971	0.4302	-1.0017	0.2589	0.2173
266031_at	no_match	no_match	0.1468	0.9102	0.5541	0.06868	0.9579	0.5337	-1.4837	0.2915	0.2644	-1.5618	0.2704	0.2229
266032_x_at	AT2G05890	transposable element gene	1.7223	0.0094	0.0624	0.7515	0.1102	0.1676	-0.1684	0.6704	0.4212	-1.1392	0.0362	0.0647
266033_at	AT2G05830	initiation factor 2B family protein / eIF-2B family pro	0.1736	0.2957	0.3208	-0.07836	0.6163	0.4293	0.3163	0.0476	0.0916	0.06438	0.5963	0.3622
266034_

266090_at	AT2G36000	chaperone protein dnaJ-related	1.0879	0.0036	0.0452	1.2208	0.0023	0.0336	0.07178	0.6926	0.4286	0.2047	0.2921	0.2347
266091_at	AT2G37920	EMB1513 (EMBRYO DEFECTIVE 1513); copper io	0.1531	0.3615	0.3553	0.2905	0.1226	0.1777	0.1511	0.2484	0.2401	0.2885	0.0615	0.0899
266092_at	AT2G37880	similar to unknown protein [Arabidopsis thaliana] (T	-1.7104	0.0885	0.1724	-1.5464	0.1127	0.1697	0.6973	0.4126	0.3219	0.8613	0.3222	0.2493
266093_at	AT2G37990	ribosome biogenesis regulatory protein (RRS1) fam	0.3763	0.1984	0.2617	0.4322	0.1516	0.1995	0.3047	0.074	0.1184	0.3606	0.0466	0.0759
266094_at	AT2G37975	similar to unknown protein [Arabidopsis thaliana] (T	0.5834	0.1061	0.1884	0.7066	0.0655	0.1279	1.3428	0.0087	0.0375	1.466	0.0064	0.0248
266095_at	AT2G38050	DET2 (DE-ETIOLATED 2)	0.2983	0.0976	0.1804	0.4848	0.0249	0.0791	0.02479	0.8667	0.4832	0.2113	0.2017	0.1861
266096_at	AT2G38020	VCL1 (VACUOLELESS 1)	0.5581	0.0011	0.036	0.4747	0.002	0.033	-0.2592	0.0174	0.0527	-0.3425	0.0067	0.0253
266097_at	AT2G37970	SOUL-1; binding	0.07727	0.5051	0.4227	0.08609	0.4609	0.3683	0.4825	0.002	0.0211	0.4913	0.0019	0.0149
266098_at	AT2G37870	protease inhibitor/seed storage/lipid transfer protein	1.3582	0.04	0.1153	1.6532	0.0217	0.0748	0.4959	0.1714	0.193	0.7909	0.0567	0.0855
266099_at	AT2G38040	CAC3 (acetyl co-enzyme A carboxylase carboxyltra	-0.4887	0.0295	0.0997	-0.4187	0.0468	0.1072	-0.6204	0.0012	0.0186	-0.5505	0.0018	0.0148
266100_at	AT2G37980	similar to unknown protein [Arabidopsis thaliana] (T	0.5681	0.1389	0.2163	0.001505	0.9963	0.5432	-0.2213	0.4079	0.3199	-0.7879	0.3303	0.0585
266101_at	AT2G37940	similar to phosphatidic acid phosphatase-related / P	0.06676	0.7872	0.5198	0.05858	0.8125	0.4937	0.1059	0.5743	0.3883	0.09775	0.6031	0.3642
266102_at	AT2G40720	pentaticcopeptide (PPR) repeat-containing protein	-0.1935	0.5527	0.4421	-0.4312	0.2226	0.2474	-0.4435	0.2121	0.2192	-0.6812	0.0849	0.1089
266103_at	AT2G45140	vesicle-associated membrane protein, putative / VA	0.3115	0.1273	0.2061	0.4341	0.0555	0.1169	0.5351	0.03	0.0705	0.6578	0.0154	0.0396
266104_at	AT2G45150	phosphatidate cytidylyltransferase family protein	-0.5334	0.0817	0.1653	-0.5584	0.0726	0.1349	-0.2567	0.2807	0.2585	-0.2818	0.2432	0.2088
266105_at	AT2G45070	SEC61 BETA (suppressors of secretion-defective 6	0.2704	0.0446	0.1217	0.6465	0.0023	0.0335	0.9075	6.00E-04	0.0158	1.2836	2.00E-04	0.0071
266106_at	AT2G45170	AIAT3/Be (AUTOPHAGY 8E); microtubule binding	-0.05072	0.9009	0.5514	0.517	0.2478	0.2624	0.5352	0.1264	0.1613	1.1029	0.0166	0.0411
266107_at	AT2G37910	cation/hydrogen exchanger, putative (CHX21)	0.2656	0.8038	0.5251	-1.3498	0.2487	0.2631	-0.09074	0.9254	0.4994	-1.7061	0.1344	0.1446
266108_at	AT2G37900	proton-dependent oligopeptide transport (POT) fam	0.3454	0.4497	0.3979	1.0238	0.0682	0.1309	-0.08525	0.7096	0.4346	0.5931	0.0497	0.079
266109_at	AT2G37890	mitochondrial substrate carrier family protein	0.3952	0.0914	0.1753	0.4351	0.0716	0.1339	-0.3848	0.0975	0.1389	-0.345	0.1257	0.1387
266110_at	AT2G02080	ATIDD4 (ARABIDOPSIS THALIANA INDETERMIN	0.1069	0.5787	0.4521	0.0715	0.7045	0.4606	-0.5858	0.0256	0.065	-0.6202	0.0213	0.0475
266111_at	AT2G02070	similar to unknown protein [Arabidopsis thaliana] (T	-0.381	0.6517	0.4766	1.2325	0.1902	0.2265	-0.6045	0.4828	0.3522	1.009	0.2666	0.2211
266112_x_at	AT2G02210;AT3G47260	[AT2G02210, transposable element gene];[AT3G47	-0.7124	0.3677	0.3583	1.3121	0.1351	0.1869	-1.0526	0.2075	0.2163	0.9719	0.2378	0.206
266113_x_at	no_match	no_match	0.6485	0.516	0.4276	-0.5591	0.5727	0.4129	0.2076	0.8309	0.473	-1	0.3341	0.2552
266114_at	no_match	no_match	0.937	0.0176	0.0794	0.8443	0.0247	0.0788	-0.3304	0.1846	0.2018	-0.4231	0.1096	0.1274
266115_at	AT2G02140	LCR72/PDF2.6 (Low-molecular-weight cysteine-rich	-1.376	0.2611	0.3003	-0.6371	0.5776	0.415	-0.3919	0.7284	0.4413	0.347	0.7581	0.4161
266116_at	AT2G02180	TOM3 (tobamovirus multiplication protein 3)	0.1933	0.4253	0.3874	0.2974	0.2441	0.2606	-0.1639	0.2781	0.257	-0.05973	0.6714	0.3879
266117_at	AT2G02130	reencr1 family protein	0.02069	0.9357	0.5611	0.0233	0.9276	0.5261	0.004922	0.9838	0.5136	0.007532	0.9749	0.4768
266118_at	AT2G02130	LCR68/PDF2.3 (Low-molecular-weight cysteine-rich	-0.07627	0.8256	0.5311	0.3051	0.3999	0.3412	1.0478	0.0319	0.0727	1.4292	0.0116	0.0338
266119_at	AT2G02100	LCR69/PDF2.2 (Low-molecular-weight cysteine-rich	1.3693	0.0319	0.1035	1.9815	0.0095	0.0532	0.8387	0.028	0.0681	1.4509	0.0043	0.0209
266120_at	AT2G02070	ATIDD6 (ARABIDOPSIS THALIANA INDETERMIN	0.03307	0.7632	0.5125	0.007737	0.9435	0.5302	0.08389	0.1816	0.1865	0.1248	0.0635	0.0916
266121_at	AT2G02160	zinc finger (CCCH-type) family protein	0.1909	0.2909	0.3179	0.4356	0.0501	0.1111	-0.7575	0.0069	0.0339	-0.5128	0.0258	0.0533
266122_at	AT2G02090	CHR19/ETL1 (chromatin remodeling 19); ATP bind	0.4344	0.083	0.1668	0.4309	0.0847	0.1465	-0.6361	0.011	0.0416	-0.6396	0.0108	0.0326
266123_at	AT2G45180	protease inhibitor/seed storage/lipid transfer protein	0.6044	0.0085	0.0548	-0.7195	0.0034	0.0374	0.01472	0.8897	0.4896	-0.1003	0.371	0.2716
266124_at	AT2G45080	CYCP3;1 (cyclin p3;1); cyclin-dependent protein kin	-0.5239	0.32	0.3344	0.3458	0.4956	0.3827	-0.1519	0.6716	0.4215	0.7178	0.097	0.1183
266125_at	AT2G45050	zinc finger (GATA type) family protein	0.258	0.1179	0.1986	0.5847	0.0108	0.0559	-0.5323	0.0149	0.0486	-0.2056	0.1886	0.1786
266126_at	AT2G45040	matrix metalloproteinase	-0.0315	0.9678	0.5692	0.1522	0.806	0.4915	0.2697	0.7314	0.4422	0.4934	0.5375	0.3404
266127_s_at	AT1G45332;AT2G45030	elongation factor/elongation factor, putative]	0.4572	0.0246	0.0912	0.4598	0.0242	0.0782	0.3473	0.056	0.101	0.3446	0.0572	0.086
266128_at	no_match	CCD7 (more axillary growth 3)	-1.5385	0.1358	0.2139	1.0238	0.2826	0.2824	-0.9799	0.3008	0.2691	1.5823	0.1277	0.1401
266129_at	AT2G44990	transcription regulatory protein SNF2, putative	0.624	0.029	0.0987	0.9351	0.0075	0.0487	-0.5949	0.0336	0.0749	-0.2837	0.2042	0.1874
266130_at	AT2G44980	scarecrow transcription factor family protein	0.09104	0.3387	0.3448	-0.3153	0.0198	0.072	-0.419	0.0072	0.0342	-0.8254	6.00E-04	0.01
266131_at	AT2G45160	SPX (SYG1/Pho81/XPR1) domain-containing prote	0.9944	0.3492	0.3495	1.2088	0.2674	0.274	0.03787	0.9698	0.5099	0.2522	0.8015	0.4291
266132_at	AT2G45120	zinc finger (C2H2 type) family protein	-2.0596	0.1409	0.2183	-0.2096	0.8612	0.5074	-1.0112	0.3839	0.3096	0.8388	0.4631	0.3113
266133_at	AT2G45110;AT1G65681	[AT2G45110, ATEXP8A (ARABIDOPSIS THALIAN	1.9162	0.1611	0.2343	0.2777	0.8157	0.4948	0.4675	0.6967	0.4301	-1.1709	0.3532	0.2641
266134_s_at	AT2G45100	RNA polymerase II transcription factor	0.3377	0.3852	0.3674	-0.8263	0.0757	0.1379	0.006557	0.9856	0.514	-1.1574	0.0289	0.0569
266135_at	AT2G45060	similar to unknown protein [Arabidopsis thaliana] (T	0.01432	0.931	0.5601	0.4067	0.0589	0.1206	-0.5307	0.002	0.0214	-0.1383	0.1365	0.1459
266136_at	AT2G45050	similar to unknown protein [Arabidopsis thaliana] (T	0.8618	0.0136	0.0719	0.4575	0.0893	0.1506	0.08563	0.3529	0.2947	-0.3187	0.0174	0.0422
266137_at	AT2G45010	similar to unknown protein [Arabidopsis thaliana] (T	0.2608	0.3052	0.3257	0.1092	0.446	0.3622	0.5059	0.0163	0.051	0.4631	0.0218	0.0482
266138_at	AT2G45060	protease inhibitor/seed storage/lipid transfer protein	0.1442	0.0065	0.0548	-0.7195	0.0034	0.0374	0.01472	0.8897	0.4896	-0.1003	0.371	0.2716
266139_at	AT2G28085	auxin-responsive family protein	-0.8186	0.4716	0.4082	0.3028	0.7836	0.4844	1.4518	0.2318	0.2304	2.5732	0.067	0.0944
266140_at	AT2G28120	nodulin family protein	-0.04292	0.9087	0.5536	0.1595	0.6738	0.4499	-0.5091	0.0165	0.0513	-0.3067	0.075	0.1008
266141_at	AT2G28060	LCR79/PDF2.1 (Low-molecular-weight cysteine-rich	0.05228	0.8742	0.5451	-1.7437	0.0333	0.0903	1.378	0.0516	0.0962	-0.498	0.4131	0.2896
266142_at	AT2G39030	GCN5-related N-acetyltransferase (GNAT) family pr	0.8303	0.0137	0.0719	0.8028	0.0153	0.0649	0.281	0.1454	0.1756	0.2535	0.1788	0.1726
266143_at	AT2G38905	hydrophobic protein, putative / low temperature and	0.15	0.6985	0.4921	-0.5655	0.1916	0.2271	-0.3531	0.2537	0.243	-1.0686	0.0157	0.0399
266144_at	AT2G12170	unknown protein	-1.1241	0.1863	0.2253	-0.7813	0.3303	0.3085	0.3339	0.6607	0.4181	0.6767	0.3918	0.2807
266145_at	no_match	no_match	0.5765	0.7307	0.5027	2.7463	0.1534	0.2006	-2.2699	0.1388	0.1703	-0.1	0.9391	0.4681
266146_at	no_match	no_match	0.4287	0.6524	0.4768	1.7813	0.1136	0.1703	-0.3296	0.6221	0.4054	1.023	0.1733	0.1692
266147_at	AT2G12220	pseudogene, C-1-tetrahydrofolate synthase, blastp	-2.4428	0.277	0.3099	0.6305	0.7618	0.478	-1.4287	0.5028	0.3605	1.6445	0.4449	0.3039
266148_x_at	AT1G36460;AT2G12240;A	[AT1G36460, transposable element gene];[AT2G12	-0.2928	0.7684	0.5141	0.9206	0.3778	0.3309	-2.0586	0.091	0.1334	-0.8451	0.4144	0.2901
266149_x_at	AT1G50850;AT2G12250	[AT1G50850, transposable element gene];[AT2G12	0.09735	0.8653	0.5423	-0.00063	0.9991	0.5438	0.09315	0.8411	0.4759	-0.00482	0.9917	0.4805
266150_x_at	AT2G12290;AT4G19700	[AT2G12290, similar to protein binding / zinc ion bir	1.1447	0.0035	0.0448	1.3758	0.0017	0.0321	-0.0507	0.702	0.4319	0.1804	0.2171	0.1947
266151_x_at	AT2G12300	transposable element gene	-0.5565	0.5921	0.4568	0.3678	0.7203	0.4656	-1.2527	0.2608	0.247	-0.3283	0.7489	0.4134
266152_s_at	AT3G31908;AT3G32377;A	[AT3G31908, pseudogene, similar to aintegumenta	0.7441	0.3591	0.3541	-0.5453	0.4903	0.3805	0.2424	0.7529	0.4491	-1.047	0.219	0.1956
266153_at	AT2G12320	transposable element gene	0.03251	0.9728	0.5705	-1.6052	0.1482	0.1968	-0.2012	0.8297	0.4726	-1.8389	0.1038	0.1233
266154_at	AT2G12190	cytochrome P450, putative	0.4948	0.2634	0.3017	0.2201	0.594	0.421	0.05234	0.8972	0.4916	-0.2223	0.5904	0.3601
266155_at	no_match	no_match	0.3013	0.4684	0.4065	0.6474	0.1607	0.2063	-0.5462	0.0857	0.1291	-0.2001	0.4523	0.307
266156_at	AT2G28110	FRA8 (FRAGILE FIBER8); transferase	1.4399	0.0333	0.1056	1.912	0.0133	0.0615	-0.1946	0.4668	0.346	0.2775	0.3157	0.2464
266157_at	AT2G28100	ATFUC1 (ALPHA-L-FUCOSIDASE 1); alpha-L-fuco	-0.123	0.792	0.5214	-0.16	0.7325	0.4689	-1.7511	0.016	0.0505	-1.788	0.0149	0.0388
266158_at	AT2G28070	ABC transporter family protein	0.4374	0.0325	0.1046	0.3054	0.0884	0.1499	-0.5584	0.0149	0.0486	-0.6905	0.0071	0.0263
266159_at	AT2G28030	aspartyl protease family protein	-0.7014	0.5363	0.4355	-1.4259	0.2415	0.2587	-1.1327	0.3365	0.2866	-1.8572	0.1481	0.1535
266160_at	AT2G28180	ATCHX8 (cation/hydrogen exchanger 8); monovale	0.4474	0.3628	0.3558	0.7494	0.1608	0.2064	-0.1311	0.7252	0.4402	0.1709	0.6488	0.3804
266161_at	AT2G28170	ATCHX7 (cation/hydrogen exchanger 7); monovale	-0.5479	0.4174	0.3836	0.1136	0.8605	0.5073	0.695	0.2779	0.2569	1.3565	0.0705	0.0973
266162_at	no_match	no_match	0.643	0.2598	0.2996	0.281	0.5971	0.4222	0.0951	0.8556	0.48	-0.2669	0.615	0.3684
266163_at	AT2G28130	similar to unnamed protein product [Vitis vinifera] (G	-0.3083	0.3159	0.332	0.1871	0.5251	0.3941	-0.1706	0.24	0.2352	0.3249	0.0584	0.0871
266164_at	AT2G28050	pentaticcopeptide (PPR) repeat-containing protein	0.385	0.4146	0.3821	-0.9927	0.079	0.1409	0.205	0.5995	0.398	-1.1727	0.0312	0.0995
266165_at	AT2G28190	CSD2 (COPPER/ZINC SUPEROXIDE DISMUTASE	0.8703	0.0145	0.0731	1.1382	0.0057	0.0436	0.5607	0.0129	0.0452	0.8285	0.0032	0.0185
266166_at	AT2G28080	glycosyltransferase family protein	0.3954	0.1788	0.2472	0.3606	0.2118	0.2408	-0.2699	0.3288	0.2828	-0.3047	0.278	0.2271
266167_at	AT2G38860	YLS5 (yellow-leaf-specific gene 5)	1.3381	0.0097	0.0633	0.7478	0.0605	0.1222	0.895	0.0176	0.053	0.3047	0.2552	0.2152
266168_at	AT2G38870	protease inhibitor, putative	-0.3261	0.3732	0.361	-0.3888	0.2983	0.2907	1.0119	0.009	0.038	0.9491	0.0113	0.0332
266169_at	AT2G38900	serine protease inhibitor, potato inhibitor I-type fami	-0.3385	0.8084	0.5263	1.4228	0.3374	0.3122	-1.5884	0.2909	0.2641	0.1728	0.9012	0.4576
266170_at	AT2G39050	hydroxyproline-rich glycoprotein family protein	0.5844	4.00E-04	0.032	0.7078	2.00E-04	0.0249	0.736	2.00E-04	0.0126	0.8594	1.00E-04	0.0059
266171_at	AT3G58880	RNA_HYP_ATNF-YB1/HAP3/HAP3A (NUCLEAR FAC	-0.2998	0.2936	0.3701	0.1728	0.2147	0.1452	0.5252	0.3692	0.3151	0.6151	0.0175	0.0423
266172_at	AT3G39010	PIP2;6/PIP2E (plasma membrane intrinsic protein 2	-0.6262	0.0327	0.1049	-0.5897	0.0392	0.0981	-0.4194	0.0778	0.122	-0.383	0.0977	0.1188
266173_at	AT2G02410	similar to unnamed protein product [Vitis vinifera] (G	0.2362	0.7464	0.5078	1.2625	0.1377	0.189	-0.8059	0.284	0.2602	0.2204	0.7524	0.4145
266174_at	AT2G02440	unknown protein	-0.2248	0.5008	0.4209	-0.7004	0.0827	0.1444	0.203	0.5409	0.3756	-0.2726	0.4208	0.2928
266175_at	AT2G02450	ANAC034/ANAC035 (Arabidopsis NAC domain con	-0.5097	0.2801	0.3114	-0.5506	0.2489	0.2632	0.724	0.0569	0.1018	0.683	0.0666	0.0941
266176_at	AT2G02250	ATPP2-B2 (Phloem protein 2-B2); carbohydrate bin	0.3701	0.3769	0.3627	-0.1233	0.7574	0.4774	0.02127	0.9572	0.5071	-0.4722	0.274	0.225
266177_at	AT2G02270	pseudogene, F-box protein (SKP1 interacting partne	-0.6819	0.382	0.3656	-0.9461	0.245	0.261	-0.4502	0.5524	0.3799	-0.7143	0.3621	0.2679
266178_at	AT2G02280	ATPP2-B4 (Phloem protein 2-B4); carbohydrate bin	0.3854	0.7161	0.4981	-0.595	0.5791	0.4158	-0.2925	0.7817	0.4579	-1.2729	0.2666	0.2211
266179_at	AT2G02300	ATPP2-B5 (Phloem protein 2-B5); carbohydrate bin	1.8983	0.072	0.1546	-0.2697	0.7473	0.474	1.1762	0.2066	0.2157	-0.9917	0.2731	0.2245
266180_at	AT2G02470	PHD finger family protein	0.1756	0.5683	0.4483	0.2117	0.4958	0.3828	0.4457	0.1901	0.2056	0.4818	0.1637	0.1635
266181_at	AT2G02390	ATGSTZ1 (GLUTATHIONE S-TRANSFERASE 18);	1.3148	0.0183	0.0806	1.1617	0.0273	0.0826	0.6555	0.0477	0.0917	0.5023	0.0966	0.118
266182_at	AT2G02370	similar to unknown protein [Arabidopsis thaliana] (T	0.6707	0.0109	0.0655	0.6428	0.0126	0.06	-0.145	0.386	0.3104	-0.173	0.3107	0.2437
266183_at	no_match	no_match	-1.0741	0.4524	0.3993	-0.0798	0.9537	0.5328	-0.4193	0.7623	0.4518	0.5761	0.6787	0.3902
266184_s_at	AT3G54700;AT2G38940	[AT3G54700, carbohydrate transmembrane transpo	-0.1297	0.7976	0.5232	0.2064	0.6851	0.4539	-0.5427	0.3153	0.2759	-0.2066	0.6849	0.3922
266185_at	AT2G38950	transcription factor jumonji (jmj) family protein / zinc	0.6055	0.005	0.0504	0.5472	0.0072	0.0478	-0.1384	0.2694	0.2519	-0.1967	0.1427	0.1499
266186_at	AT2G38960	AERO2 (ARABIDOPSIS ENDOPLASMIC RETICUL	0.1662	0.6181	0.4658	-0.1573	0.6363	0.437	0.03971	0.9036	0.4933	0.04857	0.8823	0.4521
266187_at	AT2G38970	zinc finger (C3HC4-type RING finger) family protein	-0.2369	0.5372	0.4358	-0.1091	0.7718	0.4811	-0.2396	0.3882	0.3113	-0.1117	0.6753	0.3891
266188_at	AT2G39000	GCN5-related N-acetyltransferase (GNAT) family pr	0.3733	0.062	0.143	0.3641	0.0664	0.129	-0.9117	0.0033	0.0255	-0.921	0.0032	0.0183
266189_at	AT2G39020	GCN5-related N-acetyltransferase (GNAT) family pr	0.1783	0.1865	0.253	-0.199	0.15	0.198	0.5242	8.00E-04	0.0167	0.5035	0.001	0.0121
266190_at	AT2G38840	guanylate-binding family protein	-0.1293	0.6536	0.4771	-0.1572	0.5878	0.4187	-0.07214	0.6128	0.402	-0.1	0.4896	0.3217
266191_at	AT2G39040	peroxidase, putative	0.06913	0.9629	0.568	0.06789	0.9635	0.5349	-0.9902	0.5172	0.3659	-0.9915	0.5167	0.3322
266192_at	AT2G39080	binding / catalytic	0.1537	0.2503	0.2937	0.01363	0.9109	0.5218	0.1067	0.4039	0.3181	-0.03338	0.7849	0.4243
266193_at	AT2G39080	binding / catalytic	-0.1983	0.4415	0.3944	-0.1144	0.6485	0.4411	-0.8342	0.0142	0.0475	-0.7502	0.0202	0.0458
266194_at	AT2G39090	tetratricopeptide repeat (TPR)-containing protein	0.2267	0.3097	0.3283	0.05122	0.8058	0.4915	-0.1091	0.599	0.3977	-0.2846	0.2111	0.1914
266195_at	AT2G39100	zinc finger (C3HC4-type RING finger) family protein	0.19	0.4347	0.3914	0.6653	0.0385	0.0972	-0.7972	0.022	0.0598	-0.3219	0.2156	0.1939
266196_at	AT2G39110	protein kinase, putative	1.0577	0.1934	0.2579	-0.1181	0.8701	0.5099	-0.3945	0.5915	0.3952	-1.5702	0.0813	0.106
266197_at	AT2G39120	similar to unknown protein [Arabidopsis thaliana] (T	0.2352	0.2094	0.2678	-0.1821	0.3117	0.2983	0.1425	0.3061	0.2717	-0.2748	0.0865	0.1101
266198_at	AT2G38890	similar to hypothetical protein [Vitis vinifera] (GB:CA	-1.6953	0.1597	0.2332	-1.1622	0.3026	0.2928	-0.3833	0.6978	0.4304	0.1498	0.8784	0.4509
266199_at	AT2G38910	CPK20 (calcium-dependent protein kinase 20); calc	-0.5785	0.4016	0.3761	0.8148	0.2572	0.2684	-0.9708	0.1908	0.206	0.4225	0.5312	0.3384
266200_at	AT2G38920	SPX (SYG1/Pho81/XPR1) domain-containing prote	0.5493	0.2317	0.283	-0.1693	0.6865	0.4544	-0.1484	0.7229	0.4396	-0.867	0.0903	0.1131
266201_at	AT2G39060	nodulin MtN3 family protein	-0.2513	0.8028	0.525	0.4998	0.6236	0.4322	-0.2981	0.6873	0.4268	0.4529	0.5466	0.3436
266202_at	AT2G02400	cinnamoyl-CoA reductase family	0.02112	0.827	0.5316	0.02497	0.7964	0.4885	-0.000083	0.9931	0.516	0.003017	0.975	0.4768
266203_at	AT2G02230	ATPP2-B1 (Phloem protein 2-B1); carbohydrate bin	1.8269	4.00E-04	0.032	2.6497	1.00E-04	0.0249	-0.3206	0.1156	0.1528	0.5022	0.0349	0.0632
266204_at	AT2G02410	similar to unnamed protein product [Vitis vinifera] (G	0.01972	0.9681	0.5693	0.02445	0.9605	0.5343	-0.988	0.0395	0.0822	-0.9833	0.04	0.0691
266205_s_at	AT1G08200;AT2G27860	[AT1G08200, AXS2 (UDP-D-APIOSE/UDP-D-XYL(	-0.5308	0.0117	0.0677	-0.3499	0.0442	0.1041	-0.3649	0.0204	0.0575	-0.184	0.1336	0.1441
266207_at	AT2G27730	Identical to Uncharacterized mitochondrial protein A	0.8282	0.0041	0.0468	0.8951	0.0031	0.0359	1.0323	0.0019	0.0206	1.0901	0.0015	0.0137
266208_at	AT2G27680	aldo/keto reductase family protein	-0.6144	0.0218	0.0866	-0.5727	0.0272	0.0825	-0.2891	0.0803	0.124	-0.2473	0.1171	0.1327
266209_at	AT2G27760	ATIPT2 (TRNA ISOPENTENYLTRANSFERASE);	0.3457	0.2073	0.2668	0.3527	0.2001	0.2329	-0.54	0.0788	0.1227	-0.533	0.0814	0.1061
266210_at	AT2G27750	ATC (ARABIDOPSIS THALIANA CENTRORADIAL	0.9809	0.2319	0.2831	-0.5023	0.5026	0.3857	0.1767	0.8085	0.4662	0.6353	0.4048	0.286
266211_at	AT2G27530	60S ribosomal protein L10A (RPL10aB)	-0.00362	0.9619	0.5678	0.1578	0.0907	0.1519	-0.07675	0.3412	0.2888	0.08464	0.2997	0.2385
266212_at	AT2G06820	transposable element gene	-0.00307	0.9981	0.5763	-0.9105	0.4878	0.3795	-0.06175	0.9425	0.5039	-0.9692	0.2369	0.2361
266213_at	AT2G06840	transposable element gene	0.09949	0.9398	0.5624	1.3072	0.3508	0.3182	-0.632	0.6366	0.41	0.5756	0.6661	0.3861
266213_s_at	AT2G06870;AT1G35760	[AT2G06870, transposable element gene];[AT1G35	-1.1884	0.1992	0.2619	0.4885	0.5619	0.409	-1.8997	0.07	0.1147	0.2228	0.7876	0.425
266214_at	AT2G06890	transposable element gene	-1.4258	0.2597	0.2996	-1.1129	0.3636	0.3246	1.3882	0.2705	0.2526	1.7011	0.1925	0.1806
266215_at	AT2G06850	EXGT-A4 (ENDOXYLOGLUCAN TRANSFERASE);	-1.9229	0.3579	0.3535	-0.378	0.3745	0.3296	0.4943	6.00E-04	0.0158	0.5092	6.00E-04	0.01
266216_at	AT2G28810	Dof-type zinc finger domain-containing protein	-0.02682	0.9082	0.5535	0.01998	0.9315	0.5269	0.122	0.6065	0.4002	0.1688	0.483	0.3188
266217_at	no_match	no_match	2.3382	0.0486	0.1269	0.07674	0.9311	0.5268	0.1407	0.8742	0.4852	-2.1208	0.0637	0.0917
266218_s_at	AT2G28850;AT2G28850	[AT2G28850, CYP710A4 (cytochrome P450, family	1.0056	0.3767	0.3626	0.05522	0.9591	0.534	0.7939	0.1771	0.1966	-0.1565	0.7632	0.4178
266219_at	AT2G28880	EMB1997 (EMBRYO DEFECTIVE 1997); anthranila	-0.3816	0.1284	0.207	-0.386	0.1251	0.1793	-0.3196	0.1844	0.2017	-0.3241	0.1797	0.1731
266220_at	AT2G28755	UDP-D-glucuronate carboxy-lyase-related	0.1498	0.9117	0.5545	0.6092	0.6563	0.444	0.1668	0.9018	0.493	0.6262	0.6476	0.3799
266221_at	AT2G28760	UXS6; catalytic	0.2051	0.3609	0.3551	0.3616	0.1434	0.1933	0.8412	0.006	0.0321	0.9976	0.0032	0.0184
266222_at	AT2G28780	similar to unknown protein [Arabidopsis thaliana] (T	-0.7144	0.4699	0.4072

266290_at	AT2G29490	ATGSTU1 (GLUTATHIONE S-TRANSFERASE 19)	-1.6902	0.0107	0.0549	-0.3334	0.4229	0.352	0.1938	0.6315	0.4084	1.5506	0.0143	0.038
266291_at	AT2G29320	tropinone reductase, putative / tropine dehydrogena	0.9753	0.1557	0.2302	0.5593	0.3733	0.3292	0.08578	0.7642	0.4524	-0.3303	0.284	0.2303
266292_at	AT2G29350	SAG13 (Senescence-associated gene 13); oxidore	1.2735	0.0317	0.1031	1.6062	0.015	0.0645	-0.2409	0.1998	0.2117	0.09174	0.5904	0.3601
266293_at	AT2G29360	tropinone reductase, putative / tropine dehydrogena	-0.4192	0.0824	0.166	-0.3001	0.1741	0.2155	-0.5582	0.0373	0.0797	-0.4391	0.0731	0.0992
266294_at	AT2G29500	17.6 kDa class I small heat shock protein (HSP17.6	-0.1421	0.5578	0.4441	0.6353	0.0461	0.1065	0.2383	0.3444	0.2905	1.0157	0.0103	0.0317
266295_at	AT2G29550	TUB7 (tubulin beta-7 chain)	-0.5433	0.0855	0.1696	-0.4896	0.11	0.1674	0.2063	0.2254	0.2267	0.26	0.1454	0.1518
266296_at	AT2G29420	ATGSTU7 (GLUTATHIONE S-TRANSFERASE 25)	0.2266	0.5087	0.4245	0.285	0.4136	0.3476	0.2466	0.161	0.1862	0.305	0.1009	0.1212
266297_at	AT2G29570	PCNA2 (PROLIFERATING CELL NUCLEAR ANTIG	0.2384	0.2134	0.2706	0.1359	0.4488	0.3624	-0.05957	0.729	0.4415	-0.1621	0.369	0.2708
266298_at	AT2G29590	thioesterase family protein	0.127	0.5157	0.4276	0.6542	0.0214	0.0745	0.3104	0.0683	0.1134	0.8376	0.0026	0.0169
266299_at	AT2G29450	ATGSTU5 (Arabidopsis thaliana Glutathione S-tran	-1.2998	0.0068	0.0558	-0.9887	0.0175	0.0686	-0.00177	0.969	0.5096	0.3093	0.0019	0.0151
266300_at	AT2G29420	PIN4 (PIN-FORMED 4); auxin:hydrogen symporter	-0.3766	0.1184	0.1989	-0.4387	0.0821	0.1437	-0.06734	0.6645	0.4193	-0.1294	0.4198	0.2924
266301_at	AT2G29660	AtMYB81 (myb domain protein 81); DNA binding / tr	1.366	0.2154	0.2719	-1.1274	0.2916	0.2874	1.3499	0.2198	0.2235	-1.1435	0.2857	0.2312
266302_at	AT2G29700	EIL1 (ETHYLENE-INSENSITIVE3-LIKE 1); transcrip	-0.06111	0.5003	0.4206	0.06254	0.491	0.3807	-0.6449	3.00E-04	0.0138	-0.5212	7.00E-04	0.0105
266303_at	AT2G29760	ATP binding / protein serine/threonine kinase	-0.2431	0.277	0.3099	-0.2783	0.2235	0.2478	0.3119	0.182	0.2002	0.2767	0.2256	0.1992
266304_at	AT2G29090	similar to unknown protein [Arabidopsis thaliana] (T	0.2961	0.2116	0.2693	0.02108	0.9209	0.5242	-0.02168	0.9186	0.4974	-0.2967	0.2108	0.1913
266305_at	AT2G27120	POL2B/TIL2 (TILTED2); DNA-directed DNA polyme	-2.5085	0.1546	0.2295	-0.8796	0.5722	0.4128	-1.1529	0.4171	0.3239	0.476	0.7279	0.4065
266306_at	AT2G29570	exonuclease family protein	0.3123	0.0625	0.1436	0.5841	0.0087	0.0513	0.1694	0.2212	0.2244	0.4412	0.0196	0.0449
266307_at	AT2G27000	CYP705A8 (cytochrome P450, family 705, subfamil	-0.1048	0.9239	0.558	0.8689	0.4466	0.3623	-0.4934	0.5575	0.3819	0.4803	0.5675	0.3518
266308_at	AT2G27010	CYP705A9 (cytochrome P450, family 705, subfamil	-0.2689	0.8383	0.535	0.516	0.6976	0.4581	-1.23	0.3757	0.3056	-0.4451	0.7368	0.4093
266309_at	AT2G27140	heat shock protein family	0.1131	0.7139	0.4972	0.4077	0.2288	0.2508	0.8368	0.0314	0.0721	1.1314	0.0118	0.034
266310_at	AT2G26990	FUS12 (FUSCA 12)	0.4328	0.0468	0.1245	0.6727	0.0115	0.058	-0.1188	0.479	0.3511	0.1212	0.4708	0.314
266311_at	AT2G27130	protease inhibitor/seed storage/lipid transfer protein	-0.3161	0.1442	0.2208	-0.2892	0.1727	0.2146	0.4289	0.0381	0.0806	0.4557	0.0317	0.06
266312_at	AT2G27020	PAG1 (20S proteasome alpha subunit G1); peptidas	0.7275	0.0253	0.0922	0.7037	0.0281	0.0835	0.2562	0.2248	0.2264	0.2324	0.2632	0.2193
266313_at	AT2G26980	CIPK3 (CBL-INTERACTING PROTEIN KINASE 3);	0.3522	0.2418	0.2887	0.3745	0.2181	0.2447	-0.8857	0.001	0.0175	-0.8633	0.0011	0.0124
266314_at	AT2G27040	AGO4 (ARGONAUTE 4); nucleic acid binding	0.05562	0.7285	0.502	-0.6103	0.015	0.0645	0.2137	0.0888	0.1314	-0.4522	0.009	0.0296
266315_at	AT2G27100	SE (SERRATE); transcription factor	0.404	0.0868	0.1706	0.3306	0.1383	0.1893	-0.05102	0.7249	0.4402	-0.1245	0.409	0.2879
266316_at	AT2G27080	harpin-induced protein-related / HIN1-related / harp	-0.6222	0.2781	0.3103	-0.6512	0.2595	0.2697	0.8756	0.0524	0.0971	0.8465	0.0576	0.0864
266317_at	AT2G27030	CAM5 (CALMODULIN 5); calcium ion binding	-1.6018	0.726	0.5013	0.2825	0.2559	0.2678	0.509	0.0885	0.1135	0.8717	0.0132	0.0365
266318_at	AT2G27110	FRS3 (FAR1-RELATED SEQUENCE 3); zinc ion bi	0.08535	0.7529	0.5093	-0.07976	0.7684	0.48	-0.3173	0.782	0.257	-0.3117	0.2855	0.2311
266319_s_at	AT3G10280,AT2G46720	[AT3G10280, fatty acid elongase 3-ketoacyl-CoA s	-0.1442	0.4194	0.3846	-0.5129	0.0329	0.0899	-0.1548	0.3725	0.3042	-0.5236	0.0275	0.0551
266320_at	AT2G46640	unknown protein	0.1783	0.3214	0.3352	-0.519	0.0302	0.0863	0.9613	4.00E-04	0.0147	0.6206	0.0021	0.0155
266321_at	AT2G46660	CYP78A6 (cytochrome P450, family 78, subfamily A	0.2836	0.2359	0.285	-1.1566	0.0047	0.0418	0.919	0.0107	0.041	-0.5212	0.0626	0.0908
266322_at	AT2G46690	auxin-responsive family protein	-0.463	0.2651	0.3022	0.06158	0.8716	0.5104	0.1548	0.3555	0.2959	0.6794	0.0102	0.0315
266323_at	AT2G46700	calcium-dependent protein kinase, putative / CDPK	0.08673	0.7578	0.511	0.05116	0.8583	0.5067	-0.2481	0.3214	0.2788	-0.2857	0.2628	0.2192
266324_at	AT2G46710	rac GTPase activating protein, putative	-0.9997	0.0256	0.0928	-0.3102	0.3425	0.3145	-0.8114	0.0038	0.0271	-0.1219	0.4166	0.2911
266325_at	AT2G46630	pseudogene of unknown protein	-0.3382	0.1079	0.1901	-0.2465	0.2069	0.2376	1.1117	0.0025	0.0232	1.2034	0.0018	0.0148
266326_at	AT2G46650	RS 41 (cytochrome b5 family protein #1); heme bind	-1.0674	0.0099	0.0637	-0.5422	0.0197	0.1405	0.8527	0.0126	0.0444	1.3779	0.0022	0.0158
266327_at	AT2G46680	ATHB-7 (ARABIDOPSIS THALIANA HOMEOBOX	1.1489	0.003	0.0436	1.74	6.00E-04	0.027	0.1237	0.4799	0.3514	0.7147	0.0108	0.0326
266328_at	AT2G01600	epsin N-terminal homology (ENTH) domain-contain	0.5987	0.0026	0.0426	0.3455	0.0183	0.0699	0.105	0.3069	0.272	-0.1481	0.1742	0.1698
266329_at	AT2G01590	similar to unknown protein product [Vitis vinifera] (G	-0.8108	0.0327	0.1431	-0.4031	2.00E-04	0.0249	-0.2024	0.0312	0.0719	-0.4347	0.0022	0.0157
266330_at	AT2G01530	MLP329 (MLP-LIKE PROTEIN 329)	0.4403	0.4368	0.3924	-0.4681	0.4109	0.3464	0.2748	0.6188	0.4042	-0.6336	0.2822	0.2292
266331_at	AT2G01570	RGA1 (REPRESSOR OF GA1-3 1); transcription fa	0.07102	0.8026	0.5249	0.05376	0.8497	0.5043	-0.2727	0.2716	0.2531	-0.29	0.2469	0.2107
266332_at	AT2G46410	3'-5' exonuclease/ nucleic acid binding	-0.3213	0.6446	0.4747	-1.0249	0.1874	0.2247	-1.1085	0.1609	0.1861	-1.8121	0.0484	0.0777
266333_at	AT2G32410	AXL (AXR1-LIKE); catalytic	-0.338	0.4293	0.3887	-0.3337	0.4346	0.3574	-0.9868	0.0597	0.1049	-0.9826	0.0604	0.0889
266334_at	AT2G32380	similar to unknown protein [Arabidopsis thaliana] (T	-0.2086	0.4613	0.4036	0.06548	0.8109	0.4933	0.2252	0.2171	0.2219	0.4993	0.0315	0.0598
266335_at	AT2G32440	KAO2 (ENT-KAURENOIC ACID HYDROXYLASE 2	0.1638	0.5371	0.4358	-0.4069	0.1693	0.212	-0.4262	0.1542	0.1818	-0.5969	0.0148	0.0387
266336_at	AT2G32270	ZIP3 (ZINC TRANSPORTER 3 PRECURSOR); zinc	0.4763	0.6603	0.4794	0.4614	0.67	0.4486	0.1921	0.8577	0.4804	-0.7457	0.4993	0.3257
266337_at	AT2G32390	ATGLR3.5 (GLUTAMATE RECEPTOR 6)	-0.6981	0.0216	0.0863	-0.457	0.0748	0.1371	-0.7882	0.0145	0.048	-0.5471	0.0456	0.0749
266338_at	AT2G32400	GLR5 (Glutamate receptor 5)	-0.3021	0.1747	0.2446	-0.4692	0.0627	0.1245	0.05404	0.7749	0.4558	-0.113	0.5572	0.3478
266339_s_at	AT2G01360,AT2G01390	[AT2G01360, similar to pentatricopeptide (PPR) rep	0.1519	0.8989	0.5508	1.3384	0.299	0.291	-0.2441	0.8385	0.4752	0.9425	0.4483	0.3054
266340_at	AT2G01480	similar to unknown protein [Arabidopsis thaliana] (T	-0.3914	0.1015	0.1843	-0.2035	0.3325	0.3096	-1.271	0.0023	0.0227	-1.0831	0.0042	0.0208
266341_at	AT2G01510	pentatricopeptide (PPR) repeat-containing protein	-0.2893	0.5364	0.4355	-0.3432	0.4678	0.3712	-0.4114	0.3907	0.3124	-0.4657	0.338	0.257
266342_at	AT2G01540	C2 domain-containing protein	1.1285	9.00E-04	0.0349	1.4908	3.00E-04	0.0249	-0.109	0.442	0.335	0.2533	0.1187	0.1338
266343_at	AT2G01550	transposable element gene	-0.3481	0.6906	0.4894	-1.4061	0.1588	0.205	0.4298	0.6075	0.4005	-0.6282	0.4616	0.3107
266344_at	AT2G01580	similar to unknown protein [Arabidopsis thaliana] (T	0.2859	0.3806	0.3647	-0.2194	0.4919	0.3812	0.06171	0.8421	0.4764	-0.4437	0.2013	0.1859
266345_at	AT2G01410	similar to unknown protein [Arabidopsis thaliana] (T	0.6389	0.0221	0.0872	0.4468	0.0639	0.1262	0.3628	0.1081	0.1472	0.1707	0.3867	0.2786
266346_at	AT2G01430	homeobox-leucine zipper protein 17 (HB-17) / HD-Z	-2.5153	0.0398	0.115	-0.06979	0.9376	0.5284	0.002627	0.9976	0.5172	2.4481	0.0431	0.0724
266347_at	AT2G01440	ATP-dependent helicase	0.3134	0.1893	0.2548	0.127	0.5569	0.4072	-0.7787	0.0126	0.0446	-0.9651	0.006	0.0239
266348_at	AT2G01450	ATMPK17 (Arabidopsis thaliana MAP kinase 17); M	0.2021	0.3131	0.3304	-0.1847	0.3515	0.3188	-0.5869	0.0157	0.0499	-0.9737	0.0026	0.0169
266349_at	AT2G01460	phosphoribulokinase/uridine kinase family protein	0.5174	0.0881	0.1721	0.09458	0.7025	0.46	-1.5589	0.0022	0.0222	-1.9817	9.00E-04	0.0116
266350_at	AT2G01470	STL2P (SEC12P-LIKE PROTEIN); nucleotide bindi	0.3848	0.0063	0.0543	1.0513	1.00E-04	0.0249	-0.439	7.00E-04	0.016	0.2275	0.0085	0.0287
266351_at	AT2G01490	phytanoyl-CoA dioxygenase (PhyH) family protein	0.5206	0.0035	0.0448	0.8062	7.00E-04	0.027	-0.4303	0.0044	0.0284	-0.1447	0.1236	0.1375
266352_at	AT2G01610	invertase/pectin methylesterase inhibitor family prot	1.7225	0.0041	0.0468	2.123	0.0019	0.0329	0.02986	0.9232	0.4987	0.4304	0.2133	0.1926
266353_at	AT2G01520	MLP328 (MLP-LIKE PROTEIN 328)	-1.0806	0.3203	0.3345	-2.3236	0.0714	0.1337	0.8759	0.4101	0.3207	-0.3671	0.7197	0.4039
266354_at	AT2G01500	PFS2 (PRETTY FEW SEEDS 2); transcription factc	-0.8615	0.5296	0.433	0.3078	0.818	0.4953	-0.2112	0.8734	0.4851	0.9582	0.4841	0.3193
266355_at	AT2G01400	unknown protein	-0.4969	0.156	0.2303	-0.1045	0.7322	0.4689	-0.5108	0.1474	0.1771	-0.1184	0.699	0.3971
266356_at	AT2G32360	UCC1 (UCLACYANIN 1); copper ion binding	0.2625	0.792	0.5214	1.1283	0.2922	0.2878	0.9366	0.3713	0.3036	1.8024	0.125	0.1383
266357_at	AT2G32030	BAM6/BMY5 (BETA-AMYLASE 6); beta-amylase	-1.088	0.0311	0.1023	-1.2599	0.0195	0.0719	-0.04998	0.8025	0.4643	-0.2219	0.301	0.2391
266358_at	AT2G32280	similar to unknown protein [Arabidopsis thaliana] (T	2.6326	0.0339	0.1064	2.7243	0.0305	0.0867	0.4409	0.6237	0.4059	0.5327	0.5563	0.3474
266359_at	AT2G32260	sholinehosphate cytidylyltransferase, putative / pho	-0.02921	0.7814	0.518	0.1345	0.3661	0.3257	-0.1634	0.1125	0.1502	0.01033	0.8042	0.4586
266360_at	AT2G32250	FRS2 (FAR1-RELATED SEQUENCE 2); zinc ion b	-0.2611	0.302	0.3242	-0.3621	0.176	0.217	-0.7075	0.0266	0.0663	-0.8085	0.0173	0.042
266361_at	AT2G32450	calcium-binding EF hand family protein	-0.2615	0.3267	0.3383	-0.092	0.7144	0.4634	-0.2318	0.2619	0.2475	-0.06232	0.7434	0.4114
266362_at	AT2G32430	galactosyltransferase family protein	-0.3203	0.2106	0.2687	-0.5251	0.071	0.1333	-0.00972	0.9457	0.5046	-0.2146	0.185	0.1763
266363_at	AT2G41250	haloacid dehalogenase-like hydrolase family protein	1.0786	0.0714	0.154	1.0015	0.0863	0.1481	0.2707	0.004	0.0274	0.1936	0.0132	0.0364
266364_at	AT2G41230	unknown protein	1.3004	0.0656	0.1468	-0.4889	0.3977	0.3403	1.9578	0.0136	0.0464	0.1685	0.7353	0.4089
266365_at	AT2G41220	GLU2 (Glutamate synthase)	0.8552	0.0052	0.0513	0.7917	0.0068	0.0467	-0.5937	0.0049	0.0297	-0.6572	0.0034	0.019
266366_at	AT2G41420	proline-rich family protein	-0.2762	0.1293	0.2079	-0.00457	0.9763	0.5384	1.1781	8.00E-04	0.0162	1.4497	3.00E-04	0.0088
266367_s_at	AT2G41400,AT2G41390	[AT2G41400, similar to unknown protein [Arabidops	-2.1344	0.1053	0.1875	-1.0322	0.3702	0.3276	-0.4076	0.7107	0.435	0.6945	0.5346	0.3396
266368_at	AT2G41380	embryo-abundant protein-related	1.0924	0.0253	0.0922	1.0241	0.031	0.0874	0.3191	0.2223	0.2249	0.2508	0.3199	0.2483
266369_at	AT2G41370	BOP2 (BLADE ON PETIOLE2); protein binding	1.8841	0.0722	0.1549	1.4719	0.1309	0.1835	-0.2347	0.7775	0.4565	-0.6469	0.4515	0.3066
266370_at	AT2G41350	similar to unknown protein [Arabidopsis thaliana] (T	-0.2326	0.0637	0.1446	-0.2513	0.0515	0.1126	0.5026	0.0031	0.0251	0.484	0.0036	0.0194
266371_at	AT2G41410	calmodulin, putative	0.9401	0.0133	0.0709	1.1717	0.0062	0.0451	0.2138	0.0049	0.0296	0.4453	3.00E-04	0.0083
266372_at	AT2G41310	ATRR3 (RESPONSE REGULATOR 3); transcriptior	-0.9474	0.008	0.0587	-0.6994	0.0223	0.0754	-1.1012	8.00E-04	0.0161	-0.8532	0.002	0.0153
266373_x_at	AT4G10580,AT3G31970,A	[AT4G10580, transposable element gene];[AT3G31	1.1994	0.3094	0.3282	1.5089	0.2172	0.2441	-0.5761	0.6061	0.4001	-0.2667	0.8087	0.4313
266374_at	AT2G41640	transposable element gene	-0.3785	0.7522	0.5091	-1.0999	0.3813	0.3326	0.9287	0.4533	0.3401	0.2073	0.8621	0.4464
266375_at	AT2G41630	transposable element gene	-0.8489	0.6001	0.4597	0.5766	0.7191	0.465	-1.9651	0.2032	0.2137	-0.5396	0.6978	0.3967
266376_at	AT2G41620	xyloglucan:xyloglucosyl transferase, putative / xylog	0.8687	0.028	0.097	1.0696	0.0142	0.0631	-0.2529	0.1285	0.163	-0.05194	0.7146	0.4024
266377_at	AT2G41590	transposable element gene	-0.4334	0.3036	0.325	0.04564	0.9071	0.5207	-0.7369	0.1154	0.1527	-0.2579	0.5214	0.3344
266378_at	AT2G41700	unknown protein	0.7761	0.2715	0.3064	0.3317	0.6149	0.4288	1.229	0.1137	0.1513	0.7846	0.2671	0.2212
266379_at	AT2G41690	endo-1,4-beta-xylanase/ hydrolase, hydrolyzing O-g	-1.8404	0.1905	0.2558	-0.3326	0.7901	0.4861	-0.8854	0.4774	0.3504	0.6223	0.6114	0.3672
266380_at	AT2G41680	embryo-abundant protein-related	1.0984	0.0253	0.0922	1.0241	0.031	0.0874	0.3191	0.2223	0.2249	0.2508	0.3199	0.2483
266381_at	AT2G41670	ATSUC8 (SUCROSE-PROTON SYMPORTER 8);	-0.4275	0.4989	0.42	-0.03313	0.9569	0.5335	0.322	0.6057	0.4	0.7164	0.2812	0.2287
266382_at	AT2G41595	transposable element gene	-0.7348	0.0934	0.1771	-0.6147	0.1406	0.191	-0.03877	0.9135	0.4961	0.08132	0.8202	0.4342
266383_at	AT2G41580	ATPRB1 (Arabidopsis thaliana basic pathogenesis-	1.4939	0.1676	0.2395	2.9979	0.0278	0.0831	0.1646	0.8126	0.4674	1.6686	0.0622	0.0905
266384_at	AT2G41660	similar to hypothetical protein [Vitis vinifera] (GB:CA	-1.478	0.0095	0.0626	-1.3743	0.0122	0.0593	0.3606	0.3182	0.2774	0.4644	0.2163	0.1942
266385_at	AT2G41610	PR1 (PATHOGENESIS-RELATED GENE 1)	2.7583	0.0313	0.1026	2.8472	0.0283	0.0836	0.634	0.0432	0.0867	0.7228	0.0291	0.0571
266386_at	AT2G32370	DNA binding / transcription factor	-0.08319	0.8836	0.5471	-0.281	0.6261	0.4334	-2.2075	0.0144	0.0478	-2.4053	0.0107	0.0324
266387_at	AT2G32360	ubiquitin family protein	-0.799	0.5391	0.4366	0.02636	0.9834	0.54	-1.6113	0.1395	0.1708	-0.786	0.4201	0.2926
266388_at	AT2G32340	TraB family protein	-0.4566	0.0211	0.0853	0.6117	0.0078	0.0493	-1.5627	2.00E-04	0.0126	-0.4944	0.0147	0.0386
266389_s_at	AT2G32320,AT2G31580	[AT2G32320, similar to unknown protein [Arabidops	0.6572	0.0299	0.1005	0.4335	0.095	0.1554	-0.3366	0.0143	0.0476	-0.5602	0.0023	0.016
266390_at	AT2G32310	similar to transcription factor [Arabidopsis thaliana]	0.06792	0.9501	0.5646	1.4622	0.2246	0.2482	0.1059	0.9222	0.4985	1.6361	0.1836	0.1756
266391_at	AT2G41290	strictosidine synthase family protein	-0.6657	0.0059	0.0534	-0.7014	0.0049	0.0422	-0.3973	0.0331	0.0742	-0.433	0.0253	0.0525
266392_at	AT2G41280	M10	-1.0536	0.2491	0.2931	0.3494	0.6781	0.4512	0.02455	0.9765	0.5117	1.4275	0.1419	0.1494
266393_at	AT2G41260	M17	2.3299	0.0396	0.1149	1.7181	0.0908	0.152	1.1004	0.0549	0.0998	0.4885	0.2991	0.2382
266394_at	AT2G43130	ARA4 (Arabidopsis Rab GTPase homolog A5c); GT	-0.06921	0.8025	0.5249	0.1932	0.4971	0.3832	-0.2214	0.3824	0.3089	0.04097	0.8649	0.447
266395_at	AT2G43100	aconitase C-terminal domain-containing protein	-1.3871	0.0519	0.1307	-1.4405	0.0486	0.107	1.1402	0.0071	0.0341	1.0868	0.0084	0.0285
266396_at	AT2G38790	unknown protein	-0.3707	0.4086	0.3795	0.07759	0.8563	0.5062	0.2403	0.2722	0.2535	0.6886	0.0218	0.0482
266397_at	AT2G38690	unknown protein	2.6622	0.013	0.0704	-0.3548	0.6004	0.4237	0.6719	0.3311	0.2838	-2.3451	0.0182	0.0434
266398_at	AT2G38680	pyrimidine 5'-nucleotidase family protein / uridine m	-0.4743	0.2043	0.265	-0.06368	0.8487	0.504	-0.7472	0.0754	0.1196	-0.3366	0.3427	0.2592
266399_at	AT2G38670	PECT1 (PHOSPHORYLETHANOLAMINE CYTIDY	0.7475	0.0099	0.0638	0.9251	0.0046	0.0416	0.03561	0.7869	0.4593	0.2132	0.1585	0.1603
266400_at	AT2G38660	tetrahydrofolate dehydrogenase/cyclohydrolase, pu	0.3819	0.0789	0.1618	0.4272	0.0586	0.1203	0.1111	0.5073	0.3623	0.1564	0.3637	0.2685
266401_s_at	AT2G38620,AT3G54180	[AT2G38620, CDKB1;2 (cyclin-dependent kinase B	-0.9161	0.4432	0.3951	-1.2522	0.3099	0.2973	1.2456	0.061	0.1061	0.9095	0.1321	0.1431
266402_at	AT2G38780	binding	-0.8126	9.00E-04	0.0349	-1.1773	2.00E-04	0.0249	0.308	0.0242	0.0631	-0.05663	0.5517	0.3457
266403_at	AT2G38690	acid phosphatase class B family protein	-0.8351	0.3574	0.3533	-0.5348	0.4432	0.4015	-0.5465	0.5338	0.3727	-0.2462	0.7746	0.4214
266404_at	AT2G38590	F-box family protein	0.3437	0.5485	0.4405	-0.4271	0.4616	0.3686	-0.251	0.5499	0.379	-1.0218	0.0567	0.0855
266405_at	AT2G38580	similar to hydrogen ion transmembrane transporter	-0.1004	0.6904	0.4893	0.1657	0.5187	0.3919	-0.08956	0.6689	0.4208	0.1766	0.415	0.2904
266406_at	AT2G38570	similar to hypothetical protein [Vitis vinifera] (GB:CA	-0.3665	0.4645	0.405	-0.7121	0.182	0.2211	-0.3141	0.3116	0.2743	-0.6897	0.0692	0.0964
266407_at	AT2G38560	transcription factor S-II (TFIIS) domain-containing p	0.2111	0.4872	0.4146	0.1606	0.5919	0.4203	-0.6646	0.0402	0.0831	-0.7151	0.0322	0.0606
266408_at	AT2G38520	transposable element gene	-0.1059	0.828	0.5318	0.2067	0.6745	0.45	0.3534	0.4824	0.3521	0.666	0.2187	0.1954
266409_at	AT2G38510	MATE efflux protein-related	-1.0437	0.1349	0.2133	1.0052	0.1482	0.1955	-1.4423	0.0422	0.0855	0.6066	0.2832	0.2298
266410_at	AT2G38770	EMB2765 (EMBRYO DEFECTIVE 2765)	0.647	0.0405	0.1161	0.2231	0.3614	0.3236	-0.8685	0.016	0.0505	-1.2924	0.004	0.0203
266411_at	AT2G38730	peptidyl-prolyl cis-trans isomerase, putative / cyclop	-0.3831	0.0076	0.058	-0.2562	0.0292	0.085	0.4651	6.00E-04	0.0156	0.592	2.00E-04	0.0078
266412_at	AT2G38720	microtubule associated protein (MAP65/ASE1) fam	0.04645	0.933	0.6605	0.2728	0.6277	0.4334	-0.01161	0.9832	0.5135	0.2147	0.7004	0.3975
266413_at	AT2G38740	haloacid dehalogenase-like hydrolase family protein	-0.3057	0.0928	0.1764	-0.3439	0.0687	0.1315	0.02932	0.8221	0.4703	-0.0089	0.9454	0.4697
266414_at	AT2G38700	MVD1 (mevalonate diphosphate decarboxylase 1)	-0.4541	0.0511	0.1299	-0.3402	0.1079	0.1656	-0.3575	0.0959	0.1376	-0.2436	0.2135	0.1927
266415_at	AT2G38530	LTP2 (LIPID TRANSFER PROTEIN 2); lipid binding	1.356	0.0079	0.0585	2.4773	8.00E-04	0.0284	0.5034	0.1128	0.1504	1.6248	0.0028	0.0174
266416_at	AT2G38710	AMMECR1 family	-0.05148	0.6896	0.489	-0.1545	0.2668	0.2736	-0.0121	0.8576	0.4804	-0.1151	0.143	0.1502
266417_at	AT2G38550	similar to unknown protein [Arabidopsis thaliana] (T	0.2584	0.273	0.3073	0.2521	0.2831	0.2826	-0.1516	0.0947	0.1365	-0.1579	0.0856	0.1094
266418_at	AT2G38760	ANNAT4 (ANNEXIN ARABIDOPSIS 4); calcium ion	1.1685	0.0296	0.1	-1.1161	0.0341	0.0912	0.07662	0.5116	0.3638	0.1288	0.2924	0.2348
266419_at	AT2G38760	ANNAT3 (ANNEXIN ARABIDOPSIS 3); calcium ion	-0.7248	0.0273	0.0958	-0.6103	0.0459	0.1061	0.4817	0.0017	0.0205	0.5962	7.00E-04	0.0108
266420_at	AT2G38610	KH domain-containing protein	0.1001	0.6211	0.4668	0.4858	0.0603	0.1219	-0.7799	0.014	0.0473	-0.3941	0.1029	0.1226
266421_at	AT2G38540	LP1 (nonspecific lipid transfer protein 1)	-0.4605	0.0069	0.0559	-0.2638	0.0427	0.1027	0.3102	0.0137	0.

266490_at	AT2G07000	unknown protein	-0.4148	0.7277	0.5017	-1.0793	0.386	0.3347	-0.5325	0.6565	0.4167	-1.197	0.3417	0.2588
266491_at	AT5G55875,AT2G07010	[AT5G55875, transposable element gene];[AT2G07	-0.7799	0.5052	0.4228	0.1049	0.9264	0.5258	-0.1529	0.8314	0.4731	0.732	0.3377	0.2568
266492_at	AT2G07020	protein kinase family protein	-1.7966	0.0474	0.1254	1.1764	0.1377	0.189	-1.5386	0.0726	0.1172	1.4343	0.0869	0.1104
266493_at	AT2G07030	transposable element gene	-0.3061	0.5455	0.4392	-0.6002	0.2655	0.2729	0.4322	0.4044	0.3183	0.1381	0.7808	0.4232
266494_at	AT2G07040	ATPKR2A; ATP binding / protein serine/threonine k	1.1509	0.2826	0.313	0.07619	0.9385	0.5286	-0.6211	0.2918	0.2645	-1.6958	0.0296	0.0577
266495_at	AT2G07050	CAS1 (CYCLOARTENOL SYNTHASE 1); cycloarte	-0.05093	0.7274	0.5017	-0.06474	0.6593	0.4447	-0.7051	5.00E-04	0.0155	-0.7189	5.00E-04	0.0094
266496_at	AT2G07070	transposable element gene	0.03675	0.9388	0.562	-0.7916	0.1534	0.2006	0.3115	0.464	0.3448	-0.5168	0.2508	0.213
266497_at	AT2G07080	transposable element gene	-1.2432	0.2087	0.2672	-0.1541	0.8618	0.5077	-0.9276	0.2694	0.2519	0.1615	0.8344	0.4385
266498_at	AT2G07090	oxidoreductase, 2OG-Fe(II) oxygenase family prote	-0.2723	0.5787	0.4521	-0.6342	0.2326	0.2532	0.2728	0.4846	0.3533	-0.08906	0.8141	0.4327
266499_at	AT2G07680	transposable element gene	0.5724	0.5891	0.4559	-0.5138	0.6265	0.4334	1.1574	0.3014	0.2694	0.07123	0.9453	0.4697
266500_at	AT2G06925	ATSPLA2-ALPHA;PLA2-ALPHA (PHOSPHOLIPAS	0.8739	0.0139	0.0722	1.0804	0.0067	0.0461	0.3017	0.0172	0.0524	0.5082	0.0027	0.0171
266501_at	AT2G06990	HEN2 (HUA ENHANCER 2); ATP-dependent helica	0.3049	0.2503	0.2937	0.556	0.0704	0.1327	-0.9122	0.0072	0.0343	-0.6611	0.0216	0.0478
266502_at	AT2G47720	similar to AtATG18a (Arabidopsis thaliana homolog	-0.7385	0.0521	0.131	-0.4967	0.1395	0.1903	0.06108	0.832	0.4733	0.3029	0.3245	0.2504
266503_at	AT2G47780	elongation factor (REF) protein-related	0.2827	0.3837	0.3665	0.1142	0.7131	0.4631	-0.4879	0.0616	0.1068	-0.6564	0.0257	0.0531
266504_at	AT2G47820	similar to unknown protein [Arabidopsis thaliana] (T	-0.04015	0.8861	0.5474	0.0805	0.7748	0.4821	-0.4559	0.1486	0.1781	-0.3353	0.2592	0.2174
266505_at	AT2G47830	cation efflux family protein / metal tolerance protein	0.07598	0.7324	0.5031	0.0745	0.7374	0.4704	-0.7943	0.0186	0.0546	-0.7958	0.0185	0.0436
266506_at	AT2G06950	zinc finger (CCCH-type) family protein	-0.03168	0.9202	0.5571	-0.1198	0.7075	0.4613	-0.1202	0.6735	0.422	-0.2083	0.4755	0.3159
266507_at	AT2G47860	phototropic-responsive NPH3 family protein	1.0222	0.4409	0.3941	-0.1488	0.907	0.5207	-0.04094	0.9741	0.511	-1.2119	0.364	0.2686
266508_at	AT2G47920	kinase interacting family protein	-2.5325	0.0045	0.0482	-1.4191	0.0317	0.0885	-3.2749	0.0017	0.0205	-2.1615	0.0079	0.0277
266509_at	AT2G47940	DEGP2 (DEGP PROTEASE 2); serine-type peptida	-1.1038	0.0096	0.0627	-0.9429	0.0164	0.0665	-0.9615	0.0153	0.0493	-0.8005	0.0278	0.0596
266510_at	AT2G47990	SWA1 (SLOW WALKER1); nucleotide binding	0.8422	0.1229	0.2032	1.017	0.0781	0.14	-0.4113	0.2347	0.232	-0.2366	0.4665	0.3125
266511_at	AT2G47980	zinc finger (CCCH type) helicase family protein	0.92	0.0138	0.0721	0.7617	0.0257	0.0801	-0.08469	0.6617	0.4184	-0.243	0.2472	0.2109
266512_at	AT2G47690	NADH-ubiquinone oxidoreductase-related	0.1602	0.5092	0.4246	0.3413	0.198	0.2316	-0.2491	0.3234	0.2799	-0.06807	0.7738	0.4212
266513_at	AT2G47700	zinc finger (C3HC4-type RING finger) family protein	-0.0541	0.6657	0.4812	-0.1015	0.4316	0.356	-0.2343	0.1124	0.1502	-0.2817	0.0713	0.0978
266514_at	AT2G47890	zinc finger (B-box type) family protein	0.6753	0.1656	0.238	0.7516	0.1326	0.1848	0.09869	0.8167	0.4688	0.175	0.6834	0.3917
266515_at	AT2G47900	AITLP3 (TUBBY LIKE PROTEIN 3); phosphoric die	0.1789	0.2916	0.3182	-0.2817	0.1286	0.1819	0.3481	0.0775	0.1216	-0.1124	0.4882	0.3212
266516_at	AT2G47880	glutaredoxin family protein	-2.1824	4.00E-04	0.032	-2.3632	3.00E-04	0.0249	0.3287	0.181	0.1994	0.148	0.5068	0.3285
266517_at	AT2G35120	glycine cleavage system H protein, mitochondrial, p	-0.3976	0.0442	0.1213	0.5896	0.0127	0.0602	0.2553	0.1364	0.1686	0.4473	0.0311	0.0595
266518_at	AT2G35170	MORN (Membrane Occupation and Recognition Ne	1.0603	0.0455	0.1227	1.3787	0.0203	0.0727	-0.1975	0.5483	0.3786	0.1209	0.7091	0.4005
266519_at	AT2G35155	catalytic	-0.03076	0.8096	0.5266	-0.4191	0.0248	0.0789	0.0509	0.6921	0.4284	-0.3374	0.0477	0.077
266520_at	ATCNGC6	ATCNGC6 (CYCLIC NUCLEOTIDE GATED CHAN	0.5399	0.0044	0.0482	0.6278	0.0025	0.034	-0.719	0.0011	0.0183	-0.6314	0.0018	0.0148
266521_at	AT2G24020	similar to unknown protein [Arabidopsis thaliana] (T	-0.6474	9.00E-04	0.0349	-0.6933	7.00E-04	0.0275	0.4323	0.0043	0.028	0.3865	0.0064	0.0248
266522_at	AT2G16920	PFU2/UBC23 (UBIQUITIN-CONJUGATING ENZYM	0.009827	0.9632	0.5681	0.2169	0.34	0.3134	-0.6329	0.0217	0.0593	-0.4258	0.0697	0.0967
266523_at	AT2G16950	protein transporter	0.1605	0.3837	0.3666	0.268	0.1779	0.2182	-1.0302	0.0031	0.025	-0.9226	0.0046	0.0216
266524_at	AT2G16960	importin beta-2 subunit family protein	-0.1894	0.8883	0.5479	-1.4605	0.3127	0.2989	0.2555	0.8499	0.4785	-1.0156	0.4672	0.3128
266525_at	AT2G16970	MEE15 (maternal effect embryo arrest 15); tetracyc	-0.09851	0.8769	0.5456	-1.7502	0.0427	0.1027	1.4281	0.0749	0.1192	-0.2236	0.7268	0.4061
266526_at	AT2G16980	tetracycline transporter	-0.1945	0.676	0.4847	-0.22	0.6375	0.4373	-0.08823	0.805	0.465	-0.1137	0.7509	0.414
266527_at	AT2G16840	transposable element gene	-0.6224	0.2567	0.2975	-0.4264	0.4164	0.3489	-0.6062	0.2674	0.2506	-0.4102	0.4328	0.298
266528_at	AT2G16870	disease resistance protein (TIR-NBS-LRR class), p	1.0297	0.1553	0.2299	1.1971	0.1119	0.1688	-0.2873	0.6512	0.415	-0.1199	0.8486	0.4424
266529_at	AT2G16880	pentatricopeptide (PPR) repeat-containing protein	-0.09657	0.6776	0.4851	0.1122	0.6304	0.4346	-0.7789	0.0228	0.0607	-0.5701	0.0574	0.0862
266530_at	AT2G16910	AMS (ABORTED MICROSPORES); DNA binding /	0.9383	0.5736	0.4503	-0.04883	0.9761	0.5384	0.8431	0.6116	0.4017	-0.1441	0.9296	0.4655
266531_at	AT2G16835	water channel protein, putative	1.2983	0.1204	0.2006	-1.4176	0.0981	0.1579	1.0392	0.0471	0.091	-1.6767	0.0102	0.0316
266532_at	AT2G16890	UDP-glucuronosyl/UDP-glucosyl transferase family	-0.2799	0.7115	0.4968	-1.5666	0.0903	0.1516	0.5697	0.4188	0.3248	-0.717	0.3204	0.2485
266533_s_at	AT2G16850,AT4G35100	[AT2G16850, PIP2;8/PIP3B (plasma membrane int	-0.5172	0.0047	0.0496	-0.7645	0.0011	0.0293	0.3309	0.004	0.0274	0.08353	0.2075	0.1894
266534_at	AT2G16940	RNA recognition motif (RRM)-containing protein	0.02678	0.8388	0.535	0.1129	0.4122	0.3472	-0.9822	0.0014	0.0193	-0.8961	0.0019	0.015
266535_s_at	AT2G16930,AT5G15220	[AT2G16930, ribosomal protein L27 family protein];[	0.3514	0.1933	0.2578	0.4009	0.147	0.1961	0.1641	0.3831	0.3093	0.2166	0.2659	0.2208
266536_at	AT2G16900	importin beta-2 subunit family protein	-0.04199	0.8212	0.53	0.05507	0.7676	0.4798	0.02825	0.7261	0.4405	0.1253	0.1708	0.1676
266537_at	AT2G16860	GCIP-interacting family protein	0.05356	0.3762	0.3624	0.3533	0.0028	0.0351	0.2679	0.0076	0.0352	0.5676	5.00E-04	0.0093
266538_at	AT2G35230	VQ motif-containing protein	0.09626	0.5798	0.4521	-0.00048	0.9977	0.5435	-0.1143	0.5144	0.3647	-0.211	0.2575	0.2166
266539_at	AT2G35160	SUVH5 (SU(VAR)3-9 HOMOLOG 5)	0.05033	0.9613	0.5676	1.208	0.2834	0.2827	0.2701	0.7966	0.462	1.4278	0.2172	0.1948
266540_at	AT2G35310	transcriptional factor B3 family protein	-0.8127	0.3283	0.3391	0.3272	0.6774	0.4511	-0.5192	0.4856	0.3538	0.6208	0.4108	0.2885
266541_at	AT2G35110	GRL/NAP1/NAPP (NCK-ASSOCIATED PROTEIN);	0.2864	0.212	0.3681	-0.03984	0.8641	0.5082	-0.7835	0.0061	0.0325	-1.0354	0.0022	0.0157
266542_at	AT2G35100	ARAD1 (ARABINAN DEFICIENT 1); catalytic/ trans	0.2122	0.2564	0.2973	0.1676	0.355	0.3204	-0.1097	0.3877	0.3111	-0.1543	0.2448	0.2096
266543_at	AT2G35075	similar to unnamed protein product [Vitis vinifera] (G	0.2696	0.8509	0.5384	-1.7212	0.2545	0.2669	0.824	0.5591	0.3823	-1.1568	0.4222	0.2934
266544_at	AT2G35300	late embryogenesis abundant group 1 domain-cont	-1.1169	0.2572	0.2572	0.9523	0.2527	0.2656	0.3351	0.6553	0.4163	2.4044	0.0259	0.0534
266545_at	AT2G35290	similar to unnamed protein product [Vitis vinifera] (G	-0.7127	0.2017	0.2632	-0.4301	0.4093	0.3456	0.7183	0.0372	0.0795	1.001	0.0128	0.0359
266546_at	AT2G35270	DNA-binding protein-related	-1.3141	0.2478	0.2923	-0.5396	0.6084	0.4265	-1.9352	0.1173	0.1541	-1.1607	0.2984	0.2378
266547_at	AT2G35320	ATEYA (ARABIDOPSIS THALIANA EYES ABSENT	0.5932	0.0214	0.0858	0.4396	0.0529	0.1141	0.003669	0.983	0.5134	-0.1499	0.4061	0.2866
266548_at	AT2G35210	AGD10/MEE28/RPA (MATERNAL EFFECT EMBR	0.7507	0.2699	0.3053	-0.5133	0.431	0.3557	0.7434	0.2738	0.2545	-0.5206	0.425	0.2945
266549_at	AT2G35150	phosphate-responsive 1 family protein	0.5488	0.184	0.251	0.3734	0.3364	0.3116	0.6316	0.0136	0.0464	0.4563	0.0383	0.0671
266550_s_at	AT2G35090,AT2G35070	[AT2G35090, similar to unknown protein [Arabidops	1.8273	0.1633	0.2365	2.8335	0.0573	0.119	-0.5386	0.378	0.3068	0.4676	0.4384	0.3007
266551_at	AT2G35260	similar to unknown protein [Arabidopsis thaliana] (T	-0.5436	0.0066	0.0549	-0.5041	0.0086	0.0512	-0.08498	0.4636	0.3447	-0.04554	0.6867	0.3928
266552_at	AT2G46330	AGP16 (ARABINOGALACTAN PROTEIN 16)	-0.01107	0.974	0.5708	-0.4263	0.2527	0.2656	0.3012	0.0875	0.1306	-0.114	0.442	0.3023
266553_at	AT2G46170	reticulon family protein (RTNLB9)	0.3584	0.1062	0.1885	0.3447	0.1163	0.1722	0.04587	0.8034	0.4645	0.03214	0.8612	0.4462
266554_s_at	AT2G46290,AT2G46280	initiation factor 3 subunit 2, putative / eIF-3 beta, pu	0.5784	0.0147	0.0736	0.7477	0.006	0.0447	-0.8747	0	0.0092	-0.7053	1.00E-04	0.0058
266555_at	AT2G46270	GBF3 (G-BOX BINDING FACTOR 3); transcription	0.3865	0.1925	0.2572	0.5237	0.1012	0.1605	-0.2882	0.1456	0.1758	-0.151	0.3983	0.2835
266556_at	AT2G46230	similar to unknown protein [Arabidopsis thaliana] (T	0.4055	0.0022	0.041	0.5509	7.00E-04	0.027	0.189	0.0149	0.0487	0.3344	0.0019	0.0151
266557_at	AT2G46080	similar to BPS1 (BYPASS 1) [Arabidopsis thaliana]	0.1958	0.103	0.1855	0.05558	0.5823	0.4171	0.28	0.0011	0.0181	0.1397	0.0135	0.0368
266558_at	AT2G23900	glycoside hydrolase family 28 protein / polygalactur	3.0991	0.001	0.0354	-0.6262	0.1562	0.203	0.2647	0.2137	0.2202	-3.4606	0	0.0054
266559_at	AT2G23920	unknown protein	0.7452	0.5108	0.4251	-2.8035	0.0534	0.1146	0.3697	0.7386	0.4443	-3.1791	0.0371	0.0656
266560_at	AT2G23950	leucine-rich repeat family protein / protein kinase fa	-0.01994	0.9697	0.5698	0.3569	0.5094	0.3884	-0.3261	0.474	0.3494	0.05072	0.9082	0.4594
266561_at	AT2G23960	defense-related protein, putative	-0.1484	0.8595	0.5409	0.5238	0.5417	0.4013	0.2284	0.7511	0.4485	0.9007	0.2513	0.2133
266562_at	AT2G23970	defense-related protein, putative	0.4766	0.7125	0.4972	2.1223	0.1529	0.2003	-0.415	0.6463	0.4131	1.2307	0.2157	0.194
266563_at	AT2G23990	plastocyanin-like domain-containing protein	0.7573	0.5285	0.4326	0.8493	0.4826	0.3772	0.9839	0.3399	0.2883	1.0758	0.302	0.2397
266564_at	AT2G24000	SCPL22 (serine carboxypeptidase-like 22); serine c	-0.3065	0.8594	0.5409	-0.3481	0.8406	0.5016	-0.04669	0.9744	0.5111	-0.0883	0.9515	0.4714
266565_at	AT2G24010	SCPL23 (serine carboxypeptidase-like 23); serine c	-0.767	0.4998	0.4185	-1.4289	0.2357	0.2551	1.2065	0.3043	0.2709	0.5446	0.6233	0.3713
266566_at	AT2G24040	hydrophobic protein, putative / low temperature and	0.1072	0.6891	0.4888	0.4237	0.1643	0.2086	0.5724	0.0793	0.1232	0.8889	0.0221	0.0484
266567_at	AT2G24050	MIF4G domain-containing protein / MA3 domain-co	0.05336	0.8489	0.5379	-0.3034	0.3125	0.2987	0.02324	0.9338	0.5017	-0.3335	0.2731	0.2245
266568_at	AT2G24070	similar to unknown protein [Arabidopsis thaliana] (T	-0.1598	0.8321	0.5331	-1.7798	0.0654	0.1278	0.7153	0.3223	0.2793	-0.9048	0.2267	0.1997
266569_at	AT2G24080	F-box family protein-related	0.4558	0.4594	0.4027	0.5393	0.3881	0.3359	0.4908	0.4284	0.329	0.5743	0.3611	0.2675
266570_at	AT2G24090	ribosomal protein L35 family protein	-1.1158	0	0.0312	-1.0009	0	0.0249	0.6028	2.00E-04	0.0129	0.7177	1.00E-04	0.0062
266571_at	AT2G23830	vesicle-associated membrane protein, putative / VA	2.9791	0.0246	0.0911	1.4815	0.1555	0.2024	-0.1205	0.8537	0.4795	-1.618	0.0575	0.0863
266572_at	AT2G23840	HNH endonuclease domain-containing protein	-0.1154	0.7802	0.5179	-0.266	0.5293	0.396	-0.3505	0.1248	0.1599	-0.5011	0.0504	0.0797
266573_at	AT2G23860	pseudogene, similar to VAP27, blastp match of 56	2.9313	0.0821	0.1657	1.5889	0.2789	0.2803	-0.1398	0.9176	0.4971	-1.4822	0.3078	0.2423
266574_at	AT2G23890	5' nucleotidase family protein	0.9559	0.0166	0.0774	0.5778	0.0744	0.1368	-0.5837	0.0725	0.1171	-0.9618	0.0162	0.0407
266575_at	AT2G24060	initiation factor 3 (IF-3) family protein	-0.2257	0.1156	0.1967	-0.4518	0.016	0.0658	-0.391	0.0116	0.0426	-0.6171	0.0022	0.0158
266576_at	AT2G23940	similar to unknown protein [Arabidopsis thaliana] (T	0.3315	0.0578	0.1377	0.6775	0.0057	0.0438	0.1557	0.2833	0.2599	0.5017	0.0163	0.0408
266577_at	AT2G23945	chloroplast nucleoid DNA-binding protein-related	-0.04048	0.9293	0.5598	-0.8057	0.1334	0.1856	0.3584	0.4502	0.3386	-0.4068	0.3965	0.2828
266578_at	AT2G23910	cinnamoyl-CoA reductase-related	1.1473	0.3089	0.3279	-0.5837	0.5854	0.4182	1.6937	0.1607	0.186	-0.03731	0.9716	0.4759
266579_at	AT2G23930	SNRNP-G (PROBABLE SMALL NUCLEAR RIBON	0.3642	4.00E-04	0.032	0.6709	0	0.0249	0.2996	9.00E-04	0.0172	0.6063	1.00E-04	0.0056
266580_at	AT2G46260	BTB/POZ domain-containing protein	0.2808	0.0841	0.1678	0.3743	0.038	0.0966	-0.1968	0.0398	0.0825	-0.1033	0.19	0.1792
266581_at	AT2G46140	late embryogenesis abundant protein, putative / LE	0.5557	0.03	0.1007	0.5677	0.0281	0.0835	0.8257	0.0037	0.0266	0.8377	0.0035	0.0192
266582_at	AT2G46090	diacylglycerol kinase family protein	0.09257	0.6671	0.4817	-0.1645	0.4564	0.3666	-0.4023	0.1126	0.1504	-0.6593	0.0293	0.0574
266583_at	AT2G46220	similar to unknown protein [Arabidopsis thaliana] (T	0.1369	0.4477	0.397	-0.2575	0.1889	0.2257	0.1656	0.2551	0.2437	-0.2288	0.1406	0.1485
266584_s_at	AT1G13430,AT2G14920	[AT1G13430, sulfotransferase family protein];[AT2G	-0.1476	0.8655	0.5424	0.478	0.5902	0.4196	-0.09989	0.8993	0.4921	0.5257	0.5172	0.3325
266585_at	AT2G14930	transposable element gene	-0.4026	0.7213	0.4998	0.3862	0.732	0.4688	-0.2798	0.7943	0.4615	0.509	0.6389	0.3768
266586_s_at	AT3G32950,AT5G28526,A	[AT3G32950, transposable element gene];[AT5G28	0.198	0.8713	0.5443	-2.2507	0.1211	0.1764	0.3785	0.7578	0.4507	-2.0701	0.1453	0.1518
266587_at	AT2G14880	SWIB complex BAF60b domain-containing protein	-0.6982	0.0042	0.0472	-0.7482	0.0033	0.0371	0.6243	7.00E-04	0.016	0.5742	0.001	0.0121
266588_at	AT2G14890	AGP9 (ARABINOGALACTAN PROTEIN 9)	-0.4655	0.2036	0.2644	-0.3861	0.2765	0.279	0.841	0.0031	0.0251	0.9204	0.0022	0.0158
266589_at	AT2G46250	myosin heavy chain-related	-0.1171	0.5792	0.4521	-0.1615	0.4526	0.3651	-0.2757	0.229	0.229	-0.3201	0.1749	0.1702
266590_at	AT2G46240	BAG6 (ARABIDOPSIS THALIANA BCL-2-ASSOCI	0.7921	0.197	0.2606	1.1915	0.0806	0.1424	-0.4488	0.4011	0.3171	-0.04938	0.9227	0.4636
266591_at	AT2G46225	ABIL1 (ABI-1-LIKE 1)	-0.6261	0.014	0.0723	-0.8475	0.0048	0.0421	0.6763	0.0066	0.0334	0.4549	0.0253	0.0525
266592_at	AT2G46210	delta-8 sphingolipid desaturase, putative	0.5233	0.2079	0.2669	-0.5861	0.1682	0.2113	-0.1846	0.487	0.3542	-0.2474	0.3632	0.2684
266593_at	AT2G46200	similar to unnamed protein product [Vitis vinifera] (G	0.9192	0.0128	0.0697	0.7193	0.0284	0.0838	-0.7421	0.0258	0.0652	-0.942	0.0117	0.034
266594_at	AT2G46190	similar to mitochondrial glycoprotein family protein	0.2591	0.3046	0.3254	2.3159	5.00E-04	0.0252	-1.9705	4.00E-04	0.0147	0.08635	0.6608	0.3844
266595_at	AT2G46180	GC4 (GOLGIN CANDIDATE 4)	0.05001	0.8218	0.5301	0.2207	0.3484	0.3173	-0.2436	0.3066	0.2719	-0.07284	0.7439	0.4116
266596_at	AT2G46150	similar to unknown protein [Arabidopsis thaliana] (T	0.7034	0.0953	0.1783	0.5238	0.1806	0.22	0.4331	0.2516	0.2416	0.2535	0.477	0.3165
266597_at	AT2G46130	WRKY43 (WRKY DNA-binding protein 43); transcri	1.8546	0.0921	0.176	0.3003	0.7391	0.471	0.6641	0.3061	0.2717	-0.8901	0.1912	0.1799
266598_at	AT2G46110	KPHMT/PANB1 (KETOPANTOATE HYDROXYME	-0.2772	0.4277	0.3883	-0.07062	0.8333	0.4997	-0.03447	0.8929	0.4905	0.1721	0.513	0.3309
266599_at	no_match	no_match	-0.179	0.5435	0.4384	-0.8362	0.0363	0.0941	1.1159	0.0042	0.0279	0.4588	0.0737	0.0997
266600_at	AT2G46070	ATMPK12 (Arabidopsis thaliana MAP kinase 12); M	-0.2534	0.4539	0.4	-0.4608	0.2063	0.237	-1.0691	0.0096	0.0391	-1.2766	0.0051	0.0224
266601_at	AT2G46060	transmembrane protein-related	0.4435	0.1361	0.2142	0.2322	0.3848	0.3341	-0.161	0.4792	0.3511	-0.3722	0.1457	0.1519
266602_at	AT2G46050	pentatricopeptide (PPR) repeat-containing protein	0.01713	0.9856	0.5733	-0.1796	0.8508	0.5047	-0.574	0.5003	0.3597	-0.7707	0.3766	0.2741
266603_at	AT2G46040	ARID/BRIGHT DNA-binding domain-containing prot	-0.08938	0.9339	0.5608	-0.8248	0.4611	0.3684	0.3373	0.7139	0.4362	-0.3976	0.6672	0.3865
266604_at	AT2G46030	UBC8 (UBIQUITIN-CONJUGATING ENZYME 8); u	-0.2123	0.1286	0.2071	-0.2629	0.0772	0.1393	0.2994	0.0145	0.0481	0.2489	0.0265	0.054
266605_at	AT2G46020	ATBRM/BRM/CHR2 (ARABIDOPSIS THALIANA BR	0.1946	0.1589	0.2326	0.1411	0.2785	0.2801	-0.5468	0.0015	0.0199	-0.6004	0.001	0.0123
266606_at	AT2G46310	CRF5 (CYTOKININ RESPONSE FACTOR 5); DNA	0.04672	0.9237	0.558	-0.1982	0.6875	0.4547	-0.1525	0.3455	0.2909	-0.3042	0.1005	0.121
266607_at	AT2G46300	similar to unknown protein [Arabidopsis thaliana] (T	-1.0315	0.1956	0.2595	-0.02437	0.9725	0.5372	-0.4925	0.4998	0.3596	-0.5146	0.4819	0.3184
266608_at	AT2G35500	shikimate kinase-related	-0.146	0.4686	0.4065	-0.2795	0.2005	0.233	0.04512	0.7526	0.449	-0.08838	0.5445	0.3427
266609_at	AT2G46350	SRO1 (SIMILAR TO RCD ONE 1); NAD+ ADP-ribo	-0.1286	0.4374	0.3928	0.07779	0.6298	0.4344	-0.2688	0.1581	0.1844	-0.05231	0.7437	0.4115
266610_at	AT2G14950	transposable element gene	1.0385	0.3171	0.3327	0.7988	0.4293	0.355	0.179	0.6172	0.4036	-0.06065	0.8635	0.4467
266611_at	AT2G14960	GH3.1	-0.2159	0.8125	0.5275	-1.5004	0.1531	0.2004	-0.00462	0.9959	0.5166	-1.2891	0.2049	0.1878
266612_at	AT2G14980	peroxisomal membrane protein 22 kDa, putative	0.5797	0.2314	0.283	-1.0901	0.0569	0.1187	0.2112	0.6348	0.4093	-0.2992	0.5071	0.3286
266613_at	AT2G14900	gibberellin-regulated family protein	0.3689	0.4113	0.3806	0.2651	0.5461	0.403	0.4913	0.1466	0.1766	0.3875	0.2291	0.2011
266614_at	AT2G14910	similar to amine oxidase/ copper ion binding / quino	-0.3607	0.0044	0.0482	-0.6227	6.00E-04	0.0265	-0.9042	1.00E-04	0.012	-1.1663	0	0.0055
266615_s_at	AT2G35660,AT2G29720	[AT2G35660, CTF2A; monooxygenase];[AT2G2972	0.1171	0.435	0.3916	-0.5226	0.018	0.0694	-0.4741	0.0247	0.0637	-0.8796	0.0029	0.0175
266616_at	AT2G29680	CDC6	0.1269	0.7592	0.5115	0.08164	0.8431	0.5026	-0.5994	0.1961	0.2093	-0.6447	0.1708	0.1676
266617_at	AT2G29670	binding	-0.1488	0.603	0.4605	-0.1796	0.5336	0.3978	-0.6995	0.0018	0.0206	-0.7303	0.0015	0.0139
266618_at	AT2G29480	similar to unknown protein [Arabidopsis thaliana] (T	-0.4097	0.2854	0.3146	-0.8356	0.0659	0.1284	0.3637	0.3356	0.2863	-0.06219	0.8608	0.4461
266619_at	AT2G35460	harpin-induced family protein / HIN1 family protein /	0.5637	0.4312	0.3898	0.09321	0.892	0.5163	0.3789	0.2567	0.2446	-0.09155	0.7654	0.4185
266620_at	AT2G35450	hydrolase	-0.6669	0.0121	0.0682	-0.5485	0.0231	0.0768	-1.3422	4.00E-04	0.0147	-1.2238	6.00E-04	0.01
266621_at	AT2G35450	hydrolase	-0.1186	0.2258	0.279	-0.2482	0.0402	0.0994	-0.5991	0.0019	0.021	-0.7287	9.00E-04	0.0118
266622_at	AT2G35430	zinc finger (CCCH-type) family protein	1.0607	0.1112	0.1933	1.5411	0.0415	0.1011	0.17	0.7603	0.4512

266690_at	AT2G19900	ATNADP-ME1 (NADP-MALIC ENZYME 1); malate	-0.1167	0.7161	0.4981	-0.1322	0.6811	0.4523	-0.02548	0.9176	0.4971	-0.04098	0.868	0.4477
266691_at	AT2G19890	similar to unknown protein [Arabidopsis thaliana] (T	0.6169	0.7206	0.4996	-0.3343	0.8453	0.5031	0.694	0.499	0.3593	-0.2572	0.7968	0.4279
266692_at	AT2G19960	hAT dimerisation domain-containing protein / transp	1.3467	0.3615	0.3553	-0.4161	0.7664	0.4793	0.9849	0.4746	0.3495	-0.778	0.5672	0.3517
266693_at	AT2G19800	MIOX2 (MYO-INOSITOL OXYGENASE 2)	-0.7106	0.184	0.251	-0.3249	0.504	0.3863	-0.3983	0.0887	0.1315	-0.01267	0.9467	0.47
266694_at	AT2G19790	clathrin adaptor complex small chain family protein	0.1746	0.1858	0.2525	0.3439	0.0347	0.0921	0.1014	0.2833	0.2599	0.2707	0.0298	0.958
266695_at	AT2G19810	zinc finger (CCCH-type) family protein	0.2364	0.1814	0.2492	0.6228	0.0131	0.0611	-0.5528	0.0067	0.0335	-0.1664	0.1949	0.1819
266696_at	AT2G19680	mitochondrial ATP synthase g subunit family protein	0.1068	0.4256	0.3874	0.4043	0.0284	0.0838	0.5422	0.0108	0.0413	0.8397	0.0022	0.0158
266697_at	AT2G19770	PRF5 (PROFILIN5); actin binding / actin monomer	1.1147	0.0169	0.0779	-0.4057	0.2243	0.2481	0.4835	0.1621	0.1868	-1.0368	0.0214	0.0475
266698_at	AT2G19830	SNF7.2	-0.1209	0.6279	0.4689	0.4512	0.1221	0.1773	0.2655	0.3138	0.2753	0.8376	0.0221	0.0485
266699_at	AT2G19730	60S ribosomal protein L28 (RPL28A)	0.2256	0.1075	0.1896	0.4377	0.016	0.0658	0.3272	0.031	0.0716	0.5393	0.0058	0.0236
266700_at	AT2G19740	60S ribosomal protein L31 (RPL31A)	0.7543	0.0055	0.052	0.8853	0.0031	0.0359	-0.1917	0.1452	0.1755	-0.06074	0.5978	0.3627
266701_at	AT2G19760	PFN1/PRF1 (PROFILIN 1); actin binding	-0.542	0.024	0.0903	0.08788	0.5964	0.422	0.3673	0.0743	0.1187	0.9972	0.0029	0.0175
266702_at	AT2G19860	ATHXK2 (HEXOKINASE 2); ATP binding / hexokina	0.03483	0.8371	0.5344	-0.2158	0.2457	0.2615	-0.3458	0.0309	0.0715	-0.5964	0.0049	0.022
266703_at	AT2G19880	ceramide glucosyltransferase, putative	-0.4124	0.1829	0.2502	0.3713	0.221	0.2465	-0.7742	0.0159	0.0504	-0.7332	0.0191	0.0442
266704_at	AT2G19940	semialdehyde dehydrogenase family protein	0.03973	0.737	0.5049	-0.3252	0.0421	0.1019	-0.2977	0.0031	0.0251	-0.6625	1.00E-04	0.0068
266705_at	AT2G19750	40S ribosomal protein S30 (RPS30A)	-0.00979	0.9635	0.5682	0.07397	0.7318	0.4688	0.7571	0.0197	0.0565	0.8409	0.0139	0.0375
266706_at	AT2G19320	unknown protein	-1.4353	0.0729	0.1555	-2.8691	0.0084	0.0507	-0.4825	0.4618	0.344	-1.9162	0.032	0.0603
266707_at	AT2G19310	unknown protein	0.002475	0.9962	0.5761	0.4363	0.4212	0.3512	0.1725	0.3703	0.303	0.6053	0.024	0.0509
266708_at	AT2G19200	aspartyl protease family protein	0.8991	0.3963	0.3734	0.8512	0.4197	0.3505	0.2346	0.8166	0.4687	0.1867	0.8534	0.4437
266709_at	AT2G19210	signal peptide peptidase family protein	0.9717	0.0028	0.0431	1.0764	0.0019	0.033	-0.3446	0.0806	0.1243	-0.2398	0.1807	0.1737
266710_at	AT2G19850	ATP binding / protein kinase/ protein-tyrosine kinase	-0.6569	0.597	0.4586	-0.8437	0.5022	0.3856	-0.03153	0.9794	0.5124	-0.2183	0.8581	0.4453
266711_at	AT2G19740	FAD-binding domain-containing protein	-0.6711	0.5888	0.4559	0.6707	0.589	0.4191	-0.1923	0.8746	0.4852	1.1495	0.3716	0.2719
266712_at	AT2G19750	FAD-binding domain-containing protein	1.5104	0.1325	0.211	0.8915	0.3283	0.3077	0.2787	0.7455	0.4466	-0.3401	0.6931	0.3951
266713_at	AT2G19760	FAD-binding domain-containing protein	0.9889	0.5162	0.4276	-0.1961	0.8946	0.5171	0.1581	0.915	0.4964	-1.027	0.5011	0.3263
266714_at	no_match	no_match	0.7738	0.4422	0.3946	1.4747	0.1798	0.2194	-0.3431	0.7248	0.4402	0.3578	0.7137	0.4022
266715_at	AT2G19780	RNA recognition motif (RRM)-containing protein	-1.3313	0.0139	0.0721	-1.0295	0.0318	0.0885	-0.5288	0.0636	0.1086	-0.2271	0.3358	0.256
266716_at	AT2G19820	PSAP/PSI-P/PTAC8/TMP14 (THYLAKOID MEMBR	-0.7191	0.0048	0.0496	-0.8554	0.0025	0.034	0.1215	0.392	0.3129	-0.01478	0.9128	0.4607
266717_at	AT2G19830	SNF7.2	-0.1209	0.6279	0.4689	0.4512	0.1221	0.1773	0.2655	0.3138	0.2753	0.8376	0.0221	0.0485
266718_at	AT2G19800	ATMTP1/MTP1/ZAT1 (ZINC TRANSPORTER OF A	-0.2181	0.3124	0.33	-0.2218	0.3053	0.2945	-0.4525	6.00E-04	0.0159	-0.4562	6.00E-04	0.0103
266719_at	AT2G19840	CCA1 (CIRCADIAN CLOCK ASSOCIATED 1); tran	-1.0111	0.0011	0.036	-1.1729	6.00E-04	0.027	0.04493	0.501	0.3599	-0.1169	0.127	0.1396
266720_s_at	AT2G46670,AT2G46790	ketch repeat-containing protein / pseudo-response regulator, putative	0.2455	0.7138	0.4972	0.1277	0.8477	0.5038	-0.4499	0.1309	0.1645	-0.5674	0.075	0.1008
266721_at	AT2G19720	FT1 (FUCOSYLTRANSFERASE 1); fucosyltransfer	0.3334	0.0826	0.1663	0.38	0.0585	0.1202	-0.1046	0.1258	0.1607	-0.05802	0.3444	0.26
266722_at	AT2G19210	FUT2 (fucosyltransferase 2); fucosyltransferase/ tra	0.05762	0.9604	0.5674	0.02899	0.9801	0.5393	-1.4536	0.0682	0.1133	-1.4823	0.0647	0.0926
266723_at	AT2G19190	ASK1/6 (ARABIDOPSIS SKP1-LIKE 1/6); ubiquitin-p	1.1009	0.0182	0.0566	0.4893	0.624	0.4324	-0.4644	0.644	0.4123	-0.07208	0.9415	0.4689
266724_at	AT2G19180	unknown protein	0.7167	0.4052	0.378	-0.4261	0.6099	0.4269	1.7076	0.0911	0.1335	0.5647	0.5045	0.3275
266725_at	AT2G19170	ASK1/4 (ARABIDOPSIS SKP1-LIKE 14); protein bin	0.4101	0.6029	0.4605	-3.0989	0.013	0.061	2.1502	0.0394	0.0821	-1.3588	0.1296	0.1412
266726_at	AT2G19160	ASK1/6 (ARABIDOPSIS SKP1-LIKE 1/6); ubiquitin-p	1.0056	0.1045	0.1866	-1.1872	0.2831	0.2826	2.6664	0.0361	0.0781	-0.5265	0.573	0.3535
266727_at	AT2G19350	EMB1579 (EMBRYO DEFECTIVE 1579); binding	0.5402	0.0165	0.0771	0.8227	0.0038	0.0387	-0.5352	0.005	0.0298	-0.2527	0.0573	0.0862
266728_at	AT2G19340	CAAX amino terminal protease family protein	0.3733	0.2195	0.2748	-0.2414	0.4002	0.3412	-0.6502	0.0086	0.0372	-1.2649	7.00E-04	0.0108
266729_at	AT2G19330	ribosomal protein L12 family protein	1.0866	0.2903	0.3175	-0.8439	0.3975	0.3403	0.3126	0.7304	0.4419	-1.6179	0.1282	0.1403
266730_at	AT2G19310	nucleic acid binding	-0.4919	0.6473	0.4754	-0.9025	0.416	0.3488	-0.6986	0.5217	0.3676	-1.1092	0.3277	0.2523
266731_at	AT2G19260	EXS family protein / ERD1/XPR1/SYG1 family prote	0.356	0.6306	0.4699	-0.3148	0.6696	0.4484	-0.1214	0.8188	0.4695	-0.7921	0.1856	0.1767
266732_at	AT2G19250	EXS family protein / ERD1/XPR1/SYG1 family prote	0.1983	0.6697	0.4825	-0.3543	0.6427	0.3672	-0.1635	0.4894	0.3553	-0.3194	0.2115	0.1916
266733_at	AT2G19280	similar to unknown protein [Arabidopsis thaliana] (T	0.132	0.5259	0.4316	0.1498	0.4752	0.3743	-0.6054	0.0335	0.0747	-0.5877	0.0366	0.0651
266734_at	AT2G19690	similar to unknown protein product [Vitis vinifera] (G	0.574	0.0169	0.0781	0.5752	0.0168	0.0674	-1.0675	0.0018	0.0206	-1.0663	0.0019	0.0149
266735_at	AT2G19630	pectinesterase/pectinesterase inhibitor family pro	0.3041	0.1686	0.2404	-0.4219	0.0804	0.1422	-0.3644	0.0434	0.087	-0.5023	0.019	0.0441
266736_at	AT2G19660	CYP709B1 (cytochrome P450, family 709, subfamil	-0.2109	0.8165	0.5287	-0.9412	0.3307	0.3088	1.442	0.0605	0.1056	0.7116	0.2699	0.2226
266737_at	AT2G19640	short-chain dehydrogenase/reductase (SDR) family	-0.01277	0.9759	0.5712	-0.1626	0.7038	0.4604	0.3252	0.4596	0.3429	0.1754	0.6821	0.3913
266738_at	AT2G19710	similar to unknown protein [Arabidopsis thaliana] (T	0.4241	0.3931	0.3716	0.2335	0.6264	0.4334	-0.2869	0.6529	0.3801	-0.4775	0.3421	0.259
266739_at	AT2G19720	pseudogene, similar to 68 kDa protein, blastp matcl	0.0112	0.9892	0.5743	0.9535	0.286	0.2843	-2.4295	0.035	0.0767	-1.4871	0.1275	0.1399
266740_at	AT2G19730	similar to 3' exoribonuclease family domain 1 protei	-0.05206	0.9685	0.5694	-2.3671	0.1291	0.1822	1.0383	0.4498	0.3385	-1.2767	0.3617	0.2677
266741_s_at	AT2G03030, AT2G03300	Toll-interleukin-Resistance (TIR) dom	-2.0573	0.0411	0.1168	-1.4099	0.1114	0.1685	-1.5653	0.0808	0.1244	-0.9179	0.2446	0.2096
266742_at	AT2G19750	mitochondrial transcription termination factor-relate	-0.1735	0.4652	0.4053	-0.4781	0.0904	0.1517	0.04995	0.8278	0.472	-0.2546	0.3022	0.2398
266743_at	AT2G20990	RNS1 (RIBONUCLEASE 1); endoribonuclease	0.007036	0.9879	0.5739	0.3366	0.4848	0.378	0.4336	0.3644	0.3002	0.7631	0.1463	0.1523
266744_at	AT2G20960	nucleoside phosphatase family protein / GDA1/CD3	0.2903	0.2945	0.3175	-0.8439	0.3975	0.3403	0.3126	0.7304	0.4419	-1.6179	0.1282	0.1403
266745_at	AT2G20950	PKS1 (PHYTOCHROME KINASE SUBSTRATE 1)	-0.376	0.0193	0.0823	0.1308	0.2578	0.2688	0.6076	0.0036	0.0265	0.8527	0.001	0.0121
266746_s_at	AT2G20930,AT4G02520	[AT2G02930, ATGSTF3 (GLUTATHIONE S-TRANS	0.8204	0.0315	0.1028	1.0295	0.0152	0.0646	0.2183	0.0783	0.1223	0.4274	0.01	0.0312
266747_at	AT2G20870	ketch repeat-containing F-box family protein	0.408	0.0101	0.064	0.576	0.0029	0.0355	-0.5052	0.0047	0.0292	-0.3372	0.0192	0.0444
266748_at	no_match	no_match	-1.2116	0.0871	0.171	-0.3341	0.5677	0.411	-3.7833	0.0018	0.0206	-2.9059	0.0049	0.022
266749_at	AT2G47060	serine/threonine protein kinase, putative	-0.562	0.045	0.1222	-0.517	0.057	0.1187	0.309	0.0077	0.0354	0.3539	0.0047	0.0217
266750_s_at	AT2G47040, AT2G47030	ketch repeat-containing F-box family protein	-0.8324	0.2238	0.2776	0.4497	0.4806	0.3764	-4.5570	4.00E-04	0.0145	-3.2757	0.0013	0.0133
266751_at	AT2G47020	release factor, putative	0.3657	0.3642	0.3564	0.03908	0.9182	0.5237	-0.2857	0.4209	0.3257	-0.6123	0.1272	0.1397
266752_at	AT2G47000	MDR4/PGP4 (P-GLYCOPROTEIN4); ATPase, cous	0.8058	0.036	0.1095	1.1307	0.0121	0.0589	-0.318	0.0265	0.0662	0.006849	0.9446	0.4695
266753_at	AT2G46990	IAA20 (indoleacetic acid-induced protein 20); transc	0.02547	0.9643	0.5683	-0.4666	0.4328	0.3567	0.2364	0.6817	0.4248	-0.2556	0.858	0.3835
266754_at	AT2G46980	similar to unnamed protein product [Vitis vinifera] (G	-0.03329	0.9686	0.5694	1.0452	0.2593	0.2696	-1.4383	0.145	0.1752	-0.3598	0.6746	0.3889
266755_at	AT2G47150	short-chain dehydrogenase/reductase (SDR) family	-0.7277	0.3637	0.3562	0.1356	0.8579	0.5066	-1.6769	0.0045	0.0287	-0.8136	0.0493	0.0786
266756_at	AT2G46950	CYP709B2 (cytochrome P450, family 709, subfamil	-0.637	0.2045	0.265	-0.5448	0.265	0.2726	-0.1597	0.7235	0.4398	-0.06741	0.8804	0.4515
266757_at	AT2G46940	similar to unknown protein [Arabidopsis thaliana] (T	0.5534	0.531	0.4333	-0.09622	0.9109	0.5218	0.2846	0.7378	0.4442	-0.365	0.6691	0.387
266758_at	AT2G46920	POL (POLTERGEIST); protein serine/threonine pho	0.7679	0.0204	0.0841	0.8872	0.0126	0.06	-0.285	0.0617	0.1068	-0.1656	0.209	0.1903
266759_at	no_match	no_match	-0.725	0.1493	0.225	-1.1066	0.053	0.1142	0.05898	0.8917	0.4901	-0.3227	0.4721	0.3145
266760_at	AT2G46870	NGA1 (NGATHA1); transcription factor	-0.1596	0.4563	0.401	-0.05721	0.7824	0.4843	-0.07252	0.727	0.4409	0.02983	0.885	0.4529
266761_at	AT2G47130	short-chain dehydrogenase/reductase (SDR) family	1.4833	7.00E-04	0.0334	1.1719	0.0018	0.0323	0.4942	0.0352	0.0769	0.1828	0.3112	0.2439
266762_at	AT2G47120	short-chain dehydrogenase/reductase (SDR) family	0.6188	0.4977	0.4195	0.3382	0.7048	0.4606	0.04951	0.9467	0.5048	-0.2311	0.7564	0.4156
266763_at	AT2G47070	SPL1 (SQUAMOSA PROMOTER BINDING PROTE	-0.1838	0.0893	0.1732	-0.1288	0.1929	0.2278	-0.5347	0.0029	0.0245	-0.4797	0.0043	0.0209
266764_at	AT2G47050	invertase/pectin methylesterase inhibitor family prot	0.5291	0.5153	0.4274	1.4162	0.129	0.1822	-1.5066	0.1122	0.15	-0.6195	0.4509	0.3063
266765_at	AT2G46860	ATPPA3 (ARABIDOPSIS THALIANA PYROPHOSP	-0.4021	0.6321	0.4704	-0.1349	0.8706	0.51	-0.5238	0.5372	0.3741	-0.2566	0.7578	0.4161
266766_at	AT2G46880	ATPAP14/PAP14; acid phosphatase/ protein serine	0.5789	0.2658	0.3026	-0.6854	0.2007	0.2331	0.3876	0.4099	0.3207	-0.8766	0.1061	0.1247
266767_at	AT2G46910	plastid-lipid associated protein PAP / fibrillin family p	-0.9827	0.002	0.0396	-0.8671	0.0031	0.0363	-0.1888	0.2382	0.2342	-0.07319	0.6198	0.3703
266768_s_at	AT3G62250,AT2G47110	UBQ5 (UBIQUITIN 5); protein binding	-0.05552	0.6005	0.4599	0.1753	0.1475	0.1963	0.2786	0.0464	0.0904	0.5094	0.0065	0.025
266769_s_at	AT1G18930,AT3G29440,A	[AT1G18930, transposable element gene];[AT3G29	0.1279	0.8804	0.5465	2.4085	0.0393	0.0982	0.3516	0.6823	0.425	2.6322	0.03	0.0582
266770_at	AT2G03090	ATEXPA15 (ARABIDOPSIS THALIANA EXPANSIN	-0.6328	0.0673	0.149	-0.695	0.0521	0.1132	-0.4636	0.1419	0.1729	-0.5258	0.1071	0.1255
266771_s_at	AT2G03010, similar to unknown protein [Arabidop	0.02308	0.9261	0.5585	0.4492	0.1269	0.1806	0.009256	0.9615	0.5081	0.4353	0.0733	0.0994	
266772_s_at	AT4G16540,AT2G03020	[AT4G16540, heat shock protein-related];[AT2G03	-0.936	0.2859	0.3148	-0.08283	0.9185	0.5237	-1.0594	0.2153	0.221	-0.2062	0.7888	0.4254
266773_at	AT2G29040	exostosin family protein	1.3041	0.4281	0.3884	-0.778	0.627	0.4334	0.8793	0.5349	0.3732	-1.2028	0.4061	0.2866
266774_at	AT2G29050	ATRBL1 (ARABIDOPSIS THALIANA RHOMBOID-L	0.5624	0.5173	0.4282	-0.6414	0.464	0.3697	-1.0251	0.2657	0.2497	-2.2289	0.0483	0.0776
266775_at	AT2G29060	scarecrow transcription factor family protein	0.0776	0.774	0.516	-0.1379	0.6142	0.4285	0.2765	0.3352	0.286	0.06102	0.821	0.4345
266776_at	AT2G29070	ubiquitin fusion degradation UFD1 family protein	0.9851	0.0118	0.0679	1.1858	0.0062	0.0451	-0.4147	0.0494	0.0939	-0.2141	0.2236	0.198
266777_at	AT2G29080	FTSH3 (FtsH protease 3); ATP-dependent peptidas	0.2947	0.13	0.2085	0.1417	0.4121	0.3471	-0.1546	0.3748	0.3052	-0.3076	0.1181	0.1335
266778_at	AT2G29090	CYP707A2 (cytochrome P450, family 707, subfamil	2.1277	0.0418	0.1176	2.2833	0.0339	0.0909	0.08378	0.9117	0.4957	0.2394	0.7526	0.4145
266779_at	AT2G29100	ATGLR2.9 (Arabidopsis thaliana glutamate receptor	2.1729	0.1056	0.1878	0.4756	0.6719	0.4491	1.6037	0.195	0.2087	-0.09357	0.9321	0.4662
266780_at	AT2G29110	ATGLR2.8 (Arabidopsis thaliana glutamate receptor	1.723	2.00E-04	0.0312	1.5231	3.00E-04	0.0249	-0.08158	0.5748	0.3883	-0.2815	0.103	0.1228
266781_at	AT2G28940	protein kinase family protein	1.3152	0.0078	0.0583	0.7247	0.0527	0.1139	-0.4987	0.134	0.1667	-1.0893	0.0149	0.0388
266782_at	AT2G29120	ATGLR2.7 (Arabidopsis thaliana glutamate receptor	1.2262	0.0036	0.0452	0.9514	0.0089	0.0517	-0.2087	0.3549	0.2957	-0.4835	0.0727	0.0989
266783_at	AT2G29130	LAC2 (laccase 2); copper ion binding / oxidoreducta	0.6768	0.5518	0.4419	-0.9729	0.4037	0.3429	0.3603	0.7087	0.4342	-1.2893	0.2243	0.1984
266784_at	AT2G28960	leucine-rich repeat protein kinase, putative	-0.9405	0.515	0.4272	-1.529	0.3106	0.2976	0.6173	0.664	0.4192	0.02881	0.9836	0.4789
266785_at	AT2G28970	leucine-rich repeat protein kinase, putative	-0.3218	0.7691	0.5143	-0.07746	0.9434	0.5302	-1.1193	0.336	0.2864	-0.875	0.4412	0.3019
266786_at	AT2G28980	transposable element gene	-0.281	0.6358	0.4716	0.9484	0.1593	0.2053	-0.3783	0.5288	0.3708	0.8511	0.1961	0.1826
266787_at	AT2G28990	leucine-rich repeat protein kinase, putative	0.5763	0.7382	0.5052	-1.2134	0.4926	0.3814	0.7145	0.6799	0.4243	-1.0752	0.5404	0.3411
266788_at	AT2G29000	leucine-rich repeat family protein / protein kinase fa	-0.1688	0.8594	0.5409	0.1428	0.8808	0.5134	0.2221	0.753	0.4491	0.5337	0.4634	0.3114
266789_at	AT2G29020	RabS-interacting family protein	0.5987	0.0242	0.0906	0.5637	0.0292	0.0849	-0.1973	0.0117	0.0429	-0.2322	0.0066	0.0253
266790_at	AT2G29030	ATEXPA6 (ARABIDOPSIS THALIANA EXPANSIN	-0.1679	0.4832	0.4132	-0.2954	0.246	0.2616	0.5699	0.0037	0.0268	0.4424	0.0092	0.03
266791_at	AT2G29060	zinc finger (C3HC4-type RING finger) family protein	0.2941	0.2455	0.2908	0.1952	0.4178	0.3496	-0.7978	0.021	0.0584	-0.8967	0.0143	0.038
266792_at	AT2G29080	SUT2 (sucrose transporter 2); carbohydrate transm	-0.1775	0.44	0.3937	-0.4177	0.1141	0.1706	-0.06357	0.68	0.4243	-0.3037	0.1012	0.1214
266793_at	AT2G03060	AGL30; DNA binding / transcription factor	-0.5338	0.5267	0.4318	0.2319	0.7786	0.4832	-1.614	0.0253	0.0646	-0.8484	0.1413	0.149
266794_at	AT2G29080	pentatricopeptide (PPR) repeat-containing protein	-0.6201	0.2688	0.3047	0.7625	0.1898	0.2264	-0.4429	0.4113	0.3214	0.9396	0.1238	0.1375
266795_at	AT2G03070	similar to unnamed protein product [Vitis vinifera] (G	0.2062	0.1956	0.2595	-0.1116	0.4482	0.3632	0.07638	0.1646	0.1882	-0.2415	0.0058	0.0237
266796_at	AT2G29080	mucin-related	0.2578	0.2046	0.2651	0.1941	0.318	0.3019	0.3196	0.1337	0.1665	0.2559	0.2072	0.1892
266797_at	AT2G29240	ATGRF1 (GROWTH-REGULATING FACTOR 1)	2.2261	0.0029	0.0433	1.5325	0.011	0.0563	0.039	0.9148	0.4964	-0.6546	0.1284	0.1404
266798_at	AT2G29250	ATBZIP29 (ARABIDOPSIS THALIANA BASIC LEUC	0.5956	0.0502	0.1289	0.8663	0.0157	0.0653	0.4105	0.1285	0.163	0.6813	0.0338	0.0621
266799_at	AT2G29260	ATPSK2 (PHYTOSULFOKINE 2 PRECURSOR); gr	-0.1566	0.5939	0.4575	0.7958	0.0424	0.1022	0.9996	0.021	0.0582	1.9521	0.002	0.0151
266800_at	AT2G29280	VQ motif-containing protein	-1.5206	0.0442	0.1213	-0.8523	0.1797	0.2194	1.1474	0.0265	0.0686	1.8157	0.0061	0.0242
266801_at	AT2G29270	EMB2001 (EMBRYO DEFECTIVE 2001); GTP bind	0.02729	0.8698	0.5439	-0.4004	0.0624	0.1241	0.3242	0.0845	0.128	-0.1035	0.5062	0.3283
266802_at	AT2G29500	galactosyl transferase GMA12/MNN10 family protei	-0.6106	0.038	0.1122	-0.6301	0.0346	0.0919	0.173	0.0539	0.0987	0.1536	0.0744	0.1002
266803_at	AT2G29280	APK1B (Arabidopsis protein kinase 1B); kinase	0.1327	0.6007	0.4599	-0.1974	0.4482	0.3623	-0.2047	0.0277	0.0677	-0.5348	9.00E-04	0.0116
266804_at	AT2G29600	CYP5 (cyclophilin 5); peptidyl-prolyl cis-trans isome	0.1607	0.3343	0.3425	0.2694	0.1398	0.1905	0.8733	0.004	0.0273	0.982	0.0026	0.0169
266805_at	AT2G30010	similar to PMR5 (POWDERY MILDEW RESISTANT	-1.0496	0.0076	0.0579	-1.1809	0.005	0.0424	0.6411	0.0262	0.0658	0.5098	0.052	0.0812
266806_at	AT2G30000	Identical to Uncharacterized protein At1g07170/At2	0.5604	0.0035	0.0451	0.3588	0.0169	0.0675	0.3819	0.0045	0.0286	0.1801	0.053	0.0822
266807_at	AT2G29620	unknown protein	-0.6765	0.0627	0.1436	-0.3771	0.2269	0.2497	0.3423	0.2651	0.2493	0.6417	0.0721	0.0985
266808_at	AT2G29995	similar to unknown protein [Arabidopsis thaliana] (T	-0.8613	0.0115	0.0671	-0.2944	0.2053	0.2362	0.206	0.2493	0.2405	0.773	0.0072	0.0264
266809_at	AT2G29970	heat shock protein-related	0.04044	0.8387	0.535	-0.3594	0.1259	0.1799	-0.09227	0.6463	0.4131	-0.4921	0.0575	0.0862
266810_at	AT2G44880	pentatricopeptide (PPR) repeat-containing protein	1.6187	0.0224	0.0875	-2.1578	0.0085	0.0509	2.3418	0.0029	0.0245	-1.4347	0.0163	0.0408
266811_at	AT2G44850	similar to unknown protein [Arabidopsis thaliana] (T	0.9963	0.0052	0.0514	-0.06449	0.7385	0.4708	-0.5154	4.00E-04	0.0147	-1.5762	0	0.0043
266812_at	AT2G44830	protein kinase, putative	-0.2143	0.5717	0.4495	0.5475	0.1911	0.2289	-0.2343	0.538	0.3744	0.5274	0.2045	0.1876
266813_at	AT2G44920	thylakoid lumenal 15 kDa protein, chloroplast	-0.6313	0.0663	0.1478	-0.3944	0.1925	0.2277	0.2954	0.1293	0.1635	0.5323	0.0264	0.0538
266814_at	AT2G44910	homeobox-leucine zipper protein 4 (HB-4) / HD-ZIP	0.7863	0.2914	0.318	0.7309	0.3221	0.3043	0.5223	0.4375	0.333	0.4669	0.4842	0.3193
266815_at	AT2G44900	armadillo/beta-catenin repeat family protein / F-box	0.01633	0.9345	0.5609	0.09446	0.6396	0.4381	-0.8565	0.0101	0.04	-0.7457	0.0162	0.0407
266816_at	AT2G44970	lipase-related	0.1878	0.2892	0.3169	-0.1129	0.5039	0.3862	0.1698	0.3116	0.2743	-0.1309	0.4228	0.2937
266817_at	AT2G44950	HUB1 (HISTONE MONO-UBIQUITINATION 1); pro	-0.6092	0.5338	0.4346	-0.9569	0.3456	0.3158	-1.5649	0.1556	0.1827	-1.9126	0.0996	0.1203
266818_at	AT2G44950	HUB1 (HISTONE MONO-UBIQUITINATION 1); pro	0.361	0.0668	0.1482	0.3016	0.1048	0.1635	-0.5979	0.0143	0.0477	-0.6573	0.0104	0.0318
266819_at	AT2G44870	similar to unnamed protein product [Vitis vinifera] (G	-0.4347	0.0542	0.1337	-0.5193	0.0322	0.0889	-0.08014	0.6451	0.4127	-0.1648	0.3644	0.2688
266820_at	AT2G44940	AP2 domain-containing transcription factor TINY, p	-0.6434	0.0471	0.1249	-1.0536	0.0097	0.0537	0.4961	0.0668	0.1118	0.08591	0.6875	0.393
266821_at	AT2G44940

266890_at	AT2G44620	mACP-1 (MITOCHONDRIAL ACYL CARRIER PRO	-0.1748	0.1468	0.2227	0.03905	0.7084	0.4616	0.4419	0.0098	0.0396	0.6557	0.0024	0.0161
266891_at	AT2G44690	ARAC9/AROP8/ROP8 (rho-related protein from pla	0.3605	0.1453	0.2216	0.4548	0.085	0.1468	0.1282	0.5558	0.3811	0.2225	0.3275	0.2523
266892_at	AT2G26080	ATGLDP2 (ARABIDOPSIS THALIANA GLYCINE D	-0.7804	0.0184	0.0807	-0.9873	0.0083	0.0504	-0.7149	0.0199	0.0566	-0.9218	0.0084	0.0285
266893_at	AT2G26070	RTE1 (REVERSION-TO-ETHYLENE SENSITIVITY	-0.03366	0.9029	0.5521	-0.0136	0.9607	0.5343	-0.161	0.5369	0.374	-0.1409	0.5866	0.3586
266894_at	AT2G26050	zinc ion binding	-3.6876	0.0014	0.038	0.1669	0.7387	0.4708	-3.0938	0.0027	0.0238	0.7407	0.1876	0.1779
266895_at	AT2G26040	Bet v I allergen family protein	-0.3018	0.4385	0.393	-0.9753	0.0499	0.1108	0.3455	0.3479	0.2921	-0.328	0.3702	0.2713
266896_at	AT2G45810	DEAD/DEAH box helicase, putative	0.1583	0.0986	0.1812	0.07374	0.3744	0.3296	-0.4289	0.0044	0.0283	-0.5134	0.0022	0.0158
266897_at	AT2G45585	DNA-binding protein, putative	-0.6387	0.0244	0.0908	-0.5654	0.0355	0.0929	0.6364	0.0246	0.0637	0.7097	0.0173	0.0421
266898_at	AT2G45590	similar to unnamed protein product [Vitis vinifera] (G	-0.08444	0.3933	0.3717	-0.3	0.0274	0.0826	0.5193	0.0042	0.0278	0.3037	0.0263	0.0538
266899_at	AT2G45620	mitochondrial transcription termination factor-relatec	-1.1437	0.0032	0.0442	-1.3943	0.0015	0.0314	0.1247	0.3646	0.3003	-0.1259	0.3606	0.2672
266900_at	AT2G45610	similar to unknown protein [Arabidopsis thaliana] (T	1.3479	0.2886	0.3165	-0.7889	0.5138	0.3902	1.816	0.1749	0.1953	-0.3208	0.7855	0.4245
266901_at	AT2G45650	JAZ7/TIFY5B (JASMONATE-ZIM-DOMAIN PROTE	-1.6396	0.0259	0.093	-1.3577	0.0458	0.106	0.6218	0.1492	0.1784	0.9037	0.0606	0.089
266902_at	AT2G45660	similar to unnamed protein product [Vitis vinifera] (G	-0.1571	0.8456	0.5373	-1.8472	0.0711	0.1334	1.6253	0.0982	0.1394	-0.06478	0.9359	0.4673
266903_at	AT2G45670	MEE22 (maternal effect embryo arrest 21)	0.2856	0.411	0.3805	0.2672	0.4393	0.3593	0.2602	0.2653	0.2494	0.2418	0.2954	0.2363
266904_at	AT2G45690	transketolase family protein	-0.2597	0.2762	0.3094	-0.1877	0.414	0.3478	-0.1723	0.0443	0.088	-0.1003	0.1671	0.1655
266905_at	AT2G45630	katanin, putative	-0.494	0.0432	0.1199	-0.6373	0.0196	0.0719	-0.4877	0.0035	0.026	-0.631	0.0013	0.0133
266906_at	AT2G45585	similar to unknown [Populus trichocarpa] (GB:ABK9	0.1476	0.46	0.403	0.05398	0.7801	0.4836	0.04833	0.7965	0.4623	-0.04333	0.8088	0.4313
266907_at	no_match	no_match	0.3284	0.2311	0.2827	-0.5471	0.0785	0.1404	0.01856	0.8584	0.4805	-0.8569	9.00E-04	0.0118
266908_at	AT2G45650	PID (PINOID); kinase	1.2976	0.18	0.248	1.1409	0.2268	0.2497	-0.1254	0.8615	0.4816	-0.2821	0.6971	0.3965
266909_at	AT2G46020	ATBRM/BRM/CHR2 (ARABIDOPSIS THALIANA BF	-0.812	0.0096	0.0627	0.3565	0.1101	0.1675	-1.4535	0.0011	0.0183	-0.285	0.1772	0.1715
266910_at	AT2G45520	U-box domain-containing protein	1.2262	0.0513	0.1301	0.6585	0.2136	0.2417	-2.1133	0.009	0.038	-2.681	0.0038	0.0201
266911_at	AT2G45510	protein kinase family protein / U-box domain-contair	0.6067	0.0214	0.0858	0.5999	0.0221	0.0752	-0.5571	0.0147	0.0484	-0.5639	0.0141	0.0377
266912_at	AT2G45900	similar to unknown protein [Arabidopsis thaliana] (T	0.2234	0.8465	0.5374	0.7892	0.5061	0.3871	-0.7265	0.5386	0.3747	-0.1607	0.8891	0.454
266913_at	AT2G45890	ATROPGEF4/ROPGEF4 (KINASE PARTNER PRO	0.4701	0.6909	0.4896	-1.1867	0.3411	0.314	-0.2841	0.8089	0.4662	-1.9409	0.1522	0.1563
266914_at	AT2G45880	BAM7/BMY4 (BETA-AMYLASE 7); beta-amylase	0.3744	0.0911	0.175	-0.1126	0.8417	0.4013	-0.3797	0.025	0.064	-0.8668	0.0013	0.0133
266915_at	AT2G45870	identical to UPF0187 protein AtGp45870, chloroplas	-0.6735	0.0841	0.1678	-0.4781	0.1797	0.2194	-0.2764	0.4009	0.3171	-0.08104	0.7968	0.4279
266916_at	AT2G45860	unknown protein	0.04386	0.8882	0.5479	0.1059	0.736	0.47	1.2625	0.0125	0.0444	1.3245	0.0106	0.0323
266917_at	AT2G45830	DTA2 (DOWNSTREAM TARGET OF AGL15 2)	-0.6932	0.0892	0.1731	0.408	0.2589	0.2695	-1.0624	0.0267	0.0664	-0.03882	0.9065	0.4591
266918_at	AT2G45800	LIM domain-containing protein	-1.4975	0.038	0.1122	-2.5345	0.0067	0.0463	0.3636	0.4528	0.3399	-0.6734	0.1987	0.1841
266919_at	AT2G45780	other RNA	-0.7609	0.5259	0.4316	0.08191	0.944	0.5303	-0.1728	0.8824	0.4874	0.67	0.5742	0.3539
266920_at	AT2G45760	dehydration-responsive family protein	0.7288	0.3643	0.3564	-1.1084	0.1949	0.2293	0.401	0.6851	0.3927	0.02137	0.9763	0.4772
266921_at	AT2G45970	CYP86A8 (LACERATA); fatty acid (omega-1)-hydro	-0.7482	0.0702	0.1527	-1.0161	0.0291	0.0848	-0.2693	0.3561	0.2962	-0.5372	0.1062	0.1248
266922_s_at	AT2G45950/AT3G61415	[AT2G45950, ASK20 (ARABIDOPSIS SKP1-LIKE 2	0.3524	0.2375	0.2861	0.05502	0.8391	0.5012	0.5303	0.105	0.1449	0.2329	0.411	0.2887
266923_at	AT2G45980	similar to unknown protein [Arabidopsis thaliana] (T	0.2124	0.4145	0.3821	0.3506	0.2077	0.2381	-0.528	0.0868	0.1297	-0.3899	0.1704	0.1675
266924_at	AT2G45730	initiation factor 3 gamma subunit family protein	0.1989	0.255	0.2964	-0.084	0.6049	0.4251	0.4705	0.0051	0.0301	0.1876	0.0909	0.1135
266925_at	AT2G45740	PEX11D	-0.08691	0.5299	0.4331	-0.2739	0.0964	0.1563	0.08704	0.5293	0.371	-0.09993	0.4738	0.3152
266926_at	AT2G46000	similar to unnamed protein product [Vitis vinifera] (G	-0.1657	0.4328	0.3907	-0.4012	0.1026	0.1616	0.2859	0.2073	0.2161	0.05038	0.8042	0.4299
266927_at	AT2G45960	PIP1B (plasma membrane intrinsic protein 1;2); wat	-0.5007	0.0013	0.0366	-0.9069	1.00E-04	0.0249	0.4274	0.0023	0.0224	0.02112	0.7498	0.4137
266928_at	AT2G45790	ATPMM; phosphomannomutase	0.3241	0.0084	0.06	0.5323	0.0014	0.0312	0.2569	0.0044	0.0284	0.4651	5.00E-04	0.0093
266929_at	AT2G45850	DNA-binding family protein	-0.00388	0.9855	0.5733	0.1753	0.431	0.3557	-0.2298	0.088	0.131	-0.05064	0.6466	0.3796
266930_at	AT2G45930	similar to unknown protein [Arabidopsis thaliana] (T	0.5035	0.587	0.4552	1.1297	0.2564	0.268	-0.2832	0.7567	0.4502	0.3429	0.7085	0.4004
266931_at	AT2G07730	transposable element gene	0.4257	0.4037	0.3772	-0.03594	0.941	0.5293	-0.09932	0.8317	0.4732	-0.561	0.2695	0.2225
266932_s_at	AT1G63250, DEAD box RNA	DEAD box RNA helicase, putative);[A	0.1227	0.888	0.6478	1.2337	0.2098	0.2366	-1.2913	0.1894	0.2051	-0.1803	0.8362	0.439
266933_at	AT2G07760	zinc knuckle (CCHC-type) family protein	1.3694	0.16	0.2335	0.4401	0.6092	0.4268	-0.3918	0.6479	0.4138	-2.2012	0.0504	0.0797
266934_at	AT2G18900	transducin family protein / WD-40 repeat family prot	0.6667	0.0137	0.0719	0.1386	0.4323	0.3564	-0.2752	0.0516	0.0962	-0.8033	0.0013	0.0133
266935_at	AT2G18915	HPT1 (HOMOGENTISATE PHYTYLTRANSFERAS	0.1114	0.6333	0.4707	-0.07673	0.7403	0.4714	-0.06157	0.6147	0.4025	-0.2497	0.0916	0.1141
266936_at	AT2G18920	unknown protein	0.7839	0.5142	0.4269	-1.1411	0.3568	0.3213	0.764	0.5244	0.3689	-1.1611	0.3494	0.2623
266937_at	AT2G18930	unknown protein	0.8536	0.436	0.392	-0.9948	0.3706	0.3278	0.7247	0.5036	0.3607	-1.1238	0.3186	0.2477
266938_at	AT2G18950	AHA1 (ARABIDOPSIS H+ ATPASE 1); ATPase	-0.01233	0.9637	0.5682	0.5443	0.0991	0.1588	-0.5501	0.0891	0.1319	0.006457	0.9803	0.4782
266939_at	AT2G18960	unknown protein	0.3231	0.1948	0.259	0.2287	0.3328	0.3097	-0.2492	0.0848	0.1282	-0.3436	0.0347	0.063
266940_at	AT2G18970	peroxidase, putative	2.2344	0.0229	0.0885	-1.135	0.142	0.1923	2.6193	5.00E-04	0.0148	-0.7501	0.04	0.0691
266941_at	AT2G18980	peroxidase, putative	-0.2769	0.5911	0.4565	-0.3797	0.4717	0.3728	0.2694	0.6033	0.3984	0.1685	0.7423	0.4112
266942_at	AT2G18990	TXND9 (THIOREDOXIN DOMAIN-CONTAINING P	-0.3348	0.1945	0.2587	0.2113	0.3815	0.3327	0.1974	0.4106	0.321	0.7434	0.0259	0.0533
266943_at	AT2G18820	transposable element gene	-0.1807	0.7396	0.5056	-0.08376	0.8768	0.5122	0.2139	0.6948	0.4293	0.3108	0.573	0.3535
266944_at	no_match	no_match	-0.6111	0.1446	0.2209	0.5449	0.1819	0.2211	-0.5006	0.2123	0.2193	0.6554	0.1243	0.1378
266945_at	AT2G18880	fibronectin type III domain-containing protein	-0.1212	0.7234	0.5006	0.2486	0.4796	0.3759	-0.09698	0.7534	0.4492	0.2729	0.3973	0.2831
266946_at	AT2G18890	protein kinase family protein	-1.4632	0.0136	0.0719	-1.5341	0.0116	0.0581	0.01669	0.9501	0.5056	-0.05419	0.8394	0.4398
266947_at	AT2G18830	similar to RNA recognition motif (RRM)-containing p	-1.1938	0.3354	0.343	-1.004	0.4096	0.3458	1.8627	0.1132	0.1508	2.0524	0.0898	0.1126
266948_at	AT2G18850	similar to SET domain-containing protein [Arabidops	-0.3722	0.0455	0.1227	-0.02042	0.8826	0.5138	-0.5218	0.0108	0.0412	-0.17	0.2158	0.194
266949_s_at	AT4G30260;AT2G18840	[AT4G30260, integral membrane Yip1 family prote	0.07005	0.7227	0.5003	0.4924	0.0554	0.1169	-0.2629	0.0081	0.0362	0.1595	0.0414	0.0706
266950_at	AT2G18910	hydroxyproline-rich glycoprotein family protein	-0.6955	0.0063	0.0544	-0.221	0.1708	0.2132	0.3478	0.0348	0.0765	0.8223	0.0018	0.0147
266951_at	AT2G18940	pentatricopeptide (PPR) repeat-containing protein	0.2236	0.4586	0.4023	-0.2534	0.4058	0.3439	0.08415	0.6661	0.4199	-0.3928	0.0957	0.1173
266952_at	AT2G34555	ATGA2OX3 (GIBBERELLIN 2-OXIDASE 3); gibber	-0.2786	0.703	0.4936	1.2706	0.135	0.1869	-0.2619	0.6909	0.4281	1.2873	0.1033	0.123
266953_at	AT2G34530	binding	-0.9099	0.2372	0.286	0.9594	0.217	0.2439	-0.4907	0.4956	0.358	1.3787	0.1032	0.1229
266954_at	AT2G34530	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.01944	0.9298	0.5599	0.1907	0.4094	0.3457	0.6727	0.0315	0.0721	0.844	0.0152	0.0393
266955_at	AT2G34520	RPS14 (MITOCHONDRIAL RIBOSOMAL PROTEIN	0.5004	0.0104	0.0646	0.6784	0.0035	0.0374	-0.0981	0.4226	0.3266	0.0799	0.5076	0.3288
266956_at	AT2G34510	similar to unknown protein [Arabidopsis thaliana] (T	-0.3484	0.4499	0.398	-0.2292	0.6114	0.4274	-0.2754	0.0139	0.047	-0.1562	0.0767	0.1021
266957_at	AT2G34640	PTAC12 (PLASTID TRANSCRIPTIONALLY ACTIV	-0.08646	0.4186	0.3841	-0.1518	0.1888	0.2257	0.268	0.0492	0.0935	0.2026	0.1024	0.1222
266958_at	AT2G34630	GPPS/GPS1 (GERANYLPYROPHOSPHATE SYN	0.05214	0.5803	0.4523	-0.169	0.1233	0.1782	-0.01263	0.8914	0.4901	-0.2338	0.0544	0.0834
266959_at	AT2G07690	mitochondrome maintenance family protein / MCN	0.1355	0.725	0.5011	0.173	0.6551	0.4435	-0.1586	0.6814	0.4248	-0.1211	0.7528	0.4145
266960_at	no_match	no_match	0.9328	0.2297	0.2819	0.7309	0.3295	0.3083	-0.5872	0.2089	0.2171	-0.7891	0.1147	0.1311
266961_at	AT2G07720	transposable element gene	-1.1274	0.2085	0.2672	-1.5646	0.1061	0.1644	0.5585	0.4992	0.3594	0.1214	0.8797	0.4512
266962_at	AT2G39435	similar to unknown protein [Arabidopsis thaliana] (T	-0.3687	0.4147	0.3822	-0.04737	0.9126	0.5221	-0.686	0.139	0.1705	-0.3647	0.3825	0.2768
266963_at	AT2G39450	ATMTP11/MTP11; cation transmembrane transport	-0.7152	0.0138	0.0719	-0.92	0.0057	0.0437	-0.4125	0.008	0.0359	-0.6173	0.0018	0.0148
266964_at	AT2G39480	PGP6; ATPase, coupled to transmembrane movem	-0.2986	0.1149	0.1963	0.3654	0.0698	0.1322	-1.0012	0.0018	0.0206	-0.3371	0.0689	0.0961
266965_at	AT2G39500	nodulin MtN21 family protein	0.2617	0.6799	0.4861	-0.4735	0.4667	0.3707	-0.2438	0.7003	0.4313	-0.4914	0.4513	0.3065
266966_at	AT2G39520	unknown protein	-1.4023	0.172	0.2427	-1.901	0.0875	0.1489	-0.5387	0.5581	0.3819	-1.0373	0.2865	0.2315
266967_at	AT2G39530	integral membrane protein, putative	1.3294	0.3199	0.3343	3.1583	0.0543	0.1157	0.4607	0.7142	0.4363	2.2897	0.1224	0.1367
266968_at	AT2G39360	protein kinase family protein	0.2496	0.5127	0.4261	0.3948	0.3198	0.303	0.005905	0.9535	0.5064	0.1511	0.1876	0.1779
266969_at	AT2G39540	gibberellin-regulated family protein	-0.324	0.7512	0.5088	-0.2848	0.7801	0.4836	-0.9275	0.3859	0.3104	-0.8883	0.4044	0.286
266970_at	AT2G39560	similar to hypothetical protein [Vitis vinifera] (GB:CA	-1.2322	0.1533	0.2284	-2.2628	0.0319	0.0887	-0.1325	0.8429	0.4766	-1.1631	0.1371	0.1462
266971_at	AT2G39580	binding	0.3162	0.1914	0.2564	-0.1063	0.6255	0.433	-2.625	2.00E-04	0.0126	-3.0475	1.00E-04	0.0062
266972_at	AT2G39590	40S ribosomal protein S15A (RPS15aC)	0.3285	0.7497	0.5086	-0.06847	0.9466	0.5311	-0.9665	0.3714	0.3036	-1.3635	0.2289	0.201
266973_at	AT2G39620	pentatricopeptide (PPR) repeat-containing protein	1.2959	0.2867	0.3153	0.003514	0.9975	0.5435	-1.0993	0.3562	0.2963	-2.3916	0.086	0.1098
266974_at	AT2G39370	similar to unknown protein [Arabidopsis thaliana] (T	-0.7676	0.5002	0.4206	-0.5137	0.6463	0.4402	1.4707	0.229	0.229	1.7246	0.1716	0.1682
266975_at	AT2G39380	ATEXO70H2 (EXOCYST SUBUNIT EXO70 FAMIL	-0.2717	0.3744	0.3617	-0.392	0.2231	0.2476	0.2012	0.3153	0.2759	0.08101	0.6682	0.3868
266976_at	AT2G39410	hydrolase, alpha/beta fold family protein	-1.3718	0.3419	0.3461	-0.4681	0.7318	0.4688	-1.1333	0.3049	0.2712	-0.2295	0.8235	0.4352
266977_at	AT2G39420	esterase/lipase/thioesterase family protein	0.135	0.7943	0.5223	0.1617	0.7554	0.4768	-0.1413	0.3252	0.281	-0.1147	0.4147	0.2902
266978_at	AT2G39430	disease resistance-responsive protein-related / dirig	0.1833	0.7494	0.5085	0.263	0.649	0.4413	0.03036	0.9433	0.5041	0.1101	0.7971	0.4279
266979_at	AT2G39470	PPL2 (PSBP-LIKE PROTEIN 2); calcium ion binding	-0.9965	5.00E-04	0.0325	-1.1658	3.00E-04	0.0249	0.03257	0.7143	0.4363	-0.1368	0.1741	0.1698
266980_at	AT2G39390	60S ribosomal protein L35 (RPL35B)	-0.02787	0.8937	0.5497	0.408	0.1056	0.1641	0.7531	0.0184	0.0542	1.189	0.0037	0.0198
266981_at	AT2G39460	ATRPL23A (RIBOSOMAL PROTEIN L23A); RNA b	-0.03981	0.8631	0.5418	-0.1008	0.6659	0.447	0.5734	0.057	0.102	0.5124	0.077	0.1024
266982_at	AT2G39500	similar to Os01g0974800 [Oryza sativa (japonica cu	0.1442	0.7498	0.5086	0.1328	0.7687	0.4801	0.1766	0.6971	0.4302	0.1652	0.7154	0.4026
266983_at	AT2G39400	hydrolase, alpha/beta fold family protein	0.2791	0.4202	0.385	0.7621	0.0704	0.1327	-0.3165	0.0023	0.0224	0.1665	0.0219	0.0483
266984_at	AT2G39570	ACT domain-containing protein	-0.7076	0.012	0.0681	-0.5645	0.0252	0.0794	-1.215	0	0.0092	-1.0719	0	0.0055
266985_at	AT2G39550	ATGGT-IB (GERANYLGERANYLTRANSFERASE-	0.4146	0.0668	0.1484	0.6064	0.0217	0.0747	0.03118	0.8601	0.4811	0.2229	0.2502	0.2126
266986_at	AT2G39630	glycosyl transferase family 2 protein	0.4582	0.1125	0.1942	0.2906	0.2677	0.2742	-0.2705	0.2973	0.2673	-0.438	0.1245	0.138
266987_at	AT2G39280	RAB GTPase activator	-1.3725	0.119	0.1994	-0.2214	0.7656	0.479	-3.2501	0.0094	0.0388	-2.099	0.0389	0.0679
266988_at	AT2G39310	jacalin lectin family protein	1.2487	0.0132	0.0709	1.6444	0.005	0.0425	-0.2484	0.4462	0.3367	0.1473	0.6432	0.3783
266989_at	AT2G39330	jacalin lectin family protein	1.0689	0.0086	0.0605	1.0013	0.0108	0.0559	0.3596	0.1258	0.1607	0.2921	0.1921	0.1803
266990_at	AT2G39190	ATATH8 (ABC2 homolog 8)	-0.3727	0.2299	0.282	-0.5357	0.1116	0.1687	-2.0031	0.0016	0.0202	-2.1662	0.0012	0.0127
266991_at	AT2G39290	PGP1/PGPS1/PGS1 (PHOSPHATIDYLGLYCEROL	0.1851	0.2881	0.3162	-0.2573	0.164	0.2085	0.2711	0.1474	0.1771	-0.1713	0.3206	0.2486
266992_at	AT2G39200	MLO1/2 (MILDEW RESISTANCE LOCUS O 12); ca	0.3619	0.2221	0.2764	0.3901	0.1945	0.229	-0.01949	0.9417	0.5037	0.008646	0.9741	0.4766
266993_at	AT2G39210	nodulin family protein	0.8556	0.0097	0.0633	1.3653	0.0018	0.0323	-0.6309	0.0171	0.0524	-0.1211	0.4928	0.323
266994_at	AT2G34440	AGL29; transcription factor	-2.13	0.1015	0.1842	-0.2681	0.8028	0.4904	-3.2643	0.0315	0.0721	-1.4025	0.2354	0.2047
266995_at	AT2G34500	CYP710A1 (cytochrome P450, family 710, subfami	1.038	0.1409	0.2183	1.0431	0.1394	0.1902	-0.1126	0.6319	0.4084	-0.1075	0.6469	0.3797
266996_at	AT2G34490	CYP710A2 (cytochrome P450, family 710, subfami	-0.06848	0.6376	0.4722	-0.4323	0.0325	0.0894	0.4328	0.0324	0.0734	0.06903	0.6351	0.3755
266997_at	no_match	no_match	-0.6506	0.0788	0.1617	-0.4691	0.1658	0.2096	-1.2749	0.01	0.0398	-1.0934	0.0169	0.0415
266998_at	AT2G39400	pentatricopeptide (PPR) repeat-containing protein	-2.6881	0.4542	0.4	-1.1265	0.2467	0.2619	1.3931	0.1642	0.1879	0.9547	0.3085	0.2427
266999_at	AT2G34450	high mobility group (HMG1/2) family protein	-0.6301	0.0658	0.1471	-0.1738	0.5264	0.3947	0.002902	0.9829	0.5134	0.4592	0.0228	0.0491
267000_at	AT2G34310	similar to unknown protein [Arabidopsis thaliana] (T	-0.9952	0.0012	0.036	-0.9601	0.0014	0.0312	0.08907	0.5014	0.3601	0.1242	0.3616	0.2677
267001_at	AT2G34470	UREG (urease accessory protein G); metal ion bind	0.6345	0.0086	0.0605	0.2217	0.1682	0.2114	-0.3304	0.0665	0.1115	-0.7432	0.0049	0.022
267002_s_at	AT2G34430;AT2G34420	[AT2G34430, LHB1B1 (Photosystem II light harvest	-0.2281	0.2595	0.2994	-0.4454	0.0624	0.1241	0.06187	0.504	0.3609	-0.1554	0.1392	0.1476
267003_at	AT2G34340	similar to unknown protein [Arabidopsis thaliana] (T	-0.3013	0.7167	0.4983	-0.232	0.0352	0.0926	1.5937	0.0747	0.119	-0.526	0.4733	0.3151
267004_at	AT2G34260	transducin family protein / WD-40 repeat family prot	0.7094	0.0037	0.0459	0.3824	0.0306	0.0868	0.3048	0.0425	0.0858	-0.02218	0.8411	0.4404
267005_at	AT2G34460	flavin reductase-related	-0.9754	0.0271	0.0952	-0.6759	0.0775	0.1395	-0.2391	0.2941	0.2657	0.06035	0.7759	0.4217
267006_at	AT2G34190	xanthine/uracil permease family protein	1.4217	0.1343	0.2127	0.5406	0.5155	0.3908	-0.09497	0.9064	0.4941	-0.9761	0.2677	0.2216
267007_at	AT2G34480	60S ribosomal protein L18A (RPL18aB)	0.008283	0.9507	0.5648	0.01936	0.8852	0.5147	0.08875	0.486	0.3539	0.09982	0.4372	0.3001
267008_at	AT2G39350	ABC transporter family protein	0.121	0.6871	0.4883	0.7978	0.046	0.1063	-0.294	0.3517	0.2941	0.3828	0.2422	0.2083
267009_at	AT2G39260	RNA binding	0.9106	0.0014	0.038	0.6358	0.0053	0.0431	-0.472	0.0149	0.0486	-0.7468	0.0029	0.0176
267010_at	AT2G39250	SNZ (SCHNARCHZAPFEN); DNA binding / transcri	-1.208	0.0043	0.0479	-1.3758	0.0027	0.0346	0.3087	0.0857	0.1291	0.1408	0.3588	0.2665
267011_at	AT2G39230	pentatricopeptide (PPR) repeat-containing protein	1.654	0.1479	0.2236	2.5728	0.0495	0.1103	0.04414	0.9642	0.5085	0.8747	0.3973	0.2831
267012_at	AT2G39220	PLA IIIG/PLP6 (Patatin-like protein 6); nutrient reser	0.9946	0.0236	0.0897	1.1449	0.0149	0.0643	0.3155	0.1523	0.1805	0.4658	0.0596	0.0882
267013_at	AT2G39180	protein kinase family protein	-0.9688	0.0324	0.1044	-0.5899	0.1218	0.1771	-0.2417	0.0882	0.1312	0.1372	0.2717	0.2237
267014_at	AT2G39170	similar to unnamed protein product [Vitis vinifera] (G	0.5317	0.0965	0.1795	0.4211	0.1619	0.2072	0.435	0.1515	0.18	0.3243	0.2574	0.2166
267015_at	AT2G39340	SAC3/GANP family protein	-0.1105	0.5365	0.4356	-0.0502	0.7744	0.4819	-1.4809	1.00E-04	0.0118	-1.4206	1.00E-04	0.0068
267016_at	AT2G39160	unknown protein	-0.04031	0.9775	0.5716	-1.2584	0.4018	0.3421	-0.1007	0.9438	0.5042	-1.3188	0.3817	0.2765
267017_at	AT2G39140	pseudouridine synthase family protein	0.1971	0.3715	0.3602	0.09146	0.665	0.4466	0.4869	0.0679	0.1129	0.3813	0.1236	0.1374
267018_at	AT2G39140	pseudouridine synthase family protein	0.3051	0.0387	0.1134	0.07513	0.4988	0.3831	-0.05042	0.6396	0.411	-0.2803	0.0482	0.0775
267019_at	AT2G39130	amino acid transporter family protein	-0.7404	0.0405	0.1161	-0.3404	0.2418	0.2589	-1.0659	0.0127	0.0447	-0.6659	0.0549	0.0839
267020_at	AT2G39320	OTU-like cysteine protease family protein	-0.1886	0.742	0.5065	-0.2651	0.6459	0.4402	0.7495	0.1827	0.2008	0.673	0.2219	0.197
267021_at	AT2G39300	similar to unknown protein [Arabidopsis thaliana] (T	0.4843	0.2959	0.3209	-0.1309	0.7616	0.478	0.1666	0.7006	0.4315	0.4486	0.3281	0.2524
267022_at	AT2G34230	similar to MEE20 (maternal effect embryo arrest 20	0.574	0.7427	0.5067	0.8066	0.6469	0.4405	0.7921	0.6527	0.4155	1.0247	0.564	0.3504
267023_at	AT2G34250	protein transport protein sec61, putative	0.4686	0.0337	0.1062	0.3366	0.0848	0.1465	-0.2622	0.0626	0.1075	-0.3943	0.0183	0.0434
267024_s_at	AT2G34390;AT2G29870	[AT2G34390, NIP2;1/NLM4 (NOD26-LIKE INTRINS	-0.3013	0.7167

267090_at	AT2G38270	CXIP2 (CAX-INTERACTING PROTEIN 2); electron	-0.02487	0.8907	0.5485	-0.7391	0.0122	0.0591	0.645	0.0192	0.0555	-0.06923	0.7045	0.399
267091_at	AT2G38185	zinc finger (C3HC4-type RING finger) family protein	-0.3318	0.4367	0.3923	-0.207	0.6187	0.4302	-0.6838	0.1499	0.1788	-0.559	0.2195	0.1959
267092_at	AT2G38120	AUX1 (AUXIN RESISTANT 1); amino acid transme	0.2131	0.4239	0.3868	-0.05864	0.8187	0.4954	0.1015	0.6138	0.4023	-0.1703	0.4111	0.2887
267093_at	AT2G38170	CAX1 (CATION EXCHANGER 1); calcium ion trans	0.1938	0.1623	0.2357	-0.05624	0.6457	0.4401	-0.4724	0.014	0.0473	-0.7225	0.0031	0.0181
267094_at	AT2G38080	IRX12/LAC4 (laccase 4); copper ion binding / oxido	0.04849	0.8113	0.5272	0.1211	0.5589	0.4079	-0.0566	0.726	0.4405	0.016	0.9205	0.463
267095_at	AT2G38280	FAC1 (EMBRYONIC FACTOR1); AMP deaminase	0.5009	0.0705	0.153	-0.1705	0.4511	0.3645	-0.0344	0.8745	0.4852	-0.7058	0.026	0.0534
267096_at	AT2G38180	GDSL-motif lipase/hydrolase family protein	0.7537	0.0873	0.1711	0.8384	0.0662	0.1288	-0.382	0.0888	0.1315	-0.2973	0.1565	0.159
267097_at	no_match	no_match	1.5613	0.2137	0.2707	0.4846	0.6704	0.4487	-0.8619	0.3086	0.2727	-1.9385	0.0587	0.0874
267098_at	AT2G41451	similar to unknown protein [Arabidopsis thaliana] (T	-0.1939	0.6841	0.4872	-0.5559	0.2778	0.2796	0.2581	0.5913	0.3952	-0.1038	0.8262	0.436
267099_at	AT2G41460	ARP (apurinic endonuclease-redox protein)	0.3791	0.0398	0.115	0.4989	0.0168	0.0672	0.03847	0.7577	0.4506	0.1582	0.2457	0.2101
267100_at	AT2G41470	embryo-specific protein-related	0.4664	0.0003	0.6484	0.4759	-1.3538	0.2263	0.2494	1.2409	0.2605	0.2468	-0.5793	0.5741	0.3539
267101_at	AT2G41480	peroxidase	1.3116	0.0027	0.0426	2.1473	4.00E-04	0.0251	0.7251	0.0169	0.052	1.5608	0.0011	0.0123
267102_at	AT2G41500	EMB2776/LIS (LACHESIS); nucleotide binding	0.1444	0.3742	0.3617	0.4061	0.049	0.1097	-0.934	0.0029	0.0247	-0.6744	0.0095	0.0304
267103_at	AT2G41490	GPT (UDP-GLCNAC%3ADOLICHOL+PHOSPHATI	1.0908	0.003	0.0435	0.09944	0.5876	0.4187	-0.1262	0.4965	0.3584	-1.1175	0.0027	0.0171
267104_at	AT2G41430	ERD15 (EARLY RESPONSIVE TO DEHYDRATION	-0.2775	0.397	0.3738	-0.235	0.4673	0.371	0.4154	0.081	0.1246	0.4579	0.0627	0.0908
267105_at	no_match	no_match	-0.437	0.7193	0.4992	0.1544	0.8982	0.5184	0.9303	0.3885	0.3115	1.5217	0.1891	0.1788
267106_s_at	AT2G14720;AT2G14740	AT2G14720, VSR-2 (Vacuolar sorting receptor 2);	0.4486	0.0721	0.1549	0.3564	0.126	0.18	0.07211	0.7162	0.4369	-0.02006	0.9188	0.4624
267107_at	AT2G14730	transposable element gene	0.7515	0.3784	0.3637	-1.0085	0.2549	0.2672	1.3099	0.1238	0.1593	-0.4502	0.5406	0.3412
267108_at	AT2G14830	similar to unknown protein [Arabidopsis thaliana] (T	-1.3411	0.2778	0.3101	-0.7788	0.5065	0.3873	0.7707	0.4287	0.3291	1.3329	0.2028	0.1868
267109_at	AT2G14810	unknown protein	0.5151	0.748	0.5083	-2.4819	0.1725	0.2145	2.0025	0.2518	0.2417	-0.9945	0.5426	0.3419
267110_at	AT2G14800	similar to unknown protein [Arabidopsis thaliana] (T	-0.1236	0.662	0.48	0.1221	0.6656	0.4469	-0.964	0.0111	0.0417	-0.7183	0.0291	0.0571
267111_s_at	AT1G27800;AT3G42750;A	AT1G27800, transposable element gene;[AT3G42	-0.4953	0.9191	0.5567	0.2497	0.6145	0.4286	-0.9511	0.1064	0.146	-0.6518	0.2277	0.2003
267112_at	AT2G14750	APK (APS KINASE); ATP binding / kinase/ transfer	-0.2733	0.0068	0.0556	-0.5963	0.0133	0.0615	0.5181	0.0232	0.0458	0.6452	0.0062	0.0243
267113_at	AT2G14850	similar to unknown protein [Arabidopsis thaliana] (T	-0.1844	0.314	0.3308	0.3075	0.1274	0.1811	-0.3163	0.03	0.0706	0.1755	0.1412	0.1489
267114_at	AT2G14835	zinc finger (C3HC4-type RING finger) family protein	0.1226	0.5481	0.4403	0.2635	0.2319	0.2528	-0.2589	0.0974	0.1389	-0.118	0.3814	0.2764
267115_s_at	AT2G32540;AT2G32530	AT2G32540, ATCSLB04 (Cellulose synthase-like E	-0.0549	0.8849	0.5471	-0.384	0.3413	0.3141	-0.3977	0.3263	0.2814	-0.7268	0.1106	0.1281
267116_at	AT2G32560	F-box family protein	-0.9446	0.0179	0.0801	-0.5091	0.1049	0.1636	-0.631	0.0607	0.1057	-0.1955	0.4672	0.3128
267117_at	AT2G32550	F-box family protein	1.2433	0.0043	0.0908	0.189	0.6202	0.4306	-0.5117	0.1011	0.142	0.9205	0.0188	0.044
267118_at	AT2G32590	similar to unnamed protein product [Vitis vinifera] (G	-0.1595	0.7611	0.512	0.2798	0.5986	0.4229	0.1272	0.808	0.466	0.5665	0.312	0.2444
267119_at	AT2G32610	ATCSLB01 (Cellulose synthase-like B1); transferas	-0.5408	0.6587	0.4788	-0.2754	0.8203	0.496	0.5621	0.6466	0.4132	0.8275	0.5065	0.3283
267120_at	AT2G32530	similar to protein binding / zinc ion binding [Arabido	0.2298	0.7191	0.4992	0.2858	0.6562	0.444	-0.5478	0.4095	0.3206	-0.4919	0.455	0.3079
267121_at	AT2G32540	GDSL-motif lipase/hydrolase family protein	0.459	0.7546	0.5099	1.214	0.4259	0.3534	-0.1837	0.8999	0.4924	0.5714	0.6983	0.3969
267122_at	AT2G32550	hydrolase	-0.7259	0.6297	0.4697	-0.9251	0.5429	0.4019	-0.2213	0.8282	0.4721	-0.4205	0.6826	0.3914
267123_at	AT2G32560	hydrolase, alpha/beta fold family protein	-0.7056	0.1164	0.1973	-1.2875	0.0219	0.0749	0.8845	0.0665	0.1115	0.3026	0.44	0.3013
267124_at	AT2G32570	hydrolase, alpha/beta fold family protein	-0.5957	0.7372	0.5049	0.4905	0.7818	0.484	-0.372	0.8332	0.4735	0.7143	0.6884	0.3933
267125_at	AT2G32580	hydrolase, alpha/beta fold family protein	-3.1625	0.0227	0.0882	-2.6339	0.0399	0.099	-1.0524	0.2186	0.2228	-0.5238	0.5082	0.329
267126_s_at	AT2G32590;AT2G32590	AT2G32590, ACL (ACETONE-CYANOHYDRIN LY	-0.3035	0.1013	0.1841	-0.4289	0.0401	0.0993	0.2265	0.1551	0.1824	0.1031	0.4741	0.3154
267127_at	AT2G32610	esterase, putative	-0.6824	0.0223	0.0875	-0.6742	0.0232	0.0768	0.2122	0.323	0.2797	0.2205	0.3068	0.2419
267128_at	AT2G32620	esterase, putative	0.5045	0.0731	0.1557	-0.1642	0.4758	0.3745	0.6508	0.0208	0.058	-0.01786	0.924	0.4638
267129_at	AT2G32630	CLF (CURLY LEAF); transcription factor	-0.1066	0.5816	0.4529	-0.6619	0.0224	0.0757	0.06934	0.7241	0.4399	-0.4829	0.0577	0.0865
267130_at	AT2G32390	similar to hypothetical protein Osl_015489 [Oryza s	0.02027	0.8824	0.5469	0.01677	0.9025	0.5195	-0.384	0.0405	0.0834	-0.3875	0.0394	0.0684
267131_at	AT2G32400	dehydrodolichyl diphosphate synthase, putative / DI	-2.3534	0.0234	0.0895	-0.09059	0.8974	0.5181	-1.5908	0.0382	0.0807	0.672	0.2675	0.2214
267132_at	AT2G32420	nicotinate phosphoribosyltransferase family protein	0.00919	0.9565	0.5567	-0.5704	0.0228	0.0762	-0.05688	0.5755	0.3886	-0.6181	0.0027	0.0171
267133_at	AT2G32440	unknown protein	0.3259	0.7512	0.5088	-0.6064	0.5617	0.409	-0.9885	0.2635	0.2485	-1.9208	0.065	0.0928
267134_at	AT2G32450	protein kinase family protein	0.491	0.0354	0.1087	0.4978	0.034	0.0911	-0.1228	0.328	0.2824	-0.116	0.3524	0.2638
267135_at	AT2G32430	KCK1 (KCP-RELATED PROTEIN 1)	0.0489	0.666	0.4812	0.1211	0.7243	0.4667	-0.1927	0.295	0.2661	0.07736	0.6541	0.3821
267136_at	AT2G32460	XLG1 (EXTRA-LARGE G-PROTEIN 1); signal trans	0.2663	0.0243	0.0908	0.1967	0.0598	0.1214	-0.1237	0.0803	0.124	-0.1934	0.0219	0.0483
267137_at	AT2G32410	ACPT (ARABIDOPSIS CIS-PRENYLTRANSFERAS	-0.9064	0.5153	0.4274	-1.0431	0.458	0.3673	-0.6625	0.6298	0.4079	-0.7993	0.5637	0.3503
267138_s_at	AT2G38230;ATPDX1.1	ATPDX1.1 (PYRIDOXINE BIOSYNTH	-0.6964	0.2134	0.2706	-0.2419	0.6346	0.4363	-0.8778	0.0022	0.0221	-0.4233	0.0281	0.056
267139_s_at	AT2G38195;AT2G38220	[AT2G38195, protein binding / zinc ion binding];[AT	-1.1224	0.2418	0.2887	0.533	0.5501	0.4048	-1.1003	0.2274	0.2279	0.5551	0.5121	0.3306
267140_at	AT2G38250	DNA-binding protein-related	1.3386	0.2049	0.2653	1.9588	0.0913	0.1524	0.1383	0.7042	0.4328	0.7585	0.0889	0.1119
267141_at	AT2G38090	myb family transcription factor	0.1617	0.7463	0.5078	0.1793	0.7201	0.4655	-0.3391	0.2832	0.2599	-0.3215	0.3055	0.2412
267142_at	AT2G38290	ATAMT2 (AMMONIUM TRANSPORTER 2); ammo	0.8782	0.0209	0.085	1.0665	0.0109	0.056	-0.3628	0.0864	0.1296	-0.1745	0.3376	0.2567
267143_at	AT2G38100	proton-dependent oligopeptide transport (POT) fam	0.7952	0.1053	0.1875	0.7619	0.1163	0.1722	0.6539	0.1615	0.1864	0.6205	0.1789	0.1726
267144_at	AT2G38110	ATGPX6/GPAT6 (GLYCEROL-3-PHOSPHATE AC	-0.7168	0.2169	0.2733	-0.04355	0.9334	0.5274	-0.3648	0.302	0.2696	0.3085	0.3735	0.2728
267145_at	AT2G38130	ATMAK3 (Arabidopsis thaliana MAK3 homologue);	0.2313	0.2631	0.3016	0.6686	0.0198	0.072	0.1642	0.2649	0.2492	0.6016	0.009	0.0296
267146_at	AT2G38160	similar to unknown protein [Arabidopsis thaliana] (T	0.2781	0.8075	0.5261	-0.5684	0.623	0.432	1.6371	0.1095	0.148	0.7905	0.378	0.2748
267147_at	AT2G38240	oxidoreductase, 2OG-Fe(II) oxygenase family prote	-0.0214	0.9508	0.5648	0.05268	0.8794	0.513	-0.6669	0.0677	0.1127	0.741	0.0506	0.0799
267148_at	AT2G23470	similar to EMB1879 (EMBRYO DEFECTIVE 1879)	0.8244	0.3213	0.3352	0.2123	0.7854	0.4848	-0.6571	0.2001	0.2119	-1.2692	0.0415	0.0708
267149_s_at	AT2G04310;AT2G23500;A	[AT2G04310, transposable element gene];[AT2G23	0.6523	0.6639	0.4806	0.8012	0.5959	0.4218	-0.01896	0.9898	0.5152	0.1299	0.9302	0.4657
267150_at	AT2G23510	transferase family protein	-3.528	0.0039	0.0464	-0.9216	0.1929	0.2278	-1.3331	0.0627	0.1076	1.2733	0.0708	0.0976
267151_at	AT2G30970	ASP1 (ASPARTATE AMINOTRANSFERASE 1)	-0.1169	0.3868	0.3682	0.07133	0.5858	0.4183	-0.2226	0.0846	0.128	-0.0343	0.7428	0.4113
267152_at	AT2G31040	ATP synthase protein I -related	-0.3465	0.0367	0.1105	-0.5839	0.0065	0.046	0.4071	0.0044	0.0284	0.1698	0.0733	0.0994
267153_at	AT2G30860	ATGSTF9 (Arabidopsis thaliana Glutathione S-trans	-0.1352	0.4682	0.4065	0.02934	0.8705	0.51	0.4645	0.0155	0.0495	0.629	0.0054	0.0229
267154_at	AT2G30870	ATGSTF10 (EARLY DEHYDRATION-INDUCED 13	-0.00324	0.986	0.5734	-0.03979	0.8295	0.4987	0.659	0.019	0.0553	0.6224	0.0229	0.0492
267155_at	AT2G30925	unknown protein	-0.4099	0.8244	0.5308	-1.9593	0.3209	0.3036	-1.0517	0.5669	0.3855	-2.6011	0.1981	0.1838
267156_at	AT2G30910	unknown protein	-0.8963	0.4797	0.4117	-1.8225	0.1886	0.2255	1.0217	0.425	0.3275	0.09558	0.9378	0.4678
267157_at	AT2G37630	AS1/ATMYB91/ATPHAN/MYB91 (ASYMMETRIC L	0.5369	0.2376	0.2861	0.3425	0.4262	0.3535	0.4203	0.1249	0.1599	0.2258	0.3569	0.2655
267158_at	AT2G37640	ATEXPA3 (ARABIDOPSIS THALIANA EXPANSIN	-1.263	0.0585	0.1386	-0.6682	0.2374	0.2562	-0.8522	0.1164	0.1535	-0.2574	0.5788	0.3556
267159_at	AT2G37650	scarecrow-like transcription factor 9 (SCL9)	-0.02454	0.9432	0.5632	-0.5345	0.1741	0.2155	-0.1462	0.5504	0.3792	-0.6562	0.0431	0.0725
267160_at	AT2G37670	WD-40 repeat family protein	0.05741	0.9338	0.5608	-1.6793	0.061	0.1227	1.0821	0.1711	0.1928	-0.6546	0.3706	0.2716
267161_at	no_match	no_match	0.5742	0.0894	0.1732	0.7812	0.0385	0.0972	0.518	0.1143	0.1519	0.725	0.0479	0.0773
267162_s_at	AT2G37690;AT2G05140	AT2G37690, phosphoribosylaminoimidazole carbox	0.7605	0.0175	0.0793	0.5664	0.0438	0.1036	-0.3448	0.1516	0.18	-0.5389	0.0506	0.0799
267163_at	AT2G37520	PHD finger family protein	0.199	0.2086	0.2672	0.2908	0.0939	0.1543	-0.493	0.0207	0.0579	-0.4012	0.0392	0.0682
267164_at	AT2G37700	catalytic	0.6876	0.5485	0.4405	-0.792	0.4929	0.3815	1.5999	0.2024	0.2132	0.1203	0.9143	0.4611
267165_at	AT2G37710	RLK (RECEPTOR LECTIN KINASE); kinase	0.4466	0.0235	0.0896	0.3938	0.0348	0.0921	0.2023	0.1024	0.1428	0.1495	0.1937	0.1812
267166_at	AT2G37720	similar to unknown protein [Arabidopsis thaliana] (T	-1.3348	0.2416	0.2886	-2.2232	0.0841	0.1458	1.2276	0.2752	0.2553	0.3392	0.7447	0.4119
267167_at	AT2G37740	zinc finger (C2H2 type) family protein	0.2276	0.0179	0.0802	-1.9043	0.0296	0.0855	1.7647	0.0346	0.0761	-2.3672	0.0134	0.0367
267168_at	AT2G37750	aldo/keto reductase family protein	0.6757	0.0479	0.1261	0.451	0.1332	0.1854	0.2587	0.3414	0.2889	0.03394	0.8943	0.4555
267169_at	AT2G37540	short-chain dehydrogenase/reductase (SDR) family	0.4846	0.0454	0.1226	0.1188	0.5203	0.3923	-0.1528	0.0338	0.0751	-0.5187	4.00E-04	0.0091
267170_at	AT2G37585	glycosyltransferase family 14 protein / core-2/I-bran	-0.6524	0.0487	0.1271	-0.8595	0.021	0.074	0.2156	0.4068	0.3194	0.008483	0.9727	0.4762
267171_at	AT2G37590	Dof-type zinc finger domain-containing protein	-0.1732	0.558	0.4442	0.1839	0.5353	0.3986	0.4194	0.1971	0.2099	0.7765	0.0459	0.0752
267172_at	AT2G37660	binding / catalytic/ coenzyme binding	-0.3478	0.046	0.1233	-0.8396	0.0023	0.0336	0.4108	0.0012	0.0187	-0.08103	0.1822	0.1747
267173_at	AT2G37560	ATORC2/ORC2 (ORIGIN RECOGNITION COMPLE	-0.1613	0.5757	0.451	-0.2638	0.376	0.3302	0.4568	0.0715	0.1162	0.3543	0.1318	0.1428
267174_at	AT2G37600	60S ribosomal protein L36 (RPL36A)	0.08476	0.6885	0.4887	0.1529	0.4801	0.3762	0.1637	0.1908	0.206	0.2318	0.0899	0.1127
267175_s_at	AT2G37620;AT3G53750	[AT2G37620, ACT1 (ACTIN 1); structural constituer	-0.8161	0.0094	0.0624	-0.7031	0.0157	0.0653	0.3114	0.0808	0.1244	0.4244	0.0339	0.0623
267176_at	AT2G37730	fringe-related protein	-0.315	0.5979	0.4589	-1.212	0.0925	0.1535	0.3569	0.5522	0.3799	-0.5401	0.3822	0.2767
267177_at	AT2G37580	zinc finger (C3HC4-type RING finger) family protein	0.1936	0.6383	0.4724	0.1241	0.761	0.478	0.6396	0.1166	0.1536	0.5701	0.1497	0.1544
267178_at	AT2G37750	unknown protein	0.8614	0.171	0.2421	1.0477	0.1126	0.1696	0.4903	0.0195	0.0561	0.6767	0.0065	0.0249
267179_at	AT2G37550	ASP1 (PDE1 SUPPRESSOR 1); DNA binding	0.216	0.4235	0.3868	0.2491	0.3625	0.3241	0.2111	0.4333	0.331	0.2443	0.371	0.2716
267180_at	AT2G37570	SLT1 (SODIUM- AND LITHIUM-TOLERANT 1)	-0.292	0.0514	0.1302	-0.4201	0.0167	0.0672	-0.08851	0.2885	0.2627	-0.2166	0.0402	0.0693
267181_at	AT2G37760	aldo/keto reductase family protein	1.2497	0.028	0.097	1.0359	0.0491	0.1098	0.268	0.0666	0.1116	0.0541	0.64	0.3772
267182_at	AT2G23360	transport protein-related	-0.04811	0.8496	0.538	-0.3584	0.2063	0.237	0.2129	0.4212	0.3258	-0.09733	0.7033	0.3985
267183_at	AT2G44020	mitochondrial transcription termination factor-relate	0.4865	0.0589	0.1389	0.3279	0.1525	0.2001	-0.08636	0.6664	0.42	-0.245	0.2579	0.2168
267184_at	AT2G44150	ASHH3 (HISTONE-LYSINE N-METHYLTRANSFER	-0.2482	0.1524	0.2277	0.1518	0.341	0.314	-0.2012	0.2258	0.2269	0.1988	0.2303	0.2017
267185_at	AT2G43950	OEP37; ion channel	0.1078	0.3166	0.3325	0.02358	0.8149	0.4947	0.1804	0.1283	0.1628	0.09615	0.3656	0.2694
267186_at	AT2G44090	similar to unknown protein [Arabidopsis thaliana] (T	0.04442	0.7165	0.4982	0.2469	0.0961	0.1562	-0.2192	0.1084	0.1473	-0.0167	0.8828	0.4523
267187_s_at	AT3G59970;AT2G44160	[AT3G59970, MTHFR1 (METHYLENETETRAHYDRO	-0.5706	0.0244	0.0908	-0.5496	0.0274	0.0827	0.04447	0.7943	0.4615	0.06548	0.7026	0.3982
267188_at	AT2G44050	COS1 (COI1 SUPPRESSOR1); 6,7-dimethyl-8-ribit	-0.2366	0.139	0.2164	-0.3157	0.0697	0.1322	0.3095	0.021	0.0583	0.2305	0.0515	0.0809
267189_at	AT2G44180	MAP2A (METHIONINE AMINOPEPTIDASE 2A); m	1.6819	0.0015	0.038	1.8343	0.001	0.0293	-0.3543	0.1111	0.1492	-0.2019	0.3098	0.2433
267190_at	AT2G44170	pseudogene, myristoyl-CoA:protein N-myristoyltran	0.4285	0.644	0.4745	0.6061	0.5192	0.3921	-1.0947	0.2713	0.253	-0.9171	0.3456	0.2606
267191_at	AT2G44110	MLO15 (MILDEW RESISTANCE LOCUS O 15); ca	1.8418	0.1044	0.1866	0.2953	0.754	0.4764	2.8768	0.0308	0.0715	1.3302	0.2051	0.1879
267192_at	AT2G43890	membrane protein, putative	-0.2029	0.2684	0.3045	-0.402	0.0637	0.1258	0.6912	0.0088	0.0375	0.492	0.0272	0.0548
267193_at	AT2G30900	similar to unknown protein [Arabidopsis thaliana] (T	0.3619	0.6784	0.4855	-1.1161	0.2406	0.2582	2.5843	0.0333	0.0745	1.1063	0.2441	0.2093
267194_s_at	AT2G31300;AT2G30910	[AT2G31300, ARPC1b (actin-related protein C1b);	0.2199	0.1646	0.2372	0.4137	0.033	0.09	-0.6833	0.0062	0.0327	-0.4895	0.0194	0.0447
267195_at	AT2G30940	protein kinase family protein	-1.5677	0.1715	0.2426	-1.4859	0.1899	0.2264	-0.823	0.4197	0.3252	-0.7412	0.4638	0.3115
267196_at	AT2G30950	VAR2 (VARIEGATED 2); ATP-dependent peptidase	-0.2298	0.0794	0.1624	-0.6017	0.0036	0.0378	-0.204	0.1064	0.146	-0.5759	0.0042	0.0208
267197_at	AT2G30960	unknown protein	-0.6751	0.0115	0.0669	-0.00375	0.9816	0.5396	0.05146	0.7528	0.4491	0.7228	0.009	0.0296
267198_at	AT2G30970	gibberellin-regulated family protein	-1.77	0.2549	0.2964	0.2625	0.8535	0.5057	-0.7676	0.5956	0.3967	1.265	0.3964	0.2827
267199_at	AT2G30990	similar to unknown protein [Arabidopsis thaliana] (T	0.04623	0.8585	0.5406	0.2085	0.4396	0.3594	-0.02988	0.8761	0.4856	0.1324	0.5024	0.3267
267200_at	AT2G31010	protein kinase family protein	0.2751	0.4702	0.4074	-0.511	0.213	0.2415	-0.4762	0.1089	0.1476	-1.2623	0.0055	0.0232
267201_at	AT2G31020	protein kinase family protein	1.2097	0.1074	0.1895	-0.1332	0.831	0.4991	-0.7212	0.2137	0.2202	-2.0641	0.0134	0.0367
267202_s_at	AT2G31020;AT2G31030	[AT2G31020, oxysterol-binding family protein];[AT2	0.705	0.424	0.3868	2.0703	0.0593	0.121	-0.3524	0.6796	0.4243	1.0129	0.2704	0.2229
267203_at	AT2G31035	similar to oxysterol-binding family protein [Arabidop	0.07458	0.9668	0.5694	-2.5313	0.2288	0.2508	1.2235	0.5303	0.3713	-1.3824	0.4815	0.3182
267204_at	AT2G31050	plastocyanin-like domain-containing protein	-0.1137	0.8615	0.5415	-0.3665	0.5812	0.4166	0.3372	0.6106	0.4014	0.08446	0.8968	0.4564
267205_at	AT2G30820	similar to unknown protein [Arabidopsis thaliana] (T	-0.651	0.4279	0.3883	-0.6225	0.4468	0.3624	0.4115	0.4361	0.3323	0.44	0.4075	0.2872
267206_at	AT2G30830	2-oxoglutarate-dependent dioxygenase, putative	-1.148	0.0758	0.1584	-1.0054	0.1052	0.1639	0.03838	0.9351	0.5021	0.1811	0.7035	0.3985
267207_at	AT2G30840	2-oxoglutarate-dependent dioxygenase, putative	0.4557	0.6954	0.4912	-0.3368	0.7712	0.4808	-0.3127	0.6774	0.4236	-1.1052	0.1886	0.1785
267208_at	AT2G30980	shaggy-related protein kinase delta / ASK-delta / AS	0.1673	0.1594	0.233	-0.02736	0.7917	0.4866	0.1176	0.2906	0.2639	-0.07712	0.4694	0.3135
267209_at	AT2G30930	similar to unknown protein [Arabidopsis thaliana] (T	0.06415	0.9227	0.5579	0.4383	0.595	0.3922	0.4055	0.1233	0.1589	0.7791	0.02	0.0455
267210_at	AT2G30920	ATCOQ3 (EMBRYO DEFECTIVE 3002)	0.01694	0.9246	0.5582	0.3504	0.1056	0.1641	-0.6604	0.0171	0.0524	-0.327	0.1237	0.1375
267211_at	AT2G44065	ribosomal protein L2 family protein	0.4991	0.0443	0.1213	0.6807	0.0168	0.0674	-0.08803	0.6006	0.3984	0.06358	0.5788	0.3556
267212_at	AT2G44060	late embryogenesis abundant family protein / LEA fa	0.006797	0.9496	0.5646	0.1549	0.2004	0.233	0.1783	0.6227	0.4056	0.1806	0.3264	0.232
267213_at	AT2G44120	60S ribosomal protein L7 (RPL7C)	0.2474	0.405	0.3779	0.2053	0.4833	0.3774	-0.0692	0.6227	0.4056	-0.1113	0.4402	0.3014
267214_at	AT2G43970	La domain-containing protein	0.9226	0.0022	0.041	0.7915	0.0039	0.0391	-1.0427	0	0.0092	-1.1737	0	0.0047
267215_at	AT2G20630	DC1 domain-containing protein	0.2205	0.7926	0.5184	1.4424	0.1258	0.1798	-1.0802	0.1648	0.1883	0.1417	0.8347	0.4385
267216_at	AT2G20620	DC1 domain-containing protein / PHD finger protein	1.7267	0.1088	0.191	0.119	0.8941	0.5169	0.8154	0.3864	0.3105	-0.7923	0.3987	0.2837
267217_at	AT2G20610	DC1 domain-containing protein	-0.9962	0.5964	0.4585	0.1755	0.9243	0.5252	-1.9823	0.2339	0.2317	-0.8106	0.5975	0.3626
267218_at	AT2G20615	unknown protein	-0.4477	0.61	0.463	-1.2129	0.2088	0.2387	0.3103	0.7213	0.439	-0.4549	0.6045	0.3648
267219_at	AT2G20590	similar to unnamed protein product [Vitis vinifera] (G	-0.06059	0.8403	0.5357	-0.2331	0.4548	0.3659	0.08143	0.7123	0.4357	-0.09103	0.6808	0.3908
267220_at	AT2G20500	ISPD (2-C-METHYL-D-ERYTHRITOL 4-PHOSPHA	-1.1534	0.0013	0.0376	-0.8227	0.0046	0.0416	-0.3961	0.0034	0.0258	-0.06541	0.3625	0.2681
267221_at	AT2G20480	STI (STITCHED1); ATP binding / DNA binding / DNA-c	-0.01822	0.9125	0.5547	-0.4184	0.0548	0.1162	0.1336	0.4392	0.3337	-0.2665	0.162	0.1624
267222_at	AT2G43880	polygalacturonase, putative / pectinase, putative	0.5609	0.2046	0.2651	-0.

267290_at	AT2G23740	nucleic acid binding / transcription factor/ zinc ion bi	0.1652	0.4762	0.4102	-0.1972	0.4016	0.342	-0.1667	0.4726	0.3486	-0.5291	0.0657	0.0933
267291_at	AT2G23740	nucleic acid binding / transcription factor/ zinc ion bi	-0.2641	0.0717	0.1543	-0.593	0.0055	0.0434	-0.5416	0.0075	0.035	-0.8704	0.0013	0.0133
267292_at	AT2G23740	nucleic acid binding / transcription factor/ zinc ion bi	-1.1423	0.3885	0.369	-1.6957	0.2247	0.2483	-1.1427	0.3883	0.3114	-1.6961	0.2246	0.1985
267293_at	AT2G23810	TET8 (TETRASPANIN8)	0.2156	0.3632	0.3559	0.3636	0.1588	0.2051	0.1779	0.1653	0.1886	0.326	0.036	0.0646
267294_at	AT2G23670	YCF37 (Arabidopsis homolog of Synechocystis YCf	-0.8451	0.0222	0.0874	-0.8722	0.02	0.0724	0.1457	0.5656	0.385	0.1185	0.6376	0.3764
267295_at	AT2G23800	GGPS2 (GERANYLGERANYL PYROPHOSPHATE	0.1277	0.8538	0.5392	0.5503	0.4449	0.3618	-1.391	0.0991	0.1402	-0.9684	0.2106	0.1912
267296_at	AT2G23660	LBD10 (LOB DOMAIN-CONTAINING PROTEIN 10)	0.02639	0.9852	0.5733	1.3015	0.3843	0.3339	-0.02379	0.9866	0.5143	1.2513	0.4012	0.2846
267297_at	AT2G23680	zinc finger (C3HC4-type RING finger) family protein	-0.003	0.9885	0.5741	-0.08483	0.6872	0.4546	0.3812	0.1235	0.159	0.2994	0.2011	0.1858
267298_at	AT2G23760	BLH4 (SAWTOOTH 2); DNA binding / transcription	-0.2272	0.2436	0.2898	-0.3998	0.074	0.1365	-0.04835	0.7329	0.4426	-0.2209	0.1697	0.167
267299_at	AT2G23150	UDP-glucuronosyl/UDP-glucosyl transferase family	-0.7649	0.0263	0.0937	-1.0729	0.0085	0.0509	0.1506	0.5251	0.3692	-0.1573	0.5078	0.3288
267300_at	AT2G23140	UDP-glucuronosyl/UDP-glucosyl transferase family	1.467	0.0022	0.0414	1.5823	0.0017	0.032	-0.04563	0.7129	0.4359	0.06969	0.5786	0.3555
267301_at	AT2G30110	ATUBA1 (ARABIDOPSIS THALIANA UBIQUITIN-A	0.5512	0.0235	0.0896	0.3187	0.1083	0.1658	-0.2408	0.041	0.084	-0.4732	0.0043	0.0208
267302_at	AT2G30100	ubiquitin family protein	-0.07408	0.6644	0.4808	-0.3077	0.124	0.1786	0.4874	0.0049	0.0297	0.2537	0.043	0.0724
267303_at	AT2G30090	GCN5-related N-acetyltransferase (GNAT) family pr	-0.9345	0.4739	0.4094	0.5734	0.6534	0.4429	-0.5981	0.6399	0.4111	0.9098	0.485	0.3196
267304_at	AT2G30080	ZIP6 (ZINC TRANSPORTER 6 PRECURSOR); cati	-0.2711	0.4147	0.3822	-0.4556	0.2013	0.2334	0.7108	0.0757	0.1198	0.5263	0.1524	0.1563
267305_at	AT2G30070	ATKT1 (Arabidopsis thaliana K+ uptake 1); potassi	-0.2586	0.4039	0.3773	-0.2297	0.454	0.3656	-0.6943	4.00E-04	0.0147	-0.6654	5.00E-04	0.0093
267306_at	AT2G30060	Ran-binding protein 1b (RanBP1b)	-0.2333	0.0378	0.1121	0.3076	0.0157	0.0653	0.2043	0.0554	0.1003	0.7451	6.00E-04	0.0103
267307_at	AT2G30210	LAC3 (laccase 3); copper ion binding / oxidoreducta	-0.7965	0.2375	0.2861	-0.2336	0.7048	0.4606	-0.6656	0.3107	0.2737	-0.1027	0.8666	0.4472
267308_at	AT2G30200	[acyl-carrier-protein] S-malonyltransferase/ bindi	-0.4188	0.0565	0.1362	-0.2745	0.1565	0.2032	0.1382	0.1793	0.198	0.2825	0.0293	0.0573
267309_at	AT2G19385	zinc ion binding	0.4614	0.0576	0.1375	0.9307	0.006	0.0446	0.01659	0.929	0.5003	0.4859	0.0498	0.0791
267310_at	AT2G34680	AIR9 (Auxin-Induced in Root cultures 9); protein bir	-0.6039	0.0135	0.0715	-0.5663	0.0167	0.0671	-0.3636	0.0639	0.1089	-0.326	0.0849	0.1089
267311_at	AT2G19360	proline-rich family protein	-1.3759	0.1608	0.2343	-2.0629	0.7591	0.4778	0.5365	0.6401	0.3753	-1.1032	0.2402	0.2072
267312_at	AT2G34750	initiation factor RRN3 family protein	0.4849	0.1218	0.2022	0.2129	0.4384	0.3589	-0.4254	0.0468	0.0907	-0.6974	0.0096	0.0305
267313_at	AT2G34740	protein phosphatase 2C, putative / PP2C, putative	1.2261	0.2801	0.3114	0.05114	0.961	0.5343	0.8767	0.4226	0.3266	-0.2982	0.7766	0.4219
267314_at	no_match	no_match	0.4953	0.0248	0.0914	0.6892	0.0091	0.0522	-0.6533	0.0099	0.0396	-0.4793	0.0275	0.0552
267315_at	no_match	no_match	-0.5353	0.1214	0.2018	-0.5914	0.0962	0.1562	0.576	0.1025	0.1429	0.52	0.1345	0.1411
267316_at	AT2G34710	PHB (PHABULOSA); DNA binding / transcription fa	0.4163	0.078	0.161	-0.01558	0.934	0.5276	-0.05876	0.7562	0.4501	-0.4906	0.05	0.0793
267317_at	AT2G34700	pollen Ole e 1 allergen and extensin family protein	0.2082	0.7508	0.5087	-0.3907	0.5579	0.4075	0.9338	0.2017	0.2127	0.335	0.6132	0.3677
267318_at	AT2G34770	FAH1 (FATTY ACID HYDROXYLASE 1); catalytic	-0.5058	0.4037	0.3772	-0.6002	0.3304	0.3086	-0.3522	0.0337	0.075	-0.4466	0.0158	0.04
267319_at	AT2G34660	ATMRP2 (MULTIDRUG RESISTANCE-ASSOCIAT	-0.3335	0.3866	0.3682	-0.6913	0.1145	0.1708	-0.7714	0.0099	0.0398	-1.1293	0.0025	0.0166
267320_at	AT2G19300	unknown protein	0.31	0.8213	0.53	0.05704	0.967	0.5357	-0.03734	0.9782	0.5122	0.3297	0.8103	0.4319
267321_at	AT2G19320	unknown protein	-0.5969	0.5674	0.4478	-0.1428	0.8889	0.5155	-2.04	0.0252	0.0644	-1.5859	0.0534	0.0826
267322_at	AT2G19330	leucine-rich repeat family protein	-1.2004	0.2645	0.3021	-1.6297	0.1531	0.2004	0.4854	0.4607	0.3434	0.05617	0.9294	0.4655
267323_at	AT2G19340	membrane protein, putative	0.07427	0.6886	0.4887	0.2959	0.161	0.2066	-0.4658	0.0539	0.0987	-0.2442	0.2292	0.2011
267324_at	no_match	no_match	0.6024	0.5535	0.4421	1.407	0.2059	0.2367	0.2829	0.7377	0.4442	1.0875	0.2395	0.2068
267325_at	no_match	no_match	-0.2961	0.844	0.5369	-1.6337	0.3112	0.2981	1.6187	0.315	0.2759	0.2811	0.8517	0.4431
267326_at	AT2G19380	RNA recognition motif (RRM)-containing protein	-0.3615	0.4322	0.3905	0.1822	0.6828	0.4531	-0.05683	0.8979	0.4971	0.4871	0.305	0.241
267327_at	AT2G19410	protein kinase family protein	-0.02325	0.9871	0.5736	-0.09292	0.9485	0.5316	-0.8549	0.5365	0.3739	-0.9246	0.5057	0.328
267328_at	AT2G19230	leucine-rich repeat protein kinase, putative	0.3587	0.6638	0.4806	0.2938	0.7207	0.4656	1.0012	0.261	0.2471	0.9363	0.2885	0.2326
267329_at	AT2G19250	pseudogene, similar to Magnesium-chelatase subur	-1.7709	0.276	0.3093	0.1587	0.9155	0.5229	-2.9907	0.1004	0.1414	1.0611	0.4921	0.3228
267330_at	AT2G19270	similar to unnamed protein product [Vitis vinifera] (G	0.2834	0.1461	0.2222	0.1651	0.3533	0.3197	0.1526	0.3072	0.2721	0.0343	0.8056	0.4303
267331_at	AT2G19280	pentatricopeptide (PPR) repeat-containing protein	-0.3408	0.0929	0.1766	-0.1469	0.3971	0.34	-0.6438	0.0143	0.0476	-0.4499	0.0441	0.0736
267332_at	AT2G19290	unknown protein	-0.4916	0.6551	0.4775	-0.9523	0.4034	0.3428	1.4307	0.2334	0.2314	0.9698	0.3956	0.2825
267333_at	AT2G19430	transducin family protein / WD-40 repeat family prot	0.02959	0.8906	0.5484	0.3304	0.177	0.2177	-0.1558	0.3785	0.3071	0.145	0.4095	0.288
267334_at	AT2G19420	unknown protein	-0.2981	0.8605	0.5412	-1.2996	0.4599	0.3679	0.9556	0.4176	0.3241	-0.04592	0.9675	0.475
267335_s_at	AT2G19440;AT1G64760	[At2g19440, glycosyl hydrolase family 17 protein];[	-0.8963	0.8849	0.5471	-0.2428	0.6866	0.4544	0.7434	0.2546	0.2434	0.5869	0.3533	0.2642
267336_at	AT2G19310	similar to HSP18.2 (HEAT SHOCK PROTEIN 18.2)	0.8673	0.0739	0.1564	0.754	0.1047	0.1634	0.3096	0.0299	0.0704	0.1964	0.1043	0.1236
267337_at	AT2G39980	transferase family protein	-0.7676	0.0539	0.1332	-0.3956	0.236	0.2554	-0.0923	0.2527	0.2423	0.2797	0.0155	0.0397
267338_at	AT2G39970	initiation factor	0.345	0.0963	0.1794	0.5906	0.0207	0.0735	-0.1069	0.2512	0.2415	0.1388	0.1567	0.1591
267339_at	AT2G39870	similar to unknown protein [Arabidopsis thaliana] (T	0.08893	0.6738	0.4839	0.1766	0.4189	0.3502	-0.01183	0.9548	0.5066	0.07582	0.7188	0.4036
267340_at	AT2G34690	ACD11 (ACCELERATED CELL DEATH 11)	0.1535	0.2292	0.2816	0.1676	0.1965	0.2305	-0.307	0.0471	0.091	-0.2929	0.0538	0.0829
267341_at	AT2G44200	similar to unknown protein [Arabidopsis thaliana] (T	0.009629	0.9412	0.5628	0.4199	0.0285	0.0838	0.1417	0.2151	0.2208	0.5517	0.1046	0.0214
267342_at	AT2G44520	COX10 (CYTOCHROME C OXIDASE 10); prenyltra	0.3442	0.0187	0.0813	0.2025	0.0876	0.149	-0.1079	0.2967	0.267	-0.2495	0.0502	0.0796
267343_at	AT2G44260	similar to unknown protein [Arabidopsis thaliana] (T	-0.823	0.3305	0.3403	-0.5841	0.4761	0.3746	-0.5936	0.3675	0.3018	-0.3547	0.5769	0.3548
267344_at	AT2G44230	similar to unknown protein [Arabidopsis thaliana] (T	-1.1283	0.0202	0.0839	-1.1513	0.0189	0.071	0.2107	0.022	0.0598	0.1877	0.0316	0.0599
267345_at	AT2G44240	similar to unknown protein [Arabidopsis thaliana] (T	2.9558	0.0745	0.1568	2.2263	0.1451	0.1946	2.085	0.0559	0.1009	1.3555	0.1578	0.1598
267346_at	AT2G39940	COI1 (CORONATINE INSENSITIVE 1); ubiquitin-pr	0.1388	0.6644	0.4808	0.1121	0.7248	0.4669	-0.3554	0.028	0.0681	-0.3821	0.0223	0.0486
267347_at	AT2G39950	similar to unnamed protein product [Vitis vinifera] (G	-0.07419	0.7624	0.5042	-0.442	0.123	0.18	-0.04292	0.758	0.4507	-0.4108	0.0343	0.0626
267348_at	no_match	no_match	0.2853	0.1941	0.2583	0.5827	0.0334	0.0905	0.107	0.2807	0.2585	0.4045	0.0092	03
267349_at	AT2G40010	60S acidic ribosomal protein P0 (RPP0A)	1.2327	0.145	0.2213	0.2595	0.7229	0.4664	-1.7293	0.0643	0.1093	-2.7025	0.0166	0.0412
267350_at	AT2G40030	NRPD1b (nuclear RNA polymerase D 1b); DNA bin	-0.14	0.8746	0.5451	-0.02208	0.9801	0.5393	0.07182	0.9003	0.4924	0.1897	0.7422	0.4112
267351_at	AT2G40030	NRPD1b (nuclear RNA polymerase D 1b); DNA bin	0.4757	0.0683	0.1503	0.3451	0.1466	0.1957	-0.3304	0.1602	0.1857	-0.4611	0.0742	0.1001
267352_at	AT2G40050	DC1 domain-containing protein	0.8691	0.5451	0.439	0.9159	0.5248	0.394	0.7125	0.3013	0.2694	0.7593	0.275	0.2255
267353_at	AT2G40070	similar to proline-rich family protein [Arabidopsis tha	-0.01214	0.8904	0.5484	0.025	0.7776	0.4829	0.06432	0.351	0.2938	0.1015	0.1714	0.1681
267354_at	AT2G39880	MYB25 (myb domain protein 25); DNA binding / tra	-1.3863	0.0256	0.0926	-0.8358	0.1045	0.1633	0.2186	0.6133	0.4021	0.7691	0.1264	0.1392
267355_at	AT2G39900	LIM domain-containing protein	0.6183	0.1007	0.1834	0.6981	0.0743	0.1368	0.2665	0.2925	0.2649	0.3463	0.1906	0.1796
267356_at	AT2G39930	ATISA1/ISA1 (ISOAMYLASE 1); alpha-amylase/ iso	0.1535	0.4772	0.4107	-0.07826	0.7101	0.4621	-0.5359	0.0522	0.0969	-0.7677	0.0173	0.0421
267357_at	AT2G40000	similar to unknown protein [Arabidopsis thaliana] (T	-0.4134	0.502	0.4214	-0.00929	0.9876	0.541	0.1109	0.4322	0.3306	0.515	0.0155	0.0397
267358_at	AT2G39890	ProT1 (PROLINE TRANSPORTER 1); amino acid t	-0.1243	0.6024	0.4604	-0.09545	0.6869	0.4545	-0.1846	0.4489	0.338	-0.1557	0.5183	0.3329
267359_at	AT2G40020	similar to unknown protein [Arabidopsis thaliana] (T	-0.5788	0.0059	0.0534	-0.5157	0.0088	0.0516	0.2228	0.101	0.1419	0.2859	0.0528	0.0819
267360_at	AT2G40060	protein binding / protein transporter/ structural mole	0.05872	0.6304	0.4699	0.1369	0.2918	0.2876	0.9748	3.00E-04	0.0138	1.053	2.00E-04	0.0078
267361_at	AT2G39920	acid phosphatase class B family protein	0.4381	0.518	0.4285	0.9735	0.1908	0.2268	-1.2274	0.0146	0.0482	-0.692	0.0808	0.1057
267362_at	AT2G39910	binding	-0.08964	0.6901	0.4892	0.05358	0.8103	0.4931	-0.4485	0.0984	0.1397	-0.3053	0.2179	0.195
267363_at	AT2G39970	peroxisomal membrane protein (PMP36)	0.2562	0.264	0.3019	0.4603	0.08	0.1419	-0.2361	0.2976	0.2674	-0.03192	0.8793	0.4511
267364_at	AT2G40080	ELF4 (EARLY FLOWERING 4)	1.7175	0.0421	0.118	0.8826	0.2044	0.2357	0.539	0.3087	0.2728	-0.2959	0.5572	0.3478
267365_at	AT2G44530	ribose-phosphate pyrophosphokinase, putative / ph	0.3562	0.0831	0.1668	0.2209	0.2271	0.2498	-0.1178	0.4895	0.3554	-0.253	0.1779	0.1719
267366_at	AT2G44310	calcium-binding EF hand family protein	-0.00504	0.9406	0.5627	0.01183	0.8613	0.5075	0.9386	1.00E-04	0.0119	0.9555	1.00E-04	0.0062
267367_at	AT2G44210	similar to unknown protein [Arabidopsis thaliana] (T	-0.5469	0.0673	0.149	-0.5744	0.059	0.1208	-0.521	0.0164	0.0511	-0.5485	0.0138	0.0374
267368_at	AT2G44350	ATCS (CITRATE SYNTHASE 4); citrate (Si)-synthe	0.2422	0.31	0.3285	0.1408	0.5366	0.3991	-0.1085	0.6303	0.408	-0.2099	0.371	0.2716
267369_at	AT2G44420	protein N-terminal asparagine amidohydrolase fami	1.2041	0.0417	0.1176	1.047	0.0619	0.1237	0.3418	0.2407	0.2355	0.1847	0.4983	0.3253
267370_at	AT2G44525	similar to unknown protein [Arabidopsis thaliana] (T	0.2707	0.0635	0.1444	0.1797	0.1663	0.2099	0.2719	0.0628	0.1077	0.1809	0.1641	0.1637
267371_at	AT2G44510	p21Cip1-binding protein-related	0.7588	0.0078	0.0583	0.3492	0.085	0.1468	-0.1145	0.4659	0.3456	-0.5241	0.0211	0.0472
267372_at	AT2G26290	ARSK1 (ROOT-SPECIFIC KINASE 1); kinase	-0.2569	0.7564	0.5106	-0.05665	0.9451	0.5306	-0.9618	0.2816	0.259	-0.7615	0.3806	0.276
267373_at	AT2G26280	CID7; ATP binding / damaged DNA binding	0.2578	0.2551	0.2964	-0.05722	0.7829	0.4844	0.3594	0.1379	0.1695	0.0444	0.8304	0.4372
267374_at	AT2G26230	uricase / urate oxidase / nodulin 35, putative	0.6427	0.0126	0.0692	0.7269	0.0082	0.0504	0.372	04	0.0828	-0.4562	0.0213	0.0474
267375_at	AT2G26300	GPA1 (G PROTEIN ALPHA SUBUNIT 1); signal tra	1.0506	3.00E-04	0.0312	1.0798	2.00E-04	0.0249	-0.5956	0.0024	0.0228	-0.5664	0.0029	0.0175
267376_at	AT2G26330	ER (ERECTA)	-0.3015	0.0356	0.109	-0.2674	0.0506	0.1116	0.09124	0.399	0.3161	0.1253	0.2648	0.2202
267377_at	AT2G26250	FDH (FIDDLEHEAD); acyltransferase	-0.5417	0.1877	0.2538	-0.5591	0.1768	0.2175	-0.1668	0.3027	0.2699	-0.1842	0.2619	0.2187
267378_at	AT2G26200	similar to unknown protein [Arabidopsis thaliana] (T	0.7602	0.0127	0.0696	1.0416	0.0042	04	-0.6477	0.0123	0.0441	-0.3663	0.0702	0.0971
267379_at	AT2G26340	similar to unnamed protein product [Vitis vinifera] (G	-0.4247	0.0205	0.0843	-0.5579	0.0082	0.0503	-0.04725	0.668	0.4206	-0.1804	0.1524	0.1563
267380_at	AT2G26170	CYP71A1 (MORE AXILLARY BRANCHES 1); oxy	0.1974	0.3969	0.3737	0.0682	0.7598	0.4778	0.1836	0.4278	0.3288	0.0544	0.8069	0.4307
267381_at	AT2G26190	calmodulin-binding family protein	0.2883	0.0997	0.1823	0.1206	0.4225	0.3518	0.3026	0.0886	0.1314	0.1349	0.3744	0.2732
267382_at	AT2G44300	lipid transfer protein-related	-0.1644	0.622	0.4672	-0.2452	0.4708	0.3724	0.3895	0.0453	0.0891	0.3086	0.085	0.109
267383_at	AT2G44360	similar to unnamed protein product [Vitis vinifera] (G	0.4328	0.0234	0.0895	0.3626	0.0403	0.0995	1.0468	6.00E-04	0.0158	0.9766	8.00E-04	0.0112
267384_at	AT2G44370	DC1 domain-containing protein	1.8294	0.138	0.2159	1.8962	0.1277	0.1813	0.9315	0.0989	0.14	0.9983	0.0833	0.1077
267385_at	AT2G44380	DC1 domain-containing protein	0.7049	0.0199	0.0833	0.7241	0.0183	0.0698	0.1869	0.3763	0.3059	0.206	0.3345	0.2554
267386_at	AT2G44430	DNA-binding bromodomain-containing protein	-0.2824	0.3364	0.3504	0.3507	0.2467	0.2619	-0.5361	0.0957	0.1374	0.09707	0.7142	0.4023
267387_at	AT2G44440	emsy N terminus domain-containing protein / ENT c	-0.1873	0.2056	0.2658	0.07097	0.5978	0.4225	0.0663	0.6213	0.405	0.3246	0.059	0.0876
267388_at	AT2G44450	glycosyl hydrolase family 1 protein	0.03042	0.9375	0.5616	0.2168	0.5841	0.4178	-0.03339	0.9278	0.5	0.153	0.6815	0.391
267389_at	AT2G44460	glycosyl hydrolase family 1 protein	-1.1846	0.298	0.3222	0.5244	0.6247	0.4328	-0.6925	0.5232	0.3682	1.0165	0.363	0.2683
267390_at	AT2G44470	glycosyl hydrolase family 1 protein	-1.2712	0.4255	0.3874	1.9301	0.2496	0.2636	-2.0448	0.1218	0.1577	1.1566	0.3301	0.2533
267391_at	AT2G44480	glycosyl hydrolase family 1 protein	2.2691	0.2528	0.2951	1.6176	0.3951	0.3391	1.1606	0.5322	0.3721	0.5091	0.7794	0.4228
267392_at	AT2G44490	PEN2 (PEN2 PENETRATION 2); hydrolase, hydrolyzing O	-0.2486	0.3453	0.3474	-0.2377	0.3645	0.325	-0.1437	0.125	0.1601	-0.1327	0.1483	0.1535
267393_at	AT2G44500	similar to unknown protein [Arabidopsis thaliana] (T	-0.648	0.1648	0.2373	-0.3908	0.3639	0.3248	-0.7573	0.0215	0.059	-0.5	0.0729	0.099
267394_s_at	AT2G44550;AT2G44540	[AT2G44550, ATCHIB10 (ARABIDOPSIS THALIA	0.4885	0.7285	0.502	0.9741	0.499	0.3841	-0.6	0.6711	0.4214	-0.1144	0.9347	0.4669
267395_at	AT2G44510	similar to unknown protein [Arabidopsis thaliana] (T	1.5344	0.1801	0.2481	0.1812	0.8574	0.5066	-1.5033	0.1726	0.1936	-2.8564	0.0345	0.0628
267396_at	AT2G44270	similar to unknown protein [Arabidopsis thaliana] (T	0.1641	0.4345	0.3913	0.4459	0.0779	0.1398	-0.4528	0.0188	0.055	-0.171	0.2228	0.1975
267397_at	AT1G76170	similar to unknown protein [Arabidopsis thaliana] (T	0.8284	0.1657	0.2381	0.378	0.4829	0.3773	-1.5254	0.0051	03	-1.9758	002	0.0151
267398_at	AT2G44560	ATCHIB11 (ARABIDOPSIS THALIANA GLYCOSY	-0.6512	0.4986	0.4199	1.0342	0.3032	0.2932	-0.5212	0.5839	0.3921	1.1642	0.2546	0.215
267399_at	AT2G44195	similar to unknown protein [Arabidopsis thaliana] (T	-0.3418	0.7342	0.5037	0.5897	0.5639	0.4097	-0.9836	0.3538	0.2951	-0.05214	0.9584	0.4731
267400_at	AT2G26240	Identical to UPF0136 membrane protein At2g26240	0.7106	8.00E-04	0.0338	0.645	0.0011	0.0294	0.141	0.1425	0.1733	0.07541	0.385	0.2779
267401_at	AT2G26210	ankyrin repeat family protein	0.5057	0.0075	0.0579	1.0301	5.00E-04	0.0263	-0.6049	0.0039	0.0273	-0.08051	0.4711	0.3141
267402_at	AT2G26180	IQD6 (IQ-domain 6); calmodulin binding	-0.322	0.3213	0.3352	-0.6614	0.0809	0.1426	-0.2231	0.476	0.3499	-0.5625	0.1187	0.1338
267403_at	AT2G26320	AGL33; DNA binding / transcription factor	1.7286	0.0934	0.1771	-0.9867	0.2789	0.2803	0.1391	0.8631	0.4822	-2.5763	0.0272	0.0548
267404_at	AT2G26340	ATNUDT22 (Arabidopsis thaliana Nudix hydrolase f	-0.8543	0.4062	0.3784	-0.2666	0.7866	0.4851	-1.2046	0.261	0.2471	-0.617	0.5397	0.341
267405_at	AT2G33740	CUTA	0.1673	0.4482	0.3973	0.2806	0.2318	0.2527	0.1275	0.557	0.3816	0.2408	0.2933	0.2353
267406_at	AT2G33760	EMB1611/MEE22 (EMBRYO DEFECTIVE 1611); b	0.2225	0.3584	0.3536	0.3688	0.1609	0.2064	-1.0211	0.0089	0.0378	-0.8748	0.0151	0.0392
267407_at	AT2G34880	MEE27 (maternal effect embryo arrest 27); transcri	-0.03922	0.9777	0.5717	0.1707	0.9031	0.5196	-0.7655	0.5453	0.3775	-0.5555	0.6569	0.3831
267408_at	AT2G34890	CTP synthase, putative / UTP--ammonia ligase, put	-0.6873	0.5192	0.4289	-0.3816	0.7151	0.4638	-0.05835	0.917	0.497	0.2474	0.6625	0.385
267409_at	AT2G34910	similar to unknown protein [Arabidopsis thaliana] (T	-1.2178	0.2814	0.3122	-1.6354	0.1701	0.2127	-0.5491	0.6048	0.3998	-0.9667	0.3793	0.2754
267410_at	AT2G34920	EDA18 (embryo sac development arrest 18); protei	-0.3209	0.7486	0.5084	-1.4013	0.2081	0.2383	1.6379	0.1113	0.1493	0.5575	0.5262	0.3364
267411_at	AT2G34930	disease resistance family protein	-2.3201	0.0175	0.0792	-2.1286	0.0231	0.0768	-0.1032	0.7709	0.4544	0.08833	0.8029	0.4296
267412_at	AT2G34940	vacuolar sorting receptor, putative	0.5258	0.1489	0.2246	0.6032	0.11	0.1674	-0.17	0.5948	0.3964	-0.09265	0.7689	0.4195
267413_at	AT2G34960	CAT5 (CATIONIC AMINO ACID TRANSPORTER 5	1.2178	0.0078	0.0583	0.6292	0.063	0.1249	0.4025	0.0979	0.1392	-0.1861	0.3763	0.274
267414_at	AT2G34790	EDA28/MEE23 (MATERNAL EFFECT EMBRYO AR	0.2	0.7055	0.4945	0.2268	0.6691	0.4482	-0.5392	0.3351	0.286	-0.5125	0.3569	0.2655
267415_at	AT2G34770	eIF-2gamma/eIF5/eIF2-epsilon domain-containing p	0.4492	0.1093	0.1914	0.4396	0.1149	0.1711	0.03634	0.8761	0.4856	0.02673	0.9086	0.4695
267416_at	AT2G34980	SETH1; transferase	0.364	0.6066	0.462	0.3115	0.6579	0.4444	-0.4856	0.2965	0.2669	-0.5382	0.2545	0.215
267417_at	AT2G34990	zinc finger (C3HC4-type RING finger) family protein	0.5199	0.6482	0.4759	-0.7899	0.4959	0.3828	0.3146	0.7558	0.45	-0.9952	0.3515	0.2633
267418_at	AT2G35000	zinc finger (C3HC4-type RING finger) family protein	1.1031	0.2509	0.2939	1.5993	0.1237	0.1785	0.6853	0.4515	0.3394	1.1815	0.2242	0.1984
267419_at	AT2G35010	ATO1 (ARABIDOPSIS THIOREDOXIN O1); thiol-di	0.2037	0.4578	0.4018	0.2298	0.4068	0.3444	0.2675	0.0804	0.124	0.2936	0.0629	0.0911
267420_at	AT2G35030	pentatricopeptide (PPR) repeat-containing protein	-1.2275	0.1901	0.2555	-0.3594	0.6685	0.4479	-1.3427	0.1598	0.1856	-0.4746	0.5752	0.3542
267421_at	AT2G35040	AtCAP61/PCH-like benzyme family protein	0.233	0.2341	0.2839	-0.1655	0.3763	0.3303	-0.03008	0.7868	0.4592	-0.4286	0.0146	0.0384
267422_at	AT2G35050	protein kinase family protein	0.3879	0.0376	0.112	0.1028	0.4629	0.3692	0.3209

267490_at	AT2G19130	S-locus lectin protein kinase family protein	0.604	0.0012	0.0365	0.7059	7.00E-04	0.027	0.02586	0.5481	0.3785	0.1277	0.0318	0.06	
267491_at	no_match	no_match	0.2035	0.7581	0.5111	-0.1841	0.7803	0.4836	-0.4512	0.5051	0.3613	-0.8388	0.2456	0.21	
267492_at	AT2G30620	histone H1.2	-0.2531	0.3218	0.3353	0.09586	0.6908	0.4558	0.06803	0.6021	0.3989	0.417	0.0257	0.0531	
267493_at	AT2G30400	ATOFP2/OFP2 (ARABIDOPSIS THALIANA OVATE	0.3495	0.4306	0.3894	0.5922	0.2119	0.2409	0.2703	0.3284	0.2825	0.513	0.1024	0.1222	
267494_at	AT2G30410	KIS (KIESEL); unfolded protein binding	0.07302	0.5488	0.4405	0.03885	0.7454	0.4733	0.8711	0.0015	0.0197	0.8369	0.0017	0.0145	
267495_at	no_match	no_match	-0.2705	0.6154	0.4646	-0.7549	0.2036	0.2352	-0.2496	0.6421	0.4118	-0.734	0.214	0.193	
267496_at	AT2G30550	lipase class 3 family protein	0.7339	0.0261	0.0934	0.4519	0.1011	0.1604	0.4191	0.1204	0.1565	0.1371	0.5546	0.3468	
267497_at	AT2G30540	glutaredoxin family protein	-1.5096	0.0148	0.0737	-1.4013	0.0189	0.071	0.9245	0.0031	0.0251	1.0329	0.0021	0.0154	
267498_at	AT2G45720	armadillo/beta-catenin repeat family protein	0.4379	0.1066	0.1888	0.1543	0.5052	0.3867	0.1499	0.4451	0.3362	-0.1337	0.4924	0.323	
267499_at	AT2G45500	ATP binding	1.214	0.0283	0.0974	0.9535	0.0577	0.1193	0.431	0.2989	0.2682	0.1705	0.6616	0.3847	
267500_s_at	AT2G45510,AT2G44890	[AT2G45510, CYP704A2 (cytochrome P450, family	2.3386	0.0041	0.0468	1.8615	0.0093	0.0528	-0.2558	0.1599	0.1857	-0.7329	0.0078	0.0276	
267501_at	AT2G45540	WD-40 repeat family protein / beige-related	0.1715	0.2618	0.3007	-0.09668	0.5026	0.3857	-1.2627	2.00E-04	0.0126	-1.5309	1.00E-04	0.0058	
267502_at	AT2G45550	CYP76C4 (cytochrome P450, family 76, subfamily (	-0.4691	0.4952	0.4182	-0.8578	0.2423	0.2594	0.6491	0.3582	0.2971	0.2603	0.6988	0.397	
267503_at	AT2G45560	hydrolase	0.1736	0.4433	0.3951	0.3035	0.2115	0.2407	0.02031	0.9213	0.4982	0.1503	0.4799	0.3175	
267504_at	AT2G45530	zinc finger (C3HC4-type RING finger) family protein	0.07709	0.2585	0.2988	0.195	0.0291	0.0849	-0.7211	1.00E-04	0.0109	-0.6032	2.00E-04	0.0076	
267505_at	AT2G45560	CYP76C1 (cytochrome P450, family 76, subfamily (	-0.4125	0.188	0.254	0.05797	0.8346	0.5	-1.3324	0.0036	0.0265	-0.8619	0.0167	0.0412	
267506_at	AT2G45520	similar to unnamed protein product [Vitis vinifera] (G	0.2326	0.1756	0.2452	0.205	0.2211	0.2466	1.1093	1.00E-04	0.0109	1.0816	1.00E-04	0.0061	
267507_at	AT2G45710	40S ribosomal protein S27 (RPS27A)	0.1098	0.5958	0.4583	-0.1913	0.3728	0.3289	1.3238	0.0015	0.0199	1.0226	0.0039	0.0201	
267508_at	AT2G45700	sterile alpha motif (SAM) domain-containing protein	0.0396	0.7256	0.5012	-0.04357	0.6998	0.459	-0.3592	0.0269	0.0667	-0.4424	0.0136	0.037	
267509_at	AT2G45660	AGL20 (AGAMOUS-LIKE 20); transcription factor	0.6553	0.0566	0.1363	1.0149	0.0147	0.064	-0.02927	0.8011	0.4638	0.3303	0.0385	0.0674	
267510_at	AT2G45640	SAP18 (SIN3 ASSOCIATED POLYPEPTIDE P18);	0.1814	0.3346	0.3427	0.4608	0.0496	0.1104	0.228	0.2404	0.2354	0.5073	0.0375	0.0661	
267511_at	AT2G45670	calcineurin B subunit-related	-0.3839	0.169	0.2435	-0.3494	0.2018	0.2338	-1.8608	4.00E-04	0.0147	-1.8263	5.00E-04	0.0094	
267512_at	AT2G45690	SSE1 (SHRUNKEN SEED 1)	0.4068	0.1235	0.2037	0.479	0.0836	0.1454	-0.3469	0.0768	0.121	-0.2746	0.1338	0.1442	
267513_at	AT2G45620	nucleotidyltransferase family protein	0.4707	0.0108	0.0654	0.2009	0.1272	0.1809	0.1413	0.1303	0.1641	-0.1285	0.1593	0.1608	
267514_at	AT2G45630	oxidoreductase family protein	0.3857	0.1599	0.2334	-0.08093	0.7372	0.4704	-0.1365	0.5748	0.3883	-0.6028	0.0545	0.0835	
267515_at	AT2G45680	TCP family transcription factor, putative	-0.184	0.6264	0.4685	-0.4517	0.2657	0.273	-0.1387	0.4486	0.3379	-0.4065	0.0698	0.0967	
267516_at	AT2G30520	RPT2 (ROOT PHOTOTROPISM 2); protein binding	-1.2416	0.0039	0.0463	-0.7572	0.0216	0.0747	-2.1881	5.00E-04	0.0148	-1.7037	0.0012	0.0128	
267517_at	AT2G30520	RPT2 (ROOT PHOTOTROPISM 2); protein binding	-0.5313	0.0192	0.0821	-0.7239	0.0066	0.0461	-0.5612	0.016	0.0505	-0.7538	0.0057	0.0236	
267518_at	AT2G30500	kinase interacting family protein	0.09829	0.4647	0.4051	0.1464	0.2953	0.2894	0.04083	0.742	0.4455	0.08899	0.4848	0.3196	
267519_at	AT2G30470	HSI2 (HIGH-LEVEL EXPRESSION OF SUGAR-IND	-0.2854	0.3133	0.3305	0.1423	0.5963	0.422	-0.6672	0.0456	0.0893	-0.2395	0.3614	0.2676	
267520_at	AT2G30460	similar to transporter-related (Arabidopsis thaliana)	-0.2955	0.0942	0.1777	-0.4002	0.0416	0.1013	-0.4473	0.011	0.0349	-0.552	0.0052	0.0226	
267521_at	AT2G30480	similar to hypothetical protein [Vitis vinifera] (GB:CA	0.6101	0.5262	0.4316	0.4215	0.6569	0.4441	-0.3308	0.4192	0.3249	-0.5194	0.2307	0.2018	
267522_at	AT2G30430	unknown protein	0.4631	0.6981	0.492	0.1549	0.8958	0.5174	0.06985	0.9529	0.5063	-0.2383	0.8406	0.4403	
267523_at	AT2G30630	BTB/POZ domain-containing protein	-0.2203	0.0108	0.2407	-0.2181	0.1725	0.2145	-0.4888	0.0205	0.0577	-0.4864	0.0209	0.0468	
267524_at	AT2G30600	BTB/POZ domain-containing protein	-0.6684	0.0903	0.174	-0.1581	0.6268	0.4334	-1.4252	3.00E-04	0.0141	-0.9149	0.0018	0.0147	
267525_at	AT2G30560	glycine-rich protein	1.0015	0.209	0.2674	-0.00934	0.9895	0.5416	0.415	0.5689	0.3863	-0.5958	0.4237	0.294	
267526_at	AT2G30570	PSBW (PHOTOSYSTEM II REACTION CENTER W	-0.3866	0.0946	0.1778	-0.4576	0.0612	0.1228	0.3372	0.0681	0.1132	0.2662	0.1216	0.1361	
267527_at	AT2G45610	hydrolase	-0.7341	0.6008	0.4599	-1.3646	0.3511	0.3186	1.8028	0.236	0.2328	1.1723	0.4162	0.291	
267528_at	AT2G45650	AGL6 (AGAMOUS LIKE-6); DNA binding / transcrip	0.1651	0.8702	0.5441	-0.9024	0.3951	0.3391	0.6915	0.4847	0.3533	-0.376	0.6973	0.3966	
267529_at	AT2G45490	ATAUR3 (ARABIDOPSIS); ATP binding / histone ser	0.01448	0.9838	0.573	-0.2557	0.7223	0.4661	1.0553	0.1906	0.2059	0.7851	0.3066	0.2418	
267530_at	AT2G41890	curculin-like (mannose-binding) lectin family protein	0.5781	0.0315	0.1029	0.3007	0.1667	0.2102	0.2651	0.0975	0.1389	-0.01225	0.9255	0.4643	
267531_at	AT2G41860	CPK14 (calcium-dependent protein kinase 14); calr	-1.1178	0.172	0.2427	1.1927	0.151	0.199	-0.656	0.3848	0.31	1.6545	0.0698	0.0967	
267532_at	AT2G45460	similar to unnamed protein product [Vitis vinifera] (G	0.09325	0.5105	0.425	0.2139	0.1731	0.215	0.191	0.1474	0.1771	0.3117	0.0429	0.0723	
267533_at	AT2G42070	ATNUDT23 (Arabidopsis thaliana Nudix hydrolase	-0.4715	0.0114	0.0668	-0.2823	0.0568	0.1186	-0.3733	0.0247	0.0637	-0.184	0.1589	0.1605	
267534_at	AT2G41900	zinc finger (CCCH-type) family protein	0.08222	0.7051	0.4943	0.6727	0.0292	0.0849	-0.4868	0.0737	0.1182	0.1037	0.6351	0.3755	
267535_at	AT2G41940	ZFP8 (ZINC FINGER PROTEIN 8); nucleic acid bin	0.641	0.0108	0.2402	0.4831	0.0274	0.0826	0.4336	0.0017	0.0205	0.2757	0.0087	0.0291	
267536_at	AT2G42010	PLDBETA1 (PHOSPHOLIPASE D BETA 1); phosph	0.1605	0.2351	0.2844	0.09697	0.4463	0.3623	-0.532	0.005	0.0299	-0.5955	0.0033	0.0188	
267537_at	AT2G41880	GK-1 (GUANYLATE KINASE 1); guanylate kinase	-0.126	0.5661	0.4473	-0.1441	0.5144	0.3904	-0.3395	0.0883	0.1313	-0.3576	0.0774	0.1028	
267538_at	AT2G41870	nemorin family protein	-0.359	0.2175	0.2736	-0.1553	0.5614	0.4089	-0.1331	0.4919	0.3564	0.07058	0.709	0.4005	
267539_at	AT2G42030	zinc finger (C3HC4-type RING finger) family protein	0.1847	0.4239	0.3868	0.5032	0.0725	0.1349	-0.3143	0.0112	0.0418	0.00418	0.9555	0.4724	
267540_at	AT2G32760	similar to unnamed protein product [Vitis vinifera] (G	0.03969	0.7342	0.5037	-0.3891	0.0234	0.077	0.00553	0.962	0.5081	-0.4232	0.0178	0.0427	
267541_at	AT2G32750	exostosin family protein	-0.2262	0.6535	0.4771	0.1976	0.7049	0.4606	-0.6373	0.1618	0.1866	-0.2045	0.6118	0.3674	
267542_at	AT2G32740	exostosin family protein	-0.297	0.8254	0.5311	-2.4381	0.1254	0.1795	0.2497	0.843	0.4766	-1.8914	0.1847	0.1762	
267543_at	AT2G32730	26S proteasome regulatory subunit, putative	0.714	2.00E-04	0.0312	0.5282	8.00E-04	0.0277	-0.3651	0.0032	0.0251	-0.5509	7.00E-04	0.0105	
267544_at	AT2G32720	8S #4 (cytochrome b5 family protein #4); heme bin	-0.8123	0.0093	0.0621	-0.426	0.0692	0.132	0.8458	0.0049	0.0297	1.2322	0.0012	0.0128	
267545_at	AT2G32690	pseudogene, glycine-rich protein	-0.9457	0.1873	0.2536	0.3178	0.6216	0.4313	-0.5431	0.4131	0.3222	0.7204	0.2928	0.235	
267546_at	AT2G32680	disease resistance family protein	2.1111	0.0019	0.0391	1.4769	0.0069	0.0469	0.3937	0.0142	0.0475	-0.2406	0.064	0.092	
267547_at	AT2G32670	ATVAM07/25 (Arabidopsis thaliana vesicle-associat	0.4623	0.3576	0.3533	0.5305	0.4522	0.3649	0.09997	0.883	0.4876	1.2927	0.1125	0.1294	
267548_at	AT2G32660	disease resistance family protein / LRR family protei	0.4025	0.4359	0.392	0.5318	0.3169	0.3013	0.1758	0.6392	0.4108	0.3052	0.429	0.2963	
267549_at	AT2G32640	similar to unnamed protein product [Vitis vinifera] (G	-0.7109	0.0499	0.1284	-0.9773	0.0188	0.0707	-0.6345	0.0682	0.1133	-0.9008	0.0244	0.0514	
267550_at	AT2G32600	AP4.3A; ATP binding / protein kinase	-0.2185	0.5653	0.447	0.3932	0.3231	0.3048	-0.4435	0.0123	0.0441	0.1682	0.1758	0.1706	
267551_at	AT2G32780	ubiquitin-specific protease 1, putative (UBP1)	0.9995	0.2732	0.3073	0.6294	0.4689	0.3715	-1.2188	0.1966	0.2096	-1.5889	0.1138	0.1304	
267552_at	AT2G32770	ATPAP13/PAP13; acid phosphatase	-0.6162	0.4648	0.4051	-0.3614	0.6606	0.4452	-0.9079	0.3001	0.2688	-0.6531	0.4405	0.3016	
267553_s_at	AT2G32180,AT2G32650	[AT2G32180, PTAC18 (PLASTID TRANSCRIPTION	0.194	0.375	0.3619	0.1075	0.6099	0.4269	0.1524	0.4772	0.3504	0.06589	0.7519	0.4144	
267554_at	AT2G32790	ubiquitin-conjugating enzyme, putative	-0.00579	0.9962	0.5761	0.9186	0.4678	0.3712	-0.7563	0.4551	0.3409	0.1681	0.8633	0.4467	
267555_at	AT2G32765	SUM5 (SUMO 5)	-0.5342	0.104	0.1863	-0.4289	0.1675	0.2109	0.2126	0.2768	0.2562	0.3179	0.1331	0.1438	
267556_at	AT2G32810	BGAL9 (BETA GALACTOSIDASE 9); beta-galactos	0.2011	0.2006	0.2625	0.04215	0.7644	0.4787	-0.1606	0.2887	0.2629	-0.3196	0.0718	0.0983	
267557_at	AT2G32710	KRP4 (KIP-RELATED PROTEIN 4)	0.09609	0.6877	0.4885	0.6825	0.0372	0.0953	-0.8031	0.0225	0.0605	-0.2166	0.3847	0.2778	
267558_at	AT2G32700	WD-40 repeat family protein	1.0155	0.012	0.0681	0.8113	0.0252	0.0794	0.5424	0.0198	0.0565	0.3382	0.079	0.104	
267559_at	AT2G45570	CYP76C2 (cytochrome P450, family 76, subfamily (	1.0581	0.1523	0.2276	1.3612	0.0856	0.1473	-0.4093	0.2732	0.2541	-0.1063	0.7583	0.4162	
267560_at	AT2G45580	CYP76C3 (cytochrome P450, family 76, subfamily (	0.3244	0.6028	0.4604	-0.1681	0.7845	0.4847	-0.5614	0.3459	0.2911	-1.0539	0.1156	0.1316	
267561_at	AT2G45590	protein kinase family protein	0.3232	0.0559	0.1358	0.3931	0.0315	0.0882	-0.04497	0.283	0.2598	0.02491	0.5303	0.3381	
267562_at	AT2G39670	radical SAM domain-containing protein	-0.05004	0.6813	0.4865	-0.2545	0.0891	0.1504	-0.2011	0.1218	0.1577	-0.4053	0.0169	0.0416	
267563_at	AT2G30730	serine/threonine protein kinase, putative	0.3259	0.8248	0.531	0.644	0.6647	0.4465	0.4689	0.7509	0.4485	0.787	0.5986	0.3629	
267564_at	AT2G30740	serine/threonine protein kinase, putative	-0.1753	0.2209	0.2757	-0.2528	0.1049	0.1636	-0.1738	0.0754	0.1196	-0.2512	0.026	0.0534	
267565_at	AT2G30750	CYP71A12 (CYTOCHROME P450, FAMILY 71, SU	1.7712	0.1437	0.2204	1.6863	0.159	0.2051	0.3312	0.5261	0.3695	0.2463	0.6331	0.3748	
267566_at	AT2G30760	unknown protein	-0.5347	0.6019	0.4602	0.1668	0.8685	0.5095	-1.7766	0.1015	0.1423	-1.0751	0.269	0.2223	
267567_at	AT2G30770	CYP71A13 (CYTOCHROME P450, FAMILY 71, SU	1.5003	0.0217	0.0866	2.0059	0.0081	0.0503	0.3894	0.0474	0.0914	0.895	0.0029	0.0175	
267568_at	AT2G30780	pentatricopeptide (PPR) repeat-containing protein	-0.1246	0.4701	0.4073	0.2866	0.1408	0.1913	-1.3098	0.0011	0.0183	-0.8986	0.0045	0.0213	
267569_at	AT2G30790	PSBP-2 (photosystem II subunit P-2); calcium ion b	-0.3258	0.2312	0.2828	-0.2721	0.3041	0.2937	-0.8746	7.00E-04	0.016	-0.8208	9.00E-04	0.0116	
267570_at	AT2G30800	HVT1 (HELICASE IN VASCULAR TISSUE AND TA	0.2218	0.526	0.4316	0.3336	0.3556	0.3207	-0.5317	0.1716	0.1931	-0.4198	0.2594	0.2175	
267571_at	AT2G30650	catalytic	1.1397	0.2647	0.3021	-0.1026	0.9128	0.5221	-0.8321	0.0627	0.1076	-2.0744	0.0031	0.0181	
267572_at	AT2G30660	3-hydroxyisobutyryl-coenzyme A hydrolase, putative	0.5759	0.2336	0.2839	-0.2642	0.5552	0.4067	0.6633	0.1148	0.1523	-0.1768	0.6206	0.3705	
267573_at	AT2G30670	tropinone reductase, putative / tropine dehydrogena	-0.2815	0.4281	0.3884	-0.03607	0.9156	0.5229	-0.09345	0.7845	0.4586	0.152	0.6592	0.3838	
267574_at	AT2G30680	similar to ATGSL03 (GLUCAN SYNTHASE-LIKE 3)	-1.0084	0.4448	0.3955	-0.7037	0.5864	0.4185	0.5174	0.1499	0.1788	0.8221	0.0475	0.0769	
267575_at	AT2G30690	similar to unknown protein [Arabidopsis thaliana] (T	-0.1859	0.4276	0.3882	-0.8026	0.019	0.071	0.3644	0.1589	0.185	-0.2523	0.2974	0.2373	
267576_at	AT2G30640	transposable element gene	0.251	0.3455	0.3476	0.1238	0.6261	0.4334	-0.2701	0.3143	0.2756	-0.3973	0.1661	0.1649	
267577_at	AT2G30710	RabGAP/TBC domain-containing protein	0.5563	0.0248	0.0914	0.1631	0.3621	0.3239	0.6862	0.0124	0.0442	0.293	0.1385	0.1472	
267578_at	AT2G30695	similar to unnamed protein product [Vitis vinifera] (G	-0.4315	0.1023	0.1849	-0.5349	0.0589	0.1207	0.2605	0.1083	0.1473	0.1571	0.2817	0.2289	
267579_at	AT2G42000	plant EC metallothionein-like family 15 protein	-0.05256	0.9645	0.5684	-0.9582	0.437	0.3584	0.3866	0.7454	0.4466	-0.5191	0.6646	0.3856	
267580_at	AT2G41990	similar to unknown protein [Arabidopsis thaliana] (T	-0.163	0.7662	0.5133	-0.2003	0.7158	0.4639	0.4536	0.158	0.1844	0.4164	0.1867	0.1774	
267581_at	AT2G41980	seven in absentia (SINA) family protein	-0.2983	0.231	0.2827	-0.1625	0.485	0.3781	-0.5095	0.0292	0.0694	-0.3736	0.0712	0.0978	
267582_at	AT2G41970	protein kinase, putative	1.7348	0.2173	0.2734	0.008255	0.9948	0.5429	0.1976	0.7499	0.4482	-1.5289	0.0574	0.0862	
267583_at	AT2G41960	similar to unknown protein [Arabidopsis thaliana] (T	0.06576	0.6596	0.4791	0.000342	0.9981	0.5435	-0.1039	0.281	0.2587	-0.1694	0.1123	0.1293	
267584_at	AT2G41930	kinase	-0.8419	0.3288	0.3392	0.4602	0.5764	0.4145	-0.6751	0.4233	0.3268	0.6271	0.4545	0.3078	
267585_s_at	AT2G42090	ACT9 (ACTIN 9); structural constituent of cytoskele	0.2479	0.8624	0.5416	-1.5134	0.3224	0.3045	-0.6827	0.6312	0.4083	-2.4441	0.1368	0.146	
267586_at	AT2G41950	similar to unnamed protein product [Vitis vinifera] (G	0.2274	0.1358	0.2139	-0.1938	0.1874	0.2247	0.8282	0.0025	0.0232	0.407	0.0289	0.057	
267587_at	AT2G42080	DNAJ heat shock N-terminal domain-containing pro	-0.08305	0.6784	0.4855	-0.5313	0.0461	0.1064	0.5796	0.0083	0.0365	0.1313	0.3327	0.2547	
267588_at	AT2G42060	CHP-rich zinc finger protein, putative	0.2449	0.7392	0.5054	0.2157	0.7689	0.4801	0.5094	0.4919	0.3564	0.4802	0.5156	0.3319	
267589_at	AT2G42050	transposable element gene	0.3308	0.7367	0.5047	-0.06721	0.9451	0.5306	2.6527	0.0445	0.0883	2.2546	0.0699	0.0968	
267590_at	AT2G39700	ATEXPA4 (ARABIDOPSIS THALIANA EXPANSIN	1.1777	0.0019	0.0391	1.3566	0.0011	0.0293	0.0578	0.7376	0.4442	0.2367	0.2152	0.1938	
267591_at	AT2G39705	DVL11/RTFL8 (ROTUNDIFOLIA LIKE 8)	1.5876	0.0616	0.1425	1.7688	0.0455	0.1057	0.8064	0.1368	0.1689	0.9876	0.0852	0.1092	
267592_at	AT2G39710	aspartyl protease family protein	0.492	0.2308	0.2825	0.2954	0.4443	0.3614	0.1422	0.6347	0.4093	-0.05445	0.8537	0.4438	
267593_at	AT2G33030	leucine-rich repeat family protein	-2.1039	0.1553	0.23	-2.2484	0.1351	0.1869	-2.1589	0.1473	0.1771	-2.3034	0.1282	0.1403	
267594_at	AT2G33000	ubiquitin-associated (UBA)/TS-N domain-containing	-0.01535	0.9866	0.5735	0.6204	0.5097	0.3885	0.08532	0.9256	0.4994	0.7211	0.448	0.3052	
267595_at	AT2G39580	ATGH9B8 (ARABIDOPSIS THALIANA GLYCOSYL	-1.2347	0.0361	0.1097	-1.3435	0.0279	0.0832	-0.01563	0.9639	0.5085	-0.1244	0.7207	0.4043	
267596_s_at	AT2G33060,AT2G33050	[AT2G33060, leucine-rich repeat family protein];[AT	0.3514	0.2626	0.3012	0.1699	0.5631	0.4094	0.5669	0.0131	0.0455	0.3854	0.0445	0.074	
267597_at	AT2G33020	leucine-rich repeat family protein	-0.3528	0.3797	0.3643	0.4148	0.3106	0.2976	-0.8821	0.0692	0.114	-0.1146	0.7646	0.4182	
267598_at	AT2G33010	ubiquitin-associated (UBA)/TS-N domain-containing	-1.538	0.1492	0.2249	-0.1218	0.8945	0.5171	-0.2008	0.7539	0.4493	1.2153	0.112	0.1291	
267599_at	AT2G32850	protein kinase family protein	0.6675	0.0088	0.0609	0.1717	0.287	0.2849	0.392	0.0487	0.0929	-0.1039	0.499	0.3256	
267600_at	AT2G33040	ATP synthase gamma chain, mitochondrial (ATPC)	0.08222	0.1348	0.2132	-0.1835	0.014	0.0627	0.3198	0.0019	0.0207	0.05411	0.2858	0.2312	
267601_at	AT2G32980	similar to unnamed protein product [Vitis vinifera] (G	0.09802	0.6565	0.4779	-0.04924	0.8215	0.4962	0.2192	0.24	0.2352	0.07194	0.6743	0.3888	
267602_at	AT2G32970	similar to unnamed protein product [Vitis vinifera] (G	0.2032	0.2028	0.2642	0.04332	0.762	0.4781	-0.5024	0.0198	0.0565	-0.6622	0.0077	0.0274	
267603_at	AT2G32910	ATZW10	0.2092	0.4695	0.4071	0.2487	0.3964	0.3397	-0.7906	0.0404	0.0833	-0.7294	0.0471	0.0764	
267604_at	AT2G32930	ZFN2 (ZINC FINGER PROTEIN 2); nucleic acid bin	0.5473	0.2721	0.3067	0.5581	0.2641	0.272	-0.1704	0.7121	0.4357	-0.1596	0.7293	0.4069	
267605_at	AT2G32920	ATPDIL2-3 (PDI-LIKE 2-3); protein disulfide isomer	0.9735	6.00E-04	0.0329	0.8341	0.0011	0.0293	0.08541	0.4374	0.333	-0.05395	0.6152	0.3685	
267606_at	AT2G26640	beta-ketoacyl-CoA synthase, putative	-0.4962	0.1523	0.2276	-0.5155	0.1406	0.191	-0.1337	0.503	0.3606	-0.1565	0.4489	0.3056	
267607_s_at	AT2G26740,AT2G26750	[AT2G26740, ATSEH (Arabidopsis thaliana soluble	0.5549	0.0167	0.0775	0.6489	0.0098	0.0538	-0.1824	0.2628	0.248	-0.08849	0.5619	0.3497	
267608_at	AT2G26770	plectin-related	-0.4397	0.0332	0.1056	-0.391	0.047	0.1076	-0.4199	0.0382	0.0807	-0.3713	0.0545	0.0835	
267609_at	AT2G26780	binding	0.9945	0.0017	0.0391	0.845	0.0094	0.0507	-0.9648	3.00E-04	0.0133	-1.3143	1.00E-04	0.0058	
267610_at	AT2G26650	AKT1 (ARABIDOPSIS K TRANSPORTER 1); cyclic	0.8324	0.11	0.1921	1.1476	0.0477	0.1084	-0.3903	0.2666	0.25	-0.07517	0.8161	0.4332	
267611_at	AT2G26660	SPX (SYG1/Pho81/XPR1) domain-containing prote	0.2529	0.1822	0.25	0.3518	0.0883	0.1498	0.2426	0.0039	0.0273	0.3416	0.0011	0.0124	
267612_at	AT2G26690	nitrate transporter (NTP2)	-0.5614	0.0023	0.0414	-0.6927	0.001	0.0293	-0.1129	0.1302	0.1641	-0.2443	0.0147	0.0386	
267613_at	AT2G26700	protein kinase family protein	0.9986	0.5192	0.4289	1.2957	0.4116	0.3468	-0.31	0.8373	0.4749	-0.0129	0.9932	0.481	
267614_at	AT2G26710	BAS1/CYP734A1 (PHYB ACTIVATION TAGGED S	-0.6986	0.0488	0.1271	-0.6906	0.0504	0.1115	0.2114	0.4446	0.336	0.2194	0.4289	0.2962	
267615_at	AT2G26720	plastocyanin-like domain-containing protein	0.8379	0.0506	0.1294	-0.672	0.32	0.3031	-0.4938	0.2714	0.253	0.4722	0.2898	0.2334	
267616_at	AT2G26680	similar to unnamed protein product [Vitis vinifera] (G	0.009217	0.9594	0.5672	0.09898	0.5924	0.4204	0.4422	0.0603	0.1055	0.5319	0.0354	0.0638	
267617_at	AT2G26670	HY1 (HEME OXYGENASE 1)	0.1456	0.4023	0.3765	-0.03269	0.8438	0.5027	0.2892	0.1365	0.1687	0.111	0.5149	0.3316	
267618_at	AT2G26760	CYCB1-4; cyclin-dependent protein kinase regulator	0.1668	0.8489	0.5379	-0.4278	0.6296	0.4344	0.3274	0.2103	0.1349	-0.2672	0.761	0.417	
267619_at	AT2G26730	similar to unnamed protein product [Arabidopsis thaliana] (T	-0.3681	0.2502	0.2937	-0.4557	0.1716	0.2139	-0.04794	0.8678	0.4836	-0.1356	0.6422	0.378	
267620_at	AT2G39640	glycosyl hydrolase family 17 protein	0.1689	0.7613	0.512	-0.8726	0.1682	0.2113	0.4111	0.4369	0.3327	-0.6304	0.2563	0.2159	
267621_at	no_match	no_match	3.5727	0.0365	0.1101	1.1276	0.3843	0.3339	2.812	0.4676	0.3465	-3.2571	0.0324	0.0608	

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AFFX-r2-Bs-phe-3_	no_match	no_match	-1.071	0.0745	0.1568	-0.01055	0.9823	0.5397	0.01905	0.968	0.5096	1.0795	0.073	0.0991
AFFX-r2-Bs-phe-5_	no_match	no_match	-1.2035	0.0676	0.1493	0.212	0.6838	0.4534	-0.1909	0.7132	0.4359	1.2246	0.0645	0.0924
AFFX-r2-Bs-phe-M_	no_match	no_match	-0.889	0.1293	0.2079	-0.01073	0.9827	0.5399	-0.01511	0.9724	0.5106	0.8632	0.1038	0.1233
AFFX-r2-Bs-thr-3_	no_match	no_match	-0.5844	0.2467	0.2916	0.08955	0.8456	0.5032	0.5846	0.2466	0.239	1.2585	0.0433	0.0727
AFFX-r2-Bs-thr-5_	no_match	no_match	-0.7886	0.1901	0.2555	-0.2711	0.6166	0.4294	0.00306	0.9942	0.5163	0.5205	0.2569	0.2162
AFFX-r2-Bs-thr-M_	no_match	no_match	-0.4672	0.3189	0.3338	-0.1484	0.7362	0.4701	0.4637	0.322	0.2792	0.7825	0.1295	0.1411
AFFX-r2-Ec-bioB-3_	no_match	no_match	-0.4054	0.2964	0.3212	-0.4671	0.239	0.2571	0.3061	0.4161	0.3234	0.2444	0.5094	0.3295
AFFX-r2-Ec-bioB-5_	no_match	no_match	-0.4749	0.1245	0.2043	-0.3849	0.1911	0.2269	0.2621	0.3435	0.2901	0.3521	0.2227	0.1974
AFFX-r2-Ec-bioB-M_	no_match	no_match	-0.3049	0.2565	0.2973	-0.2957	0.2688	0.2749	0.2784	0.2936	0.2654	0.2876	0.2802	0.2283
AFFX-r2-Ec-bioC-3_	no_match	no_match	-0.3812	0.1889	0.2547	-0.3711	0.1985	0.232	0.5418	0.0879	0.1308	0.5519	0.0839	0.1081
AFFX-r2-Ec-bioC-5_	no_match	no_match	-0.3726	0.1106	0.1928	-0.4714	0.061	0.1227	0.4758	0.0595	0.1047	0.377	0.1076	0.1259
AFFX-r2-Ec-bioD-3_	no_match	no_match	-0.4986	0.0958	0.1788	-0.3602	0.192	0.2274	0.1597	0.4986	0.3591	0.2981	0.2376	0.2059
AFFX-r2-Ec-bioD-5_	no_match	no_match	-0.5583	0.0504	0.1292	-0.4887	0.0725	0.1349	0.2412	0.2979	0.2676	0.3108	0.1982	0.1838
AFFX-r2-P1-cre-3_	no_match	no_match	-0.4409	0.1121	0.194	-0.5256	0.0727	0.135	0.2042	0.4002	0.3167	0.1195	0.6114	0.3672
AFFX-r2-P1-cre-5_	no_match	no_match	-0.3729	0.1357	0.2139	-0.3968	0.1182	0.1738	0.2395	0.2972	0.2672	0.2156	0.3417	0.2588
AFFX-ThrX-3_at	no_match	no_match	-0.8655	0.106	0.1884	-0.3876	0.4043	0.3432	0.537	0.2664	0.2499	1.0148	0.0713	0.0978
AFFX-ThrX-5_at	no_match	no_match	-1.1376	0.2161	0.2725	-0.2123	0.7978	0.4888	0.9699	0.2791	0.2575	1.8952	0.0708	0.0976
AFFX-ThrX-M_at	no_match	no_match	-1.1912	0.0622	0.1432	-0.4698	0.3686	0.3268	0.04963	0.92	0.4978	0.771	0.1719	0.1684
AFFX-TrpnX-3_at	no_match	no_match	0.3577	0.7711	0.515	-1.842	0.1841	0.2225	1.2133	0.1878	0.2042	-0.9863	0.2666	0.2211
AFFX-TrpnX-5_at	no_match	no_match	1.4399	0.1421	0.2191	-1.4538	0.1392	0.19	0.21	0.8033	0.4645	-2.6836	0.0272	0.0549
AFFX-TrpnX-M_at	no_match	no_match	-1.1599	0.2005	0.2624	0.6235	0.4567	0.3667	-0.8309	0.3343	0.2856	0.9525	0.277	0.2266