Electronic Supplementary Information

Embryonic exposure to 10 μg/L lead results in female-specific expression changes in genes associated with nervous system development and function and Alzheimer's disease in aged adult zebrafish brain

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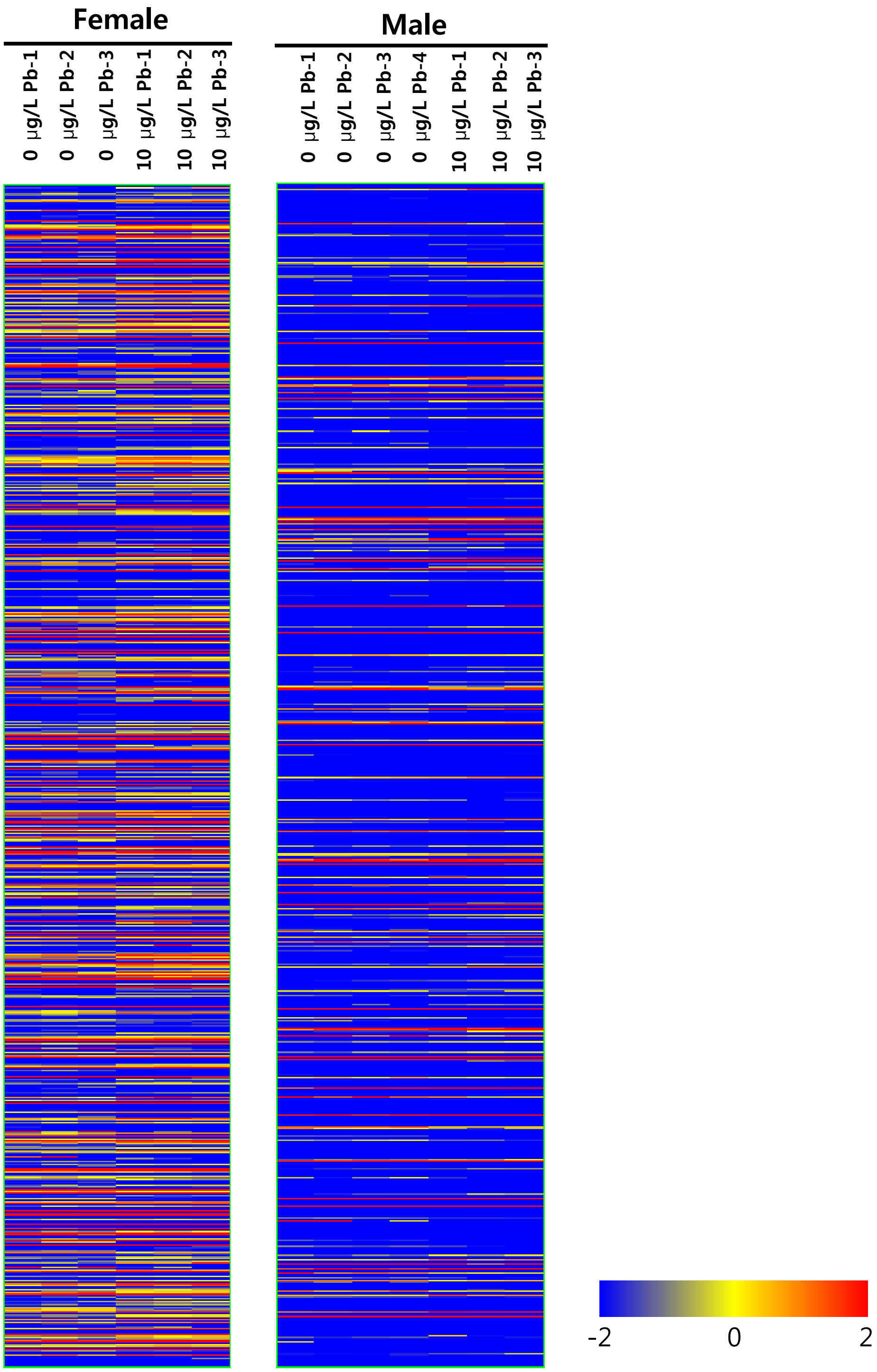
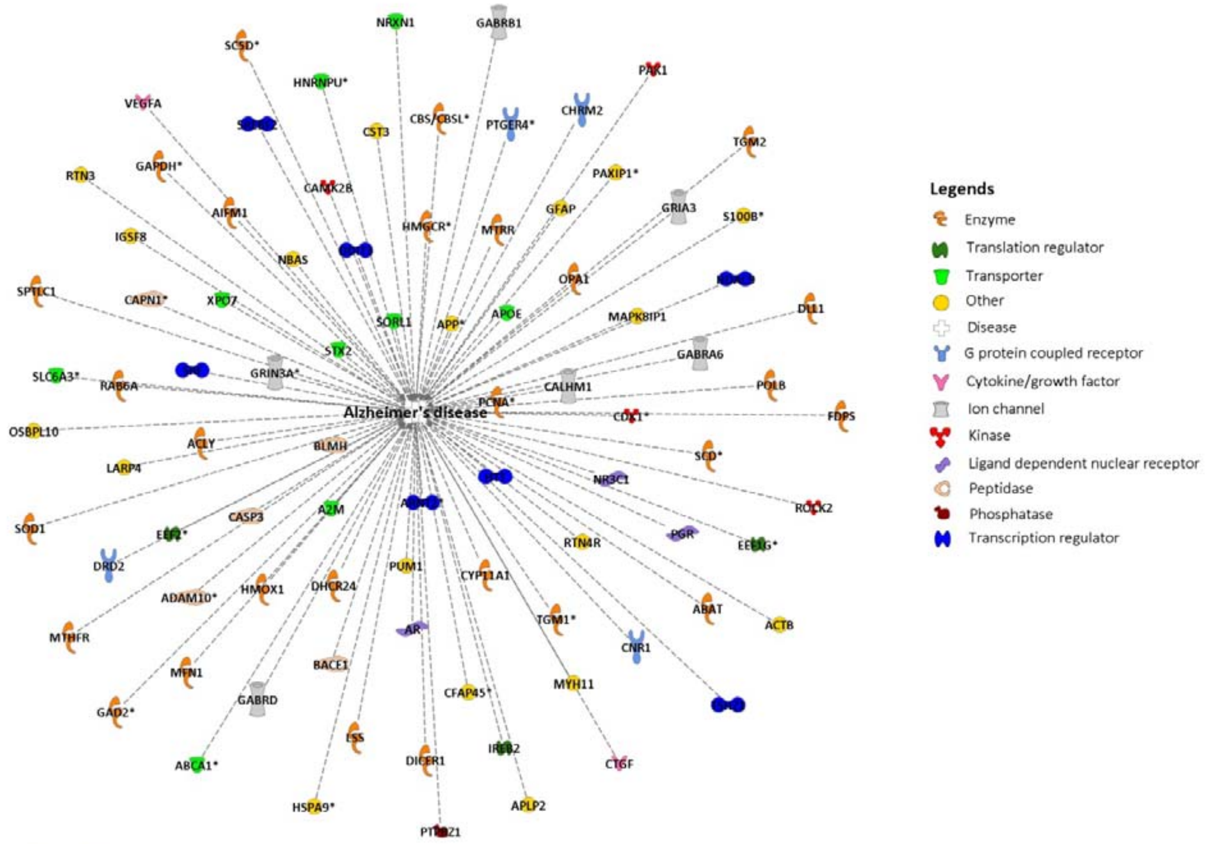


Supplementary Information Fig 1. Heat map of altered probe sets by a developmental Pb exposure in aged brain of adult female and male zebrafish. Heat map images show significantly altered probe sets (rows) by a developmental exposure to 0 µg/L Pb or 10 µg/L Pb (columns) in aged brains from adult female (left, n=3) and adult male zebrafish (right, n=4 for 0 µg/L Pb, n=3 for 10 µg/L Pb treated groups). Color range indicates different expression of each probe which is mapped to a color intensity value (blue, minimum -2 representing low expression; red, maximum 2 representing high expression).



Supplementary Information Fig 2. Altered genes in aged adult female zebrafish brain associated with Alzheimer's disease. The image shows indirect relationship (dashed line) of Alzheimer's disease with 89 molecules with altered expression profiles in adult female zebrafish exposed to 10 µg/L Pb during embryogenesis. Figure was made in IPA with molecules listed as human protein annotation.

Abbreviations: A2M, alpha-2-macroglobulin; ABAT, 4-aminobutyrate aminotransferase; ABCA1, ATP-binding cassette, subfamily A; ACLY, ATP citrate lyase; ACTB, actin, beta; ADAM10, ADAM metallopeptidase domain 10; AIFM1, apoptosis-inducing factor, mitochondrion-associated, 1; APLP2, amyloid beta (Aβ) precursor-like protein 2; APOE, apolipoprotein E; APP, amyloid beta (Aβ) precursor protein; AR, androgen receptor; ARNT2, aryl-hydrocarbon receptor nuclear translocator 2; BACE1; beta-site APP-cleaving enzyme 1; BLMH, bleomycin hydrolase; CALHM1, calcium homeostasis modulator 1; CAMK2B, calcium/calmodulin-dependent protein kinase II beta; CAPN1, calpain 1, (mu/I) large subunit; CASP3, caspase 3, apoptosis-related cysteine peptidase; CBS/CBSL, cystathionine-beta-synthase; CDK1, cyclin-dependent kinase 1; CFAP45, cilia and flagella associated protein 45; CHRM2, cholinergic receptor, muscarinic 2; CNR1, cannabinoid receptor 1 (brain); CST3, cystatin C; CTGF, connective tissue growth factor; CYP11A1, cytochrome P450, family 11, subfamily A, polypeptide 1; DDIT3, DNA-damage-inducible transcript 3; DHCR24, 24-dehydrocholesterol reductase; DICER1, dicer 1, ribonuclease type III; DLL1, delta-like 1 (Drosophila); DRD2, dopamine receptor D2; EEF2, eukaryotic translation elongation factor 2; EEF1G, eukaryotic translation elongation factor 1 gamma; FDPS, farnesyl diphosphate synthase; GABRA6, gamma-aminobutyric acid (GABA) A receptor, alpha 6; GABRB1, GABA A receptor, beta 1; GABRD, GABA A receptor, delta; GAD2, glutamate decarboxylase 2 (pancreatic islets and brain, 65kDa); GAPDH, glyceraldehyde-3-phosphate; GFAP, glial fibrillary acidic protein; GRIA3, glutamate receptor, ionotropic, AMPA 3; GRIN3A, glutamate receptor, ionotropic, N-methyl-D-aspartate 3A; HDAC9, histone deacetylase 9; HMGCR, 3-hydroxy-3-methylglutaryl-CoA reductase; HMOX1, heme oxygenase 1; HNRNPU, heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A); HSPA9, heat shock 70kDa protein 9 (mortalin); HTT, huntingtin; IGSF8, immunoglobulin superfamily, member 8; IREB2, iron-responsive element binding protein 2; LARP4, La ribonucleoprotein domain family, member 4; LSS, lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase); MAPK8IP1, mitogen-activated protein kinase 8 interacting protein 1; MFN1, mitofusin 1; MTHFR, methylenetetrahydrofolate reductase (NAD(P)H); MTRR, 5-methyltetrahydrofolate-homocysteine methyltransferase reductase; MYH11, myosin, heavy chain 11, smooth muscle; NBAS, neuroblastoma amplified sequence; NR3C1, nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor); NRXN1, neurexin 1; OPA1, optic atrophy 1 (autosomal dominant); OSBPL10, oxysterol binding protein-like 10; PAK1, p21 protein (Cdc42/Rac)-activated kinase 1; PAXIP1, PAX interacting (with transcription-activation domain) protein 1; PCNA, proliferating cell nuclear antigen; PGR, progesterone receptor; POLB, polymerase (DNA directed), beta; PTGER4, prostaglandin E receptor 4 (subtype EP4); PTPRZ1, protein tyrosine phosphatase, receptor-type, Z polypeptide 1; PUM1, pumilio RNA-binding family member 1; RAB6A, RAB6A, member RAS oncogene family; ROCK2, Rho-associated, coiled-coil containing protein kinase 2; RTN3, reticulon 3; RTN4R, reticulon 4 receptor; S100B, S100 calcium binding protein B; SC5D, sterol-C5-desaturase; SCD, stearoyl-CoA desaturase (delta-9-desaturase); SLC6A3, solute carrier family 6 (neurotransmitter transporter), member 3; SOD1, superoxide dismutase 1, soluble; SORL1, sortilin-related receptor, L(DLR class) A repeats containing; SPTLC1, serine palmitoyltransferase, long chain base subunit 1; SREBF2, sterol regulatory element binding transcription factor 2; SRF, serum response factor (c-fos serum response element-binding transcription factor); STX2, syntaxin 2; TGM1, transglutaminase 1; TGM2, transglutaminase 2; TSHZ1, teashirt zinc finger homeobox 1; VEGFA, vascular endothelial growth factor A; XPO7, exportin 7

Supplementary Information Table 1. Annotated genes altered in aged adult female zebrafish brain exposed to 10 µg/L Pb during embryogenesis.

Symbol	Probe ID	Expression Fold Change	Log_2 Expression Ratio	p-Value
A2M	A_15_P309636	-2.089	-1.063	4.37E-02
AACS	A_15_P414795	-2.178	-1.123	4.21E-03
ABAT	A_15_P108929	-2.200	-1.137	2.37E-02
ABCA1	A_15_P533082	1.920	0.941	2.04E-02
	A_15_P452790	2.672	1.418	1.83E-02
ABCA3	A_15_P347190	2.084	1.059	2.37E-02
ABCC10	A_15_P492704	2.803	1.487	4.24E-02
ABCC8	A_15_P535717	1.801	0.849	1.88E-02
ABCF1	A_15_P729266	-1.587	-0.667	1.65E-02
	A_15_P503397	-1.656	-0.727	1.33E-02
ABCF2	A_15_P623931	-1.742	-0.801	3.19E-02
ABCG4	A_15_P111605	-2.203	-1.139	5.00E-02
ABHD14B	A_15_P613857	-2.717	-1.442	9.70E-03
ABI1	A_15_P496887	1.820	0.864	1.60E-02
	A_15_P111016	2.302	1.203	2.58E-03
	A_15_P724471	1.778	0.830	1.34E-02
	A_15_P660696	1.624	0.699	1.05E-02
ABI3BP	A_15_P719151	2.282	1.190	1.07E-02
ABLIM1	A_15_P197896	2.235	1.160	8.85E-03
ACACA	A_15_P399860	-2.018	-1.013	7.39E-03
ACAD9	A_15_P179836	-1.649	-0.722	1.71E-02
ACAN	A_15_P113268	2.511	1.329	4.50E-02
ACAP3	A_15_P460881	1.928	0.947	1.22E-02
ACIN1	A_15_P731456	-2.133	-1.093	2.27E-02
	A_15_P528802	-2.192	-1.132	2.81E-02
ACLY	A_15_P166476	-1.568	-0.649	7.66E-03
ACO1	A_15_P145346	-1.684	-0.752	2.97E-02
	A_15_P192751	-1.561	-0.643	3.45E-02
ACOT9	A_15_P666416	-1.625	-0.701	5.88E-03
ACOX3	A_15_P675659	-1.511	-0.595	1.36E-02
	A_15_P727691	-1.905	-0.930	1.47E-02
	A_15_P578597	-1.760	-0.815	2.14E-03
ACSL6	A_15_P544562	-1.573	-0.653	4.65E-02
ACTA1	A_15_P341805	2.798	1.484	3.47E-02
ACTB	A_15_P541707	1.548	0.630	1.47E-02
ACTG1	A_15_P119825	2.272	1.184	2.60E-02
ACTN4	A_15_P461920	2.713	1.440	6.18E-03
	A_15_P154851	1.589	0.668	1.59E-02
ACTR1B	A_15_P158361	1.538	0.621	1.67E-02
ACTR6	A_15_P102155	-1.748	-0.806	1.71E-03
	A_15_P623521	-1.787	-0.838	6.32E-03
ACVRL1	A_15_P664971	-1.829	-0.871	3.35E-03
	A_15_P608472	-1.580	-0.660	7.62E-03
ADAM10	A_15_P111122	-2.374	-1.247	5.87E-03
	A_15_P719596	1.711	0.775	2.04E-02
	A_15_P441765	2.251	1.171	1.75E-02
	A_15_P576457	1.628	0.703	2.21E-02
ADAMTSL3	A_15_P145246	2.860	1.516	1.27E-02
ADCY1	A_15_P551767	2.421	1.276	3.87E-02
ADCYAP1	A_15_P630641	-1.634	-0.708	4.90E-02

	A_15_P347275	-1.866	-0.900	1.93E-02
ADCYAP1R1	A_15_P201096	-1.935	-0.953	2.07E-02
ADGRG1	A_15_P164066	-1.958	-0.970	1.25E-02
ADGRL3	A_15_P200296	-2.307	-1.206	9.53E-04
	A_15_P332634	-1.528	-0.612	4.45E-02
ADIPOR2	A_15_P545658	-1.901	-0.927	1.72E-03
ADK	A_15_P687771	-1.733	-0.793	1.73E-02
ADM	A_15_P168031	-2.518	-1.332	4.62E-02
ADNP	A_15_P417900	-1.677	-0.746	4.98E-02
ADO	A_15_P111812	-1.603	-0.681	2.02E-02
ADPRHL1	A_15_P153601	3.936	1.977	7.27E-03
AFF2	A_15_P553487	-1.641	-0.715	5.03E-03
AFTPH	A_15_P630386	1.935	0.952	3.83E-02
AGBL5	A_15_P194066	1.517	0.601	5.51E-03
AGFG1	A_15_P198471	-1.845	-0.884	2.25E-03
AHCY	A_15_P461855	-1.530	-0.614	4.64E-02
AHI1	A_15_P154081	-1.793	-0.842	2.02E-02
AIF1L	A_15_P691731	-2.195	-1.134	2.86E-02
	A_15_P162201	-1.614	-0.691	7.63E-03
AIFM1	A_15_P565137	3.461	1.791	7.68E-03
AK7	A_15_P109555	-2.647	-1.405	2.60E-02
AKAP11	A_15_P491677	1.741	0.800	1.93E-02
AKAP9	A_15_P505122	3.124	1.643	4.58E-02
	A_15_P552137	1.515	0.599	1.24E-02
	A_15_P538602	1.517	0.601	2.97E-02
AKR1B1	A_15_P153001	-1.644	-0.717	1.75E-02
	A_15_P118161	-1.580	-0.660	1.62E-02
AKTIP	A_15_P744866	-1.660	-0.731	3.42E-02
ALAD	A_15_P720861	-1.770	-0.824	2.13E-02
	A_15_P112185	-1.612	-0.689	1.05E-02
	A_15_P366565	-1.750	-0.807	3.79E-02
ALAS1	A_15_P160186	2.132	1.092	1.39E-02
ALCAM	A_15_P637656	-1.685	-0.753	2.73E-02
ALDH16A1	A_15_P502927	2.033	1.024	1.53E-02
ALDH3A2	A_15_P724101	-1.542	-0.625	1.91E-02
ALDH9A1	A_15_P285571	-1.757	-0.813	3.87E-02
ALDOB	A_15_P130317	1.701	0.767	3.58E-02
ALG11	A_15_P100918	-1.798	-0.847	5.65E-04
ALG14	A_15_P308941	-1.882	-0.912	1.36E-02
ALG8	A_15_P627066	-1.647	-0.720	2.66E-03
ALK	A_15_P485165	2.880	1.526	1.37E-02
ALKBH7	A_15_P110291	-1.985	-0.989	9.16E-03
ALMS1	A_15_P545487	-1.872	-0.905	2.50E-02
AMD1	A_15_P614531	2.129	1.090	2.40E-02
	A_15_P191551	1.823	0.866	1.74E-02
	A_15_P100147	2.182	1.126	4.77E-02
AMDHD2	A_15_P516282	1.573	0.653	3.49E-03
AMOTL2	A_15_P751681	2.432	1.282	2.38E-03
AMPD1	A_15_P105123	10.316	3.367	4.08E-02
AMPD3	A_15_P145394	2.306	1.206	3.82E-02
ANGPTL5	A_15_P180551	-1.591	-0.670	3.37E-02
ANK2	A_15_P211271	-1.753	-0.810	1.41E-02
	A_15_P163406	-1.546	-0.628	2.33E-02
ANKRD10	A_15_P116762	-1.572	-0.652	2.72E-03

ANKRD28	A_15_P406150	1.884	0.914	3.73E-02
ANKRD54	A_15_P100329	-1.545	-0.628	1.88E-02
ANKRD6	A_15_P240226	1.555	0.637	4.67E-02
ANKRD9	A_15_P107762	-1.636	-0.710	3.21E-03
ANLN	A_15_P102651	-1.805	-0.852	4.35E-02
ANO3	A_15_P135801	4.396	2.136	7.75E-03
ANO6	A_15_P236761	1.775	0.828	4.77E-02
ANP32B	A_15_P721891	-1.784	-0.835	4.93E-02
ANXA13	A_15_P119853	-1.801	-0.849	2.44E-02
	A_15_P113299	-1.784	-0.835	4.80E-02
	A_15_P114826	-1.699	-0.765	4.07E-02
AP1S1	A_15_P266441	-1.581	-0.661	3.83E-02
AP2M1	A_15_P668293	1.523	0.606	2.00E-02
AP5S1	A_15_P412970	-1.732	-0.793	1.66E-03
APBA2	A_15_P302076	1.775	0.828	2.94E-02
APEX1	A_15_P278451	-2.028	-1.020	3.01E-02
API5	A_15_P136951	-1.760	-0.815	3.33E-04
	A_15_P446465	-1.654	-0.726	1.75E-02
APITD1	A_15_P186051	-1.642	-0.716	2.92E-02
	A_15_P766041	-1.545	-0.628	3.47E-02
	A_15_P118152	-1.512	-0.596	2.06E-02
APLN	A_15_P632656	-1.567	-0.648	4.11E-02
APLP2	A_15_P278326	2.091	1.064	4.52E-03
APOE	A_15_P746986	1.839	0.879	4.94E-02
APP	A_15_P645791	1.767	0.821	1.38E-02
	A_15_P443870	1.856	0.892	3.29E-02
	A_15_P655926	1.704	0.769	3.84E-02
	A_15_P219381	1.640	0.713	4.01E-02
	A_15_P763436	1.898	0.925	5.40E-03
APTX	A_15_P104620	-2.096	-1.068	3.39E-02
AQR	A_15_P203446	1.919	0.940	2.16E-05
	A_15_P398980	2.015	1.011	5.78E-03
AR	A_15_P363595	1.910	0.934	5.00E-02
ARF1	A_15_P108093	-1.523	-0.607	9.09E-03
ARF3	A_15_P638706	-1.628	-0.703	1.44E-02
	A_15_P120890	-1.933	-0.951	9.38E-03
ARFGEF1	A_15_P117937	2.009	1.006	2.29E-02
ARHGAP11A	A_15_P114423	-2.493	-1.318	5.52E-03
ARHGAP27	A_15_P267576	-1.783	-0.835	3.56E-02
ARHGEF1	A_15_P392040	-2.132	-1.092	3.44E-03
ARHGEF11	A_15_P635401	1.621	0.697	2.25E-02
ARHGEF39	A_15_P256296	1.506	0.590	4.68E-02
ARHGEF7	A_15_P201406	-1.502	-0.587	1.90E-02
ARID1A	A_15_P245411	1.671	0.741	3.28E-02
ARID1B	A_15_P191621	1.538	0.621	4.42E-02
ARID3B	A_15_P495792	33.519	5.067	7.63E-03
ARID5B	A_15_P342105	1.731	0.792	3.17E-02
ARL13B	A_15_P134501	-1.804	-0.851	1.18E-02
ARL14EP	A_15_P118454	-1.727	-0.788	3.48E-02
ARL2BP	A_15_P117495	-2.281	-1.190	6.40E-03
	A_15_P654671	-1.579	-0.659	4.47E-03
ARL4C	A_15_P174756	-1.572	-0.653	1.76E-02
ARL6	A_15_P440565	-1.991	-0.994	3.29E-02
ARL6IP5	A_15_P169336	-1.592	-0.671	3.71E-02

ARMC4	A_15_P376200	3.665	1.874	4.04E-02
ARNT2	A_15_P102463	1.720	0.782	1.54E-02
	A_15_P194796	1.607	0.684	1.16E-02
ARPC4	A_15_P118217	-1.551	-0.633	1.05E-02
ARPC5	A_15_P119657	-1.552	-0.634	3.08E-02
	A_15_P647191	-1.572	-0.653	1.44E-02
ARRB2	A_15_P116117	-1.767	-0.821	1.97E-02
ARRDC3	A_15_P419295	1.681	0.749	2.49E-03
	A_15_P504717	2.211	1.144	5.89E-04
ASB13	A_15_P104961	-1.560	-0.642	1.39E-02
ASB7	A_15_P113199	2.016	1.012	9.36E-03
ASCL1	A_15_P176556	-1.780	-0.832	4.11E-02
ASH1L	A_15_P431115	1.889	0.918	3.05E-02
	A_15_P512032	1.570	0.651	5.74E-03
ASIC2	A_15_P101269	2.951	1.561	2.32E-03
	A_15_P622636	2.047	1.033	1.16E-02
	A_15_P187826	1.807	0.853	1.87E-02
ASPA	A_15_P130211	-1.526	-0.609	4.53E-02
ASPHD2	A_15_P437735	1.670	0.740	2.61E-02
ASPM	A_15_P130781	-2.058	-1.041	4.46E-02
	A_15_P664206	-2.690	-1.428	2.48E-02
ASPSCR1	A_15_P673891	1.592	0.671	1.47E-02
	A_15_P130182	2.791	1.481	1.33E-02
ASTN1	A_15_P585207	1.604	0.682	2.41E-02
ATCAY	A_15_P485237	-1.542	-0.625	4.70E-02
ATF7	A_15_P183711	-1.701	-0.766	4.75E-02
ATG5	A_15_P729966	-2.104	-1.073	9.24E-04
	A_15_P119333	-2.149	-1.104	3.54E-02
ATP11C	A_15_P190991	1.580	0.660	3.17E-02
ATP1A1	A_15_P121133	2.771	1.470	2.55E-02
ATP1B1	A_15_P729261	-2.176	-1.122	7.11E-03
	A_15_P135196	-2.043	-1.031	1.21E-02
	A_15_P442765	-2.808	-1.489	2.74E-02
ATP2A1	A_15_P381015	14.813	3.889	4.99E-02
	A_15_P104804	17.321	4.114	4.70E-02
	A_15_P450170	20.926	4.387	3.95E-02
ATP2B1	A_15_P106663	1.592	0.671	1.62E-02
ATP2B2	A_15_P435620	1.577	0.657	2.73E-02
	A_15_P521282	1.945	0.959	3.22E-02
ATP2B3	A_15_P339835	1.546	0.629	1.85E-02
	A_15_P210716	2.406	1.267	3.29E-03
	A_15_P189036	1.605	0.683	4.16E-02
ATP5SL	A_15_P410080	-1.527	-0.611	1.24E-02
ATP6AP1	A_15_P175446	-1.683	-0.751	4.02E-02
ATP6V0A2	A_15_P236631	-1.683	-0.751	3.45E-02
ATP6V1B2	A_15_P108939	-1.528	-0.612	4.58E-02
ATP6V1E1	A_15_P211946	-3.910	-1.967	3.19E-02
	A_15_P664336	-4.226	-2.079	2.98E-02
AVPR1A	A_15_P159011	-1.545	-0.628	4.24E-02
B3GALT2	A_15_P494947	1.683	0.751	4.63E-02
B3GNT2	A_15_P116745	3.745	1.905	1.90E-02
B4GALT6	A_15_P643486	-1.896	-0.923	4.57E-03
	A_15_P459585	-2.023	-1.017	1.25E-02
B9D1	A_15_P103552	-2.013	-1.009	2.73E-03

BACE1	A_15_P639466	1.761	0.816	2.15E-02
BACH2	A_15_P378925	1.568	0.649	2.46E-02
BAD	A_15_P117699	-1.771	-0.824	1.32E-02
	A_15_P114920	-2.041	-1.029	2.27E-04
	A_15_P112386	-1.557	-0.639	1.32E-02
BAHCC1	A_15_P301396	2.859	1.515	4.55E-02
BAIAP2L1	A_15_P209921	-1.594	-0.673	8.22E-03
BAZ2A	A_15_P230126	2.132	1.092	1.46E-02
BAZ2B	A_15_P749971	1.719	0.782	4.45E-02
BBS4	A_15_P136156	-2.020	-1.014	2.72E-02
BBS7	A_15_P109983	-1.570	-0.650	5.67E-03
BCAR1	A_15_P167746	2.449	1.292	7.45E-03
BCAR3	A_15_P245946	-1.563	-0.644	4.59E-02
BCL11B	A_15_P246956	3.479	1.799	3.11E-02
BCL7A	A_15_P754416	-1.529	-0.612	4.10E-02
	A_15_P104385	-1.674	-0.744	4.06E-02
	A_15_P513092	-1.603	-0.681	8.47E-03
BEND3	A_15_P643081	-1.593	-0.672	3.77E-02
BFSP2	A_15_P753306	-1.778	-0.831	3.96E-02
BHLHE22	A_15_P105549	-1.756	-0.812	3.16E-02
BHMT	A_15_P195441	2.368	1.244	3.48E-02
BLMH	A_15_P120743	-1.733	-0.793	1.22E-02
BLOC1S5	A_15_P635639	-1.506	-0.591	9.93E-03
BLVRB	A_15_P659516	-1.722	-0.784	1.98E-03
	A_15_P149371	-1.729	-0.790	3.88E-02
BMP1	A_15_P349385	1.888	0.917	4.68E-02
BOK	A_15_P109351	-2.045	-1.032	3.81E-02
BORA	A_15_P629821	-2.185	-1.128	2.37E-02
BPNT1	A_15_P173371	-1.541	-0.624	1.06E-03
	A_15_P105468	-1.556	-0.638	2.58E-03
BRCA2	A_15_P661421	-1.746	-0.804	1.63E-02
	A_15_P622366	-1.899	-0.926	1.65E-02
BRD2	A_15_P104430	1.659	0.730	2.54E-02
BRINP2	A_15_P117791	-2.023	-1.017	1.56E-02
BRPF3	A_15_P220001	1.769	0.823	2.37E-02
BTBD2	A_15_P482820	1.747	0.805	3.54E-02
BTG1	A_15_P606627	-1.917	-0.939	4.94E-02
BUD13	A_15_P377170	-1.518	-0.602	1.40E-02
C10orf88	A_15_P419715	-2.173	-1.120	2.09E-02
C11orf58	A_15_P297436	-1.505	-0.590	3.97E-02
C12orf4	A_15_P163101	-1.913	-0.936	4.43E-02
C12orf65	A_15_P625321	-1.514	-0.599	3.58E-02
C12orf73	A_15_P136426	-2.717	-1.442	2.25E-02
C15orf59	A_15_P552817	1.903	0.928	1.04E-02
	A_15_P224196	2.261	1.177	7.49E-04
C17orf85	A_15_P115674	-1.682	-0.750	2.64E-03
C1GALT1	A_15_P272341	1.670	0.740	4.51E-02
C1orf106	A_15_P189421	-1.778	-0.830	4.05E-02
	A_15_P734436	-1.640	-0.714	3.67E-02
C1orf159	A_15_P134186	-2.189	-1.130	2.37E-02
C1orf21	A_15_P114856	-1.606	-0.683	2.66E-02
C3orf14	A_15_P678656	-1.714	-0.777	3.30E-02
C5orf28	A_15_P116614	1.707	0.772	3.87E-02
C5orf30	A_15_P631526	1.800	0.848	2.79E-02

C6orf89	A_15_P169391	1.574	0.654	4.05E-02
C9orf9	A_15_P151276	-2.044	-1.032	2.96E-02
CA13	A_15_P117753	-2.166	-1.115	2.69E-03
	A_15_P107954	-1.592	-0.671	2.62E-02
	A_15_P599927	-1.632	-0.707	1.53E-02
	A_15_P687071	-1.708	-0.772	1.29E-02
CA2	A_15_P285846	-1.728	-0.789	4.34E-02
CA9	A_15_P296566	-2.180	-1.124	4.78E-02
CABIN1	A_15_P214841	-1.591	-0.670	3.82E-02
CACNA1C	A_15_P237136	1.973	0.981	3.64E-02
CACNA1E	A_15_P672704	2.044	1.032	1.68E-03
	A_15_P220516	1.632	0.706	9.64E-03
CACNA1H	A_15_P472180	1.867	0.901	1.02E-02
CACNB2	A_15_P100019	-2.455	-1.296	2.02E-02
CACNB4	A_15_P297541	1.853	0.890	1.90E-02
	A_15_P679646	1.890	0.919	4.25E-02
CACNG5	A_15_P500147	1.570	0.651	1.67E-02
CACYBP	A_15_P109742	-1.515	-0.599	3.66E-02
	A_15_P143361	-1.711	-0.775	2.09E-02
CADM2	A_15_P236176	-1.633	-0.708	3.29E-02
	A_15_P624621	-1.569	-0.649	2.49E-02
CALD1	A_15_P259751	-1.635	-0.709	3.11E-02
CALHM1	A_15_P268641	-2.232	-1.158	1.24E-03
CALR	A_15_P189106	-2.100	-1.070	8.11E-03
CALR3	A_15_P382735	-1.626	-0.702	3.38E-02
	A_15_P751936	-1.612	-0.689	3.15E-02
CALY	A_15_P518227	-1.831	-0.873	4.22E-02
CAMK2B	A_15_P146066	1.601	0.679	1.17E-02
CAMK2G	A_15_P432765	-1.738	-0.797	2.56E-03
CAMK2N2	A_15_P628146	-1.511	-0.595	8.16E-03
CAMSAP1	A_15_P180366	2.164	1.113	3.80E-02
CAND1	A_15_P209351	-1.711	-0.775	1.18E-03
CANT1	A_15_P112172	-1.798	-0.847	4.35E-02
CAPN1	A_15_P622331	-1.743	-0.801	2.12E-02
	A_15_P285396	-1.674	-0.743	3.99E-02
CAPZA1	A_15_P116774	-1.778	-0.830	1.97E-02
	A_15_P186101	-1.777	-0.829	1.31E-02
	A_15_P377630	-1.999	-0.999	5.49E-03
	A_15_P194136	-1.595	-0.674	1.89E-02
	A_15_P569927	-1.704	-0.769	2.11E-02
CASC5	A_15_P158987	-1.636	-0.710	3.37E-02
CASP3	A_15_P105110	-1.616	-0.693	1.19E-02
CBLB	A_15_P100030	-1.800	-0.848	1.56E-03
CBLL1	A_15_P136466	1.680	0.749	4.67E-02
CBLN1	A_15_P367255	-1.653	-0.725	3.60E-02
	A_15_P167956	-2.034	-1.024	1.04E-02
	A_15_P721471	-1.694	-0.761	3.88E-02
CBS	A_15_P607742	1.766	0.821	2.85E-02
	A_15_P171356	-2.260	-1.177	3.71E-02
CBX8	A_15_P103796	-1.779	-0.831	4.88E-02
	A_15_P187161	1.697	0.763	2.31E-03
CBY1	A_15_P108820	-2.517	-1.332	4.88E-02
CCDC12	A_15_P671391	-1.619	-0.695	2.13E-02
	A_15_P386025	-1.549	-0.631	2.71E-02

CCDC120	A_15_P265731	2.476	1.308	1.43E-02
CCDC146	A_15_P437365	-1.778	-0.831	9.52E-03
	A_15_P169326	-2.089	-1.063	2.58E-03
CCDC15	A_15_P243461	-1.537	-0.620	1.71E-02
CCDC170	A_15_P210171	-2.470	-1.305	6.44E-04
CCDC18	A_15_P288381	-1.888	-0.917	1.31E-03
CCDC180	A_15_P147266	-1.876	-0.907	3.60E-02
CCDC24	A_15_P194386	-1.946	-0.960	2.30E-02
CCDC79	A_15_P103996	-2.160	-1.111	5.39E-03
CCDC84	A_15_P164446	-1.634	-0.709	6.33E-06
CCDC89	A_15_P297756	-1.748	-0.805	1.91E-02
CCDC9	A_15_P176162	-1.621	-0.697	1.46E-02
CCDC96	A_15_P727066	-1.925	-0.945	2.71E-02
CCNA2	A_15_P624076	-1.720	-0.782	3.56E-02
CCND1	A_15_P132186	-1.512	-0.597	1.17E-02
	A_15_P152542	-2.008	-1.005	2.68E-02
CCND2	A_15_P142436	-2.397	-1.261	2.33E-02
CCNT2	A_15_P118694	-1.849	-0.887	1.25E-03
CCSER2	A_15_P555132	-2.838	-1.505	4.53E-02
CCT4	A_15_P600542	-1.700	-0.765	1.30E-02
	A_15_P100442	-1.715	-0.778	2.42E-02
	A_15_P734771	-1.692	-0.759	2.19E-02
CCT7	A_15_P740906	-1.839	-0.879	2.71E-02
	A_15_P509547	-2.549	-1.350	3.00E-02
CCZ1	A_15_P720201	-1.508	-0.593	3.42E-02
CD151	A_15_P100467	-3.328	-1.735	2.86E-02
	A_15_P772236	-2.113	-1.079	1.50E-02
	A_15_P106252	-2.096	-1.068	4.23E-03
CD81	A_15_P754411	-1.699	-0.765	4.13E-02
	A_15_P536662	-1.769	-0.823	3.34E-02
	A_15_P564847	-2.284	-1.192	3.32E-02
CD82	A_15_P602167	-2.181	-1.125	2.75E-02
	A_15_P331834	-1.663	-0.733	1.82E-02
CD99L2	A_15_P101501	-1.656	-0.728	1.92E-02
	A_15_P116214	-1.645	-0.718	1.33E-02
	A_15_P721581	-1.821	-0.865	5.15E-03
	A_15_P195401	-1.678	-0.747	4.32E-02
	A_15_P343975	-1.673	-0.742	9.80E-03
CDADC1	A_15_P101569	-2.013	-1.010	5.00E-02
CDC16	A_15_P321206	-1.576	-0.656	4.83E-02
CDC25A	A_15_P413270	-4.429	-2.147	4.74E-02
CDC27	A_15_P110890	1.793	0.843	4.24E-02
CDC42BPB	A_15_P109690	1.690	0.757	3.54E-03
CDC42SE1	A_15_P120964	-1.758	-0.814	1.87E-02
CDC42SE2	A_15_P630511	1.503	0.588	4.08E-02
CDC73	A_15_P408370	-1.572	-0.652	2.53E-02
CDCA8	A_15_P732617	-1.705	-0.770	2.99E-02
	A_15_P112683	-2.098	-1.069	6.43E-03
CDH7	A_15_P154631	2.887	1.530	7.41E-03
CDK1	A_15_P306636	-2.031	-1.022	1.23E-02
	A_15_P100423	-2.028	-1.020	1.99E-02
CDK11A	A_15_P440280	-1.664	-0.735	3.19E-02
	A_15_P174746	1.739	0.798	1.51E-02
CDK15	A_15_P149061	-2.699	-1.433	1.47E-03

CDKAL1	A_15_P443135	1.622	0.698	4.55E-02
	A_15_P153796	2.096	1.068	8.26E-04
	A_15_P112845	1.632	0.707	2.39E-02
CDKN1C	A_15_P111942	-1.798	-0.847	4.69E-03
CENPT	A_15_P672173	-1.992	-0.994	2.98E-02
CEP44	A_15_P383250	-1.907	-0.931	4.46E-02
CEP55	A_15_P120178	-1.713	-0.776	2.70E-02
CEP76	A_15_P203806	-1.880	-0.911	1.20E-02
	A_15_P743906	-1.588	-0.667	2.80E-02
CEP97	A_15_P207406	1.514	0.599	2.46E-02
CERS2	A_15_P255691	-1.733	-0.793	3.23E-02
CETN3	A_15_P677776	-1.522	-0.606	3.95E-02
CFAP43	A_15_P119901	-2.448	-1.292	1.39E-02
CFAP45	A_15_P157271	-2.051	-1.037	3.01E-02
	A_15_P161421	-3.059	-1.613	1.18E-02
	A_15_P657391	-1.708	-0.772	3.50E-02
CFAP58	A_15_P113343	-2.510	-1.328	3.68E-02
CGN	A_15_P622401	-1.839	-0.879	2.74E-02
CHAC1	A_15_P114147	-1.710	-0.774	4.07E-02
CHAC2	A_15_P109452	-1.505	-0.589	4.13E-02
CHAF1A	A_15_P512342	-2.008	-1.006	1.00E-02
	A_15_P113857	-2.444	-1.289	4.65E-03
	A_15_P656991	-1.522	-0.606	2.62E-02
CHAF1B	A_15_P114028	-3.202	-1.679	4.07E-02
CHD3	A_15_P178581	-1.597	-0.676	1.46E-02
CHD4	A_15_P257171	-1.593	-0.672	3.32E-02
CHD5	A_15_P177396	-1.704	-0.769	1.54E-02
CHGA	A_15_P192381	-1.639	-0.713	8.54E-03
CHP2	A_15_P274341	-2.062	-1.044	4.21E-02
CHRM2	A_15_P140116	-1.502	-0.587	4.40E-02
CHRNA9	A_15_P190376	2.109	1.077	2.50E-02
CHST8	A_15_P521397	-1.702	-0.767	2.54E-02
CHTOP	A_15_P496137	-2.756	-1.462	4.77E-02
	A_15_P170201	-2.009	-1.006	2.05E-02
CIT	A_15_P584212	2.329	1.220	2.33E-02
	A_15_P768149	1.585	0.664	1.63E-02
CKAP5	A_15_P176616	1.638	0.712	3.69E-02
CKB	A_15_P105046	1.996	0.997	1.81E-02
CKM	A_15_P280781	11.656	3.543	2.24E-02
	A_15_P107600	-2.054	-1.038	1.30E-03
	A_15_P743566	10.139	3.342	3.47E-02
	A_15_P716086	30.267	4.920	1.55E-02
	A_15_P417035	2.766	1.468	7.13E-04
	A_15_P103741	18.746	4.229	3.54E-02
	A_15_P397750	22.015	4.460	2.49E-02
CKMT2	A_15_P192711	1.888	0.917	4.35E-02
CLASP2	A_15_P100068	1.608	0.686	3.59E-02
CLCN7	A_15_P659676	-1.654	-0.726	1.41E-02
CLN5	A_15_P200046	-2.311	-1.209	3.76E-03
CLPX	A_15_P108737	2.499	1.321	9.55E-04
	A_15_P598792	2.682	1.423	8.95E-04
CLSTN1	A_15_P111698	1.542	0.624	2.60E-02
	A_15_P183661	2.204	1.140	2.21E-03
CMSS1	A_15_P120941	-2.038	-1.027	1.72E-03

CMTM4	A_15_P289521	-1.503	-0.588	3.39E-02
CMTM8	A_15_P620781	-1.638	-0.712	4.19E-02
CNBP	A_15_P504262	-1.520	-0.604	4.98E-03
CNIH1	A_15_P103577	-1.698	-0.764	2.81E-02
	A_15_P365715	-1.758	-0.814	3.52E-02
CNN3	A_15_P112885	-2.574	-1.364	3.13E-02
CNOT1	A_15_P133211	1.811	0.857	3.93E-02
CNOT11	A_15_P528377	2.191	1.132	4.77E-02
CNOT6	A_15_P112535	1.720	0.783	4.78E-02
CNR1	A_15_P206081	2.515	1.331	1.86E-02
COG7	A_15_P580087	2.656	1.409	4.83E-02
COIL	A_15_P623686	-1.602	-0.680	7.10E-03
	A_15_P114544	-1.538	-0.621	1.52E-02
COL10A1	A_15_P223226	6.170	2.625	3.40E-02
	A_15_P661781	10.567	3.401	2.16E-02
	A_15_P681766	13.323	3.736	3.96E-02
	A_15_P130226	16.527	4.047	2.57E-02
	A_15_P108588	14.806	3.888	1.46E-02
	A_15_P721941	7.829	2.969	4.74E-02
COL11A1	A_15_P504397	2.359	1.238	2.53E-02
COL14A1	A_15_P548337	1.976	0.983	1.03E-02
COL1A2	A_15_P462200	3.966	1.988	1.65E-02
	A_15_P113763	4.586	2.197	2.46E-02
	A_15_P118620	5.306	2.408	4.89E-02
COL4A5	A_15_P484155	1.805	0.852	4.34E-03
COL6A3	A_15_P764216	2.732	1.450	4.26E-02
COLEC11	A_15_P107376	-2.855	-1.513	3.71E-03
COMMD3-BMI1	A_15_P620996	-2.198	-1.136	2.88E-03
COMMD8	A_15_P496179	-1.551	-0.633	3.48E-02
COQ10A	A_15_P669831	-2.465	-1.301	7.57E-03
	A_15_P183821	-1.611	-0.688	4.42E-02
CORO1C	A_15_P453755	-1.803	-0.850	3.89E-02
	A_15_P431385	-1.926	-0.946	8.21E-03
COTL1	A_15_P323351	-2.525	-1.336	2.04E-02
COX19	A_15_P545012	-1.856	-0.892	7.80E-03
CPB1	A_15_P106371	-3.867	-1.951	2.84E-02
CPED1	A_15_P116482	-1.634	-0.709	2.33E-02
CPLX1	A_15_P349060	1.719	0.782	1.17E-02
CPNE3	A_15_P116404	-1.949	-0.963	3.15E-02
CPO	A_15_P245281	-1.648	-0.721	4.13E-02
CPPED1	A_15_P328716	-1.611	-0.688	2.38E-02
CPSF4	A_15_P111010	-1.657	-0.728	4.30E-02
CPSF7	A_15_P109490	1.850	0.888	3.96E-03
	A_15_P158721	1.866	0.900	2.87E-03
CPT1A	A_15_P106153	-1.882	-0.913	3.50E-02
	A_15_P142411	-1.724	-0.786	1.06E-02
CREBBP	A_15_P186871	1.545	0.627	2.46E-02
CRELD2	A_15_P743761	-1.946	-0.961	3.52E-02
	A_15_P672216	-1.505	-0.590	4.65E-04
CRHBP	A_15_P238406	-1.794	-0.843	3.57E-02
CRK	A_15_P117920	-2.232	-1.158	2.03E-02
CRTC1	A_15_P191906	2.156	1.108	2.05E-03
CRYGN	A_15_P627541	-2.221	-1.151	3.70E-03

	A_15_P130451	-1.509	-0.593	1.43E-02
CRYGS	A_15_P100312	-2.938	-1.555	3.82E-02
CSDC2	A_15_P154826	-1.663	-0.734	2.97E-02
CSGALNACT1	A_15_P601737	-1.557	-0.638	3.04E-02
CSGALNACT2	A_15_P113168	-1.633	-0.707	3.66E-02
CSPP1	A_15_P235566	-2.074	-1.052	1.56E-02
CSRNP2	A_15_P348695	-1.676	-0.745	4.43E-02
CSRP1	A_15_P401745	-1.782	-0.834	2.85E-02
CST3	A_15_P109240	-2.238	-1.162	4.94E-03
CTBP1	A_15_P109936	-1.729	-0.790	2.97E-02
CTBP2	A_15_P203586	2.158	1.110	3.80E-02
CTDP1	A_15_P101571	1.657	0.729	4.44E-02
CTGF	A_15_P177116	2.113	1.079	1.61E-03
CTNND2	A_15_P156726	-1.562	-0.643	1.82E-02
CTSA	A_15_P759388	-1.656	-0.728	1.27E-02
	A_15_P133606	-1.610	-0.687	1.47E-02
CTSC	A_15_P110747	2.265	1.180	2.54E-02
CUL2	A_15_P550237	-1.565	-0.647	8.01E-03
CUL4A	A_15_P660021	1.595	0.674	2.24E-02
	A_15_P669146	1.515	0.600	2.23E-02
CUL4B	A_15_P191071	-1.855	-0.891	3.98E-03
CWC22	A_15_P749036	1.539	0.622	4.81E-02
CXorf65	A_15_P405705	2.187	1.129	4.82E-02
CYB561D2	A_15_P101903	-2.027	-1.019	8.84E-03
CYB5R2	A_15_P446355	-2.301	-1.202	1.63E-02
CYGB	A_15_P626845	-1.501	-0.586	1.97E-02
CYP11A1	A_15_P101102	-2.398	-1.262	3.22E-02
CYP19A1	A_15_P112480	-3.341	-1.740	2.35E-02
CYP1B1	A_15_P631471	-2.236	-1.161	4.90E-02
	A_15_P148661	-1.745	-0.803	2.09E-02
CYP24A1	A_15_P226981	2.735	1.451	4.16E-02
CYP26B1	A_15_P132741	-1.546	-0.629	3.77E-02
	A_15_P656146	-1.689	-0.756	8.07E-03
	A_15_P734171	-2.285	-1.192	1.40E-03
CYP27A1	A_15_P117121	-2.052	-1.037	8.58E-04
CYP2J2	A_15_P116757	-3.393	-1.762	2.02E-02
CYP51A1	A_15_P106000	-1.645	-0.718	4.97E-02
CYP8B1	A_15_P111771	2.112	1.079	4.04E-02
DAB1	A_15_P451830	1.556	0.638	3.22E-02
DAB2	A_15_P551817	1.719	0.781	1.33E-02
DAD1	A_15_P141066	-2.096	-1.068	4.37E-02
	A_15_P199501	-1.898	-0.925	3.27E-05
	A_15_P626056	-1.877	-0.909	1.50E-03
DAO	A_15_P168826	-1.670	-0.740	2.95E-02
DAPK3	A_15_P104881	-2.073	-1.052	5.61E-03
DBH	A_15_P157546	-2.102	-1.072	3.18E-02
DBI	A_15_P118950	-2.176	-1.121	4.27E-02
	A_15_P201036	-2.091	-1.064	1.90E-03
	A_15_P627806	-1.775	-0.828	6.26E-03
	A_15_P150566	-1.807	-0.853	5.30E-03
DBX1	A_15_P102543	-1.961	-0.971	1.62E-02
	A_15_P625706	-2.023	-1.016	1.96E-02
DCAF5	A_15_P504632	1.575	0.655	3.60E-03
DCDC2	A_15_P106825	-3.529	-1.819	4.34E-02

	A_15_P117114	-3.744	-1.905	2.52E-02
	A_15_P720451	-4.378	-2.130	4.26E-02
DCDC2B	A_15_P365980	-4.461	-2.157	2.42E-02
DCLK1	A_15_P546657	-1.545	-0.627	3.49E-02
DCTD	A_15_P735451	-1.528	-0.611	3.70E-02
	A_15_P108274	-1.822	-0.865	1.46E-02
DCTN3	A_15_P507642	-1.531	-0.614	3.95E-02
DCXR	A_15_P170696	-1.771	-0.825	7.81E-03
DDB1	A_15_P641891	2.400	1.263	2.18E-02
DDIT3	A_15_P206471	-1.656	-0.728	1.47E-03
DDIT4	A_15_P442250	-2.179	-1.124	2.37E-03
	A_15_P194351	-1.766	-0.821	6.55E-03
	A_15_P115300	-2.165	-1.114	8.36E-03
DDT	A_15_P535062	-1.824	-0.867	2.45E-02
	A_15_P104107	-1.793	-0.842	2.55E-02
DDX19A	A_15_P661221	-2.658	-1.410	1.82E-02
	A_15_P186416	-1.752	-0.809	4.05E-02
	A_15_P711306	-1.902	-0.927	3.57E-02
	A_15_P661216	-2.680	-1.422	3.95E-02
DDX19B	A_15_P109542	-1.721	-0.783	1.32E-02
DDX21	A_15_P344750	-1.650	-0.722	4.47E-02
DDX43	A_15_P107666	1.633	0.708	1.60E-02
DDX49	A_15_P108242	-2.082	-1.058	1.82E-02
DDX54	A_15_P100156	1.508	0.593	3.23E-02
DECR2	A_15_P119292	-1.917	-0.939	1.20E-02
DEDD	A_15_P101348	-1.597	-0.675	3.05E-02
DEK	A_15_P204612	-1.593	-0.671	4.84E-02
DENND2C	A_15_P483990	-1.746	-0.804	3.19E-02
DENND2D	A_15_P217621	-2.611	-1.385	4.37E-02
	A_15_P108170	-1.810	-0.856	3.73E-02
DENND3	A_15_P581092	-2.218	-1.149	1.72E-02
DENND4B	A_15_P177901	2.117	1.082	1.14E-02
DEPTOR	A_15_P217041	1.557	0.639	2.78E-02
DERA	A_15_P149516	-1.527	-0.611	4.87E-03
DES	A_15_P112023	-3.311	-1.727	4.60E-02
DFFB	A_15_P133906	-1.598	-0.676	4.17E-03
	A_15_P119679	-1.678	-0.747	3.36E-02
DFNB31	A_15_P146271	-1.625	-0.700	3.02E-02
DGKH	A_15_P622961	1.796	0.845	4.77E-02
DGKI	A_15_P273036	1.531	0.614	2.87E-03
DHCR24	A_15_P162116	-1.772	-0.826	2.12E-02
DHPS	A_15_P204976	-1.828	-0.871	3.74E-02
DHRS11	A_15_P506752	-1.641	-0.715	2.79E-02
	A_15_P740331	-1.576	-0.656	4.69E-02
DHRS13	A_15_P111814	-1.520	-0.604	2.81E-02
DHRS4	A_15_P101345	-2.865	-1.519	4.75E-02
DHTKD1	A_15_P400725	1.756	0.812	2.58E-02
DHX29	A_15_P157371	-1.894	-0.921	2.77E-02
DHX36	A_15_P168256	-2.018	-1.013	2.25E-03
DHX8	A_15_P110464	-1.598	-0.676	2.48E-02
DICER1	A_15_P483945	1.613	0.690	3.67E-02
DIMT1	A_15_P111161	-2.143	-1.100	8.31E-03
DIS3	A_15_P113281	-1.977	-0.984	3.37E-02
DIS3L	A_15_P144396	-1.770	-0.824	9.51E-03

DISP1	A_15_P171656	1.852	0.889	4.89E-02
DLG2	A_15_P621122	-1.746	-0.804	1.03E-02
DLL1	A_15_P102804	-2.150	-1.105	1.62E-02
DLL3	A_15_P116883	-2.145	-1.101	3.40E-02
DMC1	A_15_P624416	-1.933	-0.951	3.46E-02
DMD	A_15_P336600	2.216	1.148	1.94E-02
DMRTA2	A_15_P101488	-1.698	-0.764	2.71E-02
DNA2	A_15_P299981	-1.637	-0.711	2.48E-02
DNAJA2	A_15_P739461	-1.841	-0.880	9.29E-03
DNAJB12	A_15_P214916	-1.754	-0.811	1.47E-02
DNAJC15	A_15_P202196	-1.576	-0.656	5.92E-03
DNAJC19	A_15_P106909	-1.665	-0.736	3.67E-02
DNMT3B	A_15_P364830	-1.711	-0.775	2.41E-02
	A_15_P542422	-1.794	-0.843	1.98E-02
DNPH1	A_15_P113360	1.674	0.744	4.62E-02
DOCK1	A_15_P622651	-2.020	-1.014	3.50E-02
DOCK3	A_15_P342990	1.764	0.819	9.87E-03
DOPEY1	A_15_P510477	1.802	0.849	2.26E-02
DPAGT1	A_15_P258371	-1.572	-0.653	4.06E-02
DPH2	A_15_P194551	-1.828	-0.870	5.69E-03
DPP6	A_15_P291631	-1.572	-0.653	1.37E-02
	A_15_P198396	-1.719	-0.782	3.51E-02
	A_15_P259231	1.693	0.760	3.02E-02
DPY19L1	A_15_P116231	1.832	0.873	1.71E-02
DPY19L3	A_15_P378870	1.769	0.823	4.47E-02
DPYSL3	A_15_P282486	1.897	0.924	1.39E-02
DRD2	A_15_P363870	-2.931	-1.552	7.20E-03
DSG2	A_15_P413705	3.862	1.949	2.38E-02
DTX3	A_15_P654956	-1.541	-0.624	1.51E-02
DUSP1	A_15_P116888	-1.628	-0.703	1.41E-02
	A_15_P108530	-1.859	-0.895	3.22E-02
DUSP11	A_15_P111252	-1.711	-0.775	4.78E-02
DUSP16	A_15_P768346	-1.764	-0.819	2.59E-02
	A_15_P566482	-1.771	-0.825	1.87E-02
DUSP27	A_15_P216996	2.965	1.568	3.54E-02
DYNC1H1	A_15_P756686	2.201	1.138	1.86E-02
	A_15_P567607	2.632	1.396	7.49E-03
DYNC1I2	A_15_P662321	1.551	0.633	2.27E-02
DYNC1LI2	A_15_P453740	-1.902	-0.927	7.79E-05
	A_15_P516627	-2.032	-1.023	2.10E-02
DYNLRB1	A_15_P119737	-1.580	-0.660	4.51E-02
	A_15_P102854	-1.519	-0.603	4.52E-02
DYNLT3	A_15_P350155	-1.502	-0.587	4.57E-02
DYTN	A_15_P312186	-1.511	-0.596	4.06E-02
DZIP1	A_15_P174961	-1.710	-0.774	4.93E-03
	A_15_P719296	-1.635	-0.709	1.12E-02
DZIP1L	A_15_P650711	-2.613	-1.386	3.89E-02
E2F2	A_15_P119932	-1.611	-0.688	1.65E-02
E2F3	A_15_P631421	-1.808	-0.854	4.28E-03
	A_15_P182601	-1.635	-0.709	2.27E-03
E2F8	A_15_P111660	-1.797	-0.846	4.41E-02
EBF2	A_15_P106199	-1.762	-0.817	4.59E-02
EBF3	A_15_P106593	-1.544	-0.626	3.48E-02
EBPL	A_15_P106424	-2.674	-1.419	2.50E-02

	A_15_P188281	-1.635	-0.709	8.07E-03
ECD	A_15_P202781	2.673	1.419	2.27E-02
ECH1	A_15_P152016	-1.557	-0.639	3.21E-02
EDN1	A_15_P114625	-1.899	-0.925	4.68E-02
EEF1E1	A_15_P235476	-1.823	-0.866	1.65E-02
	A_15_P290206	-1.875	-0.907	1.27E-02
EEF1G	A_15_P723016	-1.719	-0.782	6.32E-03
	A_15_P753281	-1.617	-0.693	1.54E-04
	A_15_P745251	-1.803	-0.851	2.19E-02
	A_15_P516042	-1.709	-0.773	2.72E-03
	A_15_P603937	-1.646	-0.719	8.57E-03
EEF2	A_15_P213646	1.788	0.839	2.11E-02
	A_15_P420143	2.127	1.089	1.32E-02
	A_15_P340330	1.745	0.804	3.24E-02
	A_15_P745216	1.694	0.760	3.92E-02
	A_15_P736511	2.102	1.072	2.52E-02
EFNA3	A_15_P173806	-1.694	-0.760	3.56E-02
EFNB3	A_15_P119492	-1.518	-0.602	1.49E-02
EGF	A_15_P555962	-1.512	-0.596	4.30E-03
EGFR	A_15_P198221	1.584	0.663	1.55E-04
EHHADH	A_15_P437335	3.377	1.756	3.24E-02
EHMT1	A_15_P322706	-1.791	-0.841	2.92E-02
	A_15_P180501	-1.647	-0.720	9.61E-04
EHMT2	A_15_P368615	1.686	0.754	2.93E-02
EIF2S2	A_15_P338865	-1.599	-0.677	3.88E-03
EIF3B	A_15_P187891	-1.915	-0.937	3.02E-02
	A_15_P386415	-3.050	-1.609	4.02E-03
EIF3E	A_15_P112959	-1.773	-0.827	3.73E-02
EIF3J	A_15_P100193	-1.772	-0.826	5.67E-03
	A_15_P623926	-1.527	-0.611	1.19E-02
EIF5AL1	A_15_P461690	-1.505	-0.589	2.02E-02
EIF5B	A_15_P596312	-1.747	-0.805	3.90E-03
ELK3	A_15_P172281	2.029	1.021	3.14E-03
ELOF1	A_15_P721211	-1.509	-0.593	1.99E-02
ELOVL1	A_15_P534307	-1.629	-0.704	4.22E-02
	A_15_P723936	-1.785	-0.836	2.72E-02
	A_15_P111691	-2.019	-1.014	4.51E-02
	A_15_P746691	-1.647	-0.720	4.20E-02
	A_15_P724211	-1.813	-0.858	4.90E-02
	A_15_P396970	-2.098	-1.069	1.80E-02
	A_15_P495307	-1.985	-0.989	2.55E-02
ELOVL2	A_15_P543437	-1.520	-0.604	3.80E-02
ELOVL5	A_15_P628196	-1.938	-0.955	4.15E-02
EMB	A_15_P675856	-1.847	-0.886	4.27E-02
EMC1	A_15_P100386	-1.702	-0.767	4.17E-02
EMC2	A_15_P103016	-1.864	-0.899	1.35E-02
	A_15_P627481	-1.549	-0.631	2.27E-02
	A_15_P604147	-1.972	-0.979	4.22E-02
	A_15_P753331	-1.863	-0.897	1.99E-02
	A_15_P204651	-1.915	-0.937	4.18E-02
EME1	A_15_P465495	-1.738	-0.798	1.06E-02
EMILIN1	A_15_P195646	1.960	0.971	4.71E-02
EMX1	A_15_P441625	-8.379	-3.067	1.22E-02
	A_15_P109130	-6.586	-2.719	1.56E-02

ENSA	A_15_P119872	1.822	0.865	2.85E-02
ENTPD2	A_15_P180431	-4.968	-2.313	4.85E-03
	A_15_P100174	3.246	1.699	1.74E-02
EPAS1	A_15_P622571	-1.502	-0.587	2.85E-02
EPB41L3	A_15_P101432	-1.561	-0.642	3.54E-02
EPHA2	A_15_P719576	-1.618	-0.695	8.06E-03
	A_15_P347035	2.189	1.130	1.55E-02
EPHB6	A_15_P203901	1.569	0.650	4.29E-03
EPHX2	A_15_P625571	-1.618	-0.694	2.13E-02
EPHX4	A_15_P135926	-2.078	-1.055	2.00E-02
EPYC	A_15_P111743	4.494	2.168	2.14E-02
	A_15_P102503	3.337	1.738	4.64E-02
ERAL1	A_15_P147011	-1.792	-0.841	3.95E-02
ERCC5	A_15_P171821	-2.949	-1.560	2.05E-03
ERCC6L	A_15_P207151	-1.639	-0.713	2.90E-02
ERCC8	A_15_P620911	-1.672	-0.742	1.23E-02
	A_15_P490972	-1.892	-0.920	4.38E-02
ERGIC1	A_15_P214601	-3.069	-1.618	2.00E-02
ERGIC2	A_15_P114546	-1.579	-0.659	3.32E-02
ERI1	A_15_P163301	-1.749	-0.807	2.38E-02
ERLIN1	A_15_P226466	-1.593	-0.671	4.12E-02
ESPL1	A_15_P488935	-3.054	-1.611	1.79E-02
ESYT1	A_15_P327426	-1.716	-0.779	5.21E-03
	A_15_P306516	-2.214	-1.147	2.98E-02
ETF1	A_15_P113951	-1.997	-0.998	1.61E-02
ETHE1	A_15_P111208	-1.653	-0.725	3.71E-02
ETNK2	A_15_P659066	1.802	0.849	2.00E-03
EVA1A	A_15_P344385	-2.016	-1.012	4.20E-02
	A_15_P464405	-1.660	-0.731	3.94E-02
	A_15_P173436	-2.453	-1.294	1.68E-02
EVI5	A_15_P177076	-1.729	-0.790	2.66E-02
EVX1	A_15_P574437	-2.406	-1.267	3.77E-02
EWSR1	A_15_P724261	2.046	1.033	1.46E-02
EXO1	A_15_P104116	-2.212	-1.145	1.96E-02
	A_15_P176762	-2.080	-1.057	2.27E-02
EXOC1	A_15_P184071	-1.621	-0.697	5.31E-03
EXOC3L1	A_15_P290721	-1.663	-0.733	1.57E-02
EXT2	A_15_P118401	-2.080	-1.056	1.62E-02
EXTL3	A_15_P252321	2.413	1.271	4.20E-02
EYA1	A_15_P755631	-1.854	-0.890	9.13E-03
EZH2	A_15_P131181	-1.635	-0.710	1.38E-02
FADD	A_15_P145096	1.711	0.775	3.22E-02
FADS2	A_15_P104437	-1.692	-0.759	1.78E-02
	A_15_P111237	-1.695	-0.762	8.84E-03
	A_15_P755901	-1.719	-0.781	3.15E-02
	A_15_P103127	-1.898	-0.924	4.56E-03
	A_15_P335765	-1.688	-0.756	4.23E-02
FAF2	A_15_P562627	-1.947	-0.961	6.27E-03
FAH	A_15_P680616	-1.597	-0.676	6.84E-03
FAHD1	A_15_P148431	-1.571	-0.651	4.83E-02
FAM110A	A_15_P239301	1.639	0.713	3.38E-02
FAM114A1	A_15_P530462	-1.668	-0.738	4.99E-02
FAM117B	A_15_P395630	1.794	0.843	1.40E-02
FAM120C	A_15_P415990	1.823	0.866	2.93E-02

FAM122A	A_15_P120816	-1.728	-0.789	3.85E-02
FAM135A	A_15_P726121	1.831	0.872	2.83E-02
FAM161A	A_15_P726226	1.881	0.911	2.38E-02
FAM169A	A_15_P180526	1.532	0.616	1.74E-02
FAM184B	A_15_P317661	-1.658	-0.729	2.98E-02
FAM188B	A_15_P371860	-1.684	-0.752	3.60E-02
	A_15_P189166	-2.076	-1.054	3.89E-02
FAM19A5	A_15_P500717	-1.543	-0.626	3.32E-02
FAM208B	A_15_P414255	-1.828	-0.870	8.37E-03
FAM228B	A_15_P722761	-1.629	-0.704	1.02E-02
FAM45A	A_15_P264064	-1.779	-0.831	2.24E-02
FAM46B	A_15_P115915	-1.675	-0.744	1.07E-02
	A_15_P108195	-1.605	-0.683	4.66E-02
FAM47E	A_15_P169961	-3.035	-1.602	4.17E-02
FAM53C	A_15_P660286	-1.759	-0.815	3.88E-02
FAM89B	A_15_P236306	-2.244	-1.166	4.53E-02
FAM96A	A_15_P155286	-1.835	-0.876	1.63E-02
FAM96B	A_15_P587612	-1.573	-0.653	1.29E-02
FANCF	A_15_P726681	-1.517	-0.601	9.72E-03
	A_15_P195561	-1.836	-0.876	1.03E-03
FANCL	A_15_P105630	-1.841	-0.880	3.02E-02
FAT1	A_15_P153126	1.628	0.703	4.75E-02
FAT3	A_15_P591102	1.667	0.738	1.47E-02
FBN1	A_15_P135111	3.588	1.843	4.51E-03
FBN2	A_15_P252781	2.425	1.278	4.45E-02
FBXO10	A_15_P658121	-1.905	-0.930	1.73E-02
FBXO18	A_15_P153856	-1.861	-0.896	4.32E-02
FBXO28	A_15_P196826	2.826	1.499	2.16E-02
FBXO6	A_15_P183344	-1.656	-0.728	2.20E-02
FDPS	A_15_P659061	-1.534	-0.618	2.73E-02
FDXACB1	A_15_P172021	-2.042	-1.030	6.80E-04
FEM1C	A_15_P305596	3.586	1.842	4.70E-02
FEV	A_15_P624831	-1.994	-0.996	3.37E-02
	A_15_P139831	-3.426	-1.777	4.42E-02
FGD3	A_15_P660086	2.065	1.046	2.28E-02
FGFBP2	A_15_P613677	10.838	3.438	1.85E-02
	A_15_P191376	3.096	1.631	4.01E-02
FHIT	A_15_P159851	-1.836	-0.876	6.42E-03
FHOD1	A_15_P362850	2.050	1.036	4.28E-02
FIBP	A_15_P100527	-1.508	-0.593	1.41E-02
FKBP11	A_15_P117398	2.458	1.298	4.52E-02
FKBP14	A_15_P502782	-3.161	-1.660	3.20E-02
FKBP1A	A_15_P105484	-1.524	-0.608	9.79E-03
	A_15_P116501	-1.536	-0.620	4.40E-02
FKBP5	A_15_P541507	-7.986	-2.997	3.71E-03
FLCN	A_15_P341605	1.577	0.657	4.74E-02
FLI1	A_15_P631866	-1.620	-0.696	3.50E-02
FLII	A_15_P115876	-1.732	-0.792	1.23E-02
FN3KRP	A_15_P259402	-1.686	-0.754	2.88E-02
FNDC4	A_15_P192156	-1.778	-0.830	3.10E-02
FOSB	A_15_P630281	-4.470	-2.160	2.75E-02
	A_15_P171421	-4.516	-2.175	3.33E-02
FOXJ2	A_15_P203921	1.748	0.806	2.52E-02
FOXK1	A_15_P108543	1.629	0.704	1.79E-02

FOXO1	A_15_P376310	-1.524	-0.608	3.47E-02
FOXRED1	A_15_P746082	3.085	1.625	2.31E-02
FRA10AC1	A_15_P599517	-2.229	-1.156	2.34E-03
	A_15_P121159	-1.655	-0.727	4.85E-02
FRMD8	A_15_P321179	-1.506	-0.591	2.93E-02
FST	A_15_P114697	-1.925	-0.945	1.04E-03
	A_15_P652856	-2.167	-1.116	3.13E-03
	A_15_P115175	-1.845	-0.884	1.41E-02
	A_15_P392800	-1.804	-0.851	2.63E-02
	A_15_P147116	-1.876	-0.907	1.17E-02
FTMT	A_15_P624761	-1.614	-0.691	4.23E-02
FTO	A_15_P395810	-1.575	-0.656	1.38E-03
FTSJ2	A_15_P549012	-2.384	-1.254	4.95E-02
FURIN	A_15_P437035	1.504	0.589	3.36E-02
FUT8	A_15_P287041	-1.680	-0.748	9.27E-03
	A_15_P286916	-1.861	-0.896	1.73E-02
FXYD6	A_15_P262466	-1.546	-0.629	2.23E-02
FYN	A_15_P117079	-1.706	-0.770	4.31E-02
FZD8	A_15_P109265	-1.655	-0.727	4.30E-02
G2E3	A_15_P116200	-2.013	-1.009	3.04E-02
	A_15_P332569	-2.714	-1.440	3.84E-02
G6PC3	A_15_P626461	-3.055	-1.611	1.84E-03
	A_15_P412965	-1.663	-0.733	3.28E-03
	A_15_P117585	-1.818	-0.862	4.32E-03
GABPB2	A_15_P118356	-1.810	-0.856	4.14E-03
GABRA6	A_15_P135331	4.252	2.088	4.89E-02
GABRB1	A_15_P289136	-1.832	-0.873	1.78E-02
GABRD	A_15_P491172	1.962	0.972	4.61E-02
GAD1	A_15_P106914	1.674	0.743	4.74E-02
GAD2	A_15_P699426	-1.575	-0.656	4.25E-02
	A_15_P315666	-1.564	-0.645	2.44E-02
GAL3ST3	A_15_P411645	1.779	0.831	2.10E-02
GALNT1	A_15_P116724	-1.751	-0.808	4.89E-02
GALNT2	A_15_P394965	-1.602	-0.680	2.12E-02
GAPDH	A_15_P120646	8.932	3.159	4.22E-02
	A_15_P331504	7.491	2.905	4.73E-02
GARNL3	A_15_P363610	1.853	0.890	4.09E-02
GAS8	A_15_P103540	-2.543	-1.347	7.23E-04
GATA2	A_15_P113672	-2.199	-1.137	3.96E-03
GATAD2B	A_15_P207436	1.718	0.781	4.65E-02
GATM	A_15_P731476	2.225	1.154	2.39E-03
	A_15_P528852	2.467	1.303	4.82E-03
	A_15_P578297	1.761	0.816	1.65E-02
GBGT1	A_15_P723051	-4.435	-2.149	3.49E-03
GEM	A_15_P142366	-2.370	-1.245	4.97E-02
GEMIN8	A_15_P116990	-1.747	-0.805	2.41E-02
GFAP	A_15_P658936	-3.821	-1.934	3.33E-02
GGCT	A_15_P336540	-104.233	-6.704	2.52E-05
GGH	A_15_P175246	-1.700	-0.766	9.38E-03
GHR	A_15_P189711	-1.690	-0.757	1.60E-02
GHRH	A_15_P624971	-3.198	-1.677	2.08E-02
	A_15_P135716	-4.440	-2.151	2.66E-02
GJA4	A_15_P193806	-2.137	-1.095	2.72E-02
	A_15_P258931	-1.568	-0.649	2.47E-02

GJB1	A_15_P220691	-2.983	-1.577	3.29E-02
GJC1	A_15_P743286	-1.916	-0.938	4.96E-02
GK5	A_15_P660516	-1.534	-0.618	4.00E-02
GKAP1	A_15_P724596	-1.518	-0.603	1.94E-02
	A_15_P220476	-1.679	-0.747	3.92E-02
GLDN	A_15_P213881	-1.953	-0.966	3.60E-03
GLG1	A_15_P404510	2.199	1.137	2.02E-02
	A_15_P591132	2.263	1.178	2.82E-03
GLI2	A_15_P201846	1.887	0.916	4.31E-02
GLIS1	A_15_P189156	-3.029	-1.599	4.23E-03
	A_15_P549042	-2.408	-1.268	3.15E-02
GLRX2	A_15_P678306	-1.841	-0.881	1.97E-02
GLS	A_15_P107778	1.648	0.721	2.60E-02
GLTSCR1	A_15_P110888	2.495	1.319	3.27E-02
GLUD1	A_15_P118050	-1.752	-0.809	1.27E-02
	A_15_P625671	-1.918	-0.939	2.11E-02
	A_15_P192771	-1.993	-0.995	2.10E-02
	A_15_P282316	-1.661	-0.732	4.66E-03
GMNN	A_15_P108988	-1.964	-0.974	2.41E-02
	A_15_P741676	-1.936	-0.953	1.65E-02
	A_15_P118497	-1.838	-0.878	4.47E-02
GMPS	A_15_P347201	1.822	0.866	4.97E-02
GNA11	A_15_P604552	1.511	0.596	2.81E-02
GNAI2	A_15_P179961	-1.654	-0.726	3.37E-02
GNB1	A_15_P630931	-1.559	-0.641	7.70E-03
	A_15_P107031	-1.646	-0.719	5.67E-05
GNB3	A_15_P102839	-2.836	-1.504	6.24E-03
GNB4	A_15_P397170	1.545	0.627	2.79E-02
GNMT	A_15_P721091	-1.889	-0.918	1.33E-02
	A_15_P366800	-1.995	-0.997	2.70E-02
GNRH	A_15_P103158	-3.183	-1.670	2.81E-02
GOLGA7B	A_15_P219706	-1.751	-0.808	5.93E-03
GOLT1B	A_15_P159361	-1.668	-0.738	3.27E-02
GORASP1	A_15_P466995	-1.565	-0.646	2.99E-02
GOT1	A_15_P659281	-1.908	-0.932	4.92E-04
GOT1L1	A_15_P483055	-1.847	-0.885	1.12E-02
GOT2	A_15_P167826	-1.520	-0.604	4.57E-02
GPALPP1	A_15_P100038	-1.519	-0.603	2.33E-02
GPATCH1	A_15_P116169	-2.061	-1.044	7.06E-03
GPATCH8	A_15_P116186	-1.622	-0.698	2.74E-02
GPBP1L1	A_15_P489417	-1.625	-0.701	1.46E-02
GPC4	A_15_P435125	5.455	2.448	3.51E-02
GPCPD1	A_15_P531277	-1.702	-0.768	3.14E-04
GPD2	A_15_P171486	1.596	0.675	1.02E-02
GPKOW	A_15_P114564	-1.686	-0.754	1.91E-02
GPM6B	A_15_P473825	-1.551	-0.633	2.94E-02
GPNMB	A_15_P379710	-3.012	-1.591	2.48E-03
GPR137B	A_15_P461015	1.770	0.824	3.56E-02
GPR37	A_15_P158786	-1.530	-0.614	2.50E-02
GPR68	A_15_P203266	-1.604	-0.682	4.66E-02
GPR85	A_15_P549622	1.676	0.745	1.56E-02
GPSM2	A_15_P210551	-2.055	-1.039	2.60E-02
GRAMD4	A_15_P277861	4.215	2.076	1.91E-02
	A_15_P449190	-2.360	-1.239	2.95E-03

GRAP2	A_15_P222846	-1.535	-0.618	3.79E-02
GRB10	A_15_P337115	-1.530	-0.613	1.25E-02
GREM1	A_15_P120476	-1.713	-0.777	4.71E-03
GRIA3	A_15_P193335	2.341	1.227	2.48E-03
GRIA4	A_15_P762801	1.781	0.833	1.59E-02
GRIK1	A_15_P457110	1.617	0.693	2.27E-03
GRIN3A	A_15_P286531	-1.844	-0.883	1.54E-02
	A_15_P236031	2.448	1.292	3.88E-02
GRPEL2	A_15_P367665	-2.090	-1.063	3.79E-02
GSKIP	A_15_P345170	-1.525	-0.609	4.41E-03
GTF2F1	A_15_P566512	-1.684	-0.752	1.68E-02
GTF2H2	A_15_P475200	-1.787	-0.837	4.42E-02
	A_15_P224641	-1.864	-0.899	4.41E-02
GTF3A	A_15_P660731	2.518	1.332	3.64E-02
GTPBP1	A_15_P529377	1.897	0.923	4.75E-02
GUSB	A_15_P145436	1.632	0.706	4.49E-02
GYLTL1B	A_15_P105991	1.837	0.877	2.28E-02
	A_15_P628601	1.801	0.849	1.32E-02
HAPLN4	A_15_P235191	-2.199	-1.137	4.99E-02
HAUS3	A_15_P161411	-1.799	-0.847	9.46E-03
HAUS6	A_15_P724071	-1.913	-0.936	9.77E-03
	A_15_P495772	-2.281	-1.190	1.68E-03
	A_15_P384325	-1.828	-0.871	9.52E-03
HDAC3	A_15_P115549	-1.672	-0.741	3.37E-02
HDAC5	A_15_P569902	1.691	0.758	1.02E-02
HDAC6	A_15_P510127	-2.844	-1.508	2.63E-02
HDAC9	A_15_P626381	1.609	0.687	6.87E-03
HDX	A_15_P323886	1.765	0.820	6.30E-03
HEATR1	A_15_P226756	1.598	0.676	1.06E-02
HEATR5A	A_15_P661796	-1.830	-0.872	2.95E-02
HEATR5B	A_15_P710296	1.570	0.651	3.87E-02
HECTD1	A_15_P642201	1.819	0.863	1.97E-02
	A_15_P291946	2.301	1.203	2.75E-03
HELZ2	A_15_P489190	1.877	0.908	1.80E-02
HEPACAM	A_15_P659981	1.560	0.642	3.61E-02
HERC2	A_15_P430580	1.926	0.946	3.68E-02
	A_15_P452470	1.597	0.675	5.03E-03
HERC4	A_15_P198096	1.521	0.605	4.16E-02
HEY1	A_15_P697986	-2.232	-1.158	2.09E-02
HGS	A_15_P188206	1.573	0.654	3.32E-02
HHIPL1	A_15_P534762	-1.595	-0.674	4.07E-02
HIBCH	A_15_P111993	-1.743	-0.802	8.95E-03
	A_15_P119687	1.585	0.664	1.93E-02
HIF1AN	A_15_P658911	-1.584	-0.664	1.07E-02
HIGD2A	A_15_P673821	-1.519	-0.604	4.94E-03
HIVEP2	A_15_P317711	1.777	0.830	1.80E-02
HLA-DPA1	A_15_P540002	2.864	1.518	2.84E-02
HMGA2	A_15_P739966	1.539	0.622	2.29E-02
HMGB1	A_15_P110467	-1.654	-0.726	2.09E-02
	A_15_P214388	-1.914	-0.936	1.49E-02
	A_15_P114926	-1.843	-0.882	3.16E-02
	A_15_P733031	-1.650	-0.723	1.64E-02
	A_15_P745381	-2.005	-1.004	1.70E-02
HMGB2	A_15_P742916	-1.555	-0.637	3.22E-02

HMGB3	A_15_P111896	-1.562	-0.644	1.90E-02
HMGCR	A_15_P624101	-1.998	-0.999	9.01E-03
	A_15_P206911	-2.130	-1.091	1.69E-03
	A_15_P147281	-2.644	-1.403	1.56E-02
	A_15_P237901	1.706	0.770	4.48E-02
HMGCS1	A_15_P379340	-1.570	-0.650	1.09E-02
HMGN3	A_15_P114525	-1.649	-0.721	1.50E-02
	A_15_P224341	-1.520	-0.604	4.58E-02
HMOX1	A_15_P257736	-3.448	-1.786	3.70E-02
HNRNPH1	A_15_P542637	1.605	0.682	4.91E-02
HNRNPU	A_15_P756756	-1.534	-0.618	2.27E-02
	A_15_P598547	-1.935	-0.952	2.93E-02
HOMER2	A_15_P335745	3.905	1.965	1.66E-02
HOPX	A_15_P110983	-1.810	-0.856	5.24E-03
HOXA2	A_15_P611602	-1.801	-0.849	4.43E-02
	A_15_P131556	-2.637	-1.399	2.53E-02
HPCAL4	A_15_P548087	-1.501	-0.586	2.32E-02
HPS5	A_15_P409015	3.107	1.635	4.79E-02
HS3ST1	A_15_P194941	2.539	1.344	4.90E-02
HS6ST3	A_15_P141516	-1.668	-0.738	4.08E-02
HSD17B14	A_15_P461195	-4.202	-2.071	3.39E-02
HSD17B7	A_15_P160916	-1.582	-0.661	1.95E-02
HSD3B7	A_15_P222921	-1.809	-0.855	3.72E-02
HSF5	A_15_P205801	1.812	0.858	2.11E-02
HSP90AA1	A_15_P118357	-1.795	-0.844	2.37E-02
HSP90AB1	A_15_P131441	-1.707	-0.772	4.56E-03
	A_15_P657002	-1.700	-0.765	9.56E-03
	A_15_P531677	-1.544	-0.627	8.10E-04
HSPA8	A_15_P732674	-1.811	-0.857	1.31E-02
HSPA9	A_15_P656476	-1.898	-0.924	3.94E-03
	A_15_P172211	-2.094	-1.066	7.86E-05
HSPB2	A_15_P154151	-1.566	-0.647	4.51E-02
HTT	A_15_P305441	1.524	0.608	2.19E-02
HUNK	A_15_P340925	-1.573	-0.654	3.25E-02
HUWE1	A_15_P597387	-1.687	-0.754	4.70E-02
HYOU1	A_15_P157981	-1.736	-0.796	3.82E-03
IBTK	A_15_P465385	2.130	1.091	5.18E-03
	A_15_P593817	1.735	0.795	3.44E-03
ICA1	A_15_P710738	-1.871	-0.904	1.69E-02
ICE2	A_15_P298371	-2.415	-1.272	2.40E-02
ID2	A_15_P659906	-1.803	-0.851	5.38E-03
ID3	A_15_P240461	-1.868	-0.901	1.94E-02
	A_15_P721801	-1.728	-0.789	4.94E-02
IDH1	A_15_P121313	-1.537	-0.620	1.32E-02
IDH3A	A_15_P274926	-1.561	-0.643	9.58E-03
IFT122	A_15_P154516	1.713	0.777	2.83E-02
	A_15_P763341	1.646	0.719	2.93E-02
IFT46	A_15_P212501	-1.817	-0.862	5.21E-03
IGF2BP1	A_15_P671071	-2.798	-1.485	4.54E-02
IGF2R	A_15_P161206	2.332	1.222	4.45E-03
IGFBP1	A_15_P749991	2.335	1.224	1.14E-02
	A_15_P465755	2.147	1.102	2.62E-02
	A_15_P221821	-2.016	-1.011	4.88E-02
IGFBP5	A_15_P222446	-1.565	-0.647	2.02E-02

	A_15_P186546	-1.810	-0.856	5.83E-03
IGSF8	A_15_P471785	2.755	1.462	4.54E-02
IGSF9B	A_15_P281601	1.626	0.701	1.80E-02
IL13	A_15_P257556	-2.398	-1.262	1.87E-02
IL15	A_15_P625736	-1.879	-0.910	2.09E-02
ILF2	A_15_P108833	-1.552	-0.634	1.60E-02
ILF3	A_15_P739261	-1.993	-0.995	3.47E-02
INA	A_15_P197351	-1.700	-0.766	2.03E-02
INCENP	A_15_P111936	-3.634	-1.862	2.44E-02
ING1	A_15_P501982	-1.722	-0.784	7.50E-03
ING4	A_15_P659816	-1.656	-0.728	6.82E-03
ING5	A_15_P119553	-1.617	-0.694	1.84E-02
INIP	A_15_P114972	-1.521	-0.605	3.60E-02
INPP5A	A_15_P162011	-1.558	-0.639	4.56E-02
INPP5E	A_15_P530422	3.268	1.708	7.83E-03
INPP5F	A_15_P439515	1.955	0.967	3.13E-02
INPP5J	A_15_P689526	2.194	1.133	1.82E-04
INPP5K	A_15_P545327	-1.971	-0.979	1.50E-02
	A_15_P170806	-1.583	-0.663	1.39E-02
INSM2	A_15_P202601	-1.688	-0.755	1.91E-02
INTS1	A_15_P423690	2.945	1.558	3.72E-02
INTS9	A_15_P170431	2.031	1.022	3.54E-02
IQCA1	A_15_P162901	-1.865	-0.899	6.35E-03
	A_15_P115750	-1.595	-0.674	1.74E-02
	A_15_P260381	-1.553	-0.635	3.52E-02
IQCD	A_15_P145811	-2.507	-1.326	2.55E-02
IQUB	A_15_P544127	-3.865	-1.950	4.94E-04
IREB2	A_15_P136236	2.569	1.361	4.19E-02
IRF2BP2	A_15_P118287	1.630	0.705	1.18E-02
IRS2	A_15_P429775	-1.527	-0.611	4.50E-02
IRX3	A_15_P409155	1.514	0.598	7.92E-03
IRX4	A_15_P151576	-2.319	-1.213	3.76E-02
IRX5	A_15_P112269	-1.920	-0.941	3.80E-02
ISG20L2	A_15_P148246	-1.668	-0.738	6.43E-03
ITGA11	A_15_P408315	-1.611	-0.688	4.22E-02
ITGB1	A_15_P111120	-1.562	-0.643	4.08E-02
ITIH3	A_15_P160756	-2.776	-1.473	2.69E-02
ITLN1	A_15_P290288	-2.445	-1.290	1.50E-02
ITPK1	A_15_P572037	-1.667	-0.738	4.89E-02
ITPKB	A_15_P184526	-1.862	-0.897	6.85E-04
	A_15_P457535	-1.672	-0.742	3.45E-02
	A_15_P600137	-1.569	-0.650	4.91E-02
JADE3	A_15_P103193	-1.678	-0.747	1.67E-02
JAKMIP1	A_15_P113007	-1.554	-0.636	1.16E-02
JARID2	A_15_P182346	-2.200	-1.137	2.12E-02
JMJD1C	A_15_P301731	1.934	0.951	1.80E-04
JMJD6	A_15_P188056	5.377	2.427	1.69E-02
KANSL1	A_15_P594359	2.059	1.042	2.62E-02
KANSL2	A_15_P104668	2.331	1.221	4.44E-02
KANSL3	A_15_P596102	1.636	0.710	1.20E-03
KAT6B	A_15_P601287	2.473	1.306	4.64E-02
KBTBD2	A_15_P114456	-1.555	-0.637	7.78E-03
	A_15_P282201	-1.630	-0.705	1.35E-02
KCNJ3	A_15_P488765	-1.777	-0.829	3.65E-02

KCNJ6	A_15_P157951	1.807	0.854	4.34E-03
KCNK1	A_15_P568392	1.970	0.978	1.51E-02
KCTD16	A_15_P763936	1.761	0.816	4.27E-03
KDM3B	A_15_P322221	-1.866	-0.900	3.90E-02
KDM5B	A_15_P335019	1.793	0.843	2.74E-02
KDM5C	A_15_P220391	-1.594	-0.673	4.06E-02
KDM7A	A_15_P594212	-1.643	-0.716	8.19E-03
KDSR	A_15_P113754	-1.563	-0.644	8.70E-03
KEAP1	A_15_P597762	1.665	0.736	1.20E-02
KHDRBS2	A_15_P172501	-1.693	-0.760	1.11E-02
KIAA0368	A_15_P200171	-1.643	-0.716	1.05E-02
KIAA0907	A_15_P175236	1.611	0.688	1.85E-02
	A_15_P284826	1.548	0.631	2.18E-02
KIAA1161	A_15_P250651	-1.569	-0.649	4.62E-02
KIAA1217	A_15_P100539	-1.784	-0.835	2.66E-02
KIF14	A_15_P738486	-2.186	-1.128	3.89E-02
	A_15_P193811	-2.037	-1.026	3.83E-03
	A_15_P473610	-2.812	-1.492	4.66E-02
KIF19	A_15_P709436	1.709	0.773	2.46E-03
KIF1BP	A_15_P726286	-1.561	-0.643	2.59E-02
KIF1C	A_15_P411410	1.608	0.686	3.93E-02
KIF22	A_15_P100190	-1.729	-0.790	3.90E-02
KIF26A	A_15_P686526	1.541	0.624	2.00E-02
	A_15_P591652	-1.545	-0.627	2.33E-02
KIF2C	A_15_P213841	-1.895	-0.923	2.63E-02
	A_15_P745281	-2.200	-1.137	4.52E-02
KIF5A	A_15_P489195	1.967	0.976	1.57E-02
	A_15_P214536	2.094	1.066	1.79E-02
KIFAP3	A_15_P184231	-1.514	-0.598	3.30E-02
KIRREL	A_15_P144231	2.908	1.540	4.80E-02
KLC4	A_15_P741667	2.284	1.191	6.25E-03
KLF17	A_15_P119506	-2.095	-1.067	1.46E-02
KLF3	A_15_P102825	-1.752	-0.809	1.00E-02
KLF7	A_15_P648411	-1.836	-0.876	5.80E-04
	A_15_P174151	-1.816	-0.861	1.53E-03
	A_15_P621812	-1.853	-0.890	3.74E-04
KLHDC10	A_15_P613547	1.816	0.861	4.55E-02
KLHDC2	A_15_P218021	1.784	0.835	1.47E-02
KLHL21	A_15_P183581	-2.027	-1.019	3.34E-02
KLHL24	A_15_P208591	1.993	0.995	4.15E-02
KLHL31	A_15_P115398	17.601	4.138	3.10E-02
	A_15_P210386	20.193	4.336	4.47E-02
KLHL8	A_15_P256691	1.532	0.615	4.22E-02
KMT2D	A_15_P263316	-1.762	-0.817	1.47E-02
KPNA6	A_15_P438780	-2.462	-1.300	2.20E-02
KRT15	A_15_P615937	1.682	0.751	3.22E-02
	A_15_P110571	2.444	1.289	2.44E-02
KRT17	A_15_P626517	-1.788	-0.838	1.16E-02
KRT18	A_15_P331061	-1.799	-0.848	4.09E-02
KRT8	A_15_P756471	2.335	1.223	1.76E-03
KXD1	A_15_P136501	-1.536	-0.619	1.68E-02
L1CAM	A_15_P174751	1.973	0.980	9.55E-03
	A_15_P209746	3.294	1.720	7.56E-03
	A_15_P113279	2.012	1.009	1.97E-02

L3MBTL2	A_15_P622516	-1.684	-0.752	7.62E-03
	A_15_P166576	-2.045	-1.032	9.50E-03
LACC1	A_15_P460740	-1.678	-0.747	2.54E-02
LAMA2	A_15_P241676	2.160	1.111	4.02E-02
LARGE	A_15_P663396	1.640	0.714	4.46E-02
LARP4	A_15_P529077	1.837	0.877	3.79E-02
LARP7	A_15_P365680	-1.598	-0.676	3.48E-02
LBX2	A_15_P172876	-2.650	-1.406	1.45E-02
LCLAT1	A_15_P643381	1.895	0.922	8.54E-03
LCORL	A_15_P564827	-1.557	-0.639	1.83E-02
LDB1	A_15_P112106	1.734	0.794	3.79E-02
LEPROTL1	A_15_P591577	-1.653	-0.725	1.96E-02
	A_15_P767326	-1.827	-0.869	2.77E-02
LGI1	A_15_P654841	2.184	1.127	9.86E-03
LIM2	A_15_P678141	-2.196	-1.135	3.29E-02
	A_15_P195606	-1.965	-0.975	2.63E-03
LIMA1	A_15_P624041	-1.548	-0.631	3.82E-02
LIMCH1	A_15_P470945	1.784	0.835	4.51E-02
LIMK1	A_15_P181271	-1.516	-0.600	1.60E-02
LIMS2	A_15_P404240	1.785	0.836	1.69E-02
	A_15_P149291	1.578	0.658	5.02E-03
LINGO1	A_15_P136256	1.571	0.652	1.40E-02
LIX1L	A_15_P181856	1.517	0.601	2.99E-02
LLGL2	A_15_P660301	-1.501	-0.586	1.45E-02
LMO7	A_15_P200506	2.471	1.305	3.21E-02
LMTK2	A_15_P265326	1.914	0.937	5.45E-03
LNX1	A_15_P564272	2.239	1.163	8.33E-03
LOC100996634	A_15_P202486	2.523	1.335	1.11E-02
PWP2	A_15_P662861	-1.652	-0.724	2.56E-02
LONP1	A_15_P585822	1.915	0.937	3.32E-02
LPCAT4	A_15_P729821	2.616	1.387	3.42E-02
LPPR2	A_15_P551687	1.517	0.602	2.98E-02
LPPR3	A_15_P180236	2.108	1.076	5.32E-04
LRFN3	A_15_P632156	-1.752	-0.809	1.47E-02
LRFN5	A_15_P460460	1.767	0.821	2.75E-02
LRIF1	A_15_P490717	-1.620	-0.696	3.15E-02
	A_15_P684761	-1.730	-0.791	2.36E-02
LRIG2	A_15_P536222	2.619	1.389	9.79E-03
LRIT2	A_15_P365520	1.536	0.620	1.96E-02
LRP11	A_15_P191516	1.999	0.999	2.54E-02
LRRC1	A_15_P289071	3.395	1.763	4.25E-02
LRRC15	A_15_P148076	-1.747	-0.805	2.38E-02
LRRC34	A_15_P657971	-1.742	-0.801	2.07E-02
	A_15_P667446	-1.666	-0.736	2.17E-02
LRRC47	A_15_P512117	-1.843	-0.882	4.40E-03
LRRC7	A_15_P442995	1.607	0.684	4.27E-02
LRRC8A	A_15_P755646	-1.878	-0.909	4.16E-03
LRRC8C	A_15_P424645	-1.745	-0.804	2.78E-02
	A_15_P159336	-2.117	-1.082	3.63E-02
LRRC8D	A_15_P650701	1.581	0.661	2.78E-03
LRRFIP2	A_15_P752156	-1.575	-0.656	2.41E-02
	A_15_P192922	-1.518	-0.602	2.38E-02
	A_15_P198016	-1.517	-0.601	1.61E-02
LSM11	A_15_P570362	-1.517	-0.601	3.05E-02

LSM5	A_15_P140481	-1.509	-0.594	1.71E-02
LSS	A_15_P192946	-1.753	-0.810	1.98E-02
LUC7L3	A_15_P143641	-2.110	-1.077	2.52E-03
LYRM2	A_15_P105931	-2.021	-1.015	1.07E-02
LYRM5	A_15_P225286	1.948	0.962	1.25E-02
LZTFL1	A_15_P348365	-1.770	-0.824	3.05E-02
	A_15_P512337	-1.523	-0.607	2.31E-02
MAD2L1BP	A_15_P463100	1.547	0.630	6.92E-03
MAFB	A_15_P120934	-1.752	-0.809	2.97E-02
MAFK	A_15_P120009	2.157	1.109	1.23E-02
MAGI1	A_15_P160446	1.582	0.662	1.06E-02
	A_15_P223426	2.270	1.183	3.87E-02
MAGI3	A_15_P547057	1.770	0.824	1.61E-02
MAN2B1	A_15_P328876	1.564	0.645	1.12E-02
MANEA	A_15_P103308	-1.780	-0.832	1.55E-02
MAP1A	A_15_P531432	-1.513	-0.598	2.23E-02
	A_15_P334994	-1.751	-0.808	1.14E-03
MAP2	A_15_P171551	-1.518	-0.602	4.42E-02
MAP3K12	A_15_P101314	1.632	0.707	3.00E-02
MAP3K2	A_15_P185346	1.731	0.792	3.63E-02
MAP3K7	A_15_P149956	-1.544	-0.627	5.80E-06
MAP4K4	A_15_P377715	1.567	0.648	4.49E-02
MAPK8IP1	A_15_P689181	1.677	0.746	1.40E-02
MAPRE3	A_15_P661806	1.818	0.863	5.42E-03
MAST1	A_15_P287741	2.012	1.009	4.96E-03
MAST2	A_15_P594302	-1.721	-0.783	2.30E-03
MAT2A	A_15_P173391	-1.738	-0.797	3.15E-02
MBL2	A_15_P199080	-2.342	-1.227	2.11E-02
MBOAT1	A_15_P743536	-1.718	-0.781	2.31E-02
MBOAT2	A_15_P672021	-2.043	-1.031	2.04E-02
MBOAT4	A_15_P488460	2.232	1.158	1.11E-02
MBP	A_15_P263706	-1.642	-0.715	3.16E-02
MCFD2	A_15_P142136	-1.655	-0.727	1.22E-02
	A_15_P666506	-1.568	-0.649	4.01E-02
MCMBP	A_15_P509162	2.376	1.248	3.57E-02
MCOLN1	A_15_P186816	2.399	1.262	3.04E-02
MCTP1	A_15_P603757	1.581	0.661	2.15E-02
MCTS1	A_15_P115829	-1.511	-0.596	1.43E-02
MDP1	A_15_P566822	-1.551	-0.633	4.95E-02
MEAF6	A_15_P721576	-1.557	-0.639	1.84E-02
MED22	A_15_P624301	2.057	1.040	2.07E-02
MED23	A_15_P303681	1.876	0.907	3.55E-02
MED25	A_15_P225411	2.352	1.234	2.46E-02
MED28	A_15_P630246	-1.654	-0.726	4.48E-02
MED4	A_15_P102399	-1.589	-0.668	1.04E-02
	A_15_P117538	-1.582	-0.662	1.35E-02
MEF2D	A_15_P442760	3.042	1.605	7.61E-03
MEI4	A_15_P725446	-7.368	-2.881	1.68E-02
	A_15_P191496	-3.374	-1.755	2.91E-02
MEIOB	A_15_P770001	2.634	1.397	4.93E-02
MEIS1	A_15_P151836	-1.802	-0.850	3.62E-02
MELK	A_15_P200253	-1.843	-0.882	2.95E-02
MEP1B	A_15_P460653	-1.531	-0.615	4.62E-02
MEPCE	A_15_P267076	1.553	0.635	4.13E-02

MEST	A_15_P169161	-1.771	-0.825	1.08E-02
	A_15_P102101	-1.573	-0.653	2.42E-02
MEX3C	A_15_P145491	1.939	0.956	1.87E-02
MFAP1	A_15_P211266	-1.635	-0.709	3.52E-02
MFAP4	A_15_P468400	-2.269	-1.182	2.06E-02
	A_15_P498217	-3.673	-1.877	2.12E-02
MFN1	A_15_P597247	2.648	1.405	1.01E-03
MFSD2A	A_15_P486995	-1.989	-0.992	7.79E-03
MFSD6L	A_15_P153731	3.444	1.784	2.66E-02
MGAT5B	A_15_P399210	2.694	1.430	1.00E-02
MGME1	A_15_P118396	-1.532	-0.615	6.61E-03
MIA3	A_15_P184936	1.548	0.631	4.82E-02
MICAL1	A_15_P333689	-1.809	-0.855	3.81E-03
MINK1	A_15_P151291	2.006	1.004	1.21E-02
MIOS	A_15_P109889	-3.533	-1.821	5.18E-03
MIP	A_15_P103570	-3.112	-1.638	3.70E-02
	A_15_P100341	-3.356	-1.747	1.53E-02
MKL2	A_15_P267726	1.827	0.870	2.16E-02
MLLT11	A_15_P722371	-1.564	-0.646	2.76E-02
MMD2	A_15_P409890	-1.780	-0.832	4.39E-02
MNS1	A_15_P105095	-2.235	-1.160	3.84E-02
	A_15_P289811	-2.873	-1.523	8.86E-03
MOB2	A_15_P136791	-1.772	-0.825	4.63E-02
	A_15_P740356	-1.853	-0.889	1.87E-02
	A_15_P571537	-1.722	-0.784	3.30E-02
	A_15_P506892	-1.989	-0.992	1.28E-02
	A_15_P263506	-1.960	-0.971	1.24E-02
MOCOS	A_15_P516677	-1.810	-0.856	3.45E-03
MOGAT3	A_15_P110116	-2.178	-1.123	6.08E-03
MON2	A_15_P404545	-1.672	-0.742	5.66E-03
MORN4	A_15_P162321	-1.792	-0.841	3.58E-02
MPP6	A_15_P289846	1.963	0.973	4.71E-02
MPZL2	A_15_P434270	1.844	0.883	4.86E-02
MROH1	A_15_P457595	-2.151	-1.105	3.04E-03
MRPL39	A_15_P470685	1.838	0.878	1.61E-03
MRPL9	A_15_P204981	-1.896	-0.923	2.02E-02
MRPS14	A_15_P265666	-1.551	-0.634	1.87E-02
MRPS22	A_15_P722061	-2.090	-1.064	2.81E-02
	A_15_P165204	-2.965	-1.568	4.33E-02
MRPS23	A_15_P119112	-1.711	-0.775	3.63E-02
MSI2	A_15_P179291	-1.599	-0.677	4.85E-02
	A_15_P116765	-1.570	-0.651	1.53E-02
MSMO1	A_15_P117765	-1.983	-0.987	5.96E-04
MSRB1	A_15_P149811	-1.972	-0.980	3.69E-02
	A_15_P119551	-1.694	-0.760	1.90E-02
	A_15_P392857	-1.593	-0.672	4.69E-02
MSRB2	A_15_P100974	-2.357	-1.237	6.76E-03
	A_15_P156591	-1.866	-0.900	4.17E-02
MTAP	A_15_P695231	-1.549	-0.631	2.10E-02
	A_15_P230221	-1.552	-0.634	2.10E-02
MTDH	A_15_P120409	-1.671	-0.741	1.38E-03
	A_15_P204566	-1.674	-0.743	1.29E-03
MTHFD1L	A_15_P192441	1.855	0.891	3.44E-02
MTHFR	A_15_P117151	1.544	0.627	3.59E-02

MTIF2	A_15_P172631	-1.572	-0.653	1.18E-02
MTRF1	A_15_P227096	2.297	1.199	8.82E-03
MTRR	A_15_P177246	-1.613	-0.689	4.03E-02
MTSS1L	A_15_P194976	1.526	0.610	3.79E-03
MTUS1	A_15_P200106	-1.811	-0.857	9.80E-03
MTX1	A_15_P721136	-1.643	-0.717	2.52E-02
MYBPC2	A_15_P196131	18.621	4.219	4.99E-02
	A_15_P416060	18.299	4.194	4.49E-02
MYC	A_15_P100897	-1.958	-0.969	1.42E-02
MYCBP2	A_15_P354613	1.603	0.681	2.25E-02
MYCL	A_15_P238901	-1.838	-0.878	6.14E-03
	A_15_P659166	-1.789	-0.839	4.29E-02
MYH11	A_15_P658511	-1.762	-0.818	4.20E-02
MYH4	A_15_P331879	12.430	3.636	4.80E-02
	A_15_P624916	17.966	4.167	2.60E-02
	A_15_P542682	14.041	3.812	4.11E-02
	A_15_P722036	10.497	3.392	2.53E-02
	A_15_P655096	35.296	5.141	3.77E-02
	A_15_P511817	23.429	4.550	3.47E-02
	A_15_P177831	23.112	4.531	4.54E-02
	A_15_P193441	24.484	4.614	1.78E-02
MYL1	A_15_P107336	13.058	3.707	4.61E-02
	A_15_P100247	29.453	4.880	2.39E-02
MYLPF	A_15_P331464	26.132	4.708	4.24E-02
MYO18A	A_15_P305591	2.313	1.210	1.44E-02
MYO1B	A_15_P114176	-1.801	-0.849	2.02E-03
MYO6	A_15_P191491	1.720	0.783	1.77E-02
MYO9B	A_15_P528542	1.703	0.768	5.89E-03
MYOZ1	A_15_P149696	11.061	3.467	4.62E-02
	A_15_P621961	10.525	3.396	3.12E-02
N4BP2	A_15_P200321	-1.524	-0.608	8.97E-03
	A_15_P587887	-1.567	-0.648	4.70E-02
NAA60	A_15_P162916	-1.846	-0.885	1.06E-02
NAGK	A_15_P722951	-2.176	-1.122	2.09E-02
NALCN	A_15_P229496	1.745	0.803	1.31E-02
NAMPT	A_15_P111592	1.904	0.929	1.50E-02
NANS	A_15_P119567	-1.512	-0.596	3.81E-02
	A_15_P109964	-1.931	-0.950	1.80E-02
NAPA	A_15_P323431	-1.763	-0.818	4.32E-02
NAPB	A_15_P104186	1.511	0.595	2.02E-03
NAPG	A_15_P634587	-1.570	-0.651	4.85E-02
NATD1	A_15_P107353	1.589	0.668	1.01E-02
NAV2	A_15_P460325	1.958	0.970	3.27E-03
	A_15_P555077	-2.418	-1.274	1.12E-02
NBAS	A_15_P744021	-1.652	-0.724	3.12E-02
NCAM2	A_15_P119660	-1.715	-0.778	4.26E-02
NCDN	A_15_P495692	3.046	1.607	3.90E-03
	A_15_P604642	2.434	1.283	3.63E-02
NCOR1	A_15_P147046	2.082	1.058	1.05E-02
	A_15_P380565	2.437	1.285	2.17E-02
NCS1	A_15_P103177	-1.683	-0.751	1.08E-02
	A_15_P146481	-1.770	-0.824	4.08E-02
NDRG3	A_15_P121322	1.885	0.915	3.99E-02
NDRG4	A_15_P446395	1.602	0.680	4.11E-02

NDST3	A_15_P399112	2.063	1.045	2.64E-02
NDUFS5	A_15_P209651	-1.522	-0.606	2.64E-04
	A_15_P113975	-1.557	-0.639	2.43E-03
NEK7	A_15_P118366	-1.609	-0.686	3.37E-02
NELL2	A_15_P119250	1.522	0.606	2.95E-02
	A_15_P376280	1.511	0.596	4.36E-03
NETO1	A_15_P156646	-1.653	-0.725	7.60E-03
	A_15_P257861	-1.803	-0.851	4.35E-02
NETO2	A_15_P282661	4.050	2.018	2.36E-03
NEURL1	A_15_P151501	-1.630	-0.705	1.66E-02
NEUROD6	A_15_P603012	-1.724	-0.786	1.08E-02
NFASC	A_15_P454015	-1.705	-0.770	3.08E-02
NFX1	A_15_P322186	1.605	0.682	4.86E-02
	A_15_P113887	1.533	0.617	1.43E-02
NFYA	A_15_P180056	-1.609	-0.686	1.56E-02
NGLY1	A_15_P113712	-1.563	-0.645	2.53E-02
NHLH2	A_15_P103769	-1.519	-0.603	4.83E-02
NHP2	A_15_P133591	-1.547	-0.629	3.61E-03
NHS	A_15_P258892	1.635	0.710	2.56E-02
NINJ1	A_15_P582157	-2.113	-1.079	2.13E-02
NIPBL	A_15_P106479	-3.266	-1.708	9.09E-03
NIPSNAP1	A_15_P162411	-2.045	-1.032	1.24E-02
NIT1	A_15_P348550	1.673	0.743	4.04E-02
NKX2-2	A_15_P102653	-3.306	-1.725	3.85E-02
NLGN1	A_15_P632481	-1.783	-0.835	2.21E-02
NLGN3	A_15_P145826	-1.635	-0.710	4.89E-03
NLK	A_15_P143166	-1.590	-0.669	3.28E-02
	A_15_P626081	2.067	1.048	2.69E-02
NME3	A_15_P104135	-1.628	-0.703	5.41E-03
	A_15_P105189	-1.668	-0.738	1.34E-03
NMRK2	A_15_P137531	-2.009	-1.006	4.46E-02
NOG	A_15_P117655	-2.040	-1.028	2.43E-02
	A_15_P121041	-1.529	-0.613	4.14E-02
NOLC1	A_15_P196956	-1.648	-0.721	1.75E-02
NOP2	A_15_P134332	-1.505	-0.590	1.27E-02
NOP58	A_15_P275746	-1.523	-0.607	3.64E-02
	A_15_P185356	-1.538	-0.621	8.08E-03
NOTCH3	A_15_P131536	3.892	1.961	2.81E-03
NOVA1	A_15_P502982	1.500	0.585	1.98E-02
NPBWR1	A_15_P364600	-3.926	-1.973	3.77E-02
NPEPL1	A_15_P571412	1.768	0.822	1.24E-02
NPEPPS	A_15_P257916	1.830	0.872	5.60E-03
NPTX2	A_15_P155591	1.637	0.711	3.71E-02
NR0B1	A_15_P130741	-1.801	-0.849	4.21E-02
NR1D2	A_15_P735876	-3.709	-1.891	2.42E-02
	A_15_P433290	-5.547	-2.472	1.27E-02
NR2E1	A_15_P131331	-1.842	-0.881	4.59E-02
NR2F2	A_15_P736021	-1.846	-0.885	1.73E-02
NR3C1	A_15_P194346	-1.510	-0.594	5.26E-03
NRARP	A_15_P656871	2.175	1.121	3.81E-02
NRD1	A_15_P741781	-1.684	-0.752	4.11E-03
	A_15_P614357	-1.635	-0.709	4.84E-04
NRIP1	A_15_P130756	-1.777	-0.829	5.43E-03
	A_15_P245821	1.693	0.760	3.22E-02

NRXN1	A_15_P166701	-1.814	-0.860	2.64E-03
NRXN2	A_15_P195776	1.925	0.945	2.02E-02
	A_15_P759521	2.950	1.561	3.26E-02
NSD1	A_15_P191366	1.522	0.606	1.52E-02
NSDHL	A_15_P401780	-1.556	-0.638	4.81E-02
	A_15_P210806	-2.129	-1.090	4.89E-03
	A_15_P148841	-2.229	-1.156	4.73E-03
NSF	A_15_P153006	-1.562	-0.644	3.10E-02
NT5C1A	A_15_P182621	1.931	0.950	4.68E-02
NT5C3A	A_15_P720491	-1.556	-0.637	4.44E-02
	A_15_P104284	-1.637	-0.711	4.41E-03
NT5DC1	A_15_P500437	1.543	0.626	4.34E-02
	A_15_P179746	1.644	0.717	1.28E-02
NT5E	A_15_P107850	7.202	2.848	1.42E-02
	A_15_P720086	3.234	1.693	6.04E-03
	A_15_P549377	-6.750	-2.755	1.73E-02
NTS	A_15_P282771	-2.122	-1.085	2.37E-02
NTSR1	A_15_P762141	-1.757	-0.813	3.27E-02
NUAK1	A_15_P159261	2.168	1.116	4.06E-02
NUB1	A_15_P737641	-1.955	-0.967	4.28E-03
	A_15_P347100	-1.836	-0.876	4.24E-03
	A_15_P349805	-1.879	-0.910	5.24E-03
NUCB1	A_15_P192881	-1.649	-0.721	1.34E-02
NUCKS1	A_15_P183396	-2.290	-1.195	2.07E-04
NUDT1	A_15_P114793	-2.038	-1.027	1.33E-02
NUDT19	A_15_P547622	1.759	0.815	1.29E-02
NUDT5	A_15_P304016	-2.201	-1.138	4.06E-02
	A_15_P100474	-2.340	-1.227	1.40E-02
NUF2	A_15_P118024	-1.900	-0.926	2.21E-02
NUMBL	A_15_P663876	1.619	0.695	4.87E-03
	A_15_P176736	1.528	0.612	3.97E-02
NUP160	A_15_P109150	1.610	0.687	2.85E-02
NUP54	A_15_P725561	2.185	1.128	4.05E-03
NUP93	A_15_P331624	1.925	0.945	8.55E-04
NUTF2	A_15_P380440	-2.018	-1.013	1.01E-02
	A_15_P624946	-1.537	-0.620	1.05E-02
NWD1	A_15_P386870	2.915	1.543	1.87E-02
NXNL2	A_15_P113454	-2.391	-1.258	3.60E-02
OCRL	A_15_P216106	-1.637	-0.711	5.63E-03
ONECUT1	A_15_P142826	1.848	0.886	1.77E-02
ONECUT3	A_15_P761771	2.457	1.297	4.73E-02
OPA1	A_15_P113446	-1.648	-0.720	3.11E-02
OPRD1	A_15_P658621	-1.738	-0.797	1.73E-02
ORMDL1	A_15_P579592	-1.667	-0.737	2.51E-02
OSBPL10	A_15_P118163	2.216	1.148	2.77E-02
OSBPL2	A_15_P161471	-1.835	-0.876	5.97E-03
OSBPL8	A_15_P158761	1.904	0.929	1.74E-03
OSGEP	A_15_P113817	-1.625	-0.701	4.92E-02
OSTF1	A_15_P621626	-1.507	-0.591	3.25E-02
	A_15_P145476	-1.601	-0.679	3.96E-02
OTOL1	A_15_P163266	-1.692	-0.759	2.67E-02
OTUD6B	A_15_P110221	-1.816	-0.860	2.81E-02
OTULIN	A_15_P114253	-2.215	-1.147	1.18E-02
OXSR1	A_15_P439960	-1.631	-0.705	3.75E-03

P4HA1	A_15_P639016	-1.813	-0.858	2.85E-02
PA2G4	A_15_P443250	-1.533	-0.616	4.77E-02
PABPC1	A_15_P434175	1.589	0.668	5.21E-03
PABPC3	A_15_P656726	1.822	0.866	2.11E-02
	A_15_P736096	1.557	0.639	1.23E-02
	A_15_P133836	1.763	0.818	1.19E-02
PACSIN1	A_15_P186241	-1.598	-0.676	1.14E-02
PAFAH1B1	A_15_P163541	-1.713	-0.777	1.22E-02
PAIP1	A_15_P104747	-1.988	-0.991	1.24E-04
PAK1	A_15_P282616	1.742	0.800	2.19E-02
PAK2	A_15_P446725	2.034	1.024	4.01E-02
PALB2	A_15_P497442	-1.887	-0.916	1.17E-02
	A_15_P472400	-2.253	-1.172	2.55E-02
PALM3	A_15_P768116	-1.585	-0.664	3.66E-02
PALMD	A_15_P517412	-1.833	-0.874	3.75E-02
PAN3	A_15_P105498	-2.854	-1.513	4.75E-03
PAOX	A_15_P442225	-2.060	-1.043	4.45E-03
PARN	A_15_P710006	1.809	0.856	2.68E-02
	A_15_P444255	2.496	1.319	3.63E-04
PARP12	A_15_P399300	2.016	1.011	4.28E-02
PATL2	A_15_P450205	-3.103	-1.634	3.41E-02
PAX7	A_15_P107848	1.504	0.589	1.54E-02
PAXIP1	A_15_P719551	-1.619	-0.695	2.39E-02
	A_15_P364895	-1.624	-0.699	4.98E-02
PBDC1	A_15_P157731	-1.560	-0.641	2.57E-02
PBX4	A_15_P421685	1.793	0.843	2.33E-02
PCBP2	A_15_P739351	1.566	0.647	7.25E-03
PCDH10	A_15_P131716	1.844	0.883	3.33E-02
PCDH17	A_15_P179911	-1.670	-0.740	4.20E-02
PCDH19	A_15_P101631	1.881	0.912	3.00E-02
PCDHB3	A_15_P102070	2.037	1.026	1.95E-02
PCF11	A_15_P109373	1.606	0.683	3.81E-02
PCGF5	A_15_P544282	-2.220	-1.150	4.42E-03
	A_15_P731191	-2.046	-1.033	2.86E-02
	A_15_P533207	-1.867	-0.900	1.49E-02
PCNA	A_15_P322966	-2.512	-1.329	3.92E-02
	A_15_P105183	-2.702	-1.434	2.00E-02
	A_15_P744731	-2.561	-1.357	3.60E-02
PCNX	A_15_P197881	1.743	0.802	3.70E-02
PCNXL2	A_15_P558357	1.728	0.789	3.17E-02
PCP4	A_15_P289011	-1.722	-0.784	2.45E-02
PCSK2	A_15_P685166	1.570	0.650	5.94E-03
PCYT2	A_15_P100181	-1.528	-0.611	1.44E-03
	A_15_P512947	-1.892	-0.920	4.09E-03
PDAP1	A_15_P166606	-1.607	-0.685	3.17E-02
	A_15_P223011	-1.568	-0.649	3.39E-02
PDC	A_15_P113248	2.964	1.567	4.54E-02
PDE4D	A_15_P189111	1.529	0.613	4.50E-02
PDE6H	A_15_P675851	1.918	0.939	4.68E-02
PDE8B	A_15_P484865	2.486	1.314	4.23E-02
PDGFA	A_15_P228266	1.569	0.650	1.90E-02
PDHX	A_15_P259226	1.978	0.984	1.38E-02
	A_15_P732081	1.746	0.804	1.08E-02
PDK2	A_15_P105148	-2.426	-1.279	2.39E-02

PDK4	A_15_P182791	-2.956	-1.563	3.22E-02
PDPR	A_15_P444321	2.429	1.280	2.30E-02
PDS5A	A_15_P551752	1.630	0.705	1.08E-02
PDZD2	A_15_P289931	1.721	0.784	2.97E-02
PDZD8	A_15_P283946	2.029	1.021	2.69E-02
PDZK1IP1	A_15_P746876	1.805	0.852	9.45E-04
PEAK1	A_15_P403710	1.779	0.831	4.76E-02
PER2	A_15_P456650	1.675	0.744	2.64E-02
	A_15_P286166	2.409	1.268	1.78E-02
PEX14	A_15_P368365	-1.653	-0.725	2.58E-02
PEX26	A_15_P106272	-1.506	-0.590	4.95E-02
PFDN2	A_15_P231931	-2.133	-1.093	1.45E-02
PFDN4	A_15_P115065	-2.527	-1.337	3.59E-02
PFDN5	A_15_P327881	2.230	1.157	4.34E-02
PFKP	A_15_P244116	-2.185	-1.128	4.90E-02
	A_15_P100084	-1.525	-0.609	1.24E-02
PFN2	A_15_P732686	-1.681	-0.749	2.78E-02
	A_15_P703836	-1.778	-0.830	9.49E-03
	A_15_P574682	-1.816	-0.861	1.02E-02
PGAM1	A_15_P604097	-2.008	-1.006	6.38E-03
PGGT1B	A_15_P543322	1.722	0.784	3.04E-02
	A_15_P220581	2.013	1.009	1.13E-02
	A_15_P730931	1.706	0.771	4.51E-02
PGM3	A_15_P114056	-1.863	-0.898	4.32E-02
PGR	A_15_P166236	-2.781	-1.476	1.36E-02
PHACTR4	A_15_P540932	1.507	0.592	2.08E-02
PHEX	A_15_P119527	-2.005	-1.004	4.15E-02
PHF23	A_15_P118377	-1.572	-0.653	1.79E-02
PHF6	A_15_P119247	-1.545	-0.628	3.44E-02
PHF8	A_15_P243865	1.599	0.677	2.65E-02
PHKA1	A_15_P144866	-1.886	-0.916	3.03E-02
	A_15_P111581	-1.817	-0.861	4.02E-02
PHKA2	A_15_P307301	2.029	1.021	2.73E-02
PHKG2	A_15_P209941	-1.979	-0.985	1.27E-02
	A_15_P102397	-1.691	-0.757	2.49E-02
PHLDA2	A_15_P303961	-1.562	-0.643	2.73E-04
PHLDB1	A_15_P239836	2.181	1.125	4.97E-02
PHYH	A_15_P117891	-1.580	-0.660	4.74E-03
PHYHIPL	A_15_P204166	-1.509	-0.593	3.31E-02
PI4KA	A_15_P490587	1.818	0.862	3.83E-02
	A_15_P428915	-1.570	-0.650	2.84E-02
PIAS1	A_15_P121203	1.506	0.591	1.58E-02
PID1	A_15_P365750	2.439	1.286	1.82E-02
	A_15_P613592	2.673	1.419	8.52E-04
	A_15_P767831	2.491	1.317	4.66E-02
	A_15_P720276	2.508	1.326	1.14E-02
	A_15_P114393	1.587	0.666	2.38E-03
PIGA	A_15_P201686	-1.823	-0.867	3.68E-02
PIGF	A_15_P116871	-1.637	-0.711	4.19E-02
PIGL	A_15_P287766	-1.655	-0.727	3.24E-02
PIK3C2A	A_15_P200961	-2.399	-1.262	3.04E-03
PIK3R3	A_15_P660296	1.658	0.729	1.43E-02
PIM1	A_15_P174096	-1.714	-0.778	2.05E-02
	A_15_P177156	-1.813	-0.859	2.69E-02

PIN4	A_15_P120022	-1.522	-0.606	4.03E-03
PINX1	A_15_P656736	-1.559	-0.640	2.59E-02
PIP4K2A	A_15_P424555	-2.196	-1.135	2.97E-02
	A_15_P517957	-1.722	-0.784	1.16E-02
PIP4K2C	A_15_P173491	-1.501	-0.586	3.73E-03
PIPOX	A_15_P165496	-1.775	-0.828	6.03E-03
PITX1	A_15_P626171	1.639	0.713	4.88E-02
PIWIL1	A_15_P627621	-1.571	-0.651	1.04E-02
	A_15_P189906	-1.554	-0.636	1.18E-02
PKIB	A_15_P105856	-2.119	-1.083	3.60E-02
PKN1	A_15_P667241	1.730	0.791	4.83E-02
PLA2G12B	A_15_P588037	1.590	0.669	1.56E-02
	A_15_P103131	-4.378	-2.130	3.60E-02
PLA2G15	A_15_P136741	-1.507	-0.592	4.29E-02
PLA2G4C	A_15_P445670	-2.218	-1.149	4.67E-02
PLAG1	A_15_P177601	-1.918	-0.940	5.62E-03
PLCB3	A_15_P266106	1.695	0.761	3.94E-02
PLCB4	A_15_P143701	1.695	0.762	4.72E-02
PLCH2	A_15_P220536	3.081	1.623	5.36E-03
PLD1	A_15_P102144	-2.240	-1.163	1.39E-02
PLEC	A_15_P561927	-1.789	-0.839	9.96E-03
PLEK2	A_15_P625457	1.549	0.631	2.39E-02
PLEKHA1	A_15_P103416	-1.664	-0.734	2.36E-02
PLEKHF2	A_15_P118763	1.519	0.603	1.95E-02
PLEKHG5	A_15_P269541	1.816	0.861	3.11E-02
PLEKHG7	A_15_P384021	2.703	1.434	4.51E-03
PLEKHJ1	A_15_P731216	-1.528	-0.611	6.75E-03
	A_15_P199651	-1.570	-0.651	4.76E-02
	A_15_P104056	-1.816	-0.861	1.91E-02
PLK2	A_15_P272086	1.514	0.598	3.41E-02
PLOD2	A_15_P156376	-3.164	-1.662	1.41E-02
PLSCR1	A_15_P193626	-1.520	-0.604	1.75E-03
	A_15_P117823	-1.500	-0.585	3.98E-02
PLXNA1	A_15_P655476	1.948	0.962	4.61E-02
PNKP	A_15_P571326	2.209	1.144	4.62E-02
PNN	A_15_P580782	-2.051	-1.036	1.63E-04
PNPT1	A_15_P374070	1.930	0.949	2.07E-02
PNRC1	A_15_P747431	1.956	0.968	1.16E-02
	A_15_P570672	1.605	0.683	8.42E-03
	A_15_P487440	2.302	1.203	1.43E-02
POFUT1	A_15_P195926	-2.011	-1.008	9.92E-03
POGZ	A_15_P471896	1.748	0.805	2.40E-02
POLB	A_15_P366165	-1.536	-0.619	8.99E-03
POLD3	A_15_P120857	-1.574	-0.655	8.37E-05
POLR1A	A_15_P101296	-1.512	-0.597	1.53E-03
POLR2G	A_15_P659356	-1.719	-0.781	4.09E-02
POLR2I	A_15_P117542	-1.543	-0.626	7.74E-03
	A_15_P119697	-1.631	-0.706	3.52E-03
POLR3G	A_15_P256601	-3.449	-1.786	3.30E-02
POMC	A_15_P195406	-2.942	-1.557	3.48E-02
POMP	A_15_P118871	-1.926	-0.945	4.41E-02
POMT1	A_15_P169691	-1.618	-0.694	2.93E-02
	A_15_P147271	-2.014	-1.010	1.03E-02
	A_15_P603607	-1.675	-0.744	1.30E-02

POSTN	A_15_P755806	-1.933	-0.951	2.10E-02
POU3F1	A_15_P179791	-2.420	-1.275	1.18E-02
POU3F2	A_15_P644331	-1.793	-0.843	1.55E-02
POU3F3	A_15_P119411	1.642	0.715	2.16E-02
	A_15_P658696	-1.612	-0.689	2.57E-02
PPA2	A_15_P107293	-1.668	-0.738	2.05E-02
	A_15_P276976	-1.740	-0.799	7.36E-03
	A_15_P720701	-1.560	-0.641	4.86E-02
	A_15_P115334	-1.828	-0.870	6.34E-03
PPFIA1	A_15_P442260	1.617	0.693	1.76E-02
	A_15_P686386	2.453	1.295	3.82E-02
PPFIA4	A_15_P237576	1.572	0.652	3.67E-02
PPFIBP1	A_15_P394775	-1.790	-0.840	3.99E-02
PPIA	A_15_P349860	-1.814	-0.859	2.05E-02
PPIH	A_15_P194331	-1.659	-0.730	2.87E-02
PPIL2	A_15_P101938	-1.736	-0.796	2.66E-02
	A_15_P231261	-1.599	-0.677	2.43E-02
PPIL4	A_15_P425565	1.581	0.661	1.49E-02
PPM1B	A_15_P115240	-1.659	-0.730	3.53E-03
PPM1N	A_15_P320953	1.546	0.629	3.77E-02
PPP1CC	A_15_P435865	-1.539	-0.622	4.23E-02
PPP1R12C	A_15_P164156	-2.057	-1.040	2.80E-02
	A_15_P745966	-1.505	-0.590	1.70E-02
	A_15_P217031	-1.649	-0.721	4.35E-03
PPP1R14B	A_15_P112472	-1.784	-0.835	1.49E-02
	A_15_P114799	-1.848	-0.886	1.16E-02
PPP1R21	A_15_P418240	2.098	1.069	1.66E-02
	A_15_P107530	1.705	0.770	2.50E-02
PPP1R27	A_15_P186326	5.722	2.517	2.51E-02
	A_15_P174831	9.525	3.252	2.79E-02
	A_15_P188046	3.785	1.920	4.08E-02
PPP2CB	A_15_P103368	-1.533	-0.616	4.63E-02
PPP2R5E	A_15_P116920	-1.521	-0.605	2.14E-04
	A_15_P465315	-1.519	-0.603	3.23E-03
	A_15_P133431	-1.578	-0.658	2.67E-02
PRC1	A_15_P535902	-1.592	-0.671	2.81E-02
PRDX4	A_15_P176306	21.337	4.415	3.46E-02
PREX2	A_15_P156491	-1.767	-0.822	3.93E-02
PRIM1	A_15_P209721	-1.509	-0.594	3.35E-02
PRIMPOL	A_15_P160906	-1.537	-0.620	9.08E-03
	A_15_P662856	-1.906	-0.931	7.14E-03
PRKAG1	A_15_P186276	-1.501	-0.586	3.69E-02
	A_15_P426125	-1.815	-0.860	1.26E-02
PRKCSH	A_15_P112616	-1.669	-0.739	3.34E-02
PRKRIP1	A_15_P147471	-1.544	-0.626	4.87E-03
PRMT1	A_15_P117861	-1.606	-0.684	4.38E-02
	A_15_P119062	-1.652	-0.724	2.32E-02
	A_15_P114252	-1.640	-0.714	2.06E-02
PRMT7	A_15_P659257	1.741	0.800	1.76E-02
PRODH2	A_15_P755056	-1.622	-0.698	3.36E-02
PROZ	A_15_P162991	2.030	1.022	3.30E-02
PRPF38A	A_15_P179246	-1.500	-0.585	1.95E-02
	A_15_P120917	-1.665	-0.735	2.88E-02
PRPF6	A_15_P183221	1.554	0.636	4.54E-02

PRPF8	A_15_P468270	3.819	1.933	2.55E-02
PRPSAP1	A_15_P624496	-1.548	-0.630	1.94E-02
PRRC2A	A_15_P278531	1.908	0.932	1.90E-02
PRRC2B	A_15_P472775	2.205	1.141	2.66E-03
PRRC2C	A_15_P192041	1.905	0.930	4.64E-02
PRRG1	A_15_P596527	2.683	1.424	3.52E-02
PRRX1	A_15_P104149	2.310	1.208	4.10E-02
PRSS23	A_15_P190841	-2.100	-1.071	6.07E-03
PRTFDC1	A_15_P196056	-1.787	-0.837	4.12E-02
	A_15_P417285	-2.125	-1.087	3.96E-02
PRUNE2	A_15_P541822	-1.606	-0.683	7.68E-03
PSENEN	A_15_P111406	-1.546	-0.629	2.57E-02
	A_15_P620901	-1.681	-0.750	4.16E-02
PSMB3	A_15_P104914	-1.522	-0.606	3.16E-02
PSMC3	A_15_P116353	-1.976	-0.983	4.64E-02
	A_15_P735346	-2.213	-1.146	3.11E-02
PSMC3IP	A_15_P603702	-2.357	-1.237	2.49E-02
	A_15_P222971	-1.538	-0.621	4.21E-02
PSMC6	A_15_P161001	-1.515	-0.599	1.76E-02
PSMD2	A_15_P451620	1.621	0.697	4.21E-02
PSMD7	A_15_P623716	-1.507	-0.591	2.27E-02
PSMD8	A_15_P108087	-1.549	-0.631	1.06E-02
PSME3	A_15_P536587	-1.565	-0.647	2.42E-02
	A_15_P408970	-1.508	-0.592	2.81E-03
PSMG2	A_15_P598447	-1.713	-0.776	2.76E-02
	A_15_P674051	-1.704	-0.769	1.79E-02
	A_15_P114500	-1.725	-0.787	8.20E-03
PTAR1	A_15_P110519	2.366	1.242	2.59E-02
PTBP1	A_15_P694741	-1.836	-0.876	4.59E-02
	A_15_P180241	-1.602	-0.680	3.75E-03
PTBP2	A_15_P691741	-1.535	-0.618	2.46E-02
PTGER4	A_15_P258601	-2.371	-1.246	7.06E-03
	A_15_P400790	4.065	2.023	1.98E-02
PTK2	A_15_P100452	1.796	0.845	3.06E-02
PTMA	A_15_P419522	-1.650	-0.723	8.26E-03
PTPN11	A_15_P110472	-1.513	-0.598	1.30E-02
PTPN13	A_15_P242811	-1.730	-0.791	2.33E-02
PTPRA	A_15_P101473	-1.674	-0.744	2.53E-02
PTPRB	A_15_P273376	1.675	0.745	3.51E-02
PTPRF	A_15_P749802	1.787	0.837	6.96E-03
	A_15_P404745	1.568	0.649	4.31E-02
	A_15_P534968	1.644	0.717	4.99E-02
	A_15_P660396	2.357	1.237	1.30E-02
PTPRK	A_15_P484770	1.673	0.742	1.57E-02
PTPRO	A_15_P747001	1.854	0.890	4.17E-02
	A_15_P650981	1.614	0.691	1.51E-02
PTPRZ1	A_15_P143586	-1.741	-0.800	1.85E-02
PTRHD1	A_15_P184161	-1.699	-0.765	2.93E-03
PUM1	A_15_P103730	1.523	0.607	6.90E-03
PUS7	A_15_P154861	2.517	1.332	2.06E-02
	A_15_P763276	2.124	1.087	4.17E-02
PXK	A_15_P600157	-1.512	-0.596	2.07E-02
PYROXD1	A_15_P504527	1.515	0.599	2.18E-02
QDPR	A_15_P185001	-1.861	-0.896	1.75E-02

QTRT1	A_15_P117054	-1.530	-0.614	2.94E-02
RAB11B	A_15_P398855	-1.823	-0.866	2.71E-02
RAB11FIP3	A_15_P139706	2.397	1.261	1.26E-02
RAB13	A_15_P417545	-1.580	-0.660	2.35E-02
	A_15_P163031	-1.833	-0.874	1.16E-02
	A_15_P119075	-2.079	-1.056	2.04E-02
RAB1B	A_15_P659531	-1.773	-0.827	4.55E-02
RAB24	A_15_P622311	-1.823	-0.866	2.56E-02
RAB30	A_15_P106643	-1.610	-0.687	2.59E-03
RAB36	A_15_P103940	-1.708	-0.772	3.51E-02
RAB3B	A_15_P138166	1.511	0.596	4.51E-02
RAB3GAP1	A_15_P687441	2.160	1.111	1.89E-02
RAB43	A_15_P580232	1.612	0.689	6.83E-03
RAB4B	A_15_P117624	-1.625	-0.700	3.11E-03
RAB5A	A_15_P753291	-1.598	-0.676	1.52E-02
RAB6A	A_15_P492277	-2.023	-1.016	1.07E-03
RAB8A	A_15_P625181	1.609	0.686	1.92E-02
RABL2B	A_15_P752731	-1.871	-0.904	3.96E-02
RABL3	A_15_P376375	-1.889	-0.917	3.46E-02
RAD51D	A_15_P100192	-1.706	-0.770	6.37E-03
	A_15_P149806	-1.702	-0.768	1.61E-03
RAD54L2	A_15_P566142	1.758	0.814	2.64E-02
RALA	A_15_P509027	-2.248	-1.169	6.49E-03
RAP1GAP	A_15_P102570	-1.722	-0.784	6.30E-03
RAPGEF1	A_15_P194731	1.522	0.606	2.71E-02
RASA4	A_15_P481320	-2.032	-1.023	3.90E-02
RASD1	A_15_P195831	-1.679	-0.747	2.40E-02
RASGRF2	A_15_P725351	-1.696	-0.763	2.42E-02
	A_15_P273758	-1.695	-0.761	3.56E-02
RASL10B	A_15_P145926	1.675	0.744	3.99E-02
RASL11A	A_15_P106629	1.636	0.710	3.79E-02
RASSF4	A_15_P197646	-1.957	-0.969	1.63E-02
RAVER2	A_15_P116882	1.901	0.927	4.25E-02
RBM12	A_15_P627081	-1.745	-0.803	3.31E-02
RBM14	A_15_P696956	2.292	1.197	4.00E-02
RBM15B	A_15_P273431	2.404	1.265	8.22E-03
RBM17	A_15_P101956	-1.803	-0.851	7.69E-03
	A_15_P645126	-1.686	-0.754	1.59E-02
RBM24	A_15_P284806	3.136	1.649	1.30E-02
RBM6	A_15_P109546	1.513	0.597	4.74E-02
RBMX2	A_15_P209521	-1.629	-0.704	1.79E-02
	A_15_P102501	-1.653	-0.725	9.69E-03
RBP7	A_15_P186046	4.252	2.088	4.81E-02
RDH14	A_15_P113472	-1.597	-0.675	3.81E-02
RDX	A_15_P436115	-1.977	-0.984	3.67E-02
	A_15_P133561	-1.734	-0.794	6.23E-03
RECQL	A_15_P104496	-2.038	-1.027	1.06E-02
RELL1	A_15_P144891	-1.504	-0.589	1.48E-02
RENBP	A_15_P148896	-2.315	-1.211	3.73E-02
REV3L	A_15_P221846	-2.325	-1.217	3.01E-04
RFWD2	A_15_P207316	-1.983	-0.988	9.93E-05
	A_15_P264861	-1.957	-0.969	4.10E-02
RFX1	A_15_P743086	1.507	0.592	1.90E-02
RFX7	A_15_P213286	2.200	1.138	4.86E-02

RGS16	A_15_P629676	-2.278	-1.188	2.87E-02
RGS7BP	A_15_P383215	-1.677	-0.746	4.95E-03
RHBDL1	A_15_P291271	1.523	0.606	3.47E-02
RHO	A_15_P111884	1.957	0.969	4.64E-02
RHOA	A_15_P542457	-1.553	-0.635	1.41E-02
RHOC	A_15_P133296	-1.762	-0.817	1.93E-02
RIBC1	A_15_P745806	-3.748	-1.906	9.36E-03
	A_15_P545547	-4.786	-2.259	3.64E-03
RILP	A_15_P287341	1.904	0.929	3.41E-02
RILPL2	A_15_P412351	-1.812	-0.857	3.67E-02
	A_15_P113419	-1.665	-0.736	3.69E-02
RIT1	A_15_P198426	-1.849	-0.887	1.53E-02
	A_15_P107332	-2.028	-1.020	1.41E-02
RLTPR	A_15_P167756	1.647	0.720	1.50E-02
RMI1	A_15_P207891	-1.738	-0.797	1.93E-02
	A_15_P627751	-1.830	-0.872	1.78E-02
RMI2	A_15_P477800	-1.758	-0.814	2.31E-02
RN7SK	A_15_P249301	1.844	0.883	1.14E-02
RNASEH1	A_15_P366805	-1.884	-0.914	7.78E-03
RNF141	A_15_P117363	-1.504	-0.589	2.53E-02
RNF150	A_15_P762171	-1.818	-0.862	3.51E-02
RNF175	A_15_P271786	-1.655	-0.727	3.38E-02
RNF2	A_15_P748921	2.000	1.000	2.93E-02
RNF212B	A_15_P498799	3.064	1.615	4.28E-03
RNF213	A_15_P216246	2.567	1.360	3.07E-02
RNF32	A_15_P663696	-1.681	-0.749	3.96E-02
ROBO3	A_15_P130586	1.987	0.991	7.32E-03
ROCK2	A_15_P677436	1.602	0.680	1.93E-02
RP2	A_15_P108294	-1.845	-0.884	4.05E-02
	A_15_P623736	-2.058	-1.042	2.78E-06
	A_15_P365640	-2.480	-1.310	3.57E-03
RPA1	A_15_P110325	-1.551	-0.634	1.98E-02
	A_15_P103944	-1.518	-0.603	6.30E-03
RPA2	A_15_P160886	-1.624	-0.700	4.22E-02
RPAP1	A_15_P297403	1.502	0.587	1.13E-02
RPL9	A_15_P440735	-1.532	-0.615	2.55E-02
RPLP0	A_15_P256271	-1.580	-0.659	4.78E-02
RPRML	A_15_P173141	-3.998	-1.999	4.77E-02
RPS16	A_15_P532942	-1.585	-0.665	3.18E-02
RPS23	A_15_P294871	-1.716	-0.779	5.46E-03
	A_15_P757301	-1.823	-0.866	3.69E-03
	A_15_P180326	-1.608	-0.685	3.39E-03
RPS26	A_15_P104858	-1.553	-0.635	8.30E-03
RPS6KA1	A_15_P658986	-1.623	-0.699	9.18E-04
RPUSD1	A_15_P170816	-2.326	-1.218	5.61E-03
RRAGC	A_15_P171466	-1.521	-0.605	2.91E-02
RRAS	A_15_P432420	-1.594	-0.673	3.27E-02
RREB1	A_15_P503972	-2.472	-1.306	1.92E-02
RRM2	A_15_P456255	-2.061	-1.044	2.17E-03
	A_15_P154211	-1.975	-0.982	1.95E-02
	A_15_P105192	-1.551	-0.634	3.98E-02
	A_15_P528597	-1.712	-0.776	1.73E-02
	A_15_P727796	-1.713	-0.776	2.29E-02
	A_15_P726552	-1.655	-0.727	2.68E-02

	A_15_P506957	-1.890	-0.919	2.00E-02
	A_15_P225316	-1.613	-0.690	3.58E-02
	A_15_P474705	-2.644	-1.403	1.25E-03
RSF1	A_15_P133686	-1.734	-0.794	8.77E-03
	A_15_P117577	-1.660	-0.731	3.98E-03
RSG1	A_15_P664876	-1.633	-0.708	3.67E-02
RTKN2	A_15_P134541	-3.226	-1.690	6.66E-04
RTN3	A_15_P119635	1.528	0.611	1.09E-02
RTN4R	A_15_P631726	-1.618	-0.695	3.57E-02
RTN4RL2	A_15_P620206	-2.680	-1.422	9.47E-03
	A_15_P103219	-5.270	-2.398	1.15E-02
RUNX2	A_15_P252826	-1.898	-0.925	6.11E-03
	A_15_P142811	1.784	0.835	1.07E-02
RUSC1	A_15_P121128	-1.506	-0.591	2.84E-02
RUSC2	A_15_P145946	1.909	0.933	1.53E-02
RYBP	A_15_P239201	-1.805	-0.852	9.33E-04
RYR2	A_15_P332454	2.155	1.108	2.82E-02
	A_15_P241066	2.847	1.509	2.21E-02
S100B	A_15_P100371	-1.744	-0.803	1.76E-02
	A_15_P100416	-1.852	-0.889	4.73E-02
SALL4	A_15_P512832	-2.634	-1.397	2.90E-02
SAMD12	A_15_P182941	2.634	1.397	2.40E-02
SAP130	A_15_P107163	-1.703	-0.768	2.48E-02
SAR1A	A_15_P100331	-1.787	-0.838	3.40E-02
SAT2	A_15_P153216	-1.521	-0.605	3.20E-02
SBK1	A_15_P157191	2.621	1.390	6.43E-03
SBNO1	A_15_P104943	1.754	0.811	3.83E-02
	A_15_P514902	2.967	1.569	7.74E-03
	A_15_P399740	1.694	0.760	4.64E-02
SC5D	A_15_P107141	-1.671	-0.741	4.10E-02
	A_15_P103953	-1.549	-0.631	1.41E-02
	A_15_P721231	-2.049	-1.035	1.56E-02
	A_15_P393020	-2.034	-1.024	2.85E-03
	A_15_P366960	-1.964	-0.974	1.28E-02
SCAMP2	A_15_P506417	-2.229	-1.156	4.79E-02
SCAMP4	A_15_P264546	-2.088	-1.062	4.52E-02
SCD	A_15_P104758	-1.663	-0.734	1.32E-02
	A_15_P607712	-1.932	-0.950	3.78E-03
SCGN	A_15_P106540	-2.422	-1.276	1.12E-03
SCUBE1	A_15_P159311	-1.735	-0.795	8.40E-03
SDCBP	A_15_P279771	-1.673	-0.742	4.03E-04
SDCCAG3	A_15_P265376	-1.509	-0.593	4.24E-02
SEC13	A_15_P152691	-1.516	-0.600	4.57E-03
SEC22A	A_15_P305701	-1.502	-0.587	4.93E-02
SEC24A	A_15_P181556	2.186	1.128	3.15E-02
SEC31A	A_15_P116778	1.797	0.845	2.68E-03
SEC61A1	A_15_P108417	-1.556	-0.638	1.98E-03
	A_15_P416760	1.595	0.674	3.40E-02
SEMA3A	A_15_P236951	-2.024	-1.017	4.90E-03
	A_15_P578347	-1.596	-0.674	4.24E-02
SEMA4A	A_15_P596442	-2.024	-1.017	3.11E-02
SEMA4C	A_15_P130691	2.084	1.059	1.59E-02
SEMA6A	A_15_P113425	1.996	0.997	7.92E-03
	A_15_P190066	2.167	1.116	4.64E-02

	A_15_P399235	2.620	1.390	1.14E-02
SEPN1	A_15_P627646	-1.645	-0.718	1.30E-02
	A_15_P413198	-1.675	-0.744	1.74E-03
	A_15_P175341	-1.668	-0.738	5.28E-03
SEPT12	A_15_P187421	-1.546	-0.628	1.20E-02
	A_15_P112715	-1.969	-0.978	2.13E-02
SERPINH1	A_15_P613477	-1.783	-0.835	6.43E-03
	A_15_P100880	2.594	1.375	3.52E-02
	A_15_P106877	2.882	1.527	3.50E-02
	A_15_P100253	2.168	1.117	4.25E-02
	A_15_P272571	3.693	1.885	1.71E-02
	A_15_P263671	2.436	1.284	4.61E-02
SETD1A	A_15_P231826	2.089	1.063	4.12E-02
SETD8	A_15_P179467	-2.025	-1.018	4.43E-02
SF1	A_15_P114375	-1.694	-0.760	2.38E-02
SF3B3	A_15_P240891	2.706	1.436	6.51E-03
SFRP1	A_15_P553022	-1.516	-0.600	3.11E-02
SGSH	A_15_P416555	-1.642	-0.716	5.19E-03
SH2D1A	A_15_P378150	-1.622	-0.697	2.90E-02
SH3BGRL	A_15_P682131	1.576	0.656	4.83E-02
SH3GLB1	A_15_P215021	-1.636	-0.710	3.17E-02
SH3GLB2	A_15_P151736	1.656	0.728	4.71E-02
SHC1	A_15_P406940	1.762	0.817	1.17E-02
	A_15_P516547	-1.718	-0.780	4.17E-02
SHCBP1	A_15_P151376	-2.087	-1.061	2.14E-02
SHH	A_15_P161816	-2.990	-1.580	3.19E-02
SHROOM2	A_15_P602652	-3.319	-1.731	1.06E-02
SIAE	A_15_P207946	-2.371	-1.246	4.52E-02
SKA1	A_15_P113521	-2.382	-1.252	6.60E-03
	A_15_P366560	-5.062	-2.340	2.70E-03
SKI	A_15_P111860	-1.548	-0.630	2.87E-02
SKOR1	A_15_P144411	-2.497	-1.320	4.68E-02
SLC11A2	A_15_P130351	1.690	0.757	1.95E-02
SLC12A5	A_15_P260386	1.828	0.871	2.70E-02
SLC12A9	A_15_P507387	1.741	0.800	2.09E-02
SLC16A9	A_15_P501012	-1.980	-0.986	2.96E-03
SLC17A5	A_15_P169006	-1.762	-0.817	4.21E-02
SLC17A6	A_15_P196506	-1.548	-0.630	1.39E-03
SLC18A2	A_15_P376755	-1.823	-0.866	4.29E-02
SLC22A13	A_15_P610982	-2.559	-1.356	3.38E-02
SLC22A4	A_15_P378055	1.678	0.747	4.31E-02
SLC25A12	A_15_P185186	1.847	0.885	2.13E-02
SLC25A13	A_15_P375255	-1.830	-0.872	8.17E-03
SLC25A14	A_15_P110932	1.628	0.703	4.00E-03
SLC25A17	A_15_P187261	-2.150	-1.104	5.48E-03
	A_15_P206976	-1.533	-0.616	3.34E-02
	A_15_P748976	-2.310	-1.208	1.55E-02
	A_15_P615747	-3.468	-1.794	9.26E-03
SLC25A24	A_15_P115592	-1.784	-0.835	1.58E-02
SLC25A37	A_15_P721551	1.780	0.832	1.38E-02
SLC25A4	A_15_P120885	7.449	2.897	3.88E-02
	A_15_P117984	7.651	2.936	4.57E-02
SLC25A48	A_15_P210836	-1.818	-0.863	3.31E-02
	A_15_P728101	-2.256	-1.174	3.37E-02

	A_15_P580217	-1.919	-0.940	3.38E-02
SLC26A1	A_15_P258291	-1.946	-0.961	5.03E-03
SLC27A1	A_15_P624066	-1.767	-0.822	3.01E-02
SLC27A2	A_15_P104073	-4.904	-2.294	1.80E-02
SLC27A4	A_15_P365295	-1.832	-0.874	3.46E-02
	A_15_P195796	-1.803	-0.850	1.10E-02
SLC29A1	A_15_P365795	1.664	0.734	3.34E-02
SLC29A2	A_15_P172706	-2.464	-1.301	3.08E-02
SLC29A4	A_15_P115594	-1.939	-0.956	3.01E-02
SLC2A10	A_15_P160156	-1.775	-0.827	3.29E-02
SLC30A9	A_15_P119060	-1.613	-0.689	2.30E-02
SLC35B4	A_15_P105841	-1.736	-0.795	4.21E-02
SLC35E3	A_15_P104408	-3.102	-1.633	9.75E-03
SLC35F2	A_15_P492922	-1.767	-0.821	3.09E-02
SLC38A4	A_15_P316916	-2.687	-1.426	2.52E-02
	A_15_P699556	-2.252	-1.171	2.96E-02
SLC38A5	A_15_P393205	-1.752	-0.809	4.70E-02
SLC39A10	A_15_P118323	-1.588	-0.667	1.62E-02
SLC3A2	A_15_P107639	-1.518	-0.602	2.61E-02
SLC46A3	A_15_P551062	-2.228	-1.156	6.68E-03
	A_15_P492092	1.705	0.770	1.75E-02
SLC4A4	A_15_P104924	-1.843	-0.882	2.16E-02
SLC5A6	A_15_P171546	1.784	0.835	1.02E-02
SLC6A19	A_15_P140526	-1.920	-0.941	3.31E-02
SLC6A3	A_15_P668576	2.278	1.188	2.17E-02
	A_15_P284396	1.776	0.828	4.08E-02
SLC6A9	A_15_P418868	-2.137	-1.095	3.51E-02
SLC7A10	A_15_P546612	-2.423	-1.277	3.69E-02
SLC8A1	A_15_P570817	1.815	0.860	1.50E-02
SLC8A2	A_15_P168606	1.969	0.978	1.22E-02
SLF2	A_15_P389910	-1.918	-0.940	1.03E-02
SLTM	A_15_P510672	1.522	0.606	2.82E-02
SLU7	A_15_P227181	-1.586	-0.666	4.92E-02
SMAD6	A_15_P528902	1.741	0.800	1.49E-02
	A_15_P721506	-1.579	-0.659	1.88E-04
	A_15_P164461	-1.557	-0.639	4.12E-03
SMARCAD1	A_15_P189631	-1.532	-0.616	2.41E-02
SMARCD3	A_15_P320161	-1.734	-0.794	3.43E-02
SMARCE1	A_15_P514912	1.734	0.794	4.80E-03
	A_15_P620696	1.887	0.916	1.94E-02
SMC1A	A_15_P338870	-1.756	-0.812	6.27E-03
SMC4	A_15_P133426	-2.584	-1.369	3.04E-02
SMCR8	A_15_P622466	-2.156	-1.109	9.21E-03
SMG7	A_15_P655566	1.846	0.884	4.16E-02
SMOX	A_15_P620661	-2.188	-1.130	5.04E-03
	A_15_P114049	-2.550	-1.351	9.91E-04
SMTN	A_15_P412955	-1.596	-0.674	4.58E-02
SMUG1	A_15_P160116	-2.009	-1.006	9.08E-03
SMYD1	A_15_P163436	7.715	2.948	4.81E-02
	A_15_P131246	5.347	2.419	4.16E-02
SNN	A_15_P115971	-1.633	-0.707	3.11E-02
	A_15_P101034	-1.671	-0.741	1.13E-02
SNRNP200	A_15_P730906	1.569	0.650	1.43E-02
SNRPC	A_15_P115796	-1.670	-0.740	8.85E-04

SNTB1	A_15_P416840	-1.576	-0.657	7.29E-03
SNW1	A_15_P628786	-1.593	-0.672	2.01E-02
SNX13	A_15_P548862	-1.572	-0.653	7.24E-03
SNX17	A_15_P225261	-1.585	-0.664	1.92E-03
SNX5	A_15_P660101	-1.577	-0.657	2.72E-02
SNX9	A_15_P622136	1.524	0.608	3.74E-02
SOCS3	A_15_P119415	-4.981	-2.317	3.78E-03
SOCS5	A_15_P625177	2.545	1.348	1.79E-03
SOCS7	A_15_P469000	1.644	0.717	7.34E-03
SOD1	A_15_P485200	-7.054	-2.818	1.30E-02
SOD3	A_15_P116958	-1.986	-0.990	1.11E-02
SOGA1	A_15_P437655	2.891	1.532	3.54E-02
SOGA3	A_15_P391680	-1.527	-0.611	2.75E-02
SORL1	A_15_P281646	1.590	0.669	2.86E-02
SOS1	A_15_P470220	2.397	1.261	2.08E-02
SOSTDC1	A_15_P108972	-2.531	-1.340	4.35E-02
SOX11	A_15_P131486	-1.978	-0.984	5.24E-03
SP8	A_15_P104390	-1.941	-0.957	1.60E-02
SPAG17	A_15_P258656	-4.527	-2.179	4.81E-03
SPAG9	A_15_P178796	2.414	1.272	1.20E-02
SPARCL1	A_15_P276001	-2.154	-1.107	2.83E-03
	A_15_P115365	-1.934	-0.951	4.63E-02
SPATA20	A_15_P226416	1.736	0.795	1.78E-02
SPATA5L1	A_15_P271486	1.508	0.593	2.70E-02
SPC25	A_15_P491707	-2.438	-1.285	3.36E-02
SPCS2	A_15_P690216	-1.857	-0.893	6.40E-05
	A_15_P587202	-2.201	-1.138	5.65E-03
SPDL1	A_15_P662261	-1.840	-0.879	4.03E-02
SPEF2	A_15_P134601	2.146	1.102	3.53E-02
SPEG	A_15_P112814	-1.738	-0.797	3.21E-02
	A_15_P161022	-1.733	-0.793	1.43E-02
SPG11	A_15_P371520	3.001	1.585	1.42E-02
SPHK1	A_15_P758941	2.083	1.059	2.20E-02
SPHK2	A_15_P416740	-1.874	-0.906	1.40E-02
SPHKAP	A_15_P168811	2.353	1.234	3.20E-03
SPICE1	A_15_P172431	-1.699	-0.764	4.40E-02
SPNS2	A_15_P520707	-1.619	-0.695	4.69E-02
SPOCK3	A_15_P100348	-1.717	-0.780	1.82E-03
SPP1	A_15_P629241	4.987	2.318	1.98E-02
	A_15_P109228	6.706	2.745	6.96E-03
SPRED2	A_15_P196971	1.596	0.675	1.23E-02
SPRYD3	A_15_P307241	-1.667	-0.737	1.95E-02
SPTBN2	A_15_P469535	2.275	1.186	3.20E-02
SPTLC1	A_15_P109984	-1.785	-0.836	4.79E-03
SQLE	A_15_P630396	-3.128	-1.645	1.89E-02
	A_15_P487460	-2.695	-1.430	1.43E-02
SRC	A_15_P594102	1.666	0.736	4.35E-03
SREBF2	A_15_P402025	1.695	0.761	4.53E-04
SRF	A_15_P602277	-1.551	-0.633	2.25E-02
SRP72	A_15_P155756	-1.541	-0.624	1.42E-02
SRP9	A_15_P114245	-1.512	-0.596	1.56E-02
SRR	A_15_P356910	-1.670	-0.740	3.99E-02
SRSF5	A_15_P726411	2.066	1.047	3.35E-02
SRSF9	A_15_P725956	-1.657	-0.729	1.99E-02

SS18L2	A_15_P108302	-1.747	-0.805	3.71E-02
	A_15_P288456	-1.667	-0.737	3.02E-02
SSH2	A_15_P276586	1.705	0.769	3.73E-02
SSR3	A_15_P608607	-1.804	-0.851	1.53E-02
	A_15_P766691	-1.628	-0.703	1.05E-03
SSRP1	A_15_P188651	-1.872	-0.905	6.12E-03
	A_15_P296976	-1.751	-0.808	4.64E-02
	A_15_P163651	-2.095	-1.067	2.83E-02
ST3GAL2	A_15_P116325	1.772	0.826	1.40E-02
ST6GAL1	A_15_P102648	-1.885	-0.915	3.22E-02
ST6GALNAC1	A_15_P207416	-5.029	-2.330	1.49E-02
ST7	A_15_P622941	1.672	0.742	4.22E-02
ST8SIA2	A_15_P148106	-1.603	-0.681	4.79E-02
ST8SIA4	A_15_P195466	1.514	0.598	4.36E-02
STAC3	A_15_P720456	23.335	4.544	3.39E-02
	A_15_P365985	21.560	4.430	4.99E-02
STAMBP	A_15_P121238	-1.688	-0.756	1.88E-03
STAU2	A_15_P415315	1.655	0.727	1.98E-02
STC2	A_15_P114719	-1.607	-0.685	2.62E-02
	A_15_P420940	-1.646	-0.719	3.85E-02
STIL	A_15_P622106	-3.436	-1.781	1.09E-02
STK3	A_15_P658946	1.748	0.806	1.56E-02
STK35	A_15_P744761	1.897	0.924	1.97E-02
	A_15_P323122	1.848	0.886	2.92E-02
STK39	A_15_P674141	-1.808	-0.854	1.39E-03
	A_15_P748576	-1.806	-0.853	3.34E-03
STMN3	A_15_P376180	-1.589	-0.668	4.94E-02
STOX1	A_15_P178156	-1.711	-0.775	4.77E-02
	A_15_P197251	-1.726	-0.788	2.31E-03
STX16	A_15_P528227	-1.863	-0.898	1.43E-02
STX17	A_15_P113647	-2.690	-1.427	1.33E-02
STX2	A_15_P120230	3.203	1.679	3.79E-02
STX5	A_15_P100808	-1.684	-0.752	3.29E-02
SULT2B1	A_15_P192746	-2.180	-1.124	6.43E-03
SUMF1	A_15_P107748	-1.701	-0.766	1.14E-02
SUMO3	A_15_P565462	-1.835	-0.876	4.24E-02
	A_15_P276871	-1.520	-0.604	2.68E-02
SUPT4H1	A_15_P110968	-2.050	-1.036	4.36E-02
SUZ12	A_15_P106104	-2.364	-1.241	1.17E-02
SVOP	A_15_P146006	1.689	0.757	8.06E-03
SYN1	A_15_P565967	1.793	0.842	1.79E-02
SYNE1	A_15_P202536	1.818	0.862	1.55E-02
SYNGAP1	A_15_P204881	1.650	0.723	4.80E-02
SYNGR3	A_15_P622531	-3.587	-1.843	4.28E-02
	A_15_P195991	-3.343	-1.741	4.08E-02
SYT1	A_15_P153151	-3.409	-1.769	1.84E-02
SYT7	A_15_P136141	2.137	1.095	2.75E-02
TACR2	A_15_P268616	-2.084	-1.059	1.33E-02
TACR3	A_15_P498067	-1.738	-0.798	1.06E-02
TADA1	A_15_P498337	1.981	0.986	3.58E-02
TADA2B	A_15_P659996	1.570	0.651	2.75E-02
TAF1A	A_15_P192676	-1.741	-0.800	1.33E-02
TAF3	A_15_P118156	-1.582	-0.662	3.17E-02
	A_15_P177306	-1.817	-0.862	7.02E-03

TAF6	A_15_P176536	-1.802	-0.849	3.86E-02
TAGLN3	A_15_P147731	1.707	0.771	3.56E-02
TANC2	A_15_P307226	2.242	1.165	5.86E-03
TANGO6	A_15_P599902	-1.598	-0.677	2.44E-02
TAOK1	A_15_P270501	-1.717	-0.780	2.69E-03
TAOK2	A_15_P442365	3.282	1.715	4.18E-02
TAPT1	A_15_P200291	-1.624	-0.699	1.03E-02
TARBP1	A_15_P269016	-1.509	-0.593	2.54E-02
TBC1D22A	A_15_P411165	-1.628	-0.703	2.10E-02
TBC1D24	A_15_P460040	1.741	0.800	2.17E-02
TBC1D5	A_15_P182206	-2.137	-1.096	5.11E-03
TBRG4	A_15_P484145	-1.655	-0.727	2.88E-02
TBX4	A_15_P115999	-2.101	-1.071	4.90E-02
TC2N	A_15_P197731	1.728	0.789	3.45E-02
TCEANC	A_15_P111935	-1.862	-0.897	1.09E-02
	A_15_P219546	-2.108	-1.076	4.36E-02
TCEB2	A_15_P107497	-1.607	-0.684	4.40E-02
TCF15	A_15_P101438	-2.167	-1.115	3.61E-02
TCF19	A_15_P392535	1.690	0.757	2.09E-02
TCF20	A_15_P476095	1.769	0.823	1.16E-02
	A_15_P119813	1.911	0.934	1.59E-02
TCF25	A_15_P483330	-1.609	-0.686	1.45E-02
	A_15_P746586	-1.563	-0.645	2.29E-02
TCHP	A_15_P101051	-1.610	-0.687	2.23E-02
TDG	A_15_P687141	-3.637	-1.863	2.37E-02
	A_15_P107219	-2.432	-1.282	3.48E-02
TDRD6	A_15_P221556	-1.925	-0.945	6.96E-03
TECPR2	A_15_P483420	1.857	0.893	8.41E-03
TECTA	A_15_P147536	2.342	1.227	4.17E-02
TEF	A_15_P108054	-1.987	-0.990	2.32E-02
	A_15_P200906	2.321	1.215	3.91E-02
TEP1	A_15_P337517	-1.567	-0.648	6.47E-03
TES	A_15_P666661	-1.586	-0.665	2.93E-02
TESC	A_15_P146446	-1.722	-0.784	4.53E-02
TEX9	A_15_P103365	-1.664	-0.734	1.75E-02
TFDP1	A_15_P112675	1.638	0.712	4.15E-02
TFPI	A_15_P721811	1.588	0.667	1.95E-02
TGFB3	A_15_P400260	1.893	0.920	4.57E-02
TGM1	A_15_P137266	-2.030	-1.022	4.20E-02
	A_15_P472140	-1.741	-0.800	1.03E-02
TGM2	A_15_P193006	-1.842	-0.881	3.30E-02
THAP3	A_15_P666378	-1.648	-0.720	2.39E-02
	A_15_P209756	-1.799	-0.848	4.48E-02
	A_15_P661191	-1.682	-0.750	1.45E-02
	A_15_P212828	-1.918	-0.940	3.22E-02
THBS2	A_15_P157666	3.741	1.903	2.24E-02
THG1L	A_15_P629856	-1.736	-0.796	8.94E-03
TIAL1	A_15_P323556	-1.502	-0.587	3.30E-02
TIFA	A_15_P115435	-2.298	-1.201	3.50E-02
TIMELESS	A_15_P105092	1.626	0.702	3.87E-02
TIMP2	A_15_P223056	-2.282	-1.190	4.72E-02
TIPARP	A_15_P169141	-2.817	-1.494	7.11E-03
TIRAP	A_15_P155851	-1.505	-0.590	1.65E-02
TKFC	A_15_P484065	1.818	0.863	3.13E-02

TLK1	A_15_P115908	-1.876	-0.908	1.81E-02
TLN2	A_15_P110141	-1.658	-0.729	3.72E-02
TLX1	A_15_P625936	-2.198	-1.136	4.00E-02
	A_15_P116281	-4.317	-2.110	3.02E-02
TM7SF2	A_15_P503017	-1.640	-0.713	1.60E-02
TM7SF3	A_15_P682601	-1.806	-0.853	3.70E-02
TM9SF1	A_15_P444365	-1.572	-0.652	2.50E-03
TMA16	A_15_P657798	-2.448	-1.291	4.23E-03
TMC4	A_15_P420700	3.615	1.854	4.79E-02
TMCO4	A_15_P672071	-1.547	-0.629	3.69E-02
	A_15_P265846	-1.544	-0.626	2.30E-02
TMED1	A_15_P100524	-1.878	-0.909	4.08E-02
TMED9	A_15_P172341	-1.881	-0.912	2.11E-02
TMEFF1	A_15_P108134	-1.590	-0.669	9.69E-04
	A_15_P574947	2.433	1.283	4.89E-03
	A_15_P134031	-1.942	-0.958	1.72E-03
TMEM104	A_15_P187166	-2.066	-1.047	1.04E-03
TMEM106B	A_15_P171186	-1.627	-0.703	2.21E-02
	A_15_P511987	-2.301	-1.203	2.68E-02
TMEM117	A_15_P286546	3.828	1.937	1.11E-02
TMEM125	A_15_P646976	-2.643	-1.402	2.00E-02
TMEM144	A_15_P151771	-1.947	-0.961	2.11E-02
TMEM168	A_15_P142446	3.191	1.674	3.59E-02
TMEM184C	A_15_P471450	1.581	0.660	2.19E-02
TMEM189	A_15_P109516	-1.718	-0.781	4.62E-02
TMEM235	A_15_P760396	-1.961	-0.971	1.32E-02
TMEM241	A_15_P587597	-2.203	-1.140	4.94E-02
TMEM37	A_15_P620396	-2.517	-1.332	4.04E-02
	A_15_P118238	-1.571	-0.652	2.15E-02
TMEM47	A_15_P277516	-2.325	-1.217	4.40E-02
TMEM57	A_15_P118660	-1.750	-0.808	4.86E-03
	A_15_P105470	-1.512	-0.597	1.08E-02
TMEM65	A_15_P565472	-2.030	-1.021	1.38E-02
TMOD4	A_15_P104093	-2.018	-1.013	2.77E-02
TMPO	A_15_P164056	-1.569	-0.650	2.43E-02
TMPRSS2	A_15_P108948	2.151	1.105	2.04E-02
TMTC2	A_15_P108150	-2.363	-1.240	1.17E-03
TMX2	A_15_P591182	-2.033	-1.024	4.48E-03
	A_15_P279946	-2.478	-1.309	3.76E-04
TNFAIP2	A_15_P566692	3.738	1.902	4.72E-02
TNFRSF21	A_15_P150341	-2.235	-1.160	1.47E-02
TNK1	A_15_P112196	-2.009	-1.006	3.80E-04
TNN	A_15_P731941	2.267	1.181	1.04E-02
TNNI2	A_15_P664046	16.387	4.034	3.49E-02
	A_15_P152786	11.273	3.495	3.10E-02
	A_15_P705891	13.580	3.763	2.53E-02
	A_15_P211721	19.343	4.274	3.16E-02
	A_15_P107319	14.402	3.848	4.38E-02
TNNT3	A_15_P743431	17.900	4.162	3.83E-02
	A_15_P111239	14.958	3.903	4.32E-02
	A_15_P118218	16.504	4.045	3.81E-02
	A_15_P115653	14.059	3.813	4.82E-02
	A_15_P724331	12.662	3.662	4.69E-02
TNRC6B	A_15_P421665	1.796	0.845	2.51E-02

TNS1	A_15_P105613	-1.509	-0.594	4.68E-02
TOM1	A_15_P114356	-1.686	-0.753	2.12E-03
TOMM22	A_15_P267756	-1.659	-0.731	3.67E-02
TOX	A_15_P108305	-1.586	-0.666	1.11E-02
	A_15_P530522	-1.696	-0.762	2.98E-02
TP53BP2	A_15_P580032	2.523	1.335	4.65E-02
TPD52L1	A_15_P659506	-2.014	-1.010	3.25E-02
TPD52L2	A_15_P745156	-1.795	-0.844	2.37E-02
TPM3	A_15_P727816	-1.790	-0.840	9.04E-03
	A_15_P578902	-1.801	-0.849	6.24E-03
TPP1	A_15_P744681	-1.770	-0.824	8.43E-04
TPR	A_15_P435380	2.401	1.264	4.31E-02
TPRKB	A_15_P110075	-1.655	-0.727	3.77E-02
TPX2	A_15_P471255	-3.115	-1.639	2.95E-03
TRAF6	A_15_P739941	1.835	0.876	7.19E-03
TRAF7	A_15_P630851	2.812	1.492	1.48E-03
	A_15_P143396	1.749	0.807	1.60E-02
	A_15_P529927	-2.271	-1.183	4.45E-02
TRIM32	A_15_P429585	2.304	1.204	3.97E-02
TRIM46	A_15_P204361	1.639	0.713	3.53E-02
TRIM54	A_15_P184551	4.206	2.072	4.18E-02
TRIM67	A_15_P155811	1.522	0.606	3.27E-02
TRIM8	A_15_P562942	1.571	0.652	4.34E-02
TRIO	A_15_P119874	1.912	0.935	1.11E-02
	A_15_P576982	1.811	0.857	3.02E-02
TRIOBP	A_15_P542497	-1.731	-0.791	6.43E-03
TRMT12	A_15_P174256	-1.741	-0.800	2.53E-03
TRMT5	A_15_P102338	-1.527	-0.611	4.87E-02
TRPA1	A_15_P161306	-1.927	-0.947	4.03E-02
TRPC4	A_15_P287606	-1.603	-0.681	4.56E-02
TRPC6	A_15_P445185	-2.754	-1.462	1.22E-02
TRPM7	A_15_P514522	1.666	0.736	1.56E-02
TRPS1	A_15_P597992	2.817	1.494	7.83E-03
TRPT1	A_15_P693526	1.661	0.732	2.49E-02
TSEN15	A_15_P765181	-1.758	-0.814	3.12E-02
TSFM	A_15_P749776	-1.806	-0.853	2.05E-02
	A_15_P149386	-1.688	-0.756	1.84E-02
TSHZ1	A_15_P372065	-1.845	-0.884	1.24E-02
TSNAXIP1	A_15_P174291	-1.731	-0.792	2.79E-02
TSPAN14	A_15_P118916	-2.002	-1.001	4.01E-02
TSPAN3	A_15_P176091	-1.526	-0.610	2.20E-02
TSPAN4	A_15_P148056	1.701	0.767	4.70E-02
TSPAN9	A_15_P104765	-1.727	-0.788	4.35E-02
	A_15_P106616	-13.264	-3.729	2.61E-02
TSTA3	A_15_P185032	1.786	0.837	3.24E-02
TTBK1	A_15_P179926	1.510	0.594	1.38E-02
	A_15_P202936	1.832	0.874	3.03E-02
TTC12	A_15_P103573	-1.621	-0.697	2.04E-03
TTC25	A_15_P416880	1.602	0.679	2.44E-02
TTC37	A_15_P295556	1.863	0.897	2.30E-02
TTC4	A_15_P365665	-1.529	-0.613	3.17E-02
TTC9C	A_15_P119332	-1.509	-0.594	2.80E-02
	A_15_P367385	-2.234	-1.160	1.16E-02
TTF1	A_15_P490122	-2.201	-1.138	1.53E-03

	A_15_P550547	-1.667	-0.737	3.67E-02
TTK	A_15_P210251	-1.594	-0.672	3.08E-02
TTN	A_15_P675376	13.210	3.724	4.36E-02
	A_15_P101261	3.755	1.909	4.73E-02
	A_15_P468525	18.800	4.233	2.91E-02
	A_15_P515472	19.855	4.311	4.22E-02
	A_15_P370250	13.499	3.755	4.34E-02
	A_15_P572077	6.730	2.751	3.46E-02
TTYH2	A_15_P106557	-1.682	-0.751	1.26E-02
TTYH3	A_15_P456005	-1.618	-0.694	9.99E-03
	A_15_P116086	-1.555	-0.637	2.69E-04
	A_15_P407240	-1.975	-0.982	9.79E-03
TWF1	A_15_P658836	-1.724	-0.786	4.69E-03
TWSG1	A_15_P107282	1.959	0.970	3.25E-02
	A_15_P594462	1.845	0.883	1.03E-02
TXNDC5	A_15_P226781	2.576	1.365	4.05E-02
	A_15_P722521	-1.631	-0.706	4.07E-02
TXNL4A	A_15_P116293	-1.517	-0.601	2.88E-02
TYMS	A_15_P119814	-1.928	-0.947	3.47E-02
TYRP1	A_15_P110475	2.014	1.010	5.63E-03
U2AF2	A_15_P753221	-1.607	-0.684	8.52E-03
	A_15_P151521	-1.745	-0.803	1.30E-02
	A_15_P603532	-1.973	-0.981	4.88E-02
UBA1	A_15_P726916	-1.618	-0.694	1.43E-02
UBA2	A_15_P100346	-1.508	-0.593	1.63E-02
	A_15_P515234	-1.540	-0.623	4.15E-02
UBA52	A_15_P295646	-1.644	-0.717	4.43E-02
UBE2B	A_15_P552577	1.563	0.644	2.08E-02
UBE2C	A_15_P723801	-1.960	-0.971	4.57E-02
UBE2E2	A_15_P412420	-1.513	-0.598	2.03E-02
UBE2G1	A_15_P104448	-1.553	-0.635	3.91E-03
UBE2I	A_15_P470595	-1.559	-0.641	3.86E-02
UBE2T	A_15_P205326	-1.625	-0.700	4.69E-03
UBE2V2	A_15_P111834	-2.039	-1.028	1.31E-02
UBE2Z	A_15_P112895	-1.923	-0.944	4.55E-02
UBE3C	A_15_P115490	-1.565	-0.646	1.17E-02
UBFD1	A_15_P110415	-1.532	-0.615	4.00E-02
UBP1	A_15_P182876	1.879	0.910	3.09E-02
	A_15_P629806	1.809	0.855	1.15E-02
UBR5	A_15_P595107	1.917	0.939	4.85E-02
UBTD1	A_15_P193091	-1.724	-0.786	4.90E-02
	A_15_P376390	-1.718	-0.781	3.02E-02
UBXN1	A_15_P721296	-1.848	-0.886	1.16E-02
	A_15_P367035	-1.775	-0.828	4.21E-03
UBXN10	A_15_P379610	-1.846	-0.885	3.89E-02
	A_15_P730591	-2.130	-1.091	6.54E-03
	A_15_P751306	-1.924	-0.944	6.09E-03
	A_15_P542007	-2.536	-1.343	7.33E-03
UCHL5	A_15_P235116	-1.504	-0.589	2.95E-02
UCK1	A_15_P602647	-1.584	-0.663	2.27E-02
UFM1	A_15_P531127	-1.506	-0.590	1.10E-02
UGGT1	A_15_P707286	2.971	1.571	1.55E-02
UGT1A1	A_15_P161031	-2.314	-1.210	4.52E-02
	A_15_P622316	-2.332	-1.221	6.87E-03

UHRF1	A_15_P304326	-1.595	-0.673	3.50E-02
ULK3	A_15_P495267	2.154	1.107	3.12E-02
UNC13B	A_15_P339425	-3.199	-1.678	1.55E-03
UNC13C	A_15_P310976	1.544	0.627	4.31E-02
UNC5A	A_15_P626166	1.507	0.592	7.23E-03
UPB1	A_15_P108369	-1.737	-0.797	2.36E-02
UPF1	A_15_P199676	1.524	0.608	4.84E-02
UPF3B	A_15_P120021	-2.062	-1.044	1.67E-02
UQCRB	A_15_P110872	-1.511	-0.595	2.60E-02
URAD	A_15_P142611	-1.759	-0.815	1.82E-02
USF1	A_15_P108770	-1.522	-0.606	4.55E-02
USP3	A_15_P136876	-1.689	-0.756	1.24E-03
USP44	A_15_P237076	-1.917	-0.939	2.97E-02
USP8	A_15_P283001	2.449	1.292	1.75E-02
UTS2R	A_15_P166831	-1.500	-0.585	9.09E-03
VEGFA	A_15_P147821	-1.593	-0.672	6.32E-03
VEZF1	A_15_P515907	1.845	0.883	2.94E-02
VGF	A_15_P344575	-1.505	-0.590	9.53E-03
VGLL2	A_15_P329691	-2.378	-1.250	2.18E-02
VPS8	A_15_P200601	1.540	0.623	2.29E-02
VSIG10	A_15_P419170	-1.780	-0.832	3.33E-03
VTA1	A_15_P504407	-1.642	-0.715	2.83E-02
VTI1B	A_15_P285236	-1.706	-0.771	4.81E-02
VWA5B1	A_15_P489262	1.659	0.730	8.61E-03
WDFY4	A_15_P375075	2.126	1.088	2.07E-02
WDHD1	A_15_P102190	-1.524	-0.608	2.59E-02
	A_15_P668351	-1.515	-0.599	1.40E-02
WDR37	A_15_P120560	-1.752	-0.809	2.71E-02
WDR45B	A_15_P153846	1.642	0.715	2.29E-02
WDR61	A_15_P446230	-2.287	-1.193	1.96E-02
	A_15_P114376	-1.561	-0.642	3.15E-03
WDR73	A_15_P661516	-1.506	-0.590	9.20E-03
WEE1	A_15_P106410	-1.741	-0.800	4.41E-02
WHSC1	A_15_P656956	-1.629	-0.704	6.72E-03
	A_15_P197111	-1.850	-0.887	1.33E-03
XDH	A_15_P247121	-3.700	-1.888	2.91E-02
XKR4	A_15_P169501	1.657	0.729	3.97E-02
XKR7	A_15_P205286	1.747	0.805	3.28E-02
XPC	A_15_P134231	-1.821	-0.865	4.12E-02
XPO7	A_15_P491962	1.544	0.626	2.36E-03
XRN1	A_15_P732846	-1.533	-0.616	3.41E-02
YAE1D1	A_15_P660711	-1.819	-0.863	4.87E-02
	A_15_P119359	-1.530	-0.614	3.78E-02
YAP1	A_15_P673471	-1.728	-0.789	4.71E-02
	A_15_P117829	-1.816	-0.861	2.12E-02
YBX1	A_15_P114925	-1.502	-0.587	1.27E-02
	A_15_P338810	-1.520	-0.605	3.28E-02
YEATS4	A_15_P367295	-1.742	-0.801	2.26E-02
	A_15_P721516	-1.722	-0.784	2.65E-02
YES1	A_15_P107924	-1.502	-0.587	7.73E-03
YLPM1	A_15_P101184	1.699	0.764	4.17E-02
ZAK	A_15_P114694	1.519	0.603	4.45E-02
ZBED4	A_15_P152751	-1.999	-1.000	4.57E-02
ZC3H10	A_15_P302831	1.695	0.761	5.44E-04

ZC3H18	A_15_P730526	-1.734	-0.794	1.53E-02
	A_15_P541772	-1.802	-0.850	2.31E-02
	A_15_P178211	-2.206	-1.141	1.06E-02
ZC3H4	A_15_P510572	1.579	0.659	1.50E-02
ZC4H2	A_15_P720496	-1.562	-0.643	4.14E-02
ZCCHC24	A_15_P118593	-1.546	-0.629	4.43E-02
	A_15_P432695	-2.539	-1.344	3.69E-03
ZCCHC7	A_15_P118571	-1.959	-0.970	1.72E-03
	A_15_P106053	-2.180	-1.124	2.80E-03
	A_15_P200266	-1.622	-0.698	3.60E-02
	A_15_P200261	-1.884	-0.914	1.74E-02
ZCRB1	A_15_P109294	-1.701	-0.766	1.47E-02
ZDHHC1	A_15_P730566	-1.539	-0.622	3.11E-02
ZDHHC18	A_15_P152381	-1.842	-0.882	5.26E-03
ZDHHC20	A_15_P557222	-2.013	-1.009	2.32E-04
	A_15_P507347	-2.225	-1.153	5.63E-03
	A_15_P158181	-2.466	-1.302	7.21E-03
	A_15_P509062	-2.043	-1.030	4.42E-02
ZDHHC9	A_15_P450735	-1.760	-0.816	1.92E-02
ZER1	A_15_P668116	2.744	1.456	4.90E-03
ZFAND6	A_15_P366290	-1.784	-0.835	3.68E-02
ZFP91	A_15_P498017	1.769	0.823	4.80E-03
ZFPM1	A_15_P627011	2.203	1.140	3.38E-02
ZHX2	A_15_P118662	-1.744	-0.802	7.10E-04
	A_15_P204451	-1.758	-0.814	1.96E-02
ZMPSTE24	A_15_P101841	-1.640	-0.714	2.64E-02
	A_15_P629076	-1.561	-0.643	3.64E-02
ZMYND8	A_15_P406770	-1.603	-0.680	1.12E-02
ZNF148	A_15_P346725	-1.603	-0.681	4.48E-02
ZNF362	A_15_P495962	2.421	1.276	3.34E-02
ZNF423	A_15_P346140	1.870	0.903	3.72E-02
ZNF507	A_15_P117201	-1.693	-0.760	1.95E-02
ZNF646	A_15_P103453	1.914	0.937	4.04E-02
ZNF654	A_15_P598967	-1.715	-0.778	2.52E-02
ZNF687	A_15_P246981	-2.017	-1.012	3.37E-02
ZNF704	A_15_P110629	1.632	0.707	1.87E-02
ZNF710	A_15_P392650	-1.633	-0.707	5.96E-03
ZNF729	A_15_P161866	-1.663	-0.734	3.96E-02
	A_15_P636266	3.453	1.788	4.23E-02
	A_15_P270036	2.155	1.107	3.05E-02
	A_15_P772346	-2.791	-1.481	9.41E-03
	A_15_P726301	-1.501	-0.586	4.47E-02
	A_15_P677186	2.544	1.347	1.35E-02
	A_15_P620811	-1.649	-0.721	4.52E-02
	A_15_P663806	-1.822	-0.866	4.86E-02
	A_15_P762671	3.854	1.946	8.50E-03
	A_15_P546157	-1.573	-0.653	2.33E-02
	A_15_P171626	1.574	0.654	4.87E-02
	A_15_P623046	1.950	0.964	4.88E-02
	A_15_P400205	-1.559	-0.640	8.65E-03
	A_15_P546097	-1.632	-0.707	1.22E-02
	A_15_P137801	-1.736	-0.796	1.70E-03
	A_15_P759146	2.620	1.390	7.30E-03
	A_15_P613417	1.689	0.756	4.90E-02

	A_15_P764441	-2.103	-1.072	4.80E-02
	A_15_P242936	-1.501	-0.586	3.69E-02
	A_15_P356940	2.016	1.012	4.83E-03
	A_15_P554127	-2.084	-1.059	2.87E-03
ZNF770	A_15_P374565	-1.961	-0.972	2.34E-02
	A_15_P575117	-1.944	-0.959	2.21E-02
	A_15_P576742	-1.524	-0.608	4.22E-02
	A_15_P221356	-2.874	-1.523	1.04E-02
ZNHIT6	A_15_P450475	-2.103	-1.073	3.85E-02
ZNRF2	A_15_P644531	-1.558	-0.639	1.86E-02
	A_15_P520837	-1.614	-0.690	1.36E-02

Supplementary Information Table 2. Annotated genes altered in aged adult male zebrafish brain exposed to 10 µg/L Pb during embryogenesis.

Symbol	Probe ID	Expression Fold Change	Log_2 Expression Ratio	p-Value
A2M	A_15_P733733	-1.913	-0.936	4.85E-02
AAAS	A_15_P720526	1.542	0.625	1.82E-02
AAED1	A_15_P297371	-2.128	-1.089	1.50E-02
AAMP	A_15_P629666	1.594	0.672	1.29E-03
	A_15_P107203	1.534	0.618	7.38E-04
AANAT	A_15_P119137	1.589	0.668	2.49E-03
ABCA1	A_15_P533082	-1.716	-0.779	5.62E-03
	A_15_P107891	-1.518	-0.603	1.67E-02
	A_15_P735956	-1.591	-0.670	9.09E-03
ABCA7	A_15_P492597	1.517	0.602	2.53E-02
ABCC13	A_15_P244256	-1.706	-0.771	3.89E-02
ABCG4	A_15_P624556	1.872	0.904	4.06E-02
ABHD8	A_15_P375271	1.625	0.701	3.44E-02
ABI3BP	A_15_P102132	-1.504	-0.589	4.20E-02
ACSM3	A_15_P630491	-2.240	-1.164	2.87E-02
ACTC1	A_15_P661986	1.838	0.878	2.40E-03
ADAMTS1	A_15_P219366	-1.518	-0.602	1.90E-02
ADAMTS2	A_15_P548097	-2.007	-1.005	4.60E-02
ADAMTS9	A_15_P760206	-2.775	-1.473	8.57E-03
ADD3	A_15_P434675	1.561	0.642	1.38E-03
ADGRA3	A_15_P371955	2.347	1.231	2.18E-02
ADGRV1	A_15_P106492	1.701	0.766	2.15E-02
ADRA2C	A_15_P121461	-1.547	-0.629	3.63E-02
	A_15_P111474	-1.569	-0.650	4.97E-02
ADSSL1	A_15_P537297	2.252	1.171	1.62E-02
ALAS2	A_15_P752286	-1.944	-0.959	3.37E-02
ALDH2	A_15_P109735	2.190	1.131	4.51E-02
ALDOB	A_15_P734776	2.095	1.067	4.85E-02
	A_15_P416695	1.959	0.970	3.79E-02
ANKRD31	A_15_P620426	-1.529	-0.613	3.65E-02
ANKRD33	A_15_P185801	-2.590	-1.373	1.08E-02
ANKS3	A_15_P752116	-1.560	-0.641	2.88E-02
ANTXR1	A_15_P268741	-1.534	-0.618	2.17E-02
ANXA4	A_15_P225706	-2.220	-1.151	1.58E-02
	A_15_P113967	-2.208	-1.143	9.45E-03
APLP2	A_15_P241108	1.635	0.709	4.87E-03
AQP8	A_15_P102367	-1.685	-0.752	1.07E-02
ARHGAP18	A_15_P241671	1.562	0.643	4.11E-02
ARHGAP19	A_15_P235396	-1.871	-0.904	3.77E-03
ARHGEF2	A_15_P270782	-1.511	-0.595	1.53E-02
ARL5C	A_15_P120937	-1.660	-0.731	4.10E-02
ARX	A_15_P208846	1.589	0.668	3.06E-02
ATOH1	A_15_P625371	2.191	1.132	2.70E-03
ATP13A1	A_15_P416470	2.526	1.337	2.80E-02
ATP6V1E1	A_15_P211946	1.897	0.923	2.74E-02
	A_15_P664336	1.867	0.900	2.66E-02
B3GALT4	A_15_P397070	-1.513	-0.597	1.08E-03
BACH1	A_15_P157871	-1.962	-0.973	3.31E-02
BAZ1B	A_15_P449455	-1.505	-0.590	4.07E-02
BCOR	A_15_P104859	1.504	0.589	4.87E-03
BDKRB1	A_15_P101722	-1.847	-0.885	7.01E-03

BLZF1	A_15_P182966	1.547	0.629	3.13E-02
BMP1	A_15_P190241	-2.585	-1.370	4.40E-02
BMP10	A_15_P498192	-2.093	-1.065	5.62E-03
BMP7	A_15_P131106	1.609	0.686	8.98E-03
BORA	A_15_P273421	-1.666	-0.737	2.48E-02
BRF1	A_15_P210921	1.964	0.974	2.39E-02
C10orf11	A_15_P769331	-1.523	-0.607	3.26E-02
C1orf106	A_15_P505107	1.815	0.860	8.99E-03
CA8	A_15_P105692	1.713	0.776	3.70E-03
	A_15_P170001	1.713	0.776	1.89E-02
CA9	A_15_P520122	-1.822	-0.865	4.49E-02
CACNA1S	A_15_P117067	1.830	0.872	3.01E-02
CACNA2D1	A_15_P120563	-1.838	-0.878	3.39E-04
CALR3	A_15_P732420	-1.593	-0.672	2.55E-02
CAPN5	A_15_P103655	-1.942	-0.958	3.92E-02
CASQ2	A_15_P275301	3.653	1.869	1.61E-02
CASZ1	A_15_P120437	2.955	1.563	5.02E-03
CBLB	A_15_P114158	-1.705	-0.770	1.03E-02
CCDC120	A_15_P109113	-1.715	-0.778	3.87E-02
CCDC66	A_15_P676556	-2.082	-1.058	2.90E-02
CCSAP	A_15_P176986	1.553	0.635	2.98E-02
CDC42EP1	A_15_P570272	1.883	0.913	4.40E-02
CDKN2AIPNL	A_15_P378780	1.593	0.672	4.91E-03
CDT1	A_15_P591717	1.959	0.970	1.79E-03
CELSR1	A_15_P136471	-2.035	-1.025	1.66E-02
CENPI	A_15_P450320	-1.708	-0.772	2.61E-02
CENPT	A_15_P266317	-1.899	-0.925	2.97E-02
	A_15_P414506	-1.810	-0.856	1.27E-02
CEP128	A_15_P621186	1.839	0.879	4.24E-02
CEP57	A_15_P154436	-1.824	-0.867	3.43E-02
CERCAM	A_15_P118681	-1.627	-0.702	3.27E-02
CFAP58	A_15_P555281	-1.532	-0.615	3.01E-02
CGN	A_15_P134361	1.512	0.596	1.52E-02
CHD7	A_15_P333669	1.609	0.687	4.58E-02
CHRNA1	A_15_P116128	4.386	2.133	1.66E-02
CHST13	A_15_P183876	-2.083	-1.059	2.78E-02
CLCN1	A_15_P153541	-1.723	-0.785	4.59E-02
CLDN6	A_15_P730701	4.751	2.248	4.96E-02
CNOT6L	A_15_P120537	-1.578	-0.658	7.98E-03
CNRIP1	A_15_P196886	-1.502	-0.587	3.11E-02
COBLL1	A_15_P262346	1.510	0.594	3.44E-02
COL11A1	A_15_P671961	-1.732	-0.792	6.18E-03
COL11A2	A_15_P504557	2.209	1.143	4.72E-03
COL15A1	A_15_P285771	-2.553	-1.352	1.88E-02
COL4A2	A_15_P415340	-1.627	-0.702	3.97E-02
COL7A1	A_15_P488985	-1.673	-0.743	2.03E-02
COLQ	A_15_P548462	-2.068	-1.048	3.94E-02
CPA1	A_15_P117784	2.738	1.453	1.53E-03
	A_15_P116208	2.042	1.030	9.17E-03
CPLX3	A_15_P442120	-2.805	-1.488	8.10E-03
CPSF6	A_15_P279121	1.514	0.599	1.84E-02
CRACR2A	A_15_P159116	-1.687	-0.755	1.01E-03
CSNK2A1	A_15_P284606	1.762	0.817	4.52E-02
CSRNP1	A_15_P580222	-2.161	-1.112	4.31E-02

CSRP2	A_15_P207836	1.744	0.803	4.66E-02
CTBP2	A_15_P106555	1.818	0.862	2.10E-02
C3	A_15_P310441	-1.776	-0.828	4.39E-02
CTPS1	A_15_P117541	1.614	0.691	4.59E-02
CXorf57	A_15_P437300	-1.735	-0.795	4.21E-02
CYB5R1	A_15_P750211	1.606	0.684	2.90E-02
CYP2J2	A_15_P121060	1.760	0.816	5.67E-03
CYP51A1	A_15_P738216	1.861	0.896	4.51E-02
DAZAP2	A_15_P401990	1.531	0.615	9.40E-03
DBI	A_15_P627806	1.654	0.726	4.50E-02
	A_15_P150566	1.625	0.700	3.18E-02
DDHD1	A_15_P432375	-1.612	-0.689	4.26E-02
DES	A_15_P663176	2.034	1.024	3.06E-02
DGUOK	A_15_P415885	1.669	0.739	2.11E-02
	A_15_P734571	1.606	0.684	3.89E-02
DLK1	A_15_P705461	1.541	0.624	1.44E-02
DNAH3	A_15_P155631	-1.887	-0.916	2.42E-02
DPM1	A_15_P112449	-2.312	-1.209	4.16E-02
DPY19L1	A_15_P621126	-1.948	-0.962	3.59E-02
DSN1	A_15_P607897	-1.738	-0.797	3.30E-02
DUSP10	A_15_P155101	-1.655	-0.726	2.17E-02
DUSP2	A_15_P630961	-2.159	-1.110	3.89E-02
	A_15_P108853	-2.113	-1.079	4.19E-02
DUSP23	A_15_P110079	-1.787	-0.837	1.04E-02
DUSP27	A_15_P581697	-1.597	-0.676	2.26E-02
DUSP7	A_15_P403985	-1.849	-0.887	2.77E-02
DXO	A_15_P223101	-1.533	-0.616	8.08E-03
EBP	A_15_P504977	1.553	0.635	1.64E-02
	A_15_P109540	1.565	0.646	4.83E-02
	A_15_P116121	1.795	0.844	2.87E-03
EIF3I	A_15_P597757	-1.728	-0.789	2.56E-02
ELMSAN1	A_15_P556417	1.560	0.642	2.40E-02
ELP5	A_15_P149426	1.685	0.753	2.85E-02
EMP2	A_15_P187401	-1.549	-0.631	4.43E-02
EN1	A_15_P118364	1.796	0.845	3.81E-02
ENPP2	A_15_P284306	-1.652	-0.724	3.41E-02
ENTPD2	A_15_P100727	2.066	1.047	7.31E-04
EPCAM	A_15_P109227	-1.933	-0.951	2.33E-02
EPO	A_15_P487320	2.269	1.182	3.84E-02
EPPK1	A_15_P514167	-1.522	-0.606	8.09E-03
ESR2	A_15_P192221	-1.649	-0.722	3.15E-02
ETFA	A_15_P112680	1.601	0.679	1.67E-02
ETV5	A_15_P102717	1.617	0.693	2.02E-02
	A_15_P185506	1.688	0.756	2.10E-02
EWSR1	A_15_P277286	-1.939	-0.955	2.56E-03
	A_15_P560823	-2.138	-1.096	1.40E-03
	A_15_P627836	-2.462	-1.300	3.93E-03
	A_15_P742866	-2.031	-1.022	1.35E-03
EXT1	A_15_P443670	-1.952	-0.965	2.45E-02
EZR	A_15_P203556	-2.165	-1.115	4.76E-03
F2RL1	A_15_P242841	-1.797	-0.845	1.63E-02
FAM107B	A_15_P720531	-1.907	-0.931	3.79E-03
	A_15_P293776	-1.774	-0.827	2.92E-02
	A_15_P121288	-1.958	-0.969	7.68E-04

FAM131C	A_15_P606477	1.645	0.718	4.37E-02
FAM208B	A_15_P115924	-1.585	-0.665	5.54E-03
FAM43B	A_15_P117604	-1.714	-0.777	3.54E-02
FANK1	A_15_P103581	1.860	0.895	1.09E-02
FBXL7	A_15_P413600	1.585	0.664	1.25E-02
FGF2	A_15_P109975	2.844	1.508	1.92E-02
FGF8	A_15_P105035	2.492	1.317	3.35E-02
FGG	A_15_P439455	-1.813	-0.858	2.18E-02
FHOD1	A_15_P362850	-3.701	-1.888	1.59E-02
FKTN	A_15_P135763	-1.913	-0.936	4.63E-02
FLI1	A_15_P109368	1.544	0.627	2.26E-03
FMN1	A_15_P184436	-2.975	-1.573	3.31E-02
FOXL2	A_15_P282031	1.978	0.984	3.42E-02
FOXP1	A_15_P596262	-1.692	-0.759	3.75E-02
FPGS	A_15_P209441	-1.848	-0.886	4.78E-02
FRAS1	A_15_P363650	-1.791	-0.841	4.68E-02
FRRS1	A_15_P198541	-3.433	-1.780	1.43E-02
FSHR	A_15_P113693	-2.069	-1.049	1.14E-02
FUT8	A_15_P287041	-1.504	-0.589	2.93E-02
GART	A_15_P656536	1.506	0.590	3.51E-03
GAS2	A_15_P411120	-1.514	-0.599	3.25E-02
GATSL3	A_15_P419225	-1.678	-0.747	4.80E-02
GBX2	A_15_P104642	1.830	0.872	2.16E-03
GCM2	A_15_P101196	1.857	0.893	3.00E-02
GDF10	A_15_P557412	1.752	0.809	6.30E-03
GDNF	A_15_P164611	-1.633	-0.708	4.88E-03
GGPS1	A_15_P749141	1.525	0.608	4.81E-02
GJD4	A_15_P156366	-1.513	-0.598	4.10E-02
GOLGA2	A_15_P437485	1.805	0.852	4.91E-02
GPER1	A_15_P257096	-1.734	-0.794	3.94E-02
GPT2	A_15_P562677	-1.586	-0.666	1.17E-02
GRB10	A_15_P301806	-1.730	-0.791	5.65E-03
	A_15_P182246	-1.774	-0.827	2.54E-02
GRIK1	A_15_P165896	1.655	0.727	4.66E-02
GTF2F1	A_15_P101140	3.383	1.758	2.55E-02
GUCA1C	A_15_P537302	-2.044	-1.031	4.81E-02
GYS2	A_15_P101171	-1.638	-0.712	2.79E-02
HAND2	A_15_P632716	-1.955	-0.967	3.85E-02
HBP1	A_15_P193621	-1.835	-0.875	2.54E-02
	A_15_P630166	-1.894	-0.922	2.87E-02
HBZ	A_15_P111458	-2.625	-1.392	3.71E-02
HDAC8	A_15_P116819	-1.722	-0.784	1.06E-02
HEG1	A_15_P283483	-2.532	-1.340	1.82E-02
HGS	A_15_P173116	1.500	0.585	1.78E-02
HIC1	A_15_P411550	-2.722	-1.445	2.63E-02
HIF3A	A_15_P281686	-1.898	-0.924	2.47E-02
	A_15_P101503	-2.131	-1.091	5.15E-04
	A_15_P404495	-1.977	-0.983	2.50E-02
	A_15_P165446	-1.603	-0.681	8.58E-04
	A_15_P108026	-1.744	-0.803	1.10E-03
	A_15_P621106	-1.780	-0.832	7.10E-04
	A_15_P102540	-1.914	-0.937	1.33E-02
HLA-DPA1	A_15_P109701	-1.751	-0.808	4.54E-02
HNF4A	A_15_P110568	1.638	0.712	2.47E-02

HOOK2	A_15_P112239	5.413	2.436	3.65E-02
HOXB9	A_15_P163356	-1.515	-0.600	4.01E-02
HPSE2	A_15_P102729	-1.639	-0.713	9.58E-03
HSD11B2	A_15_P768186	-2.096	-1.068	4.78E-02
	A_15_P100202	-2.098	-1.069	3.77E-02
	A_15_P613927	-2.059	-1.042	4.57E-02
HSPB9	A_15_P131406	-1.617	-0.693	2.31E-02
HUNK	A_15_P675781	-1.970	-0.978	4.07E-02
	A_15_P492182	-1.676	-0.745	3.72E-02
IGF2BP1	A_15_P599497	1.921	0.942	2.71E-02
IGFLR1	A_15_P760966	-2.364	-1.241	4.66E-02
ILVBL	A_15_P748641	-2.770	-1.470	4.08E-02
IMPG2	A_15_P113564	-2.621	-1.390	2.32E-02
INSIG2	A_15_P114064	2.092	1.065	1.84E-02
INTS2	A_15_P622716	-2.127	-1.089	3.45E-02
IQGAP1	A_15_P467920	-2.198	-1.136	3.47E-02
IQGAP2	A_15_P543077	-1.884	-0.914	9.35E-03
IRAK1	A_15_P519417	-2.066	-1.047	3.02E-02
ITGA5	A_15_P115729	-1.548	-0.630	1.56E-02
ITIH2	A_15_P160766	-1.751	-0.808	4.29E-03
ITIH3	A_15_P160756	-1.686	-0.753	3.96E-02
ITIH6	A_15_P554272	1.995	0.997	3.58E-02
ITLN1	A_15_P190506	-1.904	-0.929	4.18E-02
ITSN2	A_15_P431825	-1.962	-0.972	2.83E-02
	A_15_P409715	-2.061	-1.043	3.29E-03
KCNJ1	A_15_P399905	2.258	1.175	3.18E-02
KCNN4	A_15_P310861	-1.751	-0.808	3.55E-03
KEAP1	A_15_P737741	2.348	1.232	3.05E-02
KIAA1524	A_15_P244291	-1.551	-0.633	4.39E-02
KIF17	A_15_P237751	-1.872	-0.905	5.18E-03
KIF1C	A_15_P147756	-1.744	-0.803	7.68E-03
KLF9	A_15_P735206	-4.063	-2.023	3.81E-02
	A_15_P146191	-4.572	-2.193	3.13E-02
KRT5	A_15_P495025	3.462	1.792	1.37E-02
KY	A_15_P268561	-1.530	-0.614	3.88E-02
LEP	A_15_P159456	1.702	0.767	2.71E-02
LGI2	A_15_P444615	2.059	1.042	3.89E-03
LHPP	A_15_P378530	-1.742	-0.801	2.85E-02
	A_15_P727896	-1.582	-0.662	1.56E-02
LHX8	A_15_P189136	-1.759	-0.815	2.13E-02
LIMA1	A_15_P107878	-2.164	-1.114	1.72E-02
	A_15_P624041	-1.715	-0.778	4.10E-03
	A_15_P291286	-2.168	-1.116	3.98E-02
LLGL1	A_15_P598332	-1.692	-0.759	1.62E-02
	A_15_P742736	-2.206	-1.141	4.17E-02
LMAN2L	A_15_P723841	1.711	0.775	4.54E-02
LOC100996634	A_15_P283696	1.502	0.587	6.15E-03
LOXHD1	A_15_P695506	-2.101	-1.071	6.74E-03
LOXL1	A_15_P117879	2.670	1.417	1.80E-02
LPIN3	A_15_P551652	-2.065	-1.046	3.37E-02
LPL	A_15_P272131	1.590	0.669	4.16E-02
LRRC58	A_15_P394970	2.610	1.384	2.94E-02
	A_15_P738926	1.608	0.685	5.62E-03
LRRC8D	A_15_P198601	-1.782	-0.833	2.29E-02

LTBP3	A_15_P316846	3.199	1.677	2.08E-02
MAD2L1BP	A_15_P463100	-2.727	-1.447	2.38E-03
MAGI1	A_15_P223426	-1.648	-0.720	2.76E-02
MAN1A1	A_15_P511712	1.704	0.769	2.43E-02
MAP3K12	A_15_P570717	1.783	0.835	1.29E-02
MATN3	A_15_P184796	-2.332	-1.221	5.32E-03
	A_15_P643781	-1.722	-0.784	5.53E-03
MEGF8	A_15_P633531	-1.700	-0.766	2.14E-02
MEOX1	A_15_P105497	2.137	1.096	1.59E-02
METRN	A_15_P157116	-1.510	-0.594	4.67E-02
METTL16	A_15_P178071	-2.169	-1.117	2.03E-03
MFAP4	A_15_P357085	-3.378	-1.756	2.06E-02
	A_15_P219886	2.161	1.111	4.63E-02
MFF	A_15_P564532	1.675	0.744	4.86E-02
MFSD4	A_15_P183391	1.566	0.647	1.97E-02
MMADHC	A_15_P113004	-2.165	-1.114	1.39E-03
MOB2	A_15_P136791	-2.227	-1.155	1.44E-02
	A_15_P740356	-2.176	-1.122	8.86E-03
	A_15_P446315	-2.078	-1.055	8.47E-03
	A_15_P115255	-1.871	-0.904	1.58E-02
	A_15_P495002	-1.812	-0.858	2.51E-04
	A_15_P571537	-2.063	-1.044	3.90E-03
	A_15_P506892	-2.140	-1.098	7.93E-03
	A_15_P263506	-2.174	-1.120	8.88E-03
MORC3	A_15_P208601	-2.537	-1.343	3.82E-02
MPP7	A_15_P166681	-2.402	-1.264	1.16E-02
MSRA	A_15_P103662	1.505	0.590	1.87E-03
MSTN	A_15_P114781	1.663	0.734	2.46E-02
MTFR1	A_15_P514128	2.169	1.117	7.60E-03
MTMR1	A_15_P110989	1.635	0.709	2.31E-02
MTMR4	A_15_P155636	-2.821	-1.496	2.07E-02
MTUS1	A_15_P563767	-1.515	-0.600	4.08E-02
	A_15_P269426	-1.649	-0.722	5.26E-04
MUSK	A_15_P554302	-2.766	-1.468	3.68E-02
MYBPC1	A_15_P611332	-2.986	-1.578	1.09E-03
MYBPH	A_15_P645361	-2.218	-1.149	3.81E-02
MYCL	A_15_P732791	-1.629	-0.704	2.96E-02
MYF5	A_15_P666156	-2.172	-1.119	1.45E-02
MYH11	A_15_P116227	-1.644	-0.717	2.53E-02
MYL2	A_15_P738056	-2.250	-1.170	1.22E-02
MYLK4	A_15_P192406	-1.851	-0.888	4.58E-02
MYO5B	A_15_P107657	-1.641	-0.715	1.73E-02
MYOZ3	A_15_P135696	-1.536	-0.619	4.79E-02
NBEAL2	A_15_P297886	-1.536	-0.619	3.38E-02
NDUFB3	A_15_P575752	2.229	1.157	3.19E-03
NFE2L3	A_15_P527812	-1.587	-0.666	3.99E-02
NKX2-2	A_15_P108187	1.510	0.595	1.49E-03
NOM1	A_15_P275976	1.641	0.714	2.59E-02
NOTCH1	A_15_P131531	-2.210	-1.144	2.72E-02
NPFF	A_15_P758221	-2.022	-1.016	7.33E-04
NR5A1	A_15_P626106	1.826	0.869	3.52E-02
	A_15_P100569	2.616	1.388	3.64E-02
NR6A1	A_15_P161986	-1.631	-0.706	4.41E-02
NRIP1	A_15_P379500	-1.512	-0.596	4.76E-02

NUDT1	A_15_P102359	1.723	0.785	7.79E-03
NUDT14	A_15_P192231	-1.570	-0.651	1.84E-02
NUGGC	A_15_P181916	-1.893	-0.921	3.73E-02
OLFML1	A_15_P572617	4.349	2.121	2.97E-02
OLIG3	A_15_P598467	2.203	1.139	2.38E-04
OR8G5	A_15_P118863	-1.929	-0.948	3.51E-02
	A_15_P165706	-1.954	-0.966	3.12E-02
OSBPL3	A_15_P105684	-3.449	-1.786	2.09E-02
P2RY4	A_15_P622731	-1.657	-0.729	1.61E-02
PAH	A_15_P101511	1.768	0.822	2.64E-02
PAX3	A_15_P199351	-1.743	-0.802	3.26E-02
PCOLCE2	A_15_P410160	-1.690	-0.757	1.76E-02
PDCD6IP	A_15_P182881	1.636	0.710	4.89E-02
PDK2	A_15_P105148	-1.716	-0.779	2.42E-02
	A_15_P166716	-2.021	-1.015	3.97E-02
PFKFB4	A_15_P174861	-1.922	-0.942	4.03E-02
	A_15_P102138	-2.142	-1.099	4.68E-03
	A_15_P186271	-1.803	-0.850	4.31E-02
PFKP	A_15_P536227	1.609	0.686	7.72E-03
PGPEP1	A_15_P161876	-1.623	-0.699	1.12E-02
PHC3	A_15_P563577	-1.530	-0.613	4.00E-02
PIAS4	A_15_P581782	-2.970	-1.570	8.89E-03
PIK3R3	A_15_P207341	-2.485	-1.313	2.40E-02
	A_15_P286046	-2.552	-1.352	2.53E-02
PKNOX1	A_15_P483385	1.644	0.717	1.10E-03
PLCB3	A_15_P614617	-1.729	-0.790	1.58E-02
PLD3	A_15_P300291	-2.067	-1.048	3.10E-02
PLEKHG5	A_15_P160536	-1.699	-0.764	3.58E-02
PLEKHG7	A_15_P384021	-2.920	-1.546	5.75E-03
PLEKHM1	A_15_P486485	-1.539	-0.622	2.56E-02
PLEKHN1	A_15_P350635	-2.431	-1.282	2.62E-03
PLIN2	A_15_P598962	-2.476	-1.308	1.04E-02
	A_15_P107567	-1.991	-0.993	4.30E-03
	A_15_P150646	-2.512	-1.329	2.25E-03
POLE4	A_15_P160266	-1.693	-0.760	2.96E-02
POPDC2	A_15_P231306	-1.676	-0.745	4.38E-03
POU2F3	A_15_P659961	1.738	0.797	1.82E-02
	A_15_P134737	1.876	0.907	8.55E-03
PPAP2C	A_15_P235156	-1.902	-0.928	4.82E-02
PPT1	A_15_P100598	1.949	0.963	4.45E-02
PRDM12	A_15_P119788	1.678	0.747	3.62E-02
PREX2	A_15_P229311	-2.214	-1.146	3.28E-02
PRICKLE1	A_15_P253071	3.108	1.636	3.81E-02
PRKG1	A_15_P151231	-1.616	-0.692	1.31E-02
PRKG2	A_15_P146616	1.822	0.865	4.12E-02
PRR11	A_15_P696746	1.511	0.596	4.63E-02
PRR5	A_15_P460315	-1.799	-0.847	5.00E-02
PRSS12	A_15_P401410	-1.814	-0.859	4.40E-03
PRSS57	A_15_P138436	-1.842	-0.881	4.82E-02
PRSS57	A_15_P105846	-1.534	-0.617	2.61E-02
PSKH1	A_15_P545207	-1.511	-0.595	4.05E-02
PTK2B	A_15_P408010	2.143	1.099	2.99E-02
PTPN21	A_15_P570867	-4.381	-2.131	7.28E-03
PTPRB	A_15_P273376	2.420	1.275	3.96E-02

	A_15_P135666	-1.951	-0.964	3.44E-02
PTRH2	A_15_P666686	2.084	1.059	1.41E-02
PTX4	A_15_P696191	2.451	1.294	2.89E-02
PUS7	A_15_P763276	1.505	0.590	1.58E-02
RAB3IP	A_15_P720196	1.967	0.976	4.49E-02
	A_15_P365625	2.060	1.043	3.08E-02
RAD1	A_15_P108031	1.877	0.908	4.46E-02
RASGRP3	A_15_P742726	-1.538	-0.621	1.47E-02
RASSF3	A_15_P158771	-1.644	-0.717	3.32E-02
RAVER1	A_15_P258041	-1.736	-0.796	3.29E-02
RBM14	A_15_P696956	1.514	0.599	3.73E-02
RCBTB2	A_15_P459840	1.908	0.932	4.58E-02
RCE1	A_15_P409580	-1.630	-0.705	2.93E-02
RDH8	A_15_P186911	2.290	1.196	1.59E-02
RFWD3	A_15_P264941	-1.976	-0.983	6.76E-03
RGS3	A_15_P130216	1.561	0.642	3.98E-04
	A_15_P110651	1.657	0.729	7.26E-04
RGS9	A_15_P205901	-1.846	-0.884	4.97E-04
RNF111	A_15_P562012	-1.563	-0.645	1.17E-02
RNF182	A_15_P171456	-1.673	-0.742	1.62E-02
RNF212B	A_15_P498799	-2.729	-1.449	4.42E-02
ROBO2	A_15_P165866	-1.568	-0.649	2.23E-02
ROMO1	A_15_P100280	-2.778	-1.474	1.14E-02
ROS1	A_15_P106431	-3.028	-1.598	2.81E-02
RPL7	A_15_P263206	-1.575	-0.655	4.92E-02
RPS15A	A_15_P111486	4.208	2.073	3.72E-02
RPS6KB1	A_15_P157916	-2.750	-1.459	3.67E-03
RRAGD	A_15_P169866	1.921	0.942	3.69E-02
SALL4	A_15_P139746	-2.196	-1.135	2.27E-02
SAT1	A_15_P110641	-1.778	-0.831	4.74E-02
	A_15_P630986	-1.713	-0.776	3.60E-02
SCMH1	A_15_P344815	-1.927	-0.947	3.75E-02
SDHAF1	A_15_P758011	1.506	0.591	2.24E-02
SEC16A	A_15_P416225	2.027	1.020	3.72E-02
SELE	A_15_P184276	-1.737	-0.797	2.43E-02
SEMA3A	A_15_P116849	-1.848	-0.886	4.73E-02
SENP7	A_15_P139046	-1.739	-0.798	1.49E-02
SEPT9	A_15_P100725	1.799	0.847	1.35E-02
	A_15_P725201	1.564	0.645	3.61E-02
SERGEF	A_15_P136301	1.543	0.626	1.10E-02
SERPINA7	A_15_P116686	-2.241	-1.164	2.45E-02
SERTAD2	A_15_P307006	-1.923	-0.943	2.00E-02
SETD8	A_15_P173531	-1.501	-0.586	2.97E-02
SGK2	A_15_P626931	-1.525	-0.609	2.37E-02
SH3GL3	A_15_P660096	1.525	0.609	3.95E-02
SIGIRR	A_15_P660651	-2.022	-1.016	6.94E-03
SIM1	A_15_P158656	-2.290	-1.195	2.35E-02
SIX6	A_15_P105434	1.942	0.957	3.52E-02
SLC10A3	A_15_P719996	1.608	0.685	2.39E-03
	A_15_P581737	1.511	0.595	4.10E-03
SLC12A9	A_15_P593207	-1.543	-0.625	4.00E-02
SLC15A2	A_15_P107171	-1.594	-0.673	6.95E-03
SLC22A3	A_15_P498977	2.504	1.324	2.65E-03
SLC25A40	A_15_P101190	1.610	0.687	3.57E-02

SLC38A4	A_15_P741511	-1.566	-0.647	5.00E-02
	A_15_P158706	-1.908	-0.932	3.19E-02
	A_15_P226861	-1.568	-0.649	2.16E-02
SLC7A1	A_15_P252646	-1.584	-0.663	2.72E-02
SLF2	A_15_P285061	-1.606	-0.684	1.56E-02
SNAI3	A_15_P529407	-1.545	-0.627	2.34E-02
SOD1	A_15_P103988	1.545	0.628	1.27E-02
SOWAHC	A_15_P531242	1.508	0.593	4.58E-02
SPR	A_15_P171031	1.690	0.757	4.19E-02
SSH2	A_15_P640611	-2.600	-1.379	1.52E-02
	A_15_P302426	-2.339	-1.226	1.58E-02
	A_15_P595397	-1.956	-0.968	1.05E-03
SSTR2	A_15_P290931	2.377	1.249	4.49E-03
SSTR4	A_15_P375700	-1.546	-0.628	1.48E-02
ST14	A_15_P175546	3.206	1.681	1.50E-02
ST3GAL4	A_15_P632381	-1.670	-0.740	3.53E-02
ST6GALNAC5	A_15_P106493	1.585	0.665	4.95E-02
STK24	A_15_P725911	-2.345	-1.229	1.75E-02
STK26	A_15_P112821	-1.570	-0.651	5.22E-03
STK35	A_15_P107103	-2.237	-1.162	4.15E-02
	A_15_P744761	-1.963	-0.973	3.04E-02
	A_15_P739506	-2.210	-1.144	3.04E-02
	A_15_P183961	-1.990	-0.993	4.75E-02
	A_15_P204988	-2.427	-1.279	2.43E-02
	A_15_P323122	-2.009	-1.007	1.36E-02
STOM	A_15_P112994	1.698	0.764	7.08E-03
SULF2	A_15_P209406	1.505	0.590	2.40E-02
SUZ12	A_15_P419460	-1.713	-0.777	2.19E-02
TCP1	A_15_P116402	2.050	1.036	1.36E-02
TFAP2C	A_15_P135236	-1.790	-0.840	3.84E-02
TGDS	A_15_P762606	-1.820	-0.864	2.39E-02
	A_15_P106529	1.851	0.889	1.46E-04
	A_15_P444460	1.574	0.655	2.43E-02
THBS2	A_15_P512667	-1.646	-0.719	6.93E-03
TLCD2	A_15_P487220	1.551	0.633	3.72E-02
TLE3	A_15_P144426	1.561	0.642	3.19E-04
TMA16	A_15_P117059	1.913	0.936	1.73E-03
TMC6	A_15_P688126	1.645	0.718	6.08E-03
TMEM59L	A_15_P121289	1.867	0.900	3.25E-02
TMEM97	A_15_P436645	2.210	1.144	2.92E-02
	A_15_P165511	2.667	1.415	3.72E-02
TMPRSS9	A_15_P137966	-2.367	-1.243	1.52E-05
	A_15_P516072	-1.733	-0.793	1.88E-03
	A_15_P205161	-1.613	-0.690	4.23E-03
TNNI2	A_15_P106964	-2.646	-1.404	4.37E-02
TRAF7	A_15_P211156	1.720	0.783	7.59E-03
TRAIP	A_15_P280946	1.760	0.815	3.71E-02
TRIB3	A_15_P119740	-1.635	-0.709	3.91E-02
TRIM24	A_15_P150971	1.534	0.618	2.72E-03
TRIM35	A_15_P221264	-2.381	-1.252	1.15E-02
TRIM55	A_15_P119047	-3.052	-1.610	2.54E-02
TRMT10C	A_15_P109024	12.455	3.639	2.85E-02
TTC36	A_15_P117654	2.421	1.276	1.49E-02
TTC7A	A_15_P268447	-1.774	-0.827	1.12E-02

TTF1	A_15_P603320	2.548	1.349	4.75E-02
TTLL2	A_15_P634344	2.188	1.130	2.62E-02
	A_15_P184676	2.234	1.160	3.77E-02
	A_15_P622811	2.984	1.577	3.66E-02
TULP2	A_15_P108388	-3.899	-1.963	6.45E-03
TWIST1	A_15_P121033	1.732	0.792	3.13E-02
UOX	A_15_P107519	-2.278	-1.188	3.25E-02
USP37	A_15_P194831	1.672	0.742	4.34E-02
VGLL2	A_15_P329691	2.381	1.252	5.19E-03
VIP	A_15_P119279	1.511	0.596	3.62E-02
VWA1	A_15_P520862	-1.567	-0.648	1.01E-02
VWA2	A_15_P400665	1.603	0.681	4.17E-02
WBP1L	A_15_P620891	-1.611	-0.688	4.61E-02
WDR55	A_15_P551392	1.722	0.784	5.94E-03
WSCD2	A_15_P146036	-1.706	-0.770	1.72E-02
XDH	A_15_P288316	-1.574	-0.655	4.44E-02
	A_15_P322306	-2.663	-1.413	6.29E-05
XPO1	A_15_P473385	-1.529	-0.612	3.59E-02
ZAN	A_15_P605687	-1.911	-0.934	3.47E-02
ZAR1L	A_15_P104077	-1.521	-0.605	3.08E-02
ZBED1	A_15_P260696	-2.092	-1.065	3.32E-02
ZNF729	A_15_P270036	2.993	1.582	2.39E-02
	A_15_P442470	-3.348	-1.743	9.14E-03
	A_15_P761854	-1.640	-0.714	2.74E-02
	A_15_P613417	-1.623	-0.698	3.91E-02
	A_15_P264306	1.576	0.656	1.02E-02
ZNHIT1	A_15_P102926	-1.575	-0.655	4.03E-02
ZP3	A_15_P103400	-2.084	-1.059	1.94E-02
ZSWIM6	A_15_P158611	1.696	0.762	7.34E-03

Supplementary Table 3. Primers for qPCR analysis for microarray data confirmation

Sequence ID[a]	Zebrafish symbol	Human homolog[b]		Sequence
NM_131564.2	*appa*	*APP*[c]	forward	ACCGTCTGCTCTCACACTACTA
			reverse	TCAGTGTGAGGAGGAAGAGGAA
NM_152886.1	*appb*	*APP*[c]	forward	GGCAGATGTGTAGAAGGAAGCT
			reverse	CCCCATGCAACCATTAAGTGTG
NM_001083002.1	*arid3b*	*ARID3B*[c]	forward	CTTACATGCAGAAACGAGGTACAC
			reverse	TCTTCTTGTTGATCACCTCTACCA
NM_205704.1	*bace1*	*BACE1*[c]	forward	ATCATGGAGGGTTTCTATGTGG
			reverse	GGACGTTATAGCCACAGTCCTC
NM_198144.2	*emx1*	*EMX1*[c]	forward	AACAGCCTCAGTTTATCCGAGA
			reverse	TGTGGTGGTTTCCTTTCTTCTT
NM_001144818.1	*ggcta*	*GGCT*[c]	forward	AACTTCACACCCTGTTCACCTT
			reverse	AAGAGCCGCTGTAATTGTTTGT
NM_199729.1	*gtf2f1*	*GTF2F1*[d]	forward	GAAAGCCCATGACCACTAAAGA
			reverse	GTTCTTCCTCTCTGGATTGAGC
NM_001089425.1	*prdx4*	*PRDX4*[c]	forward	TCTACCCTCTGGACTTCACGTT
			reverse	GATCCAGGCCAGATGAGTAAAC
NM_200797.4	*romo1*	*ROMO1*[d]	forward	AGTGTAGGATCGTACGGACAGC
			reverse	AGACAGGAGAAAGTCCCAAACA
NM_212784.1	*rpl13a*	*RPL13A*[c, d]	forward	GAGAAAGGAAAAGGCCAAGCTG
			reverse	GGACAGCTCAAACAAGAACACC
NM_212762.1	*rps15a*	*RPS15A*[d]	forward	GAAGTGGCAGAACAACCTTCTC
			reverse	AAGAACCCAAGGATTTTTCCTC
NM_200164.1	*slc25a14*	*SLC25A14*[c]	forward	TAGCTTAAACTGGAAAACCACCA
			reverse	TATATCCCAACCTAATGGACGTG
NM_001007332.2	*trmt10c*	*TRMT10C*[d]	forward	ACTGGGATTGTGGAGCTAAAAA
			reverse	TGGAAACCTTTGTGTTTCCTCT
NM_001111230.1	*ttll2*	*TTLL2*[d]	forward	AAACTCAAGTCTCCAACCTTCG
			reverse	CTCTCGAGATGCTTTCCAAGTT

[a] Sequence ID of zebrafish was obtained from National Center for Biotechnology Information (NCBI) Reference Sequence (RefSeq) database. [b] Genes in zebrafish ware matched to annotated human gene symbols. qPCR analysis was conducted on selected targets for confirmation of microarray data from brain of aged adult [c] female and [d] male zebrafish exposed to 10 µg/L Pb during embryogenesis.

Supplementary Information Table 4. Annotated genes altered in aged adult female and male zebrafish brain exposed to 10 µg/L Pb during embryogenesis.

Symbol	Entrez Gene Name
A2M	alpha-2-macroglobulin
ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1
ABCG4	ATP-binding cassette, sub-family G (WHITE), member 4
ABI3BP	ABI family, member 3 (NESH) binding protein
ALDOB	aldolase B, fructose-bisphosphate
APLP2	amyloid beta (A4) precursor-like protein 2
ATP6V1E1	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E1
BMP1	bone morphogenetic protein 1
BORA	bora, aurora kinase A activator
C1orf106	chromosome 1 open reading frame 106
CA9	carbonic anhydrase IX
CALR3	calreticulin 3
CBLB	Cbl proto-oncogene B, E3 ubiquitin protein ligase
CCDC120	coiled-coil domain containing 120
CENPT	centromere protein T
CFAP58	cilia and flagella associated protein 58
CGN	cingulin
COL11A1	collagen, type XI, alpha 1
CTBP2	C-terminal binding protein 2
CYP2J2	cytochrome P450, family 2, subfamily J, polypeptide 2
CYP51A1	cytochrome P450, family 51, subfamily A, polypeptide 1
DBI	diazepam binding inhibitor (GABA receptor modulator, acyl-CoA binding protein)
DES	desmin
DPY19L1	dpy-19-like 1 (C. elegans)
DUSP27	dual specificity phosphatase 27 (putative)
ENTPD2	ectonucleoside triphosphate diphosphohydrolase 2
EWSR1	EWS RNA-binding protein 1
FAM208B	family with sequence similarity 208, member B
FHOD1	formin homology 2 domain containing 1
FLI1	Fli-1 proto-oncogene, ETS transcription factor
FUT8	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)
GRB10	growth factor receptor-bound protein 10
GRIK1	glutamate receptor, ionotropic, kainate 1
GTF2F1	general transcription factor IIF, polypeptide 1, 74kDa
HGS	hepatocyte growth factor-regulated tyrosine kinase substrate
HLA-DPA1	major histocompatibility complex, class II, DP alpha 1
HUNK	hormonally up-regulated Neu-associated kinase
IGF2BP1	insulin-like growth factor 2 mRNA binding protein 1
ITIH3	inter-alpha-trypsin inhibitor heavy chain 3
ITLN1	intelectin 1 (galactofuranose binding)
KEAP1	kelch-like ECH-associated protein 1
KIF1C	kinesin family member 1C
LIMA1	LIM domain and actin binding 1
LOC100996634	transmembrane protein FLJ37396
LRRC8D	leucine rich repeat containing 8 family, member D
MAD2L1BP	MAD2L1 binding protein
MAGI1	membrane associated guanylate kinase, WW and PDZ domain containing 1
MAP3K12	mitogen-activated protein kinase kinase kinase 12
MFAP4	microfibrillar-associated protein 4
MOB2	MOB kinase activator 2
MTUS1	microtubule associated tumor suppressor 1
MYCL	v-myc avian myelocytomatosis viral oncogene lung carcinoma derived homolog
MYH11	myosin, heavy chain 11, smooth muscle

NKX2-2	NK2 homeobox 2
NRIP1	nuclear receptor interacting protein 1
NUDT1	nudix (nucleoside diphosphate linked moiety X)-type motif 1
PDK2	pyruvate dehydrogenase kinase, isozyme 2
PFKP	phosphofructokinase, platelet
PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)
PLCB3	phospholipase C, beta 3 (phosphatidylinositol-specific)
PLEKHG5	pleckstrin homology domain containing, family G (with RhoGef domain) member 5
PLEKHG7	pleckstrin homology domain containing, family G (with RhoGef domain) member 7
PREX2	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 2
PTPRB	protein tyrosine phosphatase, receptor type, B
PUS7	pseudouridylate synthase 7 (putative)
RBM14	RNA binding motif protein 14
RNF212B	ring finger protein 212B
SALL4	spalt-like transcription factor 4
SEMA3A	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A
SETD8	SET domain containing (lysine methyltransferase) 8
SLC12A9	solute carrier family 12, member 9
SLC38A4	solute carrier family 38, member 4
SLF2	SMC5-SMC6 complex localization factor 2
SOD1	superoxide dismutase 1, soluble
SSH2	slingshot protein phosphatase 2
STK35	serine/threonine kinase 35
SUZ12	SUZ12 polycomb repressive complex 2 subunit
THBS2	thrombospondin 2
TMA16	translation machinery associated 16 homolog (S. cerevisiae)
TNNI2	troponin I type 2 (skeletal, fast)
TRAF7	TNF receptor-associated factor 7, E3 ubiquitin protein ligase
TTF1	transcription termination factor, RNA polymerase I
VGLL2	vestigial-like family member 2
XDH	xanthine dehydrogenase
ZNF729	zinc finger protein 729