

Supplementary Table 1. Significantly upregulated or downregulated gene expressions in Caco-2 cells by the treatment with *L. johsonii* MG.

Gene	Product	Ratio	p-Value log	p-value	H ₂ O ₂ -1	H ₂ O ₂ -2	H ₂ O ₂ -3	H ₂ O ₂ -LAB1	H ₂ O ₂ -LAB2	H ₂ O ₂ -LAB3
HYOU1L	hypoxia up-regulated 1	3.25	1.7033	1.228E-12	418	292	419	892	1085	1475
TYW4E	tyrosine 3-monooxygenase/tyrosinase 5-monooxygenase activation protein epsilon	3.21	1.6812	9.867E-04	346	290	346	2371	445	391
EF1B2	eukaryotic translation elongation factor 1 beta 2	3.17	1.8657	4.447E-03	194	195	194	251	1530	186
TAGLN	transgelin	2.80	1.4835	2.154E-29	238	201	238	770	758	614
PPPIA1	PTPRF interacting protein alpha 1	2.66	1.4091	2.104E-04	223	64	223	669	459	253
PSME2	proteasome activator subunit 2	2.43	1.2833	8.741E-03	201	105	201	242	1048	219
SURF4	surfactant 4	2.41	1.2716	2.039E-02	526	186	526	796	1203	227
CBS	cystathionine-beta-synthase	2.24	1.1622	9.434E-03	134	81	134	223	460	107
KLF10	Kruppel like factor 10	2.13	1.0897	2.599E-12	178	197	178	524	467	369
SAMD5	sterile alpha motif domain containing 5	2.00	1.0020	2.587E-26	439	390	439	1083	912	875
ITGA2	integrin subunit alpha 2	2.00	0.9994	1.739E-18	327	360	327	920	791	718
SPRY4	sprouty RTK signaling antagonist 4	1.98	0.9844	2.316E-05	180	338	180	572	498	491
C3	complement C3	1.88	0.9160	1.050E-12	273	222	273	590	484	511
CREG2	cellular repressor of E1A stimulated genes 2	1.87	0.9028	2.828E-15	523	422	523	1115	970	944
NFKB2	nuclear factor kappa B subunit 2	1.85	0.8902	2.837E-08	303	437	303	845	699	632
TRN1	RNA-ile	1.82	0.8721	7.318E-03	235	379	235	1635	669	586
CEACAM5	carcinoembryonic antigen related cell adhesion molecule 5	1.75	0.8089	5.410E-12	502	450	502	1190	944	811
TNFRSF12A	TNF receptor superfamily member 12A	1.75	0.8082	1.288E-10	544	695	544	1239	1067	1085
OSGIN1	oxidative stress induced growth inhibitor 1	1.74	0.7950	2.346E-17	453	446	453	991	818	830
ZNF239	zinc finger protein 239	1.73	0.7917	1.426E-09	283	236	283	585	495	497
EPHA4	EPH receptor A4	1.71	0.7754	1.199E-10	298	270	298	627	533	502
LAMC2	laminin subunit gamma 2	1.71	0.7752	5.095E-15	491	541	491	1094	966	947
TGIF1	TGFB induced factor homeobox 1	1.70	0.7619	1.716E-08	373	467	373	928	743	659
USP38	ubiquitin specific peptidase 38	1.69	0.7587	4.890E-12	410	394	410	862	714	649
NCOA7	nuclear receptor coactivator 7	1.69	0.7568	9.514E-16	487	466	487	1034	804	842
ANKRD33B	ankyrin repeat domain 33B	1.67	0.7418	3.775E-13	414	418	414	848	739	724
WOS2	omega oxidase synthase 2	1.67	0.7409	1.080E-11	379	344	379	751	645	629
GPCR5A	G protein-coupled receptor class C group 5 member A	1.66	0.7330	5.311E-04	368	626	368	988	844	716
SOC2	suppressor of cytokine signaling 2	1.64	0.7133	1.896E-11	510	512	510	1045	791	830
JUN	Jun proto-oncogene, AP-1 transcription factor subunit	1.63	0.7073	3.065E-06	236	252	236	534	453	378
ABCG2	ATP binding cassette subfamily G member 2 (junior blood group)	1.63	0.7054	1.449E-17	799	802	799	1623	1396	1382
RHOB	ras homolog family member B	1.61	0.6913	3.805E-09	390	350	390	801	660	601
PRSS23	serine protease 23	1.61	0.6834	1.412E-13	860	717	860	1654	1361	1305
TPIN1	TIMELESS interacting protein	1.60	0.6799	9.253E-08	513	379	513	879	699	753
JCAD	junctional cadherin 5 associated	1.59	0.6716	8.672E-08	456	592	456	1058	870	869
CLN5	CLN5 intracellular trafficking protein	1.59	0.6647	3.259E-07	389	322	389	675	626	549
RABEPK	Rab9 effector protein with ketch motifs	1.58	0.6591	7.350E-08	400	328	400	704	572	600
MARS2	serine protease 23	1.57	0.6505	8.469E-07	383	306	383	720	601	616
OAS3	2'-5'-oligoadenylate synthetase 3	1.57	0.6462	2.929E-07	482	373	482	786	690	715
CD3EAP	CD3e molecule associated protein	1.56	0.6451	6.105E-10	668	554	668	1275	1007	1085
MCAL2	microtubule associated monooxygenase, calponin and LIM domain containing 2	1.56	0.6444	7.683E-07	301	328	301	609	580	516
ICAM1	tumor associated calcium signal transducer 2	1.56	0.6438	6.937E-09	518	576	518	1001	851	901
LOC10274259	neuroblastoma breakpoint family member 1	1.54	0.6235	2.945E-06	449	457	449	801	757	642
RND3	Rho family GTPase 3	1.53	0.6140	1.826E-05	357	469	357	771	648	667
CLDN2	claudin 2, transcript variant 1	1.53	0.6146	1.740E-02	146	150	180	165	70	102
NES	nestin	1.53	0.6106	2.076E-09	525	462	525	941	808	801
GCLM	glutamate-cysteine ligase modifier subunit	1.52	0.6085	7.542E-06	379	426	379	717	672	590
ARHGAP45	Rho GTPase activating protein 45	1.52	0.6082	6.378E-07	324	334	324	658	535	525
AEN	apoptosis enhancing nuclease	1.52	0.6078	2.697E-11	851	770	851	1604	1355	1247
TNFRSF21	TNF receptor superfamily member 21	1.52	0.6069	1.933E-08	461	495	461	899	785	739
DDIAS	DNA damage induced apoptosis suppressor	1.52	0.6059	1.584E-10	702	608	702	1306	1075	1016
SLC8A2	solute carrier family 8 member A2	1.52	0.6047	2.586E-07	373	356	373	695	617	569
TGM2	transglutaminase 2	1.52	0.6027	4.473E-10	885	849	885	1537	1418	1294
POLR3D	RNA polymerase II subunit D	1.52	0.6009	2.098E-09	544	517	544	1022	790	827
CCN1	cellular communication network factor 1	1.52	0.5996	1.686E-04	318	297	318	513	462	457
TET3	tet methylcytosine dioxygenase 3	1.51	0.5988	9.523E-06	273	281	273	517	456	446
MMP1	matrix metalloproteinase 1	1.51	0.5926	4.129E-05	453	331	453	738	680	678
LYAR	Ly1 antibody reactive	1.51	0.5925	3.684E-10	915	805	915	1717	1254	1414
ETV5	ETS variant 5	1.50	0.5871	2.136E-03	288	419	288	600	559	513
ID2	inhibitor of DNA binding 2	1.50	0.5871	1.691E-11	959	970	959	1742	1477	1507
TRMT5	RNA methyltransferase 5	1.50	0.5857	7.021E-06	434	365	434	782	641	573
HIST1H2BH	histone cluster 1 H2B family member h	1.50	0.5845	3.439E-02	335	294	335	338	504	605
TXNIP	thioredoxin interacting protein	1.50	0.5835	3.817E-05	840	764	840	1857	1427	1189
ETS2	ETS proto-oncogene 2, transcription factor	1.50	0.5816	1.159E-04	364	446	364	713	656	572
HK2	hexokinase 2	1.50	0.5805	2.121E-07	716	864	716	1436	1257	1319
MAK16	MAK16 homolog	1.49	0.5771	5.548E-10	968	837	968	1861	1334	1362
PRMO5	PRMO5 domain containing 5	1.48	0.5679	4.316E-05	446	513	446	798	721	706
APOBEC3B	apolipoprotein B mRNA editing enzyme catalytic subunit 3B	1.48	0.5662	1.191E-10	699	663	699	1298	1034	1066
TNFAIP3	TNF alpha induced protein 3	1.48	0.5626	5.294E-07	433	415	433	816	657	636
SLC41A1	solute carrier family 41 member 1	1.48	0.5617	1.629E-06	441	477	441	832	743	673
NED09	neural precursor cell expressed, developmentally down-regulated 9	1.47	0.5600	1.533E-04	617	705	617	1088	1038	998
RBM12B	RNA binding motif protein 12B	1.47	0.5600	1.403E-05	601	455	601	1034	872	870
PAQR4	progesterin and adipoQ receptor family member 4	1.47	0.5591	4.642E-06	539	434	539	963	710	786
DYNLT3	dynein light chain Tctex-type 3	1.47	0.5574	3.898E-06	417	447	417	800	681	622
MLX	MAX dimerization protein MLX	1.47	0.5574	7.051E-10	869	891	869	1600	1290	1388
SLCO4A1	solute carrier organic anion transporter family member 4A1	1.47	0.5542	4.197E-04	292	354	292	600	474	458
KIF1A	kinesin family member 1A	1.47	0.5534	7.222E-05	519	624	519	955	844	825
CEP85	centrosomal protein 85	1.47	0.5533	7.875E-05	436	468	436	822	688	634
ZNF23P	zinc finger protein 252, pseudogene	1.47	0.5532	7.420E-05	327	307	327	616	541	463
CCZ1B	CCZ1 homolog B, vacuolar protein trafficking and biogenesis associated	1.47	0.5524	6.787E-04	426	377	426	589	671	670
FUT4	fucosyltransferase 4	1.46	0.5470	1.161E-07	614	568	614	1117	937	852
LIPG	lipase G, endothelial type	1.46	0.5447	1.739E-06	679	580	679	1171	1083	929
RBMXL1	RBMX like 1	1.46	0.5444	8.698E-05	437	339	437	680	594	565
TM4SF1	transmembrane 4 L six family member 1	1.46	0.5428	7.960E-03	466	686	466	972	895	713
ZNF1	zinc finger NFX1-type containing 1	1.45	0.5395	1.258E-08	856	752	856	1420	1227	1225
JAG1	jagged canonical Notch ligand 1	1.45	0.5388	2.727E-03	547	806	547	1111	993	954
NANP	N-acetylneuraminic acid phosphatase	1.45	0.5346	1.687E-04	328	289	328	543	482	438
OSTM1	osteoclastogenesis associated transmembrane protein 1	1.45	0.5324	5.456E-06	453	430	453	757	658	659
BMP4	bone morphogenetic protein 4	1.45	0.5318	3.925E-08	608	607	608	1096	895	941
OLR1	oxidized low density lipoprotein receptor 1	1.44	0.5298	3.353E-04	460	526	460	826	718	662
IGHMBP2	immunoglobulin mu DNA binding protein 2	1.44	0.5291	4.712E-05	455	418	455	790	636	639
EPB41L1	erythrocyte membrane protein band 4.1 like 1	1.44	0.5288	4.294E-08	662	684	662	1237	1075	977
MYBBP1A	MYB binding protein 1A	1.44	0.5281	1.032E-07	838	816	838	1429	1244	1210
EME1	essential meiotic structure-specific endonuclease 1	1.44	0.5239	7.387E-06	470	403	470	808	649	671
PHLDA1	pleckstrin homology like domain family A member 1	1.44	0.5239	3.783E-07	819	880	819	1553	1380	1218
INPP1	inositol polyphosphate-1-phosphatase	1.44	0.5234	6.153E-03	234	326	234	465	446	420
WDR3	WD repeat domain 3	1.44	0.5234	7.322E-09	939	940	939	1679	1467	1373
TARBP1	TAR (pHV-1) RNA binding protein 1	1.44	0.5227	3.067E-05	382	407	382	696	616	570
TNAGL1	tubulointerstitial nephritis antigen like 1	1.44	0.5217	1.336E-05	443	406	443	785	647	598
SFN	stratelin	1.43	0.5194	1.392E-06	722	688	722	1182	972	1041
EIF5A2	eukaryotic translation initiation factor 5A2	1.43	0.5187	4.751E-04	292	330	292	570	499	438
PXDC1	PX domain containing 1	1.43	0.5181	1.373E-05	552	643	552	1108	853	866
PKPFB3	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3	1.43	0.5181	1.924E-04	428	528	428	878	743	666
ZNF853	zinc finger protein 853	1.43	0.5180	2.168E-04	419	398	419	799	559	558
GDF11	growth differentiation factor 11	1.43	0.5175	4.075E-05	388	352	388	635	580	590
DDX31	DEAD-box helicase 31	1.43	0.5149	6.523E-06	441	454	441	841	699	689
SLC25A32	solute carrier family 25 member 32	1.43	0.5148	2.209E-05	400	405	400	694	604	588
ZNF202	zinc finger protein 202	1.43	0.5145	3.592E-05	453	397	453	834	643	630
LRWD1	leucine rich repeats and WD repeat domain containing 1	1.43	0.5141	6.663E-05	393	375	393	707	551	530
ALMS1	ALMS1 centrosome and basal body associated protein	1.43	0.5128	3.839E-04	476	405	476	741	590	745
ENTR1	endosome associated trafficking regulator 1	1.42	0.5108	7.618E-08	987	915	987	1806	1331	1391

PLS1	platein 1	1.42	0.5105	1.179E-05	552	625	552	1033	890	922
CGAS	cyclic GMP-AMP synthase	1.42	0.5095	4.776E-05	404	423	404	700	629	654
DSCC1	DNA replication and sister chromatid cohesion 1	1.42	0.5047	1.191E-04	398	339	398	636	547	531
PNKD	PNKD metallo-beta-lactamase domain containing	1.42	0.5039	2.061E-04	327	318	327	582	516	511
MAFG	MAF bZIP transcription factor G	1.42	0.5033	1.954E-03	484	644	484	981	885	745
HDAC5	histone deacetylase 5	1.42	0.5021	6.503E-05	513	601	513	1024	868	779
SPRTN	SprT-like N-terminal domain	1.41	0.4997	5.145E-05	374	353	374	635	546	551
UTP3	UTP3 small subunit processome component	1.41	0.4996	1.059E-05	506	461	506	849	715	773
INTS13	integrator complex subunit 13	1.41	0.4976	1.895E-08	1079	1042	1079	1855	1521	1516
BAIAP2	BAI1 associated protein 2	1.41	0.4970	6.509E-05	389	410	389	721	604	576
TMEM68	transmembrane protein 68	1.41	0.4956	1.495E-03	326	362	326	617	444	497
KNOP1	lysine rich nucleolar protein 1	1.41	0.4945	4.518E-06	1043	833	1043	1659	1297	1379
RASSF3	Ras association domain family member 3	1.41	0.4935	3.018E-05	524	565	524	862	731	820
UTP23	UTP23 small subunit processome component	1.41	0.4919	1.468E-03	374	277	374	561	496	497
PPM1F	protein phosphatase, Mg2+/Mn2+ dependent 1F	1.41	0.4916	2.461E-04	351	364	351	665	530	578
NUDT19	nucleic hydrolase 19	1.41	0.4909	2.809E-05	466	436	466	821	695	710
TOP2B	DNA topoisomerase III beta	1.40	0.4902	9.757E-04	369	309	369	647	493	493
HPS3	HPS3 biogenesis of lysosomal organelles complex 2 subunit 4	1.40	0.4899	1.480E-04	394	388	394	639	565	594
PIGG	phosphatidylinositol glycan anchor biosynthesis class G 3	1.40	0.4893	2.194E-04	417	341	417	657	553	563
SLC25A17	solute carrier family 25 member 17	1.40	0.4881	6.359E-05	477	439	477	788	630	655
INTS8	integrator complex subunit 8	1.40	0.4868	1.017E-05	521	482	521	894	746	710
TRMU	RNA 5-methylaminomethyl-2-thiouridylate methyltransferase	1.40	0.4866	2.231E-04	360	334	360	627	542	539
RRP12	ribosomal RNA processing 12 homolog	1.40	0.4838	3.894E-08	1060	1049	1060	1838	1544	1511
CSTF3	cleavage stimulation factor subunit 3	1.40	0.4834	1.725E-04	813	914	813	1425	1191	1149
SLC1A3	solute carrier family 1 member 3	1.40	0.4826	1.325E-05	579	591	579	992	899	821
G2E3	G2M-phase specific E3 ubiquitin protein ligase	1.40	0.4826	5.007E-04	392	416	392	680	587	541
PPAN-PRY11	PPAN-PRY11 readthrough	1.40	0.4824	1.157E-06	846	753	846	1471	1160	1144
SLC25A22	solute carrier family 25 member 22	1.40	0.4823	3.880E-06	579	567	579	1043	842	867
SPATA2	gametogenesis associated 2	1.39	0.4793	2.461E-06	754	656	754	1257	1085	1061
B3GAT3	beta-1,3-glucuronyltransferase 3	1.39	0.4790	2.591E-04	570	465	570	938	685	812
CDG5	CDP-diacylglycerol synthase 1	1.39	0.4785	2.320E-04	416	400	416	732	623	551
NOL8	nucleolar protein 8	1.39	0.4782	1.401E-03	380	323	380	708	512	524
CTot174	chromosome 1 open reading frame 174	1.39	0.4780	1.988E-05	559	489	559	960	771	751
CEP41	centriosomal protein 41	1.39	0.4779	6.649E-04	342	319	342	610	450	511
ETV4	ETS variant 4	1.39	0.4779	1.243E-05	847	959	847	1619	1399	1266
LRRCB8	leucine rich repeat containing 8 VRAC subunit 8	1.39	0.4774	3.495E-04	388	347	388	631	567	584
UQCQC1	ubiquinol-cytochrome c reductase complex assembly factor 1	1.39	0.4772	1.111E-07	1001	1018	1001	1754	1448	1496
KLHL18	kelch like family member 18	1.39	0.4771	9.582E-04	396	315	396	622	544	567
WASHC2A	WASH complex subunit 2A	1.39	0.4769	5.288E-07	864	880	864	1578	1255	1320
EXO6C	exocyst complex component 6	1.39	0.4769	3.691E-04	425	355	425	691	552	544
SKA3	spindle and kinetochore associated complex subunit 3	1.39	0.4754	5.007E-06	787	718	787	1236	1031	1078
RIOK2	ribosomal oncogene 2	1.39	0.4749	1.952E-05	537	531	537	869	741	804
IL4R	interleukin 4 receptor	1.39	0.4731	3.698E-04	462	394	462	771	652	690
IL17RB	interleukin 17 receptor B	1.39	0.4720	4.973E-05	510	501	510	899	707	681
SLC3B2	solute carrier family 9 member B2	1.39	0.4715	1.150E-03	332	329	332	567	496	440
SMC1B	structural maintenance of chromosomes 1B	1.39	0.4713	4.783E-04	367	340	367	660	509	496
IFRD1	interferon related developmental regulator 1	1.39	0.4711	3.081E-05	1041	1186	1041	1846	1510	1580
BICD2	BICD cargo adaptor 2	1.39	0.4707	5.584E-04	401	398	401	694	580	522
MYADM	myeloid associated differentiation marker	1.38	0.4695	9.916E-06	670	733	670	1202	1010	974
PNO1	partner of NOB1 homolog	1.38	0.4686	1.457E-05	843	708	843	1316	1053	1096
SM2	SM bHLH transcription factor 2	1.38	0.4679	1.577E-03	313	325	313	565	462	428
PFAS	phosphoribosylformylglycinamide synthase	1.38	0.4675	1.085E-04	531	438	531	847	711	700
PKD1	polycystin 1, transient receptor potential channel interacting	1.38	0.4667	6.555E-04	366	418	366	710	571	557
CSNK1G1	casein kinase 1 gamma 1	1.38	0.4663	7.931E-05	467	476	467	805	685	657
SLC7A8	solute carrier family 7 member 8	1.38	0.4657	9.942E-03	277	329	277	496	445	393
LNCRAD	lncRNA activating regulator of DNK1	1.38	0.4646	1.129E-03	401	442	401	695	565	605
PLRT3	plateletlet leucine rich transmembrane protein 3	1.38	0.4637	1.854E-04	681	708	681	1193	981	882
RAP2B	RAP2B, member of RAS oncogene family	1.38	0.4632	4.760E-05	651	713	651	1159	1085	1022
QSOX2	quiescin sulphydryl oxidase 2	1.38	0.4619	1.062E-05	714	720	714	1323	1074	979
FBXL14	F-box and leucine rich repeat protein 14	1.38	0.4610	1.129E-03	340	326	340	626	502	510
LYRM1	LYRM motif containing 1	1.38	0.4604	1.642E-04	543	500	543	881	679	768
GPX2	glutathione peroxidase 2	1.38	0.4600	3.048E-03	557	706	557	1041	879	827
RALGAP2A	Rai GTPase activating protein catalytic alpha subunit 2	1.37	0.4592	1.513E-05	804	843	804	1370	1124	1251
CDC47	cell division cycle associated 7	1.37	0.4586	4.061E-05	1147	916	1147	1871	1574	1491
ZNFX51	zinc finger protein 451	1.37	0.4584	8.000E-03	314	295	314	444	467	441
RAB31	RAB31, member RAS oncogene family	1.37	0.4576	2.253E-03	402	422	402	685	578	525
CL22A29	chromosome 12 open reading frame 29	1.37	0.4566	1.780E-03	428	335	428	688	522	552
TC3H8	zinc finger CCHC-type containing 8	1.37	0.4560	4.063E-03	324	327	324	490	483	503
SLF1	SMCS-SMCK complex localization factor 1	1.37	0.4559	1.689E-03	371	299	371	591	494	491
UTP15	UTP15 small subunit processome component	1.37	0.4556	2.225E-05	629	580	629	1011	867	884
SNAPC4	small nuclear RNA activating complex polypeptide 4	1.37	0.4556	3.947E-03	315	280	315	510	463	397
CCDC14	coiled-coil domain containing 14	1.37	0.4553	7.225E-05	514	500	514	928	706	727
IGF1R	insulin like growth factor 1 receptor	1.37	0.4552	7.097E-04	583	631	583	1020	846	769
LZIC	leucine zipper and CTNBP1 domain containing	1.37	0.4547	3.680E-04	661	534	661	961	900	928
IL6R	interleukin 6 receptor	1.37	0.4543	7.194E-04	366	340	366	643	531	514
SRP19	signal recognition particle 19	1.37	0.4535	7.516E-05	501	492	501	886	689	705
NUPR1	nuclear FMR1 interacting protein 1	1.37	0.4521	9.151E-04	510	456	510	835	602	704
PTER	phosphotriesterase related	1.37	0.4520	8.085E-06	529	491	529	864	692	734
ZNFX52	zinc finger protein 502	1.37	0.4520	4.241E-04	492	428	492	761	711	647
ANKK6	ankyrin repeat and sterile alpha motif domain containing 6	1.37	0.4520	4.416E-04	382	360	382	629	530	555
DMHD	DM1 locus, WD repeat containing	1.37	0.4519	1.379E-03	395	389	395	711	537	511
DZP3	DAZ interacting zinc finger protein 3	1.37	0.4514	6.927E-04	489	428	489	853	617	711
SLC25A4	solute carrier family 25 member 4	1.37	0.4512	4.262E-04	547	458	547	911	778	705
PUS7L	pseudouridine synthase 7 like	1.37	0.4509	2.888E-04	710	564	710	1011	934	935
PLA2G15	phospholipase A2 group XV	1.37	0.4502	7.904E-04	354	341	354	618	521	510
ATAD1	ATPase family AAA domain containing 1	1.37	0.4497	1.314E-02	359	337	359	491	500	596
TBC1D19	TBC1 domain family member 19	1.36	0.4473	1.051E-02	317	334	317	507	511	415
MTAP	methylthioadenosine phosphorylase	1.36	0.4465	1.371E-05	765	690	765	1263	1086	1096
REXO1	RNA exonuclease 1 homolog	1.36	0.4451	1.673E-03	362	310	362	582	506	494
SH3GLB1	SH3 domain containing GRB2 like, endophilin B1	1.36	0.4449	7.145E-05	605	578	605	954	857	827
IDS	iduronate 2-sulfatase	1.36	0.4447	3.021E-03	351	345	351	576	548	463
RPIA	ribose 5-phosphate isomerase A	1.36	0.4434	1.134E-05	780	676	780	1224	1028	1032
ITGA8	integrin subunit alpha 8	1.36	0.4431	8.213E-04	547	584	547	935	713	806
CIGALT1	core 1 synthase, glycoprotein-N-acetylgalactosamine 3 beta-galactosyltransferase 1	1.36	0.4423	1.620E-05	957	1037	957	1635	1436	1394
ODX11	OEADH-box helicase 11	1.36	0.4414	1.640E-04	577	541	577	1029	836	921
WASHC2C	WASH complex subunit 2A	1.36	0.4410	3.482E-05	757	654	757	1262	1049	1015
ALKB2	alkB homolog 2, alpha-ketoglutarate dependent dioxygenase	1.36	0.4409	6.514E-04	395	379	395	670	546	531
NETO2	neuropilin and tolloid like 2	1.36	0.4401	4.793E-04	515	478	515	838	775	673
PVR	PVR cell adhesion molecule	1.36	0.4400	1.380E-04	585	497	585	934	780	774
PAFAH2	platelet activating factor acetylhydrolase 2	1.36	0.4386	6.463E-03	368	283	368	548	444	469
NRARP	NOTCH regulated ankyrin repeat protein	1.36	0.4385	4.670E-03	370	328	370	627	581	509
PLPBP	pyridoxal phosphate binding protein	1.35	0.4376	1.037E-05	955	976	955	1625	1321	1316
ZNFX143	zinc finger protein 143	1.35	0.4362	4.316E-04	745	784	745	1215	977	1054
CHDH	choline dehydrogenase	1.35	0.4355	2.600E-03	498	393	498	819	646	692
MED10	mediator complex subunit 10	1.35	0.4352	3.567E-04	621	567	621	1037	750	851
ZC3H4	zinc finger CCHC-type containing 4	1.35	0.4350	1.715E-04	640	607	640	1164	925	915
EEF1AKM4	EEF1A lysine methyltransferase 4	1.35	0.4350	5.959E-03	350	373	350	605	458	493
TACC1	transforming acidic coiled-coil containing protein 1	1.35	0.4348	7.005E-04	478	439	478	734	640	636
GEN1	GEN1 Holliday junction 5' flap endonuclease	1.35	0.4344	1.128E-03	456	396	456	774	616	583
DOT1L	DOT1 like histone lysine methyltransferase	1.35	0.4343	1.306E-05	1046	1128	1046	1901	1488	1539
TRMT61A	RNA methyltransferase 61A	1.35	0.4342	6.889E-05	923	774	923	1511	1212	1271
CHML	CHM like Rab escort protein	1.35	0.4341	8.392E-04	479	418				

ZNF121	zinc finger protein 121	1.35	0.4325	5.725E-03	368	408	368	728	616	538
HTATSF5P2	HIV-1 Tat specific factor 1 pseudogene 2	1.35	0.4323	9.702E-04	587	479	587	964	722	724
ZNF28	zinc finger protein 28	1.35	0.4314	1.436E-03	410	348	410	642	539	537
ZNF473	zinc finger protein 473	1.35	0.4310	3.195E-03	419	339	419	658	511	523
TUBA4A	tubulin alpha 4a	1.35	0.4302	9.553E-05	741	653	741	1206	906	979
ITPR3	inositol 1,4,5-trisphosphate receptor type 3	1.35	0.4285	4.505E-04	998	1177	998	1913	1445	1452
ZNF271P	zinc finger protein 271 pseudogene	1.35	0.4285	1.193E-03	396	357	396	660	532	532
FAM114A2	family with sequence similarity 114 member A2	1.35	0.4282	4.733E-03	348	288	348	553	466	449
PPM1H	protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent 1H	1.35	0.4282	3.936E-05	833	726	833	1306	1113	1109
DKK3	Dickkopf WNT signaling pathway inhibitor 3	1.35	0.4262	4.442E-05	690	670	690	1140	967	911
PNISR	PHN interacting serine and arginine rich protein	1.34	0.4274	3.490E-02	346	241	346	534	459	372
NCR3LG1	natural killer cell cytotoxicity receptor 3 ligand 1	1.34	0.4264	3.942E-04	629	522	629	941	816	803
GDI1	GDP dissociation inhibitor 1	1.34	0.4260	4.507E-05	658	671	658	1150	956	925
PARP12	poly(ADP-ribose) polymerase family member 12	1.34	0.4258	1.853E-03	401	360	401	693	543	552
FILIP1L	filamin A interacting protein 1 like	1.34	0.4257	2.931E-04	747	723	747	1263	1027	1193
TYSD1	tyrosin domain containing 1	1.34	0.4248	6.232E-05	1073	982	1073	1891	1445	1526
KOM5B	lysine demethylase 1B	1.34	0.4238	8.739E-03	402	328	402	626	535	473
EXD2	exonuclease 3 (5') domain containing 2	1.34	0.4234	1.652E-04	617	554	617	1021	795	826
XPNPEP3	X-prolyl aminopeptidase 3	1.34	0.4234	1.588E-03	465	493	465	759	635	682
SH3PX2B	SH3 and PX domains 2B	1.34	0.4230	1.956E-03	381	403	381	654	528	577
SGO1A	suppressor of glucose, autophagy associated 1	1.34	0.4224	1.937E-05	947	972	947	1685	1353	1343
PHETA1	PH domain containing endocytic trafficking adaptor 1	1.34	0.4218	2.816E-03	399	426	399	727	629	561
KIFC3	kinesin family member C3	1.34	0.4218	2.506E-03	693	838	693	1285	958	1051
LOC107984316	ubiquitin conjugating enzyme E2 Q1	1.34	0.4213	1.988E-03	395	356	395	641	501	540
GLS	glutaminase	1.34	0.4203	2.939E-04	629	673	629	1121	990	912
RP2	RP2 activator of ARL3 GTPase	1.34	0.4197	3.733E-03	647	766	647	1062	966	959
GAREM2	GRB2 associated regulator of MAPK1 subtype 2	1.34	0.4194	3.359E-04	518	521	518	888	737	706
ADAM19	ADAM metallopeptidase domain 19	1.34	0.4194	1.408E-05	988	954	988	1630	1384	1319
LSG1	large 60S subunit nuclear export GTPase 1	1.34	0.4193	1.479E-03	1143	828	1143	1718	1425	1277
ZDHHC6	zinc finger DHHC-type containing 6	1.34	0.4188	1.020E-03	529	448	529	822	687	662
POLR1C	RNA polymerase I and III subunit C	1.34	0.4188	3.860E-03	387	357	387	667	496	492
RALGAP1L	Ral GTPase activating protein catalytic alpha subunit 1	1.34	0.4186	1.065E-02	305	273	305	502	451	393
LSMB	LSMB homolog, UB small nuclear RNA associated	1.34	0.4180	1.863E-04	614	631	614	1088	867	848
PABPC1L	poly(A) binding protein cytoplasmic 1 like	1.34	0.4178	1.057E-02	341	333	341	644	490	437
PELO	pelota mRNA surveillance and ribosome rescue factor	1.34	0.4173	6.471E-04	535	552	535	906	749	714
RAB11FIP2	RAB11 family interacting protein 2	1.34	0.4172	4.552E-05	817	753	817	1341	1086	1077
FAM83F	family with sequence similarity 83 member F	1.34	0.4170	2.465E-04	550	535	550	888	757	789
TMCC1	transmembrane and coiled-coil domain family 1	1.34	0.4170	1.143E-02	376	329	376	585	481	436
EGFR-AS1	EGFR antisense RNA 1	1.33	0.4165	7.728E-03	596	418	596	899	729	721
SK1B	salt inducible kinase 1B (putative)	1.33	0.4157	1.623E-02	322	316	322	472	485	425
NCMR	nucleosome maintenance 8 homologous recombination repair factor	1.33	0.4156	5.416E-05	840	778	840	1404	1151	1113
PPAN	pester pan homolog	1.33	0.4146	5.091E-05	766	713	766	1303	1046	1042
COP9A	COP9 signalosome subunit 7A	1.33	0.4145	1.531E-04	1208	983	1208	1838	1470	1597
CHAF1B	chromatin assembly factor 1 subunit B	1.33	0.4143	1.695E-03	471	411	471	704	619	632
LINC00667	long intergenic non-protein coding RNA 667	1.33	0.4137	4.737E-03	394	358	394	692	556	509
URB1	URB1 ribosome biogenesis homolog	1.33	0.4134	1.450E-05	1116	1008	1116	1776	1486	1462
ADAP1	ArhGAP with dual PH domains 1	1.33	0.4131	5.532E-04	912	719	912	1379	1100	1149
FBXO45	F-box protein 45	1.33	0.4128	6.504E-05	1092	922	1092	1688	1409	1384
KNTC1	kinetochore associated 1	1.33	0.4126	8.830E-04	476	476	476	794	701	648
ER12	ER12 exoribonuclease family member 2	1.33	0.4125	1.015E-02	431	335	431	696	527	506
HYAL2	hyaluronidase 2	1.33	0.4125	2.815E-04	860	724	860	1347	1089	1187
RIT1A	RBP1 interacting and tubulin associated 1	1.33	0.4122	2.067E-04	828	681	828	1245	1048	1067
SLC25A15	solute carrier family 25 member 15	1.33	0.4117	6.206E-04	906	720	906	1406	1188	1140
UTP14A	UTP14A small subunit processome component	1.33	0.4116	2.181E-03	995	751	995	1546	1119	1271
TMEM52B	transmembrane protein 52B	1.33	0.4114	3.638E-03	558	657	558	923	883	842
TNFRSF10D	TNF receptor superfamily member 10d	1.33	0.4107	3.939E-02	531	714	531	944	781	806
WDK73	WD repeat domain 73	1.33	0.4105	1.261E-02	434	335	434	680	523	493
TMEM43	transmembrane protein 43	1.33	0.4104	2.094E-05	1194	1105	1194	1914	1525	1674
ATG4B	autophagy related 4B cysteine peptidase	1.33	0.4100	1.508E-04	702	759	702	1184	1029	1045
RPS27P3	ribosomal protein S27 pseudogene 3	1.33	0.4100	1.933E-02	771	683	771	1338	810	916
ICE2	interactor of little elongation complex ELL subunit 2	1.33	0.4098	2.788E-04	765	650	765	1193	922	991
CCDC137	coiled-coil domain containing 137	1.33	0.4091	5.002E-03	442	350	442	675	551	556
C11orf24	chromosome 11 open reading frame 24	1.33	0.4087	1.087E-04	1004	886	1004	1617	1400	1312
ALAS1	5'-aminolevulinate synthase 1	1.33	0.4082	8.445E-05	1013	967	1013	1563	1389	1321
KBTBD6	ketch repeat and BTB domain containing 6	1.33	0.4081	1.411E-02	448	328	448	634	557	611
PUS7	pseudouridine synthase 7	1.33	0.4080	1.927E-04	957	830	957	1490	1260	1159
MLKL	mixed lineage kinase domain like pseudokinase	1.33	0.4077	5.590E-03	387	342	387	589	488	552
OTULINL	OTU deubiquitinase with linear linkage specificity like	1.33	0.4075	3.959E-03	345	328	345	564	482	482
ZWILCH	zwilch kinetochore protein	1.33	0.4073	1.896E-04	760	696	760	1175	1015	953
RBM18	RNA binding motif protein 18	1.33	0.4071	2.623E-03	388	279	388	645	521	516
IRAK4	interleukin 1 receptor associated kinase 4	1.33	0.4067	8.639E-03	325	338	325	531	474	440
TMEM168	transmembrane protein 168	1.33	0.4067	2.055E-03	609	670	609	997	837	873
RBM34	RNA binding motif protein 34	1.33	0.4063	1.357E-04	955	859	955	1601	1223	1324
RUVEL1	RuB like AAA ATPase 1	1.33	0.4061	6.551E-05	1199	1116	1199	1929	1508	1536
NDUFA4	NADH:ubiquinone oxidoreductase complex assembly factor 4	1.32	0.4058	2.725E-03	493	537	493	679	653	707
RAB3B	RAB3B, member RAS oncogene family	1.32	0.4054	8.468E-03	484	570	484	802	749	690
SUGP2	SURP and G-patch domain containing 2	1.32	0.4052	3.649E-03	374	380	374	657	544	510
NCES1	neuronal calcium sensor 1	1.32	0.4052	2.055E-03	419	417	419	710	573	571
TRNP1	Trs1 RNA 2'-O-methyltransferase 3	1.32	0.4050	1.014E-03	751	828	751	1280	1052	1014
ITGA6	integrin subunit alpha 6	1.32	0.4045	2.636E-05	1051	1060	1051	1776	1479	1440
FGFR1	Fibroblast growth factor receptor 1	1.32	0.4043	2.535E-03	626	634	626	975	812	793
TNFAIP8L2 SCHN1	diacylglycerol kinase zeta	1.32	0.4038	1.723E-03	536	511	536	893	654	747
PWP1	protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent 1H	1.32	0.4036	4.551E-05	995	904	995	1588	1303	1289
ZFP64	ZFP64 zinc finger protein	1.32	0.4034	3.693E-03	450	385	450	677	554	581
ERVVK3-1	endogenous retrovirus group K3 member 1	1.32	0.4028	3.145E-03	638	573	638	931	777	804
SCNM1	sodium channel modifier 1	1.32	0.4025	1.650E-03	534	516	534	891	658	747
UTP6	UTP6 small subunit processome component	1.32	0.4022	8.330E-05	1230	1097	1230	1837	1552	1646
DUS2	dihydropyrimidine synthase 2	1.32	0.4021	6.113E-04	553	508	553	868	724	747
FAM83G	family with sequence similarity 83 member G	1.32	0.4020	8.617E-04	798	904	798	1368	1118	1182
RP22	ribosome production factor 2 homolog	1.32	0.4018	7.533E-04	1003	804	1003	1590	1238	1315
SPRED1	sprouty related EVH1 domain containing 1	1.32	0.4017	2.568E-02	407	507	407	732	594	579
TUFT1	tuftsin 1	1.32	0.4016	4.639E-02	350	403	350	607	477	447
HLCS	holocarboxylase synthetase	1.32	0.4014	5.464E-04	693	606	693	1145	929	940
CSNK1D	casein kinase 1 delta	1.32	0.4014	8.745E-05	1118	1182	1118	1925	1581	1525
LANA3	laminin subunit alpha 3	1.32	0.4003	1.940E-02	399	348	399	622	478	490
STK32B	serine/threonine kinase 32B	1.32	0.3996	8.587E-03	428	399	428	616	628	620
ZNF468	zinc finger protein 468	1.32	0.3993	1.538E-03	520	457	520	799	678	657
POGK	zogo transposable element derived with KRAB domain	1.32	0.3993	8.581E-05	1033	941	1033	1700	1407	1335
CYREN	cell cycle regulator of NHEJ	1.32	0.3989	8.465E-05	1050	938	1050	1705	1348	1343
CELSR1	cadherin EGF LAG seven-pass G-type receptor 1	1.32	0.3988	1.939E-03	566	620	566	1019	780	888
ORMDL1	ORMDL sphingolipid biosynthesis regulator 1	1.32	0.3985	1.590E-02	314	322	314	509	447	407
RBIS	ribosomal biogenesis factor	1.32	0.3984	8.301E-03	471	401	471	803	563	584
WWP1	WW domain containing E3 ubiquitin protein ligase 1	1.32	0.3984	1.135E-04	813	816	813	1349	1127	1138
ZNF8-ERVVK3-1	ZNF8-ERVVK3-1 readthrough	1.32	0.3978	1.139E-03	720	664	720	1082	892	918
TPCN1	two pore segment channel 1	1.32	0.3977	5.923E-04	641	599	641	1060	925	862
E2F5	E2F transcription factor 5	1.32	0.3977	1.275E-02	431	547	431	783	659	675
CTP5B1	CTP synthase 1	1.32	0.3975	3.291E-04	871	754	871	1390	1170	1127
PDE4D	phosphodiesterase 4D	1.32	0.3975	1.794E-03	605	558	605	920	874	764
MRLP17	mitochondrial ribosomal protein L17	1.32	0.3975	5.520E-04	852	738	852	1403	1125	1060
MPM15	matrix metalloproteinase 15	1.32	0.3974	3.002E-04	887	973	887	1526	1247	1343
HEPH	hephaestin	1.32	0.3973	1.219E-03	529	548	5			

CSNK1E	casein kinase 1 epsilon	1.32	0.3960	2.195E-04	860	877	860	1493	1230	1147
SAFB2	scaffold attachment factor B2	1.32	0.3954	1.125E-04	1020	1065	1020	1709	1407	1514
FADS3	fatty acid desaturase 3	1.32	0.3954	3.036E-03	579	525	579	1018	714	771
BGAL13	beta-1,4-galactosyltransferase 3	1.31	0.3949	2.052E-04	688	714	688	1170	975	954
TP53RK	TP53 regulating kinase	1.31	0.3940	7.411E-04	562	544	562	898	782	761
METTL8	methyltransferase like 8	1.31	0.3940	7.448E-04	821	671	821	1224	994	1088
CEP170B	centrosomal protein 170B	1.31	0.3938	1.077E-03	865	963	865	1486	1353	1192
KLHL21	kelch like family member 21	1.31	0.3934	1.417E-03	700	813	700	1259	1035	991
THADA	THADA armadillo repeat containing	1.31	0.3934	7.230E-04	819	714	819	1219	1153	1043
PRPF3	pre-mRNA processing factor 3	1.31	0.3926	2.854E-04	820	752	820	1273	1130	1064
GRPEL1	GrpE like 1	1.31	0.3923	4.420E-04	969	1018	969	1541	1319	1344
GAR1	GAR1 ribonucleoprotein	1.31	0.3917	2.464E-03	518	444	518	776	685	688
HOXC12	homeobox C12	1.31	0.3910	5.066E-03	369	382	369	622	515	527
ERLIN2	ER lipid raft associated 2	1.31	0.3909	1.241E-03	864	685	864	1290	1096	1039
DYRK2	dual specificity tyrosine phosphorylation regulated kinase 2	1.31	0.3909	3.089E-04	677	632	677	1064	876	921
TPTEP2-CSNK1E	TPTEP2-CSNK1E readthrough	1.31	0.3907	2.608E-04	868	896	868	1505	1238	1184
MTX2	metaxin 2	1.31	0.3899	3.574E-03	691	595	691	1098	814	899
KIF18B	kinesin family member 18B	1.31	0.3889	2.421E-04	733	705	733	1152	982	958
NIPAL1	NIPA like domain containing 1	1.31	0.3889	1.543E-02	339	284	339	501	446	437
ZNF107	zinc finger protein 107	1.31	0.3884	7.939E-03	414	362	414	697	538	553
GOLGA1	golgin A1	1.31	0.3875	1.870E-02	397	318	397	650	477	499
GPATCH2L	G-patch domain containing 2 like	1.31	0.3875	4.987E-03	513	514	513	758	715	756
PF0N4	prefoldin subunit 4	1.31	0.3862	1.260E-02	610	554	610	1118	800	722
BRCA2	BRCA2 DNA repair associated	1.31	0.3861	1.846E-03	758	693	758	1066	980	1063
EAR52	SIAR related lipid transfer domain containing 4	1.31	0.3857	6.119E-03	569	444	569	825	684	716
EFNB2	ephrin B2	1.31	0.3857	4.894E-02	488	611	488	812	723	669
DEAH32	DEAH-box helicase 32 (putative)	1.31	0.3856	2.571E-02	395	436	395	710	532	502
ATP10B	ATPase phospholipid transporting 10D (putative)	1.31	0.3854	2.124E-04	961	1008	961	1574	1335	1367
HJURP	Holiday junction recognition protein	1.31	0.3851	4.368E-04	681	636	681	1123	917	901
ZNF641	zinc finger protein 641	1.31	0.3850	1.802E-03	508	534	508	863	717	734
LINC0205	long intergenic non-protein coding RNA 205	1.31	0.3849	1.428E-02	568	450	568	893	632	778
XPO4	exportin 4	1.31	0.3848	2.076E-03	884	698	884	1319	1096	1049
LINC01963	long intergenic non-protein coding RNA 1963	1.31	0.3848	1.005E-02	461	422	461	647	595	629
OLA	galactosidase alpha	1.31	0.3847	4.736E-03	635	683	635	1011	852	863
RFFL	ring finger and FYVE like domain containing E3 ubiquitin protein ligase	1.31	0.3847	7.032E-04	816	879	816	1421	1160	1115
TWISTNB	Twist1 neighbor	1.31	0.3845	4.832E-04	840	728	840	1271	1092	1035
SFXN4	sideroflexin 4	1.31	0.3844	1.780E-04	775	736	775	1220	1042	1051
MTG2	mitochondrial ribosome associated GTPase 2	1.31	0.3843	2.895E-03	668	565	668	1073	848	893
CACNA3H	calcium voltage-gated channel subunit alpha1 H	1.31	0.3842	3.053E-02	340	433	340	616	514	521
POLR3H	RNA polymerase II subunit H	1.31	0.3841	3.896E-04	745	686	745	1128	960	1014
STK4	serine/threonine kinase 4	1.30	0.3836	7.907E-03	411	352	411	609	527	543
ZNF76	zinc finger HMT-type containing 6	1.30	0.3836	4.869E-03	422	428	422	680	599	580
CCM2	CCM2 scaffold protein	1.30	0.3831	1.661E-03	601	589	601	1027	786	871
NFK	nucleolar protein interacting with the FHA domain of MKI67	1.30	0.3819	2.375E-03	1317	998	1317	1907	1537	1655
KLF16	Kruppel like factor 16	1.30	0.3818	1.008E-02	358	391	358	623	518	549
ZNF326	zinc finger protein 326	1.30	0.3817	5.345E-03	774	590	774	1158	952	1017
TBX3	T-box transcription factor 3	1.30	0.3815	3.004E-02	347	424	347	577	574	523
PDCD2	programmed cell death 2	1.30	0.3815	4.631E-04	1062	997	1062	1650	1306	1365
HABP4	hyaluronan binding protein 4	1.30	0.3813	2.548E-03	502	501	502	859	659	691
TRMT6	RNA methyltransferase 6	1.30	0.3804	1.455E-03	887	718	887	1307	1095	1127
UBIAD1	Uba1 pseudotransferase domain containing 1	1.30	0.3801	1.401E-03	571	573	571	979	796	785
LRCH1	leucine rich repeats and calponin homology domain containing 1	1.30	0.3797	2.226E-02	434	514	434	732	589	671
ZNF890	zinc finger protein 890	1.30	0.3793	9.904E-03	420	373	420	607	566	579
RP38	ribonuclease P/MRP subunit p38	1.30	0.3792	2.076E-03	525	491	525	845	675	704
NOL10	nucleolar protein 10	1.30	0.3791	3.437E-04	1088	956	1088	1759	1371	1414
NOL9	nucleolar protein 9	1.30	0.3789	7.555E-03	487	464	487	775	718	607
FTSJ3	FtsJ RNA 2'-O-methyltransferase 3	1.30	0.3787	3.976E-04	915	878	915	1482	1158	1289
DERPC	DERPC proline and glycine rich nuclear protein	1.30	0.3786	2.360E-03	919	752	919	1386	1171	1065
ZBTB14	zinc finger and BTB domain containing 14	1.30	0.3785	3.126E-02	390	372	390	587	447	539
MAP3K21	mitogen-activated protein kinase kinase kinase 21	1.30	0.3781	2.489E-02	376	397	376	592	497	494
PIP4K2A	phosphatidylinositol-5-phosphate 4 kinase type 2 alpha	1.30	0.3781	2.856E-03	601	510	601	941	740	748
TRIB1	tribbles pseudokinase 1	1.30	0.3780	3.156E-02	395	411	395	677	578	463
NOP16	NOP16 nucleolar protein	1.30	0.3779	1.253E-03	1295	1022	1295	1844	1571	1614
GEMIN4	gem nuclear organelle associated protein 4	1.30	0.3778	1.840E-03	719	596	719	1119	901	897
ZNF480	zinc finger protein 480	1.30	0.3773	1.165E-02	376	336	376	593	516	477
GALNT3	polypeptide N-acetylgalactosaminyltransferase 3	1.30	0.3764	2.461E-03	586	596	586	973	762	773
AKAP11	A-kinase anchoring protein 11	1.30	0.3762	7.258E-04	1015	886	1015	1511	1351	1377
SCAR33	scavenger receptor class A member 3	1.30	0.3759	1.853E-03	689	603	689	1128	904	867
CL2orf46	chromosome 12 open reading frame 45	1.30	0.3758	7.511E-03	639	544	639	931	728	870
TMEM138	transmembrane protein 138	1.30	0.3757	2.074E-02	408	316	408	587	514	504
SH3BGRL3	SH3 domain binding glutamate rich protein like 3	1.30	0.3756	1.054E-03	810	732	810	1309	1056	1125
PIR	pirin	1.30	0.3751	8.135E-03	460	437	460	778	609	570
METTL1	methyltransferase like 1	1.30	0.3749	1.662E-02	450	371	450	738	555	551
MTIF2	mitochondrial translational initiation factor 2	1.30	0.3748	1.285E-03	1243	1016	1243	1949	1509	1608
SYCP2	synaptonemal complex protein 2	1.30	0.3744	4.047E-04	1162	1035	1162	1893	1521	1506
POLR1E	RNA polymerase I subunit E	1.30	0.3742	4.511E-03	572	478	572	848	695	742
TCF7	transcription factor 7	1.30	0.3737	6.414E-04	769	788	769	1234	1106	1078
FBX05	F-box protein 5	1.30	0.3732	6.251E-03	598	670	598	997	806	851
NUP58	nucleoporin 58	1.30	0.3731	2.776E-03	746	609	746	1064	914	918
PRKX	protein kinase X-linked	1.30	0.3730	9.069E-03	423	391	423	698	589	561
KLC4	kinesin light chain 4	0.78	-0.3622	4.228E-07	628	521	628	606	485	485
SNR181	snRNP18 beta 1	0.77	-0.3842	1.233E-11	1119	1271	1119	1123	931	922
EHADH	enoyl-CoA hydratase and 3-hydroxyacyl CoA dehydrogenase	0.77	-0.3863	8.060E-14	1355	1204	1355	1262	1001	1072
ABCA1	ATP binding cassette subfamily A member 1	0.76	-0.3906	9.493E-07	658	520	658	562	480	524
WWTR1	WW domain containing transcription regulator 1	0.76	-0.4000	1.084E-13	1088	1049	1088	1050	766	854
COBLL1	corda1-like WH2 repeat protein like 1	0.75	-0.4058	1.498E-09	618	596	618	620	472	506
CLK1	CDC like kinase 1	0.75	-0.4076	7.900E-11	718	759	718	713	553	532
FOXN3	forkhead box N3	0.75	-0.4184	3.058E-08	1184	1555	1184	1225	989	1032
KDM4A	lysine demethylase 4A	0.75	-0.4232	2.566E-07	579	720	579	570	501	469
DAPK1	death associated protein kinase 1	0.74	-0.4270	1.285E-09	726	632	726	716	502	527
PGPEP1	pyroglutamate peptidase I	0.74	-0.4343	4.420E-10	557	611	557	540	459	453
EFNA1	ephrin A1	0.74	-0.4428	8.248E-14	888	881	888	839	648	612
ZNF33B	zinc finger protein 33B	0.73	-0.4584	1.414E-10	642	739	642	669	536	509
CSW115	chromosome 1 open reading frame 115	0.72	-0.4628	1.411E-16	2091	1746	2091	1807	1432	1525
TNKS1	tenin 1	0.72	-0.4726	2.088E-13	733	778	733	722	573	583
OVOL1	ovo like transcriptional repressor 1	0.72	-0.4823	2.079E-04	569	907	569	579	462	488
PRR19L	proline rich 15 like	0.71	-0.4848	5.771E-11	706	581	706	610	465	510
BCLE	BCLE transcription repressor	0.71	-0.4865	9.310E-05	656	1142	656	737	639	604
LOC730101	uncharacterized LOC730101	0.71	-0.4910	1.285E-08	987	710	987	862	611	641
PDCD4	programmed cell death 4	0.66	-0.6028	3.823E-09	911	1332	911	911	728	667
PNRC1	proline rich nuclear receptor coactivator 1	0.66	-0.6074	2.368E-04	511	1027	511	591	462	412
BMF	Bcl2 modifying factor	0.65	-0.6142	1.442E-17	1319	1612	1319	1246	925	898
DHRS3	dehydrogenase/reductase 3	0.64	-0.6483	1.455E-21	738	803	738	629	515	504
CEBPB	CCAAT enhancer binding protein beta	0.63	-0.6725	5.843E-05	899	1829	899	949	737	761
HERPUD1	homocysteine inducible ER protein with ubiquitin like domain 1	0.55	-0.8584	1.205E-12	1182	1727	1182	919	698	763
MGAT4B	alpha-1,3-mannosyl glycoprotein 4-beta-N-acetylglucosaminyltransferase B	0.40	-1.3240	1.558E-02	1613	100	1613	461	528	135