
1 **Supplementary Information:**

2 Supplementary file 1: **Supplementary Table S1.** Differentially expressed genes in
3 GSE42352 between osteosarcoma cells and mesenchyme stem cells.

4 Supplementary file 2: **Supplementary Table S2.** Genes in the blue module.

5 Supplementary file 3: **Supplementary Figure S1.** ROC curves of LASSO Cox-
6 derived genes.

7 Supplementary file 4: **Supplementary Figure S2.** Metastasis-free survival analysis of
8 LASSO Cox-derived genes.

9 Supplementary file 5: **Supplementary Figure S3.** Overall survival analysis of
10 LASSO Cox-derived genes.

11 Supplementary file 6: **Supplementary Figure S4.** Gene Set Enrichment Analysis
12 (GSEA) results on enriched KEGG pathways.

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Figure S1

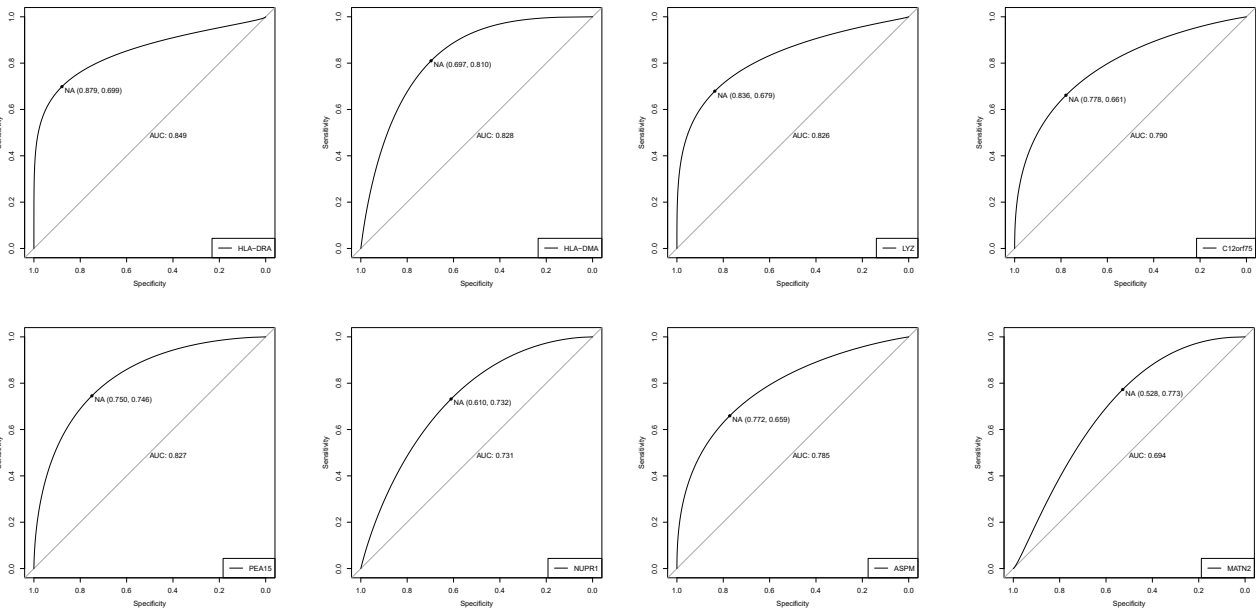


Figure S2

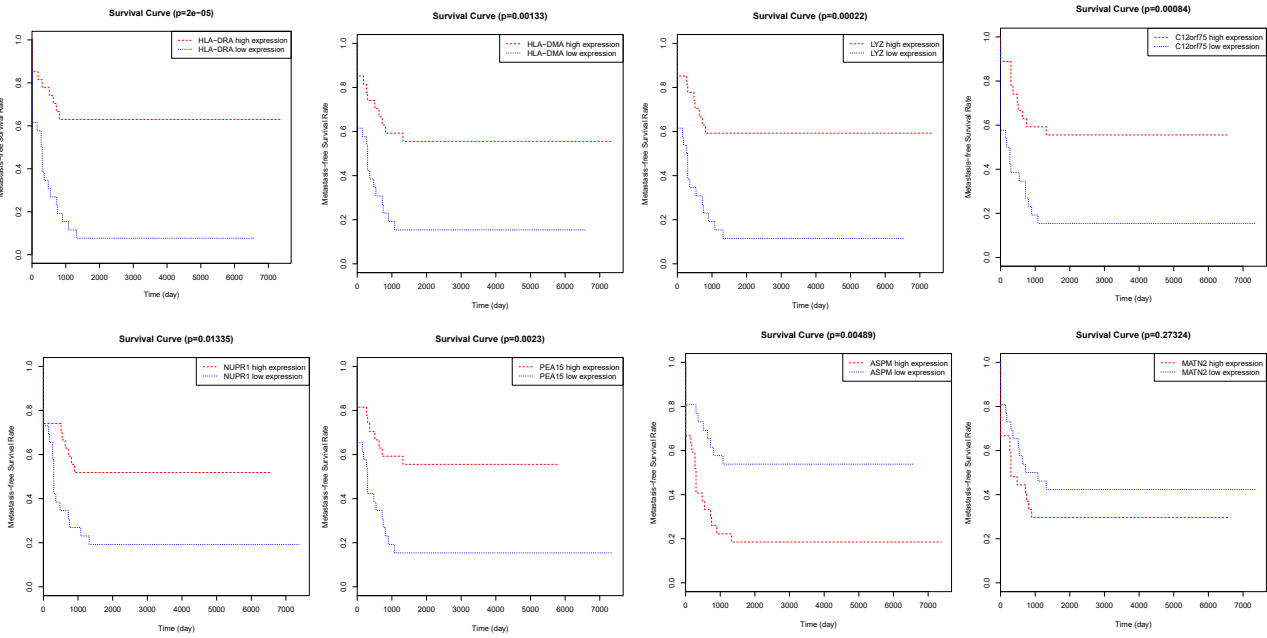


Figure S3

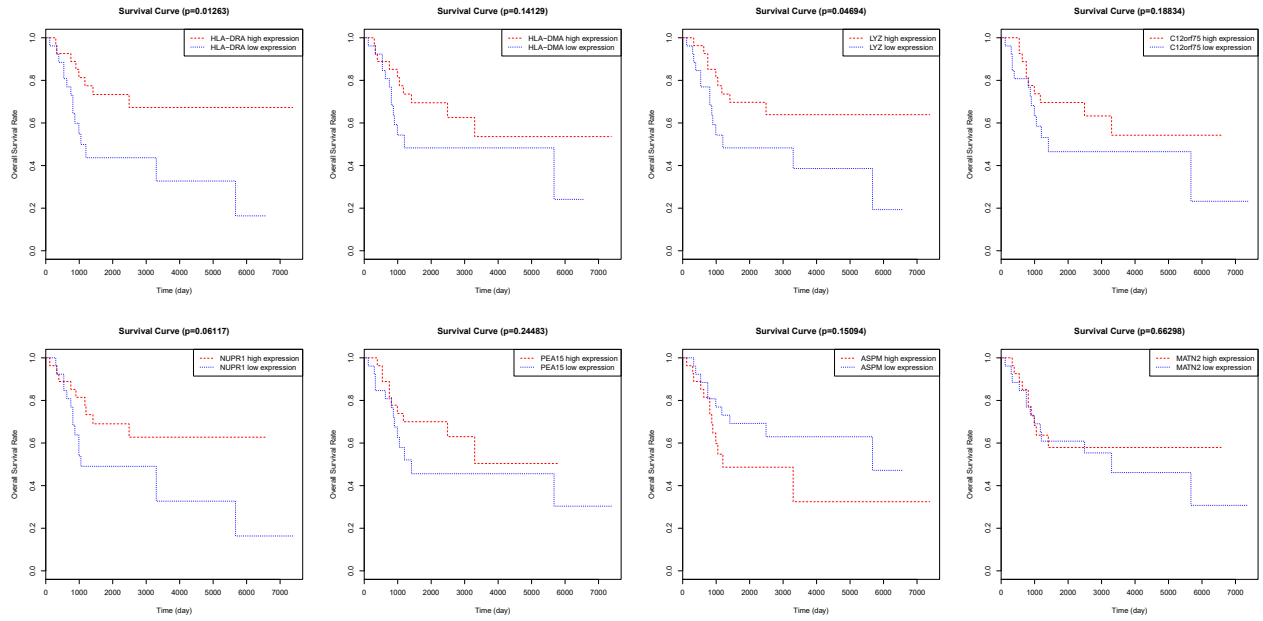


Figure S4

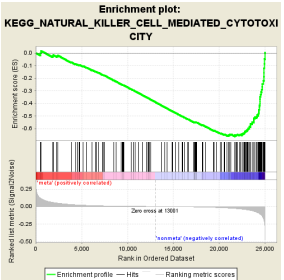
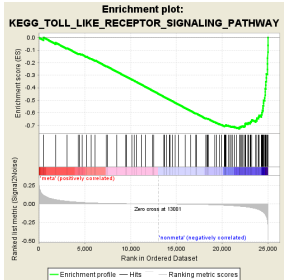
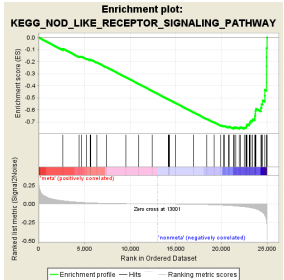
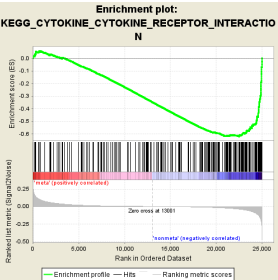
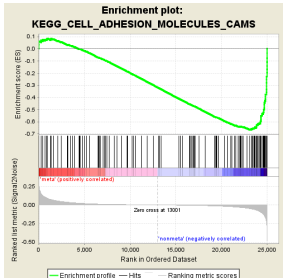
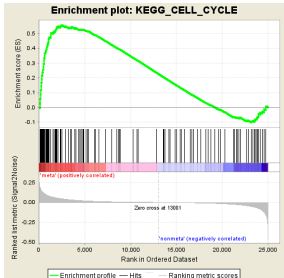
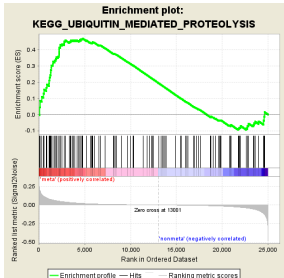


Table S1. Differentially expressed genes in GSE42352 between osteosarcoma cells and mesenchyme stem cells.

Gene Symbol	logFC	t	P.Value	adjusted P.Value
FLJ14054	2.838670456	29.99562521	9.61E-57	2.40E-52
VGLL3	1.830489786	24.37982685	1.16E-47	1.45E-43
URB	1.832495306	23.52853753	3.67E-46	2.30E-42
NPR3	1.970867298	23.11072603	2.07E-45	1.03E-41
PPAP2B	2.772724586	22.4994163	2.68E-44	9.82E-41
FN1	1.647672116	22.49362703	2.75E-44	9.82E-41
HAS1	1.346988189	21.26585058	5.42E-42	1.51E-38
LOC51334	2.040840029	20.90805803	2.62E-41	5.95E-38
PTX3	4.224430941	20.53076773	1.40E-40	2.92E-37
FLJ14834	1.847022668	19.95057606	1.91E-39	3.67E-36
SERAC1	1.195254772	19.22041236	5.44E-38	9.72E-35
PARVA	1.611932172	19.1601437	7.20E-38	1.14E-34
LTBP2	3.181064678	18.72482381	5.49E-37	8.08E-34
LIMS2	1.549272201	17.88732589	2.93E-35	3.86E-32
LMOD1	1.052252364	17.76660524	5.24E-35	6.55E-32
KRTAP1-1	2.326214522	17.46372083	2.27E-34	2.70E-31
GDF5	1.02514384	17.34496859	4.04E-34	4.59E-31
GAS6	3.343323399	17.00454965	2.13E-33	2.13E-30
EFEMP1	3.197443261	16.97738737	2.44E-33	2.34E-30
LOC652612	1.445449473	16.95042869	2.78E-33	2.58E-30
RECK	1.730552183	16.10517495	1.86E-31	1.66E-28
TPD52L1	1.576520042	15.58665489	2.56E-30	2.13E-27
CLCF1	1.313591511	15.47757436	4.45E-30	3.59E-27
KRTAP1-5	1.032442194	15.11458225	2.86E-29	2.03E-26
CRIM1	2.107463164	15.109929	2.92E-29	2.03E-26
ARSJ	1.207311045	15.0170275	4.72E-29	3.19E-26
LEPR	1.070859292	14.93120775	7.34E-29	4.83E-26
NEK7	1.489800633	14.76843248	1.70E-28	1.01E-25
FBN1	1.766075802	14.10679531	5.35E-27	2.73E-24
ABI3BP	2.94254677	13.98866173	9.96E-27	4.98E-24
PRKD1	1.384959817	13.78173992	2.96E-26	1.42E-23
ARID5B	2.263581181	13.44173922	1.79E-25	8.00E-23
CITED2	2.302310808	13.32020988	3.42E-25	1.42E-22
RDH5	2.086472913	13.11954373	9.96E-25	3.95E-22
SH2D4A	1.221523543	13.10699741	1.06E-24	4.16E-22
SERPINE1	4.113494555	13.08614983	1.19E-24	4.58E-22
HAK	3.391070669	13.04309209	1.50E-24	5.67E-22
SCUBE3	1.143707828	13.01790584	1.71E-24	6.30E-22
IGFBP4	3.985271963	12.96899278	2.23E-24	8.07E-22

RGS4	2.999303463	12.84750562	4.27E-24	1.52E-21
BST1	1.117158683	12.7199516	8.46E-24	2.90E-21
GLS	2.287130473	12.52229807	2.45E-23	8.15E-21
TBC1D2	1.731236621	12.42807179	4.06E-23	1.30E-20
PPP1R3C	2.91879272	12.42242946	4.19E-23	1.33E-20
LIMA1	2.165152332	12.41407858	4.38E-23	1.37E-20
TMEM51	-1.962574185	-12.38305937	5.18E-23	1.60E-20
PSG5	1.584381849	12.28849514	8.63E-23	2.48E-20
GPR1	1.146734396	12.27762761	9.15E-23	2.57E-20
ADAMTS1	2.395359473	12.24722541	1.08E-22	2.99E-20
WIG1	1.981630215	12.22110566	1.24E-22	3.41E-20
LOC644376	1.175326383	12.21880746	1.26E-22	3.41E-20
WASF3	2.160285493	12.19824695	1.40E-22	3.77E-20
CDC42EP3	1.571977684	12.18944194	1.47E-22	3.92E-20
RSNL2	1.254892246	12.14619714	1.86E-22	4.89E-20
TNKS1BP1	1.182006734	12.11835632	2.16E-22	5.57E-20
TNFRSF11B	3.066114227	12.09318	2.48E-22	6.32E-20
IL6	3.223192253	12.00819146	3.92E-22	9.53E-20
AVPI1	2.23213288	11.95866765	5.13E-22	1.22E-19
4-Mar	1.462163646	11.79239277	1.26E-21	2.90E-19
KRT7	1.031047365	11.75703779	1.53E-21	3.45E-19
MFAP5	3.587473169	11.70026307	2.08E-21	4.65E-19
CYB5R3	1.296398524	11.48939203	6.55E-21	1.40E-18
CNN1	1.480095688	11.30538407	1.78E-20	3.68E-18
FHL2	1.784290196	11.26665017	2.20E-20	4.51E-18
ADM2	1.607202124	11.20678448	3.05E-20	6.19E-18
PPP1R14A	1.619120634	11.17350479	3.65E-20	7.36E-18
CSRP1	2.263884298	11.11310356	5.08E-20	1.02E-17
DBC1	1.943162135	11.09224198	5.69E-20	1.12E-17
KIAA0427	1.203373751	11.09048632	5.74E-20	1.12E-17
MSRB3	1.200563215	11.03666999	7.70E-20	1.48E-17
DCUN1D3	1.340876116	10.99204334	9.82E-20	1.86E-17
STC2	3.407923858	10.9372713	1.32E-19	2.43E-17
MST150	1.044159249	10.86333222	1.98E-19	3.53E-17
LOC649708	1.010882508	10.7929296	2.91E-19	5.04E-17
FLG	1.185943823	10.78307714	3.07E-19	5.25E-17
CD151	1.639250923	10.70058588	4.81E-19	8.12E-17
KIAA1199	3.552052055	10.6910388	5.06E-19	8.50E-17
KRT19	1.412526332	10.65837215	6.05E-19	9.95E-17
HOXC8	2.151397836	10.62002273	7.46E-19	1.21E-16
MCFD2	1.083512128	10.55259219	1.08E-18	1.70E-16
KIAA1644	1.278053656	10.54726115	1.11E-18	1.73E-16
LOC388610	1.90163113	10.51708377	1.31E-18	2.02E-16
THBS1	4.278860743	10.51481434	1.32E-18	2.03E-16

ZYX	1.795137446	10.48467593	1.56E-18	2.38E-16
ALDH1L2	1.877182789	10.44919035	1.89E-18	2.85E-16
OSMR	1.335282913	10.36331179	3.02E-18	4.52E-16
NQO1	3.280276891	10.33955766	3.44E-18	5.06E-16
KIAA0830	1.005925618	10.33839303	3.46E-18	5.06E-16
RNF144	-2.065048927	-10.33746071	3.48E-18	5.06E-16
CMAH	1.078673486	10.32728545	3.68E-18	5.32E-16
AOX1	1.656609644	10.31032924	4.03E-18	5.73E-16
CAV2	1.942532274	10.29712701	4.34E-18	6.12E-16
FST	1.958953197	10.28227659	4.70E-18	6.60E-16
NAV1	1.311131165	10.22299599	6.49E-18	8.87E-16
VEGFC	2.006602045	10.20736999	7.07E-18	9.55E-16
PHLDA3	1.549999466	10.11293694	1.18E-17	1.55E-15
ANKRD13	1.024625471	10.10329613	1.25E-17	1.62E-15
ABCA8	1.652629364	10.10313828	1.25E-17	1.62E-15
FYCO1	1.114986059	10.09455172	1.31E-17	1.68E-15
IGSF4	-2.564438781	-10.09142078	1.33E-17	1.70E-15
KRT16	1.221193503	10.04253476	1.73E-17	2.15E-15
STAT4	1.224829745	10.04104764	1.75E-17	2.15E-15
ITGA11	3.169931898	10.03245257	1.83E-17	2.23E-15
NUDT18	1.003263596	10.02795318	1.88E-17	2.28E-15
MYO1C	1.192673902	9.952372163	2.83E-17	3.36E-15
MRGPRF	2.040378909	9.871766541	4.39E-17	5.13E-15
TLN1	1.067726612	9.863398304	4.60E-17	5.35E-15
CDKN1A	1.367529281	9.807792686	6.22E-17	7.10E-15
NDST1	1.350193838	9.783519425	7.10E-17	8.06E-15
FADS3	1.938039149	9.764495551	7.87E-17	8.90E-15
MYL9	2.055601506	9.762282936	7.96E-17	8.97E-15
TAGLN	2.242538033	9.750557123	8.49E-17	9.39E-15
IGFBP6	3.174424801	9.71857201	1.01E-16	1.10E-14
IGFBP2	2.925570288	9.651898141	1.45E-16	1.54E-14
WDR1	1.284315406	9.631546988	1.62E-16	1.71E-14
MAP1B	1.528553767	9.617418826	1.75E-16	1.84E-14
WNT5A	1.722752692	9.580608002	2.14E-16	2.22E-14
LHFP	1.968681252	9.57342199	2.22E-16	2.29E-14
FMN2	1.111936207	9.55816259	2.41E-16	2.48E-14
EHBP1	1.174644523	9.550514593	2.51E-16	2.58E-14
CXCL12	2.62263096	9.524329966	2.90E-16	2.96E-14
MFGE8	2.412042248	9.518361947	2.99E-16	3.04E-14
KRTHA4	1.639305593	9.486764778	3.55E-16	3.58E-14
NPAS1	1.042946669	9.48274936	3.63E-16	3.63E-14
COL8A1	1.933990041	9.428735691	4.86E-16	4.73E-14
ITGA5	2.034562327	9.392879715	5.90E-16	5.65E-14
DECR2	1.047090201	9.34146238	7.80E-16	7.27E-14

NGFB	1.164082002	9.336870538	7.99E-16	7.43E-14
MGC2654	1.090323725	9.31405431	9.04E-16	8.28E-14
DUSP14	1.296072007	9.30887986	9.30E-16	8.48E-14
MGC14376	1.576013712	9.271187601	1.14E-15	1.03E-13
PARP1	-1.394133684	-9.253063117	1.26E-15	1.13E-13
EMILIN2	-1.645165699	-9.232197201	1.41E-15	1.26E-13
SEMA4D	-1.708727717	-9.163244188	2.04E-15	1.76E-13
BZRP	1.319581363	9.162303222	2.05E-15	1.76E-13
GNG12	1.337464581	9.123497197	2.53E-15	2.14E-13
FLJ11259	1.89282336	9.120244174	2.57E-15	2.17E-13
COLEC12	-1.210906516	-9.109740432	2.72E-15	2.29E-13
CPT1C	1.011520707	9.099440636	2.88E-15	2.42E-13
PLCG2	-1.243222153	-9.098561618	2.89E-15	2.42E-13
RRAS	2.068726643	9.085740681	3.10E-15	2.58E-13
CD59	1.317328012	9.08001429	3.20E-15	2.65E-13
NUSAP1	-1.861864485	-9.035930122	4.05E-15	3.31E-13
SNX10	-2.484059702	-9.017178229	4.49E-15	3.64E-13
RRAS2	1.665416424	8.961273272	6.06E-15	4.86E-13
NEXN	1.064763861	8.929934474	7.17E-15	5.64E-13
GTF2H5	1.08616535	8.921937402	7.49E-15	5.85E-13
LOXL3	1.572704554	8.914702836	7.78E-15	6.00E-13
TXNRD1	1.716086273	8.914400845	7.79E-15	6.00E-13
CPA4	2.425352151	8.908950955	8.03E-15	6.14E-13
FOXD1	1.99947939	8.86221197	1.03E-14	7.74E-13
RABGAP1	1.373368988	8.861290877	1.04E-14	7.76E-13
ENC1	1.41093169	8.852870286	1.08E-14	8.07E-13
SH3BP4	1.775644236	8.816782826	1.32E-14	9.68E-13
PAWR	1.3005051	8.798183894	1.45E-14	1.06E-12
EPB41L3	-2.484819665	-8.795393399	1.48E-14	1.08E-12
BNIP3L	1.496529459	8.793550719	1.49E-14	1.08E-12
PLSCR4	1.667960728	8.772421681	1.67E-14	1.20E-12
CNN2	1.240623715	8.767334214	1.72E-14	1.23E-12
CYP1B1	2.79721082	8.753980546	1.84E-14	1.32E-12
CLIPR-59	2.142655563	8.721841259	2.19E-14	1.56E-12
IRS2	1.503481222	8.703802842	2.41E-14	1.70E-12
ACOX2	1.323075676	8.671938099	2.86E-14	1.99E-12
KIAA1754	1.213455109	8.653461193	3.15E-14	2.18E-12
ANXA2	1.636507473	8.623082517	3.71E-14	2.55E-12
GCNT1	1.161461064	8.583162206	4.59E-14	3.10E-12
PGRMC2	1.389054037	8.558370741	5.24E-14	3.51E-12
IL18	-2.466715628	-8.554751832	5.34E-14	3.57E-12
DSTN	1.121059872	8.55326535	5.38E-14	3.59E-12
ROR1	1.024757248	8.537112438	5.87E-14	3.88E-12
CAV1	1.947455774	8.52251949	6.34E-14	4.18E-12

ADCY4	1.175578571	8.503108969	7.03E-14	4.61E-12
CTGF	2.72226172	8.498843832	7.20E-14	4.70E-12
SPTAN1	1.308179257	8.493859846	7.39E-14	4.78E-12
LOC88523	1.239594604	8.474111126	8.21E-14	5.26E-12
GARS	1.394112351	8.465355478	8.60E-14	5.44E-12
EBF3	1.759704201	8.464028892	8.66E-14	5.45E-12
REXO2	1.364098259	8.460619607	8.82E-14	5.54E-12
SOX18	-2.235230033	-8.442173881	9.73E-14	6.06E-12
LOC645895	-1.795941066	-8.426387644	1.06E-13	6.55E-12
TPM2	2.085180789	8.414303349	1.13E-13	6.96E-12
TMEM43	1.257767828	8.410309181	1.15E-13	7.09E-12
PSAT1	1.246850278	8.404609612	1.19E-13	7.29E-12
KCTD10	1.095593886	8.396500484	1.24E-13	7.58E-12
GRAMD3	1.633679027	8.370900135	1.42E-13	8.62E-12
TGFB1I1	1.233870164	8.365334117	1.46E-13	8.85E-12
IGFBP3	3.045874353	8.356821469	1.53E-13	9.20E-12
COMT	1.081163617	8.349340424	1.59E-13	9.54E-12
PEA15	1.347355436	8.332781237	1.74E-13	1.03E-11
MCM5	-1.107930561	-8.329067543	1.77E-13	1.05E-11
PENK	2.480020797	8.326750757	1.79E-13	1.06E-11
TRIM22	1.592830244	8.31726815	1.89E-13	1.11E-11
LEF1	-1.759753874	-8.307455803	1.99E-13	1.17E-11
EFEMP2	1.804309199	8.296156205	2.11E-13	1.23E-11
GLIPR1	2.274418694	8.278621092	2.32E-13	1.33E-11
DIP13B	1.176047481	8.274889274	2.36E-13	1.35E-11
HERC5	-2.230015264	-8.251820516	2.67E-13	1.52E-11
TPM1	1.225810266	8.235066187	2.92E-13	1.65E-11
DDAH1	1.571454286	8.233860911	2.93E-13	1.66E-11
LOC201895	1.251060871	8.208321985	3.36E-13	1.87E-11
CPVL	-1.954177266	-8.192144578	3.66E-13	2.03E-11
SRXN1	1.253713621	8.177520455	3.95E-13	2.18E-11
FSTL3	1.794207434	8.157018765	4.40E-13	2.41E-11
FLJ13391	1.787699563	8.154369263	4.46E-13	2.44E-11
SERTAD2	1.123198762	8.118134026	5.40E-13	2.92E-11
CYR61	2.416492305	8.097591854	6.02E-13	3.23E-11
HNT	1.398355384	8.090456953	6.25E-13	3.35E-11
CLEC3B	1.681485798	8.086892336	6.37E-13	3.40E-11
KLF9	1.545595203	8.06798668	7.04E-13	3.73E-11
MAPK3	1.047962254	8.065542876	7.13E-13	3.77E-11
PPP3CB	1.009453419	8.055365426	7.52E-13	3.97E-11
LAMC1	1.576299451	8.02944171	8.62E-13	4.51E-11
SART2	1.54994782	7.974589635	1.15E-12	5.90E-11
MTHFD1L	1.281799597	7.965855891	1.20E-12	6.16E-11
CD248	3.01945945	7.96114963	1.23E-12	6.30E-11

PLEKHC1	1.222076731	7.908870697	1.62E-12	8.12E-11
SH3BGRL3	1.426461593	7.907235348	1.63E-12	8.16E-11
PAPPA	1.552979388	7.905570113	1.65E-12	8.21E-11
FER1L3	2.001749	7.88527815	1.83E-12	9.06E-11
RRAGD	-1.63560331	-7.871399152	1.97E-12	9.70E-11
PLAC9	2.226470908	7.856415271	2.13E-12	1.04E-10
PPT1	-2.262914273	-7.847788911	2.23E-12	1.09E-10
SPP1	-5.257964246	-7.84166753	2.30E-12	1.12E-10
TCEAL3	1.253155026	7.836806999	2.36E-12	1.14E-10
EDG2	1.089557788	7.831313514	2.43E-12	1.17E-10
GDF6	1.102079332	7.804501995	2.80E-12	1.33E-10
C9orf88	1.430187206	7.804031698	2.80E-12	1.33E-10
LRP10	1.180202456	7.789740957	3.02E-12	1.43E-10
PLVAP	-3.804436421	-7.770796032	3.33E-12	1.57E-10
E2F2	-1.71578906	-7.769710679	3.35E-12	1.57E-10
EPAS1	2.104733234	7.76921958	3.36E-12	1.57E-10
RAB11FIP5	1.209623886	7.757243081	3.58E-12	1.66E-10
COX6C	-1.067214808	-7.756665764	3.59E-12	1.67E-10
PTPRK	1.162609811	7.745129624	3.81E-12	1.76E-10
SFRS1	-1.011221326	-7.734149092	4.03E-12	1.86E-10
CAPNS1	1.002552479	7.71213241	4.52E-12	2.07E-10
LOC643509	-1.847257017	-7.70106121	4.79E-12	2.18E-10
TRIM8	1.179911606	7.69696132	4.89E-12	2.22E-10
SERPINE2	2.230328415	7.695675017	4.92E-12	2.23E-10
EFNA1	-1.838449871	-7.660001272	5.92E-12	2.66E-10
CXorf6	1.00722943	7.628125759	6.99E-12	3.10E-10
PTRF	1.860512625	7.613321811	7.54E-12	3.33E-10
TRIB3	2.372236723	7.607365373	7.78E-12	3.42E-10
TNFRSF21	-1.785189098	-7.603238096	7.95E-12	3.49E-10
LCP1	-2.823258205	-7.602850296	7.96E-12	3.49E-10
MAPRE2	-1.042898696	-7.600181817	8.07E-12	3.53E-10
SORT1	1.455901155	7.593976983	8.34E-12	3.64E-10
KNTC1	-1.07037029	-7.502633945	1.34E-11	5.68E-10
FHL1	1.723933148	7.480807999	1.49E-11	6.29E-10
LOC387882	1.941431398	7.464756056	1.62E-11	6.78E-10
RGC32	-2.438049143	-7.464109829	1.63E-11	6.79E-10
LRRC8D	1.134475681	7.460259484	1.66E-11	6.90E-10
CDH13	1.081470521	7.455482457	1.70E-11	7.05E-10
UROS	1.256618779	7.432737827	1.91E-11	7.79E-10
DENND2A	-1.602766952	-7.423813025	2.00E-11	8.13E-10
EIF3S5	1.164575757	7.419943537	2.04E-11	8.27E-10
C10orf10	1.965820343	7.397893661	2.29E-11	9.17E-10
RND3	1.526175175	7.385860674	2.43E-11	9.73E-10
CDC45	-1.444671251	-7.382777766	2.47E-11	9.87E-10

ARNT2	1.110136102	7.378150357	2.53E-11	1.01E-09
MMP9	-5.545989951	-7.376835023	2.55E-11	1.01E-09
KIAA0367	1.614196479	7.376422502	2.55E-11	1.02E-09
CDC20	-2.14881231	-7.367039198	2.68E-11	1.06E-09
HES4	-2.106810022	-7.334192544	3.17E-11	1.24E-09
LOX	2.779972589	7.332059049	3.21E-11	1.25E-09
RNASE1	-4.232054404	-7.328251391	3.27E-11	1.27E-09
NPAL3	1.006014705	7.324856221	3.33E-11	1.29E-09
APEG1	1.473936945	7.300824304	3.76E-11	1.45E-09
TOP2A	-1.673016053	-7.297242215	3.83E-11	1.48E-09
LOC130576	1.289526157	7.272719557	4.34E-11	1.66E-09
DCBLD2	1.550788747	7.241763379	5.08E-11	1.92E-09
C21orf55	-2.358120654	-7.227810653	5.45E-11	2.05E-09
GPSM2	-1.228546808	-7.224988469	5.53E-11	2.08E-09
UCP2	-1.264394184	-7.21003865	5.97E-11	2.23E-09
SPATA18	1.157869483	7.203239929	6.18E-11	2.30E-09
LEP	1.122604877	7.195639865	6.42E-11	2.38E-09
H2AFZ	-1.09773894	-7.14506805	8.30E-11	3.02E-09
C1QR1	-2.799901972	-7.144114968	8.34E-11	3.03E-09
LOC441087	-1.762756228	-7.130829441	8.92E-11	3.22E-09
FSTL1	1.528947738	7.123232132	9.27E-11	3.33E-09
TAX1BP3	1.17016973	7.091967236	1.09E-10	3.88E-09
AXL	2.420557063	7.090403312	1.09E-10	3.90E-09
CHMP1B	1.271796912	7.084180357	1.13E-10	4.01E-09
MCM8	-1.210628978	-7.080838017	1.15E-10	4.07E-09
LASP1	1.054699723	7.048084197	1.36E-10	4.75E-09
RPS27L	1.139840663	7.046132542	1.37E-10	4.79E-09
PDE7B	1.29862587	7.008023188	1.66E-10	5.72E-09
TMCO3	1.289594617	7.003830392	1.69E-10	5.83E-09
SLC14A1	1.537136412	7.001025431	1.72E-10	5.91E-09
WWP1	-1.558356154	-6.996850613	1.75E-10	6.01E-09
TYROBP	-3.896897641	-6.9821258	1.89E-10	6.42E-09
PGM1	1.725266858	6.977129948	1.94E-10	6.58E-09
MAP1A	1.351149513	6.973924381	1.97E-10	6.67E-09
LMCD1	1.37454828	6.929886321	2.45E-10	8.17E-09
PLEKHA5	-1.332115575	-6.927877791	2.48E-10	8.22E-09
SLC3A2	1.074663009	6.915953819	2.63E-10	8.68E-09
CXX1	1.065733804	6.899608671	2.86E-10	9.36E-09
VWF	-2.770367002	-6.898266299	2.88E-10	9.38E-09
TMEM47	2.075639786	6.897898911	2.88E-10	9.39E-09
HLA-DMB	-3.120076678	-6.897131869	2.89E-10	9.41E-09
CSF1R	-3.714266493	-6.890262857	2.99E-10	9.70E-09
PRSS23	2.111242591	6.889661615	3.00E-10	9.71E-09
PTHR1	-3.335338436	-6.888144576	3.02E-10	9.72E-09

FXVD6	-2.004047366	-6.888042146	3.03E-10	9.72E-09
GPR116	-1.946498061	-6.867511491	3.35E-10	1.07E-08
PALLD	1.419165989	6.864344915	3.41E-10	1.08E-08
WISP2	1.38829133	6.862263058	3.44E-10	1.09E-08
MCM4	-1.513118287	-6.860935147	3.46E-10	1.10E-08
ARHGAP1	1.019511874	6.846069094	3.73E-10	1.18E-08
CHST3	1.239401898	6.836394738	3.92E-10	1.23E-08
HERPUD1	1.122761457	6.825688847	4.13E-10	1.29E-08
OAF	-1.282032124	-6.821965921	4.21E-10	1.31E-08
IGSF3	-1.283020443	-6.816194097	4.33E-10	1.34E-08
CNTNAP1	1.453725317	6.813797453	4.38E-10	1.35E-08
PLOD2	1.41961175	6.782965078	5.11E-10	1.55E-08
C1QA	-3.932358757	-6.779444556	5.20E-10	1.58E-08
HEYL	-1.903690113	-6.774445297	5.33E-10	1.61E-08
RASGRP3	-1.018874911	-6.77131783	5.41E-10	1.64E-08
HAVCR2	-2.537221035	-6.76778502	5.51E-10	1.66E-08
LOC442578	-1.018236069	-6.749053481	6.04E-10	1.82E-08
DUSP1	2.204545132	6.744727179	6.17E-10	1.85E-08
MCM2	-1.101223328	-6.719752021	6.99E-10	2.08E-08
LAPTM5	-2.856640866	-6.712086741	7.26E-10	2.15E-08
LOC653780	-2.089079025	-6.71140447	7.28E-10	2.15E-08
HEY1	-2.233082385	-6.709709137	7.34E-10	2.17E-08
DNMT1	-1.165113442	-6.701763073	7.64E-10	2.25E-08
PHACTR2	1.144060378	6.698276738	7.77E-10	2.28E-08
S100A16	1.671693689	6.660329122	9.37E-10	2.71E-08
APOE	-3.672832031	-6.657288603	9.51E-10	2.75E-08
PTPLA	1.455871242	6.644006721	1.02E-09	2.93E-08
MGST2	-1.308986823	-6.622368179	1.13E-09	3.22E-08
ENG	1.496279512	6.619654892	1.15E-09	3.26E-08
ARHGDIB	-3.105092413	-6.610370088	1.20E-09	3.40E-08
GBE1	1.056592479	6.605314876	1.23E-09	3.48E-08
GIMAP4	-2.598114311	-6.597388607	1.28E-09	3.59E-08
MCART1	-2.661777635	-6.593317592	1.30E-09	3.65E-08
C1QB	-3.534862678	-6.572160144	1.45E-09	4.03E-08
TPX2	-1.055960986	-6.551929108	1.60E-09	4.42E-08
BRI3	1.125548346	6.549800019	1.61E-09	4.45E-08
SPOCK	2.511158816	6.546086473	1.64E-09	4.51E-08
HCAP-G	-1.247689516	-6.525668019	1.82E-09	4.94E-08
C1QC	-3.365553126	-6.495612287	2.10E-09	5.69E-08
GUSB	-1.158950535	-6.471525331	2.36E-09	6.32E-08
CHIC2	1.05491937	6.466014711	2.43E-09	6.46E-08
KIAA0746	1.60315422	6.464317797	2.45E-09	6.50E-08
SDC4	1.680686517	6.462126163	2.48E-09	6.56E-08
TIMELESS	-1.027632551	-6.459876992	2.50E-09	6.62E-08

PSME2	-1.016987689	-6.458705582	2.52E-09	6.64E-08
TUFT1	1.175018779	6.449842346	2.63E-09	6.92E-08
C1orf198	1.345922817	6.442690257	2.72E-09	7.14E-08
GCLM	1.20528705	6.439533315	2.76E-09	7.23E-08
PTGIS	1.464360035	6.439049291	2.77E-09	7.24E-08
MSX1	-1.38123399	-6.437772368	2.79E-09	7.27E-08
MEF2C	-1.733241256	-6.43606846	2.81E-09	7.32E-08
ASNS	2.035020825	6.435771913	2.81E-09	7.33E-08
LRP1	1.046554019	6.429597294	2.90E-09	7.53E-08
KIF2C	-1.234536617	-6.41369095	3.13E-09	8.07E-08
RHBDF1	1.260044806	6.404347873	3.28E-09	8.43E-08
PTTG1IP	1.119920897	6.383005316	3.64E-09	9.33E-08
TMEM97	-1.425691677	-6.374795521	3.78E-09	9.69E-08
TACC3	-1.121320216	-6.368899617	3.89E-09	9.92E-08
ASPM	-1.437011179	-6.367002867	3.93E-09	9.98E-08
DKFZp434I1020	-1.180423207	-6.364434285	3.98E-09	1.01E-07
CCDC3	-2.399265142	-6.361550169	4.03E-09	1.02E-07
NDN	1.823996301	6.357452733	4.11E-09	1.04E-07
ZNF486	-2.377297343	-6.353201172	4.20E-09	1.06E-07
NNMT	2.080394359	6.352971825	4.20E-09	1.06E-07
UNQ1940	1.433291941	6.35008366	4.26E-09	1.07E-07
AKR1C3	1.83143712	6.347414785	4.32E-09	1.08E-07
HSD17B7	-2.237413222	-6.343889755	4.39E-09	1.10E-07
FLOT2	1.024494455	6.318087328	4.97E-09	1.24E-07
ATP6V0B	-1.26463118	-6.311376634	5.14E-09	1.27E-07
STAB1	-2.405590311	-6.310072274	5.17E-09	1.28E-07
SBDSP	1.3206102	6.277900104	6.04E-09	1.48E-07
CA2	-2.908388631	-6.276583554	6.07E-09	1.48E-07
GADD45A	1.256850746	6.273636703	6.16E-09	1.50E-07
CD9	-1.52876416	-6.272143485	6.21E-09	1.51E-07
TSPAN33	-1.186847054	-6.257461107	6.66E-09	1.61E-07
ADM	2.357999574	6.256766543	6.68E-09	1.62E-07
DPYSL2	1.111175849	6.247873512	6.97E-09	1.67E-07
PALM	1.702023602	6.242316898	7.16E-09	1.72E-07
TPM4	1.085125147	6.241711415	7.18E-09	1.72E-07
CCNB2	-1.509884154	-6.241092554	7.20E-09	1.72E-07
FGD5	-1.041446476	-6.238900013	7.28E-09	1.74E-07
VASH1	-1.292168708	-6.238806394	7.28E-09	1.74E-07
MAFB	-2.166978772	-6.237961704	7.31E-09	1.74E-07
P8	1.516313567	6.229887431	7.60E-09	1.81E-07
FCER1G	-2.763166626	-6.220197944	7.96E-09	1.89E-07
DKFZp564K142	-2.212028859	-6.210573634	8.34E-09	1.97E-07
BOP1	-1.164315343	-6.201408609	8.71E-09	2.05E-07
RAGE	1.7982622	6.18507505	9.42E-09	2.20E-07

TMSL8	-2.419078991	-6.181676962	9.57E-09	2.23E-07
CRLF1	1.363372094	6.176303648	9.82E-09	2.28E-07
FGFR3	-1.51316796	-6.175521189	9.86E-09	2.29E-07
DTL	-1.173642691	-6.162490501	1.05E-08	2.41E-07
ARHGAP4	-1.170642387	-6.154511108	1.09E-08	2.49E-07
COL12A1	1.176962452	6.143647705	1.15E-08	2.61E-07
FGD3	-1.429200491	-6.141409111	1.16E-08	2.63E-07
XPOT	1.037780662	6.140088119	1.17E-08	2.65E-07
LZTS1	-1.066776833	-6.137801028	1.18E-08	2.67E-07
FLJ21127	1.078318475	6.136197918	1.19E-08	2.69E-07
ALOX5AP	-2.4130015	-6.133170439	1.21E-08	2.72E-07
CENTA2	-1.754858855	-6.124439342	1.26E-08	2.83E-07
M6PRBP1	1.041960425	6.113485783	1.32E-08	2.96E-07
SIPA1L1	1.253882352	6.105256992	1.38E-08	3.07E-07
PSCD4	-1.640406648	-6.088551641	1.49E-08	3.30E-07
LAYN	1.406709303	6.087388051	1.50E-08	3.32E-07
LCP2	-1.658406197	-6.06873233	1.64E-08	3.59E-07
ANXA5	1.072631602	6.067546037	1.65E-08	3.60E-07
ALCAM	1.439930606	6.059441536	1.71E-08	3.72E-07
ALPP	-2.209740071	-6.049943345	1.79E-08	3.88E-07
LAPTM4B	-1.300112191	-6.046346351	1.82E-08	3.94E-07
CTSH	-1.130193976	-6.025877043	2.00E-08	4.30E-07
IGSF6	-1.943984467	-6.015507263	2.11E-08	4.49E-07
CDH5	-1.278291635	-6.012058785	2.14E-08	4.55E-07
C1S	1.284806797	6.008265525	2.18E-08	4.61E-07
STIL	-1.164535592	-6.001336499	2.25E-08	4.74E-07
MCM3	-1.033251556	-5.997872083	2.29E-08	4.81E-07
EBP	-1.042617956	-5.994222104	2.33E-08	4.88E-07
CYYR1	-1.181990454	-5.9836036	2.45E-08	5.10E-07
PRKCDBP	1.559688122	5.970789544	2.60E-08	5.39E-07
PECAM1	-1.386320389	-5.962136717	2.71E-08	5.60E-07
MS4A6A	-2.502602749	-5.958088405	2.76E-08	5.70E-07
FBLN1	1.495530292	5.953358469	2.82E-08	5.81E-07
FLJ22662	-1.714176725	-5.950527667	2.86E-08	5.87E-07
FLJ90166	2.208895757	5.948700779	2.88E-08	5.90E-07
GMFG	-1.571477508	-5.947912078	2.89E-08	5.91E-07
KIAA1913	1.344437881	5.94256243	2.97E-08	6.03E-07
CRIP2	1.542693691	5.921240667	3.28E-08	6.60E-07
TYMS	-1.543835246	-5.920238853	3.29E-08	6.62E-07
PRG1	2.618153359	5.917870904	3.33E-08	6.68E-07
ACSS1	-1.146890671	-5.914144992	3.39E-08	6.77E-07
FLJ35258	1.236017017	5.909543877	3.46E-08	6.91E-07
ANTXR1	1.09558379	5.882619332	3.92E-08	7.77E-07
HBA1	-4.441753546	-5.872125031	4.12E-08	8.14E-07

RNASE6	-1.547923415	-5.868443694	4.19E-08	8.26E-07
C10orf58	-1.036839702	-5.866882066	4.22E-08	8.31E-07
CYBRD1	1.496897943	5.865073576	4.26E-08	8.37E-07
CTNNAL1	1.04908594	5.85904124	4.38E-08	8.59E-07
DLG7	-1.120046946	-5.858741114	4.39E-08	8.59E-07
SLC25A4	1.046756203	5.850220784	4.56E-08	8.91E-07
DKFZp7621137	-1.576092758	-5.846568941	4.64E-08	9.04E-07
MSH6	-1.113845461	-5.830408634	5.00E-08	9.67E-07
AIF1	-2.131881213	-5.829379745	5.03E-08	9.71E-07
S100A4	-2.759019898	-5.828523895	5.05E-08	9.74E-07
RAI14	1.26735376	5.827950383	5.06E-08	9.76E-07
TM4SF1	2.117422201	5.825251862	5.12E-08	9.87E-07
WARS	1.286854012	5.81861705	5.28E-08	1.02E-06
NCK2	-1.085454044	-5.811107968	5.47E-08	1.04E-06
SLC29A1	-1.490893704	-5.808487394	5.54E-08	1.05E-06
SP7	-2.253349913	-5.79979597	5.77E-08	1.09E-06
DAB2	1.670201338	5.79835549	5.80E-08	1.10E-06
SLC7A1	1.221147681	5.795070662	5.89E-08	1.11E-06
IRX3	1.235899663	5.791311155	6.00E-08	1.13E-06
PLEK	-1.702572138	-5.782428936	6.25E-08	1.17E-06
AQP1	-1.517249559	-5.782388194	6.25E-08	1.17E-06
ATP1B1	-1.277433095	-5.780146484	6.31E-08	1.18E-06
HBB	-4.581977906	-5.778206753	6.37E-08	1.19E-06
TUBB6	1.151790076	5.770847918	6.59E-08	1.23E-06
PAPSS2	1.335092223	5.767755489	6.69E-08	1.24E-06
FOLR2	-1.816763262	-5.75181059	7.20E-08	1.33E-06
CSRP2	-1.803713846	-5.751324616	7.21E-08	1.33E-06
ITPR3	1.548221177	5.750346965	7.25E-08	1.34E-06
BAG3	1.133577404	5.747508047	7.34E-08	1.35E-06
C9orf130	-1.285085849	-5.735661105	7.75E-08	1.42E-06
CDCA8	-1.130625858	-5.723770015	8.19E-08	1.50E-06
CPE	-2.757879392	-5.721094716	8.29E-08	1.51E-06
HLA-DRA	-3.611625081	-5.71012212	8.72E-08	1.58E-06
CKS2	-1.311510414	-5.708597099	8.78E-08	1.59E-06
BNIP3	1.465824497	5.680376836	9.99E-08	1.79E-06
TGFB3	-1.921696735	-5.670306142	1.05E-07	1.86E-06
CA12	1.690847439	5.656438673	1.12E-07	1.97E-06
SPARCL1	-1.877389984	-5.643828772	1.18E-07	2.07E-06
LHX2	-1.070653885	-5.637365532	1.22E-07	2.13E-06
HIST1H4C	-1.261917782	-5.634321788	1.23E-07	2.15E-06
GIMAP8	-1.125952216	-5.6282852	1.27E-07	2.20E-06
SDF2L1	-1.048743777	-5.624752667	1.29E-07	2.23E-06
ROR2	-1.229021004	-5.623579035	1.30E-07	2.24E-06
SPOCD1	1.317873947	5.61867048	1.32E-07	2.28E-06

ZNF14	-2.37285809	-5.617245036	1.33E-07	2.29E-06
EDG3	-1.495155373	-5.60380578	1.42E-07	2.42E-06
TMEM106C	-1.141596721	-5.59518624	1.47E-07	2.50E-06
CENPF	-1.122381131	-5.591920933	1.50E-07	2.53E-06
GGH	-1.314791973	-5.589059885	1.52E-07	2.56E-06
SULF1	2.257697163	5.580728453	1.57E-07	2.65E-06
ANGPT2	-1.274051334	-5.569698941	1.65E-07	2.77E-06
FLJ22471	1.07166751	5.568270133	1.67E-07	2.79E-06
BUB1	-1.044169174	-5.560126426	1.73E-07	2.87E-06
A2M	-2.835823015	-5.55894326	1.74E-07	2.89E-06
LMOD3	-1.759111376	-5.558724969	1.74E-07	2.89E-06
BUB1B	-1.002158027	-5.555554686	1.76E-07	2.92E-06
HSPB6	1.111518136	5.552266613	1.79E-07	2.95E-06
WAS	-1.367108908	-5.539797629	1.89E-07	3.11E-06
KIAA1598	-1.189227579	-5.536050537	1.93E-07	3.15E-06
IGF2BP3	-1.110395107	-5.535850985	1.93E-07	3.16E-06
CTSC	-1.168840816	-5.530317491	1.98E-07	3.23E-06
SLCO2B1	-1.51314036	-5.52813342	2.00E-07	3.26E-06
CRYAB	2.855455354	5.526077064	2.02E-07	3.28E-06
MATN2	-1.309987893	-5.52317398	2.04E-07	3.32E-06
SEPP1	-2.396709419	-5.52132818	2.06E-07	3.34E-06
DACT1	1.132262059	5.515640594	2.11E-07	3.42E-06
DKFZp727G131	-2.173386965	-5.513534619	2.13E-07	3.45E-06
AURKB	-1.250286379	-5.509369489	2.17E-07	3.51E-06
GUCY1A3	-1.404140426	-5.508908532	2.18E-07	3.52E-06
LOC148915	-1.144814582	-5.502439707	2.24E-07	3.61E-06
DSCR1	1.19208175	5.494875487	2.32E-07	3.73E-06
MMP13	-3.010439647	-5.490035915	2.37E-07	3.81E-06
CD14	-2.536503281	-5.487459702	2.40E-07	3.84E-06
HEM1	-1.205825315	-5.486589962	2.41E-07	3.85E-06
SLC27A3	-1.308796265	-5.47057959	2.59E-07	4.10E-06
SLC37A2	-1.610554933	-5.465099422	2.65E-07	4.20E-06
C1orf162	-1.772926895	-5.453489112	2.79E-07	4.41E-06
KIF20A	-1.136229532	-5.453347298	2.80E-07	4.41E-06
IRF8	-1.190010011	-5.432096872	3.08E-07	4.81E-06
CD33	-1.057599481	-5.427182401	3.14E-07	4.91E-06
FPRL2	-1.492225127	-5.425786827	3.16E-07	4.93E-06
GNA15	-1.310727054	-5.425316367	3.17E-07	4.93E-06
MS4A7	-1.807128197	-5.416877086	3.29E-07	5.10E-06
ANKRD37	1.12420658	5.415269602	3.32E-07	5.12E-06
CD163	-1.389152144	-5.410480145	3.39E-07	5.22E-06
NES	-1.86102522	-5.40237014	3.51E-07	5.39E-06
EDNRA	-1.677345894	-5.398544112	3.57E-07	5.47E-06
CDT1	-1.088435997	-5.394085979	3.64E-07	5.57E-06

EBI2	-1.443526637	-5.391326033	3.69E-07	5.62E-06
FLJ21438	-1.136862838	-5.370652208	4.05E-07	6.11E-06
APCDD1	-1.88344073	-5.361567512	4.21E-07	6.32E-06
RAFTLIN	1.052374626	5.358242026	4.27E-07	6.41E-06
GIMAP7	-1.306611712	-5.357061993	4.30E-07	6.44E-06
LRRC15	-1.281702216	-5.350464421	4.42E-07	6.61E-06
AMOT	-1.011434666	-5.337906591	4.68E-07	6.96E-06
HLA-DQA1	-2.552829983	-5.337402732	4.69E-07	6.98E-06
NUDT1	-1.124385198	-5.313857254	5.20E-07	7.66E-06
APOC1	-2.098256494	-5.309787855	5.30E-07	7.79E-06
SLC7A5	1.840805251	5.293568637	5.69E-07	8.31E-06
TSPAN7	-1.233953502	-5.29300602	5.71E-07	8.32E-06
MARCKSL1	-1.17816991	-5.290609164	5.77E-07	8.40E-06
NT5E	1.075469196	5.289870382	5.78E-07	8.43E-06
NPTX2	-2.289539298	-5.287866724	5.84E-07	8.48E-06
RCOR2	-1.418261702	-5.277406129	6.11E-07	8.85E-06
ACP5	-3.313573111	-5.26115133	6.56E-07	9.44E-06
RGS1	-1.75642132	-5.257935583	6.66E-07	9.55E-06
HLA-DPA1	-2.964600665	-5.257384939	6.67E-07	9.57E-06
CENPA	-1.043400661	-5.252402871	6.82E-07	9.77E-06
SCARB1	-1.139311042	-5.247624701	6.97E-07	9.94E-06
CLDN5	-1.216014239	-5.242752955	7.12E-07	1.01E-05
CEBPD	1.202084173	5.242364314	7.13E-07	1.01E-05
M160	-1.009251222	-5.232481296	7.44E-07	1.06E-05
PODN	1.1611809	5.221277466	7.82E-07	1.10E-05
HCLS1	-1.788141034	-5.200759604	8.55E-07	1.19E-05
PLTP	-1.131164593	-5.186996447	9.08E-07	1.26E-05
ERRFI1	1.247952326	5.186849114	9.09E-07	1.26E-05
LY86	-1.367209857	-5.167482712	9.89E-07	1.36E-05
AGTRL1	-1.557353766	-5.149343979	1.07E-06	1.46E-05
PPEF1	-1.272690005	-5.146345277	1.08E-06	1.47E-05
EXT1	1.004121611	5.120541832	1.21E-06	1.63E-05
LOC641704	-1.525898503	-5.118897919	1.22E-06	1.64E-05
ACTA2	2.2593088	5.110814516	1.26E-06	1.69E-05
NPNT	-1.163231503	-5.105720335	1.29E-06	1.72E-05
CRISPLD2	1.509878593	5.10371091	1.30E-06	1.74E-05
PTGES	1.573329416	5.102748075	1.31E-06	1.74E-05
MYH9	1.046196672	5.086154246	1.41E-06	1.86E-05
LRP4	-1.235582783	-5.078604463	1.45E-06	1.91E-05
FOSB	2.081881124	5.066908024	1.53E-06	1.99E-05
FLJ43339	1.316216012	5.065879534	1.53E-06	2.00E-05
SELM	1.287653577	5.056386225	1.60E-06	2.07E-05
FAM63A	-1.389911207	-5.045969017	1.67E-06	2.15E-05
FAM60A	-1.275348386	-5.043517769	1.69E-06	2.17E-05

CD74	-2.441452914	-5.041441845	1.70E-06	2.19E-05
TUBB3	1.529862771	5.028354138	1.80E-06	2.30E-05
SCRN1	1.255422338	5.026823684	1.82E-06	2.31E-05
GLRX	1.057808655	5.024364555	1.83E-06	2.33E-05
MEG3	1.194067877	5.021762014	1.85E-06	2.36E-05
CCND1	1.980458553	5.01879544	1.88E-06	2.39E-05
H19	-2.691849539	-5.012847547	1.93E-06	2.44E-05
DKFZP686A01247	1.256111471	5.012132949	1.93E-06	2.44E-05
REEP1	-1.103671849	-4.996693274	2.06E-06	2.59E-05
SNCAIP	-1.263585989	-4.994707239	2.08E-06	2.61E-05
CCT3	-1.213903026	-4.985702347	2.16E-06	2.69E-05
MVP	1.340310485	4.974171882	2.27E-06	2.81E-05
GIMAP5	-1.174580758	-4.972528529	2.29E-06	2.83E-05
CD55	-1.152366265	-4.971275265	2.30E-06	2.84E-05
SLC38A1	1.254847185	4.963124989	2.38E-06	2.93E-05
CEP27	-1.239442658	-4.96279867	2.39E-06	2.93E-05
LFNG	-1.363397034	-4.940592102	2.62E-06	3.20E-05
ZNF223	-1.637807204	-4.938593297	2.64E-06	3.23E-05
C3orf58	-1.001937466	-4.930046323	2.74E-06	3.34E-05
SPI1	-1.009686892	-4.929935655	2.74E-06	3.34E-05
RASL12	-1.010395924	-4.929847598	2.74E-06	3.34E-05
IER3	2.095123391	4.925835254	2.79E-06	3.39E-05
RENBP	-1.153620938	-4.920273886	2.86E-06	3.46E-05
CAP2	1.387549133	4.916159161	2.91E-06	3.50E-05
HSPA6	-1.57227914	-4.90874139	3.00E-06	3.60E-05
ZFP36	1.522564346	4.906492299	3.03E-06	3.63E-05
TSPAN9	-1.147980789	-4.901966777	3.09E-06	3.70E-05
SLC7A7	-1.268964602	-4.89960344	3.12E-06	3.73E-05
USP49	-2.053189834	-4.872185868	3.50E-06	4.13E-05
CHST13	-1.365357253	-4.864223807	3.62E-06	4.26E-05
GP1BB	-1.227383228	-4.850296874	3.84E-06	4.48E-05
CYBB	-1.155994897	-4.847074535	3.89E-06	4.53E-05
CD84	-1.253653967	-4.844543114	3.93E-06	4.58E-05
PDGFRA	1.403981801	4.836739848	4.06E-06	4.71E-05
DYSF	-1.090989727	-4.831990166	4.14E-06	4.79E-05
MAD2L1	-1.077941813	-4.823798991	4.29E-06	4.94E-05
PRSS35	-1.568763335	-4.823400645	4.29E-06	4.95E-05
PRC1	-1.073392349	-4.818559608	4.38E-06	5.03E-05
PAM	1.052262524	4.810025183	4.54E-06	5.19E-05
IGFBP7	1.578927597	4.798829345	4.76E-06	5.41E-05
HLA-DRB4	-2.455939998	-4.793743896	4.86E-06	5.51E-05
HIST1H1C	-1.700181701	-4.791477094	4.91E-06	5.55E-05
TBX2	-1.37415744	-4.788537873	4.97E-06	5.61E-05
BMP2	-1.142370057	-4.787904597	4.98E-06	5.61E-05

HLA-DRB3	-1.785979818	-4.767799033	5.41E-06	6.04E-05
COL13A1	-1.028475344	-4.765923185	5.46E-06	6.09E-05
GPNMB	-1.835729788	-4.762854315	5.53E-06	6.16E-05
Pfs2	-1.021291859	-4.742639084	6.01E-06	6.63E-05
HNRPA2B1	-1.451077643	-4.73939092	6.09E-06	6.70E-05
ARMCX2	1.130862962	4.738879299	6.10E-06	6.72E-05
C9orf58	-1.387596383	-4.724926207	6.47E-06	7.07E-05
YRDC	-1.148164353	-4.697720383	7.23E-06	7.83E-05
CD209	-1.156768666	-4.692411078	7.39E-06	7.99E-05
FAP	1.685383266	4.689988253	7.47E-06	8.05E-05
GPT2	1.089080324	4.675537755	7.92E-06	8.48E-05
STK6	-1.11715353	-4.663414787	8.33E-06	8.84E-05
IBSP	-2.592651508	-4.657154565	8.54E-06	9.05E-05
ODC1	1.018801769	4.653506748	8.67E-06	9.15E-05
TNFSF10	-1.284174826	-4.651764292	8.73E-06	9.20E-05
EVI2B	-1.082668745	-4.64944367	8.82E-06	9.28E-05
MT1G	-1.736450251	-4.644291684	9.00E-06	9.44E-05
LOC440704	-1.57150283	-4.632478637	9.45E-06	9.85E-05
MT1F	-1.453907958	-4.628894707	9.59E-06	9.99E-05
IFI44	-1.468682591	-4.617684599	1.00E-05	0.000103894
LYZ	-2.165790827	-4.599715065	1.08E-05	0.000110535
LOC440567	-1.580872258	-4.580169792	1.17E-05	0.000118781
LOC648622	-1.482674158	-4.572862211	1.20E-05	0.000122002
SCRG1	1.983170859	4.569656715	1.22E-05	0.000123195
ET	-1.09941051	-4.55981408	1.27E-05	0.000127527
LOC644250	-1.719150737	-4.552893339	1.31E-05	0.000130617
LOC653328	-1.790058343	-4.542563678	1.36E-05	0.000135415
HSPB2	1.052823028	4.53967622	1.38E-05	0.000136837
IFITM5	-2.19345168	-4.527657271	1.44E-05	0.000142769
IFI30	-2.077620578	-4.52301442	1.47E-05	0.000145318
SQSTM1	1.271343746	4.503599652	1.59E-05	0.000155713
FAT3	-1.361510923	-4.493875967	1.65E-05	0.000161143
PPP1R15A	1.102554451	4.471300913	1.81E-05	0.000173989
VSIG4	-1.162771455	-4.463834648	1.87E-05	0.000178427
NKD2	-1.263651762	-4.458680735	1.90E-05	0.000181574
CPXM	-1.172919554	-4.457403614	1.91E-05	0.000182404
THBS2	1.989085438	4.45561944	1.93E-05	0.000183592
FGL2	-1.153465739	-4.448898523	1.98E-05	0.000187997
DHRS3	1.040802393	4.439258718	2.06E-05	0.000194309
RDH11	-1.012431404	-4.434596354	2.10E-05	0.000197122
NOL5A	-1.12316604	-4.408684016	2.32E-05	0.000215764
DOCK2	-1.095239697	-4.404587735	2.36E-05	0.0002188
PANX3	-2.214183902	-4.393314158	2.47E-05	0.000227248
PTPLAD2	-1.563567125	-4.373864095	2.66E-05	0.00024241

LOC644914	-1.658674527	-4.353744253	2.88E-05	0.000260203
PGAM1	1.094764983	4.351992675	2.90E-05	0.000261692
MX1	-2.103897287	-4.333366174	3.12E-05	0.000278494
OLFML2B	-2.122690181	-4.324834433	3.23E-05	0.000286613
TDRD1	-1.061572726	-4.306673977	3.47E-05	0.000304851
AMICA1	-1.109397559	-4.30400346	3.50E-05	0.000307773
CCL8	-1.582152759	-4.302156883	3.53E-05	0.00030961
COL4A2	1.127749683	4.299813523	3.56E-05	0.00031212
C8orf59	-1.027209257	-4.294674919	3.63E-05	0.000317979
ADAMTS4	-1.155806171	-4.29362404	3.65E-05	0.000319058
LEPREL1	1.337896765	4.290265601	3.70E-05	0.000322463
PFKP	1.102849129	4.284731252	3.78E-05	0.000327758
MAMDC2	-1.518652488	-4.282741686	3.81E-05	0.0003295
DPT	-1.719714058	-4.280781896	3.83E-05	0.000331443
OLFML2A	-1.085334668	-4.28058042	3.84E-05	0.000331473
DKFZP564O0823	-1.079252972	-4.27767518	3.88E-05	0.000334458
GPX3	-1.199073313	-4.257381159	4.20E-05	0.000358568
SFRS10	-1.012536101	-4.248619324	4.34E-05	0.000368906
GZMA	-1.389387779	-4.245249719	4.40E-05	0.0003726
CKS1B	-1.13654489	-4.244838311	4.41E-05	0.000372984
CXADR	-1.077069306	-4.242729234	4.44E-05	0.00037548
CHSY1	-1.068794858	-4.235506252	4.57E-05	0.000384299
RPS3A	-1.358175574	-4.226263401	4.73E-05	0.000396205
ANPEP	1.231122335	4.214866832	4.95E-05	0.00041121
HCST	-1.435256085	-4.201795007	5.20E-05	0.000428954
COL24A1	-1.023516485	-4.193764126	5.36E-05	0.000440766
GAS1	1.404737061	4.19000378	5.44E-05	0.000446134
NDUFB9	-1.622066761	-4.182834863	5.59E-05	0.000455555
IRXL1	1.006788388	4.166174925	5.96E-05	0.000482033
STAT1	1.171443596	4.159645697	6.11E-05	0.000492591
CXCL10	-1.676221021	-4.136405015	6.68E-05	0.000531102
RPN2	-1.169771083	-4.121212709	7.07E-05	0.000557985
MRPL51	-1.042951855	-4.104596117	7.53E-05	0.000587876
CD36	-1.241887051	-4.101612351	7.62E-05	0.000593242
SORCS2	1.051015842	4.098023287	7.72E-05	0.00059984
LOC643284	-1.178108599	-4.096629872	7.76E-05	0.000602066
RNASET2	-1.102324965	-4.079723557	8.27E-05	0.000635358
NFIX	1.187257889	4.073720942	8.46E-05	0.000647676
HIST2H2AC	-1.196335001	-4.068858685	8.62E-05	0.000658007
MMP11	-1.536427006	-4.065693487	8.72E-05	0.000664642
C10orf116	1.706967213	4.061254461	8.86E-05	0.000674314
CDK4	-1.05500259	-4.046449796	9.37E-05	0.000707257
CDH15	-1.783192485	-4.043890559	9.46E-05	0.000713201
PPFIBP2	-1.037108154	-4.039882643	9.60E-05	0.00072223

IFITM2	1.009075635	4.038041072	9.67E-05	0.000726273
IFIT2	-1.238061571	-4.035061067	9.78E-05	0.000732717
COMP	2.44128897	4.016462135	0.000104806	0.00077961
LDHB	-1.333875561	-4.013139928	0.00010611	0.000788276
LOC648000	-1.165973811	-4.005805566	0.000109046	0.000807323
DLX3	-1.2133411	-4.004711352	0.00010949	0.000810012
ACTG1	1.578698774	3.978465418	0.000120685	0.000879043
CXCL14	-1.587751522	-3.977503064	0.000121115	0.000881153
CD68	-1.92141314	-3.956446924	0.000130912	0.000942277
ALPL	-2.273846938	-3.923981604	0.000147511	0.001044319
PDGFRL	-1.308011128	-3.910288436	0.000155099	0.001091808
COL22A1	-1.601113888	-3.908250242	0.000156259	0.001097857
COX7B	-1.156289428	-3.904914088	0.000158177	0.001110082
LOC391656	-1.015087916	-3.875302212	0.000176211	0.001220535
OMD	-1.762247935	-3.866551511	0.000181904	0.001254064
RGS16	-1.089556739	-3.858276712	0.000187448	0.001286851
G1P2	-1.523073211	-3.85798401	0.000187648	0.001287286
LOC644972	-1.527470393	-3.826493901	0.000210277	0.001418378
MLLT11	-1.128275607	-3.805655096	0.000226655	0.001514733
GREM1	1.231755802	3.802232024	0.000229459	0.001528787
PLAT	1.033772514	3.780841373	0.000247739	0.001633681
PDGFRB	1.503976048	3.769426093	0.000258053	0.001692236
CTSK	-2.613816136	-3.765245552	0.000261931	0.001715417
AGPAT5	-1.089907211	-3.763721707	0.000263358	0.001722508
RPS28	-1.632945064	-3.737970891	0.000288623	0.001862898
HLA-DQB1	-1.071544035	-3.735521122	0.000291143	0.001876255
LOC648210	-1.233498919	-3.701679502	0.00032816	0.002082065
LAMA5	-1.025775953	-3.678843582	0.000355613	0.00223133
HTRA1	1.528859601	3.673699698	0.000362091	0.00226515
IFITM3	1.082144863	3.661184485	0.00037832	0.002349625
HSPA1A	-1.691915461	-3.658204853	0.000382284	0.002368197
LOC440732	-1.561513032	-3.629227303	0.000422942	0.002578079
PRRX2	1.102954259	3.621344668	0.00043469	0.002637472
CYFIP2	-1.152029496	-3.595084118	0.000476094	0.002849427
LOC220433	-1.476675848	-3.53818415	0.000578933	0.003355473
LOC647727	-1.417938337	-3.494779004	0.000671104	0.003814521
CKB	-1.483198252	-3.473266992	0.000721749	0.004059918
LOC643287	-1.00936338	-3.469992736	0.000729766	0.004101303
ASPN	-1.985177969	-3.466842644	0.000737557	0.004138756
RHBDL2	-1.191992182	-3.466207979	0.000739137	0.004144669
MEPE	-1.683597959	-3.456087133	0.000764755	0.004263457
MGP	-1.828195853	-3.450263405	0.000779872	0.004334203
G1P3	-1.240871133	-3.447802246	0.000786345	0.004366288
RPLP1	-1.44887914	-3.44268139	0.000799975	0.004431148

BST2	-1.274625349	-3.439160466	0.000809475	0.004470891
LOC646433	-1.034564268	-3.437986742	0.000812665	0.004486529
COL10A1	-1.706240207	-3.435636267	0.00081909	0.004516347
PTMA	-1.554049731	-3.430955541	0.000832026	0.004577241
RPL7	-1.239031724	-3.423176459	0.00085395	0.004673173
LOC642115	-1.217831729	-3.417495695	0.000870303	0.00474215
S100A8	-1.266908163	-3.407715039	0.000899148	0.004870399
DCN	1.415966222	3.393008159	0.000944215	0.005068386
LOC284230	-1.648311056	-3.37433011	0.001004508	0.005337022
HLA-DMA	-1.417664165	-3.321517275	0.0011951	0.006177649
IGF2	1.246651597	3.316587024	0.001214522	0.006261213
FNDC1	1.507932801	3.304730205	0.001262446	0.006468256
SUMO2	-1.520853014	-3.299669857	0.001283433	0.006559003
SCIN	-1.013609382	-3.29873661	0.001287339	0.006576924
LOC647100	-1.356413344	-3.286337518	0.001340298	0.006790487
LOC401206	-1.40812573	-3.284167367	0.001349774	0.006830295
DKK1	1.450705782	3.282597738	0.001356667	0.006862397
SOST	-1.795494875	-3.265119589	0.001435675	0.007189951
LOC645138	-1.423420442	-3.263600668	0.00144274	0.007214564
SLC2A3	1.094730713	3.259875145	0.001460206	0.007285269
SERPINF1	-1.274063403	-3.224044129	0.00163857	0.008009578
PHGDH	1.071141315	3.218752754	0.00166657	0.008124202
MXRA5	-1.83329645	-3.199461898	0.001772467	0.008514244
VAMP8	-1.450273846	-3.195906833	0.001792653	0.008584818
LOC642989	-1.457057678	-3.174573965	0.001918352	0.009082377
CA3	-1.126468663	-3.170484159	0.001943367	0.009186893
TNNC1	-1.078328174	-3.164870672	0.001978196	0.009316307
LOC649682	-1.396076849	-3.164706924	0.001979221	0.009319376
EMP1	1.04556101	3.160665704	0.002004666	0.009423211
LOC653658	-1.526352089	-3.157987568	0.002021695	0.009490768
UQCRH	-1.024746855	-3.153485371	0.002050627	0.009597747
LOC643949	-1.076411183	-3.149028623	0.002079645	0.009708115
LOC388621	-1.518395908	-3.136144801	0.002165691	0.010047674
ALDH1A3	1.090466976	3.127770478	0.00222338	0.010271677
LOC390354	-1.13236219	-3.12673894	0.002230584	0.010301151
PTGES3	-1.200785211	-3.109779455	0.002352172	0.010767185
C14orf78	1.055959956	3.105814738	0.002381469	0.010883358
IFI27	-1.472926342	-3.095545993	0.002458931	0.011186232
LOC654194	-1.286828956	-3.092247486	0.002484304	0.011270895
LOC387753	-1.294195671	-3.079496141	0.002584691	0.011639723
HLA-H	-1.025582492	-3.073112612	0.002636345	0.011831842
EGR1	1.077887363	3.062060381	0.002728044	0.012180158
HRASLS3	1.032899018	3.039568292	0.002923838	0.012872509
ZFP36L1	-1.135776529	-3.037199828	0.002945195	0.012941462

IFI44L	-1.208591522	-3.026899775	0.003039758	0.013266038
COL6A2	1.047090069	3.026237887	0.003045929	0.013290651
LOC648294	-1.227517361	-3.023240463	0.003074023	0.013389864
THY1	1.241472794	3.016013012	0.00314275	0.013629854
PDPN	-1.053966558	-3.014997875	0.003152516	0.013665096
LOC388532	-1.083044544	-3.003427147	0.003265828	0.014046657
DLX5	-1.005313349	-2.991574746	0.003385785	0.014434409
CLEC11A	-1.248891202	-2.98978075	0.003404291	0.014499996
SFRP2	-1.021598489	-2.981373896	0.003492266	0.014786527
RPL14	-1.018878031	-2.952363459	0.003812187	0.015884901
SLN	-1.121764295	-2.948032556	0.003862198	0.016019117
RPL23	-1.488683424	-2.930278251	0.004073587	0.016732097
COX7A1	1.02573879	2.885112756	0.004660176	0.018705056
EEF1A2	-1.400984586	-2.853804252	0.005111216	0.020104925
BGLAP	-1.368202426	-2.817454337	0.005684815	0.021910117
TGFBI	1.348712577	2.803886664	0.005913572	0.022617386
LOC644969	-1.150328834	-2.787614108	0.006199001	0.023489865
TNNT1	-1.222390565	-2.769417767	0.006533014	0.024521363
HAPLN1	1.318829398	2.761836681	0.006676948	0.024930597
LOC653974	-1.160111902	-2.751828295	0.006871389	0.025473969
KSP37	-1.365028932	-2.746515436	0.006976686	0.025784214
BAMBI	-1.071280987	-2.721481031	0.007492878	0.027193231
OLFML3	1.022848168	2.709571166	0.007750427	0.027921195
ITGB2	-1.082066686	-2.671330368	0.008632605	0.03037695
LOC649518	-1.047228202	-2.608240172	0.01028834	0.034882397
MFAP4	1.161971513	2.566062401	0.011549624	0.038004147
KERA	-1.234435061	-2.440581152	0.016163622	0.049656903

Table S2. Genes in the blue module.

Gene Symbol	GB_ACC	GS.metastasis	MM.blue
ALOX5AP	NM_001629.2	-0.610267984	0.859939645
FGL2	NM_006682.1	-0.586331032	0.9225612
LYZ	NM_000239.1	-0.571063166	0.786984376
HLA-DMB	NM_002118.3	-0.564284413	0.934423876
HLA-DRA	NM_019111.3	-0.558415188	0.892501447
HLA-DMA	NM_006120.2	-0.554037962	0.918049052
AIF1	NM_001623.3	-0.547598108	0.962184529
FPRL2	NM_002030.3	-0.546448147	0.913886347
HLA-DPA1	NM_033554.2	-0.544267435	0.895859275
HLA-DQA1	XM_936120.1	-0.540946183	0.876735228
IRF8	NM_002163.2	-0.533252507	0.939018296
HCST	NM_014266.3	-0.527926303	0.944621305
PEA15	NM_003768.2	-0.526215493	0.771435047
SLCO2B1	NM_007256.2	-0.525468043	0.927096159
MS4A6A	NM_022349.2	-0.524004803	0.940906447
HLA-DRB4	NM_021983.4	-0.520342325	0.818162536
ITGB2	NM_000211.1	-0.518338483	0.92862094
CD74	NM_001025158.1	-0.517995388	0.92075136
AMICA1	NM_153206.1	-0.516780637	0.839990459
ASPM	NM_018136.2	0.512940177	-0.806495314
GIMAP4	NM_018326.2	-0.512928533	0.926220887
CD14	NM_000591.1	-0.501820306	0.953085127
DOCK2	NM_004946.1	-0.50169517	0.935162882
GIMAP7	NM_153236.3	-0.498035136	0.869237957
KIF20A	NM_005733.1	0.496409803	-0.690237901
C1orf162	NM_174896.2	-0.492915795	0.941119564
P8	NM_012385.1	-0.490375599	0.481213062
HCLS1	NM_005335.3	-0.488741173	0.846546514
HLA-DQB1	NM_002123.2	-0.48680673	0.699622368
FHL2	NM_201557.1	-0.485216466	0.527558424
CYBB	NM_000397.2	-0.484383855	0.891999512
LY86	NM_004271.3	-0.484367431	0.934314048
PRSS35	NM_153362.1	0.484127538	-0.550366111
C1QA	NM_015991.1	-0.482372191	0.948471837
HAVCR2	NM_032782.3	-0.481340543	0.897808381
WAS	NM_000377.1	-0.47850351	0.83669081
CENTA2	NM_018404.1	-0.477897308	0.939674864
TYROBP	NM_003332.2	-0.474657076	0.841197695
TPX2	NM_012112.4	0.47253331	-0.801301672
C1QC	NM_172369.2	-0.470707993	0.9303003
C1QB	NM_000491.2	-0.47055896	0.9182347
SLC7A7	NM_003982.2	-0.466259957	0.833770051

FLOT2	NM_004475.1	-0.463767102	0.62428154
RNASET2	NM_003730.3	-0.460034114	0.900475859
FCER1G	NM_004106.1	-0.456241101	0.831417291
MATN2	NM_030583.2	0.454905816	-0.413793923
KIAA0746	NM_015187.1	-0.454089605	0.673355047
FLJ11259	NM_018370.1	-0.449784753	0.854842321
VSIG4	NM_007268.1	-0.449730649	0.891742375
LCP2	NM_005565.3	-0.447028406	0.962431724
PRG1	NM_002727.2	-0.445762432	0.751723647
CCNB2	NM_004701.2	0.44506564	-0.753409815
GIMAP5	NM_018384.3	-0.441963111	0.87600546
GIMAP8	NM_175571.2	-0.433032108	0.812774606
S100A8	NM_002964.3	-0.427407355	0.491527013
CCL8	NM_005623.2	-0.427292491	0.896009788
PLEK	NM_002664.1	-0.42727759	0.897104264
LOC387882	NM_207376.1	-0.426331118	0.459446177
SCRN1	NM_014766.2	-0.411970335	0.423821682
DTL	NM_016448.1	0.411632859	-0.614822106
CXCL10	NM_001565.1	-0.409417061	0.789041299
HLA-DRB3	NM_022555.3	-0.404939375	0.714001484
MS4A7	NM_206939.1	-0.404046859	0.734908516
IGSF6	NM_005849.1	-0.402669605	0.859412352
UCP2	NM_003355.2	-0.401512578	0.663307557
TBC1D2	NM_018421.2	-0.397509749	0.680971005
CMAH	NR_002174.1	-0.38901624	0.663242309
STAB1	NM_015136.2	-0.388968813	0.80629436
TSPAN33	NM_178562.2	-0.388644361	0.798315665
TRIM22	NM_006074.2	-0.387416065	0.875816627
ARHGDI3	NM_001175.4	-0.385170369	0.905296823
BRI3	NM_015379.3	-0.376867898	0.633934468
LRRC8D	NM_018103.3	-0.37537141	0.595599942
CD163	NM_004244.3	-0.374912052	0.790306292
PLTP	NM_006227.2	-0.373061066	0.732123951
C10orf58	NM_032333.2	-0.369685641	0.424078896
IGFBP4	NM_001552.2	-0.368399999	0.730755593
TMEM51	NM_018022.1	-0.367778058	0.641596108
TPD52L1	NM_001003396.1	-0.367629657	0.435305906
FLJ21438	XM_937586.1	-0.363190818	0.797930663
AXL	NM_001699.3	-0.359558904	0.626222821
GAS6	NM_000820.1	-0.356845603	0.768423707
CXCL12	NM_001033886.1	-0.353985671	0.644059108
PPP1R3C	NM_005398.3	0.352440582	-0.25313197
EPB41L3	NM_012307.2	-0.348934536	0.603496955
TM4SF1	NM_014220.2	-0.346169344	0.747095761

APOE	NM_000041.2	-0.346121027	0.758669543
CD209	NM_021155.2	-0.339892733	0.813363023
IFITM2	NM_006435.1	-0.339484296	0.700990803
ARID5B	NM_032199.1	-0.339482504	0.498492198
PECAM1	NM_000442.2	-0.336492511	0.687967785
LIMA1	NM_016357.3	-0.334934138	0.642981023
EBI2	NM_004951.3	-0.334368702	0.587497981
Pfs2	NM_016095.1	0.333927779	-0.556114898
PTTG1IP	NM_004339.2	-0.332523831	0.606107008
BST2	NM_004335.2	-0.331968542	0.724663843
GZMA	NM_006144.2	-0.320651441	0.664774889
TYMS	NM_001071.1	0.320570597	-0.474464534
CENPF	NM_016343.3	0.312209399	-0.70049935
RNASE1	NM_198232.1	-0.307715971	0.719764386
CD9	NM_001769.2	-0.307139853	0.429993356
MCM3	NM_002388.3	0.306389385	-0.481237116
APOC1	NM_001645.3	-0.305767909	0.54106689
GRAMD3	NM_023927.1	-0.304024078	0.625799118
WDR1	NM_017491.3	-0.303935226	0.394016559
DNMT1	NM_001379.1	0.301703953	-0.334385709
CDT1	NM_030928.2	0.301009158	-0.498202203
MAD2L1	NM_002358.2	0.296199929	-0.622652226
GPNMB	NM_001005340.1	-0.28700852	0.358228461
TMEM97	NM_014573.1	0.28527108	-0.598917935
C1S	NM_001734.2	-0.285037669	0.71814387
CEBPD	NM_005195.2	-0.284898407	0.471433886
TNFSF10	NM_003810.2	-0.27750636	0.829052305
IFITM3	NM_021034.1	-0.276520596	0.651645081
IFI27	NM_005532.3	-0.276091898	0.642118922
SART2	NM_013352.1	-0.274965267	0.672334548
BOP1	NM_015201.3	0.272626939	-0.588513813
FOLR2	NM_000803.2	-0.268691112	0.766255041
IGFBP7	NM_001553.1	-0.264548113	0.690240384
C1QR1	NM_012072.2	-0.264126358	0.644649397
PHACTR2	NM_014721.1	-0.26239953	0.566505359
RPS27L	NM_015920.3	-0.260619246	0.490296335
NPTX2	NM_002523.1	0.257305638	-0.40973151
PLCG2	NM_002661.1	-0.257205587	0.595744566
BMP2	NM_001200.1	0.253665867	-0.28632222
STAT1	NM_139266.1	-0.246052141	0.675347058
MX1	NM_002462.2	-0.244784929	0.66321752
MSX1	NM_002448.1	0.244453044	-0.530152161
CLEC3B	NM_003278.1	-0.244437511	0.495423147
MGC14376	NM_032895.2	-0.242883786	0.489012679

GPX3	NM_002084.2	-0.238862683	0.450385464
HES4	NM_021170.2	0.238741901	-0.178593817
CCND1	NM_053056.1	-0.23637264	0.517521272
HBA1	NM_000558.3	-0.229691386	0.131432752
HSPA6	NM_002155.3	-0.229051658	0.39808085
FER1L3	NM_013451.2	-0.212411222	0.567635205
STAT4	NM_003151.2	-0.211778208	0.519218398
MT1F	NM_005949.1	0.210005686	0.125844709
FLJ13391	NM_032181.1	-0.208710661	0.463721941
LEF1	NM_016269.2	0.204140743	-0.349245673
HERC5	NM_016323.1	-0.201931532	0.456486231
ATP1B1	NM_001677.3	-0.198870418	0.247316422
HBB	NM_000518.4	-0.198721239	0.081643715
IFIT2	NM_001547.3	-0.182399874	0.568863715
M160	NM_174941.3	-0.18027602	0.447329229
SPATA18	NM_145263.1	-0.178734475	0.326319271
VEGFC	NM_005429.2	-0.171473902	0.424043015
AGTRL1	NM_005161.2	-0.169848242	0.501495025
PHGDH	NM_006623.2	0.165544332	-0.236764241
GARS	NM_002047.1	0.165060123	-0.138138538
GLS	NM_014905.2	-0.164168777	0.446805525
DHRS3	NM_004753.4	-0.16014066	0.199457668
RGC32	NM_014059.1	0.157402461	-0.28978528
ADCY4	NM_139247.2	-0.157162833	0.452844589
LHFP	NM_005780.1	-0.156635008	0.472249091
PRRX2	NM_016307.3	0.154224748	-0.527767755
EPAS1	NM_001430.3	-0.153422267	0.587959583
RASGRP3	NM_170672.1	-0.145796273	0.494310865
FST	NM_013409.1	-0.144519912	0.45826731
EMP1	NM_001423.1	-0.137325028	0.322232088
IFI44	NM_006417.2	-0.132896833	0.296341148
NPAS1	NM_002517.2	0.132622074	-0.282270828
LOC201895	NM_174921.1	-0.131335366	0.286333153
ANKRD13	NM_033121.1	-0.131302133	0.408508967
IFI44L	NM_006820.1	-0.128126453	0.582638755
HIST1H4C	NM_003542.3	0.122744781	-0.157686595
MLLT11	NM_006818.3	-0.118165404	-0.257972198
SULF1	NM_015170.1	-0.108995553	0.36609351
MTHFD1L	NM_015440.3	-0.106351588	0.179360632
XPOT	NM_007235.3	0.103142853	-0.364872496
BST1	NM_004334.1	-0.093256802	0.422794434
PLOD2	NM_182943.2	0.088390057	-0.257671725
NUDT1	NM_198954.1	0.084541842	-0.318077672
PALLD	NM_016081.2	-0.077646863	0.383244423

PLSCR4	NM_020353.1	-0.076208729	0.333287553
DYSF	NM_003494.2	-0.074778706	0.375515029
SERPINE2	NM_006216.2	0.070300163	0.233301619
GP1BB	NM_000407.3	0.057076949	-0.382461697
PLAT	NM_000930.2	-0.055107531	0.191110796
G1P3	NM_002038.2	-0.048256398	0.286228727
OLFML2A	NM_182487.1	0.047214477	0.325406819
LOC644376	XM_927528.1	-0.042237286	0.337622053
GPR116	NM_015234.3	0.04205511	0.37651462
MCM4	NM_005914.2	0.040906253	-0.407167416
TSPAN7	NM_004615.2	-0.036079016	0.246714144
URB	NM_199512.1	-0.033229231	0.477605762
NKD2	NM_033120.2	0.028948168	-0.186698762
OMD	NM_005014.1	0.019102079	-0.17834276
ENG	NM_000118.1	-0.019013737	0.551625862
PLVAP	NM_031310.1	0.017843116	0.208617159
CSRP2	NM_001321.1	-0.009137409	-0.259636109
GPT2	NM_133443.1	-0.00838139	-0.26954409
TMCO3	NM_017905.3	0.001758151	0.093033951
CDH5	NM_001795.2	-0.000475527	0.396547482

Abbreviations: GB_ACC, GenBank accession number; GS, Gene Significance; MM, Module Membership