

Exploring functions of long noncoding RNAs across multiple cancers through co-expression network

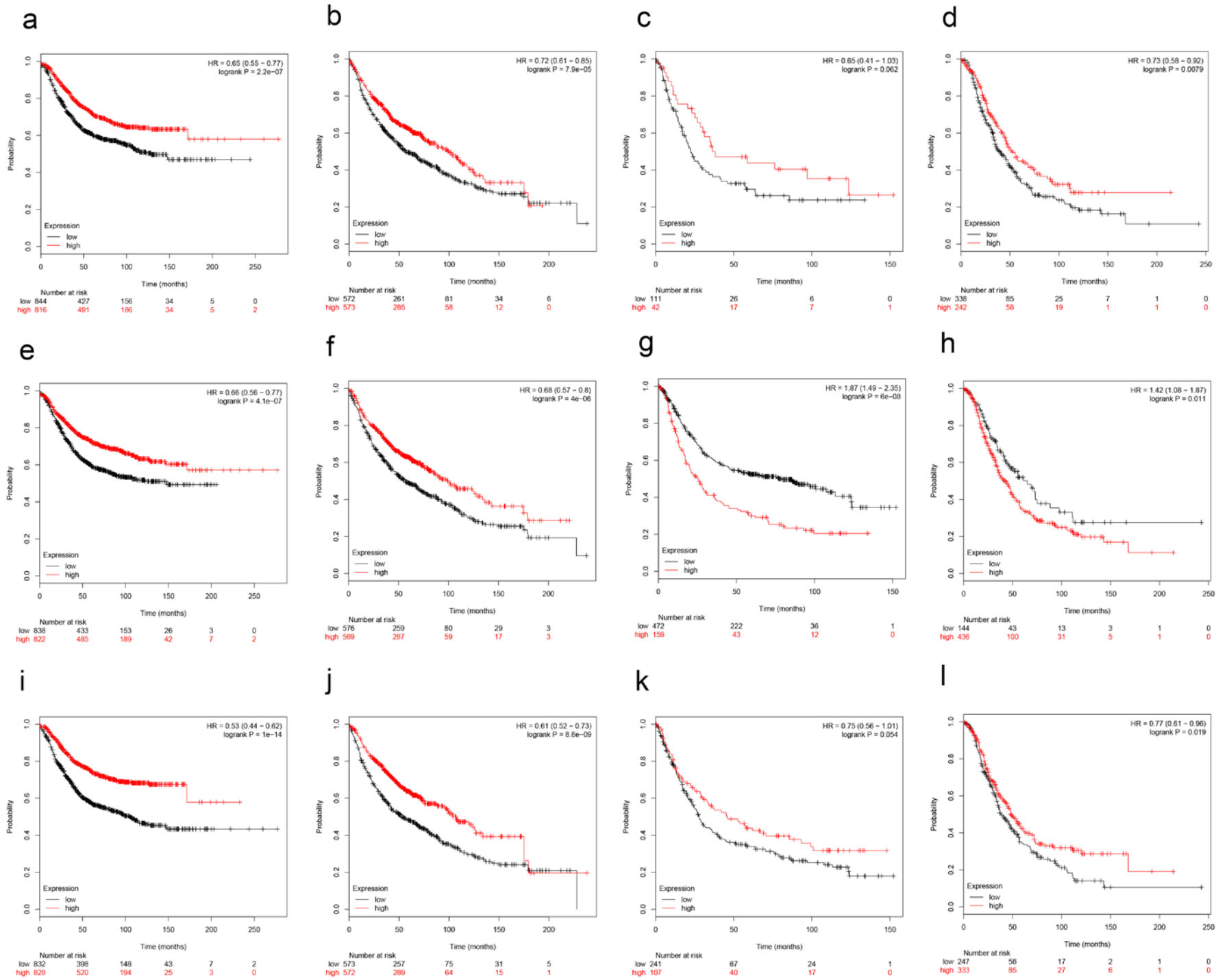
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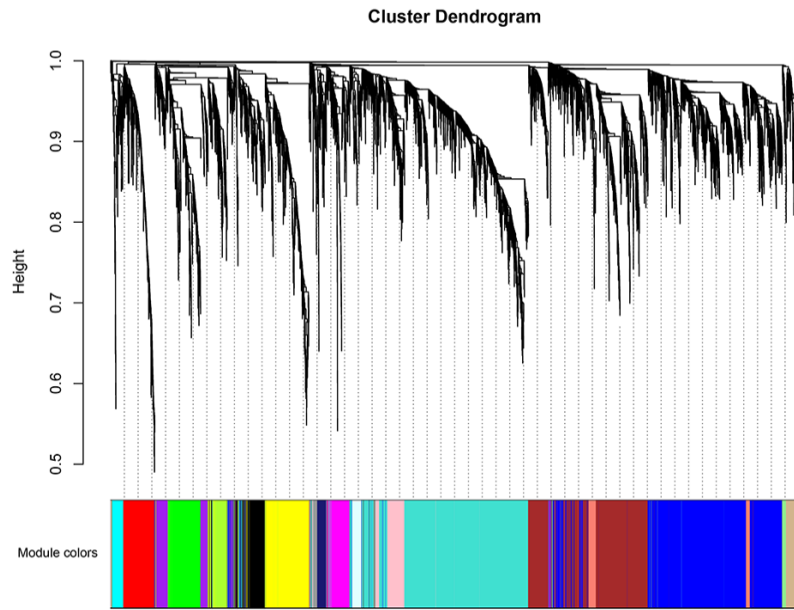
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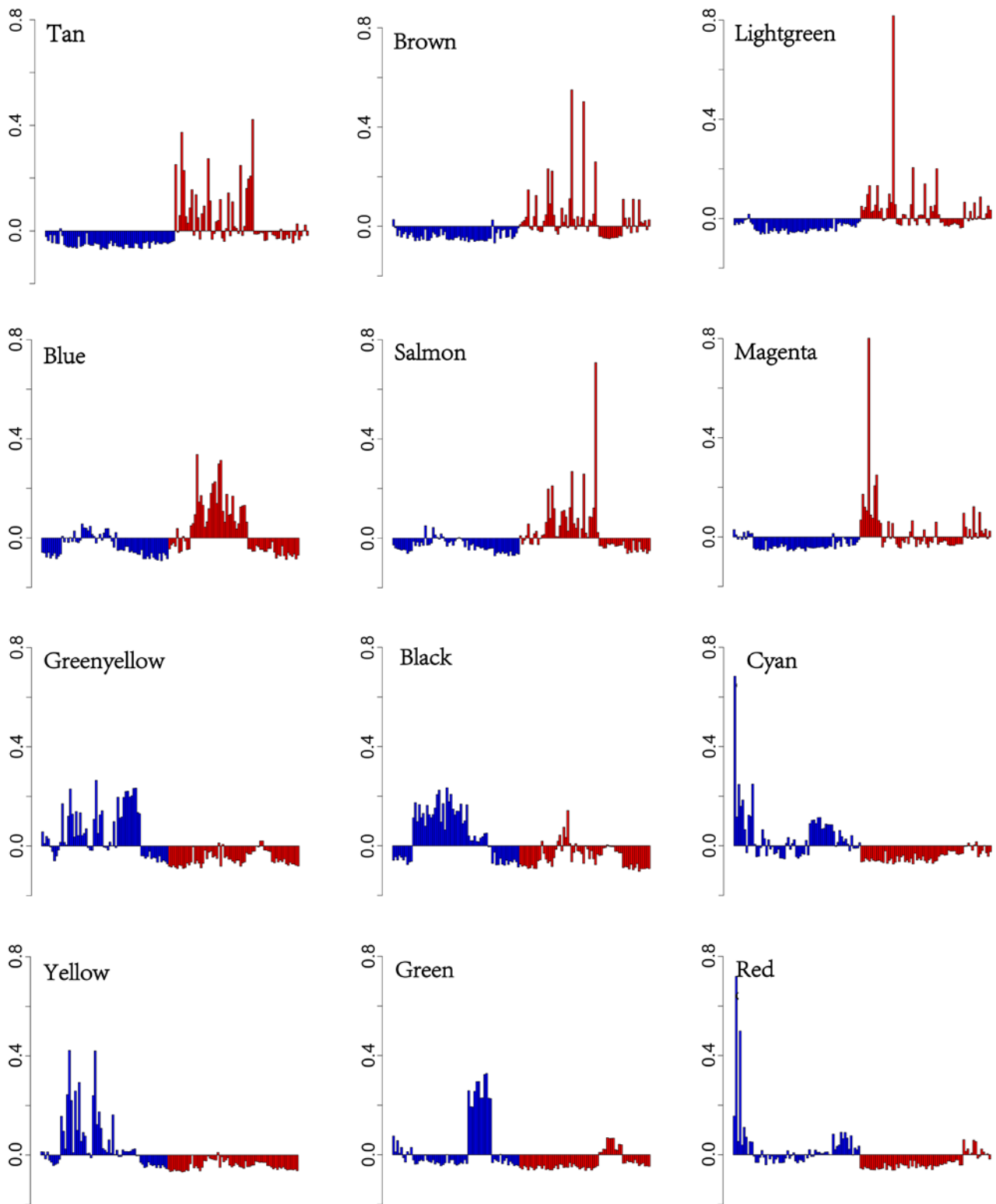
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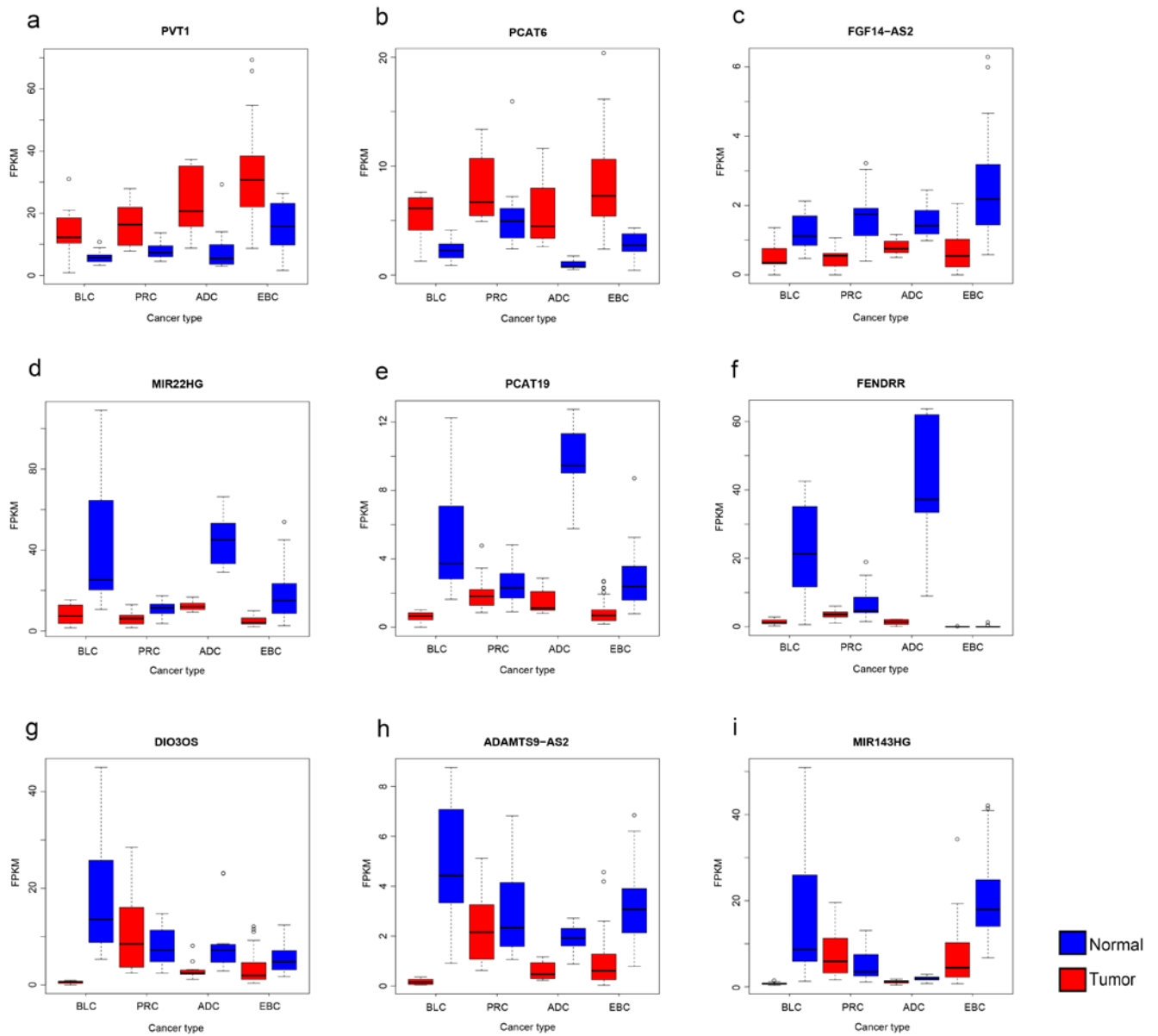
Supplementary Figure S1 | Survival analysis of low-expression and high-expression for each lncRNA using online tool Kaplan-Meier Plotter. (a, b, c, d) The Kaplan-Meier plots of ADAMTS9-AS2 in the breast cancer, lung cancer, gastric cancer and ovarian cancer. (e, f, g, h) The Kaplan-Meier plots of FGF14-AS2 in the breast cancer, lung cancer, gastric cancer and ovarian cancer. (I, j, k, l) The Kaplan-Meier plots of FGF14-AS2 in the breast cancer, lung cancer, gastric cancer and ovarian cancer. The red line denotes high expression, and the black denotes low expression. The x-axis is time, and the y axis is the proportion of subjects surviving. The digits under each plot represent the number of survival patients at each time point. The overexpression of the three lncRNAs significantly reduces risk of death when compared to their low expressions in 4 cancer types, except for FGF14-AS2 in gastric cancer and ovarian cancer, the low expression of which reduces the death rate.



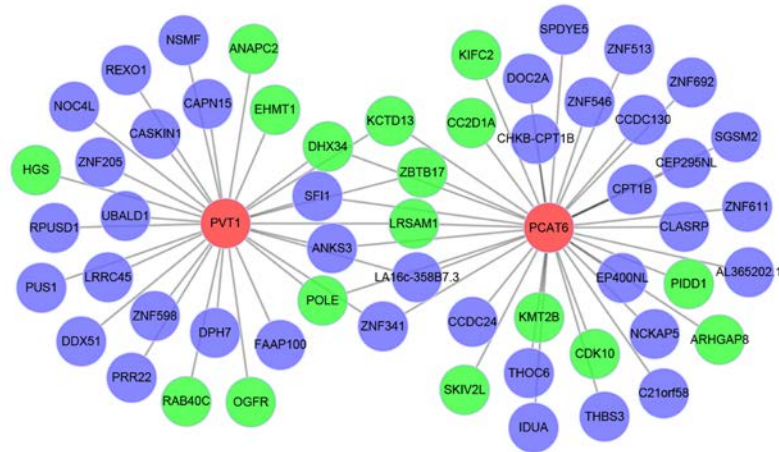
Supplementary Figure S2 | Modules defined by the weighted correlation network analysis (WGCNA). Tree on the top is the clustering dendrogram of genes, and the colorful bands represent modules in this network.



Supplementary Figure S3 | Module eigengene's profile across all samples. The x-axis depicts all samples, and the y-axis depicts the expression level of the eigengene. The red bar represents the tumor sample, and the blue denotes the normal sample.

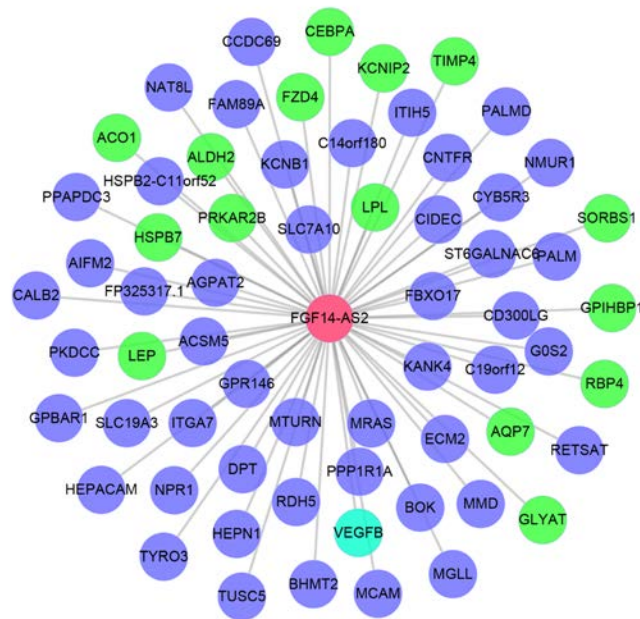


Supplementary Figure S4 | Expression levels (FPKM) of eight reported lncRNAs, (a) PVT1, (b) PCAT6, (c) FGF14-AS2. (d) MIR22HG, (e) PCAT19, (f) FENDRR, (g) DIO3OS, (h) ADAMTS9-AS2, (i) MIR143HG. The red box denotes the tumor tissue and the blue is the normal tissue. The x-axis depicts the cancer type.



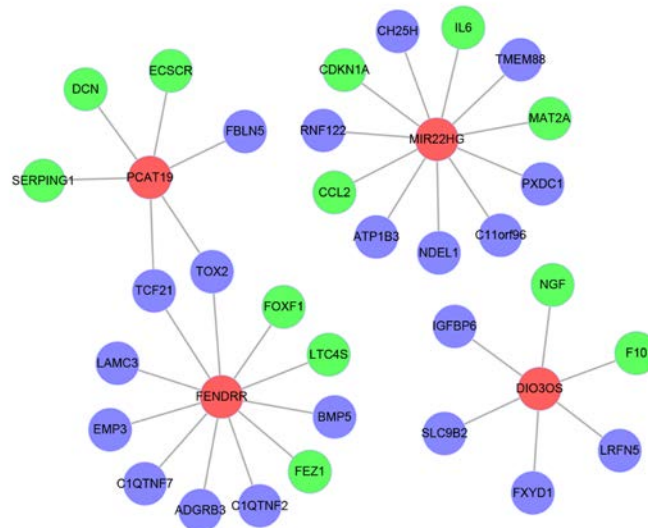
Supplementary Figure S5 | Functional investigation of genes correlated with PVT1 and PCAT6.

The red nodes denote the two lncRNAs. The green nodes denote genes involved in protein catabolic process and regulation of protein kinase cascade. The blue nodes denote other connected genes.

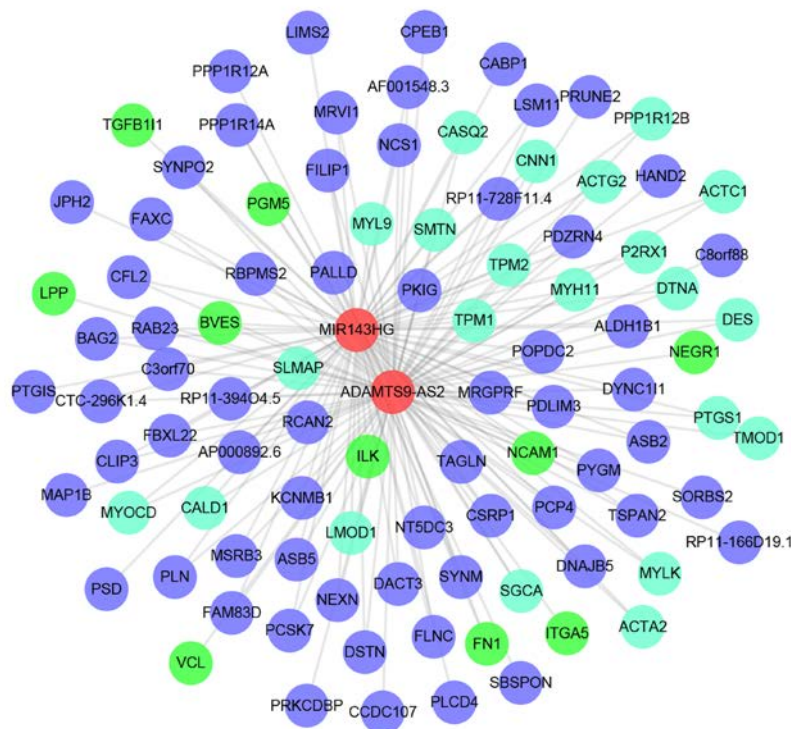


Supplementary Figure S6 | Functional investigation of genes correlated with FGF14-AS2.

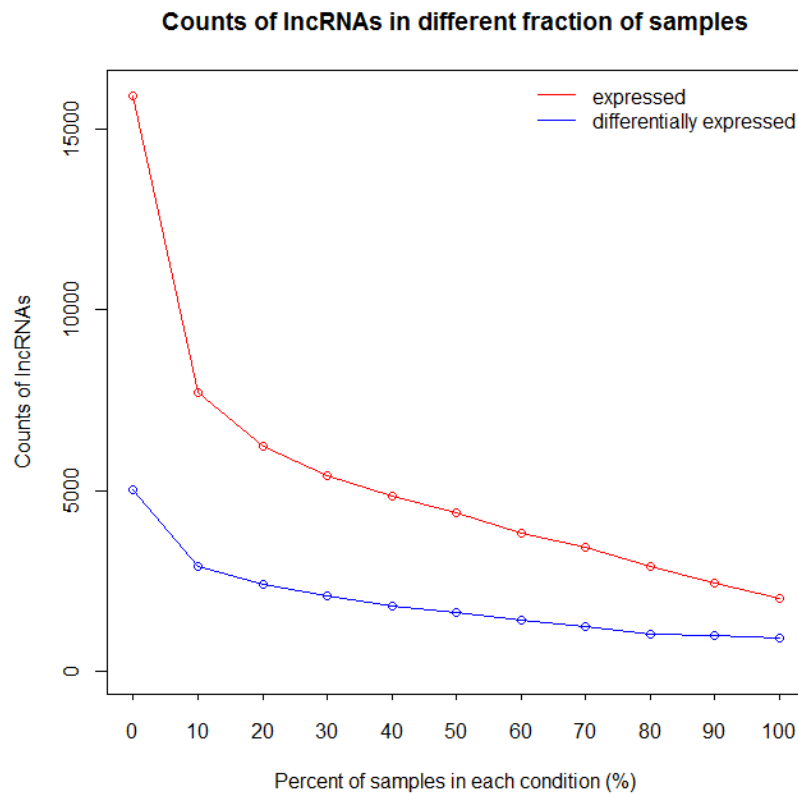
The red nodes denote the FGF14-AS2. The green nodes represent genes involved in response to stimulus. The cyan one is a famous cancer-associated gene VEGFB. The blue nodes denote other connected



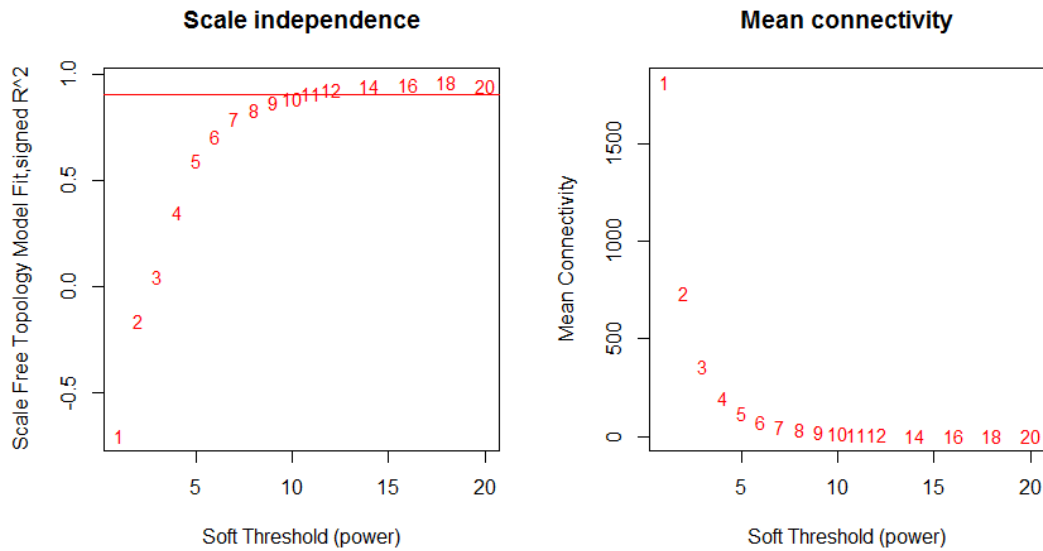
Supplementary Figure S7 | Functional investigation of genes correlated with PCAT19, FENDRR, MIR22HG and DIO3OS. The red nodes denote the four lncRNAs. The green nodes denote genes involved in response to stimulus and inflammation. The blue nodes denote other connected genes.



Supplementary Figure S8 | Functional investigation of genes correlated with MIR143HG and ADAMTS9-AS2. The red nodes denote the two lncRNAs. The green nodes denote genes involved in cell adhesion. The cyan nodes are genes showing function terms about muscle. The blue nodes denote other connected genes.



Supplementary Figure S9 | The number of expressed lncRNAs (red) and differentially expressed lncRNAs (blue) with different fraction of samples. The x-axis is the different fraction of samples, and the y-axis is the total number of expressed genes. In the work, we used the criterion $FPKM \geq 1$ to define the expressed levels. The number of expressed lncRNAs (red) decreased continuously with increase of the fraction of samples, which is similar with the number of differentially expressed genes (blue). But the number of differentially expressed genes (blue) becomes stable at 80%. Thus, to minimize the false positive and maintain a high number of differential expressed lncRNAs, we did our filter which requires the expression level of a gene exceed a threshold ($FPKM \geq 1$) in more than a fraction of samples (80%) in at least one condition in each cancer type.



Supplementary Figure S10 | Analysis of network topology for different soft thresholds. The left panel shows the scale-free topology fitting index (R^2 , y-axis) as a function of the soft-thresholding power (x-axis). The right panel displays the mean connectivity (degree, y-axis) as a function of the soft-thresholding power (x-axis). Red Arabic numerals in the panels denote different soft-thresholds. The red line in left panel means $R^2 = 0.9$. There is a trade-off between maximizing scale-free topology model fit (R^2) and maintaining a high mean number of connections. Thus, we set $\beta = 9$.

Supplementary Table S1: RNA-Seq Datasets

Accession	Study	Cancer type	Samples (pairs)	Library layout	Reads length (bp)
SRP012656	A high dimensional deep sequencing study of non-small cell lung adenocarcinoma in never-smoker Korean females	lung adenocarcinoma (ADC)	12	paired	78
SRP042620	Breast Cancer RNA-seq	ER+ breast cancer (EBC)	29	paired	50
ERP000550	Complete transcriptomic landscape of prostate cancer in the Chinese population using RNA-seq	Prostate cancer (PRC)	14	paired	90
SRP018008	Homo sapiens Transcriptome or Gene expression	Bladder cancer (BLC)	11	paired	100

Supplementary Table S2: DELs (differentially expressed lncRNAs) only altered in one cancer type

BLA				PRO				ADC				EBC			
gene_id	gene_name	log2FC	FDR	gene_id	gene_name	log2FC	FDR	gene_id	gene_name	log2FC	FDR	gene_id	gene_name	log2FC	FDR
ENSG00000151303.11	RP11-96C23.13	1.4	6.7E-04	ENSG00000154537.4	FAM27C	-1.2	1.8E-03	ENSG00000177888.5	RP5-1061H20.4	1.7	2.8E-08	ENSG00000116883.8	RP11-2681L5.5	1.3	3.3E-08
ENSG00000153363.12	LINC00467	1.3	9.3E-03	ENSG00000157306.14	RP11-66N24.4	1.3	2.4E-04	ENSG00000183250.11	LINC01547	1.8	6.7E-11	ENSG00000130600.15	H19	-1.1	4.3E-03
ENSG00000166770.10	ZNF667-AS1	-3.3	3.6E-14	ENSG00000172250.14	SERHL	1.3	9.2E-04	ENSG00000188511.12	C22orf34	-1.4	5.8E-11	ENSG00000175061.17	LRRCT5A-AS1	-1.0	8.2E-05
ENSG00000174365.19	SNHG11	1.4	2.3E-04	ENSG00000179406.6	LINC00174	1.2	1.4E-04	ENSG00000196167.9	COLCA1	1.3	1.3E-04	ENSG00000196421.7	LINC00176	1.9	2.8E-14
ENSG00000177410.12	ZFAS1	1.8	5.6E-03	ENSG00000182109.7	RP11-69E11.4	1.1	1.0E-04	ENSG00000197291.8	RAMP2-AS1	-1.3	2.6E-16	ENSG00000196668.3	LINC00173	1.5	4.0E-06
ENSG00000180139.11	ACTA2-AS1	-4.6	1.2E-17	ENSG00000184224.3	C11orf72	1.0	1.1E-04	ENSG00000203804.4	ADAMTSL4-AS1	-1.4	9.2E-07	ENSG00000197308.8	GATA3-AS1	2.4	1.0E-09
ENSG00000197182.12	MIRLET7BHG	1.6	7.8E-04	ENSG00000196295.11	AC005154.6	1.1	2.7E-05	ENSG00000204055.4	RP11-247A12.2	1.4	3.3E-03	ENSG00000205790.1	DPY9-AS1	1.1	1.2E-08
ENSG00000203497.2	PDCD4-AS1	-1.2	7.4E-04	ENSG00000197815.4	RP1-253P7.4	1.5	1.0E-06	ENSG00000204623.8	ZNRD1-AS1	1.0	2.3E-33	ENSG00000213904.8	LIPE-AS1	-1.8	3.0E-11
ENSG00000203706.8	SERTAD4-AS1	-1.8	1.3E-04	ENSG00000198590.11	C3orf35	1.5	1.1E-07	ENSG00000205037.2	RP11-863P13.4	-2.1	8.7E-10	ENSG00000214733.8	RP11-429I17.8	2.1	2.4E-12
ENSG00000204282.4	TNRC6C-AS1	1.1	1.8E-03	ENSG00000202620.2	RP11-84A19.2	1.3	5.5E-04	ENSG00000214708.4	AC090616.2	-1.6	6.4E-07	ENSG00000218416.4	PP14571	2.4	3.6E-09
ENSG00000204528.3	PSORS1C3	1.9	7.5E-03	ENSG00000203739.3	RP11-296O14.3	1.0	3.3E-04	ENSG00000219665.8	CTD-2006C1.2	1.0	8.9E-12	ENSG00000218537.1	MIF-AS1	-1.1	1.7E-03
ENSG00000204685.6	STARD7-AS1	1.0	5.3E-04	ENSG00000205861.11	C1QTNF9B-AS1	1.4	6.7E-03	ENSG00000223473.2	GS1-124K5.3	1.1	2.3E-18	ENSG00000222041.10	LINC00152	1.2	1.2E-09
ENSG00000205664.10	RP11-706O15.1	1.1	6.7E-03	ENSG00000205913.6	SRRM2-AS1	1.2	4.7E-09	ENSG00000223561.6	AC003909.1	-1.1	4.3E-03	ENSG00000223356.1	RP11-66D17.5	1.1	4.8E-08
ENSG00000210409.6	UCA1	3.3	4.5E-04	ENSG00000213121.2	RP11-306O13.1	1.7	2.6E-10	ENSG00000224023.10	FLJ37035	1.3	2.5E-03	ENSG00000223764.2	RP11-5407.3	2.5	1.7E-09
ENSG00000214773.1	RP11-717D12.1	1.8	1.7E-03	ENSG00000216921.7	AC131097.4	-1.9	1.5E-05	ENSG00000224239.1	AC090044.2	-1.1	1.9E-05	ENSG00000224195.1	RP11-574K11.5	1.2	2.9E-07
ENSG00000215386.10	MIR99AHG	-6.4	1.2E-27	ENSG00000223400.1	AP006748.1	1.9	5.8E-03	ENSG00000224397.5	LINC01272	-1.3	3.2E-05	ENSG00000224376.1	AC017104.6	1.3	1.6E-07
ENSG00000215458.8	AATBC	3.6	2.5E-09	ENSG00000223745.7	RP4-71723.3	1.5	4.0E-09	ENSG00000224888.4	RP5-1142A6.2	-1.2	4.6E-06	ENSG00000224559.2	LINC01087	2.2	1.1E-18
ENSG00000223813.2	AC007255.8	1.6	9.6E-03	ENSG00000224259.5	LINC01133	-1.7	2.3E-04	ENSG00000225342.2	AC097630.4	-1.1	7.0E-04	ENSG00000224842.2	RP11-123K19.1	1.5	4.7E-06
ENSG00000223947.1	AC016738.4	1.5	8.2E-03	ENSG00000224060.1	SH3BP5-AS1	1.2	2.9E-04	ENSG00000225473.1	ATP13A4-AS1	2.1	2.8E-03	ENSG00000225075.1	RP11-426L16.3	1.1	2.7E-05
ENSG00000224020.1	MIR181A2HG	1.3	6.4E-03	ENSG00000224843.6	LINC00240	1.3	8.7E-05	ENSG00000225792.1	AC004540.4	-2.1	9.7E-09	ENSG00000225243.5	RP1-127D3.4	-1.0	3.8E-03
ENSG00000224652.1	LINC00885	1.9	3.2E-03	ENSG00000224961.1	RP1-278O22.1	-1.1	7.6E-05	ENSG00000225873.1	LINC00694	-1.7	3.0E-05	ENSG00000225363.3	PPP1R26-AS1	1.1	1.1E-22
ENSG00000224699.8	LAMTOR5-AS1	1.6	2.0E-07	ENSG00000225177.5	RP11-390P2.4	1.4	3.3E-08	ENSG00000225938.1	RP4-575N6.4	-2.5	1.6E-22	ENSG00000225756.1	DBH-AS1	1.1	2.0E-06
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ENSG00000230185.4	C9orf147	1.6	1.5E-03	ENSG00000231711.2	LINC00899	1.2	4.5E-06	ENSG00000232814.2	COL4A2-AS1	-1.4	5.4E-06	ENSG00000230350.1	LIMD1-AS1	-1.1	1.7E-04
ENSG00000230337.1	RP4-635E18.6	2.2	6.8E-03	ENSG00000231789.2	PIK3CD-AS2	-1.5	2.7E-07	ENSG00000232878.3	DPYD-AS1	1.9	1.7E-03	ENSG00000230612.3	AC004377.1	1.2	1.1E-07
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ENSG00000231607.8	DLEU2	1.2	3.2E-04	ENSG00000232442.1	CTD-318A47.4	1.3	1.5E-06	ENSG00000233834.6	AC005083.1	1.5	4.7E-16	ENSG00000231367.5	AC016995.3	-1.0	1.8E-05
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ENSG00000231764.8	DLX6-AS1	1.8	7.8E-03	ENSG00000232774.7	FLJ22447	1.5	5.2E-13	ENSG00000234281.5	LANCL1-AS1	-2.5	4.8E-19	ENSG00000231856.2	RP11-327P2.5	-1.0	1.6E-13
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ENSG00000262061.5	RP11-1260E13.4	-2.5	6.5E-04	ENSG00000261584.1	RP11-457M11.5	2.1	2.9E-12	ENSG00000260841.1	CTC-205M6.5	-1.4	2.7E-22	ENSG00000258441.1	LINC00641	-1.2	1.8E-11
ENSG00000262251.1	RP11-199F11.2	1.6	7.2E-04	ENSG00000261770.1	CTC-459F4.1	1.6	9.5E-08	ENSG00000261338.2	RP11-378A13.1	-1.1	6.1E-05	ENSG00000258725.1	PRCI-AS1	1.0	3.0E-06
ENSG00000262848.1	RP11-517A5.5	1.3	6.6E-03	ENSG00000261829.1	RP11-223H10.1	1.7	2.4E-03	ENSG00000261634.3	RP11-352D13.6	-1.8	4.7E-05	ENSG00000259330.1	INAFM2	-1.4	1.4E-19
ENSG00000263335.1	AF001548.5	-2.7	2.4E-04	ENSG00000262089.1	RP11-589P10.5	1.1	6.8E-04	ENSG00000261662.1	RP5-1042H8.7	-1.0	2.4E-06	ENSG00000259366.1	CTD-2647L4.4	-1.6	1.7E-15
ENSG00000263494.1	AC004702.2	3.9	4.5E-05	ENSG00000262410.1	RP11-388C12.8	1.3	9.4E-07	ENSG00000261801.5	LOXLI-AS1	1.3	1.1E-07	ENSG00000259407.1	RP11-158M2.3	-1.3	7.5E-09
ENSG00000263657.1	RP11-820I9.1	2.6	2.5E-07	ENSG00000262727.1	CTC-524C5.2	1.5	2.9E-07	ENSG00000261804.1	RP11-44F14.2	1.4	1.7E-08	ENSG00000259459.5	RP11-321G12.1	1.6	1.2E-04
ENSG00000264304.1	RP11-20B24.7	1.8	2.2E-03	ENSG00000264112.1	RP11-159D12.2	1.6	4.8E-07	ENSG00000261863.1	RP11-141J13.5	-3.3	2.5E-17	ENSG00000259725.1	CTD-3032H12.1	1.1	3.6E-03
ENSG00000265100.1	RP11-147L13.2	2.0	1.2E-03	ENSG00000265246.1	RP11-663N22.1	-1.8	8.6E-05	ENSG00000263050.1	RP11-466K14.3	-2.7	4.2E-19	ENSG00000259886.1	RP11-382A20.4	1.0	3.8E-09
ENSG00000266261.1	RP11-640I15.1	2.3	8.8E-03	ENSG00000265369.3	PCATI8	1.4	4.8E-03	ENSG00000263586.1	HID1-AS1	-2.7	8.8E-12	ENSG00000260025.1	RP11-490M8.1	-1.3	2.4E-07
ENSG00000266651.1	RP11-138I1.3	1.9	3.5E-03	ENSG00000266402.3	SNHG25	1.3	8.2E-04	ENSG00000264044.1	RP11-192H23.7	1.6	1.1E-03	ENSG00000260032.1	LINC00657	-1.4	6.4E-11
ENSG00000267080.5	ASB16-AS1	1.1	1.2E-03	ENSG00000266490.1	CTD-2349P21.9	1.1	1.0E-02	ENSG00000264443.1	RP4-594I10.3	1.8	3.9E-03	ENSG00000260260.1	SNHG19	1.6	3.3E-09
ENSG00000267278.5	MAP3K14-AS1	1.2	2.0E-04	ENSG00000266644.1	RP11-927P21.2	1.5	6.3E-05	ENSG00000265474.1	AC010761.9	1.4	4.4E-03	ENSG00000260822.1	GS1-358P8.4	-1.4	8.3E-08
ENSG00000267505.1	RP13-890H12.2	1.5	6.5E-03	ENSG00000267163.1	AC084219.3	1.7	2.7E-05	ENSG00000266010.1	GATA6-AS1	-1.5	9.5E-07	ENSG00000260912.1	RP11-363E7.4	-1.1	2.1E-06
ENSG00000267565.1	CTC-559E9.8	1.4	1.6E-03	ENSG00000267470.5	ZNF571-AS1	1.0	3.0E-03	ENSG00000266283.1	RP11-627G18.1	-2.0	1.0E-14	ENSG00000260975.1	RP11-142G1.3	1.8	1.7E-10
ENSG00000267612.1	CTD-3116E22.7	2.0	6.1E-04	ENSG00000267593.1	RP11-108P20.4	-1.6	2.8E-04	ENSG00000267207.1	RP11-264B14.1	-2.1	1.1E-03	ENSG00000261054.1	RP11-602.4	-2.0	2.5E-05
ENSG00000267621.1	CTD-2540F13.2	1.8	9.9E-04	ENSG00000267655.1	CTD-2286N8.2	1.1	2.3E-03	ENSG00000267280.5	TBX2-AS1	-2.5	7.5E-26	ENSG00000261207.1	LA16c-361A3.3	1.6	7.7E-14
ENSG00000267896.1	AC018766.4	2.3	5.2E-04	ENSG00000267838.2	AC008746.12	1.2	3.7E-04	ENSG00000267519.3	CTD-3252C9.4	-1.5	5.2E-06	ENSG00000261286.1	RP11-517C16.2	1.0	1.3E-03
ENSG00000267934.1	CTB-176F20.3	1.4	3.4E-03	ENSG00000270061.1	RP11-214K3.19	1.7	4.8E-06	ENSG00000267530.2	AC006273.5	-1.3	2.3E-03	ENSG00000261312.1	AC002550.5	1.9	5.1E-06
ENSG00000268119.5	CTD-2561J22.5	1.4	8.3E-03	ENSG00000270164.1	LINC01480	1.1	9.7E-05	ENSG00000267607.1	CTD-2369P2.8	-1.8	1.3E-03	ENSG00000261353.1	CTA-14H9.5	-1.1	1.8E-06
ENSG00000268362.5	CTD-2017D11.1	1.0	1.1E-03	ENSG00000270189.1	RP11-258C19.7	1.1	4.6E-05	ENSG00000267667.1	RP11-136H19.1	-1.5	9.6E-05	ENSG00000261359.2	PYCARD-AS1	1.6	1.2E-04
ENSG00000269186.1	LINC01082	-4.1	3.4E-08	ENSG00000270580.5	PKD1P6	1.0	1.3E-03	ENSG00000267751.5	AC009005.2	1.4	3.0E-03	ENSG00000261369.1	RP11-474B12.1	1.5	3.5E-15
ENSG00000269293.2	ZSCAN16-AS1	-1.6	5.2E-05	ENSG00000270720.1	RP11-84C13.2	1.2	9.4E-04	ENSG00000267742.2	RP11-2N1.2	-3.3	4.4E-16	ENSG00000261396.1	CTD-2012K14.2	1.1	8.9E-04
ENSG00000269481.1	CTD-2521M24.6	1.8	1.7E-08	ENSG00000270787.1	AC015849.19	1.0	9.6E-04	ENSG00000268836.1	LA16c-OS12.2	-1.2	6.2E-04	ENSG00000261534.1	RP11-244O19.1	-1.4	6.4E-14
ENSG00000269609.5	RPARP-AS1	1.5	2.2E-04	ENSG00000271151.1	RP11-394I13.2	2.7	4.6E-11	ENSG00000270012.1	LLOXNCO1-7P3.1	1.1	3.7E-05	ENSG00000261567.1	RP11-680G10.1	-2.1	1.2E-16
ENSG00000269646.1	CTD-2331H12.7	2.3	1.7E-04	ENSG00000271384.1	RP11-435O5.4	1.3	3.1E-03	ENSG00000270091.1	RP11-780T.2	-1.5	1.5E-10	ENSG00000261664.5	TTC39A-AS1	1.6	2.7E-14
ENSG00000269815.1	CTD-2278I10.4	1.4	9.1E-03	ENSG00000271553.1	RP11-274B21.10	1.2	1.4E-03	ENSG00000270761.1	RP11-385F7.1	1.7	1.6E-04	ENSG00000261687.1	RP11-473C18.3	1.2	8.3E-03
ENSG00000269949.1	RP11-738E22.3	2.9	7.5E-06	ENSG00000271659.1	RP11-435O5.4	1.3	8.4E-04	ENSG00000271133.5	CTA-293F17.1	1.5	1.4E-07	ENSG00000262445.3	CTD-2545H1.2	1.0	4.7E-13
ENSG00000269952.1	RP11-324I22.3	-2.9	1.0E-05	ENSG00000271717.1	CTD-3020H12.4	1.9	2.1E-08	ENSG00000271971.1	CTD-2006H14.2	1.1	2.0E-05	ENSG00000262772.1	RP11-353N14.2	1.7	2.9E-08
ENSG00000269967.1	RP11-84A19.4	2.3	4.6E-05	ENSG00000271911.1	RP11-97C16.1	1.0	3.0E-03	ENSG00000272081.1	CTD-2376I4.2	1.2	1.9E-04	ENSG00000262903.1	RP11-235E17.6	1.0	4.3E-06
ENSG00000269973.1	RP11-95D17.1	1.4	1.7E-03	ENSG00000271941.1	RP11-188P20.3	1.5	2.9E-04	ENSG00000272145.1	NFYC-AS1	1.6	1.7E-11	ENSG00000263400.6	TMEM220-AS1	-1.6	8.9E-14
ENSG00000270010.1	CTD-2132N18.4	2.0	3.6E-04	ENSG00000272301.1	RP11-111M22.4	2.0	8.0E-08	ENSG00000272512.1	RP11-5407.17	-1.4	1.4E-05	ENSG00000263603.1	CTD-2349P21.5	1.3	1.7E-11
ENSG00000270049.1	RP11-297D21.4	1.4	1.3E-03	ENSG00000272316.1	XXbac-BPGBP6S5C20.0	1.1	4.2E-06	ENSG00000272588.1	RP11-440L14.4	1.4	5.2E-09	ENSG00000263753.6	LINC00667	-1.1	1.5E-10
ENSG00000270069.1	MIR222HG	-2.5	5.1E-06	ENSG00000272330.1	AC002044.4	1.2	7.4E-03	ENSG00000272620.1	AFAP1-AS1	5.9	8.1E-42	ENSG00000264207.1	RP11-196G18.23	1.4	5.1E-10
ENSG00000270195.1	RP11-5720I7.1	1.5	4.0E-03	ENSG00000272411.1	RP11-448B19.1	1.1	8.0E-03	ENSG00000272734.1	ADIRF-AS1	-1.4	8.2E-11	ENSG00000264982.1	RP11-34482.2	-2.2	6.6E-03
ENSG00000271579.1	RP11-116D17.3	2.5	5.3E-04	ENSG00000272574.1	RP11-359K18.4	1.5	1.7E-03	ENSG00000272783.1	RP13-1016M1.2	-3.0	1.3E-14	ENSG00000265393.1	CTD-2517M22.17	1.9	2.1E-10
ENSG00000271584.1	RP11-89C3.4	-3.4	2.2E-09	ENSG00000272732.1	RP5-1159O4.2	1.2	2.8E-04	ENSG00000272913.1	RP11-440D17.3	1.7	4.1E-13	ENSG00000265688.1	MAFG-AS1	1.5	1.6E-08
ENSG00000272129.1	RP11-250B2.6	1.7	2.9E-03	ENSG00000272780.1	RP11-260M2.1	1.0	6.9E-03	ENSG00000273100.1	RP11-302L19.3	-2.6	7.8E-23	ENSG00000266495.1	RP11-17J14.2	1.5	1.7E-03
ENSG00000272140.2	RP11-574K11.29	1.1	8.3E-03	ENSG00000272807.1	RP5-1159O4.1	1.3	4.4E-06	ENSG00000273151.1	RP11-449P15.2	1.0	1.1E-12	ENSG00000266601.1	RP11-6N17.3	-1.6	1.7E-14
ENSG00000272155.1	RP11-707M3.3	1.9	5.0E-07	ENSG00000273036.2	FAM95C	1.3	2.9E-03	ENSG00000273760.1	CHI7-360D5.3	-3.2	5.3E-14	ENSG00000266954.1	RP11-701H16.4	2.1	1.0E-15
ENSG00000272159.1	RP11-350N15.6	-3.7	5.0E-04	ENSG00000273179.1	RP11-201O4.4	3.4	7.6E-13	ENSG00000274213.1	RP11-670E13.6	-1.6	1.6E-05	ENSG00000267077.1	RP11-127I20.5	1.7	5.6E-08
ENSG00000272256.1	RP11-489E7.4	-2.7	3.1E-05	ENSG00000273212.1	AC00068.10	1.6	8.1E-03	ENSG00000274422.1	LL22NCO3-2H8.5	1.0	8.0E-03	ENSG00000267117.1	AC010525.4	1.4	5.5E-18
ENSG00000272405.1	RP11-284F21.10	2.6	3.9E-05	ENSG00000273218.1	LLNLR-246C6.1	1.1	7.6E-04	ENSG00000274653.1	RP11-347C12.11	1.6	9.8E-08	ENSG00000267194.1	RP1-193H18.2	-2.0	2.0E-15
ENSG00000272440.1	RP11-379F4.6	1.8	6.4E-03	ENSG00000273306.1	RP11-527J8.1	1.2	6.2E-04	ENSG00000275655.1	CTB-58E17.9	1.7	3.2E-05	ENSG00000267270.5	PARD6G-AS1	1.1	1.1E-05
ENSG00000272667.1	RP11-395A13.2	-1.1	5.6E-03	ENSG00000274020.1	LINC01138	1.2	2.6E-11	ENSG00000276170.4	AC124789.1	-2.7	6.2E-14	ENSG00000267282.1	CTB-129P6.4	1.2	1.2E-05
ENSG00000272870.1	RP11-798M19.6	-2.4	4.0E-08	ENSG00000274372.4	RP11-94I2.4	3.2	2.6E-12	ENSG00000276850.4	CHI7-360D5.2	-3.2	8.4E-57	ENSG00000267296.2	CEBPA-AS1	-1.9	1.3E-12
ENSG00000272870.1	CTD-2002J20.1	2.2	5.5E-04	ENSG00000274964.1	RP11-817H4.1	1.1	8.0E-03	ENSG00000277351.1	RP11-325L12.6	-1.6	4.3E-05	ENSG00000267348.2	CTB-179K24.3	1.3	2.5E-11
ENSG00000273449.1	RP11-218F10.3	1.3	1.4E-03	ENSG00000275005.1	RP11-234G16.5	1.6	1.5E-04	ENSG00000277782.1	RP11-775C24.5	-1.6	7.8E-16	ENSG00000267577.1	CTD-2587H24.5	1.1	2.5E-06
ENSG00000273723.1	RP11-93H24.3	1.8	2.1E-04	ENSG00000275413.1	CTC-529I01.1	1.8	1.1E-05	ENSG00000278918.1	CTD-2267D19.1	-1.1	4.6E-06	ENSG00000268049.1	CTD-2619I13.9	1.1	1.6E-09
ENSG00000273747.1	RP11-90B9.3	1.7	4.0E-03	ENSG00000275751.1	AC002550.6	1.2	9.7E-04	ENSG00000278934.1	CTD-2006M22.2	-1.2	1.3E-03	ENSG00000268189.2	AC005785.2	1.5	2.0E-20
ENSG00000274281.1	RP11-326N17.2	1.4	7.0E-05	ENSG00000277978.1	RP11-403P17.6	1.4	5.9E-03	ENSG00000279331.1	RBM12B-AS1	2.0	1.6E-11	ENSG00000268204.1	CTD-3214H19.6	1.2	3.1E-05
ENSG00000274565.1	CTD-3035K23.7	-2.9	1.0E-07	ENSG00000278002.1	RP11-596C23.2	1.4	1.4E-05	ENSG00000279794.1	CTD-2621I17.3	1.2	6.9E-06	ENSG00000268230.5	CTD-2619I13.8	1.7	2.0E-16
ENSG00000275393.1	RP11-104N10.2	1.1	4.4E-03	ENSG00000278932.3	BP-21264C1.2	1.7	3.5E-04	ENSG00000279805.1	CTA-212A2.1	-2.6	3.6E-23	ENSG00000268592.3	RAETIE-AS1	-1.3	9.6E-06
ENSG00000275056.1	RP11-1270L8.3	1.3	6.1E-03	ENSG00000279103.1	CTC-204F22.1	1.5	6.1E-08	ENSG00000279882.1	CTB-151G24.2	2.2	4.3E-08	ENSG00000268674.1	CTC-450M9.1	1.7	3.5E-21
ENSG00000275202.1	RP11-156K23.3	-1.1	5.0E-03	ENSG00000279289.1	RP3-331H24.6	1.3	1.5E-04	ENSG00000279940.1	RP11-243M5.5	-4.1	9.8E-27	ENSG00000268947.1	AD000684.2	1.2	9.0E-07
ENSG00000275393.1	RP11-568J23.8	2.4	6.2E-05	ENSG00000279509.1	RP11-21K12.2	1.1	2.0E-03								

Supplementary Table S3: Functional DELs only altered in one cancer type derived from PubMed

blader		pro		ADC		EBC	
gene id	gene name	gene id	gene name	gene id	gene name	gene id	gene name
ENSG00000153363.12	LINC00467	ENSG00000198590.11	C3orf35	ENSG00000196167.9	COLCA1	ENSG00000130600.15	H19
ENSG00000166770.10	ZNF667-AS1	ENSG00000205861.11	C1QTNF9B-AS1	ENSG00000204623.8	ZNRD1-AS1	ENSG00000222041.10	LINC00152
ENSG00000177410.12	ZFAS1	ENSG00000224259.5	LINC01133	ENSG00000233237.6	LINC00472	ENSG00000225756.1	DBH-AS1
ENSG00000180139.11	ACTA2-AS1	ENSG00000225937.1	PCA3	ENSG00000234380.1	LINC01426	ENSG00000230061.2	TRPM2-AS
ENSG00000214049.6	UCA1	ENSG00000231806.2	PCAT7	ENSG00000236830.6	CBR3-AS1	ENSG00000237361.2	TUSC8
ENSG00000215386.10	MIR99AHG	ENSG00000245532.5	NEAT1	ENSG00000238057.8	ZEB2-AS1	ENSG00000253552.7	HOXA-AS2
ENSG00000215458.8	AATBC	ENSG00000246763.6	RGMB-AS1	ENSG00000245694.8	CRNDE	ENSG00000270959.1	LPP-AS2
ENSG00000227372.10	TP73-AS1	ENSG00000253438.2	PCAT1	ENSG00000272620.1	AFAP1-AS1		
ENSG00000231607.8	DLEU2	ENSG00000259641.5	PCAT29	ENSG00000281406.1	BLACAT1		
ENSG00000231721.6	LINC-PINT	ENSG00000260896.5	PRCAT47				
ENSG00000231764.8	DLX6-AS1	ENSG00000265369.3	PCAT18				
ENSG00000234771.3	SLC25A25-AS1	ENSG00000280623.1	PCAT14				
ENSG00000237125.8	HAND2-AS1	ENSG00000280927.1	CTBP1-AS				
ENSG00000249082.2	C5orf66-AS1						
ENSG00000255090.5	MIR100HG						
ENSG00000255717.6	SNHG1						

Supplementary Table S4: log2FC (fold change) and FDR of onco-lncRNAs in each cancer type and their corresponding modules in the co-expression network

Onco-lncRNA and corresponding module			BLC		PRC		ADC		EBC	
gene_id	gene_name	Module	log2FC	FDR	log2FC	FDR	log2FC	FDR	log2FC	FDR
ENSG00000228434.1	AC004951.6	magenta	-	-	1.2	6.5E-04	-	-	1.4	8.1E-19
ENSG00000214719.11	AC005562.1	grey	-	-	1.4	5.4E-03	1.4	9.0E-03	-	-
ENSG00000279203.1	AC005785.5	brown	1.3	8.9E-03	1.6	2.2E-07	-	-	1.5	5.5E-20
ENSG00000279716.1	AC006128.2	blue	1.5	2.2E-04	-	-	-	-	1.6	1.7E-08
ENSG00000233251.7	AC007743.1	brown	1.1	1.1E-03	1.7	6.1E-10	-	-	1.1	7.5E-07
ENSG00000236255.1	AC009404.2	blue	1.5	6.6E-05	1.5	2.1E-09	-	-	-	-
ENSG00000226266.6	AC009961.3	blue	-	-	1.2	6.3E-07	-	-	1.3	1.7E-19
ENSG00000236039.1	AC019117.2	midnightblue	2.2	5.5E-03	-	-	1.9	3.2E-06	-	-
ENSG00000259605.3	AC074212.5	blue	-	-	1.4	5.9E-07	-	-	1.3	6.2E-07
ENSG00000235493.1	AC092415.1	brown	1.7	2.6E-03	1.9	2.3E-09	-	-	1.2	1.3E-07
ENSG00000232164.1	AC092669.3	brown	-	-	1.4	3.4E-05	1.3	2.1E-17	1.8	6.1E-12
ENSG00000237940.3	AC093642.3	blue	-	-	1.4	1.3E-03	-	-	1.5	1.0E-11
ENSG00000244567.1	AC096772.6	blue	-	-	-	-	-1.1	7.8E-13	-1.7	2.1E-19
ENSG00000233766.7	AC098617.1	greenyellow	-3.6	8.2E-05	2.5	2.4E-05	-	-	-	-
ENSG00000278000.1	AC139100.4	brown	-	-	1.6	2.4E-05	-	-	1.5	3.7E-10
ENSG00000203635.2	AC144450.2	blue	-	-	2.3	3.1E-10	-	-	1.4	6.5E-22
ENSG00000261888.1	AC144831.1	yellow	-	-	-	-	-1.9	3.5E-19	-1.6	1.1E-11
ENSG00000274370.1	AC144831.3	yellow	-	-	-	-	-1.8	5.9E-17	-2.0	8.4E-14
ENSG00000230606.10	AC159540.1	grey	-	-	2.0	1.2E-11	1.2	3.1E-03	2.0	2.3E-15
ENSG00000278766.2	AC159540.2	grey	-	-	-	-	1.2	9.5E-04	2.4	2.0E-20
ENSG00000241158.5	ADAMTS9-AS1	red	-6.6	8.9E-33	-	-	-2.6	4.0E-22	-2.6	1.3E-18
ENSG00000241684.5	ADAMTS9-AS2	red	-5.0	3.1E-35	-	-	-1.5	6.3E-09	-1.5	1.1E-08
ENSG00000280429.1	AF001548.3	red	-6.3	2.0E-19	1.3	5.1E-03	-	-	-	-
ENSG00000271880.1	AGAP11	yellow	-	-	-	-	-2.7	6.3E-20	-1.2	2.1E-04
ENSG00000246889.2	AP000487.5	blue	1.6	9.3E-04	-	-	-	-	1.0	1.6E-09
ENSG00000280143.1	AP000892.6	red	-5.5	5.1E-23	-	-	-	-	-1.9	4.4E-11
ENSG00000271816.1	BMS1P4	brown	1.4	5.2E-04	1.4	1.2E-07	-	-	-	-
ENSG00000227051.5	C14orf132	green	-2.2	1.9E-04	-	-	-2.2	1.1E-31	-	-
ENSG00000225670.4	CADM3-AS1	cyan	-5.0	8.2E-18	-	-	-1.5	1.2E-08	-	-
ENSG00000272720.1	CTA-228A9.3	brown	1.6	3.7E-05	1.7	2.0E-08	-	-	-	-
ENSG00000275719.1	CTB-147N14.6	yellow	-	-	-1.2	4.8E-03	-	-	-1.7	5.3E-09
ENSG00000267383.6	CTC-260E6.6	lightgreen	2.0	2.1E-04	1.1	4.6E-04	-	-	1.3	9.5E-10
ENSG00000267405.1	CTC-296K1.4	red	-6.3	1.5E-21	-1.3	1.0E-04	-	-	-	-
ENSG00000233937.6	CTC-338M12.4	blue	1.6	3.0E-04	-	-	1.0	6.0E-04	-	-
ENSG00000241956.9	CTC-340A15.2	brown	-	-	1.6	4.6E-06	-	-	1.5	9.5E-09
ENSG00000279759.1	CTC-425O23.5	brown	1.9	1.6E-04	1.4	1.8E-06	-	-	-	-
ENSG00000272367.1	CTC-428H11.2	cyan	-1.8	5.7E-03	1.5	5.5E-04	-	-	-	-
ENSG00000262601.1	CTC-786C10.1	yellow	-	-	-	-	-1.5	4.4E-06	-3.2	8.4E-40
ENSG00000280332.1	CTD-2013N17.6	blue	1.2	3.8E-03	1.0	1.3E-03	-	-	-	-
ENSG00000279425.1	CTD-2017D11.2	magenta	1.2	4.1E-03	1.1	8.7E-05	-	-	-	-
ENSG00000274383.1	CTD-2017F17.2	brown	-	-	2.1	5.9E-04	-	-	2.1	3.1E-10
ENSG00000262979.1	CTD-2047H16.2	brown	2.0	5.1E-05	1.1	9.3E-03	1.2	4.9E-06	3.6	7.5E-23
ENSG00000260751.2	CTD-2196E14.6	brown	1.4	1.4E-03	-	-	1.1	2.3E-07	-	-
ENSG00000270933.1	CTD-2227E11.1	grey	-	-	1.5	4.1E-04	3.6	4.5E-14	-	-
ENSG00000230698.1	CTD-2330K9.2	grey	3.6	8.0E-05	-	-	-	-	3.0	8.3E-13
ENSG00000276250.1	CTD-2349P21.12	magenta	1.5	4.9E-03	1.2	8.0E-03	-	-	-	-
ENSG00000255182.2	CTD-2517M22.14	blue	1.4	4.3E-04	1.5	9.9E-05	1.1	1.3E-06	1.5	2.1E-13
ENSG00000267523.1	CTD-2537I9.12	brown	1.2	6.4E-03	1.4	2.1E-03	-	-	1.1	1.2E-09
ENSG00000274925.1	CTD-2547G23.4	brown	1.1	6.6E-03	1.3	3.0E-05	1.5	1.0E-10	-	-
ENSG00000279117.1	CTD-2562J17.6	greenyellow	-2.1	2.5E-04	-	-	-2.5	3.5E-28	-1.3	1.6E-05
ENSG00000279789.1	CTD-2574D22.3	brown	2.0	7.9E-07	1.4	5.4E-06	1.4	1.7E-08	1.1	3.9E-15
ENSG00000269867.1	CTD-2583A14.8	turquoise	1.8	1.8E-08	-	-	-	-	1.6	2.0E-18
ENSG00000269873.1	CTD-2587H19.3	magenta	1.7	4.4E-03	1.5	6.2E-03	-	-	-	-
ENSG00000268201.1	CTD-3138B18.6	brown	-	-	1.2	7.4E-04	-	-	1.1	4.9E-16
ENSG00000265787.1	CYP4F35P	magenta	3.5	6.3E-08	2.5	2.4E-09	-	-	-	-
ENSG00000231890.7	DARS-AS1	brown	1.3	1.1E-04	1.0	8.7E-06	-	-	-	-
ENSG00000235706.7	DICER1-AS1	brown	1.0	5.2E-03	1.4	8.8E-06	-	-	-	-
ENSG00000258498.6	DIO3OS	cyan	-4.8	1.1E-28	-	-	-1.6	1.1E-04	-	-
ENSG00000245750.7	DRAIC	pink	-	-	1.9	1.2E-08	2.4	1.2E-08	1.1	6.7E-03
ENSG00000206195.10	DUXAP8	grey	-	-	1.3	1.5E-04	1.9	2.0E-04	-	-
ENSG00000203499.10	FAM83H-AS1	blue	1.9	1.2E-04	-	-	2.6	4.2E-16	-	-
ENSG00000260852.1	FBXL19-AS1	blue	2.0	1.4E-08	1.6	9.2E-10	-	-	1.1	5.6E-14
ENSG00000268388.5	FENDRR	cyan	-4.2	5.2E-33	-	-	-4.7	3.6E-31	-	-
ENSG00000272143.1	FGF14-AS2	yellow	-1.6	1.6E-03	-1.5	3.5E-04	-1.0	7.2E-07	-1.9	4.1E-10
ENSG00000250208.6	FZD10-AS1	turquoise	-2.9	4.5E-09	-	-	-1.3	7.5E-08	-	-
ENSG00000248890.1	HHIP-AS1	cyan	-3.4	1.7E-09	-	-	-1.1	1.6E-03	-	-
ENSG00000235313.1	HM13-IT1	salmon	-	-	1.4	1.4E-05	-	-	1.2	1.9E-14
ENSG00000234705.1	HMGAI1P4	blue	2.6	2.4E-06	1.1	3.0E-04	-	-	2.0	1.3E-12
ENSG00000233101.10	HOXB-AS3	magenta	2.6	2.7E-04	-	-	1.8	2.0E-03	-	-
ENSG00000227392.1	HPN-AS1	brown	-	-	2.4	5.7E-07	-	-	1.8	8.5E-17
ENSG00000236778.7	INTS6-AS1	brown	-	-	1.4	6.2E-07	-	-	1.2	3.4E-08

ENSG00000261505.1	LA16c-358B7.3	blue	-	-	1.3	1.5E-03	-	-	1.2	6.4E-13
ENSG00000226696.5	LENG8-AS1	blue	-	-	1.1	8.2E-04	1.0	5.5E-06	-	-
ENSG00000225194.2	LINC00092	turquoise	-	-	-2.0	1.2E-06	-2.1	1.4E-12	-	-
ENSG00000248360.7	LINC00504	brown	1.1	9.8E-03	1.7	2.5E-10	-	-	1.3	2.0E-08
ENSG00000281392.1	LINC00506	brown	1.2	7.9E-03	1.8	1.0E-09	-	-	1.8	4.2E-11
ENSG00000261824.6	LINC00662	brown	-	-	1.4	6.8E-10	-	-	1.3	4.2E-10
ENSG00000232677.6	LINC00665	turquoise	1.2	8.6E-04	-	-	1.1	4.5E-03	-	-
ENSG00000258647.5	LINC00930	magenta	-	-	2.1	7.9E-08	-1.5	8.6E-06	-	-
ENSG00000281657.2	LINC00976	brown	-	-	1.7	1.0E-09	-	-	1.2	6.0E-07
ENSG00000224081.7	LINC01057	magenta	1.4	8.1E-04	1.5	1.6E-06	-	-	-	-
ENSG00000212694.8	LINC01089	blue	1.3	6.0E-03	1.6	2.2E-09	-	-	-	-
ENSG00000267272.5	LINC01140	yellow	-2.0	7.9E-03	-	-	-	-	-2.5	9.5E-18
ENSG00000281404.1	LINC01176	brown	1.6	2.6E-07	1.1	1.8E-04	-	-	1.7	1.3E-17
ENSG00000280734.2	LINC01232	brown	2.0	1.6E-08	1.2	1.6E-08	1.5	1.7E-16	-	-
ENSG00000227953.6	LINC01341	magenta	1.8	2.1E-04	1.7	1.2E-05	-	-	1.8	1.9E-13
ENSG00000261326.2	LINC01355	magenta	1.2	1.3E-03	1.5	1.0E-09	1.5	6.8E-27	-	-
ENSG00000238113.6	LINC01410	brown	1.5	2.4E-03	-	-	-	-	1.7	1.4E-11
ENSG00000262468.5	LINC01569	blue	-	-	-	-	1.8	5.5E-18	1.3	1.3E-17
ENSG00000229619.3	MBNL1-AS1	red	-4.6	1.8E-13	-	-	-1.3	1.8E-09	-1.9	1.5E-22
ENSG00000214548.14	MEG3	grey	-4.4	7.5E-17	-	-	3.0	2.9E-07	-	-
ENSG00000249669.7	MIR143HG	red	-4.3	3.5E-15	-	-	-	-	-1.3	2.5E-08
ENSG00000230937.9	MIR205HG	midnightblue	-	-	-1.4	4.5E-03	3.7	7.3E-13	-	-
ENSG00000247095.2	MIR210HG	blue	1.6	2.1E-03	-	-	1.2	1.7E-03	1.1	4.5E-11
ENSG00000186594.12	MIR22HG	cyan	-2.3	8.5E-07	-	-	-1.9	9.9E-30	-2.0	7.6E-15
ENSG00000267532.3	MIR497HG	red	-3.3	4.4E-04	-	-	-	-	-1.7	5.4E-13
ENSG00000223749.7	MIR503HG	blue	-	-	-	-	1.8	3.2E-07	1.9	2.0E-06
ENSG00000261971.6	MMP25-AS1	blue	-	-	1.1	1.0E-03	-	-	1.0	1.2E-03
ENSG00000247809.7	NR2F2-AS1	red	-1.6	2.8E-04	-	-	-1.2	4.6E-10	-	-
ENSG00000238045.9	PAGR1	turquoise	-	-	-	-	1.3	5.2E-06	1.1	2.8E-17
ENSG00000267107.6	PCAT19	cyan	-2.9	4.3E-15	-	-	-2.5	2.8E-42	-	-
ENSG00000228288.6	PCAT6	blue	1.3	3.7E-04	-	-	2.3	2.4E-20	1.9	1.7E-15
ENSG00000196696.12	PDXDC2P	blue	-	-	1.6	3.9E-06	-	-	1.2	3.5E-14
ENSG00000224958.5	PGM5-AS1	red	-8.9	4.4E-35	-1.1	6.8E-04	-	-	-	-
ENSG00000260804.3	PKI55	black	-	-	-	-	-1.2	2.4E-13	-1.7	4.7E-14
ENSG00000249859.7	PVT1	blue	1.8	7.8E-04	1.6	1.5E-09	2.0	1.7E-09	1.5	1.3E-16
ENSG00000223525.1	RABGAP1L-IT1	brown	1.2	5.4E-04	-	-	-	-	1.4	3.8E-09
ENSG00000262877.4	RP11-1055B8.4	blue	-	-	1.7	6.3E-06	-	-	1.0	3.8E-04
ENSG00000280046.1	RP11-1099M24.6	brown	1.5	1.3E-04	1.2	5.6E-06	-	-	-	-
ENSG00000259884.1	RP11-1100L3.8	cyan	-	-	1.5	1.4E-03	-1.6	4.4E-05	1.5	1.5E-03
ENSG00000227388.2	RP11-112J3.16	turquoise	1.5	1.3E-03	1.1	1.9E-03	-	-	-	-
ENSG00000271771.1	RP11-1250I15.3	turquoise	1.8	8.9E-03	1.8	3.9E-05	-	-	1.1	1.7E-11
ENSG00000274605.1	RP11-12G12.7	pink	1.3	9.9E-03	-	-	1.9	6.2E-17	-	-
ENSG00000223396.2	RP11-134G8.5	brown	1.6	3.6E-03	-	-	1.3	7.5E-07	-	-
ENSG00000280234.1	RP11-145P16.2	brown	-	-	1.5	3.4E-04	-	-	1.7	2.3E-13
ENSG00000272100.1	RP11-155O18.6	salmon	2.3	8.4E-04	-	-	-	-	1.1	4.5E-06
ENSG00000260807.6	RP11-161M6.2	pink	-	-	1.1	2.7E-03	-	-	-1.2	2.2E-06
ENSG00000261560.1	RP11-166B2.3	magenta	-	-	1.0	7.7E-03	-	-	1.0	2.4E-12
ENSG00000255248.6	RP11-166D19.1	red	-5.5	9.1E-51	-	-	-	-	-1.1	3.1E-07
ENSG00000261324.2	RP11-174G6.5	pink	1.3	1.6E-04	1.5	1.6E-05	-	-	-	-
ENSG00000264608.1	RP11-192H23.8	lightgreen	2.5	2.8E-07	2.0	2.8E-09	-	-	1.7	3.1E-14
ENSG00000261716.1	RP11-196G18.22	brown	1.1	6.7E-03	1.4	7.6E-09	1.4	1.2E-10	1.3	1.4E-15
ENSG00000260436.1	RP11-20I23.7	brown	-	-	1.4	1.1E-04	-	-	1.3	4.3E-15
ENSG00000279281.1	RP11-226M10.3	magenta	1.5	4.5E-03	1.5	1.4E-05	-	-	1.3	5.2E-23
ENSG00000249731.1	RP11-259O2.3	brown	-	-	1.3	4.0E-05	1.6	7.5E-22	1.6	2.1E-09
ENSG00000260853.1	RP11-264B17.2	magenta	1.4	2.4E-03	1.1	2.1E-03	-	-	1.0	5.8E-13
ENSG00000272789.1	RP11-286H15.1	greenyellow	-4.0	1.6E-09	-	-	-4.3	1.2E-30	-	-
ENSG00000277639.1	RP11-295M3.4	grey	-	-	-2.6	2.9E-09	-	-	-2.3	8.1E-11
ENSG00000273474.1	RP11-295P9.12	magenta	2.2	1.5E-04	1.6	1.6E-05	-	-	-	-
ENSG00000270953.1	RP11-2E11.9	salmon	1.0	6.7E-03	1.2	6.6E-03	-	-	-1.1	6.3E-05
ENSG00000261663.1	RP11-304L19.11	brown	1.2	7.3E-03	-	-	-	-	1.1	2.3E-14
ENSG00000232093.1	RP11-307C12.11	blue	2.1	1.3E-03	-	-	-	-	1.4	6.6E-10
ENSG00000262580.5	RP11-334C17.5	brown	-	-	1.3	5.7E-06	-	-	1.2	2.7E-11
ENSG00000224307.1	RP11-344B5.2	green	-3.1	3.9E-06	-	-	-	-	-1.1	5.5E-08
ENSG00000259380.5	RP11-346D14.1	magenta	1.2	9.6E-03	1.8	4.8E-10	1.1	7.7E-14	1.7	1.4E-10
ENSG00000260798.1	RP11-354M1.2	blue	2.0	6.3E-03	-	-	-	-	1.4	1.4E-07
ENSG00000241288.7	RP11-379B18.5	brown	-	-	1.2	1.8E-05	-	-	1.1	1.9E-09
ENSG00000279417.1	RP11-382B18.1	magenta	-	-	1.5	5.3E-07	-	-	1.7	1.1E-10
ENSG00000266538.1	RP11-385D13.3	brown	-	-	1.6	4.1E-04	1.6	1.1E-05	1.4	2.4E-09
ENSG00000261269.1	RP11-389C8.2	yellow	-	-	-	-	-1.4	3.4E-10	-2.1	5.8E-13
ENSG00000276434.1	RP11-391H12.8	lightgreen	2.3	1.3E-04	1.1	2.6E-04	-	-	-	-
ENSG00000269936.3	RP11-394O4.5	red	-4.8	3.7E-19	1.1	9.8E-03	-	-	-1.3	3.3E-06
ENSG00000261685.2	RP11-401P9.4	green	-2.6	8.1E-13	-	-	-2.4	8.9E-48	-	-
ENSG00000279283.1	RP11-417L19.5	brown	-	-	1.9	1.5E-06	-	-	1.6	4.3E-18
ENSG00000251432.6	RP11-420A23.1	tan	1.5	3.7E-03	1.5	6.8E-05	-	-	-	-
ENSG00000264895.1	RP11-421E14.2	brown	2.1	3.5E-05	1.5	2.3E-04	-	-	2.1	2.0E-14
ENSG00000255864.5	RP11-444D3.1	yellow	-	-	-	-	-1.4	2.0E-05	-1.3	3.7E-04

ENSG00000224799.1	RP11-445O16.3	brown	1.4	2.3E-03	1.4	6.1E-05	-	-	-	-
ENSG00000260265.1	RP11-44F21.5	midnightblue	1.6	8.2E-03	-2.1	5.6E-14	-	-	-	-
ENSG00000273142.1	RP11-458F8.4	brown	1.1	6.0E-03	1.4	1.0E-05	-	-	1.3	1.6E-10
ENSG00000263235.1	RP11-461A8.4	brown	1.9	7.5E-05	1.5	1.7E-05	-	-	1.7	5.1E-14
ENSG00000272141.1	RP11-465B22.8	blue	2.6	1.1E-06	-	-	1.6	6.0E-09	2.0	1.9E-16
ENSG00000234678.1	RP11-465N4.4	magenta	1.8	4.6E-05	1.0	7.8E-04	-	-	1.3	4.5E-17
ENSG00000273478.1	RP11-465N4.5	blue	1.9	2.0E-05	-	-	-	-	1.2	2.1E-16
ENSG00000205890.3	RP11-473M20.5	blue	1.6	7.7E-04	-	-	1.6	3.7E-10	1.2	4.2E-06
ENSG00000262370.5	RP11-473M20.9	green	-2.0	1.0E-04	-	-	-1.4	5.8E-11	-	-
ENSG00000260261.1	RP11-480A16.1	blue	1.8	1.1E-07	-	-	1.6	1.7E-19	-	-
ENSG00000279089.1	RP11-481C4.2	magenta	1.6	1.4E-06	1.1	1.7E-05	-	-	-	-
ENSG00000251379.1	RP11-484O2.1	brown	1.4	3.6E-03	2.1	1.5E-11	-	-	1.5	2.6E-09
ENSG00000273302.1	RP11-493E12.2	brown	-	-	1.3	7.4E-06	-	-	1.2	1.0E-10
ENSG00000273308.1	RP11-496H1.2	blue	-	-	-	-	1.6	7.3E-09	1.4	8.9E-12
ENSG00000254815.5	RP11-496I9.1	blue	1.9	3.0E-04	1.3	1.0E-04	-	-	2.4	1.3E-13
ENSG00000278876.1	RP11-498C9.4	brown	1.9	1.6E-03	1.4	4.6E-04	1.6	2.8E-07	1.6	7.0E-12
ENSG00000240291.1	RP11-499P20.2	magenta	-	-	1.3	2.4E-05	-	-	1.2	9.0E-09
ENSG00000274849.1	RP11-49I11.4	salmon	2.4	1.2E-08	-	-	-	-	1.3	3.4E-08
ENSG00000253972.5	RP11-4K16.2	turquoise	2.2	1.9E-04	-	-	1.3	6.8E-05	1.5	9.7E-14
ENSG00000272645.2	RP11-504P24.8	brown	1.2	1.6E-05	1.1	4.1E-06	-	-	1.1	3.2E-11
ENSG00000249007.1	RP11-510N19.5	magenta	2.8	3.9E-08	1.3	3.5E-03	2.2	1.8E-05	2.4	1.2E-10
ENSG00000272183.1	RP11-523H20.3	blue	2.8	6.6E-06	-	-	2.0	1.2E-11	1.7	5.3E-12
ENSG00000261295.1	RP11-524D16__A.3	yellow	-	-	-	-	1.1	2.8E-07	-1.8	4.8E-08
ENSG00000260461.1	RP11-541N10.3	green	-	-	-	-	-1.1	1.5E-08	-1.3	8.9E-11
ENSG00000235652.7	RP11-545I5.3	brown	-	-	1.5	3.6E-08	-	-	1.0	4.3E-06
ENSG00000277566.1	RP11-545P7.9	grey60	1.7	9.1E-03	-	-	-	-	1.1	1.5E-07
ENSG00000279706.1	RP11-561O23.9	magenta	2.0	6.8E-04	-	-	-	-	1.3	4.6E-14
ENSG00000275764.1	RP11-582E3.6	brown	-	-	1.3	1.1E-07	-	-	1.2	2.7E-08
ENSG00000260244.1	RP11-588K22.2	pink	-2.0	4.1E-04	-	-	-	-	-1.6	7.8E-11
ENSG00000279806.1	RP11-58O9.2	magenta	2.7	5.0E-05	-1.8	1.4E-03	-	-	-1.4	1.6E-06
ENSG00000248429.5	RP11-597D13.9	black	-	-	1.2	2.1E-05	1.5	9.3E-06	-	-
ENSG00000279662.1	RP11-609N14.4	brown	1.5	9.7E-05	-	-	-1.4	7.8E-09	1.4	1.2E-09
ENSG00000273691.1	RP11-617F23.2	brown	1.3	9.6E-03	-	-	-	-	1.9	1.5E-20
ENSG00000279912.1	RP11-624A21.1	magenta	-	-	1.4	1.1E-06	-	-	1.7	7.0E-11
ENSG00000259345.5	RP11-624L4.1	brown	1.3	1.3E-05	-	-	-	-	1.6	3.4E-13
ENSG00000255191.1	RP11-626H12.1	black	-	-	-	-	-2.4	6.2E-11	-2.1	6.6E-12
ENSG00000275180.1	RP11-631N16.4	black	-	-	1.5	6.4E-06	1.3	1.1E-05	-	-
ENSG00000272556.1	RP11-638I8.1	brown	1.3	2.4E-03	-	-	-	-	1.1	1.0E-08
ENSG00000248787.1	RP11-666A20.4	brown	-	-	1.1	5.7E-03	-	-	1.2	6.4E-08
ENSG00000269924.1	RP11-697N18.4	blue	1.8	5.8E-04	-	-	-	-	2.0	7.2E-17
ENSG00000249614.1	RP11-703G6.1	brown	-	-	1.5	1.2E-05	1.2	1.9E-15	1.8	3.6E-10
ENSG00000279670.1	RP11-70L8.5	tan	-	-	2.5	3.9E-12	-	-	1.6	3.0E-13
ENSG00000254528.7	RP11-728F11.4	red	-3.6	3.9E-05	-	-	-1.2	4.9E-04	-	-
ENSG00000280339.1	RP11-736K20.4	yellow	-	-	-	-	-2.2	1.5E-23	-2.3	7.2E-17
ENSG00000255471.1	RP11-736K20.5	greenyellow	-	-	-	-	-2.0	1.1E-13	-2.5	1.7E-16
ENSG00000131484.4	RP11-798G7.5	brown	2.1	6.2E-04	-	-	-	-	1.0	1.7E-05
ENSG00000266918.1	RP11-798G7.8	blue	-	-	1.3	1.1E-04	1.2	6.1E-10	-	-
ENSG00000265490.1	RP11-806L2.6	magenta	2.1	4.3E-04	1.5	3.2E-05	-	-	-	-
ENSG00000276115.1	RP11-817I4.2	pink	1.2	8.8E-03	2.4	9.2E-13	-	-	-	-
ENSG00000279107.1	RP11-823P9.4	magenta	-	-	1.9	8.4E-04	-	-	1.2	4.0E-09
ENSG00000273247.5	RP11-83A24.2	brown	1.1	9.1E-03	1.1	2.4E-06	-	-	-	-
ENSG00000266717.1	RP11-855A2.3	brown	2.2	1.6E-04	-	-	-	-	1.2	2.3E-08
ENSG00000245156.1	RP11-867G23.3	brown	1.6	1.0E-03	1.5	9.3E-06	-	-	-	-
ENSG00000265218.1	RP11-927P21.1	brown	1.2	1.8E-03	1.4	7.2E-05	-	-	-	-
ENSG00000267026.5	RP11-92C4.3	turquoise	-	-	2.1	1.1E-04	2.2	9.9E-06	-	-
ENSG00000257303.1	RP11-977G19.11	magenta	3.1	2.8E-07	1.3	3.0E-03	-	-	-	-
ENSG00000215769.8	RP13-104F24.2	blue	1.9	2.7E-07	1.4	1.1E-06	-	-	-	-
ENSG00000279312.1	RP3-331H24.7	grey	-3.5	9.8E-16	1.1	3.0E-04	-2.2	8.9E-13	-	-
ENSG00000279159.1	RP3-394A18.1	grey	1.3	1.2E-03	1.1	1.8E-04	-	-	-	-
ENSG00000260418.1	RP3-406A7.7	turquoise	2.2	4.2E-05	-	-	-	-	1.3	2.2E-08
ENSG00000279453.1	RP3-425C14.4	red	-1.7	9.9E-05	-	-	-1.3	4.2E-14	-1.3	8.1E-19
ENSG00000230910.2	RP3-525N10.2	red	-3.9	7.2E-09	-	-	-2.0	2.0E-09	-	-
ENSG00000235501.5	RP4-639F20.1	red	-2.5	1.0E-04	-	-	-1.1	1.6E-05	-	-
ENSG00000261135.1	RP4-798A10.7	brown	1.9	6.9E-05	1.2	2.6E-04	-	-	-	-
ENSG00000224093.5	RP5-1033H22.2	grey	1.4	4.5E-03	-	-	1.1	5.8E-07	-	-
ENSG00000273373.1	RP5-1074L1.4	grey	1.4	1.7E-03	1.3	1.4E-04	-	-	-	-
ENSG00000270605.1	RP5-1092A3.4	magenta	1.4	1.6E-03	1.7	1.3E-10	-	-	-	-
ENSG00000260793.2	RP5-882C2.2	brown	1.7	2.2E-09	1.1	7.5E-04	-	-	1.5	3.3E-10
ENSG00000244701.1	RP5-894A10.2	brown	1.0	1.9E-04	1.5	5.2E-09	-	-	1.0	2.6E-08
ENSG00000274536.4	RP6-159A1.4	green	-2.3	1.6E-04	-	-	-1.7	2.7E-15	-	-
ENSG00000225855.6	RUSC1-AS1	brown	2.0	6.2E-07	1.3	3.7E-08	-	-	1.2	4.3E-12
ENSG00000245275.7	SAP30L-AS1	blue	-	-	-	-	1.7	7.0E-09	1.7	1.6E-24
ENSG00000251322.7	SHANK3	yellow	-1.5	5.0E-04	-	-	-2.3	3.7E-30	-1.8	2.8E-11
ENSG00000279078.1	SND1-IT1	brown	1.7	8.6E-03	1.2	2.3E-03	-	-	1.3	1.8E-14
ENSG00000242125.3	SNHG3	magenta	1.3	7.8E-03	1.2	1.6E-11	-	-	1.1	2.9E-12
ENSG00000281398.2	SNHG4	salmon	2.2	2.0E-06	-	-	1.2	5.5E-07	-	-

ENSG00000227543.4	SPAG5-AS1	lightgreen	1.3	6.1E-04	-	-	-	-	1.3	3.5E-13
ENSG00000249700.8	SRD5A3-AS1	tan	1.3	8.4E-03	-	-	1.0	1.2E-05	-	-
ENSG00000204832.9	ST8SIA6-AS1	pink	-	-	2.1	3.1E-06	-	-	1.5	2.5E-14
ENSG00000227954.6	TARID	blue	-3.5	2.5E-12	-	-	-2.8	2.4E-16	-	-
ENSG00000229950.1	TFAP2A-AS1	brown	1.5	4.2E-03	-	-	-	-	1.7	9.0E-11
ENSG00000223573.6	TINCR	blue	-	-	-1.2	7.5E-06	-2.6	1.4E-24	-	-
ENSG00000175147.11	TMEM51-AS1	magenta	2.2	4.6E-07	-	-	1.2	2.6E-05	-	-
ENSG00000248275.1	TRIM52-AS1	turquoise	-1.0	8.5E-04	-	-	-	-	-1.0	1.4E-11
ENSG00000249348.1	UGDH-AS1	brown	-	-	1.8	1.2E-11	-	-	1.3	1.5E-07
ENSG00000259248.5	USP3-AS1	turquoise	1.1	1.8E-03	1.2	1.1E-04	-	-	-	-
ENSG00000232354.7	VIPR1-AS1	green	1.4	2.5E-03	1.4	7.5E-06	-1.4	3.8E-04	-	-
ENSG00000261373.1	VPS9D1-AS1	blue	1.7	2.7E-04	1.3	2.7E-05	-	-	-	-
ENSG00000226245.1	ZNF32-AS1	turquoise	2.0	8.8E-04	1.2	6.3E-03	-	-	-	-

Supplementary Table S5: Functional onco-lncRNAs derived from PubMed

gene id	gene name
ENSG00000241684.5	ADAMTS9-AS2
ENSG00000245750.7	DRAIC
ENSG00000203499.10	FAM83H-AS1
ENSG00000268388.5	FENDRR
ENSG00000272143.1	FGF14-AS2
ENSG00000214548.14	MEG3
ENSG00000238045.9	PAGR1
ENSG00000267107.6	PCAT19
ENSG00000228288.6	PCAT6
ENSG00000249859.7	PVT1
ENSG00000227954.6	TARID
ENSG00000258498.6	DIO3OS
ENSG00000206195.10	DUXAP8
ENSG00000249669.7	MIR143HG
ENSG00000247095.2	MIR210HG
ENSG00000186594.12	MIR22HG
ENSG00000223749.7	MIR503HG
ENSG00000260804.3	PKI55
ENSG00000251322.7	SHANK3
ENSG00000223573.6	TINCR

Supplementary Table S6: log₂FC (fold change) of onco-PCGs in each cancer type

Gene id	Gene name	BLC	PRC	ADC	EBC
ENSG00000001617.11	SEMA3F	1.7	-	-1.3	-
ENSG00000002726.19	AOC1	-	-4.2	4.4	-
ENSG00000003096.13	KLHL13	-2.1	-	-	-2.9
ENSG00000003137.8	CYP26B1	-	-	-1.2	-3.0
ENSG00000003249.13	DBNDD1	1.4	-	1.3	1.3
ENSG00000004399.12	PLXND1	-1.3	-	-	-1.6
ENSG00000004776.11	HSPB6	-8.4	-1.2	-2.1	-4.2
ENSG00000004799.7	PDK4	-4.4	-	-2.5	-3.3
ENSG00000004838.13	ZMYND10	-	1.5	-1.1	1.9
ENSG00000005001.9	PRSS22	-	-	1.5	1.7
ENSG00000005102.12	MEOX1	-4.0	-	-	-2.7
ENSG00000005187.11	ACSM3	-	-	1.5	-1.4
ENSG00000005243.9	COPZ2	-3.0	-	-	-1.4
ENSG00000005249.12	PRKAR2B	-3.2	-	-	-3.5
ENSG00000005801.16	ZNF195	1.1	1.1	-	-
ENSG00000005884.17	ITGA3	1.5	-1.2	-	-
ENSG00000006016.10	CRLF1	-	-	3.2	-1.2
ENSG00000006118.14	TMEM132A	2.5	-	1.2	-
ENSG00000006210.6	CX3CL1	-1.9	-1.3	-1.7	-2.7
ENSG00000006468.13	ETV1	-1.9	-	-	-1.5
ENSG00000006555.10	TTC22	1.7	-1.6	-	-
ENSG00000006625.17	GGCT	-	-	1.3	1.2
ENSG00000007062.11	PROM1	-	-1.5	1.9	-
ENSG00000007237.18	GAS7	-3.4	-	-	-1.8
ENSG00000007908.15	SELE	-4.9	-	-3.3	-
ENSG00000008256.15	CYTH3	-1.4	-	-	-1.7
ENSG00000008300.14	CELSR3	2.8	-	-	1.5
ENSG00000008394.12	MGST1	-	-	1.1	-1.7
ENSG00000008441.16	NFIX	-2.9	-	-	-2.2
ENSG00000010319.6	SEMA3G	-2.7	-	-3.2	-3.0
ENSG00000010610.9	CD4	-1.4	-	-	-1.3
ENSG00000010810.17	FYN	-2.2	-	-1.2	-1.8
ENSG00000011465.16	DCN	-5.7	-	-1.1	-2.4

ENSG00000012223.12	LTF	-	-2.2	2.2	-3.1
ENSG00000013297.10	CLDN11	-2.5	-	-	-1.2
ENSG00000013810.18	TACC3	2.1	-	-	1.5
ENSG00000015479.17	MATR3	1.2	1.2	-	-
ENSG00000018236.14	CNTN1	-5.6	-1.0	-	-1.9
ENSG00000018280.16	SLC11A1	-2.0	-	-1.6	1.1
ENSG00000018408.14	WWTR1	-2.0	-	-	-1.4
ENSG00000018625.14	ATP1A2	-6.2	-1.2	-1.4	-3.2
ENSG00000019144.16	PHLDB1	-1.4	-	-	-1.5
ENSG00000019485.12	PRDM11	-1.2	-	-1.2	-1.5
ENSG00000019549.8	S-I2	-1.5	-1.2	-	-1.3
ENSG00000020181.17	ADGRA2	-3.8	-1.2	-1.1	-2.5
ENSG00000020577.13	SAMD4A	-2.5	-	-	-2.0
ENSG00000020633.18	RUNX3	-	-	-1.3	-1.5
ENSG00000022267.16	FHL1	-5.5	-	-3.1	-4.3
ENSG00000024422.11	EHD2	-2.2	-	-1.4	-2.6
ENSG00000025039.14	RRAGD	-1.6	-	-	-2.7
ENSG00000026025.13	VIM	-3.4	-	-	-1.8
ENSG00000027075.13	PRKCH	-	-	-1.2	-1.6
ENSG00000028137.16	TNFRSF1B	-2.0	-	-1.1	-2.1
ENSG00000029993.14	HMGB3	1.4	-	2.9	1.2
ENSG00000031081.10	ARHGAP31	-2.1	-	-1.6	-2.4
ENSG00000033327.12	GAB2	-1.3	-	-1.1	-
ENSG00000034971.14	MYOC	-7.9	-	-4.3	-
ENSG00000035403.16	VCL	-1.5	-	-	-1.6
ENSG00000035862.12	TIMP2	-4.1	-	-	-1.4
ENSG00000036448.9	MYOM2	-3.6	-	-1.8	-
ENSG00000036672.15	USP2	-3.3	-1.0	-	-
ENSG00000037280.15	FLT4	-	-	-2.0	-1.4
ENSG00000039523.17	FAM65A	-1.1	-	-1.3	-
ENSG00000041982.14	TNC	-2.8	-	-	-1.0
ENSG00000042062.11	FAM65C	-1.5	-	-1.1	-
ENSG00000046653.14	GPM6B	-2.1	-	-1.4	-1.9
ENSG00000046889.18	PREX2	-2.5	-	-1.7	-2.2
ENSG00000047457.13	CP	-	-	4.0	-2.2
ENSG00000047617.14	ANO2	-	-	-2.5	-1.6

ENSG00000047648.21	ARHGAP6	-	-	-2.4	-1.7
ENSG00000048540.14	LMO3	-2.6	-	-	-2.0
ENSG00000048740.17	CELF2	-3.1	-	-1.0	-2.7
ENSG00000049283.17	EPN3	-	-	3.4	1.8
ENSG00000049540.16	ELN	-4.1	-	-1.0	-
ENSG00000050165.17	DKK3	-3.2	-1.1	-1.1	-1.9
ENSG00000050555.17	LAMC3	-2.6	-	-3.4	-
ENSG00000050628.20	PTGER3	-3.7	-	-	-1.4
ENSG00000050767.15	COL23A1	-	-1.1	-	-1.5
ENSG00000051180.16	RAD51	1.3	-	-	1.0
ENSG00000053747.15	LAMA3	-	-	-2.3	-1.4
ENSG00000053918.15	KCNQ1	-	-1.1	-	-1.4
ENSG00000055813.5	CCDC85A	-	-	-3.1	-3.8
ENSG00000056998.18	GYG2	-	-	2.6	-4.5
ENSG00000057704.10	TMCC3	-	-	-1.2	-1.9
ENSG00000058668.14	ATP2B4	-1.2	-	-	-2.0
ENSG00000058866.14	DGKG	-2.9	-	-1.2	-
ENSG00000059804.15	SLC2A3	-3.5	-	-1.7	-1.2
ENSG00000060718.18	COL11A1	-	-	4.5	4.3
ENSG00000061656.9	SPAG4	-	-	1.7	1.3
ENSG00000061918.12	GUCY1B3	-1.8	-	-	-1.5
ENSG00000062038.13	CDH3	2.0	-1.3	2.4	-
ENSG00000062716.10	VMP1	-	-	1.1	1.4
ENSG00000063180.8	CA11	-1.9	-1.1	-	-
ENSG00000064042.17	LIMCH1	-	-	-1.5	-1.6
ENSG00000064205.10	WISP2	-5.6	-	-1.9	-1.3
ENSG00000064300.8	NGFR	-	-1.5	-	-2.2
ENSG00000064651.13	SLC12A2	-	-	1.3	-1.7
ENSG00000064655.18	EYA2	-	-	1.8	-1.8
ENSG00000064787.12	BCAS1	-	-	1.9	1.6
ENSG00000064989.12	CALCRL	-1.6	-	-2.1	-1.4
ENSG00000064999.13	ANKS1A	-	-	-1.1	-1.5
ENSG00000065054.13	SLC9A3R2	-1.8	-	-1.3	-
ENSG00000065154.11	OAT	-1.8	-1.2	-	-
ENSG00000065320.8	NTN1	-3.5	-1.8	-	-
ENSG00000065361.14	ERBB3	2.0	-	1.1	-

ENSG00000065534.18	MYLK	-5.5	-	-1.1	-1.9
ENSG00000065618.16	COL17A1	-	-2.6	3.1	-2.4
ENSG00000065833.8	ME1	-2.2	-	-	-3.1
ENSG00000066056.13	TIE1	-2.2	-	-2.3	-1.6
ENSG00000066336.11	SPI1	-2.1	-	-1.2	-
ENSG00000066468.20	FGFR2	-	-1.4	-1.3	-1.2
ENSG00000066629.16	EML1	-2.9	-	-1.7	-
ENSG00000066735.14	KIF26A	-	-	-2.2	-2.6
ENSG00000067082.14	KLF6	-1.2	-	-1.8	-1.0
ENSG00000067113.16	PPAP2A	-1.4	-	-	-2.0
ENSG00000067840.12	PDZD4	-3.4	-	-1.8	-
ENSG00000068001.13	HYAL2	-1.0	-	-2.2	-
ENSG00000068024.16	HDAC4	-1.9	-	-	-1.2
ENSG00000068028.17	RASSF1	-1.3	-	-1.1	-
ENSG00000068078.17	FGFR3	2.1	-	-	1.4
ENSG00000068383.18	INPP5A	-1.5	-	-1.0	-1.1
ENSG00000068615.16	REEP1	-5.6	-	-1.6	1.1
ENSG00000068831.18	RASGRP2	-3.3	-	-1.4	-1.2
ENSG00000069011.15	PITX1	-	-2.1	4.3	4.2
ENSG00000069535.13	MAOB	-4.6	-	-1.1	-1.3
ENSG00000069702.10	TGFBR3	-1.6	-	-2.5	-2.9
ENSG00000070193.4	FGF10	-6.9	-	-1.5	-3.2
ENSG00000070404.9	FSTL3	-2.5	-	-2.2	-1.1
ENSG00000070501.11	POLB	1.1	-	-	1.0
ENSG00000070614.14	NDST1	-	-	-1.5	-1.8
ENSG00000070731.9	ST6GAL-C2	-	-1.5	-1.5	-
ENSG00000070756.13	PABPC1	1.2	-	1.1	-
ENSG00000070778.12	PTPN21	-	-	-2.0	-1.7
ENSG00000071205.11	ARHGAP10	-1.6	-	-	-1.7
ENSG00000071242.11	RPS6KA2	-1.7	-	-1.1	-1.5
ENSG00000071246.10	VASH1	-	-	-1.0	-1.1
ENSG00000071282.11	LMCD1	-3.7	-	-2.0	-1.1
ENSG00000071539.13	TRIP13	2.6	-	1.1	1.1
ENSG00000071967.11	CYBRD1	-3.8	-	-1.4	-1.7
ENSG00000072080.10	SPP2	1.7	1.6	-	1.0
ENSG00000072163.18	LIMS2	-4.9	-	-3.0	-1.7

ENSG00000072840.12	EVC	-2.0	-	-	-1.3
ENSG00000072952.18	MRVI1	-3.7	-	-	-1.1
ENSG00000073282.12	TP63	-	-2.4	2.0	-1.9
ENSG00000073350.13	LLGL2	1.4	-	-	1.5
ENSG00000073605.18	GSDMB	2.1	1.3	1.4	-
ENSG00000073712.13	FERMT2	-3.3	-	-1.3	-1.5
ENSG00000073756.11	PTGS2	-1.8	-1.3	-	-
ENSG00000073849.14	ST6GAL1	-1.9	-	-	-1.4
ENSG00000074416.13	MGLL	-2.0	-	-	-2.5
ENSG00000074660.15	SCARF1	-1.1	-	-	-1.1
ENSG00000075213.10	SEMA3A	-2.3	-	1.0	-
ENSG00000075218.18	GTSE1	2.8	-	-	1.9
ENSG00000075239.13	ACAT1	-2.1	-	-	-1.0
ENSG00000075426.11	FOSL2	-	-	-1.5	-1.3
ENSG00000075461.5	CACNG4	-	-1.6	-	1.9
ENSG00000075702.16	WDR62	2.7	-	-	1.2
ENSG00000076067.11	RBMS2	-1.0	-	-1.2	-
ENSG00000076344.15	RGS11	-3.5	1.8	-1.1	1.3
ENSG00000076382.16	SPAG5	2.1	1.4	1.0	2.0
ENSG00000076554.15	TPD52	-	-	1.2	1.1
ENSG00000076555.15	ACACB	-2.3	-	-1.2	-3.1
ENSG00000076706.14	MCAM	-2.8	-	-1.5	-2.8
ENSG00000076944.14	STXBP2	1.4	-	-	1.4
ENSG00000077152.9	UBE2T	-	-	1.8	2.7
ENSG00000077157.20	PPP1R12B	-3.1	-	-	-1.4
ENSG00000077274.8	CAPN6	-	-1.7	-	-3.8
ENSG00000077420.15	APBB1IP	-2.3	-	-	-2.3
ENSG00000077782.19	FGFR1	-4.7	-	-	-1.3
ENSG00000077942.17	FBLN1	-2.7	-	-1.6	-1.1
ENSG00000077943.7	ITGA8	-3.6	-	-1.9	-
ENSG00000077984.5	CST7	-3.2	-	-1.4	-
ENSG00000078018.19	MAP2	-	1.2	-1.2	-1.3
ENSG00000078081.7	LAMP3	-	-1.7	-2.1	-
ENSG00000078098.13	FAP	-2.8	-	2.0	1.3
ENSG00000078401.6	EDN1	-1.1	-	-2.4	-
ENSG00000078596.10	ITM2A	-4.9	-	-1.7	-2.1

ENSG00000079308.16	TNS1	-4.6	-	-1.7	-3.9
ENSG00000079385.21	CEACAM1	-	-1.1	1.9	-
ENSG00000079435.9	LIPE	-	-1.2	-	-4.2
ENSG00000079462.7	PAFAH1B3	2.5	-	1.3	2.3
ENSG00000079819.16	EPB41L2	-2.5	-	-1.4	-2.5
ENSG00000080573.6	COL5A3	-	-	-1.2	-1.8
ENSG00000081041.8	CXCL2	-	-	-3.0	-2.8
ENSG00000081189.13	MEF2C	-2.5	-	-	-1.8
ENSG00000081277.11	PKP1	-	-1.1	-	-3.0
ENSG00000081818.3	PCDHB4	-3.4	-	-1.0	-1.3
ENSG00000081853.14	PCDHGA2	-	-	-1.3	-1.8
ENSG00000082196.20	C1QTNF3	-	1.9	1.9	1.5
ENSG00000082397.15	EPB41L3	-3.1	-	-1.0	-1.9
ENSG00000083857.13	FAT1	-	-	1.0	-2.0
ENSG00000084207.15	GSTP1	-	-1.7	-	-1.2
ENSG00000085063.14	CD59	-1.1	-	-	-1.1
ENSG00000085265.10	FCN1	-4.0	-	-1.7	-
ENSG00000085514.15	PILRA	-3.2	-	-1.2	-
ENSG00000085552.16	IGSF9	2.4	-	1.9	1.5
ENSG00000085563.14	ABCB1	-2.1	-	-2.1	-1.8
ENSG00000086289.11	EPDR1	-2.5	-	-	-2.1
ENSG00000087074.7	PPP1R15A	-1.2	-	-2.1	-
ENSG00000087085.13	ACHE	-	-	2.0	-1.1
ENSG00000087116.13	ADAMTS2	-2.7	-	-	-1.6
ENSG00000087510.6	TFAP2C	-	-	1.5	-1.5
ENSG00000087586.17	AURKA	2.2	-	1.3	1.6
ENSG00000087903.12	RFX2	-	-	-1.5	-1.2
ENSG00000088002.11	SULT2B1	-	-1.9	-1.2	-
ENSG00000088320.3	REM1	-3.2	-	-2.0	-1.8
ENSG00000088325.15	TPX2	3.0	-	1.8	2.3
ENSG00000088836.12	SLC4A11	2.1	-1.1	2.6	-
ENSG00000088882.7	CPXM1	-3.2	-1.3	-	-1.4
ENSG00000088992.17	TESC	-	-	1.6	-1.9
ENSG00000089127.12	OAS1	2.1	-	1.0	-
ENSG00000089472.16	HEPH	-3.7	-	-	-1.8
ENSG00000089486.16	CDIP1	-	-1.2	-	-1.3

ENSG00000089685.14	BIRC5	1.7	-	1.2	-
ENSG00000090006.17	LTBP4	-3.6	-	-2.7	-1.5
ENSG00000090104.11	RGS1	-2.6	-	-	1.1
ENSG00000090447.11	TFAP4	1.4	-	1.1	-
ENSG00000090530.9	P3H2	-	-	-1.6	-2.2
ENSG00000090776.5	EFNB1	-	-1.5	-1.2	-2.2
ENSG00000090975.12	PITPNM2	-1.8	-	-1.3	-1.1
ENSG00000091073.19	DTX2	1.0	-	1.0	-
ENSG00000091436.16	pk	-3.0	-	-	-1.1
ENSG00000091490.10	SEL1L3	-	-	1.1	-1.2
ENSG00000091513.14	TF	-	-1.4	-	-2.4
ENSG00000091527.15	CDV3	-1.1	-	-	-1.5
ENSG00000091972.18	CD200	-2.1	-	-1.2	-1.5
ENSG00000091986.15	CCDC80	-4.0	-	-	-1.6
ENSG00000092051.16	JPH4	-	-1.1	-1.3	-
ENSG00000092096.14	SLC22A17	-1.7	-1.6	-	-
ENSG00000092295.11	TGM1	-	-1.7	-2.6	-
ENSG00000092421.16	SEMA6A	1.8	-	-2.9	-1.0
ENSG00000092621.11	PHGDH	-	-1.2	-	-1.6
ENSG00000092758.15	COL9A3	-1.5	-	1.5	-
ENSG00000092853.13	CLSPN	2.8	-	-	1.4
ENSG00000092964.16	DPYSL2	-2.8	-	-1.2	-2.5
ENSG00000092969.11	TGFB2	-2.1	-	-1.1	-
ENSG00000093009.9	CDC45	2.4	-	-	2.0
ENSG00000094755.16	GABRP	-	-1.5	-	-2.2
ENSG00000094804.9	CDC6	2.1	-	1.9	-
ENSG00000094963.13	FMO2	-	-	-2.4	-3.1
ENSG00000095370.19	SH2D3C	-1.8	-	-2.5	-1.3
ENSG00000095383.19	TBC1D2	-	-1.3	-1.2	-
ENSG00000095585.16	BLNK	-	1.2	1.4	1.0
ENSG00000095637.20	SORBS1	-4.5	-	-	-3.6
ENSG00000095713.13	CRTAC1	-	-	-1.5	-2.1
ENSG00000095794.19	CREM	-3.0	-	-1.4	-
ENSG00000096060.14	FKBP5	-2.4	-	-	-1.2
ENSG00000096063.14	SRPK1	1.3	-	1.2	-
ENSG00000097007.17	ABL1	-1.9	-	-	-1.3

ENSG00000099204.18	ABLIM1	-	-	-1.2	-2.1
ENSG00000099250.17	NRP1	-1.6	-	-	-2.0
ENSG00000099260.10	PALMD	-	-	-1.3	-2.6
ENSG00000099849.14	RASSF7	1.4	-	-	1.8
ENSG00000099860.8	GADD45B	-3.5	-	-2.2	-
ENSG00000099864.17	PALM	-2.3	-	-1.2	-2.2
ENSG00000099953.9	MMP11	1.3	-	4.4	3.4
ENSG00000099994.10	SUSD2	-1.2	-	-1.3	-
ENSG00000099998.17	GGT5	-2.1	-	1.2	-
ENSG00000100033.16	PRODH	-	-	1.1	1.9
ENSG00000100034.13	PPM1F	-	-	-1.7	-1.0
ENSG00000100060.17	MFNG	-2.5	-	-1.4	-1.6
ENSG00000100079.6	LGALS2	-2.5	-	-1.2	-
ENSG00000100154.14	TTC28	-1.5	-	-1.2	-1.8
ENSG00000100162.14	CENPM	-	1.3	-	2.1
ENSG00000100234.11	TIMP3	-3.0	-	-1.4	-2.5
ENSG00000100243.20	CYB5R3	-	-	-1.0	-1.4
ENSG00000100290.2	BIK	-	-	1.2	1.3
ENSG00000100307.12	CBX7	-1.7	-	-1.2	-1.6
ENSG00000100321.14	SYNGR1	-1.3	-1.1	-	-
ENSG00000100422.13	CERK	-2.1	-	-	-1.4
ENSG00000100429.17	HDAC10	1.3	1.2	-	1.1
ENSG00000100479.12	POLE2	1.7	-	1.3	1.3
ENSG00000100526.19	CDKN3	-	-	1.8	1.9
ENSG00000100599.15	RIN3	-1.3	-	-	-1.5
ENSG00000100605.16	ITPK1	-1.1	-	-	-1.0
ENSG00000100625.8	SIX4	1.2	-	2.1	-
ENSG00000100626.16	GALNT16	-2.7	-	-1.4	-
ENSG00000100941.8	PNN	-	1.0	-	1.0
ENSG00000100994.11	PYGB	-2.2	-	-	-1.4
ENSG00000101003.9	GIN51	2.3	-	1.9	1.4
ENSG00000101057.15	MYBL2	2.5	-	1.8	2.7
ENSG00000101096.19	NFATC2	-2.4	-	-	-2.3
ENSG00000101104.12	PABPC1L	1.6	1.3	1.3	1.5
ENSG00000101115.12	SALL4	2.1	-	3.3	-
ENSG00000101187.15	SLCO4A1	-	-	-2.0	-1.8

ENSG00000101194.17	SLC17A9	-	-	1.4	2.4
ENSG00000101210.10	EEF1A2	-	-	5.1	3.2
ENSG00000101213.6	PTK6	2.2	-	1.8	1.2
ENSG00000101265.15	RASSF2	-1.6	-	-1.3	-1.4
ENSG00000101311.15	FERMT1	1.3	-	2.5	-
ENSG00000101331.15	CCM2L	-2.0	-	-2.8	-1.9
ENSG00000101333.16	PLCB4	-2.5	1.1	-	-
ENSG00000101335.9	MYL9	-5.8	-1.0	-1.6	-1.4
ENSG00000101336.12	HCK	-1.9	-	-1.1	-
ENSG00000101347.8	SAMHD1	-2.1	-	-	-1.3
ENSG00000101400.5	SNTA1	-1.9	-	-	-1.4
ENSG00000101412.12	E2F1	1.7	-	-	1.7
ENSG00000101443.17	WFDC2	-	-1.8	2.5	-
ENSG00000101445.9	PPP1R16B	-	-	-1.4	-3.2
ENSG00000101470.9	TNNC2	-2.4	-	1.1	-
ENSG00000101605.12	MYOM1	-3.7	-	-	-2.9
ENSG00000101665.8	SMAD7	-1.3	-	-1.2	-1.0
ENSG00000101938.14	CHRD1	-7.8	-1.2	-1.6	-4.6
ENSG00000101955.14	SRPX	-6.0	-1.3	-1.9	-3.2
ENSG00000102024.17	PLS3	-1.1	-	-	-1.6
ENSG00000102181.19	CD99L2	-2.0	-	-	-1.6
ENSG00000102265.11	TIMP1	-1.6	-	-	1.2
ENSG00000102359.5	SRPX2	-	1.1	2.1	-
ENSG00000102543.14	CDADC1	-1.4	-	-	-1.2
ENSG00000102547.18	CAB39L	-	-	-1.2	-1.7
ENSG00000102554.13	KLF5	-	-1.3	-	-1.9
ENSG00000102755.10	FLT1	-	-	-1.1	-1.7
ENSG00000102760.12	RGCC	-2.6	-	-2.9	-2.4
ENSG00000102802.9	MEDAG	-4.1	-	-1.6	-3.0
ENSG00000102804.14	TSC22D1	-1.7	-	-1.0	-1.0
ENSG00000102878.15	HSF4	-	1.7	-	1.3
ENSG00000102931.7	ARL2BP	-2.0	-	-	-1.3
ENSG00000102935.11	ZNF423	-1.8	-	-	-1.9
ENSG00000103034.14	NDRG4	-	-1.2	-2.7	-1.1
ENSG00000103175.10	WFDC1	-3.2	-	-2.4	-
ENSG00000103196.11	CRISPLD2	-4.5	-1.3	-1.7	-

ENSG00000103241.6	FOXF1	-3.9	-	-3.6	-
ENSG00000103316.10	CRYM	-2.3	-	3.3	-
ENSG00000103335.19	PIEZO1	-	-	-1.2	-1.1
ENSG00000103460.16	TOX3	2.4	-	3.7	-
ENSG00000103490.13	PYCARD	-	-1.2	-	1.4
ENSG00000103534.16	TMC5	-	-	2.2	1.2
ENSG00000103550.13	KNOP1	1.4	-	-	1.1
ENSG00000103647.12	CORO2B	-3.1	-	-2.0	-2.4
ENSG00000103710.10	RASL12	-4.4	-	-1.8	-1.9
ENSG00000103994.16	ZNF106	-	-	-1.1	-1.5
ENSG00000104140.6	RHOV	-	-1.5	2.7	-
ENSG00000104164.10	BLOC1S6	-	1.2	-	1.1
ENSG00000104219.12	ZDHHC2	-1.5	-	-	-2.0
ENSG00000104324.15	CPQ	-2.2	-	-	-1.3
ENSG00000104332.11	SFRP1	-5.5	-	-	-3.0
ENSG00000104368.17	PLAT	-	-1.0	1.6	-
ENSG00000104375.15	STK3	-	-	1.0	1.0
ENSG00000104413.15	ESRP1	1.5	-	1.3	-
ENSG00000104419.14	NDRG1	-	-1.1	-	-2.2
ENSG00000104450.12	SPAG1	-	-	1.6	1.1
ENSG00000104490.17	NCALD	-2.6	-	-	-2.2
ENSG00000104635.13	SLC39A14	-1.8	-	-	-1.6
ENSG00000104695.12	PPP2CB	-1.3	-	-	-1.2
ENSG00000104728.15	ARHGEF10	-1.6	-	-1.6	-
ENSG00000104738.16	MCM4	1.8	-	1.0	-
ENSG00000104756.15	KCTD9	-1.4	-	-	-1.4
ENSG00000104889.4	R-SEH2A	1.3	-	-	1.1
ENSG00000104967.6	NOVA2	-	-	-2.8	-1.1
ENSG00000105011.8	ASF1B	2.2	-	1.0	2.3
ENSG00000105048.16	TNNT1	-	-	1.7	3.2
ENSG00000105131.7	EPHX3	2.1	-	2.1	-
ENSG00000105137.12	SYDE1	-2.3	-	-1.3	-1.7
ENSG00000105173.13	CCNE1	1.3	-	1.8	-
ENSG00000105227.14	PRX	-	-	-4.1	-1.8
ENSG00000105270.14	CLIP3	-3.9	-	-	-1.1
ENSG00000105374.9	NKG7	-2.1	-	-2.0	-

ENSG00000105427.9	CNFN	-	-	1.9	1.4
ENSG00000105538.8	RASIP1	-2.4	-	-3.1	-2.2
ENSG00000105559.11	PLEKHA4	-2.0	-	-	-1.1
ENSG00000105609.16	LILRB5	-2.8	-	-	-1.1
ENSG00000105655.18	ISY-1	-	-1.2	-	1.2
ENSG00000105664.10	COMP	-	-	4.2	3.5
ENSG00000105707.13	HPN	-	1.8	1.2	1.7
ENSG00000105835.11	-MPT	-1.8	-	-1.4	-
ENSG00000105894.11	PTN	-3.9	-	-1.9	-
ENSG00000105926.15	MPP6	-	1.1	1.1	-1.4
ENSG00000105971.14	CAV2	-1.9	-	-2.7	-2.9
ENSG00000105974.11	CAV1	-3.9	-	-3.6	-3.4
ENSG00000105976.14	MET	-	-1.2	1.2	-2.8
ENSG00000106004.4	HOXA5	2.1	-	-1.9	-2.1
ENSG00000106006.6	HOXA6	-	-	-1.1	-1.9
ENSG00000106034.17	CPED1	-4.8	-	-1.4	-3.5
ENSG00000106066.13	CPVL	-4.1	-	-	-1.6
ENSG00000106078.17	COBL	-	-	-1.0	-1.6
ENSG00000106089.11	STX1A	1.8	-	1.7	1.6
ENSG00000106123.11	EPHB6	1.6	-1.2	-1.4	-1.9
ENSG00000106258.13	CYP3A5	1.4	-1.7	-	1.7
ENSG00000106327.12	TFR2	3.0	-	-	1.7
ENSG00000106462.10	EZH2	2.1	1.2	1.1	1.6
ENSG00000106538.9	RARRES2	-3.4	-	-	-2.0
ENSG00000106541.11	AGR2	-	-	2.9	1.6
ENSG00000106665.15	CLIP2	-1.1	-	-	-1.4
ENSG00000106772.17	PRUNE2	-7.1	-	-	-2.1
ENSG00000106809.10	OGN	-6.5	-	-2.0	-2.1
ENSG00000106819.11	ASPN	-3.1	1.4	-	1.5
ENSG00000106823.12	ECM2	-2.6	-	-1.0	-2.3
ENSG00000106852.15	LHX6	-	-	-1.3	-2.1
ENSG00000106948.16	AK-	-1.3	-	-	-1.5
ENSG00000106991.13	ENG	-	-	-1.6	-1.5
ENSG00000107104.18	KANK1	-1.1	-	-	-1.9
ENSG00000107159.12	CA9	3.0	-	3.5	-
ENSG00000107186.16	MPDZ	-1.5	-	-	-1.6

ENSG00000107263.18	RAPGEF1	-1.1	-	-	-1.6
ENSG00000107317.11	PTGDS	-5.5	-1.4	-1.5	-2.0
ENSG00000107372.12	ZFAND5	-1.2	-	-	-1.2
ENSG00000107438.8	PDLIM1	-	-1.1	-1.1	-1.1
ENSG00000107485.15	GATA3	2.0	-1.9	-	1.6
ENSG00000107562.16	CXCL12	-5.1	-	-	-1.9
ENSG00000107719.8	PALD1	-1.8	-	-1.9	-1.1
ENSG00000107736.19	CDH23	-	-	-1.3	-2.2
ENSG00000107738.19	C10orf54	-1.7	-	-1.9	-2.7
ENSG00000107742.12	SPOCK2	-	-	-2.9	-1.3
ENSG00000107796.12	ACTA2	-5.2	-	-	-1.3
ENSG00000107821.14	KAZALD1	-1.8	-	-	1.2
ENSG00000107890.16	ANKRD26	-	1.3	-	1.4
ENSG00000108176.14	D-JC12	-	-	3.1	1.3
ENSG00000108244.16	KRT23	-	-1.8	-	-1.4
ENSG00000108342.12	CSF3	-5.3	-	-4.9	-
ENSG00000108352.11	RAPGEFL1	1.9	-1.2	-	-
ENSG00000108370.15	RGS9	-4.5	-	-2.7	-
ENSG00000108381.10	ASPA	-2.3	-	-2.0	-
ENSG00000108387.14	SEPT4	-1.7	-	-1.3	-
ENSG00000108511.9	HOXB6	2.6	-	1.3	-
ENSG00000108515.17	ENO3	-	1.4	-	1.5
ENSG00000108551.4	RASD1	-2.5	-	-1.5	-1.6
ENSG00000108602.17	ALDH3A1	-	-2.3	-	-2.0
ENSG00000108622.10	ICAM2	-	-	-1.4	-1.4
ENSG00000108691.9	CCL2	-5.1	-	-2.3	-1.9
ENSG00000108821.13	COL1A1	-2.2	-	2.0	-
ENSG00000108823.15	SGCA	-5.5	-1.0	-2.1	-
ENSG00000108840.15	HDAC5	-1.0	-	-	-1.1
ENSG00000108846.15	ABCC3	2.1	-	2.4	-
ENSG00000108848.15	LUC7L3	-	1.0	-	1.3
ENSG00000108924.13	HLF	-4.8	-	-1.4	-2.8
ENSG00000108932.11	SLC16A6	-	-	-1.3	1.5
ENSG00000108947.4	EFNB3	-	-1.8	-	-1.7
ENSG00000108984.13	MAP2K6	-	1.1	-	-1.6
ENSG00000109079.9	TNFAIP1	-	-	-1.0	-1.0

ENSG00000109099.13	PMP22	-5.0	-	-1.2	-1.0
ENSG00000109107.13	ALDOC	-	-1.4	-	-2.4
ENSG00000109321.10	AREG	-	-	-2.0	1.3
ENSG00000109472.13	CPE	-3.4	-	-	-1.6
ENSG00000109501.13	WFS1	-1.0	-	-1.6	-
ENSG00000109610.5	SOD3	-5.5	-1.3	-1.2	-3.1
ENSG00000109654.14	TRIM2	-	-	1.8	-1.7
ENSG00000109667.11	SLC2A9	-	-1.1	-	-1.6
ENSG00000109686.16	SH3D19	-1.2	-	-	-2.5
ENSG00000109771.15	LRP2BP	-	1.3	-1.1	-
ENSG00000109775.10	UFSP2	-1.4	-	-	-1.0
ENSG00000109846.7	CRYAB	-5.2	-	-2.1	-3.2
ENSG00000109881.16	CCDC34	1.4	-	1.0	-
ENSG00000109906.13	ZBTB16	-4.6	-	-2.4	-2.2
ENSG00000110042.7	DTX4	1.4	-	-	-2.0
ENSG00000110047.17	EHD1	-1.2	-	-1.1	-
ENSG00000110076.18	NRXN2	-4.6	-	-	-1.2
ENSG00000110079.16	MS4A4A	-3.1	-	-	-1.3
ENSG00000110108.9	TMEM109	-1.3	-	-	-1.0
ENSG00000110328.5	GALNT18	-1.6	-	-1.6	-1.1
ENSG00000110400.10	PVRL1	-	-1.3	1.3	-1.5
ENSG00000110422.11	HIPK3	-1.3	-	-	-1.9
ENSG00000110446.9	SLC15A3	-1.6	-	-	-1.1
ENSG00000110492.15	MDK	2.0	-	1.9	-
ENSG00000110628.13	SLC22A18	1.3	-	1.7	1.4
ENSG00000110651.11	CD81	-1.6	-	-	-1.2
ENSG00000110799.13	VWF	-1.8	-	-2.3	-3.6
ENSG00000110811.19	P3H3	-2.7	-1.3	-	-
ENSG00000110848.8	CD69	-4.5	-	-1.5	-
ENSG00000110876.9	SELPLG	-2.0	-	-1.3	-
ENSG00000110880.10	CORO1C	-1.8	-	-	-1.4
ENSG00000110900.14	TSPAN11	-2.5	-	-	-2.2
ENSG00000111052.7	LIN7A	-	-	-2.4	-1.5
ENSG00000111058.7	ACSS3	-2.2	-	-1.4	-2.2
ENSG00000111077.17	TNS2	-2.8	-	-1.6	-1.3
ENSG00000111145.7	ELK3	-1.2	-	-	-1.5

ENSG00000111199.10	TRPV4	-	-1.3	1.5	-1.3
ENSG00000111206.12	FOXMI	2.4	1.2	1.5	1.6
ENSG00000111215.11	PRR4	-	1.5	-	1.2
ENSG00000111247.14	RAD51AP1	1.7	-	1.3	2.1
ENSG00000111252.10	SH2B3	-1.2	-	-1.0	-1.2
ENSG00000111269.2	CREBL2	-1.3	-	-	-1.8
ENSG00000111275.12	ALDH2	-1.8	-	-	-1.7
ENSG00000111404.6	RERGL	-6.0	-	-	-1.2
ENSG00000111450.13	STX2	-1.9	-	-1.0	-
ENSG00000111452.12	ADGRD1	-7.0	-	-1.9	-2.3
ENSG00000111665.11	CDCA3	1.4	1.2	1.2	1.9
ENSG00000111716.12	LDHB	-	-1.1	-	-2.2
ENSG00000111727.11	HCFC2	-1.2	-	-	-1.4
ENSG00000111816.7	FRK	-	-	1.1	1.4
ENSG00000111817.16	DSE	-1.7	-	-	-2.2
ENSG00000111859.16	NEDD9	-1.6	-	-1.8	-1.4
ENSG00000111897.6	SERINC1	-1.4	-	-	-1.6
ENSG00000111911.6	HINT3	-1.3	-	-	-1.0
ENSG00000111961.16	SASH1	-	-	-1.9	-2.4
ENSG00000112149.9	CD83	-2.0	-	-1.4	-1.1
ENSG00000112182.14	BACH2	-	-	-1.0	-1.5
ENSG00000112210.11	RAB23	-3.2	-	-	-1.3
ENSG00000112214.10	FHL5	-	-	-2.3	-2.5
ENSG00000112312.9	GMNN	-	-1.3	1.2	-
ENSG00000112319.17	EYA4	-4.3	-	-1.8	-
ENSG00000112320.11	SOBP	-3.0	-	-	-2.2
ENSG00000112419.14	PHACTR2	-	-	-1.2	-1.5
ENSG00000112425.13	EPM2A	-2.4	-	-	-1.5
ENSG00000112531.16	QKI	-	-	-1.0	-2.3
ENSG00000112562.18	SMOC2	-5.1	-	-	-1.3
ENSG00000112658.7	SRF	-1.7	-	-1.0	-1.3
ENSG00000112769.18	LAMA4	-2.3	-	-1.2	-2.6
ENSG00000112773.15	FAM46A	-1.6	-	-	-1.1
ENSG00000112782.15	CLIC5	-	-	-2.7	-3.0
ENSG00000112812.15	PRSS16	1.5	-1.5	-	-
ENSG00000112902.11	SEMA5A	-	-	-2.0	-2.4

ENSG00000112936.18	C7	-8.1	-	-1.4	-1.2
ENSG00000112964.13	GHR	-3.3	-	-1.8	-2.7
ENSG00000112984.11	KIF20A	3.0	-	1.9	2.2
ENSG00000113070.7	HBEGF	-1.7	-	-2.8	-1.1
ENSG00000113319.11	RASGRF2	-1.8	-	-	-1.9
ENSG00000113555.5	PCDH12	-	-	-2.2	-1.7
ENSG00000113580.14	NR3C1	-2.0	-	-	-2.2
ENSG00000113594.9	LIFR	-2.7	-	-1.7	-3.0
ENSG00000113615.12	SEC24A	-	-	1.0	-1.0
ENSG00000113657.12	DPYSL3	-3.2	-	-	-1.4
ENSG00000113721.13	PDGFRB	-2.1	-	-	-1.8
ENSG00000113810.15	SMC4	1.4	-	-	1.6
ENSG00000114019.14	AMOTL2	-2.2	-	-1.4	-2.7
ENSG00000114115.9	RBP1	-3.5	-	-	1.0
ENSG00000114200.9	BCHE	-3.3	-	-2.7	-
ENSG00000114346.13	ECT2	1.7	-	1.3	-
ENSG00000114378.16	HYAL1	-1.6	-	-1.6	-1.4
ENSG00000114631.10	PODXL2	1.7	-	2.3	-
ENSG00000114654.7	EFCC1	-2.3	-	-3.3	-
ENSG00000114698.14	PLSCR4	-2.8	-	-1.4	-2.6
ENSG00000114790.12	ARHGEF26	-1.6	1.5	-2.4	-
ENSG00000114853.13	ZBTB47	-1.7	-	-1.0	-1.7
ENSG00000114857.17	NKTR	-	1.3	-	1.0
ENSG00000115107.19	STEAP3	1.6	-1.0	1.6	-1.0
ENSG00000115226.9	FNDC4	-	-1.2	-	-2.2
ENSG00000115255.10	REEP6	-	-	1.5	1.1
ENSG00000115306.15	SPTBN1	-1.2	-	-1.8	-3.4
ENSG00000115380.18	EFEMP1	-6.3	-	-1.4	-2.1
ENSG00000115468.11	EFHD1	-2.7	-	1.3	-
ENSG00000115594.11	IL1R1	-2.1	-	-	-2.0
ENSG00000115641.18	FHL2	-	-1.0	1.6	-
ENSG00000115758.12	ODC1	-1.9	-	-	-1.5
ENSG00000115884.10	SDC1	-	-2.1	1.4	-
ENSG00000115896.15	PLCL1	-	-	-1.1	-1.7
ENSG00000115935.16	WIPF1	-1.8	-	-	-1.6
ENSG00000115947.13	ORC4	1.0	1.2	-	-

ENSG00000115956.9	PLEK	-2.2	-	-	-1.3
ENSG00000115963.13	RND3	-1.4	-	-1.1	-1.1
ENSG00000116016.13	EPAS1	-1.3	-1.0	-3.0	-3.1
ENSG00000116031.8	CD207	-	-1.9	2.8	-
ENSG00000116117.17	PARD3B	-1.5	-	-	-1.2
ENSG00000116194.12	ANGPTL1	-5.2	-	-2.5	-2.8
ENSG00000116678.18	LEPR	-	-	-1.5	-1.3
ENSG00000116711.9	PLA2G4A	-	-	1.2	-2.9
ENSG00000116741.7	RGS2	-4.5	-	-2.2	-1.6
ENSG00000116962.14	NID1	-2.0	-	-	-2.5
ENSG00000117020.16	AKT3	-2.7	-	-1.2	-
ENSG00000117069.14	ST6GAL-C5	-3.2	-	-2.3	-
ENSG00000117114.19	ADGRL2	-	-	-2.6	-2.0
ENSG00000117122.13	MFAP2	-	-	1.2	2.2
ENSG00000117245.12	KIF17	-	-	-2.1	-1.1
ENSG00000117298.14	ECE1	-1.1	-	-	-1.2
ENSG00000117308.14	GALE	1.2	-	1.4	1.7
ENSG00000117318.8	ID3	-	-1.7	-1.8	-
ENSG00000117399.13	CDC20	2.3	-	1.8	2.1
ENSG00000117472.9	TSPAN1	-	-	2.3	1.6
ENSG00000117479.12	SLC19A2	-1.8	-	-1.1	-
ENSG00000117519.15	CNN3	-2.1	-	-	-1.1
ENSG00000117525.13	F3	-2.6	-	-1.0	-
ENSG00000117632.20	STMN1	1.5	-	-	1.1
ENSG00000117724.12	CENPF	2.9	-	1.8	2.9
ENSG00000117868.15	ESYT2	-1.2	-	-	-1.1
ENSG00000118094.11	TREH	-	-	-1.3	-1.8
ENSG00000118257.16	NRP2	-3.2	-	-	-1.2
ENSG00000118407.14	FILIP1	-4.7	-	-1.4	-1.0
ENSG00000118420.16	UBE3D	1.1	1.3	-	-
ENSG00000118473.21	SGIP1	-	1.0	-	1.3
ENSG00000118495.18	PLAGL1	-3.3	-	-1.0	-2.0
ENSG00000118496.4	FBXO30	-1.2	-	-	-1.1
ENSG00000118503.14	TNFAIP3	-2.8	-	-1.9	-
ENSG00000118508.4	RAB32	-1.6	-	-	-1.2
ENSG00000118515.11	SGK1	-	-	-1.1	-1.7

ENSG00000118523.5	CTGF	-5.0	-	-1.0	-1.3
ENSG00000118526.6	TCF21	-4.0	-	-2.6	-
ENSG00000118596.11	SLC16A7	-	-	1.4	-1.0
ENSG00000118777.10	ABCG2	-1.6	-	-1.8	-
ENSG00000118804.8	FAM47E-STBD1	-1.8	-	-	-2.5
ENSG00000118922.16	KLF12	-1.2	-	-	-1.4
ENSG00000118971.7	CCND2	-2.2	-	-	-2.3
ENSG00000119138.4	KLF9	-3.8	-	-1.9	-2.3
ENSG00000119147.9	C2orf40	-5.4	-1.5	-1.6	-3.3
ENSG00000119280.16	C1orf198	-	-	-1.1	-1.2
ENSG00000119326.14	CTN-L1	-2.0	-	-1.9	-1.6
ENSG00000119333.11	WDR34	1.1	-	-	1.3
ENSG00000119508.17	NR4A3	-4.5	-	-3.0	-
ENSG00000119535.17	CSF3R	-2.3	-	-1.2	-
ENSG00000119699.7	TGFB3	-3.9	-1.3	-	-
ENSG00000119729.10	RHOQ	-1.2	-	-	-1.9
ENSG00000119862.12	LGALS1	-	-	-1.5	-1.1
ENSG00000119865.8	CNRIP1	-3.9	-	-1.3	-2.1
ENSG00000119866.20	BCL11A	1.6	-1.4	-	-1.6
ENSG00000119900.7	OGFRL1	-1.2	-	-	-1.3
ENSG00000119950.20	MXI1	-1.2	-	-	-1.2
ENSG00000119969.14	HELLS	1.9	-	1.2	1.2
ENSG00000119986.6	AVPI1	-	-1.7	-1.5	-1.6
ENSG00000120093.11	HOXB3	2.3	-	1.3	-
ENSG00000120129.5	DUSP1	-2.9	-	-2.2	-1.8
ENSG00000120156.20	TEK	-	-	-2.8	-2.6
ENSG00000120279.6	MYCT1	-3.0	-	-2.1	-2.3
ENSG00000120318.15	ARAP3	-	-	-1.8	-1.2
ENSG00000120594.16	PLXDC2	-1.7	-	-	-1.0
ENSG00000120645.11	IQSEC3	-	-	-2.0	-2.8
ENSG00000120693.13	SMAD9	-1.4	-	-1.2	-1.1
ENSG00000120738.7	EGR1	-2.7	-	-2.1	-2.2
ENSG00000120833.13	SOCS2	-2.0	-	-1.7	-1.0
ENSG00000120885.19	CLU	-2.1	-1.1	-	-1.2
ENSG00000120896.13	SORBS3	-2.7	-	-1.2	-
ENSG00000120910.14	PPP3CC	-1.4	-	-	-1.1

ENSG00000120913.23	PDLIM2	-1.8	-	-1.6	-
ENSG00000121152.9	NCAPH	2.1	-	1.3	-
ENSG00000121210.15	KIAA0922	-2.2	-	-	-1.3
ENSG00000121297.6	TSHZ3	-2.4	-	-	-1.1
ENSG00000121361.3	KCNJ8	-2.5	-	-1.5	-2.7
ENSG00000121380.12	BCL2L14	1.2	-	1.4	-
ENSG00000121440.14	PDZRN3	-4.9	-	-1.1	-2.2
ENSG00000121552.3	CSTA	-	-1.7	-	-1.7
ENSG00000121671.11	CRY2	-1.5	-	-	-1.7
ENSG00000121691.4	CAT	-	-	-1.5	-3.0
ENSG00000121716.18	PILRB	1.6	1.1	-	1.2
ENSG00000121753.12	ADGRB2	-	-	1.1	1.4
ENSG00000121769.7	FABP3	-2.4	-	2.0	-
ENSG00000121898.12	CPXM2	-5.6	-	-	-2.1
ENSG00000122026.10	RPL21	-1.4	-	-	-1.0
ENSG00000122035.6	RASL11A	-2.1	-1.1	-	-
ENSG00000122176.10	FMOD	-3.4	-	-	-2.0
ENSG00000122483.17	CCDC18	1.2	1.2	-	-
ENSG00000122484.8	RPAP2	1.0	1.3	-	1.4
ENSG00000122490.18	PQLC1	-1.1	-	-	-1.2
ENSG00000122591.11	FAM126A	-1.2	-	-	-1.2
ENSG00000122592.7	HOXA7	-	-1.4	-1.3	-2.5
ENSG00000122642.10	FKBP9	-1.4	-	-	-1.4
ENSG00000122679.8	RAMP3	-2.7	-	-3.5	-
ENSG00000122691.12	TWIST1	-2.4	1.3	-	-1.4
ENSG00000122694.15	GLIPR2	-3.6	-	-1.7	-1.8
ENSG00000122707.11	RECK	-3.6	-	-1.4	-1.9
ENSG00000122756.14	CNTFR	-	-	-2.6	-3.7
ENSG00000122862.4	SRGN	-3.3	-	-1.3	-1.3
ENSG00000122863.5	CHST3	-1.4	-	-	-2.5
ENSG00000122877.13	EGR2	-3.9	-	-1.9	-2.2
ENSG00000122952.16	ZWINT	-	-	1.4	2.1
ENSG00000122966.13	CIT	1.5	-	2.7	1.1
ENSG00000123094.15	RASSF8	-2.2	-	-1.0	-
ENSG00000123095.5	BHLHE41	1.4	-	-	-1.5
ENSG00000123096.11	SSPN	-1.6	-	-	-1.3

ENSG00000123146.19	ADGRE5	-1.3	-	-1.6	-1.6
ENSG00000123219.12	CENPK	2.3	-	1.3	1.1
ENSG00000123243.14	ITIH5	-3.7	-1.0	-2.1	-2.9
ENSG00000123342.15	MMP19	-2.0	-	-2.5	-1.9
ENSG00000123358.19	NR4A1	-3.9	-	-2.8	-
ENSG00000123473.15	STIL	2.0	-	1.9	-
ENSG00000123485.11	HJURP	2.2	-	1.9	-
ENSG00000123500.9	COL10A1	-	-	5.1	5.0
ENSG00000123685.8	BATF3	-2.2	-	-1.3	-
ENSG00000123689.5	G0S2	-3.2	-	-1.6	-3.4
ENSG00000124067.16	SLC12A4	-1.5	-	-	-1.3
ENSG00000124104.18	SNX21	-1.3	-	-	-1.1
ENSG00000124107.5	SLPI	-	-1.4	-	-1.2
ENSG00000124126.13	PREX1	-1.7	-	-1.4	-
ENSG00000124191.17	TOX2	-3.5	-	-2.2	-1.1
ENSG00000124212.5	PTGIS	-6.3	-	-1.2	-1.9
ENSG00000124215.16	CDH26	2.2	-	1.7	-
ENSG00000124216.3	S-II	-3.8	-1.1	-2.0	-1.0
ENSG00000124440.15	HIF3A	-4.4	-	-	-1.9
ENSG00000124491.15	F13A1	-3.4	-	-	-1.9
ENSG00000124615.17	MOCS1	-	-	-1.1	-2.5
ENSG00000124664.10	SPDEF	-	-	3.6	1.2
ENSG00000124762.13	CDKN1A	-	-	-1.5	-1.2
ENSG00000124766.5	SOX4	2.7	-	1.3	-
ENSG00000124785.8	NRN1	-3.8	-	-1.9	-2.6
ENSG00000124839.12	RAB17	1.3	1.2	-	1.1
ENSG00000124942.13	AH-K	-1.6	-	-1.4	-2.4
ENSG00000125148.6	MT2A	-4.8	-	-2.3	-
ENSG00000125266.6	EFNB2	-	-	-1.4	-1.7
ENSG00000125398.5	SOX9	-	-	1.0	-1.2
ENSG00000125538.11	IL1B	-3.2	-	-2.5	-
ENSG00000125730.16	C3	-2.9	-	-	-2.2
ENSG00000125740.13	FOSB	-2.6	-	-3.2	-2.3
ENSG00000125810.9	CD93	-2.4	-	-2.1	-2.6
ENSG00000125827.8	TMX4	-1.1	-	-	-1.1
ENSG00000125845.6	BMP2	-	-	-1.5	-3.3

ENSG00000125895.5	TMEM74B	2.2	-	-2.8	-
ENSG00000125968.8	ID1	-	-2.2	-2.3	-1.8
ENSG00000126016.13	AMOT	-	-1.4	1.1	-2.0
ENSG00000126218.11	F10	-6.1	-	-2.0	-
ENSG00000126351.12	THRA	-1.6	-	-1.0	-1.8
ENSG00000126458.3	RRAS	-2.0	-	-1.6	-
ENSG00000126561.16	STAT5A	-1.0	-	-	-2.2
ENSG00000126709.14	IFI6	-	-	1.1	1.9
ENSG00000126759.12	CFP	-2.1	-	-2.6	-
ENSG00000126785.12	RHOJ	-3.2	-	-2.0	-1.4
ENSG00000126803.9	HSPA2	-1.8	-1.0	-1.0	-
ENSG00000126895.13	AVPR2	-	-	-2.7	-2.3
ENSG00000126947.11	ARMCX1	-2.3	-1.6	-	-
ENSG00000127084.17	FGD3	-	-	-1.1	1.6
ENSG00000127241.16	MASP1	-5.5	-	-3.5	-
ENSG00000127329.14	PTPRB	-	-	-2.8	-1.6
ENSG00000127415.12	IDUA	1.2	-	-	1.3
ENSG00000127418.14	FGFRL1	-	1.3	-	-1.1
ENSG00000127528.5	KLF2	-4.4	-	-2.5	-1.4
ENSG00000127564.16	PKMYT1	1.9	-	1.6	3.1
ENSG00000127920.5	GNG11	-3.6	-	-2.4	-2.2
ENSG00000127951.5	FGL2	-4.2	-	-	-2.0
ENSG00000127954.12	STEAP4	-2.5	-	-	-1.4
ENSG00000127990.15	SGCE	-3.4	-	-1.5	-1.7
ENSG00000128016.5	ZFP36	-2.5	-	-2.2	-
ENSG00000128050.8	PAICS	1.1	-	1.1	-
ENSG00000128059.8	PPAT	1.1	-	1.3	-
ENSG00000128266.8	G-Z	-	-1.0	-	-2.4
ENSG00000128268.11	MGAT3	-	-	-2.4	-3.2
ENSG00000128283.6	CDC42EP1	-1.3	-	-	-1.1
ENSG00000128284.19	APOL3	-	-	-1.3	-1.2
ENSG00000128298.16	BAIAP2L2	1.7	-	-	1.2
ENSG00000128342.4	LIF	-1.9	-	-1.3	-
ENSG00000128346.10	C22orf23	-	-	-1.2	-1.2
ENSG00000128422.15	KRT17	-	-1.9	-	-1.8
ENSG00000128482.15	RNF112	-3.1	-	-1.5	-

ENSG00000128512.19	DOCK4	-1.5	-	-1.4	-1.4
ENSG00000128567.16	PODXL	-	-	-1.3	-1.9
ENSG00000128591.15	FLNC	-8.3	-1.2	-1.5	-2.4
ENSG00000128602.9	SMO	-2.0	-	-	-1.3
ENSG00000128606.12	LRRC17	-1.8	-	1.2	-
ENSG00000128849.10	CGNL1	-3.1	-	-1.7	-1.0
ENSG00000128917.6	DLL4	-	-	-1.9	-1.3
ENSG00000129009.12	ISLR	-5.0	-	-	-1.1
ENSG00000129235.10	TXNDC17	1.3	-	1.4	-
ENSG00000129244.8	ATP1B2	-3.4	-	-1.4	-
ENSG00000129250.11	KIF1C	-1.1	-	-1.3	-1.4
ENSG00000129295.8	LRRC6	-	-	1.2	1.0
ENSG00000129467.13	ADCY4	-1.8	-	-2.0	-1.0
ENSG00000129473.9	BCL2L2	-1.2	-	-	-1.4
ENSG00000129538.13	R-SE1	-2.8	-	-	-1.7
ENSG00000129596.4	CDO1	-6.7	-	-2.8	-3.6
ENSG00000129657.14	SEC14L1	-1.2	-	-1.1	-1.5
ENSG00000129680.15	MAP7D3	-1.4	-	-	-1.4
ENSG00000129757.12	CDKN1C	-2.4	-	-1.5	-2.3
ENSG00000129993.14	CBFA2T3	-1.6	-	-1.6	-
ENSG00000130052.13	STARD8	-2.0	-	-2.3	-1.6
ENSG00000130176.7	CNN1	-8.6	-1.1	-1.6	-2.1
ENSG00000130193.7	THEM6	1.2	-	1.3	-
ENSG00000130203.9	APOE	-2.3	1.2	-	-
ENSG00000130222.10	GADD45G	-3.6	-	-	2.2
ENSG00000130224.14	LRCH2	-2.6	-	-1.2	-
ENSG00000130300.8	PLVAP	-1.7	-	-	-1.4
ENSG00000130508.10	PXDN	-1.9	-	-	-1.3
ENSG00000130513.6	GDF15	-	-	2.5	2.2
ENSG00000130522.5	JUND	-2.0	-	-1.8	-
ENSG00000130558.18	OLFM1	-4.9	-	-1.2	-
ENSG00000130584.10	ZBTB46	-1.0	-	-	-1.1
ENSG00000130590.13	SAMD10	1.6	-	1.4	-
ENSG00000130635.15	COL5A1	-2.4	-	1.4	-
ENSG00000130701.3	RBBP8NL	1.9	-	-	1.6
ENSG00000130762.14	ARHGEF16	1.5	-	1.4	1.3

ENSG00000130775.15	THEMIS2	-2.4	-	-1.1	-
ENSG00000130830.14	MPP1	-2.9	-	-	-1.1
ENSG00000130844.16	ZNF331	-2.7	-	-2.3	-
ENSG00000130956.13	HABP4	-2.0	-	-	-1.5
ENSG00000130988.12	RGN	-3.5	-	-	-1.6
ENSG00000131016.16	AKAP12	-3.3	-	-2.1	-2.6
ENSG00000131018.22	SYNE1	-3.0	-	-	-1.1
ENSG00000131042.13	LILRB2	-2.2	-	-1.9	-
ENSG00000131055.4	COX4I2	-	-	-3.1	-1.7
ENSG00000131153.8	GIN52	2.0	-	-	1.6
ENSG00000131187.9	F12	2.4	-	2.0	2.3
ENSG00000131196.17	NFATC1	-2.2	-	-1.6	-1.9
ENSG00000131370.15	SH3BP5	-	-	-1.8	-1.3
ENSG00000131378.13	RFTN1	-1.5	-	-	-1.8
ENSG00000131409.12	LRRC4B	-	-	-2.2	-1.5
ENSG00000131435.12	PDLIM4	-1.9	-1.0	-	-
ENSG00000131459.12	GFPT2	-5.7	-	-1.4	-1.1
ENSG00000131471.6	AOC3	-4.2	-	-2.6	-3.9
ENSG00000131477.10	RAMP2	-2.2	-	-3.0	-1.1
ENSG00000131591.17	C1orf159	1.0	-	-	1.2
ENSG00000131711.14	MAP1B	-3.7	-	-	-1.6
ENSG00000131730.15	CKMT2	-2.3	-	-	-2.0
ENSG00000131746.12	TNS4	1.8	-2.1	2.1	-1.3
ENSG00000131747.14	TOP2A	3.3	1.7	2.4	2.9
ENSG00000131771.13	PPP1R1B	-	-	1.5	-1.3
ENSG00000131773.13	KHDRBS3	-2.0	-	-	-1.0
ENSG00000131831.17	RAI2	-3.2	-	-1.8	-
ENSG00000131873.5	CHSY1	-1.5	-	-	-1.1
ENSG00000132170.19	PPARG	-	-	-1.4	-3.3
ENSG00000132205.10	EMILIN2	-1.0	-	-	-2.1
ENSG00000132329.10	RAMP1	-4.9	-	1.7	1.5
ENSG00000132376.19	INPP5K	-	-	-1.1	-1.2
ENSG00000132386.10	SERPINF1	-3.5	-	-	-1.5
ENSG00000132470.13	ITGB4	1.1	-2.2	1.3	-
ENSG00000132613.14	MTSS1L	-	-1.0	-	-1.1
ENSG00000132622.10	HSPA12B	-3.3	-	-2.9	-2.2

ENSG00000132688.10	NES	-2.4	-	-2.4	-1.5
ENSG00000132698.13	RAB25	1.8	-	-	1.1
ENSG00000132718.8	SYT11	-3.1	-	-	-1.1
ENSG00000132746.14	ALDH3B2	-	2.6	3.9	-
ENSG00000132749.10	MTL5	2.0	-	-	1.6
ENSG00000132819.16	RBM38	-1.9	-1.2	-	-
ENSG00000132821.11	VSTM2L	-	1.5	1.9	-
ENSG00000132840.9	BHMT2	-5.3	-	-	-1.6
ENSG00000132854.18	KANK4	-	-	-1.5	-2.2
ENSG00000132965.9	ALOX5AP	-2.7	-	-	-1.1
ENSG00000132970.12	WASF3	-1.9	-	-1.4	-3.3
ENSG00000133056.13	PIK3C2B	1.2	-	-	-1.3
ENSG00000133083.14	DCLK1	-4.0	-	-	-1.4
ENSG00000133104.12	SPG20	-1.8	-	-	-1.6
ENSG00000133121.20	STARD13	-2.3	-	-1.7	-1.5
ENSG00000133138.19	TBC1D8B	-	1.5	1.0	1.3
ENSG00000133142.17	TCEAL4	-1.6	-	-	1.2
ENSG00000133169.5	BEX1	-	-1.7	-2.6	-
ENSG00000133195.11	SLC39A11	1.2	-	1.5	-
ENSG00000133392.16	MYH11	-7.7	-	-1.2	-1.8
ENSG00000133401.15	PDZD2	-	-	-2.0	-2.5
ENSG00000133466.13	C1QTNF6	-	-	1.2	1.2
ENSG00000133561.15	GIMAP6	-1.4	-	-1.8	-2.9
ENSG00000133574.9	GIMAP4	-2.2	-	-1.1	-1.5
ENSG00000133687.15	TMTC1	-2.9	-	-1.0	-2.3
ENSG00000133740.10	E2F5	1.1	-	1.2	-
ENSG00000133800.8	LYVE1	-5.7	-	-3.2	-4.0
ENSG00000133874.1	RNF122	-2.5	-	-2.2	-1.0
ENSG00000134030.13	CTIF	-	-	-1.1	-1.5
ENSG00000134057.14	CCNB1	2.0	-	1.8	1.5
ENSG00000134072.10	CAMK1	-1.4	-	-	-1.4
ENSG00000134121.9	CHL1	-	-	1.2	-3.2
ENSG00000134138.19	MEIS2	-1.9	-	-1.2	-1.2
ENSG00000134198.9	TSPAN2	-2.2	-	-1.1	-
ENSG00000134201.10	GSTM5	-5.3	-	-2.0	-3.9
ENSG00000134222.16	PSRC1	1.2	-	-	1.7

ENSG00000134245.17	WNT2B	-2.1	-	-1.3	-
ENSG00000134259.3	NGF	-3.6	-	-1.2	-
ENSG00000134317.17	GRHL1	1.5	-	1.5	-
ENSG00000134398.12	ERN2	2.4	-	3.9	-
ENSG00000134463.14	ECHDC3	-	-1.2	-	-1.5
ENSG00000134516.15	DOCK2	-2.0	-	-	-1.5
ENSG00000134531.9	EMP1	-3.4	-	-1.9	-3.1
ENSG00000134532.15	SOX5	-	-	-1.0	-2.3
ENSG00000134569.9	LRP4	-	-1.4	-1.4	-1.6
ENSG00000134668.12	SPOCD1	2.4	-	-	2.0
ENSG00000134690.10	CDCA8	2.3	-	1.9	2.0
ENSG00000134716.9	CYP2J2	-	1.3	1.7	-
ENSG00000134802.17	SLC43A3	-1.8	-	-	-1.6
ENSG00000134853.11	PDGFRA	-3.3	-	-	-1.9
ENSG00000134917.9	ADAMTS8	-3.7	-	-3.0	-
ENSG00000134954.14	ETS1	-	-	-1.3	-2.2
ENSG00000135046.13	ANXA1	-	-1.0	-1.2	-2.5
ENSG00000135047.14	CTSL	-1.7	-	-	-1.1
ENSG00000135048.13	TMEM2	-	-	-1.0	-1.3
ENSG00000135049.15	AGTPBP1	-	-	-1.2	-1.0
ENSG00000135052.16	GOLM1	-	1.2	2.3	-
ENSG00000135063.17	FAM189A2	-2.5	-	-2.0	-1.4
ENSG00000135111.14	TBX3	1.3	-	-2.9	-
ENSG00000135119.14	RNFT2	2.0	-	-	1.0
ENSG00000135218.17	CD36	-3.4	-	-2.6	-3.8
ENSG00000135318.11	NT5E	-	-	1.9	-2.3
ENSG00000135363.11	LMO2	-	-	-1.6	-1.4
ENSG00000135373.12	EHF	-	-	1.8	-1.7
ENSG00000135374.9	ELF5	-	-	1.8	-2.6
ENSG00000135424.15	ITGA7	-4.0	-	-	-3.2
ENSG00000135447.16	PPP1R1A	-	-1.0	-	-3.6
ENSG00000135451.12	TROAP	2.9	-	1.3	2.8
ENSG00000135476.11	ESPL1	2.7	-	-	1.7
ENSG00000135540.11	NHSL1	1.4	-	-1.0	-1.2
ENSG00000135549.14	PKIB	-	1.1	1.9	-
ENSG00000135604.9	STX11	-3.1	-	-2.8	-3.6

ENSG00000135636.13	DYSF	-2.2	-	-	-1.7
ENSG00000135678.11	CPM	-	-1.1	-	-1.9
ENSG00000135722.8	FBXL8	1.4	-	1.0	-
ENSG00000135750.14	KCNK1	-	-	1.0	1.5
ENSG00000135835.10	KIAA1614	-	-	-1.1	-2.1
ENSG00000135842.16	FAM129A	-4.0	-	-	-1.4
ENSG00000135862.5	LAMC1	-1.1	-	-	-2.5
ENSG00000135916.15	ITM2C	-	-1.4	-	-1.5
ENSG00000135917.13	SLC19A3	-	-	-2.5	-3.2
ENSG00000135919.12	SERPINE2	-2.3	-	1.2	-
ENSG00000135929.8	CYP27A1	-2.6	-1.3	-1.1	-
ENSG00000135951.14	TSGA10	1.2	1.1	-	-
ENSG00000135976.16	ANKRD36	-	1.5	-	1.7
ENSG00000136114.15	THSD1	-	-	-2.4	-1.3
ENSG00000136141.14	LRCH1	-1.4	-	-	-1.4
ENSG00000136143.13	SUCLA2	-1.0	-	-	-1.8
ENSG00000136158.10	SPRY2	-1.7	-	-	-3.0
ENSG00000136160.14	EDNRB	-2.9	-	-3.2	-3.4
ENSG00000136167.13	LCP1	-1.6	-	-	-1.3
ENSG00000136193.16	SCRN1	-1.2	-1.1	-	-1.1
ENSG00000136237.18	RAPGEF5	-	-	-1.3	-1.4
ENSG00000136244.11	IL6	-6.8	-	-4.5	-
ENSG00000136274.8	-CAD	-3.0	-	-1.2	-2.3
ENSG00000136425.12	CIB2	-	-1.7	-	-2.0
ENSG00000136457.9	CHAD	-	-	1.4	1.0
ENSG00000136546.13	SCN7A	-6.6	-	-2.0	-
ENSG00000136630.12	HLX	-1.4	-	-1.8	-
ENSG00000136717.14	BIN1	-3.6	-	-	-2.5
ENSG00000136732.14	GYPC	-4.5	-	-1.7	-2.5
ENSG00000136802.11	LRRC8A	-	-	-1.0	-1.3
ENSG00000136826.14	KLF4	-2.6	-	-3.3	-2.5
ENSG00000136840.18	ST6GAL-C4	-1.3	-1.2	-	-
ENSG00000136842.13	TMOD1	-4.7	-	-2.0	-2.8
ENSG00000136848.16	DAB2IP	-	-1.0	-1.3	-1.8
ENSG00000136854.17	STXBP1	-3.0	-	-	-1.8
ENSG00000136859.9	ANGPTL2	-3.4	-	-	-2.9

ENSG00000136883.12	KIF12	-	-	1.4	1.5
ENSG00000136960.12	ENPP2	-2.0	-	-1.5	-3.2
ENSG00000136997.14	MYC	-2.0	-	-1.8	-1.8
ENSG00000136999.4	NOV	-	-	-1.2	-1.5
ENSG00000137033.11	IL33	-	-	-1.4	-2.2
ENSG00000137054.15	POLR1E	-1.1	-	-	-1.3
ENSG00000137070.17	IL11RA	-1.4	-	-1.1	-1.2
ENSG00000137076.18	TLN1	-2.0	-	-1.0	-2.0
ENSG00000137077.7	CCL21	-6.0	-	-1.4	-1.5
ENSG00000137094.14	D-JB5	-4.0	-1.0	-	-
ENSG00000137124.6	ALDH1B1	-2.9	-	1.0	-
ENSG00000137193.13	PIM1	-	-	-1.2	-2.1
ENSG00000137203.10	TFAP2A	1.7	-	3.8	1.1
ENSG00000137267.5	TUBB2A	-2.3	-	-	-1.5
ENSG00000137331.11	IER3	-2.4	-1.3	-	1.5
ENSG00000137393.9	RNF144B	-	-	-1.1	-1.1
ENSG00000137460.8	FHDC1	-	-1.3	-1.0	-
ENSG00000137486.16	ARRB1	-1.8	-	-1.4	-1.0
ENSG00000137491.14	SLCO2B1	-2.2	-	-	-1.4
ENSG00000137507.11	LRRC32	-3.0	-	-2.4	-1.8
ENSG00000137573.13	SULF1	-3.0	-	2.4	-
ENSG00000137648.16	TMPRSS4	2.0	-	4.6	-
ENSG00000137672.12	TRPC6	-	-	-1.2	-1.6
ENSG00000137673.8	MMP7	-	-	2.6	-1.3
ENSG00000137699.16	TRIM29	-	-2.6	-	-1.9
ENSG00000137726.15	FXYP6	-4.9	-	-2.3	-1.3
ENSG00000137801.10	THBS1	-3.3	-	-1.3	-1.5
ENSG00000137804.12	NUSAP1	2.1	1.5	1.3	1.8
ENSG00000137807.13	KIF23	1.7	-	-	1.7
ENSG00000137809.16	ITGA11	-2.8	-	2.9	-
ENSG00000137834.14	SMAD6	-	-	-2.6	-1.5
ENSG00000137857.17	DUOX1	-	-2.2	-2.0	-
ENSG00000137868.18	STRA6	2.1	-	3.2	-
ENSG00000137872.15	SEMA6D	-	-	-2.1	-2.1
ENSG00000137878.16	GCOM1	-	-	-2.8	-2.4
ENSG00000137941.16	TTLL7	-1.8	-	-1.8	-

ENSG00000138061.11	CYP1B1	-3.9	-	1.2	-1.1
ENSG00000138135.6	CH25H	-4.9	-	-1.6	-
ENSG00000138172.10	CALHM2	-1.7	-	-1.0	-
ENSG00000138180.15	CEP55	2.2	-	1.5	-
ENSG00000138182.14	KIF20B	1.1	-	-	1.1
ENSG00000138207.12	RBP4	-6.5	-	-1.8	-4.0
ENSG00000138346.14	D-2	1.4	-	1.3	1.3
ENSG00000138356.13	AOX1	-7.6	-2.0	-1.5	-2.9
ENSG00000138411.10	HECW2	-	-	-1.7	-1.3
ENSG00000138413.13	IDH1	-	-	1.0	-1.3
ENSG00000138639.17	ARHGAP24	-2.2	-	-	-1.6
ENSG00000138641.15	HERC3	-1.3	-	-	-1.5
ENSG00000138678.10	AGPAT9	-2.6	-	-1.2	-2.5
ENSG00000138685.12	FGF2	-4.0	-	-1.9	-3.1
ENSG00000138722.9	MMRN1	-4.3	-	-1.8	-
ENSG00000138735.15	PDE5A	-2.8	-	-1.7	-
ENSG00000138772.12	ANXA3	-	-	-1.5	-1.1
ENSG00000138778.11	CENPE	2.2	-	-	3.0
ENSG00000138821.12	SLC39A8	-	-	-2.1	-1.1
ENSG00000139112.10	GABARAPL1	-2.6	-	-1.3	-2.1
ENSG00000139117.13	CPNE8	-1.4	-	-	-1.5
ENSG00000139180.10	NDUFA9	1.4	1.0	-	-
ENSG00000139263.11	LRIG3	-	-	1.6	-1.9
ENSG00000139278.9	GLIPR1	-2.7	-	-	-1.1
ENSG00000139567.12	ACVRL1	-2.2	-	-2.7	-2.1
ENSG00000139629.15	GALNT6	-	-	1.5	1.3
ENSG00000139865.16	TTC6	-	1.2	-	1.5
ENSG00000139946.9	PELI2	-2.1	-	-	-2.1
ENSG00000139970.16	RTN1	-1.8	-	-1.5	-1.8
ENSG00000139974.15	SLC38A6	-	1.1	-	1.2
ENSG00000140022.9	STON2	1.6	-	-	-1.1
ENSG00000140044.12	JDP2	-2.0	-	-1.5	-
ENSG00000140092.14	FBLN5	-4.6	-	-1.5	-2.0
ENSG00000140105.17	WARS	-	-	-1.3	-1.0
ENSG00000140254.12	DUOXA1	-	-2.6	-1.7	-
ENSG00000140263.13	SORD	1.5	-	1.3	-

ENSG00000140285.9	FGF7	-4.8	-	-	-1.7
ENSG00000140287.10	HDC	-4.5	-	-1.2	-
ENSG00000140398.13	NEIL1	-	1.2	-	1.0
ENSG00000140451.12	PIF1	1.7	-	-	1.1
ENSG00000140525.17	FANCI	1.8	-	-	1.1
ENSG00000140538.16	NTRK3	-6.0	-	-1.3	-
ENSG00000140545.14	MFGE8	-2.6	-	-	-1.9
ENSG00000140682.18	TGFB1I1	-4.0	-	-1.0	-1.0
ENSG00000140832.9	MARVELD3	1.2	-	1.4	-
ENSG00000140941.12	MAP1LC3B	-1.2	-	-	-1.1
ENSG00000140945.15	CDH13	-	-	-1.8	-1.8
ENSG00000140968.10	IRF8	-2.8	-	-	-2.1
ENSG00000141338.13	ABCA8	-2.9	-	-2.1	-1.6
ENSG00000141404.15	G-L	-2.2	-	-	-1.2
ENSG00000141447.16	OSBPL1A	-1.4	-	-	-1.5
ENSG00000141448.8	GATA6	-3.6	-	-1.9	-1.5
ENSG00000141469.16	SLC14A1	-	-2.0	-2.0	-
ENSG00000141519.14	CCDC40	-	1.0	-	1.1
ENSG00000141527.16	CARD14	1.4	-	1.6	-
ENSG00000141570.10	CBX8	1.1	-	-	1.4
ENSG00000141576.14	RNF157	-	1.5	-	-1.4
ENSG00000141579.6	ZNF750	-	-2.2	-	-1.2
ENSG00000141750.6	STAC2	-	-1.0	-	-1.8
ENSG00000141934.9	PPAP2C	1.2	-	2.6	-
ENSG00000142192.20	APP	-1.2	-	-	-1.4
ENSG00000142227.10	EMP3	-4.2	-	-1.4	-
ENSG00000142252.10	GEMIN7	1.4	-	-	1.2
ENSG00000142273.10	CBLC	1.8	-	2.9	1.4
ENSG00000142583.17	SLC2A5	-	-2.9	1.3	-
ENSG00000142627.12	EPHA2	-	-1.7	-	-2.1
ENSG00000142632.16	ARHGEF19	2.0	-1.3	1.5	-
ENSG00000142675.17	CNKSR1	1.9	-	-	1.1
ENSG00000142731.10	PLK4	2.0	-	1.1	-
ENSG00000142748.12	FCN3	-	-	-5.2	-1.8
ENSG00000142871.15	CYR61	-5.0	-	-1.4	-1.5
ENSG00000142910.15	TI-GL1	-	-	-1.2	-2.0

ENSG00000142945.12	KIF2C	2.5	-	1.8	-
ENSG00000142973.12	CYP4B1	-	-2.7	-2.2	-
ENSG00000143110.11	C1orf162	-2.4	-	-1.2	-
ENSG00000143153.12	ATP1B1	1.9	-1.1	1.5	-
ENSG00000143196.4	DPT	-9.4	-	-2.2	-3.9
ENSG00000143248.12	RGS5	-2.2	-	-	-2.0
ENSG00000143320.8	CRABP2	-	-2.6	3.6	1.9
ENSG00000143344.15	RGL1	-2.2	-	-	-2.4
ENSG00000143369.14	ECM1	-1.8	-	-	2.1
ENSG00000143382.13	ADAMTSL4	-3.3	-	-1.6	-1.8
ENSG00000143384.12	MCL1	-1.5	-	-	-1.1
ENSG00000143479.15	DYRK3	-2.5	-	-	-1.1
ENSG00000143578.15	CREB3L4	-	-	1.2	1.6
ENSG00000143590.13	EF-3	1.5	-	2.1	1.5
ENSG00000143630.9	HCN3	1.9	-	-	1.0
ENSG00000143772.9	ITPKB	-1.7	-	-1.0	-1.9
ENSG00000143867.6	OSR1	-	-	-1.6	-2.1
ENSG00000143878.9	RHOB	-2.0	-1.1	-1.6	-
ENSG00000143995.19	MEIS1	-1.6	-	-1.4	-
ENSG00000144031.11	ANKRD53	-2.9	-	-1.2	-2.3
ENSG00000144218.18	AFF3	-3.5	-	-1.6	-
ENSG00000144230.16	GPR17	-	-	-2.9	-1.6
ENSG00000144331.18	ZNF385B	-5.2	-	-1.1	-
ENSG00000144476.5	ACKR3	-2.3	-	-1.7	-1.6
ENSG00000144485.10	HES6	-	-	1.1	1.4
ENSG00000144642.20	RBMS3	-2.5	-	-1.0	-2.5
ENSG00000144655.14	CSRNP1	-2.8	-	-2.9	-1.9
ENSG00000144668.11	ITGA9	-2.9	-	-	-2.2
ENSG00000144681.10	STAC	-3.8	-	-1.3	-2.3
ENSG00000144712.11	CAND2	-	-1.0	-	-1.1
ENSG00000144724.18	PTPRG	-1.0	-	-	-2.1
ENSG00000144749.13	LRIG1	-2.6	-	-	-1.5
ENSG00000144824.19	PHLDB2	-	-	-1.4	-1.3
ENSG00000144843.11	ADPRH	-2.2	-	-1.2	-1.9
ENSG00000144857.14	BOC	-4.8	-	-	-2.3
ENSG00000144891.17	AGTR1	-2.6	1.1	-2.6	-1.2

ENSG00000144908.13	ALDH1L1	-	-	1.5	-3.2
ENSG00000144935.14	TRPC1	-2.3	-	-	-1.1
ENSG00000145147.19	SLIT2	-5.8	-	-2.4	-2.2
ENSG00000145247.11	OCIAD2	1.4	-	2.3	-
ENSG00000145284.11	SCD5	-1.9	-	-1.2	-
ENSG00000145335.15	SNCA	-2.5	-	-1.3	-1.6
ENSG00000145349.16	CAMK2D	-1.0	-	-	-1.6
ENSG00000145362.16	ANK2	-4.2	-	-1.2	-2.4
ENSG00000145386.9	CC-2	2.0	1.6	1.3	-
ENSG00000145391.13	SETD7	-1.6	-	-	-1.7
ENSG00000145423.4	SFRP2	-8.0	-	2.1	1.1
ENSG00000145431.10	PDGFC	-2.6	-	1.0	-1.9
ENSG00000145623.12	OSMR	-2.3	-	-	-1.1
ENSG00000145730.20	PAM	-2.7	-	-	-1.9
ENSG00000145861.7	C1QTNF2	-4.1	-	-2.5	-
ENSG00000145911.5	N4BP3	-	-	-1.6	1.2
ENSG00000145990.10	GFOD1	-1.6	-	-2.1	-1.0
ENSG00000146072.6	TNFRSF21	-	-1.0	1.3	-2.5
ENSG00000146122.16	DAAM2	-2.6	-	-	-2.4
ENSG00000146278.10	PNRC1	-1.8	-	-1.1	-1.4
ENSG00000146350.13	TBC1D32	1.3	-	-	1.4
ENSG00000146374.13	RSPO3	-6.3	-	-1.2	-1.7
ENSG00000146535.13	G-12	-1.7	-	-	-1.6
ENSG00000146555.18	SDK1	-	1.8	-	-2.8
ENSG00000146592.16	CREB5	-4.5	-	-1.3	-2.1
ENSG00000146670.9	CDCA5	1.6	-	1.5	1.5
ENSG00000146674.14	IGFBP3	-	-	1.5	-1.1
ENSG00000146859.6	TMEM140	-1.1	-	-	-2.1
ENSG00000146966.12	DENND2A	-2.6	-	-2.1	-1.6
ENSG00000147027.3	TMEM47	-	-	-1.3	-2.4
ENSG00000147065.16	MSN	-2.0	-	-	-1.7
ENSG00000147100.9	SLC16A2	-2.4	-1.1	-	-1.5
ENSG00000147113.16	CXorf36	-2.2	-	-2.0	-2.0
ENSG00000147119.3	CHST7	-2.3	-	-	-2.2
ENSG00000147251.15	DOCK11	-2.5	-	-	-3.5
ENSG00000147257.13	GPC3	-2.1	-	-2.7	-3.9

ENSG00000147408.14	CSGAL-CT1	-3.6	-	-	-1.2
ENSG00000147443.12	DOK2	-2.2	-	-1.3	-1.7
ENSG00000147526.19	TACC1	-1.3	-	-1.4	-2.3
ENSG00000147689.16	FAM83A	3.4	-	5.3	-
ENSG00000147799.11	ARHGAP39	1.6	-	1.2	-
ENSG00000147804.9	SLC39A4	1.3	-	1.4	-
ENSG00000147862.14	NFIB	-1.5	-	-	-2.1
ENSG00000147889.16	CDKN2A	-	-	1.4	1.1
ENSG00000148053.15	NTRK2	-3.6	-1.1	-	-2.7
ENSG00000148180.16	GSN	-3.8	-	-	-3.1
ENSG00000148339.12	SLC25A25	-2.0	-	-2.2	-2.1
ENSG00000148346.11	LCN2	3.3	-1.7	1.6	-
ENSG00000148400.9	NOTCH1	-	-1.2	-1.4	-2.1
ENSG00000148411.7	-CC2	-2.1	-	-1.2	-1.9
ENSG00000148468.16	FAM171A1	-1.4	-	-1.0	-2.0
ENSG00000148516.21	ZEB1	-3.1	-	-	-1.3
ENSG00000148541.12	FAM13C	-2.4	-	-1.5	-2.0
ENSG00000148735.14	PLEKHS1	-	1.4	2.6	-1.2
ENSG00000148773.12	MKI67	2.5	-	1.7	2.4
ENSG00000148824.18	MTG1	1.8	1.4	-	1.3
ENSG00000148841.15	ITPRIP	-2.2	-	-1.9	-1.5
ENSG00000149090.11	PAMR1	-3.9	-	-	-3.0
ENSG00000149131.15	SERPING1	-3.3	-	-1.4	-1.5
ENSG00000149218.4	ENDOD1	-1.8	-	1.0	-1.5
ENSG00000149256.14	TENM4	-	-	1.9	-1.9
ENSG00000149260.14	CAPN5	-	-	1.3	-1.4
ENSG00000149269.9	PAK1	-	-	1.0	1.5
ENSG00000149294.16	NCAM1	-6.6	-	-1.2	-3.2
ENSG00000149380.11	P4HA3	-	-	1.6	1.7
ENSG00000149451.17	ADAM33	-6.5	-	-2.2	-1.6
ENSG00000149554.12	CHEK1	1.5	-	1.3	-
ENSG00000149557.12	FEZ1	-1.7	-	-1.8	-
ENSG00000149564.11	ESAM	-	-	-2.3	-1.7
ENSG00000149573.8	MPZL2	-	-1.3	1.5	-
ENSG00000149591.16	TAGLN	-6.3	-	-	-1.2
ENSG00000149596.6	JPH2	-4.8	-1.2	-1.5	-2.9

ENSG00000149599.15	DUSP15	-	-1.0	-	1.1
ENSG00000149798.4	CDC42EP2	-1.5	-	-2.3	-1.9
ENSG00000149823.7	VPS51	-1.2	-	-	-1.3
ENSG00000149922.10	TBX6	1.8	-	1.9	-
ENSG00000150048.10	CLEC1A	-2.7	-	-1.9	-
ENSG00000150281.6	CTF1	-	-1.7	-	-1.3
ENSG00000150457.8	LATS2	-2.4	-	-1.3	-1.9
ENSG00000150477.14	KIAA1328	-	1.5	-	1.7
ENSG00000150510.15	FAM124A	-	-1.3	-2.0	-1.2
ENSG00000150551.10	LYPD1	3.3	-	2.5	-
ENSG00000150594.6	ADRA2A	-3.9	-	-	-2.7
ENSG00000150630.3	VEGFC	-1.4	-	-1.3	-1.3
ENSG00000150636.15	CCDC102B	-1.5	-	-1.4	-
ENSG00000150764.13	DIXDC1	-3.8	-	-	-1.7
ENSG00000150907.6	FOXO1	-	-	-1.0	-2.5
ENSG00000150938.9	CRIM1	-1.0	-	-1.4	-2.8
ENSG00000150995.17	ITPR1	-2.0	-	-	-1.5
ENSG00000151338.18	MIPOL1	-	1.5	-	1.5
ENSG00000151364.15	KCTD14	-	-	1.3	-1.7
ENSG00000151388.10	ADAMTS12	-	-	1.1	-1.1
ENSG00000151414.14	NEK7	-1.0	-	-	-1.7
ENSG00000151468.10	CCDC3	-2.0	-	-	-3.3
ENSG00000151491.12	EPS8	-	-	1.2	-2.2
ENSG00000151623.14	NR3C2	-2.2	-	-	-2.9
ENSG00000151689.12	INPP1	-	-	-1.0	-1.4
ENSG00000151702.16	FLI1	-2.1	-	-1.6	-1.6
ENSG00000151718.15	WWC2	-	-	-1.8	-1.0
ENSG00000151725.11	CENPU	2.1	-	1.4	2.4
ENSG00000151835.13	SACS	-2.8	-	-	-2.0
ENSG00000152049.6	KCNE4	-2.5	-	-	1.2
ENSG00000152102.17	FAM168B	-1.1	-	-	-1.7
ENSG00000152137.6	HSPB8	-4.1	-1.2	-2.0	-
ENSG00000152217.16	SETBP1	-1.8	-	-1.0	-
ENSG00000152284.4	TCF7L1	-2.6	-	-1.1	-1.4
ENSG00000152484.13	USP12	-1.4	-	-	-1.2
ENSG00000152518.6	ZFP36L2	-	-1.0	-1.1	-1.6

ENSG00000152527.13	PLEKHH2	-1.7	-	-1.6	-
ENSG00000152580.8	IGSF10	-4.8	-	-2.6	-3.1
ENSG00000152582.12	SPEF2	-1.9	-	-	1.1
ENSG00000152583.12	SPARCL1	-4.2	-	-1.8	-1.6
ENSG00000152601.17	MBNL1	-1.4	-	-	-1.7
ENSG00000152642.10	GPD1L	-	-1.0	-	-1.5
ENSG00000152669.8	CCNO	-	-	2.9	1.9
ENSG00000152784.15	PRDM8	-3.4	-2.8	-	-
ENSG00000152818.18	UTRN	-1.7	-	-	-1.9
ENSG00000152926.14	ZNF117	1.7	-	1.6	-
ENSG00000152952.11	PLOD2	-	-	1.3	-1.7
ENSG00000153071.14	DAB2	-1.9	-	-	-1.7
ENSG00000153162.8	BMP6	-	-	-2.2	-3.5
ENSG00000153179.11	RASSF3	-2.5	-	-	-1.8
ENSG00000153234.13	NR4A2	-2.5	-	-2.9	-
ENSG00000153246.11	PLA2R1	1.4	-	-	-1.2
ENSG00000153291.15	SLC25A27	-1.9	1.4	-	-
ENSG00000153446.15	C16orf89	-6.1	-1.3	1.4	-1.3
ENSG00000153814.11	JAZF1	-3.0	-	-	-1.6
ENSG00000153823.18	PID1	-5.0	-	-1.8	-3.3
ENSG00000153902.13	LGI4	-3.7	-	-2.0	-2.3
ENSG00000153956.15	CAC-2D1	-3.3	-	-	-2.3
ENSG00000154027.18	AK5	-	1.1	-	-2.0
ENSG00000154065.16	ANKRD29	-5.2	-	-2.7	-1.3
ENSG00000154133.14	ROBO4	-1.8	-	-3.4	-2.4
ENSG00000154175.16	ABI3BP	-4.7	-	-2.2	-2.0
ENSG00000154188.9	ANGPT1	-	-	-1.8	-2.5
ENSG00000154258.16	ABCA9	-	-	-1.6	-1.1
ENSG00000154262.12	ABCA6	-	1.1	-1.2	-1.4
ENSG00000154263.17	ABCA10	-	1.1	-1.4	-1.4
ENSG00000154330.12	PGM5	-7.2	-1.1	-1.7	-2.6
ENSG00000154359.12	LONRF1	-1.3	-	-1.1	-1.4
ENSG00000154511.11	FAM69A	-1.8	-	-	-1.7
ENSG00000154529.14	CNT-P3B	-	-	-1.6	-1.6
ENSG00000154553.13	PDLIM3	-6.0	-	-1.0	-1.2
ENSG00000154678.16	PDE1C	-3.3	-	-2.6	-

ENSG00000154721.14	JAM2	-4.1	-	-2.1	-1.2
ENSG00000154734.14	ADAMTS1	-4.3	-	-2.4	-2.8
ENSG00000154783.10	FGD5	-	-	-2.1	-1.9
ENSG00000154813.9	DPH3	-1.0	-	-	-1.4
ENSG00000154822.15	PLCL2	-2.2	-	-	-2.8
ENSG00000154856.12	APCDD1	-1.5	-	-	-2.3
ENSG00000154920.14	EME1	-	-	1.4	2.3
ENSG00000155016.17	CYP2U1	-1.7	-	-	-2.3
ENSG00000155066.15	PROM2	-	-1.0	3.3	-
ENSG00000155090.14	KLF10	-1.7	-1.1	-1.4	-2.0
ENSG00000155099.7	TMEM55A	-1.8	-	-	-1.7
ENSG00000155254.12	MARVELD1	-1.7	-1.0	-	-1.5
ENSG00000155324.9	GRAMD3	-	-	1.5	-1.4
ENSG00000155380.11	SLC16A1	-1.8	-	-	-2.0
ENSG00000155659.14	VSIG4	-3.6	-	-1.6	-2.0
ENSG00000155760.2	FZD7	-2.9	-	-	-2.4
ENSG00000155761.13	SPAG17	2.8	-	-	1.9
ENSG00000155846.16	PPARGC1B	-	-	-1.0	-1.5
ENSG00000155849.15	ELMO1	-2.1	-	-1.3	-
ENSG00000155850.7	SLC26A2	-	-	-1.1	-1.4
ENSG00000155876.5	RRAGA	-1.1	-	-	-1.0
ENSG00000155962.12	CLIC2	-1.9	-	-	-1.6
ENSG00000156076.9	WIF1	-	-1.7	-3.2	-
ENSG00000156218.12	ADAMTSL3	-	-	-1.8	1.7
ENSG00000156298.12	TSPAN7	-3.4	-	-2.5	-1.8
ENSG00000156802.12	ATAD2	-	-	1.5	1.0
ENSG00000156804.7	FBXO32	-2.3	-	2.3	-1.4
ENSG00000156876.9	SASS6	1.1	-	-	1.2
ENSG00000156970.12	BUB1B	2.8	-	1.7	1.7
ENSG00000157150.4	TIMP4	-	-1.7	-	-4.7
ENSG00000157240.3	FZD1	-1.9	-1.2	-	-2.0
ENSG00000157368.10	IL34	-	-	-1.5	-1.8
ENSG00000157388.13	CAC-1D	-	1.9	-1.1	1.5
ENSG00000157456.7	CCNB2	1.6	-	1.5	-
ENSG00000157510.13	AFAP1L1	-	-	-2.1	-2.2
ENSG00000157514.16	TSC22D3	-2.6	-1.2	-	-

ENSG00000157554.18	ERG	-2.4	2.1	-1.9	-2.2
ENSG00000157557.11	ETS2	-	-1.3	-1.2	-1.3
ENSG00000157570.11	TSPAN18	-	-	-2.2	-1.9
ENSG00000157613.10	CREB3L1	-2.2	-	-	1.5
ENSG00000157734.13	SNX22	-	1.5	-1.9	-
ENSG00000157827.19	FMNL2	-1.0	-	-	-2.0
ENSG00000157927.16	RADIL	-	-	-3.3	-1.1
ENSG00000157933.9	SKI	-1.2	-	-	-1.9
ENSG00000158050.4	DUSP2	-	-1.1	-2.2	-
ENSG00000158089.14	GALNT14	3.1	-1.3	2.1	-
ENSG00000158106.12	RHPN1	2.4	1.1	2.1	2.6
ENSG00000158125.9	XDH	2.7	-	4.7	-
ENSG00000158186.12	MRAS	-2.7	-	-1.1	-3.3
ENSG00000158246.7	FAM46B	-3.3	-1.2	-1.9	-
ENSG00000158292.6	GPR153	-	-	-1.5	-1.3
ENSG00000158301.18	GPRASP2	-1.6	-	-	-2.2
ENSG00000158352.15	SHROOM4	-	-	-1.7	-1.4
ENSG00000158373.8	HIST1H2BD	-	-	2.3	2.0
ENSG00000158458.19	NRG2	-	-1.4	-	-3.1
ENSG00000158517.13	NCF1	-2.7	-	-1.3	-
ENSG00000158555.14	GDPD5	-2.0	-	-	-1.8
ENSG00000158747.13	NBL1	-1.8	-1.1	-	-
ENSG00000158792.15	SPATA2L	-1.1	-	-1.1	-
ENSG00000158887.15	MPZ	-2.6	-1.2	-	-3.0
ENSG00000158966.13	CACHD1	-1.1	-	-	-2.3
ENSG00000159079.18	C21orf59	1.0	-	-	1.1
ENSG00000159167.11	STC1	-2.7	-	-1.1	-
ENSG00000159176.13	CSRP1	-4.0	-	-1.0	-1.3
ENSG00000159200.17	RCAN1	-3.1	-	-1.5	-1.7
ENSG00000159214.12	CCDC24	1.3	-	-	1.7
ENSG00000159403.15	C1R	-3.7	-	-	-1.4
ENSG00000159433.11	STARD9	-3.1	-	-2.0	-
ENSG00000159674.11	SPON2	-2.9	1.9	-	-
ENSG00000159713.10	TPPP3	-	-	-1.3	-1.2
ENSG00000159840.15	ZYX	-1.6	-	-1.1	-
ENSG00000159884.11	CCDC107	-2.8	-	-	-1.0

ENSG00000159915.12	ZNF233	-	1.2	-	1.1
ENSG00000160013.8	PTGIR	-1.9	-	-1.7	-
ENSG00000160111.12	CPAMD8	-	-1.6	-	-1.9
ENSG00000160180.15	TFF3	-	1.7	1.8	1.6
ENSG00000160182.2	TFF1	-	-2.3	-	2.4
ENSG00000160183.13	TMPRSS3	-	-	1.3	1.2
ENSG00000160233.7	LRRC3	-	-	-1.2	-1.5
ENSG00000160255.16	ITGB2	-2.1	-	-	-1.0
ENSG00000160284.14	SPATC1L	-	-1.1	-	1.1
ENSG00000160298.17	C21orf58	1.8	-	-	1.7
ENSG00000160307.9	S100B	-3.4	-	1.8	-3.8
ENSG00000160352.15	ZNF714	1.6	-	-	1.0
ENSG00000160360.11	GPSM1	-1.1	-	-1.6	-
ENSG00000160408.14	ST6GAL-C6	-1.9	-	-	-2.0
ENSG00000160539.4	PPAPDC3	-4.2	-	-	-2.1
ENSG00000160593.17	AMICA1	-2.2	-	-	-1.1
ENSG00000160606.10	TLCD1	-	-	1.3	1.5
ENSG00000160712.12	IL6R	-1.7	-	-	-1.5
ENSG00000160781.15	PAQR6	-	2.5	-	2.6
ENSG00000160789.19	LM-	-1.2	-1.1	-1.2	-
ENSG00000160801.13	PTH1R	-3.6	-	-2.4	-2.3
ENSG00000160867.14	FGFR4	-	-	-3.2	1.7
ENSG00000160888.6	IER2	-1.5	-	-1.1	-
ENSG00000160949.16	TONSL	1.9	-	1.3	1.3
ENSG00000160957.12	RECQL4	1.8	-1.5	1.7	2.3
ENSG00000160972.9	PPP1R16A	1.0	-	-	1.4
ENSG00000160973.7	FOXH1	2.8	-	2.4	1.9
ENSG00000161055.3	SCGB3A1	-	-2.3	4.1	-1.5
ENSG00000161281.10	COX7A1	-4.5	-	-1.8	-1.4
ENSG00000161544.9	CYGB	-2.5	-	-1.2	-2.2
ENSG00000161638.10	ITGA5	-4.2	-	-1.4	-
ENSG00000161647.18	MPP3	-	-	-1.1	1.1
ENSG00000161649.12	CD300LG	-	-	-4.6	-3.8
ENSG00000161798.6	AQP5	-	-	2.3	-2.3
ENSG00000161835.10	GRASP	-3.9	-	-2.9	-1.1
ENSG00000161888.11	SPC24	2.1	-	1.2	-

ENSG00000161940.10	BCL6B	-2.3	-	-2.4	-2.0
ENSG00000161958.10	FGF11	2.7	-	2.3	-
ENSG00000162062.14	C16orf59	2.4	-	2.3	2.5
ENSG00000162063.12	CCNF	1.6	-	1.2	-
ENSG00000162069.14	CCDC64B	1.3	-	1.5	1.5
ENSG00000162407.8	PPAP2B	-3.2	-	-1.5	-3.0
ENSG00000162433.14	AK4	-	-	1.7	-2.0
ENSG00000162444.11	RBP7	-4.0	-	-	-2.2
ENSG00000162493.16	PDPN	-3.1	-1.4	-	-
ENSG00000162512.15	SDC3	-1.5	-	-	-1.5
ENSG00000162520.14	SYNC	-4.4	-	-1.4	-1.3
ENSG00000162551.13	ALPL	-	-1.2	-	-2.4
ENSG00000162599.15	NFIA	-1.5	-	-	-1.0
ENSG00000162614.18	NEXN	-4.0	-	-1.2	-
ENSG00000162616.8	D-JB4	-2.4	-	-1.2	-1.4
ENSG00000162618.12	ADGRL4	-2.2	-	-	-2.3
ENSG00000162692.10	VCAM1	-3.2	-	-	-1.9
ENSG00000162706.12	CADM3	-9.0	-	-1.2	-1.8
ENSG00000162733.16	DDR2	-4.4	-	-	-3.3
ENSG00000162747.9	FCGR3B	-3.6	-	-2.5	-
ENSG00000162772.16	ATF3	-2.1	-	-2.3	-
ENSG00000162804.13	SNED1	-3.2	-	-	-1.1
ENSG00000162817.6	C1orf115	-	-	-1.9	-1.6
ENSG00000162836.11	ACP6	1.6	-	1.1	-
ENSG00000162849.15	KIF26B	-	-	3.2	1.4
ENSG00000162878.12	PKDCC	-5.8	-	-1.5	-2.8
ENSG00000162882.14	HAAO	-3.0	-1.2	-	-
ENSG00000162896.5	PIGR	1.9	-	2.1	-4.0
ENSG00000162998.4	FRZB	-1.3	-	-	-1.4
ENSG00000163017.13	ACTG2	-7.6	-	-1.5	-2.4
ENSG00000163069.12	SGCB	-2.2	-	-1.0	-1.1
ENSG00000163071.10	SPATA18	-	-1.2	-	-1.3
ENSG00000163083.5	INHBB	-1.9	-	-	-1.7
ENSG00000163132.6	MSX1	-2.9	-	-1.6	-1.3
ENSG00000163141.18	BNIPL	-	-1.9	-	1.3
ENSG00000163145.12	C1QTNF7	-4.7	-	-1.7	-

ENSG00000163171.7	CDC42EP3	-2.4	-	-	-1.3
ENSG00000163220.10	S100A9	-	-1.3	-	-2.3
ENSG00000163235.15	TGFA	-	-	1.3	-2.0
ENSG00000163239.12	TDRD10	-	-	-1.3	-1.2
ENSG00000163297.16	ANTXR2	-2.7	-	-	-2.6
ENSG00000163362.10	C1orf106	1.7	-2.0	2.0	-
ENSG00000163378.13	EOGT	-	-	-1.1	-1.5
ENSG00000163412.12	EIF4E3	-1.2	-	-	-1.9
ENSG00000163430.9	FSTL1	-2.7	-	-	-2.2
ENSG00000163431.12	LMOD1	-6.3	-	-1.3	-2.1
ENSG00000163462.17	TRIM46	-	-	1.3	1.3
ENSG00000163463.11	KRTCAP2	1.7	1.0	-	-
ENSG00000163512.13	AZI2	-1.1	-	-	-1.4
ENSG00000163513.17	TGFBR2	-1.4	-	-1.3	-3.3
ENSG00000163520.13	FBLN2	-5.7	-	-	-2.4
ENSG00000163531.15	NFASC	-3.3	-	-1.7	-1.0
ENSG00000163563.7	MNDA	-3.0	-	-1.2	-
ENSG00000163637.11	PRICKLE2	-2.3	-	-1.3	-1.6
ENSG00000163638.13	ADAMTS9	-2.7	-	-1.7	-2.1
ENSG00000163659.12	TIPARP	-1.9	-	-	-1.4
ENSG00000163686.13	ABHD6	-	-	-1.6	-2.1
ENSG00000163687.13	D-SE1L3	-4.0	-	-2.5	-2.1
ENSG00000163710.7	PCOLCE2	-6.9	-	-1.6	-3.8
ENSG00000163762.6	TM4SF18	-1.5	-	-	-1.6
ENSG00000163788.13	SNRK	-	-	-1.4	-1.3
ENSG00000163794.6	UCN	-	1.7	-	1.8
ENSG00000163814.7	CDCP1	1.7	-	1.0	-
ENSG00000163815.5	CLEC3B	-6.3	-1.3	-3.7	-3.1
ENSG00000163820.14	FYCO1	-1.3	-	-	-1.7
ENSG00000163884.3	KLF15	-	-	-1.8	-3.8
ENSG00000163909.7	HEYL	-1.9	-	-1.4	-
ENSG00000163993.6	S100P	-	-2.0	2.5	2.6
ENSG00000164023.14	SGMS2	-1.8	-	-	-1.8
ENSG00000164035.9	EMCN	-3.2	-	-2.4	-1.5
ENSG00000164038.14	SLC9B2	-2.3	-	-	-1.1
ENSG00000164056.10	SPRY1	-2.3	-	-	-2.1

ENSG00000164078.12	MST1R	2.7	-	-	1.4
ENSG00000164086.9	DUSP7	-	-	-1.1	-1.3
ENSG00000164096.12	C4orf3	-1.3	-	-	-1.5
ENSG00000164111.14	ANXA5	-2.0	-	-	-1.0
ENSG00000164116.16	GUCY1A3	-2.0	-	-	-1.9
ENSG00000164125.15	FAM198B	-1.8	-	-	-1.7
ENSG00000164221.12	CCDC112	-	1.0	-	1.1
ENSG00000164241.13	C5orf63	1.3	1.0	-	-
ENSG00000164294.13	GPX8	-1.7	-	1.1	-
ENSG00000164330.16	EBF1	-3.1	-	-	-3.0
ENSG00000164442.9	CITED2	-1.4	-	-	-1.6
ENSG00000164530.13	PI16	-10.4	-	-2.1	-3.0
ENSG00000164611.12	PTTG1	-	-	1.1	2.6
ENSG00000164619.8	BMPER	-	-	-2.7	-2.1
ENSG00000164620.8	RELL2	1.6	-	-	1.2
ENSG00000164626.8	KCNK5	-	-	2.2	-1.1
ENSG00000164647.8	STEAP1	-	-	1.4	-1.1
ENSG00000164649.19	CDCA7L	-	-1.2	-	-1.2
ENSG00000164659.14	KIAA1324L	-	-	-1.7	-1.4
ENSG00000164687.10	FABP5	-	2.2	-	-1.9
ENSG00000164691.16	TAGAP	-2.3	-	-1.1	-1.2
ENSG00000164736.5	SOX17	-4.7	-	-3.2	-2.6
ENSG00000164741.14	DLC1	-2.3	-	-2.0	-2.7
ENSG00000164764.10	SBSPON	-3.3	-	-2.2	-
ENSG00000164849.8	GPR146	-	-	-2.2	-2.9
ENSG00000164850.14	GPRI1	-3.0	-2.1	-3.0	-1.6
ENSG00000164855.15	TMEM184A	-	-	1.8	1.7
ENSG00000164867.10	NOS3	-2.3	-	-1.1	-1.7
ENSG00000164929.16	BAALC	-	-	-2.8	-2.9
ENSG00000164932.12	CTHRC1	-2.6	-	3.2	1.7
ENSG00000164946.19	FREM1	-1.6	-	-	-3.2
ENSG00000164949.7	GEM	-4.6	-	-1.3	-
ENSG00000165030.3	NFIL3	-3.2	-	-1.8	-1.5
ENSG00000165072.9	MAMDC2	-3.7	-	-2.3	-2.5
ENSG00000165092.12	ALDH1A1	-3.5	-	-	-2.8
ENSG00000165124.17	SVEP1	-4.2	-	-1.8	-3.7

ENSG00000165152.8	TMEM246	-	-2.3	-	-2.4
ENSG00000165168.7	CYBB	-2.2	-	-	-1.8
ENSG00000165197.4	FIGF	-	-	-3.0	-4.9
ENSG00000165215.6	CLDN3	-	-	1.8	1.1
ENSG00000165238.16	WNK2	-	-	2.0	-2.1
ENSG00000165304.7	MELK	2.3	-	2.1	-
ENSG00000165312.6	OTUD1	-	-	-1.6	-1.7
ENSG00000165410.14	CFL2	-4.1	-	-1.2	-
ENSG00000165424.6	ZCCHC24	-3.2	-	-	-2.4
ENSG00000165457.13	FOLR2	-3.1	-	-	-2.0
ENSG00000165474.5	GJB2	2.4	-	3.1	3.1
ENSG00000165507.8	C10orf10	-1.5	-	-1.9	-2.4
ENSG00000165548.10	TMEM63C	-	-	3.9	1.3
ENSG00000165633.12	VSTM4	-2.3	-	-1.4	-
ENSG00000165716.9	FAM69B	-1.3	-	-1.5	-
ENSG00000165757.8	KIAA1462	-2.6	-	-2.2	-2.2
ENSG00000165795.20	NDRG2	-	-1.3	-1.4	-2.3
ENSG00000165804.15	ZNF219	-	-1.1	-1.0	-1.3
ENSG00000165810.16	BTNL9	-	-	-3.8	-3.0
ENSG00000165868.12	HSPA12A	-3.5	-	-	-1.9
ENSG00000165914.14	TTC7B	-1.1	-	-1.0	-
ENSG00000165923.15	AGBL2	1.6	-	-	1.2
ENSG00000165996.13	HACD1	-2.4	-	-2.1	-
ENSG00000166025.17	AMOTL1	-2.3	-	-1.3	-2.6
ENSG00000166073.8	GPR176	-2.1	-1.3	-	-1.8
ENSG00000166086.12	JAM3	-3.9	-	-1.3	-1.5
ENSG00000166106.3	ADAMTS15	-	-	-2.0	-1.3
ENSG00000166123.13	GPT2	1.8	-	2.3	-1.3
ENSG00000166128.12	RAB8B	-1.1	-	-	-1.7
ENSG00000166147.13	FBN1	-3.6	-	-	-1.8
ENSG00000166165.12	CKB	-3.7	-	-1.0	-
ENSG00000166173.10	LARP6	-1.6	-	-1.0	-1.8
ENSG00000166250.11	CLMP	-3.8	-	-	-3.0
ENSG00000166265.11	CYYR1	-1.9	-	-1.9	-2.3
ENSG00000166292.11	TMEM100	-4.4	-	-4.8	-
ENSG00000166311.9	SMPD1	-1.5	-	-	-1.1

ENSG00000166313.18	APBB1	-3.1	-	-1.3	-1.3
ENSG00000166341.7	DCHS1	-3.2	-	-1.5	-1.7
ENSG00000166377.19	ATP9B	1.0	1.3	-	-
ENSG00000166402.8	TUB	-2.9	-	-	-1.7
ENSG00000166432.14	ZMAT1	-	1.3	-	1.0
ENSG00000166482.11	MFAP4	-6.2	-	-2.5	-1.6
ENSG00000166510.13	CCDC68	-	-1.1	-1.1	-
ENSG00000166523.7	CLEC4E	-3.6	-	-2.3	-
ENSG00000166579.15	NDEL1	-1.2	-	-1.1	-1.1
ENSG00000166592.11	RRAD	-2.9	-	-	-1.2
ENSG00000166819.11	PLIN1	-	1.5	-	-4.4
ENSG00000166825.13	ANPEP	-2.4	-	-	-1.7
ENSG00000166828.2	SCNN1G	2.0	-2.3	-	-
ENSG00000166831.8	RBPM5	-5.1	-	-1.2	-2.5
ENSG00000166851.14	PLK1	2.0	-	1.4	1.3
ENSG00000166927.12	MS4A7	-1.8	-	-	1.4
ENSG00000166963.12	MAP1A	-4.0	-	-	-1.3
ENSG00000166974.12	MAPRE2	-2.2	-	-	-1.4
ENSG00000166979.12	EVA1C	-2.0	-1.0	-	-
ENSG00000167074.14	TEF	-	-	-1.1	-2.4
ENSG00000167100.14	SAMD14	-1.6	-	-1.6	-
ENSG00000167191.11	GPRC5B	-1.4	-1.5	-	-2.7
ENSG00000167371.16	PRRT2	-3.7	-	-	2.3
ENSG00000167434.9	CA4	-	-	-5.2	-5.1
ENSG00000167513.8	CDT1	1.9	-	1.2	1.1
ENSG00000167535.7	CACNB3	1.3	-	-	1.4
ENSG00000167549.18	CORO6	-4.2	-	-1.4	1.7
ENSG00000167588.12	GPD1	-	-	-2.1	-4.5
ENSG00000167601.11	AXL	-2.8	-	-	-1.6
ENSG00000167608.11	TMC4	1.4	-	1.4	-
ENSG00000167641.10	PPP1R14A	-4.8	-	-2.3	-2.3
ENSG00000167644.11	C19orf33	2.4	-	-	2.3
ENSG00000167702.11	KIFC2	1.3	1.0	-	2.1
ENSG00000167778.8	SPRYD3	-1.1	-	-	-1.0
ENSG00000167779.7	IGFBP6	-5.3	-	-1.7	-2.6
ENSG00000167799.9	NUDT8	1.7	2.0	-	-

ENSG00000167874.6	TMEM88	-1.9	-	-3.2	-
ENSG00000167880.7	EVPL	1.4	-	-	1.6
ENSG00000167900.11	TK1	1.8	-	1.5	2.2
ENSG00000167964.12	RAB26	1.8	1.1	2.2	3.0
ENSG00000167968.12	D-SE1L2	1.5	-	-	2.4
ENSG00000167971.15	CASKIN1	-	1.1	3.2	1.2
ENSG00000167972.13	ABCA3	-2.3	-	-2.0	-
ENSG00000167994.11	RAB3IL1	-3.5	-	-	-1.0
ENSG00000167995.15	BEST1	-2.9	-	-1.2	-
ENSG00000168032.8	ENTPD3	-	-1.3	1.2	-
ENSG00000168060.14	-ALADL1	-2.7	-	-1.1	-1.3
ENSG00000168077.13	SCARA3	-1.9	-	-	-1.1
ENSG00000168079.16	SCARA5	-5.8	-	-2.5	-5.0
ENSG00000168140.4	VASN	-3.4	-	-	-1.2
ENSG00000168309.16	FAM107A	-6.1	-1.1	-4.1	-3.0
ENSG00000168329.13	CX3CR1	-	-	-1.6	-1.8
ENSG00000168350.7	DEGS2	-	-	1.7	1.8
ENSG00000168386.18	FILIP1L	-4.2	-	-1.1	-1.3
ENSG00000168447.10	SCNN1B	-	-2.2	-	-1.2
ENSG00000168461.12	RAB31	-1.4	-	-	1.4
ENSG00000168477.17	TNXB	-6.0	-	-2.9	-2.9
ENSG00000168490.13	PHYHIP	-2.7	-	-	-1.9
ENSG00000168491.9	CCDC110	-	1.5	-	1.1
ENSG00000168497.4	SDPR	-4.5	-	-3.2	-3.5
ENSG00000168528.11	SERINC2	1.5	-	1.8	1.1
ENSG00000168542.12	COL3A1	-2.0	-	1.6	-
ENSG00000168685.14	IL7R	-2.5	-	-1.6	-
ENSG00000168734.13	PKIG	-3.7	-	-1.7	-
ENSG00000168743.12	NPNT	-	-	-2.2	1.3
ENSG00000168874.12	ATOH8	-	-1.4	-2.5	-3.3
ENSG00000168899.4	VAMP5	-1.6	-	-1.3	-1.0
ENSG00000168907.13	PLA2G4F	-	-	-2.2	1.1
ENSG00000168952.15	STXBP6	-4.2	-	-3.8	-
ENSG00000168994.13	PXDC1	-1.8	-1.1	-1.5	-1.6
ENSG00000169047.5	IRS1	-	-1.3	-	-2.1
ENSG00000169071.14	ROR2	-4.9	-1.5	-	-

ENSG00000169116.11	PARM1	-2.0	-1.3	-	-2.8
ENSG00000169122.11	FAM110B	-3.4	-	-1.1	-
ENSG00000169129.14	AFAP1L2	-	-1.0	-	-1.2
ENSG00000169252.5	ADRB2	-	-	-2.3	-2.9
ENSG00000169255.13	B3GALNT1	1.6	-	-1.6	-
ENSG00000169282.17	KC-B1	-2.7	-	-	-2.3
ENSG00000169291.9	SHE	-2.7	-	-1.4	-1.2
ENSG00000169302.14	STK32A	2.1	-	2.4	-
ENSG00000169418.9	NPR1	-3.6	-	-2.3	-3.8
ENSG00000169439.11	SDC2	-2.5	-	-	-1.8
ENSG00000169442.8	CD52	-2.6	-	-1.3	-
ENSG00000169504.14	CLIC4	-3.4	-	-	-1.9
ENSG00000169508.6	GPR183	-3.0	-	-1.0	-
ENSG00000169515.5	CCDC8	-3.5	-1.1	-	-1.6
ENSG00000169554.16	ZEB2	-3.3	-	-	-2.4
ENSG00000169583.12	CLIC3	-	-2.2	-2.6	-
ENSG00000169679.14	BUB1	2.3	-	1.8	-
ENSG00000169715.14	MT1E	-2.6	-	-1.5	-
ENSG00000169744.12	LDB2	-2.7	-	-2.5	-2.4
ENSG00000169764.14	UGP2	-1.2	-	-	-2.1
ENSG00000169851.15	PCDH7	-2.2	-1.3	1.3	-
ENSG00000169855.19	ROBO1	-	-1.0	-	-1.9
ENSG00000169894.17	MUC3A	2.7	-	5.4	-
ENSG00000169902.13	TPST1	-2.0	-	-	-1.3
ENSG00000169926.9	KLF13	-	-	-1.4	-2.0
ENSG00000170049.9	KC-B3	-	1.0	-	1.0
ENSG00000170145.4	SIK2	-	-	-1.0	-2.5
ENSG00000170153.10	RNF150	-3.0	-	-	-3.1
ENSG00000170190.15	SLC16A5	-	-2.0	-1.1	-
ENSG00000170214.3	ADRA1B	-	-	-1.6	-1.7
ENSG00000170222.11	ADPRM	-1.0	-	-	-1.0
ENSG00000170271.10	FAXDC2	-2.1	-	-1.3	-1.7
ENSG00000170275.14	CRTAP	-1.9	-	-	-1.8
ENSG00000170312.15	CDK1	1.8	-	1.4	2.1
ENSG00000170323.8	FABP4	-	-	-2.7	-4.0
ENSG00000170345.9	FOS	-1.8	-	-1.8	-

ENSG00000170369.3	CST2	-	-	2.4	4.0
ENSG00000170373.8	CST1	3.4	-1.6	3.5	-
ENSG00000170417.14	TMEM182	1.2	1.8	-	1.1
ENSG00000170421.11	KRT8	-	-	1.0	1.7
ENSG00000170458.13	CD14	-2.6	-	-	-1.4
ENSG00000170464.9	D-JC18	-1.7	-	-1.1	-
ENSG00000170469.10	SPATA24	-	-	1.2	1.6
ENSG00000170476.15	MZB1	-	-	1.8	1.5
ENSG00000170525.18	PFKFB3	-	-	-1.0	-3.2
ENSG00000170571.11	EMB	-	-	1.2	-1.0
ENSG00000170891.10	CYTL1	-5.1	-1.3	-	-
ENSG00000170903.10	MSANTD4	-	-	1.2	-1.1
ENSG00000170962.12	PDGFD	-2.9	-	-	-2.1
ENSG00000170989.8	S1PR1	-3.0	-	-2.9	-2.9
ENSG00000171051.8	FPR1	-3.7	-	-2.1	-
ENSG00000171056.7	SOX7	-2.1	-1.9	-3.6	-1.6
ENSG00000171115.3	GIMAP8	-	-	-2.2	-2.4
ENSG00000171121.16	KCNMB3	-	1.0	1.4	1.3
ENSG00000171124.12	FUT3	2.8	-	2.0	-
ENSG00000171132.13	PRKCE	-	-	-2.0	-1.0
ENSG00000171163.15	ZNF692	1.3	1.1	-	1.8
ENSG00000171223.5	JUNB	-1.8	-	-2.2	-
ENSG00000171303.6	KCNK3	-	-	-3.7	-1.1
ENSG00000171345.13	KRT19	-	-2.0	-	1.3
ENSG00000171346.13	KRT15	-	-2.4	3.5	-1.6
ENSG00000171368.11	TPPP	-2.1	-	-1.8	-2.2
ENSG00000171388.11	APLN	-	-	-2.7	-1.2
ENSG00000171522.5	PTGER4	-	-	-1.7	-2.7
ENSG00000171533.11	MAP6	-2.3	-	-	-1.1
ENSG00000171596.6	NMUR1	-	-	-2.9	-1.7
ENSG00000171608.15	PIK3CD	-1.5	-	-	-1.2
ENSG00000171621.13	SPSB1	-1.6	-1.0	-	-
ENSG00000171631.14	P2RY6	-	-	2.9	1.1
ENSG00000171659.13	GPR34	-2.2	-	-	-2.1
ENSG00000171766.15	GATM	-2.0	-	1.3	-
ENSG00000171777.15	RASGRP4	-2.5	-	-1.7	-

ENSG00000171791.11	BCL2	-1.8	-	-	-1.1
ENSG00000171812.10	COL8A2	-3.8	-	1.4	-
ENSG00000171848.13	RRM2	2.2	-	1.6	-
ENSG00000171860.4	C3AR1	-2.3	-	-	-1.0
ENSG00000171867.16	PRNP	-1.7	-	-	-2.4
ENSG00000171992.12	SYNPO	-2.2	-	-1.2	-2.8
ENSG00000172005.10	MAL	-	-1.0	-2.0	-
ENSG00000172037.13	LAMB2	-1.8	-	-1.1	-1.1
ENSG00000172059.10	KLF11	-1.7	-	-1.0	-2.8
ENSG00000172137.18	CALB2	-	-	-1.7	-3.6
ENSG00000172159.15	FRMD3	-	-	-2.3	-2.5
ENSG00000172201.10	ID4	-1.2	-1.6	-2.0	-1.9
ENSG00000172216.5	CEBPB	-1.7	-1.2	-1.4	-1.1
ENSG00000172236.16	TPSAB1	-5.3	-	-	1.1
ENSG00000172260.13	NEGR1	-4.7	-	-1.1	-
ENSG00000172346.14	CSDC2	-6.1	-	-	1.4
ENSG00000172348.14	RCAN2	-4.4	-	-	-1.7
ENSG00000172349.16	IL16	-3.0	-	-	-1.4
ENSG00000172403.10	SYNPO2	-5.7	-	-1.1	-2.4
ENSG00000172458.4	IL17D	-2.2	-	-1.5	-
ENSG00000172594.12	SMPDL3A	-2.0	-	-	-1.1
ENSG00000172602.9	RND1	-	-	-1.7	1.4
ENSG00000172638.12	EFEMP2	-3.0	-	-	-1.0
ENSG00000172724.11	CCL19	-3.8	-	-	1.4
ENSG00000172889.15	EGFL7	-2.0	-	-2.7	-1.1
ENSG00000172932.14	ANKRD13D	1.1	-	-	1.3
ENSG00000172935.8	MRGPRF	-5.5	-1.1	-1.6	-2.3
ENSG00000172985.10	SH3RF3	-2.5	-	-1.0	-1.7
ENSG00000172987.12	HPSE2	-8.2	-	-1.1	-2.9
ENSG00000173137.11	ADCK5	-	-	1.2	1.4
ENSG00000173175.14	ADCY5	-4.8	-	-	-2.2
ENSG00000173198.5	CYSLTR1	1.2	1.5	-	-
ENSG00000173210.19	ABLIM3	-	-	-2.0	-2.4
ENSG00000173212.4	MAB21L3	-	1.2	-	1.8
ENSG00000173267.13	SNCG	-	-1.4	-	-1.7
ENSG00000173269.13	MMRN2	-	-	-2.1	-2.5

ENSG00000173276.13	ZBTB21	-1.8	-	-	-1.9
ENSG00000173369.15	C1QB	-2.5	-	-1.1	-
ENSG00000173376.13	NDNF	-4.2	-1.1	-1.4	-
ENSG00000173391.8	OLR1	-	-	-1.5	1.4
ENSG00000173457.10	PPP1R14B	-	-	1.3	1.4
ENSG00000173482.16	PTPRM	-	-	-1.8	-2.1
ENSG00000173511.9	VEGFB	-1.7	-	-	-1.4
ENSG00000173530.5	TNFRSF10D	-1.4	-	-1.5	-2.1
ENSG00000173546.7	CSPG4	-2.3	-	-1.9	-2.5
ENSG00000173599.13	PC	-	-	1.8	-2.8
ENSG00000173641.17	HSPB7	-7.1	-	-1.3	-4.5
ENSG00000173706.12	HEG1	-2.1	-	-1.8	-1.8
ENSG00000173715.15	C11orf80	-	-	1.4	1.0
ENSG00000173918.14	C1QTNF1	-2.7	-	-	-2.0
ENSG00000174004.5	NRROS	-2.5	-	-	-1.6
ENSG00000174059.16	CD34	-2.9	-	-1.9	-1.7
ENSG00000174080.10	CTSF	-2.3	-	-	-1.1
ENSG00000174099.10	MSRB3	-4.8	-	-1.3	-1.3
ENSG00000174125.7	TLR1	-2.0	-	-	-1.2
ENSG00000174175.16	SELP	-3.8	-	-1.8	-2.2
ENSG00000174282.11	ZBTB4	-1.2	-	-	-2.0
ENSG00000174306.21	ZHX3	-1.6	-	-	-1.1
ENSG00000174501.14	ANKRD36C	-	1.5	-	1.1
ENSG00000174516.14	PELI3	-1.4	-	-	-1.0
ENSG00000174567.7	GOLT1A	1.6	-	-	1.6
ENSG00000174600.13	CMKLR1	-2.4	-	-	-1.6
ENSG00000174640.12	SLCO2A1	-1.7	-	-2.3	-
ENSG00000174684.6	B4GAT1	-1.6	-	-1.1	-
ENSG00000174788.9	PCP2	1.5	-	-	2.3
ENSG00000174804.3	FZD4	-1.3	-	-1.8	-2.6
ENSG00000174807.3	CD248	-3.2	-	-	-2.4
ENSG00000174944.8	P2RY14	-3.9	-	-1.8	-
ENSG00000174945.13	AMZ1	-	1.6	-	1.8
ENSG00000175040.5	CHST2	-	-1.6	-	-2.9
ENSG00000175063.16	UBE2C	2.3	1.2	2.0	3.4
ENSG00000175084.11	DES	-9.8	-1.0	-2.6	-1.7

ENSG00000175164.13	ABO	1.6	-1.7	-	-
ENSG00000175183.9	CSRP2	-1.3	-1.1	-	-
ENSG00000175279.21	APITD1	1.8	-	-	1.0
ENSG00000175395.15	ZNF25	-1.5	-	-	-1.3
ENSG00000175445.14	LPL	-	-	-1.9	-4.8
ENSG00000175455.14	CCDC14	1.0	1.1	-	-
ENSG00000175592.8	FOSL1	-	-1.2	-3.1	-
ENSG00000175600.15	SUGCT	-2.1	-	2.3	-
ENSG00000175602.3	CCDC85B	-2.0	-	-1.3	-
ENSG00000175643.8	RMI2	1.6	-	1.9	1.5
ENSG00000175745.11	NR2F1	-3.2	-	-1.2	-
ENSG00000175764.14	TTLL11	-1.2	-	-	-1.5
ENSG00000175785.12	PRIMA1	-4.1	-1.7	-	-2.0
ENSG00000175832.12	ETV4	3.0	-1.0	3.1	-
ENSG00000175899.14	A2M	-3.0	-	-1.6	-2.2
ENSG00000176014.12	TUBB6	-3.8	-	-2.0	-2.0
ENSG00000176124.11	DLEU1	1.9	-	1.1	-
ENSG00000176208.8	ATAD5	1.6	-	-	1.1
ENSG00000176387.6	HSD11B2	-	-1.9	1.4	1.3
ENSG00000176435.6	CLEC14A	-1.8	-	-2.7	-1.7
ENSG00000176438.12	SYNE3	-	-	-1.4	-2.7
ENSG00000176532.3	PRR15	-	-1.5	-	1.8
ENSG00000176533.12	GNG7	-3.2	-	-	-1.4
ENSG00000176597.11	B3GNT5	-	-	-1.1	-1.5
ENSG00000176842.14	IRX5	-	-1.2	-	1.1
ENSG00000176845.12	METRNL	-1.8	-	-1.3	-
ENSG00000176903.4	PNMA1	-2.8	-1.1	-	-1.3
ENSG00000176920.11	FUT2	-	-1.6	3.4	-
ENSG00000176971.3	FIBIN	-4.8	-	-2.0	-
ENSG00000177054.13	ZDHHC13	1.1	-	1.3	-
ENSG00000177098.8	SCN4B	-	-	-3.0	-3.1
ENSG00000177202.2	SPACA4	-	-	1.3	2.4
ENSG00000177283.5	FZD8	-	-	-1.1	-1.5
ENSG00000177374.12	HIC1	-3.6	-	-1.6	-1.6
ENSG00000177432.6	-PIL5	-1.9	-	-1.1	-1.2
ENSG00000177464.4	GPR4	-	-	-2.0	-1.6

ENSG00000177469.12	PTRF	-4.3	-1.1	-2.0	-2.5
ENSG00000177606.6	JUN	-2.5	-	-1.0	-
ENSG00000177694.14	-ALADL2	-	1.3	1.4	-
ENSG00000177706.8	FAM20C	-3.2	-	-	-1.2
ENSG00000177990.11	DPY19L2	-2.4	1.4	-	-
ENSG00000178031.15	ADAMTSL1	-4.7	-	-	-1.6
ENSG00000178175.11	ZNF366	-	-	-1.5	-1.4
ENSG00000178222.12	RNF212	-2.6	-	1.8	-
ENSG00000178401.14	D-JC22	-	-	2.9	1.1
ENSG00000178573.6	MAF	-2.2	-	-	-2.1
ENSG00000178695.5	KCTD12	-2.5	-	-	-2.8
ENSG00000178726.6	THBD	-2.2	-	-2.8	-2.0
ENSG00000178773.14	CPNE7	-	2.9	2.3	3.0
ENSG00000178826.10	TMEM139	-	-1.8	-1.9	-
ENSG00000178852.15	EFCAB13	-	1.3	1.2	-
ENSG00000178878.12	APOLD1	-3.2	-	-2.3	-2.7
ENSG00000178935.5	ZNF552	1.6	-	1.0	1.8
ENSG00000178999.12	AURKB	2.4	-	1.3	2.4
ENSG00000179023.8	KLHDC7A	1.9	-	2.1	-
ENSG00000179094.13	PER1	-2.9	-	-1.6	-1.6
ENSG00000179144.4	GIMAP7	-2.3	-	-1.5	-1.3
ENSG00000179314.13	WSCD1	-	-	-1.7	-1.8
ENSG00000179388.8	EGR3	-4.2	-	-2.3	-2.0
ENSG00000179528.15	LBX2	1.8	-	1.4	1.2
ENSG00000179604.9	CDC42EP4	-	-1.1	-	-2.3
ENSG00000179776.17	CDH5	-2.0	-	-3.0	-2.4
ENSG00000179820.15	MYADM	-3.8	-	-2.2	-1.3
ENSG00000179855.5	GIPC3	-	-	-1.9	-1.5
ENSG00000179862.6	CITED4	-	-1.4	-1.2	1.0
ENSG00000179921.14	GPBAR1	-2.8	-	-2.1	-2.9
ENSG00000179979.8	CRIPAK	-	1.2	-	1.1
ENSG00000180155.18	LYNX1	-2.2	-1.1	-	-1.6
ENSG00000180198.15	RCC1	1.3	-	1.5	-
ENSG00000180346.3	TIGD2	-	-	1.1	-1.3
ENSG00000180354.15	MTURN	-1.8	-	-1.3	-2.9
ENSG00000180447.6	GAS1	-5.4	-2.1	-	-2.0

ENSG00000180543.4	TSPYL5	-1.5	-	1.0	-
ENSG00000180644.6	PRF1	-	-	-2.3	-2.1
ENSG00000180879.13	SSR4	-	-	1.3	1.0
ENSG00000180884.9	ZNF792	1.1	-	-	-1.4
ENSG00000180921.6	FAM83H	1.8	-	1.2	-
ENSG00000180953.11	ST20	-	1.1	-	1.3
ENSG00000181085.14	MAPK15	3.0	-	-	2.7
ENSG00000181191.11	PJA1	-	-1.0	-	-2.0
ENSG00000181218.5	HIST3H2A	1.4	1.2	-	2.1
ENSG00000181392.14	SYNE4	-	-	1.1	1.2
ENSG00000181444.12	ZNF467	-1.5	-	-	1.5
ENSG00000181449.3	SOX2	-	-1.3	1.9	-
ENSG00000181458.10	TMEM45A	-	1.5	-	1.1
ENSG00000181649.5	PHLDA2	-	-1.2	1.0	-
ENSG00000181754.6	AMIGO1	-	-	-1.3	-1.7
ENSG00000181804.14	SLC9A9	-2.6	-	-	-2.6
ENSG00000181826.9	RELL1	-	-	-1.0	-1.7
ENSG00000181856.14	SLC2A4	-5.2	-	-	-2.0
ENSG00000182013.17	PNMAL1	-	-1.1	2.2	-
ENSG00000182247.9	UBE2E2	-1.6	-	-	-1.5
ENSG00000182253.14	SYNM	-7.5	-	-2.0	-3.1
ENSG00000182272.11	B4GALNT4	-	-	2.2	1.7
ENSG00000182325.10	FBXL6	1.1	-	-	1.5
ENSG00000182326.14	C1S	-4.2	-	-	-1.5
ENSG00000182472.8	CAPN12	1.8	-	1.5	-
ENSG00000182492.15	BGN	-1.7	-	-	2.1
ENSG00000182511.11	FES	-1.0	-	-	-1.2
ENSG00000182534.13	MXRA7	-3.0	-	-	-1.3
ENSG00000182575.7	NXPH3	-5.5	-	-2.5	-
ENSG00000182578.13	CSF1R	-2.3	-	-	-1.5
ENSG00000182636.5	NDN	-2.2	-	-	-2.5
ENSG00000182667.14	NTM	-1.9	-	-	-1.0
ENSG00000182685.7	BRICD5	-	1.1	-	1.4
ENSG00000182771.17	GRID1	-	-	-1.5	-2.0
ENSG00000182782.7	HCAR2	-	-	-1.8	-3.0
ENSG00000182916.7	TCEAL7	-5.5	-	-1.2	-1.8

ENSG00000183010.16	PYCR1	-	-	2.5	1.4
ENSG00000183036.10	PCP4	-8.4	-	3.6	-
ENSG00000183048.11	SLC25A10	2.0	-	1.5	-
ENSG00000183087.14	GAS6	-4.1	-	-1.4	-
ENSG00000183111.11	ARHGEF37	-1.9	-	-	-1.5
ENSG00000183248.11	PRR36	2.1	1.1	1.6	1.9
ENSG00000183340.6	JRKL	-	-	1.0	-1.4
ENSG00000183421.11	RIPK4	-	-1.2	-	-1.7
ENSG00000183578.5	TNFAIP8L3	-3.8	-	-1.6	-
ENSG00000183580.9	FBXL7	-3.5	-	-1.3	-1.1
ENSG00000183688.4	FAM101B	-1.5	-	-1.6	-1.1
ENSG00000183722.7	LHFP	-3.1	-	-1.9	-2.2
ENSG00000183741.11	CBX6	-1.3	-	-	-1.1
ENSG00000183773.15	AIFM3	1.7	-	-	1.6
ENSG00000183798.4	EMILIN3	-2.7	-1.3	-	-4.4
ENSG00000183801.7	OLFML1	-3.5	-	-1.5	-1.3
ENSG00000183807.7	FAM162B	-2.0	-	-2.9	-
ENSG00000183853.17	KIRREL	-2.0	-	-	-2.4
ENSG00000183856.10	IQGAP3	3.7	-	2.0	3.0
ENSG00000183963.18	SMTN	-3.7	-	-1.0	-
ENSG00000184005.10	ST6GAL-C3	-2.6	-	-2.0	-
ENSG00000184014.7	DENND5A	-1.5	-	-	-1.7
ENSG00000184113.9	CLDN5	-4.2	-1.5	-3.9	-2.5
ENSG00000184160.7	ADRA2C	-2.5	-1.6	-1.4	-
ENSG00000184232.8	OAF	-1.8	-	-	-1.5
ENSG00000184347.14	SLIT3	-2.1	-	-1.8	-3.1
ENSG00000184349.12	EF-5	-	-1.0	1.8	-1.3
ENSG00000184371.13	CSF1	-2.2	-	-	-1.6
ENSG00000184445.11	KNTC1	1.3	-	1.3	-
ENSG00000184481.16	FOXO4	-1.0	-	-	-1.5
ENSG00000184497.12	TMEM255B	-1.9	-	-1.5	-
ENSG00000184500.14	PROS1	-3.1	-	-1.3	-2.4
ENSG00000184557.4	SOCS3	-3.0	-1.1	-2.2	-2.2
ENSG00000184588.17	PDE4B	-3.6	-	-1.4	-1.6
ENSG00000184602.5	SNN	-1.1	-	-	-2.5
ENSG00000184785.5	SMIM10	-2.6	-	-	-1.2

ENSG00000184905.8	TCEAL2	-5.0	-1.7	-2.4	-
ENSG00000184925.11	LCN12	-	1.1	1.1	-
ENSG00000185010.13	F8	-2.0	-	-1.1	-2.4
ENSG00000185022.11	MAFF	-1.9	-	-2.7	-1.3
ENSG00000185052.11	SLC24A3	-1.8	-	-	-1.2
ENSG00000185101.12	ANO9	2.0	-	-	1.5
ENSG00000185112.5	FAM43A	-3.5	-1.4	-2.1	-2.2
ENSG00000185274.11	WBSCR17	-7.0	-	-	-2.4
ENSG00000185298.12	CCDC137	1.2	-	-	1.4
ENSG00000185339.8	TCN2	-1.5	-	-	-2.2
ENSG00000185340.15	GAS2L1	-	-	-1.5	-1.1
ENSG00000185386.14	MAPK11	-1.7	-	-1.2	-
ENSG00000185432.11	METTL7A	-	-	-1.1	-1.5
ENSG00000185482.7	STAC3	-	1.2	-	1.6
ENSG00000185483.11	ROR1	-2.7	-	-	-1.9
ENSG00000185499.16	MUC1	-	-	1.1	2.0
ENSG00000185522.8	LMNTD2	1.3	-	-	1.8
ENSG00000185565.11	LSAMP	-2.2	-1.9	-	-
ENSG00000185567.6	AH-K2	-2.9	-1.0	1.5	-
ENSG00000185585.19	OLFML2A	-1.7	-1.4	-1.7	-2.2
ENSG00000185614.4	FAM212A	-	-1.9	-1.6	-
ENSG00000185842.14	D-H14	1.8	1.1	1.2	1.1
ENSG00000185885.15	IFITM1	-2.5	-1.2	-	1.0
ENSG00000185920.15	PTCH1	-1.5	-	-1.3	-2.1
ENSG00000185950.8	IRS2	-	-	-1.3	-2.1
ENSG00000185989.10	RASA3	-1.8	-	-	-1.7
ENSG00000186081.11	KRT5	-	-2.5	2.2	-2.1
ENSG00000186185.13	KIF18B	3.1	-	1.6	1.2
ENSG00000186340.14	THBS2	-2.3	-	2.4	-
ENSG00000186350.9	RXRA	-	-	-1.1	-1.1
ENSG00000186377.7	CYP4X1	1.1	-1.1	1.3	-
ENSG00000186469.8	GNG2	-2.8	-	-1.1	-3.1
ENSG00000186522.14	SEPT10	-	-	-1.0	-1.6
ENSG00000186567.12	CEACAM19	-	1.1	-1.1	-
ENSG00000186642.15	PDE2A	-4.1	-	-1.9	-3.4
ENSG00000186832.8	KRT16	2.3	-	-	-1.3

ENSG00000186847.5	KRT14	-	-2.2	-	-1.8
ENSG00000186994.11	KANK3	-2.9	-	-3.3	-
ENSG00000187017.14	ESPN	-	-	2.3	2.1
ENSG00000187193.8	MT1X	-2.5	-	-2.3	-1.7
ENSG00000187210.12	GCNT1	-	1.2	1.8	-
ENSG00000187260.15	WDR86	-	-	1.2	-1.4
ENSG00000187479.5	C11orf96	-4.8	-	-2.6	-1.7
ENSG00000187513.8	GJA4	-2.0	-	-2.1	-1.5
ENSG00000187583.10	PLEKHN1	-	-	2.3	1.7
ENSG00000187634.10	SAMD11	-2.8	-	-	2.6
ENSG00000187642.9	PERM1	1.8	-	2.4	2.5
ENSG00000187688.14	TRPV2	-1.8	-	-1.5	-1.6
ENSG00000187720.14	THSD4	-2.1	-1.5	-1.3	-
ENSG00000187741.14	FANCA	2.1	1.0	-	1.4
ENSG00000187758.7	ADH1A	2.3	-	-2.7	-
ENSG00000187800.13	PEAR1	-1.6	-	-2.5	-2.3
ENSG00000187824.8	TMEM220	-2.1	-	-	-1.4
ENSG00000187837.3	HIST1H1C	-	-	1.2	1.3
ENSG00000187951.10	ARHGAP11B	1.9	-	-	1.3
ENSG00000187955.11	COL14A1	-4.8	-	-	-2.0
ENSG00000188042.7	ARL4C	-1.7	-	-	-1.2
ENSG00000188070.9	C11orf95	-1.1	-	-	-1.7
ENSG00000188215.9	DCUN1D3	-1.3	-	-	-1.2
ENSG00000188257.10	PLA2G2A	-3.7	-	-1.5	-2.2
ENSG00000188322.4	SBK1	2.6	-	2.2	1.4
ENSG00000188536.12	HBA2	-4.1	-	-3.4	-
ENSG00000188641.12	DPYD	-1.9	-	-	-2.0
ENSG00000188643.10	S100A16	-	-1.7	-	1.1
ENSG00000188677.14	PARVB	-2.2	-	-1.2	-
ENSG00000188738.13	FSIP2	1.0	1.7	-	-
ENSG00000188783.5	PRELP	-6.1	-	-1.6	-2.3
ENSG00000188818.12	ZDHHC11	-	1.7	-	1.2
ENSG00000188878.16	FBF1	1.1	-	-	1.7
ENSG00000188921.13	HACD4	-1.4	-	-1.1	-
ENSG00000189057.10	FAM111B	1.9	-	2.0	-
ENSG00000189058.8	APOD	-4.1	-	-	-2.6

ENSG00000189067.12	LITAF	-1.0	-	-	-1.0
ENSG00000189129.13	PLAC9	-3.4	-	-2.8	-2.6
ENSG00000189143.9	CLDN4	-	-1.1	1.3	-
ENSG00000189159.15	HN1	1.4	-	-	1.9
ENSG00000189184.11	PCDH18	-2.5	-	-	-2.6
ENSG00000189320.8	FAM180A	-	-	-1.2	-1.3
ENSG00000189334.8	S100A14	-	-2.8	1.1	2.8
ENSG00000189367.14	KIAA0408	-2.8	-	-	-2.8
ENSG00000189376.11	C8orf76	1.3	-	1.1	-
ENSG00000189377.8	CXCL17	-	-2.1	1.5	-
ENSG00000189409.12	MMP23B	-4.4	-	-1.1	-
ENSG00000196118.11	C16orf93	-	-	1.2	1.9
ENSG00000196154.11	S100A4	-	-	-1.6	-1.0
ENSG00000196182.10	STK40	-1.2	-	-	-1.3
ENSG00000196188.10	CTSE	2.9	-	1.3	-
ENSG00000196196.2	HRCT1	-2.5	-	-1.5	-
ENSG00000196263.7	ZNF471	-	1.1	-	1.1
ENSG00000196296.13	ATP2A1	-	1.2	-	1.4
ENSG00000196329.10	GIMAP5	-2.1	-	-1.4	-1.8
ENSG00000196418.12	ZNF124	1.8	1.3	-	-
ENSG00000196428.12	TSC22D2	-1.1	-	-	-1.1
ENSG00000196507.10	TCEAL3	-2.0	-	-	1.2
ENSG00000196526.10	AFAP1	-1.1	-	-	-1.1
ENSG00000196549.10	MME	-	-	-1.9	-3.8
ENSG00000196557.10	CAC-1H	-3.0	-	-1.1	1.6
ENSG00000196569.11	LAMA2	-3.4	-	-	-2.2
ENSG00000196586.13	MYO6	1.2	1.5	-	-
ENSG00000196611.4	MMP1	4.8	-	3.4	-
ENSG00000196616.12	ADH1B	-5.6	-	-2.5	-4.1
ENSG00000196628.13	TCF4	-1.6	-	-	-1.2
ENSG00000196814.14	MVB12B	-	-	-1.5	-1.0
ENSG00000196834.11	POTEI	-	1.6	-	2.9
ENSG00000196843.15	ARID5A	-3.1	-	-1.8	-1.2
ENSG00000196878.12	LAMB3	-	-2.5	-	-2.6
ENSG00000196912.12	ANKRD36B	-	1.4	-	1.6
ENSG00000196924.14	FL-	-4.6	-1.1	-	-

ENSG00000196972.7	SMIM10L2B	-	-1.1	-	-2.1
ENSG00000197019.4	SERTAD1	-1.8	-	-1.8	-
ENSG00000197043.13	ANXA6	-4.0	-1.0	-	-1.1
ENSG00000197124.11	ZNF682	1.2	1.1	-	-
ENSG00000197162.9	ZNF785	1.5	-	1.1	-
ENSG00000197165.10	SULT1A2	2.4	-	-	1.3
ENSG00000197245.4	FAM110D	-3.8	-1.4	-2.4	-2.3
ENSG00000197256.10	KANK2	-3.0	-	-1.7	-1.4
ENSG00000197321.14	SVIL	-2.5	-	-	-1.4
ENSG00000197381.15	ADARB1	-3.2	-	-1.9	-1.2
ENSG00000197405.7	C5AR1	-2.8	-	-2.0	-
ENSG00000197461.13	PDGFA	-1.1	-	-	-1.3
ENSG00000197467.13	COL13A1	-3.1	-	-1.2	-
ENSG00000197471.11	SPN	-1.5	-	-1.5	-
ENSG00000197576.13	HOXA4	-	-	-2.1	-1.7
ENSG00000197614.10	MFAP5	-5.8	-	-1.8	-1.7
ENSG00000197629.5	MPEG1	-2.8	-	-	-2.1
ENSG00000197635.9	DPP4	-2.2	-	1.9	-2.3
ENSG00000197702.11	PARVA	-1.7	-	-	-1.6
ENSG00000197757.7	HOXC6	-	3.2	-	1.4
ENSG00000197766.7	CFD	-6.7	-	-2.4	-3.3
ENSG00000197774.12	EME2	1.4	1.5	-	1.9
ENSG00000197852.9	FAM212B	-	-	-2.1	-1.6
ENSG00000197872.11	FAM49A	-2.2	-	-1.2	-2.9
ENSG00000197879.14	MYO1C	-	-	-1.2	-1.7
ENSG00000197930.12	ERO1L	1.3	-	1.7	-
ENSG00000198053.11	SIRPA	-1.8	-	-	-2.4
ENSG00000198075.9	SULT1C4	-2.5	-	-1.7	-
ENSG00000198087.7	CD2AP	1.3	-	1.0	-
ENSG00000198121.13	LPAR1	-1.8	-	-	-1.7
ENSG00000198125.12	MB	-	-	3.5	1.2
ENSG00000198203.9	SULT1C2	1.7	-	2.0	-
ENSG00000198298.12	ZNF485	1.0	-	1.2	-
ENSG00000198300.12	PEG3	-4.1	-	-	-1.7
ENSG00000198353.7	HOXC4	-	2.9	-	1.6
ENSG00000198355.4	PIM3	-1.2	-	-1.1	-

ENSG00000198431.15	TXNRD1	-2.2	-	-	-1.2
ENSG00000198513.11	ATL1	-1.4	-	-	-1.3
ENSG00000198517.9	MAFK	-1.5	-	-1.4	-
ENSG00000198554.11	WDHD1	1.7	-	1.2	-
ENSG00000198598.6	MMP17	-	-	1.0	1.0
ENSG00000198624.12	CCDC69	-2.9	-	-1.1	-3.1
ENSG00000198682.12	PAPSS2	-	-	-1.1	-1.2
ENSG00000198719.8	DLL1	-1.9	-	-1.5	-1.0
ENSG00000198732.10	SMOC1	-	-1.0	-	-1.6
ENSG00000198743.5	SLC5A3	-	-	1.7	-1.7
ENSG00000198771.10	RCSD1	-2.5	-	-1.0	-1.3
ENSG00000198795.10	ZNF521	-3.6	-	-	-1.9
ENSG00000198807.12	PAX9	-	-	2.4	1.3
ENSG00000198826.10	ARHGAP11A	1.6	-	1.1	-
ENSG00000198832.10	SELM	-3.9	-1.3	-	-
ENSG00000198844.10	ARHGEF15	-2.1	-	-2.5	-2.1
ENSG00000198848.12	CES1	-7.3	-	-2.1	-3.6
ENSG00000198853.11	RUSC2	-3.0	-	-1.2	-1.1
ENSG00000198873.11	GRK5	-2.7	-	-2.6	-2.2
ENSG00000198901.13	PRC1	1.5	-	-	1.4
ENSG00000198909.7	MAP3K3	-1.4	-	-1.0	-1.2
ENSG00000198932.12	GPRASP1	-3.0	-	-	-1.4
ENSG00000198947.14	DMD	-3.4	-	-	-2.2
ENSG00000198959.11	TGM2	-2.7	-	-	-1.2
ENSG00000198961.9	PJA2	-1.7	-	-	-1.8
ENSG00000203697.11	CAPN8	-	-	2.0	1.4
ENSG00000203727.3	SAMD5	-	-	-1.5	-1.6
ENSG00000203772.7	SPRN	1.5	1.3	-	-
ENSG00000203780.10	FANK1	1.1	-	-	1.3
ENSG00000203883.6	SOX18	-2.8	-	-2.0	-1.6
ENSG00000203896.9	LIME1	1.9	1.3	-	1.5
ENSG00000204060.5	FOXO6	-	-	2.1	1.3
ENSG00000204131.8	NHSL2	-1.9	-	-	-1.4
ENSG00000204161.13	C10orf128	-3.0	-	-	-1.6
ENSG00000204262.11	COL5A2	-1.7	-	1.6	-
ENSG00000204291.10	COL15A1	-2.9	-	-	-2.5

ENSG00000204301.6	NOTCH4	-	-	-2.5	-1.6
ENSG00000204381.11	LAYN	-2.2	-1.0	-	-1.1
ENSG00000204385.10	SLC44A4	-	-	1.5	2.0
ENSG00000204410.14	MSH5	1.5	1.7	1.0	-
ENSG00000204514.9	ZNF814	1.5	1.1	-	1.2
ENSG00000204839.8	MROH6	1.5	-	2.9	1.5
ENSG00000205090.8	TMEM240	-2.8	-	-1.0	-
ENSG00000205213.13	LGR4	-	-	2.3	-2.4
ENSG00000205221.12	VIT	-8.7	-	-	-2.6
ENSG00000205362.10	MT1A	-5.3	-	-3.8	-
ENSG00000205363.5	C15orf59	-2.1	-1.5	-1.3	1.1
ENSG00000205364.3	MT1M	-4.6	-	-3.5	-1.7
ENSG00000205502.3	C2CD4B	-3.1	-	-1.9	-
ENSG00000205517.12	RGL3	1.5	1.0	-	1.1
ENSG00000205560.12	CPT1B	3.4	1.8	-	1.4
ENSG00000205795.4	CYS1	-5.2	-	-1.6	-1.1
ENSG00000205869.2	KRTAP5-1	-	-	1.7	2.7
ENSG00000205978.5	NYNRIN	-	-1.4	-	-1.7
ENSG00000206075.13	SERPINB5	-	-2.5	-	-1.3
ENSG00000206172.8	HBA1	-3.9	-	-3.4	-
ENSG00000206530.8	CFAP44	-	1.2	-	1.5
ENSG00000206535.7	LNP1	-2.5	-	-1.3	-
ENSG00000206538.7	VGLL3	-	-	-1.4	-2.9
ENSG00000211445.11	GPX3	-5.1	-1.5	-2.2	-3.9
ENSG00000211448.11	DIO2	-	-	2.9	-1.3
ENSG00000213088.9	ACKR1	-5.6	-	-2.0	-1.8
ENSG00000213145.9	CRIP1	-	-	-1.6	1.1
ENSG00000213199.7	ASIC3	-	1.9	-	2.2
ENSG00000213203.2	GIMAP1	-2.0	-	-1.6	-1.3
ENSG00000213462.4	ERV3-1	1.5	-	1.9	-
ENSG00000213626.11	LBH	-1.7	-	-1.1	-1.4
ENSG00000213639.9	PPP1CB	-1.0	-	-	-1.0
ENSG00000213865.7	C8orf44	1.4	-	1.0	-
ENSG00000213901.10	SLC23A3	1.9	1.5	-	-
ENSG00000213928.8	IRF9	1.1	1.0	-	-
ENSG00000213937.3	CLDN9	-	-	2.0	2.8

ENSG00000213949.8	ITGA1	-1.8	-	-	-1.5
ENSG00000214050.7	FBXO16	-	-	2.0	1.4
ENSG00000214140.10	PRCD	-1.6	-	-	-1.5
ENSG00000214274.9	ANG	-2.3	-1.1	-	-
ENSG00000214575.9	CPEB1	-5.0	-	-	-1.1
ENSG00000214944.9	ARHGEF28	1.3	-	-	-1.2
ENSG00000215915.9	ATAD3C	-	-1.2	-	1.6
ENSG00000216937.11	CCDC7	-	1.3	-	1.2
ENSG00000219438.8	FAM19A5	-2.6	-1.1	-	-
ENSG00000219626.8	FAM228B	-	1.4	-	1.6
ENSG00000220201.7	ZGLP1	-	1.1	-	1.7
ENSG00000221869.4	CEBPD	-3.0	-1.3	-1.5	-
ENSG00000221963.5	APOL6	1.1	-	-	-1.6
ENSG00000221968.8	FADS3	-1.8	-	-1.1	-1.5
ENSG00000223572.9	CKMT1A	2.2	-	-	1.3
ENSG00000224420.3	ADM5	-	-	-1.7	1.6
ENSG00000228594.3	C1orf233	1.9	1.5	-	-
ENSG00000228716.6	DHFR	1.6	-	1.1	-
ENSG00000228727.8	SAPCD1	-	1.8	1.4	1.4
ENSG00000233608.3	TWIST2	-5.7	-	-2.0	-2.4
ENSG00000235098.8	ANKRD65	-	-1.3	-	-1.2
ENSG00000235173.6	HGH1	1.4	-	1.1	-
ENSG00000236609.3	ZNF853	-1.8	-1.1	-	-1.5
ENSG00000236699.8	ARHGEF38	-	1.7	1.5	-
ENSG00000237440.8	ZNF737	1.6	1.1	-	-
ENSG00000237649.7	KIFC1	2.1	-	-	1.6
ENSG00000239264.8	TXNDC5	-	-	1.1	-1.3
ENSG00000239672.7	NME1	1.4	-	1.1	2.2
ENSG00000239697.10	TNFSF12	-3.3	-	-1.0	-1.0
ENSG00000240184.6	PCDHGC3	-1.6	-	-1.5	-2.1
ENSG00000240583.10	AQP1	-3.2	-	-2.0	-2.4
ENSG00000241343.9	RPL36A	-	1.1	-	1.2
ENSG00000241370.5	RPP21	-	1.0	-	1.3
ENSG00000241399.6	CD302	-1.5	-	-	-1.3
ENSG00000241484.9	ARHGAP8	2.4	1.7	-	-
ENSG00000241489.7	IDS	-	1.1	-	1.1

ENSG00000241839.9	PLEKHO2	-2.2	-	-1.1	-1.8
ENSG00000241978.9	AKAP2	-3.1	-	-1.8	-2.6
ENSG00000242265.5	PEG10	-2.3	-	-1.2	-
ENSG00000242612.6	DECR2	1.1	-	1.3	1.3
ENSG00000242732.4	RGAG4	-1.7	-	-	-1.4
ENSG00000243244.5	STON1	-2.2	-	-	-1.9
ENSG00000243364.7	EF-4	1.3	-	1.7	-
ENSG00000243449.6	C4orf48	2.8	-	1.1	-
ENSG00000243678.11	NME1-NME2	1.7	-	-	1.1
ENSG00000243989.7	ACY1	2.0	-	-	1.2
ENSG00000244405.7	ETV5	-	-1.0	-	-2.6
ENSG00000244509.3	APOBEC3C	-	-1.7	-	-1.1
ENSG00000244617.2	ASPRV1	-	-	-1.6	-1.3
ENSG00000244734.3	HBB	-2.9	-	-3.0	-4.0
ENSG00000248485.1	PCP4L1	-	-2.8	1.5	-
ENSG00000249242.7	TMEM150C	-1.9	-	1.3	-
ENSG00000249437.7	-IP	-	1.5	-	1.1
ENSG00000249709.7	ZNF564	1.2	1.0	-	-
ENSG00000249751.3	ECSCR	-2.1	-	-2.0	-
ENSG00000250067.11	YJEFN3	-	1.6	-	1.6
ENSG00000250588.6	IQCJ-SCHIP1	-2.5	-1.1	-1.6	-2.0
ENSG00000250722.5	SEPP1	-2.6	-	-	-2.3
ENSG00000253250.2	C8orf88	-3.4	-	-1.4	-
ENSG00000253276.2	CCDC71L	-1.7	-	-	-1.9
ENSG00000253304.1	TMEM200B	-4.7	-	-	-1.9
ENSG00000254122.2	PCDHGB7	-	-	-1.6	-2.7
ENSG00000254726.2	MEX3A	3.7	-	2.2	1.3
ENSG00000254996.5	ANKHD1-EIF4EBP	1.0	1.2	-	-
ENSG00000256043.2	CTSO	-1.1	-	-	-1.2
ENSG00000256235.1	SMIM3	-2.3	-	-	-2.2
ENSG00000257594.3	GALNT4	-	-	1.2	-1.1
ENSG00000258472.8	RP11-192H23.4	1.8	1.1	-	-
ENSG00000258947.6	TUBB3	2.5	-	1.4	2.1
ENSG00000259207.7	ITGB3	-2.4	-	-	-1.9
ENSG00000261052.5	SULT1A3	1.8	1.2	-	1.6
ENSG00000261371.5	PECAM1	-2.4	-	-2.0	-2.1

ENSG00000262655.3	SPON1	-3.9	-	-	-2.0
ENSG00000263155.5	MYZAP	-1.8	-	-3.5	-3.1
ENSG00000265107.2	GJA5	-2.3	-	-1.2	-1.3
ENSG00000266094.6	RASSF5	-	-1.1	-	-1.2
ENSG00000266524.2	GDF10	-	-	-3.4	-3.4
ENSG00000266964.5	FXYP1	-4.3	-	-2.7	-2.3
ENSG00000267206.5	LCN6	-5.2	-	-1.9	-
ENSG00000267795.5	SMIM22	-	-	2.4	2.3
ENSG00000269190.5	FBXO17	-3.2	-1.1	-	-1.2
ENSG00000272636.3	DOC2B	-	-	-1.5	-1.8
ENSG00000273045.5	C2orf15	1.3	-	-	1.0
ENSG00000275302.1	CCL4	-2.6	-	-1.5	-
ENSG00000275395.4	FCGBP	-	-	2.7	-2.8
ENSG00000275832.4	ARHGAP23	-	-1.3	-1.3	-1.8
ENSG00000276043.4	UHRF1	2.4	-	1.5	2.0
ENSG00000276600.4	RAB7B	-	-1.2	-	-2.0
ENSG00000277363.4	SRCIN1	2.1	-	2.0	-
ENSG00000277494.1	GPIHBP1	-4.6	-	-3.8	-3.6
ENSG00000280308.1	FKSG61	1.3	1.1	-	-
ENSG00000280789.1	PAGR1	-2.3	-	-	1.4
ENSG00000280987.2	MATR3	1.6	1.2	-	-
ENSG00000282608.1	ADORA3	-2.3	-	1.2	-

Supplementary Table S7: Oncogenes reported by COSMIC

Gene id	Gene name
ENSG00000006468.13	ETV1
ENSG00000007237.18	GAS7
ENSG00000018408.14	WWTR1
ENSG00000037280.15	FLT4
ENSG00000046889.18	PREX2
ENSG00000049540.16	ELN
ENSG00000065361.14	ERBB3
ENSG00000066468.20	FGFR2
ENSG00000067082.14	KLF6
ENSG00000068078.17	FGFR3
ENSG00000070404.9	FSTL3
ENSG00000073282.12	TP63
ENSG00000077782.19	FGFR1
ENSG00000083857.13	FAT1
ENSG00000097007.17	ABL1
ENSG00000101096.19	NFATC2
ENSG00000101213.6	PTK6
ENSG00000104419.14	NDRG1
ENSG00000105173.13	CCNE1
ENSG00000105976.14	MET
ENSG00000106462.10	EZH2
ENSG00000107485.15	GATA3
ENSG00000108821.13	COL1A1
ENSG00000108924.13	HLF
ENSG00000109906.13	ZBTB16
ENSG00000111252.10	SH2B3
ENSG00000111275.12	ALDH2
ENSG00000112531.16	QKI
ENSG00000113594.9	LIFR
ENSG00000113721.13	PDGFRB
ENSG00000116016.13	EPAS1
ENSG00000118503.14	TNFAIP3
ENSG00000118971.7	CCND2
ENSG00000119508.17	NR4A3
ENSG00000119535.17	CSF3R
ENSG00000119866.20	BCL11A
ENSG00000123473.15	STIL
ENSG00000127329.14	PTPRB
ENSG00000128602.9	SMO
ENSG00000129993.14	CBFA2T3
ENSG00000130844.16	ZNF331
ENSG00000132170.19	PPARG
ENSG00000133392.16	MYH11
ENSG00000134853.11	PDGFRA
ENSG00000135111.14	TBX3
ENSG00000135363.11	LMO2
ENSG00000136167.13	LCP1
ENSG00000136826.14	KLF4
ENSG00000136997.14	MYC
ENSG00000137193.13	PIM1
ENSG00000138413.13	IDH1
ENSG00000139263.11	LRIG3
ENSG00000140538.16	NTRK3
ENSG00000142273.10	CBLC
ENSG00000144218.18	AFF3
ENSG00000144476.5	ACKR3
ENSG00000146374.13	RSPO3
ENSG00000147065.16	MSN
ENSG00000147257.13	GPC3
ENSG00000147862.14	NFIB
ENSG00000148400.9	NOTCH1
ENSG00000150907.6	FOXO1

ENSG00000151702.16	FLI1
ENSG00000152217.16	SETBP1
ENSG00000153814.11	JAZF1
ENSG00000156076.9	WIF1
ENSG00000156970.12	BUB1B
ENSG00000157388.13	CAC-1D
ENSG00000157554.18	ERG
ENSG00000157613.10	CREB3L1
ENSG00000160789.19	LM-
ENSG00000160867.14	FGFR4
ENSG00000160957.12	RECQL4
ENSG00000162733.16	DDR2
ENSG00000163513.17	TGFBR2
ENSG00000164330.16	EBF1
ENSG00000168685.14	IL7R
ENSG00000171791.11	BCL2
ENSG00000175643.8	RMI2
ENSG00000175832.12	ETV4
ENSG00000177606.6	JUN
ENSG00000178573.6	MAF
ENSG00000179094.13	PER1
ENSG00000180644.6	PRF1
ENSG00000181449.3	SOX2
ENSG00000183722.7	LHFP
ENSG00000184481.16	FOXO4
ENSG00000185499.16	MUC1
ENSG00000185920.15	PTCH1
ENSG00000187741.14	FANCA
ENSG00000198795.10	ZNF521
ENSG00000244405.7	ETV5

Supplementary Table S8: Significantly enriched BP terms ($P \leq 0.05$) of the 12 modules

Module	Term ID	Term name	PValue
brown	GO:0045449	regulation of transcription	6.72E-13
brown	GO:0006396	RNA processing	6.93E-11
brown	GO:0006259	DNA metabolic process	1.08E-10
brown	GO:0006974	response to DNA damage stimulus	1.58E-09
brown	GO:0051276	chromosome organization	2.09E-09
brown	GO:0008380	RNA splicing	4.69E-09
brown	GO:0006281	DNA repair	1.67E-08
brown	GO:0016071	mRNA metabolic process	4.04E-08
brown	GO:0006397	mRNA processing	1.01E-07
brown	GO:0006325	chromatin organization	5.96E-07
brown	GO:0016568	chromatin modification	9.10E-07
brown	GO:0006260	DNA replication	1.50E-05
brown	GO:0006355	regulation of transcription, DNA-dependent	1.97E-05
brown	GO:0051252	regulation of RNA metabolic process	2.96E-05
brown	GO:0033554	cellular response to stress	4.00E-05
brown	GO:0006338	chromatin remodeling	4.99E-05
brown	GO:0007049	cell cycle	7.51E-05
brown	GO:0006333	chromatin assembly or disassembly	1.16E-04
brown	GO:0007017	microtubule-based process	1.34E-04
brown	GO:0006310	DNA recombination	2.04E-04
brown	GO:0022402	cell cycle process	6.66E-04
brown	GO:0000279	M phase	1.05E-03
brown	GO:0016584	nucleosome positioning	1.06E-03
brown	GO:0044265	cellular macromolecule catabolic process	1.20E-03
brown	GO:0006304	DNA modification	1.49E-03
brown	GO:0060271	cilium morphogenesis	1.49E-03
brown	GO:0022403	cell cycle phase	1.56E-03
brown	GO:0006261	DNA-dependent DNA replication	1.67E-03
brown	GO:0006305	DNA alkylation	1.97E-03
brown	GO:0006306	DNA methylation	1.97E-03
brown	GO:0031023	microtubule organizing center organization	2.04E-03

brown	GO:0040029	regulation of gene expression, epigenetic	2.84E-03
brown	GO:0009057	macromolecule catabolic process	2.95E-03
brown	GO:0010629	negative regulation of gene expression	4.25E-03
brown	GO:0010605	negative regulation of macromolecule metabolic process	4.33E-03
brown	GO:0000280	nuclear division	5.30E-03
brown	GO:0007067	mitosis	5.30E-03
brown	GO:0016458	gene silencing	5.63E-03
brown	GO:0006323	DNA packaging	5.67E-03
brown	GO:0000087	M phase of mitotic cell cycle	6.46E-03
brown	GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	6.52E-03
brown	GO:0000375	RNA splicing, via transesterification reactions	6.52E-03
brown	GO:0000398	nuclear mRNA splicing, via spliceosome	6.52E-03
brown	GO:0051297	centrosome organization	7.25E-03
brown	GO:0048285	organelle fission	7.97E-03
brown	GO:0048489	synaptic vesicle transport	8.27E-03
brown	GO:0031047	gene silencing by RNA	8.27E-03
brown	GO:0019941	modification-dependent protein catabolic process	9.11E-03
brown	GO:0043632	modification-dependent macromolecule catabolic process	9.11E-03
brown	GO:0070647	protein modification by small protein conjugation or removal	9.36E-03
brown	GO:0051603	proteolysis involved in cellular protein catabolic process	1.05E-02
brown	GO:0044257	cellular protein catabolic process	1.10E-02
brown	GO:0051301	cell division	1.11E-02
brown	GO:0000226	microtubule cytoskeleton organization	1.18E-02
brown	GO:0006298	mismatch repair	1.47E-02
brown	GO:0030031	cell projection assembly	1.49E-02
brown	GO:0045934	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1.60E-02
brown	GO:0030163	protein catabolic process	1.69E-02
brown	GO:0016567	protein ubiquitination	1.71E-02
brown	GO:0000278	mitotic cell cycle	1.78E-02
brown	GO:0051172	negative regulation of nitrogen compound metabolic process	1.92E-02
brown	GO:0007099	centriole replication	2.03E-02
brown	GO:0043087	regulation of GTPase activity	2.11E-02
brown	GO:0042384	cilium assembly	2.18E-02
brown	GO:0034621	cellular macromolecular complex subunit organization	2.20E-02

brown	GO:0006400	tRNA modification	2.22E-02
brown	GO:0016569	covalent chromatin modification	2.45E-02
brown	GO:0051253	negative regulation of RNA metabolic process	2.52E-02
brown	GO:0006511	ubiquitin-dependent protein catabolic process	2.67E-02
brown	GO:0034661	ncRNA catabolic process	2.76E-02
brown	GO:0043044	ATP-dependent chromatin remodeling	2.76E-02
brown	GO:0032392	DNA geometric change	3.06E-02
brown	GO:0032508	DNA duplex unwinding	3.06E-02
brown	GO:0032446	protein modification by small protein conjugation	3.24E-02
brown	GO:0016481	negative regulation of transcription	3.45E-02
brown	GO:0010558	negative regulation of macromolecule biosynthetic process	3.52E-02
brown	GO:0007098	centrosome cycle	3.53E-02
brown	GO:0006351	transcription, DNA-dependent	3.59E-02
brown	GO:0009451	RNA modification	3.73E-02
brown	GO:0045892	negative regulation of transcription, DNA-dependent	3.74E-02
brown	GO:0006399	tRNA metabolic process	3.96E-02
brown	GO:0032774	RNA biosynthetic process	4.03E-02
brown	GO:0051298	centrosome duplication	4.50E-02
brown	GO:0007020	microtubule nucleation	4.50E-02
brown	GO:0031327	negative regulation of cellular biosynthetic process	4.57E-02
brown	GO:0016570	histone modification	4.73E-02
blue	GO:0006350	transcription	1.40E-07
blue	GO:0046578	regulation of Ras protein signal transduction	6.53E-06
blue	GO:0051056	regulation of small GTPase mediated signal transduction	2.23E-05
blue	GO:0006355	regulation of transcription, DNA-dependent	1.85E-04
blue	GO:0046777	protein amino acid autophosphorylation	6.19E-04
blue	GO:0006468	protein amino acid phosphorylation	1.64E-03
blue	GO:0007242	intracellular signaling cascade	4.17E-03
blue	GO:0006325	chromatin organization	4.26E-03
blue	GO:0007265	Ras protein signal transduction	5.33E-03
blue	GO:0033554	cellular response to stress	5.66E-03
blue	GO:0010627	regulation of protein kinase cascade	6.90E-03
blue	GO:0008104	protein localization	8.54E-03
blue	GO:0045184	establishment of protein localization	9.05E-03

blue	GO:0006886	intracellular protein transport	9.97E-03
blue	GO:0031098	stress-activated protein kinase signaling pathway	1.03E-02
blue	GO:0019637	organophosphate metabolic process	1.05E-02
blue	GO:0032312	regulation of ARF GTPase activity	1.06E-02
blue	GO:0016310	phosphorylation	1.06E-02
blue	GO:0006913	nucleocytoplasmic transport	1.07E-02
blue	GO:0015031	protein transport	1.07E-02
blue	GO:0006644	phospholipid metabolic process	1.12E-02
blue	GO:0006289	nucleotide-excision repair	1.20E-02
blue	GO:0051169	nuclear transport	1.21E-02
blue	GO:0045814	negative regulation of gene expression, epigenetic	1.23E-02
blue	GO:0006605	protein targeting	1.28E-02
blue	GO:0006338	chromatin remodeling	1.35E-02
blue	GO:0016458	gene silencing	1.35E-02
blue	GO:0006670	sphingosine metabolic process	1.35E-02
blue	GO:0042048	olfactory behavior	1.35E-02
blue	GO:0006914	autophagy	1.37E-02
blue	GO:0016571	histone methylation	1.50E-02
blue	GO:0006974	response to DNA damage stimulus	1.55E-02
blue	GO:0034613	cellular protein localization	1.62E-02
blue	GO:0016192	vesicle-mediated transport	1.76E-02
blue	GO:0035023	regulation of Rho protein signal transduction	1.78E-02
blue	GO:0006915	apoptosis	1.78E-02
blue	GO:0070727	cellular macromolecule localization	1.81E-02
blue	GO:0007254	JNK cascade	1.86E-02
blue	GO:0007635	chemosensory behavior	1.99E-02
blue	GO:0051726	regulation of cell cycle	2.00E-02
blue	GO:0008654	phospholipid biosynthetic process	2.23E-02
blue	GO:0012501	programmed cell death	2.34E-02
blue	GO:0051338	regulation of transferase activity	2.39E-02
blue	GO:0051329	interphase of mitotic cell cycle	2.40E-02
blue	GO:0050772	positive regulation of axonogenesis	2.55E-02
blue	GO:0032318	regulation of Ras GTPase activity	2.58E-02
blue	GO:0008219	cell death	2.67E-02

blue	GO:0034504	protein localization in nucleus	2.72E-02
blue	GO:0051325	interphase	2.96E-02
blue	GO:0016265	death	3.07E-02
blue	GO:0002275	myeloid cell activation during immune response	3.13E-02
blue	GO:0006650	glycerophospholipid metabolic process	3.16E-02
blue	GO:0006399	tRNA metabolic process	3.16E-02
blue	GO:0043122	regulation of I-kappaB kinase/NF-kappaB cascade	3.17E-02
blue	GO:0045892	negative regulation of transcription, DNA-dependent	3.21E-02
blue	GO:0006396	RNA processing	3.25E-02
blue	GO:0010558	negative regulation of macromolecule biosynthetic process	3.25E-02
blue	GO:0046328	regulation of JNK cascade	3.29E-02
blue	GO:0006606	protein import into nucleus	3.31E-02
blue	GO:0043549	regulation of kinase activity	3.33E-02
blue	GO:0045859	regulation of protein kinase activity	3.36E-02
blue	GO:0009890	negative regulation of biosynthetic process	3.39E-02
blue	GO:0031327	negative regulation of cellular biosynthetic process	3.44E-02
blue	GO:0000082	G1/S transition of mitotic cell cycle	3.65E-02
blue	GO:0006383	transcription from RNA polymerase III promoter	3.75E-02
blue	GO:0035176	social behavior	3.75E-02
blue	GO:0051170	nuclear import	3.83E-02
blue	GO:0046907	intracellular transport	3.98E-02
blue	GO:0042384	cilium assembly	3.98E-02
blue	GO:0006796	phosphate metabolic process	3.98E-02
blue	GO:0006793	phosphorus metabolic process	3.98E-02
blue	GO:0051253	negative regulation of RNA metabolic process	3.98E-02
blue	GO:0050770	regulation of axonogenesis	4.00E-02
blue	GO:0006346	methylation-dependent chromatin silencing	4.11E-02
blue	GO:0046474	glycerophospholipid biosynthetic process	4.23E-02
blue	GO:0042158	lipoprotein biosynthetic process	4.38E-02
blue	GO:0006259	DNA metabolic process	4.40E-02
blue	GO:0070302	regulation of stress-activated protein kinase signaling pathway	4.59E-02
blue	GO:0010975	regulation of neuron projection development	4.96E-02
magenta	GO:0048704	embryonic skeletal system morphogenesis	6.27E-07
magenta	GO:0051252	regulation of RNA metabolic process	1.25E-06

magenta	GO:0006355	regulation of transcription, DNA-dependent	2.14E-06
magenta	GO:0048706	embryonic skeletal system development	4.93E-06
magenta	GO:0048562	embryonic organ morphogenesis	2.22E-05
magenta	GO:0048705	skeletal system morphogenesis	5.77E-05
magenta	GO:0048568	embryonic organ development	1.37E-04
magenta	GO:0009952	anterior/posterior pattern formation	2.34E-04
magenta	GO:0045449	regulation of transcription	3.01E-04
magenta	GO:0048598	embryonic morphogenesis	3.75E-04
magenta	GO:0043009	chordate embryonic development	6.75E-04
magenta	GO:0009792	embryonic development ending in birth or egg hatching	7.24E-04
magenta	GO:0006350	transcription	9.90E-04
magenta	GO:0003002	regionalization	1.77E-03
magenta	GO:0010604	positive regulation of macromolecule metabolic process	3.38E-03
magenta	GO:0060429	epithelium development	3.91E-03
magenta	GO:0010628	positive regulation of gene expression	5.08E-03
magenta	GO:0001501	skeletal system development	7.15E-03
magenta	GO:0000122	negative regulation of transcription from RNA polymerase II promoter	9.10E-03
magenta	GO:0007389	pattern specification process	9.27E-03
magenta	GO:0045893	positive regulation of transcription, DNA-dependent	9.35E-03
magenta	GO:0051254	positive regulation of RNA metabolic process	9.88E-03
magenta	GO:0045941	positive regulation of transcription	1.09E-02
magenta	GO:0045935	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	2.15E-02
magenta	GO:0050821	protein stabilization	2.50E-02
magenta	GO:0006357	regulation of transcription from RNA polymerase II promoter	2.62E-02
magenta	GO:0051173	positive regulation of nitrogen compound metabolic process	2.63E-02
magenta	GO:0010557	positive regulation of macromolecule biosynthetic process	2.91E-02
magenta	GO:0043632	modification-dependent macromolecule catabolic process	2.99E-02
magenta	GO:0019941	modification-dependent protein catabolic process	2.99E-02
magenta	GO:0034644	cellular response to UV	3.47E-02
magenta	GO:0045892	negative regulation of transcription, DNA-dependent	3.77E-02
magenta	GO:0051603	proteolysis involved in cellular protein catabolic process	3.86E-02
magenta	GO:0031328	positive regulation of cellular biosynthetic process	3.87E-02
magenta	GO:0044257	cellular protein catabolic process	3.98E-02
magenta	GO:0051253	negative regulation of RNA metabolic process	4.07E-02

magenta	GO:0009891	positive regulation of biosynthetic process	4.23E-02
magenta	GO:0045944	positive regulation of transcription from RNA polymerase II promoter	4.54E-02
magenta	GO:0030163	protein catabolic process	4.74E-02
red	GO:0003012	muscle system process	9.46E-16
red	GO:0007517	muscle organ development	5.57E-10
red	GO:0007010	cytoskeleton organization	9.16E-07
red	GO:0060537	muscle tissue development	3.34E-06
red	GO:0034329	cell junction assembly	3.43E-05
red	GO:0030036	actin cytoskeleton organization	4.51E-05
red	GO:0031032	actomyosin structure organization	5.90E-05
red	GO:0006941	striated muscle contraction	6.71E-05
red	GO:0042692	muscle cell differentiation	9.95E-05
red	GO:0007507	heart development	1.18E-04
red	GO:0006939	smooth muscle contraction	1.34E-04
red	GO:0055002	striated muscle cell development	1.35E-04
red	GO:0030705	cytoskeleton-dependent intracellular transport	1.35E-04
red	GO:0008016	regulation of heart contraction	1.72E-04
red	GO:0010927	cellular component assembly involved in morphogenesis	2.05E-04
red	GO:0055001	muscle cell development	2.05E-04
red	GO:0034330	cell junction organization	2.26E-04
red	GO:0030239	myofibril assembly	2.60E-04
red	GO:0006940	regulation of smooth muscle contraction	2.66E-04
red	GO:0007044	cell-substrate junction assembly	3.75E-04
red	GO:0030048	actin filament-based movement	3.75E-04
red	GO:0051146	striated muscle cell differentiation	3.95E-04
red	GO:0007155	cell adhesion	4.51E-04
red	GO:0022610	biological adhesion	4.60E-04
red	GO:0008015	blood circulation	5.86E-04
red	GO:0003013	circulatory system process	5.86E-04
red	GO:0050880	regulation of blood vessel size	1.26E-03
red	GO:0035150	regulation of tube size	1.26E-03
red	GO:0003018	vascular process in circulatory system	1.90E-03
red	GO:0042310	vasoconstriction	2.05E-03
red	GO:0007160	cell-matrix adhesion	2.42E-03

red	GO:0031589	cell-substrate adhesion	3.91E-03
red	GO:0030030	cell projection organization	4.40E-03
red	GO:0007015	actin filament organization	4.88E-03
red	GO:0051493	regulation of cytoskeleton organization	4.91E-03
red	GO:0006633	fatty acid biosynthetic process	7.21E-03
red	GO:0014829	vascular smooth muscle contraction	7.82E-03
red	GO:0030049	muscle filament sliding	7.82E-03
red	GO:0033275	actin-myosin filament sliding	7.82E-03
red	GO:0070252	actin-mediated cell contraction	7.82E-03
red	GO:0032989	cellular component morphogenesis	8.18E-03
red	GO:0051592	response to calcium ion	9.88E-03
red	GO:0046456	icosanoid biosynthetic process	1.16E-02
red	GO:0010035	response to inorganic substance	1.37E-02
red	GO:0006928	cell motion	1.45E-02
red	GO:0006636	unsaturated fatty acid biosynthetic process	1.49E-02
red	GO:0051271	negative regulation of cell motion	1.57E-02
red	GO:0005977	glycogen metabolic process	1.61E-02
red	GO:0031175	neuron projection development	1.71E-02
red	GO:0006073	cellular glucan metabolic process	1.74E-02
red	GO:0044042	glucan metabolic process	1.74E-02
red	GO:0033043	regulation of organelle organization	1.86E-02
red	GO:0008217	regulation of blood pressure	1.87E-02
red	GO:0051924	regulation of calcium ion transport	2.13E-02
red	GO:0007229	integrin-mediated signaling pathway	2.23E-02
red	GO:0043462	regulation of ATPase activity	2.43E-02
red	GO:0006112	energy reserve metabolic process	2.78E-02
red	GO:0045987	positive regulation of smooth muscle contraction	3.04E-02
red	GO:0051495	positive regulation of cytoskeleton organization	3.13E-02
red	GO:0060048	cardiac muscle contraction	3.36E-02
red	GO:0006690	icosanoid metabolic process	3.50E-02
red	GO:0010959	regulation of metal ion transport	3.56E-02
red	GO:0048666	neuron development	3.60E-02
red	GO:0010638	positive regulation of organelle organization	3.84E-02
red	GO:0007268	synaptic transmission	3.99E-02

red	GO:0045933	positive regulation of muscle contraction	4.04E-02
red	GO:0033559	unsaturated fatty acid metabolic process	4.30E-02
red	GO:0043244	regulation of protein complex disassembly	4.30E-02
red	GO:0019226	transmission of nerve impulse	4.30E-02
red	GO:0007264	small GTPase mediated signal transduction	4.51E-02
red	GO:0007412	axon target recognition	4.52E-02
red	GO:0003056	regulation of vascular smooth muscle contraction	4.52E-02
red	GO:0048812	neuron projection morphogenesis	4.55E-02
red	GO:0044264	cellular polysaccharide metabolic process	4.73E-02
red	GO:0003015	heart process	4.78E-02
red	GO:0060047	heart contraction	4.78E-02
red	GO:0010038	response to metal ion	4.81E-02
red	GO:0042493	response to drug	4.85E-02
yellow	GO:0009725	response to hormone stimulus	2.46E-11
yellow	GO:0009719	response to endogenous stimulus	7.84E-11
yellow	GO:0032868	response to insulin stimulus	9.37E-09
yellow	GO:0010033	response to organic substance	3.24E-08
yellow	GO:0001568	blood vessel development	1.14E-06
yellow	GO:0001944	vasculature development	1.66E-06
yellow	GO:0001525	angiogenesis	8.86E-06
yellow	GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	1.91E-05
yellow	GO:0048514	blood vessel morphogenesis	3.39E-05
yellow	GO:0007242	intracellular signaling cascade	5.31E-05
yellow	GO:0045785	positive regulation of cell adhesion	6.90E-05
yellow	GO:0030334	regulation of cell migration	1.59E-04
yellow	GO:0040012	regulation of locomotion	1.59E-04
yellow	GO:0051270	regulation of cell motion	1.68E-04
yellow	GO:0009755	hormone-mediated signaling	1.85E-04
yellow	GO:0008286	insulin receptor signaling pathway	1.89E-04
yellow	GO:0008360	regulation of cell shape	2.36E-04
yellow	GO:0030802	regulation of cyclic nucleotide biosynthetic process	2.37E-04
yellow	GO:0030808	regulation of nucleotide biosynthetic process	2.37E-04
yellow	GO:0030799	regulation of cyclic nucleotide metabolic process	2.96E-04
yellow	GO:0019933	cAMP-mediated signaling	3.56E-04

yellow	GO:0006140	regulation of nucleotide metabolic process	3.65E-04
yellow	GO:0006101	citrate metabolic process	4.05E-04
yellow	GO:0034754	cellular hormone metabolic process	4.11E-04
yellow	GO:0007243	protein kinase cascade	4.11E-04
yellow	GO:0010811	positive regulation of cell-substrate adhesion	4.13E-04
yellow	GO:0031279	regulation of cyclase activity	4.84E-04
yellow	GO:0051339	regulation of lyase activity	5.61E-04
yellow	GO:0010810	regulation of cell-substrate adhesion	6.39E-04
yellow	GO:0031667	response to nutrient levels	7.05E-04
yellow	GO:0042127	regulation of cell proliferation	7.26E-04
yellow	GO:0006631	fatty acid metabolic process	7.37E-04
yellow	GO:0006006	glucose metabolic process	8.85E-04
yellow	GO:0033500	carbohydrate homeostasis	9.00E-04
yellow	GO:0042593	glucose homeostasis	9.00E-04
yellow	GO:0019432	triglyceride biosynthetic process	9.38E-04
yellow	GO:0019216	regulation of lipid metabolic process	1.18E-03
yellow	GO:0010906	regulation of glucose metabolic process	1.20E-03
yellow	GO:0008203	cholesterol metabolic process	1.32E-03
yellow	GO:0008610	lipid biosynthetic process	1.47E-03
yellow	GO:0051350	negative regulation of lyase activity	1.66E-03
yellow	GO:0031280	negative regulation of cyclase activity	1.66E-03
yellow	GO:0007194	negative regulation of adenylate cyclase activity	1.66E-03
yellow	GO:0045761	regulation of adenylate cyclase activity	1.74E-03
yellow	GO:0010675	regulation of cellular carbohydrate metabolic process	1.75E-03
yellow	GO:0019318	hexose metabolic process	1.78E-03
yellow	GO:0009991	response to extracellular stimulus	1.93E-03
yellow	GO:0008285	negative regulation of cell proliferation	1.96E-03
yellow	GO:0006109	regulation of carbohydrate metabolic process	1.97E-03
yellow	GO:0040017	positive regulation of locomotion	1.99E-03
yellow	GO:0031589	cell-substrate adhesion	1.99E-03
yellow	GO:0051272	positive regulation of cell motion	1.99E-03
yellow	GO:0005996	monosaccharide metabolic process	2.09E-03
yellow	GO:0046463	acylglycerol biosynthetic process	2.33E-03
yellow	GO:0046460	neutral lipid biosynthetic process	2.33E-03

yellow	GO:0051056	regulation of small GTPase mediated signal transduction	2.34E-03
yellow	GO:0030817	regulation of cAMP biosynthetic process	2.40E-03
yellow	GO:0016125	sterol metabolic process	2.40E-03
yellow	GO:0030036	actin cytoskeleton organization	2.44E-03
yellow	GO:0030814	regulation of cAMP metabolic process	2.72E-03
yellow	GO:0008643	carbohydrate transport	2.83E-03
yellow	GO:0030198	extracellular matrix organization	2.88E-03
yellow	GO:0046504	glycerol ether biosynthetic process	2.98E-03
yellow	GO:0042445	hormone metabolic process	3.25E-03
yellow	GO:0019935	cyclic-nucleotide-mediated signaling	3.30E-03
yellow	GO:0007188	G-protein signaling, coupled to cAMP nucleotide second messenger	3.57E-03
yellow	GO:0022610	biological adhesion	3.60E-03
yellow	GO:0007155	cell adhesion	3.63E-03
yellow	GO:0046578	regulation of Ras protein signal transduction	3.73E-03
yellow	GO:0030029	actin filament-based process	4.24E-03
yellow	GO:0030335	positive regulation of cell migration	4.61E-03
yellow	GO:0007160	cell-matrix adhesion	4.61E-03
yellow	GO:0043467	regulation of generation of precursor metabolites and energy	4.85E-03
yellow	GO:0044093	positive regulation of molecular function	5.10E-03
yellow	GO:0006573	valine metabolic process	5.13E-03
yellow	GO:0019530	taurine metabolic process	5.13E-03
yellow	GO:0007584	response to nutrient	5.37E-03
yellow	GO:0006639	acylglycerol metabolic process	5.40E-03
yellow	GO:0006638	neutral lipid metabolic process	5.88E-03
yellow	GO:0045860	positive regulation of protein kinase activity	6.01E-03
yellow	GO:0050678	regulation of epithelial cell proliferation	6.03E-03
yellow	GO:0006662	glycerol ether metabolic process	6.40E-03
yellow	GO:0007010	cytoskeleton organization	6.48E-03
yellow	GO:0034199	activation of protein kinase A activity	6.62E-03
yellow	GO:0006468	protein amino acid phosphorylation	6.75E-03
yellow	GO:0018904	organic ether metabolic process	7.53E-03
yellow	GO:0008202	steroid metabolic process	7.68E-03
yellow	GO:0019915	lipid storage	7.80E-03
yellow	GO:0042551	neuron maturation	7.80E-03

yellow	GO:0006766	vitamin metabolic process	7.85E-03
yellow	GO:0033674	positive regulation of kinase activity	7.90E-03
yellow	GO:0008284	positive regulation of cell proliferation	8.07E-03
yellow	GO:0010907	positive regulation of glucose metabolic process	9.11E-03
yellow	GO:0043085	positive regulation of catalytic activity	9.88E-03
yellow	GO:0060173	limb development	1.01E-02
yellow	GO:0048736	appendage development	1.01E-02
yellow	GO:0030336	negative regulation of cell migration	1.02E-02
yellow	GO:0006700	C21-steroid hormone biosynthetic process	1.04E-02
yellow	GO:0007517	muscle organ development	1.05E-02
yellow	GO:0051347	positive regulation of transferase activity	1.05E-02
yellow	GO:0045913	positive regulation of carbohydrate metabolic process	1.05E-02
yellow	GO:0010676	positive regulation of cellular carbohydrate metabolic process	1.05E-02
yellow	GO:0032535	regulation of cellular component size	1.09E-02
yellow	GO:0009187	cyclic nucleotide metabolic process	1.13E-02
yellow	GO:0022604	regulation of cell morphogenesis	1.14E-02
yellow	GO:0001569	patterning of blood vessels	1.21E-02
yellow	GO:0046058	cAMP metabolic process	1.21E-02
yellow	GO:0043255	regulation of carbohydrate biosynthetic process	1.21E-02
yellow	GO:0060326	cell chemotaxis	1.24E-02
yellow	GO:0016477	cell migration	1.26E-02
yellow	GO:0060341	regulation of cellular localization	1.34E-02
yellow	GO:0016049	cell growth	1.35E-02
yellow	GO:0040013	negative regulation of locomotion	1.35E-02
yellow	GO:0040014	regulation of multicellular organism growth	1.35E-02
yellow	GO:0044057	regulation of system process	1.35E-02
yellow	GO:0007193	inhibition of adenylate cyclase activity by G-protein signaling	1.35E-02
yellow	GO:0050796	regulation of insulin secretion	1.35E-02
yellow	GO:0040008	regulation of growth	1.36E-02
yellow	GO:0043062	extracellular structure organization	1.39E-02
yellow	GO:0007568	aging	1.41E-02
yellow	GO:0048545	response to steroid hormone stimulus	1.44E-02
yellow	GO:0006091	generation of precursor metabolites and energy	1.49E-02
yellow	GO:0051271	negative regulation of cell motion	1.53E-02

yellow	GO:0001523	retinoid metabolic process	1.56E-02
yellow	GO:0016101	diterpenoid metabolic process	1.56E-02
yellow	GO:0031328	positive regulation of cellular biosynthetic process	1.72E-02
yellow	GO:0006641	triglyceride metabolic process	1.73E-02
yellow	GO:0048754	branching morphogenesis of a tube	1.73E-02
yellow	GO:0010884	positive regulation of lipid storage	1.74E-02
yellow	GO:0046580	negative regulation of Ras protein signal transduction	1.74E-02
yellow	GO:0051058	negative regulation of small GTPase mediated signal transduction	1.74E-02
yellow	GO:0007187	G-protein signaling, coupled to cyclic nucleotide second messenger	1.77E-02
yellow	GO:0010557	positive regulation of macromolecule biosynthetic process	1.81E-02
yellow	GO:0015980	energy derivation by oxidation of organic compounds	1.91E-02
yellow	GO:0045935	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1.94E-02
yellow	GO:0006721	terpenoid metabolic process	1.95E-02
yellow	GO:0009190	cyclic nucleotide biosynthetic process	1.95E-02
yellow	GO:0040018	positive regulation of multicellular organism growth	1.95E-02
yellow	GO:0009891	positive regulation of biosynthetic process	1.97E-02
yellow	GO:0051046	regulation of secretion	1.98E-02
yellow	GO:0046890	regulation of lipid biosynthetic process	2.01E-02
yellow	GO:0006107	oxaloacetate metabolic process	2.14E-02
yellow	GO:0002791	regulation of peptide secretion	2.16E-02
yellow	GO:0018108	peptidyl-tyrosine phosphorylation	2.16E-02
yellow	GO:0008361	regulation of cell size	2.26E-02
yellow	GO:0014070	response to organic cyclic substance	2.27E-02
yellow	GO:0042325	regulation of phosphorylation	2.44E-02
yellow	GO:0010817	regulation of hormone levels	2.46E-02
yellow	GO:0018212	peptidyl-tyrosine modification	2.49E-02
yellow	GO:0051173	positive regulation of nitrogen compound metabolic process	2.71E-02
yellow	GO:0040007	growth	2.74E-02
yellow	GO:0042592	homeostatic process	2.74E-02
yellow	GO:0051674	localization of cell	2.75E-02
yellow	GO:0048870	cell motility	2.75E-02
yellow	GO:0035107	appendage morphogenesis	2.77E-02
yellow	GO:0035023	regulation of Rho protein signal transduction	2.77E-02
yellow	GO:0035108	limb morphogenesis	2.77E-02

yellow	GO:0051240	positive regulation of multicellular organismal process	2.80E-02
yellow	GO:0016053	organic acid biosynthetic process	2.82E-02
yellow	GO:0046394	carboxylic acid biosynthetic process	2.82E-02
yellow	GO:0000165	MAPKKK cascade	2.82E-02
yellow	GO:0016202	regulation of striated muscle tissue development	2.84E-02
yellow	GO:0001763	morphogenesis of a branching structure	2.86E-02
yellow	GO:0030856	regulation of epithelial cell differentiation	2.90E-02
yellow	GO:0010628	positive regulation of gene expression	3.00E-02
yellow	GO:0048469	cell maturation	3.01E-02
yellow	GO:0021700	developmental maturation	3.01E-02
yellow	GO:0048634	regulation of muscle development	3.03E-02
yellow	GO:0048878	chemical homeostasis	3.03E-02
yellow	GO:0008207	C21-steroid hormone metabolic process	3.04E-02
yellow	GO:0045859	regulation of protein kinase activity	3.09E-02
yellow	GO:0032101	regulation of response to external stimulus	3.21E-02
yellow	GO:0016310	phosphorylation	3.24E-02
yellow	GO:0042330	taxis	3.32E-02
yellow	GO:0006935	chemotaxis	3.32E-02
yellow	GO:0035295	tube development	3.32E-02
yellow	GO:0051174	regulation of phosphorus metabolic process	3.42E-02
yellow	GO:0019220	regulation of phosphate metabolic process	3.42E-02
yellow	GO:0042446	hormone biosynthetic process	3.45E-02
yellow	GO:0042060	wound healing	3.48E-02
yellow	GO:0051384	response to glucocorticoid stimulus	3.48E-02
yellow	GO:0010595	positive regulation of endothelial cell migration	3.54E-02
yellow	GO:0007265	Ras protein signal transduction	3.55E-02
yellow	GO:0019748	secondary metabolic process	3.65E-02
yellow	GO:0031327	negative regulation of cellular biosynthetic process	3.79E-02
yellow	GO:0051051	negative regulation of transport	3.80E-02
yellow	GO:0016051	carbohydrate biosynthetic process	3.84E-02
yellow	GO:0043549	regulation of kinase activity	3.94E-02
yellow	GO:0045941	positive regulation of transcription	3.98E-02
yellow	GO:0046324	regulation of glucose import	4.05E-02
yellow	GO:0032526	response to retinoic acid	4.05E-02

yellow	GO:0006775	fat-soluble vitamin metabolic process	4.05E-02
yellow	GO:0006171	cAMP biosynthetic process	4.07E-02
yellow	GO:0035265	organ growth	4.07E-02
yellow	GO:0042542	response to hydrogen peroxide	4.07E-02
yellow	GO:0048771	tissue remodeling	4.07E-02
yellow	GO:0003012	muscle system process	4.23E-02
yellow	GO:0055114	oxidation reduction	4.24E-02
yellow	GO:0010604	positive regulation of macromolecule metabolic process	4.25E-02
yellow	GO:0010565	regulation of cellular ketone metabolic process	4.30E-02
yellow	GO:0031281	positive regulation of cyclase activity	4.30E-02
yellow	GO:0010827	regulation of glucose transport	4.36E-02
yellow	GO:0007166	cell surface receptor linked signal transduction	4.50E-02
yellow	GO:0009890	negative regulation of biosynthetic process	4.56E-02
yellow	GO:0022617	extracellular matrix disassembly	4.59E-02
yellow	GO:0032881	regulation of polysaccharide metabolic process	4.62E-02
yellow	GO:0009060	aerobic respiration	4.69E-02
yellow	GO:0048871	multicellular organismal homeostasis	4.76E-02
yellow	GO:0031960	response to corticosteroid stimulus	4.76E-02
yellow	GO:0006694	steroid biosynthetic process	4.76E-02
yellow	GO:0051349	positive regulation of lyase activity	4.79E-02
yellow	GO:0019932	second-messenger-mediated signaling	4.84E-02
yellow	GO:0032147	activation of protein kinase activity	4.96E-02
cyan	GO:0006959	humoral immune response	4.78E-06
cyan	GO:0032101	regulation of response to external stimulus	2.76E-05
cyan	GO:0009611	response to wounding	3.17E-05
cyan	GO:0051384	response to glucocorticoid stimulus	7.05E-05
cyan	GO:0006954	inflammatory response	7.44E-05
cyan	GO:0031960	response to corticosteroid stimulus	1.06E-04
cyan	GO:0030323	respiratory tube development	2.51E-04
cyan	GO:0060541	respiratory system development	3.27E-04
cyan	GO:0035295	tube development	1.37E-03
cyan	GO:0006956	complement activation	1.61E-03
cyan	GO:0002541	activation of plasma proteins involved in acute inflammatory response	1.72E-03
cyan	GO:0002253	activation of immune response	1.82E-03

cyan	GO:0048584	positive regulation of response to stimulus	1.95E-03
cyan	GO:0002684	positive regulation of immune system process	2.04E-03
cyan	GO:0002526	acute inflammatory response	2.12E-03
cyan	GO:0030198	extracellular matrix organization	2.64E-03
cyan	GO:0001944	vasculature development	2.66E-03
cyan	GO:0006957	complement activation, alternative pathway	3.04E-03
cyan	GO:0009612	response to mechanical stimulus	3.67E-03
cyan	GO:0050900	leukocyte migration	3.86E-03
cyan	GO:0009725	response to hormone stimulus	4.16E-03
cyan	GO:0048545	response to steroid hormone stimulus	4.23E-03
cyan	GO:0016477	cell migration	4.24E-03
cyan	GO:0006955	immune response	4.61E-03
cyan	GO:0009314	response to radiation	5.02E-03
cyan	GO:0007155	cell adhesion	5.10E-03
cyan	GO:0022610	biological adhesion	5.15E-03
cyan	GO:0002673	regulation of acute inflammatory response	5.95E-03
cyan	GO:0010033	response to organic substance	6.25E-03
cyan	GO:0002252	immune effector process	6.50E-03
cyan	GO:0048286	lung alveolus development	6.52E-03
cyan	GO:0006952	defense response	6.76E-03
cyan	GO:0051674	localization of cell	7.06E-03
cyan	GO:0048870	cell motility	7.06E-03
cyan	GO:0009719	response to endogenous stimulus	7.07E-03
cyan	GO:0050778	positive regulation of immune response	8.55E-03
cyan	GO:0045768	positive regulation of anti-apoptosis	1.19E-02
cyan	GO:0002237	response to molecule of bacterial origin	1.21E-02
cyan	GO:0043062	extracellular structure organization	1.27E-02
cyan	GO:0030334	regulation of cell migration	1.44E-02
cyan	GO:0006928	cell motion	1.60E-02
cyan	GO:0009628	response to abiotic stimulus	1.62E-02
cyan	GO:0031348	negative regulation of defense response	1.69E-02
cyan	GO:0045767	regulation of anti-apoptosis	1.87E-02
cyan	GO:0050817	coagulation	1.90E-02
cyan	GO:0007596	blood coagulation	1.90E-02

cyan	GO:0042060	wound healing	2.15E-02
cyan	GO:0040012	regulation of locomotion	2.19E-02
cyan	GO:0010572	positive regulation of platelet activation	2.20E-02
cyan	GO:0002548	monocyte chemotaxis	2.20E-02
cyan	GO:0007599	hemostasis	2.21E-02
cyan	GO:0051270	regulation of cell motion	2.22E-02
cyan	GO:0001558	regulation of cell growth	2.26E-02
cyan	GO:0051591	response to cAMP	2.26E-02
cyan	GO:0050867	positive regulation of cell activation	2.37E-02
cyan	GO:0008284	positive regulation of cell proliferation	2.71E-02
cyan	GO:0042127	regulation of cell proliferation	2.94E-02
cyan	GO:0042493	response to drug	3.19E-02
cyan	GO:0001501	skeletal system development	3.19E-02
cyan	GO:0035239	tube morphogenesis	3.35E-02
cyan	GO:0022604	regulation of cell morphogenesis	3.62E-02
cyan	GO:0060425	lung morphogenesis	3.82E-02
cyan	GO:0045597	positive regulation of cell differentiation	3.83E-02
cyan	GO:0009416	response to light stimulus	4.12E-02
cyan	GO:0045087	innate immune response	4.12E-02
cyan	GO:0050769	positive regulation of neurogenesis	4.24E-02
cyan	GO:0050878	regulation of body fluid levels	4.35E-02
cyan	GO:0070482	response to oxygen levels	4.35E-02
cyan	GO:0055093	response to hyperoxia	4.35E-02
cyan	GO:0010543	regulation of platelet activation	4.35E-02
cyan	GO:0001568	blood vessel development	4.70E-02
cyan	GO:0045893	positive regulation of transcription, DNA-dependent	4.87E-02
cyan	GO:0032103	positive regulation of response to external stimulus	4.90E-02
tan	GO:0007049	cell cycle	6.19E-36
tan	GO:0022403	cell cycle phase	5.04E-35
tan	GO:0000279	M phase	5.86E-30
tan	GO:0022402	cell cycle process	6.32E-30
tan	GO:0000278	mitotic cell cycle	2.54E-28
tan	GO:0051301	cell division	8.76E-26
tan	GO:0007067	mitosis	1.63E-23

tan	GO:0000280	nuclear division	1.63E-23
tan	GO:0000087	M phase of mitotic cell cycle	2.52E-23
tan	GO:0048285	organelle fission	4.30E-23
tan	GO:0007059	chromosome segregation	1.77E-18
tan	GO:0006259	DNA metabolic process	3.94E-16
tan	GO:0006260	DNA replication	2.65E-15
tan	GO:0006974	response to DNA damage stimulus	1.50E-10
tan	GO:0051726	regulation of cell cycle	2.36E-10
tan	GO:0000075	cell cycle checkpoint	2.66E-10
tan	GO:0006281	DNA repair	2.75E-09
tan	GO:0010564	regulation of cell cycle process	4.16E-08
tan	GO:0051276	chromosome organization	5.56E-08
tan	GO:0033554	cellular response to stress	7.87E-08
tan	GO:0051640	organelle localization	1.16E-07
tan	GO:0051329	interphase of mitotic cell cycle	2.79E-07
tan	GO:0051325	interphase	3.48E-07
tan	GO:0007051	spindle organization	3.69E-07
tan	GO:0007346	regulation of mitotic cell cycle	4.95E-07
tan	GO:0007017	microtubule-based process	5.59E-07
tan	GO:0006261	DNA-dependent DNA replication	1.72E-06
tan	GO:0051303	establishment of chromosome localization	1.97E-06
tan	GO:0050000	chromosome localization	1.97E-06
tan	GO:0000070	mitotic sister chromatid segregation	2.98E-06
tan	GO:0000819	sister chromatid segregation	3.43E-06
tan	GO:0000226	microtubule cytoskeleton organization	4.17E-06
tan	GO:0051656	establishment of organelle localization	4.81E-06
tan	GO:0000085	G2 phase of mitotic cell cycle	8.52E-06
tan	GO:0051319	G2 phase	8.52E-06
tan	GO:0051327	M phase of meiotic cell cycle	3.65E-05
tan	GO:0007126	meiosis	3.65E-05
tan	GO:0051321	meiotic cell cycle	4.09E-05
tan	GO:0007052	mitotic spindle organization	1.07E-04
tan	GO:0007093	mitotic cell cycle checkpoint	1.56E-04
tan	GO:0051383	kinetochore organization	2.38E-04

tan	GO:0031570	DNA integrity checkpoint	3.27E-04
tan	GO:0034508	centromere complex assembly	5.89E-04
tan	GO:0040001	establishment of mitotic spindle localization	1.09E-03
tan	GO:0051293	establishment of spindle localization	1.74E-03
tan	GO:0051653	spindle localization	1.74E-03
tan	GO:0051310	metaphase plate congression	2.12E-03
tan	GO:0000910	cytokinesis	2.22E-03
tan	GO:0048015	phosphoinositide-mediated signaling	2.37E-03
tan	GO:0007096	regulation of exit from mitosis	2.53E-03
tan	GO:0031577	spindle checkpoint	2.53E-03
tan	GO:0000077	DNA damage checkpoint	3.49E-03
tan	GO:0006310	DNA recombination	4.47E-03
tan	GO:0006297	nucleotide-excision repair, DNA gap filling	5.11E-03
tan	GO:0007088	regulation of mitosis	5.39E-03
tan	GO:0051783	regulation of nuclear division	5.39E-03
tan	GO:0045787	positive regulation of cell cycle	5.67E-03
tan	GO:0008283	cell proliferation	6.45E-03
tan	GO:0007010	cytoskeleton organization	6.45E-03
tan	GO:0010212	response to ionizing radiation	6.54E-03
tan	GO:0006275	regulation of DNA replication	7.16E-03
tan	GO:0030071	regulation of mitotic metaphase/anaphase transition	8.50E-03
tan	GO:0051785	positive regulation of nuclear division	1.09E-02
tan	GO:0045840	positive regulation of mitosis	1.09E-02
tan	GO:0033043	regulation of organelle organization	1.24E-02
tan	GO:0000022	mitotic spindle elongation	1.27E-02
tan	GO:0007079	mitotic chromosome movement towards spindle pole	1.27E-02
tan	GO:0051231	spindle elongation	1.27E-02
tan	GO:0051782	negative regulation of cell division	1.27E-02
tan	GO:0008156	negative regulation of DNA replication	1.36E-02
tan	GO:0042770	DNA damage response, signal transduction	1.43E-02
tan	GO:0010638	positive regulation of organelle organization	1.58E-02
tan	GO:0045842	positive regulation of mitotic metaphase/anaphase transition	1.90E-02
tan	GO:0034501	protein localization to kinetochore	1.90E-02
tan	GO:0048478	replication fork protection	1.90E-02

tan	GO:0051382	kinetochore assembly	1.90E-02
tan	GO:0051305	chromosome movement towards spindle pole	1.90E-02
tan	GO:0031536	positive regulation of exit from mitosis	2.52E-02
tan	GO:0051053	negative regulation of DNA metabolic process	2.54E-02
tan	GO:0007127	meiosis I	2.92E-02
tan	GO:0016568	chromatin modification	3.03E-02
tan	GO:0002520	immune system development	3.12E-02
tan	GO:0006271	DNA strand elongation during DNA replication	3.14E-02
tan	GO:0045005	maintenance of fidelity during DNA-dependent DNA replication	3.14E-02
tan	GO:0051052	regulation of DNA metabolic process	3.60E-02
tan	GO:0051651	maintenance of location in cell	3.73E-02
tan	GO:0000132	establishment of mitotic spindle orientation	3.75E-02
tan	GO:0051294	establishment of spindle orientation	3.75E-02
tan	GO:0022616	DNA strand elongation	3.75E-02
tan	GO:0032886	regulation of microtubule-based process	3.87E-02
tan	GO:0031400	negative regulation of protein modification process	4.01E-02
tan	GO:0042254	ribosome biogenesis	4.27E-02
tan	GO:0010605	negative regulation of macromolecule metabolic process	4.31E-02
tan	GO:0031503	protein complex localization	4.37E-02
tan	GO:0032297	negative regulation of DNA replication initiation	4.37E-02
tan	GO:0000076	DNA replication checkpoint	4.37E-02
tan	GO:0000079	regulation of cyclin-dependent protein kinase activity	4.62E-02
tan	GO:0006289	nucleotide-excision repair	4.77E-02
tan	GO:0045132	meiotic chromosome segregation	4.98E-02
greenyellow	GO:0016044	membrane organization	5.34E-08
greenyellow	GO:0001568	blood vessel development	1.31E-05
greenyellow	GO:0001944	vasculature development	1.65E-05
greenyellow	GO:0030334	regulation of cell migration	2.18E-05
greenyellow	GO:0040012	regulation of locomotion	5.94E-05
greenyellow	GO:0051270	regulation of cell motion	6.19E-05
greenyellow	GO:0048514	blood vessel morphogenesis	1.23E-04
greenyellow	GO:0016337	cell-cell adhesion	3.52E-03
greenyellow	GO:0007167	enzyme linked receptor protein signaling pathway	3.79E-03
greenyellow	GO:0045621	positive regulation of lymphocyte differentiation	3.79E-03

greenyellow	GO:0046634	regulation of alpha-beta T cell activation	4.11E-03
greenyellow	GO:0043372	positive regulation of CD4-positive, alpha beta T cell differentiation	4.21E-03
greenyellow	GO:0014706	striated muscle tissue development	4.43E-03
greenyellow	GO:0045597	positive regulation of cell differentiation	4.70E-03
salmon	GO:0006974	response to DNA damage stimulus	6.94E-06
salmon	GO:0033554	cellular response to stress	6.86E-05
salmon	GO:0007049	cell cycle	3.50E-04
salmon	GO:0006281	DNA repair	1.06E-03
salmon	GO:0006259	DNA metabolic process	2.05E-03
salmon	GO:0022403	cell cycle phase	2.20E-03
salmon	GO:0000279	M phase	2.45E-03
salmon	GO:0007059	chromosome segregation	1.06E-02
salmon	GO:0022402	cell cycle process	1.37E-02
salmon	GO:0051327	M phase of meiotic cell cycle	1.77E-02
salmon	GO:0007126	meiosis	1.77E-02
salmon	GO:0051321	meiotic cell cycle	1.87E-02
salmon	GO:0051276	chromosome organization	1.90E-02
salmon	GO:0006350	transcription	2.13E-02
salmon	GO:0051320	S phase	2.78E-02
salmon	GO:0000084	S phase of mitotic cell cycle	2.78E-02
salmon	GO:0008089	anterograde axon cargo transport	3.32E-02
salmon	GO:0033043	regulation of organelle organization	3.37E-02
lightgreen	GO:0006355	regulation of transcription, DNA-dependent	9.20E-05
lightgreen	GO:0051252	regulation of RNA metabolic process	1.13E-04
lightgreen	GO:0006350	transcription	4.31E-04
lightgreen	GO:0045449	regulation of transcription	2.71E-03
lightgreen	GO:0000279	M phase	1.98E-02
lightgreen	GO:0022403	cell cycle phase	3.58E-02
green	GO:0006955	immune response	2.04E-09
green	GO:0006952	defense response	1.90E-08
green	GO:0009611	response to wounding	4.09E-07
green	GO:0006968	cellular defense response	8.93E-06
green	GO:0045087	innate immune response	2.53E-05
green	GO:0007166	cell surface receptor linked signal transduction	9.99E-05

green	GO:0001568	blood vessel development	3.15E-04
green	GO:0001944	vasculature development	3.99E-04
green	GO:0042060	wound healing	4.59E-04
green	GO:0006954	inflammatory response	4.93E-04
green	GO:0002252	immune effector process	5.00E-04
green	GO:0010648	negative regulation of cell communication	1.20E-03
green	GO:0002449	lymphocyte mediated immunity	1.25E-03
green	GO:0045730	respiratory burst	1.25E-03
green	GO:0048878	chemical homeostasis	1.33E-03
green	GO:0009968	negative regulation of signal transduction	1.52E-03
green	GO:0002460	adaptive immune response based on somatic recombination of immune receptors built from	2.05E-03
green	GO:0002250	adaptive immune response	2.05E-03
green	GO:0006959	humoral immune response	2.34E-03
green	GO:0019724	B cell mediated immunity	2.66E-03
green	GO:0002684	positive regulation of immune system process	2.72E-03
green	GO:0006916	anti-apoptosis	2.93E-03
green	GO:0048514	blood vessel morphogenesis	3.50E-03
green	GO:0002443	leukocyte mediated immunity	3.58E-03
green	GO:0051605	protein maturation by peptide bond cleavage	3.58E-03
green	GO:0007507	heart development	4.00E-03
green	GO:0010324	membrane invagination	4.70E-03
green	GO:0006897	endocytosis	4.70E-03
green	GO:0007242	intracellular signaling cascade	5.02E-03
green	GO:0051604	protein maturation	5.04E-03
green	GO:0007202	activation of phospholipase C activity	5.09E-03
green	GO:0010863	positive regulation of phospholipase C activity	5.09E-03
green	GO:0007218	neuropeptide signaling pathway	5.26E-03
green	GO:0030514	negative regulation of BMP signaling pathway	5.27E-03
green	GO:0019835	cytolysis	5.27E-03
green	GO:0006956	complement activation	5.66E-03
green	GO:0055082	cellular chemical homeostasis	5.99E-03
green	GO:0008219	cell death	6.14E-03
green	GO:0002541	activation of plasma proteins involved in acute inflammatory response	6.16E-03
green	GO:0006935	chemotaxis	6.37E-03

green	GO:0042330	taxis	6.37E-03
green	GO:0010518	positive regulation of phospholipase activity	6.55E-03
green	GO:0016265	death	6.64E-03
green	GO:0022604	regulation of cell morphogenesis	7.38E-03
green	GO:0010517	regulation of phospholipase activity	7.39E-03
green	GO:0048584	positive regulation of response to stimulus	7.65E-03
green	GO:0006928	cell motion	7.84E-03
green	GO:0016055	Wnt receptor signaling pathway	8.00E-03
green	GO:0043066	negative regulation of apoptosis	8.16E-03
green	GO:0016477	cell migration	8.17E-03
green	GO:0043069	negative regulation of programmed cell death	9.08E-03
green	GO:0006909	phagocytosis	9.09E-03
green	GO:0060193	positive regulation of lipase activity	9.27E-03
green	GO:0060548	negative regulation of cell death	9.39E-03
green	GO:0018149	peptide cross-linking	9.68E-03
green	GO:0034405	response to fluid shear stress	9.74E-03
green	GO:0007204	elevation of cytosolic calcium ion concentration	1.16E-02
green	GO:0050778	positive regulation of immune response	1.25E-02
green	GO:0006873	cellular ion homeostasis	1.25E-02
green	GO:0016485	protein processing	1.26E-02
green	GO:0001889	liver development	1.28E-02
green	GO:0001817	regulation of cytokine production	1.29E-02
green	GO:0006958	complement activation, classical pathway	1.31E-02
green	GO:0016064	immunoglobulin mediated immune response	1.36E-02
green	GO:0008360	regulation of cell shape	1.36E-02
green	GO:0051249	regulation of lymphocyte activation	1.39E-02
green	GO:0032663	regulation of interleukin-2 production	1.44E-02
green	GO:0030510	regulation of BMP signaling pathway	1.44E-02
green	GO:0030178	negative regulation of Wnt receptor signaling pathway	1.44E-02
green	GO:0002822	regulation of adaptive immune response based on somatic recombination of immune receptors built from	1.45E-02
green	GO:0022409	positive regulation of cell-cell adhesion	1.45E-02
green	GO:0019725	cellular homeostasis	1.46E-02
green	GO:0002819	regulation of adaptive immune response	1.54E-02
green	GO:0048661	positive regulation of smooth muscle cell proliferation	1.57E-02

green	GO:0002455	humoral immune response mediated by circulating immunoglobulin	1.57E-02
green	GO:0051480	cytosolic calcium ion homeostasis	1.60E-02
green	GO:0007264	small GTPase mediated signal transduction	1.63E-02
green	GO:0050900	leukocyte migration	1.64E-02
green	GO:0060191	regulation of lipase activity	1.68E-02
green	GO:0051674	localization of cell	1.70E-02
green	GO:0048870	cell motility	1.70E-02
green	GO:0012501	programmed cell death	1.80E-02
green	GO:0008283	cell proliferation	1.83E-02
green	GO:0042592	homeostatic process	1.88E-02
green	GO:0045785	positive regulation of cell adhesion	1.94E-02
green	GO:0032101	regulation of response to external stimulus	1.98E-02
green	GO:0006875	cellular metal ion homeostasis	1.98E-02
green	GO:0031329	regulation of cellular catabolic process	2.05E-02
green	GO:0050905	neuromuscular process	2.17E-02
green	GO:0050885	neuromuscular process controlling balance	2.18E-02
green	GO:0015698	inorganic anion transport	2.18E-02
green	GO:0010551	regulation of specific transcription from RNA polymerase II promoter	2.27E-02
green	GO:0048565	gut development	2.35E-02
green	GO:0001707	mesoderm formation	2.35E-02
green	GO:0002694	regulation of leukocyte activation	2.44E-02
green	GO:0050801	ion homeostasis	2.44E-02
green	GO:0055065	metal ion homeostasis	2.51E-02
green	GO:0030595	leukocyte chemotaxis	2.52E-02
green	GO:0006022	aminoglycan metabolic process	2.53E-02
green	GO:0002526	acute inflammatory response	2.67E-02
green	GO:0048332	mesoderm morphogenesis	2.70E-02
green	GO:0030324	lung development	2.77E-02
green	GO:0032583	regulation of gene-specific transcription	2.79E-02
green	GO:0060326	cell chemotaxis	2.89E-02
green	GO:0007405	neuroblast proliferation	3.00E-02
green	GO:0006915	apoptosis	3.03E-02
green	GO:0001704	formation of primary germ layer	3.09E-02
green	GO:0050817	coagulation	3.10E-02

green	GO:0030323	respiratory tube development	3.10E-02
green	GO:0007596	blood coagulation	3.10E-02
green	GO:0050865	regulation of cell activation	3.12E-02
green	GO:0016044	membrane organization	3.17E-02
green	GO:0001701	in utero embryonic development	3.21E-02
green	GO:0010553	negative regulation of specific transcription from RNA polymerase II promoter	3.29E-02
green	GO:0048729	tissue morphogenesis	3.58E-02
green	GO:0035295	tube development	3.60E-02
green	GO:0051130	positive regulation of cellular component organization	3.65E-02
green	GO:0021695	cerebellar cortex development	3.74E-02
green	GO:0007599	hemostasis	3.82E-02
green	GO:0060541	respiratory system development	3.82E-02
green	GO:0045076	regulation of interleukin-2 biosynthetic process	4.13E-02
green	GO:0005976	polysaccharide metabolic process	4.22E-02
green	GO:0032496	response to lipopolysaccharide	4.32E-02
green	GO:0030111	regulation of Wnt receptor signaling pathway	4.41E-02
green	GO:0048660	regulation of smooth muscle cell proliferation	4.41E-02
green	GO:0009617	response to bacterium	4.88E-02
green	GO:0032582	negative regulation of gene-specific transcription	4.90E-02
black	GO:0045449	regulation of transcription	1.03E-03
black	GO:0051056	regulation of small GTPase mediated signal transduction	3.48E-03
black	GO:0007243	protein kinase cascade	5.21E-03
black	GO:0007167	enzyme linked receptor protein signaling pathway	8.51E-03
black	GO:0046578	regulation of Ras protein signal transduction	1.36E-02
black	GO:0007242	intracellular signaling cascade	1.57E-02
black	GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	1.89E-02
black	GO:0032870	cellular response to hormone stimulus	2.24E-02
black	GO:0000165	MAPKKK cascade	2.39E-02
black	GO:0009967	positive regulation of signal transduction	2.65E-02
black	GO:0051252	regulation of RNA metabolic process	2.66E-02
black	GO:0006468	protein amino acid phosphorylation	3.07E-02
black	GO:0035108	limb morphogenesis	3.17E-02
black	GO:0035107	appendage morphogenesis	3.17E-02
black	GO:0048598	embryonic morphogenesis	3.25E-02

black	GO:0006355	regulation of transcription, DNA-dependent	3.30E-02
black	GO:0009725	response to hormone stimulus	3.37E-02
black	GO:0007050	cell cycle arrest	3.58E-02
black	GO:0060173	limb development	3.58E-02
black	GO:0048736	appendage development	3.58E-02
black	GO:0007346	regulation of mitotic cell cycle	3.68E-02
black	GO:0045941	positive regulation of transcription	4.01E-02
black	GO:0010647	positive regulation of cell communication	4.58E-02
black	GO:0043009	chordate embryonic development	4.72E-02
black	GO:0016568	chromatin modification	4.82E-02
black	GO:0010628	positive regulation of gene expression	4.84E-02
black	GO:0009792	embryonic development ending in birth or egg hatching	4.93E-02
