Am J Cancer Res 2011;1(1):85-97
www.ajcr.us /ISSN:2156-6976/ajcr0000006

Original Article

Expression profiling and pathway analysis of Krüppel-like factor 4 in mouse embryonic fibroblasts

Engda G. Hagos[1], Amr M. Ghaleb[1], Amrita Kumar[2], Andrew S. Neish[2], and Vincent W. Yang[1,3]

[1]Division of Digestive Diseases, Department of Medicine, [2]Department of Pathology, and [3]Department of Hematology and Oncology, Emory University School of Medicine, Atlanta, Georgia, USA.

Received October 12, 2010; accepted October 19, 2010; Epub October 21, 2010; Published January 1, 2011

Abstract: Background: Krüppel-like factor 4 (KLF4) is a zinc-finger transcription factor with diverse regulatory functions in proliferation, differentiation, and development. KLF4 also plays a role in inflammation, tumorigenesis, and reprogramming of somatic cells to induced pluripotent stem (iPS) cells. To gain insight into the mechanisms by which KLF4 regulates these processes, we conducted DNA microarray analyses to identify differentially expressed genes in mouse embryonic fibroblasts (MEFs) wild type and null for *Klf4*. Methods: Expression profiles of fibroblasts isolated from mouse embryos wild type or null for the *Klf4* alleles were examined by DNA microarrays. Differentially expressed genes were subjected to the Database for Annotation, Visualization and Integrated Discovery (DAVID). The microarray data were also interrogated with the Ingenuity Pathway Analysis (IPA) and Gene Set Enrichment Analysis (GSEA) for pathway identification. Results obtained from the microarray analysis were confirmed by Western blotting for select genes with biological relevance to determine the correlation between mRNA and protein levels. Results: One hundred and sixty three up-regulated and 88 down-regulated genes were identified that demonstrated a fold-change of at least 1.5 and a *P*-value < 0.05 in *Klf4*-null MEFs compared to wild type MEFs. Many of the up-regulated genes in *Klf4*-null MEFs encode proto-oncogenes, growth factors, extracellular matrix, and cell cycle activators. In contrast, genes encoding tumor suppressors and those involved in JAK-STAT signaling pathways are down-regulated in *Klf4*-null MEFs. IPA and GSEA also identified various pathways that are regulated by KLF4. Lastly, Western blotting of select target genes confirmed the changes revealed by microarray data. Conclusions: These data are not only consistent with previous functional studies of KLF4's role in tumor suppression and somatic cell reprogramming, but also revealed novel target genes that mediate KLF4's functions.

Keywords: KLF4, microarray, MEF, DAVID, GSEA, IPA, SAM, FDR

Introduction

Krüppel-like factor 4 (KLF4) [1, 2] is a member of the KLF family of zinc finger transcription factors that are involved in diverse biological processes including proliferation, apoptosis, differentiation, and development [3-7]. KLF4 also plays an important role in pathological conditions such as tumorigenesis and inflammation [8-14]. Moreover, recent studies indicate that KLF4 is involved in the reprogramming of somatic cells to induced pluripotent stem (iPS) cells [15-20]. The finding that KLF4 overexpression prevents mouse embryonic stem (ES) cell differentiation suggests that KLF4 contributes to ES cell self-renewal [21].

Mice deficient for *Klf4* have been generated. *Klf4*-null (*Klf4*$^{-/-}$) mice die shortly after birth and exhibit defects in terminal differentiation of epithelial tissues such as the epidermis and colon [22, 23]. Mice with tissue-specific deletion of *Klf4* also have perturbed homeostasis in tissues from which the gene was deleted including the conjunctiva and stomach [24, 25]. In contrast, mice heterozygous for *Klf4* (*Klf4*$^{+/-}$) are normal but have increased tumor burden in the intestine when bred to *Apc*^{Min} mice that are genetically predisposed to develop intestinal adenomas [10]. Conversely, inhibition of oncogenic Notch signaling in *Apc*^{Min} mice results in an increase in *Klf4* expression accompanied by a reduction in intestinal tumor burden [9]. These results are highly suggestive of a tumor suppressive function for KLF4 in the intestinal epithelium. Recent studies demonstrating that mouse embryonic fibroblasts (MEFs) null for the *Klf4* alleles are genetically unstable as evidenced by the presence of aneuploidy, chromosome aberration, and centrosome amplification are consistent with this notion [26].

Despite growing evidence that KLF4 mediates many important physiological processes as exemplified above, the biochemical mechanisms by which KLF4 exerts many of its functions are not well established. Previous studies involving transcriptional profiling of KLF4 when it is overexpressed in a colon cancer cell line indicate that KLF4 has a global inhibitory effect on macromolecular biosynthesis and the cell cycle [27, 28]. However, no systemic evaluation has been conducted to examine the global expression profiles of KLF4 in untransformed cells. Here we compared the expression profiles of KLF4 between MEFs wild type and null for the *Klf4* alleles in an attempt to gain further insight into the mechanism of action of KLF4 in a physiological context.

Materials and methods

Isolation of mouse embryonic fibroblasts (MEFs) and cell culture

Mice heterozygous for the *Klf4* alleles (*Klf4*$^{+/-}$) on a C57BL/6 background [23] were crossbred. MEFs wild type (*Klf4*$^{+/+}$), heterozygous (*Klf4*$^{+/-}$), or null (*Klf4*$^{-/-}$) for *Klf4* were derived from day 13.5 embryos using the 3T3 protocol as previously described [29]. Briefly, 10^6 MEFs were plated on 10-cm dishes and maintained in Dulbecco's modified Eagle's Medium (DMEM), supplemented with 10% fetal bovine serum (FBS), and 1% penicillin–streptomycin at 37^{0}C in atmosphere containing 5% CO_2. Cells were passed every 3 days at a density of 10^6 cells per 10-cm dish. The breeding of mice and isolation of MEFs from mice were approved by the Emory University Institutional Animal Care and Use Committee (protocol number 098-2007).

Purification and preparation of RNA

RNA was processed from cells that had reached 80-90 confluency. Total RNA from cultured wild type and *Klf4*-null MEFs in triplicate was extracted using Trizol reagent as recommended by the manufacturer (Invitrogen; Carlsbad, CA). RNA was subjected to DNase I treatment in order to remove any contaminating genomic DNA. Final purification was performed on RNAeasy columns (Qiagen; Valencia, CA), according to the manufacturer's recommendations. The integrity of total RNA was confirmed by formaldehyde agarose gel electrophoresis. The RNA was quantified by spectrophotometric reading at 260 and 280 nm and RNA with OD_{260} /OD_{280} > 1.8 was submitted for microarray analysis.

Microarray expression analysis

Purified RNA was shipped to the Emory Biomarker Service Center, Emory University, Atlanta, GA, for microarray analysis. Concentration of the RNA was quantified by a Nanodrop spectrophotometer (Wilmington, DE) and quality was assessed using the Agilent Bioanalyzer (Foster City, CA). Samples with the RNA integrity number of > 7 were used for further microarray analysis. RNA was amplified into cRNA and labeled by *in vitro* transcription using Illumina TotalPrep RNA Amplification Kit (Ambion, Applied Biosystems; Foster City, CA). Samples were then hybridized to the Mouse WG-6 v2.0 Expression Beadchip that queries 45,281 transcripts that cover over 19,000 unique, curated genes in the NCBI RefSeq database (Build 36, Release 22). The chips were processed as per manufacturer's instructions without any modification. The arrays were scanned using the BeadStation 500 Instrument (Illumina Inc.; San Diego, CA) and data were normalized using the GenomeStudio v1.0.2 (Illumina Inc.; San Diego, CA). The data discussed in this publication have been deposited in the National Center for Biotechnology Information (NCBI's) Gene Expression Omnibus (GEO) and are accessible through GEO series accession number GSE21768.

Data normalization and statistical analysis

The background subtraction, expression summary, normalization, and log base 2 transformation of gene signals were carried out using Illumina Beadchip software (Illumina Inc.; San Diego, CA). Significant genes were identified using the significance analysis of microarrays (SAM) software [30], for which 1,000 random class assignment permutations estimated a false discovery rate (FDR) rate of 1%. This resulted in the identification of 6,218 genes with significant changes in expression between *Klf4*$^{+/+}$ and *Klf4*$^{-/-}$ MEFs.The 6,218 differentially expressed genes were annotated and biological processes were analyzed using the Database for Annotation, Visualization and Integrated Discovery (DAVID) (www.david.abcc.ncifcrf.gov). A fold-change of > 1.5 or < -1.5 and $P < 0.05$ were used as the criteria for significant gene expression changes between the *Klf4*$^{+/+}$ and *Klf4*$^{-/-}$ cells. This narrowed the number of significant genes down to 251 genes, including 163 up-regulated and 88 down-regulated ones, in *Klf4*-null cells.

Pathway analyses were conducted on the 6,218 differentially expressed genes with a FDR of 1% identified above using Gene Set Enrichment Analysis (GSEA; www.broad.mit.edu/gsea) and Ingenuity Pathway Analysis (IPA; www.ingenity.com). GSEA, based on the Kolmogorov–Smirnov statistic, was performed as described [31]. GSEA is a knowledge-based approach for interpreting genome-wide expression profiles, using 1,000 trials with randomly permuted class label to estimate a *P*-value. For each gene set, the ES (enrichment score) were normalized to account for differences in gene set size. The false discovery rate (FDR) was then calculated relative to the normalized enrichment score (NES) values to determine the false-positive rate. Significant FDR and *P*-values were less than 25% and 0.001, respectively, in accordance with GSEA recommendations.

IPA assigns biological functions to genes using the Ingenuity Pathways Knowledge Base (Ingenuity Systems, Inc., Redwood City, CA). In this, genes could be sorted several times to different groups, if their function is known as to be multimodal. The dataset containing the gene identifiers and fold-changes were uploaded into the web-based application and each gene identifier was mapped to its corresponding gene object in the Ingenuity Pathways Knowledge Base. After the analysis, generated biological function genes are ordered by *P*-value of significance and maximum number of genes.

Western blot analysis

Following protein extraction, Western blot analysis was conducted using primary antibodies against CDK2, MMP3, SUMO3, and β-actin (Santa Cruz Biotechnology, Santa Cruz, CA, USA), STAT3, pSTAT3 and SOCS3 (Cell Signaling, Danvers, MA, USA). The blots were incubated with appropriate horseradish peroxidase-conjugated secondary antibodies for 1 h at room temperature. The antibody–antigen complex was visualized by ECL chemiluminescence (Amersham, Pittsburgh, PA, USA).

Results

Changes in global gene expression patterns between wild type and Klf4-null mouse embryonic fibroblasts

To identify differentially expressed genes between wild type and *Klf4*-null MEFs, complimentary RNAs in triplicate were hybridized to the Illumina Mouse WG-6 v2.0 Expression BeadChip containing 45,218 probes that represent over 19,000 unique, curated mouse genes in the NCBI RefSeq database (Build 36, Release 22). Significance analysis of microarray (SAM) was used to analyze the original normalized dataset. This revealed a total of 6,218 genes that were differentially expressed in the *Klf4*-null cells compared to wild type MEFs with a false discovery rate (FDR) equal to or less than 1% (1% chance of genes falsely identified as differentially expressed). Among this group, 163 up-regulated and 88 down-regulated genes in *Klf4*-null compared to wild type MEFs exhibited at least a 1.5 fold-change in expression levels and a *P*-value < 0.05. Both the up- and down-regulated differentially expressed genes were submitted to DAVID (Database for Annotation, Visualization and Integrated Discovery), a web-based application (david.abcc.ncifcrf.gov) that allows access to a relational database of functional annotation [32, 33]. Shown in **Tables 1** and **2** are examples of the up-regulated and down-regulated genes in *Klf4*-null cells, respectively, that have identifiable molecular functions. Moreover, many of these genes can be clustered into major functional categories. For example, up-regulated genes in *Klf4*-null cells encode cell cycle activators, extracellular matrix proteins, proto-oncogenes, growth factors, and proteins involved in ubiquitination and inflammatory responses (**Table 1**). In contrast, a distinct group of genes is down-regulated in *Klf4*-null cells and includes those encoding JAK-STAT signaling proteins, homeobox proteins, glutathione metabolism, and ephrins (**Table 2**). The full lists of up- and down-regulated genes in *Klf4* -null MEFs are provided as supplementary materials (Tables S1 and S2, respectively).

Ingenuity biological functional analyses of the genes in wild type and Klf4-null MEFs

We next used Ingenuity Pathway Analysis (IPA;

Table 1. Examples of functional annotation clustering of genes up-regulated in *Klf4*-null MEFs

ILLUMINA_ID	Gene Symbol	Gene Name (Description)	*P*-Value	Fold-change
Cell Cycle			8.00E-03	
ILMN_1217331	Mcm6	MINICHROMOSOME MAINTENANCE DEFICIENT 6		40.36
ILMN_2723931	E2f6	E2F TRANSCRIPTION FACTOR 6		26.8
ILMN_1218470	Cdk2	CYCLIN-DEPENDENT KINASE 2		9.32
ILMN_2652909	Ddit3	DNA-DAMAGE INDUCIBLE TRANSCRIPT 3		2.07
ILMN_2742152	Gadd45a	GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE 45 ALPHA		1.92
ILMN_1227009	Gas2l1	GROWTH ARREST-SPECIFIC 2 LIKE 1		1.74
ILMN_1220454	Anapc13	ANAPHASE PROMOTING COMPLEX SUBUNIT 13		1.61
ILMN_1216213	Incenp	INNER CENTROMERE PROTEIN		1.56
ILMN_1256301	Rcc2	REGULATOR OF CHROMOSOME CONDENSATION 2		1.53
Extracellular Matrix			5.80E-06	
ILMN_2735184	Col18a1	PROCOLLAGEN, TYPE XVIII, ALPHA 1		51.5
ILMN_1223997	Crtap	CARTILAGE ASSOCIATED PROTEIN		32.74
ILMN_2753809	Mmp3	MATRIX METALLOPEPTIDASE 3		31.08
ILMN_2747959	Dcn	DECORIN		21.44
ILMN_2737685	Mmp13	MATRIX METALLOPEPTIDASE 13		13.86
ILMN_1258629	Col3a1	PROCOLLAGEN, TYPE III, ALPHA 1		5.65
ILMN_2619952	Mmp10	MATRIX METALLOPEPTIDASE 10		5.32
ILMN_1254546	Col5a2	PROCOLLAGEN, TYPE V, ALPHA 2		3.42
ILMN_1238215	Ctgf	CONNECTIVE TISSUE GROWTH FACTOR		2.28
ILMN_2687880	Col1a1	PROCOLLAGEN, TYPE I, ALPHA 1		2.06
ILMN_1258759	Col6a2	PROCOLLAGEN, TYPE VI, ALPHA 2		1.77
ILMN_2678218	Mmp2	MATRIX METALLOPEPTIDASE 2		1.75
ILMN_1217071	Mmp16	MATRIX METALLOPEPTIDASE 16		1.67
Ubiquitin			1.40E-02	
ILMN_2662401	Sumo3	SMT3 SUPPRESSOR OF MIF TWO 3 HOMOLOG 3 (YEAST)		70.01
ILMN_1225261	Uchl1	UBIQUITIN CARBOXY-TERMINAL HYDROLASE L1		3.02
ILMN_1229019	Fbxo44	F-BOX PROTEIN 44		2.12
ILMN_2749911	Ube2q2	UBIQUITIN-CONJUGATING ENZYME E2Q (PUTATIVE) 2		1.96
ILMN_2417991	Ube2i	UBIQUITIN-CONJUGATING ENZYME E2I		1.79
ILMN_1227863	Ube2n	UBIQUITIN-CONJUGATING ENZYME E2N		1.53
Proto-oncogenes			2.70E-03	
ILMN_2655260	Ptp4a3	PROTEIN TYROSINE PHOSPHATASE 4A3		4.0
ILMN_1233424	Lbcl1	RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (GEF) 2		2.03
ILMN_1224526	Lck	LYMPHOCYTE PROTEIN TYROSINE KINASE		2.0
ILMN_1237241	Araf	V-RAF MURINE SARCOMA 3611 VIRAL ONCOGENE HOMOLOG		1.83
ILMN_1212787	Pttg1	PITUITARY TUMOR-TRANSFORMING 1		1.8
ILMN_2481071	Hras1	HARVEY RAT SARCOMA VIRUS ONCOGENE 1		1.78
ILMN_1251669	Evi2a	ECOTROPIC VIRAL INTEGRATION SITE 2A		1.77
ILMN_2492264	Wisp1	WNT1 INDUCIBLE SIGNALING PATHWAY PROTEIN 1		1.76
ILMN_1221750	Mycl1	LUNG CARCINOMA MYC RELATED ONCOGENE 1		1.66
Growth Factors			2.30E-02	
ILMN_1238547	Areg	AMPHIREGULIN		21.43
ILMN_1215252	Bmp4	BONE MORPHOGENETIC PROTEIN 4		14.31
ILMN_2745480	Fgf13	FIBROBLAST GROWTH FACTOR 13		6.53
ILMN_2710698	Fgf21	FIBROBLAST GROWTH FACTOR 21		5.51
ILMN_1236725	Gdf1	GROWTH DIFFERENTIATION FACTOR 1		2.53
ILMN_2484527	Vegfa	VASCULAR ENDOTHELIAL GROWTH FACTOR A		1.97
ILMN_2736496	Fgf10	FIBROBLAST GROWTH FACTOR 10		1.73
Chemotaxis			1.50E-02	
ILMN_1231814	Ccl5	CHEMOKINE (C-C MOTIF) LIGAND 5		13.25
ILMN_2763243	Cxcl1	CHEMOKINE (C-X-C MOTIF) LIGAND 1		8.46
ILMN_2658910	Cxcl12	CHEMOKINE (C-X-C MOTIF) LIGAND 12		6.78
ILMN_1245710	Ccl2	CHEMOKINE (C-C MOTIF) LIGAND 2		5.47
ILMN_1214419	Cxcl10	CHEMOKINE (C-X-C MOTIF) LIGAND 10		2.94

(Continued Table 1)

Inflammatory Response			1.60E-02	
ILMN_1230789	C3	COMPLEMENT COMPONENT 3		8.8
ILMN_2763243	Cxcl1	CHEMOKINE (C-X-C MOTIF) LIGAND 1		8.46
ILMN_2742075	Cd14	CD14 ANTIGEN		2.68
ILMN_1254383	Atrn	ATTRACTIN		1.99
ILMN_1259252	Anxa1	ANNEXIN A1		1.99
Other Genes				
ILMN_1218967	Kif2c	KINESIN FAMILY MEMBER 2C		37.42
ILMN_2611181	Ccdc3	COILED-COIL DOMAIN CONTAINING 3		36.32
ILMN_2703267	Nes	NESTIN		18.5
ILMN_1245451	Rab6b	RAB6B, MEMBER RAS ONCOGENE FAMILY		14.71
ILMN_2713285	Fhl1	FOUR AND A HALF LIM DOMAINS 1		14.19
ILMN_2606660	Card10	CASPASE RECRUITMENT DOMAIN FAMILY, MEMBER 10		10.23
ILMN_2686327	Gas6	GROWTH ARREST SPECIFIC 6		8.94
ILMN_2689998	Fjx1	FOUR JOINTED BOX 1 (DROSOPHILA)		8.81
ILMN_1247646	H1fx	H1 HISTONE FAMILY, MEMBER X		6.91
ILMN_1217159	Lmo7	LIM DOMAIN ONLY 7		5.51
ILMN_1214327	S100a13	S100 CALCIUM BINDING PROTEIN A13		5.19
ILMN_1242829	Prdx2	PEROXIREDOXIN 2		5.10
ILMN_2868133	Gata6	GATA BINDING PROTEIN 6		4.75
ILMN_1227993	Vav3	VAV 3 ONCOGENE		2.67
ILMN_2714361	Cd34	CD34 ANTIGEN		2.32
ILMN_2687880	Col1a1	PROCOLLAGEN, TYPE I, ALPHA 1		2.02
ILMN_1214227	Krt1-10	KERATIN COMPLEX 1, ACIDIC, GENE 1-10		1.84

The criteria for Functional Annotation Clustering of Gene analysis was set at $P < 0.05$ and fold-change ³ 1.5. Shown are functional clusters of genes that were up-regulated in *Klf4*-null MEFs.

www.ingenuity.com) to test for enrichment of known gene function. IPA groups significant genes according to biological processes in which they function. The program displays the genes' significance values, the other genes with which it interacts, and how the genes' products directly and indirectly act on each other. The criteria applied for the search of major biological function categories were maximum number of genes and the *P*-value of significance. A range of *P*-values between 3.18 x10^{-14} to 5.75 x 10^{-03} is considered statistically significant. **Table 3** shows the most significant results of analysis of 6,218 differentially expressed genes with a FDR less than or equal to 1% identified by SAM. As shown, top biological functions regulated by KLF4 include tumorigenesis, cell death, neoplasia, cancer, apoptosis, proliferation and growth of cells. This result is consistent with previous findings that KLF4 is involved in tumor suppression, cellular proliferation, and apoptosis. Interestingly, one particularly large gene set is involved in neurological disorder (1,016 genes) although the *P*-value just reached statistical significance (Supplementary Table S3).

Functional pathway analysis with Gene Set Enrichment Analysis (GSEA)

We also used the GSEA functional enrichment analysis to interrogate molecular pathways enriched in the two MEFs. In this exercise, 6,218 differentially expressed genes were analyzed for gene sets enriched in *Klf4*-null and wild type cells. A total of 47 pathway gene sets, 23 in *Klf4* -null and 24 in wild type cells, were significantly enriched with a *P*-value < 0.05 and FDR < 0.25. **Tables 4** and **5** show the lists of gene sets enriched in *Klf4*-null and wild type MEFs, respectively. The complete dataset is provided as Supplementary Table S4, which also includes the specific genes in the pathway gene sets that were enriched in the *Klf4*-null or wild type MEFs. In addition, snapshots of the enriched pathways in *Klf4*-null and wild type cells are provided as Supplementary Figures S1 and S2, respectively.

Table 2. Examples of functional annotation clustering of genes down-regulated in *Klf4*-null MEFs

ILLUMINA_ID	Gene Symbol	Gene Name (Description)	*P*-Value	Fold-change
JAT-STAT Signaling			1.90E-02	
ILMN_1219155	Jak3	JANUS KINASE 3		-3.448
ILMN_2698046	Stat3	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 3		-2.273
ILMN_2618176	Socs3	SUPPRESSOR OF CYTOKINE SIGNALING 3		-1.538
Homeobox			4.20E-03	
ILMN_2860958	Dlx2	DISTAL-LESS HOMEOBOX 2		-14.286
ILMN_1219807	Hoxd4	HOMEO BOX D4		-6.667
ILMN_1242977	Hoxb5	HOMEO BOX B5		-5.263
ILMN_2636480	Hoxa5	HOMEO BOX A5		-4
Glutathione Metabolism			2.90E-03	
ILMN_2773022	Gsta4	GLUTATHIONE S-TRANSFERASE, ALPHA 4		-9.091
ILMN_2624854	Gstm2	GLUTATHIONE S-TRANSFERASE, MU 2		-5
ILMN_1228233	Gstm1	GLUTATHIONE S-TRANSFERASE, MU 1		-2.564
ILMN_2705777	Gstm5	GLUTATHIONE S-TRANSFERASE, MU 5		-2.439
ILMN_2641807	Gstm6	GLUTATHIONE S-TRANSFERASE, MU 6		-2.326
Ephrin			2.60E-02	
ILMN_1257372	Efnb1	EPHRIN B1		-2.041
ILMN_1217493	Efna4	EPHRIN A4		-1.639
ILMN_2716212	Efnb2	EPHRIN B2		-1.515
Other Genes				
ILMN_2771738	Dlk1	DELTA-LIKE 1 HOMOLOG (DROSOPHILA)		-307.819
ILMN_1256371	Fez1	FASCICULATION AND ELONGATION PROTEIN ZETA 1		-37.299
ILMN_2724942	Ptgis	PROSTAGLANDIN I2 (PROSTACYCLIN) SYNTHASE		-33.333
ILMN_1224866	Ptgs1	PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 1		-12.5
ILMN_1260020	Pcdh1	PROTOCADHERIN 1		-8.362
ILMN_3163581	En1	ENGRAILED 1		-7.692
ILMN_2699052	Nrn1	NEURITIN 1		-4.387
ILMN_1246282	Tcfap2a	TRANSCRIPTION FACTOR AP-2, ALPHA		-3.658
ILMN_2628178	Socs2	SUPPRESSOR OF CYTOKINE SIGNALING 2		-3.226
ILMN_2729197	Hic1	HYPERMETHYLATED IN CANCER 1		-3.587
ILMN_1240677	Gadd45gip1	GROWTH ARREST AND DNA-DAMAGE-INDUCED GAMMA INTERACTING PROTEIN 1		-3.026
ILMN_2623578	Nid1	NIDOGEN 1		-2.71
ILMN_2677332	Hic2	HYPERMETHYLATED IN CANCER 2		-2.515

The criteria for Functional Annotation Clustering of Gene analysis was set at $P < 0.05$ and fold-change ³ 1.5. Shown are functional clusters of genes that were down-regulated in *Klf4*-null MEFs.

In *Klf4*-null MEFs, GSEA showed a significant enrichment in gene sets associated with bile acid biosynthesis, hematopoietic cell lineage, multiple myeloma, genes expressed in medulloblastomas, cell motility, cytokine receptor, cell surface receptors, autophagy, and inflammatory response. Moreover, signaling pathways including ERBB, toll like receptors, and hedgehog signaling were enriched in *Klf4*-null cells. On the other hand, significant enrichment in gene sets associated with antigen processing and presentation, IL-2 receptor pathway, HOX genes, JAK-STAT signaling pathways, glutathione metabolism, basal transcription factors, and adipocytes differentiation were enriched in the wild type cells. **Figure 1** shows the results of enrichment of the JAK-STAT signaling pathway in wild type MEFs. In this example, GSEA mapped 134 out

Table 3. Top high-level functions identified by Ingenuity global function analysis of genes regulated by Klf4

Biological Function Classification	Number of Genes	Significance (*P*-value)
Tumorigenesis	802	2.42E-06
Cell death	753	3.18E-14
Neoplasia	751	2.45E-06
Cancer	719	5.29E-06
Apoptosis	659	5.53E-15
Proliferation of cells	614	6.31E-06
Growth of cells	525	4.10E-12
Development of cells	342	1.78E-07
Migration of cells	333	9.54E-06

The criteria applied for the search of major biological function categories were maximum number of genes and the *P*-value of significance. *P*-values in the range of 3.18×10^{-14} to 5.75×10^{-03} indicated statistical significance.

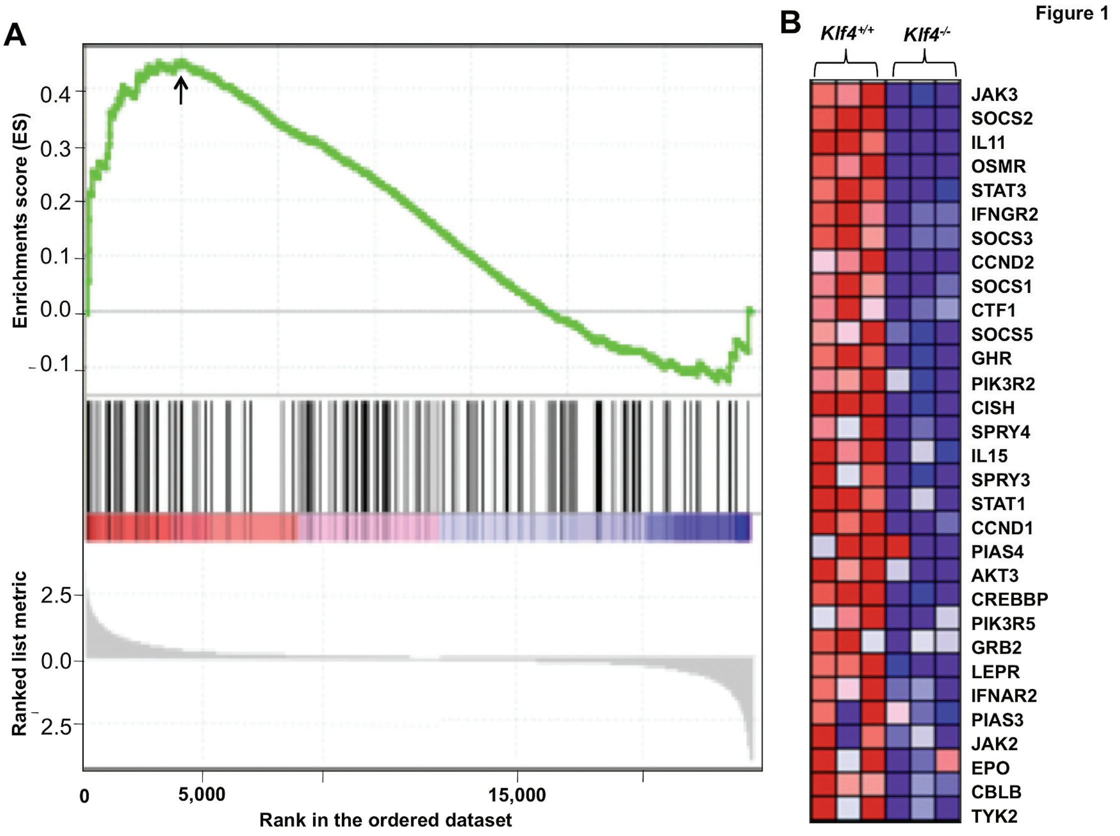

Figure 1. Gene set enrichment analysis (GSEA) for the JAK-STAT signaling pathway. **(A)** Shown are enrichment scores with a ranked list metric. The arrow indicates the enrichment score of 0.45. **(B)** Heat map of the results of microarray analysis of 32 core enrichment genes in the JAK-STAT signaling pathway in wild type (*Klf4*$^{+/+}$) and *Klf4*-null (*Klf4*$^{-/-}$) MEFs in triplicate. Red color represents up-regulated and blue color, down-regulated, genes. Significantly enriched data sets are selected according to GSEA default settings, i.e., $P < 0.001$ and a false discovery rate (FDR) < 0.

of 1,381 genes and found a highly significant correlation between the gene list and dataset ($P < 0.001$ and FDR *q*-value = 0.192). This is consistent with the results in **Table 2** showing that some of the genes involved in the JAK-STAT signaling pathway such as JAK3, STAT3, and SOCS3, are down-regulated in *Klf4*-null MEFs. Among these factors, STAT3 is required for embryonic stem cell maintenance and SOCS3 is involved in differentiation of embryonic stem

Table 4. Gene sets enriched in *Klf4*-null cells Identified by GSEA

Gene sets	Size	ES	NES	FDR *q*-value
Bile acid biosynthesis	21	-0.572	-1.844	0.213
The 50 most downregulated genes in primary invasive breast dutcal carcinoma or metastatic breast carcinoma isolated from lymph nodes, as compared to normal mammary epithelium.	25	-0.642	-1.787	0.062
Genes up-regulated in multiple myeloma cells exposed to the pro-proliferative cytokine IL-6 versus those with N-ras-activating mutations	19	-0.577	-1.775	0.133
Genes involved in hematopoietic cell lineage	65	-0.524	-1.739	0.130
B cell antigen receptors (BCRs) activate tyrosine kinases and transiently increase tyrosine phosphorylation on binding to antigen.	33	-0.533	-1.735	0.111
Genes down-regulated in hepatoma tissue of Myc+E2f1 transgenic mice	54	-0.505	-1.690	0.131
Genes involved in ERBB signaling pathway	82	-0.426	-1.684	0.118
Genes with spiked expression in subsets of MM PCs from newly diagnosed patients	21	-0.725	-1.684	0.109
Genes involved in regulation of autophagy	23	-0.570	-1.664	0.102
Genes involved in type I diabetes mellitus	19	-0.471	-1.661	0.097
Genes expressed in classic medulloblastomas.	35	-0.498	-1.661	0.093
Genes down-regulated in hepatoma tissue of Myc+Tgfa transgenic mice	54	-0.556	-1.660	0.104
Genes involved in nicotinate and nicotinamide metabolism	21	-0.701	-1.654	0.099
Any process involved in the controlled movement of a cell.	48	-0.479	-1.644	0.091
Tyrosine metabolism	27	-0.494	-1.636	0.108
Inflammatory response pathway	15	-0.792	-1.621	0.093
Genes involved in cytokine-cytokine receptor interaction	209	-0.466	-1.619	0.109
Down-regulated at 6-12 hours following treatment of WS1 human skin fibroblasts with UVC at a low dose	15	-0.601	-1.615	0.116
Any series of molecular signals initiated by the binding of an extracellular ligand to a receptor on the surface of the target cell	117	-0.470	-1.601	0.122
Genes involved in Toll-like receptor signaling pathway	96	-0.508	-1.600	0.118
Genes involved in Hedgehog signaling pathway	54	-0.601	-1.593	0.122
Reactive oxidative species related genes curated from GO	27	-0.565	-1.581	0.130
Genes down-regulated in hepatoma tissue of E2f1 transgenic mice	51	-0.506	-1.580	0.127

All genes were ranked by differential expression between *Klf4*-null and wild type MEFs using enrichment score; enrichment score normalized for differences in gene set size; and false discovery rate. Size equals the number of genes in the gene list mapped to the dataset. ES: enrichment score; NES: normalized enrichment score; FDR q-value: false discovery rate—multiple comparisons correction (q-value). The criteria for the GSEA analysis was $P < 0.05$ and false discovery rate (FDR) < 25%.

cells [21, 34, 35].

Validation of microarray data by Western blot analysis of select genes

We validated some of the microarray data by Western blot analysis of select genes in wild type and *Klf4*-null MEFs. In the microarray analysis CDK2, MMP3, and SUMO3 mRNAs were found to be up-regulated in the *Klf4*-null cells (**Table 1**). On the other hand, STAT3 and SOCS3 mRNAs were down-regulated (**Table 2**). Consistent with the microarray observations, Western blot analysis of *Klf4*-null MEFs showed excellent correlation in changes of expression for each of these genes between wild type and

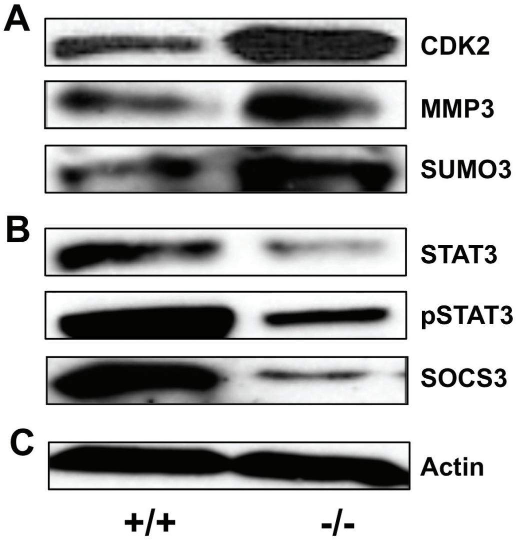

Figure 2. Confirmation of select microarray data by Western blot analysis. **(A)** Western blot analysis of genes up-regulated in *Klf4*-null including CDK2, MMP3, and SUMO3. **(B)** Western blot analysis of genes down-regulated in *Klf4*-null including STAT3, pSTAT3, and SOCS3. **(C)** Actin loading control. Shown are the representative results of 2 independent experiments. +/+ = wild type and -/- = *Klf4*-null MEFs.

Klf4-null cells (**Figure 2**). Interestingly, the level of phosphorylated STAT3 (pSTAT3) was also reduced in *Klf4*-null cells.

Discussion

Since it was initially identified some 14 years ago [1, 2], KLF4 has been shown to play an increasingly broad and important function in both physiological and pathological processes. Physiologically, KLF4 regulates proliferation, differentiation, development, apoptosis, and somatic cell reprogramming. KLF4 is also involved in disease conditions such as tumorigenesis and inflammation. Earlier studies indicate that KLF4 is a potent inhibitor of cell proliferation [1, 36] and mediates the cell cycle-checkpoint function of the tumor suppressor, p53 [37-40]. Subsequent studies confirmed this inhibitory effect by the demonstration that KLF4 exerts a tumor suppressive effect *in vivo* [9, 10]. Previous attempts at establishing the expression profiles of KLF4 were conducted in cultured cancer cells over-expressing KLF4 [27, 28]. These studies confirmed the cell cycle-checkpoint activity of KLF4 and provided additional evidence that KLF4 regulates both epithelial differentiation and macromolecular biosynthesis. In contrast, the present study shows for the first time the transcriptional profiles of KLF4 in a non-transformed cell system and as a result, identified many additional novel targets of KLF4 such as those involved in extracellular matrix, ubiquitin, growth factors, chemotaxis, JAK-STAT, and ephrin signaling (**Tables 1** and **2**). Moreover, the current study does not involve over-expression as in the previous work, thus rendering the results more physiologically relevant.

The cells used in the current study, mouse embryonic fibroblasts (MEFs), have previously been characterized [26]. Relative to wild type cells, MEFs deficient for *Klf4* had both a higher rate of proliferation and apoptosis. In addition, *Klf4*-null cells exhibited evidence of genetic instability as evidenced by the presence of aneuploidy, chromosome aberration and centrosome amplification [26]. A mechanism underlying this genetic instability in the absence of KLF4 is likely due to elevated cyclin E levels, which are normally suppressed by KLF4 [26]. The current study provides additional supporting evidence by showing that CDK2 is significantly up-regulated in *Klf4*-null cells (**Table 1** and **Figure 2**). Accompanying the increase in CDK2 levels is the up-regulation of numerous other cell cycle-promoting genes as shown in **Table 1**. Moreover, at least a subset of these genes such as MCM and E2F overlaps with those previously identified to be suppressed by KLF4 [27, 28]. The results of the present study therefore provide further mechanistic evidence for the observed inhibitory effect of KLF4 on proliferation.

Consistent with the tumor suppressive role for KLF4, results in **Table 1** also show that numerous genes involved in tumorigenesis such as proto-oncogenes and those encoding extracellular matrix proteins, growth factors, chemokines, and inflammatory response. Many of these gene families have important roles in regulating cell growth, migration, and angiogenesis. For example, several genes encoding matrix metalloproteinases (MMPs) are up-regulated in *Klf4*-null cells (**Table 1**). The up-regulation of MMPs have has been implicated in the increase in proliferation, anchorage-independent growth, tumor progression, invasion, and metastasis [41-43]. One in particular, MMP3, promotes cellular proliferation when over-expressed in transgenic mice

Table 5. Gene sets enriched in wild type cells Identified by GSEA

Gene sets	Size	ES	NES	FDR *q*-value
Prostaglandin and leukotriene metabolism	28	0.628	1.871	0.054
The intrinsic prothrombin activation pathway is activated by traumatized blood vessels and induces clot formation	22	0.659	1.732	0.095
Genes involved in antigen processing and presentation	40	0.514	1.646	0.134
Up-regulated at 3 months of age in lungs from lysosomal acid lipase (LAL) knockout mice, which display pulmonary pathology, versus wild-type controls	46	0.507	1.631	0.119
Up-regulated following stable autocrine expression of human growth hormone in mammary carcinoma cells (MCF-7)	150	0.488	1.627	0.110
Genes involved in ABC transporters - general	40	0.540	1.617	0.104
The beta subunit of the IL-2 receptor is required for IL-2 and IL-15 signal recognition and activates JAK kinase on ligand binding	35	0.545	1.572	0.134
Genes highly expressed in hepatitis C-related hepatocellular carcinoma	28	0.523	1.552	0.157
HOX genes related to hematopoiesis	31	0.500	1.539	0.159
Downregulated by nickel(II) in human peripheral lung epithelial cells	16	0.702	1.518	0.208
Genes downregulated in multiple myeloma plasma cells that secrete the light chain immunoglobulin Ig-lambda versus those that secrete Ig-kappa.	27	0.503	1.517	0.192
Genes involved in JAK-STAT signaling pathway	134	0.451	1.510	0.192
Glutathione metabolism	20	0.699	1.510	0.173
Genes involved in basal transcription factors	28	0.583	1.508	0.186
Thrombin cleaves protease-activated receptors PAR1 and PAR4 to induce calcium influx and activate platelet aggregation, a process inhibited by aspirin	21	0.500	1.490	0.199
Down-regulated in mature, differentiated adipocytes following simultaneous treatment with troglitazone and TNFalpha	25	0.731	1.482	0.201
Up-regulated in primary human adipocytes, versus preadipocytes	59	0.499	1.470	0.207
Down-regulated by infection of human colon adenocarcinoma cells (SW480) with Ad-BRCA1, versus Ad-LacZ control	16	0.555	1.466	0.203
Downregulated by ectopic expression of NF90 in GHOST(3)CXCR4 cells	33	0.612	1.466	0.194
Genes involved in taste transduction	27	0.485	1.462	0.192
Downregulated by both Et-743 and Pt-650 in HCT116 cells	21	0.438	1.460	0.190
Genes involved in arachidonic acid metabolism	40	0.434	1.454	0.204
Summary of genes up-regulated in EFTs compared with normal body atlas	27	0.499	1.453	0.200

All genes were ranked by differential expression between *Klf4*-null and wild type MEFs using enrichment score; enrichment score normalized for differences in gene set size; and false discovery rate. Size equals the number of genes in the gene list mapped to the dataset. ES: enrichment score; NES: normalized enrichment score; FDR q-value: false discovery rate—multiple comparisons correction (q-value). The criteria for the GSEA analysis was $P < 0.05$ and false discovery rate (FDR) < 25%.

[44]. Over-expression of MMP3 *in vitro* induces mesenchymal-epithelial transition (EMT) and promotes tumor progression with resultant genetic instability [45, 46]. Many of the phenotypes upon MMP3 over-expression such as genetic instability and anchorage-independent growth are shared with MEFs null for *Klf4* [26]. The up-regulation of MMPs, including MMP3 (**Table 1**; **Figure 2**), in *Klf4*-null cells may therefore be responsible for at least some of these events.

One of the most up-regulated genes in *Klf4*-null MEFs from the microarray analysis is small ubiquitin-like modifier 3 (SUMO3) (**Table 1**). Western blot analysis confirmed its elevation in *Klf4*-null cells (**Figure 2**). Post-translational modification by SUMOs is usually transient and alters protein function by affecting protein-protein interaction [47]. Recent studies indicate that the SUMO cascade is involved in the mammalian DNA damage response from genotoxic stress [48, 49]. *Klf4*-null MEFs contain a high level of phosphorylated histone H2AX (γH2AX), a marker for double-strand DNA breaks, and exhibit chromosome aberrations including dicentric chromosomes, double minute chromosomes, and chromatid breaks [26]. The elevated SUMO3 levels in these cells could therefore be a reflection of the cellular response to wide-spread DNA damage observed in *Klf4*-null MEFs.

KLF4 is one of several factors capable of reprogramming somatic cells to induced pluripotent stem (iPS) cells [15-20]. However, the mechanism by which KLF4 achieves this task is not completely understood. KLF4 interacts with two other factors, Oct4 and Sox2, to promote reprogramming [50] and may form a core circuitry with other KLFs to regulate self-renewal of embryonic stem cells [51]. KLF4 also suppresses expression of the tumor suppressor gene, p53 [52], which was recently shown to be a barrier to efficient reprogramming [53-57]. In this study, we demonstrated that the JAK-STAT signaling pathway is enriched in wild type MEFs relative to *Klf4*-null MEFs (**Tables 2** and **5**; **Figure 1**). This could provide another mechanism by which KLF4 may influence ES cell self-renewal. A previous study showed that promotion of mouse ES cell self-renewal and maintenance of pluripotency requires leukemia inhibitory factor (LIF)-stimulated STAT3 activation [21]. KLF4 is a LIF-responsive gene and over-expression of KLF4 in ES cells results in a greater capacity to self-renew [21]. A subsequent study demonstrated that KLF4 is activated by the JAK-STAT3 pathway, thus providing a mechanism by which LIF activates KLF4 [58]. It is of interest to note that both STAT3 and phospho-STAT3 levels are elevated in wild type MEFs compared to *Klf4*-null MEFs (**Figure 2**), a finding that suggests KLF4 may activate STAT3 expression, thus providing a positive feedback loop to promote ES self-renewal. Similarly, the level of SOCS3 is higher in wild type MEFs than *Klf4*-null cells (**Figure 2**). SOCS3 is also a target of LIF signaling but promotes differentiation when over-expressed [21]. KLF4 may therefore be positioned in a nodal point to mediate LIF-induced JAK-STAT signaling and to modulate the decision between self-renewal and differentiation.

In summary, our study established distinct transcriptional profiles of MEFs wild type and null for the *Klf4* alleles. Functional clustering and pathway analysis identified a rich series of potential targets that may mediate KLF4's myriads of functions. In particular, our results further strengthened the previously established role of KLF4 in maintaining genetic stability and tumor suppression. Moreover, the results provided novel insights by which KLF4 may regulate somatic cell reprogramming. Studies are warranted to further substantiate the mechanisms by which KLF4 regulates these important processes.

Acknowledgements

This work was supported in part by grants from the National Institutes of Health (DK52230, DK64399, CA84197, and CA130308). EGH was an Emory Fellowships in Research and Science Teaching (FIRST) fellow.

Please address correspondence to: Vincent W. Yang, MD, PhD, Division of Digestive Diseases, Department of Medicine, 201 Whitehead Research Building, 615 Michael Street, Atlanta, GA 30322, USA. Tel: (404) 727-5638; FAX: (404) 727-5767; E-mail: vyang@emory.edu

References

[1] Shields JM, Christy RJ and Yang VW. Identification and characterization of a gene encoding a gut-enriched Kruppel-like factor expressed during growth arrest. J Biol Chem 1996; 271: 20009-20017.

[2] Garrett-Sinha LA, Eberspaecher H, Seldin MF and de Crombrugghe B. A gene for a novel zinc-finger protein expressed in differentiated epithelial cells and transiently in certain mesenchymal cells. J Biol Chem 1996; 271: 31384-31390.

[3] McConnell BB, Ghaleb AM, Nandan MO and Yang VW. The diverse functions of Kruppel-like factors 4 and 5 in epithelial biology and pathobiology. Bioessays 2007; 29: 549-557.

[4] Ghaleb AM, Nandan MO, Chanchevalap S, Dalton WB, Hisamuddin IM and Yang VW. Kruppel-like factors 4 and 5: the yin and yang regulators of cellular proliferation. Cell Res 2005; 15: 92-96.

[5] Dang DT, Bachman KE, Mahatan CS, Dang LH, Giardiello FM and Yang VW. Decreased expression of the gut-enriched Kruppel-like factor gene in intestinal adenomas of multiple intestinal neoplasia mice and in colonic adenomas of familial adenomatous polyposis patients. FEBS Lett 2000; 476: 203-207.

[6] Black AR, Black JD and Azizkhan-Clifford J. Sp1 and kruppel-like factor family of transcription factors in cell growth regulation and cancer. J Cell Physiol 2001; 188: 143-160.

[7] Kaczynski J, Cook T and Urrutia R. Sp1- and Kruppel-like transcription factors. Genome Biol 2003; 4: 206.

[8] Feinberg MW, Cao Z, Wara AK, Lebedeva MA, Senbanerjee S and Jain MK. Kruppel-like factor 4 is a mediator of proinflammatory signaling in macrophages. J Biol Chem 2005; 280: 38247-38258.

[9] Ghaleb AM, Aggarwal G, Bialkowska AB, Nandan MO and Yang VW. Notch inhibits expression of the Kruppel-like factor 4 tumor suppressor in the intestinal epithelium. Mol Cancer Res 2008; 6: 1920-1927.

[10] Ghaleb AM, McConnell BB, Nandan MO, Katz JP, Kaestner KH and Yang VW. Haploinsufficiency of Kruppel-like factor 4 promotes adenomatous polyposis coli dependent intestinal tumorigenesis. Cancer Res 2007; 67: 7147-7154.

[11] Ghaleb AM and Yang VW. The Pathobiology of Kruppel-like Factors in Colorectal Cancer. Curr Colorectal Cancer Rep 2008; 4: 59-64.

[12] Hamik A, Lin Z, Kumar A, Balcells M, Sinha S, Katz J, Feinberg MW, Gerzsten RE, Edelman ER and Jain MK. Kruppel-like factor 4 regulates endothelial inflammation. J Biol Chem 2007; 282: 13769-13779.

[13] Kanai M, Wei D, Li Q, Jia Z, Ajani J, Le X, Yao J and Xie K. Loss of Kruppel-like factor 4 expression contributes to Sp1 overexpression and human gastric cancer development and progression. Clin Cancer Res 2006; 12: 6395-6402.

[14] Xu J, Lu B, Xu F, Gu H, Fang Y, Huang Q and Lai M. Dynamic down-regulation of Kruppel-like factor 4 in colorectal adenoma-carcinoma sequence. J Cancer Res Clin Oncol 2008; 134: 891-898.

[15] Nandan MO and Yang VW. The role of Kruppel-like factors in the reprogramming of somatic cells to induced pluripotent stem cells. Histol Histopathol 2009; 24: 1343-1355.

[16] Villarreal G, Jr., Zhang Y, Larman HB, Gracia-Sancho J, Koo A and Garcia-Cardena G. Defining the regulation of KLF4 expression and its downstream transcriptional targets in vascular endothelial cells. Biochem Biophys Res Commun 2010; 391: 984-989.

[17] Takahashi K and Yamanaka S. Induction of pluripotent stem cells from mouse embryonic and adult fibroblast cultures by defined factors. Cell 2006; 126: 663-676.

[18] Okita K, Ichisaka T and Yamanaka S. Generation of germline-competent induced pluripotent stem cells. Nature 2007; 448: 313-317.

[19] Wernig M, Meissner A, Foreman R, Brambrink T, Ku M, Hochedlinger K, Bernstein BE and Jaenisch R. In vitro reprogramming of fibroblasts into a pluripotent ES-cell-like state. Nature 2007; 448: 318-324.

[20] Maherali N, Sridharan R, Xie W, Utikal J, Eminli S, Arnold K, Stadtfeld M, Yachechko R, Tchieu J, Jaenisch R, Plath K and Hochedlinger K. Directly reprogrammed fibroblasts show global epigenetic remodeling and widespread tissue contribution. Cell Stem Cell 2007; 1: 55-70.

[21] Li Y, McClintick J, Zhong L, Edenberg HJ, Yoder MC and Chan RJ. Murine embryonic stem cell differentiation is promoted by SOCS-3 and inhibited by the zinc finger transcription factor Klf4. Blood 2005; 105: 635-637.

[22] Segre JA, Bauer C and Fuchs E. Klf4 is a transcription factor required for establishing the barrier function of the skin. Nat Genet 1999; 22: 356-360.

[23] Katz JP, Perreault N, Goldstein BG, Lee CS, Labosky PA, Yang VW and Kaestner KH. The zinc -finger transcription factor Klf4 is required for terminal differentiation of goblet cells in the colon. Development 2002; 129: 2619-2628.

[24] Swamynathan SK, Katz JP, Kaestner KH, Ashery-Padan R, Crawford MA and Piatigorsky J. Conditional deletion of the mouse Klf4 gene results in corneal epithelial fragility, stromal edema, and loss of conjunctival goblet cells. Mol Cell Biol 2007; 27: 182-194.

[25] Katz JP, Perreault N, Goldstein BG, Actman L, McNally SR, Silberg DG, Furth EE and Kaestner KH. Loss of Klf4 in mice causes altered proliferation and differentiation and precancerous changes in the adult stomach. Gastroenterology 2005; 128: 935-945.

[26] Hagos EG, Ghaleb AM, Dalton WB, Bialkowska AB and Yang VW. Mouse embryonic fibroblasts null for the Kruppel-like factor 4 gene are genetically unstable. Oncogene 2009; 28: 1197-1205.

[27] Chen X, Whitney EM, Gao SY and Yang VW. Transcriptional profiling of Kruppel-like factor 4 reveals a function in cell cycle regulation and epithelial differentiation. J Mol Biol 2003; 326: 665-677.

[28] Whitney EM, Ghaleb AM, Chen X and Yang VW. Transcriptional profiling of the cell cycle checkpoint gene kruppel-like factor 4 reveals a global inhibitory function in macromolecular biosynthesis. Gene Expr 2006; 13: 85-96.

[29] Todaro GJ and Green H. Quantitative studies of the growth of mouse embryo cells in culture and their development into established lines. J Cell Biol 1963; 17: 299-313.

[30] Tusher VG, Tibshirani R and Chu G. Significance analysis of microarrays applied to the ionizing radiation response. Proc Natl Acad Sci U S A 2001; 98: 5116-5121.

[31] Subramanian A, Tamayo P, Mootha VK, Mukherjee S, Ebert BL, Gillette MA, Paulovich A, Pomeroy SL, Golub TR, Lander ES and Mesirov JP. Gene set enrichment analysis: a knowledge-based approach for interpreting genome-wide expression profiles. Proc Natl Acad Sci U S A 2005; 102: 15545-15550.

[32] Dennis G, Jr., Sherman BT, Hosack DA, Yang J, Gao W, Lane HC and Lempicki RA. DAVID: Database for Annotation, Visualization, and Inte-

grated Discovery. Genome Biol 2003; 4: P3.

[33] Huang da W, Sherman BT and Lempicki RA. Systematic and integrative analysis of large gene lists using DAVID bioinformatics resources. Nat Protoc 2009; 4: 44-57.

[34] Niwa H, Burdon T, Chambers I and Smith A. Self-renewal of pluripotent embryonic stem cells is mediated via activation of STAT3. Genes Dev 1998; 12: 2048-2060.

[35] Matsuda T, Nakamura T, Nakao K, Arai T, Katsuki M, Heike T and Yokota T. STAT3 activation is sufficient to maintain an undifferentiated state of mouse embryonic stem cells. EMBO J 1999; 18: 4261-4269.

[36] Chen X, Johns DC, Geiman DE, Marban E, Dang DT, Hamlin G, Sun R and Yang VW. Kruppel-like factor 4 (gut-enriched Kruppel-like factor) inhibits cell proliferation by blocking G1/S progression of the cell cycle. J Biol Chem 2001; 276: 30423-30428.

[37] Zhang W, Geiman DE, Shields JM, Dang DT, Mahatan CS, Kaestner KH, Biggs JR, Kraft AS and Yang VW. The gut-enriched Kruppel-like factor (Kruppel-like factor 4) mediates the transactivating effect of p53 on the p21WAF1/Cip1 promoter. J Biol Chem 2000; 275: 18391-18398.

[38] Yoon HS, Chen X and Yang VW. Kruppel-like factor 4 mediates p53-dependent G1/S cell cycle arrest in response to DNA damage. J Biol Chem 2003; 278: 2101-2105.

[39] Yoon HS, Ghaleb AM, Nandan MO, Hisamuddin IM, Dalton WB and Yang VW. Kruppel-like factor 4 prevents centrosome amplification following gamma-irradiation-induced DNA damage. Oncogene 2005; 24: 4017-4025.

[40] Yoon HS and Yang VW. Requirement of Kruppel-like factor 4 in preventing entry into mitosis following DNA damage. J Biol Chem 2004; 279: 5035-5041.

[41] Lochter A, Sternlicht MD, Werb Z and Bissell MJ. The significance of matrix metalloproteinases during early stages of tumor progression. Ann N Y Acad Sci 1998; 857: 180-193.

[42] Morrison CJ and Overall CM. TIMP independence of matrix metalloproteinase (MMP)-2 activation by membrane type 2 (MT2)-MMP is determined by contributions of both the MT2-MMP catalytic and hemopexin C domains. J Biol Chem 2006; 281: 26528-26539.

[43] Egeblad M and Werb Z. New functions for the matrix metalloproteinases in cancer progression. Nat Rev Cancer 2002; 2: 161-174.

[44] Witty JP, Wright JH and Matrisian LM. Matrix metalloproteinases are expressed during ductal and alveolar mammary morphogenesis, and misregulation of stromelysin-1 in transgenic mice induces unscheduled alveolar development. Mol Biol Cell 1995; 6: 1287-1303.

[45] Stallings-Mann M and Radisky D. Matrix metalloproteinase-induced malignancy in mammary epithelial cells. Cells Tissues Organs 2007; 185: 104-110.

[46] Przybylo JA and Radisky DC. Matrix metalloproteinase-induced epithelial-mesenchymal transition: tumor progression at Snail's pace. Int J Biochem Cell Biol 2007; 39: 1082-1088.

[47] Morris JR. SUMO in the mammalian response to DNA damage. Biochem Soc Trans 2010; 38: 92-97.

[48] Morris JR, Boutell C, Keppler M, Densham R, Weekes D, Alamshah A, Butler L, Galanty Y, Pangon L, Kiuchi T, Ng T and Solomon E. The SUMO modification pathway is involved in the BRCA1 response to genotoxic stress. Nature 2009; 462: 886-890.

[49] Galanty Y, Belotserkovskaya R, Coates J, Polo S, Miller KM and Jackson SP. Mammalian SUMO E3-ligases PIAS1 and PIAS4 promote responses to DNA double-strand breaks. Nature 2009; 462: 935-939.

[50] Wei Z, Yang Y, Zhang P, Andrianakos R, Hasegawa K, Lyu J, Chen X, Bai G, Liu C, Pera M and Lu W. Klf4 interacts directly with Oct4 and Sox2 to promote reprogramming. Stem Cells 2009; 27: 2969-2978.

[51] Jiang J, Chan YS, Loh YH, Cai J, Tong GQ, Lim CA, Robson P, Zhong S and Ng HH. A core Klf circuitry regulates self-renewal of embryonic stem cells. Nat Cell Biol 2008; 10: 353-360.

[52] Rowland BD, Bernards R and Peeper DS. The KLF4 tumour suppressor is a transcriptional repressor of p53 that acts as a context-dependent oncogene. Nat Cell Biol 2005; 7: 1074-1082.

[53] Utikal J, Polo JM, Stadtfeld M, Maherali N, Kulalert W, Walsh RM, Khalil A, Rheinwald JG and Hochedlinger K. Immortalization eliminates a roadblock during cellular reprogramming into iPS cells. Nature 2009; 460: 1145-1148.

[54] Marion RM, Strati K, Li H, Murga M, Blanco R, Ortega S, Fernandez-Capetillo O, Serrano M and Blasco MA. A p53-mediated DNA damage response limits reprogramming to ensure iPS cell genomic integrity. Nature 2009; 460: 1149-1153.

[55] Li H, Collado M, Villasante A, Strati K, Ortega S, Canamero M, Blasco MA and Serrano M. The Ink4/Arf locus is a barrier for iPS cell reprogramming. Nature 2009; 460: 1136-1139.

[56] Kawamura T, Suzuki J, Wang YV, Menendez S, Morera LB, Raya A, Wahl GM and Belmonte JC. Linking the p53 tumour suppressor pathway to somatic cell reprogramming. Nature 2009; 460: 1140-1144.

[57] Hong H, Takahashi K, Ichisaka T, Aoi T, Kanagawa O, Nakagawa M, Okita K and Yamanaka S. Suppression of induced pluripotent stem cell generation by the p53-p21 pathway. Nature 2009; 460: 1132-1135.

[58] Niwa H, Ogawa K, Shimosato D and Adachi K. A parallel circuit of LIF signalling pathways maintains pluripotency of mouse ES cells. Nature 2009; 460: 118-122.

AJCR0000006 Supplemental Data

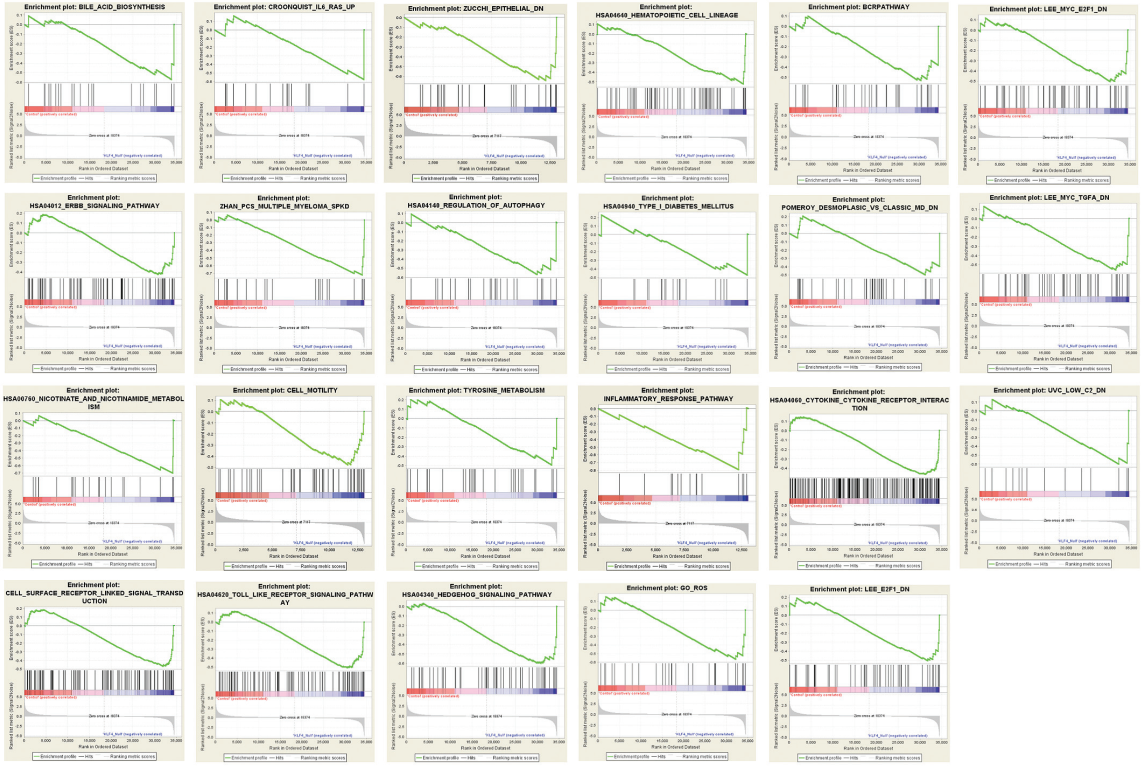

Figure S1. Snapshot of enriched gene sets identified by GSEA in *Klf4*-null MEFs.

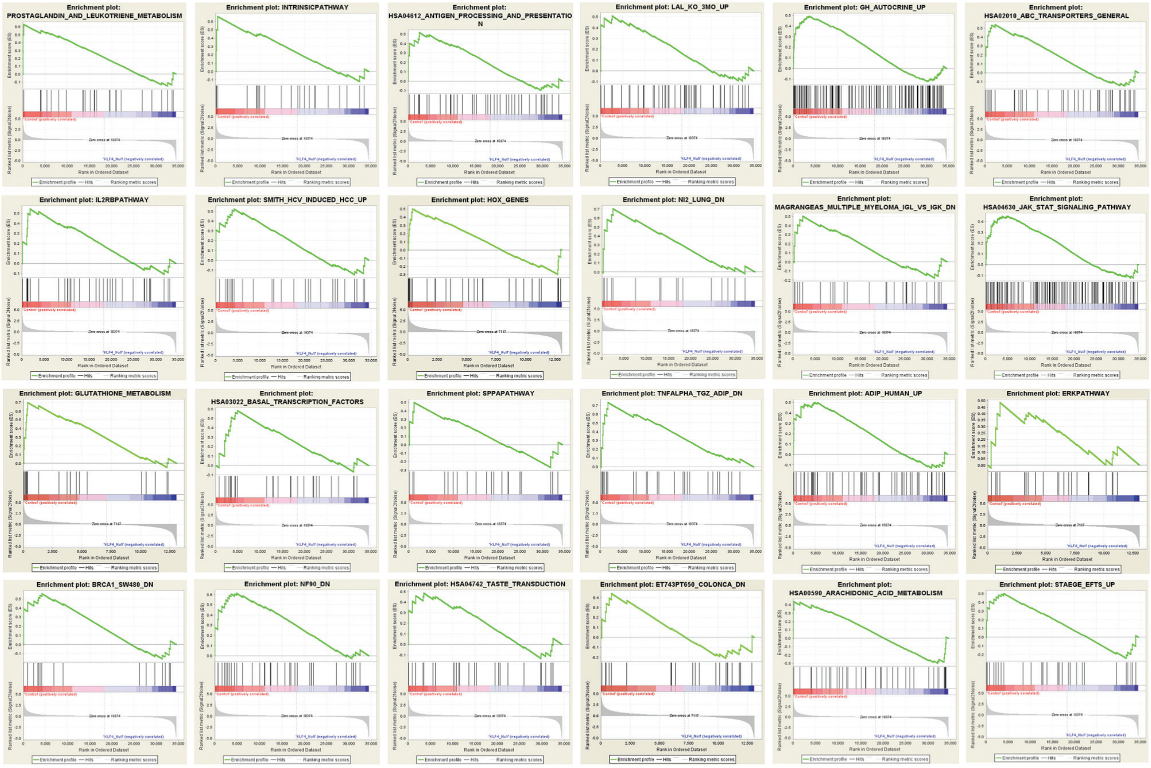

Figure S2. Snapshot of enriched gene sets identified by GSEA in wild type MEFs.

AJCR0000006 Supplemental Data

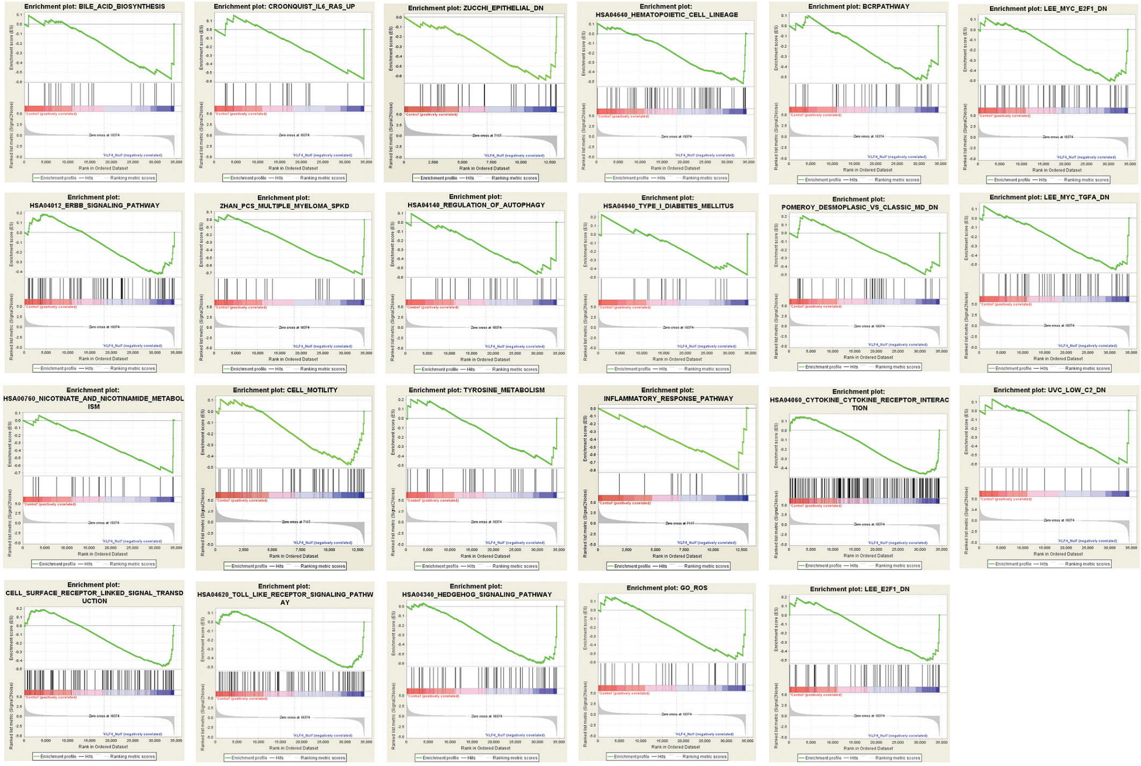

Figure S1. Snapshot of enriched gene sets identified by GSEA in *Klf4*-null MEFs.

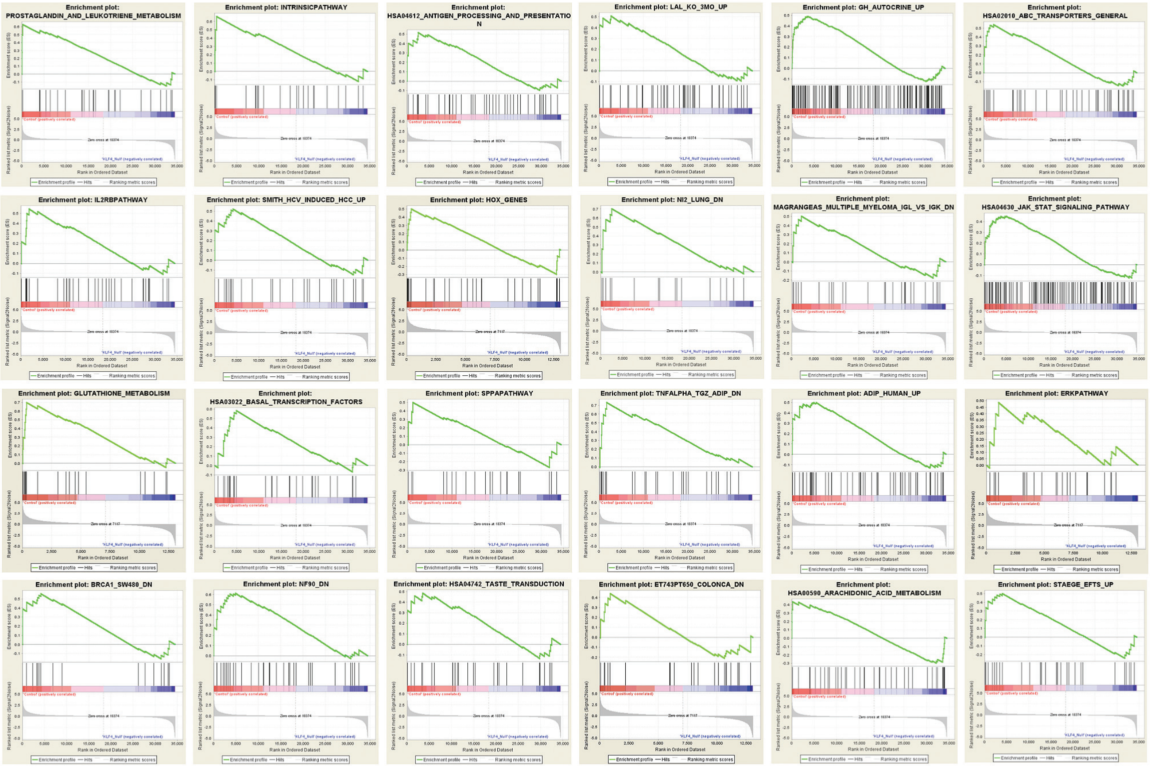

Figure S2. Snapshot of enriched gene sets identified by GSEA in wild type MEFs.

Table S1: Functional Annotation Clustering of Genes Up-Regulated in *Klf4* -Null MEFs

ILLUMINA_ID	Gene Symbol	Gene Name (Description)	*P* -value	Fold-Change
Cell Cycle			**8.00E-03**	
ILMN_1217331	Mcm6	MINICHROMOSOME MAINTENANCE DEFICIENT 6		40.36
ILMN_2723931	E2f6	E2F TRANSCRIPTION FACTOR 6		26.8
ILMN_2724570	Mapk12	MITOGEN-ACTIVATED PROTEIN KINASE 12		22.19
ILMN_1218470	Cdk2	CYCLIN-DEPENDENT KINASE 2		9.32
ILMN_1234909	Tipin	TIMELESS INTERACTING PROTEIN		5.3
ILMN_1212692	Mapk13	SAPK/ERK/KINASE 4		4.96
ILMN_2666690	Cul7	CULLIN 7		2.23
ILMN_2681776	Mapk6	MITOGEN ACTIVATED PROTEIN KINASE 4		2.11
ILMN_2652909	Ddit3	DNA-DAMAGE INDUCIBLE TRANSCRIPT 3		2.07
ILMN_2742152	Gadd45a	GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE 45 ALPHA		1.92
ILMN_1212787	Pttg1	PITUITARY TUMOR-TRANSFORMING 1		1.8
ILMN_1216721	Cdk5	CYCLIN-DEPENDENT KINASE 5		1.78
ILMN_1227009	Gas2l1	GROWTH ARREST-SPECIFIC 2 LIKE 1		1.74
ILMN_2663009	Rassf5	RAS ASSOCIATION (RALGDS/AF-6) DOMAIN FAMILY 5		1.64
ILMN_1220454	Anapc13	ANAPHASE PROMOTING COMPLEX SUBUNIT 13		1.61
ILMN_1216213	Incenp	INNER CENTROMERE PROTEIN		1.56
ILMN_1256301	Rcc2	REGULATOR OF CHROMOSOME CONDENSATION 2		1.53
Extracellular Matrix			**5.80E-06**	
ILMN_2735184	Col18a1	PROCOLLAGEN, TYPE XVIII, ALPHA 1		51.5
ILMN_1223997	Crtap	CARTILAGE ASSOCIATED PROTEIN		32.74
ILMN_2753809	Mmp3	MATRIX METALLOPEPTIDASE 3		31.08
ILMN_2747959	Dcn	DECORIN		21.44
ILMN_2737685	Mmp13	MATRIX METALLOPEPTIDASE 13		13.86
ILMN_1232899	Smoc2	SPARC RELATED MODULAR CALCIUM BINDING 2		6.91
ILMN_2727663	Tgfbi	TRANSFORMING GROWTH FACTOR, BETA INDUCED		6.75
ILMN_1258629	Col3a1	PROCOLLAGEN, TYPE III, ALPHA 1		5.65
ILMN_2619952	Mmp10	MATRIX METALLOPEPTIDASE 10		5.32
ILMN_2668463	Emilin1	ELASTIN MICROFIBRIL INTERFACER 1		3.99
ILMN_1230747	Wnt9a	WINGLESS-TYPE MMTV INTEGRATION SITE 9A		3.8
ILMN_1254546	Col5a2	PROCOLLAGEN, TYPE V, ALPHA 2		3.42
ILMN_2422848	Wnt10b	WINGLESS RELATED MMTV INTEGRATION SITE 10B		2.97

ILMN_2772556	Fbn1	FIBRILLIN 1		2.71
ILMN_2635784	Gpc1	GLYPICAN 1		2.37
ILMN_1238215	Ctgf	CONNECTIVE TISSUE GROWTH FACTOR		2.28
ILMN_2640248	Lama5	LAMININ, ALPHA 5		2.27
ILMN_2687880	Col1a1	PROCOLLAGEN, TYPE I, ALPHA 1		2.06
ILMN_2769917	Timp1	TISSUE INHIBITOR OF METALLOPROTEINASE 1		1.99
ILMN_1225835	Mfap5	MICROFIBRILLAR ASSOCIATED PROTEIN 5		1.97
ILMN_1258759	Col6a2	PROCOLLAGEN, TYPE VI, ALPHA 2		1.77
ILMN_2497957	Epb4.1l1	FIBULIN 1		1.76
ILMN_2678218	Mmp2	MATRIX METALLOPEPTIDASE 2		1.75
ILMN_1217071	Mmp16	MATRIX METALLOPEPTIDASE 16		1.67
ILMN_2774596	Lamc1	LAMININ, GAMMA 1		1.66
ILMN_1238597	Omd	OSTEOMODULIN		1.53
Ubiquitin			**1.40E-02**	
ILMN_2662401	Sumo3	SMT3 SUPPRESSOR OF MIF TWO 3 HOMOLOG 3 (YEAST)		70.01
ILMN_2763459	Tbcel	LEUCINE RICH REPEAT CONTAINING 35		3.51
ILMN_1225261	Uchl1	UBIQUITIN CARBOXY-TERMINAL HYDROLASE L1		3.02
ILMN_1229019	Fbxo44	F-BOX PROTEIN 44		2.12
ILMN_2749911	Ube2q2	UBIQUITIN-CONJUGATING ENZYME E2Q (PUTATIVE) 2		1.96
ILMN_2417991	Ube2i	UBIQUITIN-CONJUGATING ENZYME E2I		1.79
ILMN_1246522	Uchl3	UBIQUITIN CARBOXYL-TERMINAL ESTERASE L3 (UBIQUITIN THIOLESTERASE)		1.63
ILMN_2495573	Ubqln1	DNA SEGMENT, CHR 13, ERATO DOI 372, EXPRESSED		1.54
ILMN_2486783	Ube2d3	UBIQUITIN-CONJUGATING ENZYME E2D 3 (UBC4/5 HOMOLOG, YEAST)		1.54
ILMN_1227863	Ube2n	UBIQUITIN-CONJUGATING ENZYME E2N		1.53
ILMN_2516699	Ubb	UBIQUITIN B		1.51
Proto-oncogenes			**2.70E-03**	
ILMN_2655260	Ptp4a3	PROTEIN TYROSINE PHOSPHATASE 4A3		4
ILMN_1233424	Lbcl1	RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (GEF) 2		2.03
ILMN_1224526	Lck	LYMPHOCYTE PROTEIN TYROSINE KINASE		2
ILMN_1237241	Araf	V-RAF MURINE SARCOMA 3611 VIRAL ONCOGENE HOMOLOG		1.83
ILMN_1212787	Pttg1	PITUITARY TUMOR-TRANSFORMING 1		1.8
ILMN_2481071	Hras1	HARVEY RAT SARCOMA VIRUS ONCOGENE 1		1.78
ILMN_1251669	Evi2a	ECOTROPIC VIRAL INTEGRATION SITE 2A		1.77

ILMN_2492264	Wisp1	WNT1 INDUCIBLE SIGNALING PATHWAY PROTEIN 1		1.76
ILMN_1221750	Mycl1	LUNG CARCINOMA MYC RELATED ONCOGENE 1		1.66
Growth Factors			**2.30E-02**	
ILMN_1238547	Areg	AMPHIREGULIN		21.43
ILMN_1215252	Bmp4	BONE MORPHOGENETIC PROTEIN 4		14.31
ILMN_1254114	Artn	ARTEMIN		8.65
ILMN_2763243	Cxcl1	CHEMOKINE (C-X-C MOTIF) LIGAND 1		8.46
ILMN_2745480	Fgf13	FIBROBLAST GROWTH FACTOR 13		6.53
ILMN_2710698	Fgf21	FIBROBLAST GROWTH FACTOR 21		5.51
ILMN_1246073	Lefty1	LEFT RIGHT DETERMINATION FACTOR 1		4.72
ILMN_2659994	Gdnf	GLIAL CELL LINE DERIVED NEUROTROPHIC FACTOR		3.1
ILMN_1236725	Gdf1	GROWTH DIFFERENTIATION FACTOR 1		2.53
ILMN_2698449	Hbegf	HEPARIN-BINDING EGF-LIKE GROWTH FACTOR		2.36
ILMN_2484527	Vegfa	VASCULAR ENDOTHELIAL GROWTH FACTOR A		1.97
ILMN_2697220	Figf	C-FOS INDUCED GROWTH FACTOR		1.74
ILMN_2736496	Fgf10	FIBROBLAST GROWTH FACTOR 10		1.73
Cell Adhesion			**1.80E-03**	
ILMN_2774764	Cntnap4	CONTACTIN ASSOCIATED PROTEIN 4		7.88
ILMN_2627041	Cx3cl1	CHEMOKINE (C-X3-C MOTIF) LIGAND 1		2.5
ILMN_2670172	Itga5	INTEGRIN ALPHA 5 (FIBRONECTIN RECEPTOR ALPHA)		2.32
ILMN_2640248	Lama5	LAMININ, ALPHA 5		2.27
ILMN_1223697	Cd44	CD44 ANTIGEN		2.1
ILMN_1243254	Adam12	A DISINTEGRIN AND METALLOPEPTIDASE DOMAIN 12 (MELTRIN ALPHA)		1.92
ILMN_2707976	Cdh26	CADHERIN-LIKE 26		1.88
ILMN_2725411	Cd9	CD9 ANTIGEN		1.84
ILMN_1257880	Itga7	INTEGRIN ALPHA 7		1.77
ILMN_2492264	Wisp1	WNT1 INDUCIBLE SIGNALING PATHWAY PROTEIN 1		1.76
ILMN_2663613	Itgb5	INTEGRIN BETA 5		1.74
ILMN_2659503	Cdh13	CADHERIN 13		1.69
ILMN_1241893	Wisp2	WNT1 INDUCIBLE SIGNALING PATHWAY PROTEIN 2		1.69
ILMN_1232768	Vcam1	VASCULAR CELL ADHESION MOLECULE 1		1.56
ILMN_1237629	Cntn2	CONTACTIN 2		1.51

Collagen			**2.10E-02**	
ILMN_2735184	Col18a1	PROCOLLAGEN, TYPE XVIII, ALPHA 1		19.16
ILMN_1258629	Col3a1	PROCOLLAGEN, TYPE III, ALPHA 1		5.65
ILMN_1254546	Col5a2	PROCOLLAGEN, TYPE V, ALPHA 2		3.04
ILMN_2687880	Col1a1	PROCOLLAGEN, TYPE I, ALPHA 1		2.06
ILMN_2707616	Col22a1	COLLAGEN, TYPE XXII, ALPHA 1		1.87
ILMN_1258759	Col6a2	PROCOLLAGEN, TYPE VI, ALPHA 2		1.77
ILMN_1225073	Cthrc1	COLLAGEN TRIPLE HELIX REPEAT CONTAINING 1		1.53
Inflammatory Response			**1.60E-02**	
ILMN_1230789	C3	COMPLEMENT COMPONENT 3		8.8
ILMN_2763243	Cxcl1	CHEMOKINE (C-X-C MOTIF) LIGAND 1		8.46
ILMN_2742075	Cd14	CD14 ANTIGEN		2.68
ILMN_1254383	Atrn	ATTRACTIN		1.99
ILMN_1259252	Anxa1	ANNEXIN A1		1.99
ILMN_1255385	Chst1	CARBOHYDRATE (KERATAN SULFATE GAL-6) SULFOTRANSFERASE 1		1.82
Chemotaxis			**1.50E-02**	
ILMN_1231814	Ccl5	CHEMOKINE (C-C MOTIF) LIGAND 5		13.25
ILMN_2772998	Enpp2	ECTONUCLEOTIDE PYROPHOSPHATASE/PHOSPHODIESTERASE 2		12.7
ILMN_2658910	Cxcl12	CHEMOKINE (C-X-C MOTIF) LIGAND 12		6.78
ILMN_1245710	Ccl2	CHEMOKINE (C-C MOTIF) LIGAND 2		5.47
ILMN_1253797	Slit2	SLIT HOMOLOG 2 (DROSOPHILA)		3.1
ILMN_1214419	Cxcl10	CHEMOKINE (C-X-C MOTIF) LIGAND 10		2.94
ILMN_1235571	Cyr61	CYSTEINE RICH PROTEIN 61		2.9
ILMN_1216285	Creb3	CAMP RESPONSIVE ELEMENT BINDING PROTEIN 3		1.55
Development			**3.10E-02**	
ILMN_1234990	Gap43	GROWTH ASSOCIATED PROTEIN 43		37.4
ILMN_1226016	Scx	SCLERAXIS		29.89
ILMN_1215252	Bmp4	BONE MORPHOGENETIC PROTEIN 4		14.3
ILMN_2769657	Picalm	PHOSPHATIDYLINOSITOL BINDING CLATHRIN ASSEMBLY PROTEIN		4.98
ILMN_1246073	Lefty1	LEFT RIGHT DETERMINATION FACTOR 1		4.71
ILMN_2684289	Sema3a	SEMA DOMAIN, IMMUNOGLOBULIN DOMAIN (IG), SHORT BASIC DOMAIN, SECRETED,		3.89
ILMN_1230747	Wnt9a	WINGLESS-TYPE MMTV INTEGRATION SITE 9A		3.8

ILMN_2422848	Wnt10b	WINGLESS RELATED MMTV INTEGRATION SITE 10B		2.97
ILMN_2675833	Dlx3	DISTAL-LESS HOMEOBOX 3		2.96
ILMN_1245731	Hhex	HEMATOPOIETICALLY EXPRESSED HOMEOBOX		2.82
ILMN_1238558	Arid3b	AT RICH INTERACTIVE DOMAIN 3B (BRIGHT LIKE)		2.35
ILMN_1225378	Htatip2	HIV-1 TAT INTERACTIVE PROTEIN 2, HOMOLOG (HUMAN)		1.99
ILMN_1252870	Rorb	RAR-RELATED ORPHAN RECEPTOR BETA		1.89
ILMN_2722938	Myd116	MYELOID DIFFERENTIATION PRIMARY RESPONSE GENE 116		1.84
ILMN_2697220	Figf	C-FOS INDUCED GROWTH FACTOR		1.74
ILMN_1223414	Ptp4a1	PROTEIN TYROSINE PHOSPHATASE 4A1		1.72
ILMN_1215746	Cchcr1	COILED-COIL ALPHA-HELICAL ROD PROTEIN 1		1.65
ILMN_2734034	Prrx2	PAIRED RELATED HOMEOBOX 2		1.55
ILMN_2630811	Rere	ARGININE GLUTAMIC ACID DIPEPTIDE (RE) REPEATS		1.54
ILMN_2706755	Foxd1	FORKHEAD BOX D1		1.54
ILMN_1238875	Strbp	SPERMATID PERINUCLEAR RNA BINDING PROTEIN		1.54
ILMN_1253420	Psme4	PROTEASOME (PROSOME, MACROPAIN) ACTIVATOR SUBUNIT 4		1.5
Other Genes				
ILMN_1218967	Kif2c	KINESIN FAMILY MEMBER 2C		37.42
ILMN_2611181	Ccdc3	COILED-COIL DOMAIN CONTAINING 3		36.32
ILMN_1217009	Rab15	RAB15, MEMBER RAS ONCOGENE FAMILY		33.76
ILMN_2621448	Adh7	ALCOHOL DEHYDROGENASE 7 (CLASS IV), MU OR SIGMA POLYPEPTIDE		22.19
ILMN_1245531	Neto2	NEUROPILIN (NRP) AND TOLLOID (TLL)-LIKE 2		21.94
ILMN_1225602	S100a1	S100 CALCIUM BINDING PROTEIN A1		20.27
ILMN_2703267	Nes	NESTIN		18.5
ILMN_1245451	Rab6b	RAB6B, MEMBER RAS ONCOGENE FAMILY		14.71
ILMN_2713285	Fhl1	FOUR AND A HALF LIM DOMAINS 1		14.19
ILMN_2606660	Card10	CASPASE RECRUITMENT DOMAIN FAMILY, MEMBER 10		10.23
ILMN_2646891	Centd1	CENTAURIN, DELTA 1		9.05
ILMN_2686327	Gas6	GROWTH ARREST SPECIFIC 6		8.94
ILMN_2689998	Fjx1	FOUR JOINTED BOX 1 (DROSOPHILA)		8.81
ILMN_1230080	S100a7a	S100 CALCIUM BINDING PROTEIN A15		6.95
ILMN_1247646	H1fx	H1 HISTONE FAMILY, MEMBER X		6.91
ILMN_1217159	Lmo7	LIM DOMAIN ONLY 7		5.51
ILMN_1214327	S100a13	S100 CALCIUM BINDING PROTEIN A13		5.19
ILMN_1242829	Prdx2	PEROXIREDOXIN 2		5.10

ILMN_2868133	Gata6	GATA BINDING PROTEIN 6		4.75
ILMN_2614590	Tmem45a	TRANSMEMBRANE PROTEIN 45A		4.71
ILMN_1224014	Tmem100	TRANSMEMBRANE PROTEIN 100		4.42
ILMN_1230586	Traf1	TNF RECEPTOR-ASSOCIATED FACTOR 1		3.73
ILMN_1215807	Glipr1	GLI PATHOGENESIS-RELATED 1 (GLIOMA)		3.44
ILMN_2633670	Tmem62	TRANSMEMBRANE PROTEIN 62		3.03
ILMN_2773901	Glipr2	GLI PATHOGENESIS-RELATED 2		3.02
ILMN_1227993	Vav3	VAV 3 ONCOGENE		2.67
ILMN_2714361	Cd34	CD34 ANTIGEN		2.32
ILMN_2687880	Col1a1	PROCOLLAGEN, TYPE I, ALPHA 1		2.02
ILMN_1214227	Krt1-10	KERATIN COMPLEX 1, ACIDIC, GENE 1-10		1.84

The criteria for Functional Annotation Clustering of Gene analysis was set at $P < 0.05$ and fold-change less than or equal to 1.5. Shown are functional clusters of genes that were up-regulated in *Klf4* -null MEFs.

Table S2: Functional Annotation Clustering of Genes Down-Regulated in *Klf4*-Null MEFs

ILLUMINA_ID	Gene Symbol	Gene Name (Description)	*P*-Value	Fold-Change
Jak-Stat Signaling Pathway			**1.90E-02**	
ILMN_1256180	Osmr	ONCOSTATIN M RECEPTOR		-4.000
ILMN_1219155	Jak3	JANUS KINASE 3		-3.448
ILMN_2628178	Socs2	SUPPRESSOR OF CYTOKINE SIGNALING 2		-3.226
ILMN_1243862	Il11	INTERLEUKIN 11		-3.226
ILMN_2698046	Stat3	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 3		-2.273
ILMN_2618176	Socs3	SUPPRESSOR OF CYTOKINE SIGNALING 3		-1.538
Homeobox			**4.20E-03**	
ILMN_2860958	Dlx2	DISTAL-LESS HOMEOBOX 2		-14.286
ILMN_3163581	En1	ENGRAILED 1		-7.692
ILMN_1219807	Hoxd4	HOMEO BOX D4		-6.667
ILMN_1242977	Hoxb5	HOMEO BOX B5		-5.263
ILMN_2762935	Rhox5	REPRODUCTIVE HOMEOBOX 5		-5.263
ILMN_1218266	Meis1	MYELOID ECOTROPIC VIRAL INTEGRATION SITE 1		-4.348
ILMN_2636480	Hoxa5	HOMEO BOX A5		-4.000
ILMN_2618302	Hoxa2	HOMEO BOX A2		-3.448
ILMN_1229029	Dlx1	DISTAL-LESS HOMEOBOX 1		-3.030
ILMN_2621038	Hoxa7	HOMEO BOX A7		-2.564
ILMN_1239460	Onecut2	ONE CUT DOMAIN, FAMILY MEMBER 2		-2.273
ILMN_2678094	Prrx1	PAIRED RELATED HOMEOBOX 1		-2.273
ILMN_2774121	Mrg1	MYELOID ECOTROPIC VIRAL INTEGRATION SITE-RELATED GENE 1		-2.128
ILMN_1242943	Mrg2	MYELOID ECOTROPIC VIRAL INTEGRATION SITE-RELATED GENE 2		-2.128
ILMN_2662351	Hoxd3	HOMEO BOX D3		-2.083
Glutathione Metabolism			**2.90E-03**	
ILMN_2773022	Gsta4	GLUTATHIONE S-TRANSFERASE, ALPHA 4		-9.091
ILMN_2624854	Gstm2	GLUTATHIONE S-TRANSFERASE, MU 2		-5.000
ILMN_2729458	Idh1	ISOCITRATE DEHYDROGENASE 1 (NADP+), SOLUBLE		-2.564
ILMN_1228233	Gstm1	GLUTATHIONE S-TRANSFERASE, MU 1		-2.564
ILMN_2705777	Gstm5	GLUTATHIONE S-TRANSFERASE, MU 5		-2.439
ILMN_2641807	Gstm6	GLUTATHIONE S-TRANSFERASE, MU 6		-2.326
ILMN_1229964	Gstz1	GLUTATHIONE TRANSFERASE ZETA 1 (MALEYLACETOACETATE ISOMERASE)		-2.174

Ephrin			**2.60E-02**	
ILMN_1257372	Efnb1	EPHRIN B1		-2.041
ILMN_1217493	Efna4	EPHRIN A4		-1.639
ILMN_2716212	Efnb2	EPHRIN B2		-1.515
Developmental protein			**3.20E-04**	
ILMN_2422615	Ebf3	EARLY B-CELL FACTOR 3		-18.519
ILMN_2860958	Dlx2	DISTAL-LESS HOMEOBOX 2		-14.286
ILMN_3163581	En1	ENGRAILED 1		-7.692
ILMN_2630993	Ppap2b	PHOSPHATIDIC ACID PHOSPHATASE TYPE 2B		-7.143
ILMN_1219807	Hoxd4	HOMEO BOX D4		-6.667
ILMN_1242977	Hoxb5	HOMEO BOX B5		-5.263
ILMN_2703433	Foxc2	FORKHEAD BOX C2		-4.545
ILMN_1218266	Foxc2	MYELOID ECOTROPIC VIRAL INTEGRATION SITE 1		-4.348
ILMN_2636480	Hoxa5	HOMEO BOX A5		-4.000
ILMN_2776850	Gas7	GROWTH ARREST SPECIFIC 7		-3.846
ILMN_2618302	Hoxa2	HOMEO BOX A2		-3.448
ILMN_1228557	Id2	INHIBITOR OF DNA BINDING 2		-3.030
ILMN_1229029	Dlx1	DISTAL-LESS HOMEOBOX 1		-2.941
ILMN_2716389	Smpd3	SPHINGOMYELIN PHOSPHODIESTERASE 3, NEUTRAL		-2.632
ILMN_2621038	Hoxa7	HOMEO BOX A7		-2.564
ILMN_2765047	Chrd	CHORDIN		-2.381
ILMN_2624731	Egfl7	EGF-LIKE DOMAIN 7		-2.326
ILMN_2721198	Ggnbp1	GAMETOGENETIN BINDING PROTEIN 1		-2.273
ILMN_2643531	Angptl6	ANGIOPOIETIN-LIKE 6		-2.273
ILMN_1234976	Prrx1	PAIRED RELATED HOMEOBOX 1		-2.222
ILMN_1257372	Efnb1	EPHRIN B1		-2.041
ILMN_2662351	Hoxd3	HOMEO BOX D3		-2.041
ILMN_2659224	Cspg4	CHONDROITIN SULFATE PROTEOGLYCAN 4		-2.000
ILMN_1232901	Vamp5	VESICLE-ASSOCIATED MEMBRANE PROTEIN 5		-1.961
ILMN_2485120	Vti1a	INHIBITOR OF DNA BINDING 1		-1.961
ILMN_1235053	Mlf1	MYELOID LEUKEMIA FACTOR 1		-1.887
ILMN_1237197	Nrp1	NEUROPILIN 1		-1.887

Other Genes				
ILMN_2771738	Dlk1	DELTA-LIKE 1 HOMOLOG (DROSOPHILA)		-307.819
ILMN_2644350	Thy1	THYMUS CELL ANTIGEN 1, THETA		-67.239
ILMN_1244206	Prl2c4	PROLIFERIN 2		-42.157
ILMN_2661576	Bicc1	BICAUDAL C HOMOLOG 1 (DROSOPHILA)		-37.988
ILMN_1256371	Fez1	FASCICULATION AND ELONGATION PROTEIN ZETA 1 (ZYGIN I)		-37.299
ILMN_2724942	Ptgis	PROSTAGLANDIN I2 (PROSTACYCLIN) SYNTHASE		-33.333
ILMN_2661576	Bicc1	BICAUDAL C HOMOLOG 1 (DROSOPHILA)		-33.333
ILMN_2693606	Nr1h5	NUCLEAR RECEPTOR SUBFAMILY 1, GROUP H, MEMBER 5		-21.170
ILMN_2729103	Adamts2	A DISINTEGRIN-LIKE AND METALLOPEPTIDASE (REPROLYSIN TYPE) WITH THROMBO		-15.967
ILMN_1224866	Ptgs1	PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 1		-12.500
ILMN_1249767	Thbd	THROMBOMODULIN		-10.099
ILMN_1260020	Pcdh1	PROTOCADHERIN 1		-8.362
ILMN_1235133	Syn1	SYNAPSIN I		-6.305
ILMN_1232183	Mgmt	O-6-METHYLGUANINE-DNA METHYLTRANSFERASE		-4.859
ILMN_2634538	Peli2	PELLINO 2		-4.575
ILMN_1249776	Insl3	INSULIN-LIKE 3		-4.447
ILMN_2699052	Nrn1	NEURITIN 1		-4.387
ILMN_2674533	Renbp	RENIN BINDING PROTEIN		-4.011
ILMN_2674122	Pkia	PROTEIN KINASE INHIBITOR, ALPHA		-3.780
ILMN_1246282	Tcfap2a	TRANSCRIPTION FACTOR AP-2, ALPHA		-3.658
ILMN_2729197	Hic1	HYPERMETHYLATED IN CANCER 1		-3.587
ILMN_1235499	Pros1	PROTEIN S (ALPHA)		-3.367
ILMN_1240677	Gadd45gip1	GROWTH ARREST AND DNA-DAMAGE-INDUCED GAMMA INTERACTING PROTEIN 1		-3.026
ILMN_1218934	Rdm1	RAD52 MOTIF 1		-3.010
ILMN_2674367	Agrn	AGRIN		-2.932
ILMN_2623578	Nid1	NIDOGEN 1		-2.710
ILMN_2624328	Adamts7	A DISINTEGRIN-LIKE AND METALLOPEPTIDASE (REPROLYSIN TYPE) WITH THROMBO		-2.707
ILMN_2677332	Hic2	HYPERMETHYLATED IN CANCER 2		-2.515
ILMN_2677859	Insl6	INSULIN-LIKE 6		-2.229
ILMN_1230145	Acvr2b	ACTIVIN RECEPTOR IIB		-2.141

The criteria for Functional Annotation Clustering of Gene analysis was set at $P < 0.05$ and fold-change less than or equal to1.5. Shown are functional clusters of genes that were down-regulated in *Klf4* -null MEFs.

Table S3 Functional annotation identified by Ingenuity global function analysis of genes regulated by Klf4

Functional Annotation	P-value	Name of Genes	Number of Genes
neurological disorder	5.75E-03	ABCC4, ABCC5, ABCC10, ABCD1, ABCD4, ACADM, ACBD3, ACER3, ACP1, ACP2, ACSL1, ACSL4, ACTB, ADA, ADAM12, ADAM15, ADCY7, ADCY8, ADCY9, ADCYAP1R1, ADH7, ADRB2, AEBP1, AEBP2, AEN, AHCY, AHI1, AIG1, AIM1 (includes EG:202), AK5,	1016
tumorigenesis	2.42E-06	ABCA5, ABCC4, ABR, ACTB, ACTR10, ACVR1, ACY1, ADA, ADAM12, ADAM17, ADAMTS1, ADARB1, ADORA2B, ADRB2, AGPAT2, AHCY, AIG1, AIM2, AIM1 (includes EG:202), AK2, AKAP1, AKAP12, AKAP8L, AKR1B10, AKT3, ALAD, ALDH2, ALDH5A1,	802
cell death	3.18E-14	AAK1, ABCC4, ABCC5, ACSL4, ACTB, ACVR1, ACVR1B, ACVR2B, ADA, ADAM12, ADAMTSL4, ADCYAP1R1, ADM, ADORA2B, ADRB2, AFP, AGPAT2, AHSA1, AIFM2, AIM2, AKAP1, AKAP12, AKT3, ALCAM, ALDH2, ALDOC, ALOX12, ANGPT2, ANGPTL4, ANKRD1, ANP32A, ANTXR1, ANTXR2, ANXA1, ANXA7	753
neoplasia	2.45E-06	ABCA5, ABCC4, ABR, ACTB, ACTR10, ACY1, ADA, ADAM12, ADAM17, ADAMTS1, ADARB1, ADORA2B, ADRB2, AGPAT2, AHCY, AIG1, AIM2, AIM1 (includes EG:202), AK2, AKAP1, AKAP12, AKAP8L, AKR1B10, AKT3, ALAD, ALDH2, ALDH5A1, ALDOC, AMFR,	751
cancer	5.29E-06	ABCA5, ABCC4, ABR, ACTR10, ACY1, ADA, ADAM12, ADAMTS1, ADARB1, ADORA2B, ADRB2, AGPAT2, AHCY, AIG1, AIM2, AIM1 (includes EG:202), AK2, AKAP1, AKAP12, AKAP8L, AKR1B10, AKT3, ALAD, ALDH2, ALDH5A1, ALDOC, AMFR, ANGPT2,	719
apoptosis	5.53E-15	ACSL4, ACVR1, ACVR1B, ACVR2B, ADA, ADAM12, ADAMTSL4, ADCYAP1R1, ADM, ADRB2, AFP, AGPAT2, AHSA1, AIFM2, AIM2, AKAP1, AKAP12, AKT3, ALCAM, ALDH2, ALDOC, ALOX12, ANGPT2, ANGPTL4, ANKRD1, ANP32A, ANXA1, ANXA7, APBB2, APH1B, APPL1, AREG, ARF6, ARL11, ARMC10, A	659
cell death of eukaryotic cells	1.42E-12	AAK1, ABCC4, ACTB, ACVR1B, ACVR2B, ADA, ADAM12, ADCYAP1R1, ADM, ADRB2, AFP, AGPAT2, AHSA1, AIM2, AKAP1, AKT3, ALDH2, ALOX12, ANGPT2, ANKRD1, ANP32A, ANTXR1, ANTXR2, ANXA1, APH1B, AREG, ARF6, ARL11, ARMC10, ARRB2,	624
proliferation of cells	6.31E-06	ABCC4, ACP1, ACSL6, ADA, ADAM15, ADAM17, ADAMTS1, ADC, ADCYAP1R1, ADM, ADORA2B, ADRB2, AEBP1, AFP, AGTRAP, AIM2, AKR1B1, AKT3, ALOX12, ANGPT2, ANGPTL4, ANGPTL6, ANP32A, ANXA1, ANXA7, APPL1, APPL2, ARAF, ARD1A, AREG, ARHGAP24, ARHGEF2, ARIH2, ARTN, ASAH2,	614
tumor	5.51E-04	ABCC4, ABR, ACTR10, ACVR1, ACY1, ADA, ADAM12, ADAM17, ADAMTS1, ADARB1, ADORA2B, ADRB2, AGPAT2, AIG1, AIM2, AK2, AKAP1, AKAP12, AKAP8L, AKT3, ALAD, ALDH5A1, ALDOC, ANGPT2, ANGPTL4, ANO6, ANP32A, ANTXR1, ANXA1, ANXA5,	555
apoptosis of eukaryotic cells	7.67E-14	ACVR1B, ACVR2B, ADA, ADAM12, ADCYAP1R1, ADM, ADRB2, AFP, AGPAT2, AHSA1, AIM2, AKAP1, AKT3, ALDH2, ALOX12, ANGPT2, ANKRD1, ANP32A, ANXA1, APH1B, AREG, ARF6, ARL11, ARMC10, ARRB2, ASAH2, ASNS, ATF2, ATF3, ATMIN, ATP1A1,	541
growth of cells	4.10E-12	ABCC5, ACP1, ACTB, ACVR1B, ADAM12, ADAM15, ADAM17, ADFP, ADIPOR2, ADM, ADORA2B, AHCY, AHSA1, AK2, AKAP12, AKR1B1, AKT3, ALCAM, ALOX12, ANP32A, ANXA1, ANXA7, APBB2, ARAF, AREG, ARL3, ARL11, ARMC10, ARRB2, ATF2, ATF3,	525

primary tumor	1.00E-03	ABCC4, ABR, ACTR10, ACY1, ADA, ADAM12, ADAMTS1, ADARB1, ADORA2B, ADRB2, AGPAT2, AIG1, AIM2, AK2, AKAP1, AKAP12, AKAP8L, AKT3, ALAD, ALDH5A1, ALDOC, ANGPT2, ANO6, ANTXR1, ANXA1, ANXA5, AQP1, AREG, ARFGEF2, ARIH2, ARL11,	518
malignant tumor	9.24E-04	ABCC4, ABR, ACTR10, ACY1, ADA, ADAM12, ADAMTS1, ADARB1, ADORA2B, ADRB2, AGPAT2, AIG1, AIM2, AK2, AKAP1, AKAP12, AKAP8L, AKT3, ALAD, ALDH5A1, ALDOC, ANGPT2, ANO6, ANTXR1, ANXA1, AQP1, AREG, ARFGEF2, ARIH2, ARL11, ARL4D,	504
proliferation of eukaryotic cells	4.71E-05	ABCC4, ACP1, ACSL6, ADA, ADAM15, ADAMTS1, ADC, ADCYAP1R1, ADM, ADRB2, AEBP1, AFP, AGTRAP, AIM2, AKR1B1, AKT3, ANGPT2, ANGPTL4, ANGPTL6, ANXA1, ARD1A, AREG, ARHGAP24, ARIH2, ARTN, ATF4, ATP6V0A2, B4GALT1, BACH2	488
transcription	2.57E-03	ACTR2, ACTR1B (includes EG:10120), ACVR1, ACVR1B, ACVR2B, ADRB2, AEBP1, AEBP2, AFF4, AGRN, AMPH, ANKRD1, ANP32A, AP1G2, APBB2, APOL3 (includes EG:80833), ATF2, ATF3, ATF4, ATF7IP, ATP2C1, AZI2, BACH2 (includes EG:60468),	468
cell death of cell lines	9.67E-15	AAK1, ABCC4, ACTB, ACVR1B, ACVR2B, ADM, AFP, AGPAT2, AHSA1, AIM2, AKAP1, AKT3, ALDH2, ALOX12, ANGPT2, ANKRD1, ANTXR1, ANTXR2, APH1B, AREG, ARL11, ARMC10, ARRB2, ASNS, ATF2, ATF3, ATMIN, ATP2A2, BACH2 (includes EG:60468),	467
apoptosis of cell lines	4.63E-13	ACVR1B, ACVR2B, ADM, AFP, AGPAT2, AHSA1, AIM2, AKAP1, AKT3, ALDH2, ALOX12, ANGPT2, ANKRD1, APH1B, AREG, ARL11, ARMC10, ARRB2, ASNS, ATF2, ATF3, ATMIN, BACH2 (includes EG:60468), BCAR1, BCL2, BCL10, BCL2L11, BDNF, BHLHE40,	399
differentiation of cells	2.22E-05	ACADM, ACVR1, ACVR1B, ACVR2B, ADA, ADD1, ADORA2B, ADRB2, ALG5, ANXA1, AREG, ATF2, ATF3, ATF4, ATP7A, AXIN2, B4GALNT1, BAIAP2, BCL2, BCL2L11, BDH2, BDNF, BHLHE40, BIN1, BLNK, BMP1, BMP4, BMPER, BSG, BTC, C5ORF13, CAND1,	399
carcinoma	3.96E-05	ABCC4, ACTR10, ACY1, ADAM12, ADAMTS1, ADRB2, AGPAT2, AIG1, AIM2, AKAP1, AKT3, ALDH5A1, ALDOC, ANGPT2, ANO6, ANTXR1, ANXA1, AQP1, AREG, ARL11, ARRB2, ASS1, ATF2, ATP1B1, ATP2C1, AXIN2, BAT1, BCL2, BCL10, BHLHE40, BRCA2,	382
cell death of tumor cell lines	4.67E-11	ABCC4, ACVR1B, ACVR2B, ADM, AFP, AGPAT2, AHSA1, AIM2, AKAP1, AKT3, ALOX12, ANGPT2, ANKRD1, AREG, ARL11, ARMC10, ARRB2, ASNS, ATF2, ATF3, ATMIN, ATP2A2, BACH2 (includes EG:60468), BCAR1, BCL2, BCL10, BCL2L11, BDNF,	359
growth of eukaryotic cells	2.56E-06	ABCC5, ACP1, ADAM17, ADM, AHSA1, AKAP12, AKR1B1, AKT3, ANP32A, ANXA1, ANXA7, AREG, ARL11, ARMC10, ATF2, ATF3, BCAR1, BCL2, BCL2L11, BDNF, BMP4, BSG, BTC, C3, C8ORF4, CAMK2N1, CASP8, CAST, CBFB, CBX7, CCND1, CCNE1, CD14, CD44, CD82, CD274, CDC7, CDCA4, CDH	350
cell death of normal cells	9.58E-05	ABCC4, ADA, ADAM12, ADCYAP1R1, ADM, ADRB2, ALOX12, ANGPT2, ANP32A, ANXA1, ARF6, ARRB2, ASAH2, ATF2, ATF3, ATP1A1, ATP2C1, B4GALNT1, BACE1, BCL2, BCL10, BCL2L11, BDNF, BID, BLNK, BMP4, BNIP3L, C3, C14ORF153, C8ORF4,	347
development of cells	1.78E-07	ACP1, ACVR1, ADA, ADAM17, ADD1, AFF4, AGFG1 (includes EG:3267), ANGPT2, ANGPTL2, ANTXR1, ANXA5, ANXA7, ARHGDIG, ARHGEF2, ARRB2, ATF3, ATP1B1, ATRN, B4GALT1, BAIAP2, BCAR1, BCL2, BCL10, BCL2L11, BDNF, BLNK, BMP4, CAPG,	342

movement of cells	1.77E-05	ABHD2, ACP1, ACVR1, ADAM9, ADAM12, ADAM15, ADAM17, ADM, ADRB2, AKT3, ALCAM, ALOX12, ANGPT2, ANGPTL4, ANXA1, AOC3, APBB2, AREG, ARF6, ARHGAP24, ARRB2, B4GALT1, BCAR1, BCL2, BDNF, BMP4, BTC, C3, C5ORF13, CAPNS1, CBFB, CCK, CCL5, CCL7, CCL8, CCL9, CCL13, CCL	335
migration of cells	9.54E-06	ABHD2, ACP1, ACVR1, ADAM9, ADAM12, ADAM15, ADAM17, ADM, ADRB2, AKT3, ALCAM, ALOX12, ANGPT2, ANGPTL4, ANXA1, AOC3, APBB2, AREG, ARF6, ARHGAP24, ARRB2, B4GALT1, BCAR1, BCL2, BDNF, BMP4, BTC, C3, C5ORF13, CAPNS1, CBFB, CCK, CCL5, CCL7, CCL8, CCL9, CCL13, CCL	333
cell division process of cells	9.23E-06	ACVR1, ACVR1B, ADM, ADORA2B, AKAP9, AKAP12, ANAPC4, ANGPTL2, APBB2, ARAF, AREG, ATF2, ATF3, AXIN2, BCAR1, BCL2, BCL2L11, BHLHE40, BID, BLNK, BMP4, BRCA2, BRCC3, BTC, BTRC, C13ORF15, CAMK1, CAMK2D, CAMK2N1, CAMKK1, CARD10, CASP2, CAST, CCK, CCNB1IP1, CCND1	320
apoptosis of tumor cell lines	3.54E-11	ACVR1B, ACVR2B, ADM, AFP, AGPAT2, AHSA1, AIM2, AKAP1, AKT3, ALOX12, ANGPT2, ANKRD1, AREG, ARL11, ARMC10, ARRB2, ASNS, ATF2, ATF3, ATMIN, BACH2 (includes EG:60468), BCAR1, BCL2, BCL10, BCL2L11, BDNF, BHLHE40, BID,	315
movement of eukaryotic cells	3.69E-04	ACP1, ACVR1, ADAM9, ADAM12, ADAM15, ADAM17, ADM, ADRB2, AKT3, ALCAM, ALOX12, ANGPT2, ANGPTL4, ANXA1, AOC3, APBB2, ARF6, ARHGAP24, ARRB2, B4GALT1, BCAR1, BDNF, BMP4, BTC, C3, C5ORF13, CAPNS1, CBFB, CCK, CCL5,	302
apoptosis of normal cells	1.80E-06	ADA, ADAM12, ADCYAP1R1, ADM, ADRB2, ANGPT2, ANP32A, ANXA1, ARF6, ARRB2, ASAH2, ATF2, ATF3, ATP1A1, ATP2C1, B4GALNT1, BCL2, BCL10, BCL2L11, BDNF, BID, BLNK, BMP4, BNIP3L, C3, C8ORF4, CABLES2, CAMK2D, CAPN1, CAPNS1, CASP2,	301
migration of eukaryotic cells	2.34E-04	ACP1, ACVR1, ADAM9, ADAM12, ADAM15, ADAM17, ADM, ADRB2, AKT3, ALCAM, ALOX12, ANGPT2, ANGPTL4, ANXA1, AOC3, APBB2, ARF6, ARHGAP24, ARRB2, B4GALT1, BCAR1, BDNF, BMP4, BTC, C3, C5ORF13, CAPNS1, CBFB, CCK, CCL5,	300
developmental process of organism	3.33E-04	ACVR1, ACVR1B, ADA, ADAMTS1, ADD1, ADH5 (includes EG:128), ANGPT2, ANGPTL2, APH1A (includes EG:226548), AQP1, ARIH2, ATF2, ATP1B1, BCL2, BCL2L11, BDNF, BMP1, BMP4, BTC, CBFB, CCDC47, CCND1, CD164, CDH5, CDK6, CDKN1B, CDON, CHD7, CHD8, CHRD, CHST2, CHST11,	288
growth of cell lines	1.83E-07	ABCC5, ACP1, ADAM17, ADM, AHSA1, AKAP12, AKT3, ANP32A, ANXA1, ANXA7, AREG, ARL11, ARMC10, ATF2, ATF3, BCAR1, BCL2, BCL2L11, BMP4, BTC, C8ORF4, CAMK2N1, CAST, CBFB, CBX7, CCND1, CCNE1, CD44, CD274, CDCA4, CDH13, CDK2, CDK6, CDKN1A, CDKN1B, CEBPD, CHKA, CLI	287
proliferation of cell lines	1.32E-05	ADC, ADM, AFP, AIM2, AKT3, ANXA1, ARD1A, AREG, ARIH2, ATP6V0A2, BACH2 (includes EG:60468), BCAR1, BCL2, BDNF, BID, BMP4, BRCA2, BTC, BTRC, C5ORF13, CASP2, CASP8, CBFB, CCDC6, CCL13, CCND1, CCNE1, CCNG2, CD9, CD44, CD81,	286
death of animal	9.24E-06	ABCA3, ADA, ADAM12, ADH7, ADH5 (includes EG:128), ADK, ADRB2, AEBP1, AKT3, ALOX12, AMPH, ANGPT2, ANGPTL6, ANXA1, APH1A (includes EG:226548), AQP11, B4GALNT1, BACE1, BCL2, BCL2L11, BID, BLMH, BNIP3L, BRCA2, C3, C1GALT1,	283

developmental process of tissue	2.24E-07	ACVR1, ACVR1B, ACVR2B, ADAM12, ADAM15, ADAMTS1, ADCYAP1R1, ADRB2, AEBP1, ANGPT2, APH1A (includes EG:226548), AREG, ARHGEF10, ATF3, ATP7A, B4GALNT1, B4GALT1, BACE1, BBS1, BCL2, BCL2L11, BDNF, BMP4, CAPNS1, CASP9, CCNF, CD9, CD44, CD81, CDK5, CDK5R1, CDKN1A	280
death of mammalia	7.57E-06	ABCA3, ADA, ADAM12, ADH7, ADH5 (includes EG:128), ADK, ADRB2, AEBP1, AKT3, ALOX12, AMPH, ANGPT2, ANGPTL6, ANXA1, APH1A (includes EG:226548), AQP11, B4GALNT1, BACE1, BCL2, BCL2L11, BID, BLMH, BNIP3L, BRCA2, C3, C1GALT1,	279
developmental process of tumor cell lines	4.38E-07	ADAM17, ADM, AHSA1, AKAP12, AKT3, ALG5, ANXA1, ANXA7, AREG, ARL11, ATF2, ATF3, B4GALNT1, BCAR1, BCL2, BCL2L11, BDH2, BDNF, BMP4, BTC, CAMK2N1, CAPN1, CAST, CBX7, CCND1, CCNE1, CD14, CD44, CD82, CD274, CDCA4, CDH13, CDK2, CDK6, CDK5R1, CDKN1A, CDKN1B, CEBP	277
death of rodents	5.72E-06	ABCA3, ADA, ADAM12, ADH7, ADH5 (includes EG:128), ADK, ADRB2, AEBP1, AKT3, ALOX12, AMPH, ANGPT2, ANGPTL6, ANXA1, APH1A (includes EG:226548), AQP11, B4GALNT1, BACE1, BCL2, BCL2L11, BID, BLMH, BNIP3L, BRCA2, C3, C1GALT1,	277
death of mice	6.21E-06	ABCA3, ADA, ADAM12, ADH7, ADH5 (includes EG:128), ADK, ADRB2, AEBP1, AKT3, ALOX12, AMPH, ANGPT2, ANGPTL6, ANXA1, APH1A (includes EG:226548), AQP11, B4GALNT1, BACE1, BCL2, BCL2L11, BID, BLMH, BNIP3L, BRCA2, C3, C1GALT1,	276
survival of cells	5.95E-05	ACVR2B, ADK, ADORA2B, AGRN, AK5, AKAP8L, ALCAM, ALOX12, ANTXR1, ANTXR2, AREG, ARTN, ATF2, ATF4, ATP7A, AURKAIP1, BANF1, BCAR1, BCL2, BCL2L11, BDNF, BHLHE40, BMP4, BRCA2, BTC, C7ORF16, CAMK2D, CAMK2N1, CASP2, CASP6,	256
cell division process of eukaryotic cells	2.15E-05	ADM, ADORA2B, AKAP9, AKAP12, APBB2, ARAF, AREG, ATF2, ATF3, AXIN2, BCAR1, BCL2, BCL2L11, BHLHE40, BID, BLNK, BMP4, BRCA2, BTRC, C13ORF15, CAMK1, CAMK2N1, CAMKK1, CARD10, CASP2, CAST, CCK, CCNB1IP1, CCND1, CCNE1, CCNF, CCNG1, CCNG2, CD44, CD274, CDC7, CDC2	254
cell movement	4.57E-03	ACP1, ACTB, ACTR2, ADM, ALOX12, ALOX5AP, AMFR, ANGPT2, ANXA1, AOC3, ARF6, ARRB2, ARTN, B4GALT1, BCAR1, BDNF, BMP4, BSG, BTN1A1, C3, CALD1, CAMK2N2, CAPN1, CAPZB, CASP8, CAST, CBFB, CCL5, CCL7, CCL8, CCL13, CCL25, CCND1,	253
cell stage	4.52E-05	ACVR1, ACVR1B, ADORA2B, AKAP9, AKAP12, ANAPC4, APBB2, ARAF, AREG, ATF2, ATF3, AXIN2, BCL2, BCL2L11, BHLHE40, BID, BMP4, BRCA2, BRCC3, BTC, BTRC, C13ORF15, CAMK1, CAMK2D, CAMK2N1, CAMKK1, CCK, CCNB1IP1, CCND1, CCNE1, CCNF, CCNG1, CCNG2, CD44, CDC7, CDC16,	250
developmental disorder	1.41E-03	ACSL4, ACTG2 (includes EG:72), ADA, ADAMTS10 (includes EG:81794), ADM, ADRB2, ANGPT2, ANKH, ARAF, ARL6, ARSA, ATF3, ATF4, ATP6AP2, ATP7A, BACE1, BBS1, BBS7, BCL2, BCOR, BDNF, BMP4, BRWD3, BTRC, C3, CACNA1C, CAMK2D, CCL13,	250
modification of protein	1.50E-04	ACP1, ACVR1B, ADAM17, ADM, ALG8, ALG9, ALG12, AMFR, APH1B, ARAF, ARD1A, ARRB2, ATG3, ATG10, ATG12, ATXN10, BCL2, BCL10, BMP4, BSG, CAMK2D, CAND1, CAPN1, CARD10, CAST, CCK, CCL5, CCND1, CCNE1, CCT4, CCT6A, CD9, CD34, CD44,	248

development of tissue	3.37E-07	ACVR1, ACVR1B, ACVR2B, ADAM12, ADAMTS1, ADCYAP1R1, ADRB2, AEBP1, ANGPT2, APH1A (includes EG:226548), AREG, ARHGEF10, ATP7A, B4GALNT1, B4GALT1, BACE1, BBS1, BCL2, BCL2L11, BDNF, BMP4, CAPNS1, CASP9, CCNF, CD9, CD44, CD81, CDK5, CDK5R1, CDON, CHKB, CHST11,	239
development of organ	2.14E-04	ABR, ACADM, ACVR1, ACVR2B, ADA, ADAMTS1, ADAMTS2, ADM, AEBP1, APH1A (includes EG:226548), AQP11, AREG, ARF6, ASL, ATF3, ATP7A, BBS1, BCL2, BCL2L11, BCOR, BDNF, BMP4, BRCA2, C1GALT1, CASP2, CASP7, CASP8, CASP9, CBFB, CCND1, CCNF, CDK5, CDK5R1, CFL1, CHD7,	238
survival of eukaryotic cells	3.50E-05	ACVR2B, ADK, AGRN, AK5, AKAP8L, ALOX12, ANTXR1, ANTXR2, AREG, ARTN, ATF2, ATP7A, AURKAIP1, BCAR1, BCL2, BCL2L11, BDNF, BHLHE40, BMP4, BRCA2, BTC, C7ORF16, CAMK2D, CAMK2N1, CASP2, CASP7, CASP8, CASP9, CBFB, CCL5, CCND1, CCNG1, CCRK, CD44, CD81, CD82, CDH5,	237
infectious disorder of cells	4.84E-04	ACADSB, AEBP2, AFG3L1, AMDHD2, ANAPC2, AP1G2, AP2M1, ARGLU1, ARHGEF19, ARPC1A, ATG12, ATG16L2, ATMIN, ATP6V0C, B4GALNT4, BICD2, BMP1, C3, C6ORF1, CAD, CAMK1D, CAPN6, CCDC51, CCL5, CCT2, CD44, CD93, CD164, CDC42EP3, CHST1, CLNS1A, CLOCK, CLTA, COL5A1, CRYA	236
development of organism	9.75E-04	ACVR1, ACVR1B, ADA, ADD1, ANGPT2, ANGPTL2, APH1A (includes EG:226548), ARIH2, ATF2, ATP1B1, BCL2, BCL2L11, BDNF, BMP1, BMP4, BTC, CBFB, CCDC47, CCND1, CD164, CDH5, CDK6, CDON, CHD7, CHD8, CHRD, CHST2, CHST11, CLPTM1, CNR1, COL18A1, COMMD1 (includes EG:150	236
infection of cells	3.10E-04	ACADSB, AEBP2, AFG3L1, AMDHD2, ANAPC2, AP1G2, AP2M1, ARGLU1, ARHGEF19, ARPC1A, ATG12, ATG16L2, ATMIN, ATP6V0C, B4GALNT4, BICD2, BMP1, C6ORF1, CAD, CAMK1D, CAPN6, CCDC51, CCL5, CCT2, CD44, CD93, CD164, CDC42EP3, CHST1, CLNS1A, CLOCK, CLTA, COL5A1, CRYAB, C	234
infectious disorder of eukaryotic cells	3.10E-04	ACADSB, AEBP2, AFG3L1, AMDHD2, ANAPC2, AP1G2, AP2M1, ARGLU1, ARHGEF19, ARPC1A, ATG12, ATG16L2, ATMIN, ATP6V0C, B4GALNT4, BICD2, BMP1, C3, C6ORF1, CAD, CAMK1D, CAPN6, CCDC51, CCL5, CCT2, CD44, CD93, CD164, CDC42EP3, CHST1, CLNS1A, CLOCK, CLTA, COL5A1, CRYA	234
infection of eukaryotic cells	1.67E-04	ACADSB, AEBP2, AFG3L1, AMDHD2, ANAPC2, AP1G2, AP2M1, ARGLU1, ARHGEF19, ARPC1A, ATG12, ATG16L2, ATMIN, ATP6V0C, B4GALNT4, BICD2, BMP1, C6ORF1, CAD, CAMK1D, CAPN6, CCDC51, CCL5, CCT2, CD44, CD93, CD164, CDC42EP3, CHST1, CLNS1A, CLOCK, CLTA, COL5A1, CRYAB, C	233
cell stage of cells	6.06E-05	ACVR1, ACVR1B, ADORA2B, AKAP9, AKAP12, ANAPC4, APBB2, ARAF, AREG, ATF2, ATF3, AXIN2, BCL2, BCL2L11, BHLHE40, BID, BMP4, BRCA2, BRCC3, BTC, BTRC, C13ORF15, CAMK1, CAMK2D, CAMK2N1, CAMKK1, CCK, CCNB1IP1, CCND1, CCNE1, CCNF, CCNG1, CCNG2, CD44, CDC7, CDC16,	229
infectious disorder of cell lines	2.08E-04	ACADSB, AEBP2, AFG3L1, AMDHD2, ANAPC2, AP1G2, AP2M1, ARGLU1, ARHGEF19, ARPC1A, ATG12, ATG16L2, ATMIN, ATP6V0C, B4GALNT4, BICD2, BMP1, C3, C6ORF1, CAD, CAMK1D, CAPN6, CCDC51, CCL5, CCT2, CD164, CDC42EP3, CHST1, CLNS1A, CLOCK, CLTA, COL5A1, CRYAB, CSPP1, CT	229

migration of normal cells	1.29E-03	ACP1, ACVR1, ADAM9, ADAM15, ADAM17, ADM, ADRB2, ANGPT2, ANGPTL4, ANXA1, AOC3, APBB2, ARF6, ARHGAP24, ARRB2, B4GALT1, BCAR1, BDNF, BMP4, C3, CAPNS1, CCK, CCL5, CCL7, CCL8, CCL9, CCL13, CCL25, CCND1, CD9, CD34, CD44,	229
infection of cell lines	1.28E-04	ACADSB, AEBP2, AFG3L1, AMDHD2, ANAPC2, AP1G2, AP2M1, ARGLU1, ARHGEF19, ARPC1A, ATG12, ATG16L2, ATMIN, ATP6V0C, B4GALNT4, BICD2, BMP1, C6ORF1, CAD, CAMK1D, CAPN6, CCDC51, CCL5, CCT2, CD164, CDC42EP3, CHST1, CLNS1A, CLOCK, CLTA, COL5A1, CRYAB, CSPP1, CTDP1,	228
developmental process of animal	1.92E-03	ACVR1, ACVR1B, ADA, ADAMTS1, ADD1, ADH5 (includes EG:128), ANGPT2, ANGPTL2, APH1A (includes EG:226548), AQP1, ATP1B1, BCL2, BCL2L11, BDNF, BMP4, BTC, CBFB, CCDC47, CCND1, CDH5, CDK6, CDKN1B, CDON, CHD7, CHD8, CHRD, CHST11, CNR1, COL4A2, COMMD1 (includes E	225
colorectal cancer	2.07E-05	ABCA5, ADAMTS1, AHCY, AIM1 (includes EG:202), AKT3, ANGPTL2, ANK3, ANTXR1, AOC3, ATP2A2, AXIN2, C14ORF143, C15ORF23, C15ORF48, C17ORF81, C9ORF167, CACNA2D1, CALD1, CAMK2N1, CAPG, CCT4, CD9, CD274, CDKN3, CDKN1A, CDKN1B,	212
growth of tumor cell lines	2.28E-05	ADAM17, ADM, AHSA1, AKAP12, AKT3, ANXA1, ANXA7, AREG, ARL11, ATF2, ATF3, BCAR1, BCL2, BCL2L11, BTC, CAMK2N1, CBX7, CCND1, CCNE1, CD44, CD274, CDCA4, CDH13, CDK2, CDK6, CDKN1A, CDKN1B, CEBPD, CLIP1, COL18A1, COL6A3, CRABP2, CREB1, CREG1, CTGF, CTSD, CUL7 (	212
cell cycle progression	1.38E-04	ADORA2B, AKAP9, ANXA1, APBB2, ASNS, ATF3, BCAR1, BCL2, BCL2L11, BLNK, BMP4, BRCA2, BTC, BTRC, CALM2, CAMK2N1, CARD10, CASP2, CAST, CCK, CCNB1IP1, CCNC, CCND1, CCNE1, CCNF, CCNG1, CCNG2, CD44, CD274, CDC7, CDC16, CDC23	212
proliferation of tumor cell lines	5.09E-05	ADC, ADM, AFP, AIM2, AKT3, ANXA1, ARD1A, AREG, ARIH2, BCAR1, BCL2, BDNF, BID, BRCA2, BTC, CASP2, CASP8, CCL13, CCND1, CCNE1, CCNG2, CD44, CD81, CDK5, CDK5R1, CDKN1A, CDKN1B, CHKA, COL1A1, CRK, CTGF, CTSB, CUL4A, CXCL12,	200
Huntington's disease	3.11E-05	ACADM, ACP1, ACTB, ADCY7, AEBP1, AHCY, AIG1, ALDH2, ALDH6A1, AP1S1, AQP1, ARIH2, ARL3, ATP2A2, ATP5C1, ATP5O, ATP6AP2, BAIAP2, BCL2, BCL7A, BDNF, BHLHE40, C3, C14ORF156, C4A, C5ORF13, CA11, CA12, CAPNS1, CASP2, CASP6,	199
cell division process of cell lines	5.53E-05	ADM, AKAP9, AKAP12, APBB2, ARAF, AREG, ATF2, AXIN2, BCAR1, BCL2, BHLHE40, BID, BMP4, BRCA2, BTRC, CAMK1, CAMK2N1, CAMKK1, CARD10, CASP2, CAST, CCK, CCND1, CCNE1, CCNG1, CCNG2, CD44, CDC7, CDC25A, CDC25C, CDH13, CDK2, CDK6, CDK5RAP3 (includes EG:80279), CD	199
organogenesis	2.77E-05	ACADM, ACVR1, ACVR2B, ADAMTS1, ADM, ATF4, B4GALT1, BCL2, BCL2L11, BCOR, BDNF, BMP4, BRCA2, CASP7, CASP8, CCND1, CDKN1B, CHD7, COL18A1, COL3A1, COL5A1, COL5A2, COL8A1, CREB1, CRK, CRKL, CRYAB, CUL1, CXADR, CXCL13, DCN, DGCR6, DLC1, DLX1, DLX2, ECE1, ECE2,	179
morphogenesis of cells	6.39E-09	ACP1, ADD1, ANGPT2, ANGPTL2, ANTXR1, ANXA5, ANXA7, ARHGDIG, ARHGEF2, ARRB2, ATRN, BAIAP2, BCAR1, BCL2, BCL10, BDNF, BMP4, CAPG, CAPZB, CASP8, CASP9, CAST, CCL5, CCL7, CCL8, CCL13, CCND1, CCNE1, CD9, CD44, CD47, CD82, CD151, CDC42EP1, CDC42EP2, CDH13, CDK5	178

shape change	1.02E-08	ACP1, ANGPT2, ANGPTL2, ANTXR1, ANXA5, ANXA7, AP2M1, ARF6, ARHGAP17, ARHGDIG, ARRB2, ATRN, BAIAP2, BCAR1, BCL2, BCL10, BDNF, BMP4, CAPG, CASP8, CASP9, CAST, CCL5, CCL7, CCL8, CCL13, CCNE1, CD9, CD44, CD47, CD151, CDC42EP1, CDC42EP2, CDK5, CDK5R1, CDKN1B, C	178
cell stage of eukaryotic cells	1.92E-04	ADORA2B, AKAP9, AKAP12, ARAF, AREG, ATF2, ATF3, AXIN2, BCL2, BCL2L11, BHLHE40, BID, BMP4, BRCA2, BTRC, C13ORF15, CAMK1, CAMK2N1, CAMKK1, CCK, CCNB1IP1, CCND1, CCNE1, CCNG1, CCNG2, CD44, CDC7, CDC25A, CDC25C, CDH13,	177
disease of tumor cell lines	5.42E-04	ACADSB, ADAM17, AFG3L1, ANAPC2, AP2M1, ARGLU1, ARHGEF19, ARPC1A, ATF2, ATF3, ATG12, ATG16L2, BICD2, C6ORF1, CAMK1D, CAPN6, CCND1, CCT2, CD82, CD151, CD274, CDKN1A, CHST1, CLNS1A, COL18A1, CSPP1, CTDP1, CTSB, CTSZ (includes EG:1522), CXADR, CYR61, DDX3X, D	175
reproductive system disorder	4.87E-03	ACTB, ADRB2, AIG1, ANGPT2, ANK3, ANXA5, ATF4, ATP1B1, BCL2, BRCA2, BSG, C13ORF15, CAPN6, CASP8, CBX6, CD14, COL18A1, COL6A2, CREB1, CTGF, CX3CL1, CXADR, CXCL10, CXCL13, CYR61, DBP, DCN, DNMT1, DNMT3B, DST, DUSP1, ECT2,	169
arrest in cell division process of cells	2.58E-05	AKAP9, AKAP12, APBB2, ATF2, ATF3, BCL2, BHLHE40, BID, BMP4, BTRC, CAMK1, CAMK2N1, CAMKK1, CCND1, CCNE1, CCNG1, CCNG2, CD44, CD274, CDC7, CDC25A, CDC25C, CDC2L6, CDH13, CDK2, CDK6, CDK5RAP3 (includes EG:80279), CDKN3, CDKN1A, CDKN1B, CDKN2C, CDKN2D, CEBPD,	165
survival of cell lines	1.36E-05	ACVR2B, ADK, AK5, AKAP8L, ALOX12, ANTXR1, ANTXR2, ATF2, ATP7A, AURKAIP1, BCL2, BDNF, BHLHE40, BMP4, BRCA2, BTC, C7ORF16, CAMK2D, CAMK2N1, CASP2, CASP9, CCND1, CCRK, CD44, CD81, CD82, CDH13, CDK2, CDK6, CDK8, CDKN1A, CDKN1B, CDKN2D, CHKA, CREB1, CXCL12, CX	162
differentiation of cell lines	1.57E-04	ALG5, AREG, ATF2, B4GALNT1, BCL2, BDH2, BDNF, BHLHE40, BLNK, BMP4, BTC, CBFB, CBR2, CBY1, CCND1, CD9, CD14, CD81, CD164, CDK2, CDK6, CDK5R1, CDKN1A, CDKN1B, CDKN2D, CDON, CEBPD, CHKA, CHRD, CREBBP, CREG1, CRK, CTGF, CTSB, CUL4A, CXCL12, DAB2, DCN, DDIT3,	161
movement of cell lines	3.21E-05	ACP1, ADAM12, ADAM15, ADAM17, AKT3, ALCAM, ALOX12, ARRB2, BCAR1, BTC, C3, C5ORF13, CBFB, CCL5, CCL13, CD44, CD47, CD82, CD151, CDH5, CDKN1A, CDKN1B, CLIC4, CNR1, COL18A1, CRK, CRKL, CTSB, CX3CL1, CXCL2, CXCL10, CXCL12, CYR61, DCBLD2, DDX3X, DICER1, DNAJA3	160
development of blood vessel	8.83E-10	ACP1, ACVR1, ADA, ADAM17, ADAMTS1, ADORA2B, ANGPT2, ANGPTL2, ANGPTL4, APH1A (includes EG:226548), ARHGAP24, ATP7A, B4GALT1, BCL2, BDNF, BMP4, BTC, C1GALT1, CASP8, CCL13, CCND1, CD151, CDH5, CHD7, COL18A1, COL1A1, COL3A1, COL4A2, COL5A1, CRKL, CSPG4, CTGF,	159
migration of cell lines	1.73E-05	ACP1, ADAM12, ADAM15, ADAM17, AKT3, ALCAM, ALOX12, ARRB2, BCAR1, BTC, C3, C5ORF13, CBFB, CCL5, CCL13, CD44, CD47, CD82, CD151, CDH5, CDKN1A, CDKN1B, CLIC4, CNR1, COL18A1, CRK, CRKL, CTSB, CX3CL1, CXCL2, CXCL10, CXCL12, CYR61, DCBLD2, DDX3X, DICER1, DNAJA3	158

digestive organ tumor	4.50E-03	ACY1, ADAM12, ADORA2B, AIM2, AKAP1, AKT3, ANTXR1, ANXA1, BAT1, BCL2, BTRC, C14ORF143, CASP8, CD14, CD59, CD274, CDC2L6, CDK2, CDK5, CDK6, CDK8, CDK10, CDKN3, CDKN1A, CDKN1B, CHRNA1, CHRNB1, COBLL1, COL1A1, COL6A3, COPS5, CREB1, CREBBP, CTSB, CTSD, CUGBP1,	151
adhesion of eukaryotic cells	1.77E-03	ACP1, ADAM9, ADAM12, ADAM15, ADAM17, ADRB2, ALOX12, ANGPT2, ANXA1, ANXA5, AOC3, B4GALT1, BMP4, BSG, C3, CASP8, CCL5, CCL13, CCL25, CCNC, CCND1, CD9, CD34, CD44, CD47, CD59, CD81, CD82, CD151, CDK5R1, CERCAM, COL18A1, COL7A1, CORO1A, CTGF, CX3CL1, CXCL2, C	150
developmental process of mammalia	3.03E-03	ACVR1, ADAMTS1, ADH5 (includes EG:128), ANGPT2, ANGPTL2, APH1A (includes EG:226548), AQP1, ATP1B1, BCL2, BCL2L11, BDNF, BMP4, BTC, CBFB, CCND1, CDH5, CDK6, CDKN1B, COL4A2, COMMD1 (includes EG:150684), CREB1, CXCL12, CXXC1,	145
transformation	3.54E-03	ACP1, ADM, AFF4, AKT3, ANGPTL2, ANP32A, ARAF, ARHGEF3, ATF3, BCAR1, BCKDHA, BCL2, BCL10, BIN1, CBFB, CCDC6, CCND1, CCNE1, CDC25A, CDK2, CDK6, CDKN1A, CDKN1B, CLTC, COL1A1, CREBBP, CRK, CYP2D6, CYTH1, DMTF1, DNAJA3,	145
developmental process of rodents	2.79E-03	ACVR1, ADAMTS1, ADH5 (includes EG:128), ANGPT2, ANGPTL2, APH1A (includes EG:226548), AQP1, ATP1B1, BCL2, BCL2L11, BDNF, BMP4, BTC, CBFB, CCND1, CDH5, CDK6, CDKN1B, COL4A2, COMMD1 (includes EG:150684), CREB1, CXCL12, CXXC1,	144
benign tumor	5.55E-03	ADAM12, ADARB1, AIG1, AK2, AKAP8L, ANXA1, ANXA5, ARFGEF2, ARIH2, ARL4D, ATF2, ATP1A1, ATRN, ATRNL1, BCL2, BCL10, BTRC, CAPN6, CCND1, CDC7, CDKN1A, CDKN1B, CDKN2C, CLEC16A, CNR1, COL18A1, COL6A3, COX6A2, CRABP2, CTGF, CTSB, CYP1B1, CYR61, DNMT1, DNMT3B, DO	144
developmental process of mice	3.25E-03	ACVR1, ADAMTS1, ADH5 (includes EG:128), ANGPT2, ANGPTL2, APH1A (includes EG:226548), AQP1, ATP1B1, BCL2, BCL2L11, BDNF, BMP4, BTC, CBFB, CCND1, CDH5, CDK6, CDKN1B, COL4A2, COMMD1 (includes EG:150684), CREB1, CXCL12, CXXC1,	143
transformation of cells	2.33E-03	ACP1, ADM, AFF4, AKT3, ANGPTL2, ANP32A, ARAF, ARHGEF3, ATF3, BCAR1, BCKDHA, BCL2, BCL10, BIN1, CBFB, CCDC6, CCND1, CCNE1, CDC25A, CDK2, CDK6, CDKN1A, CDKN1B, CLTC, COL1A1, CREBBP, CRK, CYTH1, DMTF1, DNAJA3, DNMT1,	141
infection of tumor cell lines	2.75E-03	ACADSB, AFG3L1, ANAPC2, AP2M1, ARGLU1, ARHGEF19, ARPC1A, ATG12, ATG16L2, BICD2, C6ORF1, CAMK1D, CAPN6, CCT2, CHST1, CLNS1A, CSPP1, CTDP1, CTSZ (includes EG:1522), DDX3X, DLST, DNAJA2, DTX4, DYSF, EDNRA, EGF, EGFR, ETHE1, EXOSC5, FAM76B, FBXO21, FGD6, FHL3	141
interphase of eukaryotic cells	8.35E-05	AKAP12, ARAF, ATF2, ATF3, BCL2, BCL2L11, BHLHE40, BID, BMP4, BTRC, C13ORF15, CAMK1, CAMK2N1, CAMKK1, CCND1, CCNE1, CCNG1, CCNG2, CD44, CDC7, CDC25A, CDC25C, CDH13, CDK2, CDK6, CDK5RAP3 (includes EG:80279), CDKN1A, CDKN1B, CDKN2D, CEBPD, CHKA, COPS5, CREG1	139
cell stage of cell lines	3.70E-04	AKAP9, AKAP12, ARAF, ATF2, AXIN2, BCL2, BHLHE40, BID, BMP4, BRCA2, BTRC, CAMK1, CAMK2N1, CAMKK1, CCK, CCND1, CCNE1, CCNG1, CCNG2, CDC7, CDC25A, CDC25C, CDH13, CDK2, CDK6, CDK5RAP3 (includes EG:80279), CDKN1A, CDKN1B,	139

cell division process of tumor cell lines	7.03E-04	AKAP9, APBB2, ATF2, AXIN2, BCAR1, BCL2, BHLHE40, BMP4, BRCA2, BTRC, CAMK1, CAMK2N1, CAMKK1, CARD10, CASP2, CCK, CCND1, CCNE1, CCNG1, CCNG2, CD44, CDC7, CDC25A, CDC25C, CDH13, CDK2, CDK6, CDK5RAP3 (includes EG:80279), CDKN1A, CDKN1B, CDKN2C, CEBPD, CHKA, C	136
infection of cervical cancer cell lines	2.91E-03	ACADSB, AFG3L1, ANAPC2, AP2M1, ARGLU1, ARHGEF19, ARPC1A, ATG12, ATG16L2, BICD2, C6ORF1, CAMK1D, CAPN6, CCT2, CHST1, CLNS1A, CSPP1, CTDP1, CTSZ (includes EG:1522), DDX3X, DLST, DNAJA2, DTX4, DYSF, EDNRA, EGF, EGFR, ETHE1, EXOSC5, FAM76B, FBXO21, FGD6, FHL3	136
invasion of cells	1.48E-04	ADAM9, ADAM17, ADM, AKT3, ANXA1, AREG, ARF6, ATF3, ATP6V0C, BATF3, BCAR1, BCL2, BMP4, BSG, BTC, CCND1, CD9, CD14, CD44, CD82, CD151, CDKN1B, CHRD, COL18A1, CRK, CSPG4, CTSB, CTSD, CXCL10, CXCL12, DKK3, DLC1, DNMT3B, EGF, EGFR, ENG, ENPP2, ENTPD5, EPHA2, E	135
angiogenesis	2.12E-09	ACP1, ACVR1, ADA, ADAM17, ADAMTS1, ADORA2B, ANGPT2, ANGPTL2, ANGPTL4, APH1A (includes EG:226548), ARHGAP24, ATP7A, B4GALT1, BCL2, BDNF, BMP4, BTC, C1GALT1, CASP8, CCL13, CCND1, CD151, CDH5, COL18A1, COL4A2, CSPG4, CTGF, CTSB, CX3CL1, CXCL12, CYR61, DDAH1,	132
invasion of eukaryotic cells	5.03E-04	ADAM9, ADAM17, ADM, AKT3, ANXA1, AREG, ARF6, ATF3, BATF3, BCAR1, BCL2, BMP4, BSG, BTC, CCND1, CD9, CD14, CD44, CD82, CD151, CDKN1B, CHRD, COL18A1, CRK, CSPG4, CTSB, CTSD, CXCL10, CXCL12, DKK3, DLC1, DNMT3B, EGF, EGFR,	127
arrest in cell division process of eukaryotic cells	2.05E-04	AKAP9, AKAP12, ATF2, BCL2, BHLHE40, BID, BMP4, BTRC, CAMK1, CAMK2N1, CAMKK1, CCND1, CCNE1, CCNG1, CCNG2, CD44, CDC7, CDC25A, CDC25C, CDH13, CDK2, CDK5RAP3 (includes EG:80279), CDKN1A, CDKN1B, CDKN2C, CDKN2D, CEBPD, CHKA, CLIP1, COL1A1, COPS5, CREB1, CUL1,	125
survival of tumor cell lines	1.78E-04	ACVR2B, ADK, AK5, AKAP8L, ALOX12, ANTXR1, ANTXR2, ATF2, AURKAIP1, BCL2, BDNF, BHLHE40, BRCA2, C7ORF16, CAMK2D, CAMK2N1, CASP2, CCND1, CCRK, CD44, CD81, CD82, CDK2, CDK6, CDK8, CDKN1A, CDKN1B, CDKN2D, CHKA, CREB1, CXCL12, CXCR7, DGKA, DUSP1, DUSP5, DUSP14,	124
colony formation of cells	5.29E-04	AKAP12, ANKRD1, ANXA1, ANXA7, ATF3, BACH2 (includes EG:60468), BCL2, BCL2L11, BNIP3L, CBFB, CCL13, CCND1, CCNE1, CCNG2, CD9, CD44, CD82, CDA, CDKN1A, CDKN1B, CLTC, CNOT7, CRTC1, CTSD, CXCL12, CYR61, DCK, DCN, DDIT3, DLC1,	124
cell death of neurons	2.05E-03	ADA, ADCYAP1R1, ALOX12, ATF3, ATP2C1, B4GALNT1, BACE1, BCL2, BCL2L11, BDNF, BID, CAPNS1, CASP2, CASP6, CASP7, CASP8, CASP9, CAST, CCL5, CD200, CDK2, CDK5, CDK6, CDK5R1, CDKN1A, CDKN1B, CDKN2D, CREB1, CREBBP, CTSB, CTSD, CX3CL1, CXCL12, DLX1, DLX2, E2F1, E	124
cell division process of normal cells	3.95E-04	ADORA2B, AREG, ATF2, ATF3, BCL2, BCL2L11, BLNK, BMP4, BRCA2, C13ORF15, CCK, CCNB1IP1, CCND1, CCNE1, CCNF, CCNG2, CD44, CD274, CDC7, CDC25C, CDK2, CDK5, CDKN1A, CDKN1B, CDKN2D, CEBPD, CHKA, COL1A1, CREB1, CXCL10, CYP26B1, DCN, DNM1L, E2F1, E2F2, E2F3, EGF,	120

shape change of eukaryotic cells	1.01E-07	ACP1, ANGPT2, ANGPTL2, ANTXR1, ANXA5, ARHGDIG, ARRB2, ATRN, BCAR1, BCL2, BCL10, BDNF, CAPG, CAST, CCL5, CCL7, CCL8, CCL13, CCNE1, CD9, CD44, CD47, CD151, CDK5, CDK5R1, CDKN1B, COL18A1, CORO1A, CRK, CRKL, CSPG4, CX3CL1, CXCL12, CYR61, DCN, DICER1, DPYSL2,	119
colony formation of eukaryotic cells	1.34E-04	AKAP12, ANKRD1, ANXA1, ANXA7, ATF3, BACH2 (includes EG:60468), BCL2, BCL2L11, BNIP3L, CBFB, CCL13, CCND1, CCNE1, CCNG2, CD9, CD44, CD82, CDA, CDKN1A, CDKN1B, CLTC, CNOT7, CRTC1, CTSD, CYR61, DCK, DCN, DDIT3, DLC1, DYNC1H1,	118
interphase of cell lines	1.65E-04	AKAP12, ARAF, ATF2, BCL2, BHLHE40, BID, BMP4, BTRC, CAMK1, CAMK2N1, CAMKK1, CCND1, CCNE1, CCNG1, CCNG2, CDC7, CDC25A, CDC25C, CDH13, CDK2, CDK6, CDK5RAP3 (includes EG:80279), CDKN1A, CDKN1B, CDKN2D, CEBPD, CHKA, COPS5, CREG1, CUL4A, CXCL12, CYR61, DCN, DD	117
developmental process of embryonic tissue	5.85E-04	ACVR1, ACVR1B, ACVR2B, ANGPT2, APH1A (includes EG:226548), AREG, BCL2, BDNF, BMP4, CASP9, CD44, CRKL, CUL7 (includes EG:9820), CX3CL1, CXCL12, DAB2, DPPA4, ECE1, ECE2, EDNRA, EGF, EGFR, EGR2, EN1, ENAH, ENPP2, ETS2, EYA1, F2RL1,	113
arrest in cell stage of cells	8.95E-04	AKAP12, ATF2, BCL2, BHLHE40, BID, BMP4, BTRC, CAMK1, CAMK2N1, CAMKK1, CCND1, CCNE1, CCNG1, CD44, CDC7, CDC25A, CDC25C, CDC2L6, CDH13, CDK2, CDK5RAP3 (includes EG:80279), CDKN1A, CDKN1B, CDKN2D, CEBPD, CHKA, CLIP1, COPS5, CUL4A, CYP26B1, CYR61, DCN, DDIT3,	113
colon cancer	1.78E-03	ABCA5, ADAMTS1, AHCY, AKT3, ANTXR1, AOC3, ATP2A2, AXIN2, C14ORF143, C15ORF23, C15ORF48, C17ORF81, CALD1, CAMK2N1, CCT4, CD274, CDKN3, CDKN1A, CEP55, CNNM2, COG8, COL3A1, COL6A2, CPEB4, CTSB, DGKA, DHDDS, DLGAP5, DNAJB9, DUSP5, EBP, EFNB1, EGFR, EIF4A2, EN	112
cell death of fibroblast cell lines	5.44E-06	ABCC4, ACTB, ATF2, ATF3, BACH2 (includes EG:60468), BCL2, BCL2L11, BID, BNIP3L, BRCA2, CAPNS1, CASP2, CASP8, CASP9, CCND1, CCNE1, CCNG1, CDK6, CDKN1A, CDKN1B, CLIC4, COPS5, COX5A, CTSB, CTSD, CUL7 (includes EG:9820), CYR61,	111
movement of tumor cell lines	2.65E-05	ADAM15, ADAM17, AKT3, ALOX12, ARRB2, BCAR1, C5ORF13, CCL5, CCL13, CD44, CD47, CD82, CD151, CDKN1B, CRK, CRKL, CX3CL1, CXCL2, CXCL10, CXCL12, DCBLD2, DNAJA3, DPYSL2, EFNB1, EGF, EGFR, EGR1, ENPP2, ESR1, ETV5, FGFR1, GAB1, GAS6, GDNF, GFER, GIPC1, GJA1, GOL	110
cell movement of cell lines	9.01E-05	ACP1, ADM, ARRB2, BSG, C3, CAPN1, CASP8, CCL5, CCL7, CCL8, CCL13, CCL25, CD9, CD44, CD47, CD81, CD82, CD151, CDH13, CDKN1B, CNR1, CREB3, CRKL, CTSB, CX3CL1, CXCL10, CXCL12, CXCL13, DGKA, DKK3, DLC1, EGF, EGFR, ENPP2, ESR1, FIGF, FLNA, FOSL2, GAB1, GAS6, G	110
invasion of cell lines	6.82E-04	ADAM9, ADAM17, ADM, AKT3, ANXA1, AREG, ARF6, ATF3, BATF3, BCAR1, BCL2, BMP4, BSG, BTC, CD9, CD44, CD82, CD151, CDKN1B, CHRD, COL18A1, CRK, CSPG4, CTSB, CTSD, CXCL12, DKK3, DLC1, DNMT3B, EGF, EGFR, ENPP2, ENTPD5, EPHA2,	110
migration of tumor cell lines	2.19E-05	ADAM15, ADAM17, AKT3, ALOX12, ARRB2, BCAR1, C5ORF13, CCL5, CCL13, CD44, CD47, CD82, CD151, CDKN1B, CRK, CRKL, CX3CL1, CXCL2, CXCL10, CXCL12, DCBLD2, DNAJA3, DPYSL2, EFNB1, EGF, EGFR, EGR1, ENPP2, ESR1, FGFR1, GAB1, GAS6, GDNF, GFER, GIPC1, GJA1, GOLGA2, H	109

growth of plasma membrane projections	2.92E-04	ADAM17, ADRB2, ANP32A, ARHGAP17, ARTN, BAIAP2, BCAR1, BCL2, BDNF, BMP4, CD9, CD47, CDK2, CDK5, CDK5R1, CDKN1A, CNPY2, CNR1, CNTN2, CREB1, CRK, CXCL12, DNAJA3, DOK4, DPYSL2, E2F1, EFNB1, EFNB2, EGF, EGFR, EIF4EBP1, ELMO2, EPHA2, EPN1, FEZ1, FGFR1, GAB1, GA	108
growth of neurites	2.51E-04	ADAM17, ADRB2, ANP32A, ARHGAP17, ARTN, BAIAP2, BCL2, BDNF, BMP4, CD9, CD47, CDK2, CDK5, CDK5R1, CDKN1A, CNPY2, CNR1, CNTN2, CREB1, CRK, CXCL12, DNAJA3, DOK4, DPYSL2, E2F1, EFNB1, EFNB2, EGF, EGFR, EIF4EBP1, ELMO2,	107
degradation of protein	1.62E-04	ACY1, ADAM17, ADAMTS2, ADAMTS4, ADAMTS7, ALOX12, AMFR, ANAPC2, ANAPC4, ARIH2, AURKAIP1, BACE1, BLMH, BMP1, BTRC, CAPN1, CAPNS1, CASP2, CASP6, CASP7, CASP8, CASP9, CAST, CDC23 (includes EG:8697), CTSB, CTSD, CTSZ (includes EG:1522), DHCR24, DLD, DNAJC1, DP	105
protein kinase cascade	9.45E-04	ADAM9, ADORA2B, ADRB2, AIDA, APOL3 (includes EG:80833), ARAF, ATP2C1, ATP6AP2, AZI2, BCL10, C7ORF16, CRKL, DOK1, DOK4, DUSP4, DUSP22, ECOP, ECT2, EDA2R, EEF1D, EGF, EGFR, F2R, FGF13, FGFR1, FLNA, GJA1, GPS2, HIPK2, HMGA2,	105
cell cycle progression of eukaryotic cells	1.93E-03	AKAP9, APBB2, BCAR1, BCL2, BCL2L11, BLNK, BMP4, BTRC, CAMK2N1, CARD10, CASP2, CAST, CCND1, CCNE1, CCNF, CCNG1, CCNG2, CD44, CDC25C, CDK2, CDK5, CDK6, CDKN1A, CDKN1B, CDKN2C, CDKN2D, COL1A1, CREB1, CRK, CUL1, CUL7 (includes EG:9820), DMTF1, DUSP1, E2F1, E2	104
formation of tissue	2.19E-06	ACVR1, ADAM12, ADAM15, ANGPT2, ANTXR2, APH1A (includes EG:226548), ARHGAP22, ARHGAP24, ATF3, ATF4, BDNF, BMP4, CASP8, CBFB, CD44, CD276, CFL1, CHRD, CHST3, COL18A1, COL4A2, CTGF, CTNNBIP1, CX3CL1, CXCL12, DAG1,	103
cell stage of tumor cell lines	7.24E-04	AKAP9, ATF2, AXIN2, BCL2, BHLHE40, BRCA2, BTRC, CAMK1, CAMK2N1, CAMKK1, CCK, CCND1, CCNE1, CCNG1, CCNG2, CDC7, CDC25A, CDC25C, CDH13, CDK2, CDK6, CDK5RAP3 (includes EG:80279), CDKN1A, CDKN1B, CEBPD, CHKA, COPS5, CREG1, CYLD, CYR61, DCN, DDIT3, DLGAP5, DUS	103
arrest in cell division process of cell lines	1.25E-03	AKAP9, AKAP12, ATF2, BCL2, BHLHE40, BID, BMP4, BTRC, CAMK1, CAMK2N1, CAMKK1, CCND1, CCNE1, CCNG1, CCNG2, CDC7, CDC25A, CDC25C, CDH13, CDK2, CDK5RAP3 (includes EG:80279), CDKN1A, CDKN1B, CDKN2C, CDKN2D, CEBPD, CHKA, CLIP1, COPS5, CUL1, CUL4A, CYR61, DCN, D	103
development of skeleton	1.71E-05	ACP2, ACVR1, ACVR2B, ADAMTS4, ADRB2, AEBP1, ANKH, ATF2, AXIN2, BCL2, BMP4, CBFB, CD276, CHD7, CHRD, CHST11, COL12A1, COL1A1, COL5A2, CTGF, DLK1, E2F1, EBP, EGFR, EGR2, EIF2AK3, EN1, ENPP1, ERCC2, ESR1, ETS2, EXT2, EYA1, FBN1,	102
uterine cancer	4.42E-03	ADAM12, ADARB1, AGPAT2, AIG1, AK2, AKAP8L, ARFGEF2, ARIH2, ARL4D, ATRN, ATRNL1, BCL10, BTRC, CAPN6, CDC7, CDC2L6, CDK2, CDK5, CDK6, CDK8, CDK10, CLEC16A, COL6A3, CRABP2, CTSB, CYP1B1, CYR61, DOK1, DST, EGFR, EIF4EBP1,	101
outgrowth of neurites	2.80E-05	ADAM17, ADRB2, ANP32A, ARHGAP17, BAIAP2, BCL2, BDNF, BMP4, CD9, CD47, CDK2, CDK5, CDK5R1, CDKN1A, CNPY2, CNR1, CREB1, CRK, CXCL12, DNAJA3, DOK4, DPYSL2, E2F1, EFNB1, EFNB2, EGF, EGFR, ELMO2, EPHA2, EPN1, FEZ1,	100

arrest in cell stage of eukaryotic cells	2.89E-04	AKAP12, ATF2, BCL2, BHLHE40, BID, BMP4, BTRC, CAMK1, CAMK2N1, CAMKK1, CCND1, CCNE1, CCNG1, CD44, CDC7, CDC25A, CDC25C, CDH13, CDK2, CDK5RAP3 (includes EG:80279), CDKN1A, CDKN1B, CDKN2D, CEBPD, CHKA, CLIP1, COPS5, CUL4A, CYP26B1, CYR61, DCN, DDIT3, DLGAP5,	100
formation of filaments	1.21E-05	AKAP1, ARF6, ARHGEF2, ARHGEF3, BACE1, BCAR1, CALD1, CAPN1, CDC42EP2, CDKN1A, CDKN1B, CFL1, COL18A1, COL5A1, CRK, CTGF, DAB2, DLC1, DLGAP5, DPYSL2, EDNRA, EGF, EGFR, F2R, FHL1, FMN1, GAP43, GAS7, GNAO1, GNAQ, GNB1, GNG12, GPI, GSN, HGF, HSPA5, HTT, IDE, IN	99
differentiation of tumor cell lines	6.54E-04	ALG5, ATF2, B4GALNT1, BCL2, BDH2, BDNF, BMP4, BTC, CCND1, CD14, CDK2, CDK6, CDK5R1, CDKN1A, CDKN1B, CEBPD, CHKA, CREBBP, CREG1, CRK, CTGF, CUL4A, DAB2, DDIT3, DLK1, DMTF1, DUSP1, E2F1, EGF, EGFR, EGR1, ELAVL2, ERBB2IP	99
development of embryonic tissue	2.41E-03	ACVR1, ACVR1B, ACVR2B, ANGPT2, APH1A (includes EG:226548), AREG, BCL2, BDNF, BMP4, CD44, CRKL, CX3CL1, CXCL12, DAB2, ECE1, ECE2, EDNRA, EGF, EGFR, EGR2, EN1, ENAH, ENPP2, ETS2, EYA1, FGF10, FGFR1, FGFR2, FOSL2, FOXC2, FOXF1, FTO,	99
developmental process of muscle	4.52E-06	ACVR2B, ADAM12, ADRB2, AEBP1, BDNF, BMP4, CDK5, CDKN1A, CDON, CHKB, COL6A3, CRYAB, CXCL10, DUSP1, E2F1, EGR3, ETV1, F2RL1, FEM1C, FGFR1, FHL3, FLNB, FOSL2, FOXC2, FOXF1, FOXO1, FXR1, GAA, GAB1, GATA4, GATA6, GEFT,	97
adhesion of cell lines	9.72E-05	ACP1, ADAM9, ADAM12, ADAM15, ADAM17, ANGPT2, ANXA1, ANXA5, B4GALT1, BSG, C3, CASP8, CCL13, CCNC, CD9, CD44, CD47, CD59, CD81, CD82, CD151, CTGF, CX3CL1, CXCL2, CXCL10, CXCL12, CYR61, CYTH1, CYTIP, DAB2, DCN, DKK3, E2F1,	96
invasion of tumor cell lines	6.00E-04	ADAM9, ADAM17, ADM, AKT3, ANXA1, AREG, ARF6, ATF3, BATF3, BCAR1, BCL2, BMP4, BSG, BTC, CD9, CD44, CD82, CD151, CDKN1B, CHRD, COL18A1, CRK, CSPG4, CTSB, CTSD, CXCL12, DKK3, DLC1, DNMT3B, EGF, EGFR, ENPP2, ENTPD5, EPHA2,	96
disease of kidney cell lines	1.20E-03	AEBP2, AMDHD2, ANAPC2, AP1G2, ATMIN, ATP6V0C, B4GALNT4, BMP1, CAD, CCDC51, CCL5, CD164, CDC42EP3, CHST1, CLOCK, CLTA, COL5A1, CRYAB, CSNK1E, CTDP1, CTSB, DAZAP2 (includes EG:9802), DCP2, EIF2B5, ENC1, ERCC1, ETS2, EXOSC10, FXR1, GATAD2A, GINS4, HBEGF, HMG	96
developmental process of tumor	5.94E-06	ADAM17, ANGPTL4, ARRB2, B4GALNT1, BCL2, CCND1, CD44, CD59, CD274, CDH5, CDKN1A, CDKN1B, CDKN2C, CNR1, COL18A1, CRABP2, CREB1, CREBBP, CRYAB, CTSB, DNMT1, DNMT3B, E2F1, E2F3, EGFR, EGR1, EPHA2, ESR1, ETS2, F2R, FGFR1, FGFR2, GADD45A, GDNF, GJA1, HGF, HRAS,	94
developmental process of fibroblast cell lines	3.42E-04	ACP1, AKAP12, ANP32A, AREG, BCAR1, BMP4, CAST, CBFB, CBR2, CBY1, CCND1, CDH13, CDK2, CDK6, CDKN1A, CDKN1B, COL1A1, CRK, CUL1, CUL7 (includes EG:9820), DDIT3, DDX3X, DLK1, DMTF1, E2F1, E2F2, E2F3, EBF1, EEF1D, EGF, EGFR,	94
disease of embryonic cell lines	6.37E-04	AEBP2, AMDHD2, ANAPC2, AP1G2, ATMIN, ATP6V0C, B4GALNT4, BMP1, CAD, CCDC51, CD44, CD164, CDC42EP3, CHST1, CLOCK, CLTA, COL5A1, CRYAB, CTDP1, DAG1, DAZAP2 (includes EG:9802), DCP2, EGFR, EIF2B5, ENC1, ERCC1, ETS2, EXOSC10, FXR1, GATAD2A, GINS4, HMGCS1, HNRP	94

cell death of breast cancer cell lines	1.83E-06	ABCC4, ADM, AIM2, ATF2, BCAR1, BCL2, BCL10, BCL2L11, BHLHE40, BID, BNIP3L, CASP2, CASP6, CASP7, CASP8, CASP9, CCND1, CD44, CD47, CDKN1A, CRABP2, CTGF, CYB5A, CYLD, CYR61, DAB2, DDIT4, DUSP1, DUSP4, E2F1, EGF, EGFR,	93
colony formation of cell lines	7.22E-05	AKAP12, ANKRD1, ANXA1, ANXA7, ATF3, BACH2 (includes EG:60468), BCL2, BCL2L11, CBFB, CCL13, CCND1, CCNE1, CCNG2, CD44, CD82, CDKN1A, CDKN1B, CLTC, CNOT7, CRTC1, CTSD, CYR61, DCK, DLC1, DYNC1H1, E2F1, EGF, EGFR, EGLN2, EGR1, ETV6, FBLN1, FOXO3, GADD45A, GJA	93
disease of epithelial cell lines	9.94E-04	AEBP2, AMDHD2, ANAPC2, AP1G2, ATMIN, ATP6V0C, B4GALNT4, BMP1, CAD, CCDC51, CD164, CDC42EP3, CHST1, CLOCK, CLTA, COL5A1, CRYAB, CTDP1, CXCL2, DAZAP2 (includes EG:9802), DCP2, EIF2B5, ENC1, ERCC1, ETS2, EXOSC10, FXR1,	93
infection of kidney cell lines	1.40E-03	AEBP2, AMDHD2, ANAPC2, AP1G2, ATMIN, ATP6V0C, B4GALNT4, BMP1, CAD, CCDC51, CCL5, CD164, CDC42EP3, CHST1, CLOCK, CLTA, COL5A1, CRYAB, CTDP1, CTSB, DAZAP2 (includes EG:9802), DCP2, EIF2B5, ENC1, ERCC1, ETS2, EXOSC10, FXR1, GATAD2A, GINS4, HMGCS1, HNRPDL, ID	93
differentiation of connective tissue cells	1.41E-04	ACVR1, ACVR2B, ADRB2, AREG, ATF4, AXIN2, BCL2, BMP4, CAPNS1, CASP8, CAST, CBY1, CCL9, CCND1, CD200, CD276, CDK6, CHRD, CREB1, DDIT3, DICER1, DLK1, EBF1, EGFR, ENPP1, FGF10, FGFR1, FIGF, FOSL2, GAS7, GDF5, GDNF, GPX1, IL11,	92
arrest in interphase of eukaryotic cells	4.11E-04	AKAP12, ATF2, BCL2, BHLHE40, BID, BMP4, BTRC, CAMK1, CAMK2N1, CAMKK1, CCND1, CCNE1, CCNG1, CD44, CDC7, CDC25A, CDC25C, CDH13, CDK2, CDK5RAP3 (includes EG:80279), CDKN1A, CDKN1B, CDKN2D, CEBPD, CHKA, COPS5, CUL4A, CYR61, DCN, DDIT3, DUSP1, E2F1, E2F2, E2F3	92
infectious disorder of embryonic cell lines	1.22E-03	AEBP2, AMDHD2, ANAPC2, AP1G2, ATMIN, ATP6V0C, B4GALNT4, BMP1, CAD, CCDC51, CD164, CDC42EP3, CHST1, CLOCK, CLTA, COL5A1, CRYAB, CTDP1, DAG1, DAZAP2 (includes EG:9802), DCP2, EIF2B5, ENC1, ERCC1, ETS2, EXOSC10, FXR1, GATAD2A, GINS4, HMGCS1, HNRPDL, IDH1, IR	92
infectious disorder of epithelial cell lines	1.67E-03	AEBP2, AMDHD2, ANAPC2, AP1G2, ATMIN, ATP6V0C, B4GALNT4, BMP1, CAD, CCDC51, CD164, CDC42EP3, CHST1, CLOCK, CLTA, COL5A1, CRYAB, CTDP1, DAZAP2 (includes EG:9802), DCP2, EIF2B5, ENC1, ERCC1, ETS2, EXOSC10, FXR1, GATAD2A, GINS4, HMGCS1, HNRPDL, IDH1, IRF3, KH	91
cell death of connective tissue cells	5.92E-04	ADAM12, ADM, ARRB2, ATF2, ATF3, BCL2, BCL2L11, BID, CABLES2, CAPNS1, CASP2, CASP7, CASP8, CASP9, CCL9, CCND1, CD44, CDKN1A, CDKN1B, CDKN2C, CLIC4, CREB1, CTSD, CYP1B1, DCN, DDIT3, DHCR24, DUSP1, E2F1, EGF, EGFR, EGR1, ESR1, FLNA, FOXO1, GAB1, GABBR1, GLO1	88
formation of plasma membrane projections	6.92E-05	AKAP12, ARF6, ARHGAP24, BAIAP2, BDNF, CAPNS1, CAST, CCL13, CD44, CD47, CD82, CDC42EP1, CDC42EP2, CDKN1B, CRK, CRKL, CTGF, CXCL12, CYR61, DAG1, DPYSL2, EFNB1, EGF, ENAH, EXOC7, FGD3, FGD4, GAB1, GAP43, GDNF, HGF, HRAS,	87
arrest in cell stage of cell lines	4.41E-04	AKAP12, ATF2, BCL2, BHLHE40, BID, BMP4, BTRC, CAMK1, CAMK2N1, CAMKK1, CCND1, CCNE1, CCNG1, CDC7, CDC25A, CDC25C, CDH13, CDK2, CDK5RAP3 (includes EG:80279), CDKN1A, CDKN1B, CDKN2D, CEBPD, CHKA, CLIP1, COPS5, CUL4A, CYR61, DCN, DDIT3, DLGAP5, DUSP1, E2F1, E	87

formation of cells	3.57E-03	ADAM12, ARHGAP22, BDNF, CASP8, CCL5, CD9, CD44, CD47, CD81, CDKN1A, COL18A1, CREBBP, CXCL12, DLK1, EFNB1, EGF, EGR1, ENAH, ENPP2, EPC1, ERCC1, FGF13, FGFR1, FST, FZD1, GDNF, GGT1, GNAO1, GNAQ, HAS2, HGF, HOPX, HRAS,	86
arrest in cell cycle progression	2.53E-03	AKAP9, APBB2, ATF3, BCL2, BMP4, BTRC, CCND1, CCNE1, CCNG1, CCNG2, CD274, CDC25A, CDK2, CDK6, CDKN3, CDKN1A, CDKN1B, CDKN2C, CDKN2D, COL1A1, COMMD5, CREB1, CREBBP, CUL1, CUL4A, DMTF1, E2F1, E2F2, E2F3, EGFR, EIF4G2, ERN1, FANCA, FANCC, FOXO3, GADD45A, GAS7	85
interphase of tumor cell lines	3.90E-04	ATF2, BCL2, BHLHE40, BTRC, CAMK1, CAMK2N1, CAMKK1, CCND1, CCNE1, CCNG1, CCNG2, CDC7, CDC25A, CDC25C, CDH13, CDK2, CDK6, CDK5RAP3 (includes EG:80279), CDKN1A, CDKN1B, CEBPD, CHKA, COPS5, CREG1, CYR61, DCN, DDIT3, DUSP1, E2F1, EGF, EGFR, EPB41L1, FOXO3, GAD	84
apoptosis of neurons	2.21E-03	ADA, ADCYAP1R1, ATF3, ATP2C1, B4GALNT1, BCL2, BCL2L11, BDNF, BID, CASP2, CASP6, CASP9, CCL5, CD200, CDK2, CDK5, CDK5R1, CDKN1A, CDKN2D, CREB1, CREBBP, CTSB, CXCL12, DLX1, DLX2, E2F1, EN1, ETV6, F2R, FBXW7, FOXO3, GDF5,	84
tumorigenesis of cells	2.21E-03	ADAM17, ARHGDIG, ARMC10, ATF2, ATF3, BCL2, C3, CASP2, CASP9, CAST, CCND1, CCNE1, CD44, CD82, CD151, CD274, CDKN1A, CDKN2C, CDKN2D, COL18A1, CSNK1E, CTSB, CXADR, CXCL2, CYLD, CYR61, DLC1, DOK1, E2F1, EGF, EGFR, EGR1, EMP2,	84
formation of eukaryotic cells	2.48E-03	ADAM12, ARHGAP22, BDNF, CASP8, CCL5, CD9, CD44, CD47, CD81, CDKN1A, COL18A1, CREBBP, CXCL12, DLK1, EGF, EGR1, ENAH, ENPP2, EPC1, ERCC1, FGF13, FGFR1, FST, FZD1, GDNF, GGT1, GNAO1, GNAQ, HGF, HOPX, HRAS, ID1, IFNGR1,	84
apoptosis of fibroblast cell lines	1.00E-04	ATF2, ATF3, BACH2 (includes EG:60468), BCL2, BCL2L11, BID, BNIP3L, CAPNS1, CASP2, CASP8, CASP9, CCNE1, CCNG1, CDKN1A, CDKN1B, CLIC4, COPS5, COX5A, CUL7 (includes EG:9820), CYR61, DDIT3, DDX3X, DUSP4, E2F1, E2F2, EGFR, EGR1,	83
adenocarcinoma	2.42E-03	ACY1, AGPAT2, ALDOC, ANXA1, BRCA2, BTRC, CAMK2N1, CBLN1, CCND1, CD14, CDC2L6, CDK2, CDK5, CDK6, CDK8, CDK10, CDKN1B, CDKN2C, DICER1, DLK1, DYNLRB1, E2F1, EDNRA, EGFR, ENG, ESR1, FGFR1, FOXA3, GJA1, GLG1, GPI,	83
development of muscle	9.43E-05	ADAM12, AEBP1, BDNF, BMP4, CDK5, CDON, CHKB, COL6A3, CRYAB, CXCL10, DUSP1, EGR3, ETV1, F2RL1, FGFR1, FHL3, FLNB, FOSL2, FOXC2, FOXF1, FOXO1, FXR1, GAA, GAB1, GATA4, GATA6, GEFT, GJA1, GJC1, HBEGF, HGF, HLX, HMGA2,	82
arrest in interphase of cell lines	4.09E-04	AKAP12, ATF2, BCL2, BHLHE40, BID, BMP4, BTRC, CAMK1, CAMK2N1, CAMKK1, CCND1, CCNE1, CCNG1, CDC7, CDC25A, CDC25C, CDH13, CDK2, CDK5RAP3 (includes EG:80279), CDKN1A, CDKN1B, CDKN2D, CEBPD, CHKA, COPS5, CUL4A, CYR61, DCN, DDIT3, DUSP1, E2F1, EGF, EGFR, EP400	82
cell death of epithelial cell lines	8.30E-07	AAK1, ATF3, BCL2, BCL10, BID, BNIP3L, CASP2, CASP7, CASP8, CASP9, CD44, CDKN1B, CEBPD, CLIC4, CRYAB, CUL7 (includes EG:9820), DAB2, DAP3, DDIT3, DLST, E2F6, ECOP, EGF, EGFR, EMP1, EMP2, EMP3, ESR1, FOXO3, HIPK2, HK1, HRAS,	81
apoptosis of breast cancer cell lines	9.39E-06	ADM, AIM2, ATF2, BCAR1, BCL2, BCL10, BCL2L11, BHLHE40, BID, BNIP3L, CASP2, CASP6, CASP7, CASP8, CASP9, CCND1, CD44, CDKN1A, CRABP2, CTGF, CYB5A, CYLD, CYR61, DDIT4, DUSP1, DUSP4, E2F1, EGF, EGFR, EPHA2, ESR1, ETS2, FBLN1,	81

cell stage of normal cells	1.08E-03	ADORA2B, AREG, ATF2, ATF3, BCL2, BCL2L11, BMP4, BRCA2, C13ORF15, CCK, CCNB1IP1, CCND1, CCNE1, CCNG2, CD44, CDC7, CDC25C, CDK2, CDKN1A, CDKN1B, CEBPD, CHKA, CYP26B1, DCN, E2F1, E2F2, E2F3, EGF, EGR1, ERCC1, FANCA,	80
developmental process of connective tissue	2.75E-03	ACVR1, ADAMTS1, ADRB2, ATP7A, BCL2, BCL2L11, BMP4, CD9, CD44, CD81, CHST11, DLX2, E2F1, EGF, EGR1, EGR2, EN1, ENPP1, EXT2, FGF10, FGFR2, FOXC2, GGT1, GHR, GJA1, GPC3, GSN, HIP1, HIP1R, HOXA2, HOXA11, HOXD3, HOXD8, HOXD10,	79
transport of protein	1.47E-05	ADRB2, AP1G2, AP1GBP1, AP2M1, AP3B2, AP3S2, AP4B1, APPBP2, ARF2, ARF6, CASP9, CCHCR1, CDK5, CFL1, COL1A1, CTSA, DNAJA2, DRD1, EIF5A, ERGIC1, ERGIC3, GDI2, GOSR1, GOSR2, HLA-DMA, HSPA9, HTT, IGF2R, IPO9, KDELR2, KIF1B,	76
development of heart	6.19E-05	ACADM, ACVR1, ACVR2B, ADM, BCOR, BDNF, BMP4, CASP7, CASP8, CCND1, CHD7, COL3A1, COL5A1, CRK, CRKL, CXADR, DLC1, ECE1, ECE2, EDNRA, ENG, FBN1, FOXC2, GAA, GATA4, GJA1, GJC1, GNAQ, HAS2, HOPX, ID1, ID2, ID3, INSR, JMJD6,	76
adhesion of tumor cell lines	1.60E-05	ACP1, ADAM9, ADAM12, ADAM15, ADAM17, ANXA1, B4GALT1, BSG, CASP8, CCL13, CD9, CD44, CD47, CD59, CD81, CD82, CD151, CX3CL1, CXCL2, CXCL10, CXCL12, CYR61, CYTH1, CYTIP, DAB2, DCN, DKK3, E2F1, EFNB1, EGF, EGFR, EGR1, EMILIN1,	75
arrest in cell division process of tumor cell lines	1.51E-03	ATF2, BCL2, BHLHE40, BMP4, BTRC, CAMK1, CAMK2N1, CAMKK1, CCND1, CCNE1, CCNG1, CDC7, CDC25A, CDC25C, CDH13, CDK2, CDK5RAP3 (includes EG:80279), CDKN1A, CDKN1B, CDKN2C, CEBPD, CHKA, CYR61, DCN, DDIT3, DLGAP5, DUSP1, E2F1, EGF, EGFR, EPB41L1, FOXO3, GADD45A,	75
gonadal tumor	1.94E-03	ADA, AGPAT2, BCL2, BCL10, BTRC, C13ORF15, C4A, CD274, COL18A1, CP, CTNNAL1, DAB2, DHTKD1, DNMT1, DTNA, DYNLRB1, E2F3, EGFR, EPHB6, F2R, FAM171A1, FGFR2, FGFR1OP (includes EG:11116), FLRT2, FOXN2, FZD3, GATA4, GATA6, GSTM1, GSTM5, HDAC11, HIST2H2AA3, HMGA2	75
modification of DNA	2.19E-03	ATF2, ATF7IP, BRCA2, CCNO, CDK2, CDKN1A, CDKN2D, COPS5, CREBBP, CSNK1E, DNMT1, DNMT3B, E2F1, EGF, ERCC1, ERCC2, ERCC4, FANCA, FANCC, FEN1, FTH1, GADD45A, GATAD2A, GTF2H4, GTF3A, HGF, HMGN1, HSPA1B, IGF2, IGF2R, MBD4, MCM4, MCM6, MGMT, MLH1, MNAT1, MPG, MR	75
cell cycle progression of cell lines	3.93E-03	AKAP9, APBB2, BCAR1, BCL2, BMP4, BTRC, CAMK2N1, CARD10, CASP2, CAST, CCND1, CCNE1, CCNG1, CCNG2, CD44, CDC25C, CDK2, CDK6, CDKN1A, CDKN1B, CDKN2C, CRK, CUL1, CUL7 (includes EG:9820), DMTF1, DUSP1, E2F1, E2F2, EGF, EGFR, EGR1, ESR1, EZH2, FANCA, FGFR1, FOX	75
cell death of kidney cell lines	7.49E-04	AAK1, BCL2, BCL10, BID, BNIP3L, BRCA2, CASP2, CASP7, CASP8, CASP9, CCBL1, CD44, DAP3, DDIT3, DLST, DUSP4, E2F6, ECOP, EGF, EGFR, EMP1, EMP2, EMP3, GNB2, HGF, HIPK2, HK1, HRAS, HSPA5, HTT, IER3, IRF1, IRS1, ITPR1, MAP2K6, MCL1,	74
formation of actin filaments	5.78E-06	AKAP1, ARF6, ARHGEF2, ARHGEF3, BCAR1, CALD1, CAPN1, CDC42EP2, CDKN1A, CFL1, COL18A1, CRK, CTGF, DAB2, EDNRA, EGF, EGFR, F2R, FMN1, GAP43, GAS7, GNAO1, GNAQ, GNB1, GNG12, GPI, GSN, HGF, INPP5B, ITGA3, ITGA5, ITGA6, LAT2,	73
cell movement of tumor cell lines	2.33E-03	ARRB2, BSG, C3, CAPN1, CASP8, CCL5, CCL7, CCL8, CCL13, CCL25, CD9, CD44, CD81, CD82, CD151, CDH13, CDKN1B, CREB3, CTSB, CX3CL1, CXCL12, DKK3, DLC1, EGF, EGFR, ESR1, FIGF, FLNA, GAS6, GNB1, GNB2, GPI, HGF, IGF2BP1, ING4, IRS1,	73

proliferation of epithelial cells	2.88E-03	ANGPTL6, B4GALT1, BTRC, CCND1, CCNG2, CD9, CDH13, CDK2, CDK6, CDKN1A, CDKN1B, COL8A1, CRYAB, E2F1, EDNRA, EGF, EGFR, EPHA2, ESR1, FGF10, FGFR1, FGFR2, FOXF1, FOXF2, FST, HGF, HMGN1, HRAS, ID1, ID2, IGFBP4, INSR, ITGA3,	72
apoptosis of connective tissue cells	1.69E-03	ADAM12, ADM, ARRB2, ATF2, ATF3, BCL2, BCL2L11, BID, CABLES2, CAPNS1, CASP2, CASP8, CASP9, CCL9, CCND1, CD44, CDKN1A, CDKN1B, CDKN2C, CLIC4, CREB1, CTSD, DCN, DDIT3, DHCR24, DUSP1, E2F1, EGF, EGFR, ESR1, FOXO1, GAB1, GABBR1, GLO1, HRAS, INSR, MAPK1, MBD4,	71
ovarian tumor	2.79E-03	AGPAT2, BCL2, BCL10, BTRC, C13ORF15, C4A, CD274, COL18A1, CP, CTNNAL1, DAB2, DHTKD1, DNMT1, DTNA, DYNLRB1, E2F3, EGFR, EPHB6, F2R, FAM171A1, FGFR1OP (includes EG:11116), FLRT2, FOXN2, FZD3, GATA4, GATA6, GSTM1, GSTM5,	71
colony formation of tumor cell lines	2.50E-05	ANKRD1, ANXA1, ANXA7, ATF3, BACH2 (includes EG:60468), BCL2, BCL2L11, CCL13, CCNG2, CD44, CD82, CDKN1A, CDKN1B, CNOT7, CTSD, CYR61, DLC1, DYNC1H1, E2F1, EGF, EGFR, EGLN2, EGR1, FBLN1, FOXO3, GADD45A, GJA1, HAS2, HGF,	70
developmental disorder of animal	3.03E-05	ARSA, CCND1, CHRD, CLCN7, CSNK1E, DLK1, DOK1, E2F1, EDNRA, EGF, EGFR, EGR3, ERCC2, ESR1, FGFR1, FMR1, FOSL2, GDNF, GGT1, GNAQ, HIP1, HIP1R, HIPK2, HOXA5, HRAS, HSPG2 (includes EG:3339), HTT, IGF2BP1, INSIG2, INSL3, INSR, ITGA7,	70
G1 phase of cell lines	1.63E-03	AKAP12, BCL2, BHLHE40, BTRC, CAMK1, CAMKK1, CCND1, CCNE1, CCNG1, CCNG2, CDC25A, CDC25C, CDK2, CDK6, CDK5RAP3 (includes EG:80279), CDKN1A, CDKN1B, CDKN2D, COPS5, CREG1, CYR61, DCN, DDIT3, DUSP1, E2F1, E2F3, EGF, EGFR, EP400, EPB41L1, GHR, GJA1, GPI, GPS2,	70
apoptosis of epithelial cell lines	1.35E-07	ATF3, BCL2, BCL10, BID, BNIP3L, CASP2, CASP8, CASP9, CD44, CEBPD, CLIC4, CRYAB, CUL7 (includes EG:9820), DAB2, DAP3, DDIT3, E2F6, ECOP, EGF, EGFR, ESR1, FOXO3, HIPK2, HRAS, HSPA5, HSPB8, HTT, IER3, INSR, IRF1, IRS1, ITGA5,	69
cell spreading	4.83E-05	ACP1, ANTXR1, ATRN, BCAR1, BCL10, CAST, CCL5, CD44, CD47, CORO1A, CRK, CRKL, CSPG4, CXCL12, CYR61, EFNB1, EGF, EPHA2, FBN1, FHL3, GAP43, HGF, HRAS, IGBP1, ING4, ITGA3, ITGA5, ITGA6, ITGB5, ITGB1BP1, LAMA5, LPAR1, LPP,	69
growth of fibroblast cell lines	9.03E-04	ACP1, AKAP12, ANP32A, AREG, BCAR1, BMP4, CAST, CBFB, CCND1, CDH13, CDK6, CDKN1A, CDKN1B, COL1A1, CRK, CUL1, CUL7 (includes EG:9820), DDX3X, DMTF1, E2F1, E2F2, E2F3, EEF1D, EGF, EGFR, ERRFI1, ETV6, F2R, GADD45GIP1, GAK,	69
shape change of cell lines	2.53E-04	ACP1, ANGPTL2, ANTXR1, ANXA5, ARHGDIG, BCAR1, BCL2, BCL10, CAST, CCNE1, CD151, CDKN1B, CRK, CYR61, DICER1, DPYSL2, EDNRA, EFNA5, EFNB1, EGF, EGFR, EPHA2, FGD4, FHL3, GAP43, GNAQ, GNG12, ING4, INSR, ITGA5, ITGA6, LPAR1,	68
cell death of fibroblasts	1.50E-03	ARRB2, ATF2, ATF3, BCL2, BCL2L11, BID, CABLES2, CAPNS1, CASP2, CASP7, CASP8, CASP9, CCND1, CDKN1A, CDKN1B, CDKN2C, CLIC4, CTSD, CYP1B1, DDIT3, DHCR24, DUSP1, E2F1, EGF, EGFR, FLNA, FOXO1, GAB1, GPX4, HMOX1, HRAS, IGF2, IGF2R,	68
shape change of normal cells	1.46E-05	ANGPT2, ARRB2, ATRN, BCL2, BDNF, CAPG, CAST, CCL5, CCL7, CCL8, CCL13, CD9, CD44, CD47, CDK5, CDK5R1, COL18A1, CORO1A, CRK, CRKL, CX3CL1, CXCL12, CYR61, DCN, EFNB1, EGF, EPHB4, F2R, FBN1, FGFR1, GAP43, GDNF, GSN, HGF,	67

developmental process of muscle cells	8.97E-04	ACADM, ACVR1, AKR1B1, BIN1, BMP4, CBY1, CD9, CD81, CDKN1A, CDON, CEBPD, CXADR, DNAJB6, DUSP1, E2F1, EGFR, EPC1, EPHB4, EZH2, FGF10, FGFR1, FOSL2, FOXO1, GATA4, GNAQ, HGF, HMOX1, HOPX, ID2, ID3, IGF2, ITGA6, ITGA7, KLF4,	66
inhibition of apoptosis	8.97E-04	ADAM17, ADM, ALOX12, ANXA1, ANXA5, BCL2, BDNF, BFAR, BNIP1, BNIP2, CD59, CDKN1A, CDKN2D, CFL1, CIAPIN1, CRYAB, DHCR24, DNAJB9, DUSP1, FOXC2, FOXO1, GDNF, GLO1, GNAQ, GPX1, GSTP1, HBXIP, HGF, HMOX1, HSPA5, HSPA9,	66
cell death of embryonic cell lines	3.88E-05	AAK1, BCL2, BCL10, BID, BNIP3L, CASP2, CASP7, CASP8, CASP9, CD44, COPS5, DAP3, DLST, DPPA4, E2F1, E2F6, ECOP, EGF, EMP1, EMP2, EMP3, HIPK2, HK1, HRAS, HSPA5, HTT, IER3, IRF1, IRS1, MAP2K6, MCL1, PAK2, PEA15, PKN2, PMP22, PPARD,	65
developmental disorder of rodents	1.00E-04	ARSA, CCND1, CHRD, CLCN7, DLK1, DOK1, E2F1, EDNRA, EGF, EGFR, EGR3, ERCC2, FGFR1, FMR1, FOSL2, GDNF, GGT1, GNAQ, HIP1, HIP1R, HIPK2, HOXA5, HRAS, HSPG2 (includes EG:3339), HTT, IGF2BP1, INSIG2, INSL3, ITGA7, ITGA11, LIF, MAP2K6,	65
arrest in cell stage of tumor cell lines	3.35E-04	ATF2, BCL2, BHLHE40, BTRC, CAMK1, CAMK2N1, CAMKK1, CCND1, CCNE1, CCNG1, CDC7, CDC25A, CDC25C, CDH13, CDK2, CDK5RAP3 (includes EG:80279), CDKN1A, CDKN1B, CEBPD, CHKA, CYR61, DCN, DDIT3, DLGAP5, DUSP1, EGF, EGFR, EPB41L1, FOXO3, GADD45A, GOLGA2, GPS2, GSPT1	65
migration of endothelial cells	1.52E-05	ACP1, ADAM15, ADM, ANGPT2, ANGPTL4, ARHGAP24, ARRB2, CD9, CD81, CD151, CDH5, CDH13, COL18A1, COL4A2, CXCL12, CYR61, DCN, EFNB2, EGFL7, ENG, EPHB4, FGF13, FGFR1, FIGF, FOXC2, GAB1, GIPC1, HGF, ID1, IGF2, IGF2R, ITGA3,	64
arrest in growth of cells	2.31E-05	AKAP12, AKT3, ALCAM, BCL2L11, BMP4, CBX7, CCND1, CCNE1, CDC7, CDH13, CDK2, CDK6, CDKN1A, CDKN1B, CDKN2C, CDKN2D, DAB2, DDIT3, DMTF1, E2F1, EGF, EGR1, ELAC2, ENG, EZH2, FOXO3, GADD45A, GADD45GIP1, HIPK2, HMOX1, HRAS, ID3, IL6ST, IRF1, ITGB4, KLF4, KRT10, L	64
cell death of muscle cells	7.60E-04	ADAM12, ADM, ADRB2, BCL2, BCL2L11, BMP4, BNIP3L, C14ORF153, CACNB2, CAMK2D, CAPN1, CASP8, CASP9, CDC42EP3, CDKN1A, CDKN1B, COQ6, CXCL12, DAG1, E2F1, EEF1D, GATA4, GATA6, GNAQ, GNPTG, GPX1, HGF, HK1, HLA-B, HLA-DMA, HSPB6, HSPB8, ID2, IL6ST, IRF1, LIF, MAP	63
replication of DNA	4.54E-03	AKAP8L, AREG, BCL2, BRCA2, BTC, C4ORF16, CCNE1, CDC7, CDC25A, CDK2, CDKN1A, CDKN1B, DNAJC2, DUT (includes EG:1854), E2F1, E2F2, EGF, ERCC1, FEN1, GTPBP4, HBEGF, HELB, HMGA2, HMGN1, HRAS, ID1, ID3, INSR, KIAA0101, KRT7,	63
growth of rodents	5.78E-03	ADAMTS1, ADH5 (includes EG:128), AQP1, BDNF, CDKN1B, COL4A2, DLK1, DRD1, E2F1, E2F3, EGF, EGFR, EIF2AK3, EXT2, EZH2, FGFR2, FOSL2, GHR, GNB5, GPC3, GRB10, HIP1, HIP1R, HMOX1, HOXA5, HSPA5, IGF2, IGF2BP1, IGF2R, IRS1, ITPR3, LIF,	63
developmental process of embryonic cells	1.32E-04	ACVR1, ADA, ATP1B1, BAIAP2, BCL2L11, BDNF, BMP4, CDC7, CDKN1B, DAB2, DNMT1, EDNRA, EGF, EIF4G2, ENG, EPHB4, ERF, EZH2, FGFR1, FGFR2, FOXC2, GAS7, GATA4, GATA6, HBEGF, HGF, HHEX, HMGN1, HOPX, HTT, ID1, ID3, IGF2, IL6ST,	62
arrest in interphase of tumor cell lines	1.58E-04	ATF2, BCL2, BHLHE40, BTRC, CAMK1, CAMK2N1, CAMKK1, CCND1, CCNE1, CCNG1, CDC7, CDC25A, CDC25C, CDH13, CDK2, CDK5RAP3 (includes EG:80279), CDKN1A, CDKN1B, CEBPD, CHKA, CYR61, DCN, DDIT3, DUSP1, EGF, EGFR, EPB41L1, FOXO3, GADD45A, GPS2, GSPT1, HAS2, HGF, HRA	62

apoptosis of kidney cell lines	2.25E-04	BCL2, BCL10, BID, BNIP3L, CASP2, CASP8, CASP9, CD44, DAP3, DDIT3, DUSP4, E2F6, ECOP, EGF, EGFR, GNB2, HGF, HIPK2, HRAS, HSPA5, HTT, IER3, IRF1, IRS1, ITPR1, MAP2K6, MCL1, PAK1, PAK2, PEA15, PKN2, PPARD, PPP1R15A (includes EG:23645),	62
developmental disorder of mice	3.18E-04	ARSA, CCND1, CHRD, CLCN7, DLK1, DOK1, E2F1, EGF, EGFR, EGR3, ERCC2, FGFR1, FMR1, FOSL2, GGT1, GNAQ, HIP1, HIP1R, HIPK2, HOXA5, HRAS, HSPG2 (includes EG:3339), HTT, IGF2BP1, INSIG2, INSL3, ITGA7, ITGA11, LIF, MAP2K6, MAP3K4,	62
growth of mice	5.62E-03	ADAMTS1, ADH5 (includes EG:128), AQP1, BDNF, CDKN1B, COL4A2, DLK1, DRD1, E2F1, E2F3, EGF, EGFR, EIF2AK3, EXT2, EZH2, FGFR2, FOSL2, GHR, GNB5, GPC3, GRB10, HIP1, HIP1R, HOXA5, HSPA5, IGF2, IGF2BP1, IGF2R, IRS1, ITPR3, LIF, LMNA,	62
disease of tumor	3.02E-06	ADAM17, ANP32A, ARRB2, ATF2, ATF3, ATP2A2, BCL2, BRCA2, BTRC, CCND1, CD44, CDKN1A, CDKN1B, CDKN2C, CRYAB, CTSB, CYP1B1, DCN, E2F1, E2F2, EGFR, EGR1, EPHA2, ESR1, FOXP3, HGF, HIP1, HMGA2, HRAS, ID2, IFNGR1, IGF2, ITGB5, MAP2K6,	61
cell spreading of eukaryotic cells	3.67E-05	ACP1, ANTXR1, ATRN, BCAR1, BCL10, CAST, CD44, CD47, CORO1A, CRK, CRKL, CSPG4, CXCL12, CYR61, EFNB1, EGF, EPHA2, FBN1, FHL3, GAP43, HGF, HRAS, IGBP1, ING4, ITGA3, ITGA5, ITGA6, ITGB5, ITGB1BP1, LAMA5, LPAR1, LPP, MPRIP,	61
endocrine gland tumor	4.83E-03	ADAMTS1, ANGPT2, ATP1A1, BCL2, CCND1, CD59, CDC2L6, CDK2, CDK5, CDK6, CDK8, CDK10, CDKN1A, CDKN1B, CDKN2C, COPS5, CTSD, CYR61, E2F3, EFNB2, EGFR, ENG, EPHB4, FGFR1, HBEGF, HDAC11, HLA-G, IFITM1, IL15, ITGA3, ITGA5,	61
S phase of eukaryotic cells	1.01E-03	ARAF, BCL2, BCL2L11, BHLHE40, BID, C13ORF15, CAMK2N1, CCND1, CCNE1, CCNG1, CCNG2, CDC7, CDC25A, CDC25C, CDK2, CDK6, CDKN1A, CDKN1B, COPS5, CXCL12, DDX3X, DMTF1, E2F1, E2F2, E2F3, E2F6, EGF, EGFR, FOXO3, GAB1, GADD45A,	60
cell division process of fibroblast cell lines	2.00E-03	ADM, AKAP12, ARAF, AREG, AXIN2, BID, BMP4, CAST, CCND1, CCNE1, CDC25A, CDK2, CDKN1A, CDKN1B, CDKN2D, COPS5, CRK, DDX3X, DMTF1, E2F1, E2F2, E2F3, E2F6, EGF, EGFR, EP400, GADD45A, GATA6, GPI, HRAS, ID1, ID2, ID3, IGF2, INSR,	59
tumorigenesis of tumor	4.77E-06	ADAM17, ANP32A, ARRB2, ATF2, ATF3, ATP2A2, BCL2, BRCA2, BTRC, CCND1, CD44, CDKN1A, CDKN1B, CDKN2C, CTSB, CYP1B1, DCN, E2F1, E2F2, EGFR, EGR1, EPHA2, FOXP3, HGF, HIP1, HMGA2, HRAS, IFNGR1, IGF2, ITGB5, MAP2K6, MMP2, MMP3,	58
development of tumor	7.15E-05	ADAM17, ANGPTL4, BCL2, CCND1, CDH5, CDKN1B, CDKN2C, COL18A1, CTSB, E2F1, E2F3, EGFR, EGR1, EPHA2, ESR1, FGFR2, GDNF, HGF, HRAS, ID1, IER3, IL18, INSR, IRF1, ITGB5, LATS1, LCK, MGAT3, MGMT, MLH1, MMP2, MMP3, MMP14, MYD88,	58
growth of tumor	1.89E-04	ANGPTL4, ARRB2, B4GALNT1, BCL2, CD44, CD59, CD274, CDKN1A, CDKN1B, CNR1, COL18A1, CRABP2, CREB1, CREBBP, CTSB, DNMT1, DNMT3B, EGFR, EPHA2, F2R, FGFR1, FGFR2, GADD45A, GJA1, HGF, HRAS, HSPA4, IGF2, IL18, IRF1, ITGA5, ITGB5,	58
proliferation of muscle cells	2.53E-03	ABCC4, ADM, AGTRAP, AKR1B1, BMP4, CDH13, CDKN1A, CDKN1B, CEBPD, COMT, CTNNBIP1, CXADR, E2F3, EGF, EGFR, ESR1, FGFR2, GATA4, GATA6, GNAQ, GPX1, HBEGF, HGF, HMGA2, ID2, IL15, ITGA5, ITGA6, KLF4, LIF, LRP1, MMP14, MNAT1,	58
cell viability of cell lines	5.43E-03	ANTXR1, ANTXR2, BCL2, BNIP2, CDKN1A, CLNS1A, DAB2, DDIT3, DPP3, E2F1, EGF, ESR1, FTH1, GPC1, GPX1, GSTP1, HGF, HIP1, HMOX1, HRAS, HSPA5, IFNZ, IGFBP7, LCK, LMNA, MCL1, MT1E, MT1F, NFKBIA, P4HB, PLAU, PLAUR, PRNP, PTEN, PTPN6,	57

survival of cervical cancer cell lines	1.71E-03	ACVR2B, ADK, AK5, AKAP8L, AURKAIP1, BCL2, BRCA2, CAMK2D, CAMK2N1, CCRK, CDK6, CDK8, CHKA, DGKA, DUSP5, DUSP14, DUSP22, DYRK3, EIF2AK4, INPP5B, KHK, LCK, MAP3K4, MINPP1, MPG, MTMR7, NEK3, PFKFB2, PFKM, PLK2, PPAP2A, PPM1B,	56
formation of actin stress fibers	2.05E-04	AKAP1, ARHGEF2, ARHGEF3, BCAR1, CALD1, CAPN1, CDKN1A, COL18A1, CRK, CTGF, DAB2, EDNRA, EGF, EGFR, F2R, GNAO1, GNAQ, GNB1, GNG12, GPI, HGF, ITGA3, ITGA5, ITGA6, LIMK1, LPAR1, LPAR4, MAPK11, MPRIP, NET1, NF1, PALLD,	55
apoptosis of muscle cells	6.10E-04	ADM, ADRB2, BCL2, BCL2L11, BMP4, BNIP3L, CAMK2D, CAPN1, CASP8, CASP9, CDC42EP3, CDKN1A, COQ6, CXCL12, DAG1, E2F1, EEF1D, GATA4, GATA6, GNAQ, GNPTG, GPX1, HGF, HLA-B, HLA-DMA, HSPB6, ID2, IL6ST, IRF1, LIF, MAP2K6, MCL1,	55
apoptosis of embryonic cell lines	6.22E-06	BCL2, BCL10, BID, BNIP3L, CASP2, CASP8, CASP9, CD44, COPS5, DAP3, E2F1, E2F6, ECOP, EGF, HIPK2, HRAS, HSPA5, HTT, IER3, IRF1, IRS1, MAP2K6, MCL1, PAK2, PEA15, PKN2, PPARD, PPP1R15A (includes EG:23645), PPP3R1, PRMT2, PTGIS,	54
interphase of normal cells	1.24E-04	ATF2, ATF3, BCL2, BCL2L11, C13ORF15, CCND1, CCNE1, CCNG2, CD44, CDC7, CDC25C, CDK2, CDKN1A, CDKN1B, CEBPD, CHKA, DCN, E2F1, E2F2, E2F3, EGF, ERCC1, FANCC, GAB1, GADD45A, GATA6, GPC1, GRB10, HMGN1, ID2, ID3, IGFBP7,	54
apoptosis of fibroblasts	3.69E-03	ARRB2, ATF2, ATF3, BCL2, BCL2L11, BID, CABLES2, CAPNS1, CASP2, CASP8, CASP9, CCND1, CDKN1A, CDKN1B, CDKN2C, CLIC4, CTSD, DDIT3, DHCR24, DUSP1, E2F1, EGF, EGFR, FOXO1, GAB1, HRAS, INSR, MBD4, MCL1, MT1E, MT1F, NEK1, NOTCH1, NUPR1, OPA1, PITPNA, POLB, PRMT2	54
metastasis	4.86E-03	ACTB, ADAM17, AKAP12, ARHGDIG, ARRB2, ATF2, ATF3, CD44, CD151, CD274, COL18A1, CXCL2, CYP1B1, EGF, EGFR, ENPP2, EPHA2, F2R, FIGF, FUS, HGF, HMGCR, HTATIP2, IFNAR2, IGF2BP1, ITGB4, LAMA5, LCK, LETMD1, MAPK1, MMP2,	54
arrest in growth of eukaryotic cells	3.59E-04	AKAP12, AKT3, BMP4, CBX7, CCND1, CCNE1, CDC7, CDK2, CDK6, CDKN1A, CDKN1B, CDKN2D, DAB2, DMTF1, E2F1, EGF, EGR1, ELAC2, ENG, EZH2, FOXO3, GADD45GIP1, HMOX1, HRAS, ID3, IL6ST, IRF1, ITGB4, KLF4, KRT10, LIF, LMNA, MAP2K6, MAPK1,	53
G1 phase of tumor cell lines	6.17E-04	BCL2, BHLHE40, BTRC, CAMK1, CAMKK1, CCND1, CCNE1, CCNG1, CCNG2, CDC25A, CDC25C, CDK2, CDK6, CDK5RAP3 (includes EG:80279), CDKN1A, CDKN1B, COPS5, CREG1, CYR61, DCN, DDIT3, DUSP1, EGF, EGFR, EPB41L1, GJA1, GPS2, GSPT1,	53
development of connective tissue	6.09E-03	ACVR1, ADAMTS1, ADRB2, ATP7A, BCL2, BMP4, CD9, CD81, CHST11, DLX2, E2F1, EGR2, EN1, ENPP1, FGF10, FGFR2, FOXC2, GJA1, GPC3, HIP1, HIP1R, HOXA2, HOXA11, HOXD3, HOXD8, HOXD10, HOXD13, MAPK3, MMP2, MMP13, MMP14, MSX1, NDST1, PDGFC, PDGFRA, PRRX1, PRRX2, PTGE	53
tumorigenesis of cell lines	3.93E-04	ADAM17, ARMC10, ATF2, ATF3, BCL2, CAST, CCND1, CD44, CD82, CD151, CD274, CDKN1A, COL18A1, CSNK1E, CTSB, CXADR, CXCL2, CYR61, DLC1, EGFR, EGR1, ENPP2, ERF, F2R, GPI, HAS2, HGF, HRAS, HTATIP2, IL18, IRF1, LAMA5, LPP, MAD1L1,	52
quantity of cell lines	1.34E-03	BCL2, BHLHE40, CBFB, CCND1, CCNE1, CD63, CDC25A, CDK5RAP3 (includes EG:80279), CDKN1A, CDKN1B, COL18A1, CUL4A, E2F1, EDNRA, EGF, EGFR, ERRFI1, ESR1, FGF13, HMOX1, HRAS, IFNZ, IGFBP6, IGFBP7, IL11, INPPL1, JUNB, KLF4, LIF,	52

arrest in G1 phase of cell lines	4.26E-03	AKAP12, BCL2, BHLHE40, BTRC, CAMK1, CAMKK1, CCND1, CCNE1, CCNG1, CDC25A, CDK2, CDK5RAP3 (includes EG:80279), CDKN1A, CDKN1B, CDKN2D, COPS5, CYR61, DCN, DDIT3, DUSP1, E2F1, EGF, EGFR, EP400, EPB41L1, GHR, GPS2, GSPT1, HRAS, ID3, ITGA5, JAK3, KLF4, LMNA, MA	51
neurological process of neurites	8.16E-04	ALCAM, ANK3, APBB2, ARTN, BACE1, BDNF, CDK5, CDK5R1, CXCL12, DPYSL2, EFNA5, EFNB1, EGR2, ENAH, ETV1, FEZ1, FOXD1, GALNS, GAP43, GDNF, GRIA1, HGF, HOXA1, HOXA2, HRAS, KLF7, LAMC1, MAPK1, MAPK3, MAPK8IP3, NCAM1,	50
differentiation of embryonic cells	6.33E-05	ACVR1, ADA, BAIAP2, BCL2L11, BDNF, BMP4, CDKN1B, DAB2, DNMT1, EGF, EIF4G2, EPHB4, ERF, EZH2, FGFR1, FGFR2, GAS7, GATA4, GATA6, HBEGF, HGF, HHEX, HMGN1, HOPX, HTT, ID3, IGF2, IL6ST, JUNB, LIF, MAPK1, MAPK8IP3, METRN, MMP2,	49
neurological process of axons	1.27E-03	ALCAM, ANK3, APBB2, ARTN, BACE1, BDNF, CDK5, CDK5R1, CXCL12, DPYSL2, EFNA5, EFNB1, EGR2, ENAH, ETV1, FEZ1, FOXD1, GALNS, GAP43, GDNF, GRIA1, HGF, HOXA1, HOXA2, HRAS, KLF7, LAMC1, MAPK1, MAPK3, MAPK8IP3, NCAM1,	49
pancreatic tumor	2.86E-03	AKAP1, CD59, CDC2L6, CDK2, CDK5, CDK6, CDK8, CDK10, CDKN1A, COPS5, CREBBP, CTSB, CTSD, CYR61, EGFR, GATA4, GATA6, HBEGF, HLA-G, HOXA5, IFITM1, IL15, ITGA3, ITGAE, ITGB4, KLF4, KRT7, KRT10, MAPK13, MLL3, MSLN, PALLD,	49
proliferation of breast cancer cell lines	3.86E-03	AIM2, BCAR1, BRCA2, BTC, CCND1, CCNE1, CDKN1A, CHKA, CYR61, DCN, E2F1, EGF, EGFR, EPHA2, ESR1, ETS2, FOXO1, GPER, GPX1, HAS2, HOXA1, HSPB8, ID1, ID2, IER3, IGF2, ITGA5, LATS1, MAGED1, MAPK6, MAPK11, MAPK12, MED1, MMP14,	49
ossification	8.21E-04	ACVR1, ACVR2B, ADRB2, ANKH, ATF2, AXIN2, BCL2, BMP4, CBFB, CD276, COL1A1, CTGF, E2F1, EGFR, EGR2, EIF2AK3, EN1, ENPP1, ERCC2, ESR1, EXT2, FETUB, FGFR2, FOSL2, FOXC2, GJA1, GLA, HSPG2 (includes EG:3339), MEF2C, MMP13,	48
cell death of prostate cancer cell lines	4.92E-03	ALOX12, BCL2, BCL2L11, CASP7, CASP8, CASP9, CDK5, CDK5R1, COX5A, CREB1, DDIT3, DKK3, E2F1, EGF, EGFR, EGR1, ETS2, FOXO1, FOXO3, FST, GADD45A, GLIPR1, HBEGF, HGF, HOXC6, HSPB8, ID1, IGFBP4, IGFBP7, ITGB5, NFKB2, PLAU,	48
organization of filaments	3.43E-04	ADAMTS2, AGFG1 (includes EG:3267), AKAP2, ARHGEF2, ATP7A, BCAR1, BCL2, CDK2AP2, CDKN1B, CFL1, COL1A1, COL3A1, COL5A1, COL5A2, CORO1A, DNAJB6, ENAH, EPB41, EVL, FES, FLNA, FNBP1, FOXC2, GHR, GOLGA2, HAS2, ITGB4, LOX,	47
morphogenesis of tissue	2.52E-03	ACVR2B, AREG, CHST11, CX3CL1, DAG1, DLX2, EGFR, FGF10, FGFR2, FOXC2, FTO, GAA, GAB1, GATA4, GDNF, GREM1, GRSF1, HOXA2, HOXB4, HOXD13, IL11, INSR, IPP, IRX3, IRX5, LAMA5, LIF, LY6E, MEOX2, NDST1, NOTCH1, PTPN11, ROR2, RXRA,	47
cardiovascular process of organism	2.46E-04	ADORA2B, ANGPT2, ANGPTL2, BTC, CCND1, CD14, CDH5, COL18A1, CX3CL1, CXCL12, CYR61, EFNB1, EFNB2, ELK3, EPHB4, ESR1, FIGF, HGF, HRAS, IGF2R, IL15, IL18, KLF5, LAMC1, MED1, MMP2, MMP14, NR2F2, NRP1, NRP2, PGF, PRL2C2, PTEN,	46
S phase of cell lines	5.58E-04	ARAF, BCL2, BHLHE40, BID, CAMK2N1, CCND1, CCNE1, CCNG1, CCNG2, CDC7, CDC25A, CDC25C, CDK6, CDKN1A, CDKN1B, COPS5, CXCL12, DDX3X, DMTF1, E2F1, E2F2, E2F3, E2F6, EGF, EGFR, FOXO3, GADD45A, GATA6, HGF, HMOX1, ID1, IRS1, MCM10, MPG, MTCH2, MXD4, MXI1, MYBL2,	46

neuroepithelial tumor	4.43E-03	AKAP12, AKT3, CDC2L6, CDK2, CDK5, CDK6, CDK8, CDK10, CDKN1B, CDKN2C, CLK2, CLK4, E2F1, EDNRA, EGFR, ENC1, EPHA3, ESR1, FNTB, GRIA1, GRIA3, HBEGF, HIPK2, HRAS, HSPA5, ID2, IGF2, ITGB5, LPAR1, MGMT, MLH1, MLL3, MMP14, NES,	46
cell division process of connective tissue cells	1.72E-04	ATF2, ATF3, BCL2, BRCA2, CCND1, CCNE1, CCNF, CDC7, CDC25C, CDK2, CDKN1A, CDKN1B, E2F1, E2F2, E2F3, EGF, FANCA, FANCC, FIGF, GAB1, GADD45A, GRB10, HBEGF, HMGN1, HRAS, ID2, ID3, IGF2, IGFBP7, IL11, INSR, IRS1, JUNB, MAP2K6,	45
arrest in growth of cell lines	4.08E-04	AKAP12, AKT3, BMP4, CBX7, CCND1, CCNE1, CDK2, CDK6, CDKN1A, CDKN1B, DAB2, DMTF1, E2F1, EGF, ELAC2, ENG, EZH2, GADD45GIP1, HMOX1, HRAS, IL6ST, IRF1, ITGB4, KLF4, KRT10, LIF, LMNA, MAP2K6, MAPK1, MAPK3, NOTCH1, PTEN, RASSF5,	45
formation of cellular protrusions	7.22E-05	ARF6, ARHGAP24, BAIAP2, BDNF, CAPNS1, CAST, CD44, CD82, CDKN1B, CRK, CRKL, CTGF, CYR61, DAG1, EGF, FGD4, GAB1, GDNF, HGF, HRAS, HSP90AA1, IQGAP1, ITGA3, ITGA6, ITGB4, LASP1, LPAR1, MPRIP, NISCH, NRP1, PFN1, PKP1, PLAU,	44
neuroendocrine tumor	2.41E-03	BCL2, CCND1, CD59, CDC2L6, CDK2, CDK5, CDK6, CDK8, CDK10, CDKN1A, CDKN2C, COPS5, CTSD, CYR61, E2F3, EGFR, HBEGF, HLA-G, IFITM1, IL15, ITGA3, ITGAE, ITGB4, KRT7, KRT10, MLL3, MSLN, NCAM1, PALLD, PDGFRA, PLAT, PLAU, POLE3,	44
apoptosis of prostate cancer cell lines	6.23E-03	ALOX12, BCL2, BCL2L11, CASP7, CASP8, CASP9, CDK5, CDK5R1, COX5A, CREB1, DKK3, E2F1, EGF, EGFR, EGR1, ETS2, FOXO1, FOXO3, FST, GADD45A, GLIPR1, HBEGF, HGF, HOXC6, HSPB8, ID1, IGFBP4, IGFBP7, ITGB5, PLAU, PLAUR, PTEN,	44
cell division process of fibroblasts	1.54E-05	ATF2, ATF3, BCL2, BRCA2, CCND1, CCNE1, CCNF, CDC7, CDC25C, CDK2, CDKN1A, CDKN1B, E2F1, E2F2, E2F3, EGF, FANCA, FANCC, FIGF, GAB1, GADD45A, GRB10, HBEGF, HMGN1, HRAS, ID2, ID3, IGF2, IL11, INSR, IRS1, JUNB, MAP2K6, MBD4,	43
arrest in cell division process of normal cells	1.57E-03	ATF2, CCND1, CD44, CDC25C, CDK2, CDKN1A, CDKN1B, CHKA, COL1A1, CREB1, CYP26B1, DCN, E2F1, E2F2, E2F3, ERCC1, FANCA, FANCC, FOXO3, GADD45A, GPC1, HRAS, ID2, IGFBP7, JAK3, LY6C1, MAP2K6, MBD4, MLH1, MNAT1, MYBL2, NFKBIA,	43
tumorigenesis of organ	2.23E-03	AKAP12, AREG, BCL2, BRCA2, CCNE1, CDK2, CDKN1A, CDKN1B, CDKN2C, CUL1, CYP1B1, DNMT1, E2F1, EPHA2, ESR1, GADD45A, GSTP1, HBEGF, HGF, HRAS, KLF9, KRT10, LCK, MMP3, NDRG1, NOTCH1, PPARD, PTEN, PTTG1, RBL1, SIGIRR, SKP2, SPP1, TCIRG1, TGFBR2, TIMP1, TSC2, TXN	43
guidance of axons	1.18E-03	ALCAM, ANK3, APBB2, ARTN, BDNF, CDK5, CDK5R1, CXCL12, DPYSL2, EFNA5, EFNB1, EGR2, ENAH, ETV1, FEZ1, FOXD1, GALNS, GAP43, HGF, HOXA1, HOXA2, HRAS, KLF7, MAPK1, MAPK3, MAPK8IP3, NRP1, NRP2, PDIA3, PLXNA2, PTPRF,	42
catabolism of protein	2.92E-03	ACY1, AMFR, ANAPC2, ANAPC4, ARIH2, BTRC, CAST, CDC23 (includes EG:8697), DHCR24, EGLN2, FBXO2, FBXO6, FLNA, GJA1, ITCH, KIAA0368, PJA1, PSENEN, PSMB3, PSMC2, RELA, RNF6, RNF40, SELS, SGSM3, SIAH1, SIAH2, SKP2, SQSTM1,	42
angiogenesis of organism	5.70E-07	ANGPT2, ANGPTL2, BTC, CCND1, CDH5, COL18A1, CX3CL1, CXCL12, CYR61, EFNB2, ELK3, EPHB4, FIGF, HGF, HRAS, IGF2R, IL15, IL18, KLF5, LAMC1, MED1, MMP2, MMP14, NR2F2, NRP1, NRP2, PGF, PRL2C2, PTEN, PTGS2, RELA, SERPINF1, SMOC2,	41
branching morphogenesis	3.45E-06	AREG, B4GALT1, BCL2, BMP4, CD44, CRK, CX3CL1, DICER1, DLX2, EFNA5, EFNB2, EGF, EPHB4, ESR1, EYA1, FGF10, FGFR1, GAB1, GDNF, GPC3, GREM1, GZF1, HGF, HOXA11, HOXD13, IL11, ITGA5, ITGA6, LAMA5, MFGE8, MMP14, NOTCH1, NOTCH4,	41

attachment of cells	1.25E-05	ACP1, ADAM15, BCAR1, BTC, CD44, CDH13, CXCL12, DAB2, DCN, EFNB1, EGF, EGFR, EGR1, ENG, F11R, HRAS, HSPG2 (includes EG:3339), IGF2, ITGA3, ITGA5, ITGA6, ITGB5, LOX, LRP1, LRPAP1, MMP2, PLAU, PLAUR, PLD1, PTEN, PTGER2, PTK2B,	41
morphogenesis of animal	1.30E-03	BMP4, CDON, CHD7, CHST11, CRABP2, CYP26B1, DICER1, ECE1, EN1, FGF10, FGFR1, FMN1, GATA4, GATAD2A, GDF5, GNAQ, GREM1, HOXA9, HOXA11, HOXD10, HOXD13, KIAA1715, LMBR1, LRP4, LRP5, MED1, MSX1, NOTCH1, PBX2, PRRX1, PRRX2, PTCH1, PTHLH, RARG, SLC31A1, SMAD2, SM	41
serous ovarian carcinoma	2.70E-03	AGPAT2, BCL10, C13ORF15, C4A, CP, CTNNAL1, DAB2, DHTKD1, DTNA, E2F3, EPHB6, F2R, FAM171A1, FGFR1OP (includes EG:11116), FLRT2, FOXN2, FZD3, GATA6, GSTM5, HIST2H2AA3, IGFBP4, LRIG1, MFAP5, NOTCH4, PAPSS2, PDGFRA, PPAP2A, RECK, RNF144B, RRAS, SEMA3C, SLIT2,	41
organization of cytoskeleton	6.15E-03	ATP2C1, BCAR1, CCL13, CD44, CD47, CD82, CFL1, CRKL, CXCL12, DLC1, EFNA5, EFNB1, ENG, EPHA2, F2RL1, FLNA, GAS6, GDNF, HGF, LCK, MARCKS (includes EG:4082), MSN, MYH9, NF1, PAK1, PLAU, PLAUR, PLS3, PLXNB2, PTK2B, PTPN1,	41
disease of primary tumor	7.76E-04	ARRB2, ATF2, BRCA2, BTRC, CCND1, CD44, CDKN1A, CDKN1B, CDKN2C, CTSB, CYP1B1, DCN, E2F1, E2F2, EGFR, EGR1, FOXP3, HGF, HIP1, HMGA2, HRAS, ITGB5, MMP3, MMP14, NF1, PRDM2, PTEN, PTGS2, PTPN1, RRM2, SOCS1, SOCS3, STAT3,	40
morphology of tissue	1.72E-03	BDNF, CCND1, CDKN1B, COL18A1, EBF1, FMR1, FOXC2, FOXO1, GJA1, GSN, HGF, HTT, ID2, IL6ST, INSR, KIF3A, KRT10, LDLR, LFNG, LIF, LTBP4, MMP2, NCAM1, OTX1, PDGFRA, PLEC1, PLOD3, PRRX1, PRRX2, PTEN, RARG, RXRA, SERPINH1, SLC31A1,	40
development of limb	4.93E-03	CHD7, CHST11, CRABP2, CYP26B1, DICER1, E2F1, ECE1, EN1, FGF10, FGFR1, FMN1, GDF5, GJA1, GNAQ, GREM1, HGF, HOXA9, HOXA11, HOXD10, HOXD13, KIAA1715, LMBR1, LRP4, LRP5, MED1, MSX1, NOTCH1, PBX2, PGF, PRRX1, PRRX2, PTCH1,	40
neuroendocrine carcinoma	1.69E-04	BCL2, CD59, CDC2L6, CDK2, CDK5, CDK6, CDK8, CDK10, CDKN1A, CDKN2C, COPS5, CTSD, CYR61, EGFR, HBEGF, HLA-G, IFITM1, IL15, ITGA3, ITGAE, ITGB4, KRT7, KRT10, MLL3, MSLN, NCAM1, PALLD, PDGFRA, PLAT, PLAU, POLE3, PSMB5, PTEN, PTGES, RELA, RRM2, SPP1, TIMP1, TY	39
formation of filopodia	3.50E-04	AKAP12, ARHGAP24, BAIAP2, CAPNS1, CCL13, CD47, CTGF, CYR61, DAG1, ENAH, FGD3, FGD4, GAP43, HGF, HRAS, ITGA3, ITGA6, ITGB4, LAMA5, MARCKS (includes EG:4082), MTSS1, MYD88, MYO10, NEO1, NF1, PAK1, PKP1, PPP1R9A, PTK2B, PVR,	39
migration of endothelial cell lines	4.40E-04	ALCAM, ALOX12, BTC, CBFB, CD151, CDH5, CDKN1B, COL18A1, CTSB, CX3CL1, CXCL12, CYR61, DICER1, EGF, EGFR, FGF13, FIGF, FOXO1, FOXO3, HGF, HHEX, HOXA9, ID1, ID3, IL18, MEOX2, NCL, NRP1, PLAU, PTEN, PTGS2, PTK2B, PTN, SDC2,	39
tumorigenesis of primary tumor	1.28E-03	ARRB2, ATF2, BRCA2, BTRC, CCND1, CD44, CDKN1A, CDKN1B, CDKN2C, CTSB, CYP1B1, DCN, E2F1, E2F2, EGFR, EGR1, FOXP3, HGF, HIP1, HMGA2, HRAS, ITGB5, MMP3, MMP14, NF1, PRDM2, PTEN, PTGS2, PTPN1, RRM2, SOCS1, SOCS3, STAT3, STX2, TGFBR2, THBS1, THBS2, WNT10B, XRC	39

morphogenesis of embryo	2.27E-03	BMP4, CDON, CHD7, CHST11, CRABP2, CYP26B1, DICER1, ECE1, EN1, FGF10, FGFR1, FMN1, GATA4, GATAD2A, GDF5, GNAQ, GREM1, HOXA9, HOXA11, HOXD10, HOXD13, KIAA1715, LMBR1, LRP4, LRP5, MED1, MSX1, NOTCH1, PBX2, PRRX1, PRRX2, PTCH1, RARG, SMAD2, SMARCA4, TBX3, TBX	39
arrest in G1 phase of tumor cell lines	3.00E-03	BCL2, BHLHE40, BTRC, CAMK1, CAMKK1, CCND1, CCNE1, CCNG1, CDC25A, CDK2, CDK5RAP3 (includes EG:80279), CDKN1A, CDKN1B, CYR61, DCN, DDIT3, DUSP1, EGF, EGFR, EPB41L1, GPS2, GSPT1, ID3, ITGA5, KLF4, MLH1, MNAT1, MTBP, MYBL2,	38
developmental disorder of muscle cells	3.00E-03	ADRB2, ANGPT2, CAMK2D, CDKN1B, DUSP1, EDNRA, EGF, FOXF1, FOXF2, FOXO3, GATA4, GATA6, GNAQ, GPX1, HBEGF, HSPB8, IER3, IGF2, IL11, IL18, LIF, MAP2K5, MAP2K6, MAPK1, MSX1, NFKBIA, PLAU, PPP3CA, PPP3R1, PTEN, PTGES, PTGS2,	38
disease of malignant tumor	1.01E-03	ARRB2, ATF2, BRCA2, BTRC, CD44, CDKN1A, CDKN1B, CDKN2C, CTSB, CYP1B1, DCN, E2F1, E2F2, EGFR, EGR1, FOXP3, HGF, HIP1, HRAS, ITGB5, MMP3, MMP14, NF1, PRDM2, PTEN, PTGS2, PTPN1, RRM2, SOCS1, SOCS3, STAT3, STX2, TGFBR2, THBS1,	37
development of kidney	2.27E-03	ACVR2B, ADAMTS1, APH1A (includes EG:226548), AQP11, AREG, BCL2, BCL2L11, BDNF, BMP4, C1GALT1, CX3CL1, EYA1, FBN1, FGFR1, FGFR2, FOXC2, FOXD1, GDNF, GFRA1, GPC3, GREM1, HOXA11, IL11, INSR, JMJD6, KIF3A, LRP4, MMP14, NF1, OSR1,	37
developmental process of endothelial cell lines	2.08E-04	ALCAM, ALOX12, ATF3, BTC, CCL13, CD151, CDH5, CDKN1B, CLIC4, COL18A1, COL1A1, CXCL12, CYR61, DGKA, ECT2, EGF, EGFR, FES, FOXO1, FOXO3, HGF, ID1, ID3, MMP2, NAB2, NRP1, PTEN, PTN, SLIT2, SMOC2, TFAP2A, THBS1, THBS2, TIMP2,	36
developmental process of adipocytes	4.41E-04	ADRB2, CAST, CBY1, CCND1, CREB1, DDIT3, DLK1, EBF1, ENPP1, FGF10, GPX1, IL11, INSR, IRS1, LIF, MED1, METTL8, MMP3, NOTCH1, PARP2, PPARD, PRG4 (includes EG:10216), RARRES2, RGS2, RUNX1T1, SCAND1, SMAD2, SOCS1, SOD2, TBL1X,	36
ubiquitination of protein	8.82E-04	AMFR, ATG3, BCL10, CAND1, CAPN1, CARD10, CAST, CUL1, FBXO2, FBXW7, G2E3, GSPT1, ITCH, MGRN1, MUL1, PCNP, PPARD, PPIL2, RNF144B, SIAH1, SIAH2, SMURF1, STUB1, TPP2, TRAF6, UBA1, UBB, UBE2D3, UBE2E1, UBE2L3, UBE2N,	36
tumorigenesis of malignant tumor	1.67E-03	ARRB2, ATF2, BRCA2, BTRC, CD44, CDKN1A, CDKN1B, CDKN2C, CTSB, CYP1B1, DCN, E2F1, E2F2, EGFR, EGR1, FOXP3, HGF, HIP1, HRAS, ITGB5, MMP3, MMP14, NF1, PRDM2, PTEN, PTGS2, PTPN1, RRM2, SOCS1, SOCS3, STAT3, STX2, TGFBR2, THBS1,	36
cell spreading of cell lines	3.01E-03	ACP1, ANTXR1, BCAR1, BCL10, CAST, CYR61, EGF, EPHA2, FHL3, GAP43, ING4, ITGA5, LPAR1, MPRIP, PAK1, PALLD, PFN1, PLAU, PPFIA1, PTK2B, PTPN12, PTPN14, PVR, RTN4, SIRPA, SNAI2, SPHK1, SPP1, TESK1, TGFBI, THBS1, TIAM1, TSPAN7,	36
migration of fibroblast cell lines	2.05E-05	ACP1, BCAR1, CDKN1A, CDKN1B, CLIC4, CRKL, CXCL10, DDX3X, EGF, EGFR, FIGF, GNG12, HAS2, HBEGF, IL18, ITGA3, ITGA5, ITGB1BP1, LRPAP1, MEOX2, MMP14, MYLK, PALLD, PDGFD, PDGFRA, PLAU, PLAUR, PTEN, PTGS2, PTPN11, PTPN12, PVR,	35
developmental process of kidney cell lines	4.75E-04	ABCC5, CDKN1A, CHKA, CRK, DLGAP5, DLST, EGF, ESR1, F2RL1, FOXC2, GAB1, GAK, GDNF, HAS2, HBEGF, HGF, HRAS, ITGA5, LMNA, LOX, MT1E, MT1F, NFYB, NINL, PKP3, PMP22, PTP4A3, PTPN14, SLC30A1, STEAP2, TPM2, TPP2, TSC2, UNC5B,	35
differentiation of adipocytes	7.64E-04	ADRB2, CAST, CBY1, CCND1, CREB1, DDIT3, DLK1, EBF1, ENPP1, FGF10, GPX1, INSR, IRS1, LIF, MED1, METTL8, MMP3, NOTCH1, PARP2, PPARD, PRG4 (includes EG:10216), RARRES2, RGS2, RUNX1T1, SCAND1, SMAD2, SOCS1, SOD2, TBL1X,	35

migration of connective tissue cells	1.20E-03	BCAR1, CAPNS1, CCND1, CD44, CDKN1B, COL1A1, CYR61, EGF, F2R, FLNB, GRLF1, HBEGF, HGF, IGBP1, ITGA5, ITGB1BP1, LPP, LRP1, LRPAP1, MAPK1, MRC2, PALLD, PLAUR, PLEC1, PRKAR1A, PTN, PTPN2, RAMP2, SDC4, SPP1, STAT3, TGFBR2,	35
interphase of fibroblast cell lines	1.48E-03	AKAP12, ARAF, BID, BMP4, CCND1, CCNE1, CDC25A, CDK2, CDKN1A, CDKN1B, CDKN2D, COPS5, DDX3X, DMTF1, E2F1, E2F2, E2F3, E2F6, EGF, EP400, GADD45A, GATA6, GPI, HRAS, IRS1, LATS1, LMNA, MAP2K6, PPAP2C, PTPN11, PTTG1, PVR,	35
development of lung	2.73E-03	ACVR2B, ADA, ADAMTS2, BMP4, DICER1, FGF10, FGFR1, FGFR2, FOXF1, GPC3, GREM1, HOXA5, IGF2, JMJD6, LAMA5, LOX, MMP2, MMP14, NOTCH1, PDGFRA, PDPN, PPP1CA, PPP3R1, PTGES, RBP1, RQCD1, SMAD2, SP1, TBX4, TBX5, TGFB2,	35
cell division process of breast cancer cell lines	4.78E-03	BHLHE40, CAMK1, CAMKK1, CCND1, CCNE1, CCNG1, CDC25A, CDC25C, CDKN1A, CDKN1B, CUL7 (includes EG:9820), DCN, EGF, EGFR, ESR1, EZH2, FOXO3, HAS2, HBEGF, HRAS, LATS1, MLH1, PTEN, PTHLH, RRAD, RXRA, SIAH1, SKP2, SMARCA4,	35
pancreatic carcinoma	5.54E-05	CD59, CDC2L6, CDK2, CDK5, CDK6, CDK8, CDK10, CDKN1A, COPS5, CTSD, CYR61, HBEGF, HLA-G, IFITM1, IL15, ITGA3, ITGAE, ITGB4, KRT7, KRT10, MLL3, MSLN, PALLD, PDGFRA, PLAT, PLAU, POLE3, PTEN, PTGES, RELA, RRM2, SPP1, TIMP1, TYMS	34
attachment of eukaryotic cells	3.08E-04	ACP1, ADAM15, BCAR1, BTC, CD44, CDH13, CXCL12, DCN, EFNB1, EGF, EGFR, EGR1, ENG, HRAS, HSPG2 (includes EG:3339), IGF2, ITGA3, ITGA5, ITGA6, ITGB5, LOX, LRP1, LRPAP1, MMP2, PLAU, PLAUR, PLD1, PTGER2, PTK2B, TGFBI, THBS2,	34
formation of lamellipodia	8.27E-04	ARHGAP24, BAIAP2, BDNF, CD44, CD82, CDKN1B, CRK, CRKL, CTGF, CYR61, EGF, FGD4, GAB1, GDNF, HGF, HRAS, HSP90AA1, ITGA6, ITGB4, LASP1, LPAR1, MPRIP, NISCH, NRP1, PLAU, PVR, PVRL1, PVRL3, SDC4, SEMA3A, SPHK1, SWAP70, TPM1,	34
disease of liver	1.04E-03	ATF4, BCL2, CCND1, CCNE1, CD14, CDKN1B, DNMT3B, E2F1, ENG, FGFR1, FGFR2, GADD45A, HGF, IRS1, LHX2, MED1, MMP13, MT1E, MT1F, MYD88, NDRG1, NFE2L1, PDGFC, PLAU, SCG5, SKP2, SOCS1, SPP1, STAT1, TGFBR2, TIMP1, TSC2, VEGFA,	34
quantity of tumor cell lines	1.62E-03	BCL2, BHLHE40, CCND1, CDC25A, CDK5RAP3 (includes EG:80279), CDKN1A, CDKN1B, CUL4A, E2F1, EGF, ESR1, FGF13, HMOX1, IFNZ, IGFBP6, IGFBP7, INPPL1, JUNB, KLF4, LIF, MCTS1, MYBL2, PEG3, PTGS2, PTHLH, RBBP4, SKP2, TIMP3, TPP2, TSC2,	34
morphogenesis of limb	3.63E-03	CHD7, CHST11, CRABP2, CYP26B1, DICER1, ECE1, EN1, FGF10, FGFR1, FMN1, GDF5, GNAQ, GREM1, HOXA9, HOXA11, HOXD10, HOXD13, KIAA1715, LMBR1, LRP4, LRP5, MED1, MSX1, NOTCH1, PBX2, PRRX1, PRRX2, PTCH1, RARG, SMARCA4, TBX3, TBX4,	34
migration of fibroblasts	5.51E-04	BCAR1, CAPNS1, CCND1, CDKN1B, COL1A1, CYR61, EGF, F2R, FLNB, GRLF1, HBEGF, HGF, IGBP1, ITGA5, ITGB1BP1, LPP, LRP1, LRPAP1, MAPK1, MRC2, PALLD, PLAUR, PLEC1, PRKAR1A, PTPN2, RAMP2, SDC4, SPP1, STAT3, TGFBR2, THBS1,	33
arrest in cell stage of normal cells	8.96E-04	ATF2, CCND1, CD44, CDC25C, CDK2, CDKN1A, CDKN1B, CHKA, CYP26B1, DCN, E2F1, E2F2, E2F3, EGF, ERCC1, FANCC, FOXO3, GADD45A, GPC1, IGFBP7, JAK3, MAP2K6, MBD4, MLH1, MNAT1, MYBL2, PTEN, PTTG1, RELA, RPS6KA2, SP1, TFDP1, XPC	33
developmental process of colon cancer cell lines	1.42E-03	AHSA1, AREG, BCL2, BCL2L11, CAMK2N1, CCND1, CDKN1A, CDKN1B, COL18A1, CTSD, DUSP5, EGF, EGFR, EGR2, ENC1, FDXR, FES, GADD45A, GREM1, IGF2, IGF2R, ITGA5, KLF4, NDRG1, PDLIM4, PTEN, PTPN1, SDC2, STAT3, SUFU, TAX1BP3,	33

formation of extracellular matrix	7.60E-04	ADAMTSL4, ADM, APBB2, ATP7A, B4GALT1, CCDC80, COL18A1, COL4A6, CYR61, DCN, EMILIN1, ERCC2, FBLN1, FOXF1, FOXF2, HSPG2 (includes EG:3339), KAZALD1, NF1, NFKB2, NID1, OLFML2B, PDGFRA, PTX3, RECK, ROR2, SMARCA4, SMOC1,	32
activation of NFkB binding site	9.69E-04	ATF3, BCL2, BTRC, CD14, CREBBP, EGF, F2RL1, HGF, IER3, IL18, LY96, MAP3K14, MAVS, MYD88, NFKB2, NFKBIA, NFKBIB, NFKBID, NFKBIE, PRKRA, PRMT2, RALA, RELA, SMAD1, TLR6, TNFAIP3, TNFRSF25, TNFRSF1A, TRADD, TRAF6, VCAM1,	32
dephosphorylation of amino acids	1.92E-03	BCL2, CDC25C, CTDP1, DUSP1, DUSP3, DUSP4, DUSP5, DUSP22, EYA1, MTMR7, PDP2, PPAP2A, PPM1B, PPM1F, PPP1CA, PPP1CB, PPP2CB, PPP3CA, PPP3R1, PTEN, PTPN1, PTPN2, PTPN6, PTPN11, PTPN12, PTPN14, PTPN18, PTPN22, PTPRE, PTPRF,	32
developmental process of embryonic stem cells	1.92E-03	BAIAP2, BCL2L11, BMP4, CDC7, DNMT1, EIF4G2, ENG, EPHB4, EZH2, GATA4, GATA6, HHEX, HTT, ID1, ID3, IL6ST, LIF, MAPK1, MAPK8IP3, NMT1, NR4A2, PTEN, PTPN11, PTTG1, RBL1, SOX2, SRF, STAT3, TERF1, TLN1, VEGFA, WWTR1	32
experimentally-induced diabetes	1.92E-03	ALOX12, ANXA1, ANXA5, AQP1, C3, CCNG1, CD200, CEBPD, CNGB1, CP, DDAH1, DUSP1, EXOC7, FGFR1, HLA-C, HMGCL, ID1, IFITM3, IRF1, KLF4, MT1F, PDLIM4, PPAP2B, PPT2, PSMC2, PTPN1, RSAD2, SCARB1, SCN1B, SPP1, TIMP1, VEGFA	32
carcinoma in situ	3.59E-03	ABCC4, ANO6, ASS1, BHLHE40, C3, COL7A1, CX3CL1, ENTPD5, FCGR3A, FGFR2, FLNA, GPC1, GPRC5A, HMGA2, HRAS, IER3, IRF1, ITGB4, KRT7, LY6E, MFGE8, MIPEP, MXRA8, MYL9 (includes EG:10398), PTEN, RBL1, SGK269, SMARCD3, SMS,	32
arrest in developmental process of tumor cell lines	4.37E-03	CBX7, CCND1, CCNE1, CDK2, CDKN1A, CDKN1B, DAB2, E2F1, EZH2, GADD45GIP1, HMOX1, IL6ST, IRF1, KLF4, KRT10, LIF, MAP2K6, MAPK1, MAPK3, NOTCH1, PTEN, RASSF5, RBL1, RUNX1T1, SKP2, SMARCA4, SOCS1, SOCS3, STAT1, STAT3, TGFBR2,	32
cell stage of connective tissue cells	1.57E-04	ATF2, ATF3, BRCA2, CCND1, CCNE1, CDC7, CDC25C, CDK2, CDKN1A, CDKN1B, E2F1, E2F2, E2F3, FIGF, GAB1, GADD45A, GRB10, HMGN1, ID2, ID3, IGFBP7, IRS1, JUNB, MAP2K6, MBD4, MYBL2, PLK2, RELA, SKP2, TFDP1, TFE3	31
cell spreading of normal cells	2.60E-03	ATRN, CAST, CD44, CD47, CORO1A, CRK, CRKL, CXCL12, EFNB1, EGF, FBN1, HGF, HRAS, IGBP1, ITGA3, ITGA5, ITGA6, ITGB5, ITGB1BP1, LAMA5, LPP, PALLD, PTK2B, SDC4, SEMA3A, SRF, STAT3, THBS1, THBS2, TIAM1, TLN1	31
proliferation of carcinoma cell lines	4.80E-03	AKT3, ANXA1, BID, CASP2, CDK5, CDK5R1, CDKN1A, CXCL12, CYR61, DLC1, E2F1, EGF, EGFR, EGR1, ERCC1, FANCC, GAS6, HGF, HK1, IGF2, IL18, ITPR1, NDUFAF2, NEK2, PLAU, PTGS2, RAP1GAP (includes EG:5909), RELA, SKP2, SLC25A6, TSPO	31
arrest in growth of tumor cell lines	5.82E-03	CBX7, CCND1, CCNE1, CDK2, CDKN1A, CDKN1B, DAB2, E2F1, EZH2, GADD45GIP1, HMOX1, IL6ST, IRF1, KLF4, KRT10, LIF, MAP2K6, MAPK1, MAPK3, NOTCH1, PTEN, RASSF5, RBL1, SKP2, SMARCA4, SOCS1, SOCS3, STAT1, STAT3, TGFBR2, UBE2D3	31
cell stage of fibroblasts	4.34E-05	ATF2, ATF3, BRCA2, CCND1, CCNE1, CDC7, CDC25C, CDK2, CDKN1A, CDKN1B, E2F1, E2F2, E2F3, FIGF, GAB1, GADD45A, GRB10, HMGN1, ID2, ID3, IRS1, JUNB, MAP2K6, MBD4, MYBL2, PLK2, RELA, SKP2, TFDP1, TFE3	30
targeting of protein	1.63E-04	AP3M1, CCHCR1, EIF5A, ERBB2IP (includes EG:55914), GIPC1, GPHN, HPS4, HSPA9, LTBP2, MYO6, NUPL2, OPTN, PEX6, PEX7, PEX19, PICK1, PPP1R3C, PTPN11, RAB27A, STXBP4, SYNJ2BP, TIMM9, TIMM44, TOMM22, TRNT1, TSPO, XPO5, XPO6,	30

proliferation of endothelial cell lines	3.95E-04	ATP6V0A2, CBFB, CDH13, CDKN1A, CDKN1B, COL18A1, DAB2, DGKA, DICER1, EGF, EGFR, ENG, F2R, FGF13, FIGF, FOXO1, HGF, HHEX, NCL, NRP1, NRP2, PTEN, PTN, PTPN1, PTX3, SEMA3A, SEMA3F, SKP2, TNFRSF25, VEGFA	30
proliferation of dermal cells	1.44E-03	ANGPTL6, CCNG2, CDH13, CDK2, CDKN1A, EGF, EPHA2, FGF10, FST, HGF, IGFBP4, INSR, JUNB, KLK8, KRT10, LRIG1, PPARD, PTCH1, PTEN, PTGER2, PTGS2, PTHLH, PTPRK, RBL1, RXRA, SGK3, SLC7A11, SNAI2, TOM1L1, VDR	30
ductal carcinoma	3.52E-03	AGPAT2, ANXA1, CCND1, CDKN1A, COX4I1, CP110, CSPP1, DDHD2, DDX19B, EPHA2, EYA1, FAM96B, GSPT1, HSPB8, IER3, ING4, MKI67, MT1E, MT1F, PPFIA1, PXDN, RBM4B, SAT2, SERPINF1, STAU2, TNXB, TPD52, TRIM16, WWTR1, ZNF703	30
growth of colon cancer cell lines	5.27E-03	AHSA1, AREG, BCL2, BCL2L11, CAMK2N1, CCND1, CDKN1A, COL18A1, CTSD, DUSP5, EGF, EGFR, EGR2, ENC1, FDXR, FES, GADD45A, IGF2, IGF2R, ITGA5, KLF4, PDLIM4, PTEN, PTPN1, SDC2, STAT3, SUFU, TAX1BP3, TGFBR2, TIAM1	30
interphase of connective tissue cells	2.03E-05	ATF2, ATF3, CCND1, CCNE1, CDC7, CDC25C, CDK2, CDKN1A, CDKN1B, E2F1, E2F2, E2F3, GAB1, GADD45A, GRB10, HMGN1, ID2, ID3, IGFBP7, IRS1, JUNB, MAP2K6, MBD4, MYBL2, PLK2, RELA, SKP2, TFDP1, TFE3	29
angiogenesis of animal	4.18E-04	ANGPT2, ANGPTL2, BTC, CCND1, CDH5, CXCL12, CYR61, EFNB2, ELK3, HGF, HRAS, KLF5, MED1, MMP2, MMP14, NR2F2, NRP1, NRP2, PGF, PTEN, RELA, SERPINF1, SMOC2, SPHK1, THBS1, TNFRSF1A, VEGFA, VEGFC, WARS	29
ruffling	5.53E-04	ARF6, ARHGAP17, BAIAP2, CAPG, CCL13, CRK, CXCL12, EFNB1, EGF, GSN, HGF, HMOX1, HRAS, INPPL1, INSR, IRS1, MTSS1, MYO1C, PAK1, PLAU, PLAUR, PTEN, PTK2B, SPHK1, SPP1, SWAP70, TIAM1, TSC2, WASF1	29
proliferation of epidermal cells	1.22E-03	ANGPTL6, CCNG2, CDH13, CDK2, CDKN1A, EGF, EPHA2, FGF10, FST, HGF, INSR, JUNB, KLK8, KRT10, LRIG1, PPARD, PTCH1, PTEN, PTGER2, PTGS2, PTHLH, PTPRK, RBL1, RXRA, SGK3, SLC7A11, SNAI2, TOM1L1, VDR	29
assembly of extracellular matrix	3.85E-03	ADAMTSL4, APBB2, ATP7A, B4GALT1, CCDC80, COL18A1, COL4A6, CYR61, DCN, EMILIN1, ERCC2, FBLN1, FOXF1, FOXF2, HSPG2 (includes EG:3339), KAZALD1, NF1, NFKB2, NID1, OLFML2B, PDGFRA, RECK, SMARCA4, SMOC1, SMOC2, TGFB2, TGFBI,	29
developmental process of epithelial cell lines	5.79E-03	ABCC5, AREG, BTC, CCND1, CDK2, CDKN1A, CHKA, CXCL2, DAB2, DLGAP5, DLST, EGF, ENG, ESR1, ETV6, HGF, ID2, NINL, NOTCH1, PTHLH, PTP4A3, RBBP9, RXRA, SPP1, TFE3, TGFB2, TGFBR3, TPP2, UNC5B	29
interphase of fibroblasts	1.30E-05	ATF2, ATF3, CCND1, CCNE1, CDC7, CDC25C, CDK2, CDKN1A, CDKN1B, E2F1, E2F2, E2F3, GAB1, GADD45A, GRB10, HMGN1, ID2, ID3, IRS1, JUNB, MAP2K6, MBD4, MYBL2, PLK2, RELA, SKP2, TFDP1, TFE3	28
Dupuytren contracture	1.31E-03	ADAMTS1, ADAMTS2, ADAMTS4, ADAMTS6, COL12A1, COL16A1, COL17A1, COL18A1, COL1A1, COL22A1, COL3A1, COL4A2, COL4A5, COL4A6, COL5A1, COL5A2, COL6A2, COL6A3, COL7A1, COL8A1, MMP2, MMP3, MMP13, MMP14, MMP16, TIMP1, TIMP2,	28
delay in initiation of cell division process of eukaryotic cells	1.31E-03	BCL2, CASP2, CCND1, CCNE1, CDC25C, CDKN1A, CDKN1B, CREG1, DLGAP5, ECT2, ELAC2, GADD45A, GRB10, IGFBP7, IL15, INSR, JUNB, KLF4, KLF9, LIMK1, MPG, PTEN, PTTG1, RAD21, RASSF5, SOD2, STAT1, TFDP1	28

neoplasia of cells	3.38E-03	ARHGDIG, ATF2, ATF3, CD44, CD151, CD274, COL18A1, CXCL2, EGF, ENPP2, F2R, FIGF, HGF, HRAS, HTATIP2, IGF2BP1, ITGB4, LAMA5, MAD1L1, MAPK1, NFKBIA, NFKBIB, PPARD, SOCS1, TGFBR2, TIMP1, TXNIP, WISP1	28
migration of smooth muscle cells	4.21E-03	ADM, CCL5, CD47, CDKN1B, DUSP1, EGF, EGFL7, FGFR1, HBEGF, HGF, IGFBP4, IL18, ITGB5, LDLR, MAPK1, MAPK3, MEOX2, NEO1, PLAT, PLAU, PLAUR, PTGS2, PTPRF, RAMP2, SDC4, SPP1, THBS1, TIMP1	28
invasion of normal cells	5.19E-03	CCND1, CD151, CXCL10, EGF, ENG, ETV6, EZH2, FST, GAB1, HGF, HRAS, IL18, ITGA5, ITGA6, ITGB4, LRP1, LRPAP1, MMP14, NF1, SPP1, STAT3, THBS2, TIMP1, TIMP2,	28
morphogenesis of eukaryotic cells	6.19E-05	BDNF, CCND1, CD82, COL18A1, CRK, CXCL2, EFNB2, EGF, EPHB4, GAB1, GDNF, HGF, ITGA6, MMP2, NFKB2, NOTCH1, NOTCH4, PTEN, PTK2B, PVRL2, RELA, SLC1A3, SPR, STC1, TFAP2A, TIMP2, VCAM1	27
growth of kidney cell lines	4.62E-04	ABCC5, CDKN1A, CHKA, DLGAP5, DLST, EGF, ESR1, F2RL1, GAK, HAS2, HRAS, ITGA5, LMNA, LOX, MT1E, MT1F, NINL, PKP3, PMP22, PTP4A3, SLC30A1, STEAP2,	27
angiogenesis of mammalia	8.23E-04	ANGPT2, ANGPTL2, BTC, CCND1, CDH5, CXCL12, CYR61, EFNB2, ELK3, HGF, HRAS, KLF5, MED1, MMP2, MMP14, NR2F2, PGF, PTEN, RELA, SERPINF1, SMOC2, SPHK1, THBS1, TNFRSF1A, VEGFA, VEGFC, WARS	27
growth of epithelial cell lines	2.32E-03	ABCC5, AREG, BTC, CCND1, CDK2, CDKN1A, CHKA, CXCL2, DAB2, DLGAP5, DLST, EGF, ENG, ESR1, ETV6, HGF, NINL, NOTCH1, PTHLH, PTP4A3, RBBP9, RXRA, TFE3, TGFB2, TGFBR3, TPP2, UNC5B	27
angiogenesis of mice	6.53E-04	ANGPT2, ANGPTL2, BTC, CCND1, CDH5, CXCL12, CYR61, EFNB2, ELK3, HGF, HRAS, KLF5, MED1, MMP2, MMP14, NR2F2, PGF, PTEN, RELA, SMOC2, SPHK1, THBS1, TNFRSF1A, VEGFA, VEGFC, WARS	26
cardiovascular process of tumor	6.53E-04	ADAM17, ANGPTL4, B4GALNT1, BCL2, CDH5, COL18A1, CRYAB, CTSB, EPHA2, FGFR2, HGF, HRAS, IL18, ITGB5, MMP2, MMP3, MMP14, NRP1, PGF, PLAU, THBS1,	26
closure of tissue	8.72E-04	BCL10, BMP4, CFL1, CREBBP, DLC1, ENAH, FTO, FZD3, FZD6, GRLF1, HIPK2, IRX3, IRX5, ITGA3, ITGA6, PDGFRA, PFN1, PLXNB2, PTGS1, PTGS2, PTK7, RGMA, TRAF6,	26
differentiation of embryonic stem cells	1.15E-03	BAIAP2, BCL2L11, BMP4, DNMT1, EIF4G2, EPHB4, EZH2, GATA4, GATA6, HHEX, HTT, ID3, IL6ST, LIF, MAPK1, MAPK8IP3, NMT1, NR4A2, PTPN11, RBL1, SOX2, SRF, STAT3,	26
arrest in interphase of normal cells	4.02E-03	ATF2, CCND1, CD44, CDC25C, CDK2, CDKN1A, CDKN1B, CHKA, DCN, E2F1, E2F2, E2F3, ERCC1, FANCC, GADD45A, GPC1, IGFBP7, JAK3, MAP2K6, MBD4, MNAT1,	26
dwarfism	3.92E-05	CHST3, COL1A1, E2F1, EBP, EGFR, FGFR1, FGFR2, FLNA, GGT1, GHR, HIP1, HIP1R, HOXA5, HSPG2 (includes EG:3339), ITGA11, LBR, LIF, MAP2K6, MMP13, PAPSS2, PEX7, PTHLH, ROR2, SMPD3, VEGFA	25
proliferation of keratinocytes	1.84E-04	CCNG2, CDH13, CDKN1A, EGF, EPHA2, FGF10, FST, HGF, INSR, JUNB, KLK8, KRT10, LRIG1, PPARD, PTCH1, PTEN, PTGER2, PTGS2, PTHLH, PTPRK, RXRA, SGK3, SNAI2,	25
closure of embryonic tissue	1.23E-03	BCL10, BMP4, CFL1, CREBBP, DLC1, ENAH, FTO, FZD3, FZD6, GRLF1, HIPK2, IRX3, IRX5, ITGA3, ITGA6, PFN1, PLXNB2, PTGS1, PTGS2, PTK7, RGMA, TRAF6, TSC2,	25
cell division process of bone cancer cell lines	2.71E-03	BHLHE40, CCND1, CCNE1, CCNG1, CDC25A, CDK6, CDK5RAP3 (includes EG:80279), CDKN1A, CDKN2C, DUSP1, E2F1, EGF, GJA1, GPS2, IGF2, LATS1, MAP2K6, MNAT1, MTBP, MYBL2, PKMYT1, RBL1, RPL23, TOPBP1, TP53BP1	25

morphogenesis of skeleton	3.46E-03	ACVR2B, CHST11, EYA1, FMN1, FOXC2, HOXA2, HOXA5, HOXA7, HOXB4, HOXB5, HOXB6, HOXD3, HOXD4, HOXD8, HOXD10, HSPG2 (includes EG:3339), OSR2, PRKRA, PRRX1, PRRX2, RECQL4, RYK, TBX4, TFAP2A, WNT9A	25
developmental process of breast cell lines	1.30E-03	AREG, BCL2L11, C8ORF4, CCND1, CDK2, CHKA, DAB2, EGF, EGFR, EPHA2, ETS2, GAS6, HAS2, HRAS, HSPB8, IER3, IGF2, NOTCH1, NOTCH4, RELB, SPP1, STAT3,	24
retraction of plasma membrane projections	2.25E-03	BCAR1, BDNF, CRK, F2R, GNAQ, GPI, GSN, HGF, HRAS, IL6ST, ITGA3, LIF, LPAR4, MSN, MYH9, OTX1, RDX, RICS, RRAD, RRAS, RYK, SEMA3A, SEMA3D, TIAM1	24
adenomyosis	3.75E-03	AIG1, CBX6, CD14, DST, ESR1, GPI, GPX1, HBA2, IL15, IQGAP1, LGMN, MFAP3L, MTHFD2, NFIC, NME7, PDS5B, PEG3, PMEPA1, PRDX5, RHOU, STX7, TBL1X, THBS1,	24
metastasis of cells	4.76E-03	ARHGDIG, ATF2, ATF3, CD44, CD151, CD274, COL18A1, CXCL2, EGF, ENPP2, F2R, FIGF, HGF, HTATIP2, IGF2BP1, ITGB4, LAMA5, MAPK1, NFKBIA, NFKBIB, SOCS1,	24
development of extraembryonic tissue	5.99E-03	ACVR1B, ADAMTS1, APH1A (includes EG:226548), BMP4, CCNF, COL18A1, ENPP2, ETV6, FGF13, FOXO1, GATA6, HGF, MMP2, NRP1, NRP2, PTEN, PTPN11, PTX3, SFRS5, SMAD2, TFDP1, THBS1, TIMP3, VEGFA	24
differentiation of tissue	5.99E-03	BMP4, CDKN1A, CUL7 (includes EG:9820), DAB2, DPPA4, EGFR, ETS2, EXT2, FEM1C, FOSL2, HRAS, KLF5, LIF, MEOX2, MSX1, NDRG1, PDK4, PEG3, PRKG2, RARG, SGPL1,	24
nuclear export	5.99E-03	AGFG1 (includes EG:3267), ANP32A, BAT1, CAMK1, CCHCR1, DDX19B, EIF5A, HHEX, HSPA9, KHDRBS1, LSG1, MALT1, NUDT4, NUP50, NUP98, NUP107, NUPL2, PTPN11, RANGRF, SMG6, XPO5, XPO6, XPO7, XPOT	24
re-entry into cell division process of cells	5.99E-03	BCL2, BRCA2, CAST, CCND1, CCNE1, CCNF, CDC25A, CDC25C, CDKN1A, CDKN1B, CDKN2D, E2F1, E2F2, EGF, EGFR, FOXO3, GAS6, HMG20B, ID1, ID2, ID3, RBL1, SKP2,	24
pancreatic adenocarcinoma	4.43E-06	CD59, CDKN1A, COPS5, CTSD, CYR61, HBEGF, HLA-G, IFITM1, ITGA3, ITGAE, ITGB4, KRT7, KRT10, MLL3, MSLN, PLAT, PLAU, PTEN, PTGES, RELA, RRM2, SPP1, TIMP1	23
angiogenesis of tumor	1.83E-04	ADAM17, ANGPTL4, BCL2, CDH5, COL18A1, CTSB, EPHA2, FGFR2, HGF, HRAS, IL18, ITGB5, MMP2, MMP3, MMP14, NRP1, PGF, THBS1, THBS2, TIMP1, VASH1, VEGFA,	23
neurological disorder of tissue	1.83E-03	B4GALNT1, BACE1, BCL2, C3, CCL5, CREB1, CXCL10, DAG1, EIF2AK3, HTT, IL18, ITGB4, LPAR1, MYD88, NDRG1, PITPNA, PLAT, PMP22, SNCA, SPG7, SPHK1, SPP1,	23
infiltrating duct breast carcinoma	2.41E-03	AGPAT2, CCND1, COX4I1, CP110, CSPP1, DDHD2, DDX19B, EPHA2, EYA1, FAM96B, GSPT1, ING4, MT1E, MT1F, PPFIA1, RBM4B, SAT2, SERPINF1, STAU2, TNXB, TPD52,	23
cell death of gonadal cell lines	5.17E-03	ANTXR1, ANTXR2, BTC, CASP8, CCL5, CDKN1A, DDIT3, DUSP1, EGF, GHR, HRAS, ITGA5, MAP3K11, MCL1, MGMT, PAK2, PDIA3, PLD1, PLSCR1, POLB, SGMS1, SGMS2,	23
growth of breast cell lines	3.07E-05	AREG, BCL2L11, C8ORF4, CCND1, CDK2, EGF, EGFR, EPHA2, ETS2, GAS6, HAS2, HRAS, HSPB8, IER3, IGF2, NOTCH1, NOTCH4, RELB, SPP1, STAT3, TGFBR3, TIMP2	22
morphogenesis of embryonic tissue	1.06E-03	ACVR2B, AREG, CX3CL1, EGFR, FGF10, FTO, GATA4, GDNF, GREM1, HOXD13, IL11, INSR, IRX3, IRX5, MEOX2, NOTCH1, ROR2, SMAD2, TBX3, TCF7, TGFB2, TIMP2	22
disease of carcinoma	2.57E-03	ARRB2, ATF2, BRCA2, CDKN1B, E2F1, EGR1, HGF, HIP1, HRAS, ITGB5, MMP3, MMP14, PTEN, PTGS2, PTPN1, SOCS1, SOCS3, STAT3, STX2, TGFBR2, VEGFA,	22
re-entry into cell division process of eukaryotic cells	2.57E-03	BCL2, BRCA2, CAST, CCND1, CCNE1, CCNF, CDC25A, CDC25C, CDKN1A, CDKN1B, CDKN2D, E2F1, E2F2, EGFR, FOXO3, GAS6, HMG20B, ID1, ID2, ID3, RBL1, SKP2	22

cardiomyopathy of mice	5.61E-03	ACSL1, ANGPT2, BNIP3L, CACNB2, CASP8, CAST, CREB1, DICER1, DYSF, GNAQ, INSR, LMNA, LTBP4, MAP2K5, PPP1CA, PTPN11, RCE1, RXRA, SGCB, SOD2, TNNT2,	22
formation of epithelial tissue	5.61E-03	ADAM15, ANTXR2, ARHGAP22, ARHGAP24, ATF3, BDNF, CBFB, CD44, COL18A1, COL4A2, CX3CL1, CXCL12, FGF13, MMP14, PLAU, PLAUR, PTEN, PTK2B, PTN, SDC2,	22
migration of brain cancer cell lines	1.72E-04	BCAR1, C5ORF13, CRK, CXCL12, EGF, EGR1, ENPP2, GAS6, HGF, LPAR1, MAPK8IP3, MMP14, PLAU, PLAUR, PTEN, PTN, PVR, SEMA3F, SIRPA, VEGFA, VEGFC	21
sprouting of eukaryotic cells	2.59E-04	ANGPT2, ANGPTL2, BCL2, BDNF, CDK5R1, COL18A1, CYR61, DCN, DICER1, EPHB4, GAP43, GDNF, NAB2, NDST1, REM1, RNASEN, RTN4, SPP1, THBS1, VEGFA, VEGFC	21
S phase of fibroblast cell lines	3.82E-04	ARAF, BID, CCND1, CCNE1, CDC25A, CDKN1B, COPS5, DDX3X, DMTF1, E2F1, E2F2, E2F3, E2F6, EGF, GADD45A, GATA6, IRS1, PPAP2C, PTPN11, RBL1, SKP2	21
arrest in cell division process of connective tissue cells	7.84E-04	ATF2, CCND1, CDC25C, CDKN1A, CDKN1B, E2F1, E2F2, E2F3, FANCA, FANCC, GADD45A, HRAS, IGFBP7, MAP2K6, MBD4, MYBL2, PARP2, RELA, SKP2, TFDP1,	21
cell stage of bone cancer cell lines	7.84E-04	BHLHE40, CCND1, CCNE1, CDC25A, CDK6, CDK5RAP3 (includes EG:80279), CDKN1A, DUSP1, E2F1, GJA1, GPS2, LATS1, MAP2K6, MNAT1, MTBP, MYBL2, PKMYT1, RBL1, RPL23, TOPBP1, TP53BP1	21
development of endothelial cells	7.84E-04	COL18A1, CXCL2, EFNB2, ENG, EPHB4, FGF13, GPX1, HGF, MEOX2, NOTCH1, NOTCH4, PTK2B, RELA, SEMA3A, STC1, THBS1, TIMP2, VASH1, VCAM1, VEGFA,	21
formation of endothelial tube	1.51E-03	ADAM15, ARHGAP22, ARHGAP24, ATF3, BDNF, CBFB, CD44, COL18A1, COL4A2, CX3CL1, CXCL12, FGF13, MMP14, PLAU, PLAUR, PTEN, PTK2B, PTN, SDC2, TGFBR2,	21
skeletal and muscular process of tissue	1.51E-03	ACVR1, ADRB2, BCL2, BMP4, CD9, CD81, E2F1, EGFR, EGR2, ENPP1, FGFR2, FOSL2, GAA, GJA1, MMP13, MMP14, PTK2B, RBL1, RSAD2, SMURF1, STAT1	21
neurological disorder of nervous tissue	2.74E-03	B4GALNT1, BACE1, BCL2, C3, CCL5, CREB1, CXCL10, DAG1, EIF2AK3, HTT, IL18, ITGB4, LPAR1, MYD88, NDRG1, PITPNA, PLAT, PMP22, SPG7, SPP1, TLR2	21
mineralization of bone	3.62E-03	ACVR1, ACVR2B, ADRB2, ANKH, BMP4, CD276, EIF2AK3, EN1, ENPP1, ERCC2, ESR1, FETUB, FGFR2, GLA, MMP13, PHEX, PTHLH, PTN, SOX9, TNFRSF11B, VDR	21
development of hair follicle	4.72E-03	ACVR1B, ATP7A, BCL2, CCND1, E2F1, EGF, EGFR, FOXQ1, FST, GFRA1, HGF, LRP4, NOTCH1, NSDHL, PTGS2, PTHLH, RELA, SGK3, SOX9, TGFB2, TRAF6	21
tumorigenesis of carcinoma	4.72E-03	ARRB2, ATF2, BRCA2, CDKN1B, E2F1, EGR1, HGF, HIP1, HRAS, ITGB5, MMP3, MMP14, PTEN, PTGS2, PTPN1, SOCS1, SOCS3, STAT3, STX2, TGFBR2, WNT10B	21
angiogenesis of cells	6.43E-05	CCL13, CD151, COL18A1, CTSB, DGKA, ECT2, FGF13, FIGF, LAMA5, MEOX2, PLAUR, SEMA3A, SMOC2, TGFB2, THBS1, THBS2, TIMP2, VASH1, VEGFA, VEGFC	20
migration of colon cancer cell lines	1.63E-04	BCAR1, CD44, CD82, CRK, CRKL, CXCL10, EFNB1, EGFR, HGF, IGF2, IGFBP4, ING4, ITGA6, ITGB4, KLF4, PPFIA1, PTPN11, PTPN12, ST6GAL1, VEGFA	20
arrest in cell division process of fibroblasts	3.75E-04	ATF2, CCND1, CDC25C, CDKN1A, CDKN1B, E2F1, E2F2, E2F3, FANCA, FANCC, GADD45A, HRAS, MAP2K6, MBD4, MYBL2, PARP2, RELA, SKP2, TFDP1, XRCC6	20
disease of mammary gland	3.75E-04	BRCA2, BTRC, CCND1, CDC25A, CDK2, CDKN1B, EGFR, ESR1, HGF, HRAS, MFGE8, MMP3, MMP14, NOTCH1, PAK1, PTEN, PTGER2, PTGS2, PTPRE, TIMP1	20
cardiovascular process of cornea	1.57E-03	ADAMTS1, ANGPTL4, CCL13, CDH5, COL18A1, CSPG4, CYR61, EGF, EPHA2, FGF13, FIGF, HGF, IGF2, IL18, PRL2C2, SERPINF1, THBS1, VCAM1, VEGFA, VEGFC	20

initiation of cell division process of cells	1.57E-03	BLNK, CCND1, CCNE1, CDK2, CDK6, CDKN1A, CDKN1B, COPS5, CXCL12, E2F1, E2F2, E2F3, E2F6, GAB1, GATA6, IRS1, NOTCH1, PDGFRA, PTPN2, SKP2	20
cell cycle progression of connective tissue cells	2.15E-03	BCL2, CCND1, CCNF, CDC25C, CDKN1A, CDKN1B, E2F1, FANCA, FANCC, GADD45A, HRAS, ID2, IGF2, INSR, JUNB, PARP2, RBL1, SKP2, TFDP1, XRCC6	20
development of metanephros	2.90E-03	APH1A (includes EG:226548), AREG, BCL2, BDNF, BMP4, CX3CL1, EYA1, FGFR1, FGFR2, FOXC2, GDNF, GPC3, GREM1, HOXA11, IL11, INSR, NF1, OSR1, SLIT2, TIMP2	20
closure of neural tube	5.07E-03	BCL10, CFL1, CREBBP, DLC1, ENAH, FTO, FZD3, FZD6, GRLF1, IRX3, IRX5, ITGA3, ITGA6, PFN1, PLXNB2, PTK7, RGMA, TRAF6, TSC2, VANGL2	20
S phase of fibroblasts	1.50E-04	CCND1, CCNE1, CDC7, CDK2, CDKN1A, CDKN1B, E2F1, E2F2, E2F3, GAB1, GRB10, ID2, ID3, IRS1, JUNB, PLK2, SKP2, TFDP1, TFE3	19
tubulation of endothelial cell lines	1.50E-04	ALCAM, ALOX12, BTC, CDH5, CLIC4, COL1A1, CXCL12, CYR61, EGF, FES, FOXO1, FOXO3, HGF, ID1, ID3, NAB2, PTN, SLIT2, VEGFA	19
interphase of bone cancer cell lines	2.37E-04	BHLHE40, CCND1, CCNE1, CDC25A, CDK6, CDK5RAP3 (includes EG:80279), CDKN1A, DUSP1, E2F1, GJA1, GPS2, MAP2K6, MNAT1, MTBP, MYBL2, RBL1, RPL23, TOPBP1,	19
initiation of cell stage of cells	1.15E-03	CCND1, CCNE1, CDK2, CDK6, CDKN1A, CDKN1B, COPS5, CXCL12, E2F1, E2F2, E2F3, E2F6, GAB1, GATA6, IRS1, NOTCH1, PDGFRA, PTPN2, SKP2	19
proliferation of chondrocytes	1.62E-03	CCND1, CDKN1A, CTGF, DICER1, FOSL2, GABBR1, GDF5, GGT1, GHR, IL18, IRS1, NFKB2, PPBP, PRKG2, PTHLH, RBL1, RELA, STAT1, STC1	19
formation of membrane ruffles	2.24E-03	ARHGAP24, ARHGEF2, BCAR1, CCND1, COL18A1, EGF, FLNA, GAS6, ITGA6, ITGB4, LTBP2, PAK1, PIP5K1B, PLEKHA1, RICS, RND1, SNTA1, USP6NL, VAV3	19
cell spreading of tumor cell lines	4.11E-03	BCL10, EGF, GAP43, ING4, ITGA5, MPRIP, PAK1, PFN1, PLAU, PPFIA1, PTPN14, PVR, SIRPA, SNAI2, SPHK1, TESK1, THBS1, TIAM1, VCAM1	19
cell movement of endothelial cells	5.44E-03	ANGPT2, CD81, CD151, CSPG4, CXCL12, DGKA, FGFR1, HGF, IGF2R, ITGA3, ITGA5, ITGA6, PDGFRA, PRL2C2, SEMA3A, SEMA3F, THBS1, VEGFA, VEGFC	19
invasion of melanoma cell lines	4.67E-05	BCAR1, BMP4, CD151, CHRD, CSPG4, CTSB, CXCL12, ENPP2, HGF, LAMA5, MMP2, MMP14, MMP16, PTEN, RHOC, SDCBP, SPP1, STAT3	18
disease of epidermis	3.44E-04	BCL2, CCND1, COL17A1, E2F1, KRT10, NFKBIA, NOTCH1, PPARD, PTEN, PTGS2, RARG, RBL1, RELB, TGFBR2, TNFRSF1A, VEGFA, XPA, XPC	18
cell cycle progression of fibroblasts	1.15E-03	BCL2, CCND1, CCNF, CDC25C, CDKN1A, CDKN1B, FANCA, FANCC, GADD45A, HRAS, ID2, IGF2, INSR, JUNB, PARP2, RBL1, SKP2, XRCC6	18
cell death of organ	1.15E-03	AKT3, CD14, FBN1, GSTZ1 (includes EG:2954), MAP2K5, MED1, MT1E, MT1F, NFE2L1, PTPN1, RXRA, SCG5, SIGIRR, SOCS1, SOD2, STAT1, STAT3, TRAF1	18
skeletal and muscular process of bone	3.21E-03	ACVR1, ADRB2, BCL2, BMP4, CD9, CD81, E2F1, EGR2, ENPP1, FGFR2, GJA1, MMP13, MMP14, PTK2B, RBL1, RSAD2, SMURF1, STAT1	18
attachment of cell lines	4.35E-03	ADAM15, BTC, CD44, CDH13, EFNB1, EGF, EGFR, EGR1, IGF2, ITGA3, ITGA5, ITGA6, LOX, LRP1, PLAU, PLAUR, PLD1, PTGER2	18
cell death of sensory neurons	7.68E-04	BCL2, BDNF, CASP9, CDK5, CDKN2D, CREB1, DLX1, DLX2, GJB2, HIPK2, HTT, KLF7, LRP1, LRPAP1, NFKBIA, PRNP, RELA	17
re-entry into cell division process of cell lines	1.67E-03	BRCA2, CAST, CCND1, CCNE1, CDC25A, CDC25C, CDKN1B, E2F1, E2F2, EGFR, FOXO3, GAS6, HMG20B, ID1, ID2, ID3, SKP2	17

sprouting of normal cells	1.67E-03	ANGPT2, BCL2, BDNF, CDK5R1, COL18A1, CYR61, DCN, EPHB4, GAP43, GDNF, NAB2, NDST1, REM1, RTN4, SPP1, VEGFA, VEGFC	17
morphogenesis of normal cells	2.39E-03	BDNF, COL18A1, CXCL2, EFNB2, EPHB4, GAB1, HGF, NFKB2, NOTCH1, NOTCH4, PTK2B, PVRL2, RELA, SLC1A3, SPR, STC1, VCAM1	17
ossification of tissue	6.19E-03	ACVR1, ADRB2, BCL2, BMP4, E2F1, EGFR, EGR2, ENPP1, FGFR2, FOSL2, GJA1, MMP13, MMP14, PTK2B, RBL1, RSAD2, SMURF1	17
attachment of tumor cell lines	4.63E-04	ADAM15, CD44, CDH13, EFNB1, EGF, EGFR, EGR1, IGF2, ITGA3, ITGA5, ITGA6, LRP1, PLAU, PLAUR, PLD1, PTGER2	16
hyperproliferation of epidermis	7.30E-04	BCL2, CCND1, E2F1, NFKBIA, NOTCH1, PPARD, PTEN, PTGS2, RARG, RBL1, RELB, TFAP2A, TGFBR2, TNFRSF1A, XPA, XPC	16
development of metanephric bud	1.12E-03	AREG, BCL2, BDNF, BMP4, CX3CL1, EYA1, FGFR1, FGFR2, FOXC2, GDNF, GPC3, GREM1, HOXA11, IL11, SLIT2, TIMP2	16
moiety attachment of essential amino acids	1.67E-03	ACVR1B, BCL2, CDK5, DUSP1, HK1, MAPK1, MYLK, PLOD3, PRMT3, PRMT7, SBK1, SGK1, SGK3, SUV39H1, TNKS, TTK	16
initiation of cell division process of eukaryotic cells	2.42E-03	BLNK, CCND1, CCNE1, CDK2, CDK6, CDKN1A, CDKN1B, COPS5, E2F1, E2F2, E2F3, E2F6, GAB1, GATA6, IRS1, SKP2	16
G2 phase of normal cells	4.80E-03	ATF2, CCNG2, CDC25C, ERCC1, FANCC, GADD45A, GPC1, GRB10, HMGN1, IRS1, JUNB, MAP2K6, MBD4, MYBL2, RELA, XPC	16
initiation of S phase of eukaryotic cells	7.35E-05	CCND1, CCNE1, CDK2, CDK6, CDKN1A, CDKN1B, COPS5, E2F1, E2F2, E2F3, E2F6, GAB1, GATA6, IRS1, SKP2	15
cell movement of smooth muscle cells	1.07E-03	CCND1, ENPP2, HGF, IL6ST, LDLR, LOX, MMP2, PLAU, PLAUR, PTPN1, PTPN11, STAT3, THBS1, TRIB1, WISP2	15
hyperplasia of epidermis	1.07E-03	BCL2, CCND1, E2F1, NFKBIA, NOTCH1, PPARD, PTEN, PTGS2, RARG, RBL1, RELB, TGFBR2, TNFRSF1A, XPA, XPC	15
shape change of endothelial cells	1.07E-03	ANGPT2, BCL2, COL18A1, CRK, CYR61, DCN, EFNB1, EPHB4, NAB2, NDST1, PTK2B, REM1, SPP1, VEGFA, VEGFC	15
development of endothelial cell lines	1.63E-03	ATF3, CCL13, CD151, CDKN1B, COL18A1, CYR61, DGKA, ECT2, HGF, MMP2, PTEN, SMOC2, TFAP2A, TIMP2, VEGFA	15
branching of normal cells	2.43E-03	BDNF, BMP4, COL18A1, EGF, FGF10, GAS6, GDNF, HGF, HOXA11, NFKBIA, SMAD1, STX2, TIMP1, TIMP2, VEGFA	15
dilated cardiomyopathy of mice	3.52E-03	ACSL1, CASP8, CAST, CREB1, DICER1, GNAQ, INSR, LMNA, MAP2K5, PPP1CA, PTPN11, RCE1, RXRA, TNNT2, ZMPSTE24	15
entry into cell division process	1.03E-04	CCND1, CDK2, CDKN1A, CDKN1B, E2F1, E2F2, E2F3, ID3, JUNB, PLK2, RBL1, SKP2,	14
dwarfism of mice	9.86E-04	E2F1, EGFR, FGFR1, GGT1, HIP1, HIP1R, HOXA5, ITGA11, LIF, MAP2K6, PTHLH, ROR2, SMPD3, VEGFA	14
entry into cell stage of fibroblast cell lines	9.86E-04	ARAF, CCND1, CCNE1, CDC25A, CDK2, DDX3X, DMTF1, E2F1, E2F3, E2F6, EGF, PPAP2C, PTPN11, SKP2	14
morphology of connective tissue	9.86E-04	CCND1, FMR1, FOXC2, GSN, KIF3A, LTBP4, MMP2, PDGFRA, PRRX1, PRRX2, SMAD1, SOX9, TGFBR2, THBS1	14

entry into cell division process of fibroblast cell lines	1.56E-03	ARAF, CCND1, CCNE1, CDC25A, CDK2, DDX3X, DMTF1, E2F1, E2F3, E2F6, EGF, PPAP2C, PTPN11, SKP2	14
arrest in interphase of connective tissue cells	2.39E-03	ATF2, CCND1, CDC25C, CDKN1A, E2F1, E2F2, E2F3, GADD45A, IGFBP7, MAP2K6, MBD4, MYBL2, RELA, TFDP1	14
G1 phase of bone cancer cell lines	3.54E-03	CCND1, CCNE1, CDK6, CDK5RAP3 (includes EG:80279), CDKN1A, DUSP1, GJA1, GPS2, MNAT1, MTBP, MYBL2, RBL1, RPL23, TOPBP1	14
arrest in interphase of bone cancer cell lines	5.11E-03	CCND1, CCNE1, CDK5RAP3 (includes EG:80279), CDKN1A, DUSP1, GPS2, MAP2K6, MNAT1, MTBP, MYBL2, RBL1, RPL23, TOPBP1, TP53BP1	14
developmental process of	5.11E-03	ADA, CDKN1B, EGF, ENG, ERF, FGFR2, HBEGF, HOPX, JUNB, RXRA, SOX2, SP1, SRF,	14
emigration of leukocytes	5.11E-03	ANXA1, CCL13, CD44, CD99L2, CXCL2, CXCL12, CYTIP, F11R, LAMA5, RELA, SIRPA, SPP1, TNFRSF1A, VCAM1	14
binding of tumor cells	2.79E-04	CD14, CD44, CD47, CXCL12, DAG1, GFRA1, ITGA3, ITGA5, PDIA3, PLAUR, SEMA3B,	13
differentiation of embryonic tissue	8.76E-04	BMP4, CUL7 (includes EG:9820), DAB2, DPPA4, ETS2, FOSL2, HRAS, LIF, MEOX2, NDRG1, RARG, SGPL1, SPHK1	13
morphogenesis of cell lines	1.44E-03	CCND1, CD82, COL18A1, CRK, EGF, GAB1, GDNF, HGF, ITGA6, MMP2, PTEN, TFAP2A,	13
vascularization of cornea	1.44E-03	ADAMTS1, CCL13, COL18A1, CYR61, EGF, HGF, IGF2, IL18, PRL2C2, SERPINF1, THBS1, VEGFA, VEGFC	13
developmental process of	2.29E-03	BDNF, CDK5, CDON, EGR2, ITGA6, LAMC1, MAP2K6, NAB1, NAB2, NF1, NFKBIA,	13
migration of cervical cancer cell lines	3.49E-03	CD151, CXCL2, CXCL12, DCBLD2, EGF, ESR1, GFER, HGF, MYO10, PLD1, SLC9A3R1, TFAP2A, WDR44	13
arrest in interphase of fibroblasts	5.17E-03	ATF2, CCND1, CDC25C, CDKN1A, E2F1, E2F2, E2F3, GADD45A, MAP2K6, MBD4, MYBL2, RELA, TFDP1	13
entry into S phase of	2.00E-04	CCND1, CDK2, CDKN1A, CDKN1B, E2F1, E2F2, E2F3, ID3, JUNB, PLK2, TFDP1, TFE3	12
cell division process of liver	3.97E-04	BCL2, CCND1, CCNE1, E2F2, EGF, EGR1, ERCC1, HGF, INSR, PTPRF, SKP2, VEGFA	12
cell death of liver	7.33E-04	CD14, GSTZ1 (includes EG:2954), MED1, MT1E, MT1F, NFE2L1, PTPN1, RXRA, SCG5, SIGIRR, SOCS1, SOD2	12
follicular thyroid carcinoma	7.33E-04	ADAMTS1, ANGPT2, EFNB2, EGFR, ENG, EPHB4, FGFR1, ITGA5, MMP2, PTTG1, SPP1,	12
endochondral ossification	1.28E-03	ATF2, COL1A1, CTGF, E2F1, HSPG2 (includes EG:3339), MEF2C, MMP14, NAB1, NAB2, PEX7, PTHLH, SMURF1	12
organization of collagen fibrils	1.28E-03	ADAMTS2, ATP7A, COL1A1, COL3A1, COL5A1, COL5A2, FOXC2, LOX, NF1, SERPINH1,	12
entry into S phase of fibroblast	2.12E-03	ARAF, CCND1, CDC25A, DDX3X, DMTF1, E2F1, E2F3, E2F6, EGF, PPAP2C, PTPN11,	12
formation of tumor cell lines	2.12E-03	CDKN1A, COL18A1, EGR1, FZD1, GNAO1, GNAQ, HRAS, KIF23, LIMK1, RGS12,	12
necrosis of organ	2.12E-03	CD14, GSTZ1 (includes EG:2954), MED1, MT1E, MT1F, NFE2L1, RXRA, SCG5, SIGIRR, SOCS1, SOD2, TRAF1	12
invasion of pancreatic cancer	3.36E-03	ADM, CTSD, EGF, EPHA2, GDNF, HGF, NRP1, PLAT, PLAU, SEL1L, TIMP1, TIMP2	12
sprouting of endothelial cells	3.36E-03	ANGPT2, BCL2, COL18A1, CYR61, DCN, EPHB4, NAB2, NDST1, REM1, SPP1, VEGFA,	12
phosphorylation of L-threonine	5.13E-03	ACVR1B, BCL2, CDK5, DUSP1, HK1, MAPK1, MYLK, SBK1, SGK1, SGK3, TNKS, TTK	12
shape change of epithelial	1.63E-05	CRK, CRKL, EGF, FBN1, FGFR1, GSN, HGF, ITGA3, LAMA5, STAT3, TIAM1	11
migration of microvascular	2.75E-04	ADM, COL18A1, EFNB2, FOXC2, GAB1, RECK, TGFBR2, TIMP1, TIMP2, VAV3, VEGFA	11

G2 phase of connective tissue	5.61E-04	ATF2, CDC25C, GADD45A, GRB10, HMGN1, IRS1, JUNB, MAP2K6, MBD4, MYBL2,	11
apoptosis of sensory neurons	5.61E-04	CASP9, CDKN2D, CREB1, DLX1, DLX2, HIPK2, KLF7, LRP1, LRPAP1, PRNP, RELA	11
binding of cancer cells	5.61E-04	CD44, CXCL12, DAG1, GFRA1, ITGA3, ITGA5, PDIA3, PLAUR, SEMA3B, THBS1, VCAM1	11
necrosis of liver	5.61E-04	CD14, GSTZ1 (includes EG:2954), MED1, MT1E, MT1F, NFE2L1, RXRA, SCG5, SIGIRR,	11
proliferation of neuronal	1.06E-03	BDNF, CDON, CFL1, CNR1, E2F1, E2F3, EGF, GDNF, NCAM1, VEGFA, WNT7B	11
morphogenesis of endothelial	1.87E-03	COL18A1, CXCL2, EFNB2, EPHB4, HGF, NOTCH1, NOTCH4, PTK2B, RELA, STC1,	11
morphology of bone	3.11E-03	CCND1, FMR1, FOXC2, KIF3A, MMP2, PDGFRA, PRRX1, PRRX2, SMAD1, TGFBR2,	11
trafficking of leukocytes	3.11E-03	ANXA1, AOC3, CCL5, CCL13, CD44, CXCL10, CXCL13, ENPP2, NEDD9, NT5E,	11
Ehlers-Danlos syndrome	5.64E-05	ADAMTS2, ADAMTS4, ATP7A, COL1A1, COL3A1, COL5A1, COL5A2, TNXB, ZMPSTE24,	10
chemotaxis of neurons	1.57E-04	BDNF, CXCL12, EFNB1, GDNF, GFRA1, NRP2, RGS3, SEMA3A, SEMA3F, SLIT2	10
G2 phase of fibroblasts	7.90E-04	ATF2, CDC25C, GADD45A, GRB10, HMGN1, JUNB, MAP2K6, MBD4, MYBL2, RELA	10
initiation of S phase of cell	7.90E-04	CDK6, CDKN1A, CDKN1B, COPS5, E2F1, E2F2, E2F3, E2F6, GATA6, IRS1	10
cell division process of	1.53E-03	BCL2, CCND1, CCNE1, E2F2, EGF, ERCC1, HGF, INSR, PTPRF, SKP2	10
expression of E2F binding site	2.73E-03	CCND1, E2F1, E2F2, E2F3, E2F6, RBL1, REEP5, SP1, TFDP1, TFDP2	10
gastrulation of mice	2.73E-03	ACVR1, DAB2, EXT2, HTT, LAMA5, NUP98, SCXB, SMAD2, SRF, TJP2	10
hyperactive behavior of mice	2.73E-03	BDNF, CLOCK, DKK3, FGFR1, FMR1, FXR2, GABBR1, HTT, LRP1, TGFBR2	10
size of thymus gland	4.59E-03	B4GALNT1, CCND1, CDKN1B, HOXA9, JAK3, MAD1L1, MGMT, MLH1, SOCS1, VCAM1	10
attachment of connective	1.91E-04	BCAR1, HRAS, LRP1, LRPAP1, MMP2, PTK2B, TGFBI, THBS2, TIMP2	9
chemotaxis of axons	1.91E-04	ARTN, BDNF, NRP1, NRP2, PICK1, SEMA3A, SEMA3B, SEMA3F, SLIT2	9
neurological disorder of nerves	2.20E-03	B4GALNT1, BACE1, DAG1, ITGB4, MYD88, NDRG1, PMP22, SPG7, TLR2	9
transcription of E2F binding	2.20E-03	E2F1, E2F2, E2F3, E2F6, RBL1, REEP5, SP1, TFDP1, TFDP2	9
cell spreading of epithelial	2.16E-04	CRK, CRKL, FBN1, HGF, ITGA3, LAMA5, STAT3, TIAM1	8
attachment of fibroblasts	6.33E-04	BCAR1, HRAS, LRP1, LRPAP1, MMP2, TGFBI, THBS2, TIMP2	8
growth of fibrosarcoma cell	6.33E-04	CDKN1A, EGR1, HGF, IL18, PLAU, RELA, SDC2, STAT1	8
maturation of blood vessel	6.33E-04	ANGPT2, CDH5, ENPP2, ETV6, FOXO3, MMP2, RECK, VEGFA	8
chemotaxis of brain cells	1.52E-03	BDNF, CXCL12, EFNB1, NRP2, RGS3, SEMA3A, SEMA3F, SLIT2	8
survival of gonadal cell lines	1.52E-03	ANTXR1, ANTXR2, ATP7A, BCL2, ITGA5, MGMT, RAD51C, XRCC1	8
apoptosis of heart cell lines	5.88E-03	ANKRD1, BCL2, BNIP2, DDIT3, HGF, IL18, SPHK1, TXNIP	8
branching morphogenesis of	5.88E-03	CRK, EFNB2, EGF, EPHB4, GAB1, GDNF, HGF, NOTCH1	8
cell viability of neuroblastoma	5.88E-03	BCL2, DPP3, GPC1, HMOX1, P4HB, PRNP, SNCA, SQSTM1	8
proliferation of skin cancer cell	5.88E-03	CDKN1A, CDKN1B, CRK, EGF, HGF, PTCH1, PTGER2, THBS1	8
cell division process of kidney	7.62E-04	CDKN1A, CDKN1B, CXCL10, EGF, ITGB4, MAPK1, PTGS2	7
developmental process of	7.62E-04	BMP4, CUL7 (includes EG:9820), ETS2, F2RL1, MAPK1, NDRG1, PBRM1	7
activation of E2F binding site	2.04E-03	CDCA4, E2F1, E2F2, E2F3, E2F6, RBL1, TFDP1	7
developmental disorder of	2.04E-03	BTRC, CDKN1B, E2F1, EGFR, ESR1, FGF10, PAK1	7
diabetic retinopathy	2.04E-03	AKR1B1, HGF, PTGS1, PTGS2, SERPINF1, VCAM1, VEGFA	7
initiation of S phase of	2.04E-03	COPS5, E2F1, E2F2, E2F3, E2F6, GATA6, IRS1	7

neurological disorder of sciatic	2.04E-03	DAG1, ITGB4, MYD88, NDRG1, PMP22, SPG7, TLR2	7
quantity of caveolae	2.04E-03	DAB2, EGF, EGFR, HRAS, PIP5K1B, SYNJ2, VEGFA	7
G2/M phase transition of	4.49E-03	ATF2, CDC25C, GADD45A, IRS1, JUNB, MBD4, RELA	7
binding of vesicles	4.49E-03	ACTR1A, DCTN4, DCTN6, GGA2, MYO5A, RBP1, SNCA	7
development of lymphoid	4.49E-03	CXCL13, ID2, MAP3K14, NFKB2, RELA, RELB, TNFRSF1A	7
scattering of tumor cell lines	4.49E-03	CRK, EGF, EGFR, ETV5, GDNF, HGF, MMP14	7
transactivation of E2F binding	1.45E-04	CDCA4, E2F1, E2F2, E2F3, E2F6, TFDP1	6
apoptosis of germ cell tumor	8.13E-04	BCL2, CCNG1, CDKN1B, CXCL12, GATA4, MEF2C	6
cell division process of	8.13E-04	CDKN1B, CXCL10, EGF, ITGB4, MAPK1, PTGS2	6
degradation of Gelatin	8.13E-04	ADAM12, ADAM15, CSPG4, MMP14, MMP16, TIMP3	6
biosynthesis of chondroitin	2.62E-03	B4GALNT1, CHST3, CHST7, CHST11, CHST12, CSGALNACT1	6
cell movement of skin cancer	2.62E-03	CD151, EGF, FIGF, HGF, ITGA6, ITGB4	6
chemorepulsion of neurites	2.62E-03	NRP1, NRP2, SEMA3A, SEMA3B, SEMA3F, SLIT2	6
degeneration of myofiber	2.62E-03	CD9, CD81, CUGBP1, DTNA, PLAU, STRA13	6
initiation of S phase of	2.62E-03	CCND1, CCNE1, CDK2, GAB1, IRS1, SKP2	6
neurological process of brain	2.62E-03	BDNF, DLG4, MYO5A, RBL1, THBS1, THBS2	6
organic aciduria	2.62E-03	BCKDHA, BCKDHB, DBT, DLD, MLYCD, SOD2	6
shape change of dermal cells	2.62E-03	EGF, FBN1, GSN, ITGA3, STAT3, TIAM1	6
termination of cell cycle	2.62E-03	CDKN1A, CDKN1B, CDKN2C, E2F1, ID2, TFDP1	6
termination of cell division	2.62E-03	CDKN1A, CDKN1B, CDKN2C, E2F1, ID2, TFDP1	6
G0 phase of fibroblast cell	6.33E-03	BMP4, CCNE1, CDKN1A, CDKN1B, COPS5, PVR	6
G2/M phase transition of	6.33E-03	ATF2, CDC25C, GADD45A, JUNB, MBD4, RELA	6
adhesion of lung cancer cell	6.33E-03	ADAM9, B4GALT1, CXCL12, SEMA3F, THBS1, VCAM1	6
chemoattraction of neurons	6.31E-04	CXCL12, EFNB1, GDNF, GFRA1, RGS3	5
chemotaxis of skin cancer cell	6.31E-04	CD151, EGF, FIGF, ITGA6, ITGB4	5
cell cycle progression of	3.06E-03	CCND1, CCNE1, E2F2, EGF, SKP2	5
demyelination of nerves	3.06E-03	B4GALNT1, DAG1, ITGB4, NDRG1, PMP22	5
quantity of clathrin-coated pits	3.06E-03	DAB2, EGF, EGFR, PIP5K1B, SYNJ2	5
renal lesion	3.06E-03	EGFR, MT1E, MT1F, PLAT, TSC2	5
tubulo-interstitial fibrosis of	3.06E-03	C3, CD59A, MMP2, PTHLH, SKP2	5
assembly of sarcomere	2.76E-03	CAMK2D, GATA4, HBEGF, LIF	4
demyelination of sciatic nerve	2.76E-03	DAG1, ITGB4, NDRG1, PMP22	4
developmental process of	2.76E-03	E2F1, GAB1, SRF, STC1	4
differentiation of glial	2.76E-03	BMP4, EGFR, EIF2B5, NOTCH1	4
differentiation of primitive	2.76E-03	HRAS, RARG, SGPL1, SPHK1	4
differentiation of trophoblast	2.76E-03	BMP4, CUL7 (includes EG:9820), ETS2, NDRG1	4
formation of endodermal cells	2.76E-03	FZD1, GNAO1, GNAQ, SMAD2	4

hypoplasia of exocrine gland	2.76E-03	BTRC, CDKN1B, ESR1, FGF10	4
loss of mesencephalic neurons	2.76E-03	BDNF, CASP8, CASP9, GDNF	4
maple syrup urine disease,	2.76E-03	BCKDHA, BCKDHB, DBT, DLD	4
transformation of embryonic	2.76E-03	FGFR1, FGFR2, HAS2, HRAS	4

P -values are from IPA Tool. The criteria applied for the search of major biological function categories were maximum number of genes and the *P* -value of significa

Table S4: Gene sets Identified by GSEA

Specific genes enriched in *Klf4* -null MEFs

NAME	PROBE	RUNNING ES	CORE ENRICHMENT
BILE_ACID_BIOSYNTHESIS			
row_17	AKR1D1	-0.492	Yes
row_18	SOAT2	-0.471	Yes
row_19	ALDH2	-0.405	Yes
row_20	ADH7	0.001	Yes
ZUCCHI_EPITHELIAL_DN			
row_18	STRN4	-0.597	Yes
row_19	PPM1G	-0.591	Yes
row_20	PDLIM1	-0.550	Yes
row_21	ANXA1	-0.480	Yes
row_22	PICALM	-0.363	Yes
row_23	CXCL1	-0.195	Yes
row_24	AREG	0.001	Yes
CROONQUIST_IL6_RAS_U			
row_17	CCL4	-0.468	Yes
row_18	CCL5	0.001	Yes
HSA04640_HEMATOPOIETIC_CELL_LINEAGE			
row_57	ITGA6	-0.469	Yes
row_58	CSF1	-0.461	Yes
row_59	CD9	-0.459	Yes
row_60	CD44	-0.392	Yes
row_61	CD34	-0.310	Yes
row_62	ITGA5	-0.222	Yes
row_63	CD14	-0.123	Yes
row_64	ITGA3	0.005	Yes
BCRPATHWAY			
row_25	VAV1	-0.508	Yes
row_26	BTK	-0.507	Yes
row_27	RAC1	-0.484	Yes
row_28	MAPK3	-0.476	Yes
row_29	CALM2	-0.433	Yes
row_30	JUN	-0.387	Yes
row_31	PPP3CA	-0.335	Yes
row_32	BLNK	0.001	Yes
LEE_MYC_E2F1_DN			
row_44	ABCD3	-0.489	Yes
row_45	IGF1	-0.479	Yes
row_46	G0S2	-0.481	Yes
row_47	CYP7B1	-0.460	Yes

row_48	MCM10	-0.440	Yes
row_49	PXMP2	-0.421	Yes
row_50	ELOVL5	-0.396	Yes
row_51	RGS16	-0.326	Yes
row_52	EGFR	-0.206	Yes
row_53	NETO2	0.001	Yes

HSA04012_ERBB_SIGNALING_PATHWAY

row_67	EREG	-0.415	Yes
row_68	ERBB2	-0.408	Yes
row_69	CAMK2B	-0.410	Yes
row_70	AKT2	-0.402	Yes
row_71	MAP2K4	-0.386	Yes
row_72	MAPK3	-0.373	Yes
row_73	PAK3	-0.357	Yes
row_74	EIF4EBP1	-0.344	Yes
row_75	JUN	-0.328	Yes
row_76	SRC	-0.310	Yes
row_77	ARAF	-0.304	Yes
row_78	PAK1	-0.269	Yes
row_79	HBEGF	-0.209	Yes
row_80	EGFR	-0.137	Yes
row_81	AREG	0.000	Yes

ZHAN_PCS_MULTIPLE_MYELOMA_SPKD

row_16	IFIT3	-0.671	Yes
row_17	CTGF	-0.614	Yes
row_18	LGALS3BP	-0.484	Yes
row_19	TSPAN7	-0.257	Yes
row_20	AREG	0.000	Yes

HSA04140_REGULATION_OF_AUTOPHAGY

row_18	PRKAA1	-0.532	Yes
row_19	ULK2	-0.509	Yes
row_20	GABARAPL1	-0.463	Yes
row_21	PIK3R4	-0.389	Yes
row_22	ATG3	0.005	Yes

HSA04940_TYPE_I_DIABETES_MELLITUS

row_15	CPE	-0.377	Yes
row_16	FAS	-0.360	Yes
row_17	HSPD1	-0.336	Yes
row_18	ICA1	0.007	Yes

POMEROY_DESMOPLASIC_VS_CLASSIC_MD_DN

row_31	NUCB1	-0.430	Yes
row_32	SFRS2IP	-0.404	Yes
row_33	PSMB5	-0.347	Yes

row_34	CRABP2	0.000	Yes

LEE_MYC_TGFA_DN

row_45	G0S2	-0.535	Yes
row_46	CYP7B1	-0.516	Yes
row_47	MCM10	-0.500	Yes
row_48	PXMP2	-0.484	Yes
row_49	ELOVL5	-0.464	Yes
row_50	RGS16	-0.404	Yes
row_51	EGFR	-0.298	Yes
row_52	PTP4A3	-0.184	Yes
row_53	NETO2	0.001	Yes

HSA00760_NICOTINATE_AND_NICOTINAMIDE_METABOLISM

row_17	NT5C2	-0.620	Yes
row_18	NNMT	-0.478	Yes
row_19	ENPP1	-0.242	Yes
row_20	NT5E	0.007	Yes

CELL_MOTILITY

row_36	FLNA	-0.457	Yes
row_37	BCL9L	-0.451	Yes
row_38	ACTN4	-0.429	Yes
row_39	MSN	-0.411	Yes
row_40	F2R	-0.383	Yes
row_41	THBS1	-0.353	Yes
row_42	F11R	-0.330	Yes
row_43	ANXA1	-0.293	Yes
row_44	CTGF	-0.250	Yes
row_45	CXCL10	-0.194	Yes
row_46	ENPP2	-0.109	Yes
row_47	CCL5	0.002	Yes

TYROSINE_METABOLISM

row_24	ALDH3B1	-0.410	Yes
row_25	FAH	-0.308	Yes
row_26	ADH7	0.001	Yes

INFLAMMATORY_RESPONSE_PATHWAY

row_10	THBS1	-0.678	Yes
row_11	LAMC1	-0.564	Yes
row_12	LCK	-0.436	Yes
row_13	LAMA5	-0.264	Yes
row_14	COL3A1	0.011	Yes

HSA04060_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION

row_176	ACVR1B	-0.461	Yes
row_177	CCL27	-0.457	Yes

row_178	TSLP	-0.454	Yes
row_179	TNFSF4	-0.452	Yes
row_180	CSF1	-0.450	Yes
row_181	TNFSF11	-0.446	Yes
row_182	LTBR	-0.441	Yes
row_183	IL23A	-0.438	Yes
row_184	CXCR6	-0.433	Yes
row_185	IL17RA	-0.435	Yes
row_186	TGFB2	-0.434	Yes
row_187	EDA2R	-0.429	Yes
row_188	IL18RAP	-0.426	Yes
row_189	TGFB1	-0.420	Yes
row_190	TNFRSF10B	-0.413	Yes
row_191	ACVR1	-0.410	Yes
row_192	IL12RB1	-0.413	Yes
row_193	LIF	-0.401	Yes
row_194	TNFRSF9	-0.392	Yes
row_195	IFNGR1	-0.377	Yes
row_196	HGF	-0.362	Yes
row_197	CCL7	-0.346	Yes
row_198	VEGFA	-0.329	Yes
row_199	CX3CL1	-0.312	Yes
row_200	VEGFC	-0.288	Yes
row_201	EGFR	-0.262	Yes
row_202	CXCL10	-0.234	Yes
row_203	TGFBR2	-0.203	Yes
row_204	CXCL12	-0.168	Yes
row_205	IL6ST	-0.130	Yes
row_206	CCL2	-0.091	Yes
row_207	CXCL1	-0.047	Yes
row_208	CCL5	0.001	Yes

UVC_LOW_C2_DN

row_12	MYO10	-0.534	Yes
row_13	SLIT2	-0.362	Yes
row_14	CXCL12	0.004	Yes

CELL_SURFACE_RECEPTOR_LINKED_SIGNAL_TRANSDUCTION

row_98	ARHGEF2	-0.460	Yes
row_99	ISGF3G	-0.451	Yes
row_100	IL18RAP	-0.454	Yes
row_101	TNFRSF10B	-0.445	Yes
row_102	FLNA	-0.437	Yes
row_103	ECGF1	-0.428	Yes
row_104	IL12RB1	-0.416	Yes
row_105	LIF	-0.397	Yes
row_106	RAMP2	-0.380	Yes
row_107	HGF	-0.355	Yes

row_108	STC2	-0.330	Yes
row_109	STC1	-0.303	Yes
row_110	ANXA1	-0.274	Yes
row_111	CD14	-0.241	Yes
row_112	LY6E	-0.200	Yes
row_113	CXCL10	-0.157	Yes
row_114	ADRB2	-0.113	Yes
row_115	IL6ST	-0.057	Yes
row_116	CCL2	0.003	Yes

HSA04620_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY

row_73	RAC1	-0.500	Yes
row_74	CCL4	-0.495	Yes
row_75	NFKB1	-0.497	Yes
row_76	TLR8	-0.489	Yes
row_77	CHUK	-0.491	Yes
row_78	AKT2	-0.487	Yes
row_79	MAP2K4	-0.476	Yes
row_80	MAP2K3	-0.466	Yes
row_81	MAPK3	-0.455	Yes
row_82	IRAK1	-0.448	Yes
row_83	TRAF3	-0.435	Yes
row_84	JUN	-0.426	Yes
row_85	RELA	-0.416	Yes
row_86	CASP8	-0.405	Yes
row_87	TLR2	-0.396	Yes
row_88	SPP1	-0.375	Yes
row_89	NFKBIA	-0.358	Yes
row_90	NFKB2	-0.324	Yes
row_91	CD14	-0.277	Yes
row_92	MAPK12	-0.223	Yes
row_93	CXCL10	-0.166	Yes
row_94	MAPK13	-0.094	Yes
row_95	CCL5	0.001	Yes

HSA04340_HEDGEHOG_SIGNALING_PATHWAY

row_41	CSNK1G1	-0.586	Yes
row_42	STK36	-0.586	Yes
row_43	RAB23	-0.586	Yes
row_44	GLI3	-0.580	Yes
row_45	SUFU	-0.567	Yes
row_46	PTCH1	-0.552	Yes
row_47	WNT3A	-0.532	Yes
row_48	BTRC	-0.530	Yes
row_49	WNT10A	-0.496	Yes
row_50	WNT10B	-0.426	Yes
row_51	WNT9A	-0.321	Yes
row_52	BMP4	-0.164	Yes

row_53	WNT7B	0.002	Yes

GO_ROS

row_22	LTC4S	-0.524	Yes
row_23	STK25	-0.488	Yes
row_24	PDLIM1	-0.416	Yes
row_25	DUSP1	-0.279	Yes
row_26	CCL5	0.001	Yes

LEE_E2F1_DN

row_43	MCM10	-0.485	Yes
row_44	PXMP2	-0.473	Yes
row_45	ELOVL5	-0.457	Yes
row_46	ITPR1	-0.424	Yes
row_47	GSTO1	-0.386	Yes
row_48	EGFR	-0.305	Yes
row_49	PPCS	-0.166	Yes
row_50	NETO2	0.001	Yes

Specific genes enriched in wild type MEFs

PROSTAGLANDIN_AND_LEUKOTRIENE_METABOLISM

row_0	PTGIS	0.276	Yes
row_1	CBR3	0.497	Yes
row_2	PTGS1	0.628	Yes

INTRINSICPATHWAY

row_0	PROS1	0.255	Yes
row_1	COL4A6	0.502	Yes
row_2	COL4A5	0.659	Yes

HSA04612_ANTIGEN_PROCESSING_AND_PRESENTATION

row_0	TAP2	0.277	Yes
row_1	LGMN	0.401	Yes
row_2	PSME1	0.432	Yes
row_3	TAP1	0.448	Yes
row_4	CIITA	0.480	Yes
row_5	HSP90AA1	0.514	Yes

LAL_KO_3MO_UP

row_0	PLA2G7	0.221	Yes
row_1	GPNMB	0.426	Yes
row_2	TREM2	0.487	Yes
row_3	FKBP5	0.478	Yes
row_4	SLC40A1	0.507	Yes

GH_AUTOCRINE_UP

row_0	ID3	0.053	Yes

row_1	SCAMP5	0.104	Yes
row_2	ALCAM	0.154	Yes
row_3	IGFBP7	0.193	Yes
row_4	COL4A6	0.232	Yes
row_5	TLE2	0.267	Yes
row_6	BLVRB	0.295	Yes
row_7	GRIA1	0.324	Yes
row_8	SFXN5	0.344	Yes
row_9	ID1	0.368	Yes
row_10	PPA2	0.386	Yes
row_11	VTI1A	0.391	Yes
row_12	UQCR	0.394	Yes
row_13	ADK	0.408	Yes
row_14	MOBKL2B	0.420	Yes
row_15	SPATA7	0.429	Yes
row_16	MRPL28	0.431	Yes
row_17	SH3KBP1	0.439	Yes
row_18	CFL2	0.442	Yes
row_19	BSG	0.444	Yes
row_20	MOGAT2	0.451	Yes
row_21	SSR4	0.459	Yes
row_22	SAR1B	0.465	Yes
row_23	PIR	0.467	Yes
row_24	AXL	0.469	Yes
row_25	GMPR	0.475	Yes
row_26	PSMB2	0.481	Yes
row_27	SLC43A1	0.485	Yes
row_28	GPR12	0.482	Yes
row_29	G3BP	0.488	Yes

HSA02010_ABC_TRANSPORTERS_GENERAL

row_0	TAP2	0.192	Yes
row_1	ABCD4	0.294	Yes
row_2	ABCA3	0.353	Yes
row_3	ABCC10	0.418	Yes
row_4	ABCC5	0.465	Yes
row_5	ABCC3	0.503	Yes
row_6	ABCA7	0.534	Yes
row_7	TAP1	0.540	Yes

IL2RBPATHWAY

row_0	JAK3	0.217	Yes
row_1	SOCS3	0.274	Yes
row_2	MAPK1	0.353	Yes
row_3	SOCS1	0.429	Yes
row_4	IRS1	0.499	Yes
row_5	CRKL	0.545	Yes

SMITH_HCV_INDUCED_HCC_UP

row_0	GSTA4	0.309	Yes
row_1	SDHC	0.378	Yes
row_2	PMVK	0.386	Yes
row_3	PDCD5	0.416	Yes
row_4	PIR	0.450	Yes
row_5	IMPA2	0.469	Yes
row_6	COPS5	0.485	Yes
row_7	ANXA7	0.510	Yes
row_8	NOLA2	0.523	Yes

HOX_GENES

row_0	HOXD4	0.092	Yes
row_1	HOXB5	0.176	Yes
row_2	HOXA5	0.251	Yes
row_3	HOXA2	0.319	Yes
row_4	MEIS1	0.376	Yes
row_5	PRRX1	0.414	Yes
row_6	HOXA7	0.461	Yes
row_7	HOXD3	0.500	Yes

NI2_LUNG_DN

row_0	TRAP1	0.257	Yes
row_1	CEBPD	0.470	Yes
row_2	ABCC3	0.584	Yes
row_3	LGTN	0.639	Yes
row_4	HSP90AA1	0.702	Yes

MAGRANGEAS_MULTIPLE_MYELOMA_IGL_VS_IGK_DN

row_0	GSTM5	0.178	Yes
row_1	TJP2	0.328	Yes
row_2	SMARCA1	0.407	Yes
row_3	CSNK2A2	0.466	Yes
row_4	UBE4A	0.503	Yes

HSA04630_JAK_STAT_SIGNALING_PATHWAY

row_0	JAK3	0.054	Yes
row_1	SOCS2	0.111	Yes
row_2	IL11	0.166	Yes
row_3	OSMR	0.214	Yes
row_4	STAT3	0.253	Yes
row_5	IFNGR2	0.270	Yes
row_6	SOCS3	0.281	Yes
row_7	CCND2	0.300	Yes
row_8	SOCS1	0.319	Yes
row_9	CTF1	0.338	Yes
row_10	SOCS5	0.358	Yes
row_11	GHR	0.369	Yes

row_12	PIK3R2	0.382	Yes
row_13	CISH	0.392	Yes
row_14	SPRY4	0.406	Yes
row_15	IL15	0.398	Yes
row_16	SPRY3	0.408	Yes
row_17	STAT1	0.418	Yes
row_18	CCND1	0.426	Yes
row_19	PIAS4	0.429	Yes
row_20	AKT3	0.435	Yes
row_21	CREBBP	0.441	Yes
row_22	PIK3R5	0.437	Yes
row_23	GRB2	0.442	Yes
row_24	LEPR	0.449	Yes
row_25	IFNAR2	0.440	Yes
row_26	PIAS3	0.438	Yes
row_27	JAK2	0.443	Yes
row_28	EPO	0.448	Yes
row_29	CBLB	0.447	Yes
row_30	TYK2	0.451	Yes

GLUTATHIONE_METABOLISM

row_0	GSTA4	0.165	Yes
row_1	GSTM2	0.297	Yes
row_2	IDH1	0.384	Yes
row_3	GSTM5	0.469	Yes
row_4	GSTM1	0.555	Yes
row_5	GSTZ1	0.625	Yes
row_6	GSTO2	0.699	Yes

HSA03022_BASAL_TRANSCRIPTION_FACTORS

row_0	GTF2H4	0.132	Yes
row_1	GTF2F2	0.182	Yes
row_2	TAF13	0.264	Yes
row_3	TBPL2	0.333	Yes
row_4	GTF2E1	0.375	Yes
row_5	TAF7L	0.420	Yes
row_6	TAF9B	0.466	Yes
row_7	GTF2I	0.511	Yes
row_8	GTF2H3	0.528	Yes
row_9	TAF6L	0.562	Yes
row_10	GTF2A1	0.583	Yes

SPPAPATHWAY

row_0	PTGS1	0.273	Yes
row_1	GNB1	0.391	Yes
row_2	MAPK1	0.500	Yes

TNFALPHA_TGZ_ADIP_DN

row_0	IDH1	0.218	Yes
row_1	ALAD	0.362	Yes
row_2	RGS2	0.495	Yes
row_3	IDH3G	0.591	Yes
row_4	CDKN2C	0.662	Yes

ADIP_HUMAN_UP

row_0	ADORA2B	0.136	Yes
row_1	ALDH6A1	0.247	Yes
row_2	LPL	0.345	Yes
row_3	RXRA	0.383	Yes
row_4	ACSL1	0.381	Yes
row_5	CRYAB	0.410	Yes
row_6	PFKFB3	0.437	Yes
row_7	LYPLA1	0.465	Yes
row_8	RXRB	0.469	Yes
row_9	KCNH2	0.483	Yes
row_10	LBP	0.476	Yes
row_11	CTSG	0.464	Yes
row_12	GPD1	0.475	Yes
row_13	DGAT1	0.482	Yes
row_14	PLCD1	0.490	Yes
row_15	ATP8A2	0.496	Yes
row_16	ABCE1	0.499	Yes
row_17	FABP5	0.493	Yes
row_18	SMARCB1	0.499	Yes

ERKPATHWAY

row_0	STAT3	0.180	Yes
row_1	PDGFRA	0.290	Yes
row_2	GNB1	0.401	Yes

BRCA1_SW480_DN

row_0	GRB10	0.390	Yes
row_1	COL16A1	0.462	Yes
row_2	RXRB	0.475	Yes
row_3	BAX	0.486	Yes
row_4	SEMA3B	0.515	Yes
row_5	GRB2	0.537	Yes
row_6	PIN1	0.555	Yes

NF90_DN

row_0	SLC1A3	0.276	Yes
row_1	CXCR7	0.355	Yes
row_2	IRX5	0.449	Yes
row_3	ASNS	0.485	Yes
row_4	RAD52	0.514	Yes
row_5	CUGBP2	0.545	Yes

row_6	AXL	0.567	Yes
row_7	CREBBP	0.589	Yes
row_8	NMT1	0.606	Yes
row_9	GAL	0.606	Yes
row_10	POLD2	0.612	Yes
HSA04742_TASTE_TRANSDUCTION			
row_0	TAS1R2	0.322	Yes
row_1	GNB1	0.410	Yes
row_2	PRKX	0.461	Yes
row_3	TAS1R3	0.452	Yes
row_4	PRKACA	0.485	Yes
ET743PT650_COLONCA_DN			
row_0	ALCAM	0.180	Yes
row_1	TIAM1	0.255	Yes
row_2	ID1	0.339	Yes
row_3	COMMD1	0.394	Yes
row_4	ATBF1	0.438	Yes
HSA00590_ARACHIDONIC_ACID_METABOLISM			
row_0	PTGIS	0.192	Yes
row_1	CBR3	0.345	Yes
row_2	PTGS1	0.434	Yes
STAEGE_EFTS_UP			
row_0	CYP26B1	0.191	Yes
row_1	CCK	0.337	Yes
row_2	KCNAB3	0.410	Yes
row_3	EGR2	0.436	Yes
row_4	TMEM29	0.462	Yes
row_5	CCND1	0.484	Yes
row_6	ZDHHC21	0.492	Yes
row_7	CLEC11A	0.499	Yes

The criteria for the GSEA analysis was $P < 0.05$ and false discovery rate (FDR) <25%.