

Pathway crosstalk analysis in prostate cancer based on protein-protein network data

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Received March 9, 2016 / Accepted July 18, 2016

Prostate cancer (PCa) is one of the major leading cause in men and no effective biomarkers or therapy have been approved for it to date. This study aimed to explore the molecular mechanisms and identify the potential molecular biomarkers of PCa.

The microarray profile GSE38241 including 18 prostate cancer metastasis and 21 normal prostate samples was retrieved from the Gene Expression Omnibus (GEO) database. Differentially expressed genes (DEGs) were identified by Limma. DEGs functions were investigated by Gene Ontology (GO) and pathway enrichment analysis. Moreover, protein-protein interaction (PPI) network of DEGs was constructed, followed by functional analysis of modules. Additionally, pathway crosstalk network was constructed by integrating PPI network and Kyoto encyclopedia of genes and genomes (KEGG) pathways.

Totally, 334 up- and 703 down-regulated DEGs were identified. The functions of up-regulated DEGs were significantly enriched in GO terms of cell cycle phase and cell cycle process. While down-regulated DEGs mainly participated in actin filament-based process. Among these pathways in the pathway crosstalk network, T cell receptor signaling pathway, chemokine signaling pathways, endometrial cancer and glioma were found to play critical roles during PC progression.

Cell division cycle 45 (CDC45), baculoviral IAP repeat containing 5 (BIRC5) and cell division cycle associated 5 (CDCA5) may be useful markers for predicting tumor metastasis and therapeutic targets for the treatment of PCa patients. Moreover, the pathway crosstalk network provides the groundwork that targeting multiple pathways might be more effective than targeting one pathway alone.

Key words: prostate cancer, differentially expressed genes, protein-protein interaction network, pathway crosstalk

Prostate cancer (PCa) is a kind of malignancy resulting from the pathological changes in men's prostate tissue [1]. PCa is the most commonly diagnosed cancer for men in American and is by far the second leading cause of cancer-related death in men [2]. Moreover, recurrence rate remains about 15% within 5 years after prostatectomy and approximately 40% within 10 years [3]. The mortality rate of PCa patients is higher even after prostatectomy, hormone therapy or radiation [4]. Despite the high incidence rate as well as high mortality rate, the etiology of PCa still remains largely unknown. Thus, more efforts should be devoted for exploring the molecular mechanism and identifying molecular targets to prevent PCa metastases during the early stage to improve the prognosis of PCa patients.

Recently, considerable researches were undertaken to explore the molecular mechanism of PCa. Some genes have been identified to be aberrant in PCa. The six-transmembrane epi-

thelial antigen of prostate 1 (STEAP1) gene overexpression has been reported in PCa [5]. Recently, Neto *et al.* have reported a significant, direct link between human epidermal growth factor receptor 2 (HER2)/neu over-expression and recurrence and death risk in PCa patients [4]. Additionally, the mutation in β -catenin has been reported in PCa [6]. A previous study has suggested that insulin-like growth factor-1 (IGF-1) signaling involved in PCa development through blocking apoptosis and promoting cancer cell proliferation and invasion [7, 8]. Recent study has demonstrated that focal adhesion pathway is of special importance to the development and the progression of human PCa [9]. Additionally, Wnt/ β -catenin is one of the most influential pathways on both human and rat PCa cell growth [10]. However, PCa complexity is not only the combination of proteins in the pathways but also the interactions of the crosstalk of these pathways [11, 12]. Recently, the cross-talk among different signaling pathways has been

demonstrated to play a crucial role in PCA: the inhibition of IGF-1 reduced the β -catenin signaling. Wnt/ β -catenin inhibition subsequently resulted in an inhibition of the T-cell factor/lymphoid enhancer factor dependent transcriptional activity and effective inhibition of PCa cell growth [13]. The cooperation of Wnt signaling pathway and Notch signaling pathway is also found in PCa [14].

In the current study, microarray data GSE38241 [15] was employed to identify differentially expressed genes (DEGs) between PCa metastasis and normal prostate samples. Through some studies have analyzed the datasets for biomarkers and small molecules drugs of metastatic prostate carcinoma [9, 16], a large amount of information in the dataset still remain to be discovered. In this study, in addition to the Gene Ontology (GO) and pathway enrichment analysis of DEGs, the protein-protein interaction (PPI) network was constructed, followed by functional analysis of modules. Additionally, the pathway crosstalk network was constructed among PCa-related pathways by integrating PPI and Kyoto encyclopedia of genes and genomes (KEGG) pathways information. Therefore, this research will light the further understanding of molecular mechanisms of PCa. Meanwhile, this may provide new insight into the therapy for it.

Materials and methods

Data source. The mRNAs expression profile of GSE38241 [15] which was generated by Aryee *et al.* based on GPL4133 (Agilent-014850 Whole Human Genome Microarray 4x44K G4112F (Feature Number version) was downloaded from the Gene Expression Omnibus (GEO) database (<http://www.ncbi.nlm.nih.gov/geo/>). A total of 39 mRNA chips were available, including 18 PC metastasis samples and 21 normal prostate samples. The raw data files and the probe annotation files were obtained and used for further analysis.

Data preprocessing. The probe ID was converted into gene symbol based on the annotation of the platform. Probes with at least one defective expression values were abandoned. For each sample, the expression values of all probe set that map to a given gene were reduced and averaged to a single value. Then, the data were normalized using PreprocessCore package [17]. Finally, the gene expression matrix was obtained.

Identification of DEGs. Based on data preprocessing, the limma package [18] in R language was performed to identify DEGs between PCa metastasis samples and normal prostate samples. $|\log_2 \text{fold change (FC)}| > 1$ and $\text{FDR} < 0.05$ were used as the cut-off criterion of DEGs. The raw p values were adjusted to false discovery rates (FDR) on the basis of Benjamini & Hochberg method [19].

GO and pathway enrichment analysis of DEGs. According to GO Database (<http://www.geneontology.org/>), GO annotation was performed to analyze the functions of DEGs between PCa metastasis samples and normal prostate samples. GO analysis has been used as functional enrichment studies of large-scale genes frequently [20]. GenCLiP 2.0, which is

a web-based text-mining server for gene clustering and molecular networks construction, was applied to perform the GO analysis [21]. A $p \leq 0.05$ and $\text{Hit} \geq 10$ were the cutoff criterions for GO categories.

KEGG databases cover all kinds of biochemistry pathways [22]. GenCLiP 2.0 was applied for KEGG pathway enrichment analysis of DEGs. A $p \leq 0.05$ was chosen as the cut off value.

PPI network construction and functional analysis of modules. The Human Protein Reference Database (HPRD) [23] is a protein database accessible through the internet. A total of 39240 PPI pairs were obtained from HPRD. The Search Tool for the Retrieval of Interacting Genes (STRING) [24] database offers both experimental and predicted interaction information. STRING database was applied to construct the PPI network.

Then, the edges and nodes of the PPI network were so complicated, there is a need for further analysis to expose the enriched functional modules of the PPI network using Cytoscape and ClusterOne [25, 26]. Finally, GO and pathway enrichment analysis of modules was performed.

Significance analysis of pathway crosstalk under PPI and KEGG data. All human pathways were collected from KEGG database. The pathway of PCa was screened as host pathway. The candidate pathways were obtained with at least a protein overlap between any given pair of pathways.

Pearson correlation coefficient (PCC) was applied to calculate the similarity of gene expression and weight pairwise gene co-expression in PCa. Then, p-values mapping to nodes and edges in the PPI network were calculated and obtained. The following formula [27] was performed to assess and measure statistical significance of functional interactions by a scoring scheme.

$$S(e) = f(\text{diff}(x), \text{corr}(x, y), \text{diff}(y)) \\ = -2 \sum_{i=1}^k \log_e(p_i)$$

Where the $\text{diff}(x)$ and $\text{diff}(y)$ represented the quantitative assessment in differential gene expression of gene x and gene y, respectively; $\text{corr}(x, y)$ represented their correlation strength between gene x and gene y based on the expression levels; f represented a general method in data integration taking account of multiple data sets across a variety of statistical power; Where $k = 3$, p_1 and p_2 indicated the statistical significance (p-values) of differential expression of two nodes, while p_3 referred to their co-expression strength (p-value).

To determine the significance of a pathway P, the scores of all edges $S(e)$ of every pathway were summarized as S_p . To assess statistical significance of this pathway, p-values were obtained and calculated from 1000 randomly generated pathways with the same size. Score frequency that larger than S_p was used as the significant p-value of pathway P to describe its importance. We considered the pathway with the p-value < 0.05 as the significant pathway.

Disease Ontology (DO) annotation of DEGs. To identify a direct link between human cancer and DEGs, TargetMine (<http://targetmine.nibio.go.jp/>) which is an integrated data warehouse for known disease-associated genes was used for retrieval of candidate target genes and proteins for cancer from large-scale experiments. Additionally, DEGs have been reported to play roles in cancer pathogenesis would be identified to validate the results.

Results

Identification of DEGs. Heatmap in Figure 1 displayed the differential gene expression between prostate cancer

metastasis and normal prostate samples (Supplemental Table 1). After preprocessing, 1037 DEGs were identified, including 334 up – and 703 down-regulated DEGs (Supplemental Table 2). Alpha-methylacyl-CoA racemase (AMACR, $\log_2FC = 3.263$) and actin, gamma 2, smooth muscle, enteric (ACTG2, $\log_2FC = -5.945$) had the highest fold changes among the up – and down-regulated genes, respectively.

GO and pathways enriched by DEGs. The top 3 clusters of GO terms which were most significantly enriched by DEGs were shown in Table 1. Up-regulated DEGs were significantly enriched in cell cycle phase ($p = 4.56E-12$), chromosome segregation ($p = 1.80E-10$) and cell cycle process ($p = 2.49E-08$).

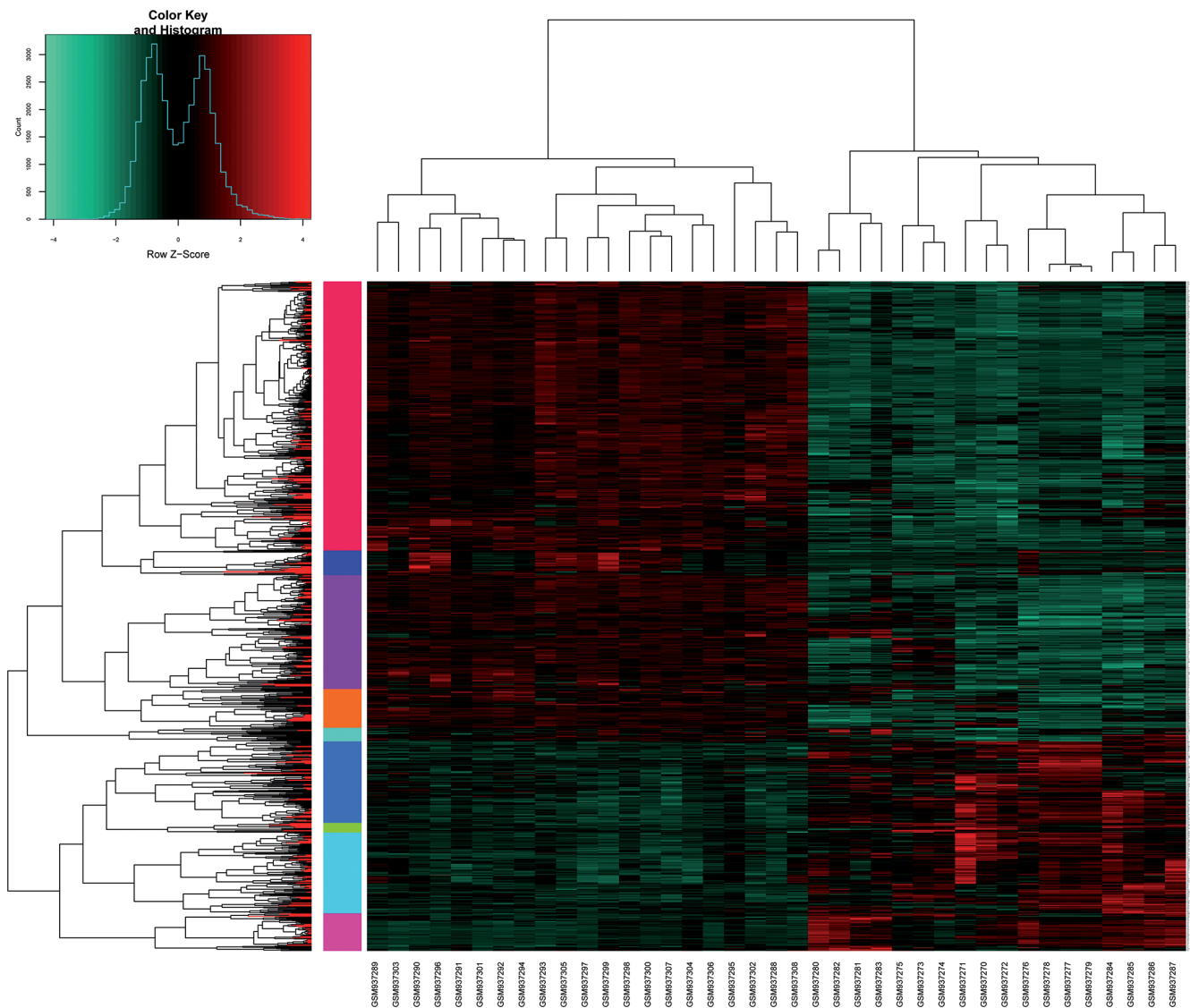


Figure 1. Heatmap of differential gene expression between prostate cancer metastasis and normal prostate samples. Each row represents the relative levels of expression of a single gene across all samples; each column represents the levels of expression for a single sample. The colors red and green denote high and low expression, respectively.

While down-regulated DEGs mainly participated in muscle contraction ($p = 4.39E-81$), muscle system process ($p = 2.61E-76$), muscle structure development ($p = 6.46E-48$) and cardiovascular system development ($p = 3.17E-31$).

The KEGG pathways obtained with $p \leq 0.05$ of the up- and down-regulated genes were shown in Table 1. On the basis of the results, the up-regulated DEGs were enriched in pathways significantly such as leishmania infection ($p = 3.45E-07$), antigen procession and presentation ($p = 1.09E-05$) and type I diabetes mellitus ($p = 5.11E-05$). Besides, the down-regulated DEGs were significantly enriched in dilated cardiomyopathy ($p = 5.24E-14$), hypertrophic cardiomyopathy (HCM) ($p = 8.67E-14$) and arrhythmogenic right ventricular cardiomyopathy (ARVC) ($p = 1.36E-07$). These pathways of the down-regulated DEGs were mainly associated with cardiomyopathy. The detailed information

of DEGs enriched in GO terms and pathways were shown in Supplemental Table 3.

PPI and functional analysis of modules. To identify the connection between DEGs and distinct functional modules, the STRING tool was performed to obtain the PPI network of DEGs. The PPI network as well as module of up-regulated DEGs was shown in Figure 2. DEGs highly connected (known as high degree nodes) to others would be more important in the network. While gene modules function as conserved molecular “circuits” responsible for specific biological function. In the module, there were 41 nodes and 713 edges. The density of the module was 0.575. Additionally, the PPI network and module of down-regulated DEGs was shown in Figure 3. In the module, there were 39 nodes and 311 edges. The density of the module was 0.308.

We then performed the GO and KEGG pathway enrichment analysis of DEGs in modules. Similarly, the top three

Table 1. The top 3 cluster Gene Ontology (GO) functional enrichment and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway of differentially expressed genes.

Category	GO term	Hit	p value	
GO terms of up-regulated genes	Cluster 1 Enrichment Score: 10.40	Cell cycle phase	24	4.56E-12
		Mitotic cell cycle	29	3.45E-10
	Cluster 2 Enrichment Score: 7.98	Chromosome segregation	12	1.80E-10
		Condensed chromosome	11	3.14E-07
		Chromosome,centromeric region	11	2.05E-08
	Cluster 3 Enrichment Score: 7.20	Cell cycle process	38	2.49E-08
		Cell cycle	11	1.60E-07
	Pathways of up-regulated genes	Leishmania infection	7	3.49E-07
		Allograft rejection	5	2.61E-04
		Antigen	7	1.09E-05
Type I diabetes mellitus		6	5.11E-05	
Asthma		5	9.30E-05	
Viral myocarditis		5	1.07E-03	
Graft versus host disease		5	4.26E-04	
Intestinal immune network for IgA production		5	8.92E-04	
Autoimmune thyroid disease		5	1.29E-03	
Systemic lupus erythematosus		6	2.20E-02	
GO terms of down-regulated genes	Cluster 1 Enrichment Score: 56.04	Muscle contraction	70	4.39E-81
		Muscle system process	73	2.61E-76
		System process	143	6.73E-13
	Cluster 2 Enrichment Score: 31.11	Muscle structure development	79	6.46E-48
		Tissue development	129	3.26E-25
		Organ development	181	2.17E-22
	Cluster 3 Enrichment Score: 25.25	Circulatory system development	92	3.17E-31
		Cardiovascular system development	92	3.17E-31
		Anatomical structure formation involved in morphogenesis	78	1.76E-15
		Dilated cardiomyopathy	19	5.24E-14
Pathways of down-regulated genes	Hypertrophic cardiomyopathy (HCM)	18	8.67E-14	
	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	13	1.36E-07	
	Cardiac muscle contraction	9	4.87E-03	

clusters of GO terms and pathways enriched by up- and down-regulated DEGs were shown in Table 2. The detailed information were shown in Supplemental Table 4.

The up-regulated DEGs, such as cell division cycle 45 (CDC45), baculoviral IAP repeat containing 5 (BIRC5) and cell division cycle associated 5 (CDCA5), were significantly enriched in GO functions of cell cycle phase ($p = 1.10E-88$), mitotic cell cycle ($p = 7.82E-88$) and cell cycle process ($p = 6.84E-77$). The up-regulated DEGs were significantly enriched in pathways such as cell cycle ($p = 6.09E-05$) and DNA replication ($p = 6.61E-06$). While the down-regulated DEGs mainly participated in GO terms of actin filament-based process ($p = 4.53E-130$), cytoskeletal protein binding ($p = 5.69E-92$) and myofibril ($p = 4.02E-54$), and remarkably enriched in pathways

such as dilated cardiomyopathy ($p = 7.19E-13$), hypertrophic cardiomyopathy (HCM) ($p = 1.56E-11$) and cardiac muscle contraction ($p = 4.68E-07$).

Significance analysis of pathway crosstalk under PPI and KEGG data. To identify the important pathways altered in PCa, a statistical method on pathway level was used. The significance analysis of crosstalk effects in pathways was based on the PPI database and KEGG database. The molecular crosstalk between host and candidate pathways showed that many significant pathways containing T cell receptor signaling pathway, chemokine signaling pathway, endometrial cancer and glioma were obtained (Figure 4). This results indicated the connection between immune and PC, and also suggested the commonness of cancer. Addi-

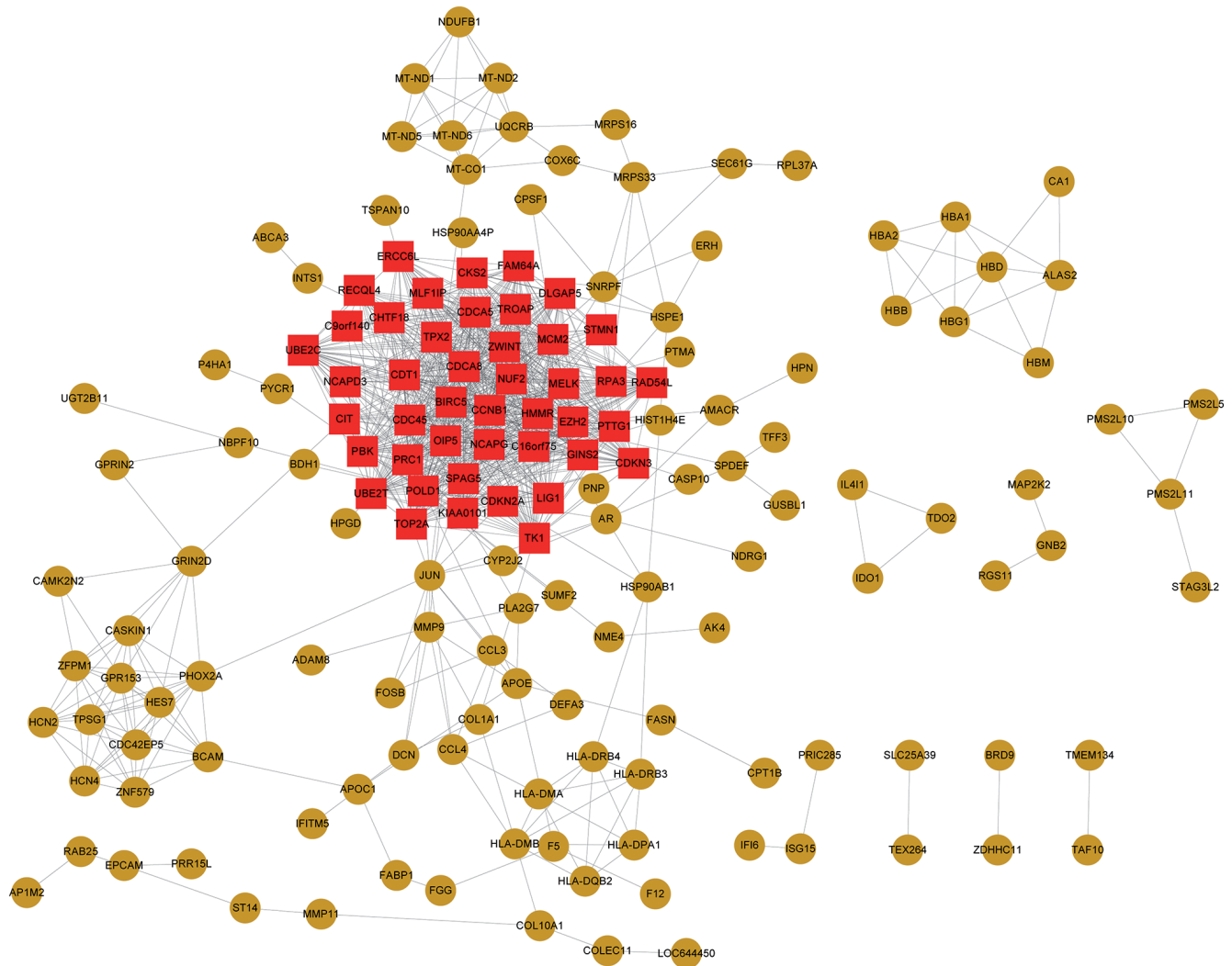


Figure 2. Protein-protein interaction (PPI) network of up-regulated differentially expressed genes. The red square nodes represent the module of the PPI network. Other nodes represent up-regulated differentially expressed genes outside the module. In the module, there were 41 nodes and 713 edges. The density of the module was 0.575.

tionally, the associations between DEGs and pathways were provided in Supplemental Table 5.

DO terms of DEGs. Multiple DO terms of DEGs were obtained (as shown in Supplemental Table 6). Especially, the cancer-related terms including PCa, carcinoma, cell type cancer and malignant glioma were enriched by down-regulated DEGs, besides, cancer, malignant ovarian surface epithelial-stromal neoplasm, ovary epithelial cancer, and ovarian carcinoma were enriched by up-regulated DEGs.

Discussion

PCa is a highly prevalent cancer in older men of the western countries [28]. In the current study, we employed

bioinformatics methods to explore the molecular mechanisms and identify the potential molecular biomarkers to PCa. Our results suggested that 334 up – and 703 down-regulated DEGs were screened out. Moreover, the functions of up-regulated DEGs were significantly enriched in cell cycle phase and cell cycle process. While down-regulated DEGs mainly participated in actin filament-based process and dilated cardiomyopathy.

In our study, we found DEGs were mostly enriched in GO terms of cell cycle phase, cell cycle process and cell cycle. It is well known that cancer is characterized by uncontrolled cell proliferation due to dysregulation of the cell-cycle [29]. Moreover, replication of damaged DNA leads to mutations in the genome and the development of diseases such as cancer

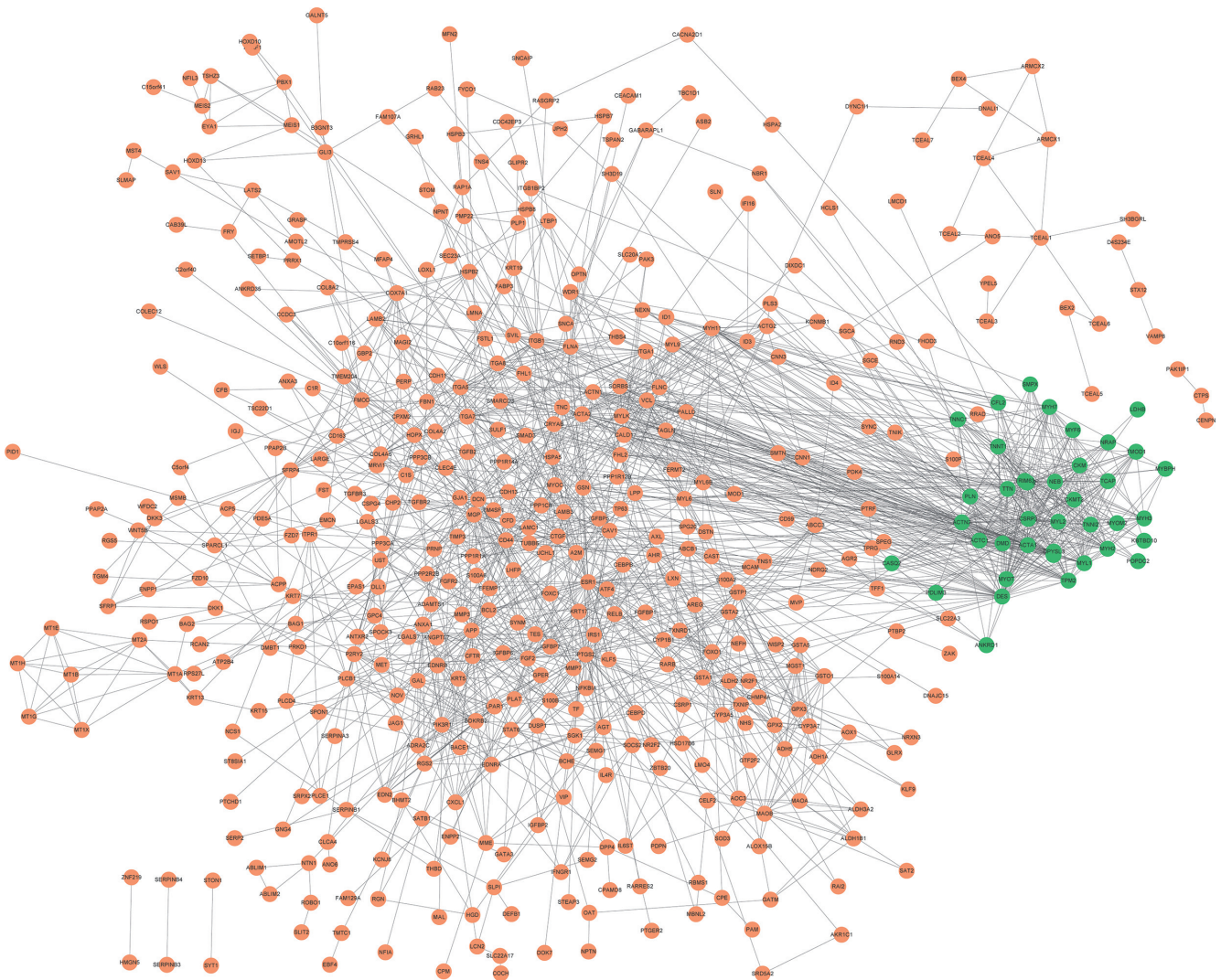


Figure 3. The protein-protein interaction (PPI) network of down-regulated differentially expressed genes.

The green circle nodes represent the module of the PPI network. Other nodes represent down-regulated differentially expressed genes outside the module. In the module, there were 39 nodes and 311 edges. The density of the module was 0.308.

[30]. CDC45, BIRC5, CDCA5 as DEGs were shown to be significantly up-regulated in PCa metastases samples in the present study. CDC45 plays an important role in the initiation as well as the extension of DNA replication [31, 32], and participated in the pathway of DNA damage-dependent signal transduction [33]. A former study has demonstrated that CDC45 expression level is strongly higher in human cancer-derived cells than in primary human cells [34]. BIRC5 gene has been reported to be associated with PCa previously [35, 36]. Our result was in accordance with previous study. Additionally, DO term annotation revealed that multiple DEGs played roles in various cancers including PCa. This may confirm the result accuracy to some extent as well. In addition, the CDCA5 gene was suggested to play some roles in cell cycle progression

via the interaction with chromatin in some immortalized cell lines [37]. Besides, Nguyen *et al.* have indicated that CDCA5 is an oncogene that is highly expressed in lung cancers [38]. These results strongly suggested that dysregulation of these genes related with cell cycle might be crucial for the progression of PCa.

In the pathway crosstalk network, several significant immunity and cancer-related pathways crosstalk with PCa, such as T cell receptor signaling pathway and chemokine signaling pathway. The T cell receptor plays a key role in the immune system. Immunotherapy of cancer is dependent on a proper target antigen and antigen presentation to the patient's immune system. Antigen presenting cells are responsible for uptake, processing and presentation of anti-

Table 2. The Gene Ontology (GO) functional enrichment and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis of differentially expressed genes.

Category	Term	Hit	P values	
GO terms of up-regulated genes	Cluster 1 Enrichment Score: 79.07	Cell cycle phase	23	1.10E-88
		Mitotic cell cycle	28	7.82E-88
		Cell cycle process	34	6.84E-77
		Cell cycle	36	9.22E-66
	Cluster 2 Enrichment Score: 53.78	Cell division	20	3.49E-61
		Mitosis	18	2.26E-53
		Nuclear division	18	2.26E-53
		Organelle fission	18	4.20E-50
	Cluster 3 Enrichment Score: 36.23	Chromosome organization	20	4.52E-38
		Chromosome	18	1.48E-35
		Chromosomal part	17	3.05E-37
	Pathways of up-regulated genes	Cell cycle	5	6.09E-05
		DNA replication	4	6.61E-06
Mismatch repair		3	6.60E-05	
Nucleotide excision repair		3	4.70E-04	
Homologous recombination		3	1.21E-04	
GO terms of down-regulated genes	Cluster 1 Enrichment Score: 80.41	Actin filament-based process	27	4.53E-130
		Cellular component movement	22	3.32E-32
	Cluster 2 Enrichment Score: 53.87	Cytoskeletal protein binding	26	5.69E-92
		Myofibril	30	4.02E-54
		Contractile fiber	30	3.09E-53
		Actin binding	17	4.53E-19
	Cluster 3 Enrichment Score: 46.94	Sarcomere	27	2.80E-48
		Contractile fiber part	27	4.72E-47
Pathways of down-regulated genes	Dilated cardiomyopathy	10	7.19E-13	
	Hypertrophic cardiomyopathy (HCM)	9	1.56E-11	
	Cardiac muscle contraction	6	4.68E-07	
	Tight junction	5	1.49E-04	
	Viral myocarditis	4	1.53E-04	
	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	3	3.03E-03	
	Arginine and proline metabolism	2	1.93E-02	
	Calcium signal pathway	3	3.24E-02	

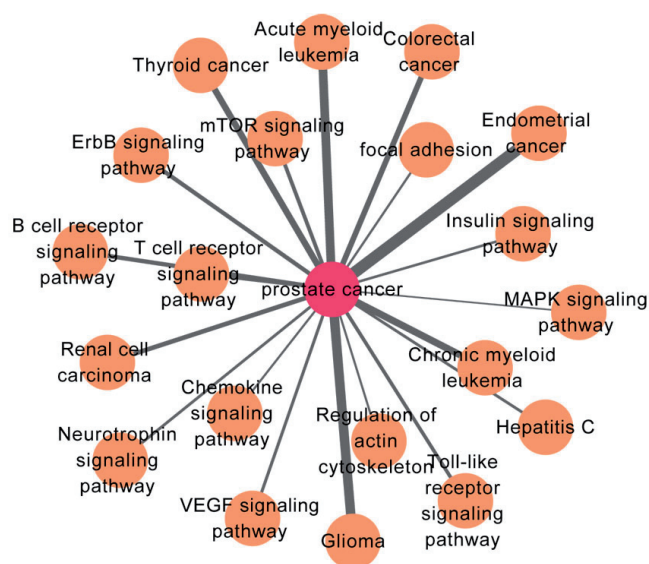


Figure 4. The pathway-crosstalk network of prostate cancer. The rose red node in the middle represents the host pathway of prostate cancer; Peripheral orange nodes are the pathways interacting with the host pathway; The thickness of the edges is proportional to the significance between two interaction pathways.

gens to T cells [39]. Chemokines are shown to play roles in regulating recruitment of immune cells during inflammatory responses [40]. Considerable evidence has also showed that the chemokine signaling pathway plays crucial roles in the tumor progression and microenvironment [41]. Moreover, chemokines as well as their receptors exhibit differential expression following PCa progression [42]. Thus, a combination of targeting multiple pathways might be a promising therapy strategy for PCa.

Additionally, we found several cancer-related pathways crosstalk with PCa, such as endometrial cancer and glioma. Recent studies found the alteration of tumor suppressor gene named PTEN or MMAC1 in human PCa cell lines obtained from metastatic tissues [43, 44]. Mutations of PTEN/MMAC1 have also been reported in endometrial carcinoma [45] and glioma [46]. Moreover, the mutations in this gene are frequent in endometrial carcinoma but rare in other common gynecological cancers [47]. Suzuki *et al.* have demonstrated that alteration of PTEN/MMAC1 might play an important role in the pathogenesis of many human malignancies [48]. In light of these results, we infer that PTEN/MMAC1 may be a biomarker for metastatic PCa, endometrial cancer and glioma.

In conclusion, the identified DEGs, especially CDC45, BIRC5 and CDCA5, may be pivotal genes for PCa, and these genes related with cell cycle may be useful markers for predicting tumor metastasis and therapeutic targets for the treatment of PCa patients. Moreover, B cell receptor signaling pathway, T cell receptor signaling pathway, endometrial

cancer and glioma were found to play important roles during PCa progression in the crosstalk network among PCa-related pathways. Our studies shed new light on the mechanism and treatment of PCa. However, the consequence described above, not only genes, but also pathways associated with PCa will be evaluated and verified conjointly through animal and clinical experiments in later work.

Supplementary information is available in the online version of the paper.

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Supplemental table 1. Gene list in heatmap.

Gene	Cluster
TPST2	1
SH3BGR	1
P2RY2	1
AVPI1	1
LGALS7B	1
LGALS7	1
IGJ	1
CFTR	1
LMCD1	1
CTGF	1
TNC	1
STAT6	1
EFS	1
GLIPR2	1
SLC20A2	1
GFOD1	1
RAB34	1
GSTP1	1
ID4	1
RGN	1
RARRES2	1
DZIP1	1
FGF2	1
ANKRD35	1
MAOB	1
SLC24A3	1
NR2F1	1
PDE5A	1
MEIS2	1
RASGRP2	1
PPAPDC3	1
SORBS1	1
KANK2	1
CBX7	1
SLIT2	1
GSN	1
IGFBP6	1
DKK3	1
SLC16A5	1
SPOCK3	1
PAGE4	1
GLIS1	1
TBC1D1	1
PLCL1	1
CFL2	1
ATP2B4	1
DPYSL3	1
DBNDD2	1

RAB23	1
RARB	1
DNAJC15	1
PPAP2B	1
PMP22	1
TIMP3	1
FAM162B	1
CYP4B1	1
LRCH2	1
ACOX2	1
MET	1
KRT23	1
PDPN	1
PCOLCE2	1
FST	1
MAL	1
CUGBP2	1
PID1	1
LPHN2	1
MOXD1	1
MFAP4	1
SOD3	1
FILIP1L	1
RERG	1
CD59	1
PNMA1	1
TCEAL4	1
CALD1	1
LMNA	1
AMOTL2	1
NDRG2	1
MYL6	1
LOC72826	1
LOC39133	1
MEIS1	1
S100A6	1
REEP2	1
RP9P	1
DYNC1I1	1
DOK7	1
PPP1CB	1
C22orf28	1
PPP1R1A	1
ART3	1
FABP3	1
CHP2	1
PRDM6	1
COL4A6	1
CAV1	1
SMTN	1

KCNMB1	1
FLNC	1
MYL9	1
CSRP1	1
FLNA	1
ACTBL2	1
ACTC1	1
PDZRN4	1
ATP1A2	1
SLMAP	1
CLIC4	1
PRICKLE2	1
LOC39995	1
PLN	1
FRMD6	1
FZD7	1
PALLD	1
FERMT2	1
TNIK	1
FBXO30	1
UST	1
GPR87	1
TP63	1
FGFR2	1
C9orf125	1
KRT15	1
LAMB3	1
TNS4	1
FLRT3	1
TCEAL2	1
PTPLA	1
HSPB8	1
TCEAL7	1
PTCHD1	1
EYA1	1
GALNT5	1
FOXC1	1
NEXN	1
COX7A1	1
MXRA7	1
TAGLN	1
MSRB3	1
MYLK	1
ACTA2	1
PTRF	1
ARHGAP2	1
TPM2	1
CNN1	1
DES	1
MYH11	1

PPP1R12B	1
SYNM	1
PCP4	1
AOC3	1
ACTG2	1
SRD5A2	1
TNS1	1
DACT3	1
JPH2	1
SYNPO2	1
LMOD1	1
FHL1	1
TSPAN2	1
PAM	1
TMEM35	1
GPR124	1
EDNRA	1
SGCA	1
MYOF	1
SH3BGRL	1
SCHIP1	1
GATM	1
BHMT2	1
VCL	1
DSTN	1
PPP1R14A	1
HSPB2	1
CSPG4	1
MCAM	1
ITGA5	1
NPTN	1
CDC42EP3	1
SPEG	1
MGC24103	1
S100A2	1
S100A14	1
GATA3	1
KRT13	1
ANXA8L2	1
GAS1	1
CDKL1	1
FIBIN	1
PLCB1	1
LOXL1	1
COL8A2	1
SH3D19	1
PPP2R2B	1
HSPB7	1
HOXD13	1
ANO5	1

CES1	1
C2orf40	1
MYOC	1
LARGE	1
C8orf84	1
RRAD	1
DUSP26	1
HSPB3	1
ASB5	1
RAB31	1
PLS3	1
GJA1	1
SPON1	1
AMIGO2	1
KANK1	1
BAG2	1
ITGA1	1
ITGB1BP2	1
DNAJB4	1
SVIL	1
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C15orf41	1
PLCD4	1
TGFBR3	1
TGFBR2	1
A2M	1
C1S	1
C1R	1
FHL2	1
MGP	1
SULF1	1
CDH11	1
TWIST2	1
ANGPTL1	1
MAMDC2	1
CFD	1
GPX3	1
HSD11B1	1
DKK1	1
RARRES1	1
GFPT2	1
MMP7	1
SERPINB1	1
IFI16	1
STOM	1
IL33	1
KCNJ8	1
GPC4	1
CDC37L1	1
ECHDC1	1

ADH5	1
GTF2F2	1
RAP1A	1
ITGB1	1
CUTC	1
IGFBP7	1
DCN	1
EFEMP1	1
AXL	1
EMCN	1
PDLIM3	1
GALNAC4	1
DMD	1
SULF2	1
COL4A2	1
CPXM2	1
EDNRB	1
CCDC3	1
TMEM204	1
PTBP2	1
APP	1
IGFBP2	1
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SEC23A	1
RP6?213H	1
GULP1	1
NPNT	1
B3GNT8	1
ASB2	1
ROBO1	1
GLI3	1
DNAJB5	1
ITGA7	1
TUBB6	1
FREQ	1
LMO4	1
WFDC1	1
PDLIM4	1
WFDC2	1
RND3	1
FOXF1	1
DKFZP586	1
GBP2	1
PTGER2	1
CLIC6	1
RSPO1	1
DIO3	1
MRVI1	1
WISP2	1
C16orf45	1

PKIG	1
LRFN5	1
TNFRSF12	1
STEAP3	1
SMARCD3	1
LOC34123	1
TF	1
AKR1C1	1
SNX7	1
RNASE4	1
REEP1	1
TMOD1	1
RILPL2	1
CAST	1
LTBP1	1
LAMB2	1
FLJ10357	1
TMEM47	1
CAND2	1
ZNF655	1
EPB41L3	1
BAG1	1
ALDH2	1
BDKRB2	1
B3GNT3	1
CXCL1	1
CFB	1
LOC38776	1
GEM	1
GPX2	1
CHRDL2	1
OLFM4	1
GABRP	1
VTCN1	1
SNCAIP	1
PCDH8	1
PRRX2	1
C17orf91	1
RDH10	1
PLAT	1
TM4SF1	1
SRPX2	1
OAT	1
FBN1	1
SFRP4	1
CDH13	1
THBD	1
SNCA	1
HCLS1	1
CD163	1

ADH1C	1
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CYB5R2	1
CRYAB	1
UCHL1	1
FAM129A	1
DEFB1	1
C3orf57	1
C10orf116	1
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NFIA	1
ABLIM1	1
VAMP8	1
KRT19	1
SOCS2	1
MME	1
ALOX15B	1
PAK1IP1	1
PON3	1
MT1M	1
MT1E	1
MT1L	1
MT1B	1
MT1G	1
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MT1X	1
MT2A	1
RSPO3	1
CRISPLD1	1
VILL	1
CACNA2E	1
ZNF334	1
KIAA1210	1
DPP4	1
KIAA0513	1
FLJ46111	1
DKFZP564	1
CPAMD8	1
MSMB	1
NTN1	1
ABCB1	1
SAT2	1
SCPEP1	1
JAKMIP1	1
SYT1	1
MYOM2	1
ANGPTL7	1

SYT10	1
ZNF219	1
KIF1C	1
FCGBP	1
ALDH1B1	1
ZNF185	1
KRT7	1
VSIG2	1
S100B	1
PLP1	1
CDH19	1
MRAP2	1
ESR1	1
GSTA5	1
GSTA2	1
GSTA1	1
SLC39A2	1
VIP	1
SLC38A1	2
BCHE	2
NRXN3	2
MYL2	2
MYL1	2
KBTBD10	2
TNNC1	2
SLN	2
TTN	2
MYF6	2
SMPX	2
NRAP	2
CSRP3	2
ANKRD1	2
CKM	2
ACTA1	2
MYH7	2
MYBPH	2
MYOT	2
CASQ2	2
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NEB	2
TCAP	2
CA3	2
TNNC2	2
MYH2	2
TNNI2	2
TRIM63	2
ACTN2	2
TNNT1	2
MYL6B	2
CKMT2	2

SUMF2	2
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MGST1	2
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GAL	2
THBS4	2
KLF5	3
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MBNL2	3
CARD10	3
ABCA8	3
PLEKHO1	3
DIXDC1	3
HOXD10	3
GABRE	3
SPG20	3
BNC2	3
NHS	3
GPRASP1	3
ANTXR2	3
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NOV	3
SPARCL1	3
MEIS3P1	3
TSHZ3	3
FSTL1	3
BACE1	3
SFRP1	3
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EPAS1	3
AHR	3
NTN4	3
IL6ST	3
TPBG	3
ENPP2	3
RCAN2	3
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ZAK	3
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PRNP	3
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SYNC	3
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HECTD2	3
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SMAD3	3
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COCH	3
HSPA5	3
ACPP	3
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CHMP4A	3
BEX4	3
BEX2	3
DLL1	3
PRUNE2	3
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FOXN3	3
RAMP1	3
TXNIP	3
TPM1	3
TCEAL6	3
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TCEAL5	3
LARP6	3
RNF150	3
FAM107A	3
C5orf4	3
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COLEC12	3
RELB	3
CEACAM	3
IL4R	3
CEBPD	3
MVP	3
SERPINA3	3
LXN	3
SERPINB4	3

SERPINB3	3
LCN2	3
DMBT1	3
ST8SIA1	3
SERP2	3
HSD17B6	3
PSMD7	3
ANXA3	3
PIK3R1	3
METTL7A	3
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YPEL5	3
PBX1	3
NR2F2	3
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FOXO1	3
TPRG1	3
PTGS2	3
PDK4	3
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LATS2	3
LAMC1	3
ITGA8	3
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PPP3CB	3
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SCRN1	3
KCNB1	3
FYCO1	3
STON1	3
RAI2	3
MFN2	3
WNT5B	3
GPR177	3
CYP3A7	3
CYP3A5	3
EBF4	3
C1orf190	3
DKFZp667	3
ZBTB20	3
AQP1	3
IRS1	3
HOPX	3
GSTO1	3
CNN3	3
RGS5	3
LHFP	3
TMEM14C	3

RPS27L	3
HGD	3
ALDH3A2	3
AJAP1	3
CPE	3
SLC22A3	3
SH3BGRL	3
SLC22A17	3
LOC10014	3
LOC10012	3
MAGI2	3
CPM	3
ABCC3	3
KRT5	3
GRASP	3
POPDC2	3
KRT17	3
FGFBP1	3
GRHL1	3
GPR64	3
TXNRD1	3
RBM3	3
CLEC4E	3
CCL23	3
MMP3	3
ABLIM2	3
TFCP2L1	3
SORD	3
HSPA2	3
NFKBIA	3
CEBPB	3
SGK1	3
TGM4	4
TFF1	4
BASP1	4
AGR2	4
SEMG2	4
SEMG1	4
GPER	4
AOX1	4
NBR1	4
GNG4	4
SUSD5	4
ATF4	4
SLC16A9	4
PDE8B	4
SAV1	4
CENPN	4
SLC12A2	4
PPAP2A	4

MAOA	4
ZHX3	4
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CLCA4	4
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JAG1	4
ADAMTS	4
CTPS	4
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NEFH	4
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NUAK1	4
FMOD	4
NKX3?1	4
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NSBP1	4
ANXA1	4
LEPREL1	4
DMKN	4
C1orf133	4
LGALS3	4
TES	4
PPP1R3C	4
PERP	4
TSPYL5	4
CD44	4
IFFO2	4
SATB1	4
POTEF	4
RP4?691N	4
ODZ2	4
ITPR1	4
BCL2	4
D4S234E	4
AMD1	4
ADRA2C	4
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DUSP23	5
ATAD4	5
HLA?DRB	5
HLA?DPA	5
LGALS2	5
HLA?DQE	5
AREG	5

AGT	5
HLA?DRB	5
CCL4	5
PCP4L1	5
LY6K	5
EDN2	5
SGCE	5
OPTN	5
ENPP1	5
GLRX	5
CYP1B1	5
SLPI	5
BATF	5
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MEX3A	6
PTMAP7	6
PCBD1	6
P4HA1	6
UQCRB	6
CRISP2	6
TMEM184	6
POU5F1P3	6
GPR160	6
EPCAM	6
TSPAN13	6
C15orf61	6
ATP8A2	6
FAM83H	6
DUSP5P	6
PRC1	6
CIT	6
PYCR1	6
NDUFB1	6
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APOC1	6
COL1A1	6
FGG	6
FABP1	6
COLEC11	6
ISX	6
UGT2B11	6
CTAG1A	6
LASS4	6
TFF3	6

DIO1	6
LOC44257	6
TMSB15A	6
C1QTNF3	6
TRPM4	6
PECI	6
RAB25	6
BDH1	6
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ABCC5	6
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PDIA5	6
FLJ39632	6
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GAS5	6
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RPL37A	6
LOC91316	6
LOC10017	6
LOC65308	6
GUSBL1	6
TMC4	6
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C20orf74	6
HERC2P4	6
FAAH	6
ELK4	6
LOC14780	6
ELOVL1	6
HSP90AB3	6
HSP90AB1	6
EIF2S3	6
LOC64465	6
GTF2H2D	6
POTED	6
POTEC	6
POTEG	6
POTEB	6
SPDEF	6
ANKRD37	6
MESP1	6
ERH	6
PPFIA4	6
PFKFB4	6
MKMK2	6
SEC61G	6
NDRG1	6
WWC1	6
NCAPD3	6
SGK196	6

MAP2K2	6
ST14	6
C16orf13	6
ARHGEF1	6
RECQL4	6
PPP1R14B	6
TTLL12	6
AR	6
NME4	6
AP1M2	6
SLC25A39	6
SLC19A1	6
LPIN3	6
INTS1	6
PMS2L3	6
CHTF18	6
C6orf129	6
NSUN5B	6
NSUN5	6
NSUN5C	6
PMS2L5	6
PMS2L11	6
PMS2L2	6
PILRB	6
PILRA	6
ZDHHC11	6
LOC64525	6
RAB24	6
MCCC2	6
MLPH	6
CCDC125	6
FAM64A	6
AMACR	6
LOC72998	6
C9orf140	6
TRAP1	6
ABCA3	6
CAMKK2	6
BAIAP2L1	6
PVT1	7
MRPS16	7
C19orf48	7
LOC44034	7
LOC73012	7
AK3L1	7
PRR7	7
CELSR3	7
SLC35E2	7
RP11?3451	7
WBP1	7

TDO2	7
ACAD8	7
HLA?DMB	7
COL10A1	7
KIAA1683	8
KCNQ10T	8
GSDMB	8
GHRLOS	8
ZNF692	8
LOC39949	8
CPT1B	8
RP11?2161	8
CPSF1	8
SNHG7	8
CPNE7	8
LOC72841	8
LOC10013	8
FLJ27365	8
LOC85391	8
HIST1H4E	8
RGL2	8
RGS11	8
B4GALNT	8
ANKZF1	8
SLC45A2	8
NBPF20	8
HSF4	8
ROGDI	8
ZNF841	8
LOC44035	8
STAG3L2	8
BRD9	8
PCDHGB2	8
PCDHGA2	8
JUN	8
SOX4	8
HSPA6	8
TMEM45E	8
HPN	8
DLX1	8
APLN	8
MARCKS1	8
ESM1	8
TMEFF2	8
PRIC285	8
LOC25578	8
CASKIN1	8
LOC40135	8
LOC43995	8
GRIN2D	8

C9orf62	8
CAMK2N2	8
ZFPM1	8
PHOX2A	8
LOC40165	8
HES7	8
LOC44046	8
GPR150	8
TSPAN10	8
ZNF579	8
LCE1D	8
GPR153	8
C17orf96	8
ND6	8
ND5	8
CCDC11	8
LOC44246	8
ND2	8
ND1	8
LIG1	8
FOSB	8
TPSG1	8
HCN4	8
HCN2	8
LCE5A	8
FLJ22184	8
IFITM5	8
DUX4	8
DNM1P35	8
BCAM	8
CDC42EP2	8
ND3	8
COX1	8
ZNF541	8
MMP11	8
HBD	8
ALAS2	8
HBM	8
HBA2	8
HBA1	8
HBB	8
CA1	8
MRPS33	8
GINS2	8
COX6C	8
LOC44073	8
C12orf45	8
CGREF1	8
MUCL1	8
TMEM134	8

DCXR	8
TEX264	8
TCEA3	8
NMRAL1	8
ICA1	8
TAF10	8
DUS1L	8
PTK6	8
FASN	8
LOC38856	8
GNB2	8
METRN	8
PCDHB2	8
ADAM8	8
CYP2J2	8
YIPF6	8
HBG1	8
LOC10012	8
HPGD	8
ABCC11	8
GLYATL1	8
SERHL2	8
ITPR3	8
IL4I1	8
SULT1C2	8
DEFA3	8
MMP9	8
RP13?36C	8
NUDT8	8
TMEM106	9
LRRC36	9
FOXD1	9
B3GAT1	9
GPRIN2	9
CORO2A	9
ADRB2	9
ZFP62	9
MLEC	9
PLA2G7	9
MCM2	9
C16orf75	9
TK1	9
CDC45L	9
STMN1	9
CDT1	9
TOP2A	9
CDC2	9
CKS2	9
SNRPF	9
ERCC6L	9

PTTG1	9
CDCA8	9
UBE2C	9
BIRC5	9
CDKN2A	9
OIP5	9
CDCA5	9
MLF1IP	9
NUF2	9
NCAPG	9
MELK	9
ZWINT	9
KIAA0101	9
UBE2T	9
SPAG5	9
RAD54L	9
F12	9
PACSIN1	9
CDH24	9
HMMR	9
CCNB1	9
TPX2	9
CDKN3	9
PBK	9
DLGAP5	9
TROAP	9
HIG2	9
RPA3	9
NP	9
CCL3L3	9
CCL3	9
IDO1	9
REG1A	9
HLA?DM	9
ISG15	9
CASP10	9
IFI6	9

Supplemental table 2. The fold change and p-value of up-regulated and down-regulated differentially expressed genes (DEGs)

Gene id	Gene name	logFC	P.Value	adj.P.Val	B
569	AMACR	3,263	9,53E-13	3,62E-11	18,868
7294	HBB	2,973	1,24E-08	1,29E-07	9,389
4520	DEFA3	2,800	1,71E-08	1,69E-07	9,071
10452	LOC73012	2,695	1,86E-06	1,04E-05	4,410
10969	MCCC2	2,676	1,25E-11	3,16E-10	16,290
14608	RECQL4	2,293	1,33E-10	2,48E-09	13,923
1442	BIRC5	2,193	4,04E-09	4,80E-08	10,513
9605	LOC10013	2,179	4,16E-12	1,24E-10	17,392
7477	HIG2	2,152	7,08E-09	7,92E-08	9,953
4014	CRISP2	2,150	3,88E-05	1,57E-04	1,420
13670	POTEB	2,128	2,44E-05	1,04E-04	1,877
843	AR	2,088	1,02E-08	1,08E-07	9,589
16747	STMN1	2,071	1,84E-11	4,41E-10	15,903
13675	POTEG	2,032	6,47E-06	3,16E-05	3,180
5407	ESM1	2,029	6,02E-17	1,05E-14	28,522
810	APOE	2,022	1,29E-10	2,41E-09	13,953
11916	ND3	2,004	8,54E-18	2,05E-15	30,462
3563	CHTF18	1,949	1,08E-16	1,71E-14	27,937
18276	UBE2C	1,936	5,65E-10	8,74E-09	12,478
8545	KIAA0101	1,910	1,19E-11	3,03E-10	16,344
3455	CGREF1	1,883	8,25E-09	9,07E-08	9,799
3076	CCL3	1,882	1,34E-17	3,05E-15	30,013
16683	STAG3L2	1,870	7,03E-14	4,13E-12	21,476
12979	PCDHGB2	1,853	8,40E-09	9,20E-08	9,782
7292	HBA1	1,848	1,20E-11	3,07E-10	16,330
9615	LOC10017	1,847	1,24E-07	9,52E-07	7,097
10051	LOC44073	1,844	1,84E-10	3,27E-09	13,601
10311	LOC65308	1,839	2,89E-10	4,88E-09	13,149
10363	LOC72841	1,831	6,41E-13	2,59E-11	19,266
6809	GLYATL1	1,791	9,68E-06	4,52E-05	2,783
7296	HBD	1,787	8,11E-07	4,97E-06	5,234
7426	HERC2P4	1,782	5,69E-10	8,78E-09	12,472
12913	PBK	1,780	2,39E-08	2,24E-07	8,741
3344	CDT1	1,762	5,24E-09	6,06E-08	10,253
7716	HPN	1,756	1,10E-13	5,97E-12	21,024
1272	B4GALNT1	1,751	6,44E-11	1,31E-09	14,652
13671	POTEC	1,737	3,66E-06	1,90E-05	3,742
670	ANKRD37	1,720	1,04E-06	6,20E-06	4,986
16440	SPAG5	1,718	5,69E-12	1,64E-10	17,079

8376 JUN	1,712	3,66E-11	8,00E-10	15,217
11862 NCAPG	1,707	1,15E-08	1,20E-07	9,466
17366 TK1	1,697	1,02E-05	4,73E-05	2,735
9281 LOC10012	1,691	4,59E-03	1,08E-02	-3,170
17447 TMEFF2	1,688	1,35E-11	3,36E-10	16,217
10480 LOC85391	1,674	3,46E-06	1,82E-05	3,797
11638 MUCL1	1,668	5,56E-06	2,76E-05	3,330
3953 CPNE7	1,655	7,18E-08	5,91E-07	7,643
11307 MMP11	1,644	1,91E-10	3,39E-09	13,562
14228 PTTG1	1,628	1,69E-09	2,28E-08	11,383
785 APLN	1,610	2,39E-15	2,38E-13	24,853
14985 RPA3	1,610	1,14E-13	6,13E-12	20,991
7439 HES7	1,607	3,93E-14	2,56E-12	22,059
18306 UBE2T	1,605	3,46E-09	4,21E-08	10,667
11861 NCAPD3	1,596	1,05E-13	5,77E-12	21,072
11273 MLF1IP	1,593	2,56E-08	2,38E-07	8,671
6140 FLJ27365	1,592	3,17E-10	5,22E-09	13,057
354 ADRB2	1,587	1,33E-10	2,48E-09	13,924
5482 EZH2	1,582	8,29E-10	1,21E-08	12,095
16479 SPDEF	1,582	5,65E-11	1,17E-09	14,783
19125 ZFPM1	1,579	1,10E-14	8,47E-13	23,330
11914 ND1	1,573	4,27E-11	9,16E-10	15,064
12159 NME4	1,570	6,03E-16	7,47E-14	26,228
11100 MEX3A	1,564	2,00E-06	1,11E-05	4,338
11915 ND2	1,561	1,87E-12	6,31E-11	18,196
3959 CPSF1	1,554	1,57E-13	7,82E-12	20,675
7225 GUSBL1	1,554	6,27E-10	9,53E-09	12,375
14171 PTK6	1,548	9,85E-09	1,05E-07	9,623
4321 CYP2J2	1,548	6,85E-08	5,66E-07	7,689
5487 F12	1,544	9,65E-08	7,61E-07	7,348
13421 PLA2G7	1,542	8,05E-05	3,01E-04	0,707
15667 SGK196	1,537	7,93E-16	9,27E-14	25,955
4722 DLX1	1,528	2,67E-17	5,55E-15	29,329
19480 ZNF579	1,523	5,20E-12	1,51E-10	17,171
18382 UGT2B11	1,518	2,38E-03	6,06E-03	-2,552
7925 IFITM5	1,517	2,33E-13	1,09E-11	20,279
19067 ZDHHC11	1,505	1,65E-09	2,23E-08	11,405
9083 LCE5A	1,505	9,31E-13	3,54E-11	18,892
2694 CA1	1,504	2,92E-05	1,22E-04	1,697
3258 CDC42EP	1,503	7,90E-13	3,09E-11	19,056
3326 CDKN2A	1,497	1,25E-13	6,57E-12	20,900
19708 ZWINT	1,497	3,62E-09	4,37E-08	10,622
11082 METRN	1,495	2,25E-13	1,06E-11	20,312

15042 RPL37A	1,485	2,39E-12	7,71E-11	17,950
13672 POTES	1,478	1,45E-03	3,93E-03	-2,080
5825 FASN	1,473	6,77E-06	3,28E-05	3,135
6988 GPR160	1,471	4,33E-08	3,78E-07	8,147
264 ADAM8	1,468	6,95E-07	4,36E-06	5,386
805 APOC1	1,462	6,03E-06	2,97E-05	3,250
12923 PCBD1	1,460	1,29E-16	2,00E-14	27,766
6211 FLJ39632	1,453	1,72E-07	1,26E-06	6,773
14252 PVT1	1,452	1,91E-08	1,86E-07	8,960
3898 COX1	1,449	1,61E-11	3,93E-10	16,041
10049 LOC44046	1,436	1,60E-11	3,91E-10	16,047
7585 HLA-DRB	1,433	8,63E-09	9,43E-08	9,755
4636 DIO1	1,433	2,94E-05	1,23E-04	1,691
17241 TFF3	1,427	7,64E-05	2,87E-04	0,758
9070 LCE1D	1,423	8,98E-12	2,40E-10	16,624
10202 LOC64445	1,421	5,52E-06	2,74E-05	3,338
6307 FOSB	1,420	6,65E-22	5,25E-19	39,783
6982 GPR150	1,416	7,09E-13	2,84E-11	19,164
7788 HSP90AB1	1,415	2,09E-18	6,38E-16	31,858
17838 TPSG1	1,413	2,06E-12	6,82E-11	18,096
1256 B3GAT1	1,412	4,83E-05	1,91E-04	1,207
4130 CTAG1A	1,412	9,79E-03	2,10E-02	-3,874
10526 LPIN3	1,405	2,80E-11	6,31E-10	15,487
9310 LOC10012	1,403	1,74E-13	8,52E-12	20,570
7139 GSDMB	1,398	4,02E-07	2,69E-06	5,930
5748 FAM64A	1,398	5,39E-09	6,23E-08	10,225
7054 GPRIN2	1,396	7,19E-05	2,72E-04	0,818
4959 DUS1L	1,393	2,22E-09	2,87E-08	11,111
4825 DNMT1P35	1,392	2,38E-12	7,71E-11	17,951
3606 CKS2	1,387	1,55E-06	8,85E-06	4,593
7293 HBA2	1,387	7,37E-11	1,47E-09	14,516
12413 NUF2	1,382	1,14E-08	1,20E-07	9,475
3233 CDC2	1,382	2,54E-09	3,23E-08	10,976
6983 GPR153	1,378	1,80E-11	4,32E-10	15,927
7915 IFI6	1,375	1,05E-07	8,18E-07	7,268
7622 HMMR	1,372	7,86E-07	4,84E-06	5,264
2670 C9orf62	1,371	3,09E-14	2,10E-12	22,298
3590 CIT	1,368	1,35E-13	6,99E-12	20,823
12511 OIP5	1,368	4,12E-11	8,92E-10	15,097
5320 EPCAM	1,364	2,64E-10	4,51E-09	13,238
1869 C16orf13	1,363	1,02E-15	1,15E-13	25,706
3270 CDCA5	1,352	9,18E-09	9,92E-08	9,694
1192 ATP8A2	1,351	9,57E-06	4,48E-05	2,795

5384 ERH	1,351	8,18E-13	3,18E-11	19,021
14301 RAB11B	1,350	1,37E-03	3,74E-03	-2,029
14266 PYCR1	1,346	8,20E-13	3,18E-11	19,019
10009 LOC40165	1,345	8,99E-11	1,76E-09	14,318
2791 CAMKK2	1,343	1,27E-10	2,38E-09	13,971
14962 RP13-36C	1,339	1,26E-02	2,61E-02	-4,104
11918 ND6	1,331	2,30E-12	7,50E-11	17,987
7300 HBM	1,329	2,20E-05	9,43E-05	1,978
66 ABCC11	1,323	3,29E-03	8,08E-03	-2,858
2726 CACNA1I	1,322	1,44E-06	8,29E-06	4,667
13851 PRC1	1,320	4,05E-12	1,21E-10	17,420
13271 PHOX2A	1,313	2,95E-12	9,23E-11	17,737
7363 HCN2	1,310	2,22E-11	5,21E-10	15,717
6118 FLJ22184	1,303	1,03E-12	3,86E-11	18,794
17594 TMEM45E	1,300	1,54E-03	4,16E-03	-2,142
10443 LOC72998	1,296	3,60E-10	5,83E-09	12,929
10839 MAP2K2	1,291	2,35E-13	1,10E-11	20,268
2477 C6orf129	1,285	8,31E-14	4,72E-12	21,308
11327 MMP9	1,283	2,14E-04	7,18E-04	-0,241
5502 FAAH	1,282	8,65E-09	9,44E-08	9,753
2636 C9orf140	1,279	9,07E-11	1,77E-09	14,309
3262 CDC45L	1,278	4,91E-08	4,23E-07	8,020
18001 TRPM4	1,272	3,99E-08	3,52E-07	8,227
16649 ST14	1,272	1,70E-10	3,05E-09	13,681
7299 HBG1	1,271	1,28E-04	4,56E-04	0,256
17420 TMC4	1,262	1,11E-11	2,86E-10	16,413
2945 CCDC125	1,261	3,92E-10	6,29E-09	12,843
14703 RGS11	1,258	1,34E-12	4,81E-11	18,528
9661 LOC1478C	1,257	2,56E-09	3,25E-08	10,968
14928 ROGDI	1,255	3,80E-10	6,12E-09	12,875
492 ALAS2	1,252	2,38E-07	1,68E-06	6,452
12345 NSUN5B	1,250	2,27E-14	1,60E-12	22,604
3847 COLEC11	1,243	3,68E-05	1,49E-04	1,472
743 AP1M2	1,243	1,56E-10	2,84E-09	13,764
3377 CELSR3	1,243	1,30E-09	1,81E-08	11,643
7715 HPGD	1,243	3,61E-03	8,75E-03	-2,945
10026 LOC43995	1,239	1,21E-12	4,42E-11	18,632
11917 ND5	1,234	9,97E-14	5,49E-12	21,126
13770 PPP1R14E	1,234	5,76E-09	6,60E-08	10,158
17671 TMSB15A	1,230	2,98E-04	9,63E-04	-0,563
3332 CDKN3	1,229	1,82E-08	1,78E-07	9,010
12344 NSUN5	1,229	7,71E-17	1,28E-14	28,276
13725 PPFIA4	1,227	3,71E-06	1,93E-05	3,729

14319 RAB24	1,227	9,30E-15	7,39E-13	23,498
17219 TEX264	1,225	2,70E-12	8,54E-11	17,828
3273 CDCA8	1,220	9,25E-13	3,53E-11	18,898
13339 PILRB	1,217	1,46E-10	2,68E-09	13,829
4990 DUX4	1,215	3,12E-10	5,17E-09	13,074
14616 REG1A	1,214	7,34E-03	1,63E-02	-3,608
11485 MRPS16	1,214	2,04E-18	6,38E-16	31,884
17987 TROAP	1,213	3,53E-09	4,27E-08	10,648
2162 C1QTNF3	1,212	5,00E-13	2,10E-11	19,515
4714 DLGAP5	1,212	4,39E-08	3,83E-07	8,132
15877 SLC19A1	1,211	2,79E-15	2,70E-13	24,700
7571 HLA-DM/	1,210	1,81E-08	1,77E-07	9,016
7365 HCN4	1,208	1,39E-10	2,56E-09	13,881
8489 KCNQ10	1,207	1,17E-06	6,92E-06	4,868
5779 FAM83H	1,206	2,50E-12	8,02E-11	17,905
7801 HSPA6	1,205	1,65E-04	5,71E-04	0,008
127 ACAD8	1,205	2,71E-08	2,50E-07	8,614
11076 MESP1	1,202	2,96E-06	1,57E-05	3,953
13553 PMS2L5	1,200	2,22E-15	2,27E-13	24,927
14688 RGL2	1,200	2,11E-12	6,98E-11	18,071
12779 P4HA1	1,199	3,12E-09	3,85E-08	10,771
3085 CCNB1	1,195	2,53E-08	2,36E-07	8,684
3814 COL1A1	1,193	8,08E-08	6,52E-07	7,525
14401 RAD54L	1,192	4,11E-09	4,87E-08	10,496
3966 CPT1B	1,191	1,43E-07	1,07E-06	6,957
1075 ATAD4	1,191	1,37E-03	3,73E-03	-2,025
72 ABCC5	1,186	6,81E-08	5,64E-07	7,696
17455 TMEM106	1,184	6,94E-07	4,35E-06	5,388
8676 KIAA1683	1,182	2,88E-05	1,20E-04	1,712
1302 BAIAP2L1	1,180	8,15E-13	3,17E-11	19,025
13889 PRIC285	1,180	2,29E-12	7,50E-11	17,990
16411 SOX4	1,178	4,45E-07	2,94E-06	5,829
13338 PILRA	1,175	1,06E-14	8,25E-13	23,364
15533 SERHL2	1,173	3,10E-03	7,65E-03	-2,801
2011 C19orf48	1,171	4,64E-05	1,84E-04	1,245
1897 C16orf75	1,169	1,45E-06	8,37E-06	4,656
10198 LOC64438	1,169	3,18E-08	2,89E-07	8,454
18473 UQCRB	1,168	1,78E-11	4,30E-10	15,937
2851 CASKIN1	1,165	1,61E-13	8,00E-12	20,647
13550 PMS2L11	1,165	1,35E-15	1,47E-13	25,423
10222 LOC64525	1,159	2,05E-13	9,75E-12	20,408
17845 TPX2	1,156	3,37E-10	5,50E-09	12,997
6008 FGG	1,155	2,20E-03	5,66E-03	-2,478

5219 ELK4	1,154	3,22E-15	3,00E-13	24,557
9145 LGALS2	1,153	2,07E-07	1,49E-06	6,589
10488 LOC91316	1,152	1,07E-10	2,04E-09	14,148
19651 ZNF841	1,151	2,37E-08	2,23E-07	8,747
4450 DCXR	1,151	1,57E-05	6,98E-05	2,305
18953 YIPF6	1,150	1,83E-05	7,99E-05	2,158
10904 MARCKS1	1,149	4,55E-15	3,97E-13	24,212
3803 COL10A1	1,143	2,60E-04	8,53E-04	-0,431
17779 TOP2A	1,140	5,00E-07	3,25E-06	5,713
19443 ZNF541	1,138	8,75E-06	4,13E-05	2,883
18716 WBP1	1,136	6,52E-11	1,32E-09	14,639
16822 SUMF2	1,135	4,54E-11	9,69E-10	15,001
1866 C15orf61	1,134	1,02E-15	1,15E-13	25,701
4982 DUSP5P	1,131	3,26E-10	5,35E-09	13,029
17867 TRAP1	1,131	3,49E-17	6,88E-15	29,065
7896 IDO1	1,131	2,91E-07	2,02E-06	6,251
13178 PFKFB4	1,130	1,20E-09	1,68E-08	11,725
18135 TTLL12	1,128	1,44E-07	1,08E-06	6,947
1955 C17orf96	1,125	9,11E-09	9,87E-08	9,700
5167 EIF2S3	1,124	1,28E-11	3,21E-10	16,270
7584 HLA-DRB	1,122	1,15E-07	8,88E-07	7,175
16815 SULT1C2	1,121	1,15E-04	4,15E-04	0,356
17535 TMEM184	1,119	3,21E-05	1,32E-04	1,607
7821 HSPE1	1,119	8,55E-11	1,68E-09	14,368
16299 SNHG7	1,117	2,74E-08	2,52E-07	8,601
5231 ELOVL1	1,116	1,10E-13	5,97E-12	21,024
13689 POU5F1P3	1,116	9,19E-07	5,55E-06	5,110
6845 GNB2	1,114	1,03E-14	8,09E-13	23,396
10980 MCM2	1,114	5,51E-08	4,67E-07	7,906
8173 INTS1	1,113	5,16E-14	3,21E-12	21,785
5496 F5	1,113	1,40E-02	2,86E-02	-4,202
10209 LOC64465	1,112	1,59E-08	1,59E-07	9,143
12964 PCDHB2	1,110	2,44E-05	1,04E-04	1,874
7107 GRIN2D	1,110	1,78E-11	4,30E-10	15,937
12410 NUDT8	1,110	5,08E-05	2,00E-04	1,157
7311 hCG_1641	1,109	1,86E-13	9,02E-12	20,505
13129 PEBP4	1,107	1,76E-05	7,74E-05	2,193
3078 CCL4	1,106	1,30E-06	7,61E-06	4,763
17484 TMEM134	1,105	6,16E-09	7,00E-08	10,091
7581 HLA-DQB	1,103	5,28E-06	2,64E-05	3,381
12972 PCDHGA2	1,103	5,93E-11	1,22E-09	14,735
3291 CDH24	1,102	1,88E-13	9,06E-12	20,495
6718 GINS2	1,100	3,71E-07	2,51E-06	6,010

13131 PECE	1,096	6,09E-07	3,88E-06	5,517
2930 CCDC11	1,096	1,82E-11	4,36E-10	15,916
6704 GHRLOS	1,093	3,01E-09	3,74E-08	10,806
16943 TAF10	1,090	2,67E-11	6,06E-10	15,532
9049 LASS4	1,090	9,68E-10	1,39E-08	11,940
13552 PMS2L3	1,088	6,93E-18	1,75E-15	30,669
9959 LOC39949	1,087	4,42E-07	2,92E-06	5,837
12801 PACSIN1	1,082	4,18E-09	4,94E-08	10,479
6316 FOXD1	1,082	1,08E-08	1,14E-07	9,530
10298 LOC64983	1,079	1,32E-11	3,30E-10	16,236
16085 SLC45A2	1,076	1,98E-04	6,73E-04	-0,168
19119 ZFP62	1,075	3,29E-04	1,05E-03	-0,658
7872 ICA1	1,075	3,78E-08	3,35E-07	8,281
11291 MLPH	1,072	3,81E-06	1,97E-05	3,704
14174 PTMAP7	1,071	1,74E-12	5,97E-11	18,264
10044 LOC44035	1,069	3,25E-08	2,94E-07	8,432
3892 CORO2A	1,067	2,36E-08	2,22E-07	8,750
19564 ZNF692	1,067	3,14E-06	1,66E-05	3,895
9750 LOC25578	1,067	2,64E-14	1,82E-12	22,455
13087 PDIA5	1,067	2,02E-07	1,45E-06	6,615
3077 CCL3L3	1,065	1,85E-21	1,18E-18	38,781
11953 NDUFB1	1,064	4,48E-14	2,83E-12	21,927
11851 NBPF20	1,063	8,67E-08	6,93E-07	7,455
10043 LOC44034	1,062	3,13E-10	5,18E-09	13,069
7787 HSP90AB	1,060	4,63E-14	2,90E-12	21,895
10588 LRRC36	1,060	1,86E-06	1,04E-05	4,410
17166 TDO2	1,057	6,61E-03	1,49E-02	-3,510
18880 WWC1	1,056	4,08E-05	1,64E-04	1,371
14320 RAB25	1,055	1,72E-12	5,91E-11	18,278
17479 TMEM132	1,053	8,03E-06	3,83E-05	2,967
2788 CAMK2N	1,050	4,93E-11	1,04E-09	14,918
16326 SNRPF	1,049	4,82E-13	2,05E-11	19,551
11501 MRPS33	1,049	1,31E-08	1,35E-07	9,335
48 ABCA3	1,047	9,60E-12	2,53E-10	16,556
7781 HSF4	1,046	6,25E-11	1,27E-09	14,682
8262 ISX	1,046	9,49E-05	3,48E-04	0,547
16030 SLC35E2	1,044	1,08E-05	4,98E-05	2,680
8799 KLHDC9	1,044	2,71E-11	6,14E-10	15,517
14015 PRR7	1,043	2,46E-11	5,62E-10	15,616
11264 MKNK2	1,040	1,28E-08	1,32E-07	9,360
14947 RP11-216I	1,039	4,48E-09	5,27E-08	10,409
10098 LOC44246	1,037	1,66E-07	1,22E-06	6,811
6568 GAS5	1,036	1,72E-06	9,74E-06	4,487

7572 HLA-DME	1,033	8,46E-07	5,15E-06	5,192
1344 BCAM	1,030	1,75E-11	4,23E-10	15,957
1726 C12orf45	1,029	1,80E-11	4,32E-10	15,926
10002 LOC40135	1,029	2,24E-13	1,06E-11	20,318
1517 BRD9	1,028	3,07E-10	5,10E-09	13,088
7540 HIST1H4E	1,027	1,46E-04	5,13E-04	0,125
18051 TSPAN13	1,026	1,58E-06	9,03E-06	4,572
9183 LIG1	1,026	5,63E-11	1,17E-09	14,786
8319 ITPR3	1,025	1,17E-09	1,65E-08	11,748
12224 NP	1,024	1,92E-05	8,34E-05	2,112
5376 ERCC6L	1,023	4,60E-09	5,39E-08	10,383
17109 TCEA3	1,022	1,57E-07	1,17E-06	6,863
452 AK3L1	1,022	5,62E-08	4,76E-07	7,886
697 ANKZF1	1,021	9,27E-11	1,81E-09	14,287
2221 C20orf74	1,021	8,03E-05	3,00E-04	0,710
9902 LOC38856	1,019	3,15E-10	5,21E-09	13,062
1392 BDH1	1,018	5,67E-12	1,63E-10	17,084
7575 HLA-DPA	1,017	8,65E-08	6,92E-07	7,457
11064 MELK	1,017	8,26E-08	6,65E-07	7,503
8251 ISG15	1,016	1,38E-04	4,88E-04	0,181
11928 NDRG1	1,016	5,78E-04	1,73E-03	-1,202
14953 RP11-345I	1,015	2,41E-06	1,31E-05	4,154
13551 PMS2L2	1,013	5,34E-17	9,49E-15	28,641
7183 GTF2H2D	1,013	4,92E-09	5,72E-08	10,316
15950 SLC25A35	1,010	1,18E-13	6,29E-12	20,954
8095 IL4I1	1,010	6,71E-08	5,58E-07	7,709
12346 NSUN5C	1,010	6,07E-17	1,05E-14	28,513
5504 FABP1	1,009	1,34E-02	2,75E-02	-4,160
11271 MLEC	1,008	5,84E-09	6,69E-08	10,144
18048 TSPAN10	1,008	6,65E-14	3,99E-12	21,531
15457 SEC61G	1,008	4,39E-07	2,91E-06	5,843
3915 COX6C	1,006	2,19E-11	5,15E-10	15,731
902 ARHGEF1	1,004	9,57E-10	1,38E-08	11,952
12167 NMRAL1	1,004	1,65E-11	4,03E-10	16,012
10099 LOC44257	1,003	1,30E-11	3,26E-10	16,254
2854 CASP10	1,003	1,58E-04	5,50E-04	0,050
9787 LOC28423	1,003	1,21E-11	3,08E-10	16,324
177 ACP5	-1,002	1,98E-04	6,71E-04	-0,166
19536 ZNF655	-1,003	2,68E-09	3,37E-08	10,922
16717 STEAP3	-1,003	3,11E-09	3,84E-08	10,774
621 ANGPTL7	-1,003	2,55E-09	3,24E-08	10,973
13810 PPP3CA	-1,003	2,96E-05	1,23E-04	1,685
4857 DOK7	-1,004	5,21E-14	3,23E-12	21,775

16182 SLIT2	-1,004	1,48E-11	3,65E-10	16,125
17221 TF	-1,005	1,41E-06	8,16E-06	4,685
15897 SLC22A17	-1,007	1,40E-05	6,30E-05	2,418
15865 SLC16A9	-1,008	2,80E-06	1,49E-05	4,007
12293 NR2F2	-1,008	2,99E-08	2,73E-07	8,516
16618 SSBP2	-1,008	4,57E-10	7,21E-09	12,691
16777 STX12	-1,009	4,01E-14	2,59E-12	22,038
7181 GTF2F2	-1,010	1,20E-10	2,26E-09	14,028
17840 TPST2	-1,010	3,04E-15	2,90E-13	24,614
8333 JAGN1	-1,011	1,18E-09	1,66E-08	11,742
17254 TGF2	-1,011	2,86E-10	4,83E-09	13,161
14716 RGS5	-1,011	5,91E-06	2,91E-05	3,270
3848 COLEC12	-1,011	1,10E-02	2,32E-02	-3,978
17259 TGFBR3	-1,012	5,29E-10	8,23E-09	12,545
17832 TPRG1	-1,012	3,29E-12	1,02E-10	17,628
4681 DKFZP586c001000	-1,013	3,92E-10	6,29E-09	12,844
19113 ZFP36L1	-1,013	2,22E-10	3,85E-09	13,413
17652 TMOD1	-1,014	3,23E-11	7,17E-10	15,341
8384 KANK2	-1,015	3,45E-14	2,31E-12	22,186
9150 LGALS7B	-1,016	1,43E-08	1,45E-07	9,251
17290 THBS4	-1,017	4,57E-03	1,08E-02	-3,166
5285 ENPP1	-1,017	4,13E-08	3,63E-07	8,193
6338 FOXN3	-1,017	1,04E-07	8,15E-07	7,273
3319 CDKL1	-1,018	1,21E-11	3,07E-10	16,329
5245 EMCN	-1,018	1,16E-06	6,85E-06	4,880
7088 GRHL1	-1,020	1,49E-06	8,54E-06	4,634
320 ADH1A	-1,021	3,88E-06	2,00E-05	3,685
16669 ST8SIA1	-1,021	3,83E-05	1,55E-04	1,433
6374 FRMD6	-1,022	1,86E-17	4,03E-15	29,690
111 ABLIM1	-1,022	2,66E-06	1,42E-05	4,059
14025 PRRX2	-1,022	4,93E-10	7,73E-09	12,615
3604 CKMT2	-1,022	3,44E-05	1,41E-04	1,538
16287 SNCAIP	-1,023	7,21E-11	1,44E-09	14,539
13703 PPAP2A	-1,024	1,24E-02	2,57E-02	-4,087
8793 KLHDC5	-1,025	9,28E-14	5,20E-12	21,199
18595 VCL	-1,027	1,35E-10	2,51E-09	13,908
1266 B3GNT8	-1,027	9,64E-17	1,56E-14	28,053
3613 CLCA4	-1,027	4,60E-06	2,34E-05	3,516
12043 NFIA	-1,027	4,77E-08	4,12E-07	8,050
14032 PRSS23	-1,027	1,11E-04	4,02E-04	0,391
8279 ITGA8	-1,028	6,25E-08	5,23E-07	7,781
16898 SYT10	-1,031	1,03E-08	1,09E-07	9,575
10442 LOC72997	-1,033	1,33E-10	2,48E-09	13,922

7886 ID3	-1,033	6,97E-08	5,75E-07	7,672
4165 CTPS	-1,035	2,28E-07	1,63E-06	6,491
15539 SERP2	-1,036	6,82E-05	2,59E-04	0,869
9249 LMNA	-1,037	1,75E-12	5,98E-11	18,260
2733 CACNA2I	-1,038	3,47E-09	4,21E-08	10,666
15095 RPS27L	-1,039	2,94E-09	3,66E-08	10,831
18143 TTN	-1,040	1,91E-04	6,51E-04	-0,133
14110 PSMD7	-1,041	1,61E-08	1,61E-07	9,134
1238 AXL	-1,041	2,60E-09	3,29E-08	10,954
7906 IFFO2	-1,042	1,54E-07	1,15E-06	6,882
17724 TNIK	-1,043	2,35E-15	2,37E-13	24,870
8239 IRS1	-1,043	1,62E-06	9,21E-06	4,550
15699 SH3BGRL	-1,044	5,91E-11	1,22E-09	14,737
1850 C15orf41	-1,045	1,36E-12	4,88E-11	18,511
9255 LMO4	-1,045	1,82E-09	2,44E-08	11,308
53 ABCA8	-1,046	3,22E-09	3,96E-08	10,739
7164 GSTO1	-1,048	1,93E-09	2,55E-08	11,253
18622 VILL	-1,048	3,89E-10	6,25E-09	12,853
5074 EDNRA	-1,049	1,14E-12	4,21E-11	18,690
18963 YPEL5	-1,049	8,65E-11	1,70E-09	14,357
116 ABR	-1,050	1,99E-09	2,62E-08	11,220
7453 HGD	-1,052	6,74E-04	1,98E-03	-1,349
13048 PDE11A	-1,054	4,31E-06	2,21E-05	3,580
12552 OPTN	-1,055	6,81E-07	4,28E-06	5,407
12121 NKX3-1	-1,057	6,23E-06	3,05E-05	3,217
1416 BEX4	-1,057	7,04E-08	5,81E-07	7,662
5286 ENPP2	-1,057	3,74E-04	1,18E-03	-0,784
13332 PIK3R1	-1,058	1,12E-11	2,87E-10	16,406
6071 FLJ10357	-1,059	3,41E-09	4,17E-08	10,681
12828 PAK3	-1,060	1,12E-08	1,17E-07	9,498
14458 RARRES2	-1,062	3,01E-09	3,74E-08	10,807
10962 MCAM	-1,063	6,78E-14	4,03E-12	21,512
13443 PLCE1	-1,064	1,24E-09	1,72E-08	11,696
2867 CASQ2	-1,065	5,00E-08	4,29E-07	8,003
18212 TWIST2	-1,067	5,24E-11	1,10E-09	14,858
18734 WDR1	-1,069	2,81E-16	3,85E-14	26,989
5115 EFS	-1,069	1,28E-07	9,77E-07	7,066
215 ACTN1	-1,070	8,66E-10	1,26E-08	12,052
476 AKR1C1	-1,070	1,58E-09	2,15E-08	11,449
13866 PRDM6	-1,070	3,25E-10	5,34E-09	13,033
18239 TXNRD1	-1,071	2,57E-08	2,39E-07	8,665
17755 TNS1	-1,072	1,66E-11	4,05E-10	16,007
14773 RILPL2	-1,073	1,18E-10	2,24E-09	14,045

14971 RP4-691N	-1,075	1,47E-05	6,56E-05	2,375
12215 NOV	-1,075	3,33E-06	1,75E-05	3,835
704 ANO5	-1,077	2,16E-14	1,54E-12	22,655
55 ABCB1	-1,077	3,05E-18	8,85E-16	31,482
5844 FBN1	-1,078	6,67E-05	2,54E-04	0,891
7408 HECTD2	-1,078	2,35E-13	1,10E-11	20,267
5632 FAM162B	-1,079	1,57E-10	2,85E-09	13,759
16379 SOD3	-1,080	5,13E-07	3,33E-06	5,688
172 ACOX2	-1,083	2,07E-08	1,99E-07	8,884
5039 EBF4	-1,085	1,79E-12	6,10E-11	18,236
13811 PPP3CB	-1,087	2,86E-12	9,00E-11	17,769
9166 LHFP	-1,088	5,69E-07	3,66E-06	5,585
17581 TMMEM35	-1,091	4,12E-12	1,22E-10	17,404
7066 GPX3	-1,092	6,47E-09	7,32E-08	10,043
8101 IL6ST	-1,093	1,87E-12	6,31E-11	18,195
7940 IFNGR1	-1,093	1,78E-07	1,30E-06	6,737
3352 CEACAM	-1,094	5,06E-08	4,34E-07	7,991
12303 NRAP	-1,096	6,77E-04	1,99E-03	-1,354
1325 BATF	-1,098	9,70E-06	4,53E-05	2,782
18681 VSIG2	-1,098	3,45E-08	3,09E-07	8,372
18353 UCHL1	-1,100	2,08E-04	7,01E-04	-0,214
13442 PLCD4	-1,101	2,47E-10	4,25E-09	13,305
13389 PKIG	-1,102	2,25E-10	3,91E-09	13,398
5075 EDNRB	-1,102	4,40E-09	5,18E-08	10,428
12365 NTN1	-1,102	1,80E-16	2,65E-14	27,431
14163 PTGS2	-1,103	1,24E-05	5,64E-05	2,542
4976 DUSP23	-1,104	1,56E-04	5,45E-04	0,061
17809 TPBG	-1,104	2,17E-10	3,78E-09	13,435
180 ACP	-1,105	5,14E-03	1,19E-02	-3,276
10698 LY6K	-1,105	1,15E-02	2,42E-02	-4,024
15916 SLC24A3	-1,105	6,32E-18	1,66E-15	30,761
639 ANKRD1	-1,109	1,53E-03	4,12E-03	-2,134
112 ABLIM2	-1,109	1,06E-05	4,92E-05	2,693
18863 WNT5B	-1,110	4,29E-11	9,19E-10	15,058
2088 C1orf190	-1,110	3,69E-15	3,38E-13	24,421
16605 SRPX2	-1,110	3,22E-09	3,96E-08	10,738
7907 IFI16	-1,111	3,12E-08	2,84E-07	8,473
14858 RNF150	-1,111	7,98E-10	1,17E-08	12,133
3281 CDH13	-1,112	1,57E-07	1,17E-06	6,863
17399 TM4SF1	-1,112	5,67E-06	2,81E-05	3,310
1430 BHMT2	-1,116	4,06E-17	7,69E-15	28,914
2870 CAST	-1,119	5,88E-10	9,02E-09	12,440
15619 SFRP4	-1,122	6,35E-05	2,43E-04	0,940

907 ARHGEF3	-1,124	1,76E-10	3,15E-09	13,646
12367 NTN4	-1,127	2,35E-07	1,67E-06	6,464
17591 TMEM43	-1,127	5,65E-15	4,79E-13	23,995
852 AREG	-1,127	3,80E-04	1,19E-03	-0,798
15305 SAV1	-1,128	4,19E-10	6,67E-09	12,778
8783 KLF5	-1,128	7,67E-12	2,10E-10	16,781
716 ANTXR2	-1,133	3,71E-14	2,46E-12	22,114
9023 LAMC1	-1,134	2,45E-10	4,21E-09	13,316
4732 DMD	-1,134	1,60E-13	7,95E-12	20,656
14424 RAMP1	-1,134	1,01E-03	2,85E-03	-1,736
16046 SLC38A1	-1,135	1,24E-06	7,26E-06	4,812
1261 B3GNT3	-1,135	3,92E-06	2,02E-05	3,674
17499 TMEM14C	-1,136	5,57E-06	2,77E-05	3,327
5507 FABP3	-1,136	9,09E-16	1,04E-13	25,818
16364 SNX7	-1,136	1,18E-07	9,12E-07	7,145
13448 PLCL1	-1,137	3,87E-09	4,62E-08	10,557
8331 JAG1	-1,138	7,46E-08	6,10E-07	7,604
505 ALDH3A2	-1,139	5,95E-11	1,23E-09	14,731
2711 CAB39L	-1,139	1,65E-09	2,23E-08	11,408
9036 LARGE	-1,139	4,24E-11	9,11E-10	15,071
12478 OCC-1	-1,140	2,56E-09	3,24E-08	10,970
1480 BNC2	-1,140	1,35E-17	3,05E-15	30,010
11063 MEIS3P1	-1,145	7,60E-12	2,09E-10	16,790
3432 CFD	-1,146	5,85E-04	1,74E-03	-1,214
2275 C22orf28	-1,147	3,11E-15	2,94E-13	24,590
8096 IL4R	-1,147	6,41E-04	1,90E-03	-1,302
11324 MMP3	-1,147	1,42E-05	6,38E-05	2,405
1289 BAG1	-1,147	6,51E-11	1,32E-09	14,640
19240 ZNF219	-1,149	3,94E-14	2,56E-12	22,055
6999 GPR177	-1,150	6,84E-10	1,03E-08	12,288
1000 ART3	-1,155	1,60E-10	2,88E-09	13,743
15160 RSPO1	-1,155	1,56E-13	7,78E-12	20,682
823 APP	-1,159	4,77E-06	2,41E-05	3,482
1366 BCL2	-1,159	5,95E-12	1,70E-10	17,035
7152 GSTA1	-1,160	1,18E-08	1,23E-07	9,443
7975 IGFBP7	-1,160	1,04E-06	6,20E-06	4,986
12917 PBX1	-1,161	4,28E-12	1,26E-10	17,366
12050 NFKBIA	-1,162	3,28E-08	2,96E-07	8,423
4219 CXCL1	-1,162	5,34E-03	1,23E-02	-3,311
17738 TNNI2	-1,163	2,77E-04	9,03E-04	-0,493
16202 SMAD3	-1,163	4,80E-17	8,67E-15	28,748
6250 FLJ46111	-1,168	7,19E-14	4,21E-12	21,453
5998 FGFBP1	-1,168	1,70E-12	5,88E-11	18,288

19143 ZHX3	-1,170	1,49E-12	5,26E-11	18,420
11854 NBR1	-1,170	1,90E-12	6,38E-11	18,176
4405 DBNDD2	-1,170	4,16E-15	3,68E-13	24,302
500 ALDH1B1	-1,172	3,59E-12	1,09E-10	17,540
15445 SEC23A	-1,173	1,02E-11	2,68E-10	16,494
15706 SH3D19	-1,175	2,31E-12	7,51E-11	17,983
9890 LOC38776	-1,175	8,22E-04	2,37E-03	-1,539
1602 C10orf116	-1,176	2,37E-04	7,85E-04	-0,340
773 APCDD1	-1,176	2,45E-07	1,73E-06	6,423
8718 KIF1C	-1,177	2,08E-14	1,49E-12	22,692
18235 TXNIP	-1,177	1,73E-05	7,63E-05	2,210
12331 NSBP1	-1,181	7,15E-16	8,59E-14	26,058
6857 GNG4	-1,183	1,42E-05	6,39E-05	2,404
18224 TXNDC13	-1,185	2,54E-15	2,49E-13	24,794
7324 hCG_1783	-1,186	1,88E-13	9,06E-12	20,495
7970 IGFBP2	-1,186	2,55E-08	2,37E-07	8,675
14982 RP9P	-1,188	3,86E-22	3,63E-19	40,314
9019 LAMB2	-1,188	3,98E-12	1,19E-10	17,437
5792 FAM92A1	-1,188	1,90E-12	6,37E-11	18,180
12329 NRXN3	-1,190	7,51E-04	2,19E-03	-1,454
6474 GABARA1	-1,191	8,47E-09	9,26E-08	9,774
6524 GALNAC2	-1,192	2,95E-11	6,61E-10	15,434
17352 TIMP3	-1,192	3,83E-09	4,59E-08	10,566
7361 HCLS1	-1,195	1,50E-05	6,69E-05	2,354
615 ANGPTL1	-1,195	1,03E-10	1,98E-09	14,183
10505 LOXL1	-1,196	3,35E-08	3,01E-07	8,403
6729 GJA1	-1,198	2,02E-12	6,75E-11	18,115
15237 S100B	-1,198	8,03E-12	2,18E-10	16,735
14624 RELB	-1,199	1,16E-05	5,31E-05	2,609
14328 RAB31	-1,202	4,99E-11	1,05E-09	14,907
6670 GFPT2	-1,202	3,86E-09	4,62E-08	10,558
11692 MYH2	-1,202	1,29E-03	3,55E-03	-1,972
5072 EDN2	-1,203	9,88E-07	5,93E-06	5,038
10794 MAGI2	-1,204	2,41E-10	4,16E-09	13,330
11652 MVP	-1,204	4,18E-06	2,14E-05	3,611
3363 CEBPB	-1,207	3,72E-06	1,93E-05	3,726
3832 COL4A6	-1,208	3,82E-15	3,47E-13	24,387
8461 KCNJ8	-1,208	3,13E-10	5,18E-09	13,068
15302 SAT2	-1,208	3,30E-16	4,39E-14	26,829
2306 C2orf40	-1,209	3,06E-09	3,79E-08	10,792
1082 ATF4	-1,210	6,82E-08	5,65E-07	7,693
11706 MYL6B	-1,212	3,27E-08	2,95E-07	8,427
10544 LRFN5	-1,212	4,57E-09	5,36E-08	10,389

4206 CUTC	-1,212	7,60E-13	2,99E-11	19,096
6535 GALNT5	-1,214	1,31E-15	1,44E-13	25,450
16371 SOCS2	-1,214	1,56E-05	6,94E-05	2,312
2701 CA3	-1,215	3,13E-03	7,73E-03	-2,811
3793 COCH	-1,217	1,80E-08	1,77E-07	9,020
11412 MRAP2	-1,219	8,37E-13	3,24E-11	18,998
18999 ZBTB20	-1,220	5,45E-07	3,52E-06	5,628
5019 DZIP1	-1,220	5,34E-12	1,55E-10	17,144
6786 GLRX	-1,221	3,11E-05	1,29E-04	1,636
6384 FRY	-1,222	5,14E-08	4,39E-07	7,975
3663 CLEC4E	-1,223	1,20E-06	7,07E-06	4,843
8904 KRT19	-1,224	2,21E-04	7,40E-04	-0,274
18624 VIP	-1,224	1,01E-04	3,69E-04	0,482
11302 MME	-1,226	1,64E-04	5,68E-04	0,013
3676 CLIC6	-1,228	1,10E-11	2,84E-10	16,423
8580 KIAA0513	-1,228	1,08E-16	1,71E-14	27,945
14438 RAP1A	-1,230	6,11E-07	3,89E-06	5,515
1953 C17orf91	-1,232	1,45E-11	3,59E-10	16,144
16523 SPOCK3	-1,233	1,69E-10	3,04E-09	13,684
6004 FGFR2	-1,235	8,09E-22	6,13E-19	39,593
4717 DLL1	-1,237	1,26E-07	9,62E-07	7,084
14150 PTGER2	-1,238	1,00E-07	7,86E-07	7,312
10947 MBNL2	-1,239	1,66E-10	3,00E-09	13,701
13777 PPP1R1A	-1,240	8,94E-09	9,70E-08	9,720
17908 TRIM2	-1,240	2,79E-10	4,74E-09	13,184
8889 KRT17	-1,240	8,09E-09	8,93E-08	9,819
7223 GULP1	-1,240	5,18E-09	6,00E-08	10,264
12082 NHS	-1,241	3,57E-16	4,66E-14	26,750
4108 CSRP1	-1,241	8,41E-11	1,66E-09	14,384
17286 THBD	-1,242	2,17E-07	1,55E-06	6,543
4773 DNAJB4	-1,245	7,29E-08	5,98E-07	7,628
12377 NUAK1	-1,250	6,98E-14	4,11E-12	21,483
13769 PPP1R14A	-1,250	4,01E-11	8,69E-10	15,125
13061 PDE5A	-1,250	4,19E-14	2,70E-12	21,994
13436 PLCB1	-1,250	7,47E-12	2,06E-10	16,807
6023 FIBIN	-1,251	2,18E-09	2,83E-08	11,130
13674 POTEF	-1,252	1,02E-07	8,01E-07	7,293
9055 LATS2	-1,253	8,97E-10	1,30E-08	12,016
17820 TPM1	-1,255	2,06E-12	6,82E-11	18,099
5308 EPAS1	-1,255	2,60E-12	8,31E-11	17,863
18576 VAMP8	-1,255	1,11E-05	5,13E-05	2,646
11685 MYF6	-1,256	3,53E-04	1,12E-03	-0,727
2830 CARD10	-1,257	2,29E-12	7,50E-11	17,990

216	ACTN2	-1,260	7,48E-04	2,18E-03	-1,450
8368	JPH2	-1,264	2,05E-18	6,38E-16	31,877
5312	EPB41L3	-1,264	5,81E-10	8,95E-09	12,451
1874	C16orf45	-1,267	1,40E-12	4,99E-11	18,486
3507	CHMP4A	-1,269	4,50E-09	5,29E-08	10,405
2290	C2orf12	-1,270	3,15E-09	3,88E-08	10,762
8479	KCNMB1	-1,271	7,91E-16	9,27E-14	25,957
15833	SLC12A2	-1,271	4,64E-07	3,05E-06	5,787
4684	DKFZp667	-1,272	7,98E-16	9,27E-14	25,948
11705	MYL6	-1,274	1,56E-12	5,44E-11	18,378
11512	MRVI1	-1,280	4,45E-07	2,94E-06	5,828
16062	SLC39A2	-1,280	1,44E-06	8,29E-06	4,668
13923	PRKD1	-1,281	6,54E-10	9,88E-09	12,332
7244	H1F0	-1,281	1,72E-05	7,58E-05	2,219
17560	TMEM204	-1,283	3,11E-09	3,84E-08	10,774
7664	HOPX	-1,283	8,42E-06	4,00E-05	2,921
1415	BEX2	-1,284	7,45E-04	2,17E-03	-1,446
958	ARMCX1	-1,286	3,14E-09	3,87E-08	10,765
13296	PID1	-1,287	3,28E-10	5,39E-09	13,022
11746	MYOM2	-1,287	5,16E-10	8,06E-09	12,569
16222	SMARCD1	-1,289	1,01E-07	7,93E-07	7,303
11542	MSRB3	-1,290	2,31E-21	1,38E-18	38,566
4678	DKFZP564	-1,294	6,77E-12	1,89E-10	16,906
11929	NDRG2	-1,295	1,71E-12	5,90E-11	18,281
6496	GABRP	-1,295	2,90E-09	3,62E-08	10,845
4329	CYP3A5	-1,296	3,04E-08	2,78E-07	8,499
3625	CLDN1	-1,297	6,68E-11	1,35E-09	14,615
1359	BCHE	-1,300	2,00E-03	5,20E-03	-2,385
3199	CD59	-1,300	2,27E-16	3,20E-14	27,200
3248	CDC37L1	-1,300	1,66E-15	1,74E-13	25,216
17026	TBC1D1	-1,301	2,25E-14	1,59E-12	22,613
18549	UST	-1,305	1,52E-18	4,98E-16	32,176
5537	FAM107A	-1,306	7,95E-07	4,88E-06	5,253
503	ALDH2	-1,311	7,53E-08	6,16E-07	7,595
9874	LOC34688	-1,312	7,37E-13	2,93E-11	19,125
3391	CENPN	-1,312	8,26E-07	5,05E-06	5,215
9090	LCN2	-1,317	1,78E-03	4,71E-03	-2,278
16845	SUSD5	-1,317	9,86E-12	2,59E-10	16,530
14024	PRRX1	-1,319	3,07E-16	4,17E-14	26,901
8417	KCNB1	-1,320	1,23E-11	3,12E-10	16,306
13659	PON3	-1,321	1,16E-05	5,32E-05	2,607
2800	CAND2	-1,327	2,87E-15	2,75E-13	24,672
19317	ZNF334	-1,327	1,79E-12	6,10E-11	18,237

4363 D4S234E	-1,328	1,75E-08	1,72E-07	9,050
14533 RBM3	-1,331	1,87E-05	8,15E-05	2,136
6929 GPC4	-1,332	1,40E-14	1,03E-12	23,089
3421 CES1	-1,333	3,57E-10	5,79E-09	12,937
17666 TMPRSS4	-1,334	1,25E-05	5,68E-05	2,534
4428 DCN	-1,334	3,81E-04	1,19E-03	-0,801
447 AJAP1	-1,335	2,52E-14	1,75E-12	22,503
13148 PERP	-1,335	4,61E-09	5,39E-08	10,380
3279 CDH11	-1,337	2,36E-08	2,22E-07	8,753
7041 GPR87	-1,338	1,26E-17	2,93E-15	30,073
4734 DMKN	-1,339	5,91E-12	1,69E-10	17,042
11660 MXRA7	-1,339	1,20E-20	5,64E-18	36,949
16897 SYT1	-1,340	9,64E-11	1,87E-09	14,247
11708 MYL9	-1,341	4,34E-12	1,28E-10	17,352
4785 DNAJC15	-1,345	2,69E-12	8,54E-11	17,830
3071 CCL23	-1,346	4,09E-10	6,53E-09	12,803
3364 CEBPD	-1,347	1,21E-05	5,52E-05	2,565
4693 DKK1	-1,349	4,81E-09	5,60E-08	10,339
3446 CFTR	-1,349	4,98E-05	1,96E-04	1,177
18689 VTCN1	-1,350	7,42E-08	6,08E-07	7,610
8289 ITGB1BP2	-1,351	2,12E-11	5,02E-10	15,762
11560 MT1M	-1,351	1,90E-04	6,49E-04	-0,129
9442 LOC10013	-1,351	1,34E-02	2,75E-02	-4,160
7703 HOXD13	-1,352	2,93E-17	5,95E-15	29,238
9858 LOC34123	-1,354	3,65E-10	5,90E-09	12,916
9963 LOC39995	-1,357	4,86E-17	8,71E-15	28,734
5000 DYNC1H1	-1,358	9,20E-15	7,36E-13	23,508
15125 RRAD	-1,359	1,43E-08	1,45E-07	9,250
12256 NPNT	-1,360	3,82E-05	1,54E-04	1,436
1143 ATP2B4	-1,363	1,53E-17	3,39E-15	29,882
15384 SCPEP1	-1,364	3,80E-12	1,14E-10	17,485
14595 RDH10	-1,365	9,26E-08	7,33E-07	7,389
14133 PTBP2	-1,366	5,08E-13	2,14E-11	19,498
7800 HSPA5	-1,366	5,91E-07	3,78E-06	5,548
6255 FLNC	-1,368	3,48E-15	3,20E-13	24,480
13013 PCP4L1	-1,368	8,07E-05	3,02E-04	0,705
13760 PPP1CB	-1,372	3,18E-11	7,07E-10	15,358
17116 TCEAL7	-1,376	1,14E-18	3,86E-16	32,462
725 ANXA3	-1,376	1,67E-06	9,44E-06	4,521
10672 LTBP1	-1,377	2,04E-08	1,97E-07	8,899
10829 MAOA	-1,378	7,81E-06	3,73E-05	2,995
2650 C9orf3	-1,378	3,24E-15	3,00E-13	24,550
5411 ESR1	-1,379	3,91E-15	3,51E-13	24,362

14813 RNASE4	-1,380	2,26E-06	1,24E-05	4,219
14045 PRUNE2	-1,380	3,29E-05	1,35E-04	1,583
6772 GLIPR2	-1,380	4,40E-06	2,24E-05	3,562
11115 MFN2	-1,382	1,92E-14	1,38E-12	22,772
12774 P2RY2	-1,383	3,15E-14	2,12E-12	22,278
6364 FREQ	-1,384	6,67E-19	2,44E-16	32,988
4654 DIXDC1	-1,387	1,14E-16	1,78E-14	27,889
6966 GPR124	-1,392	1,78E-16	2,65E-14	27,441
11170 MGC2410	-1,393	2,02E-12	6,75E-11	18,116
6514 GAL	-1,398	3,85E-03	9,25E-03	-3,004
7973 IGFBP5	-1,399	6,43E-12	1,81E-10	16,958
1317 BASP1	-1,401	2,89E-04	9,37E-04	-0,534
5096 EFEMP1	-1,401	1,45E-05	6,48E-05	2,387
6654 GEM	-1,401	3,14E-06	1,66E-05	3,894
16390 SORD	-1,403	2,32E-02	4,43E-02	-4,657
7156 GSTA5	-1,411	1,01E-09	1,44E-08	11,900
4273 CYB5R2	-1,413	9,80E-10	1,40E-08	11,928
13891 PRICKLE2	-1,415	3,98E-17	7,61E-15	28,934
5884 FBXO30	-1,417	2,99E-17	6,01E-15	29,218
321 ADH1C	-1,417	4,64E-07	3,05E-06	5,788
15303 SATB1	-1,418	5,91E-10	9,06E-09	12,435
4638 DIO3	-1,418	1,11E-12	4,15E-11	18,711
13949 PRNP	-1,419	3,20E-11	7,10E-10	15,351
6773 GLIS1	-1,421	8,15E-11	1,61E-09	14,416
3286 CDH19	-1,427	5,55E-13	2,29E-11	19,410
4963 DUSP1	-1,432	1,18E-06	6,97E-06	4,860
4809 DNALI1	-1,437	2,27E-05	9,71E-05	1,947
11061 MEIS2	-1,439	9,06E-16	1,04E-13	25,822
15888 SLC20A2	-1,446	1,22E-14	9,27E-13	23,224
16489 SPG20	-1,452	5,95E-15	5,00E-13	23,944
14921 ROBO1	-1,452	8,08E-16	9,32E-14	25,936
7030 GPR64	-1,453	1,10E-04	3,97E-04	0,404
10529 LPP	-1,456	5,48E-13	2,27E-11	19,422
573 AMD1	-1,460	1,55E-05	6,87E-05	2,322
16751 STOM	-1,461	5,77E-12	1,66E-10	17,065
11108 MFAP4	-1,462	3,45E-06	1,81E-05	3,801
11556 MT1G	-1,462	2,15E-04	7,22E-04	-0,246
2060 C1orf133	-1,462	6,98E-17	1,20E-14	28,375
17699 TNFRSF11B	-1,465	1,43E-07	1,07E-06	6,959
411 AGT	-1,468	2,60E-04	8,53E-04	-0,431
10689 LXN	-1,470	1,26E-04	4,49E-04	0,271
16194 SLN	-1,472	2,66E-04	8,71E-04	-0,453
19642 ZNF827	-1,473	8,50E-05	3,16E-04	0,655

705 ANO6	-1,475	7,84E-14	4,54E-12	21,368
8623 KIAA121C	-1,476	9,83E-09	1,05E-07	9,625
14318 RAB23	-1,480	2,01E-17	4,32E-15	29,610
2612 C8orf84	-1,484	9,92E-09	1,06E-07	9,616
18020 TSC22D1	-1,485	3,83E-09	4,59E-08	10,566
11977 NEB	-1,487	2,25E-04	7,51E-04	-0,290
6767 GLI3	-1,487	1,31E-16	2,02E-14	27,749
16810 SULF2	-1,490	6,09E-09	6,94E-08	10,103
8269 ITGA1	-1,491	1,87E-08	1,82E-07	8,982
8337 JAKMIP1	-1,491	4,93E-06	2,48E-05	3,449
16286 SNCA	-1,492	3,26E-08	2,95E-07	8,429
6575 GATA3	-1,495	3,26E-19	1,21E-16	33,697
6447 FYCO1	-1,497	2,16E-16	3,09E-14	27,252
7700 HOXD10	-1,499	1,55E-12	5,44E-11	18,380
11554 MT1E	-1,500	6,51E-07	4,11E-06	5,452
18823 WFDC2	-1,501	3,63E-12	1,10E-10	17,529
10354 LOC72826	-1,505	1,87E-12	6,31E-11	18,196
13511 PLS3	-1,506	3,80E-14	2,50E-12	22,091
1284 BACE1	-1,510	1,39E-14	1,03E-12	23,094
13103 PDPN	-1,511	1,90E-13	9,16E-12	20,479
5582 FAM129A	-1,513	1,54E-07	1,15E-06	6,881
4016 CRISPLD1	-1,518	1,55E-07	1,15E-06	6,876
2906 CBX7	-1,521	5,63E-16	7,16E-14	26,295
12466 OAT	-1,522	1,83E-09	2,44E-08	11,304
3842 COL8A2	-1,523	3,78E-13	1,65E-11	19,793
12944 PCDH8	-1,528	8,52E-07	5,18E-06	5,185
17676 TMTC1	-1,528	2,11E-15	2,16E-13	24,979
4881 DPP4	-1,530	2,10E-07	1,51E-06	6,573
7797 HSPA2	-1,531	7,62E-07	4,71E-06	5,296
323 ADH5	-1,533	1,09E-14	8,43E-13	23,339
3190 CD44	-1,533	6,44E-07	4,07E-06	5,462
14980 RP6-213H	-1,535	3,10E-08	2,82E-07	8,479
9041 LARP6	-1,538	1,79E-10	3,20E-09	13,628
15557 SERPINB3	-1,540	4,57E-03	1,08E-02	-3,165
3944 CPM	-1,542	1,40E-09	1,93E-08	11,569
7809 HSPB7	-1,543	1,65E-14	1,20E-12	22,922
17258 TGFBR2	-1,555	1,26E-13	6,61E-12	20,892
12826 PAK1IP1	-1,555	8,30E-05	3,09E-04	0,677
8287 ITGB1	-1,562	1,96E-08	1,90E-07	8,938
19219 ZNF185	-1,564	4,85E-10	7,63E-09	12,632
4729 DMBT1	-1,567	1,92E-03	5,02E-03	-2,347
14827 RND3	-1,567	1,46E-11	3,61E-10	16,137
16261 SMTN	-1,567	1,27E-11	3,21E-10	16,274

3750 CNN3	-1,567	1,72E-11	4,18E-10	15,970
16257 SMPX	-1,568	5,52E-06	2,75E-05	3,336
6253 FLNA	-1,570	3,54E-13	1,55E-11	19,860
18981 ZAK	-1,572	7,01E-18	1,75E-15	30,658
4102 CSPG4	-1,572	2,20E-16	3,12E-14	27,233
11552 MT1A	-1,577	5,77E-05	2,24E-04	1,032
2452 C5orf4	-1,580	4,18E-09	4,94E-08	10,480
17110 TCEAL1	-1,587	2,56E-13	1,18E-11	20,185
428 AHR	-1,589	2,21E-12	7,28E-11	18,026
9149 LGALS7	-1,590	7,84E-10	1,15E-08	12,151
547 ALOX15B	-1,590	6,34E-04	1,88E-03	-1,290
16195 SLPI	-1,592	4,86E-05	1,92E-04	1,201
15551 SERPINB1	-1,592	4,00E-11	8,67E-10	15,128
1232 AVPI1	-1,594	1,02E-15	1,15E-13	25,702
10809 MAMDC2	-1,595	1,45E-11	3,59E-10	16,144
10522 LPHN2	-1,596	7,73E-17	1,28E-14	28,272
15666 SGK1	-1,600	5,30E-03	1,23E-02	-3,305
15904 SLC22A3	-1,601	3,72E-08	3,30E-07	8,297
17736 TNNC2	-1,602	2,63E-05	1,11E-04	1,803
7046 GPRASP1	-1,605	1,76E-17	3,85E-15	29,746
15497 SEMG2	-1,609	3,47E-03	8,45E-03	-2,906
14693 RGN	-1,615	7,70E-18	1,90E-15	30,565
583 AMIGO2	-1,616	3,57E-12	1,09E-10	17,546
16877 SYNC	-1,617	7,68E-13	3,02E-11	19,084
6667 GFOD1	-1,623	6,71E-11	1,35E-09	14,611
14611 REEP2	-1,626	2,36E-16	3,28E-14	27,161
4977 DUSP26	-1,632	2,07E-09	2,71E-08	11,182
6281 FMOD	-1,636	4,81E-09	5,60E-08	10,339
9612 LOC10014	-1,637	2,33E-07	1,66E-06	6,473
829 AQP1	-1,637	1,00E-14	7,92E-13	23,421
17267 TGM4	-1,639	3,90E-04	1,22E-03	-0,822
17951 TRIM63	-1,641	3,29E-06	1,73E-05	3,847
4151 CTGF	-1,643	7,22E-05	2,73E-04	0,814
7065 GPX2	-1,644	1,03E-11	2,68E-10	16,488
3674 CLIC4	-1,646	3,37E-16	4,44E-14	26,806
7810 HSPB8	-1,654	1,63E-15	1,72E-13	25,233
15661 SGCE	-1,656	2,49E-08	2,32E-07	8,699
13125 PDZRN4	-1,657	1,13E-13	6,06E-12	21,006
11217 MGST1	-1,661	4,57E-06	2,32E-05	3,523
9360 LOC10012	-1,664	1,55E-07	1,15E-06	6,875
3827 COL4A2	-1,668	1,00E-10	1,94E-09	14,207
8091 IL33	-1,675	5,37E-10	8,33E-09	12,529
14479 RASGRP2	-1,677	3,54E-18	9,97E-16	31,336

18074 TSPYL5	-1,678	9,15E-07	5,53E-06	5,114
6583 GATM	-1,683	2,69E-14	1,85E-12	22,435
13071 PDE8B	-1,686	6,32E-06	3,09E-05	3,204
13097 PDLIM3	-1,690	9,41E-14	5,26E-12	21,184
15558 SERPINB4	-1,692	1,90E-03	4,99E-03	-2,340
6457 FZD7	-1,698	3,72E-14	2,46E-12	22,112
6031 FILIP1L	-1,699	2,98E-10	5,00E-09	13,118
17232 TFPC2L1	-1,701	2,09E-06	1,15E-05	4,296
18 A2M	-1,703	1,86E-04	6,35E-04	-0,108
16755 STON1	-1,703	4,91E-13	2,07E-11	19,533
4373 DACT3	-1,705	3,48E-21	1,96E-18	38,165
15239 S100P	-1,714	3,72E-03	8,98E-03	-2,974
6935 GPER	-1,715	8,15E-07	4,99E-06	5,228
7757 HSD11B1	-1,716	3,34E-05	1,37E-04	1,568
70 ABCC3	-1,718	1,13E-11	2,91E-10	16,390
14711 RGS2	-1,721	6,03E-06	2,97E-05	3,250
18817 WFDC1	-1,722	2,90E-12	9,10E-11	17,755
7153 GSTA2	-1,723	2,08E-09	2,73E-08	11,174
11557 MT1H	-1,724	1,54E-05	6,84E-05	2,329
18058 TSPAN2	-1,724	1,20E-22	1,18E-19	41,455
5957 FERMT2	-1,726	2,59E-17	5,43E-15	29,361
16191 SLMAP	-1,728	9,89E-17	1,59E-14	28,028
14224 PTRF	-1,732	8,92E-21	4,40E-18	37,241
11743 MYOF	-1,732	9,36E-18	2,22E-15	30,371
13765 PPP1R12E	-1,740	1,13E-19	4,64E-17	34,743
15584 SETBP1	-1,744	6,52E-12	1,83E-10	16,944
13098 PDLIM4	-1,748	3,24E-15	3,00E-13	24,552
4196 CUGBP2	-1,750	1,37E-21	9,34E-19	39,075
8787 KLF9	-1,755	9,80E-10	1,40E-08	11,928
14638 RERG	-1,755	2,77E-18	8,14E-16	31,579
267 ADAMTS	-1,760	4,20E-08	3,68E-07	8,178
10537 LRCH2	-1,762	1,19E-14	9,07E-13	23,250
12818 PAGE4	-1,764	8,86E-08	7,06E-07	7,433
4111 CSRP3	-1,768	8,62E-04	2,47E-03	-1,585
17114 TCEAL5	-1,768	2,03E-12	6,76E-11	18,112
4902 DPYSL3	-1,775	8,35E-18	2,03E-15	30,484
13492 PLEKHO1	-1,776	3,82E-15	3,47E-13	24,385
15162 RSPO3	-1,778	3,09E-15	2,93E-13	24,599
6322 FOXF1	-1,780	7,56E-14	4,41E-12	21,403
6397 FST	-1,782	3,35E-16	4,43E-14	26,813
18186 TUBB6	-1,792	3,92E-17	7,57E-15	28,950
3524 CHRDL2	-1,804	2,73E-08	2,52E-07	8,606
14214 PTPRK	-1,805	2,07E-09	2,71E-08	11,183

9245 LMCD1	-1,807	1,89E-09	2,51E-08	11,271
13709 PPAPDC3	-1,811	2,10E-18	6,38E-16	31,852
13503 PLN	-1,814	3,82E-16	4,95E-14	26,682
14182 PTPLA	-1,814	4,83E-21	2,57E-18	37,844
5476 EYA1	-1,819	1,29E-20	5,89E-18	36,882
5050 ECHDC1	-1,824	7,64E-15	6,20E-13	23,694
13664 POPDC2	-1,826	9,77E-20	4,10E-17	34,885
6340 FOXO1	-1,830	1,11E-11	2,86E-10	16,411
16524 SPON1	-1,830	6,37E-08	5,32E-07	7,761
2764 CALD1	-1,848	6,36E-20	2,73E-17	35,308
8317 ITPR1	-1,851	1,53E-08	1,54E-07	9,185
9945 LOC39133	-1,854	1,24E-14	9,35E-13	23,212
12497 ODZ2	-1,855	2,36E-06	1,28E-05	4,174
13704 PPAP2B	-1,860	3,13E-12	9,69E-11	17,679
13507 PLP1	-1,861	2,68E-12	8,53E-11	17,833
14455 RARB	-1,865	6,51E-14	3,91E-12	21,553
13785 PPP1R3C	-1,867	2,07E-08	1,99E-07	8,880
2627 C9orf125	-1,867	2,52E-21	1,46E-18	38,483
5986 FGF2	-1,870	4,36E-21	2,39E-18	37,942
4044 CRYAB	-1,871	2,35E-08	2,21E-07	8,757
11096 METTL7A	-1,874	2,14E-12	7,04E-11	18,061
11079 MET	-1,876	1,01E-18	3,49E-16	32,578
15225 S100A14	-1,877	6,84E-16	8,33E-14	26,102
17201 TES	-1,880	3,66E-12	1,11E-10	17,522
12265 NPTN	-1,880	1,76E-18	5,69E-16	32,028
8396 KBTBD10	-1,889	6,16E-07	3,91E-06	5,507
3972 CPXM2	-1,890	9,22E-11	1,80E-09	14,293
11701 MYL2	-1,894	5,50E-05	2,15E-04	1,080
7806 HSPB2	-1,908	3,97E-15	3,54E-13	24,348
13798 PPP2R2B	-1,909	2,50E-14	1,74E-12	22,511
11561 MT1X	-1,909	3,21E-06	1,69E-05	3,873
14610 REEP1	-1,910	3,89E-15	3,51E-13	24,369
7986 IGJ	-1,914	6,78E-04	1,99E-03	-1,355
14139 PTCHD1	-1,915	2,47E-18	7,36E-16	31,694
12292 NR2F1	-1,924	8,58E-17	1,40E-14	28,169
12839 PAM	-1,925	5,40E-22	4,63E-19	39,987
17239 TFF1	-1,929	4,50E-06	2,29E-05	3,539
11559 MT1L	-1,931	3,73E-06	1,94E-05	3,723
2981 CCDC3	-1,934	8,25E-07	5,04E-06	5,217
8383 KANK1	-1,945	1,56E-15	1,67E-13	25,282
11553 MT1B	-1,956	7,00E-06	3,38E-05	3,102
9146 LGALS3	-1,958	6,41E-12	1,81E-10	16,961
6314 FOXC1	-1,962	1,18E-17	2,78E-15	30,138

17735 TNNC1	-1,965	4,36E-06	2,22E-05	3,570
13542 PMP22	-1,967	7,49E-13	2,96E-11	19,110
1022 ASB2	-1,968	2,44E-15	2,40E-13	24,834
1395 BDKRB2	-1,972	6,26E-10	9,52E-09	12,377
18038 TSHZ3	-1,980	5,77E-16	7,21E-14	26,271
11700 MYL1	-1,985	3,70E-05	1,50E-04	1,467
3430 CFB	-1,988	1,47E-04	5,15E-04	0,121
880 ARHGAP2	-1,993	2,60E-25	4,66E-22	47,372
16384 SORBS1	-2,011	2,38E-15	2,38E-13	24,857
6594 GBP2	-2,021	8,45E-15	6,83E-13	23,593
6492 GABRE	-2,025	2,53E-12	8,09E-11	17,893
959 ARMCX2	-2,029	2,67E-12	8,51E-11	17,837
4524 DEFB1	-2,033	3,01E-05	1,25E-04	1,671
7887 ID4	-2,033	6,66E-18	1,73E-15	30,708
11378 MOXD1	-2,036	9,04E-10	1,31E-08	12,008
3141 CD163	-2,041	4,74E-05	1,88E-04	1,225
4301 CYP1B1	-2,044	1,99E-04	6,74E-04	-0,170
15697 SH3BGR	-2,057	2,00E-19	7,74E-17	34,178
2382 C3orf57	-2,063	3,03E-10	5,03E-09	13,103
14415 RAI2	-2,072	2,51E-09	3,21E-08	10,987
11060 MEIS1	-2,073	5,78E-16	7,21E-14	26,270
15698 SH3BGRL	-2,076	7,31E-17	1,24E-14	28,328
12046 NFIL3	-2,078	1,32E-12	4,77E-11	18,541
17741 TNNT1	-2,086	5,81E-04	1,73E-03	-1,207
3442 CFL2	-2,089	1,28E-15	1,41E-13	25,474
4333 CYP4B1	-2,099	1,27E-14	9,53E-13	23,190
13562 PNMA1	-2,111	7,31E-13	2,91E-11	19,134
4939 DSTN	-2,112	4,42E-14	2,80E-12	21,940
11671 MYBPH	-2,112	2,61E-05	1,10E-04	1,809
17106 TCAP	-2,125	1,13E-03	3,14E-03	-1,842
13094 PDK4	-2,138	1,90E-07	1,38E-06	6,672
15861 SLC16A5	-2,142	7,05E-19	2,53E-16	32,934
13432 PLAT	-2,142	2,90E-06	1,54E-05	3,971
17807 TP63	-2,153	5,52E-26	1,82E-22	48,850
10511 LPAR1	-2,163	7,94E-14	4,58E-12	21,354
3256 CDC42EP1	-2,170	1,29E-12	4,67E-11	18,563
11562 MT2A	-2,176	1,27E-05	5,75E-05	2,519
11740 MYOC	-2,179	2,92E-13	1,32E-11	20,052
17112 TCEAL3	-2,186	1,38E-13	7,09E-12	20,804
2879 CAV1	-2,188	9,88E-14	5,46E-12	21,136
17115 TCEAL6	-2,190	4,69E-14	2,94E-12	21,880
16967 TAGLN	-2,198	2,18E-19	8,28E-17	34,091
15387 SCRNI	-2,212	5,24E-15	4,51E-13	24,070

16577 SRD5A2	-2,219	8,15E-19	2,87E-16	32,790
8927 KRT5	-2,221	3,26E-17	6,48E-15	29,133
7080 GRASP	-2,223	1,47E-17	3,30E-15	29,920
591 AMOTL2	-2,225	9,08E-12	2,41E-10	16,613
11215 MGP	-2,232	2,95E-10	4,96E-09	13,127
6022 FHOD3	-2,243	3,95E-14	2,56E-12	22,052
718 ANXA1	-2,243	1,27E-14	9,54E-13	23,185
17683 TNC	-2,243	2,67E-11	6,06E-10	15,533
730 ANXA8L2	-2,246	2,97E-12	9,27E-11	17,732
1290 BAG2	-2,260	6,88E-16	8,33E-14	26,095
17113 TCEAL4	-2,262	4,65E-17	8,48E-15	28,779
6398 FSTL1	-2,262	5,78E-18	1,56E-15	30,849
7147 GSN	-2,264	1,53E-14	1,12E-12	23,001
1025 ASB5	-2,271	6,25E-15	5,19E-13	23,894
4695 DKK3	-2,274	6,07E-16	7,48E-14	26,221
3931 CPAMD8	-2,277	7,99E-11	1,58E-09	14,436
14576 RCAN2	-2,297	8,63E-10	1,26E-08	12,055
7769 HSD17B6	-2,319	3,22E-06	1,70E-05	3,868
16809 SULF1	-2,320	9,77E-11	1,89E-09	14,234
8276 ITGA5	-2,327	4,08E-18	1,13E-15	31,194
11748 MYOT	-2,330	2,17E-13	1,03E-11	20,350
16856 SVIL	-2,343	3,90E-15	3,51E-13	24,366
3935 CPE	-2,353	8,34E-08	6,70E-07	7,493
3916 COX7A1	-2,389	7,70E-21	3,89E-18	37,386
16708 STAT6	-2,395	3,09E-13	1,39E-11	19,994
14332 RAB34	-2,400	6,01E-18	1,60E-15	30,810
2170 C1S	-2,408	4,20E-11	9,03E-10	15,080
352 ADRA2C	-2,418	1,60E-08	1,60E-07	9,140
15617 SFRP1	-2,448	3,21E-15	3,00E-13	24,559
6451 FZD10	-2,458	7,64E-17	1,28E-14	28,285
5919 FCGBP	-2,470	2,08E-08	1,99E-07	8,879
8931 KRT7	-2,485	3,38E-11	7,45E-10	15,297
734 AOC3	-2,488	2,79E-24	3,93E-21	45,095
2168 C1R	-2,511	2,06E-12	6,82E-11	18,096
17595 TMEM47	-2,515	2,60E-15	2,54E-13	24,770
11325 MMP7	-2,520	1,34E-05	6,07E-05	2,460
11693 MYH3	-2,549	1,45E-10	2,65E-09	13,840
668 ANKRD35	-2,554	1,06E-21	7,72E-19	39,325
15545 SERPINA1	-2,585	1,15E-04	4,15E-04	0,356
4330 CYP3A7	-2,615	2,96E-10	4,97E-09	13,125
407 AGR2	-2,621	1,69E-08	1,67E-07	9,084
207 ACTC1	-2,644	2,07E-13	9,82E-12	20,398
10804 MAL	-2,693	1,63E-19	6,45E-17	34,378

11696 MYH7	-2,693	4,12E-06	2,11E-05	3,625
4774 DNAJB5	-2,696	5,43E-21	2,82E-18	37,728
15658 SGCA	-2,701	6,11E-22	5,02E-19	39,867
7974 IGFBP6	-2,709	4,36E-18	1,19E-15	31,129
9132 LEPREL1	-2,721	8,71E-14	4,92E-12	21,262
13010 PCOLCE2	-2,784	2,47E-12	7,95E-11	17,915
17111 TCEAL2	-2,876	1,19E-19	4,80E-17	34,688
7807 HSPB3	-2,893	1,39E-08	1,41E-07	9,282
6260 FLRT3	-2,915	1,08E-26	7,12E-23	50,395
8278 ITGA7	-2,927	1,10E-20	5,28E-18	37,037
16891 SYNPO2	-2,930	1,18E-25	3,34E-22	48,123
12028 NEXN	-2,932	5,27E-20	2,31E-17	35,495
3601 CKM	-3,016	1,35E-07	1,02E-06	7,011
11989 NEFH	-3,031	4,63E-08	4,01E-07	8,080
15496 SEMG1	-3,033	1,08E-05	4,99E-05	2,676
737 AOX1	-3,038	2,40E-11	5,52E-10	15,640
206 ACTBL2	-3,048	1,20E-18	4,00E-16	32,410
16483 SPEG	-3,073	1,61E-16	2,42E-14	27,545
8909 KRT23	-3,081	1,33E-16	2,03E-14	27,735
15353 SCHIP1	-3,103	1,68E-21	1,11E-18	38,876
14457 RARRES1	-3,104	4,80E-08	4,14E-07	8,044
17821 TPM2	-3,132	4,74E-22	4,25E-19	40,115
3518 CHP2	-3,169	1,35E-14	1,00E-12	23,124
1130 ATP1A2	-3,171	7,81E-13	3,07E-11	19,067
9105 LDHB	-3,200	7,48E-13	2,96E-11	19,111
11688 MYH11	-3,226	3,45E-20	1,54E-17	35,912
7166 GSTP1	-3,266	1,92E-25	3,99E-22	47,661
8885 KRT13	-3,289	3,27E-13	1,45E-11	19,940
6563 GAS1	-3,310	3,21E-13	1,43E-11	19,958
11537 MSMB	-3,319	1,44E-08	1,46E-07	9,242
15232 S100A6	-3,330	6,61E-16	8,10E-14	26,136
9021 LAMB3	-3,370	2,32E-23	2,54E-20	43,049
10830 MAOB	-3,424	1,45E-25	3,57E-22	47,931
204 ACTA2	-3,471	2,19E-24	3,33E-21	45,327
16451 SPARCL1	-3,492	1,46E-13	7,39E-12	20,743
18844 WISP2	-3,507	1,31E-14	9,74E-13	23,156
9257 LMOD1	-3,552	1,97E-23	2,28E-20	43,208
6018 FHL2	-3,569	3,42E-18	9,77E-16	31,370
203 ACTA1	-3,666	1,39E-08	1,42E-07	9,281
6017 FHL1	-3,689	1,68E-23	2,07E-20	43,360
12833 PALLD	-3,709	1,95E-21	1,20E-18	38,732
7884 ID1	-3,716	4,26E-17	7,93E-15	28,865
11711 MYLK	-3,719	1,10E-21	7,72E-19	39,295

17757 TNS4	-3,769	5,12E-26	1,82E-22	48,923
4564 DES	-3,972	1,35E-23	1,77E-20	43,575
15228 S100A2	-4,303	8,03E-23	8,33E-20	41,844
16889 SYNM	-4,307	2,02E-25	3,99E-22	47,613
12520 OLFM4	-4,496	4,65E-12	1,37E-10	17,283
3748 CNN1	-4,905	5,37E-29	5,29E-25	55,354
8887 KRT15	-4,909	4,17E-25	6,85E-22	46,922
13012 PCP4	-5,670	1,21E-31	2,38E-27	60,887
209 ACTG2	-5,945	4,19E-26	1,82E-22	49,113

Pathways enriched by up-regulated and down-regulated differentially expressed genes

Terms	Hit	p value	Gene List
Up-regulated genes			
Leishmania infection	7	3,45E-07	HLA-DMA;HLA-DMB;HLA-DPA1;HLA-DRB3;HLA-DRB4;JUN;MARCKSL1
Allograft rejection	5	0,000260628	HLA-DMA;HLA-DMB;HLA-DPA1;HLA-DRB3;HLA-DRB4
Antigen	7	1,09E-05	HLA-DMA;HLA-DMB;HLA-DPA1;HLA-DRB3;HLA-DRB4;HSP90AB1;HSPA6
Type I diabetes mellitus	6	5,11E-05	HLA-DMA;HLA-DMB;HLA-DPA1;HLA-DRB3;HLA-DRB4;ICA1
Asthma	5	9,30E-05	HLA-DMA;HLA-DMB;HLA-DPA1;HLA-DRB3;HLA-DRB4
Viral myocarditis	5	0,001069719	HLA-DMA;HLA-DMB;HLA-DPA1;HLA-DRB3;HLA-DRB4
Graft versus host disease	5	0,000426181	HLA-DMA;HLA-DMB;HLA-DPA1;HLA-DRB3;HLA-DRB4
Intestinal immune network for IgA production	5	0,000892171	HLA-DMA;HLA-DMB;HLA-DPA1;HLA-DRB3;HLA-DRB4
Autoimmune thyroid disease	5	0,001288187	HLA-DMA;HLA-DMB;HLA-DPA1;HLA-DRB3;HLA-DRB4
Systemic lupus erythematosus	6	0,021962707	HIST1H4E;HLA-DMA;HLA-DMB;HLA-DPA1;HLA-DRB3;HLA-DRB4
Down-regulated genes			
Dilated cardiomyopathy	19	5,24E-14	ACTC1;CACNA2D1;DES;DMD;ITGA1;ITGA5;ITGA7;ITGA8;ITGB1;LMNA;MYH7;MYL2;PLN;SGCA;TGFB2;TNNC1;TPM1;TPM2;TTN
Hypertrophic cardiomyopathy (HCM)	18	8,67E-14	ACTC1;CACNA2D1;DES;DMD;ITGA1;ITGA5;ITGA7;ITGA8;ITGB1;LMNA;MYH7;MYL2;SGCA;TGFB2;TNNC1;TPM1;TPM2;TTN
(ARVC)	13	1,36E-07	ACTN1;ACTN2;CACNA2D1;DES;DMD;GJA1;ITGA1;ITGA5;ITGA7;ITGA8;ITGB1;LMNA;SGCA
Cardiac muscle contraction	9	0,004866729	ACTC1;ATP1A2;CACNA2D1;COX7A1;MYH7;MYL2;TNNC1;TPM1;TPM2

The Gene Ontology (GO) functional enrichment and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis of t

Category	Hit	P-Value	Gene List
GO terms			
cluster1		Enrichment Score: 80.41	
actin filament-based process	27	4,53E-130	ACTA1;ACTC1;ACTN2;ANKRD1;CFL2;CSR3;DES;DMD;DPYSL3;KLHL41;MYH2;MYH3;MYH7;MYL1;MYL2;NEB;PDLIM3;PLN;TCAP;TMOD1;TNNC1;TNNC2;TNNI2;TNNT1;TPM1;TPM2;TTN
cellular component movement	22	3,32E-32	ACTA1;ACTC1;ACTN2;DES;DMD;DPYSL3;MYH2;MYH3;MYH7;MYL1;MYL2;NEB;PLN;TCAP;TMOD1;TNNC1;TNNC2;TNNI2;TNNT1;TPM1;TPM2;TTN
cluster2		Enrichment Score: 53.87	
cytoskeletal protein binding	26	5,69E-92	ACTA1;ACTC1;ACTN2;ANKRD1;CFL2;CSR3;DES;DMD;MYH2;MYH3;MYH7;MYL2;MYOT;NEB;NRAP;PDLIM3;TCAP;TMOD1;TNNC1;TNNC2;TNNI2;TNNT1;TPM1;TPM2;TRIM63;TTN
myofibril	30	4,02E-54	ACTA1;ACTC1;ACTN2;ANKRD1;CASQ2;CSR3;DES;DMD;KLHL41;MYH2;MYH3;MYH7;MYL1;MYL2;MYOM2;MYOT;NEB;NRAP;PDLIM3;SMPX;TCAP;TMOD1;TNNC1;TNNC2;TNNI2;TNNT1;TPM1;TPM2;TRIM63;TTN
contractile fiber	30	3,09E-53	ACTA1;ACTC1;ACTN2;ANKRD1;CASQ2;CSR3;DES;DMD;KLHL41;MYH2;MYH3;MYH7;MYL1;MYL2;MYOM2;MYOT;NEB;NRAP;PDLIM3;SMPX;TCAP;TMOD1;TNNC1;TNNC2;TNNI2;TNNT1;TPM1;TPM2;TRIM63;TTN
actin binding	17	4,53E-19	ACTN2;CFL2;DMD;MYH2;MYH3;MYH7;MYL2;MYOT;NEB;NRAP;TMOD1;TNNC1;TNNC2;TNNI2;TPM1;TPM2;TTN
cluster3		Enrichment Score: 46.94	
sarcomere	27	2,80E-48	ACTA1;ACTC1;ACTN2;ANKRD1;CASQ2;CSR3;DES;DMD;KLHL41;MYH2;MYH7;MYL1;MYL2;MYOM2;MYOT;NEB;PDLIM3;SMPX;TCAP;TNNC1;TNNC2;TNNI2;TNNT1;TPM1;TPM2;TRIM63;TTN
contractile fiber part	27	4,72E-47	ACTA1;ACTC1;ACTN2;ANKRD1;CASQ2;CSR3;DES;DMD;KLHL41;MYH2;MYH7;MYL1;MYL2;MYOM2;MYOT;NEB;PDLIM3;SMPX;TCAP;TNNC1;TNNC2;TNNI2;TNNT1;TPM1;TPM2;TRIM63;TTN
Pathways			
Dilated cardiomyopathy	10	7,19E-13	ACTC1;DES;DMD;MYH7;MYL2;PLN;TNNC1;TPM1;TPM2;TTN
Hypertrophic cardiomyopathy (HCM)	9	1,56E-11	ACTC1;DES;DMD;MYH7;MYL2;TNNC1;TPM1;TPM2;TTN
Cardiac muscle contraction	6	4,68E-07	ACTC1;MYH7;MYL2;TNNC1;TPM1;TPM2
Tight junction	5	0,000148737	ACTN2;MYH2;MYH3;MYH7;MYL2
Viral myocarditis	4	0,000153213	DMD;MYH2;MYH3;MYH7
Arrhythmogenic right ventricular cardiomyopathy (ARVC)	3	0,003029789	ACTN2;DES;DMD
Arginine and proline metabolism	2	0,019264137	CKM;CKMT2
Calcium signal pathway	3	0,03236325	PLN;TNNC1;TNNC2

Supplemental table 5. Pathways and genes involving in crosstalk pathways

Pathways	Gene list
hsa04662:B cell receptor signaling pathway	MAP2K2,JUN,CHP2,PPP3CB,PIK3R1,NFKBIA,PPP3CA
hsa04620:Toll-like receptor signaling pathway	CCL3,MAP2K2,JUN,CCL4,PIK3R1,NFKBIA
hsa05211:Renal cell carcinoma	MAP2K2,JUN,MET,EPAS1,PIK3R1,TGFB2,PAK3,RAP1A
hsa04062:Chemokine signaling pathway	CCL3L3,CCL3,GNB2,CCL4,RASGRP2,PLCB1,PIK3R1,CCL23,NFKBIA,RAP1A,GNG4,CXCL1
hsa04810:Regulation of actin cytoskeleton	MAP2K2,FGFR2,MYLK,FGF2,ITGA7,ITGA5,CFL2,GSN,MYL9,PIK3R1,PPP1CB,VCL,BDKRB2,ACTN1,PAK3,ITGA1,ITGB1,ITGA8,MYL2,ACTN2
hsa04910:Insulin signaling pathway	MAP2K2,MKMK2,FASN,SORBS1,FOXO1,PIK3R1,PPP1CB,PPP1R3C,IRS1,SOCS2
hsa04510:Focal adhesion	JUN,COL1A1,LAMB3,MYLK,ITGA7,MET,ITGA5,FLNC,COL4A6,CAV1,FLNA,LAMB2,MYL9,BCL2,PIK3R1,TNC,PPP1CB,COL4A2,VCL,LAMC1,ACTN1,PAK3,ITGA1,ITGB1,ITGA8,RAP1A,MYL2,ACTN2,THBS4
hsa05210:Colorectal cancer	JUN,BIRC5,SMAD3,TGFBR2,BCL2,PIK3R1,TGFB2
hsa04660:T cell receptor signaling pathway	MAP2K2,JUN,MET,EPAS1,PIK3R1,TGFB2,PAK3,RAP1A
hsa04010:MAPK signaling pathway	ELK4,MAP2K2,STMN1,JUN,MKMK2,CACNA1D,HSPA6,FGFR2,FGF2,RASGRP2,ZAK,FLNC,CHP2,TGFBR2,FLNA,PPP3CB,TGFB2,CACNA2D1,ATF4,RAP1A,HSPA2,DUSP1,RELB,PPP3CA
hsa05213:Endometrial cancer	MAP2K2,PIK3R1
hsa04370:VEGF signaling pathway	MAP2K2,CHP2,PPP3CB,PIK3R1,PTGS2,PPP3CA
hsa04722:Neurotrophin signaling pathway	MAP2K2,JUN,BCL2,PIK3R1,NFKBIA,ATF4,RAP1A,IRS1
hsa05214:Glioma	CDKN2A,MAP2K2,PIK3R1
hsa05220:Chronic myeloid leukemia	CDKN2A,MAP2K2,SMAD3,TGFBR2,PIK3R1,TGFB2,NFKBIA
hsa05221:Acute myeloid leukemia	MAP2K2,PIK3R1
hsa04012:ErbB signaling pathway	MAP2K2,JUN,PIK3R1,PAK3,AREG
hsa05216:Thyroid cancer	MAP2K2
hsa04150:mTOR signaling pathway	IRS1,CAB39L
hsa05160:Hepatitis C	PPP2R2B,PIK3R1,CLDN1,NFKBIA

Disease Ontology (DO) annotation of up-regulated differentially expressed genes

DO Term	p value	p value	Hit	Gene list
DOID:5656	cranial nerve disease	6,40E-04	5	MMP11,MMP9,ND1,ND6,PHOX2A
DOID:3526	cerebral infarction	6,72E-04	4	APOE,F5,FABP1,LGALS2
DOID:0050686	organ system cancer	7,43E-04	53	90AB1,HSPE1,IDO1,ITPR3,JUN,KIAA0101,LGALS2,MARCKSL1,MCM2,MELK,MMP11,MMP9,ND3,NDRG1,PBK,PTTG1,RECQL4,REG1A,SLC19A1,SOX4,STMN1,TK1,TMSB15A,UBE2C,UBE2T,ZDHHC11
DOID:162	cancer	1,40E-03	61	12,F5,FASN,FGG,HPGD,HPN,HSP90AB1,HSPE1,IDO1,ISG15,ITPR3,JUN,KCNQ1OT1,KIAA0101,LGALS2,MARCKSL1,MCM2,MELK,MMP11,MMP9,ND3,NDRG1,PBK,PTK6,PTTG1,RECQL4,REG1A,SLC19A1,SOX4,STMN1,TK1,TMSB15A,UBE2C,UBE2T,ZDHHC11
DOID:3454	brain infarction	1,56E-03	4	APOE,F5,FABP1,LGALS2
DOID:0060158	acquired metabolic disease	1,67E-03	20	ADRB2,APLN,APOC1,APOE,AR,CA1,CDKN2A,CDKN3,F5,FAAH,FASN,HLA-DMA,HLA-DMB,ITPR3,MCM2,MMP9,ND1,PCBD1,PVT1,REG1A
DOID:9351	diabetes mellitus	1,99E-03	16	ADRB2,APLN,APOC1,APOE,AR,CA1,CDKN2A,F5,HLA-DMA,HLA-DMB,ITPR3,MMP9,ND1,PCBD1,PVT1,REG1A
DOID:14566	disease of cellular proliferation	2,20E-03	61	12,F5,FASN,FGG,HPGD,HPN,HSP90AB1,HSPE1,IDO1,ISG15,ITPR3,JUN,KCNQ1OT1,KIAA0101,LGALS2,MARCKSL1,MCM2,MELK,MMP11,MMP9,ND3,NDRG1,PBK,PTK6,PTTG1,RECQL4,REG1A,SLC19A1,SOX4,STMN1,TK1,TMSB15A,UBE2C,UBE2T,ZDHHC11
DOID:3389	Papillon-Lefevre disease	2,28E-03	2	CCL3,CCL3L3
DOID:2151	malignant ovarian surface epithelial-stromal neoplasm	2,89E-03	5	CDKN2A,EPCAM,MCM2,MMP9,TK1
DOID:2152	ovary epithelial cancer	2,89E-03	5	CDKN2A,EPCAM,MCM2,MMP9,TK1
DOID:4001	ovarian carcinoma	2,89E-03	5	CDKN2A,EPCAM,MCM2,MMP9,TK1
DOID:0050013	carbohydrate metabolism disease	3,25E-03	16	ADRB2,APLN,APOC1,APOE,AR,CA1,CDKN2A,F5,HLA-DMA,HLA-DMB,ITPR3,MMP9,ND1,PCBD1,PVT1,REG1A
DOID:4194	glucose metabolism disease	3,25E-03	16	ADRB2,APLN,APOC1,APOE,AR,CA1,CDKN2A,F5,HLA-DMA,HLA-DMB,ITPR3,MMP9,ND1,PCBD1,PVT1,REG1A
DOID:0014667	disease of metabolism	3,57E-03	22	ADRB2,APLN,APOC1,APOE,AR,CA1,CDKN2A,CDKN3,F5,FAAH,FASN,HLA-DMA,HLA-DMB,ITPR3,MCM2,MMP9,ND1,ND2,ND3,PCBD1,PVT1,REG1A
DOID:684	hepatocellular carcinoma	3,58E-03	14	APOE,AR,BCAM,BIRC5,CCL3,CDKN2A,DLGAP5,EPCAM,EZH2,JUN,KIAA0101,MCM2,MMP9,UBE2C
DOID:686	liver carcinoma	3,58E-03	14	APOE,AR,BCAM,BIRC5,CCL3,CDKN2A,DLGAP5,EPCAM,EZH2,JUN,KIAA0101,MCM2,MMP9,UBE2C
DOID:4766	embryoma	4,07E-03	21	APOE,AR,BCAM,BIRC5,CASP10,CCNB1,CDKN2A,COX1,DLGAP5,EPCAM,EZH2,F5,FASN,HSPE1,IDO1,JUN,KCNQ1OT1,MELK,MMP9,NDRG1,TK1
DOID:5158	pleural cancer	4,21E-03	3	BIRC5,CDKN2A,MMP9
DOID:7474	malignant pleural mesothelioma	4,21E-03	3	BIRC5,CDKN2A,MMP9
DOID:688	embryonal cancer	4,24E-03	21	APOE,AR,BCAM,BIRC5,CASP10,CCNB1,CDKN2A,COX1,DLGAP5,EPCAM,EZH2,F5,FASN,HSPE1,IDO1,JUN,KCNQ1OT1,MELK,MMP9,NDRG1,TK1
DOID:0080001	bone disease	4,87E-03	16	ADRB2,APOE,AR,BIRC5,CASP10,CCL3,CCL4,DEFA3,F5,FASN,HLA-DMA,HLA-DMB,ISG15,JUN,MMP9,SLC19A1
DOID:2600	laryngeal carcinoma	5,27E-03	4	BIRC5,CCNB1,CDKN2A,MMP9
DOID:0050687	cell type cancer	5,50E-03	33	PCAM,EZH2,F12,F5,FASN,HSPE1,IDO1,ISG15,JUN,KCNQ1OT1,MCM2,MELK,MMP11,MMP9,NDRG1,PTK6,PTTG1,REG1A,STMN1,TK1
DOID:3571	liver cancer	5,86E-03	14	APOE,AR,BCAM,BIRC5,CCL3,CDKN2A,DLGAP5,EPCAM,EZH2,JUN,KIAA0101,MCM2,MMP9,UBE2C
DOID:4450	renal cell carcinoma	6,14E-03	9	AP1M2,AR,BIRC5,CCNB1,CDKN2A,EPCAM,EZH2,HPN,MMP9
DOID:4451	renal carcinoma	6,14E-03	9	AP1M2,AR,BIRC5,CCNB1,CDKN2A,EPCAM,EZH2,HPN,MMP9
DOID:7148	rheumatoid arthritis	6,77E-03	13	ADRB2,APOE,AR,BIRC5,CASP10,CCL3,DEFA3,HLA-DMA,HLA-DMB,ISG15,JUN,MMP9,SLC19A1
DOID:2994	germ cell cancer	6,80E-03	21	APOE,AR,BCAM,BIRC5,CASP10,CCNB1,CDKN2A,COX1,DLGAP5,EPCAM,EZH2,F5,FASN,HSPE1,IDO1,JUN,KCNQ1OT1,MELK,MMP9,NDRG1,TK1
DOID:3342	bone inflammation disease	7,02E-03	14	ADRB2,APOE,AR,BIRC5,CASP10,CCL3,CCL4,DEFA3,HLA-DMA,HLA-DMB,ISG15,JUN,MMP9,SLC19A1
DOID:3093	nervous system cancer	7,14E-03	11	APLN,AR,BIRC5,CDKN2A,EPCAM,EZH2,MELK,MMP11,MMP9,NDRG1,TMSB15A
DOID:3302	chordoma	7,68E-03	2	AR,CDKN2A
DOID:3303	notochordal cancer	7,68E-03	2	AR,CDKN2A
DOID:6204	follicular adenoma	7,68E-03	2	CDKN2A,MCM2

DOID:5113	nutritional deficiency disease	7,78E-03	3 CDKN2A,CDKN3,MCM2
DOID:10534	stomach cancer	7,95E-03	13 AR,B3GAT1,BIRC5,CCL4,CDKN2A,EZH2,HPGD,ITPR3,JUN,MMP11,MMP9,PTTG1,REG1A
DOID:3119	gastrointestinal system cancer	8,44E-03	26 APOE,AR,B3GAT1,BCAM,BIRC5,CCL3,CCL4,CCNB1,CDKN2A,DLGAP5,EPCAM,EZH2,HPGD,HSPE1,ITPR3,JUN,KIAA0101,LGALS2,MCM2,MMP11,MMP9,NDRG1,PTTG1,REG1A,SOX4,UBE2C
DOID:540	strabismus	8,88E-03	3 MMP11,MMP9,PHOX2A
DOID:9352	type 2 diabetes mellitus	9,51E-03	13 ADRB2,APLN,APOC1,APOE,AR,CA1,CDKN2A,F5,HLA-DMA,HLA-DMB,ITPR3,MMP9,PVT1
DOID:1319	brain cancer	9,94E-03	4 APLN,BIRC5,MELK,MMP9
DOID:3652	Leigh disease	1,01E-02	2 ND2,ND3
DOID:591	phobic disorder	1,01E-02	2 AR,CAMKK2
DOID:8574	lichen disease	1,01E-02	2 IDO1,MMP9
DOID:9201	lichen planus	1,01E-02	2 IDO1,MMP9
DOID:74	hematopoietic system disease	1,02E-02	9 AR,BIRC5,CA1,F5,FABP1,FGG,MMP9,RECQL4,UBE2T
DOID:3620	central nervous system cancer	1,04E-02	6 APLN,BIRC5,CDKN2A,MELK,MMP11,MMP9
DOID:848	arthritis	1,10E-02	13 ADRB2,APOE,AR,BIRC5,CASP10,CCL3,DEFA3,HLA-DMA,HLA-DMB,ISG15,JUN,MMP9,SLC19A1
DOID:2876	laryngeal squamous cell carcinoma	1,13E-02	3 BIRC5,CCNB1,CDKN2A
DOID:178	vascular disease	1,22E-02	17 ADRB2,APLN,APOC1,APOE,CDKN2A,F5,FABP1,FGG,HSPE1,JUN,LGALS2,MMP9,ND1,ND2,PHOX2A,TK1,TRAP1
DOID:10211	cholelithiasis	1,27E-02	3 APOC1,APOE,AR
DOID:1279	ocular motility disease	1,27E-02	3 MMP11,MMP9,PHOX2A
DOID:319	spinal cord disease	1,27E-02	3 AR,MMP9,SLC19A1
DOID:11801	protein-energy malnutrition	1,28E-02	2 CDKN2A,MCM2
DOID:2891	thyroid adenoma	1,28E-02	2 CDKN2A,MCM2
DOID:3390	palmoplantar keratosis	1,28E-02	2 CCL3,CCL3L3
DOID:4231	histiocytoma	1,28E-02	2 CDKN2A,MCM2
DOID:5041	esophageal cancer	1,36E-02	9 AR,BIRC5,CCNB1,CDKN2A,EPCAM,MMP9,NDRG1,PTTG1,UBE2C
DOID:0060262	gallbladder disease	1,42E-02	3 APOC1,APOE,AR
DOID:2596	larynx cancer	1,45E-02	4 BIRC5,CCNB1,CDKN2A,MMP9
DOID:10923	sickle cell anemia	1,57E-02	2 ADRB2,BCAM,F5
DOID:9834	hyperopia	1,57E-02	3 MMP11,MMP9,PHOX2A
DOID:4418	cutaneous fibrous histiocytoma	1,58E-02	2 AR,MMP9
DOID:3376	bone osteosarcoma	1,60E-02	5 CDKN2A,JUN,MMP9,RECQL4,SLC19A1
DOID:263	kidney cancer	1,64E-02	9 AP1M2,AR,BIRC5,CCNB1,CDKN2A,EPCAM,EZH2,HPN,MMP9
DOID:120	female reproductive organ cancer	1,72E-02	12 AR,BIRC5,CDKN2A,COX1,EPCAM,FASN,HSPE1,JUN,MCM2,MMP9,NDRG1,TK1
DOID:2871	endometrial carcinoma	1,77E-02	7 AR,BIRC5,CDKN2A,COX1,HSPE1,MMP9,NDRG1
DOID:305	carcinoma	1,77E-02	16 ADAM8,BIRC5,CCL3,CDKN2A,EPCAM,F12,FASN,JUN,MMP11,MMP9,NDRG1,PTK6,PTTG1,REG1A,STMN1,TK1
DOID:0060089	endocrine organ benign neoplasm	1,79E-02	4 CDKN2A,MCM2,MMP9,PTTG1
DOID:3565	meningioma	1,79E-02	4 BIRC5,CDKN2A,MMP11,MMP9
DOID:4074	pancreas adenocarcinoma	1,79E-02	4 ADAM8,CDKN2A,JUN,NDRG1
DOID:5517	stomach carcinoma	1,81E-02	6 BIRC5,CCL4,CDKN2A,MMP9,PTTG1,REG1A
DOID:1287	cardiovascular system disease	1,81E-02	18 ADRB2,APLN,APOC1,APOE,AR,CDKN2A,F5,FABP1,FGG,HSPE1,JUN,LGALS2,MMP9,ND1,ND2,PHOX2A,TK1,TRAP1
DOID:6713	cerebrovascular disease	1,91E-02	3 APOE,F5,FABP1,LGALS2
DOID:2438	dermis tumor	1,91E-02	2 AR,MMP9
DOID:3905	lung carcinoma	1,94E-02	8 ADRB2,BIRC5,CDKN2A,CTAG1A,MARCKSL1,MMP9,STMN1,TK1
DOID:0050134	cutaneous mycosis	1,99E-02	1 APOE
DOID:10247	pleurisy	1,99E-02	1 MMP9
DOID:14283	primary hypertrophic osteoarthropathy	1,99E-02	1 HPGD
DOID:2231	factor XII deficiency	1,99E-02	1 F12
DOID:2451	protein S deficiency	1,99E-02	1 F5

DOID:2519	testicular disease	1,99E-02	1 AR
DOID:2732	Rothmund-Thomson syndrome	1,99E-02	1 RECQL4
DOID:3540	choroid plexus cancer	1,99E-02	1 BIRC5
DOID:3763	hermaphroditism	1,99E-02	1 AR
DOID:4232	extraosseous Ewing's sarcoma	1,99E-02	1 CDKN2A
DOID:4415	fibrous histiocytoma	1,99E-02	1 MCM2
DOID:4674	androgen insensitivity syndrome	1,99E-02	1 AR
DOID:4985	extraosseous Ewings sarcoma-primitive neuroepithelial tur	1,99E-02	1 CDKN2A
DOID:5003	eunuchism	1,99E-02	1 AR
DOID:5289	uterus leiomyosarcoma	1,99E-02	1 CDKN2A
DOID:7475	diverticulitis	1,99E-02	1 IDO1
DOID:8913	dermatophytosis	1,99E-02	1 APOE
DOID:9362	status asthmaticus	1,99E-02	1 ADRB2
DOID:5223	infertility	2,03E-02	4 AR,BIRC5,CRISP2,F5
DOID:184	bone cancer	2,05E-02	6 AR,CDKN2A,JUN,MMP9,RECQL4,SLC19A1
DOID:170	endocrine gland cancer	2,09E-02	13 ABCC5,ADAM8,APOC1,B3GAT1,BIRC5,CCNB1,CDKN2A,JUN,MCM2,MMP11,MMP9,NDRG1,PTTG1
DOID:1891	optic nerve disease	2,26E-02	2 ND1,ND6
DOID:9279	hyperhomocysteinemia	2,26E-02	2 APOE,F5
DOID:9840	esotropia	2,26E-02	2 MMP11,MMP9
DOID:3347	osteosarcoma	2,27E-02	5 CDKN2A,JUN,MMP9,RECQL4,SLC19A1
DOID:2394	ovarian cancer	2,31E-02	6 BIRC5,CDKN2A,EPCAM,MCM2,MMP9,TK1
DOID:1380	endometrial cancer	2,34E-02	7 AR,BIRC5,CDKN2A,COX1,HSPE1,MMP9,NDRG1
DOID:363	uterine cancer	2,34E-02	7 AR,BIRC5,CDKN2A,COX1,HSPE1,MMP9,NDRG1
DOID:0060085	organ system benign neoplasm	2,37E-02	9 AR,BCAM,BIRC5,CDKN2A,ESM1,MCM2,MMP9,NDRG1,PTTG1
DOID:65	connective tissue disease	2,49E-02	17 ADRB2,APOE,AR,BIRC5,CASP10,CCL3,CCL4,DEFA3,F5,FASN,HLA-DMA,HLA-DMB,ISG15,ITPR3,JUN,MMP9,SLC19A1
DOID:201	connective tissue cancer	2,63E-02	8 AR,BIRC5,CDKN2A,JUN,MCM2,MMP9,RECQL4,SLC19A1
DOID:4905	pancreatic carcinoma	2,73E-02	5 ABCC5,ADAM8,CDKN2A,JUN,NDRG1
DOID:4645	retinal cancer	2,91E-02	3 AR,CDKN2A,EPCAM
DOID:768	retinoblastoma	2,91E-02	3 AR,CDKN2A,EPCAM
DOID:771	retinal cell cancer	2,91E-02	3 AR,CDKN2A,EPCAM
DOID:9835	refractive error	2,91E-02	3 MMP11,MMP9,PHOX2A
DOID:0080014	chromosomal disease	2,98E-02	5 APOE,AR,FAAH,SLC19A1,STMN1
DOID:700	mitochondrial metabolism disease	3,04E-02	2 ND2,ND3
DOID:9588	encephalitis	3,04E-02	2 APOE,CCL3
DOID:326	ischemia	3,05E-02	4 APOE,HSPE1,MMP9,TRAP1
DOID:0060116	sensory system cancer	3,21E-02	4 AR,CDKN2A,EPCAM,EZH2
DOID:2174	ocular cancer	3,21E-02	4 AR,CDKN2A,EPCAM,EZH2
DOID:870	neuropathy	3,22E-02	6 MMP11,MMP9,ND1,ND6,NDRG1,PHOX2A
DOID:4866	salivary gland adenoid cystic carcinoma	3,46E-02	2 CDKN2A,SOX4
DOID:0050624	gastrointestinal system benign neoplasm	3,62E-02	3 BIRC5,CDKN2A,NDRG1
DOID:0060086	female reproductive organ benign neoplasm	3,62E-02	3 AR,CDKN2A,PTTG1
DOID:0060095	uterine benign neoplasm	3,62E-02	3 AR,CDKN2A,PTTG1
DOID:13223	uterine fibroid	3,62E-02	3 AR,CDKN2A,PTTG1
DOID:552	pneumonia	3,74E-02	4 APOE,CDKN2A,FGG,MMP9
DOID:8692	myeloid leukemia	3,84E-02	9 ABCA3,BIRC5,CCL3,CCNB1,CDKN2A,IDO1,JUN,MMP9,PTTG1
DOID:3829	pituitary adenoma	3,88E-02	3 CDKN2A,MMP9,PTTG1
DOID:11612	polycystic ovary syndrome	3,93E-02	4 ADRB2,AR,F5,MMP9
DOID:0060443	endothelial dystrophy	3,93E-02	1 BIRC5

DOID:10541	microinvasive gastric cancer	3,93E-02	1 REG1A
DOID:10863	paralytic squint	3,93E-02	1 PHOX2A
DOID:10869	fourth cranial nerve palsy	3,93E-02	1 PHOX2A
DOID:11555	Fuchs' endothelial dystrophy	3,93E-02	1 BIRC5
DOID:13620	patent foramen ovale	3,93E-02	1 F5
DOID:14748	Sotos syndrome	3,93E-02	1 F12
DOID:1659	supratentorial cancer	3,93E-02	1 BIRC5
DOID:2216	factor V deficiency	3,93E-02	1 F5
DOID:2671	transitional cell carcinoma	3,93E-02	1 BIRC5
DOID:318	progressive muscular atrophy	3,93E-02	1 AR
DOID:3362	coronary aneurysm	3,93E-02	1 MMP9
DOID:3500	gallbladder adenocarcinoma	3,93E-02	1 CDKN2A
DOID:3541	cerebral ventricle cancer	3,93E-02	1 BIRC5
DOID:368	cerebrum cancer	3,93E-02	1 BIRC5
DOID:3717	gastric adenocarcinoma	3,93E-02	1 REG1A
DOID:4012	papillary transitional carcinoma	3,93E-02	1 BIRC5
DOID:4449	macular retinal edema	3,93E-02	1 APOE
DOID:5165	uterine corpus sarcoma	3,93E-02	1 CDKN2A
DOID:5199	ureteral obstruction	3,93E-02	1 FABP1
DOID:5200	urinary tract obstruction	3,93E-02	1 FABP1
DOID:6929	retinal edema	3,93E-02	1 APOE
DOID:801	hemarthrosis	3,93E-02	1 MMP9
DOID:899	choledochal cyst	3,93E-02	1 REG1A
DOID:9460	uterine corpus cancer	3,93E-02	1 CDKN2A
DOID:9499	disseminated eosinophilic collagen disease	3,93E-02	1 BIRC5
DOID:9651	systolic heart failure	3,93E-02	1 MMP9
DOID:9768	heart aneurysm	3,93E-02	1 MMP9
DOID:10763	hypertension	4,27E-02	10 ADRB2,APLN,APOE,CDKN2A,F5,JUN,MMP9,ND1,ND2,PHOX2A
DOID:10124	corneal disease	4,37E-02	2 BIRC5,MMP9
DOID:381	arthropathy	4,37E-02	2 CCL4,MMP9
DOID:0050622	reproductive organ benign neoplasm	4,41E-02	3 AR,CDKN2A,PTTG1
DOID:127	leiomyoma	4,41E-02	3 AR,CDKN2A,PTTG1
DOID:0070004	myeloma	4,57E-02	7 AR,BIRC5,CCL3,CCL4,CDKN2A,F5,PTTG1
DOID:4960	bone marrow cancer	4,57E-02	7 AR,BIRC5,CCL3,CCL4,CDKN2A,F5,PTTG1
DOID:2377	multiple sclerosis	4,77E-02	6 APOE,IDO1,MMP9,ND1,ND5,STMN1
DOID:0050615	respiratory system cancer	4,81E-02	13 ADAM8,ADRB2,BIRC5,CCNB1,CDKN2A,CTAG1A,HPGD,MARCKSL1,MMP9,SLC19A1,STMN1,TK1,UBE2T
DOID:37	skin disease	4,83E-02	8 ADRB2,APOC1,CCL3,CCL3L3,F12,IDO1,MMP9,RECQL4
DOID:3996	urinary system cancer	4,83E-02	10 AP1M2,AR,BIRC5,CCNB1,CDKN2A,EPCAM,EZH2,HPN,MMP9,ZDHHC11
DOID:225	syndrome	4,85E-02	11 ADRB2,AR,CASP10,CRISP2,F12,F5,HPGD,KCNQ1OT1,MLPH,MMP9,RECQL4
DOID:161	keratosis	4,86E-02	2 CCL3,CCL3L3
DOID:14330	Parkinson's disease	4,93E-02	5 APOE,CDKN2A,ND1,ND2,ND5