Screening and identification of key biomarkers in clear cell renal cell carcinoma based on bioinformatics analysis

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Abstract

Clear cell renal cell carcinoma (ccRCC) is one of the most common types of malignancy of the urinary system. The pathogenesis and effective diagnosis of ccRCC have become popular topics for research in the previous decade. In the current study, an integrated bioinformatics analysis was performed to identify core genes associated in ccRCC. An expression dataset (GSE105261) was downloaded from the Gene Expression Omnibus database, and included 26 ccRCC and 9 normal kidney samples. Assessment of the microarray dataset led to the recognition of differentially expressed genes (DEGs), which was subsequently used for pathway and gene ontology (GO) enrichment analysis. This data was utilized in the construction of the protein-protein interaction network and module analysis was conducted using Human Integrated Protein-Protein Interaction rEference (HIPPIE) and Cytoscape software. In addition, target gene - miRNA regulatory network and target gene - TF regulatory network were constructed and analysed. Finally, hub genes were validated by survival analysis, expression analysis, stage analysis, mutation analysis, immune histochemical analysis, receiver operating characteristic (ROC) curve analysis, RT-PCR and immune infiltration analysis. The results of these analyses led to the identification of a total of 930 DEGs, including 469 up regulated and 461 down regulated genes. The pathways and GO found to be enriched in the DEGs (up and down regulated genes) were dTMP de novo biosynthesis, glycolysis, 4-hydroxyproline degradation, fatty acid beta-oxidation (peroxisome), cytokine, defense response, renal system development and organic acid metabolic process. Hub genes were identified from PPI network according to the node degree, betweenness centrality, stress centrality, closeness centrality and clustering coefficient. Similarly, target genes were identified from target gene - miRNA regulatory network and target gene - TF regulatory network according to the node degree. Furthermore, survival analysis, expression analysis, stage analysis, mutation analysis, immune histochemical analysis, ROC curve analysis, RT-PCR and immune infiltration analysis revealed that CANX, SHMT2, IFI16, P4HB, CALU, CDH1, ERBB2, NEDD4L, TFAP2A and SORT1 may be associated in the tumorigenesis, advancement or prognosis of ccRCC. In conclusion, the 10 hub genes diagnosed in the current study may help researchers in exemplify the molecular mechanisms

linked with the tumorigenesis and advancement of ccRCC, and may be powerful and favorable candidate biomarkers for the prognosis, diagnosis and treatment of ccRCC.

Key words: clear cell renal cell carcinoma; bioinformatics analysis; pathway and gene ontology (GO) enrichment analysis; Gene Expression Omnibus; protein - protein interaction network

Introduction

Clear cell renal cell carcinoma (ccRCC) is the most common malignancy of the kidney [Heng et al. 2009]. ccRCC ranks 14th in cancer deaths worldwide, responsible for about 403,262 new cases and 175,098 deaths last year [Bray et al. 2018]. Although we have made great development on the early prognosis, diagnosis and new therapy, ccRCC still is one of challengeable diseases in this world [Jiang et al. 2006; Pan et al. 2004; Wood and Margulis, 2009]. However, the molecular mechanisms of ccRCC are not well understood. And due to the absence of specific biomarkers, most ccRCC patients are diagnosed at a late stage, leading to particularly poor outcomes of patients [Patel et al. 2016]. Even worse, some of ccRCC patients suffer from tumor recurrence due to the cancer drug resistance [Mickisch et al. 1990] and nephrectomy [Eggerer et al. 2006]. Therefore, it is of outstanding importance to find novel biomarkers, pathways and effective targets for ccRCC patients.

Similar to that of other cancers, the process of ccRCC initiation, progression and invasion of cancer cells associates' genetic aberrations, and changes in the cancer microenvironment [Slaton et al. 2001]. The literature has also reported that the development and occurrence of ccRCC are closely associated with a variety of genes such as von Hippel-Lindau (VHL) [Nickerson et al. 2008], AL-1/4.1B [Yamada et al. 2006], HIF1A [Wiesener et al. 2001], FOXM1 [Xue et al. 2012] and KISS1R [Chen et al. 2011], and cellular pathways such as IL-6/STAT-3 pathway [Cuadros et al. 2014], notch and TGF- β signaling pathways [Sjölund et al. 2011], MYC pathway [Tang et al. 2009], EGFR/MMP-9 signaling pathway [Liang et al. 2012] and phosphoinositide 3-kinase/Akt pathway [Soubrier et al. 2006]. Thus, it is vital to identify effective early diagnostic methods progression development, in order to intervene in the advancement of the disease at the early stages.

Microarray technology is a high-throughput and powerful tool to make large quantities of data such as gene expression and DNA methylation [Giltane and Rimm, 2004]. To explore the differential expressed genes (DEGs) in metastatic ccRCC, diagnose new high-specificity and high-sensitivity tumor biomarkers,

and identify effective therapeutic targets, *in silico* methods were used to study ccRCC. In the current study, GSE105261 was downloaded and analyzed from the Gene Expression Omnibus (GEO) database to obtain DEGs between metastatic ccRCC tissues and normal renal tissues. Subsequently, pathway enrichment analysis, gene ontology (GO) enrichment analysis, protein-protein interaction (PPI) network analysis, module analysis, target gene - miRNA regulatory network analysis and target gene - TF regulatory network analysis were performed to characterize the molecular mechanisms underlying carcinogenesis and progression of ccRCC. Validation of hub genes was performed by using survival analysis, expression analysis, stage analysis, mutation analysis, immune histochemical analysis (IHC) receiver operating characteristic (ROC) curve, RT-PCR and immune infiltration analysis. In conclusion, the present study identified a number of important genes that are associated with the molecular mechanism of ccRCC by integrated bioinformatical analysis, and these genes and regulatory networks may assist with identifying potential gene therapy targets for ccRCC. Our study results should provide novel insights for predicting the risk of ccRCC.

Materials and methods

Microarray data source, data preprocessing and identification of DEGs

In the current study, gene microarray datasets comparing the gene expression profiles between metastatic ccRCC tissues and normal renal tissues were downloaded from the GEO (<http://www.ncbi.nlm.nih.gov/gds/>). The accession number was GSE105261 was submitted by Nam et al (2019). The microarray data of GSE105261 was assessed using the GPL10558 Illumina HumanHT-12 V4.0 expression beadchip. The gene microarray data comprised 26 metastatic ccRCC tissue samples and 9 normal renal tissue samples. IDAT files were converted to expression measures and normalized via the beadarray package in R bioconductor [Dunning et al. 2006]. The aberrantly expressed mRNAs were subsequently determined using the Limma package in R bioconductor [Ritchie et al. 2015], based on the Benjamini and Hochberg method [Kvam et al. 2012]. DEGs between metastatic ccRCC tissues and normal renal tissues were defined by the cut-off criterion of fold change >1.11 for up regulated genes, fold change >1.00 for down regulated genes and a P-value of <0.05.

Pathway enrichment analysis of DEGs

Pathway enrichment analyses of DEGs were performed according to the enrichment analysis tool of ToppGene (ToppFun) (<https://toppgene.cchmc.org/enrichment.jsp>) [Chen et al 2009] which integrates various pathway databases such as Kyoto Encyclopedia of Genes and Genomes (KEGG; <http://www.genome.jp/kegg/>) [Aoki-Kinoshita and Kanehisa, 2007], Pathway Interaction Database (PID, <http://pid.nci.nih.gov/>) [Schaefer et al 2009], Reactome (<https://reactome.org/PathwayBrowser/>) [Croft et al 2011], Molecular signatures database (MSigDB, <http://software.broadinstitute.org/gsea/msigdb/>) [Liberzon et al 2011], GenMAPP (<http://www.genmapp.org/>) [Dahlquist et al 2002], Pathway Ontology (<https://bioportal.bioontology.org/ontologies/PW>) [Petri et al 2014], PantherDB (<http://www.pantherdb.org/>) [Mi et al 2013] and Small Molecule Pathway Database (SMPDB, <http://smpdb.ca/>) with the cutoff criterion of p value <0.05.

GO enrichment analysis of DEGs

ToppGene (ToppFun) (<https://toppgene.cchmc.org/enrichment.jsp>) [Chen et al 2009] is an online biological information database that integrates biological data and analysis tools. GO (<http://www.geneontology.org/>) [Harris et al 2004] was used to perform bioinformatics analysis and annotate function enrichment of genes. ToppGene was applied to perform the function enrichment and biological analyses of these DEGs with categories of biological processes (BP), cellular component (CC) and molecular function (MF). P<0.05 was considered statistically significant.

PPI network construction and module analysis

Human Integrated Protein-Protein Interaction rEference (HIPPIE) (<http://cbdm.uni-mainz.de/hippie/>) [Alanis-Lobato et al. 2017] is a online tool that studies genetic interactions and can assess PPI network and this online tool integrates various PPI databases such as IntAct (<https://www.ebi.ac.uk/intact/>) [Orchard et al. 2014], BioGRID (<https://thebiogrid.org/>) [Chatr-Aryamontri et al. 2017], HPRD (<http://www.hprd.org/>) [Keshava Prasad et al. 2009], MINT (<https://mint.bio.uniroma2.it/>) [Licata et al. 2012], BIND (<http://download.baderlab.org/BINDTranslation/>) [Isserlin et al. 2011], MIPS (<http://mips.helmholtz-muenchen.de/proj/ppi/>) [Pagel et al. 2005] and DIP

(<http://dip.doe-mbi.ucla.edu/dip/Main.cgi>) [Salwinski et al. 2004]. Therefore, the HIPPIE database in Cytoscape version 3.7.2 (<http://www.cytoscape.org/>) [Shannon et al 2003] was used to identify and map potential associations between the DEGs (up and down regulated genes). Network Analyzer is an application of Cytoscape, and was used for calculating the topological properties such as node degree [Wang et al 2014], betweenness centrality [Peng et al 2015], stress centrality [Carson and Lu, 2015], closeness centrality [Jalili et al 2016] and clustering coefficient [Wiles et al 2010] of hub genes in PPI network. Modules in the PPI network were extracted from Cytoscape using the PEWCC1 [Zaki et al 2013], with the following criteria: Degree cut-off, 2; node score cut-off, 0.2; k-core, 2; and maximum depth, 100.

Construction of target genes - miRNA regulatory network

The micro RNA (miRNAs) interacts with targeted genes were predicted by two established miRNA target prediction databases such as DIANA-TarBase (<http://diana.imis.athena-innovation.gr/DianaTools/index.php?r=tarbase/index>) [Vlachos et al 2015] and miRTarBase (<http://mirtarbase.mbc.nctu.edu.tw/php/download.php>) [Chou et al 2018]. The miRNAs predicted by online tool NetworkAnalyst (<https://www.networkanalyst.ca/>) [Zhou et al 2019] selected as the targeted genes and converted the results visualized by using Cytoscape version 3.7.2 (<http://www.cytoscape.org/>) [Shannon et al 2003]. In the network, a blue diamond node represented the miRNA and a green and red circular nodes represented the up and down regulated target gene, their interaction was represented by an line. The numbers of lines in the networks indicated the contribution of one miRNA to the surrounding target genes, and the higher the degree, the more central the target gene was within the network.

Construction of target genes - TF regulatory network

The transcription factors (TFs) interacts with targeted genes were predicted by established TF target prediction database JASPAR (<http://jaspar.genereg.net/>) [Khan et al 2018]. The TFs predicted by online tool NetworkAnalyst (<https://www.networkanalyst.ca/>) [Zhou et al 2019] selected as the targeted genes and converted the results visualized by using Cytoscape version 3.7.2 (<http://www.cytoscape.org/>) [Shannon et al 2003]. In the network, a blue and

yellow triangle node represented the TF and a green and red circular nodes represented the up and down regulated target gene, their interaction was represented by an line. The numbers of lines in the networks indicated the contribution of one TF to the surrounding target genes, and the higher the degree, the more central the target gene was within the network.

Validation of hub genes

After hub genes identified from microarray expression profile dataset, UALCAN (<http://ualcan.path.uab.edu/analysis.html>) [Chandrashekar et al 2017], cBio Cancer Genomics Portal (<http://www.cbioportal.org/>) [Gao et al 2013] and The Human Protein Atlas (HPA) (<https://www.proteinatlas.org/>) [Uhlen et al 2010] were used to validate the selected up regulated and down regulated hub genes. UALCAN is an online tool for gene expression analysis between cancer patients and normal person's data from The Cancer Genome Atlas (TCGA). UALCAN provides data such as survival period, gene expression and tumor staging. cBio Cancer Genomics Portal is an online tool for genetic alterations in cancer patients from TCGA database. cBio Cancer Genomics Portal provides data such as DNA mutations, methylations, gene amplifications, homozygous deletions, protein alterations and phosphorous abundance. The Human Protein Atlas (HPA) is an online tool for map all the human proteins in tissues, cells and organs. HPA provides data about expressions of hub genes in cancer tissue and its normal tissue. Receiver operating characteristic (ROC) curve was performed to evaluate the diagnosis value of hub genes in ccRCC using R package "pROC" [Robin et al 2011]. Total RNA of hub genes were segregated from cultured ccRCC cells using TRIzol reagent (Invitrogen) and converted into complementary DNA (EY001; Shanghai Iyumbio Co). LightCycler 96 Real-Time PCR Systems (Roche) was used to performed RT-PCR. The operations for the real-time polymerase chain reaction (RT-PCR) were as follows: 50C for 3 minutes, 95C for 3 minutes, 95C for 10 seconds, followed by 40 cycles of 95C for 10 seconds and 60C for 30 seconds. The sequences of the primers are shown in Table 1. The relative expression levels of genes were normalized to those of human β -actin, estimated using the $2^{-\Delta\Delta CT}$ method and were log-transformed [Livak and Schmittgen, 2001]. The hub genes were further analyzed using online tool the TIMER

(<https://cistrome.shinyapps.io/timer/>) [Li et al. 2017] for immune infiltration analysis. Immune cell types such as B cells, CD4+ T cells, CD8+ T cells, neutrophils, macrophages, and dendritic cells were assessed by TIMER on renal cancer sample data, and the correlation between 10 hub genes expression and immune infiltration.

Results

Identification of DEGs

The gene expression dataset GSE33455 was downloaded from the GEO database. After the standardization (normalization) of the microarray data, differentially expressed genes were identified between metastatic ccRCC tissues and normal renal tissues. Box plots were constructed before normalization and after normalization of microarray data (Fig. 1A and Fig. 1B). Upon preprocessing, 930 DEGs (P value <0.05; fold change > 1.11 for up regulated genes; fold change < -1 for down regulated genes) were identified, including 469 up regulated and 461 down regulated genes (Table 1). The volcano plot of gene expression profile data was shown in Fig. 2. The heat maps of the up regulated and down regulated genes are presented in Fig. 3 and Fig. 4.

Pathway enrichment analysis

Pathway enrichment analyses of DEGs (up and down regulated genes) was performed using ToppGene. As for pathway enrichment, the up regulated genes were enriched in dTMP de novo biosynthesis, glycolysis, phagosome, complement and coagulation cascades, HIF-1-alpha transcription factor network, IL12-mediated signaling events, extracellular matrix organization, cytokine signaling in immune system, gluconeogenesis, one carbon pool by folate, ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins, ensemble of genes encoding core extracellular matrix including ECM glycoproteins, collagens and proteoglycans, integrin signalling pathway, plasminogen activating cascade, hypertension, reverse cholesterol transport and pyrimidine metabolism are listed in Table 2. Similarly, the down regulated genes were enriched in 4-hydroxyproline degradation, fatty acid beta-oxidation (peroxisome), metabolic pathways, aldosterone-regulated sodium reabsorption, FOXA2 and FOXA3 transcription factor networks, p75(NTR)-mediated signaling, transmembrane transport of small

molecules, SLC-mediated transmembrane transport, urea cycle and metabolism of amino groups, valine/leucine and isoleucine degradation, platelet amyloid precursor protein pathway, ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins, blood coagulation, 5-hydroxytryptamine degradation, pathway of urea cycle and metabolism of amino groups, gluconeogenesis pathway, polythiazide pathway and ramipril pathway are listed in Table 3.

GO enrichment analysis of DEGs

GO enrichment analysis for the up and down regulated DEGs were performed, respectively. Specifically, GO includes three items, including the BP, CC, and MF. Up regulated genes were mainly enriched in the BP, CC and MF including response to cytokine, defense response, vesicle organization, cell surface, signaling receptor binding and extracellular matrix structural constituent are listed in Table 4. Similarly, down regulated genes were mainly enriched in the BP, CC and MF including renal system development, organic acid metabolic process, apical part of cell, intrinsic component of plasma membrane, ion transmembrane transporter activity and transmembrane transporter activity are listed in Table 5.

PPI network construction

The PPI network of up regulated genes consisted of 6829 nodes and 16639 edges is shown in Fig. 5. When ‘node degree distribution ≥ 150 ’, ‘betweenness centrality ≥ 0.00567913 ’, ‘stress centrality ≥ 16321080 ’, ‘closeness centrality ≥ 0.33036363 ’ and ‘clustering coefficient = 0’ were set as the cut-off criterion, a total of 12 genes (EGLN3, PCLAF, VCAM1, CANX, SHMT2, IFI16, GAPDH, MS4A7, FGF11, IKBIP, SCD and TRIM9) were selected as hub genes from DEGs and detailed listed of hub genes are given in Table 6. The statistical results and scatter plot for node degree distribution, betweenness centrality, stress centrality, closeness centrality and clustering coefficient are presented in Fig. 6A - 6E. It was found that the pathway and GO enrichment analysis of 12 hub genes are mainly referred to HIF-1 signaling pathway, extracellular matrix organization, phagosome, dTMP de novo biosynthesis, innate immune system, response to cytokine, pathways in cancer, endoplasmic reticulum part, defense response and adaptive immune system. The PPI network of down regulated genes consisted of 5108 nodes and 9299 edges is shown in Fig. 7. When ‘node degree distribution $\geq$

150', 'betweenness centrality ≥ 0.01687101 ', 'stress centrality ≥ 8184666 ', 'closeness centrality ≥ 0.30386246 ' and 'clustering coefficient = 0' were set as the cut-off criterion, a total of 12 genes (CDH1, ERBB2, ATP1A1, ALB, NEDD4L, PHGDH, RTN4, ACOT11, ANKRD9, VTCN1, SLC22A7 and MST1L) were selected as hub genes from DEGs and detailed listed of hub genes are given in Table 6. The statistical results and scatter plot for node degree distribution, betweenness centrality, stress centrality, closeness centrality and clustering coefficient are presented in Fig. 8A - 8E. It was found that the pathway and GO enrichment analysis of 12 hub genes are mainly referred to Rap1 signaling pathway, tight junction, aldosterone-regulated sodium reabsorption, FOXA2 and FOXA3 transcription factor networks, ion transport, metabolic pathways, p75(NTR)-mediated signaling, metabolism of lipids and lipoproteins, plasma membrane bounded cell projection part, signaling receptor binding, transmembrane transport of small molecules and ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins.

Module analysis

Total 2083 modules were obtained from the PPI network for up regulated genes based on the PEWCC1 analysis in Cytoscape. We chose the four most significant modules for further analysis (Fig.9). Module 8 consisted of 41 nodes and 108 edges, module 11 consisted of 34 nodes and 90 edges, module 21 consisted of 26 nodes and 62 edges, and module 32 consisted of 18 nodes and 64 edges. Pathway and GO enrichment analysis showed that GAPDH, VIM, STAT1, COL6A1, ENO2, SERPINH1, CAV1 and SPARC were included in module 8, module 11, module 21 and module 32, and participated in HIF-1 signaling pathway, aurora B signaling, pathways in cancer, focal adhesion, cell surface, extracellular matrix, response to cytokine and response to other organism. Total 932 modules were obtained from the PPI network for down regulated genes based on the PEWCC1 analysis in Cytoscape. We chose the four most significant modules for further analysis (Fig.10). Module 3 consisted of 25 nodes and 65 edges, module 5 consisted of 22 nodes and 47 edges, module 6 consisted of 17 nodes and 46 edges, and module 8 consisted of 15 nodes and 31 edges. Pathway and GO enrichment analysis showed that ERBB2, CDH1, NEDD4L, KLK6, PLCG2, RTN4, SCNN1A and COL4A3 were included in module 3, module 5, module 6 and module 8, and participated in tight junction, rap1 signaling pathway, aldosterone-regulated

sodium reabsorption, alpha-synuclein signaling, ion transport, chemical homeostasis, cation transport and renal system development.

Construction of target genes - miRNA regulatory network

Most of miRNAs were responsible for progression of CCRCC [Liu et al 2010]. In order to investigate the regulatory network of target genes - miRNA for CCRCC, DIANA-TarBase and miRTarBase were utilized to obtain miRNAs for the top 5 up regulated and down regulated genes. The up regulated genes and miRNAs is shown in Fig. 11. Specifically, that SOD2 regulates 257 miRNAs (ex; hsa-mir-4424), CCND1 regulates 197 miRNAs (ex; hsa-mir-5009-3p), SCD regulates 167 miRNAs (ex; hsa-mir-3671), VEGFA regulates 108 miRNAs (ex; hsa-mir-4497) and SH3PXD2A regulates 105 miRNAs (ex; hsa-mir-6818-5p) are listed in Table 7. The pathway and GO enrichment analysis revealed that up regulated target genes were enriched in reactive oxygen species degradation, Focal adhesion, defense response, regulation of immune system process and molecular function regulator. Similarly, down regulated genes and miRNAs is shown in Fig. 12. Specifically, BTG2 regulates 227 miRNAs (ex; hsa-mir-4319), VAV3 regulates 164 miRNAs (ex; hsa-mir-5001-5p), LDLR regulates 123 miRNAs (ex; hsa-mir-3121-3p), FOXC1 regulates 103 miRNAs (ex; hsa-mir-5688) and SYT7 regulates 75 miRNAs (ex; hsa-mir-4270) are listed in Table 7. The pathway and GO enrichment analysis revealed that down regulated target genes were enriched in response to endogenous stimulus, leukocyte transendothelial migration, metabolism of lipids and lipoproteins, renal system development and insulin secretion pathway.

Construction of target genes - TF regulatory network

Many of the TFs were responsible for advancement of CCRCC [Higgins et al 2003]. The current study focused on the five hub genes, and further assessed their TF-target associations. The TF-target regulatory network was based on interactions in the JASPAR database. A target genes - TF regulated network was established, including connections and top five up regulated genes, which are presented in Fig. 13. Specifically, THBS2 regulates 217 TFs (ex; FOXC1), VCAN regulates 173 TFs (ex; GATA2), MLKL regulates 102 TFs (ex; YY1), RHBDF2 regulates 100 TFs (ex; FOXL1) and COL11A1 regulates 90 TFs (ex; E2F1) are listed in Table

8. The pathway and GO enrichment analysis revealed that up regulated target genes were enriched in phagosome, direct p53 effectors, protein-containing complex binding, secretion and extracellular matrix organization. Similarly, target genes - TF regulated network was established, including connections and top five down regulated genes, which are presented in Fig. 14. Specifically, FOXQ1 regulates 175 TFs (ex; GATA2), EFHD1 regulates 126 TFs (ex; YY1), NCOA7 regulates 86 TFs (ex; FOXL1), PTH1R regulates 84 TFs (ex; USF2) and MUC20 regulates 83 TFs (ex; NFIC) are listed in Table 8. The pathway and GO enrichment analysis revealed that down regulated target genes were enriched in epithelium development, mitochondrion, signaling receptor binding, signaling by GPCR and signaling events mediated by hepatocyte growth factor receptor (c-Met).

Validation of hub genes

The present study validated the effect of CANX, SHMT2, IFI16, P4HB, CALU, CDH1, ERBB2, NEDD4L, TFAP2A and SORT1 on the prognosis of patients with ccRCC using the UALCAN. According to the median expression level of CANX, SHMT2, IFI16, P4HB, CALU, CDH1, ERBB2, NEDD4L, TFAP2A and SORT1, the patients were divided into a high-expression and a low-expression group. The Kaplan-Meier analysis demonstrated that patients with low CANX expression had shorter survival time than patients with high CANX levels ($p = 0.043$) (Fig. 15A), high SHMT2 expression had shorter survival time than patients with low SHMT2 levels ($p = 0.039$) (Fig. 15B), high IFI16 expression had shorter survival time than patients with low IFI16 levels ($p < 0.0001$) (Fig. 15C), high P4HB expression had shorter survival time than patients with low P4HB levels ($p < 0.0001$) (Fig. 15D), high CALU expression had shorter survival time than patients with low CALU levels ($p = 0.0065$) (Fig. 15E), low CDH1 expression had shorter survival time than patients with higher CDH1 levels ($p = 0.0037$) (Fig. 16A), low ERBB2 expression had shorter survival time than patients with higher ERBB2 levels ($p = 6e-04$) (Fig. 16B), low NEDD4L expression had shorter survival time than patients with high NEDD4L levels ($p = 0.0044$) (Fig. 16C), high TFAP2A expression had shorter survival time than patients with low TFAP2A levels ($p < 0.0001$) (Fig. 16D) and low SORT1 expression had shorter survival time than patients with higher SORT1 levels ($p = 0.00099$) (Fig. 16E). UALCAN for expression analysis of tumor vs. normal tissue demonstrated that CANX, SHMT2, IFI16, P4HB and CALU were significantly over expressed in ccRCC compared to normal (Fig. 17),

while CDH1, ERBB2, NEDD4L, TFAP2A and SORT1 were significantly low expressed in ccRCC compared to normal (Fig. 18). In addition, UALCAN box plots of gene expression by pathological stages based on the TCGA database results shows that CANX, SHMT2, IFI16, P4HB and CALU were more expressed in all stages of ccRCC compared to normal (Fig. 19), while CDH1, ERBB2, NEDD4L, TFAP2A and SORT1 were less expressed in all stages of ccRCC compared to normal (Fig. 20). We used cBioportal tool to identify the specific alterations in hub genes. Percentages of alteration in hub genes such as 8 % CANX (missense mutation, truncating mutation and amplification), 0.3 % SHMT2 (missense mutation), 0.3 % IFI16 (amplification), 0.3% P4HB (amplification), 0.6 % CALU (missense mutation and amplification), 0.3% % CDH1 (missense mutation), 1.1 % ERBB2 (missense mutation, truncating mutation and amplification), 0.6 % NEDD4L (truncating mutation and amplification), 0 % TFAP2A and 0.3 % SORT1 (missense mutation) (Fig.21). In addition, the immunohistochemistry staining obtained from The Human Protein Atlas indicated that the expression of CANX, SHMT2, IFI16, P4HB and CALU were enhanced in ccRCC tissue compared to normal tissue and CDH1, ERBB2, NEDD4L, TFAP2A and SORT1 in ccRCC tissue compared to normal tissue (Fig. 22) and showed consistent conclusions. To further investigate the efficiency of hub genes as potential biomarker of ccRCC, ROC curve between CCRCC patients and controls was performed to analyze the sensitivity and specificity of hub genes in diagnosing ccRCC. The result (Fig. 23) showed that areas under the curve (AUC) of hub genes were CANX (AUC = 0.936), SHMT2 (AUC = 0.915), IFI16 (AUC = 0.932), P4HB (AUC = 0.974), CALU (AUC = 0.944), CDH1 (AUC = 0.880), ERBB2 (AUC = 0.962), NEDD4L (AUC = 0.885), TFAP2A (AUC = 0.799) and SORT1 (AUC = 0.932). The AUC values were more than 0.6, which had great diagnostic value for ccRCC. To verify the reliability of the high-throughput sequencing data, several candidate mRNAs of interest were initially identified for further analysis, including CANX, SHMT2, IFI16, P4HB, CALU, CDH1, ERBB2, NEDD4L, TFAP2A and SORT1. The results demonstrated that CANX, SHMT2, IFI16, P4HB and CALU were up regulated and that CDH1, ERBB2, NEDD4L, TFAP2A and SORT1 were down regulated in ccRCC patients relative to those in the healthy group (Fig. 24). These results demonstrated that the expression patterns of CANX, SHMT2, IFI16, P4HB, CALU, CDH1, ERBB2, NEDD4L, TFAP2A and SORT1 were consistent with those attained by high-throughput sequencing analysis. In the

ccRCC, the high expression levels of the CDH1, ERBB2, NEDD4L, TFAP2A and SORT1 all negatively associated with tumor purity (Fig. 25A-E), whereas low expression of CDH1, ERBB2, NEDD4L, TFAP2A and SORT1 were all positively associated with tumor purity (Fig. 25F-J). It can be inferred from this result that all ten hub genes are probably expressed not in the microenvironment, but expressed in the tumor cells.

Discussion

ccRCC is a common malignant neoplasm of the kidney [Gerlinger et al 2014]. The histological type of disease, determined after surgery and chemotherapy, has a key impact on the survival and prognosis of patients with ccRCC. Pathologically determined cancer usually leads to a poor prognosis with metastasis and more difficult surgery or chemotherapy. Furthermore, the 5-year survival rate only reaches 10% [Li et al 2016]. Consequently, a comprehensive understanding of the molecular mechanism behind the occurrence and progression of ccRCC is of essential for management and therapy, as is the progression of new targeted therapies to progress over all survival time. With the popular use of high through output sequencing technologies and microarrays, the expression levels of genes in the human genome are openly incorporated in public databases. Therefore, there is an insistent need for sensitive and new biomarkers of ccRCC and also microarray data can be scrutinized in order to promote the genetic research of ccRCC.

In the current study, based on the original microarray data, we identified 930 DEGs, including 469 up regulated and 461 down regulated genes between metastatic ccRCC tissues and normal renal tissues. Genes such as CKMT1A [Fan et al 2018] and P4HA1 [Zhou et al 2017] were associated with invasion of various cancer cells, but these genes may be liable for invasion of ccRCC cells. Genes such as RAB25 [Liu and Ding, 2014], KCNJ1 [Guo et al 2015], SFRP1 [Ricketts et al 2014], CLDN8 [Osunkoya et al 2009], ATP1A1 [Zhang et al 2017], NDUFA4L2 [Wang et al 2017], SLC16A3 [Fisel et al 2013], ANGPTL4 [Dong et al 2017] and PLOD2 [Kurozumi et al 2016] were responsible for progression of ccRCC.

In pathway enrichment analysis, up regulated genes were enriched in dTMP de novo biosynthesis, phagosome, HIF-1-alpha transcription factor network, extracellular matrix organization, gluconeogenesis, ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins, integrin signalling pathway and hypertension. Genes such as TYMS (thymidylatesynthetase) [Colavito et al 2009], HLA-A (major histocompatibility complex, class I, A) [Schendel et al 1997], HLA-B (major histocompatibility complex, class I, B) [Ibrahim et al 2003], HLA-G (major histocompatibility complex, class I, G) [Seliger and Schlaf, 2007], TAP1 [Dovhey et al 2000], CD14 [Li et al 2014], SCARB1 [Pośpiech et al 2015], HK2 [Yoshino et al 2013], PLIN2 [Cao et al 2018], ADM (adrenomedullin) [Gao et al 2016], VEGFA (vascular endothelial growth factor A) [Dorević et al 2009], BHLHE41 [Bigot et al 2016], BNIP3 [Huang et al 2014], CXCR4 [D'Alterio et al 2010], CA9 [Bleumer et al 2007], LDHA (lactate dehydrogenase A) [Girgis et al 2014], MMP9 [Liang et al 2012], VCAM1 [Shioi et al 2006], COL3A1 [Su et al 2014], COL6A1 [Wan et al 2015], COL23A1 [Xu et al 2018], VCAN (versican) [Mitsui et al 2017], LAMA4 [Wragg et al 2016], SERPINH1 [Qi et al 2018], TIMP1 [Lu et al 2014], LOX (lysyl oxidase) [Di Stefano et al 2016], PFKP (phosphofructokinase, platelet) [Wang et al 2016], CTHRC1 [Jin et al 2016], ANGPT2 [Gayed et al 2015], POSTN (periostin) [Chuanyu et al 2017], IGFBP3 [Ricketts et al 2009], CXCL10 [Polimeno et al 2013], ESM1 [Leroy et al 2010], LGALS1 [White et al 2017], TGFA (transforming growth factor alpha) [Argilés et al 1992], TGFBI [Lebdai et al 2015], TGM2 [Erdem et al 2014], CAV1 [Butz et al 2015], SOD2 [Gao et al 2013] and GAPDH (glyceraldehyde-3-phosphate dehydrogenase) [Vilà et al 2000] were responsible for progression of ccRCC. SHMT2 was associated with pathogenesis of hepatocellular carcinoma [Woo et al 2016], but expression of this gene may be important for advancement of ccRCC. SNP in genes such as HLA-DQA1 [Kohno et al 2011], HLA-DQB1 [Chan et al 2007], FCGR2A [Gavin et al 2017], THBS4 [Lin et al 2016], C1QA [Azzato et al 2010] and RAC2 [Hertz et al 2016] were responsible for advancement of various cancer, but these polymorphic genes may be liable for progression of ccRCC. Genes such as ITGA5 [Yoo et al 2016], ITGB2 [Liu et al 2018], C3 (complement C3) [Chen et al 2013], THBS2 [Wei et al 2017], CD36 [Ladanyi et al 2018], HMOX1 [Ghosh et al 2016], SERPINE1 [Azimi et al 2017], PLOD1 [Li et al 2017], COL1A1 [Zhang et al 2018], COL1A2 [Ao et al 2018], COL4A1 [Huang et al 2018], COL4A2 [JingSong et al 2017],

COL5A1 [Liu et al 2018], COL5A2 [Zeng et al 2018], COL6A3 [Ao et al 2018], COL8A1 [Ma et al 2012], BMP1 [Wu et al 2014], P4HB [Xia et al 2017], ALDOC (aldolase, fructose-bisphosphate C) [Li et al 2016], PGF (placental growth factor) [Zhang et al 2015], SERPINE2 [Wang et al 2015], CXCL9 [Bronger et al 2016], FGF11 [Ye et al 2016], CCL5 [Mi et al 2011], SEMA6A [Lim et al 2017], VWF (von Willebrand factor) [Wang et al 2005], CTSZ (cathepsin Z) [Lines et al 2012], INHBB (inhibin subunit beta B) [Zou et al 2018], FNDC1 [Das and Ogunwobi, 2017], PXDN (peroxidase) [Zheng and Liang, 2018] and FSTL1 [Yang et al 2017] were important for invasion of various cancer cells, but these genes may be involved in invasion of ccRCC cells. High expression of genes such as CANX (calnexin) [Kobayashi et al 2015], OLR1 [Wang et al 2017], CP (ceruloplasmin) [Balmaña et al 2015], SLC2A1 [Santassusagna et al 2018], FGG (fibrinogen gamma chain) [Zhu et al 2009], ENO2 [Soh et al 2011], C1QTNF6 [Takeuchi et al 2011], TNFSF13B [Qian et al 2014], CSPG4 [Poli et al 2013] and C1QL1 [Celestino et al 2018] were responsible for pathogenesis of various cancer, but over expression of these genes may be linked with progression of ccRCC. Genes such as COL11A1 [Wu et al 2015], PLOD3 [Baek et al 2019] and SFRP4 [Warrier et al 2014] were associated with drug resistance in various cancer, but these genes may be linked with chemo resistance in ccRCC. HLA-DQA2, HLA-F (major histocompatibility complex, class I, F), FCGR1A, CYBB (cytochrome b-245 beta chain), C1R, TUBA3D, EGLN3, COL6A2, COL15A1, SPARC (secreted protein acidic and cysteine rich), P4HA2, COLGALT1, TPI1, SEMA5B, SERPINF2, ANXA4, CCL4L2, FCN3, C1QB, C1QC and TNFAIP6 were identified as novel biomarkers for pathogenesis of ccRCC in these pathways. Similarly, down regulated genes were enriched in 4-hydroxyproline degradation, metabolic pathways, FOXA2 and FOXA3 transcription factor networks, transmembrane transport of small molecules, urea cycle and metabolism of amino groups, platelet amyloid precursor protein pathway, blood coagulation, pathway of urea cycle and metabolism of amino groups and polythiazide pathway. Low expression of genes such as GPHN (gephyrin) [Zhang et al 2019], ASS1 [Qiu et al 2014], INPP5J [Zhu et al 2015], PCK1 [Liu et al 2018] and NEDD4L [Qu et al 2016] were linked with development of various cancer, but less expression of these genes may be liable for progression of ccRCC. Genes such as EPHX2 [Vainio et al 2011], ACY1 [Shi et al 2013] CKB (creatine kinase B) [Li et al 2013], UGT8 [Cao et al 2018], ALDOB (aldolase, fructose-bisphosphate B) [Tian

et al 2017], **HYAL1** [Tan et al 2011], G6PC [Guo et al 2015], GLDC (glycine decarboxylase) [Berezowska et al 2017], QPRT (quinolinatephosphoribosyltransferase) [Hinsch et al 2009], AQP6 [Ma et al 2016], SLC12A1 [Teng et al 2016], SLC44A4 [Mattie et al 2016], NIPAL1 [Sasahira et al 2018], PLG (plasminogen) [Stillfried et al 2007], COL4A3 [Jiang et al 2013] and **KNR1** [Quesada-Calvo et al 2017] were important for progression of various cancer, but these genes may be linked with pathogenesis of ccRCC. Genes such as HMGCS2 [Su et al 2017], PTGDS (prostaglandin D2 synthase) [Shyu et al 2013] and PLAT (plasminogen activator, tissue type) [Strojan et al 1998] were involved in invasion of various cancer cells, but these genes may be responsible for invasion of ccRCC cells. Single nucleotide polymorphism (SNP) in genes such as ADH1A [Cui et al 2018] and ADH1C [Hidaka et al 2015] were linked with advancement of gastric cancer, but these polymorphic genes may be associated with pathogenesis of ccRCC. Genes such as ATP6V1G3 [Shinmura et al 2015], FBP1 [Ning et al 2016], ARG2 [Ochocki et al 2018], GATM (glycine amidinotransferase) [Pflueger et al 2015], DDC (dopa decarboxylase) [Papadopoulos et al 2015], PHGDH (phosphoglycerate dehydrogenase) [Yoshino et al 2017], MAN1C1 [Li et al 2018], ALB (albumin) [Koparal et al 2018], ABCB1 [Diekstra et al 2015], AQP1 [Morrissey et al 2015], SLC47A2 [Gao et al 2019], FXRD2 [Gaut et al 2013] and LCN2 [Perrin et al 2011] were important for pathogenesis of ccRCC. Methylation inactivation of tumor suppressor genes such as ST6GAL1 [Antony et al 2014], OGDHL (oxoglutarate dehydrogenase like) [Khalaj-Kondori et al 2019], ALDH1A2 [Kim et al 2005], **SCNN1B** [Qian et al 2017] and RHCG (Rh family C glycoprotein) [Ming et al 2018] were liable for advancement of various cancer, but loss of these genes may be important for progression of ccRCC. PRODH2, HOGA1, ALDH4A1, CDS1, ACAA1, GGT6, PIPOX (pipecolic acid and sarcosine oxidase), ACOX2, CKMT1B, CKMT2, HPD (4-hydroxyphenylpyruvate dioxygenase), PLA2G4F, ATP6V1C2, ATP6V0D2, PLCG2, ALDH6A1, AMT (aminomethyltransferase), AOX1, CYP4F2, ATP6V0A4, SORD (sorbitol dehydrogenase), ATP6V1B1, CYP4A11, DHRS4L1, FTCD (formimidoyltransferasecyclodeaminase), SUCLG1, HSD17B8, RDH10, GPAT3, PAH (phenylalanine hydroxylase), TM7SF2, AGMAT (agmatinase), HADH (hydroxyacyl-CoA dehydrogenase), PCCA (propionyl-CoA carboxylase subunit alpha), DCXR (dicarbonyl and L-xylulosereductase), SLC29A2, SLC22A6, SLC22A8, CLCNKA (chloride voltage-gated channel Ka), CLCNKB (chloride

voltage-gated channel Kb), SCNN1A, SCNN1G, SLC13A3, AQP2, SLC22A12, SLC4A1, SLC6A12, SLC9A2, SLC12A3, SLC13A1, SLC26A7, SLC34A1, FXRD4, SLC30A2, SLC22A7, SLC36A2, WNK4, SLC7A8 and COL4A4 were identified as novel biomarkers for pathogenesis of ccRCC in these pathways.

In GO enrichment analysis, up regulated genes were enriched in response to cytokine, vesicle organization and signaling receptor binding. Genes such as IL32 [Lee et al 2012], FCER1G [Chen et al 2017], VIM (vimentin) [Yamasaki et al 2012], WAS (Wiskott-Aldrich syndrome) [Liu et al 2015], CSF1R [Soares et al 2009], XAF1 [Kempkensteffen et al 2009], FSCN1 [Zhang et al 2018], AXL (AXL receptor tyrosine kinase) [Zucca et al 2018], CCND1 [Sukov et al 2009], STAT1 [Zhu et al 2012], ACKR3 [Mahmoodi et al 2017], RUNX1 [Xiong et al 2014], CD70 [Ruf et al 2015], ACLY (ATP citrate lyase) [Teng et al 2018], ENPP3 [Thompson et al 2018], DYSF (dysferlin) [Ha et al 2019], CD163 [Ma et al 2018], CAV2 [Yamasaki et al 2013], CMTM3 [Xie et al 2014], PDGFRB (platelet derived growth factor receptor beta) [Shim et al 2015], SLC6A3 [Hansson et al 2017], STC2 [Ma et al 2015], PTHLH (parathyroid hormone like hormone) [Yao et al 2014], NRP1 [Cao et al 2008], EDNRB (endothelin receptor type B) [Wuttig et al 2012], CD2 [Tienari et al 2005] and NETO2 [Oparina et al 2012] were responsible for progression of ccRCC. Methylation inactivation of tumor suppressor genes such as MSC (musculin) [Pirini et al 2017] and TRIM9 [Mishima et al 2015] were important for progression of various cancer, but loss of these genes may be liable for advancement of ccRCC. Elevated expression of genes such as SAA1 [Kim et al 2015], UBD (ubiquitin D) [Zhao et al 2015], PARP14 [Iansante et al 2015], IFI16 [Alimirah et al 2007], ISG15 [Burks et al 2015], PLVAP (plasmalemma vesicle associated protein) [Wang et al 2014], TNFRSF6B [Chen et al 2010], SIRPA (signal regulatory protein alpha) [Nagahara et al 2015], IL18BP [Carbotti et al 2013], PRDX4 [Ummanni et al 2012], APOC1 [Su et al 2018], TAPBP (TAP binding protein) [Shao et al 2013], RAB31 [Sui et al 2015], SAA2 [Kim et al 2015], C10orf99 [Pan et al 2014], LAG3 [Huang et al 2016] and TYMP (thymidine phosphorylase) [Derwinger et al 2013] were associated with development of various cancer, but increase expression of these genes may be involved in progression of ccRCC. Genes such as SNX10 [Cervantes-Anaya et al 2017], LAPTM5 [Chen et al 2017], ABCA1 [Chen et al 2017], RNASET2 [Acquati et al 2011], RARRES2 [Liu-Chittenden et al 2017] and BTN3A1 [Zocchi

et al 2017] were liable for pathogenesis of various cancer, but expression of these genes may be linked with development of ccRCC. Genes such as BIRC3 [Mendoza-Rodríguez et al 2017] and BST2 [Kuang et al 2017] were responsible for drug resistance in various cancer, but these genes may be associated with chemo resistance in ccRCC. Genes such as POU5F1 [Cai et al 2016], PSMB8 [Yang et al 2018], GBP1 [Li et al 2015], GBP2 [Zhang et al 2018], DPYSL3 [Yang et al 2018], CORO1C [Lim et al 2017], FABP5 [Wang et al 2016], EHD2 [Kim et al 2017], HSPA6 [Shin et al 2017], SLC2A5 [Weng et al 2018], PROS1 [Che Mat et al 2016], DOCK2 [El Haibi et al 2010], CD68 [Eiró et al 2012], NCKAP1L [Xiong et al 2019] and GJA1 [Busby et al 2018] were liable for invasion of various cancer cells, but these genes may be important for invasion of ccRCC cells. SNP in genes such as IL2RB [Jia et al 2019], CD86 [Azimzadeh et al 2013] and BTN3A2 [Zhu et al 2017] were associate with advancement of various cancer, but these polymorphic genes may be liable for pathogenesis of ccRCC. HLA-H (major histocompatibility complex, class I, H (pseudogene)), IFI27, RHEX (regulator of hemoglobinization and erythroid cell expansion), PSMB9, IL20RB, ISG20, GBP5, NOL3, OAS2, LCP1, HCLS1, TYROBP (TYRO protein tyrosine kinase binding protein), PLEK (pleckstrin), NLGN1, SLC15A4, PYGL (glycogen phosphorylase L), LHFPL2, STEAP3, ADGRE5, LY96, SAA4, HILPDA (hypoxia inducible lipid droplet associated), APOL2, FYB1, CD8A and PRAME (preferentially expressed antigen in melanoma) were identified as novel biomarkers for pathogenesis of ccRCC in these GO categories. Similarly, down regulated genes were enriched in in renal system development, apical part of cell and ion transmembrane transporter activity. Methylation inactivation of tumor suppressor genes such as CDKN1C [Yang et al 2009] and MAL (mal, T cell differentiation protein) [Suzuki et al 2013] were linked with progression of various cancer, but loss of these genes may be liable for development of ccRCC. Genes such as MECOM (MDS1 and EVI1 complex locus) [Hou et al 2016], HPGD (15-hydroxyprostaglandin dehydrogenase) [Fink et al 2014], PROM1 [Qiu et al 2015], CA2 [Luo et al 2017], ACPP (acid phosphatase, prostate) [Chuang et al 2010], MUC20 [Chen et al 2016], IGFBP2 [Zumkeller et al 1993], PTH1R [Liang et al 2012], REEP6 [Park et al 2016], DPEP1 [Tachibana et al 2017], LDLR (low density lipoprotein receptor) [Caruso et al 2002], MAL2 [Li et al 2017], HSPA2 [Zhang et al 2015], CLDN16 [Kuo et al 2010] and SLC4A11 [Qin et al 2017] were important for advancement of various cancer, but expression of these genes may be

important for advancement of ccRCC. Genes such as HOXD11 [Sharpe et al 2014], FOXC1 [Han et al 2015], CTSH (cathepsin H) [Jevnikar et al 2013], TACSTD2 [Noorlag et al 2015], IRX2 [Berinstein et al 2012], ERBB2 [Kondratyev et al 2012], CLIC5 [Flores-Téllez et al 2015], ANK2 [Cao et al 2018], ANXA3 [Zhou et al 2017], MPC1 [Zhou et al 2017] and PPARGC1A [Li et al 2017] were involved in the invasion of various cancers cells, but these genes may be associated with invasion of ccRCC. Genes such as GATA3 [Cooper et al 2010], GPC3 [Valsechi et al 2014], TCF21 [Gooskens et al 2015], REN (renin) [Deckers et al 2015], EPCAM (epithelial cell adhesion molecule) [Zimpfer et al 2014], MUC1 [Aubert et al 2009], CEACAM1 [Kammerer et al 2004], CASR (calcium sensing receptor) [Joeckel et al 2014], CD9 [Garner et al 2016], CDH1 [Ricketts et al 2009], CRHBP (corticotropin releasing hormone binding protein) [Tezval et al 2016] and KCNJ15 [Liu et al 2019] were responsible for development of CCRCC. Decrease expression of genes such as RBP4 [Karunanithi et al 2017], EMX2 [Qiu et al 2013], RAB17 [Qi et al 2015], SLC25A25 [Li et al 2016] and PRSS8 [Zhang et al 2016] were associated with advancement of various cancer, but low expression of these genes may be important for pathogenesis of ccRCC. Genes such as TFAP2A [Tang et al 2017] and SLC27A2 [Chen et al 2018] were associated with chemo resistance in various cancer such as gastric cancer and ovarian cancer, but these genes may be linked with drug resistance in ccRCC. SNP in SLC16A5 was linked with advancement of testicular cancer [Drögemölle et al 2017], but this polymorphic gene may be liable for progression of ccRCC. UMOD (uromodulin), FRAS1, KLHL3, NPHS2, PROM2, RAPGEF3, SHROOM3, TJP3, CA4, MARVELD2, SCN2A, SLC25A4, TMC4 and GPD1L were identified as novel biomarkers for pathogenesis of ccRCC in these GO categories.

In PPI network, up regulated genes such as EGLN3, PCLAF (PCNA clamp associated factor), VCAM1, CANX, SHMT2, IFI16 and GAPDH were identified as hub genes showing the highest node degree, betweenness, stress and closeness. Up regulated genes such as MS4A7, FGF11, IKBIP (IKBKB interacting protein), SCD (stearoyl-CoA desaturase) and TRIM9 were identified as hub genes showing the lowest clustering coefficient. High expression of SCD was linked with progression of prostate cancer [Kim et al 2011], but increase expression of this gene may be liable for advancement of ccRCC. PCLAF, MS4A7 and IKBIP were identified as novel biomarkers for pathogenesis of ccRCC. Similarly, down

regulated genes such as CDH1, ERBB2, ATP1A1, ALB, NEDD4L, PHGDH and RTN4 were identified as hub genes showing the highest node degree, betweenness, stress and closeness. Down regulated genes such as ACOT11, ANKRD9, VTCN1, SLC22A7 and MST1L were identified as hub genes showing the lowest clustering coefficient. RTN4 was important for pathogenesis for ccRCC [Pu et al 2018]. VTCN1 was associated with invasion of bladder cancer cells [Chand et al 2019], but this gene may be responsible for invasion of ccRCC cells. ACOT11, ANKRD9 and MST1L were identified as novel biomarkers for pathogenesis of ccRCC.

In module analysis, up regulated genes such as PCLAF, GAPDH, ENO2, TPI1, VIM, SERPINH1, P4HB, LGALS1, STAT1, CAV1, VEGFA, PDGFRB, COL6A1, SPARC, COL6A2, BMP1, PLOD1, COL1A2, MMP9, TIMP1, COL5A1 and COL1A1 were identified as hub genes showing the highest node degree in all four significant modules. Similarly, down regulated genes such as ERBB2, PLCG2, PLXNB1, KIT, CDH1, RTN4, CGN, SHROOM3, LAD1, NEDD4L, SCNN1A, SCNN1G, SCNN1B, USP2, MATN2, KLK6, COL4A3 and COL4A4 were identified as hub genes showing the highest node degree in all four significant modules. Genes such as KIT (KIT proto-oncogene receptor tyrosine kinase) [Wang and Mills, 2005] and LAD1 [Van Vlodrop et al 2017] were involved in pathogenesis of ccRCC. Genes such as PLXNB1 [Worzfeld et al 2012] and USP2 [Qu et al 2015] were associated with invasion of breast cancer cells, but these genes may be involved in invasion of ccRCC cells. KLK6 was associated with progression of breast cancer [Sidiropoulos et al 2016], but this gene may be involved in pathogenesis of ccRCC. PLXNB1, CGN (cingulin) and MATN2 were identified as novel biomarker for pathogenesis of ccRCC.

In target gene - miRNA network, up regulated genes such as SOD2, CCND1, SCD, VEGFA and SH3PXD2A were identified as target genes showing the highest number of integration with miRNAs. Methylation inactivation of tumor suppressor SH3PXD2A was liable for advancement of colorectal cancer [Ma et al 2018], but loss of this gene may be responsible for progression of ccRCC. Similarly, down regulated genes such as BTG2, VAV3, LDLR, FOXC1 and SYT7 were identified as target genes showing the highest number of integration with miRNAs. BTG2 was responsible for pathogenesis of CCRCC [Struckmann et al 2004]. Genes such as VAV3 [Jiang et al 2017] and SYT7 [Liu et al 2019] were

important for invasion of various cancer cells such as breast cancer and lung cancer, but these genes may be associated with invasion of ccRCC cells.

In target gene - TF network, up regulated genes such as THBS2, VCAN, MLKL (mixed lineage kinase domain like pseudokinase), RHBDF2 and COL11A1 were identified as target genes showing the highest number of integration with TFs. RHBDF2 was important for invasion of gastric cancer cells [Ishimoto et al 2017], but this gene may be liable for invasion of ccRCC cells. MLKL was identified as novel biomarker for pathogenesis of ccRCC. Similarly, down regulated genes such as FOXQ1, EFHD1, NCOA7, PTH1R and MUC20 were identified as target genes showing the highest number of integration with TFs. Genes such as FOXQ1 [Liu et al 2017] and NCOA7 [Xie et al 2016] were involved in the invasion of various cancer cells, but these genes may be linked with invasion of CCRCC cells. Methylation inactivation of tumor supressor EFHD1 was associated with development of colorectal cancer [Takane et al 2014], but loss of this gene may be responsible for advancement of ccRCC.

CANX, SHMT2, IFI16, P4HB, CALU, CDH1, ERBB2, NEDD4L, TFAP2A and SORT1 were screened. CALU (calumenin) was asspiciated with invasion of lung cancer cells [Nagano et al 2015], but this gene may be involved in the progression of ccRCC. These include high expression of, TFAP2A, SHMT2, IFI16, P4HB and CALU were predicting shorter survival of ccRCC, while low expression of CANX, CDH1, ERBB2, NEDD4L, and SORT1 were predicting longer survival of CCRCC. Low expression of genes such as CDH1, ERBB2, NEDD4L, TFAP2A and SORT1 were associated with advancement of ccRCC, while high expression of genes such as CANX, SHMT2, IFI16, P4HB and, CALU were associated with advancement of ccRCC. All 10 hub genes were showed altered expressed in all four stage of ccRCC. The mutation analysis found that mutations or alterations in all ten hub genes could result in importantly reduced disease-free survival and poorer clinical outcomes in ccRCC. All ten hub genes were validated by ICH analysis and RT-PCR. ROC curve analysis revealed that the combination of these hub genes was a good predictive model for ccRCC. Immune infiltration analysis revealed that hub genes were positively and negatively associated with tumor purity.

In conclusion, a risk assessment tool for assessing the prognosis of patients with ccRCC was developed and validated in the current study. The 10 identified prognostic genes were associated with several cellular processes and signaling pathways and may be recommended as promising prognostic biomarkers or a diagnostic biomarkers or therapeutic targates of ccRCC. The current risk assessment tool may help identify patients with a high risk of ccRCC, and the proposed prognostic and diagnostic genes as well as therapeutic targates may help elucidate the progression of ccRCC.

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Conflict of interest

The authors declare that they have no conflict of interest.

Ethical approval

This article does not contain any studies with human participants or animals performed by any of the authors.

Informed consent

No informed consent because this study does not contain human or animals participants.

Author Contributions

Basavaraj Vastrad was associated with methodology, manuscript preparation, review and editing. Chanabasayya Vastrad was performed software, supervision, formal analysis and validation.

Availability of data and materials

The datasets supporting the conclusions of this article are available in the GEO (Gene Expression Omnibus) (<https://www.ncbi.nlm.nih.gov/geo/>) repository.

[(GSE105261) (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE105261>)]

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

Author Contributions

B. V. - Writing original draft, and review and editing

C. V. - Software and investigation

I. K. - Supervision and resources

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Tables

Table 1. Primers used for quantitative PCR

Gene	Primer sequence (5'→3')	
	Forward	Reverse
CANX	CCAAGGTTACTTACAAAGCTCCA	GGCCCGAGACATCAACACA
SHMT2	CCCTTCTGCAACCTCACGAC	TGAGCTTATAGGGCATAGACTCG
IFI16	AGACTGAAGACTGAACCTGAAGA	GAACCCATTGCGGCAAACATA
P4HB	GGTGCTGCGGAAAAGCAAC	ACCTGATCTCGGAACCTTCTG
CALU	AATAGACGCGGATAAAGATGGGT	GCCATTGGTTTTCAACATTGTCA
CDH1	CGAGAGCTACACGTTACGG	GGGTGTCGAGGGAAAAATAGG
ERBB2	TGCAGGGAAACCTGGAAGTC	ACAGGGGTGGTATTGTTTCAGC
NEDD4L	GACATGGAGCATGGATGGGAA	GTTTCGGCCTAAATTGTCCACT
TFAP2A	AGGTCAATCTCCCTACACGAG	GGAGTAAGGATCTTTCGACTGG
SORT1	GAAGTCGTGGAGGAAGAATCTTT	TGGTGTTGTCTGATCCCCATT

Table 2 The statistical metrics for key differentially expressed genes (DEGs)

Illumina Id	Gene Symbol	logFC	pValue	adj.P.Val	tvalue	Regulation	Gene Name
ILMN_1756573	NDUFA4L2	4.94406	4.77E-13	4.77E-13	11.1406	Up	NDUFA4, mitochondrial complex associated like 2
ILMN_2364022	SLC16A3	2.44418	1.18E-12	1.18E-12	10.7782	Up	solute carrier family 16 member 3
ILMN_1693334	P4HA1	1.58446	7.79E-11	7.79E-11	9.17547	Up	prolyl 4-hydroxylase subunit alpha 1
ILMN_1707727	ANGPTL4	3.45004	1.52E-09	1.52E-09	8.10967	Up	angiopoietin like 4
ILMN_2410924	PLOD2	2.05884	1.99E-09	1.99E-09	8.0163	Up	procollagen-lysine,2-oxoglutarate 5-dioxygenase 2
ILMN_2059797	NOL3	1.67226	4.13E-09	4.13E-09	7.76188	Up	nucleolar protein 3
ILMN_1746085	IGFBP3	2.67781	4.5E-09	4.5E-09	7.73213	Up	insulin like growth factor binding protein 3
ILMN_2396875	IGFBP3	2.8935	4.55E-09	4.55E-09	7.72867	Up	insulin like growth factor binding protein 3
ILMN_1771599	PLOD2	2.1839	4.59E-09	4.59E-09	7.72525	Up	procollagen-lysine,2-oxoglutarate 5-dioxygenase 2
ILMN_2142284	SLC25A43	1.02494	9.99E-09	9.99E-09	7.45822	Up	solute carrier family 25 member 43
ILMN_1793476	CAVIN3	1.9016	1.07E-08	1.07E-08	7.43626	Up	caveolae associated protein 3

ILMN_1715508	NNMT	3.11765	1.51E-08	1.51E-08	7.31646	Up	nicotinamide N-methyltransferase
ILMN_1751079	TAP1	1.63045	1.64E-08	1.64E-08	7.28954	Up	transporter 1, ATP binding cassette subfamily B member
ILMN_1785732	TNFAIP6	2.63898	1.67E-08	1.67E-08	7.28345	Up	TNF alpha induced protein 6
ILMN_1726720	NUSAP1	1.54149	1.68E-08	1.68E-08	7.28041	Up	nucleolar and spindle associated protein 1
ILMN_2222234	PRDX4	1.23203	1.77E-08	1.77E-08	7.26408	Up	peroxiredoxin 4
ILMN_2058251	VIM	1.51006	1.98E-08	1.98E-08	7.22621	Up	vimentin
ILMN_1676899	YEATS2	1.09882	2.21E-08	2.21E-08	7.18878	Up	YEATS domain containing 2
ILMN_1796216	VASH1	1.28255	2.26E-08	2.26E-08	7.18126	Up	vasohibin 1
ILMN_1813925	NOL3	1.91111	2.33E-08	2.33E-08	7.17066	Up	nucleolar protein 3
ILMN_2386444	ANGPTL4	2.56814	2.51E-08	2.51E-08	7.14519	Up	angiopoietin like 4
ILMN_2375879	VEGFA	2.38125	3.53E-08	3.53E-08	7.03026	Up	vascular endothelial growth factor A
ILMN_1659990	HILPDA	2.86186	3.94E-08	3.94E-08	6.99305	Up	hypoxia inducible lipid droplet associated hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7
ILMN_1653042	HSD3B7	1.62702	4.35E-08	4.35E-08	6.95931	Up	
ILMN_1747195	PSMB8	1.23692	5.09E-08	5.09E-08	6.90689	Up	proteasome subunit beta 8
ILMN_1723486	HK2	1.8379	5.42E-08	5.42E-08	6.88577	Up	hexokinase 2
ILMN_1700896	SAP30	1.31403	6.04E-08	6.04E-08	6.84918	Up	Sin3A associated protein 30
ILMN_1719303	P4HB	1.43032	7.09E-08	7.09E-08	6.79531	Up	prolyl 4-hydroxylase subunit beta
ILMN_1794370	SEMA5B	2.32877	9.03E-08	9.03E-08	6.71438	Up	semaphorin 5B
ILMN_2390299	PSMB8	1.1645	9.75E-08	9.75E-08	6.68881	Up	proteasome subunit beta 8
ILMN_1782538	VIM	1.30824	1.02E-07	1.02E-07	6.67538	Up	vimentin
ILMN_3253456	FNDC3B	1.0949	1.09E-07	1.09E-07	6.65048	Up	fibronectin type III domain containing 3B
ILMN_1684620	SPAG4	1.88709	1.2E-07	1.2E-07	6.61983	Up	sperm associated antigen 4
ILMN_1679060	POU5F1	1.04576	1.37E-07	1.37E-07	6.57595	Up	POU class 5 homeobox 1
ILMN_1803882	VEGFA	2.05198	1.62E-07	1.62E-07	6.52026	Up	vascular endothelial growth factor A
ILMN_1725139	CA9	3.40323	1.66E-07	1.66E-07	6.51089	Up	carbonic anhydrase 9
ILMN_1776181	BIRC3	1.93943	2.02E-07	2.02E-07	6.44613	Up	baculoviral IAP repeat containing 3
ILMN_3261938	TMSB10	1.38146	2.13E-07	2.13E-07	6.42779	Up	thymosin beta 10
ILMN_1749014	ACLY	1.14395	2.39E-07	2.39E-07	6.38987	Up	ATP citrate lyase
ILMN_2076463	SLC15A4	1.3177	2.69E-07	2.69E-07	6.35149	Up	solute carrier family 15 member 4
ILMN_1807106	LDHA	1.03504	3.23E-07	3.23E-07	6.29087	Up	lactate dehydrogenase A
ILMN_1742450	TAPBP	1.04643	3.6E-07	3.6E-07	6.25463	Up	TAP binding protein
ILMN_1710937	IFI16	1.42017	4.32E-07	4.32E-07	6.19402	Up	interferon gamma inducible protein 16
ILMN_1727043	COLGALT1	1.46297	4.85E-07	4.85E-07	6.15597	Up	collagen beta(1-O)galactosyltransferase 1
ILMN_1815184	ASPM	1.2583	5.53E-07	5.53E-07	6.11212	Up	abnormal spindle microtubule assembly
ILMN_2156172	HK2	1.01448	5.59E-07	5.59E-07	6.10861	Up	hexokinase 2
ILMN_3178302	FNDC3B	1.06409	5.89E-07	5.89E-07	6.09174	Up	fibronectin type III domain containing 3B
ILMN_2042771	PTTG1	1.87482	6.01E-07	6.01E-07	6.08473	Up	pituitary tumor-transforming 1
ILMN_1682799	STAMBPL1	1.17181	6.04E-07	6.04E-07	6.08331	Up	STAM binding protein like 1
ILMN_1714861	CD68	1.60258	6.9E-07	6.9E-07	6.03928	Up	CD68 molecule
ILMN_1661264	SHMT2	1.43305	7.35E-07	7.35E-07	6.01835	Up	serine hydroxymethyltransferase 2
ILMN_3205656	GAPDH	1.47146	7.43E-07	7.43E-07	6.01484	Up	glyceraldehyde-3-phosphate dehydrogenase
ILMN_2324994	IKBIP	1.03433	7.58E-07	7.58E-07	6.00842	Up	IKBKB interacting protein

ILMN_2140059	LAMA4	1.86994	7.92E-07	7.92E-07	5.99366	Up	laminin subunit alpha 4
ILMN_1721559	FABP6	2.42448	8.27E-07	8.27E-07	5.97929	Up	fatty acid binding protein 6
ILMN_1691731	PARP14	1.07132	9.16E-07	9.16E-07	5.94582	Up	poly(ADP-ribose) polymerase family member 14
ILMN_1667825	MLKL	1.24968	1.04E-06	1.04E-06	5.90442	Up	mixed lineage kinase domain like pseudokinase
ILMN_1674376	ANGPTL4	1.78774	1.13E-06	1.13E-06	5.87699	Up	angiotensinogen like 4
ILMN_1805737	PFKP	1.38959	1.14E-06	1.14E-06	5.87356	Up	phosphofructokinase, platelet
ILMN_2104356	COL1A2	2.82778	1.15E-06	1.15E-06	5.86931	Up	collagen type I alpha 2 chain
ILMN_1661599	DDIT4	1.59116	1.17E-06	1.17E-06	5.86429	Up	DNA damage inducible transcript 4
ILMN_1796409	C1QB	2.47943	1.18E-06	1.18E-06	5.86295	Up	complement C1q B chain
ILMN_1758146	SIRPA	1.41529	1.18E-06	1.18E-06	5.86269	Up	signal regulatory protein alpha
ILMN_1656670	HLA-G	1.49902	1.54E-06	1.54E-06	5.77401	Up	major histocompatibility complex, class I, G
ILMN_1806040	TYMS	1.23046	1.56E-06	1.56E-06	5.77054	Up	thymidylatesynthetase
ILMN_1774836	PLOD3	1.10246	1.62E-06	1.62E-06	5.75815	Up	procollagen-lysine,2-oxoglutarate 5-dioxygenase 3
ILMN_2372974	SIRPA	1.27302	1.67E-06	1.67E-06	5.74721	Up	signal regulatory protein alpha
ILMN_1792679	ITGA5	1.60851	0.000002	0.000002	5.6889	Up	integrin subunit alpha 5
ILMN_1723978	LGALS1	1.76798	2.08E-06	2.08E-06	5.67618	Up	galectin 1
ILMN_2055156	PAG1	1.07748	2.2E-06	2.2E-06	5.6574	Up	phosphoprotein membrane anchor with glycosphingolipidmicrodoma 1
ILMN_2373062	RHBDF2	1.09229	2.22E-06	2.22E-06	5.6534	Up	rhomboid 5 homolog 2
ILMN_1671565	RNASET2	1.99934	2.24E-06	2.24E-06	5.65098	Up	ribonuclease T2
ILMN_1795442	LAMA4	1.76315	2.38E-06	2.38E-06	5.63054	Up	laminin subunit alpha 4
ILMN_1701308	COL1A1	3.00318	2.39E-06	2.39E-06	5.62941	Up	collagen type I alpha 1 chain
ILMN_2109708	TYMP	1.7576	2.4E-06	2.4E-06	5.62768	Up	thymidine phosphorylase
ILMN_1691717	RHBDF2	1.24569	2.53E-06	2.53E-06	5.61056	Up	rhomboid 5 homolog 2
ILMN_1343295	GAPDH	1.09798	2.56E-06	2.56E-06	5.6067	Up	glyceraldehyde-3-phosphate dehydrogenase
ILMN_1745954	CORO1C	1.12047	2.56E-06	2.56E-06	5.60642	Up	coronin 1C
ILMN_3286809	DUXA	1.67303	2.57E-06	2.57E-06	5.60558	Up	double homeobox A
ILMN_1715693	#N/A	1.05965	2.61E-06	2.61E-06	5.60117	Up	NA
ILMN_2401057	CANX	1.05553	2.62E-06	2.62E-06	5.59898	Up	calnexin
ILMN_1741404	MSC	1.30164	2.67E-06	2.67E-06	5.59355	Up	musculin
ILMN_1723480	BST2	1.4402	2.7E-06	2.7E-06	5.58912	Up	bone marrow stromal cell antigen 2
ILMN_1729117	COL5A2	2.19145	2.72E-06	2.72E-06	5.58674	Up	collagen type V alpha 2 chain
ILMN_1696187	PYGL	1.10652	2.75E-06	2.75E-06	5.58365	Up	glycogen phosphorylase L
ILMN_1695880	LOX	2.28574	2.81E-06	2.81E-06	5.57675	Up	lysyl oxidase
ILMN_2371379	ACLY	1.13473	2.93E-06	2.93E-06	5.56221	Up	ATP citrate lyase
ILMN_2149226	CAV1	1.9489	2.95E-06	2.95E-06	5.56074	Up	caveolin 1
ILMN_1802252	GAPDH	1.29903	3.03E-06	3.03E-06	5.55202	Up	glyceraldehyde-3-phosphate dehydrogenase
ILMN_2392261	FABP6	2.29734	3.09E-06	3.09E-06	5.54474	Up	fatty acid binding protein 6
ILMN_1766054	ABCA1	1.20416	3.19E-06	3.19E-06	5.5342	Up	ATP binding cassette subfamily A member 1
ILMN_3223126	TYMP	1.36237	3.24E-06	3.24E-06	5.52992	Up	thymidine phosphorylase
ILMN_1784661	CEMIP2	1.30351	3.24E-06	3.24E-06	5.52973	Up	cell migration inducing hyaluronidase 2
ILMN_3259146	BST2	1.32517	3.29E-06	3.29E-06	5.52479	Up	bone marrow stromal cell antigen 2
ILMN_1667791	PPFIA4	1.16547	3.31E-06	3.31E-06	5.5224	Up	PTPRF interacting protein alpha 4

ILMN_2211003	GAS2L3	1.09327	3.41E-06	3.41E-06	5.51277	Up	growth arrest specific 2 like 3
ILMN_1690939	TYMP	1.17281	3.46E-06	3.46E-06	5.5077	Up	thymidine phosphorylase
ILMN_1802708	BTN3A1	1.16251	3.59E-06	3.59E-06	5.49533	Up	butyrophilin subfamily 3 member A1
ILMN_3283772	GAPDH	1.43167	3.6E-06	3.6E-06	5.4944	Up	glyceraldehyde-3-phosphate dehydrogenase
ILMN_1728934	PRC1	1.1121	3.74E-06	3.74E-06	5.48201	Up	protein regulator of cytokinesis 1
ILMN_1726809	BHLHE41	1.56511	3.77E-06	3.77E-06	5.47926	Up	basic helix-loop-helix family member e41
ILMN_1686097	TOP2A	1.7593	3.81E-06	3.81E-06	5.47585	Up	DNA topoisomerase II alpha
ILMN_1785902	C1QC	2.29005	3.82E-06	3.82E-06	5.47556	Up	complement C1q C chain
ILMN_1674063	OAS2	1.53953	3.96E-06	3.96E-06	5.46312	Up	2'-5'-oligoadenylate synthetase 2
ILMN_2285996	PCLAF	1.30212	4.12E-06	4.12E-06	5.4499	Up	PCNA clamp associated factor
ILMN_1763000	ADAP2	1.33192	4.14E-06	4.14E-06	5.44902	Up	ArfGAP with dual PH domains 2
ILMN_1803686	ADA	1.22708	4.14E-06	4.14E-06	5.44881	Up	adenosine deaminase
ILMN_2148913	TMEM45A	2.33426	4.36E-06	4.36E-06	5.43196	Up	transmembrane protein 45A
ILMN_2049766	NFE2L3	1.38406	4.4E-06	4.4E-06	5.42854	Up	nuclear factor, erythroid 2 like 3
ILMN_1797822	SEL1L3	1.35291	4.41E-06	4.41E-06	5.42764	Up	SEL1L family member 3
ILMN_3245057	ASAP1	1.08719	4.43E-06	4.43E-06	5.4261	Up	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1
ILMN_1711566	TIMP1	1.53339	4.45E-06	4.45E-06	5.42515	Up	TIMP metalloproteinase inhibitor 1
ILMN_2360730	CAV2	1.16113	4.49E-06	4.49E-06	5.42229	Up	caveolin 2
ILMN_1668861	TPI1	1.11755	4.77E-06	4.77E-06	5.4018	Up	triosephosphateisomerase 1
ILMN_3256478	LOC100129034	1.28187	4.99E-06	4.99E-06	5.38731	Up	uncharacterized LOC100129034
ILMN_2183409	SCARB1	2.14881	5.54E-06	5.54E-06	5.3526	Up	scavenger receptor class B member 1
ILMN_1659027	SLC2A1	1.68329	5.65E-06	5.65E-06	5.346	Up	solute carrier family 2 member 1
ILMN_2054019	ISG15	1.22476	6.52E-06	6.52E-06	5.299	Up	ISG15 ubiquitin-like modifier
ILMN_2376108	PSMB9	1.43378	6.81E-06	6.81E-06	5.28455	Up	proteasome subunit beta 9
ILMN_2049021	PTTG3P	1.49427	6.95E-06	6.95E-06	5.2777	Up	pituitary tumor-transforming 3, pseudogene
ILMN_1684114	TPIIP2	1.03393	0.000007	0.000007	5.27544	Up	triosephosphateisomerase 1 pseudogene 2
ILMN_1773125	ENTPD1	1.01684	7.02E-06	7.02E-06	5.2746	Up	ectonucleoside triphosphate diphosphohydrolase 1
ILMN_1810420	DYSF	1.03094	7.57E-06	7.57E-06	5.24985	Up	dysferlin
ILMN_2253732	ST8SIA4	1.10406	7.79E-06	7.79E-06	5.24019	Up	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4
ILMN_1760849	NETO2	1.77586	8.04E-06	8.04E-06	5.22989	Up	neuropilin and tolloid like 2
ILMN_1658044	EDNRB	1.61524	8.34E-06	8.34E-06	5.21785	Up	endothelin receptor type B
ILMN_1701402	IKBIP	1.23484	8.7E-06	8.7E-06	5.20357	Up	IKBKB interacting protein
ILMN_1752520	SLFN11	1.21423	8.8E-06	8.8E-06	5.20007	Up	schlafen family member 11
ILMN_2186806	HLA-A	1.31697	8.82E-06	8.82E-06	5.19927	Up	major histocompatibility complex, class I, A
ILMN_1684391	PLOD1	1.42722	8.98E-06	8.98E-06	5.19337	Up	procollagen-lysine,2-oxoglutarate 5-dioxygenase 1
ILMN_1667626	EGLN3	1.70461	9.25E-06	9.25E-06	5.18352	Up	egl-9 family hypoxia inducible factor 3
ILMN_2364521	AXL	1.41259	9.64E-06	9.64E-06	5.1697	Up	AXL receptor tyrosine kinase
ILMN_1689329	SCD	2.18899	9.76E-06	9.76E-06	5.16587	Up	stearoyl-CoA desaturase
ILMN_2381697	P4HA2	1.30823	0.00001	0.00001	5.15654	Up	prolyl 4-hydroxylase subunit alpha 2
ILMN_1783909	COL6A2	2.02474	1.03E-05	1.03E-05	5.14808	Up	collagen type VI alpha 2 chain
ILMN_1670238	CDC45	1.04184	1.05E-05	1.05E-05	5.14082	Up	cell division cycle 45
ILMN_1729905	GAL3ST1	2.02699	0.000012	0.000012	5.09681	Up	galactose-3-O-sulfotransferase 1
ILMN_1681644	BIRC3	1.13485	1.22E-05	1.22E-05	5.09125	Up	baculoviral IAP repeat containing 3

ILMN_1653028	COL4A1	1.59509	1.23E-05	1.23E-05	5.08837	Up	collagen type IV alpha 1 chain
ILMN_1706434	YBX3P1	1.03827	1.23E-05	1.23E-05	5.08824	Up	Y-box binding protein 3 pseudogene 1
ILMN_1773079	COL3A1	2.18638	1.41E-05	1.41E-05	5.045	Up	collagen type III alpha 1 chain
ILMN_3297126	TYMP	1.08379	1.41E-05	1.41E-05	5.04313	Up	thymidine phosphorylase
ILMN_1695763	PDIA5	1.25348	1.43E-05	1.43E-05	5.03899	Up	protein disulfideisomerase family A member 5
ILMN_1701877	AXL	1.48063	1.47E-05	1.47E-05	5.03062	Up	AXL receptor tyrosine kinase
ILMN_1789007	APOC1	2.68207	1.48E-05	1.48E-05	5.02827	Up	apolipoprotein C1
ILMN_1727194	CALU	1.38389	1.54E-05	1.54E-05	5.01586	Up	calumenin
ILMN_1666894	CSPG4	1.31496	1.55E-05	1.55E-05	5.01184	Up	chondroitin sulfate proteoglycan 4
ILMN_1747744	LHFPL2	1.55023	1.58E-05	1.58E-05	5.00721	Up	LHFPL tetraspan subfamily member 2
ILMN_1754894	C1orf162	1.70236	1.58E-05	1.58E-05	5.0063	Up	chromosome 1 open reading frame 162
ILMN_2170949	SNX10	1.27107	1.62E-05	1.62E-05	4.99722	Up	sorting nexin 10
ILMN_1724994	COL4A2	1.18498	1.63E-05	1.63E-05	4.99688	Up	collagen type IV alpha 2 chain
ILMN_2162860	SLFN11	1.0252	1.63E-05	1.63E-05	4.99547	Up	schlafen family member 11
ILMN_1693452	GAL3ST4	1.54035	0.000017	0.000017	4.98202	Up	galactose-3-O-sulfotransferase 4
ILMN_1666665	COL23A1	2.4199	1.84E-05	1.84E-05	4.95664	Up	collagen type XXIII alpha 1 chain
ILMN_1801710	APBB1IP	1.14872	1.88E-05	1.88E-05	4.9486	Up	amyloid beta precursor protein binding family B member 1 interacting protein
ILMN_1676528	BTN3A2	1.36607	1.94E-05	1.94E-05	4.93914	Up	butyrophilin subfamily 3 member A2
ILMN_1737918	C1QA	1.70527	1.95E-05	1.95E-05	4.93684	Up	complement C1q A chain
ILMN_2087646	HLX	1.12732	2.05E-05	2.05E-05	4.92087	Up	H2.0 like homeobox
ILMN_1663866	TGFB1	2.53587	0.000021	0.000021	4.91149	Up	transforming growth factor beta induced
ILMN_1760062	IFI44	1.10951	2.15E-05	2.15E-05	4.90442	Up	interferon induced protein 44
ILMN_1655549	SIGLEC10	1.27398	2.18E-05	2.18E-05	4.90028	Up	sialic acid binding Ig like lectin 10
ILMN_1765796	ENO2	2.23108	2.27E-05	2.27E-05	4.88639	Up	enolase 2
ILMN_1814074	PHKA2	1.19935	2.36E-05	2.36E-05	4.87373	Up	phosphorylase kinase regulatory subunit alpha 2
ILMN_3239060	KRBA1	1.46945	0.000024	0.000024	4.86771	Up	KRAB-A domain containing 1
ILMN_2193980	ABCB6	1.03109	0.000024	0.000024	4.86711	Up	ATP binding cassette subfamily B member 6 (Langereis blood group)
ILMN_1725090	CTHRC1	2.33548	2.41E-05	2.41E-05	4.8658	Up	collagen triple helix repeat containing 1
ILMN_1765557	OLFML2B	1.64275	2.47E-05	2.47E-05	4.85784	Up	olfactomedin like 2B
ILMN_1809467	VAMP5	1.01708	2.92E-05	2.92E-05	4.80246	Up	vesicle associated membrane protein 5
ILMN_1688848	TMEM44	1.25007	2.92E-05	2.92E-05	4.80194	Up	transmembrane protein 44
ILMN_1749131	ENPP3	2.86159	2.97E-05	2.97E-05	4.79645	Up	ectonucleotidepyrophosphatase/phosphodiesterase 3
ILMN_1653292	PFKFB4	1.5745	3.07E-05	3.07E-05	4.78542	Up	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4
ILMN_2388070	TMEM44	1.12288	3.08E-05	3.08E-05	4.78425	Up	transmembrane protein 44
ILMN_2282641	TBXAS1	1.20472	3.15E-05	3.15E-05	4.77709	Up	thromboxane A synthase 1
ILMN_1679731	SLC15A4	1.06167	3.26E-05	3.26E-05	4.76548	Up	solute carrier family 15 member 4
ILMN_1751444	NCAPG	1.03865	3.49E-05	3.49E-05	4.74262	Up	non-SMC condensin I complex subunit G
ILMN_3294222	RPS2P32	1.11198	3.62E-05	3.62E-05	4.73055	Up	ribosomal protein S2 pseudogene 32
ILMN_3178258	FABP5P2	1.18322	3.67E-05	3.67E-05	4.72583	Up	fatty acid binding protein 5 pseudogene 2
ILMN_1760247	CD70	2.66251	3.83E-05	3.83E-05	4.71218	Up	CD70 molecule
ILMN_1724658	BNIP3	1.42129	3.96E-05	3.96E-05	4.70078	Up	BCL2 interacting protein 3
ILMN_1795778	P4HA2	1.19549	3.97E-05	3.97E-05	4.70004	Up	prolyl 4-hydroxylase subunit alpha 2

ILMN_3266606	FABP5	1.53586	4.03E-05	4.03E-05	4.69543	Up	fatty acid binding protein 5
ILMN_1761199	SLCO2B1	1.20476	4.06E-05	4.06E-05	4.69261	Up	solute carrier organic anion transporter family member 2B1
ILMN_1753196	PTTG1	1.08478	4.19E-05	4.19E-05	4.68239	Up	pituitary tumor-transforming 1
ILMN_2130441	HLA-H	1.0139	4.26E-05	4.26E-05	4.67681	Up	major histocompatibility complex, class I, H (pseudogene)
ILMN_3250067	ANGPT2	1.54336	4.26E-05	4.26E-05	4.67674	Up	angiopoietin 2
ILMN_1709683	RASSF2	1.12733	4.39E-05	4.39E-05	4.66644	Up	Ras association domain family member 2
ILMN_1809928	COL6A2	1.55958	4.53E-05	4.53E-05	4.65583	Up	collagen type VI alpha 2 chain
ILMN_1711408	ANXA4	1.07774	4.67E-05	4.67E-05	4.64606	Up	annexin A4
ILMN_1743103	SH3PXD2A	1.13633	0.000047	0.000047	4.6434	Up	SH3 and PX domains 2A
ILMN_1778401	HLA-B	1.1877	4.85E-05	4.85E-05	4.63331	Up	major histocompatibility complex, class I, B
ILMN_1774077	GBP2	1.32679	4.91E-05	4.91E-05	4.62869	Up	guanylate binding protein 2
ILMN_1801939	CCNB2	1.10026	0.00005	0.00005	4.62289	Up	cyclin B2
ILMN_1796349	SMPDL3A	1.69404	5.18E-05	5.18E-05	4.61135	Up	sphingomyelinphosphodiesterase acid like 3A
ILMN_1729288	C1QTNF6	1.13107	5.51E-05	5.51E-05	4.59034	Up	C1q and TNF related 6
ILMN_1770922	TMEM45A	2.08327	0.000056	0.000056	4.58525	Up	transmembrane protein 45A
ILMN_3210741	FABP5	1.18918	5.66E-05	5.66E-05	4.58134	Up	fatty acid binding protein 5
ILMN_2206722	FER1L4	1.20957	5.67E-05	5.67E-05	4.58098	Up	fer-1 like family member 4, pseudogene
ILMN_1713182	C3	2.2001	5.71E-05	5.71E-05	4.57819	Up	complement C3
ILMN_1758128	CYGB	1.23911	5.86E-05	5.86E-05	4.56972	Up	cytoglobin
ILMN_1660871	NEK6	1.01736	5.91E-05	5.91E-05	4.56673	Up	NIMA related kinase 6
ILMN_2087656	SLCO2B1	1.34201	5.97E-05	5.97E-05	4.56341	Up	solute carrier organic anion transporter family member 2B1
ILMN_1773262	ESM1	1.68554	6.22E-05	6.22E-05	4.5496	Up	endothelial cell specific molecule 1
ILMN_2146761	FABP5	1.35616	6.25E-05	6.25E-05	4.54835	Up	fatty acid binding protein 5
ILMN_3242038	GPX8	1.19396	6.27E-05	6.27E-05	4.54686	Up	glutathione peroxidase 8 (putative)
ILMN_1712075	SYNM	1.08359	6.39E-05	6.39E-05	4.54087	Up	synemin
ILMN_1775268	HECW2	1.03701	6.47E-05	6.47E-05	4.53653	Up	HECT, C2 and WW domain containing E3 ubiquitin protein ligase
ILMN_1800412	BMP1	1.06289	6.76E-05	6.76E-05	4.52152	Up	bone morphogenetic protein 1
ILMN_2138765	PLIN2	1.88978	6.77E-05	6.77E-05	4.52138	Up	perilipin 2
ILMN_1772359	LAPTM5	1.76934	6.81E-05	6.81E-05	4.51918	Up	lysosomal protein transmembrane 5
ILMN_1798360	ACKR3	1.51285	7.22E-05	7.22E-05	4.49977	Up	atypical chemokine receptor 3
ILMN_1790778	PNMA2	1.68887	7.43E-05	7.43E-05	4.49006	Up	PNMA family member 2
ILMN_1677814	ABCC3	1.50561	7.55E-05	7.55E-05	4.48473	Up	ATP binding cassette subfamily C member 3
ILMN_1775486	SSPN	1.04765	7.57E-05	7.57E-05	4.48362	Up	sarcospan
ILMN_1745299	FABP7	4.32652	7.65E-05	7.65E-05	4.48036	Up	fatty acid binding protein 7
ILMN_1785272	COL1A2	2.1374	8.31E-05	8.31E-05	4.45239	Up	collagen type I alpha 2 chain
ILMN_2066849	CALHM6	1.04561	8.62E-05	8.62E-05	4.43988	Up	calcium homeostasis modulator family member 6
ILMN_1658835	CAV2	1.20931	8.75E-05	8.75E-05	4.43495	Up	caveolin 2
ILMN_1663390	CDC20	1.36173	9.41E-05	9.41E-05	4.41043	Up	cell division cycle 20
ILMN_1762861	HLA-F	1.25867	9.48E-05	9.48E-05	4.40795	Up	major histocompatibility complex, class I, F
ILMN_2056032	CD99	1.12127	9.65E-05	9.65E-05	4.40172	Up	CD99 molecule (Xg blood group)
ILMN_2203271	FPR3	1.42948	9.77E-05	9.77E-05	4.39778	Up	formyl peptide receptor 3
ILMN_2301083	UBE2C	1.85946	0.000098	0.000098	4.39651	Up	ubiquitin conjugating enzyme E2 C
ILMN_1737184	CDCA7	1.29367	9.94E-05	9.94E-05	4.39173	Up	cell division cycle associated 7

ILMN_1772876	ZNF395	1.43855	0.000104	0.000104	4.37736	Up	zinc finger protein 395
ILMN_1846306	AC090204.1	1.1125	0.000104	0.000104	4.37711	Up	novel transcript
ILMN_1755974	ALDOC	1.71554	0.000107	0.000107	4.36824	Up	aldolase, fructose-bisphosphate C
ILMN_1774207	ANGPT2	1.58125	0.000109	0.000109	4.35935	Up	angiopoietin 2
ILMN_2221808	DGCR5	1.70798	0.00011	0.00011	4.35671	Up	DiGeorge syndrome critical region gene 5
ILMN_1761425	OLFML2A	1.6147	0.000116	0.000116	4.34057	Up	olfactomedin like 2A
ILMN_2331231	TNFRSF6B	1.42469	0.000127	0.000127	4.30988	Up	TNF receptor superfamily member 6b
ILMN_1738552	SLC1A3	1.4439	0.000128	0.000128	4.3055	Up	solute carrier family 1 member 3
ILMN_1747016	CEP55	1.05497	0.000129	0.000129	4.30342	Up	centrosomal protein 55
ILMN_2115005	FGD2	1.17986	0.00013	0.00013	4.30045	Up	FYVE, RhoGEF and PH domain containing 2
ILMN_1797731	MS4A6A	1.69103	0.000133	0.000133	4.29334	Up	membrane spanning 4-domains A6A
ILMN_1669409	VSIG4	1.26735	0.000133	0.000133	4.29241	Up	V-set and immunoglobulin domain containing 4
ILMN_1706505	COL5A1	2.03224	0.00014	0.00014	4.27583	Up	collagen type V alpha 1 chain
ILMN_1697543	SPINK13	1.91623	0.00014	0.00014	4.27578	Up	serine peptidase inhibitor, Kazal type 13 (putative)
ILMN_1778977	TYROBP	1.65758	0.00014	0.00014	4.27516	Up	TYRO protein tyrosine kinase binding protein
ILMN_1736863	TMEM140	1.05368	0.000144	0.000144	4.26649	Up	transmembrane protein 140
ILMN_2336781	SOD2	1.45404	0.000144	0.000144	4.26505	Up	superoxide dismutase 2
ILMN_1781626	C1S	1.89512	0.000148	0.000148	4.2577	Up	complement C1s
ILMN_1687583	CAV1	1.37754	0.000148	0.000148	4.25642	Up	caveolin 1
ILMN_2201678	FSTL1	1.55863	0.000151	0.000151	4.25045	Up	folliculin like 1
ILMN_1685714	INHBB	1.189	0.000153	0.000153	4.2454	Up	inhibin subunit beta B
ILMN_1732967	PPP1R18	1.1586	0.000159	0.000159	4.23196	Up	protein phosphatase 1 regulatory subunit 18
ILMN_1660691	RAB31	1.10772	0.000161	0.000161	4.22914	Up	RAB31, member RAS oncogene family
ILMN_1811468	IRX3	1.5522	0.000161	0.000161	4.22824	Up	iroquoishomeobox 3
ILMN_1666269	CTSZ	1.25835	0.000166	0.000166	4.2176	Up	cathepsin Z
ILMN_1674250	NCKAP1L	1.28467	0.000168	0.000168	4.21456	Up	NCK associated protein 1 like
ILMN_1691884	STC2	1.87134	0.000172	0.000172	4.20457	Up	stanniocalcin 2
ILMN_1714730	UBE2C	1.66373	0.000176	0.000176	4.19741	Up	ubiquitin conjugating enzyme E2 C
ILMN_2083946	TGFA	1.1968	0.000177	0.000177	4.19595	Up	transforming growth factor alpha
ILMN_1659913	ISG20	1.22099	0.000178	0.000178	4.19412	Up	interferon stimulated exonuclease gene 20
ILMN_1787815	TRIB3	1.91824	0.000202	0.000202	4.15065	Up	tribblespseudokinase 3
ILMN_2371458	ACKR3	1.32766	0.000207	0.000207	4.14184	Up	atypical chemokine receptor 3
ILMN_1751228	TMEM74B	1.04368	0.000209	0.000209	4.13918	Up	transmembrane protein 74B
ILMN_1808777	EHD2	1.17555	0.000214	0.000214	4.13129	Up	EH domain containing 2
ILMN_2289849	FCGR2A	1.23891	0.000216	0.000216	4.12823	Up	Fc fragment of IgG receptor IIa
ILMN_2331087	MS4A7	1.2497	0.000223	0.000223	4.11668	Up	membrane spanning 4-domains A7
ILMN_1764629	SLC39A14	1.55329	0.000228	0.000228	4.1094	Up	solute carrier family 39 member 14
ILMN_1807825	LY86	1.21142	0.000229	0.000229	4.10813	Up	lymphocyte antigen 86
ILMN_1751028	SERPINH1	1.28658	0.000234	0.000234	4.10064	Up	serpin family H member 1
ILMN_1661266	HLA-DQB1	2.11462	0.000236	0.000236	4.09781	Up	major histocompatibility complex, class II, DQ beta 1
ILMN_2123743	FCER1G	1.57111	0.000248	0.000248	4.08069	Up	Fc fragment of IgE receptor Ig
ILMN_1801077	PLIN2	2.00889	0.000254	0.000254	4.07206	Up	perilipin 2
ILMN_1762260	C3	1.77617	0.000259	0.000259	4.0658	Up	complement C3

ILMN_2117508	CTHRC1	1.77956	0.00026	0.00026	4.06421	Up	collagen triple helix repeat containing 1
ILMN_1781514	PCDH17	1.17569	0.000262	0.000262	4.06156	Up	protocadherin 17
ILMN_1808707	FSCN1	1.15049	0.000273	0.000273	4.04703	Up	fascin actin-bundling protein 1
ILMN_1805175	TGFA	1.08466	0.000278	0.000278	4.04057	Up	transforming growth factor alpha
ILMN_3239475	LINC00887	1.48462	0.000283	0.000283	4.0342	Up	long intergenic non-protein coding RNA 887
ILMN_1666932	FCGR2A	1.19248	0.000285	0.000285	4.03172	Up	Fc fragment of IgG receptor IIa
ILMN_1758315	SLC9A9	1.04143	0.000288	0.000288	4.02847	Up	solute carrier family 9 member A9
ILMN_1686623	CSF1R	1.48226	0.000297	0.000297	4.01746	Up	colony stimulating factor 1 receptor
ILMN_2212878	ESM1	1.84894	0.000307	0.000307	4.00643	Up	endothelial cell specific molecule 1
ILMN_1802106	APOBEC3G	1.11028	0.000312	0.000312	4.00122	Up	apolipoprotein B mRNA editing enzyme catalytic subunit 3G
ILMN_2176063	FCGR1A	1.19164	0.000316	0.000316	3.99617	Up	Fc fragment of IgG receptor Ia
ILMN_2379599	CD163	1.64579	0.000318	0.000318	3.99437	Up	CD163 molecule
ILMN_2215640	TUBA3D	1.1396	0.000318	0.000318	3.99417	Up	tubulin alpha 3d
ILMN_1764850	HPCAL1	1.04958	0.000322	0.000322	3.9896	Up	hippocalcin like 1
ILMN_1656940	ABLIM3	1.36169	0.000331	0.000331	3.98055	Up	actin binding LIM protein family member 3
ILMN_1742618	XAF1	1.05607	0.000338	0.000338	3.97371	Up	XIAP associated factor 1
ILMN_1727402	HCLS1	1.39657	0.000361	0.000361	3.94999	Up	hematopoietic cell-specific Lyn substrate 1
ILMN_1708934	ADM	1.4677	0.000376	0.000376	3.93676	Up	adrenomedullin
ILMN_1733538	RGS10	1.11145	0.000377	0.000377	3.93537	Up	regulator of G protein signaling 10
ILMN_1699574	NRP1	1.02284	0.000378	0.000378	3.9344	Up	neuropilin 1
ILMN_1724533	LY96	1.49669	0.000382	0.000382	3.9308	Up	lymphocyte antigen 96
ILMN_1799139	PLOD2	1.23951	0.000388	0.000388	3.92564	Up	procollagen-lysine,2-oxoglutarate 5-dioxygenase 2
ILMN_2406501	SOD2	1.45843	0.000416	0.000416	3.90123	Up	superoxide dismutase 2
ILMN_1739521	NLGN1	1.4261	0.000426	0.000426	3.89265	Up	neuroligin 1
ILMN_1796734	SPARC	1.34964	0.000448	0.000448	3.87509	Up	secreted protein acidic and cysteine rich
ILMN_1722622	CD163	1.62857	0.00049	0.00049	3.84429	Up	CD163 molecule
ILMN_1655077	PRDM1	1.06934	0.000497	0.000497	3.83916	Up	PR/SET domain 1
ILMN_1673363	ADGRE5	1.07059	0.000499	0.000499	3.8377	Up	adhesion G protein-coupled receptor E5
ILMN_1810844	RARRES2	1.46953	0.000504	0.000504	3.83438	Up	retinoic acid receptor responder 2
ILMN_1710740	C2	1.44544	0.00051	0.00051	3.82986	Up	complement C2
ILMN_1682993	NKG7	1.55585	0.000515	0.000515	3.82689	Up	natural killer cell granule protein 7
ILMN_3243156	AHNAK2	1.50864	0.000515	0.000515	3.82673	Up	AHNAK nucleoprotein 2
ILMN_1748473	GIMAP4	1.04777	0.000521	0.000521	3.82232	Up	GTPase, IMAP family member 4
ILMN_1660654	CDCA2	1.013	0.000535	0.000535	3.81329	Up	cell division cycle associated 2
ILMN_1657111	AHNAK2	1.7878	0.000538	0.000538	3.81131	Up	AHNAK nucleoprotein 2
ILMN_1714602	CD86	1.09549	0.000538	0.000538	3.81094	Up	CD86 molecule
ILMN_1726589	CD248	1.1485	0.000539	0.000539	3.81089	Up	CD248 molecule
ILMN_1700031	PRAME	1.16394	0.00056	0.00056	3.79746	Up	preferentially expressed antigen in melanoma
ILMN_2085862	SLC15A3	1.08851	0.000571	0.000571	3.79006	Up	solute carrier family 15 member 3
ILMN_2334296	IL18BP	1.1418	0.00058	0.00058	3.78457	Up	interleukin 18 binding protein
ILMN_1791280	HSPB8	1.47988	0.000587	0.000587	3.78089	Up	heat shock protein family B (small) member 8
ILMN_1763433	TRIM9	1.26772	0.000609	0.000609	3.76761	Up	tripartite motif containing 9
ILMN_1683450	CDCA5	1.0293	0.000619	0.000619	3.76219	Up	cell division cycle associated 5

ILMN_1768940	COL15A1	1.18329	0.000636	0.000636	3.75252	Up	collagen type XV alpha 1 chain
ILMN_2320888	CXCR4	1.28425	0.000675	0.000675	3.73154	Up	C-X-C motif chemokine receptor 4
ILMN_1721035	MS4A6A	1.5269	0.000687	0.000687	3.72503	Up	membrane spanning 4-domains A6A
ILMN_1765668	IL20RB	2.20963	0.000688	0.000688	3.72488	Up	interleukin 20 receptor subunit beta
ILMN_1653039	CERNA2	1.1913	0.000693	0.000693	3.72195	Up	competing endogenous lncRNA 2 for microRNA let-7b
ILMN_1795762	PLEK	1.32035	0.000695	0.000695	3.72121	Up	pleckstrin
ILMN_1723912	IFI44L	1.30542	0.000699	0.000699	3.719	Up	interferon induced protein 44 like
ILMN_1722524	GALNT14	1.02917	0.0007	0.0007	3.71874	Up	polypeptide N-acetylgalactosaminyltransferase 14
ILMN_1706643	COL6A3	1.79502	0.000734	0.000734	3.70166	Up	collagen type VI alpha 3 chain
ILMN_1745356	CXCL9	1.98853	0.000759	0.000759	3.69001	Up	C-X-C motif chemokine ligand 9
ILMN_1765446	EMP3	1.10761	0.000776	0.000776	3.68189	Up	epithelial membrane protein 3
ILMN_1705442	CMTM3	1.10209	0.00081	0.00081	3.66665	Up	CKLF like MARVEL transmembrane domain containing 3
ILMN_3240308	C3	1.40282	0.000815	0.000815	3.66461	Up	complement C3
ILMN_2307861	COL6A3	1.73176	0.000819	0.000819	3.66305	Up	collagen type VI alpha 3 chain
ILMN_3248910	MIR155HG	1.08233	0.000828	0.000828	3.65912	Up	MIR155 host gene
ILMN_1654396	ITGB2	1.34885	0.000835	0.000835	3.65591	Up	integrin subunit beta 2
ILMN_3237946	PXDN	1.44552	0.000841	0.000841	3.65356	Up	peroxidase
ILMN_1788203	HEY1	1.05761	0.000847	0.000847	3.65114	Up	hes related family bHLH transcription factor with YRPW motif 1
ILMN_1787345	FKBP11	1.1234	0.000876	0.000876	3.6391	Up	FK506 binding protein 11
ILMN_2297765	KCNMA1	1.3253	0.000882	0.000882	3.6366	Up	potassium calcium-activated channel subfamily M alpha 1
ILMN_1791759	CXCL10	1.87472	0.000892	0.000892	3.63247	Up	C-X-C motif chemokine ligand 10
ILMN_1813206	CP	1.82714	0.000899	0.000899	3.62975	Up	ceruloplasmin
ILMN_2396444	CD14	1.2457	0.000932	0.000932	3.61675	Up	CD14 molecule
ILMN_1684349	IL2RB	1.02228	0.000947	0.000947	3.61112	Up	interleukin 2 receptor subunit beta
ILMN_2359800	MS4A6A	1.38835	0.001012	0.001012	3.58752	Up	membrane spanning 4-domains A6A
ILMN_1796094	CD36	1.23196	0.001037	0.001037	3.57859	Up	CD36 molecule
ILMN_1733270	CD163	1.15526	0.001052	0.001052	3.57361	Up	CD163 molecule
ILMN_2066858	TNFSF13B	1.1572	0.00107	0.00107	3.56733	Up	TNF superfamily member 13b
ILMN_1714428	FBXO17	1.07446	0.001078	0.001078	3.56493	Up	F-box protein 17
ILMN_1767665	GPX8	1.07714	0.001099	0.001099	3.55785	Up	glutathione peroxidase 8 (putative)
ILMN_1727087	GJA1	1.23393	0.001144	0.001144	3.54356	Up	gap junction protein alpha 1
ILMN_1740015	CD14	1.30292	0.001193	0.001193	3.52825	Up	CD14 molecule
ILMN_1766675	CDH6	1.391	0.001207	0.001207	3.52425	Up	cadherin 6
ILMN_2058782	IFI27	1.19889	0.001221	0.001221	3.51994	Up	interferon alpha inducible protein 27
ILMN_1685608	NPTX2	2.68465	0.001266	0.001266	3.50692	Up	neuronal pentraxin 2
ILMN_2388547	EPSTI1	1.02127	0.001301	0.001301	3.49725	Up	epithelial stromal interaction 1
ILMN_1685433	COL8A1	1.90914	0.001306	0.001306	3.49575	Up	collagen type VIII alpha 1 chain
ILMN_2383349	STEAP3	1.3782	0.00132	0.00132	3.49185	Up	STEAP3 metalloredutase
ILMN_1801377	SLC29A4	1.08142	0.001337	0.001337	3.48716	Up	solute carrier family 29 member 4
ILMN_2363658	PXDN	1.2356	0.001358	0.001358	3.48153	Up	peroxidase
ILMN_1801504	RUNX1	1.04486	0.001445	0.001445	3.45909	Up	runt related transcription factor 1
ILMN_1766169	BCAT1	1.1835	0.001466	0.001466	3.45403	Up	branched chain amino acid transaminase 1
ILMN_2194577	PLVAP	1.06736	0.001527	0.001527	3.43921	Up	plasmalemma vesicle associated protein

ILMN_2165354	DCLK1	1.23529	0.001545	0.001545	3.43497	Up	doublecortin like kinase 1
ILMN_1758418	TNFSF13B	1.12964	0.001576	0.001576	3.42772	Up	TNF superfamily member 13b
ILMN_1732151	COL6A1	1.44291	0.001611	0.001611	3.41959	Up	collagen type VI alpha 1 chain
ILMN_2175912	ITGB2	1.25987	0.001641	0.001641	3.41298	Up	integrin subunit beta 2
ILMN_2082273	RGS5	1.34163	0.001718	0.001718	3.39624	Up	regulator of G protein signaling 5
ILMN_2196328	POSTN	1.08922	0.00183	0.00183	3.3731	Up	periostin
ILMN_1682312	CYBB	1.10292	0.001833	0.001833	3.37253	Up	cytochrome b-245 beta chain
ILMN_1651554	RGS5	1.26361	0.001837	0.001837	3.37161	Up	regulator of G protein signaling 5
ILMN_1760027	WAS	1.08759	0.001868	0.001868	3.36566	Up	Wiskott-Aldrich syndrome
ILMN_1763452	EVI2B	1.05627	0.001891	0.001891	3.36099	Up	ecotropic viral integration site 2B
ILMN_1810628	PRUNE2	1.23824	0.001907	0.001907	3.35795	Up	prune homolog 2
ILMN_1767556	DEPP1	1.27113	0.00201	0.00201	3.33862	Up	DEPP1, autophagy regulator
ILMN_1656310	IDO1	1.13878	0.002133	0.002133	3.31688	Up	indoleamine 2,3-dioxygenase 1
ILMN_1801766	MCUB	1.01585	0.002219	0.002219	3.30224	Up	mitochondrial calcium uniporter dominant negative beta subunit
ILMN_1687301	VCAN	1.563	0.002224	0.002224	3.30138	Up	versican
ILMN_1766955	VCAM1	1.36333	0.002227	0.002227	3.30096	Up	vascular cell adhesion molecule 1
ILMN_3244117	STMN3	1.39191	0.002315	0.002315	3.28657	Up	stathmin 3
ILMN_1719938	FGF11	1.21081	0.002338	0.002338	3.28293	Up	fibroblast growth factor 11
ILMN_1713529	SEMA6A	1.17651	0.002534	0.002534	3.25305	Up	semaphorin 6A
ILMN_1716957	C1QL1	1.42756	0.002559	0.002559	3.24938	Up	complement C1q like 1
ILMN_2402392	COL8A1	1.71362	0.002672	0.002672	3.23341	Up	collagen type VIII alpha 1 chain
ILMN_1800512	HMOX1	1.15558	0.00268	0.00268	3.2322	Up	hemeoxygenase 1
ILMN_1799725	DOCK2	1.08482	0.002721	0.002721	3.22658	Up	dedicator of cytokinesis 2
ILMN_2368530	IL32	1.12531	0.002784	0.002784	3.21809	Up	interleukin 32
ILMN_2325337	APOL2	1.34833	0.00287	0.00287	3.20671	Up	apolipoprotein L2
ILMN_1671928	PROS1	1.20795	0.002891	0.002891	3.20406	Up	protein S
ILMN_2307903	VCAM1	1.52088	0.002903	0.002903	3.20244	Up	vascular cell adhesion molecule 1
ILMN_3239965	IDO1	1.14742	0.003064	0.003064	3.18221	Up	indoleamine 2,3-dioxygenase 1
ILMN_1690209	RHEX	1.16857	0.003133	0.003133	3.17394	Up	regulator of hemoglobinization and erythroid cell expansion
ILMN_1700183	APLN	1.14594	0.003155	0.003155	3.17121	Up	apelin receptor
ILMN_2128668	FOXJ3	1.13384	0.003199	0.003199	3.16611	Up	forkhead box J3
ILMN_1718866	C5orf46	2.00995	0.003316	0.003316	3.15262	Up	chromosome 5 open reading frame 46
ILMN_1792506	PLA1A	1.22203	0.003337	0.003337	3.15016	Up	phospholipase A1 member A
ILMN_2331082	MS4A7	1.14497	0.003394	0.003394	3.14377	Up	membrane spanning 4-domains A7
ILMN_1779228	CDH2	1.03098	0.003443	0.003443	3.13845	Up	cadherin 2
ILMN_2211065	TMEM91	1.43891	0.003456	0.003456	3.13703	Up	transmembrane protein 91
ILMN_1655595	SERPINE2	1.07558	0.003483	0.003483	3.13401	Up	serpin family E member 2
ILMN_1815057	PDGFRB	1.05591	0.003493	0.003493	3.133	Up	platelet derived growth factor receptor beta
ILMN_3203444	CERCAM	1.12463	0.003569	0.003569	3.1249	Up	cerebral endothelial cell adhesion molecule
ILMN_1736670	PPP1R3C	1.37197	0.003616	0.003616	3.11989	Up	protein phosphatase 1 regulatory subunit 3C
ILMN_1670926	CHST15	1.13933	0.003619	0.003619	3.11955	Up	carbohydrate sulfotransferase 15
ILMN_1780060	FCN3	1.1591	0.003733	0.003733	3.10789	Up	ficolin 3
ILMN_1688480	CCND1	1.01744	0.003922	0.003922	3.08914	Up	cyclin D1

ILMN_1734276	PMEPA1	1.1069	0.003991	0.003991	3.08258	Up	prostate transmembrane protein, androgen induced 1
ILMN_1701114	GBP1	1.03115	0.00433	0.00433	3.05151	Up	guanylate binding protein 1
ILMN_1683179	RRAD	1.18869	0.004357	0.004357	3.04913	Up	RRAD, Ras related glycolysis inhibitor and calcium channel regulat
ILMN_1796316	MMP9	2.15361	0.00465	0.00465	3.02426	Up	matrix metallopeptidase 9
ILMN_2186137	RRAD	1.28976	0.004803	0.004803	3.01186	Up	RRAD, Ras related glycolysis inhibitor and calcium channel regulat
ILMN_1666078	HLA-H	1.09189	0.004863	0.004863	3.00706	Up	major histocompatibility complex, class I, H (pseudogene)
ILMN_1779324	GZMA	1.29778	0.004892	0.004892	3.00476	Up	granzyme A
ILMN_1796537	FYB1	1.05329	0.005027	0.005027	2.9943	Up	FYN binding protein 1
ILMN_1673521	KISS1R	1.64287	0.005093	0.005093	2.98931	Up	KISS1 receptor
ILMN_1662932	LCP1	1.23358	0.005311	0.005311	2.97314	Up	lymphocyte cytosolic protein 1
ILMN_2261600	FCGR1A	1.0377	0.005533	0.005533	2.95734	Up	Fc fragment of IgG receptor Ia
ILMN_1752755	VWF	1.12259	0.005627	0.005627	2.95079	Up	von Willebrand factor
ILMN_2098126	CCL5	1.38477	0.005635	0.005635	2.95027	Up	C-C motif chemokine ligand 5
ILMN_1802192	C10orf99	1.66943	0.005738	0.005738	2.94322	Up	chromosome 10 open reading frame 99
ILMN_2304512	SAA1	2.3196	0.005808	0.005808	2.93852	Up	serum amyloid A1
ILMN_1691364	STAT1	1.03074	0.005814	0.005814	2.93813	Up	signal transducer and activator of transcription 1
ILMN_1656011	RGS1	1.60073	0.006121	0.006121	2.91813	Up	regulator of G protein signaling 1
ILMN_1672611	CDH11	1.07048	0.006407	0.006407	2.90034	Up	cadherin 11
ILMN_2114568	GBP5	1.23897	0.006627	0.006627	2.88713	Up	guanylate binding protein 5
ILMN_1697189	PNCK	2.61168	0.006717	0.006717	2.88188	Up	pregnancy up-regulated nonubiquitousCaM kinase
ILMN_1699071	MAP3K7CL	1.01879	0.006764	0.006764	2.87914	Up	MAP3K7 C-terminal like
ILMN_1852151	#N/A	1.02269	0.007393	0.007393	2.84423	Up	NA
ILMN_1813338	LAG3	1.0695	0.007502	0.007502	2.83847	Up	lymphocyte activating 3
ILMN_3235832	CCL4L2	1.07587	0.007548	0.007548	2.83607	Up	C-C motif chemokine ligand 4 like 2
ILMN_2325338	APOL2	1.058	0.007606	0.007606	2.83304	Up	apolipoprotein L2
ILMN_1709795	RAC2	1.0549	0.007701	0.007701	2.82815	Up	Rac family small GTPase 2
ILMN_1715068	AQP9	1.18514	0.007769	0.007769	2.82467	Up	aquaporin 9
ILMN_1679262	DPYSL3	1.32112	0.007987	0.007987	2.81373	Up	dihydropyrimidinase like 3
ILMN_2413779	SEZ6L2	1.2184	0.008415	0.008415	2.793	Up	seizure related 6 homolog like 2
ILMN_2370241	TEX11	1.11289	0.008543	0.008543	2.78702	Up	testis expressed 11
ILMN_1677198	C1R	1.29186	0.008548	0.008548	2.78681	Up	complement C1r
ILMN_3243714	#N/A	1.12432	0.008767	0.008767	2.77673	Up	NA
ILMN_1723035	OLR1	1.06884	0.009687	0.009687	2.73683	Up	oxidized low density lipoprotein receptor 1
ILMN_2163873	FNDC1	1.03976	0.010153	0.010153	2.71795	Up	fibronectin type III domain containing 1
ILMN_1705750	TGM2	1.09984	0.010383	0.010383	2.70896	Up	transglutaminase 2
ILMN_1801584	CXCR4	1.05022	0.010761	0.010761	2.69453	Up	C-X-C motif chemokine receptor 4
ILMN_1768482	CD8A	1.30393	0.011092	0.011092	2.68225	Up	CD8a molecule
ILMN_2351466	NTM	1.125	0.011197	0.011197	2.67845	Up	neurotrimin
ILMN_1769388	GJB2	1.18122	0.01146	0.01146	2.66905	Up	gap junction protein beta 2
ILMN_2065773	SCG5	1.27548	0.011639	0.011639	2.66273	Up	secretogranin V
ILMN_1809813	PGF	1.64335	0.011795	0.011795	2.65732	Up	placental growth factor
ILMN_1773352	CCL5	1.22065	0.01189	0.01189	2.65406	Up	C-C motif chemokine ligand 5
ILMN_1806165	HSPA6	1.1867	0.012355	0.012355	2.63841	Up	heat shock protein family A (Hsp70) member 6

ILMN_1776516	ITPKA	1.12694	0.012587	0.012587	2.63082	Up	inositol-trisphosphate 3-kinase A
ILMN_3181328	#N/A	1.73878	0.012858	0.012858	2.62212	Up	NA
ILMN_2314169	PTH LH	1.86592	0.013169	0.013169	2.61231	Up	parathyroid hormone like hormone
ILMN_1739496	PRRX1	1.06772	0.013906	0.013906	2.58993	Up	paired related homeobox 1
ILMN_1758731	CYP2J2	2.0314	0.014868	0.014868	2.5623	Up	cytochrome P450 family 2 subfamily J member 2
ILMN_1778444	FKBP5	1.02677	0.014872	0.014872	2.56218	Up	FK506 binding protein 5
ILMN_1810172	SFRP4	1.25218	0.015169	0.015169	2.55398	Up	secreted frizzled related protein 4
ILMN_1695025	CD2	1.02692	0.015269	0.015269	2.55124	Up	CD2 molecule
ILMN_1701017	SAA1	1.45216	0.015478	0.015478	2.5456	Up	serum amyloid A1
ILMN_1678842	THBS2	1.40843	0.016961	0.016961	2.50743	Up	thrombospondin 2
ILMN_1678841	UBD	1.32192	0.017456	0.017456	2.49539	Up	ubiquitin D
ILMN_1789507	COL11A1	1.12097	0.017805	0.017805	2.48705	Up	collagen type XI alpha 1 chain
ILMN_1785699	PTH LH	1.67411	0.020347	0.020347	2.43061	Up	parathyroid hormone like hormone
ILMN_3214389	HLA-DQB1	1.01342	0.021318	0.021318	2.41075	Up	major histocompatibility complex, class II, DQ beta 1
ILMN_2353732	CD8A	1.20437	0.021726	0.021726	2.40264	Up	CD8a molecule
ILMN_1740005	SERPINF2	1.12852	0.022691	0.022691	2.384	Up	serpin family F member 2
ILMN_1808405	HLA-DQA1	1.06566	0.022716	0.022716	2.38352	Up	major histocompatibility complex, class II, DQ alpha 1
ILMN_2105797	SLC6A3	1.24259	0.022936	0.022936	2.37938	Up	solute carrier family 6 member 3
ILMN_1680339	PDGFRL	1.02747	0.024207	0.024207	2.35611	Up	platelet derived growth factor receptor like
ILMN_3249667	HLA-DQA2	1.0902	0.02571	0.02571	2.32999	Up	major histocompatibility complex, class II, DQ alpha 2
ILMN_1736078	THBS4	1.07147	0.026696	0.026696	2.31358	Up	thrombospondin 4
ILMN_1671337	SLC2A5	1.17798	0.026741	0.026741	2.31286	Up	solute carrier family 2 member 5
ILMN_1795325	ACTG2	1.11261	0.02682	0.02682	2.31157	Up	actin, gamma 2, smooth muscle, enteric
ILMN_2325837	CD3D	1.03049	0.027768	0.027768	2.29636	Up	CD3d molecule
ILMN_1699852	CES4A	1.05401	0.028527	0.028527	2.28454	Up	carboxylesterase 4A
ILMN_2315044	FGG	1.73985	0.029489	0.029489	2.26994	Up	fibrinogen gamma chain
ILMN_1668055	SAA4	1.05153	0.033879	0.033879	2.20829	Up	serum amyloid A4, constitutive
ILMN_1844464	#N/A	1.01818	0.042329	0.042329	2.10742	Up	NA
ILMN_1744381	SERPINE1	1.09191	0.044409	0.044409	2.08535	Up	serpin family E member 1
ILMN_1710734	GZMK	1.11368	0.044511	0.044511	2.08429	Up	granzyme K
ILMN_1728262	SAA2	1.07888	0.049886	0.049886	2.03131	Up	serum amyloid A2
ILMN_2064150	PRRG2	-2.43973	2.4E-15	2.4E-15	-13.4169	Down	proline rich and Gla domain 2
ILMN_1715476	CKMT1B	-1.74432	7.19E-14	7.19E-14	-11.9239	Down	creatine kinase, mitochondrial 1B
ILMN_1674135	RALGPS1	-1.18155	1.04E-13	1.04E-13	-11.769	Down	Ral GEF with PH domain and SH3 binding motif 1
ILMN_1812073	ATP6V1B1	-4.36136	1.14E-13	1.14E-13	-11.7304	Down	ATPase H+ transporting V1 subunit B1
ILMN_1732066	CKMT1A	-1.57898	4.43E-13	4.43E-13	-11.1713	Down	creatine kinase, mitochondrial 1A
ILMN_1736527	TFCP2L1	-2.27455	6.11E-13	6.11E-13	-11.0409	Down	transcription factor CP2 like 1
ILMN_2364072	CLCNKA	-5.00306	1.15E-12	1.15E-12	-10.7865	Down	chloride voltage-gated channel Ka
ILMN_1787576	CLCNKA	-4.83518	1.2E-12	1.2E-12	-10.7718	Down	chloride voltage-gated channel Ka
ILMN_1678186	ATP6V0A4	-3.83117	1.33E-12	1.33E-12	-10.7281	Down	ATPase H+ transporting V0 subunit a4
ILMN_1732149	AQP2	-5.6941	1.72E-12	1.72E-12	-10.6276	Down	aquaporin 2
ILMN_2183692	PHYHD1	-1.22598	1.75E-12	1.75E-12	-10.6213	Down	phytanoyl-CoA dioxygenase domain containing 1
ILMN_1791826	RAB25	-2.87927	2.5E-12	2.5E-12	-10.48	Down	RAB25, member RAS oncogene family

ILMN_1725597	FXYP4	-5.05753	3.38E-12	3.38E-12	-10.3621	Down	FXYP domain containing ion transport regulator 4
ILMN_1740585	UMOD	-5.41077	4.75E-12	4.75E-12	-10.23	Down	uromodulin
ILMN_1749415	KCNJ1	-2.99725	5.56E-12	5.56E-12	-10.1696	Down	potassium voltage-gated channel subfamily J member 1
ILMN_2149164	SFRP1	-3.29025	6.07E-12	6.07E-12	-10.1354	Down	secreted frizzled related protein 1
ILMN_1751785	DMRT2	-3.28567	6.48E-12	6.48E-12	-10.1107	Down	doublesex and mab-3 related transcription factor 2
ILMN_2072568	CLDN8	-4.13227	8.58E-12	8.58E-12	-10.0028	Down	claudin 8
ILMN_1739126	TMEM213	-3.48802	9.05E-12	9.05E-12	-9.98257	Down	transmembrane protein 213
ILMN_2406151	UMOD	-5.45165	9.47E-12	9.47E-12	-9.965	Down	uromodulin
ILMN_2394287	ATP6V0A4	-2.89309	1.03E-11	1.03E-11	-9.93441	Down	ATPase H+ transporting V0 subunit a4
ILMN_2415189	ATP1A1	-1.48865	1.39E-11	1.39E-11	-9.82018	Down	ATPase Na+/K+ transporting subunit alpha 1
ILMN_1813350	HSD11B2	-3.27711	1.39E-11	1.39E-11	-9.8184	Down	hydroxysteroid 11-beta dehydrogenase 2
ILMN_2049184	DNASE1L3	-2.04535	1.7E-11	1.7E-11	-9.74361	Down	deoxyribonuclease 1 like 3
ILMN_1798742	CLCNKB	-2.89447	1.7E-11	1.7E-11	-9.74351	Down	chloride voltage-gated channel Kb
ILMN_1765310	TCEAL2	-1.83889	2.31E-11	2.31E-11	-9.62648	Down	transcription elongation factor A like 2
ILMN_1746676	CLDN8	-3.55129	2.47E-11	2.47E-11	-9.6024	Down	claudin 8
ILMN_2357944	KCNJ1	-2.77041	2.6E-11	2.6E-11	-9.5835	Down	potassium voltage-gated channel subfamily J member 1
ILMN_2413833	TOX3	-1.41846	2.7E-11	2.7E-11	-9.5686	Down	TOX high mobility group box family member 3
ILMN_2104295	TMEM178A	-1.5487	3.23E-11	3.23E-11	-9.50192	Down	transmembrane protein 178A
ILMN_1744211	PLA2G4F	-1.6303	3.86E-11	3.86E-11	-9.43578	Down	phospholipase A2 group IVF
ILMN_1801697	SYNE4	-1.26958	4.07E-11	4.07E-11	-9.41594	Down	spectrin repeat containing nuclear envelope family member 4
ILMN_2210934	NR3C2	-1.63615	4.55E-11	4.55E-11	-9.37421	Down	nuclear receptor subfamily 3 group C member 2
ILMN_1752935	TMEM30B	-2.11753	4.63E-11	4.63E-11	-9.36797	Down	transmembrane protein 30B
ILMN_1814917	TLE2	-1.15227	8.42E-11	8.42E-11	-9.14707	Down	transducin like enhancer of split 2
ILMN_1696657	LRRN2	-2.38643	8.42E-11	8.42E-11	-9.14702	Down	leucine rich repeat neuronal 2
ILMN_1725852	S100A2	-1.7948	9.66E-11	9.66E-11	-9.09655	Down	S100 calcium binding protein A2
ILMN_1738849	SLC9A2	-1.20954	1.1E-10	1.1E-10	-9.04952	Down	solute carrier family 9 member A2
ILMN_1739001	TACSTD2	-4.64171	1.11E-10	1.11E-10	-9.04545	Down	tumor associated calcium signal transducer 2
ILMN_2241124	ADGRF1	-1.6207	1.13E-10	1.13E-10	-9.03939	Down	adhesion G protein-coupled receptor F1
ILMN_1791123	TMPRSS2	-3.06504	1.26E-10	1.26E-10	-9.00037	Down	transmembrane serine protease 2
ILMN_1660729	ATP6V1C2	-1.16374	1.31E-10	1.31E-10	-8.9851	Down	ATPase H+ transporting V1 subunit C2
ILMN_1682326	PCP4	-1.96434	1.54E-10	1.54E-10	-8.92731	Down	Purkinje cell protein 4
ILMN_1731783	ATP1A1	-1.72998	1.67E-10	1.67E-10	-8.8965	Down	ATPase Na+/K+ transporting subunit alpha 1
ILMN_1685194	CLDN10	-2.60027	2.44E-10	2.44E-10	-8.75976	Down	claudin 10
ILMN_1657011	SLC25A25-AS1	-1.43676	2.93E-10	2.93E-10	-8.69404	Down	SLC25A25 antisense RNA 1
ILMN_1753729	KNG1	-4.08681	3.55E-10	3.55E-10	-8.62565	Down	kininogen 1
ILMN_1788942	GGT6	-1.80113	3.83E-10	3.83E-10	-8.598	Down	gamma-glutamyltransferase 6
ILMN_1761999	FYB2	-1.2687	5.26E-10	5.26E-10	-8.48477	Down	FYN binding protein 2
ILMN_1807211	NICN1	-1.11116	5.28E-10	5.28E-10	-8.48341	Down	nicotin 1
ILMN_1775566	ATP1A1	-1.80538	5.62E-10	5.62E-10	-8.46123	Down	ATPase Na+/K+ transporting subunit alpha 1
ILMN_2148469	RASL11B	-2.20338	7.88E-10	7.88E-10	-8.34141	Down	RAS like family 11 member B
ILMN_3248882	DANCR	-1.26115	8.4E-10	8.4E-10	-8.31889	Down	differentiation antagonizing non-protein coding RNA
ILMN_1721770	PAPPA	-1.79303	9.2E-10	9.2E-10	-8.28638	Down	pappalysin 1

ILMN_1741597	NUPR2	-2.16198	9.27E-10	9.27E-10	-8.28406	Down	nuclear protein 2, transcriptional regulator
ILMN_1672605	MTURN	-2.12831	9.46E-10	9.46E-10	-8.27678	Down	maturin, neural progenitor differentiation regulator homolog
ILMN_1715463	SOSTDC1	-1.46942	9.56E-10	9.56E-10	-8.27287	Down	sclerostin domain containing 1
ILMN_1678403	TMEM178A	-1.12036	1.01E-09	1.01E-09	-8.25277	Down	transmembrane protein 178A
ILMN_1849399	PARTICL	-1.3149	1.08E-09	1.08E-09	-8.23141	Down	promoter of MAT2A antisense radiation-induced circulating long no coding RNA
ILMN_1767711	CASR	-1.44337	1.11E-09	1.11E-09	-8.21882	Down	calcium sensing receptor
ILMN_1725311	GCGR	-2.56099	1.17E-09	1.17E-09	-8.20174	Down	glucagon receptor
ILMN_1764309	ADH1A	-2.89162	1.23E-09	1.23E-09	-8.18455	Down	alcohol dehydrogenase 1A (class I), alpha polypeptide
ILMN_1689699	#N/A	-1.18037	1.27E-09	1.27E-09	-8.17414	Down	NA
ILMN_1744929	PTGER1	-2.61548	1.29E-09	1.29E-09	-8.16666	Down	prostaglandin E receptor 1
ILMN_1661799	HIGD1A	-1.62483	1.38E-09	1.38E-09	-8.14419	Down	HIG1 hypoxia inducible domain family member 1A
ILMN_1694106	GPD1L	-1.50546	2.16E-09	2.16E-09	-7.98786	Down	glycerol-3-phosphate dehydrogenase 1 like
ILMN_1803367	MECOM	-2.02632	2.33E-09	2.33E-09	-7.96005	Down	MDS1 and EVI1 complex locus
ILMN_3236481	HIGD1A	-1.77486	2.35E-09	2.35E-09	-7.95812	Down	HIG1 hypoxia inducible domain family member 1A
ILMN_1798496	HOXB8	-2.35089	2.39E-09	2.39E-09	-7.9523	Down	homeobox B8
ILMN_1730809	SLC29A2	-1.28181	2.44E-09	2.44E-09	-7.94488	Down	solute carrier family 29 member 2
ILMN_1674522	HIGD1A	-1.57769	2.46E-09	2.46E-09	-7.94148	Down	HIG1 hypoxia inducible domain family member 1A
ILMN_1782412	IRX2	-1.44472	2.5E-09	2.5E-09	-7.93656	Down	iroquoishomeobox 2
ILMN_2230016	HIGD1A	-1.21282	2.88E-09	2.88E-09	-7.88648	Down	HIG1 hypoxia inducible domain family member 1A
ILMN_1730454	FOLR3	-2.0559	2.98E-09	2.98E-09	-7.87542	Down	folate receptor 3
ILMN_2413015	EMX1	-1.48584	3.45E-09	3.45E-09	-7.82425	Down	empty spiracles homeobox 1
ILMN_1655261	ERP27	-2.26076	3.48E-09	3.48E-09	-7.82086	Down	endoplasmic reticulum protein 27
ILMN_2160209	EPCAM	-2.41651	3.56E-09	3.56E-09	-7.81365	Down	epithelial cell adhesion molecule
ILMN_1755649	SLC16A5	-2.6913	3.67E-09	3.67E-09	-7.80302	Down	solute carrier family 16 member 5
ILMN_1704294	CDH3	-1.24267	4.15E-09	4.15E-09	-7.76073	Down	cadherin 3
ILMN_1745817	NELL1	-1.4884	4.61E-09	4.61E-09	-7.72405	Down	neural EGFL like 1
ILMN_1707670	CLDN16	-1.67981	5.3E-09	5.3E-09	-7.67598	Down	claudin 16
ILMN_1715301	FXYP2	-3.39361	5.43E-09	5.43E-09	-7.66772	Down	FXYP domain containing ion transport regulator 2
ILMN_2163723	KRT7	-2.16448	5.5E-09	5.5E-09	-7.66311	Down	keratin 7
ILMN_1753026	PLPPR1	-1.59013	6.11E-09	6.11E-09	-7.62723	Down	phospholipid phosphatase related 1
ILMN_1744299	ADGRF1	-1.39364	8.5E-09	8.5E-09	-7.51353	Down	adhesion G protein-coupled receptor F1
ILMN_1728570	TCF21	-1.68102	9.64E-09	9.64E-09	-7.47045	Down	transcription factor 21
ILMN_1693912	SLC47A2	-2.76292	1.09E-08	1.09E-08	-7.42718	Down	solute carrier family 47 member 2
ILMN_1762531	FGF9	-2.30479	1.29E-08	1.29E-08	-7.37088	Down	fibroblast growth factor 9
ILMN_1777644	INPP5J	-2.43241	1.32E-08	1.32E-08	-7.36382	Down	inositol polyphosphate-5-phosphatase J
ILMN_2051972	GPC3	-1.2178	1.45E-08	1.45E-08	-7.33074	Down	glypican 3
ILMN_1732782	SCN2A	-1.44922	1.59E-08	1.59E-08	-7.29921	Down	sodium voltage-gated channel alpha subunit 2
ILMN_1669114	WNK4	-1.54216	1.8E-08	1.8E-08	-7.25802	Down	WNK lysine deficient protein kinase 4
ILMN_1736015	JADE1	-1.24167	1.9E-08	1.9E-08	-7.23978	Down	jade family PHD finger 1
ILMN_1758323	ACPP	-1.74012	1.92E-08	1.92E-08	-7.23608	Down	acid phosphatase, prostate
ILMN_1766712	TCF21	-1.25274	1.95E-08	1.95E-08	-7.23042	Down	transcription factor 21
ILMN_1719250	SLC44A4	-2.22914	2.14E-08	2.14E-08	-7.19838	Down	solute carrier family 44 member 4

ILMN_3249032	EPCAM	-3.08359	2.24E-08	2.24E-08	-7.18363	Down	epithelial cell adhesion molecule
ILMN_1748378	NPHS2	-2.52369	2.38E-08	2.38E-08	-7.16345	Down	NPHS2, podocin
ILMN_2355486	FAM3B	-1.68363	2.46E-08	2.46E-08	-7.15206	Down	family with sequence similarity 3 member B
ILMN_1787265	ZNF503	-1.53017	2.49E-08	2.49E-08	-7.14708	Down	zinc finger protein 503
ILMN_1730977	SLC44A4	-2.20365	2.69E-08	2.69E-08	-7.12129	Down	solute carrier family 44 member 4
ILMN_2371001	ATP6V1G3	-1.99984	2.81E-08	2.81E-08	-7.10735	Down	ATPase H ⁺ transporting V1 subunit G3
ILMN_1761312	CRHBP	-1.20411	2.84E-08	2.84E-08	-7.10319	Down	corticotropin releasing hormone binding protein
ILMN_1742272	REN	-1.3207	2.98E-08	2.98E-08	-7.08643	Down	renin
ILMN_1780671	PLEKHG3	-1.38249	3.12E-08	3.12E-08	-7.07106	Down	pleckstrin homology and RhoGEF domain containing G3
ILMN_1791728	SLC25A25	-1.79501	3.36E-08	3.36E-08	-7.04637	Down	solute carrier family 25 member 25
ILMN_3285762	SLC4A1	-2.14805	3.68E-08	3.68E-08	-7.01577	Down	solute carrier family 4 member 1 (Diego blood group)
ILMN_1742330	PLXNB1	-1.24841	3.71E-08	3.71E-08	-7.01345	Down	plexin B1
ILMN_1714577	OGDHL	-2.71492	3.87E-08	3.87E-08	-6.99909	Down	oxoglutarate dehydrogenase like
ILMN_1753101	VTCN1	-2.26595	3.92E-08	3.92E-08	-6.99414	Down	V-set domain containing T cell activation inhibitor 1
ILMN_1711124	MARVELD2	-1.34592	4.08E-08	4.08E-08	-6.98099	Down	MARVEL domain containing 2
ILMN_1778308	COL4A4	-1.14212	4.6E-08	4.6E-08	-6.941	Down	collagen type IV alpha 4 chain
ILMN_1779448	EFHD1	-2.63315	4.7E-08	4.7E-08	-6.93354	Down	EF-hand domain family member D1
ILMN_3268403	ZNF667-AS1	-1.34062	4.91E-08	4.91E-08	-6.919	Down	ZNF667 antisense RNA 1 (head to head)
ILMN_1674193	EMX1	-1.38735	4.93E-08	4.93E-08	-6.91727	Down	empty spiracles homeobox 1
ILMN_1739594	ACOT11	-1.36868	5.32E-08	5.32E-08	-6.89159	Down	acyl-CoA thioesterase 11
ILMN_1760412	SHISA2	-1.28449	6.08E-08	6.08E-08	-6.84674	Down	shisa family member 2
ILMN_3236756	ACSF2	-2.01091	6.22E-08	6.22E-08	-6.83938	Down	acyl-CoA synthetase family member 2
ILMN_2153916	HSPA2	-1.98884	6.41E-08	6.41E-08	-6.82918	Down	heat shock protein family A (Hsp70) member 2
ILMN_1815154	MYH10	-1.57869	6.79E-08	6.79E-08	-6.81014	Down	myosin heavy chain 10
ILMN_1769547	DIO1	-2.15622	7.17E-08	7.17E-08	-6.79188	Down	iodothyroninedeiodinase 1
ILMN_1812096	CADM4	-1.2623	7.37E-08	7.37E-08	-6.78267	Down	cell adhesion molecule 4
ILMN_1693119	LYPD6B	-1.39319	7.37E-08	7.37E-08	-6.78243	Down	LY6/PLAUR domain containing 6B
ILMN_1727606	TMEM52B	-1.90215	7.88E-08	7.88E-08	-6.75991	Down	transmembrane protein 52B
ILMN_1697460	REEP6	-1.30552	8.36E-08	8.36E-08	-6.74013	Down	receptor accessory protein 6
ILMN_3247560	BSPRY	-1.28718	8.37E-08	8.37E-08	-6.73969	Down	B-box and SPRY domain containing
ILMN_3233179	HS6ST1	-1.29682	8.71E-08	8.71E-08	-6.72649	Down	heparansulfate 6-O-sulfotransferase 1
ILMN_1766499	HSPA2	-2.3088	8.81E-08	8.81E-08	-6.72263	Down	heat shock protein family A (Hsp70) member 2
ILMN_1814215	SCNN1G	-2.10375	8.9E-08	8.9E-08	-6.71943	Down	sodium channel epithelial 1 gamma subunit
ILMN_1680453	ITM2C	-1.82221	8.99E-08	8.99E-08	-6.71592	Down	integral membrane protein 2C
ILMN_1793954	#N/A	-1.30965	1.05E-07	1.05E-07	-6.66463	Down	NA
ILMN_1690616	SMIM5	-1.42234	1.07E-07	1.07E-07	-6.65736	Down	small integral membrane protein 5
ILMN_2366041	ITM2C	-1.75291	1.11E-07	1.11E-07	-6.6466	Down	integral membrane protein 2C
ILMN_1713995	SCNN1A	-3.51323	1.14E-07	1.14E-07	-6.63788	Down	sodium channel epithelial 1 alpha subunit
ILMN_2320330	MAL	-4.03816	1.15E-07	1.15E-07	-6.63429	Down	mal, T cell differentiation protein
ILMN_1688162	SLC12A1	-1.42068	1.2E-07	1.2E-07	-6.62071	Down	solute carrier family 12 member 1
ILMN_1686562	KIF13B	-1.28171	1.21E-07	1.21E-07	-6.61626	Down	kinesin family member 13B
ILMN_1659610	TJP3	-1.55042	1.22E-07	1.22E-07	-6.61265	Down	tight junction protein 3
ILMN_2153837	SCNN1G	-2.61565	1.25E-07	1.25E-07	-6.60723	Down	sodium channel epithelial 1 gamma subunit

ILMN_1711928	ACSF2	-1.75754	1.29E-07	1.29E-07	-6.59513	Down	acyl-CoA synthetase family member 2
ILMN_1745079	TRIM2	-1.57218	1.4E-07	1.4E-07	-6.56894	Down	tripartite motif containing 2
ILMN_2399769	WLS	-1.12947	1.42E-07	1.42E-07	-6.56319	Down	wntlessWnt ligand secretion mediator
ILMN_2323508	AIF1L	-2.62225	1.46E-07	1.46E-07	-6.55376	Down	allograft inflammatory factor 1 like
ILMN_2047511	ADAP1	-1.47805	1.47E-07	1.47E-07	-6.55194	Down	ArfGAP with dual PH domains 1
ILMN_1780255	KLK6	-1.29553	1.49E-07	1.49E-07	-6.54668	Down	kallikrein related peptidase 6
ILMN_1740234	GSTO2	-2.22554	1.52E-07	1.52E-07	-6.53966	Down	glutathione S-transferase omega 2
ILMN_1679011	SLC12A3	-1.27707	1.75E-07	1.75E-07	-6.49318	Down	solute carrier family 12 member 3
ILMN_1716803	RALYL	-1.45705	1.78E-07	1.78E-07	-6.48832	Down	RALY RNA binding protein like
ILMN_2094952	NUAK2	-1.35141	1.79E-07	1.79E-07	-6.48598	Down	NUAK family kinase 2
ILMN_1811593	NIPAL1	-1.18978	1.83E-07	1.83E-07	-6.47955	Down	NIPA like domain containing 1
ILMN_2352131	ERBB2	-1.42232	1.98E-07	1.98E-07	-6.45289	Down	erb-b2 receptor tyrosine kinase 2
ILMN_1803219	TMC4	-1.26871	2.15E-07	2.15E-07	-6.42616	Down	transmembrane channel like 4
ILMN_1770725	AIF1L	-2.6693	2.2E-07	2.2E-07	-6.41758	Down	allograft inflammatory factor 1 like
ILMN_2229379	KIT	-1.5562	2.25E-07	2.25E-07	-6.40965	Down	KIT proto-oncogene receptor tyrosine kinase
ILMN_2069224	PVALB	-2.70404	2.29E-07	2.29E-07	-6.40411	Down	parvalbumin
ILMN_3246328	PTH1R	-1.8657	2.3E-07	2.3E-07	-6.40361	Down	parathyroid hormone 1 receptor
ILMN_2160210	EPCAM	-3.17996	2.33E-07	2.33E-07	-6.39886	Down	epithelial cell adhesion molecule
ILMN_2406656	GATA3	-1.12016	2.44E-07	2.44E-07	-6.38399	Down	GATA binding protein 3
ILMN_2185427	PRR35	-1.7792	2.51E-07	2.51E-07	-6.37408	Down	proline rich 35
ILMN_1701497	CD5L	-1.97816	2.52E-07	2.52E-07	-6.37225	Down	CD5 molecule like
ILMN_3247998	STAP1	-1.28133	2.57E-07	2.57E-07	-6.36657	Down	signal transducing adaptor family member 1
ILMN_2414786	DIO1	-1.91483	2.65E-07	2.65E-07	-6.35543	Down	iodothyroninedeiodinase 1
ILMN_2135258	RAPGEF3	-1.16851	2.7E-07	2.7E-07	-6.34984	Down	Rap guanine nucleotide exchange factor 3
ILMN_1748970	PRR15L	-1.90253	2.79E-07	2.79E-07	-6.33903	Down	proline rich 15 like
ILMN_1661491	SH3GL2	-1.77461	2.82E-07	2.82E-07	-6.33536	Down	SH3 domain containing GRB2 like 2, endophilin A1
ILMN_1759910	SERPINA5	-2.47801	3.34E-07	3.34E-07	-6.27921	Down	serpin family A member 5
ILMN_1671260	WLS	-1.203	3.94E-07	3.94E-07	-6.22417	Down	wntlessWnt ligand secretion mediator
ILMN_1793182	SLC36A2	-2.48406	4.24E-07	4.24E-07	-6.20031	Down	solute carrier family 36 member 2
ILMN_1661994	ESRRG	-1.92177	4.44E-07	4.44E-07	-6.18528	Down	estrogen related receptor gamma
ILMN_2391264	DMKN	-1.65451	4.58E-07	4.58E-07	-6.17451	Down	dermokine
ILMN_1732000	LINC00982	-1.3081	5.09E-07	5.09E-07	-6.14002	Down	long intergenic non-protein coding RNA 982
ILMN_1706483	C1orf116	-1.78787	5.44E-07	5.44E-07	-6.11761	Down	chromosome 1 open reading frame 116
ILMN_1748827	TMEM238	-1.21043	5.69E-07	5.69E-07	-6.10309	Down	transmembrane protein 238
ILMN_1743065	HACD3	-1.36027	5.78E-07	5.78E-07	-6.09751	Down	3-hydroxyacyl-CoA dehydratase 3
ILMN_1694548	ANXA3	-1.94135	5.81E-07	5.81E-07	-6.09616	Down	annexin A3
ILMN_1751425	ERMP1	-1.39043	5.9E-07	5.9E-07	-6.09078	Down	endoplasmic reticulum metallopeptidase 1
ILMN_2286400	CAPS	-1.17672	5.95E-07	5.95E-07	-6.08803	Down	calcyphosine
ILMN_1740717	ADH1C	-2.11151	6.61E-07	6.61E-07	-6.05365	Down	alcohol dehydrogenase 1C (class I), gamma polypeptide
ILMN_1685540	SHROOM3	-1.83583	7.02E-07	7.02E-07	-6.03353	Down	shroom family member 3
ILMN_1688886	GPC5	-1.23071	7.39E-07	7.39E-07	-6.0167	Down	glypican 5
ILMN_1778319	DMKN	-1.64094	7.69E-07	7.69E-07	-6.00335	Down	dermokine
ILMN_2234697	BEX1	-1.82902	7.76E-07	7.76E-07	-6.00064	Down	brain expressed X-linked 1

ILMN_1740917	SCNN1B	-1.35446	8.14E-07	8.14E-07	-5.98453	Down	sodium channel epithelial 1 beta subunit
ILMN_1782389	LAD1	-2.98786	8.5E-07	8.5E-07	-5.97048	Down	ladinin 1
ILMN_1804593	HEPACAM2	-1.27205	9.18E-07	9.18E-07	-5.94501	Down	HEPACAM family member 2
ILMN_1778687	RHCG	-1.87723	9.19E-07	9.19E-07	-5.94485	Down	Rh family C glycoprotein
ILMN_1795166	PTH1R	-2.9444	9.46E-07	9.46E-07	-5.93521	Down	parathyroid hormone 1 receptor
ILMN_1801476	CDS1	-1.48053	1.04E-06	1.04E-06	-5.90246	Down	CDP-diacylglycerol synthase 1
ILMN_1687768	NCOA7	-1.53484	1.05E-06	1.05E-06	-5.90208	Down	nuclear receptor coactivator 7
ILMN_1729734	MFSD4A	-1.14461	1.1E-06	1.1E-06	-5.88572	Down	major facilitator superfamily domain containing 4A
ILMN_2099259	MST1L	-1.2963	1.16E-06	1.16E-06	-5.86659	Down	macrophage stimulating 1 like
ILMN_1813561	SCIN	-2.60012	1.19E-06	1.19E-06	-5.86031	Down	scinderin
ILMN_2400644	SRGAP3	-1.20792	1.2E-06	1.2E-06	-5.85562	Down	SLIT-ROBO Rho GTPase activating protein 3
ILMN_1736154	LZTS3	-1.16418	1.21E-06	1.21E-06	-5.85305	Down	leucine zipper tumor suppressor family member 3
ILMN_2285404	DMKN	-1.80713	1.23E-06	1.23E-06	-5.84728	Down	dermokine
ILMN_1726273	ATP6V1G3	-1.41384	1.24E-06	1.24E-06	-5.84673	Down	ATPase H+ transporting V1 subunit G3
ILMN_1662731	COL4A3	-1.36348	1.26E-06	1.26E-06	-5.84155	Down	collagen type IV alpha 3 chain
ILMN_1790160	KIT	-1.43029	1.27E-06	1.27E-06	-5.83769	Down	KIT proto-oncogene receptor tyrosine kinase
ILMN_1772809	SLC4A1	-1.51728	1.31E-06	1.31E-06	-5.82676	Down	solute carrier family 4 member 1 (Diego blood group)
ILMN_1719906	HADH	-1.18826	1.33E-06	1.33E-06	-5.82295	Down	hydroxyacyl-CoA dehydrogenase
ILMN_1659991	SLC34A1	-2.05392	1.47E-06	1.47E-06	-5.78965	Down	solute carrier family 34 member 1
ILMN_2388263	HEPACAM2	-1.42307	1.57E-06	1.57E-06	-5.76816	Down	HEPACAM family member 2
ILMN_1767446	RNF150	-1.47325	1.57E-06	1.57E-06	-5.76733	Down	ring finger protein 150
ILMN_3241087	INPP5J	-1.29256	1.62E-06	1.62E-06	-5.75709	Down	inositol polyphosphate-5-phosphatase J
ILMN_1757660	CAPS	-1.36331	1.63E-06	1.63E-06	-5.75574	Down	calcyphosine
ILMN_1677962	GPHN	-1.12197	1.65E-06	1.65E-06	-5.75253	Down	gephyrin
ILMN_1713807	MAN1C1	-1.22431	1.72E-06	1.72E-06	-5.73771	Down	mannosidase alpha class 1C member 1
ILMN_1750062	PPARGC1A	-2.04285	1.79E-06	1.79E-06	-5.72483	Down	PPARG coactivator 1 alpha
ILMN_2095597	CDH16	-2.20398	1.88E-06	1.88E-06	-5.70913	Down	cadherin 16
ILMN_1656369	TCIM	-2.21357	1.88E-06	1.88E-06	-5.70876	Down	transcriptional and immune response regulator
ILMN_1758816	UGT8	-1.13738	0.000002	0.000002	-5.68863	Down	UDP glycosyltransferase 8
ILMN_2283325	WLS	-1.29225	2.03E-06	2.03E-06	-5.68418	Down	wntlessWnt ligand secretion mediator
ILMN_2327860	MAL	-4.24043	2.08E-06	2.08E-06	-5.67611	Down	mal, T cell differentiation protein
ILMN_1755741	DACH1	-1.27402	2.1E-06	2.1E-06	-5.67157	Down	dachshund family transcription factor 1
ILMN_1681601	SUCNR1	-1.11912	2.11E-06	2.11E-06	-5.67021	Down	succinate receptor 1
ILMN_1690040	TM7SF2	-1.57569	2.17E-06	2.17E-06	-5.66219	Down	transmembrane 7 superfamily member 2
ILMN_1748538	ALDH1A2	-1.99755	2.2E-06	2.2E-06	-5.65684	Down	aldehyde dehydrogenase 1 family member A2
ILMN_3245062	SHROOM3	-1.30962	2.25E-06	2.25E-06	-5.64887	Down	shroom family member 3
ILMN_2082865	PLLP	-1.87389	2.42E-06	2.42E-06	-5.62584	Down	plasmolipin
ILMN_1786381	AQP6	-1.55138	2.44E-06	2.44E-06	-5.62305	Down	aquaporin 6
ILMN_1736184	GSTM3	-2.06909	2.47E-06	2.47E-06	-5.61914	Down	glutathione S-transferase mu 3
ILMN_1794875	GPAT3	-1.93	2.53E-06	2.53E-06	-5.61036	Down	glycerol-3-phosphate acyltransferase 3
ILMN_1799889	ATP6V0D2	-1.55067	2.55E-06	2.55E-06	-5.60828	Down	ATPase H+ transporting V0 subunit d2
ILMN_1670779	DPEP1	-1.91652	2.59E-06	2.59E-06	-5.60284	Down	dipeptidase 1
ILMN_1681437	DCXR	-1.48894	2.66E-06	2.66E-06	-5.59485	Down	dicarbonyl and L-xyluloseductase

ILMN_1746801	CGN	-2.20998	2.67E-06	2.67E-06	-5.59343	Down	cingulin
ILMN_1716815	CEACAM1	-1.77661	2.88E-06	2.88E-06	-5.56801	Down	carcinoembryonic antigen related cell adhesion molecule 1
ILMN_1747716	ALDOB	-3.89192	2.97E-06	2.97E-06	-5.55791	Down	aldolase, fructose-bisphosphate B
ILMN_1807894	SLC7A8	-1.5444	3.23E-06	3.23E-06	-5.53047	Down	solute carrier family 7 member 8
ILMN_2363744	PACRG	-1.24376	3.53E-06	3.53E-06	-5.50092	Down	parkin coregulated
ILMN_1740426	RASD1	-2.62182	3.59E-06	3.59E-06	-5.49557	Down	ras related dexamethasone induced 1
ILMN_2401779	FAM102A	-1.27491	3.61E-06	3.61E-06	-5.49375	Down	family with sequence similarity 102 member A
ILMN_2237428	SCD5	-1.4676	3.68E-06	3.68E-06	-5.48767	Down	stearoyl-CoA desaturase 5
ILMN_1677314	MUC1	-1.28986	3.73E-06	3.73E-06	-5.48325	Down	mucin 1, cell surface associated
ILMN_2166457	HPGD	-1.11002	3.75E-06	3.75E-06	-5.48131	Down	15-hydroxyprostaglandin dehydrogenase
ILMN_1787673	PLLP	-1.66935	3.84E-06	3.84E-06	-5.47338	Down	plasmolipin
ILMN_1719616	DNASE1	-1.92403	3.92E-06	3.92E-06	-5.46633	Down	deoxyribonuclease 1
ILMN_1707077	SORT1	-1.26959	3.95E-06	3.95E-06	-5.46401	Down	sortilin 1
ILMN_1788416	ABHD17C	-1.17626	4.24E-06	4.24E-06	-5.44057	Down	abhydrolase domain containing 17C
ILMN_1761946	PROM2	-2.16356	4.26E-06	4.26E-06	-5.43917	Down	prominin 2
ILMN_3307693	WFDC2	-2.71753	4.4E-06	4.4E-06	-5.4283	Down	WAP four-disulfide core domain 2
ILMN_1674908	HOXB5	-1.37565	4.64E-06	4.64E-06	-5.41089	Down	homeobox B5
ILMN_1711015	CRYAA	-2.30411	4.91E-06	4.91E-06	-5.39242	Down	crystallin alpha A
ILMN_1712112	RCAN1	-2.05079	5.05E-06	5.05E-06	-5.38333	Down	regulator of calcineurin 1
ILMN_2113490	NTN4	-1.87775	5.11E-06	5.11E-06	-5.37917	Down	netrin 4
ILMN_1815719	PLCG2	-1.42874	5.15E-06	5.15E-06	-5.37695	Down	phospholipase C gamma 2
ILMN_1738921	ACAA1	-1.16704	5.45E-06	5.45E-06	-5.35784	Down	acetyl-CoA acyltransferase 1
ILMN_1653278	MUC20	-2.14802	5.5E-06	5.5E-06	-5.35527	Down	mucin 20, cell surface associated
ILMN_2094856	RANBP3L	-1.2556	5.95E-06	5.95E-06	-5.32917	Down	RAN binding protein 3 like
ILMN_1743357	XPNPEP2	-1.84548	6.09E-06	6.09E-06	-5.32123	Down	X-prolylaminopeptidase 2
ILMN_2367239	RCAN1	-1.61029	6.67E-06	6.67E-06	-5.29165	Down	regulator of calcineurin 1
ILMN_2354478	CYFIP2	-1.44283	7.05E-06	7.05E-06	-5.27323	Down	cytoplasmic FMR1 interacting protein 2
ILMN_1776519	RAP1GAP	-2.35951	7.13E-06	7.13E-06	-5.26945	Down	RAP1 GTPase activating protein
ILMN_2361603	NDRG2	-1.40641	7.79E-06	7.79E-06	-5.24024	Down	NDRG family member 2
ILMN_2052871	TMEM116	-1.1147	0.000008	0.000008	-5.23127	Down	transmembrane protein 116
ILMN_2371724	CEACAM1	-1.35971	8.09E-06	8.09E-06	-5.22778	Down	carcinoembryonic antigen related cell adhesion molecule 1
ILMN_2184612	C3orf52	-1.15775	8.57E-06	8.57E-06	-5.20878	Down	chromosome 3 open reading frame 52
ILMN_1746618	PAQR7	-1.20057	8.87E-06	8.87E-06	-5.19736	Down	progesterone and adipoQ receptor family member 7
ILMN_1675656	PPFIBP2	-1.30768	9.35E-06	9.35E-06	-5.17977	Down	PPFIA binding protein 2
ILMN_1786197	NR2F1	-1.42838	9.43E-06	9.43E-06	-5.17703	Down	nuclear receptor subfamily 2 group F member 1
ILMN_2096985	ALDH6A1	-1.85409	1.03E-05	1.03E-05	-5.14735	Down	aldehyde dehydrogenase 6 family member A1
ILMN_2181892	BEX2	-1.66026	1.06E-05	1.06E-05	-5.13736	Down	brain expressed X-linked 2
ILMN_1777797	AFM	-1.89377	1.09E-05	1.09E-05	-5.12955	Down	afamin
ILMN_1718565	CDKN1C	-1.14458	1.09E-05	1.09E-05	-5.12838	Down	cyclin dependent kinase inhibitor 1C
ILMN_2048607	ANKRD9	-1.13598	0.000011	0.000011	-5.12755	Down	ankyrin repeat domain 9
ILMN_1783756	SLC22A8	-1.47431	1.11E-05	1.11E-05	-5.12466	Down	solute carrier family 22 member 8
ILMN_1666967	MPC1	-1.32106	1.16E-05	1.16E-05	-5.10841	Down	mitochondrial pyruvate carrier 1
ILMN_1779616	SUCLG1	-1.14001	1.17E-05	1.17E-05	-5.10668	Down	succinate-CoA ligase alpha subunit

ILMN_1784287	TGFB3	-1.23448	1.23E-05	1.23E-05	-5.09024	Down	transforming growth factor beta receptor 3
ILMN_2188862	GDF15	-1.95276	1.26E-05	1.26E-05	-5.08068	Down	growth differentiation factor 15
ILMN_1809291	TSPAN7	-1.54927	1.35E-05	1.35E-05	-5.05758	Down	tetraspanin 7
ILMN_1733627	NEDD4L	-1.13671	1.48E-05	1.48E-05	-5.02709	Down	neural precursor cell expressed, developmentally down-regulated 4 like, E3 ubiquitin protein ligase
ILMN_1912287	SUCNR1	-1.49518	1.49E-05	1.49E-05	-5.02537	Down	succinate receptor 1
ILMN_3246401	AIF1L	-2.44496	1.54E-05	1.54E-05	-5.01393	Down	allograft inflammatory factor 1 like
ILMN_2391419	SYNE2	-1.16851	1.57E-05	1.57E-05	-5.00756	Down	spectrin repeat containing nuclear envelope protein 2
ILMN_1785284	ALDH6A1	-2.00498	1.61E-05	1.61E-05	-5.00104	Down	aldehyde dehydrogenase 6 family member A1
ILMN_1770641	KLHL3	-1.2408	1.67E-05	1.67E-05	-4.9889	Down	kelch like family member 3
ILMN_1761260	COBLL1	-1.48282	0.000017	0.000017	-4.9812	Down	cordon-bleu WH2 repeat protein like 1
ILMN_1812031	PALM	-1.27171	1.78E-05	1.78E-05	-4.96598	Down	paralectin
ILMN_2143685	CLDN7	-1.96341	1.81E-05	1.81E-05	-4.96046	Down	claudin 7
ILMN_1778964	CLIC5	-1.4425	1.82E-05	1.82E-05	-4.96023	Down	chloride intracellular channel 5
ILMN_1677384	PTGER3	-1.74448	1.84E-05	1.84E-05	-4.95593	Down	prostaglandin E receptor 3
ILMN_1705627	USP2	-1.13564	1.98E-05	1.98E-05	-4.93171	Down	ubiquitin specific peptidase 2
ILMN_1743445	FAM107A	-2.01235	2.09E-05	2.09E-05	-4.91327	Down	family with sequence similarity 107 member A
ILMN_1705172	SLC26A7	-1.26899	2.09E-05	2.09E-05	-4.91318	Down	solute carrier family 26 member 7
ILMN_2376847	PDE1A	-1.41652	2.15E-05	2.15E-05	-4.90428	Down	phosphodiesterase 1A
ILMN_1778924	PDE1A	-1.54941	2.22E-05	2.22E-05	-4.89333	Down	phosphodiesterase 1A
ILMN_2390853	CTSH	-1.11373	2.29E-05	2.29E-05	-4.88307	Down	cathepsin H
ILMN_2415421	SLC30A2	-1.50808	2.32E-05	2.32E-05	-4.87902	Down	solute carrier family 30 member 2
ILMN_1714384	PCCA	-1.27333	2.34E-05	2.34E-05	-4.87603	Down	propionyl-CoA carboxylase subunit alpha
ILMN_1656560	PARM1	-1.31002	2.42E-05	2.42E-05	-4.86541	Down	prostate androgen-regulated mucin-like protein 1
ILMN_3289297	TACC1	-1.15606	2.59E-05	2.59E-05	-4.84244	Down	transforming acidic coiled-coil containing protein 1
ILMN_1730995	AFAP1L2	-1.11282	2.81E-05	2.81E-05	-4.81496	Down	actin filament associated protein 1 like 2
ILMN_2223941	FBLN5	-1.52398	2.87E-05	2.87E-05	-4.80774	Down	fibulin 5
ILMN_1664176	FBLN5	-1.29775	2.96E-05	2.96E-05	-4.79832	Down	fibulin 5
ILMN_1813270	ELF5	-2.07101	3.01E-05	3.01E-05	-4.79272	Down	E74 like ETS transcription factor 5
ILMN_1749868	FAM171A1	-1.24585	3.06E-05	3.06E-05	-4.78659	Down	family with sequence similarity 171 member A1
ILMN_3243185	RERGL	-1.25613	3.21E-05	3.21E-05	-4.77075	Down	RERG like
ILMN_1677920	LTF	-1.41147	3.26E-05	3.26E-05	-4.76583	Down	lactotransferrin
ILMN_1695157	CA4	-1.9515	3.26E-05	3.26E-05	-4.76536	Down	carbonic anhydrase 4
ILMN_1775163	PDE1A	-1.35698	3.58E-05	3.58E-05	-4.73414	Down	phosphodiesterase 1A
ILMN_1692517	SORD	-1.32566	3.65E-05	3.65E-05	-4.72848	Down	sorbitol dehydrogenase
ILMN_1664464	PTGDS	-1.875	3.69E-05	3.69E-05	-4.72433	Down	prostaglandin D2 synthase
ILMN_1709590	PGM5	-1.13293	3.73E-05	3.73E-05	-4.72043	Down	phosphoglucomutase 5
ILMN_1771120	TMEM45B	-1.17039	3.82E-05	3.82E-05	-4.71272	Down	transmembrane protein 45B
ILMN_3241729	EMX2OS	-1.44004	3.84E-05	3.84E-05	-4.71152	Down	EMX2 opposite strand/antisense RNA
ILMN_1660000	SNRPN	-1.40601	3.86E-05	3.86E-05	-4.70935	Down	small nuclear ribonucleoprotein polypeptide N
ILMN_1665331	AMT	-1.19917	3.88E-05	3.88E-05	-4.70787	Down	aminomethyltransferase
ILMN_2351638	BEX4	-1.22376	3.95E-05	3.95E-05	-4.70201	Down	brain expressed X-linked 4
ILMN_1715324	HSD17B8	-1.23134	0.000041	0.000041	-4.7089	Down	hydroxysteroid 17-beta dehydrogenase 8

ILMN_1763196	WDR72	-2.08191	4.27E-05	4.27E-05	-4.67561	Down	WD repeat domain 72
ILMN_1683883	ACY1	-1.86309	4.28E-05	4.28E-05	-4.67499	Down	aminoacylase 1
ILMN_1683923	MT1H	-1.18871	4.44E-05	4.44E-05	-4.66234	Down	metallothionein 1H
ILMN_1831106	LINC02381	-1.3621	4.48E-05	4.48E-05	-4.65933	Down	long intergenic non-protein coding RNA 2381
ILMN_1757467	H1F0	-1.32614	4.53E-05	4.53E-05	-4.6558	Down	H1 histone family member 0
ILMN_1781388	PGM5	-1.1462	0.000046	0.000046	-4.65109	Down	phosphoglucosylmutase 5
ILMN_1712419	DCDC2	-1.4737	0.000046	0.000046	-4.65093	Down	doublecortin domain containing 2
ILMN_1714446	PLG	-1.76826	4.88E-05	4.88E-05	-4.63097	Down	plasminogen
ILMN_1656501	DUSP5	-1.32354	4.96E-05	4.96E-05	-4.62541	Down	dual specificity phosphatase 5
ILMN_2380938	SYT7	-1.43609	5.43E-05	5.43E-05	-4.59515	Down	synaptotagmin 7
ILMN_1662214	PAH	-2.12338	5.47E-05	5.47E-05	-4.59311	Down	phenylalanine hydroxylase
ILMN_2120695	TSPAN7	-1.60273	5.73E-05	5.73E-05	-4.57704	Down	tetraspanin 7
ILMN_2121408	HBEGF	-1.31614	6.48E-05	6.48E-05	-4.53604	Down	heparin binding EGF like growth factor
ILMN_1770653	MAL2	-1.96134	0.000065	0.000065	-4.53493	Down	mal, T cell differentiation protein 2 (gene/pseudogene)
ILMN_1690733	EGF	-1.25729	6.92E-05	6.92E-05	-4.51394	Down	epidermal growth factor
ILMN_1786720	PROM1	-2.90137	7.36E-05	7.36E-05	-4.49332	Down	prominin 1
ILMN_3239925	PP7080	-1.65294	7.97E-05	7.97E-05	-4.46639	Down	uncharacterized LOC25845
ILMN_1685917	EMCN	-1.33929	8.18E-05	8.18E-05	-4.45772	Down	endomucin
ILMN_1656537	SNRPN	-1.26872	8.35E-05	8.35E-05	-4.45058	Down	small nuclear ribonucleoprotein polypeptide N
ILMN_1728799	FBP1	-1.96508	8.43E-05	8.43E-05	-4.44725	Down	fructose-bisphosphatase 1
ILMN_1725193	IGFBP2	-1.51036	8.62E-05	8.62E-05	-4.43992	Down	insulin like growth factor binding protein 2
ILMN_1756501	ST6GAL1	-1.51539	0.000087	0.000087	-4.43667	Down	ST6 beta-galactoside alpha-2,6-sialyltransferase 1
ILMN_1776998	DNAJA4	-1.33964	9.34E-05	9.34E-05	-4.41281	Down	DnaJ heat shock protein family (Hsp40) member A4
ILMN_2395451	ASS1	-1.76334	9.87E-05	9.87E-05	-4.39413	Down	argininosuccinate synthase 1
ILMN_1681670	SLC25A4	-1.2506	0.000102	0.000102	-4.38211	Down	solute carrier family 25 member 4
ILMN_1800898	ARG2	-1.97678	0.000107	0.000107	-4.36751	Down	arginase 2
ILMN_1746158	HOXD11	-1.18553	0.000108	0.000108	-4.36318	Down	homeobox D11
ILMN_1676822	C2orf40	-1.36672	0.000109	0.000109	-4.36049	Down	chromosome 2 open reading frame 40
ILMN_1657746	BPHL	-1.17415	0.000111	0.000111	-4.35438	Down	biphenyl hydrolase like
ILMN_1755582	PCSK1N	-1.82614	0.000112	0.000112	-4.35179	Down	proproteinconvertasubtilisin/kexin type 1 inhibitor
ILMN_2218104	PAH	-1.27756	0.000113	0.000113	-4.34889	Down	phenylalanine hydroxylase
ILMN_1694840	MATN2	-1.2143	0.000123	0.000123	-4.32081	Down	matrilin 2
ILMN_1704537	PHGDH	-1.4879	0.000123	0.000123	-4.31895	Down	phosphoglycerate dehydrogenase
ILMN_2211780	SLC25A4	-1.27515	0.000135	0.000135	-4.28753	Down	solute carrier family 25 member 4
ILMN_1787266	SPINK1	-2.84593	0.000139	0.000139	-4.27795	Down	serine peptidase inhibitor, Kazal type 1
ILMN_1668194	LMTK3	-1.20788	0.000145	0.000145	-4.26418	Down	lemur tyrosine kinase 3
ILMN_3275388	ASS1	-1.57049	0.000146	0.000146	-4.2619	Down	argininosuccinate synthase 1
ILMN_1804798	BEX4	-1.12065	0.000149	0.000149	-4.25467	Down	brain expressed X-linked 4
ILMN_1770085	BTG2	-1.47741	0.000151	0.000151	-4.2496	Down	BTG anti-proliferation factor 2
ILMN_1695423	CD9	-1.13453	0.000152	0.000152	-4.2473	Down	CD9 molecule
ILMN_2413816	GRB14	-1.35508	0.000157	0.000157	-4.23614	Down	growth factor receptor bound protein 14
ILMN_2179083	LOXL4	-1.31935	0.000158	0.000158	-4.23447	Down	lysyl oxidase like 4
ILMN_1715401	MT1G	-3.08478	0.000164	0.000164	-4.22154	Down	metallothionein 1G

ILMN_1693341	SNURF	-1.16368	0.000165	0.000165	-4.21988	Down	SNRPN upstream reading frame
ILMN_2124802	MT1H	-2.90933	0.000165	0.000165	-4.219	Down	metallothionein 1H
ILMN_1708778	ASS1	-1.93446	0.000169	0.000169	-4.21129	Down	argininosuccinate synthase 1
ILMN_1766083	SLC22A12	-1.86737	0.000176	0.000176	-4.19752	Down	solute carrier family 22 member 12
ILMN_1723042	CLDN3	-1.38753	0.000196	0.000196	-4.16005	Down	claudin 3
ILMN_1699887	ST14	-1.16357	0.000204	0.000204	-4.14674	Down	suppression of tumorigenicity 14
ILMN_1738401	FOXC1	-1.11773	0.000205	0.000205	-4.14565	Down	forkhead box C1
ILMN_2043079	ILDR1	-1.38035	0.000206	0.000206	-4.14407	Down	immunoglobulin like domain containing receptor 1
ILMN_1686573	DEFB1	-2.72304	0.000214	0.000214	-4.13036	Down	defensin beta 1
ILMN_1689200	DHDH	-1.57393	0.000215	0.000215	-4.12885	Down	dihydrodiol dehydrogenase
ILMN_1781374	TUFT1	-1.30415	0.000219	0.000219	-4.12279	Down	tuftelin 1
ILMN_1764266	CKMT2	-1.73274	0.000227	0.000227	-4.11123	Down	creatine kinase, mitochondrial 2
ILMN_1703123	CSRNP1	-1.17081	0.000252	0.000252	-4.07489	Down	cysteine and serine rich nuclear protein 1
ILMN_3241522	ASS1	-1.41625	0.000253	0.000253	-4.07313	Down	argininosuccinate synthase 1
ILMN_1676014	DHRS4L1	-1.22166	0.000257	0.000257	-4.06747	Down	dehydrogenase/reductase 4 like 1
ILMN_2371911	MUC1	-1.87082	0.000259	0.000259	-4.06579	Down	mucin 1, cell surface associated
ILMN_2353117	SLC22A7	-1.39089	0.000267	0.000267	-4.05452	Down	solute carrier family 22 member 7
ILMN_3209070	ASS1	-1.30238	0.000268	0.000268	-4.05325	Down	argininosuccinate synthase 1
ILMN_1745688	HPD	-1.65253	0.000293	0.000293	-4.02279	Down	4-hydroxyphenylpyruvate dioxygenase
ILMN_1815203	HMGCS2	-2.42292	0.000307	0.000307	-4.00674	Down	3-hydroxy-3-methylglutaryl-CoA synthase 2
ILMN_2374865	ATF3	-1.69066	0.000319	0.000319	-3.99299	Down	activating transcription factor 3
ILMN_1836218	PP7080	-1.50866	0.000364	0.000364	-3.94711	Down	uncharacterized LOC25845
ILMN_1735156	SLC4A11	-1.38614	0.000413	0.000413	-3.90348	Down	solute carrier family 4 member 11
ILMN_1796925	CXADR	-1.12927	0.000417	0.000417	-3.90018	Down	CXADR, Ig-like cell adhesion molecule
ILMN_1770940	CDH1	-1.78858	0.000424	0.000424	-3.89452	Down	cadherin 1
ILMN_1765966	CHGB	-1.30484	0.000434	0.000434	-3.88659	Down	chromogranin B
ILMN_1687848	C7	-2.18011	0.000439	0.000439	-3.88202	Down	complement C7
ILMN_2178492	CYP4F2	-1.11804	0.000467	0.000467	-3.86075	Down	cytochrome P450 family 4 subfamily F member 2
ILMN_1756439	SCRN1	-1.15754	0.000475	0.000475	-3.85512	Down	secernin 1
ILMN_2337923	TPD52L1	-1.49215	0.000482	0.000482	-3.84953	Down	TPD52 like 1
ILMN_2225537	PTGR1	-1.32257	0.000496	0.000496	-3.84006	Down	prostaglandin reductase 1
ILMN_1704531	PTGR1	-1.28676	0.000502	0.000502	-3.83543	Down	prostaglandin reductase 1
ILMN_1739813	HYAL1	-1.45677	0.000529	0.000529	-3.81735	Down	hyaluronidase 1
ILMN_3238534	AC129507.4	-1.41833	0.00053	0.00053	-3.81662	Down	novel transcript, antisense to RPH3AL
ILMN_1744949	RHOBTB3	-1.2253	0.000542	0.000542	-3.80835	Down	Rho related BTB domain containing 3
ILMN_1682717	IER3	-1.19689	0.0006	0.0006	-3.77317	Down	immediate early response 3
ILMN_2408748	SLC22A12	-2.56984	0.000625	0.000625	-3.75854	Down	solute carrier family 22 member 12
ILMN_1683263	TSPAN8	-2.06895	0.000639	0.000639	-3.75066	Down	tetraspanin 8
ILMN_1663569	FTCD	-1.91884	0.000669	0.000669	-3.73445	Down	formimidoyltransferasecyclodeaminase
ILMN_1658519	SLC13A3	-1.24431	0.000719	0.000719	-3.70906	Down	solute carrier family 13 member 3
ILMN_2079890	G6PC	-1.25758	0.000727	0.000727	-3.70523	Down	glucose-6-phosphatase catalytic subunit
ILMN_1692223	LCN2	-2.07725	0.00081	0.00081	-3.66682	Down	lipocalin 2
ILMN_1730229	CGNL1	-1.27356	0.000837	0.000837	-3.65502	Down	cingulin like 1

ILMN_1677200	CYFIP2	-1.13802	0.000867	0.000867	-3.64255	Down	cytoplasmic FMR1 interacting protein 2
ILMN_1714383	TPD52L1	-1.44462	0.000904	0.000904	-3.62776	Down	TPD52 like 1
ILMN_1814719	RBP4	-1.22835	0.00094	0.00094	-3.61391	Down	retinol binding protein 4
ILMN_1756992	MUC1	-1.69362	0.000962	0.000962	-3.60554	Down	mucin 1, cell surface associated
ILMN_1806667	FRAS1	-1.35998	0.000982	0.000982	-3.59814	Down	Fraser extracellular matrix complex subunit 1
ILMN_2187746	EMX2	-1.71942	0.001064	0.001064	-3.56961	Down	empty spiracles homeobox 2
ILMN_1721818	CLDN10	-1.73056	0.001067	0.001067	-3.56862	Down	claudin 10
ILMN_1664861	ID1	-1.21892	0.001077	0.001077	-3.56513	Down	inhibitor of DNA binding 1, HLH protein
ILMN_2405391	SLC22A6	-1.30215	0.001098	0.001098	-3.55821	Down	solute carrier family 22 member 6
ILMN_2390017	SLC22A6	-1.41605	0.001123	0.001123	-3.55009	Down	solute carrier family 22 member 6
ILMN_1738414	G6PC	-1.11236	0.001148	0.001148	-3.54208	Down	glucose-6-phosphatase catalytic subunit
ILMN_1806754	GLDC	-1.48283	0.001159	0.001159	-3.53868	Down	glycine decarboxylase
ILMN_1805665	FLRT3	-1.79836	0.001173	0.001173	-3.53436	Down	fibronectinleucine rich transmembrane protein 3
ILMN_1675756	KCNJ15	-1.25965	0.001199	0.001199	-3.52669	Down	potassium voltage-gated channel subfamily J member 15
ILMN_1774375	SMIM24	-2.32682	0.001221	0.001221	-3.51995	Down	small integral membrane protein 24
ILMN_1739050	PIPOX	-1.17186	0.001325	0.001325	-3.49053	Down	pipecolic acid and sarcosine oxidase
ILMN_1671478	CKB	-1.49736	0.001361	0.001361	-3.4808	Down	creatine kinase B
ILMN_1748983	RTN4	-1.33032	0.001374	0.001374	-3.47752	Down	reticulon 4
ILMN_1680874	TUBB2B	-1.81269	0.001385	0.001385	-3.47451	Down	tubulin beta 2B class IIb
ILMN_1682763	ALB	-1.56887	0.001404	0.001404	-3.46966	Down	albumin
ILMN_1685703	ACOX2	-1.13309	0.001498	0.001498	-3.44603	Down	acyl-CoA oxidase 2
ILMN_2167259	FAM151A	-1.60866	0.00152	0.00152	-3.44086	Down	family with sequence similarity 151 member A
ILMN_1682273	SHISA3	-1.11692	0.001846	0.001846	-3.36987	Down	shisa family member 3
ILMN_1796461	PRSS8	-1.68831	0.001891	0.001891	-3.36105	Down	serine protease 8
ILMN_1776363	ANK2	-1.13471	0.001921	0.001921	-3.35532	Down	ankyrin 2
ILMN_1784040	NAPSA	-1.34749	0.002031	0.002031	-3.33491	Down	napsin A aspartic peptidase
ILMN_1777591	HOGA1	-1.26181	0.002079	0.002079	-3.32633	Down	4-hydroxy-2-oxoglutarate aldolase 1
ILMN_1782939	ALB	-1.92681	0.002141	0.002141	-3.31549	Down	albumin
ILMN_1765574	TFAP2A	-1.34115	0.00227	0.00227	-3.29383	Down	transcription factor AP-2 alpha
ILMN_2167252	FAM151A	-1.13242	0.002377	0.002377	-3.27689	Down	family with sequence similarity 151 member A
ILMN_1696099	ALDH4A1	-1.13043	0.002385	0.002385	-3.27556	Down	aldehyde dehydrogenase 4 family member A1
ILMN_2116877	OLFM4	-1.33642	0.002461	0.002461	-3.2639	Down	olfactomedin 4
ILMN_2199439	CA2	-1.15415	0.002466	0.002466	-3.26312	Down	carbonic anhydrase 2
ILMN_1669046	FOXQ1	-1.27849	0.002478	0.002478	-3.26142	Down	forkhead box Q1
ILMN_1662795	CA2	-1.13535	0.00277	0.00277	-3.21999	Down	carbonic anhydrase 2
ILMN_1681103	AQP1	-1.23027	0.00279	0.00279	-3.21723	Down	aquaporin 1 (Colton blood group)
ILMN_3307841	AGR2	-1.2673	0.002917	0.002917	-3.20065	Down	anterior gradient 2, protein disulphide isomerase family member
ILMN_1766914	MFAP4	-1.24939	0.003075	0.003075	-3.18085	Down	microfibril associated protein 4
ILMN_1685387	PIGR	-2.10586	0.003379	0.003379	-3.14554	Down	polymeric immunoglobulin receptor
ILMN_2053415	LDLR	-1.39265	0.00355	0.00355	-3.12684	Down	low density lipoprotein receptor
ILMN_1780831	SLC6A12	-1.30463	0.003909	0.003909	-3.09045	Down	solute carrier family 6 member 12
ILMN_1657435	MT1M	-1.2828	0.004135	0.004135	-3.06909	Down	metallothionein 1M
ILMN_1812070	ABCB1	-1.18055	0.004608	0.004608	-3.0277	Down	ATP binding cassette subfamily B member 1

ILMN_1714335	RDH10	-1.1366	0.004641	0.004641	-3.02503	Down	retinol dehydrogenase 10
ILMN_1700268	QPRT	-1.21328	0.004814	0.004814	-3.01096	Down	quinolinatephosphoribosyltransferase
ILMN_1686259	PRODH2	-1.63319	0.005136	0.005136	-2.9861	Down	proline dehydrogenase 2
ILMN_1709237	EPHX2	-1.25507	0.005535	0.005535	-2.95718	Down	epoxide hydrolase 2
ILMN_1656368	ALDH4A1	-1.30428	0.005894	0.005894	-2.93283	Down	aldehyde dehydrogenase 4 family member A1
ILMN_2173611	MT1E	-1.80554	0.008045	0.008045	-2.81086	Down	metallothionein 1E
ILMN_1700831	SLC27A2	-1.47991	0.0082	0.0082	-2.80332	Down	solute carrier family 27 member 2
ILMN_1707169	AGMAT	-1.29745	0.008378	0.008378	-2.79478	Down	agmatinase
ILMN_2145396	AKR7A3	-1.19095	0.010499	0.010499	-2.70446	Down	aldo-ketoreductase family 7 member A3
ILMN_1685403	MMP7	-1.85489	0.012538	0.012538	-2.63243	Down	matrix metalloproteinase 7
ILMN_2192072	MMP7	-1.90906	0.012614	0.012614	-2.62996	Down	matrix metalloproteinase 7
ILMN_1731948	PCK1	-1.47192	0.015572	0.015572	-2.54308	Down	phosphoenolpyruvatecarboxykinase 1
ILMN_1738742	PLAT	-1.11487	0.015949	0.015949	-2.53314	Down	plasminogen activator, tissue type
ILMN_1802131	SLC13A1	-1.37298	0.017687	0.017687	-2.48985	Down	solute carrier family 13 member 1
ILMN_2399463	VAV3	-1.48039	0.0181	0.0181	-2.48014	Down	vav guanine nucleotide exchange factor 3
ILMN_2052373	RAB17	-1.31335	0.019902	0.019902	-2.44002	Down	RAB17, member RAS oncogene family
ILMN_1767113	AOX1	-1.14694	0.019979	0.019979	-2.43837	Down	aldehyde oxidase 1
ILMN_1735816	CYP4A11	-1.98039	0.020866	0.020866	-2.41989	Down	cytochrome P450 family 4 subfamily A member 11
ILMN_1718766	MT1F	-1.30358	0.028287	0.028287	-2.28826	Down	metallothionein 1F
ILMN_1767523	IL17RB	-1.23763	0.029927	0.029927	-2.26342	Down	interleukin 17 receptor B
ILMN_1729180	GATM	-1.32587	0.042896	0.042896	-2.10132	Down	glycine amidinotransferase
ILMN_2228463	DDC	-1.25	0.044558	0.044558	-2.0838	Down	dopa decarboxylase

Table 3 The enriched pathway terms of the up regulated differentially expressed genes

BIOCYC

Pathway ID	Pathway Name	P-value	FDR B&H	FDR B&Y	Bonferroni	Gene Count	Gene
547484	dTMP de novo biosynthesis (mitochondrial)	1.63E-03	7.99E-02	3.58E-01	7.99E-02	2	TYMS,SHMT2
782396	glycolysis	4.76E-03	1.17E-01	5.22E-01	2.33E-01	3	PFKP,ALDOC,E NO2
1108784	reactive oxygen species degradation	2.19E-02	2.62E-01	1.00E+00	1.00E+00	2	GPX8,SOD2
142445	acetyl-CoA biosynthesis from citrate	2.41E-02	2.62E-01	1.00E+00	1.00E+00	1	ACLY
1108783	purine deoxyribonucleosides degradation	4.65E-02	2.62E-01	1.00E+00	1.00E+00	1	ADA

142152	glycine/serine biosynthesis	4.65E-02	2.62E-01	1.00E+00	1.00E+00	1	SHMT2
142451	lactate fermentation (reoxidation of cytosolic NADH)	4.65E-02	2.62E-01	1.00E+00	1.00E+00	1	LDHA
545346	heme degradation	9.09E-02	2.62E-01	1.00E+00	1.00E+00	1	HMOX1
782399	UTP and CTP dephosphorylation II	9.09E-02	2.62E-01	1.00E+00	1.00E+00	1	ENTPD1
545277	dermatansulfate biosynthesis (late stages)	9.09E-02	2.62E-01	1.00E+00	1.00E+00	1	CHST15
Pathway Interaction Database							
138045	HIF-1-alpha transcription factor network	1.90E-11	1.88E-09	9.72E-09	1.88E-09	15	HK2,HMOX1,PLIN2,ADM,VEGFA,CP,SLC2A1,BHLHE41,ITGB2,BNIP3,CXCR4,CA9,EGLN3,LDHA,SERPINE1
137922	IL12-mediated signaling events	5.47E-04	2.71E-02	1.40E-01	5.42E-02	7	HLA-A,HLX,IL2RB,STAT1,CD3D,CD8A,GZMA
137956	HIF-2-alpha transcription factor network	1.11E-03	2.75E-02	1.42E-01	1.10E-01	5	VEGFA,POU5F1,SLC2A1,EGLN3,SERPINE1
169349	Validated transcriptional targets of AP1 family members Fra1 and Fra2	1.11E-03	2.75E-02	1.42E-01	1.10E-01	5	HMOX1,MMP9,COL1A2,CCND1,GJA1
137939	Direct p53 effectors	3.98E-03	6.84E-02	3.54E-01	3.94E-01	9	DDIT4,IGFBP3,VCAN,PRDM1,TAP1,CAV1,TGFA,SERPINE1,STEAP3
169353	Validated targets of C-MYC transcriptional repression	1.42E-02	9.36E-02	4.85E-01	1.00E+00	5	PDGFRB,CCL5,COL1A2,CCND1,LGALS1
137932	IL6-mediated signaling events	8.00E-02	3.30E-01	1.00E+00	1.00E+00	3	FGG,STAT1,TIMP1

138080	Aurora B signaling	2.34E-01	6.61E-01	1.00E+00	1.00E+00	2	VIM,NCAPG
137934	E2F transcription factor network	2.46E-01	6.78E-01	1.00E+00	1.00E+00	3	TYMS,CES4A,SERPINE1
138001	mTORsignaling pathway	4.23E-01	7.19E-01	1.00E+00	1.00E+00	2	DDIT4,BNIP3
REACTOME							
1270244	Extracellular matrix organization	1.70E-14	3.90E-12	2.78E-11	1.17E-11	34	FGG,MMP9,PLOD1,PLOD2,VCAM1,COL1A1,COL1A2,COL3A1,COL4A1,COL4A2,COL5A1,COL5A2,COL6A1,COL6A2,COL6A3,COL8A1,COL11A1,COL15A1,COL23A1,VCAN,SPARC,ITGA5,ITGB2,BMP1,P4HA2,PLOD3,LAMA4,COLGALT1,SERPINH1,TIMP1,P4HA1,P4HB,LOX,SERPINE1
1269310	Cytokine Signaling in Immune system	9.76E-11	1.12E-08	7.98E-08	6.73E-08	49	IL32,HLA-A,HLA-B,PDGFRB,HLA-DQA1,HLA-DQA2,HLA-DQB1,HLA-F,HLA-G,HLA-H,HMOX1,SAA1,FCGR1A,CCL5,FGG,MMP9,VCAM1,APBB1IP,VEGFA,COL1A2,VIM,VWF,BIRC3,IFI27,CSF1R,ISG15,TNFSF13B,XAF1,FSCN1,IL2RB,CXCL10,PSMB8,PSMB9,TNFRSF6B,IL20RB,GBP1,GBP2,CCND1,ISG20,ITGB2,STAT1,GBP5,BST2,OAS2,IL18BP,TIMP1,CD86,C

							D36,CD70
1269203	Innate Immune System	6.73E-06	2.32E-04	1.65E-03	4.64E-03	56	HLA-A,HLA-B,PDGFRB,ACLY,HLA-H,LY96,FABP5,TYROBP,SAA1,FCER1G,FCGR1A,FCGR2A,FGG,MMP9,ALDOC,LY86,HSPA6,APBB1IP,VWF,WAS,PRDX4,BIRC3,FCN3,IFI16,SLC2A5,TRIB3,ISG15,SLC15A4,RNAS ET2,IL2RB,CTSZ,PROS1,CYBB,PSMB8,PSMB9,SIRPA,ITGB2,BS T2,C1QA,C1QB,C1QC,C1R,PYGL,C1S,C2,C3,DOCK2,RAB31,OLR1,CD14,CD86,CD36,CD68,ADGRE5,TNFAIP6,NCKAP1L
1269171	Adaptive Immune System	2.34E-05	5.99E-04	4.26E-03	1.62E-02	39	HLA-A,HLA-B,PDGFRB,HLA-DQA1,HLA-DQA2,HLA-DQB1,HLA-F,HLA-G,HLA-H,LY96,TYROBP,FCGR1A,HECW2,VCAM1,WAS,TRIB3,TRIM9,FYB1,CYBB,PA G1,PSMB8,PSMB9,FBXO17,ITGB2,SIGLEC10,C3,TAP1,TAPBP,CANX,UBE2C,LAG3,BTN3A2,BTN3A1,CD3D,CD8A,CD14,CD86,CD36,CDC20
1269318	Signaling by Interleukins	1.40E-04	3.11E-03	2.21E-02	9.64E-02	27	IL32,PDGFRB,HMOX1,SAA1,CCL5,FGG,MMP9,VCAM1,APBB1

							P, VEGFA, COL1A2, VIM, VWF, CSF1R, FSCN1, IL2RB, CXCL10, PSMB8, PSMB9, IL20RB, CCND1, ITGB2, STAT1, IL18BP, TIMP1, CD86, CD36
1269340	Hemostasis	2.48E-04	4.96E-03	3.53E-02	1.71E-01	30	EHD2, SERPINE2, FCER1G, CD99, FGG, PLEK, SERPINF2, APBB1IP, VEGFA, VWF, ANGPT2, IL2RB, PROS1, SPARC, SIRPA, ITGA5, ITGB2, KCNMA1, RAC2, DOCK2, RARRS2, CALU, CAV1, OLR1, CD2, SLC16A3, TIMP1, CD36, SERPINE1, LHFPL2
1269192	Class I MHC mediated antigen processing & presentation	5.90E-04	1.02E-02	7.24E-02	4.07E-01	20	HLA-A, HLA-B, HLA-F, HLA-G, HLA-H, LY96, FCGR1A, HECW2, TRIM9, CYBB, PSMB8, PSMB9, FBXO17, TAP1, TAPBP, CANX, UBE2C, CD14, CD36, CDC20
1269957	Metabolism of carbohydrates	4.55E-03	5.92E-02	4.21E-01	1.00E+00	15	HK2, PFKFB4, PFKP, PHKA2, CHST15, ALDOC, SLC2A1, SLC2A5, PPP1R3C, VCAN, CSPG4, GAPDH, PYGL, ENO2, TPI1
1270303	Axon guidance	1.16E-02	1.15E-01	8.15E-01	1.00E+00	22	PDGFRB, TYROBP, SEMA6A, FGG, MMP9, APBB1IP, VEGFA, COL4A1, COL4A2, COL6A1, COL6A2, COL6A3, VWF, ABLIM3, IL2RB, PSMB8, PSMB9, ITGA5, NRP1, ST8SI

							A4,RAC2,DPYS L3
1269903	Transmembrane transport of small molecules	1.23E-01	4.39E-01	1.00E+0 0	1.00E+00	21	HK2,SLCO2B1,H MOX1,SLC15A3, CP,SLC1A3,AQP 9,SLC2A1,SLC2 A5,SLC6A3,SLC 15A4,ABCC3,SL C9A9,PSMB8,PS MB9,SLC29A4,A BCB6,RUNX1,S LC16A3,STEAP3 ,SLC39A14
Gen MAPP							
MAP00010	Glycolysis Gluconeogenesis	1.32E-03	2.13E-02	8.43E-02	3.84E-02	6	HK2,PFKP,ALD OC,LDHA,ENO2 ,TPI1
MAP00670	One carbon pool by folate	1.85E-03	2.13E-02	8.43E-02	5.37E-02	3	TYMS,SHMT2,N DUFA4L2
MAP00860	Porphyrin and chlorophyll metabolism	6.59E-02	2.12E-01	8.42E-01	1.00E+00	2	HMOX1,CP
MAP00330	Arginine and proline metabolism	2.25E-01	4.35E-01	1.00E+0 0	1.00E+00	2	P4HA1,P4HB
MAP00240	Pyrimidine metabolism	2.77E-01	4.47E-01	1.00E+0 0	1.00E+00	2	TYMS,TYMP
MAP00380	Tryptophan metabolism	2.95E-01	4.50E-01	1.00E+0 0	1.00E+00	2	IDO1,CYP2J2
MAP00562	Inositol phosphate metabolism	3.64E-01	4.76E-01	1.00E+0 0	1.00E+00	1	ITPKA
MAP00590	Prostaglandin and leukotriene metabolism	3.64E-01	4.76E-01	1.00E+0 0	1.00E+00	1	TBXAS1
MAP00640	Propanoate metabolism	3.79E-01	4.76E-01	1.00E+0 0	1.00E+00	1	LDHA
MAP00910	Nitrogen metabolism	3.94E-01	4.76E-01	1.00E+0 0	1.00E+00	1	CA9
MSigDB C2 BIOCARTA							
M5889	Ensemble of genes encoding extracellular matrix and extracellular matrix-	1.51E-16	1.72E-14	9.16E-14	1.72E-14	70	PGF,SERPINE2, SEMA5B,CXCL9 ,CTHRC1,FGF11 ,CCL5,SEMA6A,

	associated proteins						C1QTNF6,FGG, MMP9,SERPINF 2,PLOD1,PLOD2 ,COL1A1,VEGF A,COL1A2,COL 3A1,COL4A1,CO L4A2,COL5A1,C OL5A2,COL6A1, COL6A2,COL6A 3,COL8A1,COL1 1A1,SFRP4,COL 15A1,VWF,ANG PT2,ANXA4,CC L4L2,FCN3,COL 23A1,POSTN,IG FBP3,TNFSF13B ,VCAN,CSPG4,C TSZ,SPARC,INH BB,CXCL10,C1Q L1,BMP1,FNDC1 ,PXDN,C1QA,C1 QB,C1QC,EGLN 3,P4HA2,PLOD3, LAMA4,ESM1,S ERPINH1,LGAL S1,TGFA,TGFBI, TGM2,THBS2,T HBS4,FSTL1,TI MP1,P4HA1,LO X,ANGPTL4,SE RPINE1,TNFAIP 6
M5884	Ensemble of genes encoding core extracellular matrix including ECM glycoproteins, collagens and proteoglycans	1.17E-11	4.45E-10	2.37E-09	1.34E-09	29	CTHRC1,FGG,C OL1A1,COL1A2, COL3A1,COL4A 1,COL4A2,COL5 A1,COL5A2,CO L6A1,COL6A2,C OL6A3,COL8A1, COL11A1,COL1 5A1,VWF,COL2 3A1,POSTN,IGF BP3,VCAN,SPA RC,FNDC1,PXD N,LAMA4,ESM1 ,TGFB1,THBS2,T HBS4,TNFAIP6
M7146	Classical Complement Pathway	1.11E-08	3.16E-07	1.68E-06	1.27E-06	7	C1QA,C1QB,C1 QC,C1R,C1S,C2, C3
M5885	Ensemble of genes	3.97E-07	7.54E-06	4.01E-05	4.53E-05	41	PGF,SERPINE2,

	encoding ECM-associated proteins including ECM-affiliated proteins, ECM regulators and secreted factors						SEMA5B,CXCL9,FGF11,CCL5,SEMA6A,C1QTNF6,MMP9,SERPINF2,PLOD1,PLOD2,VEGFA,SFRP4,ANGPT2,ANXA4,CCL4L2,FCN3,TNFSF13B,CSPG4,CTSZ,INHBB,CXCL10,C1QL1,BMP1,C1QA,C1QB,C1QC,EGLN3,P4HA2,PLOD3,SERPINH1,LGALS1,TGFA,TGM2,FSTL1,TIMP1,P4HA1,LOX,ANGPTL4,SERPINE1
M3468	Genes encoding enzymes and their regulators involved in the remodeling of the extracellular matrix	1.63E-04	2.06E-03	1.10E-02	1.85E-02	16	SERPINE2,MMP9,SERPINF2,PLOD1,PLOD2,CTSZ,BMP1,EGLN3,P4HA2,PLOD3,SERPINH1,TGM2,TIMP1,P4HA1,LOX,SERPINE1
M3008	Genes encoding structural ECM glycoproteins	7.51E-04	7.78E-03	4.14E-02	8.56E-02	13	CTHRC1,FGG,VWF,POSTN,IGFBP3,SPARC,FND C1,PXDN,LAMAC1,TGFB1,THBS2,THBS4,TNFAIP6
M5880	Genes encoding proteins affiliated structurally or functionally to extracellular matrix proteins	2.40E-03	1.95E-02	1.04E-01	2.74E-01	11	SEMA5B,SEMA6A,C1QTNF6,ANXA4,FCN3,CSPG4,C1QL1,C1QA,C1QB,C1QC,LGALS1
M5883	Genes encoding secreted soluble factors	3.32E-02	1.40E-01	7.46E-01	1.00E+00	14	PGF,CXCL9,FGF11,CCL5,VEGFA,SFRP4,ANGPT2,CCL4L2,TNFSF13B,INHBB,CXCL10,TGFA,FSTL1,ANGPTL4
M3270	Integrin Signaling Pathway	4.39E-02	1.67E-01	8.87E-01	1.00E+00	5	WAS,ITGA5,ASAP1,CAV1,P4HB

M16801	Genes related to regulation of the actin cytoskeleton	1.99E-01	5.15E-01	1.00E+00	1.00E+00	2	ACTG2,FSCN1
Panther DB							
P00034	Integrin signalling pathway	7.64E-08	4.28E-06	1.97E-05	4.28E-06	18	COL1A1,COL1A2,COL3A1,COL4A1,COL4A2,COL5A1,COL5A2,COL6A1,COL6A2,COL6A3,COL8A1,COL11A1,COL15A1,ITGA5,ITGB2,RAC2,LAMA4,CAV1
P00050	Plasminogen activating cascade	5.61E-04	1.57E-02	7.25E-02	3.14E-02	4	FGG,MMP9,SERPINF2,SERPINE1
P00011	Blood coagulation	2.34E-03	4.36E-02	2.01E-01	1.31E-01	5	FGG,SERPINF2,VWF,PROS1,SERPINE1
P00031	Inflammation mediated by chemokine and cytokine signaling pathway	1.50E-02	2.10E-01	9.69E-01	8.41E-01	10	ACTG2,CCL5,COL6A1,COL6A2,COL6A3,VWF,PR3,CXCL10,CXCR4,RAC2
P00053	T cell activation	3.33E-02	3.70E-01	1.00E+00	1.00E+00	5	HLA-DQA1,HLA-DQA2,WAS,CD3D,CD86
P04393	Ras Pathway	2.15E-01	5.48E-01	1.00E+00	1.00E+00	3	MAP3K7CL,STAT1,RAC2
P00026	Heterotrimeric G-protein signaling pathway-Gi alpha and Gs alpha mediated pathway	2.79E-01	6.62E-01	1.00E+00	1.00E+00	5	PHKA2,RGS5,PYGL,RGS1,RGS10
P00057	Wntsignaling pathway	5.81E-01	8.07E-01	1.00E+00	1.00E+00	7	ACTG2,SFRP4,MAP3K7CL,CCND1,CDH2,CDH6,CDH11
P00045	Notch signaling pathway	5.86E-01	8.07E-01	1.00E+00	1.00E+00	1	HEY1
P00060	Ubiquitin proteasome pathway	6.58E-01	8.07E-01	1.00E+00	1.00E+00	1	UBE2C

Pathway Ontology							
PW:0000021	hypertension	5.07E-05	2.09E-03	1.02E-02	3.75E-03	3	HMOX1,SOD2,LOX
PW:0000498	reverse cholesterol transport	5.64E-05	2.09E-03	1.02E-02	4.18E-03	4	ABCA1,CAV1,CAV2,SCARB1
PW:0000640	glycolysis pathway	1.04E-04	2.57E-03	1.26E-02	7.71E-03	5	HK2,PFKFB4,PFKP,GAPDH,ENO2
PW:0000243	vascular endothelial growth factor signaling	2.20E-03	3.26E-02	1.59E-01	1.63E-01	4	PGF,VEGFA,NRP1,EGLN3
PW:0000010	lipid metabolic	3.21E-03	3.96E-02	1.94E-01	2.38E-01	2	SAA4,ANGPTL4
PW:0000534	glycogen degradation	1.81E-02	1.19E-01	5.82E-01	1.00E+00	3	PHKA2,PPP1R3C,PYGL
PW:0000032	pyrimidine metabolic	3.12E-02	1.40E-01	6.85E-01	1.00E+00	2	TYMS,ENTPD1
PW:0000482	lipoprotein metabolic	3.63E-02	1.40E-01	6.85E-01	1.00E+00	2	APOC1,SCARB1
PW:0000459	apelin signaling	6.90E-02	1.50E-01	7.34E-01	1.00E+00	1	APLNR
PW:0000490	transforming growth factor-beta Smad dependent signaling	4.62E-01	5.03E-01	1.00E+00	1.00E+00	1	RUNX1
SMPDB							
SMP00040	Glycolysis	3.10E-03	1.98E-01	9.40E-01	1.98E-01	3	HK2,GAPDH,TPI1
SMP00046	Pyrimidine Metabolism	1.16E-01	5.32E-01	1.00E+00	1.00E+00	2	TYMS,TYMP
SMP00048	Nicotinate and Nicotinamide Metabolism	2.49E-01	5.32E-01	1.00E+00	1.00E+00	1	NNMT
SMP00063	Tryptophan Metabolism	3.33E-01	5.32E-01	1.00E+00	1.00E+00	1	IDO1
SMP00276	Argatroban Pathway	3.33E-01	5.32E-01	1.00E+00	1.00E+00	1	FGG
SMP00035	Bile Acid Biosynthesis	3.33E-01	5.32E-01	1.00E+00	1.00E+00	1	HSD3B7
SMP00381	Nisoldipine Pathway	3.49E-01	5.32E-01	1.00E+00	1.00E+00	1	EDNRB

SMP00034	Sphingolipid Metabolism	4.22E-01	5.83E-01	1.00E+00	1.00E+00	1	GAL3ST1
SMP00006	Tyrosine Metabolism	4.36E-01	5.83E-01	1.00E+00	1.00E+00	1	CYBB
SMP00032	Valine, Leucine and Isoleucine Degradation	5.11E-01	5.83E-01	1.00E+00	1.00E+00	1	BCAT1

Table 4 The enriched pathway terms of the down regulated differentially expressed genes

BIOCYC							
Pathway ID	Pathway Name	P-value	FDR B&H	FDR B&Y	Bonferro ni	Gene Count	Gene
142337	4-hydroxyproline degradation	4.06E-05	2.80E-03	1.35E-02	2.80E-03	3	PRODH2,HOGA1,ALDH4A1
782404	fatty acid beta-oxidation (peroxisome)	1.36E-04	4.71E-03	2.27E-02	9.41E-03	4	ACAA1,ACOX2,SLC27A2,HADH
545340	glycine cleavage	1.41E-03	2.43E-02	1.17E-01	9.70E-02	2	AMT,GLDC
545319	creatine-phosphate biosynthesis	1.41E-03	2.43E-02	1.17E-01	9.70E-02	2	CKMT1B,CKMT2
545295	retinoate biosynthesis I	1.22E-02	1.69E-01	8.12E-01	8.42E-01	2	ALDH1A2,RBP4
782382	gluconeogenesis	4.14E-02	1.86E-01	8.98E-01	1.00E+00	2	FBP1,ALDOB
142255	CDP-diacylglycerol biosynthesis	6.37E-02	2.11E-01	1.00E+00	1.00E+00	2	CDS1,GPAT3
142269	superpathway of cholesterol biosynthesis	1.03E-01	2.19E-01	1.00E+00	1.00E+00	2	HMGCS2,TM7SF2
142419	phospholipases	1.32E-01	2.33E-01	1.00E+00	1.00E+00	2	PLA2G4F,PLCG2
835392	superpathway of tryptophan utilization	1.54E-01	2.53E-01	1.00E+00	1.00E+00	2	DDC,QPRT
KEGG							
132956	Metabolic	2.85E-10	7.21E-08	4.41E-07	7.21E-08	63	GPHN,EPHX2,CDS1,ACAA1,GGT6,PIPO

	pathways						X,HMGCS2,ACY1,A COX2,ADH1A,ADH 1C,CKB,CKMT1B,C KMT2,PRODH2,AT P6V1G3,FBP1,HPD, HOGA1,UGT8,PLA2 G4F,ATP6V1C2,AT P6V0D2,PLCG2,AL DOB,ALDH6A1,AM T,HYAL1,AOX1,ST 6GAL1,CYP4F2,AR G2,ATP6V0A4,ASS1 ,OGDHL,ALDH4A1, G6PC,INPP5J,SORD ,ATP6V1B1,CYP4A 11,DHRS4L1,GATM ,FTCD,SUCLG1,PT GDS,DDC,PHGDH, ALDH1A2,GLDC,H SD17B8,CKMT1A, MAN1C1,RDH10,GP AT3,QPRT,PAH,TM 7SF2,AGMAT,HAD H,PCCA,DCXR,PCK 1
130626	Aldosterone- regulated sodium reabsorption	4.35E-09	5.50E-07	3.36E-06	1.10E-06	10	SCNN1A,SCNN1B,S CNN1G,NR3C2,HSD 11B2,ATP1A1,FX YD2,FXD4,KCNJ1, NEDD4L
147586	Collecting duct acid secretion	7.25E-08	5.05E-06	3.09E-05	1.84E-05	8	ATP6V1G3,CLCNK B,ATP6V1C2,ATP6 V0D2,SLC4A1,ATP6 V0A4,ATP6V1B1,C A2
212237	Mineral absorption	1.12E-04	4.04E-03	2.47E-02	2.83E-02	7	MT1E,MT1F,MT1G, MT1H,MT1M,ATP1 A1,FXD2
83071	Tight junction	3.55E-04	9.98E-03	6.10E-02	8.98E-02	12	ERBB2,CGN,CLDN 3,CLDN7,CLDN16,T JP3,MYH10,NEDD4 L,CLDN10,CLDN8, MARVELD2,CGNL 1
83083	Leukocyte transendothelial migration	3.50E-03	4.43E-02	2.71E-01	8.86E-01	8	RAPGEF3,VAV3,PL CG2,CLDN3,CLDN7 ,CLDN16,CLDN10,C LDN8

83088	Taste transduction	3.51E-02	1.93E-01	1.00E+00	1.00E+00	5	PDE1A,SCN2A,SCN N1A,SCNN1B,SCN N1G
82973	Glutathione metabolism	1.14E-01	3.88E-01	1.00E+00	1.00E+00	3	GGT6,GSTO2,GST M3
868086	Rap1 signaling pathway	1.77E-01	4.80E-01	1.00E+00	1.00E+00	7	RAPGEF3,FGF9,ID1 ,KIT,RAP1GAP,EGF ,CDH1
83050	Calcium signaling pathway	2.08E-01	5.06E-01	1.00E+00	1.00E+00	6	ERBB2,PDE1A,PLC G2,SLC25A4,PTGE R1,PTGER3
Pathway Interaction Database							
137911	FOXA2 and FOXA3 transcription factor networks	2.60E-03	1.03E-01	5.08E-01	2.05E-01	5	ALB,ALDOB,G6PC, HADH,PCK1
138019	p75(NTR)-mediated signaling	1.05E-02	2.08E-01	1.00E+00	8.33E-01	5	SORT1,PLG,MMP7, BEX1,RTN4
138006	ATF-2 transcription factor network	1.19E-01	7.05E-01	1.00E+00	1.00E+00	3	ATF3,PPARGC1A,D USP5
138085	Coregulation of Androgen receptor activity	1.28E-01	7.05E-01	1.00E+00	1.00E+00	3	VAV3,SNURF,TMP RSS2
137930	Signaling events mediated by Hepatocyte Growth Factor Receptor (c-Met)	2.08E-01	7.75E-01	1.00E+00	1.00E+00	3	MUC20,SH3GL2,CD H1
138068	Signaling events mediated by Stem cell factor receptor (c-Kit)	3.15E-01	7.75E-01	1.00E+00	1.00E+00	2	STAP1,KIT
137913	Alpha-synuclein signaling	5.07E-01	7.75E-01	1.00E+00	1.00E+00	1	KLK6
137948	BMP receptor signaling	5.49E-01	7.75E-01	1.00E+00	1.00E+00	1	SOSTDC1
138080	Aurora B signaling	5.78E-01	7.75E-01	1.00E+00	1.00E+00	1	TACC1

138072	Nephrin/Neph1 signaling in the kidney podocyte	4.37E-01	7.75E-01	1.00E+00	1.00E+00	1	NPHS2
REACTOME							
1269903	Transmembrane transport of small molecules	2.42E-10	1.54E-07	1.08E-06	1.54E-07	43	SLC29A2,ABCB1,SLC22A6,ATP6V1G3,SLC22A8,CLCNKA,CLCNKB,SCNN1A,SCNN1B,SCNN1G,ALB,ATP6V1C2,ATP6V0D2,RHCG,SLC13A3,AQP1,AQP2,AQP6,SLC47A2,SLC22A12,SLC4A1,SLC6A12,SLC9A2,SLC12A1,SLC12A3,SLC13A1,SLC26A7,SLC34A1,ATP6V0A4,ATP1A1,FXND2,G6PC,ATP6V1B1,FXND4,SLC30A2,SLC22A7,SLC36A2,WNK4,NEDD4L,LCN2,SLC44A4,SLC7A8,NIPAL1
1269907	SLC-mediated transmembrane transport	3.27E-07	6.92E-05	4.87E-04	2.08E-04	22	SLC29A2,SLC22A6,SLC22A8,ALB,RHCG,SLC13A3,SLC47A2,SLC22A12,SLC4A1,SLC6A12,SLC9A2,SLC12A1,SLC12A3,SLC13A1,SLC26A7,SLC34A1,G6PC,SLC30A2,SLC22A7,SLC36A2,SLC44A4,SLC7A8
1269950	Ion channel transport	5.50E-05	3.89E-03	2.73E-02	3.50E-02	15	ATP6V1G3,CLCNKA,CLCNKB,SCNN1A,SCNN1B,SCNN1G,ATP6V1C2,ATP6V0D2,ATP6V0A4,ATP1A1,FXND2,ATP6V1B1,FXND4,WNK4,NEDD4L
1270158	Metabolism of amino acids and derivatives	1.64E-04	7.43E-03	5.23E-02	1.04E-01	20	PIPOX,CKB,CKMT1B,CKMT2,HPD,ALDH6A1,AMT,ARG2,SLC6A12,ASS1,ALDH4A1,GAT

							M,FTCD,DDC, PHGDH,GLDC,DIO 1,CKMT1A,PAH,AG MAT
1270001	Metabolism of lipids and lipoproteins	3.52E-03	6.58E-02	4.63E-01	1.00E+00	30	EPHX2,CDS1,ACAA 1,HMGCS2,SCD5,A COX2,HPGD,UGT8, ALB,PLA2G4F,HSD 11B2,HACD3,CYP4 F2, ACSF2,PTGR1,ACO T11,INPP5J,CYP4A1 1,PTGDS, GPD1L,PPARGC1A, HSD17B8,SLC27A2, DPEP1, GPAT3,SLC44A4,L DLR,TM7SF2,HAD H,PCCA
1270303	Axon guidance	9.96E-02	4.21E-01	1.00E+0 0	1.00E+00	17	ERBB2,SCN2A,FGF 9,VAV3,PLXNB1,C OL4A3,COL4A4,AN K2,SH3GL2,MYH10 ,SRGAP3,KIT,RAP1 GAP,HBEGF,DUSP5 ,NTN4,EGF
1269340	Hemostasis	1.08E-01	4.32E-01	1.00E+0 0	1.00E+00	19	PDE1A,RAPGEF3,P LAT,VAV3,ALB,PL CG2,PLG,CXADR,G ATA3,CEACAM1,K NG1,KIF13B,GRB14 ,SLC7A8,EGF,CD9, TSPAN7,EPCAM,SE RPINA5
1269203	Innate Immune System	4.24E-01	7.30E-01	1.00E+0 0	1.00E+00	30	ERBB2,PDE1A,ACA A1,ACPP,ATP6V1G 3,PIGR,FGF9,VAV3, ATP6V1C2,ATP6V0 D2,PLCG2,MUC20,F OLR3,OLFM4,CYFI P2,ATP6V0A4,MUC 1,CTSH,ATP6V1B1, CEACAM1,DEFB1,I ER3,C7,KIT,SLC27 A2,HBEGF,DUSP5, LCN2,EGF,LTF
1269543	Signaling by GPCR	9.89E-01	1.00E+0 0	1.00E+0 0	1.00E+00	19	ERBB2,PDE1A,FGF 9,VAV3,PLXNB1,S UCNR1,CRHBP,GC GR,PTGER1,PTGER

Gen MAPP							
MAP00220	Urea cycle and metabolism of amino groups	2.39E-05	8.86E-04	3.72E-03	8.86E-04	5	ACY1,CKB,CKMT2,ARG2,ASS1
MAP00280	Valineleucine and isoleucine degradation	2.17E-04	4.01E-03	1.68E-02	8.01E-03	5	ACAA1,HMGCS2,ALDH6A1,AOX1,PCCA
MAP00350	Tyrosine metabolism	4.37E-04	5.39E-03	2.26E-02	1.62E-02	5	ADH1A,ADH1C,HPD,AOX1,DDC
MAP00330	Arginine and proline metabolism	1.34E-03	1.24E-02	5.19E-02	4.94E-02	5	CKB,CKMT2,ARG2,ASS1,AGMAT
MAP00010	Glycolysis Gluconeogenesis	5.40E-03	3.99E-02	1.68E-01	2.00E-01	5	ADH1A,ADH1C,FBP1,ALDOB,G6PC
MAP00910	Nitrogen metabolism	1.03E-02	4.21E-02	1.77E-01	3.79E-01	3	AMT,CA2,CA4
MAP00071	Fatty acid metabolism	1.77E-02	5.46E-02	2.30E-01	6.56E-01	4	ACAA1,ADH1A,ADH1C,CYP4A11
MAP00360	Phenylalanine metabolism	4.67E-02	1.23E-01	5.18E-01	1.00E+00	2	HPD,DDC
MAP00590	Prostaglandin and leukotriene metabolism	6.37E-02	1.46E-01	6.13E-01	1.00E+00	2	CYP4F2,PTGDS
MAP00361	gamma Hexachlorocyclohexane degradation	4.73E-01	5.01E-01	1.00E+00	1.00E+00	1	ACPP

M6487	Platelet Amyloid Precursor Protein Pathway	1.88E-04	1.07E-02	4.95E-02	1.07E-02	4	PLAT,PLG,COL4A3,COL4A4
M5889	Ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins	5.64E-03	8.03E-02	3.72E-01	3.21E-01	35	MATN2,S100A2,MFAP4,LOXL4,FGF9,P LAT,GPC5,PLG,MM P7,PLXNB1,PARM1 ,MUC20,COL4A3,C OL4A4,FRAS1,FBL N5,SFRP1,HYAL1,G DF15,ANXA3,CRHB P,IGFBP2,MUC1,CT SH,EMCN,ST14,NE LL1,GPC3,KNG1,H BEGF,NTN4,EGF,P APPA,MST1L,SERP INA5
M5885	Ensemble of genes encoding ECM-associated proteins including ECM-affiliated proteins, ECM regulators and secreted factors	1.39E-02	1.32E-01	6.11E-01	7.92E-01	26	S100A2,LOXL4,FGF 9,PLAT,GPC5,PLG, MMP7,PLXNB1,PA RM1,MUC20,SFRP1 ,HYAL1,GDF15,AN XA3,CRHBP,MUC1, CTSH,EMCN,ST14, GPC3,KNG1,HBEGF ,EGF,PAPPA,MST1 L,SERPINA5
M5880	Genes encoding proteins affiliated structurally or functionally to extracellular matrix proteins	3.42E-02	2.08E-01	9.60E-01	1.00E+00	8	GPC5,PLXNB1,PAR M1,MUC20,ANXA3, MUC1,EMCN,GPC3
M3468	Genes encoding enzymes and their regulators involved in the remodeling of the extracellular matrix	3.64E-02	2.08E-01	9.60E-01	1.00E+00	10	LOXL4,PLAT,PLG, MMP7,HYAL1,CTS H,ST14,KNG1,PAPP A,SERPINA5
M3008	Genes encoding structural ECM glycoproteins	1.38E-01	5.63E-01	1.00E+00	1.00E+00	7	MATN2,MFAP4,FR AS1,FBLN5,IGFBP2 ,NELL1,NTN4
M5884	Ensemble of genes encoding core extracellular matrix including ECM glycoproteins,	1.49E-01	5.66E-01	1.00E+00	1.00E+00	9	MATN2,MFAP4,CO L4A3,COL4A4,FRA S1,FBLN5,IGFBP2, NELL1,NTN4

	collagens and proteoglycans						
M2404	Mechanism of Gene Regulation by Peroxisome Proliferators via PPARα(alpha)	3.63E-01	5.88E-01	1.00E+00	1.00E+00	2	PPARGC1A,NR2F1
M5883	Genes encoding secreted soluble factors	4.80E-01	6.43E-01	1.00E+00	1.00E+00	8	S100A2,FGF9,SFRP1,GDF15,CRHBP,HBEFG,EGF,MST1L
M5493	Genes related to Wnt-mediated signal transduction	5.83E-01	6.44E-01	1.00E+00	1.00E+00	2	SFRP1,TLE2
Panther DB							
P00011	Blood coagulation	5.63E-02	5.49E-01	1.00E+00	1.00E+00	3	PLAT,PLG,KNG1
P04372	5-Hydroxytryptamine degradation	5.78E-02	5.49E-01	1.00E+00	1.00E+00	2	ALDH4A1,ALDH1A2
P00009	Axon guidance mediated by netrin	1.39E-01	5.49E-01	1.00E+00	1.00E+00	2	PLCG2,NTN4
P00004	Alzheimer disease-presenilin pathway	2.34E-01	7.69E-01	1.00E+00	1.00E+00	4	MMP7,TRIM2,CDH1,CDH3
P00047	PDGF signaling pathway	3.02E-01	8.03E-01	1.00E+00	1.00E+00	4	VAV3,PLCG2,SRGAP3,ELF5
P00005	Angiogenesis	4.16E-01	8.03E-01	1.00E+00	1.00E+00	4	PLCG2,SFRP1,CRYAA,GRB14
P00018	EGF receptor signaling pathway	4.39E-01	8.03E-01	1.00E+00	1.00E+00	3	ERBB2,PLCG2,HBEFG
P00016	Cytoskeletal regulation by Rho GTPase	4.47E-01	8.03E-01	1.00E+00	1.00E+00	2	MYH10,TUBB2B
P00012	Cadherin signaling pathway	4.60E-01	8.03E-01	1.00E+00	1.00E+00	4	ERBB2,CDH1,CDH3,CDH16
P00029	Huntington disease	5.06E-01	8.03E-01	1.00E+00	1.00E+00	3	PRODH2,CYFIP2,TUBB2B

Pathway Ontology							
PW:0000076	pathway of urea cycle and metabolism of amino groups	1.36E-04	9.00E-03	4.30E-02	9.00E-03	4	CKB,ARG2,ASS1,GATM
PW:0000641	gluconeogenesis pathway	4.24E-04	1.40E-02	6.68E-02	2.80E-02	4	FBP1,ALDOB,G6PC,PCK1
PW:0000419	water transport	7.86E-04	1.64E-02	7.84E-02	5.19E-02	3	AQP1,AQP2,AQP6
PW:0000050	arginine and proline metabolic	9.95E-04	1.64E-02	7.84E-02	6.57E-02	4	CKB,ARG2,ASS1,GATM
PW:0000052	tyrosine metabolic	4.68E-03	5.15E-02	2.46E-01	3.09E-01	3	HPD,AOX1,DDC
PW:0000025	glycolysis/gluconeogenesis	2.48E-02	1.79E-01	8.56E-01	1.00E+00	3	FBP1,G6PC,PCK1
PW:0000047	glycine, serine and threonine metabolic	3.64E-02	2.04E-01	9.73E-01	1.00E+00	2	GATM,PHGDH
PW:0000071	valine, leucine and isoleucine degradation	5.21E-02	2.12E-01	1.00E+00	1.00E+00	2	ACAA1,AOX1
PW:0000490	transforming growth factor-beta Smad dependent signaling	1.10E-01	2.50E-01	1.00E+00	1.00E+00	2	ATF3,TGFBR3
PW:0000674	insulin secretion pathway	3.28E-01	4.17E-01	1.00E+00	1.00E+00	1	SYT7
SMPDB							
SMP00080	Polythiazide Pathway	1.99E-06	2.82E-05	1.61E-04	3.38E-04	5	CLCNKA,AQP1,SLC12A3,ATP1A1,FXR
SMP00154	Ramipril Pathway	7.14E-06	3.92E-05	2.24E-04	1.21E-03	7	SCNN1A,SCNN1B,NR3C2,AQP2,ATP1A1,FXR,REN
SMP00004	Glycine, Serine and Threonine Metabolism	1.96E-03	9.53E-03	5.45E-02	3.34E-01	4	AMT,GATM,PHGDH,GLDC
SMP00032	Valine, Leucine and Isoleucine Degradation	3.90E-03	1.84E-02	1.05E-01	6.64E-01	4	HMGCS2,ALDH6A1,AOX1,PCCA

									P1,P4HB,CD86,LOX,CD36,SERPINE1,CD70,HCLS1
GO:0006952	BP	defense response	2.18E-22	4.23E-19	3.91E-18	1.27E-18	99	IL32,HLA-A,HLA-B,HLA-DQA1,HLA-DQA2,HLA-DQB1,ENPP3,HLA-F,VSIG4,HLA-G,HLA-H,APOBEC3G,HMOX1,LY96,ADA,CD163,ADM,TYROBP,SAA1,SAA2,SAA4,FCER1G,FCGR1A,FCGR2A,SCD,CXCL9,CCL5,FGG,MMP9,SERPINF2,APOL2,LY86,VCAM1,VIM,DDIT4,WAS,UBD,FPR3,SHMT2,BIRC3,PARP14,FCN3,IFI16,IFI27,CSF1R,ISG15,CSPG4,XAF1,SLFN11,CYBB,IDO1,GAPDH,INHBB,CXCL10,AXL,PSMB8,PSMB9,IL20RB,GBP1,GBP2,ISG20,SIRPA,ITGB2,C10orf99,STAT1,PRDM1,GJA1,BNIP3,GBP5,BST2,CXCR4,SIGLEC10,C1QA,C1QB,C1QC,C1R,C1S,C2,C3,IFI44L,TAP1,TAPBP,RARRES2,LALG3,OAS2,CAV1,OLR1,EDNRB,TGM2,CD8A,CD14,TIMP1,CD86,CD36,SCARB1,SERPINE1,CD68,ADGRE5,TNFAIP6	
GO:0051707	BP	response to other organism	2.64E-20	2.08E-17	1.92E-16	1.54E-16	88	ABCA1,HLA-A,HLA-B,HLA-DQA1,HLA-DQA2,HLA-DQB1,HLA-F,VSIG4,HLA-G,HLA-H,APOBEC3G,LY96,ADM,TYROBP,SAA1,FCER1G,FCGR1A,SCD,CXCL9,CCL5,FGG,LY86,FCBP5,VCAM1,VIM,DDIT4,WAS,UB	

									D,IFI44,SHMT2,BI RC3,PARP14,FCN3 ,IFI16,IFI27,CSF1R ,ISG15,XAF1,SLFN 11,CYBB,SPARC,I DO1,GAPDH,CXC L10,AXL,PSMB8,P SMB9,GBP1,GBP2, ISG20,SIRPA,ITGB 2,C10orf99,STAT1 PRDM1,GJA1,GJB 2,BNIP3,GBP5,BST 2,CXCR4,SIGLEC1 0,C1QA,C1QB,C1Q C,C1R,PYGL,C1S, C2,C3,IFI44L,TAP1 ,RARRES2,GAS2L 3,LAG3,OAS2,CA V1,RGS1,EDNRB, CD8A,CD14,CD86, CD36,SCARB1,GZ MA,SERPINE1,CD 68,DCLK1
GO:0002682	BP	regulation of immune system process	9.91E-20	4.80E-17	4.44E-16	5.76E-16	92	CMTM3,HLA- A,HLA-B,HLA- DQA1,HLA- DQA2,HLA- DQB1,ENPP3,HLA -F,VSIG4,HLA- G,HLA- H,HLX,APOBEC3 G,EVI2B,HMOX1, LY96,DYSF,ADA, PGF,TYROBP,FCE R1G,FCGR1A,FCG R2A,CD99,CCL5,F GG,MMP9,VCAM1 ,COL1A1,VEGFA, COL1A2,COL3A1, WAS,FPR3,BIRC3, PARP14,FCN3,IFI1 6,RHEX,CSF1R,IS G15,TNFSF13B,FY B1,PROS1,PAG1,P LVAP,IDO1,RASS F2,CXCL10,AXL,P SMB8,PSMB9,IL20 RB,GBP1,SIRPA,IT GB2,C10orf99,STA T1,PRDM1,GBP5,B ST2,SIGLEC10,C1 QA,C1QB,C1QC,C 1R,C1S,C2,C3,TAP 1,RAC2,RARRES2, LAG3,CAV1,RUN X1,BTN3A2,BTN3 A1,LGALS1,CD2,C D3D,THBS4,CD8A ,CD14,CD86,LOX, CD36,SCARB1,SE	

									RPINE1,CD68,CD70,HCLS1,NCKAP1L
GO:0046903	BP	secretion	2.24E-18	1.00E-15	9.25E-15	1.30E-14	91	ABCA1,HK2,ACLY,HLA-F,HLA-H,HMOX1,DYSF,ADA,FABP5,ADM,TYROBP,SAA1,SERPINE2,FCER1G,FCGR2A,SNX10,CCL5,FGG,PLEK,MMP9,SERPINF2,ALDO C,HSPA6,VEGFA,VWF,SCG5,PPFIA4,ANXA4,PRDX4,POU5F1,NLGN1,SLC1A3,AQP9,SLC2A1,SLC2A5,SLC6A3,POSTN,CSF1R,IGFBP3,ISG15,TRIM9,SLC15A4,TNFSF13B,RNASET2,CTSZ,PROS1,CYBB,ABCC3,SPARC,GAPDH,CYP2J2,INHBB,AXL,GBP1,CCND1,SIRPA,ITGB2,GJA1,KISS1R,GBP5,BST2,SIGLEC10,KCNMA1,PYGL,C3,RAC2,CA9,DOCK2,RAB31,RARRES2,RHBDF2,CANX,OAS2,CAV1,RUNX1,OLR1,BTN3A2,BTN3A1,EDNRB,CD2,CD14,TIMP1,CD36,ENTPD1,SERPINE1,CD68,LHFPL2,STEAP3,ADGRE5,TNFAIP6,NCKAP1L	
GO:0098542	BP	defense response to other organism	8.80E-18	3.65E-15	3.38E-14	5.12E-14	72	HLA-A,HLA-B,HLA-DQA1,HLA-DQA2,HLA-DQB1,HLA-F,VSIG4,HLA-G,HLA-H,APOBEC3G,LY96,TYROBP,SAA1,FCER1G,FCGR1A,SCD,CXCL9,CCL5,FGG,LY86,VCAM1,VIM,DDIT4,WAS,UBD,SHMT2,BIRC3,PARP14,FCN3,IFI16,IFI27,CSF1R,ISG15,XAF1,SLFN11	

									,CYBB,GAPDH,CX CL10,AXL,PSMB8, PSMB9,GBP1,GBP 2,ISG20,SIRPA,IT GB2,C10orf99,STA T1,PRDM1,BNIP3, GBP5,BST2,SIGLE C10,C1QA,C1QB,C 1QC,C1R,C1S,C2,C 3,IFI44L,TAP1,RA RRES2,LAG3,OAS 2,CAV1,CD8A,CD 14,CD86,CD36,SC ARB1,SERPINE1
GO:0001775	BP	cell activation	2.25E-17	8.70E-15	8.05E-14	1.31E-13	81	PDGFRB,HLA- DQA1,ACLY,HLA- DQB1,ENPP3,HLA -F,VSIG4,HLA- G,HLA- H,CYGB,HLX,HM OX1,DYSF,ADA,F ABP5,TYROBP,SA A1,SERPINE2,FCE R1G,FCGR2A,CCL 5,FGG,PLEK,MMP 9,ALDOC,HSPA6, VCAM1,APBB1IP, COL1A1,COL1A2, COL3A1,VWF,WA S,UBD,PRDX4,SL C2A5,SLC15A4,TN FSF13B,RNASET2, FYB1,IL2RB,CTSZ ,CYBB,PAG1,IDO1 ,CXCL10,AXL,IL2 ORB,SIRPA,ITGB2, PRDM1,GJA1,BST 2,CXCR4,SIGLEC1 0,C1QA,PYGL,C3, RAC2,DOCK2,RA B31,LAG3,CAV1,R UNX1,LCP1,OLR1, BTN3A1,LGALS1, CD2,CD3D,CD8A, CD14,TIMP1,CD86 ,CD36,ENTPD1,CD 68,CD70,ADGRE5, TNFAIP6,NCKAP1 L	
GO:0140352	BP	export from cell	6.63E-14	1.48E-11	1.37E-10	3.86E-10	79	ABCA1,ACLY,HL A-F,HLA- H,HMOX1,DYSF,F ABP5,ADM,TYRO BP,SAA1,SERPINE 2,FCER1G,FCGR2 A,CCL5,FGG,PLE K,MMP9,SERPINF 2,ALDOC,HSPA6, VEGFA,VWF,SCG	

								5,PPFIA4,ANXA4, PRDX4,POU5F1,N LGN1,SLC1A3,SL C2A1,SLC2A5,POS TN,CSF1R,IGFBP3 ,ISG15,TRIM9,SLC 15A4,TNFSF13B,R NASET2,CTSZ,PR OS1,CYBB,SPARC ,GAPDH,CYP2J2,I NHBB,AXL,GBP1, SIRPA,ITGB2,GJA 1,KISS1R,GBP5,BS T2,SIGLEC10,PYG L,C3,RAC2,DOCK 2,RAB31,RARRES 2,RHBDF2,CANX, RUNX1,OLR1,BT N3A2,BTN3A1,CD 2,CD14,TIMP1,CD 36,ENTPD1,SERPI NE1,CD68,LHFPL2 ,STEAP3,ADGRE5, TNFAIP6,NCKAP1 L
GO:0016477	BP	cell migration	1.22E-12	2.14E-10	1.98E-09	7.06E-09	77	PDGFRB,CORO1C ,CYGB,HMOX1,D YSF,ADA,PGF,SA A1,SAA2,SAA4,SE RPINE2,FCER1G,F CGR2A,SEMA5B, CD99,CXCL9,ASP M,CTHRC1,CCL5, SEMA6A,MMP9,V CAM1,COL1A1,V EGFA,COL1A2,CO L3A1,VIM,COL5A 1,FNDC3B,DDIT4, ANGPT2,VASH1,P OSTN,HSD3B7,CS F1R,IGFBP3,VCA N,CSPG4,FSCN1,S OD2,PROS1,SPAR C,PLVAP,CXCL10, AXL,SIRPA,ITGA5 ,ITGB2,C10orf99,S TAT1,NRP1,GJA1, KISS1R,BST2,CXC R4,ACKR3,RAC2, DPYSL3,RARRES2 ,CD248,LAMA4,C AV1,LCP1,OLR1,E DNRB,CD2,THBS4 ,SLC16A3,TIMP1,L OX,SCARB1,SERP INE1,TMSB10,TNF AIP6,CDH2,DCLK 1,NCKAP1L

GO:0016050	CC	vesicle organizati on	1.15E-10	1.31E-08	1.21E-07	6.68E-07	73	ABCA1,ACLY,EN PP3,CORO1C,HLA -F,HLA- H,HMOX1,DYSF,C D163,FABP5,EHD2 ,ADM,TYROBP,SA A1,SERPINE2,FCE R1G,FCGR1A,FCG R2A,SNX10,CCL5, FGG,PLEK,MMP9, SERPINF2,ALDOC ,HSPA6,VEGFA,SF RP4,VWF,WAS,PR DX4,POU5F1,APO C1,NLGN1,FCN3,S LC2A5,TRIM9,SL C15A4,ASIP,RNAS ET2,CTSZ,PROS1, CYBB,SPARC,AX L,SIRPA,ITGB2,BS T2,ACKR3,PYGL, C3,TAP1,TAPBP,R AC2,DOCK2,RAB3 1,RARRES2,CANX ,CAV1,CAV2,OLR 1,TGFA,CD14,TIM P1,CD36,SCARB1, SERPINE1,CD68,L HFPL2,STEAP3,A DGRE5,TNFAIP6, NCKAP1L
GO:0009986	CC	cell surface	2.46E-23	1.44E-20	9.99E-20	1.44E-20	73	ABCA1,HLA- A,HLA- B,PDGFRB,HLA- DQA1,HLA- DQB1,ENPP3,HLA -F,HLA-G,HLA- H,ADA,CD163,TY ROBP,SERPINE2,F CER1G,FCGR1A,F CGR2A,CXCL9,FG G,SERPINF2,HILP DA,VCAM1,VEGF A,SFRP4,VWF,PPF IA4,ANXA4,NLGN 1,SLC1A3,COL23A 1,SLC6A3,CSF1R, VCAN,CSPG4,IL2 RB,CTSZ,SPARC,P LVAP,VAMP5,CX CL10,AXL,SIRPA,I TGA5,ITGB2,NRP 1,KISS1R,BST2,CX CR4,ACKR3,NTM, KCNMA1,C3,CD24 8,LAG3,CAV1,CA V2,BTN3A2,BTN3 A1,LGALS1,TGFA, CD2,CD3D,CD8A, CD14,P4HB,CD86,

								CD36,SCARB1,EN TPD1,CDH2,ENO2, CDH6,CDH11
GO:0031012	CC	extracellul ar matrix	1.19E-19	2.31E-17	1.61E-16	6.93E-17	51	SERPINE2,CTHRC 1,FGG,MMP9,SER PINF2,PLOD1,COL 1A1,VEGFA,COL1 A2,COL3A1,COL4 A1,COL4A2,COL5 A1,COL5A2,COL6 A1,COL6A2,COL6 A3,COL8A1,COL1 1A1,COL15A1,VW F,OLFML2B,ANX A4,COL23A1,POS TN,VCAN,CSPG4, CTS2,SPARC,BMP 1,OLFML2A,PXD N,C1QA,C1QB,C1 QC,PLOD3,RARR ES2,CD248,LAMA 4,RUNX1,SERPIN H1,LGALS1,TGFB I,TGM2,THBS2,TH BS4,TIMP1,LOX,E NTPD1,SERPINE1, CDH2
GO:0044433	CC	cytoplasm ic vesicle part	1.16E-13	9.66E-12	6.71E-11	6.76E-11	72	HLA-A,HLA- B,HLA- DQA1,HLA- DQA2,ACLY,HLA- DQB1,CORO1C,H LA-F,HLA-G,HLA- H,LY96,DYSF,AD A,CD163,FABP5,E HD2,TYROBP,SA A1,FCER1G,FCGR 1A,FCGR2A,PLA1 A,SNX10,FGG,MM P9,SERPINF2,ALD OC,HSPA6,VEGFA ,VWF,FGD2,PRDX 4,SLC2A5,SLC15A 4,RNASET2,CTS2, AHNAK2,PROS1,C YBB,SLC9A9,SPA RC,VAMP5,SIRPA, ITGB2,PMEP1,GJ A1,BST2,PYGL,C3 ,TAP1,TAPBP,RAC 2,DOCK2,RAB31,R ARRES2,ABCB6,C AV1,CAV2,OLR1, TGFA,CD3D,CD14 ,TIMP1,CD36,SCA RB1,SERPINE1,CD 68,LHFPL2,STEAP 3,ADGRE5,TNFAI

								P6,NCKAP1L
GO:0097478	CC	leaflet of membrane bilayer	3.04E-13	1.97E-11	1.37E-10	1.78E-10	44	ABCA1,HLA-A,HLA-B,HLA-DQA1,HLA-DQA2,HLA-DQB1,ENPP3,HLA-F,HLA-G,HLA-H,ADA,CD163,SERPINE2,FCER1G,FCGR1A,FCGR2A,CXCL9,FGG,VCAM1,VWF,NLGN1,IL2RB,CXCL10,ITGA5,ITGB2,CXCR4,ACKR3,KCNMA1,TAPBP,NPTX2,CD248,CANX,LAG3,CAV2,RGS1,BTN3A2,BTN3A1,CD2,CD3D,CD8A,CD14,P4HB,CD86,CD36
GO:0044432	CC	endoplasmic reticulum part	8.41E-13	4.92E-11	3.42E-10	4.92E-10	66	ABCA1,HLA-A,HLA-B,HLA-DQA1,HLA-DQA2,HLA-DQB1,HLA-F,HLA-G,HLA-H,HMOX1,SCD,FGG,APOL2,PLOD1,PLOD2,COL1A1,COL1A2,COL3A1,COL4A1,COL4A2,COL5A1,COL5A2,COL6A1,COL6A2,COL6A3,COL8A1,COL11A1,COL15A1,GPX8,CP,IFI27,COL23A1,HSD3B7,IGFBP3,STC2,VCAN,RNASET2,CTS2,PRSS1,CYBB,CYP2J2,IKBIP,GJA1,PDI5,C3,TAP1,TAPBP,TBXAS1,P4HA2,PLOD3,RHBDF2,CALU,CANX,ABCB6,CAV1,COLGALT1,SEZ6L2,SERPINH1,LGALS1,TGFA,FSTL1,TIMP1,P4HA1,P4HB,CERCAM,CDH2
GO:0030141	CC	secretory granule	8.46E-12	4.50E-10	3.13E-09	4.95E-09	49	ACLY,HLA-H,FABP5,TYROBP,SERPINE2,FCER1G,FCGR2A,PLA1A,SNX10,FGG,MMP9,SERPINF2,HILP

									DA,ALDOC,HSPA 6,COL1A1,VEGFA, VWF,SCG5,PRDX 4,SLC2A5,IGFBP3, SLC15A4,RNASET 2,CTSZ,PROS1,CY BB,SPARC,SIRPA, ITGB2,BST2,PYGL ,C3,DOCK2,RAB31 ,RARRES2,CAV1 CAV2,OLR1,THBS 2,CD14,TIMP1,CD 36,SERPINE1,CD6 8,LHFPL2,ADGRE 5,TNFAIP6,NCKA P1L
GO:0098805	CC	whole membrane	1.00E-10	3.67E-09	2.55E-08	5.87E-08	72	ABCA1,HK2,HLA- A,HLA-B,HLA- DQA1,HLA- DQA2,HLA- DQB1,CORO1C,H LA-F,HLA-G,HLA- H,HMOX1,LY96,S LC15A3,DYSF,CD 163,FABP5,EHD2, TYROBP,FCER1G, FCGR1A,FCGR2A, PLA1A,SNX10,CO L6A1,FGD2,BIRC3 ,CP,IFI27,SLC2A1, SLC2A5,SLC6A3,S LC15A4,CYBB,AB CC3,SLC9A9,PAG 1,SPARC,PLVAP,S IRPA,ITGB2,PMEP A1,LAPTM5,GJA1, BNIP3,BST2,KCN MA1,TAP1,TAPBP ,RAC2,RAB31,AB CB6,CAVIN3,CAV 1,CAV2,SERPINH1 ,OLR1,EDNRB,TG FA,CD2,CD3D,CD 8A,CD14,CD36,SC ARB1,CD68,LHFP L2,STEAP3,ADGR E5,CDH2,ENO2,N CKAP1L	
GO:0031226	CC	intrinsic component of plasma membrane	1.02E-07	1.81E-06	1.26E-05	5.99E-05	65	ABCA1,PDGFRB,S LCO2B1,HLA- DQA1,HLA- DQA2,HLA- H,EVI2B,LY96,CD 163, CEMIP2,TYROBP, FCER1G,CD99,AP LNR, SEMA6A,VCAM1, GAL3ST1,CP,NLC	

									N1, SLC1A3,AQP9,SLC2A1,SLC2A5,SLC6A3, CSF1R,CSPG4,IL2RB,CYBB,ABCC3,VAMP5,AXL,SIRPA,ITGA5,ITGB2,PCDH17,LAPTM5,NRP1,GJA1,GJB2,KISS1R, KCNMA1,NKG7,TAPBP,TMEM45A,CANX,CALHM6,CAV1,CAV2,OLR1,EDNRB, TGM2,SSPN,CD2,CD8A,CD14,SLC16A3, CD36,SCARB1,ENTPD1,CD70,ADGRE5, SLC39A14,CDH2,DCLK1,NCKAP1L
GO:0005794	CC	Golgi apparatus	1.81E-04	1.96E-03	1.36E-02	1.06E-01	51	ABCA1,HLA-A,HLA-B,PDGFRB,HLA-DQA1 ,HLA-DQA2,HLA-DQB1,HLA-F,HLA-G ,HLA-H,DYSF,CHST15,VCAM1,COL1A1,FGD2,GAL3ST1,NLGN1,SLC2A1,POSTN, STC2,VCAN,CSPG4,CTSZ,PROS1,CYBB, VAMP5,RASSF2,GBP1,GBP2,ITGA5,PMEPA1,PTHLH,BMP1,GJA1,GBP5,BST2,STMN3,ST8SIA4,TAPBP,GALNT14,RAB31,PLOD3,CALU,ABCB6,GAL3ST4,CAV1,CAV2,TGFA,TGFB1,CD14,CD36	
GO:0099081	CC	supramolecular polymer	2.32E-03	1.56E-02	1.09E-01	1.00E+00	44	NUSAP1,CORO1C,HLA-G,ACTG2,DYSF,SSAA1,ASPM,VCAM1,COL1A1,COL1A2,COL3A1,COL4A1,COL4A2,VIM,COL5A1,COL5A2,COL6A1,COL6A3,CO	

									L8A1,COL11A1,WAS,NLGN1,ABLIM3,SLC2A1,FSCN1,AHNAK2,SPAG4,NEK6,IDO1,NRP1,GJA1,RAC2,CA9,DPYSL3,NPTX2,GAS2L3,SYNM,TUBA3D,PRC1,LCP1,LDHA,CD36,SCARB1,HCLS1
GO:0005102	MF	signaling receptor binding	4.11E-17	4.13E-14	3.09E-13	4.13E-14	90	CMTM3,ABCA1,IL32,HLA-A,HLA-B,PDGFRB,HLA-DQA1,HLA-DQA2,HLA-DQB1,HLA-F,HLA-G,HLA-H,LY96,PGF,ADM,TYROBP,SAA1,SAA2,SAA4,SERPINE2,FCGR1A,FCGR2A,SEMA5B,CXCL9,CTHRC1,FGF11,CCL5,SEMA6A,FGG,MMP9,HILPDA,APOL2,VCAM1,VEGFA,COL3A1,COL5A1,VWF,ANGPT2,NLGN1,SLC6A3,RHEX,ISG15,STC2,TNFSF13B,ASIP,FYB1,INHBB,CXCL10,ITGA5,ITGB2,C10orf99,PTHLH,STAT1,NRP1,C1QL1,BMP1,GJA1,PXDN,C3,TAP1,TAPBP,DOCK2,RARRES2,NOL3,CANX,LAG3,LAMA4,ESM1,IL18BP,CAV1,CAV2,LCP1,TYMP,BTN3A2,BTN3A1,EDNRB,TGFA,TGFB1,CD2,THBS4,CD8A,TIMP1,NETO2,P4HB,CD86,LOX,CD36,SERPINE1,CD70,PRAME	
GO:0005201	MF	extracellular matrix structural constituent	1.23E-14	6.17E-12	4.62E-11	1.23E-11	25	CTHRC1,FGG,COL1A1,COL1A2,COL3A1,COL4A1,COL4A2,COL5A1,COL5A2,COL6A1,COL6A2,COL6A3,COL8A1,COL11A1,COL15A1,VWF,COL23A1,POSTN,VCA	

								N,SPARC,PXDN,L AMA4,TGFBI,THB S2,THBS4
GO:0042803	MF	protein homodim erization activity	5.99E-10	1.20E-07	9.00E-07	6.01E-07	51	HLA- G,APOBEC3G,HM OX1,PGF,TYMS,F CER1G,CCL5,FGG ,PLEK,SERPINF2,P LOD1,VEGFA,VW F,OLFML2B,PRDX 4,COL23A1,CSF1R ,STC2,TRIM9,BHL HE41,PLVAP,GAP DH,INHBB,GBP1, GBP2,STAT1,OLF ML2A,BNIP3,GBP 5,BST2,KCNMA1, C1QB,PYGL,TAP1, HSPB8,CAV2,RUN X1,TYMP,LGALS1 ,CD2,CD3D,CD8A, HEY1,SCARB1,GZ MA,CDH2,ENO2,C DH6,TOP2A,CDH1 1,TPII
GO:0098772	MF	molecular function regulator	1.35E-06	9.69E-05	7.26E-04	1.36E-03	67	PTTG1,CMTM3,IL 32,RRAD,PGF,AD M,SAA1,SAA2,SA A4,SERPINE2,SE MA5B,CXCL9,FGF 11,CCL5,SEMA6A, SERPINF2,VEGFA ,COL6A3,WAS,FG D2,RGS5,SCG5,AN XA4,BIRC3,APOC 1,PPP1R3C,IGFBP 3,TRIB3,STC2,SH3 PXD2A,TNFSF13B ,ADAP2,PROS1,G APDH,INHBB,CX CL10,CCND1,SIRP A,C10orf99,PTHLH ,ASAP1,NRP1,SPI NK13,BMP1,PXDN ,BST2,C3,MCUB,R AC2,DOCK2,NOL3 ,CALU,IL18BP,CA V1,TYMP,SERPIN H1,RGS1,RGS10,T GFA,THBS4,TIMP 1,CCNB2,ANGPTL 4,SERPINE1,CD70, CDC20,NCKAP1L
GO:0044877	MF	protein- containing complex binding	8.77E-06	3.39E-04	2.54E-03	8.80E-03	50	PTTG1,ABCA1,HL A- A,CORO1C,PFKP, FCER1G,FCGR1A, FCGR2A,MMP9,A

									POL2,VCAM1,COL3A1,VIM,COL5A1,VWF,WAS,UBD,ABLM3,SLC6A3,ISG15,CSPG4,FSCN1,FYB1,CDCA5,PROS1,SPARC,PSMB9,CCND1,ITGA5,ITGB2,MLKL,KCNMA1,TAPBP,DOCK2,SYNM,ESM1,CAV1,LCP1,SERPINH1,OLR1,TGFB1,THBS4,CD8A,P4HB,CD36,SCARB1,CD20,CDH2,HCLS1,NCKAP1L
GO:0016491	MF	oxidoreductase activity	1.93E-05	5.37E-04	4.02E-03	1.93E-02	39	HK2,CYGB,PFKFB4,HMOX1,PFKP,SCD,ALDOC,PLOD1,PLOD2,VCAM1,DDIT4,GPX8,PRDX4,CP,HSD3B7,SH3PXD2A,SOD2,CYBB,IDO1,GAPDH,CYP2J2,NDUFA4L2,BCAT1,PXDN,PDIAS,TBXAS1,EGLN3,P4HA2,PLOD3,CAV1,LDHA,P4HA1,P4HB,LOX,SCARB1,GZMA,STEAP3,ENO2,TPI1	
GO:0030234	MF	enzyme regulator activity	1.05E-04	1.95E-03	1.46E-02	1.05E-01	40	PTTG1,SERPINE2,CCL5,SERPINF2,COL6A3,WAS,RGS5,SCG5,ANXA4,BIRC3,APOC1,PPP1R3C,IGFBP3,TRIB3,SH3PXD2A,ADAP2,PROS1,GAPDH,CXCL10,CCND1,SIRPA,ASAP1,NRP1,SPINK13,BST2,C3,RAC2,DOCK2,NOLL3,CALU,CAV1,SERPINH1,RGS1,REGS10,TIMP1,CCNB2,ANGPTL4,SERPINE1,CDC20,NCKAP1L	
GO:0008233	MF	peptidase activity	4.72E-02	1.79E-01	1.00E+00	1.00E+00	34	PTTG1,SERPINE2,STAMBPL1,MMP9,SERPINF2,VEGFA,COL6A3,VASH1,SHMT2,BIRC3,IFI16,CTSZ,PROS1,GAPDH,PSMB8,PS	

								MB9,STAT1,SPIN K13,BMP1,BST2,C 1R,C1S,C2,C3,EGL N3,RHBD2,NOL3 ,CAV1,SERPINH1, TIMP1,GZMA,GZ MK,SERPINE1,CD C20
GO:0016773	MF	phosphotr ansferase activity, alcohol group as acceptor	5.46E-02	1.87E-01	1.00E+0 0	1.00E+00	37	HK2,PDGFRL,PDG FRB,CORO1C,PFK FB4,PFKP,PHKA2, SAA1,FCGR1A,CC L5,ALDOC,VEGF A,FGD2,CSF1R,TR IB3,CSPG4,PNCK, NEK6,GAPDH,RA SSF2,CXCL10,AX L,CCND1,ITPKA,N RP1,MLKL,KISS1 R,CXCR4,HSPB8,R AC2,CAV1,TGFA, CCNB2,ENO2,DCL K1,TPI1,NCKAP1L
GO:0060089	MF	molecular transducer activity	6.26E-02	2.02E-01	1.00E+0 0	1.00E+00	45	ABCA1,PDGFRL,P DGFRB,HLA- DQA1,HLA- DQA2,HLA- DQB1,LY96,FCER 1G,FCGR1A,FCGR 2A,APLNR,CCL5,S EMA6A,VEGFA,F PR3,NLGN1,CSF1 R,IL2RB,CXCL10, AXL,TNFRSF6B,I L20RB,CCND1,IT GB2,NRP1,KISS1R ,PXD, CXCR4, AC KR3,NPTX2,LAG3, IL18BP,EDNRB,T GFA,CD2,CD3D,C D8A,CD14,NETO2, CCNB2,CD86,CD3 6,SCARB1,SERPIN E1,ADGRE5

Table 6 The enriched GO terms of the down-regulated differentially expressed genes

GO ID	CATEGORY	GO Name	P Value	FDR B&H	FDR B&Y	Bonferroni	Gene Count	Gene
GO:0072001	BP	renal system development	1.40E-17	7.69E-14	7.07E-13	7.69E-14	36	CDKN1C,MECOM, CLCNKB,HOXD11 ,HPGD,UMOD,FO XC1,COL4A3,COL 4A4,FRAS1,SFRP1, AQP1,AQP2,ARG2 ,SLC12A1,SLC34A

								1,ASS1,CTSH,GAT A3,KLHL3,PROM1 ,NPHS2,ALDH1A2, GPC3,KCNJ1,WN K4,CA2,TCF21,RB P4,RDH10,REN,TF AP2A,EMX2,TACS TD2,IRX2,EPCAM
GO:0006082	BP	organic acid metabolic process	5.34E-16	9.78E-13	8.99E-12	2.94E-12	68	EPHX2,ACAA1,G GT6,PIPOX,SCD5, ACY1,ACOX2,AD H1A,ADH1C,CKB, CKMT1B,CKMT2, PRODH2,FBP1,HP D,HPGD,HOGA1,P LA2G4F,ALDOB,A LDH6A1,AMT,HA CD3,HYAL1,ST6G AL1,CYP4F2,ACS F2,SLC22A12,SLC 4A1,ARG2,PTGR1, SLC34A1,ACOT11, ASS1,OGDHL,MP C1,ALDH4A1,G6P C,SORD,ATP6V1B 1,CYP4A11,GATM ,FTCD,GSTO2,SU CLG1,PTGDS,DDC ,PHGDH,CEACAM 1,PPARGC1A,ALD H1A2,BPHL,IER3, GLDC,KIT,HSD17 B8,SLC27A2,CKM T1A,DPEP1,RDH1 0,SLC7A8,EGF,QP RT,PAH,AGMAT, HADH,PCCA,DCX R,PCK1
GO:0001822	BP	kidney development	7.66E-16	1.05E-12	9.67E-12	4.21E-12	33	CDKN1C,CLCNKB ,HOXD11,HPGD,U MOD,FOXC1,COL 4A3,COL4A4,FRA S1,SFRP1,AQP1,A QP2,ARG2,SLC12 A1,SLC34A1,ASS1 ,CTSH,GATA3,KL HL3,PROM1,NPHS 2,ALDH1A2,GPC3, KCNJ1,WNK4,CA2 ,TCF21,RDH10,RE N,TFAP2A,TACST D2,IRX2,EPCAM
GO:0043436	BP	oxoacid metabolic process	3.12E-15	2.86E-12	2.63E-11	1.72E-11	66	EPHX2,ACAA1,G GT6,PIPOX,SCD5, ACY1,ACOX2,AD H1A,ADH1C,CKB, CKMT1B,CKMT2, PRODH2,FBP1,HP

									D,HPGD,HOGA1,P LA2G4F,ALDOB,A LDH6A1,AMT,HA CD3,HYAL1,ST6G AL1,CYP4F2,ACS F2,SLC4A1,ARG2, PTGR1,SLC34A1, ACOT11,ASS1,OG DHL,MPC1,ALDH 4A1,SORD,ATP6V 1B1,CYP4A11,GA TM,FTCD,GSTO2, SUCLG1,PTGDS,D DC,PHGDH,CEAC AM1,PPARGC1A, ALDH1A2,BPHL,I ER3,GLDC,KIT,HS D17B8,SLC27A2,C KMT1A,DPEP1,RD H10,SLC7A8,EGF, QPRT,PAH,AGMA T,HADH,PCCA,DC XR,PCK1
GO:0006811	BP	ion transport	7.06E-14	5.55E-11	5.10E-10	3.88E-10	85	PCP4,SLC25A25,A BCB1,SLC22A6,A TP6V1G3,CLIC5,S LC22A8,CLCNKA, CLCNKB,RAPGEF 3,SCN2A,SCNN1A, SCNN1B,SCNN1G, PLA2G4F,ATP6V1 C2,ATP6V0D2,PL CG2,HSPA2,RHCG ,ANK2,SLC25A4,F OLR3,ANXA3,CY P4F2,SLC13A3,TM C4,AQP1,AQP2,A QP6,CRHBP,SLC2 2A12,SLC4A1,AR G2,SLC6A12,SLC9 A2,SLC12A1,SLC1 2A3,SLC13A1,SLC 26A7,SLC34A1,AT P6V0A4,CLDN16, MPC1,ATP1A1,FX YD2,G6PC,TMEM 30B,ATP6V1B1,PR SS8,SPINK1,CYP4 A11,BSPRY,FXYD 4,SLC30A2,PTGER 3,SLC22A7,SLC36 A2,CEACAM1,GP D1L,KLHL3,PPAR GC1A,KCNJ1,KCN J15,WNK4,CA2,SL C27A2,CA4,NEDD 4L,RTN4,RBP4,CA SR,LCN2,SLC44A4 ,SYT7,LDLR,CLD N10,SLC7A8,USP2	

									.PLLP,EGF,SLC16 A5,NIPAL1,LTF,S LC4A11
GO:0048878	BP	chemical homeostasis	2.93E-12	1.61E-09	1.48E-08	1.61E-08	64	EPHX2,ACOX2,C KB,ATP6V1G3,SC NN1A,SCNN1B,SC NN1G,UMOD,NR3 C2,ATP6V1C2,AT P6V0D2,PLCG2,R HCG,NAPSA,ANK 2,HACD3,CYP4F2, SUCNR1,AQP1,AQ P2,SLC4A1,SLC6A 12,MT1E,MT1F,M T1G,MT1H,MT1M, SLC9A2,SLC12A1, SLC12A3,SLC34A 1,ATP6V0A4,CLD N16,ATP1A1,CTS H,G6PC,ATP6V1B 1,CYP4A11,GCGR, PTGER1,SLC30A2, PTGER3,PTH1R,G PD1L,KLHL3,PPA RGC1A,TMEM178 A,C7,WNK4,KNG1 ,CA2,CA4,NEDD4 L,RTN4,RBP4,CAS R,FAM3B,LCN2,L DLR,SLC7A8,LTF, CDH1,PCK1,SLC4 A11	
GO:0060429	BP	epithelium development	2.36E-11	9.97E-09	9.17E-08	1.30E-07	66	CDKN1C,FOXQ1, MECOM,ABCB1,H OXB5,TFCP2L1,C LIC5,HOXD11,RA PGEF3,CGN,SCNN 1B,SCNN1G,UMO D,FLRT3,FOXC1,R HCG,COL4A4,FRA S1,SHROOM3,SFR P1,AGR2,ID1,SOS TDC1,CLDN3,AQP 1,SYNE4,ARG2,CR YAA,DMRT2,CTS H,PRSS8,GATA3,S T14,PHGDH,CEAC AM1,KLHL3,PRO M1,NPHS2,ALDH1 A2,GPC3,WNK4,C A2,KRT7,RAB25,T CF21,HBEGF,RTN 4,RDH10,CASR,RE N,SLC44A4,TFAP2 A,GSTM3,TGFBR3 ,NTN4,EGF,ELF5, MST1L,MARVEL D2,EMX1,TACST D2,IRX2,CDH1,EP	

									CAM,CDH3,PCK1
GO:0006812	BP	cation transport	2.22E-09	5.56E-07	5.11E-06	1.22E-05	60	PCP4,SLC25A25,ABCB1,ATP6V1G3,SLC22A8,RAPGEF3,SCN2A,SCNN1A,SCNN1B,SCNN1G,ATP6V1C2,ATP6V0D2,PLCG2,HSPA2,RHCG,ANK2,SLC25A4,ANXA3,SLC13A3,AQP1,AQP2,CRHBP,SLC22A12,ARG2,SLC6A12,SLC9A2,SLC12A1,SLC12A3,SLC13A1,SLC34A1,ATP6V0A4,CLDN16,ATP1A1,FXYD2,ATP6V1B1,PRSS8,SPINK1,BSPRY,FXYD4,SLC30A2,PTGER3,SLC36A2,GPD1L,KLHL3,PPARGC1A,KCNJ1,KCNJ15,WNK4,NEDD4L,RTN4,CASR,LCN2,SLC44A4,SYT7,SLC7A8,USP2,EGF,NIPAL1,LTF,SLC4A11	
GO:0055085	BP	transmembrane transport	4.37E-09	9.62E-07	8.84E-06	2.41E-05	70	SLC25A25,SLC29A2,ABCB1,SORT1,SLC22A6,ATP6V1G3,CLIC5,SLC22A8,CLCNKA,CLCNKB,RAPGEF3,SCN2A,SCNN1A,SCNN1B,SCNN1G,ATP6V1C2,ATP6V0D2,PLCG2,HSPA2,RHCG,ANK2,SLC25A4,ANXA3,MFSD4A,SLC13A3,TMC4,AQP1,AQP2,AQP6,SLC47A2,CRHBP,SLC22A12,SLC4A1,SLC6A12,SLC9A2,SLC12A1,SLC12A3,SLC13A1,SLC26A7,SLC34A1,ATP6V0A4,CLDN16,MPKC1,ATP1A1,FXYD2,ATP6V1B1,PRSS8,FXYD4,SLC30A2,PTGER3,SLC22A7,SLC36A2,CEACAM1,GPD1L,PPARGC1A,GPC3,KCNJ1,KCNJ15,WNK4,CAC2,SLC27A2,NEDD	

									4L,RBP4,CASR,SLC44A4,SLC7A8,SLC16A5,NIPAL1,LT F,SLC4A11
GO:0009719	BP	response to endogenous stimulus	6.13E-08	9.63E-06	8.85E-05	3.37E-04	67	CDKN1C,ERBB2,ESRRG,ADH1C,SORT1,ATP6V1G3,RAPGEF3,HPGD,CGN,FGF9,NR3C2,ATP6V1C2,ATP6V0D2,FLRT3,HSD11B2,ALDOB,FOXC1,PAQR7,SFRP1,HYAL1,GDF15,ANXA3,SH3GL2,ID1,SOSTDC1,AQP1,CRHBP,IGFBP2,SLC34A1,ASIP,ATP6V0A4,ASS1,RASL11B,ATP1A1,CTSH,SNRPN,SORD,ATP6V1B1,GATA3,GATM,CGR,PTGER1,DDC,CEACAM1,PPARGC1A,ALDH1A2,BTG2,GPC3,KIT,CA2,RAP1GAP,TCF21,RBP4,GRB14,CASR,SHISA2,REN,LDLR,NR2F1,TGFBR3,CD9,FAM107A,PALM,PAPPA,HADH,CDH1,PCK1	
GO:0045177	CC	apical part of cell	6.33E-24	1.86E-21	1.29E-20	3.72E-21	50	ERBB2,MAL,ACPP,ABCB1,CLIC5,CLCNKB,PROM2,RAPGEF3,SCNN1A,SCNN1B,SCNN1G,UMOD,PLAT,ATP6V0D2,MUC20,RHCG,SHROOM3,ANK2,CYP4F2,AQP1,AQP2,AQP6,SLC22A12,SLC12A1,IGFBP2,SLC12A3,SLC34A1,ATP6V0A4,ATP1A1,MUC1,TJP3,ATP6V1B1,CYP4A11,PTH1R,CEACAM1,PROM1,REEP6,CA2,CA4,DPEP1,RAB17,CASR,REN,SLC44A4,LDLR,MAL2,CD9,MARVELD2,CDH1,EPCAM	
GO:0031226	CC	intrinsic component of	2.18E-09	1.60E-07	1.11E-06	1.28E-06	69	ERBB2,SLC29A2,SLC22A6,CLCNKA,	

		plasma membrane							CLCNKB,PIGR,PR OM2,HS6ST1,SCN 2A,SCNN1A,SCNN 1B,SCNN1G,GPC5, FLRT3,PLXNB1,IL 17RB,RHCG,SLC2 5A4,FOLR3,TMC4, CLDN3,AQP1,AQP 2,AQP6,SLC4A1,S LC6A12,SLC12A3, SLC13A1,SLC26A 7,SLC34A1,ATP1A 1,FXYD2,MUC1,C XADR,PRRG2,PRS S8,FXYD4,GCGR, PTGER1,PTGER3, PLPPR1,ST14,SLC 22A7,PTH1R,CEA CAM1,PROM1,NP HS2,GPC3,KCNJ1, KCNJ15,C7,KIT,C A4,HBEGF,RTN4, CASR,SYT7,LDLR ,SLC7A8,TGFBR3, CD9,SLC16A5,TSP AN7,TSPAN8,TM7 SF2,PALM,TMPRS S2,CDH16,SLC4A1 1
GO:0099081	CC	supramolecular polymer	2.22E-05	5.88E-04	4.09E-03	1.31E-02	51	PCP4,ERBB2,ACP P,PGM5,ABCB1,M FAP4,CLIC5,PRO M2,RAPGEF3,CG N,SCNN1A,MUC2 0,COL4A3,COL4A 4,DCDC2,SHROO M3,FBLN5,ANK2, NICN1,AQP1,CRH BP,SLC22A12,SLC 4A1,SLC9A2,SLC3 4A1,ATP6V0A4,SC IN,CTSH,CXADR, ATP6V1B1,MYH1 0,TUBB2B,AIF1L, PTGER3,PTH1R,C EACAM1,DEFB1,P ROM1,PVALB,SY NE2,CA2,CA4,KIF 13B,DPEP1,KRT7, GSTM3,FAM107A, PALM,BEX4,PAC RG,DCXR	
GO:0120038	CC	plasma membrane bounded cell projection part	8.42E-05	1.71E-03	1.19E-02	4.95E-02	55	GPHN,JADE1,LMT K3,WLS,NDRG2,A BHD17C,ABCB1,S ORT1,CKB,PROM 2,RAPGEF3,SCN2 A,SCNN1A,UMOD ,PLA2G4F,FLRT3,	

									MUC20,DCDC2,ANK2,ANXA3,SH3GL2,AQP1,CRHBP,SLC22A12,SLC34A1,ATP6V0A4,CTSH,INPP5J,CXADR,MYH10,LZTS3,ANKRD9,AIF1L,PTGER3,PTH1R,CEACAM1,DEFB1,PROM1,PPARGC1A,SYNE2,CA4,KIF13B,DPEP1,RAP1GAP,RAB25,RAB17,RTN4,CASR,SYT7,GSMT3,MAL2,FAM107A,PALM,PACRG,CDH1
GO:0098805	CC	whole membrane	6.96E-04	9.74E-03	6.78E-02	4.09E-01	51	ERBB2,MAL,ACPP,WLS,ABHD17C, SORT1,SLC22A6, ATP6V1G3,PIGR,PROM2,UMOD,PLA2G4F,ATP6V1C2,ATP6V0D2,FYB2,PARM1,ANK2,SLC25A4,ANXA3,SH3GL2,AQP1,AQP2,SYNE4,SLC26A7,SLC34A1,ATP6V0A4,ASS1,ATP1A1,CXADR,ATP6V1B1,PROSS8,SLC30A2,CEACAM1,NPHS2,BPHL,REEP6,SYNE2,ITM2C,SLC27A2,CA4,RAB17,HBEGF,GRB14,SYT7,LDLR,MAL2,PLLP,EGF,CD9,CDH1,SERPINA5	
GO:0005739	CC	mitochondrion	3.67E-02	1.34E-01	9.32E-01	1.00E+00	45	ACAA1,HMGCS2,SLC25A25,ADH1C,CKB,CKMT1B,CKMT2,PRODH2,TFCP2L1,HOGA1,ALDH6A1,HSPA2,AMT,ANK2,SLC25A4,HACD3,AGR2,OLFM4,ACSF2,ARG2,HIGD1A,ACOT11,EFHD1,ASS1,OGDHL,MPC1,ALDH4A1,SORD,KLK6,GATM,SUCLG1,STAPI,PPARGC1A,BPHL,IER3,GLDC,SYNE2,HSD17B8,SLC27A2,CKMT1A,	

								AGMAT,HADH,P ACRG,PCCA,PCK 1
GO:0005794	CC	Golgi apparatus	3.90E-02	1.38E-01	9.58E-01	1.00E+00	40	MAL,ACPP,HEPA CAM2,LMTK3,WL S,NDRG2,SORT1, CLIC5,HPD,HS6ST 1,UMOD,ALB,GPC 5,PARM1,MUC20, GDF15,RHOBTB3, SH3GL2,ID1,ST6G AL1,AQP2,CRHBP ,ATP1A1,MUC1,T MEM30B,FTCD,PT GDS,DEFB1,GPC3, PCSK1N,ITM2C,C A4,RAP1GAP,NED D4L,MAN1C1,GR B14,TFAP2A,LDL R,H1F0,CDH1
GO:0005789	CC	endoplasmic reticulum membrane	4.42E-02	1.53E-01	1.00E+00	1.00E+00	28	CDS1,ERMP1,SCD 5,WLS,SORT1,HP D,NR3C2,FLRT3,H SD11B2,ALDOB,H ACD3,CYP4F2,G6 PC,CYP4A11,FTC D,PTGDS,REEP6,T MEM178A,SYNE2, DIO1,SLC27A2,C3 orf52,RTN4,RDH10 ,GPAT3,SHISA2,T M7SF2,SHISA3
GO:0031967	CC	organelle envelope	4.69E-02	1.58E-01	1.00E+00	1.00E+00	32	HMGCS2,SLC25A 25,SLC29A2,SORT 1,CKMT1B,CKMT 2,PRODH2,SLC25 A4,HACD3,AQP1, SYNE4,HIGD1A,R ANBP3L,EFHD1,A SS1,MPC1,SORD, GATM,SCRN1,SU CLG1,PTGDS,PTG ER3,NELL1,BPHL, SYNE2,DNASE1,H SD17B8,CKMT1A, RTN4,FAM3B,TM 7SF2,HADH
GO:0045202	CC	synapse	1.73E-01	3.52E-01	1.00E+00	1.00E+00	32	GPHN,ERBB2,ND RG2,SLC29A2,AB HD17C,RAPGEF3, SCN2A,PLAT,NR3 C2,FLRT3,PLG,AN K2,PPFIBP2,SH3G L2,AQP1,CRHBP,C YFIP2,ATP1A1,CX ADR,ATP6V1B1,L YPD6B,MYH10,LZ

									TS3,TUBB2B,DDC ,RTN4,CASR,SYT7 ,MAL2,FAM107A, PALM,CDH1
GO:0015075	MF	ion transmembrane transporter activity	6.02E-12	6.59E-09	4.99E-08	6.59E-09	59	SLC25A25,ABCB1, SLC22A6,ATP6V1 G3,CLIC5,SLC22A 8,CLCNKA,CLCN KB,RAPGEF3,SCN 2A,SCNN1A,SCNN 1B,SCNN1G,ATP6 V1C2,ATP6V0D2,P LCG2,HSPA2,RHC G,ANK2,SLC25A4, ANXA3,SLC13A3, TMC4,AQP1,AQP6 ,CRHBP,SLC22A1 2,SLC4A1,SLC6A1 2,SLC9A2,SLC12A 1,SLC12A3,SLC13 A1,SLC26A7,SLC3 4A1,ATP6V0A4,C LDN16,MPC1,ATP 1A1,FXYD2,ATP6 V1B1,PRSS8,FX D4,SLC30A2,SLC2 2A7,SLC36A2,CEA CAM1,GPD1L,PPA RGC1A,KCNJ1,KC NJ15,WNK4,SLC2 7A2,NEDD4L,SLC 44A4,SLC7A8,SLC 16A5,NIPAL1,SLC 4A11	
GO:0022857	MF	transmembrane transporter activity	1.42E-11	7.78E-09	5.90E-08	1.56E-08	64	SLC25A25,SLC29 A2,ABCB1,SLC22 A6,ATP6V1G3,CLI C5,SLC22A8,CLC NKA,CLCNKB,RA PGEF3,SCN2A,SC NN1A,SCNN1B,SC NN1G,ATP6V1C2, ATP6V0D2,PLCG2 ,HSPA2,RHCG,AN K2,SLC25A4,ANX A3,MFSD4A,SLC1 3A3,TMC4,AQP1, AQP2,AQP6,SLC4 7A2,CRHBP,SLC2 2A12,SLC4A1,SLC 6A12,SLC9A2,SLC 12A1,SLC12A3,SL C13A1,SLC26A7,S LC34A1,ATP6V0A 4,CLDN16,MPC1,A TP1A1,FXYD2,AT P6V1B1,PRSS8,FX YD4,SLC30A2,SL C22A7,SLC36A2,C	

									EACAM1,GPD1L,P PARGC1A,KCNJ1, KCNJ15,WNK4,SL C27A2,NEDD4L,R BP4,SLC44A4,SLC 7A8,SLC16A5,NIP AL1,SLC4A11
GO:0015318	MF	inorganic molecular entity transmembrane transporter activity	5.93E-11	2.16E-08	1.64E-07	6.49E-08	55	ABCB1,SLC22A6, ATP6V1G3,CLIC5, SLC22A8,CLCNK A,CLCNKB,RAPG EF3,SCN2A,SCNN 1A,SCNN1B,SCNN 1G,ATP6V1C2,AT P6V0D2,PLCG2,H SPA2,ANK2,ANX A3,SLC13A3,TMC 4,AQP1,AQP2,AQP 6,CRHBP,SLC4A1, SLC6A12,SLC9A2, SLC12A1,SLC12A 3,SLC13A1,SLC26 A7,SLC34A1,ATP6 V0A4,CLDN16,MP C1,ATP1A1,FXYD 2,ATP6V1B1,PRSS 8,FXYD4,SLC30A2 ,SLC36A2,CEACA M1,GPD1L,PPARG C1A,KCNJ1,KCNJ 15,WNK4,SLC27A 2,NEDD4L,RBP4,S LC7A8,SLC16A5,N IPAL1,SLC4A11	
GO:0005215	MF	transporter activity	6.83E-10	1.50E-07	1.13E-06	7.48E-07	65	SLC25A25,SLC29 A2,ABCB1,SLC22 A6,ATP6V1G3,CLI C5,SLC22A8,CLC NKA,CLCNKB,RA PGEF3,SCN2A,SC NN1A,SCNN1B,SC NN1G,ATP6V1C2, ATP6V0D2,PLCG2 ,HSPA2,RHCG,AN K2,SLC25A4,ANX A3,MFSD4A,SLC1 3A3,TMC4,AQP1, AQP2,AQP6,SLC4 7A2,CRHBP,SLC2 2A12,SLC4A1,SLC 6A12,SLC9A2,SLC 12A1,SLC12A3,SL C13A1,SLC26A7,S LC34A1,ATP6V0A 4,CLDN16,MPC1,A TP1A1,FXYD2,TM EM30B,ATP6V1B1 ,PRSS8,FXYD4,SL C30A2,SLC22A7,S	

									LC36A2,CEACAM1,GPD1L,PPARGC1A,KCNJ1,KCNJ15,WNK4,SLC27A2,NEDD4L,RBP4,SLC44A4,SLC7A8,SLC16A5,NIPAL1,SLC4A11
GO:0008324	MF	cationtransmembrane transporter activity	4.24E-08	5.81E-06	4.40E-05	4.65E-05	43	ATP6V1G3,SLC22A8,RAPGEF3,SCN2A,SCNN1A,SCNN1B,SCNN1G,ATP6V1C2,ATP6V0D2,PLCG2,HSPA2,RHCG,ANK2,ANXA3,SLC13A3,AQP1,CRHBP,SLC22A12,SLC6A12,SLC9A2,SLC12A1,SLC12A3,SLC13A1,SLC34A1,ATP6V0A4,CLDN16,ATP1A1,FXVD2,ATP6V1B1,PRSS8,FXVD4,SLC30A2,SLC36A2,GPD1L,PPARGC1A,KCNJ1,KCNJ15,WNK4,NEDD4L,SLC44A4,SLC7A8,NIPAL1,SLC4A11	
GO:0016491	MF	oxidoreductase activity	5.27E-07	4.12E-05	3.13E-04	5.77E-04	43	GPHN,ACAA1,PIPOX,SCD5,ACOX2,ADH1A,ADH1C,PRODH2,FBP1,HPD,HPGD,LOXL4,HSAD11B2,ALDOB,ALDH6A1,AOX1,CYP4F2,PHYHD1,SLC4A1,ARG2,PTGR1,AKR7A3,OGDHL,ALDH4A1,SORD,CYP4A11,DHRS4L1,GSTO2,PHGDH,GPD1L,PPARGC1A,ALDH1A2,DHDH,IER3,GLDC,DIO1,HSD17B8,RDH10,PAH,TM7SF2,HAADH,CDH3,DCXR	
GO:0042803	MF	protein homodimerization activity	6.24E-07	4.55E-05	3.45E-04	6.83E-04	44	GPHN,EPHX2,ACPP,MECOM,ACOX2,ADH1C,CKMT1B,SLC22A6,HPGD,HOGA1,NR3C2,FLRT3,FBLN5,GDF15,AGR2,SH3GL2,AOX1,OLFM4,ID1,ST6GAL1,SLC4A1,D	

								MRT2,SLC34A1,A TF3,PTH1R,CEAC AM1,GPD1L,GLD C,PVALB,TOX3,KI T,CKMT1A,RAP1 GAP,RTN4,GRB14, CASR,LCN2,TFAP 2A,GSTM3,QPRT, PAH,CDH1,CDH3, TPD52L1
GO:0046983	MF		8.91E-05	3.05E-03	2.31E-02	9.75E-02	52	GPHN,EPHX2,ERB B2,ACPP,MECOM, ACOX2,ADH1C,C KMT1B,SLC22A6, HPGD,HOGA1,NR 3C2,ATP6V1C2,FL RT3,FBLN5,GDF1 5,AGR2,SH3GL2,A OX1,OLFM4,ID1,S T6GAL1,SLC4A1, DMRT2,SLC34A1, ATF3,GATA3,TUB B2B,SUCLG1,PTH 1R,CEACAM1,GP D1L,GLDC,PVAL B,TOX3,KIT,CKM T1A,RAP1GAP,TC F21,RTN4,RBP4,G RB14,CASR,LCN2, TFAP2A,GSTM3,Q PRT,PAH,CDH1,C DH3,SLC4A11,TP D52L1
		protein dimerization activity						
GO:0005102	MF		1.72E-02	1.13E-01	8.56E-01	1.00E+00	48	GPHN,ERBB2,CA DM4,CHGB,WLS,P IGR,FGF9,PLAT,V AV3,FLRT3,PLG,P LXNB1,COL4A3,F BLN5,SFRP1,GDF 15,AGR2,AQP1,IG FBP2,ASIP,RASL1 1B,CTSH,CXADR, TCIM,GATA3,PTG ER1,STAP1,CEAC AM1,DEFB1,PPAR GC1A,PCSK1N,TA CC1,KNG1,SLC27 A2,TCF21,HBEGF, VTCN1,GRB14,CA SR,FAM3B,REN,T GFBR3,EGF,CD9,T SPAN8,PALM,NC OA7,PACRG
		signaling receptor binding						
GO:0016772	MF	transferase activity, transferring phosphorus-	3.33E-01	4.71E-01	1.00E+00	1.00E+00	39	PCP4,GPHN,CDK N1C,ERBB2,CDS1, LMTK3,CKB,CKM T1B,CKMT2,FBP1, VAV3,ALDOB,PA

containing groups

RM1,MUC20,SFRP
1,HACD3,GDF15,S
OSTDC1,SLC4A1,
HIGD1A,OGDHL,
G6PC,TCIM,SUCL
G1,STAP1,CEACA
M1,PPARGC1A,AF
AP1L2,IER3,KIT,
WNK4,CKMT1A,D
USP5,NUAK2,TGF
BR3,EGF,LTF,PCK
1,TPD52L1

Table 7 Topology table for up and down regulated genes

Regulation	Node	Degree	Betweenness	Stress	Closeness	Clustering Coefficient
Up	EGLN3	1241	0.250861	618983568	0.404015	4.70E-04
Up	PCLAF	773	0.121066	345354730	0.388354	0.001528
Up	VCAM1	635	0.084524	285800222	0.37613	0.00151
Up	CANX	580	0.103284	158725614	0.383724	0.001329
Up	SHMT2	452	0.078303	125276880	0.362636	9.15E-04
Up	IFI16	430	0.051866	175081688	0.345328	3.06E-04
Up	VIM	412	0.064665	112344794	0.372903	0.00235
Up	GAPDH	314	0.042337	74755204	0.374479	0.006101
Up	POU5F1	306	0.037123	85607058	0.342469	7.60E-04
Up	HECW2	291	0.044433	70940852	0.343002	6.25E-04
Up	STAT1	241	0.034048	48465066	0.362694	0.004114
Up	CAV1	226	0.033122	50583308	0.346539	0.003243
Up	ISG15	215	0.024125	41496992	0.355143	0.004173
Up	RUNX1	211	0.022575	55449940	0.333154	8.74E-04
Up	P4HB	189	0.01965	28844720	0.358332	0.01081
Up	LDHA	186	0.01632	28658140	0.356534	0.008672
Up	CDC20	168	0.021063	22994446	0.361503	0.007613
Up	GJA1	157	0.0144	23837330	0.347563	0.005362
Up	CALU	150	0.015791	16321080	0.358012	0.006711
Up	FKBP5	146	0.018408	24990784	0.333904	8.50E-04

Up						
Up	SERPINH1	138	0.014797	15568792	0.367856	0.013118
Up						
Up	CCND1	132	0.015711	24603794	0.333643	0.002027
Up						
Up	CORO1C	130	0.013058	15644794	0.348326	0.005844
Up						
Up	TOP2A	127	0.011452	16198434	0.351538	0.007874
Up						
Up	PDGFRB	125	0.012851	16164934	0.336789	0.007064
Up						
Up	FGF11	121	0.005679	22341998	0.318103	0
Up						
Up	CEP55	118	0.015742	15857008	0.330364	7.50E-04
Up						
Up	TPI1	115	0.008287	10492332	0.351122	0.023862
Up						
Up	PFKP	115	0.009519	14517030	0.34283	0.003635
Up						
Up	TGM2	113	0.011909	15773390	0.336838	0.005078
Up						
Up	ACLY	113	0.00634	12309858	0.346486	0.004914
Up						
Up	HSPA6	113	0.010399	12254720	0.349467	0.005373
Up						
Up	HEY1	112	0.009254	10104082	0.346222	0.011176
Up						
Up	LGALS1	108	0.012329	11357092	0.346328	0.00848
Up						
Up	APLNR	100	0.015068	22701820	0.30225	0
Up						
Up	ASPM	97	0.01057	6806314	0.34437	0.007947
Up						
Up	SH3PXD2A	96	0.009857	15593536	0.32401	0.013377
Up						
Up	ENO2	96	0.006829	6344414	0.34144	0.021053
Up						
Up	WAS	94	0.008596	15861768	0.315821	0.005495
Up						
Up	BIRC3	90	0.009748	5657548	0.342245	0.005486
Up						
Up	NEK6	90	0.008065	15967028	0.314178	0
Up						
Up	P4HA2	89	0.010792	8215390	0.322677	0.00401
Up						
Up	FSCN1	86	0.005916	8794990	0.339183	0.005882
Up						
Up	PLOD1	85	0.009079	7007482	0.34228	0.011167
Up						
Up	TRIM9	83	0.009788	14728732	0.315792	0
Up						
Up	CDH2	82	0.006066	10559296	0.320494	0.004216
Up						
Up	PRDX4	81	0.006747	5790826	0.367579	0.024667
Up						
Up	FABP5	80	0.006212	8279522	0.330124	0.010127
Up						
Up	SOD2	80	0.006325	5713596	0.328978	0.007659
Up						
Up	DCLK1	79	0.005538	8878238	0.314337	0.019799
Up						
Up	UBE2C	78	0.004803	5328674	0.321946	0.011579

Up						
Up	COL1A1	76	0.008556	5264666	0.333692	0.025176
Up	CD70	76	0.009952	11798154	0.306445	0
Up	ALDOC	72	0.00605	4687934	0.333741	0.007825
Up	PSMB9	72	0.00503	10153670	0.309925	0.016977
Up	IKBIP	71	0.009496	12035366	0.317644	0
Up	HK2	67	0.007144	4838368	0.354331	0.010403
Up	ST8SIA4	67	0.012248	10613948	0.304598	0.001923
Up	ITGA5	64	0.007049	4549876	0.337405	0.011409
Up	SAP30	60	0.005375	8332564	0.30117	5.65E-04
Up	PSMB8	60	0.001772	4706212	0.309083	0.024198
Up	NRP1	60	0.006352	4581992	0.323856	0.010889
Up	ITGB2	60	0.006909	8408980	0.312108	0.003025
Up	VSIG4	60	0.009002	9655374	0.307218	0
Up	P4HA1	60	0.004723	3583150	0.322402	0.010889
Up	PYGL	59	0.004024	3261034	0.325742	0.013158
Up	NCAPG	59	0.00726	4228574	0.343002	0.007013
Up	CXCR4	59	0.005519	3172672	0.323472	0.011278
Up	ABCA1	59	0.006954	4170432	0.33078	0.004091
Up	PRAME	58	0.003847	9114872	0.30977	0
Up	PTTG1	56	0.002826	3805260	0.319818	0.016073
Up	PPP1R18	56	0.005233	9332000	0.308873	0
Up	TYMS	56	0.005351	2996512	0.321612	0.011181
Up	CDCA5	55	0.005455	6645530	0.313298	0
Up	PLOD3	55	0.003993	4132842	0.359787	0.029753
Up	BMP1	54	0.005621	3469862	0.312982	0.006787
Up	TNFSF13B	52	0.007315	4566696	0.301516	0
Up	PLOD2	52	0.001898	2696008	0.318534	0.013878
Up	ASAP1	51	0.004311	11188980	0.314149	0
Up	C3	51	0.006877	3016876	0.312566	0.006803
Up	ADGRE5	51	0.007976	4431076	0.305116	0
Up	TAP1	50	0.004416	2660904	0.329041	0.031028

Up						
Up	PNMA2	50	0.00679	9320814	0.298182	0
Up	DYSF	50	0.005968	3687554	0.315019	0.003265
Up	SLC2A1	49	0.004706	3366462	0.364477	0.028677
Up	PRC1	48	0.003382	7811278	0.306914	0
Up	COL1A2	48	0.003186	2140154	0.326897	0.047872
Up	VEGFA	47	0.003434	2412154	0.322677	0.020202
Up	STAMBPL1	47	0.003942	6736508	0.302425	0
Up	MMP9	46	0.005149	2849206	0.294794	0.031712
Up	COL4A2	45	0.004953	2384394	0.328851	0.026578
Up	YEATS2	45	0.005294	3904858	0.318311	0.00202
Up	CAVIN3	45	0.001603	1865142	0.320886	0.030655
Up	PAG1	44	0.003677	4777982	0.306914	0
Up	CDC45	44	0.004057	2465132	0.336423	0.013742
Up	GBP2	44	0.002774	4915582	0.301024	0.002114
Up	CCL5	43	0.006384	5183190	0.30373	0.004878
Up	TRIB3	42	0.003345	5234840	0.311282	0
Up	IGFBP3	42	0.004054	1963526	0.323687	0.010976
Up	LOX	40	0.00319	1638028	0.316466	0.019915
Up	COL5A1	40	0.00319	1686710	0.319653	0.083926
Up	CCNB2	39	0.003508	5193684	0.304993	0
Up	SFRP4	39	0.002727	4437368	0.297675	0.00135
Up	RAC2	38	0.003994	1890586	0.32475	0.012698
Up	BHLHE41	38	0.003164	2889870	0.308384	0
Up	HMOX1	37	0.003665	2478934	0.313658	0
Up	SCARB1	37	0.003471	2004158	0.332165	0.022523
Up	PRDM1	36	0.00224	3278888	0.309981	0
Up	DPYSL3	36	0.003109	3462742	0.310221	0
Up	BCAT1	36	0.00465	3217572	0.293059	0.004762
Up	PDIA5	36	0.004182	3523962	0.301676	0
Up	FYB1	35	0.002533	2629956	0.306418	0.026891
Up	HSPB8	35	0.00327	5410658	0.300282	0

Up						
	NOL3	35	0.002975	2283256	0.304789	0
Up						
	AXL	35	0.00175	3151542	0.314903	0
Up						
	NUSAP1	35	0.002216	2415062	0.315252	0.00713
Up						
	RAB31	35	0.002622	3061892	0.310179	0
Up						
	LAMA4	35	0.003133	1677138	0.313269	0.006723
Up						
	COL4A1	34	0.001753	939612	0.308775	0.03629
Up						
	APOL2	34	0.003705	4816772	0.304164	0
Up						
	FCGR2A	33	0.002738	3690508	0.292958	0
Up						
	FGG	33	0.002097	1714754	0.309265	0.006452
Up						
	CD14	33	0.003112	1651182	0.295406	0.004032
Up						
	CA9	33	8.76E-04	2086168	0.299163	0
Up						
	HCLS1	32	0.002509	3320462	0.309013	0.012097
Up						
	SPARC	32	0.002648	958126	0.316011	0.068966
Up						
	BNIP3	32	0.003568	1412256	0.308454	0.004598
Up						
	VCAN	32	0.00354	1994154	0.286416	0.013793
Up						
	FSTL1	32	0.003411	2520918	0.28323	0.002016
Up						
	CSF1R	31	0.001788	5278582	0.295573	0
Up						
	RASSF2	31	0.002706	5132438	0.292343	0
Up						
	COL6A1	31	0.001955	1495894	0.316539	0.055914
Up						
	IL2RB	30	0.001287	1181950	0.312523	0.022989
Up						
	SYNM	30	0.001487	2621784	0.304925	0
Up						
	EHD2	30	0.002568	7246662	0.282467	0
Up						
	EDNRB	30	0.003502	1635350	0.298652	0.004598
Up						
	STEAP3	30	0.003515	3529838	0.291956	0
Up						
	COLGALT1	30	0.001441	1523026	0.341218	0.087356
Up						
	VWF	29	0.002415	1103608	0.309925	0.031339
Up						
	C1QA	29	0.002151	1556280	0.298743	0.039409
Up						
	CD36	29	0.002123	1536556	0.306294	0.017094
Up						
	LCP1	29	0.001451	1033906	0.309644	0.008547
Up						
	ANGPTL4	29	0.001413	2145348	0.308817	0
Up						
	LAPTM5	28	0.00227	1407336	0.292118	0

Up						
	SCD	28	0.001169	2006452	0.31757	0
Up						
	SERPINE1	27	0.001838	1930778	0.29431	0
Up						
	SERPINE2	27	0.001862	901128	0.304707	0.008547
Up						
	COL6A2	27	0.002437	1081274	0.295598	0.039886
Up						
	NETO2	26	0.001475	1753206	0.299675	0
Up						
	DOCK2	25	0.001128	1182226	0.306914	0.006667
Up						
	FCGR1A	25	0.00217	4375574	0.268316	0.007905
Up						
	FOXJ3	25	6.74E-04	1121012	0.310517	0
Up						
	PXDN	25	0.003044	1475620	0.31425	0
Up						
	BST2	24	0.001571	2179708	0.301063	0
Up						
	GJB2	24	0.002067	1007162	0.300242	0.008658
Up						
	CHST15	24	0.003287	1534180	0.301649	0
Up						
	ANXA4	24	9.85E-04	1339322	0.306817	0
Up						
	AHNAK2	24	7.76E-04	1314420	0.295662	0
Up						
	CD2	23	0.001748	900106	0.295266	0.007905
Up						
	PPP1R3C	23	0.001997	2482774	0.304517	0
Up						
	COL3A1	23	3.79E-04	356310	0.296266	0.02381
Up						
	C1QB	23	0.001553	816086	0.297506	0.063241
Up						
	CDCA2	23	0.00101	802328	0.313456	0.011858
Up						
	TNFAIP6	23	0.003378	1803632	0.264529	0.007905
Up						
	HPCAL1	23	0.001819	1836010	0.304816	0
Up						
	ACTG2	22	3.36E-04	562288	0.303676	0
Up						
	PDGFRL	22	0.002598	3054050	0.27729	0.004329
Up						
	GBP1	21	0.001519	786404	0.314874	0.040936
Up						
	CD8A	21	8.31E-04	550400	0.301263	0.013072
Up						
	COL8A1	21	9.20E-04	1901460	0.291931	0
Up						
	PHKA2	21	0.001558	1835824	0.293336	0
Up						
	ADA	21	0.001684	4352826	0.29501	0
Up						
	TYMP	21	0.001622	621310	0.310136	0.011696
Up						
	KRBA1	21	0.002055	2692044	0.278365	0
Up						
	ABCB6	21	9.12E-04	1055500	0.286801	0

Up						
Up	MLKL	20	0.001328	2108362	0.292156	0
Up	CSPG4	20	9.72E-04	1070402	0.298691	0
Up	SLFN11	20	7.17E-04	1671762	0.29588	0
Up	SIRPA	19	0.001672	1240544	0.304952	0
Up	TGFA	19	0.001017	953844	0.302384	0
Up	SERPINF2	19	0.001729	773772	0.30396	0.022059
Up	IL32	19	0.001197	1527896	0.283147	0.007353
Up	KCNMA1	19	0.001302	533224	0.296678	0.014706
Up	GZMA	19	4.01E-04	707304	0.297779	0
Up	ACKR3	19	0.001304	1364720	0.308315	0
Up	IL20RB	19	0.003086	3594924	0.281454	0
Up	EPSTI1	19	9.89E-04	1419634	0.301156	0
Up	HLX	19	7.40E-04	1095088	0.291022	0
Up	SLC6A3	18	4.86E-04	658350	0.279952	0
Up	CD3D	18	0.00106	459006	0.302989	0.044118
Up	SEMA6A	18	8.15E-04	1022722	0.285481	0
Up	STC2	18	0.001672	2857556	0.300573	0
Up	PRUNE2	18	0.001003	1174026	0.297675	0
Up	ANGPT2	17	3.98E-04	238974	0.310489	0.038095
Up	NFE2L3	17	0.002027	1800236	0.283701	0
Up	FNDC3B	17	7.76E-04	548870	0.308873	0
Up	CEMIP2	17	0.001229	1332096	0.300123	0
Up	TMSB10	17	0.001291	1788146	0.288536	0
Up	CERCAM	17	0.002141	3021970	0.272028	0
Up	NTM	17	0.001497	953496	0.292043	0
Up	DDIT4	16	3.01E-04	497928	0.299176	0
Up	THBS2	16	0.001864	1630020	0.264263	0.010989
Up	PLEK	16	7.47E-04	808376	0.279643	0
Up	CP	16	0.001153	1816470	0.256224	0
Up	SLC1A3	16	2.63E-04	490442	0.294794	0
Up	GAS2L3	16	5.51E-04	785248	0.298013	0

Up						
Up	TAPBP	15	9.57E-05	210154	0.306143	0.076923
Up	CAV2	15	3.33E-04	320382	0.309995	0.085714
Up	RRAD	15	7.44E-04	1094198	0.29691	0
Up	TIMP1	15	0.001214	1045180	0.28479	0.019048
Up	PARP14	15	7.22E-04	1108570	0.292845	0
Up	CD68	15	0.001414	614446	0.293072	0.009524
Up	OLR1	14	8.31E-04	2871724	0.290106	0
Up	INHBB	14	0.002366	2692990	0.224426	0
Up	PROS1	14	0.001399	2153000	0.28062	0
Up	SLC15A4	14	0.001107	1356644	0.278297	0.010989
Up	GBP5	14	0.001818	962746	0.271984	0
Up	CD99	14	6.96E-04	1420324	0.289466	0
Up	RHEX	14	0.001583	1674786	0.272615	0
Up	APBB1IP	14	7.92E-04	1195142	0.269099	0
Up	C1QC	13	1.49E-04	122974	0.287187	0.236364
Up	XAF1	13	7.41E-04	488728	0.297584	0.051282
Up	RGS10	13	9.13E-04	1196502	0.291856	0
Up	GPX8	13	5.56E-04	242082	0.320539	0.012821
Up	C1QL1	13	0.001212	1372944	0.281756	0
Up	NDUFA4L2	13	0.001536	1770950	0.290662	0
Up	C1R	12	7.88E-04	357766	0.282362	0.066667
Up	C1S	12	4.03E-04	296532	0.288584	0.066667
Up	CMTM3	12	9.81E-04	853872	0.294641	0
Up	PCDH17	12	0.001393	2373104	0.282	0.030303
Up	CYBB	12	9.57E-04	862182	0.288158	0.030303
Up	RGS1	12	4.74E-04	608456	0.282502	0
Up	PFKFB4	12	3.22E-04	395238	0.286548	0
Up	NLGN1	11	0.001536	2575952	0.245405	0
Up	TYROBP	11	0.002056	5782242	0.227274	0
Up	FCER1G	11	9.49E-04	3462918	0.258604	0
Up	HLA-B	11	9.80E-04	1905804	0.323702	0.044444

Up						
	GZMK	11	1.44E-04	206976	0.280978	0
Up						
	RNASET2	11	6.06E-04	341502	0.296472	0
Up						
	CTSZ	11	4.80E-04	818626	0.288121	0
Up						
	ADAP2	11	1.66E-04	237282	0.301356	0
Up						
	SLC39A14	11	3.65E-04	405316	0.299451	0
Up						
	SLC16A3	11	4.12E-04	601534	0.287454	0
Up						
	SIGLEC10	11	9.65E-04	1026750	0.292594	0
Up						
	COL23A1	11	6.13E-05	102790	0.274966	0
Up						
	SLC2A5	11	0.001324	765956	0.278558	0
Up						
	VASH1	11	9.11E-04	453536	0.291918	0.036364
Up						
	FABP7	11	6.21E-04	749168	0.273084	0
Up						
	PMEPA1	10	6.14E-04	815466	0.291594	0
Up						
	ABLM3	10	4.54E-04	692634	0.290106	0
Up						
	GAL3ST1	10	0.001599	612452	0.305116	0.022222
Up						
	SEZ6L2	10	0.001566	1571342	0.268179	0
Up						
	ISG20	10	0.001577	4827420	0.240534	0
Up						
	ABCC3	10	3.77E-04	183334	0.304259	0.111111
Up						
	CD86	9	0.001758	2203938	0.240128	0
Up						
	HLA-A	9	0.001114	1817730	0.310447	0.142857
Up						
	CXCL9	9	7.38E-04	1509160	0.230592	0
Up						
	TGFBI	9	6.84E-05	62158	0.277369	0.166667
Up						
	ZNF395	9	5.21E-04	344296	0.295112	0.027778
Up						
	PLVAP	9	9.79E-04	505398	0.275221	0
Up						
	RHBDF2	9	9.07E-04	985704	0.276034	0
Up						
	VAMP5	9	8.97E-04	954858	0.274247	0
Up						
	SLC15A3	9	1.80E-04	99438	0.26759	0.027778
Up						
	LY96	8	9.99E-05	46154	0.268052	0
Up						
	PPFIA4	8	6.56E-04	747738	0.2544	0
Up						
	CXCL10	8	1.99E-05	11676	0.229901	0.066667
Up						
	APOC1	8	3.41E-05	28664	0.242881	0
Up						
	MCUB	8	8.16E-04	406738	0.289049	0

Up						
	SCG5	8	3.27E-04	395966	0.257676	0
Up						
	NCKAP1L	8	5.94E-05	109118	0.269631	0
Up						
	ITPKA	8	3.90E-05	64982	0.275399	0
Up						
	SEMA5B	8	1.15E-05	37592	0.258996	0
Up						
	PGF	7	2.97E-05	11986	0.266982	0.5
Up						
	PTHLH	7	5.95E-04	533186	0.290947	0
Up						
	RGS5	7	3.62E-04	395546	0.282549	0
Up						
	C2	7	4.23E-04	294228	0.271012	0.095238
Up						
	ADM	7	3.08E-04	199958	0.202933	0
Up						
	MAP3K7CL	7	5.91E-04	793984	0.254476	0
Up						
	CDCA7	7	4.12E-04	746674	0.285183	0
Up						
	DEPP1	7	3.86E-05	63950	0.235503	0
Up						
	CDH6	7	8.80E-04	779332	0.258378	0
Up						
	COL5A2	7	1.60E-04	78688	0.283795	0.190476
Up						
	COL6A3	7	6.17E-05	34098	0.286922	0.238095
Up						
	NNMT	7	2.88E-04	374258	0.268231	0
Up						
	BTN3A2	6	0.001465	2156620	0.177696	0
Up						
	SEL1L3	6	3.43E-04	388138	0.28409	0
Up						
	HSD3B7	6	3.06E-04	156390	0.274678	0
Up						
	POSTN	6	8.83E-04	1647972	0.261108	0
Up						
	SLC25A43	6	1.18E-05	50446	0.29524	0
Up						
	FKBP11	6	3.44E-04	142160	0.27874	0
Up						
	CD163	5	1.54E-05	29836	0.266774	0
Up						
	CDH11	5	3.93E-05	22038	0.281083	0.1
Up						
	PLIN2	5	5.87E-04	853182	0.242492	0
Up						
	THBS4	5	2.17E-05	35412	0.271217	0
Up						
	MSC	5	8.98E-06	31596	0.276011	0
Up						
	IFI27	5	2.77E-05	15026	0.278854	0.1
Up						
	C1QTNF6	5	3.02E-04	411964	0.250726	0
Up						
	COL15A1	5	6.69E-06	10178	0.26978	0
Up						
	PRRX1	5	3.46E-04	409894	0.253097	0

Up						
	NKG7	5	5.99E-04	634982	0.254239	0
Up						
	OAS2	5	3.14E-04	268994	0.27339	0
Up						
	COL11A1	5	2.98E-04	127330	0.244648	0.2
Up						
	SPAG4	4	2.93E-04	365682	0.228883	0
Up						
	IDO1	4	3.26E-04	302534	0.270453	0
Up						
	STMN3	4	3.33E-04	460682	0.238541	0
Up						
	KISS1R	4	9.60E-07	4022	0.254466	0
Up						
	ENPP3	4	3.00E-04	441202	0.282222	0
Up						
	PLA1A	4	3.02E-04	244638	0.272364	0
Up						
	NPTX2	4	8.79E-04	1097298	0.237843	0
Up						
	EMP3	4	6.11E-04	816550	0.242242	0
Up						
	LY86	3	3.22E-04	151172	0.263182	0
Up						
	FCN3	3	0	0	0.198049	0
Up						
	SMPDL3A	3	8.10E-06	7232	0.23587	0
Up						
	CYP2J2	3	2.89E-05	29690	0.239757	0
Up						
	GALNT14	3	9.03E-05	22690	0.273456	0
Up						
	C1orf162	3	5.86E-04	707674	0.211101	0
Up						
	IFI44	3	2.93E-04	594734	0.282421	0.333333
Up						
	TMEM140	3	2.28E-04	235350	0.252957	0
Up						
	SSPN	3	1.33E-05	9876	0.226054	0
Up						
	CTHRC1	3	3.23E-05	44374	0.255668	0
Up						
	CD248	3	4.43E-06	8834	0.269109	0
Up						
	SNX10	3	1.20E-05	11216	0.271984	0
Up						
	TMEM44	3	2.99E-04	408262	0.251141	0
Up						
	HLA-G	2	1.67E-06	1780	0.250569	0
Up						
	ENTPD1	2	1.32E-06	6534	0.266701	0
Up						
	BTN3A1	2	0.001757	2587908	0.21602	0
Up						
	LAG3	2	1.09E-06	3636	0.237437	0
Up						
	CYGB	2	8.70E-07	562	0.22331	0
Up						
	ESM1	2	0	0	0.237884	1
Up						
	SLC9A9	2	4.15E-05	62316	0.266753	0

Up						
Up	OLFML2A	2	7.36E-06	19348	0.262868	0
Up	GIMAP4	2	6.02E-05	26088	0.260838	0
Up	FGD2	2	1.61E-06	1674	0.222886	0
Up	SAA4	2	7.04E-06	2916	0.24537	0
Up	MS4A7	2	1	2	1	0
Up	TBXAS1	2	2.10E-07	918	0.234782	0
Up	AQP9	2	3.78E-05	13852	0.254751	0
Up	C5orf46	2	2.93E-04	256380	0.189328	0
Up	GAL3ST4	2	5.30E-07	2588	0.275399	0
Up	HILPDA	2	2.20E-07	194	0.231272	0
Up	IRX3	2	4.90E-07	1012	0.243036	0
Up	IL18BP	1	0	0	0.210217	0
Up	TMEM91	1	0	0	0.265517	0
Up	PNCK	1	0	0	0.22987	0
Up	CES4A	1	0	0	0.26364	0
Up	EVI2B	1	0	0	0.229684	0
Up	TMEM74B	1	0	0	0.211409	0
Up	MS4A6A	1	0	0	0.229152	0
Up	HLA-F	1	0	0	0.247587	0
Up	SLCO2B1	1	0	0	0.260539	0
Up	FABP6	1	0	0	0.204704	0
Down	CDH1	693	0.259198	121547616	0.379624	5.41E-04
Down	ERBB2	333	0.129232	34741382	0.371994	0.002728
Down	ATP1A1	266	0.083063	54590882	0.34782	9.08E-04
Down	ALB	207	0.055828	45805024	0.312193	9.57E-05
Down	NEDD4L	193	0.056299	24086984	0.32576	0.001047
Down	PHGDH	161	0.03776	39008354	0.326219	6.99E-04
Down	TFAP2A	142	0.040402	21539610	0.320852	3.00E-04
Down	SORT1	138	0.041548	12963050	0.316444	2.18E-04
Down	RTN4	138	0.039431	12047478	0.339605	0.001852
Down	MYH10	132	0.02967	23545456	0.324018	1.19E-04

Down						
Down	SNRPN	131	0.037526	23772714	0.301952	0
Down	TUBB2B	120	0.026126	25106302	0.310897	0
Down	HSPA2	114	0.025534	22209396	0.316877	0
Down	CKB	110	0.020008	21499552	0.306405	0
Down	FOXQ1	106	0.027135	16594892	0.288075	0
Down	CGN	105	0.021225	6407394	0.324866	0.01685
Down	KIT	104	0.014148	7895564	0.295655	0.006212
Down	PTGER3	104	0.03145	7182912	0.302544	7.47E-04
Down	KIF13B	102	0.013459	5340844	0.300224	0.01359
Down	USP2	101	0.0296	10802748	0.324059	0.002376
Down	ATP6V1B1	94	0.025425	7025326	0.302994	0.003203
Down	ASS1	92	0.025855	7606678	0.319543	0.002996
Down	H1FO	91	0.024115	12162840	0.320751	0.001709
Down	SYNE4	85	0.02798	10088088	0.280781	0
Down	HACD3	80	0.0161	10621238	0.326136	0.002215
Down	SH3GL2	76	0.019507	6445552	0.295004	7.40E-04
Down	PCK1	72	0.015641	7415072	0.301934	0
Down	ATF3	71	0.016871	11739154	0.305742	0
Down	PLG	69	0.018702	4703886	0.304809	0.009498
Down	PLCG2	68	0.013403	4602800	0.316503	0.022115
Down	PPARGC1A	67	0.014083	6986164	0.305101	0.002261
Down	SLC25A4	66	0.010651	9642660	0.295158	0
Down	CYFIP2	64	0.014579	6579308	0.309875	4.96E-04
Down	SYNE2	59	0.011317	4805146	0.315034	0.006429
Down	GATA3	59	0.011633	9509276	0.289814	0
Down	SORD	59	0.013366	10570060	0.280472	0
Down	MUC1	56	0.009802	5383238	0.314761	0.007687
Down	DPEP1	56	0.014861	8387070	0.248754	0
Down	FOXC1	54	0.012235	5753298	0.294271	0.003017
Down	FAM107A	54	0.013618	5623864	0.283724	0
Down	MATN2	53	0.011547	3641806	0.280333	0.004706

Down						
Down	DNAJA4	52	0.007892	3152852	0.291791	8.16E-04
Down	AQP1	50	0.007986	3253014	0.281901	0.007092
Down	FBP1	49	0.00957	2744702	0.301201	0.0037
Down	PTH1R	49	0.013169	11691028	0.263731	0
Down	TUFT1	49	0.011961	6085424	0.264155	0
Down	ANK2	49	0.009814	6256720	0.282323	0
Down	HOXB5	49	0.010007	5586258	0.276405	0
Down	QPRT	48	0.010041	8926142	0.265671	0
Down	DACH1	47	0.008754	4094378	0.289303	0.00404
Down	ID1	47	0.011365	5847118	0.283092	0
Down	CD9	46	0.010479	3381142	0.286922	0.007729
Down	LTF	46	0.010058	6762572	0.289863	0
Down	TACC1	45	0.0088	7476958	0.279594	0
Down	RALYL	45	0.009411	3995994	0.269998	0
Down	ESRRG	44	0.0082	3062428	0.300579	0.005807
Down	KNG1	44	0.009694	3149642	0.277641	0.002323
Down	GSTM3	43	0.011572	4841836	0.299078	0.00122
Down	LDLR	42	0.008576	1929946	0.291691	0.001282
Down	SLC27A2	40	0.008563	8184666	0.267051	0
Down	NR3C2	39	0.004711	4737272	0.279855	0
Down	CHGB	39	0.007807	5897340	0.273847	0
Down	NELL1	39	0.009639	4282098	0.280952	0.002699
Down	PLAT	38	0.005702	1426874	0.278797	0.026984
Down	NR2F1	38	0.008207	4443108	0.275105	0
Down	GPHN	37	0.007555	2518432	0.288942	0
Down	MECOM	36	0.004729	3361560	0.289567	0
Down	RHOBTB3	36	0.007177	4574840	0.282198	0
Down	HEPACAM2	36	0.007047	5381200	0.259073	0
Down	SERPINA5	35	0.006542	3295844	0.263826	0.005682
Down	REEP6	35	0.006464	3863054	0.272163	0
Down	SLC4A1	34	0.005923	1174244	0.294356	0.020161

Down						
	PIGR	34	0.005291	4018712	0.264897	0
Down						
	OLFM4	34	0.013147	2836492	0.260718	0
Down						
	MMP7	33	0.006905	1257552	0.275269	0.005682
Down						
	PLXNB1	32	0.007588	1225364	0.292815	0.014113
Down						
	RCAN1	32	0.005243	4275550	0.283423	0
Down						
	ACAA1	32	0.007909	5938134	0.262195	0
Down						
	ALDOB	32	0.005835	2439078	0.285314	0
Down						
	TRIM2	31	0.004417	2954728	0.267374	0
Down						
	HIGD1A	31	0.004466	3128148	0.282652	0
Down						
	TGFBR3	30	0.005544	3457546	0.263785	0
Down						
	PCCA	30	0.004533	4536562	0.269027	0
Down						
	HADH	30	0.00621	3633032	0.29327	0
Down						
	ADAP1	29	0.005442	1985674	0.271322	0.005698
Down						
	ALDH4A1	29	0.005056	2262930	0.271887	0
Down						
	VAV3	29	0.003608	1238938	0.298027	0.041872
Down						
	SUCLG1	29	0.005674	5044508	0.27603	0
Down						
	SRGAP3	29	0.004324	1643774	0.278279	0.002849
Down						
	IL17RB	29	0.006084	2158032	0.264704	0
Down						
	FBLN5	28	0.004828	1996618	0.242231	0
Down						
	ACY1	28	0.005734	1281792	0.28932	0.009231
Down						
	RAB25	28	0.004743	3067438	0.269569	0
Down						
	SHROOM3	28	0.0043	1455902	0.314683	0.021164
Down						
	GPD1L	28	0.005237	1133948	0.288059	0.005291
Down						
	EGF	27	0.005617	1510972	0.303862	0.02
Down						
	SCNN1A	27	0.00265	652674	0.295879	0.086667
Down						
	CDKN1C	27	0.003245	2121992	0.268106	0
Down						
	KRT7	27	0.004209	3253364	0.278782	0
Down						
	UGT8	27	0.006099	1169348	0.273538	0.002849
Down						
	FRAS1	27	0.004978	2590188	0.265464	0
Down						
	JADE1	26	0.004512	4191992	0.270932	0
Down						
	MAL2	26	0.005189	3107026	0.274645	0.006154

Down						
Down	PACRG	26	0.002869	2179072	0.281247	0
Down	BEX2	26	0.003986	2762224	0.251209	0
Down	TLE2	25	0.005151	1615190	0.262466	0
Down	COBLL1	25	0.006927	1259472	0.299923	0.013333
Down	RAP1GAP	25	0.003142	2780928	0.262263	0
Down	AGR2	25	0.004428	2938102	0.27463	0
Down	TPD52L1	24	0.00325	1859252	0.267655	0.008658
Down	SCNN1B	24	0.001929	456866	0.287766	0.125541
Down	ACPP	24	0.004335	933510	0.297765	0.004329
Down	AGMAT	24	0.005348	1164806	0.26781	0
Down	MUC20	24	0.004232	846616	0.261885	0
Down	GRB14	23	0.002336	1770164	0.269941	0.003953
Down	BTG2	23	0.003085	1609024	0.264251	0
Down	CEACAM1	23	0.003388	4540864	0.258599	0
Down	CA2	23	0.003426	2095062	0.278446	0
Down	GPC3	23	0.004913	2502320	0.271728	0
Down	ERMP1	23	0.006078	4006476	0.277052	0
Down	BSPRY	23	0.006604	5560000	0.262615	0
Down	DCXR	22	0.004077	2335628	0.279455	0
Down	NUAK2	22	0.003371	2297660	0.286019	0
Down	PTGDS	22	0.00385	2407208	0.265298	0.010526
Down	ABCB1	22	0.003098	2258662	0.273877	0
Down	PALM	22	0.004914	2035486	0.281698	0
Down	ALDH6A1	22	0.005156	1462366	0.273671	0
Down	ST14	21	0.002164	2288906	0.25142	0
Down	ATP6V1C2	21	0.001995	742188	0.256307	0.042857
Down	CXADR	21	0.003743	1043682	0.309498	0.005848
Down	COL4A3	21	0.003993	1239518	0.2641	0.071429
Down	SCIN	21	0.002634	2420842	0.277899	0
Down	GLDC	21	0.002807	2356188	0.266855	0
Down	TSPAN7	21	0.0025	1427020	0.260265	0

Down						
Down	KLK6	21	0.002767	1275570	0.251793	0.017544
Down	S100A2	20	0.002173	1858288	0.257474	0
Down	KLHL3	20	0.002334	1030546	0.275165	0.019608
Down	LCN2	20	0.00203	1298144	0.260812	0
Down	LOXL4	20	0.002814	1412830	0.264004	0
Down	HSD17B8	20	0.006167	3274386	0.270644	0
Down	WLS	20	0.003621	2556742	0.264952	0
Down	STAP1	19	0.001868	841268	0.262764	0.011696
Down	TCEAL2	19	0.003857	1032296	0.309272	0.023392
Down	MARVELD2	19	0.003958	825126	0.304955	0.017544
Down	DUSP5	19	0.003407	1736698	0.259694	0
Down	ST6GAL1	19	0.00459	2161064	0.225851	0
Down	PAPPA	19	0.00319	812264	0.272571	0.007353
Down	SCNN1G	18	9.79E-04	301622	0.286696	0.183333
Down	WNK4	18	0.002873	817250	0.293152	0.052288
Down	CTSH	18	0.002584	1594094	0.253777	0
Down	NDRG2	18	0.003172	593632	0.30276	0.019608
Down	SCRN1	18	0.003446	2072176	0.25403	0
Down	PLEKHG3	18	0.001461	1475860	0.271105	0
Down	IER3	17	0.002196	1268854	0.271438	0
Down	PPFIBP2	17	0.003027	1380392	0.276962	0
Down	CKMT2	17	0.00215	494980	0.264237	0.038095
Down	SLC30A2	16	0.003628	2929896	0.237551	0
Down	RAPGEF3	16	0.001606	885728	0.244383	0
Down	EFHD1	16	0.003496	2194774	0.263949	0
Down	HBEGF	15	0.001718	451640	0.264732	0.038462
Down	RBP4	15	0.003202	480066	0.273333	0.019048
Down	NCOA7	15	0.002247	976248	0.281636	0
Down	RAB17	15	0.007207	2889818	0.240401	0
Down	ANXA3	15	0.001632	1364618	0.253726	0
Down	BEX1	15	0.001584	326354	0.297835	0.028571

Down						
Down	LRRN2	15	0.002353	1633262	0.243041	0
Down	CGNL1	15	0.002235	1434228	0.26743	0
Down	FGF9	14	0.002072	1555996	0.240616	0
Down	CDH3	14	3.50E-04	88384	0.289632	0.136364
Down	GSTO2	14	0.002795	398288	0.25902	0
Down	ACSF2	14	0.002419	1195996	0.244125	0
Down	PTGR1	14	0.001925	348784	0.25972	0.032967
Down	CDS1	13	0.002645	845130	0.262886	0
Down	SYT7	13	0.002143	325910	0.304208	0.012821
Down	CRHBP	13	0.001962	891290	0.239147	0
Down	CLIC5	13	0.001019	645778	0.255638	0
Down	MAL	13	0.002099	2137006	0.246108	0
Down	HOGA1	13	0.002539	1198636	0.228672	0
Down	COL4A4	13	5.57E-04	239346	0.243938	0.153846
Down	DEFB1	13	0.004132	2319076	0.213857	0
Down	RNF150	13	0.001052	876476	0.247773	0
Down	MFSD4A	13	0.002876	1257778	0.226242	0
Down	CLDN3	12	0.001707	675402	0.277324	0.030303
Down	ZNF503	12	0.002122	2134426	0.231259	0
Down	AOX1	12	0.002077	275630	0.25478	0
Down	WFDC2	12	0.002335	1479712	0.230954	0
Down	FAM171A1	12	7.83E-04	699540	0.25931	0
Down	GPAT3	12	0.001338	1012372	0.274172	0
Down	AKR7A3	11	0.002542	1002028	0.233508	0
Down	RASD1	11	0.001718	871562	0.237075	0
Down	TJP3	11	0.001523	1110118	0.257917	0
Down	PGM5	11	0.001355	902092	0.25147	0
Down	LAD1	11	0.001188	740102	0.316071	0.109091
Down	C3orf52	11	0.003199	624072	0.26954	0
Down	PLLPL	11	0.001787	1301558	0.242867	0
Down	TCF21	10	0.002071	641674	0.229932	0

Down						
Down	SLC9A2	10	8.41E-04	726412	0.251943	0
Down	REN	10	0.002421	850118	0.221468	0
Down	GDF15	10	9.45E-04	466572	0.226182	0
Down	SFRP1	10	9.71E-04	817552	0.229166	0
Down	EPCAM	10	0.001066	916664	0.251694	0
Down	AFAP1L2	10	5.07E-04	375040	0.27112	0
Down	ITM2C	10	0.001334	841336	0.232909	0
Down	NTN4	10	8.27E-04	488546	0.255496	0
Down	TACSTD2	10	0.001358	390396	0.265408	0.044444
Down	OGDHL	9	0.001286	950648	0.252543	0
Down	PIPOX	9	0.001991	855924	0.236678	0
Down	BPHL	9	0.001671	1064486	0.249253	0
Down	NICN1	9	0.003141	1226328	0.162532	0
Down	DMKN	9	0.001404	803042	0.28404	0
Down	FAM3B	9	0.002241	957248	0.245242	0
Down	EPHX2	8	0.001201	462590	0.228415	0
Down	CLDN7	8	8.49E-04	177266	0.25085	0.035714
Down	CA4	8	6.10E-04	218822	0.240196	0
Down	ATP6V0A4	8	0.001327	220926	0.249412	0
Down	IGFBP2	8	0.001385	722692	0.248888	0
Down	KCNJ1	8	3.60E-04	511496	0.244853	0
Down	EMX2	8	0.001673	178282	0.221516	0
Down	FLRT3	8	9.46E-04	423750	0.260371	0
Down	C1orf116	8	0.001256	239608	0.303881	0.035714
Down	ELF5	8	0.001593	1276782	0.20525	0
Down	RASL11B	8	8.86E-04	253820	0.284358	0
Down	CADM4	8	0.001251	333302	0.239079	0
Down	PROM1	8	5.53E-04	353608	0.251532	0
Down	FYB2	8	0.001133	191080	0.220222	0
Down	HMGCS2	8	3.54E-04	363446	0.273892	0
Down	SOSTDC1	7	0.001193	349552	0.188798	0

Down						
Down	SCN2A	7	0.001967	573630	0.221748	0
Down	CSRNP1	7	0.001524	346600	0.259205	0
Down	NAPSA	7	0.001076	500638	0.251631	0
Down	AIF1L	7	2.72E-04	211538	0.263649	0
Down	MFAP4	7	0.001534	861684	0.249608	0
Down	PTGER1	7	0.001278	216604	0.25198	0.095238
Down	HYAL1	7	5.62E-04	312888	0.227374	0
Down	TFCP2L1	7	8.00E-04	229068	0.202886	0
Down	DDC	6	1.74E-04	137232	0.237518	0
Down	PCP4	6	3.16E-04	204552	0.237031	0
Down	ALDH1A2	6	2.03E-04	85214	0.238307	0
Down	HSD11B2	6	1.14E-04	75100	0.252192	0
Down	HS6ST1	6	9.22E-04	440850	0.254411	0
Down	PCSK1N	6	8.26E-04	255270	0.19903	0
Down	HPD	6	8.85E-04	695972	0.219066	0
Down	TMEM213	6	0.001355	456676	0.222106	0
Down	INPP5J	6	4.81E-04	360496	0.224774	0
Down	SLC13A3	6	8.76E-04	555818	0.235202	0
Down	ERP27	6	5.35E-04	239288	0.222972	0
Down	GATM	6	4.27E-04	241476	0.229724	0
Down	EMX1	6	0.001575	473232	0.202337	0
Down	SCD5	6	4.15E-04	357470	0.237396	0
Down	PDE1A	6	6.15E-04	407204	0.265533	0
Down	KCNJ15	5	4.99E-04	434290	0.227832	0
Down	DNASE1	5	7.53E-05	92538	0.261724	0
Down	PAH	5	7.86E-04	409870	0.175669	0
Down	PRRG2	5	1.27E-04	85098	0.245467	0
Down	RALGPS1	5	1.88E-04	169748	0.269341	0
Down	ARG2	5	4.96E-04	156490	0.223756	0
Down	ACOT11	5	1	6	1	0
Down	CLDN10	5	5.46E-04	261576	0.227567	0

Down						
Down	PLA2G4F	5	5.86E-04	102882	0.24758	0
Down	GCGR	5	6.16E-05	44128	0.235126	0
Down	FAM102A	5	8.38E-04	479684	0.249498	0
Down	ACOX2	5	4.51E-04	109454	0.222232	0
Down	SLC6A12	4	4.06E-04	176300	0.226162	0
Down	HOXB8	4	5.17E-05	29510	0.209422	0
Down	C7	4	4.91E-04	94544	0.259734	0
Down	SHISA2	4	4.00E-04	149318	0.221016	0
Down	FTCD	4	5.34E-05	21182	0.230776	0.166667
Down	ILDR1	4	6.88E-05	16866	0.252995	0
Down	ADH1A	4	3.93E-04	171160	0.226797	0
Down	TM7SF2	4	3.41E-05	18656	0.22774	0
Down	AMT	4	1.31E-04	53966	0.240049	0
Down	CYP4A11	4	0.001179	240162	0.218558	0
Down	TMPRSS2	4	2.44E-05	15064	0.232314	0
Down	RDH10	4	1.56E-04	64698	0.248002	0
Down	TOX3	4	7.24E-04	84984	0.260345	0
Down	SPINK1	4	7.93E-04	482734	0.215815	0
Down	SLC7A8	3	3.93E-04	129966	0.226595	0
Down	LMTK3	3	1.37E-04	75538	0.248123	0
Down	PHYHD1	3	9.73E-05	53214	0.245894	0
Down	RHCG	3	0	0	0.188693	0
Down	CLCNKA	3	0	0	0.189628	0
Down	RANBP3L	3	4.74E-05	27784	0.226898	0
Down	PRSS8	3	6.05E-05	72732	0.25213	0
Down	DCDC2	3	7.86E-04	377482	0.239732	0
Down	CDH16	3	9.54E-06	23934	0.249779	0
Down	MPC1	3	1.79E-05	9352	0.219567	0
Down	ANKRD9	2	1	2	1	0
Down	EMCN	2	3.93E-04	142098	0.19322	0
Down	CAPS	2	2.90E-04	293354	0.279963	0

Down						
Down	ABHD17C	2	3.63E-06	5564	0.217336	0
Down	SLC16A5	2	1.25E-05	10006	0.244806	0
Down	SLC44A4	2	1.01E-05	3798	0.203551	0
Down	PAQR7	2	1.33E-05	7712	0.239947	0
Down	MT1F	2	8.36E-06	1256	0.203567	0
Down	DHDH	2	5.79E-06	3378	0.208641	0
Down	TMEM45B	2	3.93E-04	59996	0.196624	0
Down	DNASE1L3	2	9.45E-06	5968	0.200971	0
Down	TCIM	2	1.60E-05	11436	0.231458	0
Down	MT1H	2	3.93E-04	137864	0.187194	0
Down	VTCN1	2	1	2	1	0
Down	MT1M	2	3.93E-04	224492	0.2036	0
Down	PROM2	2	2.17E-04	33892	0.283818	0
Down	MTURN	2	1.08E-04	118012	0.254297	0
Down	GPC5	2	3.93E-04	188742	0.23971	0
Down	MAN1C1	2	3.11E-05	10948	0.232463	0
Down	SLC29A2	2	1.40E-05	9546	0.203559	0
Down	DIO1	2	0	0	0	0
Down	SLC22A7	1	0	0	1	0
Down	SUCNR1	1	0	0	0.210001	0
Down	FOLR3	1	0	0	0.166514	0
Down	MST1L	1	0	0	1	0
Down	MT1G	1	0	0	0.196601	0
Down	MT1E	1	0	0	0.226857	0
Down	SHISA3	1	0	0	0.200852	0
Down	C2orf40	1	0	0	0.191772	0
Down	LYPD6B	1	0	0	0.183516	0
Down	PVALB	1	0	0	0.18903	0
Down	BEX4	1	0	0	0.227955	0
Down	TMC4	1	0	0	0.198657	0
Down	DMRT2	1	0	0	1	0

Down						
Down	FAM151A	1	0	0	0.239687	0
Down	GGT6	1	0	0	0.215824	0
Down	HPGD	1	0	0	0.239687	0
Down	FXYD2	1	0	0	0.258074	0
Down	TMEM178A	1	0	0	0.217197	0

Table 7 miRNA - target gene interaction table

Regulation	Target Genes	Degree	MicroRNA	Regulation	Target Genes	Degree	MicroRNA
UP	SOD2	257	hsa-mir-4424	Down			
UP	CCND1	197	hsa-mir-5009-3p	Down	BTG2	227	hsa-mir-4319
UP	SCD	167	hsa-mir-3671	Down	VAV3	164	hsa-mir-5001-5p
UP	VEGFA	108	hsa-mir-4497	Down	LDLR	123	hsa-mir-3121-3p
UP	SH3PXD2A	105	hsa-mir-6818-5p	Down	FOXC1	103	hsa-mir-5688
UP	C3	93	hsa-mir-4432	Down	SYT7	75	hsa-mir-4270
UP	FNDC3B	89	hsa-mir-3689b-3p	Down	AGMAT	74	hsa-mir-548p
UP	DDIT4	82	hsa-mir-5688	Down	TGFBR3	67	hsa-mir-1238-3p
UP	CANX	80	hsa-mir-6825-5p	Down	PLCG2	66	hsa-mir-4458
UP	OLR1	80	hsa-mir-4433b-3p	Down	ERBB2	66	hsa-mir-4677-5p
UP	THBS2	79	hsa-mir-4326	Down	PIGR	66	hsa-mir-6720-5p
UP	ADM	77	hsa-mir-4495	Down	RHOBTB3	64	hsa-mir-4664-5p
UP	SERPINH1	76	hsa-mir-5197-3p	Down	TMEM30B	64	hsa-mir-548ae-5p
UP	FKBP5	72	hsa-mir-4443	Down	HOXB5	58	hsa-mir-6133
UP	CALU	67	hsa-mir-4289	Down	SLC4A1	57	hsa-mir-588
UP	LHFPL2	65	hsa-mir-1260a	Down	SORD	55	hsa-mir-6847-3p
UP	ENTPD1	64	hsa-mir-6503-3p	Down	CLIC5	54	hsa-mir-2276-5p
UP	OLFML2A	64	hsa-mir-4709-5p	Down	EMCN	54	hsa-mir-6769b-3p
UP	RRAD	62	hsa-mir-3934-5p	Down	G6PC	53	hsa-mir-3666
UP	STC2	62	hsa-mir-147a	Down	ITM2C	50	hsa-mir-4747-5p
UP	PAG1	60	hsa-mir-548ax	Down	TFAP2A	49	hsa-mir-6165
UP	RUNX1	60	hsa-mir-2115-3p	Down	DMRT2	48	hsa-mir-4436b-5p

UP	CAV1	58	hsa-mir-4468	Down	RDH10	46	hsa-mir-7977
UP	TMEM91	58	hsa-mir-3689c	Down	SCD5	44	hsa-mir-5691
UP	CEP55	57	hsa-mir-3666	Down	ALDH6A1	43	hsa-mir-3064-5p
UP	SYNM	57	hsa-mir-4705	Down	RCAN1	43	hsa-mir-6873-3p
UP	HSPA6	57	hsa-mir-6499-3p	Down	ANKRD9	42	hsa-mir-4294
UP	VCAM1	53	hsa-mir-3127-5p	Down	MUC20	42	hsa-mir-4433a-3p
UP	FSCN1	53	hsa-mir-3180	Down	AQP6	42	hsa-mir-4478
UP	PNMA2	52	hsa-mir-7849-3p	Down	PLLP	41	hsa-mir-3975
UP	FOXJ3	51	hsa-mir-3139	Down	PAQR7	41	hsa-mir-6781-3p
UP	CD3D	51	hsa-mir-4284	Down	RHCG	41	hsa-mir-6821-3p
UP	BCAT1	50	hsa-mir-548ac	Down	EPHX2	40	hsa-mir-6817-3p
UP	BTN3A2	50	hsa-mir-5693	Down	TRIM2	40	hsa-mir-6828-5p
UP	CCL5	48	hsa-mir-5095	Down	CYP4A11	39	hsa-mir-6880-5p
UP	CDH6	48	hsa-mir-4664-5p	Down	FOXQ1	38	hsa-mir-4782-5p
UP	HMOX1	47	hsa-mir-3180-5p	Down	QPRT	38	hsa-mir-5693
UP	SLC2A1	47	hsa-mir-5703	Down	SLC16A5	38	hsa-mir-7111-3p
UP	NETO2	45	hsa-mir-548az-5p	Down	UGT8	37	hsa-mir-4477a
UP	PMEP1	44	hsa-mir-4436b-3p	Down	HOXD11	37	hsa-mir-5698
UP	HLA-B	44	hsa-mir-3620-5p	Down	GPC5	36	hsa-mir-548j-3p
UP	LDHA	43	hsa-mir-4305	Down	H1F0	36	hsa-mir-664a-3p
UP	RGS5	42	hsa-mir-6868-3p	Down	SCIN	35	hsa-mir-3150a-3p
UP	STMN3	42	hsa-mir-6766-5p	Down	TJP3	35	hsa-mir-4419a
UP	COL4A1	41	hsa-mir-8070	Down	SLC29A2	34	hsa-mir-4450
UP	CERCAM	41	hsa-mir-4295	Down	GSTO2	33	hsa-mir-1184
UP	SLC29A4	41	hsa-mir-548al	Down	SLC22A6	33	hsa-mir-3911
UP	COL8A1	39	hsa-mir-6847-3p	Down	EMX2	33	hsa-mir-6727-3p
UP	TRIB3	39	hsa-mir-1299	Down	NIPAL1	33	hsa-mir-6807-5p
UP	HLA-A	39	hsa-mir-6127	Down	MARVELD2	31	hsa-mir-1179
UP	SLC25A43	38	hsa-mir-4459	Down	RTN4	31	hsa-mir-4524b-5p
UP	SLC2A5	38	hsa-mir-6834-5p	Down	CLDN16	31	hsa-mir-4659b-3p
UP	GIMAP4	37	hsa-mir-548ae-5p	Down	SHROOM3	30	hsa-mir-3607-3p

UP	EGLN3	37	hsa-mir-5590-3p	Down	NEDD4L	30	hsa-mir-7843-3p
UP	PFKP	37	hsa-mir-3609	Down	TFCP2L1	29	hsa-mir-3160-5p
UP	SHMT2	36	hsa-mir-4322	Down	HOXB8	29	hsa-mir-3191-3p
UP	C1QTNF6	36	hsa-mir-4733-3p	Down	ILDR1	29	hsa-mir-548aq-3p
UP	TGFA	36	hsa-mir-6817-3p	Down	KLHL3	29	hsa-mir-5701
UP	NPTX2	35	hsa-mir-5197-5p	Down	SLC25A25	29	hsa-mir-604
UP	CYGB	34	hsa-mir-1255a	Down	FGF9	29	hsa-mir-6833-3p
UP	STEAP3	33	hsa-mir-6803-5p	Down	HBEGF	27	hsa-mir-4659b-3p
UP	EHD2	33	hsa-mir-6779-5p	Down	FAM107A	26	hsa-mir-6826-3p
UP	VASH1	32	hsa-mir-3977	Down	PCK1	25	hsa-let-7f-2-3p
UP	CD99	32	hsa-mir-4707-3p	Down	NICN1	25	hsa-mir-4753-5p
UP	CXCL10	32	hsa-mir-3065-5p	Down	TUFT1	25	hsa-mir-759
UP	RASSF2	32	hsa-mir-3612	Down	ATP1A1	24	hsa-mir-3685
UP	UBD	31	hsa-mir-4469	Down	SHISA2	24	hsa-mir-4284
UP	PRUNE2	30	hsa-mir-548ag	Down	SFRP1	24	hsa-mir-4700-5p
UP	RAB31	30	hsa-mir-5190	Down	KIT	23	hsa-mir-4490
UP	IL20RB	30	hsa-mir-4446-5p	Down	ALDH1A2	23	hsa-mir-4733-5p
UP	SIGLEC10	30	hsa-mir-5699-3p	Down	RNF150	23	hsa-mir-5003-3p
UP	TPI1	29	hsa-mir-1207-5p	Down	PPARGC1A	23	hsa-mir-5585-3p
UP	COL5A1	29	hsa-mir-6883-5p	Down	WDR72	23	hsa-mir-5590-5p
UP	SSPN	29	hsa-mir-3689d	Down	HIGD1A	22	hsa-mir-3074-3p
UP	PXDN	28	hsa-mir-6749-3p	Down	ATF3	22	hsa-mir-3614-3p
UP	PSMB9	28	hsa-mir-6890-3p	Down	ZNF503	22	hsa-mir-3689c
UP	CORO1C	27	hsa-mir-1199-5p	Down	RAB25	22	hsa-mir-4520-3p
UP	GAPDH	27	hsa-mir-769-3p	Down	ACPP	22	hsa-mir-5197-5p
UP	VIM	27	hsa-mir-3135b	Down	KCNJ15	22	hsa-mir-6771-3p
UP	COL1A2	27	hsa-mir-4725-3p	Down	EGF	22	hsa-mir-6893-5p
UP	ITGA5	26	hsa-mir-3130-5p	Down	NUAK2	22	hsa-mir-7154-3p
UP	TAPBP	26	hsa-mir-5690	Down	COBLL1	21	hsa-mir-520d-5p
UP	FSTL1	25	hsa-mir-3689b-5p	Down	TACC1	21	hsa-mir-5692c
UP	GPX8	25	hsa-mir-4724-5p	Down	ACY1	21	hsa-mir-6764-5p

UP	STAMBPL1	24	hsa-mir-548p	Down	DUSP5	20	hsa-mir-363-3p
UP	CHST15	24	hsa-mir-660-3p	Down	GSTM3	20	hsa-mir-6791-3p
UP	P4HB	24	hsa-mir-378d	Down	SLC12A3	19	hsa-mir-4524a-3p
UP	SAA1	24	hsa-mir-4441	Down	IER3	19	hsa-mir-4703-5p
UP	SLC39A14	23	hsa-mir-4729	Down	RAB17	19	hsa-mir-4749-5p
UP	SEMA6A	23	hsa-mir-4289	Down	COL4A3	19	hsa-mir-548ap-3p
UP	PCDH17	23	hsa-mir-548ba	Down	S100A2	18	hsa-mir-296-5p
UP	SEL1L3	22	hsa-mir-7111-3p	Down	ATP6V1G3	18	hsa-mir-362-3p
UP	CDCA7	22	hsa-mir-4804-3p	Down	LTF	18	hsa-mir-3664-5p
UP	TGFB1	22	hsa-mir-5588-3p	Down	COL4A4	18	hsa-mir-4302
UP	TMEM74B	22	hsa-mir-1470	Down	DMKN	18	hsa-mir-4701-3p
UP	CYBB	22	hsa-mir-4640-3p	Down	PAPPA	18	hsa-mir-4770
UP	PRDM1	21	hsa-mir-3157-3p	Down	SLC36A2	18	hsa-mir-6771-5p
UP	CAV2	21	hsa-mir-365a-5p	Down	HSPA2	18	hsa-mir-6811-3p
UP	FGG	21	hsa-mir-6089	Down	PHGDH	17	hsa-mir-1178-5p
UP	SLFN11	21	hsa-mir-6077	Down	EMX1	17	hsa-mir-2110
UP	IL2RB	21	hsa-mir-6127	Down	IL17RB	17	hsa-mir-4722-5p
UP	NCAPG	20	hsa-mir-664b-3p	Down	NCOA7	17	hsa-mir-4789-5p
UP	SERPINE1	20	hsa-mir-6882-5p	Down	PLEKHG3	17	hsa-mir-548c-3p
UP	SNX10	20	hsa-mir-3160-5p	Down	BSPRY	17	hsa-mir-5690
UP	CD86	20	hsa-mir-7110-3p	Down	ATP6V1B1	17	hsa-mir-6129
UP	HSPB8	20	hsa-mir-6079	Down	CDH1	17	hsa-mir-888-5p
UP	HLX	20	hsa-mir-1260b	Down	FBLN5	16	hsa-mir-2277-3p
UP	CDH2	19	hsa-mir-1244	Down	ERMP1	16	hsa-mir-4720-3p
UP	SIRPA	19	hsa-mir-2355-5p	Down	DCDC2	16	hsa-mir-5692a
UP	CD36	19	hsa-mir-4438	Down	SLC22A12	16	hsa-mir-3199
UP	OAS2	19	hsa-mir-4306	Down	SCRN1	15	hsa-mir-1273e
UP	IFI44L	19	hsa-mir-3921	Down	RASD1	15	hsa-mir-139-3p
UP	TMEM44	19	hsa-mir-3613-3p	Down	PALM	15	hsa-mir-6753-5p
UP	ALDOC	19	hsa-mir-7106-3p	Down	FAM102A	14	hsa-mir-296-3p
UP	AXL	18	hsa-mir-4421	Down	SYNE2	14	hsa-mir-21-5p

UP	APOL2	18	hsa-mir-588	Down	GATM	14	hsa-mir-297
UP	SPARC	18	hsa-mir-4792	Down	TPD52L1	14	hsa-mir-203a-3p
UP	HILPDA	18	hsa-mir-6790-3p	Down	ATP6V0D2	14	hsa-mir-665
UP	CD68	18	hsa-mir-4282	Down	ST6GAL1	13	hsa-mir-526b-5p
UP	COL23A1	18	hsa-mir-4680-5p	Down	ASS1	13	hsa-mir-606
UP	AHNAK2	17	hsa-mir-6165	Down	ACSF2	13	hsa-mir-4459
UP	PPFIA4	17	hsa-mir-4700-5p	Down	DNASE1L3	13	hsa-mir-7156-3p
UP	TOP2A	17	hsa-mir-203a-3p	Down	TMEM45B	13	hsa-mir-3679-3p
UP	PRC1	17	hsa-mir-633	Down	SLC26A7	12	hsa-mir-409-3p
UP	FBXO17	17	hsa-mir-4514	Down	MAN1C1	12	hsa-mir-8055
UP	GJA1	16	hsa-mir-4266	Down	SCNN1G	12	hsa-mir-937-5p
UP	HSD3B7	16	hsa-mir-377-5p	Down	BEX4	12	hsa-mir-3941
UP	IKBIP	16	hsa-mir-16-1-3p	Down	SLC25A4	11	hsa-mir-4775
UP	MSC	16	hsa-mir-4481	Down	SLC27A2	11	hsa-mir-4469
UP	NCKAP1L	16	hsa-mir-5685	Down	MT1E	11	hsa-mir-545-3p
UP	DUXA	16	hsa-mir-3199	Down	PARM1	11	hsa-mir-4422
UP	STAT1	15	hsa-mir-7158-3p	Down	ESRRG	11	hsa-mir-5580-5p
UP	ABCA1	15	hsa-mir-33a-5p	Down	ELF5	11	hsa-mir-520a-5p
UP	LOX	15	hsa-mir-3591-5p	Down	C3orf52	11	hsa-mir-4279
UP	PRRX1	15	hsa-mir-4791	Down	PDE1A	11	hsa-mir-8063
UP	CDC20	14	hsa-mir-188-5p	Down	PROM1	11	hsa-mir-4452
UP	GAS2L3	14	hsa-mir-4690-5p	Down	FTCD	11	hsa-mir-7155-5p
UP	ACLY	14	hsa-mir-361-5p	Down	C1orf116	11	hsa-mir-6833-5p
UP	SCARB1	14	hsa-mir-223-3p	Down	PTGER3	11	hsa-mir-514b-3p
UP	HPCAL1	14	hsa-mir-6165	Down	PROM2	11	hsa-mir-3689d
UP	PLEK	14	hsa-mir-520a-5p	Down	DNAJA4	10	hsa-mir-218-5p
UP	VCAN	13	hsa-mir-6777-3p	Down	SORT1	10	hsa-mir-376a-3p
UP	SERPINF2	13	hsa-mir-6833-3p	Down	ADAP1	10	hsa-mir-8070
UP	LAMA4	13	hsa-mir-7705	Down	MAL2	10	hsa-mir-4719
UP	COL4A2	12	hsa-mir-29a-3p	Down	AQP2	10	hsa-mir-4779
UP	HECW2	12	hsa-mir-7977	Down	CKB	9	hsa-mir-346

UP	ADAP2	12	hsa-mir-5095	Down	TCF21	9	hsa-mir-5088-5p
UP	DPYSL3	12	hsa-mir-3667-3p	Down	PCCA	9	hsa-mir-455-5p
UP	COL1A1	12	hsa-mir-516b-3p	Down	PLA2G4F	9	hsa-mir-2116-3p
UP	POU5F1	12	hsa-mir-6754-3p	Down	IRX2	9	hsa-mir-4504
UP	TYMS	11	hsa-mir-433-3p	Down	SLC30A2	9	hsa-mir-5589-5p
UP	PDIA5	11	hsa-mir-513a-5p	Down	HADH	8	hsa-mir-151a-3p
UP	NNMT	11	hsa-mir-6500-3p	Down	WLS	8	hsa-mir-3682-3p
UP	IGFBP3	11	hsa-mir-1909-5p	Down	ID1	8	hsa-mir-520h
UP	ST8SIA4	11	hsa-mir-487a-5p	Down	FXYD2	8	hsa-mir-4999-5p
UP	NRP1	10	hsa-mir-338-3p	Down	TMEM213	8	hsa-mir-3166
UP	SAP30	10	hsa-mir-5096	Down	TUBB2B	7	hsa-mir-877-5p
UP	MMP9	9	hsa-mir-451a	Down	MYH10	7	hsa-mir-1274a
UP	UBE2C	9	hsa-mir-140-3p	Down	CGN	7	hsa-mir-4705
UP	CXCR4	9	hsa-mir-133b	Down	MUC1	7	hsa-mir-455-3p
UP	ASAP1	9	hsa-mir-136-3p	Down	KRT7	7	hsa-mir-199a-3p
UP	LAPTM5	9	hsa-mir-4656	Down	CGNL1	7	hsa-mir-130b-5p
UP	KRBA1	9	hsa-mir-4766-5p	Down	CLDN10	7	hsa-mir-6801-3p
UP	CES4A	9	hsa-mir-4269	Down	PRR15L	7	hsa-mir-590-3p
UP	LCP1	8	hsa-mir-520a-3p	Down	RASL11B	7	hsa-mir-4652-3p
UP	COL3A1	8	hsa-mir-29c-3p	Down	GATA3	6	hsa-mir-29b-3p
UP	BTN3A1	8	hsa-mir-106b-5	Down	NR3C2	6	hsa-mir-944
UP	PLOD2	8	hsa-mir-136-5p	Down	HPGD	6	hsa-mir-4289
UP	PDGFRB	8	hsa-mir-29b-3p	Down	CKMT1A	6	hsa-mir-107
UP	C1R	8	hsa-mir-6817-3p	Down	RAPGEF3	6	hsa-mir-4286
UP	NLGN1	8	hsa-mir-5088-5p	Down	KCNJ1	6	hsa-mir-5009-3p
UP	PLOD1	7	hsa-mir-23b-3p	Down	HS6ST1	6	hsa-mir-3185
UP	CTHRC1	7	hsa-mir-630	Down	SUCNR1	6	hsa-mir-4501
UP	PTTG1	7	hsa-mir-655-3p	Down	XPNPEP2	6	hsa-mir-4502
UP	COL5A2	7	hsa-mir-222-3p	Down	CDKN1C	5	hsa-mir-221-3p
UP	CD248	7	hsa-mir-758-3p	Down	ACAA1	5	hsa-mir-10a-5p
UP	TGM2	7	hsa-mir-127-3p	Down	ABCB1	5	hsa-mir-451a

UP	HK2	7	hsa-mir-7-5p	Down	CA2	4	hsa-mir-99b-3p
UP	C1S	7	hsa-mir-548s	Down	CXADR	4	hsa-mir-342-3p
UP	FABP7	7	hsa-mir-16-1-3p	Down	FAM171A1	4	hsa-mir-103a-3p
UP	ZNF395	7	hsa-mir-125b-5p	Down	MMP7	4	hsa-mir-148a-3p
UP	SLC15A4	7	hsa-mir-302d-5p	Down	RALGPS1	4	hsa-mir-377-3p
UP	GJB2	7	hsa-mir-5704	Down	GGT6	4	hsa-mir-7702
UP	FCGR2A	7	hsa-mir-512-5p	Down	HSD17B8	3	hsa-mir-16-5p
UP	ESM1	7	hsa-mir-6887-3p	Down	OLFM4	3	hsa-let-7c-5p
UP	ASPM	6	hsa-let-7a-5p	Down	USP2	3	hsa-let-7f-5p
UP	CCNB2	6	hsa-let-7c-3p	Down	GPD1L	3	hsa-mir-210-3p
UP	IFI16	6	hsa-let-7c-5p	Down	PLAT	3	hsa-mir-204-5p
UP	COL6A1	6	hsa-mir-1301-3p	Down	BEX1	3	hsa-mir-15b-5p
UP	GBP2	6	hsa-mir-4709-5p	Down	SUCLG1	3	hsa-mir-339-5p
UP	ANXA4	6	hsa-mir-548u	Down	LOXL4	3	hsa-mir-124-3p
UP	PRDX4	6	hsa-mir-1229-3p	Down	MT1F	3	hsa-mir-219a-5p
UP	P4HA1	6	hsa-mir-941	Down	GPC3	3	hsa-mir-520c-3p
UP	CDCA2	6	hsa-mir-18a-3p	Down	CDS1	3	hsa-mir-223-3p
UP	YEATS2	5	hsa-mir-205-5p	Down	DIO1	3	hsa-mir-224-5p
UP	TMSB10	5	hsa-mir-101-5p	Down	ST14	3	hsa-mir-27b-3p
UP	NEK6	5	hsa-mir-1307-3p	Down	ANK2	3	hsa-mir-122-5p
UP	BNIP3	5	hsa-mir-27a-3p	Down	CDH3	3	hsa-mir-9-5p
UP	COL6A2	5	hsa-mir-3928-3p	Down	CYFIP2	3	hsa-mir-149-5p
UP	NTM	5	hsa-mir-501-5p	Down	TACSTD2	3	hsa-mir-155-5p
UP	ABCB6	4	hsa-mir-7113-5p	Down	PAH	3	hsa-mir-590-3p
UP	ANGPTL4	4	hsa-mir-1-1	Down	SPINK1	2	hsa-mir-1-1
UP	IFI44	4	hsa-mir-146a-5p	Down	TOX3	2	hsa-mir-149-5p
UP	IFI27	4	hsa-mir-942-5p	Down	INPP5J	2	hsa-mir-346
UP	CDCA5	4	hsa-mir-331-3p	Down	SH3GL2	2	hsa-mir-330-3p
UP	TMEM45A	4	hsa-mir-181a-5p	Down	CASR	2	hsa-mir-31-5p
UP	CMTM3	4	hsa-mir-24-3p	Down	CKMT1B	2	hsa-mir-92a-3p
UP	COL15A1	4	hsa-mir-29c-3p	Down	RAP1GAP	2	hsa-mir-192-5p

UP	CTSZ	4	hsa-mir-615-3p	Down	NTN4	2	hsa-mir-196a-5p
UP	SMPDL3A	4	hsa-mir-376a-5p	Down	AGR2	2	hsa-mir-197-3p
UP	TIMP1	4	hsa-mir-3155b	Down	NR2F1	2	hsa-mir-181b-5p
UP	PYGL	4	hsa-mir-155-5p	Down	BEX2	2	hsa-mir-204-5p
UP	RHBDF2	4	hsa-mir-98-5p	Down	DACH1	2	hsa-mir-217
UP	BMP1	4	hsa-mir-29b-3p	Down	AIF1L	2	hsa-mir-1229-3p
UP	ABCC3	4	hsa-mir-197-3p	Down	ALDOB	2	hsa-mir-378a-3p
UP	HLA-DQA1	4	hsa-mir-122-5p	Down	PGM5	2	hsa-mir-124-3p
UP	FPR3	4	hsa-mir-572	Down	NDRG2	2	hsa-mir-650
UP	TNFAIP6	4	hsa-mir-2052	Down	IGFBP2	2	hsa-mir-126-3p
UP	EMP3	3	hsa-mir-1-3p	Down	SLC6A12	2	hsa-mir-342-3p
UP	ISG15	3	hsa-mir-146a-5p	Down	CD9	2	hsa-mir-326
UP	ISG20	3	hsa-mir-1-1	Down	CLDN7	2	hsa-mir-484
UP	LGALS1	3	hsa-mir-22-3p	Down	OGDHL	2	hsa-mir-130b-5p
UP	TRIM9	3	hsa-mir-1-3p	Down	TM7SF2	2	hsa-mir-193b-3p
UP	SERPINE2	3	hsa-mir-30e-3p	Down	GPHN	1	hsa-let-7b-5p
UP	PLOD3	3	hsa-mir-320b	Down	KLK6	1	hsa-let-7f-5p
UP	CSF1R	3	hsa-mir-34a-5p	Down	ARG2	1	hsa-mir-16-5p
UP	CXCL9	3	hsa-mir-26b-5p	Down	CRHBP	1	hsa-mir-16-5p
UP	ITGB2	3	hsa-mir-146a-5p	Down	LMTK3	1	hsa-mir-16-5p
UP	ADA	3	hsa-mir-140-5p	Down	SLC9A2	1	hsa-mir-16-5p
UP	BIRC3	3	hsa-mir-375	Down	HYAL1	1	hsa-mir-25-3p
UP	IL32	3	hsa-mir-205-5p	Down	ACOX2	1	hsa-mir-26b-5p
UP	HLA-G	3	hsa-mir-205-5p	Down	ANXA3	1	hsa-mir-26b-5p
UP	HEY1	3	hsa-mir-30b-5p	Down	AOX1	1	hsa-mir-26b-5p
UP	CDH11	3	hsa-mir-200c-3p	Down	GRB14	1	hsa-mir-26b-5p
UP	ENO2	3	hsa-mir-99b-5p	Down	MT1M	1	hsa-mir-26b-5p
UP	FGF11	3	hsa-mir-18a-3p	Down	PACRG	1	hsa-mir-26b-5p
UP	SLCO2B1	3	hsa-mir-640	Down	PVALB	1	hsa-mir-26b-5p
UP	APLN	2	hsa-mir-10b-5p	Down	SCN2A	1	hsa-mir-26b-5p
UP	SLC16A3	2	hsa-mir-16-5p	Down	SLC22A8	1	hsa-mir-26b-5p

UP	PDGFRL	2	hsa-mir-25-3p	Down	SNRPN	1	hsa-mir-26b-5p
UP	APOBEC3G	2	hsa-mir-26b-5p	Down	SNURF	1	hsa-mir-26b-5p
UP	CA9	2	hsa-mir-98-5p	Down	PCSK1N	1	hsa-mir-31-5p
UP	PHKA2	2	hsa-mir-149-5p	Down	HOGA1	1	hsa-mir-92a-3p
UP	P4HA2	2	hsa-mir-9-5p	Down	PIPOX	1	hsa-mir-197-3p
UP	HLA-F	2	hsa-mir-324-3p	Down	AFAP1L2	1	hsa-mir-34a-5p
UP	TNFSF13B	2	hsa-mir-215-5p	Down	PLXNB1	1	hsa-mir-214-3p
UP	INHBB	2	hsa-mir-34a-5p	Down	LYPD6B	1	hsa-mir-218-5p
UP	KCNMA1	2	hsa-mir-211-5p	Down	ACOT11	1	hsa-mir-124-3p
UP	C2	2	hsa-mir-142-3p	Down	CTSH	1	hsa-mir-124-3p
UP	ANGPT2	2	hsa-mir-542-3p	Down	FRAS1	1	hsa-mir-124-3p
UP	VAMP5	2	hsa-mir-9-5p	Down	MFAP4	1	hsa-mir-124-3p
UP	BHLHE41	2	hsa-mir-186-5p	Down	SCNN1A	1	hsa-mir-125b-5p
UP	CD8A	2	hsa-mir-196b-5p	Down	ALDH4A1	1	hsa-mir-128-3p
UP	PFKFB4	2	hsa-mir-92b-3p	Down	KNG1	1	hsa-mir-128-3p
UP	PROS1	2	hsa-mir-494-3p	Down	ADH1A	1	hsa-mir-132-3p
UP	TBXAS1	2	hsa-mir-34b-3p	Down	ADH1C	1	hsa-mir-132-3p
UP	CDC45	2	hsa-mir-455-3p	Down	LCN2	1	hsa-mir-138-5p
UP	CYP2J2	1	hsa-let-7b-5p	Down	DDC	1	hsa-mir-145-5p
UP	NUSAP1	1	hsa-let-7b-5p	Down	ATP6V1C2	1	hsa-mir-9-5p
UP	C1QB	1	hsa-mir-26b-5p	Down	AQP1	1	hsa-mir-320a
UP	GAL3ST1	1	hsa-mir-26b-5p	Down	WNK4	1	hsa-mir-296-5p
UP	PSMB8	1	hsa-mir-26b-5p	Down	CHGB	1	hsa-mir-375
UP	RNASET2	1	hsa-mir-26b-5p	Down	AMT	1	hsa-mir-335-5p
UP	SFRP4	1	hsa-mir-26b-5p	Down	CD5L	1	hsa-mir-335-5p
UP	PTHLH	1	hsa-mir-33a-5p	Down	FAM151A	1	hsa-mir-335-5p
UP	TYMP	1	hsa-mir-92a-3p	Down	FAM3B	1	hsa-mir-335-5p
UP	TNFRSF6B	1	hsa-mir-34a-5p	Down	FXYD4	1	hsa-mir-335-5p
UP	ABLIM3	1	hsa-mir-214-3p	Down	GDF15	1	hsa-mir-335-5p
UP	OLFML2B	1	hsa-mir-30b-5p	Down	KIF13B	1	hsa-mir-335-5p
UP	CSPG4	1	hsa-mir-124-3p	Down	NPHS2	1	hsa-mir-335-5p

UP	GBP1	1	hsa-mir-124-3p	Down	PRRG2	1	hsa-mir-335-5p
UP	PARP14	1	hsa-mir-124-3p	Down	PRSS8	1	hsa-mir-335-5p
UP	SLC1A3	1	hsa-mir-124-3p	Down	PTGDS	1	hsa-mir-335-5p
UP	SLC9A9	1	hsa-mir-124-3p	Down	REN	1	hsa-mir-335-5p
UP	TUBA3D	1	hsa-mir-124-3p	Down	RERGL	1	hsa-mir-335-5p
UP	EVI2B	1	hsa-mir-142-3p	Down	SOSTDC1	1	hsa-mir-335-5p
UP	EPSTI1	1	hsa-mir-146a-5p	Down	VTGN1	1	hsa-mir-335-5p
UP	RGS1	1	hsa-mir-374a-5p	Down	GLDC	1	hsa-mir-423-3p
UP	PPP1R18	1	hsa-mir-324-5p	Down	ALB	1	hsa-mir-492
UP	APOC1	1	hsa-mir-335-5p	Down	EFHD1	1	hsa-mir-193b-3p
UP	C10orf99	1	hsa-mir-335-5p	Down	DHRS4	1	hsa-mir-181d-5p
UP	C1QA	1	hsa-mir-335-5p	Down	LRRN2	1	hsa-mir-671-5p
UP	CD14	1	hsa-mir-335-5p	Down	TMEM116	1	hsa-mir-127-5p
UP	COL11A1	1	hsa-mir-335-5p	Down	DCXR	1	hsa-mir-744-5p
UP	FABP6	1	hsa-mir-335-5p	Down	TSPAN7	1	hsa-mir-744-5p
UP	FGD2	1	hsa-mir-335-5p				
UP	FNDC1	1	hsa-mir-335-5p				
UP	GAL3ST4	1	hsa-mir-335-5p				
UP	GZMK	1	hsa-mir-335-5p				
UP	IL18BP	1	hsa-mir-335-5p				
UP	NDUFA4L2	1	hsa-mir-335-5p				
UP	NKG7	1	hsa-mir-335-5p				
UP	PPP1R3C	1	hsa-mir-335-5p				
UP	RARRES2	1	hsa-mir-335-5p				
UP	TMEM140	1	hsa-mir-335-5p				
UP	XAF1	1	hsa-mir-335-5p				
UP	TAP1	1	hsa-mir-346				
UP	HCLS1	1	hsa-mir-484				
UP	ITPKA	1	hsa-mir-193b-3p				
UP	RAC2	1	hsa-mir-193b-3p				
	FCER1G	1	hsa-mir-1225-3p				

Degree – No of miRNA interact with target gene. We taken any one miRNA in table.

Table 9 TF - target gene interaction table

Regulation	TF	Degree	Target Gene	Regulation	TF	Degree	Target Gene
Up	FOXC1	217	THBS2	Down	GATA2	175	FOXQ1
Up	GATA2	173	VCAN	Down	YY1	126	EFHD1
Up	YY1	102	MLKL	Down	FOXL1	86	NCOA7
Up	FOXL1	100	RHBDF2	Down	USF2	84	PTH1R
Up	E2F1	90	COL11A1	Down	NFIC	83	MUC20
Up	HINFP	86	RUNX1	Down	SRF	78	HADH
Up	TFAP2A	86	NDUFA4L2	Down	E2F1	77	CGN
Up	NFIC	82	GAS2L3	Down	NFKB1	75	FXVD4
Up	TP53	77	SNX10	Down	JUN	69	PRSS8
Up	PPARG	73	EVI2B	Down	PPARG	68	RHCG
Up	USF2	72	NCKAP1L	Down	RELA	67	TFAP2A
Up	NFKB1	71	PTHLH	Down	STAT3	64	MMP7
Up	RELA	71	FOXJ3	Down	CREB1	63	FTCD
Up	JUN	69	LHFPL2	Down	POU2F2	63	ERP27
Up	SRF	68	C1S	Down	MEF2A	59	ATP6V0A4
Up	POU2F2	60	BTN3A2	Down	HINFP	57	DACH1
Up	SREBF1	58	CAV2	Down	HNF4A	55	EMCN
Up	CREB1	53	APOL2	Down	SREBF1	55	AMT
Up	NFYA	52	SEL1L3	Down	HOXA5	47	MARVELD2
Up	STAT3	48	HLA-DQB1	Down	TP53	46	CD9
Up	HNF4A	47	RASSF2	Down	NFYA	44	ACAA1
Up	HOXA5	44	HLA-F	Down	TFAP2C	41	CYFIP2
Up	MEF2A	43	SAA4	Down	TEAD1	36	BEX4
Up	GATA3	42	PXDN	Down	ELK1	35	SYT7

Up	MAX	42	IL18BP	Down	MAX	34	NEDD4L
Up	FOS	40	IDO1	Down	RUNX2	34	TACC1
Up	FOXA1	38	ADA	Down	NR3C1	34	INPP5J
Up	TFAP2C	37	VEGFA	Down	STAT1	33	REEP6
Up	CEBPB	35	GAL3ST1	Down	JUND	31	AOX1
Up	RUNX2	34	ALDOC	Down	SREBF2	30	TOX3
Up	NR3C1	34	OLFML2A	Down	PRRX2	29	TSPAN7
Up	PRRX2	33	TMEM140	Down	BRCA1	29	MECOM
Up	SP1	33	IRX3	Down	USF1	29	PPARGC1A
Up	USF1	33	PSMB9	Down	ESR1	29	SYNE2
Up	ESR1	33	TGFA	Down	PAX2	29	EGF
Up	TEAD1	32	DYSF	Down	IRF2	28	REN
Up	ARID3A	31	VAMP5	Down	TP63	28	IER3
Up	TP63	31	LOX	Down	ARID3A	26	BEX2
Up	ELK4	30	DPYSL3	Down	CEBPB	26	PLG
Up	KLF5	29	HEY1	Down	PRDM1	26	SORT1
Up	ELK1	28	PLOD2	Down	FOXA1	26	PAH
Up	JUND	27	BCAT1	Down	SP1	25	ATP1A1
Up	BRCA1	26	LDHA	Down	E2F6	24	MUC1
Up	PAX2	26	MS4A6A	Down	KLF5	24	HS6ST1
Up	SREBF2	25	ISG15	Down	NKX3-2	23	TMPRSS2
Up	E2F6	24	TYMP	Down	FOS	23	ACY1
Up	IRF2	24	SCD	Down	ELK4	23	DNASE1L3
Up	EN1	23	CXCL9	Down	ZNF354C	21	RASL11B
Up	ZNF354C	22	CAV1	Down	FOXF2	19	NAPSA
Up	NR2F1	21	TYROBP	Down	EN1	19	LDLR
Up	FOXF2	21	TEX11	Down	SPIB	16	CKB
Up	SPIB	18	POU5F1	Down	SOX10	13	UGT8
Up	NKX3-2	18	HCLS1	Down	SOX5	12	LTF
Up	SOX10	14	SPARC	Down	PDX1	9	CA2
Up	EGR1	13	C1QC	Down	NKX2-5	9	QPRT

Up	PDX1	12	VASH1	Down	NRF1	9	SCNN1B
Up	NRF1	12	BNIP3	Down	EGR1	9	ID1
Up	SOX17	12	VIM	Down	SOX17	9	FAM171A1
Up	FOXI1	10	CALU	Down	SRF	8	COBLL1
Up	NKX2-5	9	NPTX2	Down	REL	7	ALDH4A1
Up	ELF5	9	SERPINF2	Down	E2F4	4	CASR
Up	REL	8	RRAD	Down	ARNT	4	ANXA3
Up	NOBOX	8	CANX	Down	KLF4	4	MYH10
Up	SOX5	8	NTM	Down	FOXD1	3	SHISA3
Up	NFATC2	7	TBXAS1	Down	FEV	3	HYAL1
Up	SRF	6	CD86	Down	FOXI1	3	RALYL
Up	MYB	6	HMOX1	Down	NKX3-1	3	PTGER3
Up	NKX3-1	4	CMTM3	Down	NR2E3	3	KNG1
Up	NR4A2	3	C2	Down	GATA1	3	SERPINA5
Up	NR2E3	3	HLA-A	Down	SOX9	2	TFCP2L1
Up	GATA1	3	UBD	Down	FOXO3	2	SLC22A12
Up	NFYB	3	TOP2A	Down	NOBOX	2	RNF150
Up	SOX9	2	COL15A1	Down	NFATC2	2	HEPACAM2
Up	FEV	2	ISG20	Down	NFYB	2	GPC3
Up	E2F4	2	CDCA7	Down	ESR2	1	CRHBP
Up	HNF1B	2	C1R	Down	GABPA	1	FAM102A
Up	ARNT	1	RARRES2	Down	RUNX1	1	SLC4A11
Up	MYCN	1	RARRES2	Down	HNF1B	1	TMEM213
Up	MYC	1	RARRES2	Down	MYB	1	SHROOM3
Up	ZFX	1	PPP1R18				
Up	KLF4	1	NETO2				

Degree – No of TF interact with target gene. We taken any one TF in table

Figures

Fig. 1. Box plots of the gene expression data before normalization (A) and after normalization (B). Horizontal axis represents the sample symbol and the vertical axis represents the gene expression values. The black line in the box plot represents the median value of gene expression. (A1 – A9 = normal renal tissues samples; B1 – B26 = metastatic ccRCC tissues samples)

Fig. 2. Volcano plot of differentially expressed genes. Genes with a significant change of more than two-fold were selected.

Fig. 3. Heat map of up regulated differentially expressed genes. Legend on the top left indicate log fold change of genes. (A1 – A9 = normal renal tissues samples; B1 – B26 = metastatic ccRCC tissues samples)

Fig. 4. Heat map of down regulated differentially expressed genes. Legend on the top left indicate log fold change of genes. (A1 – A9 = normal renal tissues samples; B1 – B26 = metastatic ccRCC tissues samples)

Fig. 5. Protein-protein interaction network of up regulated genes. Green nodes denotes up regulated genes.

Fig. 6. Scatter plot for up regulated genes. (A- Node degree; B- Betweenness centrality; C- Stress centrality ; D- Closeness centrality; E- Clustering coefficient)

Fig. 7. Protein-protein interaction network of down regulated genes. Red nodes denotes down regulated genes.

Fig. 8. Scatter plot for down regulated genes. (A- Node degree; B- Betweenness centrality; C- Stress centrality ; D- Closeness centrality; E- Clustering coefficient)

Fig. 9. Modules in PPI network. The green nodes denote the up regulated genes

Fig. 10. Modules in PPI network. The red nodes denote the down regulated genes

Fig. 11. The network of up regulated target gene and their related miRNAs. The green circles nodes are the up regulated target gene, and orange diamond nodes are the miRNAs

Fig. 12. The network of down regulated target gene and their related miRNAs. The red circles nodes are the down regulated target gene, and blue diamond nodes are the miRNAs

Fig. 13. Target gene - TF network of predicted target up regulated genes. (Orange triangle - TFs and green circles - target up regulated genes)

Fig. 14. Target gene - TF network of predicted target down regulated genes. (Blue triangle - TFs and red circles - target down regulated genes)

Fig. 15. Overall survival analysis of hub genes (up regulated). Overall survival analyses were performed using the UALCAN online platform. A) CANX B) SHMT2 C) IFI16 D) P4HB E) CALU

Fig. 16. Overall survival analysis of hub genes (down regulated). Overall survival analyses were performed using the UALCAN online platform. A) CDH1 B) ERBB2 C) NEDD4L D) TFAP2A E) SORT1

Fig. 17. Box plots (expression analysis) hub genes (up regulated genes) were produced using the UALCAN platform. A) CANX B) SHMT2 C) IFI16 D) P4HB E) CALU

Fig. 18. Box plots (expression analysis) hub genes (down regulated genes) were produced using the UALCAN platform. A) CDH1 B) ERBB2 C) NEDD4L D) TFAP2A E) SORT1

Fig. 19. Box plots (stage analysis) of hub genes (up regulated) were produced using the UALCAN platform. A) CANX B) SHMT2 C) IFI16 D) P4HB E) CALU

Fig. 20. Box plots (stage analysis) of hub genes (down regulated) were produced using the UALCAN platform. A) CDH1 B) ERBB2 C) NEDD4L D) TFAP2A E) SORT1

Fig. 21. Mutation analyses of hub genes were produced using the CbioPortal online platform

Fig. 22 Immuno histochemical analyses of hub genes were produced using the human protein atlas (HPA) online platform. A) CANX B) SHMT2 C) IFI16 D) P4HB E) CALU F) CDH1 G) ERBB2 H) NEDD4L I) TFAP2A J) SORT1

Fig. 23. ROC curve validated the sensitivity, specificity of hub genes as a predictive biomarker for GBM prognosis. A) CANX B) SHMT2 C) IFI16 D) P4HB E) CALU F) CDH1 G) ERBB2 H) NEDD4L I) TFAP2A J) SORT1

Fig. 24. Validation of microarray data by quantitative PCR. A) CANX B) SHMT2 C) IFI16 D) P4HB E) CALU F) CDH1 G) ERBB2 H) NEDD4L I) TFAP2A J) SORT1

Fig. 25. Scatter plot for Immune infiltration of A) ADAM15 B) BATF C) NOTCH3 D) ITGAX E) SDC1 F) RPL4 G) EEF1G H) RPL3 I) RBMX J) ABCC2 in renal cancer