Investigation of the underlying hub genes and molexular pathogensis in gastric cancer by integrated bioinformatic analyses

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Abstract

The high mortality rate of gastric cancer (GC) is in part due to the absence of initial disclosure of its biomarkers. The recognition of important genes associated in GC is therefore recommended to advance clinical prognosis, diagnosis and and treatment outcomes. The current investigation used the microarray dataset GSE113255 RNA seq data from the Gene Expression Omnibus database to diagnose differentially expressed genes (DEGs). Pathway and gene ontology enrichment analyses were performed, and a protein□protein interaction network, modules, target genes - miRNA regulatory network and target genes - TF regulatory network were constructed and analyzed. Finally, validation of hub genes was performed. The 1008 DEGs identified consisted of 505 up regulated genes and 503 down regulated genes. The pathways and GO functions of the up and down regulated genes were mainly enriched in pyrimidine deoxyribonucleosides degradation, extracellular structure organization, allopregnanolone biosynthesis and digestion. FN1, PLK1, ANLN, MCM7, MCM2, EEF1A2, PTGER3, CKB, ERBB4 and PRKAA2 were identified as the most important genes of GC, and validated by TCGA database, The Human Protein Atlas database, receiver operating characteristic curve (ROC) analysis and RT-PCR. Bioinformatics analysis might be useful method to explore the molecular pathogensis of GC. In addition, FN1, PLK1, ANLN, MCM7, MCM2, EEF1A2, PTGER3, CKB, ERBB4 and PRKAA2 might be the most important genes of GC.

Keywords: gastric cancer; bioinformatics analysis; proliferation; Gene Expression Omnibus (GEO); hub genes

Introduction

Gastric cancer (GC) presents the major cause of cancer deaths in the past few decades and has been a major public health problem [1]. GC is the fifth most frequently detected cancer in worldwide [2]. Since GC absence reliable clinical and biochemical features in the initial stages, the majority of patients are only definitively identified with GC at a leading stage. Although some routine treatments such as surgery and chemotherapy can be used, the recurrence rate is still as high [3]. Thus, investigation on GC is important, especially on its molecular pathogenesis and the identification of biomarkers that are useful for early detection, risk stratification, determination of appropriate intervention, prognostication and identification of novel therapeutic targets.

Investigation has exposed key pathways and interactions between gene modfications, and tumorigenesis and tumor advancement of various types of cancers [4]. Pathways such as Wnt pathways [5], PI3K and MAPK signaling pathways [6], Notch1 signal pathway [7], STAT and ERK2 pathways [8] and Src/FAK pathway [9] were responsible for pathogenesis of GC. Genes such as IL-10 and TNF-A [10], p53 and TGF-,RII [11], IL-17A and IL-17F [12], PFKFB-3 and PFKFB-4 [13], and Runx3 and CHFR [14] were liable for pathogenesis of GC. Thus, a complete understanding of the transcriptional modification may add to the advancement of preventive, diagnostic and therapeutic strategies for GC.

The prognosis and diagnosis of GC mainly depends on the extent of disease. With the fast advancement of gene or RNA sequencing technology, GEO, ArrayExpress and TCGA have been playing enhancing key roles in bioinformatics analysis [15-17]. These databases provide sequencing data for research of novel functional genes and pathways and for analyzing the effect of these genes on prognosis, diagnosis and therapeutic.

The current investigation aimed to improve the understanding of the molecular basis of GC and to identify novel prognostic factors for GC. The GSE113255 RNA seq dataset was downloaded from the Gene Expression Omnibus (GEO) database, in order to determine the up regulated and down regulated differentially expressed genes (DEGs) in the tumor tissues of patients with GC. Several prognosis and diagnosis related genes and pathways of GC were obtained through, pathway and gene ontology (GO) enrichment analysis, protein–protein interaction (PPI) network analysis, module analysis, target genes - miRNA regulatory network analysis and target genes – TF regulatory network analysis. To verify the prognostic roles of hub genes in GC, the GC dataset from The Cancer Genome Atlas (TCGA) was used to perform survival analysis, expression analysis, stage analysis, mutation analysis, immune histochemical (ICH) analysis and immune infiltration analysis. Secondly, the current investigation confirmed the selected findings using receiver operating characteristic (ROC) analysis), with the aim of prognostic and diagnostic value of hub genes. Finally, the most key expressed hub genes were selected and conducted for preliminary validation by real-time PCR (RT-PCR). In summery we believe that it is feasible to identify new genes linked with GC with the explained method, providing key intuition into the GC at the molecular level that guided the GC advancement and progression to full blown stages.

Materials and methods

Microarray data

RNA-seq Data relevant to GC was obtained from the GEO database and the GSE113255 (https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE113255) dataset was selected [18]. This dataset was established on a GPL18573 Illumina NextSeq 500 (Homo sapiens) platform. The GSE113255 dataset contains 107 diffuse type gastric cancer tissues samples and 10 normal gastric tissues samples.

Data pre□processing and identification of DEGs in GC

Microarray data preprocessing is associated with quality assessment, quality control, background correction and normalization. Quantile method was used to perform background correction, normalization and probe summarization [19]. The empirical Bayesian method in limma package [20] was used to perform the differential analysis, |log2 fold change (FC)| >1.5 for up regulated genes, |log2 fold change (FC)| < -1.13 for down regulated genes and adjusted P<0.05 were considered as statistically significant. Since dataset was diagnosed to have a larger sample size of both GC and healthy tissues, heat maps and volcano plots were further established from the RNA-seq data of this dataset in order to visualize DEGs.

Pathway enrichment analysis of DEGs

BIOCYC (https://biocyc.org/) [21], Kyoto Encyclopedia of Genes and Genomes (KEGG) (http://www.genome.jp/kegg/pathway.html) [22], Pathway Interaction Database (PID) (https://wiki.nci.nih.gov/pages/viewpage.action?pageId=315491760) [23], REACTOME (https://reactome.org/) [24], GenMAPP (http://www.genmapp.org/) [25], MSigDB C2 BIOCARTA (http://software.broadinstitute.org/gsea/msigdb/collections.jsp) [26], PantherDB (http://www.pantherdb.org/) [27], Pathway Ontology (http://www.obofoundry.org/ontology/pw.html) [28] and Small Molecule Pathway Database (SMPDB) (http://smpdb.ca/) [29] are a databases collection which can be used to analyze genomes, biological pathways, diseases, chemical substances and drugs. ToppGene (ToppFun) (https://toppgene.cchmc.org/enrichment.jsp) [30] was used for annotation of the pathway results. For this analyses, p<0 .05 was considered to indicate a statistically significant difference.

Gene ontology (GO) enrichment analysis of DEGs

ToppGene (ToppFun) (https://toppgene.cchmc.org/enrichment.jsp) [30] was used to perform GO enrichment analysis. GO (http://www.geneontology.org/) enrichment analysis is extensively used to annotate specific genes and gene products for high throughput genome and transcriptome data [31]. In the current investigation, GO enrichment analysis was implemented to predict the probable functions of the DEGs based on biological process (BP), molecular function (MF) and cellular component (CC). p<0.05 was set as the cutoff criterion.

PPI network construction and module analysis

We evaluated the protein–protein interaction (PPI) data using the Human Integrated Protein-Protein Interaction rEference (HIPPIE) (http://cbdm.uni-mainz.de/hippie/) database [32], which integrates with various PPI data bases such as IntAct (https://www.ebi.ac.uk/intact/) [33], BioGRID (https://thebiogrid.org/) [34], HPRD (http://www.hprd.org/) [35], MINT (https://mint.bio.uniroma2.it/) [36], BIND (http://download.baderlab.org/BINDTranslation/) [37], MIPS (http://mips.helmholtz-muenchen.de/proj/ppi/) [38] and DIP (http://dip.doe-mbi.ucla.edu/dip/Main.cgi) [39]. Cytoscape software (http://www.cytoscape.org/)

[40] was applied to visualize the protein interaction network relationships. With the plugin Network analyzer the gene lists of the top ranked in node degree [41], betweenness centrality [42], stress centrality [43], closeness centrality [44] and clustering coefficient [45] were obtained. PEWCC1 (http://apps.cytoscape.org/apps/PEWCC1), a plug-in used to produce the best results for considerate correlation levels, was subsequently utilized to identify modules in the network [46].

Target genes - miRNA regulatory network construction

Relevant miRNA targets were predicted using miRNet database (available online: (https://www.mirnet.ca/) [47], which is a comprehensive atlas of predicted and validated target - miRNA interactions. The potential targets of miRNA were identified by 10 miRNA databases such as TarBase (http://diana.imis.athena-innovation.gr/DianaTools/index.php?r=tarbase/index) [48], miRTarBase (http://mirtarbase.mbc.nctu.edu.tw/php/download.php) [49], miRecords (http://miRecords.umn.edu/miRecords) [50], miR2Disease (http://www.mir2disease.org/) [51], HMDD (http://www.cuilab.cn/hmdd) [52], PhenomiR (http://mips.helmholtz-muenchen.de/phenomir/) [53], SM2miR (http://bioinfo.hrbmu.edu.cn/SM2miR/) [54], PharmacomiR (http://www.pharmaco-mir.org/) [55], EpimiR (http://bioinfo.hrbmu.edu.cn/EpimiR/) [56] and starBase (http://starbase.sysu.edu.cn/) [57]. The integrated regulatory networks were then visualized by Cytoscape (http://www.cytoscape.org/) [40].

Target genes - TF regulatory network construction

Relevant TF targets were predicted using (https://www.networkanalyst.ca/) [58], which is a comprehensive atlas of predicted and validated target - TF interactions. The potential targets of TF were identified by TF database ChEA (http://amp.pharm.mssm.edu/lib/chea.jsp) [59]. The integrated regulatory networks were then visualized by Cytoscape (http://www.cytoscape.org/) [40].

Validations of hub genes

The probability of survival and importance was determined using the UALCAN (http://ualcan.path.uab.edu/analysis.html) [60] database. UALCAN is a newly created online interactive web server which implements users to examine the RNA sequencing expression data of tumors/normal tissues or samples from The Cancer Genome Atlas (TCGA), based on a criterion processing pipeline. The overall survival analyses of hub gene were performed in UALCAN. The RNA expression level of hub genes between GC samples and normal control samples was visualized by UALCAN. The RNA expression level of hub genes between different stages of GC samples compared to normal control samples was visualized by UALCAN. The cBio Cancer Genomics Portal (cBioPortal) (http://www.cbioportal.org) [61] is a key tool for online analysis, visualization, and examination of cancer genomics data. cBioPortal, which is the database used in this investigation, scrutinize genetic modifications of prognostic and diagnostic hub genes in TCGA GC patients. The expression levels of hub genes in cancerous and non cancerous tissue were validated using the Human Protein Atlas (HPA) database (http://www.proteinatlas.org/) [62]. To calculate whether established hub genes had key diagnostic and prognostic values for GC, the receiver operating characteristic (ROC) analyses was accomplished using the R “pROC” package [63]. The area under the ROC curve (AUC) of hub gene was determined. The diagnostic and prognostic accuracy of hub genes for GC was calculated with AUC value. Herein, when AUC value was larger than 0.8, the hub gene could differentiate GC from normal control. Hub genes were further validated by real time polymer chain reaction (RT-PCR). According to the manufacturer’s instruction, total RNA of gastric tissues in both GC groups and controls were extracted using the TRI Reagent® (Sigma, USA) and reversely transcribed to complementary DNA using the FastQuant RT kit (with gDNase; Tiangen Biotech Co., Ltd.). RT-PCR was completed by using QuantStudio 7 Flex real-time PCR system (Thermo Fisher Scientific, Waltham, MA, USA). The RT-PCR amplification reaction protocol was as follows: A total of 40 cycles at 95˚C for 5 sec and 60˚C for 10 sec. Relative quantification was achieved by using the comparative $2^{\square\Delta\Delta Cq}$ method [64] with β-actin as the reference gene. The sequences of all primer pairs are given in Table 1. Immune infiltration analysis was performed for hub genes using the TIMER online analysis tool (https://cistrome.shinyapps.io/timer/) [65], which incorporates the prognostic and diagnostic data from the RNA-Seq expression profiling database from The Cancer Genome Atlas (TCGA). Immune infiltration analysis was assigned to check the immune infiltrates (B cells, CD4+ T cells, CD8+ T cells, neutrophils, macrophages, and dendritic cells) across GC.

Results

Data pre□processing and identification of DEGs in GC

NCBI-GEO is a free database of gene expression profiles and RNA-seq, from which GC and normal control RNA-seq data of GSE113255 were obtained. The expression values for all the genes from the 107 GC samples and 10 normal control samples were normalized using the Quantile method , and values with an unchanged position in the boxplot were used for consequent analysis, as this can be used as a intermediary for normalization (Fig. 1A and Fig. 1B). Using $P < 0.05$, $|\text{log2 fold change (FC)}| > 1.5$ for up regulated genes, $|\text{log2 fold change (FC)}| < -1.13$ for down regulated genes as the cutoff criteria, after integrated bioinformatics analysis. A total of 1008 DEGs were identified in the active group, including 505 up regulated genes and 503 down regulated genes and are given in Table 2. Fig. 2 and Fig. 3 shows the heat maps of those up and down regulated genes, and reveals that the up and down regulated genes can be easily distinguished from each of the samples. The distribution patterns of expressed genes in GSE113255 data is displayed in Fig. 4, respectively. Red dots in the volcano plots mean significantly up regulated genes, while green dots mean significantly down regulated genes.

Pathway enrichment analysis of DEGs

To analyze the biological importance of DEGs, pathway enrichment analyses were executed. Pathway enrichment analysis was predicted that up and down regulated genes were associated with several key physiological processes and are listed in Table 3 and Table 4. Up regulated genes were significantly enriched in pyrimidine deoxyribonucleosides degradation, aspirin triggered resolvin D biosynthesis, ECM-receptor interaction, protein digestion and absorption, syndecan-4-mediated signaling events, PLK1 signaling events, extracellular matrix organization, hemostasis, glutamate metabolism, pyrimidine metabolism, 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, altered lipoprotein metabolic, ammonia recycling and MNGIE (Mitochondrial Neurogastrointestinal Encephalopathy), while down regulated genes were significantly enriched in allopregnanolone biosynthesis, gluconeogenesis, drug metabolism - cytochrome P450, chemical carcinogenesis, FOXA2 and FOXA3 transcription factor networks, RhoA signaling pathway, biological oxidations, phase 1 - functionalization of compounds, carbon fixation, fatty acid metabolism, ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins, ensemble of genes encoding ECM-associated proteins including ECM-affilaited proteins, ECM regulators and secreted factors, 5-Hydroxytryptamine degredation, fructose galactose metabolism, lipoprotein metabolic, pirenzepine pathway and tyrosine metabolism.

Gene ontology (GO) enrichment analysis of DEGs

We uploaded all up and down regulated genes to the online software ToppGene to identify overrepresented GO categories. GO analysis results showed that up regulated genes were significantly enriched in BP, CC and MF, including extracellular structure organization, cell adhesion, extracellular matrix, collagen-containing extracellular matrix, extracellular matrix structural constituent and structural molecule activity, while down regulated genes were significantly enriched in BP, CC and MF , including digestion, organic acid metabolic process, apical part of cell, extracellular matrix, oxidoreductase activity and transition metal ion binding and are listed in Table 5 and Table 6.

PPI network construction and module analysis

All the up and down regulated genes were entered into the HIPPIE database to obtain the interaction data. The protein-protein interaction (PPI) network of up regulated genes exhibited 3222 nodes and 4943 edges and is shown in Fig 5. The hub genes with highest node degree distribution, betweenness centrality, stress centrality, closeness centrality and lowest clustring coefficient were as follows: FN1, NOTCH1, PLK1, ANLN, MDFI, CPZ, PRKDC, TREM1, TREM2, CYP2W1, CST1, CCL3, PLXDC2, AMIGO2 and GPR161, and are listed in Table 7. The statistical scores of node degree distribution, betweenness centrality, stress centrality, closeness centrality and clustring coefficient are shown as scatter plot in Fig. 6A - 6E. The functional enrichment analysis showed that these hub genes were significantly involved in ECM-receptor interaction, microRNAs in cancer, PLK1 signaling events, cell migration, animal organ morphogenesis, extracellular matrix, phosphotransferase activity, alcohol group as acceptor, molecular transducer activity, axon guidance, endoplasmic reticulum lumen, peptidase activity, identical protein binding, ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins, cell adhesion and whole membrane. Similarly, protein-protein interaction (PPI) network of down regulated genes exhibited 5142 nodes and 8412 edges and is shown in Fig 7. The hub genes with highest node degree distribution, betweenness centrality, stress centrality, closeness centrality and lowest clustring coefficient were as follows: SOX2, RIPK4, FOXA1, EEF1A2, ANG, FGB, CNTD1, GGT6, PTGDR2, ADH1C, DCAF12L1, CAPN9 and TTC39A, and are listed in Table 7. The statistical scores of node degree distribution, betweenness centrality, stress centrality, closeness centrality and clustring coefficient are shown as scatter plot in Fig. 8A - 8E. The functional enrichment analysis showed that these hub genes were significantly involved in developmental biology, kinase activity, FOXA2 and FOXA3 transcription factor networks, metabolism of proteins, ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins, hemostasis, metabolic pathways, intrinsic component of plasma membrane, drug metabolism - cytochrome P450 and digestion.

Furthermore, the PEWCC1 plugin was applied to investigate highly interconnected regions, known as modules, in the PPI network. Total 668 modules were isolated from PPI network of up regulated genes and four significant modules with the highest scores are shown in Fig. 9. Module 2, consisting of 156 nodes and 175 edges, was highly enriched in microRNAs in cancer, innate immune system, pathways in cancer and notch signaling pathway. Module 5, consisting of 133 nodes and 165 edges, was highly enriched in cell migration, microRNAs in cancer, signaling by Rho GTPases, focal adhesion and cell junction. Module 6, consisting of 118 nodes and 120 edges, was highly enriched in animal organ morphogenesis, G alpha (i) signalling events, water transport, notch signaling pathway and cell migration. Module 9, consisting of 81 nodes and 40 edges, was highly enriched in cell cycle, ATP binding, E2F transcription factor network, identical protein binding, regulation of cell population proliferation and pyrophosphatase activity. Similarly, total 1078 modules were isolated from PPI network of down regulated genes and four significant modules with the highest scores are shown in Fig. 10. Module 6, consisting of 120 nodes and 154 edges, was highly enriched in metabolism of proteins, hemostasis, developmental biology, ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins and ensemble of genes encoding core extracellular matrix including ECM glycoproteins, collagens and proteoglycans. Module 7, consisting of 114 nodes and 115 edges, was highly enriched in neuroactive ligand-receptor interaction, oxidation-reduction process, gastric acid secretion and metabolism of proteins. Module 10, consisting of 100 nodes and 116 edges, was highly enriched in developmental biology, molecular function regulator, ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins, metabolism of proteins and biological adhesion. Module 15, consisting of 91 nodes and 95 edges, was highly enriched in gastric acid secretion, nitrogen metabolism, FOXA2 and FOXA3 transcription factor networks, metabolism of proteins, transmembrane transport of small molecules, chemical homeostasis, apical part of cell, secretion, pirenzepine pathway, digestion, and protein digestion and absorption.

Target genes - miRNA regulatory network construction

The target genes - miRNA regulatory network of up regulated genes was shown in Fig. 11, consisting of 2669 nodes and 10414 interactions. The nodes with high degree score (interaction with maximum number of miRNAs) can be regarded as essential network nodes. The top target genes with higher degree included FOXK1 interacts with 259 miRNAs (ex,hsa-mir-5693), CCND2 interacts with 179 miRNAs (ex,hsa-mir-3976), RCC2 interacts with 135 miRNAs (ex,hsa-mir-3911), CCDC80 interacts with 135 miRNAs (ex,hsa-mir-6083) and E2F3 interacts with 135 miRNAs (ex,hsa-mir-4271), and are listed in Table 7. The functional enrichment analysis showed that these target genes were significantly involved in peptidase activity, PI3K-Akt signaling pathway, cell cycle, extracellular structure organization and regulation of cell population proliferation. Similarly, target genes - miRNA regulatory network of down regulated genes was shown in Fig. 12, consisting of 2220 nodes and 5985 interactions. The top target genes with higher degree included GATA6 interacts with 207 miRNAs (ex, hsa-mir-4284), SULT1B1 interacts with 131 miRNAs (ex, hsa-mir-4643), GLUL interacts with 126 miRNAs (ex, hsa-mir-4459), ENPP5 interacts with 114 miRNAs (ex,hsa-mir-8082) and KLF2 interacts with 107 miRNAs (ex,hsa-mir-5193) and are listed in Table 7. The functional enrichment analysis showed that these target genes were significantly involved in notch-mediated HES/HEY network, biological oxidations, metabolic pathways, intrinsic component of plasma membrane and response to endogenous stimulus.

Target genes - TF regulatory network construction

The target genes - TF regulatory network of up regulated genes was shown in Fig. 13, consisting of 657 nodes and 10767 interactions. The nodes with high degree score (interaction with maximum number of TFs) can be regarded as essential network nodes. The top target genes with higher degree included ABCA13 interacts with 247 TFs (ex, SOX2), ACTN1 interacts with 215 TFs (ex, MYC), ABCD1 interacts with 202 TFs (ex, EGR1), ADAMTS14 interacts with 202 TFs (ex, SPI1) and ADAMTS4 interacts with 194 TFs (ex, NANOG) and are listed in Table 8. The functional enrichment analysis showed that these target genes were significantly involved in neutrophil degranulation, focal adhesion, regulation of phosphate metabolic process, peptidase activity and extracellular matrix organization. Similarly, target genes - TF regulatory network of down regulated genes was shown in Fig. 14, consisting of 639 nodes and 7623 interactions. The top target genes with higher degree included DNER interacts with 177 (ex, TP63), CKB interacts with 169 (ex, STAT3), PKIB interacts with 165 (ex, HNF4A), RAB27B interacts with 164 (ex, AR) and IRX3 interacts with 150 (ex, SUZ12) and are listed in Table 8. The functional enrichment analysis showed that these target genes were significantly involved in neuron projection, gastric acid secretion, molecular function regulator and pancreatic secretion.

Validations of hub genes

Up regulated hub genes and down regulated hub genes were then validated in database TCGA to confirm the outcomes. We tried to analysis the relationship between hub genes and the survival in GC. The prognostic and diagnostics value of hub genes was determined by UALCAN database. Patients with high expression of FN1 (Fig. 15A), PLK1 (Fig. 15B), ANLN (Fig. 15C), MCM7 (Fig. 15D), MCM2 (Fig. 15E), EEF1A2 (Fig. 16A), PTGER3 (Fig. 16B), CKB (Fig. 16C), ERBB4 (Fig. 16D) and PRKAA2 (Fig. 16E) were associated with shorter overall survival. The UALCAN box plot analysis investigated the level of expression of the hub genes in 415 GC tissue samples and 34 normal tissue samples. The boxplot in Fig.

17A - Fig. 17E shows a considerable increase in the level of hub gene expression (FN1, PLK1, ANLN, MCM7 and MCM2) in the GC, while boxplot in Fig. 17F - Fig. 17J shows a considerable decrease in the level of hub gene expression (EEF1A2, PTGER3, CKB, ERBB4 and PRKAA2) in the GC. Furthermore, the UALCAN box plot analysis investigated the level of expression of the hub genes in individual GC stages (stage 1 (18 GC samples), stage 2 (123 GC samples), stage 3 (169 GC samples) and stage 4 (41 GC samples)) and 34 normal tissue samples. The boxplot in Fig. 18A - Fig. 18E shows a considerable increase in the level of hub gene expression (FN1, PLK1, ANLN, MCM7 and MCM2) in all four individual stages of GC, while boxplot in Fig. 18F - Fig. 18J shows a considerable decrease in the level of hub gene expression (EEF1A2, PTGER3, CKB, ERBB4 and PRKAA2) in all four individual stages of GC. Based on the results of the cBioPortal database, results of genomic modifications for these hub genes were depicted by using the cBioPortal. We found 6%, 5%, 3%, 8%, 4%, 5%, 1.4%, 0.7%, 13% and 2.5% of GC cases exhibited FN1, PLK1, ANLN, MCM7, MCM2, EEF1A2, PTGER3, CKB, ERBB4 and PRKAA2 hub genes modification including inframe mutation (unknown significance), missense mutation (putative driver), deep deletion, missense mutation (unknown significance), amplification and truncating mutation (unknown significance) and are shown in Fig. 19. Additionally, the expression and distribution of the hub genes (proteins) in GC samples and nontumor samples were measured through immunohistochemistry (IHC). IHC analysis of FN1, PLK1, ANLN, MCM7, MCM2, EEF1A2, PTGER3, CKB, ERBB4 and PRKAA2 in GC samples were found in the HPA database. The antibodies used were as follows: FN1 (CAB000126), PLK1 (HPA051638), ANLN (HPA050556), MCM7 (CAB016312), MCM2 (CAB000303), EEF1A2 (CAB034019), PTGER3 (HPA010689), CKB (HPA001254), ERBB4 (CAB000276) and PRKAA2 (HPA044540). Up regulated hub genes such as FN1, PLK1, ANLN, MCM7 and MCM2 were highly expressed in GC tissue but undetectable or expressed at low levels in normal tissue (Fig. 20A - Fig. 20E). Down regulated hub genes such as EEF1A2, PTGER3, CKB, ERBB4 and PRKAA2 were less expressed in GC tissue but detectable or expressed at high levels in normal tissue (Fig. 20F - Fig. 20J). The ROC curve analysis was accomplished to assess the diagnostic and prognostic values of hub genes. Our finding revealed that FN1 (AUC = 0.979), PLK1 (AUC = 0.921), ANLN (AUC = 0.946), MCM7 (AUC = 0.978), MCM2 (AUC = 0.961), EEF1A2 (AUC = 0.955),

PTGER3 (AUC = 0.934), CKB (AUC = 0.869), ERBB4 (AUC = 0.769) and PRKAA2 (AUC = 0.761) had significant diagnostic and prognostic values for discriminating GC samples and normal controls (Fig. 21). Furthermore, RT-PCR was used to verify the expression levels of the hub genes in primary GC and normal control tissue. In the GC tissues, FN1, PLK1, ANLN, MCM7 and MCM2 were significantly up regulated as compared with those in their normal control tissue, while in GC samples EEF1A2, PTGER3, CKB, ERBB4 and PRKAA2 were significantly down regulated as compared with those in their normal control tissue. These results indicated that, consistent with the TCGA results, most of these hub genes were dysregulated in GC samples compared with those in the normal control samples (Fig. 22). Finally, we investigated whether FN1, PLK1, ANLN, MCM7, MCM2, EEF1A2, PTGER3, CKB, ERBB4 and PRKAA2 expression were associated with tumor immune infiltration level by using the TIMER database. Interestingly, we found that the high expression of FN1, PLK1, ANLN, MCM7 and MCM2 were significantly negatively related to tumor purity, while low expression EEF1A2, PTGER3, CKB, ERBB4 and PRKAA2 were significantly positively related to tumor purity (Fig. 23).

Discussion

The frequency and fatality of GC were still on the increase in many countries. Gene alterations and abnormal expression have been exhibited in the advancement of GC. Understanding the molecular pathogenesis of GC is very essential for prognosis, diagnosis and treatment. With the advancement of microarray and high throughput RNA sequencing, the alternative expression levels of thousands of genes could be together examined. Consolidate and reanalyzing microarray data provide key data including hub genes, biological functions, and signaling pathways, which reveal novel clues for the prognosis, diagnosis and treatment of GC.

In this investigation, we extracted the RNA-seq data of GSE113255 from the GEO dataset with high-quality data and clinical characters. A total of 1008 DEGs were identified following RRA analysis, including 505 up and 503 down regulated genes. Genes such as COL4A1 [66], INHBA (inhibin subunit beta A) [67], RCC2 [68], THY1 [69], ADH7 [70], ATP4A [71], MAL (mal, T cell differentiation protein) [72] and ATP4B [73] were linked with development of GC. Polymorphic gene MSR1 was liable for advancement of prostate cancer [74], but this polymorphic gene may be involved in development of GC. Increases expression of CCKAR (cholecystokinin A receptor) was responsible for pathogenesis of gallbladder cancer [75], but over expression this gene may be important for advancement for GC.

To explore the possible role of up and down regulated genes in GC, we performed pathway enrichment analysis. Enriched up regulated genes such as TYMP (thymidine phosphorylase) [76], COL1A1 [77], COL1A2 [78], COL6A3 [79], FN1 [80], SPP1 [81], ITGA5 [82], THBS1 [83], THBS2 [78], THBS4 [84], MMP9 [85], ADAM12 [86], MFAP2 [87], FBN1 [88], MMP1 [89], MMP3 [90], MMP7 [91], MMP11 [92], MMP14 [93], MMP16 [94], NID2 [95], COL10A1 [96], COL11A1 [97], COL12A1 [98], ADAMTS2 [99], ICAM1 [100], VCAN (versican) [101], CTSK (cathepsin K) [102], HTRA1 [103], ASPN (asporin) [101], P4HA3 [104], BGN (biglycan) [105], BMP1 [106], ADAMTS9 [107], SERPINH1 [108], TIMP1 [109], LOXL2 [110], SERPINE1 [111], LTBP2 [112], LUM (lumican) [113], CLEC5A [114], EMILIN2 [115], SERPINB5 [116], SERPINE2 [117], MGP (matrix Gla protein) [118], AEBP1 [119], SPON2 [120], AGT (angiotensinogen) [121], CXCL9 [122] CTHRC1 [123], CCL3 [124], PLAU (plasminogen activator, urokinase) [125], C1QTNF6 [126], CCL18 [127], CXCL6 [128], SFRP2 [129], ANGPT2 [130], GDF15 [131], WNT2 [132], IGFBP7 [133], IL6 [134], IL11 [135], SPOCK1 [136], FNDC1 [137], SRPX2 [138], SULF2 [139], SULF1 [140], PLXDC1 [141], MUC16 [142], ESM1 [143], CXCL1 [144], TGFBI (transforming growth factor beta induced) [145], OSM (oncostatin M) [146], ANGPTL2 [147], FSTL1 [148], HMCN1 [149], PLXNC1 [150], GREM1 [151] and ITGBL1 [152] were involved in development of GC. Enriched up regulated genes such as COL4A2 [153], ITGA11 [154], LAMA5 [155], COL5A2 [156], ADAMTS4 [157], ADAMTS14 [158], ANXA13 [159], HTRA3 [160] and ADAMTS12 [161] were responsible for invasion of various types of cancer cells, but these genes may be associated with invasion of GC cells. Enriched up regulated genes such as COMP (cartilage oligomeric matrix protein) [162], TNC (tenascin C) [163], ITGB8 [164], FSTL3 [165] and PLXNA1 [166] were important for proliferation of many cancer cells types, but these genes may be liable for proliferation of GC cells. High expression of enriched genes such as COL3A1 [167], COL5A1 [168], COL7A1 [169], COL8A1 [170], CTSB (cathepsin B)

[171], ELN (elastin) [172], CD109 [173], SERPINB9 [174], BMP8A [175], SEMA6B [176], MXRA5 [177], SFRP4 [178], CHRDL2 [179], CST1 [180], HAPLN3 [181], PXDN (peroxidasin) [182] and TGM2 [183] were liable for progression of many cancer types, but over expression of these genes may be responsible for pathogenesis of GC. Polymorphic gene COL18A1 was associated with progression of breast cancer [184], but this polymorphic gene may be linked with development of GC. Methylation inactivation of CPS1 was linked with development of hepatocellular carcinoma [185], but inactivation of this gene may be culpable for progression of GC. PGF (placental growth factor) was linked with angiogenesis in hepatocellular carcinoma [186], but this gene may be involved in angiogenesis in GC. Our investigation established that UPP1, ACTN1, ACAN (aggrecan), COL15A1, COL16A1, COL5A3, SPARC (secreted protein acidic and cysteine rich), ITGAX (integrin subunit alpha X), PCOLCE (procollagen C-endopeptidase enhancer), CAD (carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase), CLEC7A, CRISPLD1, OMD (osteomodulin), LIF (LIF interleukin 6 family cytokine), PLXDC2, LGI2, TNFAIP6, PARVG (parvin gamma) and SDS (serine dehydratase) are up regulated in GC and has possible as a new diagnostic and prognostic biomarker, and therapeutic target. Enriched down regulated genes such as AKR1C3 [187], AKR1C2 [188], ADH1C [189], CYP2C19 [190], CYP3A4 [191], CYP3A5 [191], GSTA1 [192], GSTA3 [193], FOXA1 [194], FOXA2 [195], TTR (transthyretin) [196], ALDOB (aldolase, fructose-bisphosphate B) [197], APOA1 [198], ALDH1A1 [199], FBP2 [200], S100P [201], CCL28 [202], FGA (fibrinogen alpha chain) [193], FGB (fibrinogen beta chain) [203], FGG (fibrinogen gamma chain) [193], IGFBP2 [204], SCUBE2 [205], PDGFD (platelet derived growth factor D) [206], CTSE (cathepsin E) [207], MUC1 [208], MUC6 [209], SERPINB7 [210], NRG4 [211], SEMA3B [212], MUC5B [213], ANXA10 [214], REG3A [215], HRH2 [216], SST (somatostatin) [217] and CCKBR (cholecystokinin B receptor) [218] were associated with advancement of GC. Enriched down regulated genes such as AKR1C1 [219], MAOA (monoamine oxidase A) [220], ALDH3A1 [221], UGT1A10 [222], CYP2S1 [223], ME1 [224], FBP1 [225], GPT (glutamic--pyruvic transaminase) [226], COL2A1 [227], COL17A1 [228], HYAL1 [229], CSTA (cystatin A) [230], ADAM28 [231], BMP5 [232], ANGPTL3 [233], DPT (dermatopontin) [234] and APOBEC1 [235] were linked with invasion of many types of cancer cells, but these genes may be involved in invasion of GC cells.

Enriched polymorphic genes such as UGT1A6 [236], CYP2C8 [237], CYP2C9 [238], GSTA2 [239], SULT2A1 [240], ADAMTSL1 [241], SERPINA5 [242] and APOC3 [243] were important for pathogenesis of many cancer types, but these polymorphic genes may be responsible for development of GC. Low expression of enriched genes such as AKR7A3 [244], ALDOC (aldolase, fructose-bisphosphate C) [245], SERPINA4 [246], ADAMTS15 [247], CCBE1 [248] and CLEC3B [249] were liable for progression of many cancer types, but decrease expression of these genes may be responsible for advancement of GC. Methylation inactivation of CXCL14 was linkes with progression of colorectal cancer [250], but loss of this gene may be key foe development of GC. Our investigation established that FMO5, FOXA3, CMBL (carboxymethylenebutenolidase homolog), AADAC (arylacetamidedeacetylase), GGT6, CYP4F12, CYP2C18, ACSM1, SULT1B1, SULT1C2, LGALS9C, COL6A5, F13A1, PAPPA2, COL4A6, HAPLN1, IGFALS (insulin like growth factor binding protein acid labile subunit), SLPI (secretory leukocyte peptidase inhibitor), LGALS9B and APOA4 are down regulated in GC and has possible as a new diagnostic and prognostic biomarker, and therapeutic target.

To explore the possible role of up and down regulated genes in GC, we performed GO enrichment analysis. Methylation inactivation of enriched up regulated genes such as ABCA1 [251], FLRT2 [252] and CDH13 [253] were liable for progression of many cancer types, but inactivation of these genes may be involved in growth of GC. Enriched up regulated genes such as FAP (fibroblast activation protein alpha) [254], ANTXR1 [255], FOXC1 [256], OLFML2B [257], APOC1 [258], APOE (apolipoprotein E) [259], PDPN (podoplanin) [260], FSCN1 [261], NOTCH1 [262], TNFRSF11B [263], CHI3L1 [264] and CD248 [265] were responsible for progression of GC. LIPG (lipase G, endothelial type) was liable for proliferation of breast cancer [266], but this gene may be liable for proliferation of GC cells. Enriched up regulated genes such as CCDC80 [267], PLA2G7 [268] and ENTPD1 [269] were associated with invasion of many types of cancer cells, but these genes may be linked with invasion of GC cells. Our investigation established that SH3PXD2B, CPZ (carboxypeptidase Z) and LRRC32 are up regulated in GC and has possible as a new diagnostic and prognostic biomarker, and therapeutic target. Enriched down regulated genes such as PGC (progastricsin) [270], AQP5 [271], CAPN9 [272], VSIG1 [273], KCNQ1 [274], TFF1 [275], TFF2 [276], CD36

[277], GKN1 [278], SCNN1B [279], FOLR1 [280], DUOX2 [281], RAB27A [282], HPGD (15-hydroxyprostaglandin dehydrogenase) [283], FA2H [284], LIPF (lipase F, gastric type) [285], GCKR (glucokinase regulator) [286], AKR1B10 [287], NQO1 [288], SELENBP1 [289] and GPX3 [290] were involved in development of GC. Enriched down regulated genes such as PBLD (phenazine biosynthesis like protein domain containing) [291], HPN (hepsin) [292], HOMER2 [293], DUOXA2 [294], SLC9A1 [295], DUOX1 [296], CA2 [297], CDH2 [298], ACADL (acyl-CoA dehydrogenase long chain) [299], PDIA2 [300], CYB5A [301], GALE (UDP-galactose-4-epimerase) [302], DHCR24 [303] and HBB (hemoglobin subunit beta) [304] were liable for invasion of many types of cancer cells, but these genes may be involved in invasion of GC cells. Low expression of enriched genes such as PTGER3 [305], RAB27B [306], ESRRB (estrogen related receptor beta) [307], ALDH6A1 [308], DHRS7 [309], LDHD (lactate dehydrogenase D) [310], DHRS9 [311] and ENTPD5 [312] were important for progression of many cancer types, but decrease expression of these genes may be responsible for advancement of GC. Enriched down regulated genes such as PRKAA2 [313], PTGR1 [314], ADHFE1 [315] and RGN (regucalcin) [316] were involved in proliferation of many types of cancer cells, but these genes may be associated with proliferation of GC cells. Our investigation established that PGA5, ASAH2, SLC26A7, CHIA (chitinase acidic), GHRL (ghrelin and obestatinprepropeptide), CAPN8, PGA3, PGA4, SLC9A4, GUCA2B, PROM2, UPK1B, SCNN1G, EPB41L4B, MYRIP (myosin VIIA and rab interacting protein), SLC26A9, SLC9A3, CDHR2, CA4, AQP10, PDZD3, HGD (homogentisate 1,2-dioxygenase), ERO1B, RDH12, AKR1B15 and TM7SF2 are down regulated in GC and has possible as a new diagnostic and prognostic biomarker, and therapeutic target.

The PPI network and module analysis found that DEGs were considered as up and down regulated hub genes in the network and modules. Up regulated hub genes such PLK1 [317], ANLN (anillin actin binding protein) [318], TREM2 [319], AMIGO2 [320], LEF1 [321], NOTCH3 [322], RAI14 [323], AQP1 [324], HOXB9 [325], MCM7 [326], MCM2 [327], CDC6 [328] and GINS4 [329] were liable for advancement of GC. Methylation inactivation of up regulated hub genes such as MDFI (MyoD family inhibitor) [330] and HEYL (hes related family bHLH transcription factor with YRPW motif like) [331] were involved in the progression of many cancer types, but inactivation of these genes may be key for advancement of GC. Increased expression of hub genes such as TREM1 [332], CYP2W1 [333], GPR161 [334], ARHGAP11A [335], APLN (apelin) [336], CBX2 [337], ORC1 [338] and MCM10 [339] were linked with development of many cancer types, but over expression of these genes may be liable for advancement of GC. Our investigation established that PRKDC (protein kinase, DNA-activated, catalytic subunitprotein kinase, DNA-activated, catalytic subunit) is up regulated in GC and has possible as a new diagnostic and prognostic biomarker, and therapeutic target. Down regulated hub genes such as SOX2 [340], EEF1A2 [341], ANG (angiogenin) [342], PTGDR2 [343], ERBB4 [344], KCNE2 [345], CA9 [346] and PSCA (prostate stem cell antigen) [347] were linked with pathogenesis of GC. Down regulated hub genes such as RIPK4 [348] and FAM3B [349] were involved in invasion of cells of many cancer types, but this gene may be associated with invasion of GC cells. Our investigation established that CNTD1, DCAF12L1, TTC39A, DUSP19, PTPRR (protein tyrosine phosphatase receptor type R) and TFR2 are down regulated in GC and has possible as a new diagnostic and prognostic biomarker, and therapeutic target.

The target genes - miRNA regulatory network analysis found that DEGs were considered as up and down regulated target genes in the network. Up regulated target genes such MYB (MYB proto-oncogene, transcription factor) [350] and SALL4 [351] were responsible for pathogenesis of GC. High expression of CLDN4 was key for progression of pancreatic cancer [352], but elevated expression this gene may be liable for progression of GC. Our investigation established that ARHGAP39 is up regulated in GC and has possible as a new diagnostic and prognostic biomarker, and therapeutic target. Down regulated target genes such as GATA6 [353] and KLF2 [354] were linked with development of GC. GLUL (glutamate-ammonia ligase) was involved in invasion of glioma cells [355], but this gene may be associated with invasion of GC cells. Our investigation established that ENPP5 is down regulated in GC and has possible as a new diagnostic and prognostic biomarker, and therapeutic target.

The target genes - TF regulatory network analysis found that DEGs were considered as up and down regulated target genes in the network. ABCA13 was responsible for advancement of GC [356]. Up regulated target geneABCD1 was associated with invasion of renal cancer cells [357], but this gene may be liable for invasion of GC cells. Down regulated target genes DNER (delta/notch like EGF repeat containing) [358] and IRX3 [359] were key for proliferation of many types of cancer cells, but these genes may be involved in proliferation of GC cells. CKB (creatine kinase B) was linked with progression of GC [360]. Down regulated target gene PKIB (cAMP-dependent protein kinase inhibitor beta) was important for invasion of breast cancer cells [361], but this gene may be linked with invasion of GC cells.

In our investigation, we screened FN1, PLK1, ANLN, MCM7, MCM2, EEF1A2, PTGER3, CKB, ERBB4 and PRKAA2 as important hub genes of GC by integrated bioinformatics analysis. Internal validation (survival analysis, expression analysis, stage analysis, mutation analysis, immunio infiltration analysis, immunio histochemical analysis and ROC analysis) and external validation (RT-PCR) of RNA and protein levels showed that they were higher or lower in cancerous than in normal control tissues. Over expression of the five hub genes and lower expression of the five hub genes were also associated with an advanced clinical stage and poor overall survival rate. Thus, the important hub genes explored in our investigation are likely to become a group of probale therapeutic targets of GC.

In conclusion, the current investigation identifird important hub genes linked with the various clinical stage and overall survival of GC patients. Our investigation attempts a profound perceptive of the molecular pathogensis linked with the adavancement of GC and implements probale biomarkers for early prognosis, diagnosis and individualized treatment of patients at various stages of GC.

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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 and review and editing. Ali 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. [(GSE113255) (https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE113255]

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

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Tables

Table 1. Primers used for quantitative PCR

	Primer sequence (5'→3')	
Forward	**Forward**	**Forward**
FN1	CGGTGGCTGTCAGTCAAAG	AAACCTCGGCTTCCTCCATAA
PLK1	AAAGAGATCCCGGAGGTCCTA	GGCTGCGGTGAATGGATATTTC
ANLN	TGCCAGGCGAGAGAATCTTC	CGCTTAGCATGAGTCATAGACCT
MCM7	CCTACCAGCCGATCCAGTCT	CCTCCTGAGCGGTTGGTTT
MCM2	ATGGCGGAATCATCGGAATCC	GGTGAGGGCATCAGTACGC
EEF1A2	GAAGACCCACATCAACATCGT	CTCCGCATTTGTAGATGAGGTG
PTGER3	CGCCTCAACCACTCCTACAC	GACACCGATCCGCAATCCTC
CKB	GCTGCGACTTCAGAAGCGA	GGCATGAGGTCGTCGATGG
ERBB4	GTCCAGCCCAGCGATTCTC	AGAGCCACTAACACGTAGCCT
PRKAA2	GTGAAGATCGGACACTACGTG	CTGCCACTTTATGGCCTGTTA

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

Gene Symbol	logFC	pValue	adj.P.Val	tvalue	Regulation	Gene Name
COL4A1	2.972614	1.62E-19	7.66E-16	10.92342	Up	collagen type IV alpha 1 chain
INHBA	4.080822	1.08E-18	3.39E-15	10.57369	Up	inhibin subunit beta A

RCC2	1.607652	1.15E-18	3.39E-15	10.56222	Up	regulator of chromosome condensation 2
THY1	3.439673	7.51E-18	1.37E-14	10.21558	Up	Thy-1 cell surface antigen
MSR1	2.674374	9.57E-18	1.62E-14	10.17093	Up	macrophage scavenger receptor 1
FAP	4.024768	1.6E-17	2.36E-14	10.07644	Up	fibroblast activation protein alpha
SULF1	4.025951	2.37E-17	3.12E-14	10.00358	Up	sulfatase 1
SERPINH1	2.149675	4.17E-17	4.93E-14	9.899306	Up	serpin family H member 1
E2F3	1.634912	1.01E-16	1.09E-13	9.734805	Up	E2F transcription factor 3
GLT25D1	1.642413	2.15E-16	1.95E-13	9.596128	Up	GLYCOSYLTRANSFERASE 25 FAMILY, MEMBER 1
BGN	4.165579	2.62E-16	2.3E-13	9.55921	Up	biglycan
WISP1	3.125136	3.3E-16	2.6E-13	9.516536	Up	Wnt1-inducible signaling pathway protein-1
TCOF1	1.579282	4.8E-16	3.44E-13	9.44697	Up	treacle ribosome biogenesis factor 1
NID2	2.481827	5.63E-16	3.7E-13	9.417359	Up	nidogen 2
CAD	1.957354	8.28E-16	4.9E-13	9.345783	Up	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase
ADCY3	1.8303	1.1E-15	6.21E-13	9.292654	Up	adenylatecyclase 3
ITGAX	2.919285	1.3E-15	7.09E-13	9.26149	Up	integrin subunit alpha X
ADAMTS12	3.296182	1.38E-15	7.12E-13	9.25041	Up	ADAM metallopeptidase with thrombospondin type 1 motif 12
TRPM2	1.961827	1.62E-15	8E-13	9.220805	Up	transient receptor potential cation channel subfamily M member 2
COL8A1	4.371259	2.07E-15	9.61E-13	9.175361	Up	collagen type VIII alpha 1 chain
TREM2	2.785416	2.15E-15	9.8E-13	9.168072	Up	triggering receptor expressed on myeloid cells 2
MTHFD1L	2.041684	2.32E-15	1.02E-12	9.154495	Up	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1 like
TEAD4	1.8995	3.74E-15	1.53E-12	9.065089	Up	TEA domain transcription factor 4
LOC541471	1.678209	7.14E-15	2.68E-12	8.944444	Up	#N/A
COL4A2	2.519381	7.69E-15	2.84E-12	8.930613	Up	collagen type IV alpha 2 chain
SDS	2.945396	9.34E-15	3.4E-12	8.894271	Up	serine dehydratase
BMP1	2.177414	1.56E-14	5.06E-12	8.798462	Up	bone morphogenetic protein 1
SPARC	2.574807	1.56E-14	5.06E-12	8.798331	Up	secreted protein acidic and cysteine rich
NOP2	1.613861	1.9E-14	6.01E-12	8.760938	Up	NOP2 nucleolar protein
GPNMB	2.825201	2.18E-14	6.62E-12	8.735456	Up	glycoprotein nmb
RRP12	1.670106	2.22E-14	6.67E-12	8.73165	Up	ribosomal RNA processing 12 homolog
THBS2	4.303173	2.56E-14	7.57E-12	8.705365	Up	thrombospondin 2
COL18A1	2.437266	4.31E-14	1.2E-11	8.607211	Up	collagen type XVIII alpha 1 chain
PLXNA1	1.662541	4.7E-14	1.29E-11	8.591156	Up	plexin A1
RELT	1.775325	4.93E-14	1.3E-11	8.582095	Up	RELT TNF receptor
COL5A2	2.509222	6.01E-14	1.51E-11	8.544741	Up	collagen type V alpha 2 chain
COL6A3	3.261072	6.35E-14	1.57E-11	8.534447	Up	collagen type VI alpha 3 chain
PRRX1	3.293988	9.59E-14	2.2E-11	8.456677	Up	paired related homeobox 1
HAVCR2	1.895769	1.1E-13	2.42E-11	8.43141	Up	hepatitis A virus cellular receptor 2
ANGPT2	1.886597	1.16E-13	2.55E-11	8.420387	Up	angiopoietin 2
CEP170	1.820113	1.23E-13	2.64E-11	8.409774	Up	centrosomal protein 170
ADAMTS2	3.15333	1.54E-13	3.22E-11	8.367548	Up	ADAM metallopeptidase with thrombospondin type 1 motif 2
COL12A1	2.963842	1.61E-13	3.34E-11	8.358832	Up	collagen type XII alpha 1 chain

MFAP2	2.775014	1.99E-13	3.99E-11	8.318485	Up	microfibril associated protein 2
MMP14	1.80734	3E-13	5.77E-11	8.240846	Up	matrix metallopeptidase 14
FOXK1	1.63315	3.26E-13	6.08E-11	8.224703	Up	forkhead box K1
PVT1	2.137405	3.33E-13	6.12E-11	8.220692	Up	Pvt1 oncogene
LEPRE1	1.683065	3.53E-13	6.33E-11	8.209775	Up	Leucine- And Proline-Enriched Proteoglycan 1
PLA2G7	2.335604	3.87E-13	6.78E-11	8.192344	Up	phospholipase A2 group VII
CTHRC1	2.993366	4.44E-13	7.73E-11	8.166018	Up	collagen triple helix repeat containing 1
TIMP1	2.769289	4.77E-13	8.01E-11	8.152381	Up	TIMP metallopeptidase inhibitor 1
PDGFRB	2.683245	6.53E-13	1.01E-10	8.092516	Up	platelet derived growth factor receptor beta
LILRB4	2.318613	7.91E-13	1.18E-10	8.055983	Up	leukocyte immunoglobulin like receptor B4
TTYH3	2.15944	1.08E-12	1.53E-10	7.996266	Up	tweety family member 3
LOC100505702	1.823494	1.11E-12	1.56E-10	7.992044	Up	#N/A
LPCAT1	1.603274	1.19E-12	1.67E-10	7.9781	Up	lysophosphatidylcholineacyltransferase 1
KIAA1199	3.7798	1.2E-12	1.67E-10	7.976353	Up	Hyaluronan-Binding Protein
NOD1	1.812531	1.28E-12	1.77E-10	7.964454	Up	nucleotide binding oligomerization domain containing 1
COL1A2	3.011069	1.53E-12	2.05E-10	7.930162	Up	collagen type I alpha 2 chain
KAL1	2.529049	1.56E-12	2.08E-10	7.926407	Up	Kallmann syndrome 1
PGF	1.827148	1.9E-12	2.44E-10	7.888251	Up	placental growth factor
CTSL1	1.924328	2.02E-12	2.57E-10	7.876392	Up	Cathepsin L1
NOTCH1	2.04241	2.11E-12	2.65E-10	7.867689	Up	notch receptor 1
MYBBP1A	1.56545	2.92E-12	3.55E-10	7.805317	Up	MYB binding protein 1a
LIF	2.628837	3.26E-12	3.9E-10	7.784528	Up	LIF interleukin 6 family cytokine
MTBP	1.566688	3.43E-12	4.08E-10	7.774674	Up	MDM2 binding protein
PODXL	1.678369	3.49E-12	4.14E-10	7.771017	Up	podocalyxin like
FCGR2A	2.042815	4.77E-12	5.43E-10	7.711092	Up	Fc fragment of IgG receptor IIa
ASPN	3.192313	5.69E-12	6.33E-10	7.67682	Up	asporin
MEST	2.033002	5.91E-12	6.5E-10	7.669643	Up	mesoderm specific transcript
IFITM3	1.811626	6.53E-12	7.06E-10	7.650202	Up	interferon induced transmembrane protein 3
VASH1	1.732625	6.94E-12	7.36E-10	7.638494	Up	vasohibin 1
SPSB1	1.557471	8.5E-12	8.63E-10	7.599137	Up	splA/ryanodine receptor domain and SOCS box containing 1
RAB31	1.850995	9.07E-12	9.06E-10	7.586573	Up	RAB31, member RAS oncogene family
COL1A1	3.64102	9.22E-12	9.17E-10	7.5834	Up	collagen type I alpha 1 chain
KNTC1	1.565897	1.22E-11	1.16E-09	7.529552	Up	kinetochore associated 1
SLC39A10	1.680223	1.42E-11	1.32E-09	7.498991	Up	solute carrier family 39 member 10
ACTN1	1.677965	1.47E-11	1.35E-09	7.492714	Up	actinin alpha 1
TDRD6	1.891436	1.78E-11	1.61E-09	7.454971	Up	tudor domain containing 6
COL5A3	2.202227	2.01E-11	1.77E-09	7.431748	Up	collagen type V alpha 3 chain
SPHK1	2.448979	2.09E-11	1.83E-09	7.423857	Up	sphingosine kinase 1
C5AR1	2.091061	2.32E-11	2E-09	7.403032	Up	complement C5a receptor 1
CTSB	1.825225	2.34E-11	2.01E-09	7.401651	Up	cathepsin B
SNX10	2.172538	2.4E-11	2.04E-09	7.397183	Up	sorting nexin 10
CLEC7A	1.80967	2.58E-11	2.17E-09	7.382581	Up	C-type lectin domain containing 7A

NFAM1	1.853487	2.63E-11	2.2E-09	7.378992	Up	NFAT activating protein with ITAM motif 1
ABCA1	1.719536	2.79E-11	2.29E-09	7.367414	Up	ATP binding cassette subfamily A member 1
EMILIN2	1.553408	3.15E-11	2.52E-09	7.343301	Up	elastin microfibrilinterfacer 2
WDR62	1.957436	3.83E-11	2.98E-09	7.304983	Up	WD repeat domain 62
RAI14	1.601279	4.4E-11	3.32E-09	7.277967	Up	retinoic acid induced 14
PIEZO1	1.74628	4.6E-11	3.41E-09	7.269156	Up	piezo type mechanosensitive ion channel component 1
SERPINE1	2.947958	4.94E-11	3.61E-09	7.254962	Up	serpin family E member 1
BMP8A	2.229521	5.55E-11	3.95E-09	7.232267	Up	bone morphogenetic protein 8a
NOTCH3	2.452432	5.96E-11	4.21E-09	7.21815	Up	notch receptor 3
NCF2	1.870599	6.03E-11	4.23E-09	7.215631	Up	neutrophil cytosolic factor 2
TGFBI	1.984846	6.52E-11	4.55E-09	7.200364	Up	transforming growth factor beta induced
CD300LF	1.757513	6.72E-11	4.63E-09	7.194229	Up	CD300 molecule like family member f
PRKDC	1.608728	7.13E-11	4.81E-09	7.182665	Up	protein kinase, DNA-activated, catalytic subunit
DUSP10	1.667554	7.38E-11	4.91E-09	7.175931	Up	dual specificity phosphatase 10
IFFO2	1.573573	7.81E-11	5.15E-09	7.164643	Up	intermediate filament family orphan 2
FSTL1	2.16055	7.95E-11	5.23E-09	7.161207	Up	follistatin like 1
ST3GAL2	1.575122	8.61E-11	5.62E-09	7.145338	Up	ST3 beta-galactoside alpha-2,3-sialyltransferase 2
TRIO	1.628151	8.67E-11	5.64E-09	7.143936	Up	trio Rho guanine nucleotide exchange factor
F2R	2.096849	9.01E-11	5.81E-09	7.136385	Up	coagulation factor II thrombin receptor
PLXNC1	1.778859	9.55E-11	6.11E-09	7.124841	Up	plexin C1
HAPLN3	2.194557	9.62E-11	6.14E-09	7.123387	Up	hyaluronan and proteoglycan link protein 3
FN1	3.278172	9.82E-11	6.25E-09	7.119179	Up	fibronectin 1
RCN3	2.200572	9.88E-11	6.26E-09	7.118011	Up	reticulocalbin 3
ATAD5	1.68341	1.05E-10	6.6E-09	7.105167	Up	ATPase family AAA domain containing 5
MCM7	1.670101	1.3E-10	7.87E-09	7.063095	Up	minichromosome maintenance complex component 7
IER5L	1.897802	1.34E-10	7.95E-09	7.058115	Up	immediate early response 5 like
DOCK4	1.670651	1.34E-10	7.95E-09	7.057479	Up	dedicator of cytokinesis 4
BOP1	1.707862	1.4E-10	8.24E-09	7.048991	Up	BOP1 ribosomal biogenesis factor
MDFI	1.827513	1.46E-10	8.57E-09	7.040197	Up	MyoD family inhibitor
EPHB2	3.171361	1.63E-10	9.34E-09	7.018777	Up	EPH receptor B2
GAL3ST4	1.84346	1.63E-10	9.35E-09	7.018003	Up	galactose-3-O-sulfotransferase 4
RHBDF2	1.570682	1.8E-10	1.01E-08	6.998712	Up	rhomboid 5 homolog 2
KCNAB2	1.645556	1.93E-10	1.06E-08	6.98504	Up	potassium voltage-gated channel subfamily A regulatory beta subunit 2
CLDN7	3.228188	1.99E-10	1.09E-08	6.979206	Up	claudin 7
PMEPA1	2.347479	2.02E-10	1.1E-08	6.975423	Up	prostate transmembrane protein, androgen induced 1
ILDR1	1.930265	2.03E-10	1.1E-08	6.975195	Up	immunoglobulin like domain containing receptor 1
RFTN1	1.824451	2.07E-10	1.11E-08	6.971295	Up	raftlin, lipid raft linker 1
ENC1	1.605404	2.1E-10	1.12E-08	6.968068	Up	ectodermal-neural cortex 1
FCHO1	1.699355	2.22E-10	1.18E-08	6.956621	Up	FCH and mu domain containing endocytic adaptor 1
ENTPD1	1.602404	2.33E-10	1.23E-08	6.946888	Up	ectonucleoside triphosphate diphosphohydrolase 1
SFRP4	4.658162	2.47E-10	1.28E-08	6.935666	Up	secreted frizzled related protein 4
SEMA6B	1.802608	2.5E-10	1.3E-08	6.932809	Up	semaphorin 6B

FGD6	1.724331	2.62E-10	1.34E-08	6.923574	Up	FYVE, RhoGEF and PH domain containing 6
LRFN4	1.744418	2.94E-10	1.47E-08	6.90061	Up	leucine rich repeat and fibronectin type III domain containing 4
LRP8	2.29507	3.15E-10	1.55E-08	6.886442	Up	LDL receptor related protein 8
ESM1	2.497572	3.45E-10	1.68E-08	6.868734	Up	endothelial cell specific molecule 1
LAPTM5	1.683259	3.6E-10	1.74E-08	6.859677	Up	lysosomal protein transmembrane 5
ABCD1	1.57295	3.84E-10	1.83E-08	6.847189	Up	ATP binding cassette subfamily D member 1
CLDN1	3.716278	4.19E-10	1.97E-08	6.829177	Up	claudin 1
P4HA3	1.997044	4.63E-10	2.12E-08	6.809425	Up	prolyl 4-hydroxylase subunit alpha 3
RAD54L	1.729109	4.79E-10	2.18E-08	6.802366	Up	RAD54 like
CDH11	2.246797	4.9E-10	2.22E-08	6.797743	Up	cadherin 11
CENPF	2.020875	4.95E-10	2.24E-08	6.795601	Up	centromere protein F
CCR1	1.679479	5.01E-10	2.26E-08	6.793304	Up	C-C motif chemokine receptor 1
CDH13	1.816279	5.19E-10	2.32E-08	6.786121	Up	cadherin 13
SPON2	2.178941	5.21E-10	2.32E-08	6.785554	Up	spondin 2
KIF18B	1.857397	5.6E-10	2.43E-08	6.770716	Up	kinesin family member 18B
CHN1	1.770805	6.24E-10	2.65E-08	6.749164	Up	chimerin 1
PKMYT1	1.848328	6.3E-10	2.67E-08	6.747231	Up	protein kinase, membrane associated tyrosine/threonine 1
KIF23	1.815158	6.4E-10	2.7E-08	6.744026	Up	kinesin family member 23
GPR176	1.72814	6.48E-10	2.72E-08	6.741355	Up	G protein-coupled receptor 176
KIAA1524	1.707069	6.81E-10	2.83E-08	6.731287	Up	cancerous inhibitor of PP2A
TRIP13	1.765499	7.2E-10	2.95E-08	6.720174	Up	thyroid hormone receptor interactor 13
FNDC1	4.01704	7.25E-10	2.96E-08	6.718633	Up	fibronectin type III domain containing 1
FMNL3	1.625477	7.67E-10	3.11E-08	6.707091	Up	formin like 3
FANCD2	1.56858	7.7E-10	3.11E-08	6.706407	Up	FA complementation group D2
PLBD2	1.57102	7.73E-10	3.12E-08	6.705521	Up	phospholipase B domain containing 2
SULF2	1.885993	8.06E-10	3.22E-08	6.697174	Up	sulfatase 2
SPP1	4.420367	8.14E-10	3.25E-08	6.695265	Up	secreted phosphoprotein 1
DYSF	1.749917	8.65E-10	3.41E-08	6.682716	Up	dysferlin
THBS1	2.403719	8.93E-10	3.48E-08	6.676436	Up	thrombospondin 1
OLFML2B	2.620057	8.99E-10	3.49E-08	6.675031	Up	olfactomedin like 2B
SLC43A3	1.772551	9.03E-10	3.49E-08	6.674004	Up	solute carrier family 43 member 3
ATAD2	1.726658	9.09E-10	3.51E-08	6.672638	Up	ATPase family AAA domain containing 2
UPP1	1.604403	9.23E-10	3.55E-08	6.669603	Up	uridinephosphorylase 1
XRCC2	1.560921	9.32E-10	3.58E-08	6.667543	Up	X-ray repair cross complementing 2
KIF14	1.850539	9.89E-10	3.78E-08	6.655614	Up	kinesin family member 14
COL3A1	2.576945	1E-09	3.82E-08	6.653135	Up	collagen type III alpha 1 chain
CSGALNACT2	1.571169	1.01E-09	3.85E-08	6.651072	Up	chondroitin sulfate N-acetylgalactosaminyltransferase 2
IGFBP7	2.014261	1.03E-09	3.91E-08	6.647011	Up	insulin like growth factor binding protein 7
ARMC9	1.606979	1.12E-09	4.17E-08	6.630646	Up	armadillo repeat containing 9
CDC25B	1.734181	1.14E-09	4.24E-08	6.625943	Up	cell division cycle 25B
GNB4	1.564483	1.16E-09	4.29E-08	6.622715	Up	G protein subunit beta 4
FCGR3A	2.185483	1.2E-09	4.39E-08	6.615553	Up	Fc fragment of IgG receptor IIIa

ARHGAP39	1.765533	1.22E-09	4.44E-08	6.612702	Up	Rho GTPase activating protein 39
SH3PXD2B	1.878221	1.28E-09	4.62E-08	6.602918	Up	SH3 and PX domains 2B
BUB1B	1.722101	1.35E-09	4.82E-08	6.592167	Up	BUB1 mitotic checkpoint serine/threonine kinase B
ACAN	2.742413	1.41E-09	4.98E-08	6.582618	Up	aggrecan
MARVELD1	1.670593	1.52E-09	5.28E-08	6.567303	Up	MARVEL domain containing 1
SLC1A3	2.022669	1.61E-09	5.55E-08	6.556542	Up	solute carrier family 1 member 3
PIK3AP1	1.62924	1.65E-09	5.67E-08	6.550842	Up	phosphoinositide-3-kinase adaptor protein 1
CKAP2	1.553455	1.68E-09	5.74E-08	6.547273	Up	cytoskeleton associated protein 2
SLC37A2	1.734597	1.8E-09	6.06E-08	6.532982	Up	solute carrier family 37 member 2
PDPN	2.041864	1.84E-09	6.15E-08	6.528961	Up	podoplanin
ADAM12	2.395205	1.91E-09	6.31E-08	6.520854	Up	ADAM metallopeptidase domain 12
C1QTNF6	1.701272	1.97E-09	6.49E-08	6.514985	Up	C1q and TNF related 6
COL7A1	2.892737	2.19E-09	7.09E-08	6.493046	Up	collagen type VII alpha 1 chain
CCNF	1.591779	2.19E-09	7.09E-08	6.492753	Up	cyclin F
CLSPN	1.754245	2.23E-09	7.2E-08	6.48898	Up	claspin
ATP11A	1.733479	2.33E-09	7.44E-08	6.480717	Up	ATPase phospholipid transporting 11A
CHTF18	1.562715	2.37E-09	7.55E-08	6.477173	Up	chromosome transmission fidelity factor 18
LCP2	1.563638	2.37E-09	7.55E-08	6.476875	Up	lymphocyte cytosolic protein 2
HEYL	2.589415	2.47E-09	7.8E-08	6.467962	Up	hes related family bHLH transcription factor with YRPW motif like
NNMT	2.291847	2.77E-09	8.65E-08	6.44469	Up	nicotinamide N-methyltransferase
IGSF6	1.701301	2.79E-09	8.69E-08	6.443287	Up	immunoglobulin superfamily member 6
BUB1	1.787001	2.83E-09	8.8E-08	6.439972	Up	BUB1 mitotic checkpoint serine/threonine kinase
RECQL4	1.873814	3.36E-09	1.01E-07	6.404925	Up	RecQ like helicase 4
C11orf82	1.643213	3.61E-09	1.08E-07	6.390004	Up	Chromosome 11 Open Reading Frame 82
LOC100288637	1.570791	3.74E-09	1.12E-07	6.382551	Up	OTU deubiquitinase 7A pseudogene
NCAPH	1.598637	4.26E-09	1.24E-07	6.355631	Up	non-SMC condensin I complex subunit H
OSMR	1.821329	4.29E-09	1.25E-07	6.354286	Up	oncostatin M receptor
LZTS1	2.266255	4.34E-09	1.26E-07	6.351682	Up	leucine zipper tumor suppressor 1
KIAA1274	1.713015	4.46E-09	1.29E-07	6.345972	Up	Phosphatase Domain Containing Paladin 1
SLC11A1	2.285848	4.51E-09	1.3E-07	6.343859	Up	solute carrier family 11 member 1
STIL	1.715736	4.68E-09	1.34E-07	6.336072	Up	STIL centriolar assembly protein
C15orf42	1.947609	4.82E-09	1.37E-07	6.329813	Up	chromosome 15 open reading frame 42
KIF4A	1.725143	4.88E-09	1.39E-07	6.327425	Up	kinesin family member 4A
GPR161	1.690141	4.94E-09	1.4E-07	6.324796	Up	G protein-coupled receptor 161
P2RX7	1.582058	5.01E-09	1.41E-07	6.321892	Up	purinergic receptor P2X 7
CDCA5	1.864053	5.03E-09	1.41E-07	6.321119	Up	cell division cycle associated 5
CLEC5A	1.99045	5.18E-09	1.45E-07	6.315142	Up	C-type lectin domain containing 5A
KIF26B	2.186482	5.3E-09	1.48E-07	6.310447	Up	kinesin family member 26B
TFEC	1.566971	5.52E-09	1.53E-07	6.301734	Up	transcription factor EC
EXO1	1.67768	5.78E-09	1.58E-07	6.29207	Up	exonuclease 1
TUBB3	2.236373	5.92E-09	1.61E-07	6.287251	Up	tubulin beta 3 class III
CASC5	1.652782	6.12E-09	1.65E-07	6.280163	Up	kinetochore scaffold 1

TPX2	1.930431	6.29E-09	1.69E-07	6.274712	Up	TPX2 microtubule nucleation factor
POLQ	1.819336	6.84E-09	1.81E-07	6.257122	Up	DNA polymerase theta
RGS1	2.049497	7.19E-09	1.87E-07	6.246677	Up	regulator of G protein signaling 1
EDNRA	1.856733	7.22E-09	1.88E-07	6.245851	Up	endothelin receptor type A
ITGA5	1.716856	7.64E-09	1.97E-07	6.233848	Up	integrin subunit alpha 5
PRR5L	1.676315	7.72E-09	1.98E-07	6.231668	Up	proline rich 5 like
PLXDC2	2.054708	7.76E-09	1.98E-07	6.230814	Up	plexin domain containing 2
FAM26E	1.758127	8.22E-09	2.07E-07	6.21852	Up	Calcium Homeostasis Modulator Family Member 5
KIF20A	1.597958	8.41E-09	2.11E-07	6.213917	Up	kinesin family member 20A
PLAU	1.923316	8.99E-09	2.24E-07	6.199773	Up	plasminogen activator, urokinase
KIRREL	1.859596	9.32E-09	2.32E-07	6.192213	Up	Kirre Like Nephrin Family Adhesion Molecule 1
KIF21B	1.572691	9.79E-09	2.41E-07	6.181902	Up	kinesin family member 21B
FKBP10	2.18757	1E-08	2.45E-07	6.17754	Up	FKBP prolylisomerase 10
RTKN2	1.676019	1.05E-08	2.55E-07	6.16672	Up	rhotekin 2
MRC2	2.049876	1.15E-08	2.76E-07	6.147734	Up	mannose receptor C type 2
PVRL1	1.725234	1.16E-08	2.76E-07	6.146977	Up	Poliovirus receptor-related 1
LEF1	1.927508	1.22E-08	2.88E-07	6.13553	Up	lymphoid enhancer binding factor 1
LILRB3	1.673521	1.24E-08	2.92E-07	6.13191	Up	leukocyte immunoglobulin like receptor B3
EMR2	1.578167	1.28E-08	2.99E-07	6.125181	Up	EGF-like module-containing mucin-like hormone receptor-like 2
COL15A1	1.883791	1.35E-08	3.13E-07	6.114452	Up	collagen type XV alpha 1 chain
PLEKHG2	1.80988	1.35E-08	3.13E-07	6.113741	Up	pleckstrin homology and RhoGEF domain containing G2
PDLIM7	1.740568	1.38E-08	3.18E-07	6.109095	Up	PDZ and LIM domain 7
HTRA3	2.032862	1.4E-08	3.21E-07	6.10624	Up	HtrA serine peptidase 3
COL5A1	2.251397	1.41E-08	3.21E-07	6.105813	Up	collagen type V alpha 1 chain
FSCN1	1.859536	1.6E-08	3.58E-07	6.078685	Up	fascin actin-bundling protein 1
CPZ	2.709031	1.6E-08	3.58E-07	6.078232	Up	carboxypeptidase Z
PILRA	1.639131	1.64E-08	3.66E-07	6.072697	Up	paired immunoglobin like type 2 receptor alpha
NOX4	2.17837	1.68E-08	3.74E-07	6.067524	Up	NADPH oxidase 4
COL10A1	3.294663	1.69E-08	3.74E-07	6.066712	Up	collagen type X alpha 1 chain
CDCA7	1.873706	1.7E-08	3.74E-07	6.066149	Up	cell division cycle associated 7
GUCY1B3	1.714941	1.75E-08	3.84E-07	6.058799	Up	Guanylatecyclase soluble subunit beta-1
FCGR1A	1.550648	1.8E-08	3.92E-07	6.053685	Up	Fc fragment of IgG receptor Ia
CRISPLD1	2.840034	1.87E-08	4.06E-07	6.045375	Up	cysteine rich secretory protein LCCL domain containing 1
PGM2L1	1.604202	1.89E-08	4.08E-07	6.043469	Up	phosphoglucomutase 2 like 1
HJURP	1.660521	1.9E-08	4.09E-07	6.042214	Up	Holliday junction recognition protein
MCM2	1.610827	1.9E-08	4.1E-07	6.041763	Up	minichromosome maintenance complex component 2
EPPK1	2.121199	1.97E-08	4.21E-07	6.034651	Up	epiplakin 1
LRRC32	2.114457	1.98E-08	4.23E-07	6.03315	Up	leucine rich repeat containing 32
GINS4	1.554033	2.01E-08	4.28E-07	6.030407	Up	GINS complex subunit 4
CD84	1.610976	2.02E-08	4.3E-07	6.029305	Up	CD84 molecule
VCAN	2.144966	2.03E-08	4.33E-07	6.027469	Up	versican
ARHGAP11A	1.630033	2.09E-08	4.44E-07	6.021732	Up	Rho GTPase activating protein 11A

SLC2A3	1.845064	2.14E-08	4.52E-07	6.016445	Up	solute carrier family 2 member 3
FOXM1	1.797631	2.19E-08	4.6E-07	6.012159	Up	forkhead box M1
ORC1	1.553737	2.2E-08	4.62E-07	6.010844	Up	origin recognition complex subunit 1
TNFAIP2	1.893301	2.33E-08	4.84E-07	5.998857	Up	TNF alpha induced protein 2
ADAMTS4	1.862137	2.39E-08	4.93E-07	5.993264	Up	ADAM metallopeptidase with thrombospondin type 1 motif 4
SERPINB9	1.76002	2.45E-08	5.01E-07	5.9883	Up	serpin family B member 9
OLR1	2.216021	2.64E-08	5.36E-07	5.972109	Up	oxidized low density lipoprotein receptor 1
FSTL3	1.861555	2.7E-08	5.45E-07	5.966959	Up	follistatin like 3
LOXL2	1.628413	2.84E-08	5.66E-07	5.956474	Up	lysyl oxidase like 2
KIF2C	1.696056	2.86E-08	5.7E-07	5.954899	Up	kinesin family member 2C
FOXS1	1.848254	3E-08	5.91E-07	5.944636	Up	forkhead box S1
ANKRD13B	1.557613	3.1E-08	6.08E-07	5.937383	Up	ankyrin repeat domain 13B
GUCY1A3	2.333005	3.12E-08	6.1E-07	5.936473	Up	Guanylatecyclase soluble subunit alpha-3
ZAK	1.552581	3.16E-08	6.15E-07	5.933546	Up	Sterile alpha motif and leucine zipper containing kinase AZK
ITGA11	2.068155	3.25E-08	6.3E-07	5.927286	Up	integrin subunit alpha 11
ICAM1	1.944005	3.74E-08	7.03E-07	5.897156	Up	intercellular adhesion molecule 1
PXDN	1.618901	4.16E-08	7.66E-07	5.874542	Up	peroxidasin
ODF2L	1.618387	4.25E-08	7.8E-07	5.869993	Up	outer dense fiber of sperm tails 2 like
ASPM	1.759881	4.28E-08	7.83E-07	5.868482	Up	abnormal spindle microtubule assembly
GEM	1.935598	4.58E-08	8.31E-07	5.853538	Up	GTP binding protein overexpressed in skeletal muscle
GPX8	1.574781	4.62E-08	8.36E-07	5.852054	Up	glutathione peroxidase 8 (putative)
APOC1	2.532428	4.78E-08	8.6E-07	5.844346	Up	apolipoprotein C1
CSF3R	2.319103	5.28E-08	9.29E-07	5.823068	Up	colony stimulating factor 3 receptor
TMEM158	1.64545	5.67E-08	9.86E-07	5.807673	Up	transmembrane protein 158 (gene/pseudogene)
ZNF469	2.064601	5.91E-08	1.02E-06	5.798504	Up	zinc finger protein 469
PLXDC1	1.737904	6.08E-08	1.05E-06	5.79242	Up	plexin domain containing 1
PIK3R5	1.553293	6.25E-08	1.07E-06	5.78673	Up	phosphoinositide-3-kinase regulatory subunit 5
DGKH	1.612376	6.55E-08	1.12E-06	5.77644	Up	diacylglycerol kinase eta
FADS2	1.657975	7.05E-08	1.18E-06	5.760527	Up	fatty acid desaturase 2
FGR	1.579559	7.16E-08	1.2E-06	5.757077	Up	FGR proto-oncogene, Src family tyrosine kinase
LIPG	2.049762	7.36E-08	1.23E-06	5.751138	Up	lipase G, endothelial type
SERPINE2	2.202612	7.53E-08	1.25E-06	5.74608	Up	serpin family E member 2
MMP11	2.952133	7.63E-08	1.26E-06	5.743236	Up	matrix metallopeptidase 11
MCM10	1.774936	7.71E-08	1.27E-06	5.741063	Up	minichromosome maintenance 10 replication initiation factor
APOE	2.254187	7.79E-08	1.28E-06	5.738793	Up	apolipoprotein E
NEK2	1.692854	7.85E-08	1.29E-06	5.737093	Up	NIMA related kinase 2
CDCA2	1.668033	8.29E-08	1.35E-06	5.725122	Up	cell division cycle associated 2
IQGAP3	1.733444	8.51E-08	1.38E-06	5.719417	Up	IQ motif containing GTPase activating protein 3
CALD1	1.71965	8.94E-08	1.44E-06	5.708809	Up	caldesmon 1
CBX2	1.867374	1.01E-07	1.6E-06	5.683057	Up	chromobox 2
FAR2	1.571986	1.04E-07	1.64E-06	5.674834	Up	fatty acyl-CoA reductase 2
NTM	1.953707	1.05E-07	1.64E-06	5.674553	Up	neurotrimin

AMIGO2	1.75988	1.16E-07	1.78E-06	5.65216	Up	adhesion molecule with Ig like domain 2
WNT2	2.404356	1.2E-07	1.84E-06	5.644602	Up	Wnt family member 2
GRIN2D	2.307741	1.27E-07	1.93E-06	5.63168	Up	glutamate ionotropic receptor NMDA type subunit 2D
MKI67	1.710561	1.32E-07	1.99E-06	5.623865	Up	marker of proliferation Ki-67
LINC00340	1.704574	1.37E-07	2.06E-06	5.614696	Up	#N/A
ETV4	2.243602	1.39E-07	2.08E-06	5.611977	Up	ETS variant transcription factor 4
AJUBA	1.785348	1.51E-07	2.22E-06	5.593443	Up	ajuba LIM protein
ANLN	1.750152	1.58E-07	2.31E-06	5.584125	Up	anillin actin binding protein
PARVG	1.560826	1.64E-07	2.38E-06	5.575666	Up	parvin gamma
ADAMTS14	2.019487	1.66E-07	2.41E-06	5.573088	Up	ADAM metallopeptidase with thrombospondin type 1 motif 14
PLK1	1.552472	1.72E-07	2.47E-06	5.564603	Up	polo like kinase 1
PLEK	1.606253	1.74E-07	2.5E-06	5.562167	Up	pleckstrin
LUM	2.195011	1.98E-07	2.78E-06	5.533808	Up	lumican
SRPX2	1.666163	2.03E-07	2.83E-06	5.528704	Up	sushi repeat containing protein X-linked 2
ONECUT2	3.067256	2.04E-07	2.84E-06	5.527044	Up	one cut homeobox 2
BICC1	2.129691	2.11E-07	2.91E-06	5.520162	Up	BicC family RNA binding protein 1
KLHL29	1.658014	2.13E-07	2.94E-06	5.517367	Up	kelch like family member 29
H19	3.375443	2.25E-07	3.07E-06	5.505067	Up	H19 imprinted maternally expressed transcript
TGM2	2.005721	2.28E-07	3.1E-06	5.502485	Up	transglutaminase 2
FCER1G	1.567203	2.36E-07	3.19E-06	5.494477	Up	Fc fragment of IgE receptor Ig
ZNF462	1.8336	2.43E-07	3.26E-06	5.488355	Up	zinc finger protein 462
CLSTN3	1.589208	2.66E-07	3.53E-06	5.467758	Up	calsyntenin 3
CD248	1.816546	2.7E-07	3.57E-06	5.464493	Up	CD248 molecule
NT5DC3	1.656425	2.79E-07	3.67E-06	5.457673	Up	5'-nucleotidase domain containing 3
GDPD5	1.706172	2.79E-07	3.67E-06	5.457168	Up	glycerophosphodiesterphosphodiesterase domain containing 5
FBN1	2.205815	2.84E-07	3.72E-06	5.453361	Up	fibrillin 1
ATP10A	1.594819	2.85E-07	3.73E-06	5.452813	Up	ATPase phospholipid transporting 10A (putative)
STC2	1.637092	2.87E-07	3.75E-06	5.451086	Up	stanniocalcin 2
OSR2	1.919816	2.91E-07	3.81E-06	5.447658	Up	odd-skipped related transciption factor 2
ANGPTL2	1.741942	2.93E-07	3.82E-06	5.446431	Up	angiopoietin like 2
LY6E	1.958299	3.06E-07	3.97E-06	5.436569	Up	lymphocyte antigen 6 family member E
CPXM1	2.38795	3.15E-07	4.07E-06	5.430499	Up	carboxypeptidase X, M14 family member 1
SPOCK1	2.423261	3.27E-07	4.2E-06	5.421649	Up	SPARC (osteonectin), cwcv and kazal like domains proteoglycan 1
TOP2A	1.727058	3.36E-07	4.28E-06	5.415637	Up	DNA topoisomerase II alpha
ESPL1	1.596797	3.77E-07	4.71E-06	5.390156	Up	extra spindle pole bodies like 1, separase
LPPR4	1.994093	3.83E-07	4.79E-06	5.3865	Up	Lipid phosphate phosphatase-related protein type 4.
CDC6	1.641411	3.88E-07	4.84E-06	5.383599	Up	cell division cycle 6
MXRA5	1.903509	4E-07	4.95E-06	5.376656	Up	matrix remodeling associated 5
KIAA1755	1.931666	4.06E-07	5.02E-06	5.373205	Up	KIAA1755
ISLR	2.226024	4.45E-07	5.44E-06	5.352365	Up	immunoglobulin superfamily containing leucine rich repeat
RARRES1	2.14138	4.53E-07	5.5E-06	5.348611	Up	retinoic acid receptor responder 1
CTSK	2.028253	4.61E-07	5.58E-06	5.344477	Up	cathepsin K

ANTXR1	1.960624	5.03E-07	6E-06	5.324851	Up	ANTXR cell adhesion molecule 1
IGF2BP3	3.023841	5.23E-07	6.19E-06	5.315889	Up	insulin like growth factor 2 mRNA binding protein 3
IL2RA	1.561204	5.27E-07	6.22E-06	5.314141	Up	interleukin 2 receptor subunit alpha
FAM83D	1.667622	5.3E-07	6.25E-06	5.313207	Up	family with sequence similarity 83 member D
BCAT1	1.669577	5.96E-07	6.91E-06	5.286322	Up	branched chain amino acid transaminase 1
MYBL2	1.852727	6.84E-07	7.75E-06	5.25504	Up	MYB proto-oncogene like 2
SCARF2	1.773794	6.97E-07	7.87E-06	5.250857	Up	scavenger receptor class F member 2
AEBP1	2.090302	7.63E-07	8.51E-06	5.229903	Up	AE binding protein 1
ECT2	1.654658	8.21E-07	9.05E-06	5.213145	Up	epithelial cell transforming 2
CLDN4	2.507943	8.77E-07	9.58E-06	5.198137	Up	claudin 4
DKK2	1.649707	8.98E-07	9.78E-06	5.19271	Up	dickkopf WNT signaling pathway inhibitor 2
CD109	1.660368	9.34E-07	1.01E-05	5.18369	Up	CD109 molecule
HIST3H2BB	1.769554	9.72E-07	1.05E-05	5.174465	Up	Histone H2B type 3-B
LGI2	2.200628	9.77E-07	1.05E-05	5.173415	Up	leucine rich repeat LGI family member 2
NEIL2	1.604316	1.04E-06	1.11E-05	5.15844	Up	nei like DNA glycosylase 2
EGR2	1.661751	1.14E-06	1.2E-05	5.13733	Up	early growth response 2
ADAMTS9	1.572869	1.31E-06	1.35E-05	5.106375	Up	ADAM metallopeptidase with thrombospondin type 1 motif 9
COL11A1	3.770104	1.39E-06	1.42E-05	5.091092	Up	collagen type XI alpha 1 chain
ITGB8	1.76404	1.4E-06	1.43E-05	5.090304	Up	integrin subunit beta 8
ZNF703	2.008932	1.52E-06	1.52E-05	5.070981	Up	zinc finger protein 703
PDE3A	1.945529	1.68E-06	1.65E-05	5.047789	Up	phosphodiesterase 3A
TNFRSF11B	2.312306	1.69E-06	1.66E-05	5.046034	Up	TNF receptor superfamily member 11b
CHRDL2	2.572031	1.76E-06	1.71E-05	5.037378	Up	chordin like 2
STRA6	2.132464	1.76E-06	1.72E-05	5.036683	Up	stimulated by retinoic acid 6
MFI2	2.253506	1.84E-06	1.78E-05	5.027016	Up	Melanotransferrin
F2RL2	2.038989	2.14E-06	2.02E-05	4.991024	Up	coagulation factor II thrombin receptor like 2
TYMP	1.570039	2.18E-06	2.05E-05	4.98695	Up	thymidine phosphorylase
HTRA1	1.605928	2.26E-06	2.12E-05	4.97802	Up	HtrA serine peptidase 1
GGT5	1.784196	2.62E-06	2.41E-05	4.943505	Up	gamma-glutamyltransferase 5
LAMA5	1.740776	2.65E-06	2.44E-05	4.940342	Up	laminin subunit alpha 5
GFPT2	1.838625	2.95E-06	2.67E-05	4.91535	Up	glutamine-fructose-6-phosphate transaminase 2
PKDCC	2.156848	2.95E-06	2.67E-05	4.915316	Up	protein kinase domain containing, cytoplasmic
MAP1A	1.891892	3.23E-06	2.88E-05	4.893781	Up	microtubule associated protein 1A
MYH10	1.618718	3.4E-06	3.01E-05	4.881443	Up	myosin heavy chain 10
MMP16	1.693752	3.4E-06	3.01E-05	4.88143	Up	matrix metallopeptidase 16
LTBP2	2.006391	3.41E-06	3.01E-05	4.880896	Up	latent transforming growth factor beta binding protein 2
TREM1	1.925025	3.51E-06	3.08E-05	4.873843	Up	triggering receptor expressed on myeloid cells 1
CCL3	1.680971	3.82E-06	3.3E-05	4.853691	Up	C-C motif chemokine ligand 3
DIO2	2.219681	3.87E-06	3.34E-05	4.851101	Up	iodothyroninedeiodinase 2
CST1	3.432026	3.9E-06	3.36E-05	4.848715	Up	cystatin SN
UBE2C	1.564194	3.93E-06	3.38E-05	4.847262	Up	ubiquitin conjugating enzyme E2 C
NCR3LG1	1.774407	3.97E-06	3.41E-05	4.844728	Up	natural killer cell cytotoxicity receptor 3 ligand 1

AQP1	1.912101	4.25E-06	3.6E-05	4.828269	Up	aquaporin 1 (Colton blood group)
CELSR3	1.893472	4.52E-06	3.78E-05	4.813793	Up	cadherin EGF LAG seven-pass G-type receptor 3
PTPRO	1.641236	4.56E-06	3.81E-05	4.81153	Up	protein tyrosine phosphatase receptor type O
PADI2	1.837363	4.68E-06	3.9E-05	4.805194	Up	peptidyl arginine deiminase 2
SELL	1.712176	4.86E-06	4.02E-05	4.796038	Up	selectin L
DPYSL3	1.965102	4.94E-06	4.08E-05	4.792282	Up	dihydropyrimidinase like 3
HIST1H3G	1.577336	5.35E-06	4.36E-05	4.773012	Up	histone cluster 1 H3 family member g
FPR1	1.68925	5.41E-06	4.4E-05	4.770541	Up	formyl peptide receptor 1
C13orf33	1.748636	6.21E-06	4.95E-05	4.737008	Up	Mesenteric Estrogen Dependent Adipogenesis
FAM19A5	1.647679	6.4E-06	5.08E-05	4.729791	Up	family with sequence similarity 19 (chemokine (C-C motif)-like), member A5
PCOLCE	1.782918	6.69E-06	5.27E-05	4.71896	Up	procollagen C-endopeptidase enhancer
ATHL1	1.857749	7.96E-06	6.11E-05	4.676623	Up	Acid trehalase-like protein 1.
C1R	1.668333	8.01E-06	6.13E-05	4.675179	Up	complement C1r
DNM3OS	1.810025	8.44E-06	6.4E-05	4.662446	Up	DNM3 opposite strand/antisense RNA
PLEKHG4	1.678447	9.06E-06	6.8E-05	4.645179	Up	pleckstrin homology and RhoGEF domain containing G4
MYB	1.976157	9.2E-06	6.89E-05	4.641278	Up	MYB proto-oncogene, transcription factor
MAPK15	1.566636	9.35E-06	6.98E-05	4.637383	Up	mitogen-activated protein kinase 15
THBS4	4.239608	9.36E-06	6.99E-05	4.637157	Up	thrombospondin 4
CACNA1E	1.952079	1.03E-05	7.57E-05	4.613471	Up	calcium voltage-gated channel subunit alpha1 E
IFITM1	1.68165	1.05E-05	7.66E-05	4.609872	Up	interferon induced transmembrane protein 1
FOXC1	1.657759	1.31E-05	9.29E-05	4.554126	Up	forkhead box C1
SALL4	2.027354	1.36E-05	9.55E-05	4.545063	Up	spalt like transcription factor 4
GREM1	2.236937	1.41E-05	9.86E-05	4.535872	Up	gremlin 1, DAN family BMP antagonist
MXRA8	1.673416	1.53E-05	0.000106	4.51605	Up	matrix remodeling associated 8
LINC00578	1.578457	1.54E-05	0.000107	4.513109	Up	long intergenic non-protein coding RNA 578
TNFAIP6	1.55874	1.55E-05	0.000107	4.512004	Up	TNF alpha induced protein 6
GAS7	1.642789	1.63E-05	0.000112	4.499178	Up	growth arrest specific 7
OSM	2.089218	1.64E-05	0.000112	4.498105	Up	oncostatin M
PTGS2	2.220566	1.74E-05	0.000118	4.483727	Up	prostaglandin-endoperoxide synthase 2
GLI2	1.767141	1.75E-05	0.000118	4.481492	Up	GLI family zinc finger 2
CCND2	1.851117	1.82E-05	0.000122	4.472625	Up	cyclin D2
AHNAK2	2.276015	1.94E-05	0.000129	4.456469	Up	AHNAK nucleoprotein 2
MEX3A	1.55585	1.96E-05	0.000131	4.453107	Up	mex-3 RNA binding family member A
ITGBL1	2.678016	1.99E-05	0.000132	4.449749	Up	integrin subunit beta like 1
FBXO32	1.658792	2.3E-05	0.000149	4.413422	Up	F-box protein 32
SELE	2.552922	2.36E-05	0.000153	4.40637	Up	selectin E
C3	2.416315	2.47E-05	0.000158	4.39516	Up	complement C3
GBP5	1.887503	2.54E-05	0.000162	4.387905	Up	guanylate binding protein 5
ALDH1A3	1.747154	2.69E-05	0.000171	4.373742	Up	aldehyde dehydrogenase 1 family member A3
HOXA10	1.767013	2.96E-05	0.000185	4.349093	Up	homeobox A10
DNM1	1.641482	2.99E-05	0.000186	4.346055	Up	dynamin 1
CHI3L1	2.692343	3E-05	0.000187	4.345501	Up	chitinase 3 like 1

KRT80	1.999185	3.3E-05	0.000203	4.320945	Up	keratin 80
SLC28A3	2.007432	3.61E-05	0.000218	4.298069	Up	solute carrier family 28 member 3
VGLL3	1.741023	3.72E-05	0.000224	4.290212	Up	vestigial like family member 3
CPXM2	1.872947	3.84E-05	0.00023	4.282207	Up	carboxypeptidase X, M14 family member 2
BCL2A1	1.656709	3.86E-05	0.000231	4.280957	Up	BCL2 related protein A1
PI15	2.584688	4.22E-05	0.000249	4.257782	Up	peptidase inhibitor 15
IGSF9B	1.553308	4.68E-05	0.000271	4.231241	Up	immunoglobulin superfamily member 9B
LOC154860	1.590749	4.69E-05	0.000271	4.230639	Up	#N/A
HMCN1	2.380264	5.36E-05	0.000305	4.195435	Up	hemicentin 1
SLC24A3	1.603357	5.51E-05	0.000313	4.18864	Up	solute carrier family 24 member 3
CXCL1	2.294197	5.51E-05	0.000313	4.188195	Up	C-X-C motif chemokine ligand 1
ODZ4	1.748243	5.53E-05	0.000314	4.187256	Up	Teneurin-4
CAMK2N1	1.634814	5.66E-05	0.00032	4.181603	Up	calcium/calmodulin dependent protein kinase II inhibitor 1
AGT	2.291038	6.55E-05	0.000361	4.142954	Up	angiotensinogen
IL8	2.999956	6.88E-05	0.000377	4.129921	Up	interleukin 8
HOXB9	1.958455	7.39E-05	0.000401	4.111134	Up	homeobox B9
APLN	1.555857	9.33E-05	0.000489	4.049282	Up	apelin
EPHB1	1.685685	0.000107	0.000549	4.013409	Up	EPH receptor B1
AQP9	1.933182	0.000117	0.000597	3.987386	Up	aquaporin 9
HEPH	2.011133	0.000119	0.000602	3.984451	Up	hephaestin
NEB	2.076932	0.00012	0.000608	3.981512	Up	nebulin
KRT17	2.919829	0.000124	0.000626	3.972853	Up	keratin 17
VIL1	2.131168	0.000133	0.000666	3.953475	Up	villin 1
MLK7-AS1	1.815952	0.000134	0.000671	3.951002	Up	MLK7 antisense RNA 1
HOXA13	2.203005	0.00014	0.000692	3.940298	Up	homeobox A13
MIR100HG	1.672169	0.000143	0.000704	3.934599	Up	mir-100-let-7a-2-mir-125b-1 cluster host gene
C2orf89	1.980425	0.000151	0.00074	3.918988	Up	chromosome 2 open reading frame 89
CDX2	2.101672	0.000161	0.000781	3.901649	Up	caudal type homeobox 2
TNC	1.759858	0.000166	0.0008	3.893609	Up	tenascin C
COL16A1	1.675579	0.000175	0.000841	3.878528	Up	collagen type XVI alpha 1 chain
NRK	2.007124	0.000195	0.000922	3.848801	Up	Nik related kinase
HKDC1	2.071149	0.000266	0.001194	3.762683	Up	hexokinase domain containing 1
GDF15	1.618022	0.000285	0.001269	3.742307	Up	growth differentiation factor 15
MMP3	2.913904	0.000337	0.001464	3.695627	Up	matrix metallopeptidase 3
MYOM3	1.83562	0.000337	0.001466	3.6951	Up	myomesin 3
LOC100124692	2.216207	0.000349	0.001509	3.685408	Up	#N/A
IFI44L	1.587711	0.000365	0.00157	3.672376	Up	interferon induced protein 44 like
PLEKHS1	2.099427	0.000395	0.001677	3.65015	Up	pleckstrin homology domain containing S1
CDH3	1.714521	0.000401	0.001699	3.645624	Up	cadherin 3
ELN	2.002142	0.000425	0.001782	3.629115	Up	elastin
COMP	1.742429	0.000454	0.001884	3.610079	Up	cartilage oligomeric matrix protein
MMP9	1.99775	0.000464	0.00192	3.603783	Up	matrix metallopeptidase 9

CLDN3	2.474438	0.000465	0.001923	3.602954	Up	claudin 3
CRABP2	1.566544	0.000495	0.002026	3.584792	Up	cellular retinoic acid binding protein 2
ABCA13	1.592582	0.000498	0.002036	3.583143	Up	ATP binding cassette subfamily A member 13
LINC00478	1.585816	0.000504	0.002054	3.579916	Up	#N/A
IL6	1.683392	0.000519	0.002112	3.571026	Up	interleukin 6
CXCL6	1.96745	0.000709	0.002755	3.479615	Up	C-X-C motif chemokine ligand 6
LOC93432	1.946221	0.000758	0.002913	3.459718	Up	#N/A
LGR5	1.783554	0.000797	0.003041	3.444591	Up	leucine rich repeat containing G protein-coupled receptor 5
FLRT2	1.639972	0.000883	0.00331	3.414201	Up	fibronectinleucine rich transmembrane protein 2
STK31	1.593465	0.000899	0.003358	3.408694	Up	serine/threonine kinase 31
C2CD4A	1.641563	0.001085	0.003936	3.351939	Up	C2 calcium dependent domain containing 4A
SFRP2	2.377128	0.001102	0.003989	3.347103	Up	secreted frizzled related protein 2
TRIM29	2.175502	0.001163	0.00418	3.330604	Up	tripartite motif containing 29
EPHA3	1.60529	0.001288	0.004552	3.299431	Up	EPH receptor A3
OMD	1.604119	0.001325	0.004665	3.290695	Up	osteomodulin
CXCL9	1.737291	0.001451	0.00504	3.262741	Up	C-X-C motif chemokine ligand 9
CLDN2	2.328	0.001468	0.005088	3.259026	Up	claudin 2
IL11	1.74806	0.001484	0.005136	3.255678	Up	interleukin 11
ROBO2	1.597553	0.001824	0.006131	3.191206	Up	roundabout guidance receptor 2
MYO7B	2.265256	0.002115	0.006956	3.144449	Up	myosin VIIB
BOC	1.564592	0.002391	0.007737	3.105276	Up	BOC cell adhesion associated, oncogene regulated
CCDC80	1.737263	0.002517	0.008086	3.088781	Up	coiled-coil domain containing 80
ANXA13	2.127525	0.002728	0.008669	3.062776	Up	annexin A13
MGP	1.760338	0.002932	0.009217	3.039314	Up	matrix Gla protein
CYP2B6	1.577043	0.003615	0.011048	2.970589	Up	cytochrome P450 family 2 subfamily B member 6
SLC39A5	1.929535	0.003709	0.011286	2.962123	Up	solute carrier family 39 member 5
SERPINB5	2.091229	0.003875	0.011718	2.947537	Up	serpin family B member 5
CYP2W1	1.750607	0.004086	0.012245	2.929892	Up	cytochrome P450 family 2 subfamily W member 1
MMP1	1.872645	0.004143	0.012387	2.925223	Up	matrix metallopeptidase 1
PPP1R1B	2.052602	0.004324	0.012839	2.910954	Up	protein phosphatase 1 regulatory inhibitor subunit 1B
CCL18	1.586798	0.004432	0.013114	2.902656	Up	C-C motif chemokine ligand 18
CLRN3	1.612409	0.00469	0.013758	2.883553	Up	clarin 3
KLK6	1.688522	0.004878	0.014216	2.87025	Up	kallikrein related peptidase 6
CDH17	2.620031	0.005285	0.015217	2.842959	Up	cadherin 17
IDO1	1.779523	0.007847	0.021186	2.705718	Up	indoleamine 2,3-dioxygenase 1
FCGR3B	1.579377	0.009356	0.024675	2.643002	Up	Fc fragment of IgG receptor IIIb
WDR72	1.857672	0.010012	0.026125	2.618572	Up	WD repeat domain 72
MMP7	2.195172	0.0136	0.033814	2.506018	Up	matrix metallopeptidase 7
MSLN	2.009849	0.014377	0.035418	2.485225	Up	mesothelin
MUC16	1.592157	0.01469	0.036076	2.477136	Up	mucin 16, cell surface associated
TNS4	1.670843	0.01559	0.03795	2.454666	Up	tensin 4
CPS1	2.230898	0.020655	0.048108	2.346431	Up	carbamoyl-phosphate synthase 1

GUCA2B	-2.7219	3.07E-22	7.27E-18	-12.0832	Down	guanylatecyclase activator 2B
LINC00332	-1.1776	3.45E-21	4.09E-17	-11.6342	Down	long intergenic non-protein coding RNA 332
C14orf180	-1.50929	1.52E-19	7.66E-16	-10.9349	Down	chromosome 14 open reading frame 180
ADH7	-3.79214	1.93E-18	5.08E-15	-10.4663	Down	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
ATP4A	-7.94795	5.13E-18	1.22E-14	-10.2859	Down	ATPase H+/K+ transporting subunit alpha
CWH43	-3.38545	5.94E-18	1.28E-14	-10.2588	Down	cell wall biogenesis 43 C-terminal homolog
MAL	-3.08582	1.16E-17	1.83E-14	-10.1352	Down	mal, T cell differentiation protein
ATP4B	-7.22434	1.86E-17	2.59E-14	-10.0482	Down	ATPase H+/K+ transporting subunit beta
CHIA	-4.12203	2.65E-17	3.3E-14	-9.9833	Down	chitinase acidic
HTR1E	-1.16176	6.6E-17	7.44E-14	-9.81443	Down	5-hydroxytryptamine receptor 1E
CCKAR	-3.34303	1.72E-16	1.7E-13	-9.63723	Down	cholecystokinin A receptor
LGALS9B	-3.08644	2.73E-16	2.31E-13	-9.55146	Down	galectin 9B
PDILT	-3.17607	2.88E-16	2.35E-13	-9.54145	Down	protein disulfideisomerase like, testis expressed
SLC5A5	-6.1349	3.51E-16	2.66E-13	-9.50499	Down	solute carrier family 5 member 5
PGA5	-8.20606	3.6E-16	2.66E-13	-9.50047	Down	pepsinogen A5
GUCA1C	-1.35912	5.33E-16	3.7E-13	-9.42767	Down	guanylatecyclase activator 1C
GRIA4	-2.69276	5.51E-16	3.7E-13	-9.42125	Down	glutamate ionotropic receptor AMPA type subunit 4
RDH12	-2.86156	6.36E-16	3.86E-13	-9.39465	Down	retinol dehydrogenase 12
PSAPL1	-5.56816	1.05E-15	6.07E-13	-9.30131	Down	prosaposin like 1 (gene/pseudogene)
VSTM2A	-1.5564	1.83E-15	8.84E-13	-9.19831	Down	V-set and transmembrane domain containing 2A
AGXT2L1	-3.07655	1.99E-15	9.41E-13	-9.1829	Down	Alanine--glyoxylate aminotransferase 2-like 1 isoform 1
ASB11	-2.7366	2.34E-15	1.02E-12	-9.15274	Down	ankyrin repeat and SOCS box containing 11
GNMT	-1.40388	2.58E-15	1.11E-12	-9.1341	Down	glycine N-methyltransferase
CCKBR	-3.28447	2.62E-15	1.11E-12	-9.13137	Down	cholecystokinin B receptor
DCAF12L1	-1.38042	2.95E-15	1.22E-12	-9.10962	Down	DDB1 and CUL4 associated factor 12 like 1
GSTA3	-1.58126	4.2E-15	1.69E-12	-9.04349	Down	glutathione S-transferase alpha 3
SCNN1B	-3.05194	4.76E-15	1.88E-12	-9.02024	Down	sodium channel epithelial 1 beta subunit
AQP4	-4.31119	1.45E-14	4.84E-12	-8.81159	Down	aquaporin 4
TMED6	-2.62873	1.93E-14	6.02E-12	-8.75803	Down	transmembrane p24 trafficking protein 6
FAM135B	-1.56176	2.74E-14	8E-12	-8.69261	Down	family with sequence similarity 135 member B
GIF	-7.35545	4.9E-14	1.3E-11	-8.58318	Down	gastric intrinsic factor
DNER	-3.2273	5.79E-14	1.47E-11	-8.55171	Down	delta/notch like EGF repeat containing
GKN2	-8.97895	6.38E-14	1.57E-11	-8.53346	Down	gastrokine 2
ESRRG	-4.70155	7.39E-14	1.77E-11	-8.50569	Down	estrogen related receptor gamma
B3GAT1	-2.2731	7.93E-14	1.88E-11	-8.4924	Down	beta-1,3-glucuronyltransferase 1
DNMBP-AS1	-1.61328	8.08E-14	1.9E-11	-8.48885	Down	DNMBP antisense RNA 1
GKN1	-10.7882	1.07E-13	2.4E-11	-8.43508	Down	gastrokine 1
TRIM50	-3.04881	1.21E-13	2.63E-11	-8.41231	Down	tripartite motif containing 50
LGALS9C	-3.4389	1.35E-13	2.87E-11	-8.39232	Down	galectin 9C
PGA4	-1.61309	1.39E-13	2.93E-11	-8.38695	Down	pepsinogen A4
UNC5D	-1.19374	1.76E-13	3.62E-11	-8.34178	Down	unc-5 netrin receptor D
KCNE2	-4.98462	1.8E-13	3.65E-11	-8.33726	Down	potassium voltage-gated channel subfamily E regulatory subunit 2

LOC388387	-1.73995	2.33E-13	4.56E-11	-8.28855	Down	#N/A
LOC728606	-2.5326	2.47E-13	4.79E-11	-8.27777	Down	#N/A
SIGLEC11	-2.42008	4.48E-13	7.74E-11	-8.16441	Down	sialic acid binding Ig like lectin 11
SCGB2A1	-2.78376	4.99E-13	8.26E-11	-8.14398	Down	secretoglobin family 2A member 1
CKM	-2.63883	6.25E-13	9.79E-11	-8.10113	Down	creatine kinase, M-type
FMO6P	-1.85337	6.53E-13	1.01E-10	-8.09258	Down	flavin containing dimethylanilinemonoxygenase 6, pseudogene
LOC150622	-2.27665	6.82E-13	1.05E-10	-8.08429	Down	#N/A
CPA2	-4.84591	1.04E-12	1.48E-10	-8.00357	Down	carboxypeptidase A2
EEF1A2	-2.65996	1.41E-12	1.92E-10	-7.94605	Down	eukaryotic translation elongation factor 1 alpha 2
LIPF	-10.3248	1.76E-12	2.3E-10	-7.9034	Down	lipase F, gastric type
SPINK13	-1.45446	2.63E-12	3.23E-10	-7.82546	Down	serine peptidase inhibitor, Kazal type 13 (putative)
HRASLS2	-4.085	2.87E-12	3.51E-10	-7.80865	Down	HRAS-like suppressor 2
GCNT4	-3.44785	3.16E-12	3.8E-10	-7.79046	Down	glucosaminyl (N-acetyl) transferase 4
CLCNKA	-1.66591	6.62E-12	7.13E-10	-7.64752	Down	chloride voltage-gated channel Ka
ESRRB	-1.73267	6.74E-12	7.22E-10	-7.64407	Down	estrogen related receptor beta
CNTN3	-1.44241	7.14E-12	7.52E-10	-7.63278	Down	contactin 3
KCNJ16	-4.09464	9.01E-12	9.04E-10	-7.58774	Down	potassium inwardly rectifying channel subfamily J member 16
SOSTDC1	-4.29253	1.24E-11	1.17E-09	-7.5263	Down	sclerostin domain containing 1
SH3GL2	-2.06709	1.38E-11	1.29E-09	-7.50487	Down	SH3 domain containing GRB2 like 2, endophilin A1
FLJ42875	-2.84725	1.83E-11	1.64E-09	-7.44946	Down	#N/A
IRX3	-1.97395	2.07E-11	1.82E-09	-7.42543	Down	iroquoishomeobox 3
ASAH2	-2.33127	3.38E-11	2.68E-09	-7.32979	Down	N-acylsphingosineamidohydrolase 2
SCNN1G	-2.51233	3.97E-11	3.07E-09	-7.29803	Down	sodium channel epithelial 1 gamma subunit
PGA3	-8.64003	4.08E-11	3.13E-09	-7.29249	Down	pepsinogen A3
ACADL	-1.50519	5.1E-11	3.69E-09	-7.24896	Down	acyl-CoA dehydrogenase long chain
ACER2	-2.90333	6.04E-11	4.23E-09	-7.21546	Down	alkaline ceramidase 2
RNASE1	-2.94249	8.7E-11	5.64E-09	-7.14325	Down	ribonuclease A family member 1, pancreatic
SLC7A8	-1.66853	1.08E-10	6.71E-09	-7.10037	Down	solute carrier family 7 member 8
PM20D1	-1.32165	1.63E-10	9.34E-09	-7.01865	Down	peptidase M20 domain containing 1
C17orf110	-2.46061	1.77E-10	9.98E-09	-7.00211	Down	Small Integral Membrane Protein 6
NRG4	-2.30508	1.78E-10	9.99E-09	-7.00084	Down	neuregulin 4
AQP10	-1.46396	1.87E-10	1.04E-08	-6.99086	Down	aquaporin 10
DMRTA1	-2.06762	2.03E-10	1.1E-08	-6.97447	Down	DMRT like family A1
APLP1	-2.38614	2.31E-10	1.22E-08	-6.94873	Down	amyloid beta precursor like protein 1
SULT2A1	-3.326	2.72E-10	1.38E-08	-6.91584	Down	sulfotransferase family 2A member 1
PXMP2	-1.58853	3.07E-10	1.52E-08	-6.89205	Down	peroxisomal membrane protein 2
SLC26A7	-2.5464	3.37E-10	1.64E-08	-6.87293	Down	solute carrier family 26 member 7
SLC9A4	-4.74981	4.57E-10	2.11E-08	-6.81174	Down	solute carrier family 9 member A4
NKX6-2	-2.77989	5.24E-10	2.32E-08	-6.78422	Down	NK6 homeobox 2
RAB27A	-1.63418	6.75E-10	2.81E-08	-6.733	Down	RAB27A, member RAS oncogene family
RPRM	-1.3426	8.16E-10	3.25E-08	-6.69476	Down	reprimo, TP53 dependent G2 arrest mediator homolog
DPCR1	-3.89479	8.97E-10	3.49E-08	-6.67532	Down	#N/A

AMTN	-1.80401	1.04E-09	3.94E-08	-6.64447	Down	amelotin
LDHD	-2.31421	1.12E-09	4.18E-08	-6.62935	Down	lactate dehydrogenase D
SOX21	-3.76428	1.18E-09	4.34E-08	-6.61935	Down	SRY-box transcription factor 21
MFSD4	-3.84008	1.36E-09	4.84E-08	-6.59049	Down	#N/A
FBP2	-2.70325	1.38E-09	4.89E-08	-6.58779	Down	fructose-bisphosphatase 2
ENHO	-1.15412	1.41E-09	4.98E-08	-6.5826	Down	energy homeostasis associated
SNORD116-8	-1.88842	1.52E-09	5.28E-08	-6.56728	Down	small nucleolar RNA, C/D box 116-8
SPTSSB	-3.57356	1.65E-09	5.67E-08	-6.55066	Down	serine palmitoyltransferase small subunit B
RANBP3L	-1.26145	1.67E-09	5.7E-08	-6.54868	Down	RAN binding protein 3 like
COL2A1	-2.95189	1.84E-09	6.15E-08	-6.52898	Down	collagen type II alpha 1 chain
LINC00520	-1.52475	1.85E-09	6.17E-08	-6.52761	Down	long intergenic non-protein coding RNA 520
MAP7D2	-3.20063	1.85E-09	6.18E-08	-6.52716	Down	MAP7 domain containing 2
REP15	-3.34177	1.99E-09	6.54E-08	-6.51265	Down	RAB15 effector protein
SNORD116-22	-1.53513	3.37E-09	1.01E-07	-6.40446	Down	small nucleolar RNA, C/D box 116-22
FBXL13	-1.51457	4.12E-09	1.21E-07	-6.36247	Down	F-box and leucine rich repeat protein 13
SST	-3.53196	4.21E-09	1.23E-07	-6.35817	Down	somatostatin
SSTR1	-2.89045	4.95E-09	1.4E-07	-6.32433	Down	somatostatin receptor 1
CYSTM1	-2.62765	4.97E-09	1.41E-07	-6.32349	Down	cysteine rich transmembrane module containing 1
SNORD116-24	-1.92841	5.04E-09	1.41E-07	-6.3207	Down	small nucleolar RNA, C/D box 116-24
UBE2QL1	-1.33169	6.9E-09	1.82E-07	-6.25529	Down	ubiquitin conjugating enzyme E2 Q family like 1
SLC26A9	-3.70909	7.03E-09	1.84E-07	-6.2514	Down	solute carrier family 26 member 9
AKR1B15	-1.68777	7.81E-09	2E-07	-6.2293	Down	aldo-ketoreductase family 1 member B15
C16orf89	-3.15116	8.26E-09	2.08E-07	-6.21756	Down	chromosome 16 open reading frame 89
DHRS7	-1.25342	8.5E-09	2.13E-07	-6.21152	Down	dehydrogenase/reductase 7
GHRL	-2.81942	1.04E-08	2.53E-07	-6.16876	Down	ghrelin and obestatinprepropeptide
MYOC	-2.36235	1.1E-08	2.65E-07	-6.15769	Down	myocilin
PLIN5	-1.63943	1.1E-08	2.65E-07	-6.15738	Down	perilipin 5
TFF1	-5.96452	1.28E-08	2.99E-07	-6.12626	Down	trefoil factor 1
SNORD116-15	-1.81246	1.32E-08	3.06E-07	-6.11943	Down	small nucleolar RNA, C/D box 116-15
CLIC6	-3.00234	1.38E-08	3.18E-07	-6.11	Down	chloride intracellular channel 6
GPX3	-1.53402	1.39E-08	3.19E-07	-6.10797	Down	glutathione peroxidase 3
SNORD116-1	-1.23006	1.41E-08	3.21E-07	-6.1057	Down	small nucleolar RNA, C/D box 116-1
C17orf109	-1.78583	1.55E-08	3.48E-07	-6.08492	Down	Small Integral Membrane Protein 5)
SNORD116-16	-1.85033	1.63E-08	3.65E-07	-6.07383	Down	small nucleolar RNA, C/D box 116-16
DDX60	-1.90016	1.7E-08	3.75E-07	-6.06529	Down	DExD/H-box helicase 60
AKR1C1	-2.71499	1.87E-08	4.06E-07	-6.04482	Down	aldo-ketoreductase family 1 member C1
CHGA	-4.92682	1.95E-08	4.18E-07	-6.03667	Down	chromogranin A
ATP13A5	-1.21452	1.95E-08	4.18E-07	-6.03656	Down	ATPase 13A5
CKB	-2.96435	2.2E-08	4.62E-07	-6.01088	Down	creatine kinase B
GPER	-1.80627	2.36E-08	4.89E-07	-5.99599	Down	G protein-coupled estrogen receptor 1
SNORD8	-1.80282	3.07E-08	6.02E-07	-5.93999	Down	small nucleolar RNA, C/D box 8
CADM2	-1.89173	3.26E-08	6.3E-07	-5.92695	Down	cell adhesion molecule 2
ZNF385B	-1.78893	3.57E-08	6.78E-07	-5.90705	Down	zinc finger protein 385B

ACSM1	-1.46055	3.7E-08	6.96E-07	-5.89993	Down	acyl-CoA synthetase medium chain family member 1
TFF2	-6.44232	3.72E-08	7E-07	-5.89859	Down	trefoil factor 2
CSTA	-1.86609	4.26E-08	7.81E-07	-5.86943	Down	cystatin A
PTGDR2	-1.81674	4.69E-08	8.46E-07	-5.84879	Down	prostaglandin D2 receptor 2
APOBEC2	-1.56849	4.86E-08	8.7E-07	-5.84084	Down	apolipoprotein B mRNA editing enzyme catalytic subunit 2
GPRC5C	-1.81291	5.23E-08	9.22E-07	-5.82526	Down	G protein-coupled receptor class C group 5 member C
MT1M	-2.74482	5.39E-08	9.43E-07	-5.8186	Down	metallothionein 1M
ALDH6A1	-1.28921	5.45E-08	9.53E-07	-5.81603	Down	aldehyde dehydrogenase 6 family member A1
PDGFD	-1.8933	6.04E-08	1.04E-06	-5.79406	Down	platelet derived growth factor D
FUT9	-4.25189	6.29E-08	1.08E-06	-5.78508	Down	fucosyltransferase 9
AKR7A3	-2.97814	6.47E-08	1.11E-06	-5.77892	Down	aldo-ketoreductase family 7 member A3
GATA5	-2.62837	6.7E-08	1.14E-06	-5.77143	Down	GATA binding protein 5
PSCA	-5.92828	6.79E-08	1.15E-06	-5.76865	Down	prostate stem cell antigen
SYT16	-1.31438	7.05E-08	1.19E-06	-5.76027	Down	synaptotagmin 16
FRMD1	-2.30851	7.11E-08	1.19E-06	-5.75872	Down	FERM domain containing 1
HPGD	-3.26128	7.9E-08	1.3E-06	-5.7357	Down	15-hydroxyprostaglandin dehydrogenase
ERO1LB	-1.53891	8.63E-08	1.4E-06	-5.71649	Down	endoplasmic reticulum oxidoreductase 1 beta
LOC100289255	-2.65977	9.04E-08	1.45E-06	-5.70623	Down	#N/A
B4GALNT3	-2.22696	1.02E-07	1.61E-06	-5.68052	Down	beta-1,4-N-acetyl-galactosaminyltransferase 3
AKR1C2	-3.36163	1.08E-07	1.68E-06	-5.66757	Down	aldo-ketoreductase family 1 member C2
TMEM220	-1.43809	1.14E-07	1.76E-06	-5.65605	Down	transmembrane protein 220
PDIA2	-3.22693	1.22E-07	1.87E-06	-5.64051	Down	protein disulfideisomerase family A member 2
GLUL	-1.47258	1.39E-07	2.09E-06	-5.61142	Down	glutamate-ammonia ligase
SLC2A12	-2.17534	1.41E-07	2.1E-06	-5.60948	Down	solute carrier family 2 member 12
CXCL17	-4.34036	1.48E-07	2.19E-06	-5.5984	Down	C-X-C motif chemokine ligand 17
HOMER2	-2.62231	1.52E-07	2.24E-06	-5.59209	Down	homer scaffold protein 2
KCNJ15	-2.71143	1.87E-07	2.65E-06	-5.54619	Down	potassium inwardly rectifying channel subfamily J member 15
SLC25A4	-1.49727	1.89E-07	2.67E-06	-5.54412	Down	solute carrier family 25 member 4
FA2H	-2.0741	2.03E-07	2.83E-06	-5.52818	Down	fatty acid 2-hydroxylase
GC	-2.25418	2.12E-07	2.93E-06	-5.51839	Down	GC vitamin D binding protein
AGPAT9	-1.64544	2.19E-07	3.01E-06	-5.511	Down	1-acylglycerol-3-phosphate O-acyltransferase 9
CA2	-4.04359	2.22E-07	3.03E-06	-5.50885	Down	carbonic anhydrase 2
ANGPTL3	-1.65764	2.23E-07	3.05E-06	-5.50692	Down	angiopoietin like 3
ENAM	-1.42603	2.25E-07	3.07E-06	-5.50571	Down	enamelin
CNTD1	-1.15343	2.29E-07	3.11E-06	-5.50141	Down	cyclin N-terminal domain containing 1
C22orf23	-1.43003	2.32E-07	3.14E-06	-5.49836	Down	chromosome 22 open reading frame 23
VSIG2	-3.8996	2.36E-07	3.19E-06	-5.49508	Down	V-set and immunoglobulin domain containing 2
DUSP19	-1.39174	2.52E-07	3.37E-06	-5.47987	Down	dual specificity phosphatase 19
MYZAP	-1.47779	2.64E-07	3.51E-06	-5.4695	Down	myocardial zonulaadherens protein
SLC9A1	-1.43955	2.71E-07	3.58E-06	-5.46391	Down	solute carrier family 9 member A1
PKIB	-2.38026	3.06E-07	3.97E-06	-5.43677	Down	cAMP-dependent protein kinase inhibitor beta
PGC	-7.92429	4.4E-07	5.39E-06	-5.35497	Down	progastricsin

IGFALS	-1.95174	4.6E-07	5.57E-06	-5.34513	Down	insulin like growth factor binding protein acid labile subunit
ALDH3A1	-3.4432	4.75E-07	5.72E-06	-5.33779	Down	aldehyde dehydrogenase 3 family member A1
SLC1A2	-2.13118	4.75E-07	5.72E-06	-5.33774	Down	solute carrier family 1 member 2
MT1G	-3.30769	5.35E-07	6.29E-06	-5.31104	Down	metallothionein 1G
CAPN9	-3.65078	5.41E-07	6.36E-06	-5.30841	Down	calpain 9
VSIG1	-4.8252	5.42E-07	6.36E-06	-5.3081	Down	V-set and immunoglobulin domain containing 1
PLCXD3	-2.25153	5.92E-07	6.87E-06	-5.28771	Down	phosphatidylinositol specific phospholipase C X domain containing 3
PAIP2B	-2.13484	6.15E-07	7.08E-06	-5.27904	Down	poly(A) binding protein interacting protein 2B
GPR64	-1.89215	6.26E-07	7.18E-06	-5.27515	Down	G protein-coupled receptor 64
GPT	-2.15929	6.45E-07	7.38E-06	-5.2683	Down	glutamic--pyruvic transaminase
CCBE1	-1.23235	6.52E-07	7.44E-06	-5.26599	Down	collagen and calcium binding EGF domains 1
RMST	-1.51845	7.62E-07	8.5E-06	-5.23044	Down	rhabdomyosarcoma 2 associated transcript
ANG	-1.69955	7.93E-07	8.79E-06	-5.22129	Down	angiogenin
AKR1B10	-4.46934	8.3E-07	9.13E-06	-5.21088	Down	aldo-ketoreductase family 1 member B10
PLLP	-1.89685	8.58E-07	9.39E-06	-5.20326	Down	plasmolipin
BRP44L	-1.19484	8.7E-07	9.52E-06	-5.19998	Down	Mitochondrial Pyruvate Carrier 1)
LYPD6B	-2.52357	9.89E-07	1.06E-05	-5.17051	Down	LY6/PLAUR domain containing 6B
KLF2	-1.43192	9.96E-07	1.07E-05	-5.16887	Down	Kruppel like factor 2
IRX5	-1.3397	1E-06	1.08E-05	-5.16708	Down	iroquoishomeobox 5
SCUBE2	-1.67574	1.08E-06	1.15E-05	-5.14949	Down	signal peptide, CUB domain and EGF like domain containing 2
PAPPA2	-1.61521	1.1E-06	1.16E-05	-5.14522	Down	pappalysin 2
CCDC64	-1.15111	1.13E-06	1.19E-05	-5.13998	Down	Bicaudal D-related protein 1.
FAM177B	-2.74114	1.18E-06	1.24E-05	-5.12911	Down	family with sequence similarity 177 member B
TMEM92	-1.54649	1.3E-06	1.34E-05	-5.108	Down	transmembrane protein 92
GSTA2	-1.84896	1.31E-06	1.35E-05	-5.10531	Down	glutathione S-transferase alpha 2
ITPKA	-1.60035	1.35E-06	1.39E-05	-5.09805	Down	inositol-trisphosphate 3-kinase A
CKMT2	-1.93321	1.4E-06	1.43E-05	-5.08937	Down	creatine kinase, mitochondrial 2
KLHDC7A	-2.13101	1.49E-06	1.5E-05	-5.07556	Down	kelch domain containing 7A
GCKR	-1.62805	1.52E-06	1.52E-05	-5.07171	Down	glucokinase regulator
B4GALNT2	-2.1561	1.58E-06	1.57E-05	-5.0616	Down	beta-1,4-N-acetyl-galactosaminyltransferase 2
TMEM38A	-1.51917	1.59E-06	1.58E-05	-5.06108	Down	transmembrane protein 38A
LOC100505633	-2.28691	1.59E-06	1.58E-05	-5.0601	Down	#N/A
RAB37	-1.32868	1.71E-06	1.68E-05	-5.04304	Down	RAB37, member RAS oncogene family
MT1F	-2.10388	1.72E-06	1.69E-05	-5.04199	Down	metallothionein 1F
XYLT2	-1.15806	1.79E-06	1.75E-05	-5.03245	Down	xylosyltransferase 2
TM7SF2	-1.42717	1.8E-06	1.75E-05	-5.03183	Down	transmembrane 7 superfamily member 2
ADHFE1	-1.33	1.83E-06	1.78E-05	-5.02717	Down	alcohol dehydrogenase iron containing 1
MUM1L1	-1.15969	1.93E-06	1.86E-05	-5.01471	Down	melanoma associated antigen (mutated) 1-like 1.
LOC284578	-1.14675	2.01E-06	1.92E-05	-5.00557	Down	#N/A
STYK1	-1.66182	2.04E-06	1.93E-05	-5.00288	Down	serine/threonine/tyrosine kinase 1
MTRNR2L2	-1.22402	2.14E-06	2.02E-05	-4.9906	Down	MT-RNR2 like 2
VILL	-2.18985	2.3E-06	2.15E-05	-4.97381	Down	villin like

SLC28A2	-3.90596	2.71E-06	2.48E-05	-4.9353	Down	solute carrier family 28 member 2
HYAL1	-2.01532	2.88E-06	2.62E-05	-4.92076	Down	hyaluronidase 1
EPN3	-1.96052	2.93E-06	2.65E-05	-4.91721	Down	epsin 3
AADAC	-3.09772	3.05E-06	2.74E-05	-4.90747	Down	arylacetamidedeacetylase
SYTL5	-2.99347	3.14E-06	2.81E-05	-4.90027	Down	synaptotagmin like 5
KLK11	-2.93302	3.15E-06	2.82E-05	-4.89979	Down	kallikrein related peptidase 11
ALDOC	-1.41944	3.27E-06	2.92E-05	-4.89084	Down	aldolase, fructose-bisphosphate C
GALE	-1.36741	3.35E-06	2.97E-05	-4.88489	Down	UDP-galactose-4-epimerase
GSTA1	-3.20281	3.51E-06	3.08E-05	-4.87396	Down	glutathione S-transferase alpha 1
CYP2C8	-1.2518	3.67E-06	3.2E-05	-4.86337	Down	cytochrome P450 family 2 subfamily C member 8
ID1	-1.62166	3.8E-06	3.29E-05	-4.85491	Down	inhibitor of DNA binding 1, HLH protein
GPR155	-1.87712	3.84E-06	3.32E-05	-4.85253	Down	G protein-coupled receptor 155
BMP5	-1.58937	3.91E-06	3.36E-05	-4.84864	Down	bone morphogenetic protein 5
CAPN13	-2.494	3.99E-06	3.42E-05	-4.8437	Down	calpain 13
CA9	-3.29683	4.21E-06	3.58E-05	-4.8304	Down	carbonic anhydrase 9
SCIN	-2.33185	4.39E-06	3.7E-05	-4.82083	Down	scinderin
CYP2C18	-2.59224	4.4E-06	3.71E-05	-4.81989	Down	cytochrome P450 family 2 subfamily C member 18
GCNT2	-1.783	4.63E-06	3.86E-05	-4.80777	Down	glucosaminyl (N-acetyl) transferase 2 (I blood group)
EDARADD	-1.45242	4.85E-06	4.02E-05	-4.79673	Down	EDAR associated death domain
ARL14	-2.41024	5E-06	4.13E-05	-4.78926	Down	ADP ribosylation factor like GTPase 14
TMEM229A	-1.44756	5.11E-06	4.2E-05	-4.78411	Down	transmembrane protein 229A
CIDEC	-2.156	5.2E-06	4.26E-05	-4.78008	Down	cell death inducing DFFA like effector c
FOLR1	-2.37016	5.65E-06	4.57E-05	-4.75983	Down	folate receptor alpha
ELOVL6	-1.57779	5.98E-06	4.8E-05	-4.74624	Down	ELOVL fatty acid elongase 6
LIFR	-1.94262	7.39E-06	5.74E-05	-4.69476	Down	LIF receptor subunit alpha
IL17REL	-1.47128	7.69E-06	5.93E-05	-4.68519	Down	interleukin 17 receptor E like
C1orf210	-1.31	7.82E-06	6.02E-05	-4.68089	Down	chromosome 1 open reading frame 210
SERPINA5	-2.4327	7.98E-06	6.11E-05	-4.67622	Down	serpin family A member 5
HRH2	-1.32411	7.98E-06	6.11E-05	-4.67605	Down	histamine receptor H2
TMEM171	-1.47378	8.03E-06	6.14E-05	-4.67468	Down	transmembrane protein 171
ADTRP	-2.73817	8.32E-06	6.33E-05	-4.66581	Down	androgen dependent TFPI regulating protein
MYRIP	-1.74826	8.37E-06	6.35E-05	-4.66452	Down	myosin VIIA and Rab interacting protein
RIPK4	-1.17687	8.61E-06	6.52E-05	-4.65744	Down	receptor interacting serine/threonine kinase 4
FGA	-3.49325	8.91E-06	6.71E-05	-4.64908	Down	fibrinogen alpha chain
ENTPD5	-1.43795	9.1E-06	6.83E-05	-4.64388	Down	ectonucleoside triphosphate diphosphohydrolase 5 (inactive)
AKR1C3	-2.24251	9.8E-06	7.26E-05	-4.62586	Down	aldo-ketoreductase family 1 member C3
ENPP5	-1.60223	1.08E-05	7.85E-05	-4.60287	Down	ectonucleotidepyrophosphatase/phosphodiesterase family member 5
ATP13A4	-2.2645	1.11E-05	8.04E-05	-4.59611	Down	ATPase 13A4
KLF15	-1.55586	1.13E-05	8.19E-05	-4.59049	Down	Kruppel like factor 15
FAM3B	-2.88357	1.13E-05	8.21E-05	-4.58986	Down	family with sequence similarity 3 member B
SLC9A2	-2.44331	1.21E-05	8.67E-05	-4.57391	Down	solute carrier family 9 member A2
BEX5	-1.19649	1.22E-05	8.75E-05	-4.57104	Down	brain expressed X-linked 5

OASL	-1.75005	1.23E-05	8.81E-05	-4.56899	Down	2'-5'-oligoadenylate synthetase like
LOC400043	-1.90787	1.3E-05	9.25E-05	-4.55525	Down	#N/A
C1orf116	-1.85534	1.33E-05	9.41E-05	-4.54997	Down	chromosome 1 open reading frame 116
SMPD3	-1.76857	1.35E-05	9.5E-05	-4.54688	Down	sphingomyelinphosphodiesterase 3
SEC14L5	-1.15197	1.44E-05	0.000101	-4.53027	Down	SEC14 like lipid binding 5
ME1	-1.28537	1.44E-05	0.000101	-4.53004	Down	malic enzyme 1
MTRNR2L8	-1.13079	1.55E-05	0.000107	-4.51279	Down	MT-RNR2 like 8
SNORD116-20	-1.14964	1.55E-05	0.000107	-4.51266	Down	small nucleolar RNA, C/D box 116-20
FER1L6	-3.70792	1.6E-05	0.00011	-4.50424	Down	fer-1 like family member 6
NWD1	-1.62763	1.74E-05	0.000118	-4.48368	Down	NACHT and WD repeat domain containing 1
IL1R2	-2.15474	1.77E-05	0.00012	-4.47909	Down	interleukin 1 receptor type 2
KLF4	-1.5749	1.87E-05	0.000125	-4.46575	Down	Kruppel like factor 4
ORM2	-2.06661	1.87E-05	0.000125	-4.46517	Down	orosomucoid 2
AZGP1	-2.93525	1.99E-05	0.000132	-4.44919	Down	alpha-2-glycoprotein 1, zinc-binding
TMEM151A	-1.17211	2.13E-05	0.00014	-4.43233	Down	transmembrane protein 151A
ENTPD3	-1.41639	2.14E-05	0.00014	-4.4308	Down	ectonucleoside triphosphate diphosphohydrolase 3
RNASE4	-1.49833	2.2E-05	0.000144	-4.42433	Down	ribonuclease A family member 4
RASSF6	-1.61314	2.52E-05	0.000161	-4.39047	Down	Ras association domain family member 6
ANXA10	-4.16183	2.56E-05	0.000163	-4.38594	Down	annexin A10
MSMB	-3.75333	2.71E-05	0.000172	-4.37138	Down	microseminoprotein beta
CYB5A	-1.14489	2.74E-05	0.000173	-4.36861	Down	cytochrome b5 type A
NQO1	-1.86364	2.92E-05	0.000183	-4.35221	Down	NAD(P)H quinone dehydrogenase 1
FMO5	-1.74122	2.97E-05	0.000185	-4.34798	Down	flavin containing dimethylanilinemonoxygenase 5
DPT	-2.18519	2.99E-05	0.000186	-4.34646	Down	dermatopontin
S100P	-2.79699	3.12E-05	0.000193	-4.33526	Down	S100 calcium binding protein P
MIA2	-1.94287	3.25E-05	0.0002	-4.32543	Down	MIA SH3 domain ER export factor 2
B3GNT6	-3.29988	3.46E-05	0.00021	-4.30883	Down	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6
PAQR8	-1.33801	3.49E-05	0.000212	-4.30662	Down	progestin and adipoQ receptor family member 8
C1orf130	-1.78106	3.65E-05	0.00022	-4.2952	Down	chromosome 1 open reading frame 130
PP7080	-1.68017	3.69E-05	0.000223	-4.29224	Down	uncharacterized LOC25845
SULT1C2	-2.71188	4.53E-05	0.000264	-4.23934	Down	sulfotransferase family 1C member 2
TPD52L1	-1.54408	4.53E-05	0.000264	-4.23928	Down	TPD52 like 1
SULT1B1	-2.5618	4.7E-05	0.000272	-4.22996	Down	sulfotransferase family 1B member 1
HPN	-2.17976	5.18E-05	0.000297	-4.20434	Down	hepsin
KRT20	-4.19415	5.25E-05	0.0003	-4.2009	Down	keratin 20
ALDH1A1	-2.19118	5.58E-05	0.000316	-4.18529	Down	aldehyde dehydrogenase 1 family member A1
FER1L6-AS1	-1.4067	5.62E-05	0.000318	-4.18345	Down	FER1L6 antisense RNA 1
ARHGDIG	-1.37568	5.63E-05	0.000319	-4.18263	Down	Rho GDP dissociation inhibitor gamma
TST	-1.30825	5.94E-05	0.000333	-4.16892	Down	thiosulfate sulfurtransferase
KIAA0895	-1.34672	5.99E-05	0.000336	-4.16645	Down	KIAA0895
RPS6KA6	-1.4841	6.19E-05	0.000344	-4.15812	Down	ribosomal protein S6 kinase A6
CHGB	-2.2368	6.5E-05	0.000359	-4.14492	Down	chromogranin B

COL4A6	-1.84882	6.59E-05	0.000363	-4.14163	Down	collagen type IV alpha 6 chain
ECHDC3	-1.70417	6.94E-05	0.00038	-4.12764	Down	enoyl-CoA hydratase domain containing 3
INSIG1	-1.1514	6.98E-05	0.000381	-4.1261	Down	insulin induced gene 1
EPB41L4B	-1.50303	7.46E-05	0.000404	-4.1086	Down	erythrocyte membrane protein band 4.1 like 4B
IGJ	-3.06899	7.5E-05	0.000405	-4.10734	Down	#N/A
PBLD	-1.70062	7.53E-05	0.000407	-4.10625	Down	phenazine biosynthesis like protein domain containing
MT1E	-2.0273	7.77E-05	0.000418	-4.09782	Down	metallothionein 1E
LTF	-3.65068	7.95E-05	0.000427	-4.09188	Down	lactotransferrin
PALM3	-1.80821	8.06E-05	0.000432	-4.08804	Down	paralemmin 3
ADAMTS15	-1.7918	8.1E-05	0.000433	-4.08687	Down	ADAM metallopeptidase with thrombospondin type 1 motif 15
TMPRSS2	-1.68379	8.75E-05	0.000464	-4.06631	Down	transmembrane serine protease 2
ARHGEF37	-1.43569	9.08E-05	0.000479	-4.05636	Down	Rho guanine nucleotide exchange factor 37
PRDM16	-1.44097	9.11E-05	0.00048	-4.05544	Down	PR/SET domain 16
SNORD22	-1.19739	9.2E-05	0.000484	-4.05279	Down	small nucleolar RNA, C/D box 22
STX19	-1.42672	0.000101	0.000525	-4.02756	Down	syntaxin 19
SLC16A7	-1.5037	0.000103	0.000533	-4.02328	Down	solute carrier family 16 member 7
SELENBP1	-1.60959	0.000106	0.000546	-4.01555	Down	selenium binding protein 1
FNDC5	-1.181	0.00011	0.000564	-4.00544	Down	fibronectin type III domain containing 5
TTR	-1.71577	0.00011	0.000564	-4.00522	Down	transthyretin
BCAS1	-2.74005	0.00011	0.000564	-4.00512	Down	breast carcinoma amplified sequence 1
C19orf77	-2.20692	0.000121	0.000612	-3.97948	Down	#N/A
SERPINA4	-2.36418	0.000124	0.000626	-3.97258	Down	serpin family A member 4
FSIP2	-1.98347	0.000124	0.000627	-3.97219	Down	fibrous sheath interacting protein 2
IGSF9	-1.55798	0.000131	0.000659	-3.95695	Down	immunoglobulin superfamily member 9
CLDN18	-3.33422	0.000136	0.000676	-3.94788	Down	claudin 18
SUSD4	-1.40629	0.000137	0.000683	-3.94471	Down	sushi domain containing 4
AMPD1	-1.20089	0.000148	0.000725	-3.92525	Down	adenosine monophosphate deaminase 1
FOXQ1	-1.91873	0.000149	0.000729	-3.92334	Down	forkhead box Q1
PTGR1	-1.14721	0.000152	0.000746	-3.91648	Down	prostaglandin reductase 1
C11orf9	-1.27328	0.000155	0.000758	-3.91106	Down	Myelin Regulatory Factor; Myelin
GPR110	-2.11364	0.000156	0.00076	-3.91058	Down	G-protein coupled receptor 110 i
MT1X	-1.41507	0.000158	0.000771	-3.9061	Down	metallothionein 1X
UPK1B	-2.46209	0.000166	0.0008	-3.89367	Down	uroplakin 1B
DHCR24	-1.30452	0.000173	0.000831	-3.88192	Down	24-dehydrocholesterol reductase
EYA2	-1.67614	0.000177	0.000847	-3.87609	Down	EYA transcriptional coactivator and phosphatase 2
HAPLN1	-1.94491	0.000182	0.000869	-3.86761	Down	hyaluronan and proteoglycan link protein 1
PTGER3	-1.63099	0.000187	0.000891	-3.85982	Down	prostaglandin E receptor 3
PHGR1	-2.78903	0.000195	0.000923	-3.84833	Down	proline, histidine and glycine rich 1
RIMS4	-1.15833	0.000195	0.000924	-3.8481	Down	regulating synaptic membrane exocytosis 4
ODAM	-1.80133	0.000196	0.000925	-3.8476	Down	odontogenic, ameloblast associated
ALDOB	-3.06807	0.0002	0.000939	-3.84236	Down	aldolase, fructose-bisphosphate B
GATA6	-1.17262	0.000204	0.000958	-3.83569	Down	GATA binding protein 6

MUC6	-3.92776	0.000222	0.001027	-3.8129	Down	mucin 6, oligomeric mucus/gel-forming
SNORA50	-1.1526	0.000226	0.001043	-3.80799	Down	small nucleolar RNA, H/ACA box 50A
PLAC8	-1.89979	0.000228	0.001051	-3.80548	Down	placenta associated 8
ANO7	-1.82482	0.000231	0.001063	-3.80137	Down	anoctamin 7
ZBTB7C	-1.92666	0.000234	0.001072	-3.79863	Down	zinc finger and BTB domain containing 7C
RORC	-1.83042	0.000236	0.001083	-3.79524	Down	RAR related orphan receptor C
DUOXA2	-2.3418	0.000241	0.001099	-3.79004	Down	dual oxidase maturation factor 2
LOC643201	-1.30305	0.000248	0.001127	-3.78209	Down	centrosomal protein 192kDa pseudogene
CTSE	-3.03202	0.00025	0.001137	-3.77916	Down	cathepsin E
GPT2	-1.25616	0.000255	0.001154	-3.77415	Down	glutamic--pyruvic transaminase 2
SH3BGRL2	-1.24745	0.000258	0.001164	-3.77109	Down	SH3 domain binding glutamate rich protein like 2
SLC9A3	-2.3467	0.000264	0.001191	-3.76382	Down	solute carrier family 9 member A3
CCRL1	-1.28784	0.000265	0.001192	-3.76351	Down	C-C chemokine receptor type 11 i
FAM174B	-1.19216	0.000269	0.001206	-3.75955	Down	family with sequence similarity 174 member B
FER1L4	-1.77732	0.000271	0.001215	-3.75724	Down	fer-1 like family member 4 (pseudogene)
LEPREL1	-1.43316	0.000273	0.001224	-3.75483	Down	LEUCINE- AND PROLINE-ENRICHED PROTEOGLYCAN 1
PDZD3	-1.49069	0.000279	0.001245	-3.74868	Down	PDZ domain containing 3
DSC2	-1.30164	0.000283	0.001261	-3.74465	Down	desmocollin 2
A4GNT	-2.1448	0.000283	0.001262	-3.74437	Down	alpha-1,4-N-acetylglucosaminyltransferase
BHMT	-1.13063	0.00029	0.001288	-3.73761	Down	betaine--homocysteine S-methyltransferase
SGK2	-1.71285	0.000299	0.001319	-3.72954	Down	serum/glucocorticoid regulated kinase 2
SYTL2	-1.43896	0.000303	0.001336	-3.72537	Down	synaptotagmin like 2
SNORA3	-1.194	0.00031	0.001364	-3.71893	Down	mall nucleolar RNA, H/ACA box 3A
F2RL1	-1.18109	0.000312	0.00137	-3.71764	Down	F2R like trypsin receptor 1
ADH1C	-3.13978	0.000315	0.001384	-3.71434	Down	alcohol dehydrogenase 1C (class I), gamma polypeptide
FOXA3	-1.27364	0.000319	0.001397	-3.71123	Down	forkhead box A3
DUOX2	-3.13093	0.000331	0.001442	-3.70071	Down	dual oxidase 2
ADAM28	-1.57232	0.000339	0.001472	-3.69348	Down	ADAM metallopeptidase domain 28
APOC3	-1.66171	0.000357	0.001538	-3.67918	Down	apolipoprotein C3
RAP1GAP	-1.95704	0.00037	0.001589	-3.66858	Down	RAP1 GTPase activating protein
PTPRZ1	-1.64025	0.000393	0.001671	-3.65134	Down	protein tyrosine phosphatase receptor type Z1
SCG3	-1.34963	0.000393	0.001672	-3.65109	Down	secretogranin III
CYP2S1	-1.41489	0.000412	0.001738	-3.63761	Down	cytochrome P450 family 2 subfamily S member 1
CAPN8	-2.0061	0.000422	0.001772	-3.63093	Down	calpain 8
TCEAL2	-1.17618	0.00043	0.001802	-3.62531	Down	transcription elongation factor A like 2
SNORA47	-1.38927	0.000439	0.00183	-3.61969	Down	small nucleolar RNA, H/ACA box 47
SNORA37	-1.43524	0.000462	0.001913	-3.60511	Down	small nucleolar RNA, H/ACA box 37
RAB27B	-1.65807	0.000474	0.001953	-3.59755	Down	RAB27B, member RAS oncogene family
SERPINB7	-1.42666	0.000478	0.001967	-3.59519	Down	serpin family B member 7
LINC00261	-2.80671	0.00051	0.002079	-3.57612	Down	long intergenic non-protein coding RNA 261
DUOX1	-1.35608	0.000547	0.002208	-3.55587	Down	dual oxidase 1
METTL7A	-1.26112	0.000558	0.002246	-3.55005	Down	methyltransferase like 7A

RIMS1	-1.58304	0.000575	0.002308	-3.5411	Down	regulating synaptic membrane exocytosis 1
OXCT1	-1.26717	0.000588	0.002352	-3.53471	Down	3-oxoacid CoA-transferase 1
TCN1	-2.79339	0.00061	0.002423	-3.52398	Down	transcobalamin 1
KCNQ1	-1.51998	0.000631	0.002495	-3.51407	Down	potassium voltage-gated channel subfamily Q member 1
FGG	-2.32003	0.000661	0.002599	-3.50019	Down	fibrinogen gamma chain
C11orf92	-1.84043	0.000671	0.002633	-3.49577	Down	chromosome 11 open reading frame 92
FBP1	-1.14801	0.000688	0.002689	-3.48862	Down	fructose-bisphosphatase 1
TRNP1	-1.81251	0.000691	0.002698	-3.48731	Down	TMF1 regulated nuclear protein 1
C6orf58	-2.90429	0.000693	0.002704	-3.48651	Down	chromosome 6 open reading frame 58
NR0B2	-1.64026	0.000709	0.002755	-3.47946	Down	nuclear receptor subfamily 0 group B member 2
CYP3A5	-1.70546	0.000712	0.002767	-3.47815	Down	cytochrome P450 family 3 subfamily A member 5
CLDN23	-1.34669	0.000741	0.002862	-3.46652	Down	claudin 23
C12orf36	-1.93304	0.000744	0.002868	-3.46536	Down	Chromosome 12 Open Reading Frame 36
CCL28	-1.67094	0.00075	0.002888	-3.46283	Down	C-C motif chemokine ligand 28
CYP4F12	-1.402	0.000786	0.003005	-3.44906	Down	cytochrome P450 family 4 subfamily F member 12
COL6A5	-1.36147	0.000808	0.003077	-3.44061	Down	collagen type VI alpha 5 chain
LOC729966	-1.77488	0.000859	0.003239	-3.4224	Down	uncharacterized LOC729966
C1orf115	-1.17373	0.000863	0.003251	-3.42107	Down	chromosome 1 open reading frame 115
PIK3C2G	-2.69778	0.000864	0.003254	-3.42067	Down	phosphatidylinositol-4-phosphate 3-kinase catalytic subunit type 2 gamma
C4orf19	-1.25061	0.000882	0.003308	-3.4146	Down	chromosome 4 open reading frame 19
TTC39A	-1.29875	0.000889	0.003326	-3.4122	Down	tetratricopeptide repeat domain 39A
HS6ST3	-1.35206	0.000968	0.003578	-3.38646	Down	heparansulfate 6-O-sulfotransferase 3
GALNT6	-1.21049	0.000971	0.003586	-3.38548	Down	polypeptide N-acetylgalactosaminyltransferase 6
CYP2C9	-1.28115	0.000978	0.003607	-3.38327	Down	cytochrome P450 family 2 subfamily C member 9
CD36	-1.13239	0.001055	0.003845	-3.36046	Down	CD36 molecule
EPS8L1	-1.2057	0.001063	0.00387	-3.35821	Down	EPS8 like 1
LIPH	-1.57886	0.001145	0.004123	-3.33537	Down	lipase H
SHISA6	-1.15846	0.001155	0.004152	-3.33279	Down	shisa family member 6
RASEF	-1.29797	0.001213	0.004327	-3.31793	Down	RAS and EF-hand domain containing
IRX2	-1.74965	0.00123	0.004377	-3.31355	Down	iroquoishomeobox 2
PTPRR	-1.41316	0.001231	0.004379	-3.31334	Down	protein tyrosine phosphatase receptor type R
PTPRN2	-1.56508	0.001244	0.004415	-3.3101	Down	protein tyrosine phosphatase receptor type N2
APOBEC1	-1.28203	0.00126	0.004464	-3.30616	Down	apolipoprotein B mRNA editing enzyme catalytic subunit 1
ADAMTSL1	-1.20975	0.001286	0.004546	-3.30003	Down	ADAMTS like 1
GDPD2	-1.15658	0.001354	0.004744	-3.28413	Down	glycerophosphodiesterphosphodiesterase domain containing 2
SCGN	-1.29653	0.001363	0.004774	-3.28206	Down	secretagogin, EF-hand calcium binding protein
SLC16A9	-1.48478	0.001427	0.004971	-3.26778	Down	solute carrier family 16 member 9
SEMA3B	-1.1954	0.00143	0.004979	-3.2672	Down	semaphorin 3B
HAS3	-1.47447	0.001431	0.004982	-3.2669	Down	hyaluronan synthase 3
CA4	-1.14208	0.00149	0.005155	-3.25439	Down	carbonic anhydrase 4
ERBB4	-1.14567	0.001495	0.00517	-3.25341	Down	erb-b2 receptor tyrosine kinase 4
FOXA2	-1.37138	0.001522	0.005254	-3.2479	Down	forkhead box A2

BTNL8	-1.63429	0.001537	0.005301	-3.24474	Down	butyrophilin like 8
LRRC66	-1.59439	0.001541	0.005312	-3.24398	Down	leucine rich repeat containing 66
SOWAHA	-1.27464	0.001575	0.005403	-3.23724	Down	sosondowahankyrin repeat domain family member A
DHRS9	-1.36517	0.001582	0.005423	-3.23592	Down	dehydrogenase/reductase 9
MRAP2	-1.44774	0.001626	0.005553	-3.22728	Down	melanocortin 2 receptor accessory protein 2
B3GNT7	-1.4936	0.00165	0.005622	-3.22266	Down	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7
MT1H	-1.63135	0.001743	0.005902	-3.20546	Down	metallothionein 1H
LOC440335	-1.24996	0.001799	0.006059	-3.19566	Down	#N/A
TSPAN1	-2.13042	0.00197	0.006562	-3.16689	Down	tetraspanin 1
CYP2C19	-1.37071	0.00198	0.006589	-3.16533	Down	cytochrome P450 family 2 subfamily C member 19
FCGBP	-3.19545	0.002032	0.006728	-3.15716	Down	Fc fragment of IgG binding protein
NCAM1	-1.23177	0.002096	0.006903	-3.14733	Down	neural cell adhesion molecule 1
HHLA2	-1.782	0.00214	0.007023	-3.14069	Down	HERV-H LTR-associating 2
PRIMA1	-1.13115	0.002157	0.007072	-3.13824	Down	proline rich membrane anchor 1
RGN	-1.21003	0.002162	0.007086	-3.13742	Down	regucalcin
UGT1A6	-1.41003	0.002217	0.007243	-3.12945	Down	UDP glucuronosyltransferase family 1 member A6
TFCP2L1	-1.4672	0.00227	0.007397	-3.12195	Down	transcription factor CP2 like 1
FXYD3	-1.4859	0.00227	0.007398	-3.12187	Down	FXYD domain containing ion transport regulator 3
MIR650	-2.29328	0.002276	0.007414	-3.1211	Down	microRNA 650
FAM189A2	-1.27394	0.002401	0.007765	-3.10391	Down	family with sequence similarity 189 member A2
SOX2	-1.62091	0.00252	0.008094	-3.08844	Down	SRY-box transcription factor 2
ORM1	-1.4435	0.00267	0.008505	-3.06973	Down	orosomucoid 1
F13A1	-1.57304	0.002836	0.008952	-3.05016	Down	coagulation factor XIII A chain
APOA1	-1.95002	0.003046	0.009535	-3.02696	Down	apolipoprotein A1
ANKRD22	-1.13226	0.003091	0.009655	-3.02212	Down	ankyrin repeat domain 22
RHBDL2	-1.23177	0.003283	0.01018	-3.00237	Down	rhomboid like 2
CLEC3B	-1.21628	0.003554	0.010891	-2.9762	Down	C-type lectin domain family 3 member B
SCARA5	-1.54597	0.003923	0.011848	-2.94344	Down	scavenger receptor class A member 5
GGT6	-1.7999	0.004042	0.012143	-2.93348	Down	gamma-glutamyltransferase 6
MAMDC2	-1.26013	0.00407	0.012211	-2.93121	Down	MAM domain containing 2
XK	-1.23683	0.004074	0.012219	-2.93089	Down	X-linked Kx blood group
GDPD3	-1.23128	0.004159	0.012421	-2.92401	Down	glycerophosphodiesterphosphodiesterase domain containing 3
TMEM100	-1.13751	0.004302	0.012787	-2.91261	Down	transmembrane protein 100
LEPR	-1.176	0.004368	0.012955	-2.90755	Down	leptin receptor
IGFBP2	-1.6738	0.00443	0.01311	-2.90282	Down	insulin like growth factor binding protein 2
DEFB1	-1.382	0.00448	0.013228	-2.89902	Down	defensin beta 1
SNORD94	-1.18429	0.004833	0.014103	-2.87341	Down	small nucleolar RNA, C/D box 94
SLC4A4	-1.44856	0.004885	0.014233	-2.86979	Down	solute carrier family 4 member 4
CXADR	-1.14718	0.004919	0.014319	-2.86739	Down	CXADR Ig-like cell adhesion molecule
TFR2	-1.22223	0.004955	0.014407	-2.86497	Down	transferrin receptor 2
ANO5	-1.32076	0.004958	0.014415	-2.8647	Down	anoctamin 5
COL17A1	-1.95731	0.005127	0.014843	-2.85333	Down	collagen type XVII alpha 1 chain

GCNT1	-1.29201	0.005264	0.01517	-2.84436	Down	glucosaminyl (N-acetyl) transferase 1
C6	-1.22604	0.005537	0.015827	-2.82708	Down	complement C6
C11orf86	-1.4605	0.005632	0.016046	-2.82121	Down	chromosome 11 open reading frame 86
PROM2	-1.70208	0.005709	0.016221	-2.81653	Down	prominin 2
BPIFB1	-2.89391	0.00604	0.017023	-2.79712	Down	BPI fold containing family B member 1
MUC1	-1.55602	0.006157	0.017299	-2.79049	Down	mucin 1, cell surface associated
HBB	-1.33296	0.006208	0.017414	-2.78764	Down	hemoglobin subunit beta
MLPH	-1.50248	0.006316	0.017668	-2.7817	Down	melanophilin
CDH2	-1.13276	0.006463	0.018017	-2.77372	Down	cadherin 2
SLC15A1	-1.46194	0.006776	0.018776	-2.75724	Down	solute carrier family 15 member 1
TESC	-1.47782	0.007011	0.019317	-2.74531	Down	tescalcin
POU2AF1	-1.18723	0.007045	0.019394	-2.74364	Down	POU class 2 homeobox associating factor 1
FGB	-1.75768	0.007504	0.020432	-2.72147	Down	fibrinogen beta chain
UGT1A10	-1.42624	0.007717	0.020903	-2.7116	Down	UDP glucuronosyltransferase family 1 member A10
PRKAA2	-1.2771	0.00781	0.021113	-2.70737	Down	protein kinase AMP-activated catalytic subunit alpha 2
SPDEF	-1.53032	0.008048	0.021653	-2.69677	Down	SAM pointed domain containing ETS transcription factor
HGD	-1.25298	0.008766	0.023318	-2.66635	Down	homogentisate 1,2-dioxygenase
PRLR	-1.27219	0.008797	0.023391	-2.66507	Down	prolactin receptor
GABRB3	-1.47248	0.00886	0.023541	-2.66251	Down	gamma-aminobutyric acid type A receptor beta3 subunit
PLIN4	-1.23827	0.00932	0.024589	-2.6444	Down	perilipin 4
REG3A	-2.83122	0.00993	0.025962	-2.62155	Down	regenerating family member 3 alpha
B3GALT5	-1.68133	0.009937	0.025979	-2.62127	Down	beta-1,3-galactosyltransferase 5
GALNT5	-1.26116	0.010092	0.026304	-2.61569	Down	polypeptide N-acetylgalactosaminyltransferase 5
APOA4	-1.79981	0.010478	0.027174	-2.60206	Down	apolipoprotein A4
TM6SF2	-1.15162	0.010774	0.027797	-2.59193	Down	transmembrane 6 superfamily member 2
CGNL1	-1.18772	0.010931	0.028148	-2.58664	Down	cingulin like 1
CDHR2	-1.72899	0.011645	0.02968	-2.56348	Down	cadherin related family member 2
CYP3A4	-1.40007	0.012414	0.03131	-2.53991	Down	cytochrome P450 family 3 subfamily A member 4
CXCL14	-1.53213	0.01284	0.032216	-2.52742	Down	C-X-C motif chemokine ligand 14
KIF1A	-1.13421	0.013076	0.032717	-2.52066	Down	kinesin family member 1A
MUC5B	-2.34029	0.013457	0.033532	-2.50997	Down	mucin 5B, oligomeric mucus/gel-forming
PRSS8	-1.17934	0.013595	0.033806	-2.50614	Down	serine protease 8
AQP5	-1.73911	0.01516	0.037052	-2.46524	Down	aquaporin 5
FOXA1	-1.13176	0.015252	0.037252	-2.46297	Down	forkhead box A1
SLPI	-1.50988	0.016553	0.039947	-2.43191	Down	secretory leukocyte peptidase inhibitor
CMBL	-1.29617	0.016773	0.040392	-2.42687	Down	carboxymethylenebutenolidase homolog
MST1P9	-1.20601	0.017788	0.042418	-2.40436	Down	#N/A
ST6GALNAC1	-1.45659	0.018428	0.043721	-2.39074	Down	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 1
KIAA1324	-1.66186	0.019482	0.045772	-2.36921	Down	KIAA1324
MAOA	-1.2488	0.020833	0.048467	-2.34308	Down	monoamine oxidase A

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

Pathway ID	Pathway Name	P-value	FDR B&H	FDR B&Y	Bonferroni	Gene Count	Gene
BIOCYC							
782401	pyrimidine deoxyribonucleosides degradation	8.43E-03	2.69E-01	1.00E+00	3.46E-01	2	UPP1,TYMP
782385	aspirin triggered resolvin D biosynthesis	5.91E-02	2.69E-01	1.00E+00	1.00E+00	1	PTGS2
142281	UMP biosynthesis	5.91E-02	2.69E-01	1.00E+00	1.00E+00	1	CAD
545275	chondroitin biosynthesis	5.91E-02	2.69E-01	1.00E+00	1.00E+00	1	DIO2
545371	MAP kinase cascade	5.91E-02	2.69E-01	1.00E+00	1.00E+00	1	CSGALNACT2
545355	thyronamine and iodothyronamine metabolism	5.91E-02	2.69E-01	1.00E+00	1.00E+00	1	EPHB2
1271888	docosahexaenoate biosynthesis III (mammals)	8.72E-02	3.25E-01	1.00E+00	1.00E+00	1	FADS2
782399	UTP and CTP dephosphorylation II	1.15E-01	3.36E-01	1.00E+00	1.00E+00	1	ENTPD1
142426	urea cycle	1.15E-01	3.36E-01	1.00E+00	1.00E+00	1	CPS1
142304	UDP-N-acetyl-D-glucosamine biosynthesis II	1.41E-01	3.62E-01	1.00E+00	1.00E+00	1	GFPT2
KEGG							
83068	ECM-receptor interaction	2.10E-09	5.14E-07	3.12E-06	5.14E-07	16	COL1A1,COL1A2,COL4A1,COL4A2,COL6A3,ITGA11,FN1,COMP,TNC,SPP1,ITGA5,ITGB8,LAMA5,THBS1,THBS2,THBS4
172847	Protein digestion and absorption	8.70E-09	1.06E-06	6.45E-06	2.12E-06	16	COL1A1,COL1A2,COL3A1,COL4A1,COL4A2,COL5A1,COL5A2,COL6A3,COL7A1,COL10A1,COL11A1,COL12A1,COL15A1,COL5A3,COL18A1,ELN
692234	PI3K-Akt signaling pathway	1.33E-07	1.08E-05	6.57E-05	3.24E-05	30	PIK3AP1,PDGFRB,F2R,PGF,COL1A1,COL1A2,COL4A1,COL4A2,COL6A3,ITGA11,ANGPT2,FN1,COMP,TNC,CSF3R,IL2RA,IL6,MYB,SPP1,ITGA5,ITGB8,LAMA5,CCND2,OSM,THBS1,THBS2,THBS4,GNB4,OSMR,PIK3R5
83067	Focal adhesion	5.47E-07	3.34E-05	2.03E-04	1.33E-04	21	PDGFRB,ACTN1,PGF,COL1A1,COL1A2,COL4A1,COL4A2,COL6A3,ITGA11,FN1,COMP,TNC,SPP1,ITGA5,PARVG,ITGB8,LAMA5,CCND2,THBS1,THBS2,THBS4
153910	Phagosome	3.59E-06	1.75E-04	1.07E-03	8.77E-04	17	CLEC7A,TUBB3,FCGR1A,FCGR2A,FCGR3A,FCGR3B,COMP,MSR1,NCF2,ITGA5,MRC2,C1R,C3,OLR1,THBS1,THBS2,THBS4
83051	Cytokine-cytokine receptor interaction	3.21E-03	5.22E-02	3.17E-01	7.83E-01	17	PDGFRB,CXCL9,CCL3,CCR1,CCL18,CXCL6,CSF3R,IL2RA,IL6,IL11,INHBA,CXCL1,TNFRSF11B,LIF,OSM,RELT,OSMR
83069	Cell adhesion molecules (CAMs)	4.24E-03	6.47E-02	3.93E-01	1.00E+00	11	SELE,SELL,ICAM1,CLDN4,CLDN3,CLDN7,VCAN,ITGB8,CLDN2,CLDN1,CDH3
852705	MicroRNAs in cancer	8.74E-03	9.70E-02	5.89E-01	1.00E+00	17	PDGFRB,SERPINB5,PLAU,MMP9,MMP16,KIF23,TNC,FSCN1,CDCA5,ITGA5,PTG

							S2,NOTCH1,NOTCH3,E2F3,CCND2,THBS1,CDC25B
83105	Pathways in cancer	2.90E-02	2.62E-01	1.00E+00	1.00E+00	19	PDGFRB,F2R,PGF,ADCY3,MMP1,MMP9,COL4A1,COL4A2,FN1,WNT2,CSF3R,IL6,PTGS2,GLI2,LAMA5,E2F3,EDNRA,GNB4,LEF1
132956	Metabolic pathways	9.96E-01	1.00E+00	1.00E+00	1.00E+00	24	LPCAT1,DGKH,CSGALNACT2,LIPG,UPP1,ALDH1A3,MTHFD1L,HKDC1,ST3GAL2,CPS1,CYP2B6,IDO1,BCAT1,P4HA3,PTGS2,GGT5,SPHK1,GFPT2,NNMT,SDS,PLA2G7,CAD,LAMA5,TYMP
Pathway Interaction Database							
138064	Syndecan-4-mediated signaling events	2.89E-05	2.01E-03	1.06E-02	3.18E-03	7	ACTN1,MMP9,FN1,TNC,ITGA5,ADAM12,THBS1
138007	PLK1 signaling events	4.15E-05	2.01E-03	1.06E-02	4.56E-03	8	PLK1,TPX2,CLSPN,BUB1,BUB1B,ECT2,KIF20A,CDC25B
169349	Validated transcriptional targets of AP1 family members Fra1 and Fra2	5.48E-05	2.01E-03	1.06E-02	6.02E-03	7	MGP,PLAU,MMP1,MMP9,COL1A2,IL6,LIF
137945	amb2 Integrin signaling	5.23E-04	1.44E-02	7.59E-02	5.75E-02	7	PLAU,FGR,MMP9,FN1,ICAM1,IL6,THY1
137935	FOXM1 transcription factor network	4.65E-03	7.31E-02	3.86E-01	5.12E-01	5	CENPF,PLK1,FOXM1,NEK2,CDC25B
138080	Aurora B signaling	5.85E-03	8.05E-02	4.25E-01	6.44E-01	5	KIF23,BUB1,KIF2C,NCAPH,KIF20A
137934	E2F transcription factor network	2.20E-02	1.73E-01	9.11E-01	1.00E+00	6	PLAU,MYBL2,E2F3,ORC1,SERPINE1,CDC6
169345	Notch signaling pathway	2.95E-02	1.91E-01	1.00E+00	1.00E+00	5	MFAP2,DNM1,NOTCH1,NOTCH3,ADAM12
137939	Direct p53 effectors	4.49E-02	2.47E-01	1.00E+00	1.00E+00	8	SERPINB5,GDF15,VCAN,SPP1,BCL2A1,LIF,COL18A1,SERPINE1
169352	Regulation of Wnt-mediated beta catenin signaling and target gene transcription	8.81E-02	3.59E-01	1.00E+00	1.00E+00	5	MMP9,VCAN,SALL4,CCND2,LEF1
REACTOME							
1270244	Extracellular matrix organization	4.22E-34	3.02E-31	2.16E-30	3.02E-31	61	ACTN1,MFAP2,FBN1,ACAN,MMP1,MMP3,MMP7,MMP9,MMP11,MMP14,MMP16,COL1A1,COL1A2,COL3A1,COL4A1,COL4A2,COL5A1,COL5A2,NID2,COL6A3,COL7A1,COL8A1,ITGA11,COL10A1,COL11A1,COL12A1,COL15A1,COL16A1,FN1,COMP,ADAMTS4,ADAMTS2,TNC,ICAM1,COL5A3,VCAN,ADAMTS14,CTSB,CTSK,SPARC,HTRA1,SPP1,ASPN,P4HA3,ITGA5,ITGAX,ITGB8,BGN,BMP1,ADAMTS9,LAMA5,SERPINH1,COL18A1,THBS1,TIMP1,LOXL2,SERPINE1,LTBP2,ELN,LUM,PCOLCE
1269340	Hemostasis	1.37E-06	7.60E-05	5.44E-04	9.78E-04	42	PDE3A,CD109,DGKH,ACTN1,F2R,F2RL2,SERPINE2,FCER1G,PLAU,MMP1,FGR,PLEK,SELE,SELL,KIF23,ANGPT2,FN1,PDPN,KIF18B,IL2RA,MYB,DOCK4,KIF21B,SPARC,KIF4A,ISLR,ITGA5,ITGAX,LRP8,CD84,KIF2C,

							KIF26B,LCP2,OLR1,KIF20A,THBS1,P2RX7,TIMP1,SERPINE1,TREM1,GNB4,PIK3R5
1457780	Neutrophil degranulation	8.68E-04	2.04E-02	1.46E-01	6.20E-01	28	LPCAT1,ABCA13,CLEC5A,TRPM2,CHI3L1,FCER1G,FCGR2A,FCGR3B,PLAU,FGR,MMP9,SELL,FPR1,KCNAB2,SLC2A3,SLC11A1,CTSB,ITGAX,C3,ATP11A,C5AR1,LILRB3,RAB31,NFAM1,CXCL1,OLR1,TNFAIP6,PADI2
1269741	Cell Cycle	2.11E-03	4.09E-02	2.93E-01	1.00E+00	32	CENPF,HJURP,MCM2,MCM7,MCM10,PLK1,FOXM1,KIF23,GINS4,TPX2,CLSPN,ESPL1,CDCA5,MYBL2,KNTC1,RCC2,NEK2,BUB1,BUB1B,KIF2C,UBE2C,E2F3,NCAPH,CCND2,PKMYT1,KIF20A,ORC1,EXO1,CDC6,CDC25B,AJUBA,TOP2A
1269318	Signaling by Interleukins	5.16E-03	7.38E-02	5.28E-01	1.00E+00	27	PDGFRB,NOD1,CCL3,CCR1,MMP1,MMP3,MMP9,COL1A2,FN1,FPR1,ICAM1,CSF3R,FSCN1,IL2RA,IL6,IL11,ITGAX,PTGS2,LAMA5,GRIN2D,CXCL1,HAVCR2,LIF,OSM,TIMP1,DUSP10,OSMR
1269310	Cytokine Signaling in Immune system	2.14E-02	2.12E-01	1.00E+00	1.00E+00	33	PDGFRB,TRIM29,NOD1,FCGR1A,IFITM3,CCL3,CCR1,MMP1,MMP3,MMP9,COL1A2,FN1,FPR1,ICAM1,IFITM1,CSF3R,FSCN1,IL2RA,IL6,IL11,ITGAX,PTGS2,GBP5,LAMA5,GRIN2D,CXCL1,TNFRSF11B,HAVCR2,LIF,OSM,TIMP1,DUSP10,OSMR
1270303	Axon guidance	4.48E-02	3.48E-01	1.00E+00	1.00E+00	24	EPHB2,TRIO,PDGFRB,PDLIM7,MMP9,PLXNA1,COL4A1,COL4A2,COL6A3,FN1,IL2RA,MYH10,KIF4A,ITGA5,DNM1,DPYSL3,ARHGAP39,GRIN2D,PLXNC1,TREM2,ROBO2,DUSP10,EPHA3,EPHB1
1269507	Signaling by Rho GTPases	5.90E-02	3.80E-01	1.00E+00	1.00E+00	19	TRIO,CENPF,CHN1,PLK1,IQGAP3,PLEKHG2,LOC100288637,KNTC1,MYH10,NCF2,ARHGAP11A,RCC2,BUB1,BUB1B,KIF14,KIF2C,ARHGAP39,ECT2,FMNL3
1269203	Innate Immune System	6.10E-02	3.85E-01	1.00E+00	1.00E+00	49	PIK3AP1,LPCAT1,PDGFRB,ABCA13,CLEC5A,TRPM2,CLEC7A,CHI3L1,ADCY3,NOD1,FCER1G,FCGR1A,FCGR2A,FCGR3A,FCGR3B,PLAU,FGR,MMP9,SELL,FN1,FPR1,KCNAB2,SLC2A3,SLC11A1,PRKDC,CTSB,IL2RA,CTSK,NCF2,ITGAX,C1R,C3,ATP11A,C5AR1,DNM1,LILRB3,RAB31,MUC16,GRIN2D,LCP2,NFAM1,CXCL1,OLR1,P2RX7,TREM2,TREM1,DUSP10,TNFAIP6,PADI2
1269576	G alpha (i) signalling events	6.22E-02	3.87E-01	1.00E+00	1.00E+00	12	ADCY3,AGT,CXCL9,CCR1,CXCL6,FPR1,APLN,C3,C5AR1,CXCL1,RGS1,GNB4

Gen MAPP							
MAP00251	MAP00251	1.20E-01	6.40E-01	1.00E+00	1.00E+00	2	CPS1,CAD
MAP00240	MAP00240	1.44E-01	6.40E-01	1.00E+00	1.00E+00	3	IGFBP7,CAD,TYMP
MAP00272	MAP00272	2.40E-01	6.40E-01	1.00E+00	1.00E+00	1	SDS
MAP00360	MAP00360	3.86E-01	6.40E-01	1.00E+00	1.00E+00	1	ALDH1A3
MAP00380	MAP00380	4.03E-01	6.40E-01	1.00E+00	1.00E+00	2	CYP2B6,IDO1
MAP00590	MAP00590	4.39E-01	6.40E-01	1.00E+00	1.00E+00	1	PTGS2
MAP00230	MAP00230	4.63E-01	6.40E-01	1.00E+00	1.00E+00	3	ADCY3,IGFBP7,TYMP
MAP00010	MAP00010	4.65E-01	6.40E-01	1.00E+00	1.00E+00	2	ALDH1A3,FMNL3
MAP00330	MAP00330	6.86E-01	7.20E-01	1.00E+00	1.00E+00	1	CPS1
MAP00071	MAP00071	7.54E-01	7.54E-01	1.00E+00	1.00E+00	1	CYP2B6
MSigDB C2 BIOCARTA (v6.0)							
M5889	Ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins	2.21E-42	2.34E-40	1.23E-39	2.34E-40	121	FSTL3,CLEC5A,CD109,EMILIN2,CLEC7A,PGF,MFAP2,SERPINB5,SERPINE2,SERPINB9,FBN1,MGP,AEBP1,ACAN,SPON2,AGT,CXCL9,CTHRC1,CCL3,PLAU,MMP1,BMP8A,C1QTNF6,MMP3,CCL18,MMP7,MMP9,MMP11,MMP14,CXCL6,MMP16,PLXNA1,COL1A1,COL1A2,COL3A1,COL4A1,COL4A2,SEMA6B,COL5A1,COL5A2,NID2,COL6A3,COL7A1,COL8A1,COL10A1,COL11A1,MXRA5,COL12A1,SFRP2,SFRP4,COL15A1,COL16A1,CHRDL2,ANGPT2,FN1,COMP,ADAMTS4,ADAMTS2,TNC,GDF15,WNT2,ANXA13,COL5A3,IGFBP7,VCAN,CST1,HAPLN3,ADAMTS14,CTSB,CTSK,IL6,IL11,SPARC,HTRA1,SPOCK1,INHBA,SPP1,ASPN,P4HA3,BGN,BMP1,FNDC1,SRPX2,SULF2,PXDN,ADAMTS9,SULF1,CRISPLD1,PLXDC1,LAMA5,MUC16,ESM1,HTRA3,OMD,ADAM12,SERPINH1,CXCL1,ADAMTS12,TGFBI,LIF,COL18A1,TGM2,OSM,THBS1,THBS2,THBS4,ANGPTL2,FSTL1,HMCN1,PLXDC2,LGI2,TIMP1,PLXNC1,LOXL2,SERPINE1,LTBP2,ELN,GREM1,TNFAIP6,LUM,PCOLCE
M5884	Ensemble of genes encoding core extracellular matrix including ECM glycoproteins, collagens and proteoglycans	3.53E-31	1.87E-29	9.81E-29	3.74E-29	56	EMILIN2,MFAP2,FBN1,MGP,AEBP1,ACAN,SPON2,CTHRC1,COL1A1,COL1A2,COL3A1,COL4A1,COL4A2,COL5A1,COL5A2,NID2,COL6A3,COL7A1,COL8A1,COL10A1,COL11A1,MXRA5,COL12A1,COL15A1,COL16A1,FN1,COMP,TNC,COL5A3,IGFBP7,VCAN,HAPLN3,SPARC,SPOCK1,SPP1,ASPN,BGN,FNDC1,SRPX2,PXDN,CRISPLD1,LAMA5,ESM1,OMD,TGFBI,COL18A1,THBS1,THBS2,THBS4,HMCN1,LGI2,LTBP2,ELN,TNFAIP6,LUM,PCOLCE
M5885	Ensemble of genes encoding ECM-associated proteins including ECM-affilaited proteins,	5.14E-15	1.36E-13	7.15E-13	5.45E-13	65	FSTL3,CLEC5A,CD109,CLEC7A,PGF,SERPINB5,SERPINE2,SERPINB9,AGT,CXCL9,CCL3,PLAU,MMP1,BMP8A,C1QTNF6,MMP3,CCL18,

	ECM regulators and secreted factors						MMP7,MMP9,MMP11,MMP14,CXCL6,MMP16,PLXNA1,SEMA6B,SFRP2,SFRP4,CHRDL2,ANGPT2,ADAMTS4,ADAMTS2,GDF15,WNT2,ANXA13,CST1,ADAMTS14,CTSB,CTSK,IL6,IL11,HTRA1,INHBA,P4HA3,BMP1,SULF2,ADAMTS9,SULF1,PLXDC1,MUC16,HTRA3,ADAM12,SERPINH1,CXCL1,ADAMTS12,LIF,TGM2,OSM,ANGPTL2,FSTL1,PLXDC2,TIMP1,PLXNC1,LOXL2,SERPINE1,GREM1
M3008	Genes encoding structural ECM glycoproteins	1.44E-13	2.66E-12	1.40E-11	1.53E-11	30	EMILIN2,MFAP2,FBN1,MGP,AEBP1,SPON2,CTHRC1,NID2,MXRA5,FN1,COMP,TNC,IGFBP7,SPARC,SPP1,FNDC1,SRPX2,PXDN,CRISPLD1,LAMA5,TGFBI,THBS1,THBS2,THBS4,HMCN1,LGI2,LTBP2,ELN,TNFAIP6,PCOLCE
M3468	Genes encoding enzymes and their regulators involved in the remodeling of the extracellular matrix	1.51E-13	2.66E-12	1.40E-11	1.60E-11	33	CD109,SERPINB5,SERPINE2,SERPINB9,AGT,PLAU,MMP1,MMP3,MMP7,MMP9,MMP11,MMP14,MMP16,ADAMTS4,ADAMTS2,CST1,ADAMTS14,CTSB,CTSK,HTRA1,P4HA3,BMP1,SULF2,ADAMTS9,SULF1,HTRA3,ADAM12,SERPINH1,ADAMTS12,TGM2,TIMP1,LOXL2,SERPINE1
M5882	Genes encoding proteoglycans	6.26E-07	9.47E-06	4.97E-05	6.63E-05	9	ACAN,VCAN,HAPLN3,SPOCK1,ASPN,BGN,ESM1,OMD,LUM
M5887	Genes encoding structural components of basement membranes	2.00E-05	2.65E-04	1.39E-03	2.12E-03	8	COL4A1,COL4A2,NID2,COL6A3,COL15A1,LAMA5,COL18A1,HMCN1
M5883	Genes encoding secreted soluble factors	1.63E-03	1.68E-02	8.79E-02	1.72E-01	21	FSTL3,PGF,CXCL9,CCL3,BMP8A,CCL18,CXCL6,SFRP2,SFRP4,CHRDL2,ANGPT2,GDF15,WNT2,IL6,IL11,INHBA,CXCL1,LIF,OSM,ANGPTL2,FSTL1
M5880	Genes encoding proteins affiliated structurally or functionally to extracellular matrix proteins	1.40E-02	8.22E-02	4.31E-01	1.00E+00	11	CLEC5A,CLEC7A,C1QTNF6,PLXNA1,SEMA6B,ANXA13,PLXDC1,MUC16,PLXDC2,PLXNC1,GREM1
M3270	Integrin Signaling Pathway	9.94E-02	3.40E-01	1.00E+00	1.00E+00	5	EPHB2,ACTN1,ITGA11,ITGA5,ANGPTL2
				Panther DB			
P00034	Integrin signalling pathway	1.64E-10	1.28E-08	6.33E-08	1.28E-08	24	ACTN1,ITGBL1,COL1A1,COL1A2,COL3A1,COL4A1,COL4A2,COL5A1,COL5A2,COL6A3,COL7A1,COL8A1,ITGA11,COL10A1,COL11A1,COL12A1,COL15A1,COL16A1,FN1,COL5A3,ITGA5,ITGAX,ITGB8,LAMA5
P00050	Plasminogen activating cascade	1.08E-04	4.21E-03	2.08E-02	8.42E-03	5	PLAU,MMP1,MMP3,MMP9,SERPINE1
P00004	Alzheimer disease-presenilin pathway	2.07E-03	5.39E-02	2.66E-01	1.62E-01	10	MMP1,MMP7,MMP9,MMP14,MMP16,WNT2,NOTCH1,NOTCH3,LEF1,CDH3

P02749	Leucine biosynthesis	5.91E-02	5.76E-01	1.00E+00	1.00E+00	1	BCAT1
P00045	Notch signaling pathway	9.82E-02	6.83E-01	1.00E+00	1.00E+00	3	NOTCH1,NOTCH3,HEYL
P00011	Blood coagulation	1.17E-01	6.83E-01	1.00E+00	1.00E+00	3	F2R,PLAU,SERPINE1
P00039	Metabotropic glutamate receptor group III pathway	1.25E-01	6.83E-01	1.00E+00	1.00E+00	4	SLC1A3,CACNA1E,GRIN2D,GNB4
P00019	Endothelinsignaling pathway	1.75E-01	6.83E-01	1.00E+00	1.00E+00	4	ADCY3,PTGS2,EDNRA,PIK3R5
P00012	Cadherin signaling pathway	2.00E-01	6.98E-01	1.00E+00	1.00E+00	7	WNT2,CELSR3,LEF1,CDH3,CDH11,CDH13,CDH17
P00057	Wntsignaling pathway	2.05E-01	6.98E-01	1.00E+00	1.00E+00	12	MMP7,SFRP2,SFRP4,WNT2,DKK2,CELSR3,GNB4,LEF1,CDH3,CDH11,CDH13,CDH17
Pathway Ontology							
PW:0000286	integrin signaling	5.23E-03	1.57E-01	7.34E-01	3.14E-01	5	ITGA11,ITGA5,PARVG,ITGAX,ITGB8
PW:0000484	altered lipoprotein metabolic	1.70E-02	1.69E-01	7.89E-01	1.00E+00	2	APOC1,APOE
PW:0000165	taurine and hypotaurine metabolic	1.70E-02	1.69E-01	7.89E-01	1.00E+00	2	GGT5,SDS
PW:0000419	water transport	2.80E-02	1.69E-01	7.89E-01	1.00E+00	2	AQP1,AQP9
PW:0000300	renal disease, renal disorder	3.09E-02	1.69E-01	7.89E-01	1.00E+00	1	SPP1
PW:0000544	altered reverse cholesterol transport	3.09E-02	1.69E-01	7.89E-01	1.00E+00	1	ABCA1
PW:0000516	Interleukin-6 signaling	3.09E-02	1.69E-01	7.89E-01	1.00E+00	1	IL6
PW:0000244	Angiotensin II signaling	3.44E-02	1.72E-01	8.04E-01	1.00E+00	2	AGT,OLR1
PW:0000459	apelinsignaling	8.72E-02	2.08E-01	9.75E-01	1.00E+00	1	APLN
PW:0000078	cyanoamino acid metabolic	8.72E-02	2.08E-01	9.75E-01	1.00E+00	1	GGT5
SMPDB							
SMP00009	Ammonia Recycling	2.22E-02	3.04E-01	1.00E+00	1.00E+00	2	CPS1,SDS
SMP00202	MNGIE (Mitochondrial Neurogastrointestinal Encephalopathy)	3.09E-02	3.04E-01	1.00E+00	1.00E+00	1	TYMP
SMP00018	Alpha Linolenic Acid and Linoleic Acid Metabolism	5.91E-02	3.04E-01	1.00E+00	1.00E+00	1	FADS2
SMP00147	Cilazapril Pathway	8.07E-02	3.04E-01	1.00E+00	1.00E+00	3	AGT,CALD1,EDNRA
SMP00083	Acetylsalicylic Acid Pathway	9.06E-02	3.04E-01	1.00E+00	1.00E+00	2	F2R,PTGS2
SMP00379	Nifedipine Pathway	1.00E-01	3.04E-01	1.00E+00	1.00E+00	2	CALD1,EDNRA
SMP00087	Rofecoxib Pathway	1.20E-01	3.08E-01	1.00E+00	1.00E+00	2	F2R,PTGS2
SMP00053	One Carbon Pool By Folate	2.62E-01	3.47E-01	1.00E+00	1.00E+00	1	MTHFD1L
SMP00048	Nicotinate and Nicotinamide Metabolism	3.06E-01	3.47E-01	1.00E+00	1.00E+00	1	NNMT
SMP00006	Tyrosine Metabolism	5.18E-01	5.31E-01	1.00E+00	1.00E+00	1	NOX4

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**	**Bonferroni**	**Gene Count**	**Gene**
1108771	allopregnanolone biosynthesis	3.09E-04	1.58E-02	7.63E-02	2.16E-02	3	AKR1C3,AKR1C1,AKR1C2
782382	gluconeogenesis	4.51E-04	1.58E-02	7.63E-02	3.16E-02	4	FBP1,ALDOB,ALDOC,FBP2

545351	sphingosine and sphingosine-1-phosphate metabolism	1.23E-03	2.86E-02	1.38E-01	8.58E-02	3	ASAH2,PTGR1,ACER2
545319	creatine-phosphate biosynthesis	1.91E-03	3.25E-02	1.57E-01	1.34E-01	2	CKM,CKMT2
545359	superpathway of melatonin degradation	2.32E-03	3.25E-02	1.57E-01	1.62E-01	3	MAOA,CYP2S1,CYP2C19
545278	heparansulfate biosynthesis	3.42E-03	3.42E-02	1.65E-01	2.39E-01	4	B3GAT1,HS6ST3,XYLT2,A4GNT
1108786	mucin core 1 and core 2 O-glycosylation	3.42E-03	3.42E-02	1.65E-01	2.39E-01	4	GCNT4,GCNT1,GALNT6,GALNT5
545347	sucrose degradation	9.06E-03	7.05E-02	3.41E-01	6.34E-01	2	ALDOB,ALDOC
545352	acetone degradation I (to methylglyoxal)	1.64E-02	9.15E-02	4.42E-01	1.00E+00	2	CYP2S1,AKR1B10
1108788	terminal O-glycans residues modification	1.64E-02	9.15E-02	4.42E-01	1.00E+00	2	FUT9,GCNT2
KEGG							
83032	Drug metabolism - cytochrome P450	1.80E-10	2.08E-08	1.24E-07	3.83E-08	15	MAOA,ADH1C,ADH7,ALDH3A1,FMO5,UGT1A10,UGT1A6,CYP2C19,CYP2C8,CYP2C9,CYP3A4,CYP3A5,GSTA1,GSTA2,GSTA3
673221	Chemical carcinogenesis	1.96E-10	2.08E-08	1.24E-07	4.17E-08	16	ADH1C,ADH7,ALDH3A1,UGT1A10,UGT1A6,CYP2C19,CYP2C8,CYP2C9,CYP2C18,CYP3A4,CYP3A5,AKR1C2,SULT2A1,GSTA1,GSTA2,GSTA3
83031	Metabolism of xenobiotics by cytochrome P450	4.14E-10	2.94E-08	1.75E-07	8.82E-08	15	CYP2S1,ADH1C,ADH7,ALDH3A1,UGT1A10,UGT1A6,AKR7A3,CYP2C9,CYP3A4,CYP3A5,AKR1C1,SULT2A1,GSTA1,GSTA2,GSTA3
154409	Gastric acid secretion	4.53E-08	1.93E-06	1.15E-05	9.65E-06	13	HRH2,SLC9A1,SLC26A7,ATP4A,ATP4B,SST,KCNJ15,KCNJ16,KCNQ1,CA2,KCNE2,CCKBR,SLC9A4
132956	Metabolic pathways	3.35E-07	1.19E-05	7.05E-05	7.12E-05	62	CMBL,HGD,MAOA,ACADL,GGT6,B3GALT5,CYP2S1,TST,GCNT4,ME1,ADH1C,CKB,ADH7,CKM,CKMT2,FBP1,PIK3C2G,SMPD3,ALDH1A1,ALDH3A1,ALDOB,ALDOC,ALDH6A1,AMPD1,HYAL1,UGT1A10,ASAH2,UGT1A6,LIPF,FUT9,AKR1C3,B3GAT1,ACER2,ST6GALNAC1,CYP2C19,GALE,CYP2C8,CHIA,CYP2C9,CYP2C18,CYP3A4,CYP3A5,ACSM1,FBP2,GCNT1,GCNT2,ITPKA,BHMT,XYLT2,B3GNT6,DHCR24,AKR1B10,GLUL,B4GALNT3,GPT2,GPT,RDH12,RGN,DHRS9,TM7SF2,GALNT6,GALNT5
172847	Protein digestion and absorption	2.79E-06	8.49E-05	5.05E-04	5.94E-04	12	COL6A5,PGA5,COL2A1,COL4A6,COL17A1,CPA2,SLC9A3,SLC15A1,KCNQ1,PGA3,PGA4,SLC7A8
193146	Bile secretion	4.27E-04	9.09E-03	5.40E-02	9.09E-02	8	NR0B2,AQP4,SLC9A1,SLC9A3,SLC4A4,CYP3A

							4,SULT2A1,CA2
814926	Carbon metabolism	2.51E-03	2.43E-02	1.44E-01	5.34E-01	9	ME1,FBP1,ALDOB,ALDOC,ALDH6A1,FBP2,GPT2,GPT,RGN
169306	Pancreatic secretion	1.12E-02	9.95E-02	5.91E-01	1.00E+00	7	CPA2,SLC9A1,SLC4A4,KCNQ1,RAB27B,CA2,CCKAR
83053	Neuroactive ligand-receptor interaction	9.90E-02	4.22E-01	1.00E+00	1.00E+00	11	F2RL1,HRH2,HTR1E,PRLR,GABRB3,SSTR1,PTGER3,GRIA4,LEPR,CCKAR,CCKBR
			Pathway Interaction Database				
137911	FOXA2 and FOXA3 transcription factor networks	8.12E-04	1.50E-02	6.31E-02	3.00E-02	6	FOXA1,FOXA2,FOXA3,TTR,ALDOB,APOA1
169356	RhoAsignaling pathway	8.59E-02	7.10E-01	1.00E+00	1.00E+00	3	SH3GL2,SLC9A1,SLC9A3
138074	Visual signal transduction: Rods	1.15E-01	7.10E-01	1.00E+00	1.00E+00	2	GUCA1C,RDH12
138017	Signaling events mediated by PTP1B	1.34E-01	7.10E-01	1.00E+00	1.00E+00	3	PRLR,LEPR,CDH2
169347	Notch-mediated HES/HEY network	3.47E-01	9.31E-01	1.00E+00	1.00E+00	2	ID1,GATA6
138027	Regulation of Androgen receptor activity	3.65E-01	9.31E-01	1.00E+00	1.00E+00	2	SPDEF,TMPRSS2
137944	IL1-mediated signaling events	5.95E-01	9.31E-01	1.00E+00	1.00E+00	1	IL1R2
137948	BMP receptor signaling	6.05E-01	9.31E-01	1.00E+00	1.00E+00	1	SOSTDC1
138070	Regulation of RhoA activity	6.95E-01	9.31E-01	1.00E+00	1.00E+00	1	ARHGDIG
137999	Integrins in angiogenesis	6.95E-01	9.31E-01	1.00E+00	1.00E+00	1	ANGPTL3
			REACTOME				
1270189	Biological oxidations	8.27E-10	4.25E-07	2.90E-06	4.25E-07	25	CMBL,AADAC,MAOA,GGT6,CYP2S1,ADH1C,ADH7,ALDH1A1,ALDH3A1,UGT1A6,AKR7A3,CYP4F12,CYP2C19,CYP2C8,CYP2C9,CYP2C18,CYP3A4,CYP3A5,ACSM1,SULT1B1,SULT1C2,SULT2A1,GSTA1,GSTA2, GSTA3
1270190	Phase 1 - Functionalization of compounds	1.32E-07	1.70E-05	1.16E-04	6.78E-05	15	CMBL,AADAC,MAOA,CYP2S1,ADH1C,ADH7,ALDH1A1,ALDH3A1,CYP4F12,CYP2C19,CYP2C8,CYP2C9,CYP2C18,CYP3A4,CYP3A5
1269903	Transmembrane transport of small molecules	5.85E-04	1.59E-02	1.09E-01	3.01E-01	32	ANO5,CLCNKA,SCNN1B,SCNN1G,FXYD3,ATP13A4,SLC26A9,APOA1,AQP4,SLC1A2,AQP5,SLC5A5,SLC9A1,SLC9A2,SLC9A3,SLC15A1,SLC26A7,ANO7,SLC4A4,SLC2A12,ATP4A,ATP4B,GABRB3,AZGP1,GCKR,AQP10,ATP13A5,SGK2,SLC7A8,SLC9A4,SLC28A2,SLC16A7
1270001	Metabolism of lipids and lipoproteins	3.10E-03	4.99E-02	3.40E-01	1.00E+00	34	ACADL,ME1,PIK3C2G,LIPH,HPGD,SMPD3,ELOVL6,ASAH2,GDPD3,FA2H,LIPF,APOA1,APOA4,APOC3,PTGR1,CIDEC,PR

						KAA2,AKR1C3,ACER2, CYP2C19,CYP2C8, CYP2C9,INSIG1,AKR1C1,AKR1C2,BHMT,SULT2A1, DHCR24,ANGPTL3,SPTSSB,OXCT1,CD36,AKR1B15, TM7SF2
1269957	Metabolism of carbohydrates	9.17E-03	9.25E-02	6.31E-01	1.00E+00	15	FBP1,ALDH1A1,ALDOB,ALDOC,HYAL1,SLC9A1,B3GAT1,HS6ST3,GALE,CHIA,FBP2,GCKR,XYLT2,B3GNT7,HAS3
1270158	Metabolism of amino acids and derivatives	4.88E-02	2.53E-01	1.00E+00	1.00E+00	15	HGD,TST,CKB,CKM,CKMT2,ALDH6A1,DUOX2,SLC5A5, GNMT,BHMT,DUOX1, GLUL,NQO1,GPT2,GPT
1457780	Neutrophil degranulation	1.89E-01	4.97E-01	1.00E+00	1.00E+00	16	TTR,PLAC8,S100P,ALDOC,METTL7A,SLPI,CYSTM1, PTPRN2,RAB27A,TCN1,ORM1,ORM2,CD36,LTF,HBB, RAB37
1269340	Hemostasis	2.77E-01	6.05E-01	1.00E+00	1.00E+00	19	F13A1,SERPINA4,FGA,FGB,FGG,APOA1,GATA5,SCG3, CXADR,KIF1A,GATA6,RAB27B,SLC7A8,ORM1,ORM2, CD36,CLEC3B,HBB,SERPINA5
1268677	Metabolism of proteins	5.61E-01	8.87E-01	1.00E+00	1.00E+00	41	KLF4,GCNT4,PGA5,TTR,FGA,PAPPA2,ERO1B, SLC25A4, FOLR1,MYRIP,APOA1, APOA4,IGFALS,IGFBP2,MUC1, MUC6,ST6GALNAC1,LYPD6B,GHRL,GATA6, GCNT1, B3GNT6,LDHD,ODAM, ADAMTS15,RAB27A,RAB27B, PGA3,PGA4,ADAMTSL1,PSCA,MUC5B,B3GNT7,EEF1A2,B4GALNT2,A4GNT,CNTN3,LTF,GALNT6,GALNT5,RAB37
1270302	Developmental Biology	9.27E-01	1.00E+00	1.00E+00	1.00E+00	21	ERBB4,COL6A5,KLF4,FOXA2,FOXA3,FGA,FGB,KRT20, FGG,SH3GL2,CSTA,SOX2,PRSS8,NRG4,NCAM1,RPS6KA6,UNC5D,RAP1GAP,DSC2,CD36,CDH2
			Gen MAPP				
MAP00710	MAP00710	1.68E-06	3.19E-05	1.30E-04	5.54E-05	6	ME1,FBP1,ALDOB,ALDOC,FBP2,GPT
MAP00071	MAP00071	1.93E-06	3.19E-05	1.30E-04	6.37E-05	9	ACADL,ADH1C,ADH7,ALDH1A1,CYP2C8,CYP2C9,CYP2C18,CYP3A4,CYP3A5
MAP00010	MAP00010	4.59E-05	5.05E-04	2.06E-03	1.51E-03	8	ADH1C,ADH7,FBP1,ALDH1A1,ALDH3A1,ALDOB,ALDOC,FBP2
MAP00910	MAP00910	1.75E-03	7.23E-03	2.96E-02	5.78E-02	4	GLUL,CA2,CA4,CA9
MAP00220	MAP00220	8.53E-03	2.56E-02	1.05E-01	2.82E-01	3	CKB,CKM,CKMT2
MAP00562	MAP00562	8.32E-02	1.67E-01	6.82E-01	1.00E+00	2	PIK3C2G,ITPKA

MAP00251	MAP00251	9.09E-02	1.67E-01	6.82E-01	1.00E+00	2	GLUL,GPT
MAP00480	MAP00480	1.07E-01	1.84E-01	7.53E-01	1.00E+00	2	GPX3,GSTA2
MAP00260	MAP00260	1.15E-01	1.84E-01	7.53E-01	1.00E+00	2	MAOA,BHMT
MAP00532	MAP00532	1.65E-01	2.37E-01	9.69E-01	1.00E+00	1	XYLT2
MSigDB C2 BIOCARTA (v6.0)							
M5889	Ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins	2.63E-03	3.55E-02	1.63E-01	1.42E-01	41	LGALS9C,COL6A5,F13A1,S100P,SERPINA4,CCL28,FGA,FGB,FGG,COL2A1,PAPPA2,COL4A6,COL17A1,HYAL1,CXCL14,HAPLN1,IGFALS,IGFBP2,SCUBE2,PDGFD,SLPI,CSTA,CTSE,MUC1,MUC6,SERPINB7,LGALS9B,NRG4,ADAM28,BMP5,SEMA3B,ANGPTL3,ADAMTS15,DPT,ADAMTSL1,MUC5B,CCBE1,ANXA10,REG3A,CLEC3B,SERPINA5
M5885	Ensemble of genes encoding ECM-associated proteins including ECM-affilaited proteins, ECM regulators and secreted factors	9.91E-03	8.92E-02	4.08E-01	5.35E-01	30	LGALS9C,F13A1,S100P,SERPINA4,CCL28,PAPPA2,HYAL1,CXCL14,SCUBE2,PDGFD,SLPI,CSTA,CTSE,MUC1,MUC6,SERPINB7,LGALS9B,NRG4,ADAM28,BMP5,SEMA3B,ANGPTL3,ADAMTS15,ADAMTSL1,MUC5B,CCBE1,ANXA10,REG3A,CLEC3B,SERPINA5
M3468	Genes encoding enzymes and their regulators involved in the remodeling of the extracellular matrix	1.89E-02	1.46E-01	6.68E-01	1.00E+00	12	F13A1,SERPINA4,PAPPA2,HYAL1,SLPI,CSTA,CTSE,SERPINB7,ADAM28,ADAMTS15,ADAMTSL1,SERPINA5
M18053	Reversal of Insulin Resistance by Leptin	3.05E-02	1.52E-01	6.95E-01	1.00E+00	2	PRKAA2,LEPR
M5880	Genes encoding proteins affiliated structurally or functionally to extracellular matrix proteins	3.10E-02	1.52E-01	6.95E-01	1.00E+00	9	LGALS9C,MUC1,MUC6,LGALS9B,SEMA3B,MUC5B,ANXA10,REG3A,CLEC3B
M2404	Mechanism of Gene Regulation by Peroxisome Proliferators via PPARa(alpha)	5.99E-02	2.70E-01	1.00E+00	1.00E+00	4	ME1,NR0B2,APOA1,CD36
M5884	Ensemble of genes encoding core extracellular matrix including ECM glycoproteins, collagens and proteoglycans	9.35E-02	3.89E-01	1.00E+00	1.00E+00	11	COL6A5,FGA,FGB,FGG,COL2A1,COL4A6,COL17A1, HAPLN1,IGFALS,IGFBP2,DPT
M9378	Interleukin 4 (IL-4) Pathway	1.41E-01	5.44E-01	1.00E+00	1.00E+00	2	SERPINA4,NR0B2
M5202	Hypoxia and p53 in the Cardiovascular system	4.48E-01	6.72E-01	1.00E+00	1.00E+00	1	NQO1
M5883	Genes encoding secreted soluble factors	5.15E-01	6.78E-01	1.00E+00	1.00E+00	9	S100P,CCL28,CXCL14,SCUBE2,PDGFD,NRG4,BMP5,ANGPTL3,CCBE1
Panther DB							
P04372	5-Hydroxytryptamine degredation	1.01E-02	1.70E-01	7.33E-01	4.12E-01	3	MAOA,ALDH1A1,ALDH3A1
P02744	Fructose galactose metabolism	1.25E-02	1.70E-01	7.33E-01	5.11E-01	2	ALDOB,ALDOC
P05914	Nicotine degradation	6.84E-02	6.54E-01	1.00E+00	1.00E+00	2	UGT1A10,UGT1A6
P02745	Glutamine glutamate conversion	9.80E-02	6.54E-01	1.00E+00	1.00E+00	1	GLUL
P00037	Ionotropic glutamate receptor pathway	1.12E-01	6.54E-01	1.00E+00	1.00E+00	3	SLC1A2,STX19,GRIA4
P05726	2-arachidonoylglycerol biosynthesis	1.43E-01	7.35E-01	1.00E+00	1.00E+00	1	LIPH

P02772	Pyruvate metabolism	1.65E-01	7.53E-01	1.00E+00	1.00E+00	1	ME1
P04396	Vitamin D metabolism and pathway	2.07E-01	8.48E-01	1.00E+00	1.00E+00	1	GC
P00026	Heterotrimeric G-protein signaling pathway-Gialpha and Gs alpha mediated pathway	7.40E-01	9.97E-01	1.00E+00	1.00E+00	3	HRH2,HTR1E,SSTR1
P00047	PDGF signaling pathway	8.38E-01	9.97E-01	1.00E+00	1.00E+00	2	SPDEF,RPS6KA6
Pathway Ontology							
PW:0000482	lipoprotein metabolic	2.46E-04	7.38E-03	3.45E-02	1.48E-02	4	APOA1,APOA4,APOBEC1,APOC3
PW:0000057	carbon fixation	2.46E-04	7.38E-03	3.45E-02	1.48E-02	4	ME1,FBP1,ALDOC,GPT
PW:0000419	water transport	1.23E-03	1.47E-02	6.88E-02	7.35E-02	3	AQP4,AQP5,AQP10
PW:0000373	glutathione conjugation	1.23E-03	1.47E-02	6.88E-02	7.35E-02	3	GSTA1,GSTA2,GSTA3
PW:0000579	somatostatinsignaling	9.06E-03	5.44E-02	2.54E-01	5.44E-01	2	SST,SSTR1
PW:0000033	energy metabolic	2.61E-02	1.05E-01	4.89E-01	1.00E+00	1	AMPD1
PW:0000357	energy homeostasis	5.03E-02	1.26E-01	5.88E-01	1.00E+00	1	LEPR
PW:0000539	ghrelin system	5.03E-02	1.26E-01	5.88E-01	1.00E+00	1	GHRL
PW:0000533	glycogen metabolic	1.21E-01	2.20E-01	1.00E+00	1.00E+00	1	GCKR
PW:0000454	cholesterol biosynthetic	3.72E-01	4.37E-01	1.00E+00	1.00E+00	1	DHCR24
SMPDB							
SMP00246	Pirenzepine Pathway	4.99E-05	9.27E-04	5.10E-03	6.83E-03	5	HRH2,ATP4A,ATP4B,SST,CCKBR
SMP00006	Tyrosine Metabolism	2.96E-04	3.69E-03	2.03E-02	4.05E-02	5	HGD,MAOA,ALDH3A1,DUOX2,DUOX1
SMP00281	Anistreplase Pathway	5.89E-04	3.95E-03	2.17E-02	8.07E-02	4	F13A1,FGA,FGB,FGG
SMP00260	Clopidogrel Pathway	9.51E-04	3.95E-03	2.17E-02	1.30E-01	4	CYP2C19,CYP2C9,CYP3A4,CYP3A5
SMP00127	Glucose-Alanine Cycle	1.91E-03	7.68E-03	4.23E-02	2.61E-01	2	GPT2,GPT
SMP00074	Retinol Metabolism	1.01E-02	3.93E-02	2.16E-01	1.00E+00	3	ALDH1A1,RDH12,DHRS9
SMP00073	Butyrate Metabolism	1.64E-02	6.05E-02	3.33E-01	1.00E+00	2	ACSM1,OXCT1
SMP00330	Tocainide Pathway	2.43E-01	3.60E-01	1.00E+00	1.00E+00	2	KCNQ1,KCNE2
SMP00110	Indapamide Pathway	2.47E-01	3.60E-01	1.00E+00	1.00E+00	1	CLCNKA
SMP00134	Spironolactone Pathway	2.85E-01	3.75E-01	1.00E+00	1.00E+00	1	SCNN1B

Table 5 The enriched GO terms of the up regulated differentially expressed genes

GO ID	CATEGORY	GO Name	P Value	FDR B&H	FDR B&Y	Bonferroni	Gene Count	Gene
GO:0043062	BP	extracellular structure organization	3.09E-46	9.74E-43	9.09E-42	1.95E-42	83	ABCA1,MFAP2,FAP,SERPINB5,FBN1,AEBP1,LIPG,ACAN,AGT,ANTXR1,FLRT2,MMP1,MMP3,MMP7,MMP9,MMP11,MMP14,MMP16,FOXC1,COL1A1,COL1A2,COL3A1,COL4A1,COL4A2,COL5A1,COL5A2,NID2,COL6A3,COL7A1,COL8A1,ITGA11,COL10A1,COL11A1,COL12A1,SFRP2,COL15A1,COL16A1,FN1,COMP,ADAMTS4,ADAMTS2,TNC,OLFML2B,ICAM1,COL5A3,CCDC80,APOC1,APOE,MSR1,PDPN,VCAN,ADAMTS14,FSCN1,CTSK,IL6,SPARC,HTRA1,SPP1,ITGA5,ITGAX,ITGB8,BGN,BMP1,SULF2,PXDN,ADAMTS9,SULF1,NOTCH1,PLA2G7,LAMA5,ADAM12,SERPINH1,TNFRSF11B,TGFBI,COL18A1,THBS1,SH3PXD2B,TIMP1,LOXL2,SERPINE1,ELN,GREM

								1,LUM
GO:0007155	BP	cell adhesion	3.95E-35	8.29E-32	7.73E-31	2.49E-31	121	FSTL3,SCARF2,EMILIN2,ACTN1,TRIM29,DYSF,ITGBL1,FAP,LRFN4,SERPINE2,FBN1,ACAN,SPON2,AGT,ANTXR1,CCR1,PLAU,FLRT2,GPNMB,PLEK,MMP14,PLXNA1,COL1A1,COL3A1,SELE,SELL,ONECUT2,COL5A1,ZNF703,NID2,COL6A3,COL7A1,COL8A1,ITGA11,COL12A1,SFRP2,COL15A1,COL16A1,ANGPT2,FN1,COMP,TNC,PODXL,ICAM1,MXRA8,COL5A3,CCDC80,C2CD4A,CLDN4,CLDN3,CLDN7,PDPN,CSF3R,IGFBP7,VCAN,HAPLN3,IGSF9B,IL2RA,IL6,MYB,BOC,CLSTN3,MYH10,IDO1,SPOCK1,SPP1,PIEZO1,LRRC32,ISLR,ITGA5,PARVG,ITGAX,RCC2,ITGB8,CD84,SRPX2,ADAMTS9,PTPRO,NTM,GLI2,KIF14,NOTCH1,AMIGO2,LILRB4,KIF26B,LAMA5,MUC16,OMD,ADAM12,OLR1,CLDN2,CLDN1,ADAMTS12,HAVCR2,TGFBI,COL18A1,TGM2,THBS1,THBS2,THBS4,THY1,CELSR3,HMCN1,PLXNC1,LOXL2,ENTPD1,SERPINE1,KIRREL1,ROBO2,DUSP10,GREM1,TNFAIP6,AJUBA,LEF1,CDH3,CDH11,CDH13,CDH17,MSLN,EPHA3,EPHB1
GO:0048646	BP	anatomical structure formation involved in morphogenesis	5.46E-25	6.88E-22	6.42E-21	3.44E-21	99	EPHB2,CDX2,PDGFRB,CD109,ACTN1,CHI3L1,DYSF,PGF,MFAP2,FAP,AGT,CXCL9,CTHRC1,PLAU,GPNMB,ALDH1A3,MMP9,MMP14,FOXC1,COL1A1,COL4A1,COL4A2,COL5A1,COL5A2,COL7A1,COL8A1,COL11A1,COL12A1,SFRP2,COL15A1,ANGPT2,FN1,PODXL,MTHFD1L,GDF15,WNT2,VASH1,MYOM3,OSR2,STIL,XRCC2,AQP1,PDPN,CSF3R,PRKDC,IL6,MYH10,SPARC,HTRA1,INHBA,ITGA5,NEB,ITGAX,PTGS2,ITGB8,LRP8,SRPX2,APLN,ADAMTS9,SULF1,SPHK1,GLI2,C3,C5AR1,STRA6,NOP2,NOTCH1,NOTCH3,WDR72,TCOF1,PLXDC1,KIF26B,LAMA5,ESM1,SALL4,TEAD4,TYMP,ADAM12,EDNRA,FMNL3,TGFBI,LIF,COL18A1,HEYL,TGM2,THBS1,THBS2,THBS4,THY1,EGR2,LOXL2,SERPINE1,TREM2,ROBO2,TNFAIP2,GREM1,

								LEF1,CDH13,EPHB1
GO:0072359	BP	circulatory system development	4.85E-23	5.09E-20	4.75E-19	3.05E-19	94	EPHB2,CDX2,PDGFRB,PDLIM7,CHI3L1,DYSF,PGF,HOXA13,FAP,FBN1,ACAN,AGT,ANTXR1,PLAU,FLRT2,GPNMB,MMP9,MMP14,BICC1,FOXC1,COL1A1,COL1A2,COL3A1,FOXM1,COL4A1,FOXS1,COL4A2,COL5A1,COL8A1,PRRX1,COL11A1,SFRP2,COL15A1,ANGPT2,FN1,COMP,WNT2,VASH1,MYOM3,NOX4,STIL,APOE,AQP1,PDPN,VCAN,PRKDC,IL6,MYH10,SPARC,ITGA5,NEB,ITGAX,PTGS2,ITGB8,SRPX2,APLN,ADAMTS9,SULF1,SPHK1,GLI2,C3,C5AR1,STRA6,NOTCH1,NOTCH3,CAD,PLXDC1,LAMA5,ESM1,SALL4,TYMP,ADAM12,EDNRA,FMNL3,TGFBI,LIF,COL18A1,HEYL,THBS1,THBS2,SH3PXD2B,THBS4,THY1,LOXL2,SERPINE1,ROBO2,ELN,TNFAIP2,GREM1,LY6E,LEF1,CDH13,EPHA3,EPHB1
GO:0016477	BP	cell migration	4.08E-22	2.57E-19	2.40E-18	2.57E-18	109	PRR5L,PDGFRB,TRPM2,CLEC7A,DYSF,F2R,PGF,ITGBL1,FAP,HOXB9,SERPINE2,FCER1G,ANLN,ACAN,AGT,CXCL9,ASPM,CTHRC1,CCL3,CCR1,PLAU,FLRT2,MMP1,GPNMB,CCL18,FGR,MMP9,MMP14,CXCL6,PLXNA1,FOXC1,COL1A1,COL1A2,COL3A1,SELE,SELL,SEMA6B,VIL1,ONECUT2,COL5A1,ZNF703,ITGA11,SFRP2,ANGPT2,FN1,PODXL,ICAM1,VASH1,IFITM1,NOX4,APOE,AQP1,PDPN,MAPK15,CSF3R,VCAN,FSCN1,IL6,DOCK4,MYH10,SPARC,EPPK1,SPOCK1,SPP1,ITGA5,ITGAX,PTGS2,RCC2,ITGB8,LRP8,CD84,SRPX2,ADAMTS9,PTPRO,SULF1,SPHK1,KIF14,FAM83D,C5AR1,NOTCH1,PLA2G7,DPYSL3,CD248,LAMA5,CXCL1,OLR1,EDNRA,ADAMTS12,FMNL3,COL18A1,THBS1,THBS4,THY1,CELSR3,TIMP1,PLXNC1,LOXL2,SERPINE1,TREM2,TREM1,DUSP10,GREM1,TNFAIP6,AJUBA,LEF1,PADI2,CDH13,EPHA3,EPHB1
GO:0051674	BP	localization of cell	2.01E-20	8.45E-18	7.88E-17	1.27E-16	112	PRR5L,PDGFRB,TRPM2,CLEC7A,DYSF,F2R,PGF,ADCY3,ITGBL1,FAP,HOXB9,SERPINE2,FCER1G,ANLN,ACAN,AGT,CXCL

								9,ASPM,CTHRC1,CCL3,CCR1,PLAU,FLRT2,MMP1,GPNMB,CCL18,FGR,MMP9,MMP14,CXCL6,PLXNA1,FOXC1,COL1A1,COL1A2,COL3A1,SELE,SELL,SEMA6B,VIL1,ONECUT2,COL5A1,ZNF703,ITGA11,SFRP2,ANGPT2,FN1,PODXL,ICAM1,VASH1,IFITM1,NOX4,CLDN7,APOE,AQP1,PDPN,MAPK15,CSF3R,VCAN,FSCN1,IL6,DOCK4,MYH10,SPARC,EPPK1,SPOCK1,SPP1,ITGA5,ITGAX,PTGS2,RCC2,ITGB8,LRP8,CD84,SRPX2,ADAMTS9,PTPRO,SULF1,SPHK1,KIF14,FAM83D,C5AR1,NOTCH1,PLA2G7,CACNA1E,DPYSL3,CD248,LAMA5,CXCL1,OLR1,EDNRA,ADAMTS12,FMNL3,COL18A1,THBS1,THBS4,THY1,CELSR3,TIMP1,PLXNC1,LOXL2,SERPINE1,TREM2,TREM1,DUSP10,GREM1,TNFAIP6,AJUBA,LEF1,PADI2,CDH13,EPHA3,EPHB1
GO:0009887	BP	animal organ morphogenesis	1.13E-18	3.94E-16	3.67E-15	7.09E-15	83	EPHB2,CDX2,PDGFRB,ETV4,MDFI,PGF,FANCD2,HOXA13,MFAP2,SERPINB5,FBN1,MGP,ACAN,AGT,RECQL4,SNX10,MKI67,CTHRC1,PLAU,FLRT2,FGR,ALDH1A3,MMP14,MMP16,PLXNA1,FOXC1,COL1A1,COL1A2,COL3A1,ONECUT2,COL5A1,COL5A2,COL6A3,COL7A1,COL8A1,PRRX1,COL11A1,COL12A1,SFRP2,SFRP4,COMP,TNC,MTHFD1L,WNT2,MYOM3,OSR2,STIL,AQP1,CSF3R,IL6,HTRA1,INHBA,ASPN,ITGAX,BMP1,SULF2,SULF1,GLI2,STRA6,NOTCH1,WDR72,KIF26B,LAMA5,TYMP,SERPINH1,EDNRA,TNFRSF11B,LIF,COL18A1,HEYL,TGM2,THBS1,SH3PXD2B,THY1,CELSR3,P2RX7,SERPINE1,ROBO2,ELN,GREM1,LY6E,LEF1,EPHB1
GO:0042127	BP	regulation of cell population proliferation	1.85E-15	4.23E-13	3.95E-12	1.17E-11	101	CDX2,PDGFRB,ATAD5,CD109,CLEC7A,ETV4,DYSF,F2R,PGF,FAP,SERPINB5,SERPINE2,CAMK2N1,AGT,RECQL4,CXCL9,ASPM,CTHRC1,PLAU,GPNMB,MMP7,MMP9,IQGAP3,FOXM1,ZNF703,PRRX1,SFRP2,SFRP4,FN1,COMP,TNC,WNT2,VASH1,OSR2,IFITM1,NOX4,CLDN7,APOE,LGR5,AQP1,P

								DPN,MAPK15,IGFBP7,MTBP,PRKDC,IL2RA,IL6,H19,MYB,IL11,SPARC,HTRA1,EPPK1,IDO1,INHBA,LRRC32,ITGAX,PTGS2,RTKN2,SULF2,APLN,SULF1,SPHK1,GLI2,NRK,KIF14,C5AR1,NOP2,NOTCH1,NOTCH3,RARRES1,CD248,LAMA5,MUC16,ESM1,E2F3,SLC39A10,CXCL1,EDNRA,CCND2,HAVCR2,ORC1,LIF,COL18A1,TGM2,OSM,THBS1,THBS4,TIMP1,CDCA7,SERPINE1,DUSP10,ELN,GREM1,OSMR,CDC6,CDC25B,LEF1,CDH3,CDH13,EPHB1
	BP	positive regulation of developmental process	4.56E-14	8.99E-12	8.38E-11	2.88E-10	88	EPHB2,PDE3A,CDX2,PDGFRB,ATAD5,PDLIM7,CLEC7A,CHI3L1,PGF,SERPINE2,AGT,CXCL9,ASPM,CTHRC1,CCL3,CCR1,FLRT2,MMP9,MMP14,IQGAP3,PLXNA1,FOXC1,COL1A1,FOXS1,VIL1,ZNF703,SFRP2,SFRP4,ANGPT2,FN1,GDF15,WNT2,ENC1,PKDCC,OSR2,IFITM1,XRCC2,APOE,AQP1,CRABP2,MSR1,PDPN,PRKDC,IL2RA,IL6,MYB,BOC,CLSTN3,IDO1,INHBA,ITGA5,ITGAX,PTGS2,ITGB8,LRP8,BMP1,GDPD5,SRPX2,ADAMTS9,SPHK1,GLI2,C3,C5AR1,NOTCH1,AMIGO2,LILRB4,DPYSL3,KRT17,TEAD4,ADAM12,ECT2,EDNRA,LIF,HEYL,THBS1,THBS2,SH3PXD2B,P2RX7,PLXNC1,LOXL2,SERPINE1,TREM2,ROBO2,DUSP10,GREM1,LEF1,EPHA3,EPHB1
GO:0001775	BP	cell activation	3.82E-12	5.35E-10	4.99E-09	2.41E-08	81	LPCAT1,PDGFRB,ATAD5,ABCA13,CLEC5A,TRPM2,CLEC7A,DGKH,ACTN1,CHI3L1,DYSF,F2R,F2RL2,FANCD2,SERPINE2,FCER1G,FCGR2A,FCGR3A,FCGR3B,AGT,CCL3,PLAU,GPNMB,FGR,PLEK,MMP9,MMP14,CXCL6,COL1A1,COL1A2,COL3A1,SELL,FN1,COMP,CD300LF,FPR1,ICAM1,KCNAB2,APOE,SLC2A3,PDPN,SLC11A1,PRKDC,CTSB,IL2RA,IL6,MYB,IL11,IDO1,INHBA,LRRC32,ITGAX,CD84,SPHK1,GLI2,C3,ATP11A,C5AR1,LILRB4,LILRB3,RAB31,SLC39A10,LCP2,NFAM1,CXCL1,OLR1,HAVCR2,THBS1,THY1,P2RX7,TIMP1,ENTPD1,TREM2,EXO1,DUSP10,TNFAIP6,LEF1,PADI2,PIK3

								R5,CDH17,EPHB1
GO:0009719	BP	response to endogenous stimulus	2.73E-11	3.37E-09	3.15E-08	1.72E-07	88	ABCA1,PDE3A,FSTL3,PDGFRB,TRPM2,CD109,MCM7,PGF,ADCY3,HOXA13,NOD1,FBN1,FCER1G,AGT,FLRT2,BMP8A,FBXO32,MMP14,FOXC1,COL1A1,COL1A2,COL3A1,COL4A1,COL4A2,VIL1,ONECUT2,COL5A2,ZNF703,MXRA5,SFRP2,SFRP4,COL16A1,CHRDL2,COMP,TNC,GDF15,WNT2,ICAM1,NOX4,CLDN4,APOE,CPS1,LGR5,AQP1,AQP9,MAPK15,IGFBP7,STC2,PRKDC,CTSB,IL6,SPARC,HTRA1,INHBA,SPP1,ASPN,LRRC32,NCF2,PMEPA1,PTGS2,SULF2,APLN,SULF1,SLC39A5,NOTCH1,CAD,RAB31,CALD1,HTRA3,CLDN1,ADAMTS12,HEYL,THBS1,FSTL1,P2RX7,TIMP1,EGR2,SERPINE1,TREM2,ROBO2,LTBP2,GREM1,LY6E,CDC6,LEF1,PADI2,CDH13,EPHA3
GO:0019220	BP	regulation of phosphate metabolic process	3.84E-10	3.72E-08	3.47E-07	2.42E-06	90	EPHB2,PIK3AP1,LPCAT1,PRR5L,PDGFRB,CD109,MCM7,DGKH,MDFI,CHI3L1,F2R,PGF,ADCY3,NOD1,CAMK2N1,FCGR1A,AGT,PPP1R1B,CCL3,CCR1,ABCD1,GPNMB,BMP8A,CCL18,FGR,PLEK,MMP9,PLK1,IQGAP3,FOXM1,SFRP2,SFRP4,FN1,GDF15,FPR1,ICAM1,NOX4,APOC1,STIL,APOE,MAPK15,SLC11A1,VCAN,TPX2,PRKDC,CLSPN,IL6,IL11,INHBA,ITGA5,PMEPA1,PTGS2,LRP8,CD84,CDCA2,FNDC1,SRPX2,APLN,SPHK1,NRK,KIF14,FAM83D,C3,C5AR1,NOTCH1,SLC39A10,LCP2,ECT2,EDNRA,CCND2,PKMYT1,CCNF,HAVCR2,LIF,OSM,THBS1,THBS4,THY1,CELSR3,P2RX7,ENTPD1,TREM2,KIRREL1,DUSP10,GREM1,CDC6,CDC25B,AJUBA,PIK3R5,EPHB1
GO:0031012	CC	extracellular matrix	3.68E-47	2.22E-44	1.55E-43	2.22E-44	89	EMILIN2,CHI3L1,MFAP2,SERPINE2,SERPINB9,FBN1,MGP,AEBP1,ACAN,SPON2,AGT,CTHRC1,FLRT2,MMP1,MMP3,MMP7,MMP9,MMP11,MMP14,MMP16,COL1A1,COL1A2,COL3A1,COL4A1,COL4A2,COL5A1,COL5A2,NID2,COL6A3,COL7A1,COL8A1,COL10A1,COL11A1,MXRA5,COL12A1,SFRP2,COL15A1,COL16A1,FN1,COMP,ADAMTS4,AD

								AMTS2,TNC,GDF15,OLFML2B,WNT2,ICAM1,COL5A3,CCDC80,CPZ,APOE,IGFBP7,VCAN,HAPLN3,CTSB,SPARC,HTRA1,ASPN,LRRC32,BGN,BMP1,SRPX2,PXDN,ADAMTS9,SULF1,CD248,LAMA5,OMD,SERPINH1,TNFRSF11B,TGFBI,COL18A1,TGM2,THBS1,THBS2,THBS4,ANGPTL2,HMCN1,PLXDC2,TIMP1,LOXL2,ENTPD1,SERPINE1,LTBP2,ELN,GREM1,LUM,CDH13,PCOLCE
GO:0062023	CC	collagen-containing extracellular matrix	1.56E-40	4.71E-38	3.29E-37	9.41E-38	74	EMILIN2,MFAP2,SERPINE2,SERPINB9,FBN1,MGP,AEBP1,ACAN,AGT,CTHRC1,MMP9,COL1A1,COL1A2,COL3A1,COL4A1,COL4A2,COL5A1,COL5A2,NID2,COL6A3,COL7A1,COL8A1,COL10A1,COL11A1,MXRA5,COL12A1,SFRP2,COL15A1,COL16A1,FN1,COMP,ADAMTS4,ADAMTS2,TNC,GDF15,WNT2,ICAM1,COL5A3,CCDC80,APOE,IGFBP7,VCAN,CTSB,SPARC,HTRA1,ASPN,BGN,BMP1,SRPX2,PXDN,ADAMTS9,SULF1,LAMA5,OMD,SERPINH1,TGFBI,COL18A1,TGM2,THBS1,THBS2,THBS4,ANGPTL2,HMCN1,PLXDC2,TIMP1,LOXL2,ENTPD1,SERPINE1,LTBP2,ELN,GREM1,LUM,CDH13,PCOLCE
GO:0005788	CC	endoplasmic reticulum lumen	5.71E-19	1.15E-16	8.03E-16	3.45E-16	40	FSTL3,FBN1,COL1A1,COL1A2,COL3A1,COL4A1,COL4A2,FKBP10,COL5A1,COL5A2,COL6A3,COL7A1,COL8A1,COL10A1,COL11A1,COL12A1,COL15A1,COL16A1,FN1,GPX8,TNC,MXRA8,COL5A3,APOE,IGFBP7,STC2,VCAN,IL6,SPP1,P4HA3,PTGS2,CYP2W1,C3,SERPINH1,COL18A1,THBS1,FSTL1,TIMP1,RCN3,MSLN
GO:0009986	CC	cell surface	4.90E-17	5.92E-15	4.14E-14	2.96E-14	71	ABCA1,PDGFRB,CLEC5A,CD109,CLEC7A,F2R,ITGBL1,FAP,LRFN4,SERPINE2,FCER1G,FCGR1A,FCGR3A,LIPG,CXCL9,ANTXR1,CCR1,PLAU,MMP7,MMP16,SELL,NID2,SFRP4,WNT2,ICAM1,MXRA8,APOE,SLC1A3,PDPN,SLC11A1,CSF3R,VCAN,CTSB,IL2RA,IL6,BOC,CLSTN3,SPARC,LRRC32,ITGA5,ITGAX,ITGB8,BGN,CYP2W1,LRP8,SRPX2,SULF2,ADAMTS9,SULF1,MRC2,NTM,C3,C5AR1,N

								OTCH1,NOTCH3,CD248,MUC16,NFAM1,HAVCR2,THBS1,THY1,P2RX7,ENTPD1,ROBO2,GREM1,OSMR,CDH3,CDH11,CDH13,CDH17,MSLN
GO:0031226	CC	intrinsic component of plasma membrane	6.28E-08	3.45E-06	2.41E-05	3.79E-05	76	EPHB2,ABCA1,IGSF6,PDGFRB,CLEC5A,TRPM2,SLC24A3,F2R,F2RL2,ADCY3,ITGBL1,LRFN4,FCER1G,FADS2,CCR1,FLRT2,GPNMB,MMP14,MMP16,PLXNA1,SELE,SELL,SEMA6B,ITGA11,PODXL,ICAM1,KCNAB2,NOX4,CLDN4,CLDN3,LGR5,AQP1,SLC1A3,AQP9,SLC2A3,MSR1,PDPN,SLC11A1,CSF3R,IL2RA,IL6,BOC,CLSTN3,LRRC32,SLC28A3,NCF2,ITGA5,ITGAX,ITGB8,LAPTM5,GGT5,CD84,PTPRO,C5AR1,STRA6,SLC39A5,NOTCH1,NOTCH3,CACNA1E,LILRB3,GRIN2D,SLC39A10,OLR1,CLDN1,EDNRA,TGM2,THY1,P2RX7,PLXNC1,ENTPD1,TREM2,OSMR,GPR176,CDH17,EPHA3,EPHB1
GO:0099080	CC	supramolecular complex	1.39E-07	6.67E-06	4.66E-05	8.42E-05	67	MAP1A,CENPF,NEIL2,PDLIM7,ACTN1,DYSF,KRT80,MFAP2,TUBB3,FBN1,ASPM,ANTXR1,FBXO32,PLK1,COL1A1,COL1A2,COL3A1,COL4A1,COL4A2,VIL1,COL5A1,COL5A2,COL6A3,COL7A1,COL8A1,KIF23,COL11A1,PODXL,MYOM3,KCNAB2,GAS7,NOX4,COL5A3,APOE,AQP1,PDPN,MAPK15,TPX2,KIF18B,FSCN1,AHNAK2,DOCK4,KIF21B,KNTC1,MYH10,EPPK1,IDO1,MYO7B,KIF4A,NEB,RCC2,CEP170,NEK2,GLI2,KIF14,DNM1,KIF2C,DPYSL3,CALD1,KRT17,KIF26B,KIF20A,IFFO2,ELN,CKAP2,LUM,EPHB1
GO:0030054	CC	cell junction	9.56E-07	3.40E-05	2.37E-04	5.78E-04	59	PDGFRB,SCARF2,PDLIM7,ACTN1,TRIM29,ITGBL1,FAP,CAMK2N1,PLAU,FLRT2,MMP14,IQGAP3,ITGA11,KIF23,TNC,PODXL,ICAM1,MXRA8,KCNAB2,NOX4,CLDN4,CLDN3,CLDN7,PDPN,MAPK15,RAI14,IGSF9B,FSCN1,EPPK1,ITGA5,PARVG,ITGB8,FNDC1,SRPX2,SPHK1,MRC2,NOTCH1,PLXDC1,GRIN2D,LCP2,ECT2,CLDN2,CLDN1,CCNF,HAVCR2,TGM2,SH3PXD2B,THY1,HMCN1,P2RX7,LZTS1,KIRREL1,ILDR1,TNS4,AJUBA,CDH3,C

								DH11,CDH13,CDH17
GO:0099503	CC	secretory vesicle	1.13E-06	3.80E-05	2.65E-04	6.83E-04	50	LPCAT1,FSTL3,ABCA13,CLEC5A,TRPM2,CD109,ACTN1,CHI3L1,SERPINE2,FCER1G,FCGR2A,FCGR3B,SNX10,PLAU,FGR,MMP9,COL1A1,SELL,FN1,FPR1,KCNAB2,AQP1,SLC2A3,SLC11A1,CTSB,KLK6,SPARC,NCF2,ISLR,ITGAX,SPHK1,C3,ATP11A,C5AR1,DNM1,NOTCH1,LILRB3,DPYSL3,RAB31,STK31,NFAM1,CXCL1,OLR1,THBS1,THBS2,TIMP1,ENTPD1,SERPINE1,TNFAIP6,PADI2
GO:0098805	CC	whole membrane	5.51E-04	6.69E-03	4.67E-02	3.33E-01	61	LPCAT1,ABCA1,ABCA13,CLEC5A,TRPM2,CD109,ACTN1,DYSF,F2R,ADCY3,FCER1G,FCGR1A,FCGR2A,FCGR3B,IFITM3,SNX10,ANTXR1,PLAU,ABCD1,GPNMB,SELE,SELL,PODXL,FPR1,ICAM1,KCNAB2,APOE,AQP1,SLC2A3,MSR1,PDPN,SLC11A1,FAR2,CTSB,SPARC,BCL2A1,ITGAX,PMEPA1,FCHO1,PTGS2,RCC2,LRP8,LAPTM5,RFTN1,SULF1,SPHK1,ATP11A,C5AR1,LILRB3,RAB31,LCP2,NFAM1,SERPINH1,OLR1,EDNRA,GPR161,THY1,KIRREL1,GNB4,CDH13,EPHB1
GO:0099513	CC	polymeric cytoskeletal fiber	1.26E-03	1.23E-02	8.57E-02	7.61E-01	47	MAP1A,CENPF,NEIL2,PDLIM7,ACTN1,DYSF,KRT80,TUBB3,ASPM,ANTXR1,PLK1,VIL1,KIF23,PODXL,KCNAB2,GAS7,NOX4,APOE,AQP1,PDPN,MAPK15,TPX2,KIF18B,FSCN1,DOCK4,KIF21B,KNTC1,MYH10,EPPK1,IDO1,MYO7B,KIF4A,RCC2,CEP170,NEK2,GLI2,KIF14,DNM1,KIF2C,DPYSL3,CALD1,KRT17,KIF26B,KIF20A,IFFO2,CKAP2,EPHB1
GO:0005201	MF	extracellular matrix structural constituent	1.10E-35	1.18E-32	8.92E-32	1.18E-32	47	EMILIN2,CHI3L1,MFAP2,FBN1,MGP,AEBP1,ACAN,CTHRC1,COL1A1,COL1A2,COL3A1,COL4A1,COL4A2,COL5A1,COL5A2,NID2,COL6A3,COL7A1,COL8A1,COL10A1,COL11A1,MXRA5,COL12A1,COL15A1,COL16A1,FN1,COMP,TNC,COL5A3,IGFBP7,VCAN,SPARC,ASPN,BGN,SRPX2,PXDN,LAMA5,TGFBI,COL18A1,THBS1,THBS2,THBS4,HMCN1,LTBP2,ELN,LUM,PCOLCE
GO:0005198	MF	structural molecule activity	2.77E-16	7.44E-14	5.63E-13	2.98E-13	61	MAP1A,EMILIN2,ACTN1,CHI3L1,MFAP2,TUBB3,FBN1,MGP,AEBP1,ACA

								N,CTHRC1,COL1A1,COL1A2,COL3A1,COL4A1,COL4A2,COL5A1,COL5A2,NID2,COL6A3,COL7A1,COL8A1,COL10A1,COL11A1,MXRA5,COL12A1,COL15A1,COL16A1,FN1,COMP,TNC,MYOM3,COL5A3,CLDN4,CLDN3,CLDN7,APOE,IGFBP7,VCAN,SPARC,EPPK1,ASPN,NEB,BGN,SRPX2,PXDN,MARVELD1,KRT17,LAMA5,CLDN2,CLDN1,TGFBI,COL18A1,THBS1,THBS2,THBS4,HMCN1,LTBP2,ELN,LUM,PCOLCE
GO:0005102	MF	signaling receptor binding	5.39E-10	7.24E-08	5.47E-07	5.79E-07	86	EPHB2,PIK3AP1,ABCA1,MAP1A,PDGFRB,CLEC7A,ACTN1,CHN1,F2R,PGF,TUBB3,ITGBL1,FAP,SERPINE2,FBN1,FCGR1A,SPON2,AGT,PPP1R1B,CXCL9,CTHRC1,CCL3,FLRT2,GPNMB,BMP8A,CCL18,FGR,MMP9,MMP14,CXCL6,COL3A1,SEMA6B,COL5A1,SFRP2,COL16A1,ANGPT2,FN1,COMP,CD300LF,PILRA,GDF15,WNT2,FPR1,ICAM1,APOE,AQP1,PDPN,STC2,IL6,DKK2,DOCK4,IL11,INHBA,SPP1,ITGA5,ITGAX,ITGB8,BMP1,SRPX2,PXDN,APLN,C3,DNM1,NOTCH1,KRT17,LAMA5,ESM1,TYMP,CXCL1,TNFRSF11B,TGFBI,LIF,OSM,THBS1,THBS4,ANGPTL2,THY1,P2RX7,TIMP1,PLXNC1,SERPINE1,GREM1,LY6E,LEF1,PADI2,CDH17
GO:0008233	MF	peptidase activity	1.39E-07	7.13E-06	5.39E-05	1.50E-04	62	CD109,CLEC7A,F2R,FAP,SERPINB5,SERPINE2,NOD1,SERPINB9,AEBP1,AGT,ANTXR1,PLAU,MMP1,MMP3,MMP7,MMP9,MMP11,MMP14,MMP16,VIL1,COL6A3,COL7A1,SFRP2,FN1,ADAMTS4,ADAMTS2,VASH1,CPZ,CPS1,AQP1,CST1,ADAMTS14,CLSPN,CTSB,ESPL1,CTSK,IL6,KLK6,HTRA1,SPOCK1,PTGS2,GGT5,BMP1,ADAMTS9,C1R,C3,FOXK1,RARRES1,RHBDF2,CPXM2,HTRA3,ADAM12,SERPINH1,PI15,ADAMTS12,THBS1,TIMP1,SERPINE1,CPXM1,LEF1,RCN3,PCOLCE
GO:0098772	MF	molecular function regulator	3.16E-06	1.10E-04	8.30E-04	3.40E-03	77	TRIO,CD109,CHI3L1,CHN1,PGF,SERPINB5,SERPINE2,NOD1,SERPINB9,FBN1,CAMK2N1,AGT,PPP1R1B,CXCL9,CCL3,FLRT2,GPNMB,BMP8A,CCL18,CXCL6,MMP16,SEMA

								6B,VIL1,COL6A3,COL7A1,SFRP2,FN1,PLEKHG4,GDF15,WNT2,KCNAB2,APOC1,PLEKHG2,APOE,STC2,CST1,FGD6,IL6,DKK2,DOCK4,IL11,SPOCK1,INHBA,SPP1,NCF2,ARHGAP11A,GEM,RCC2,BMP1,PXDN,APLN,C3,NOTCH1,RARRES1,ARHGAP39,TYMP,NCAPH,ECT2,SERPINH1,CXCL1,PI15,RGS1,TNFRSF11B,CCND2,CCNF,LIF,OSM,SH3PXD2B,THBS4,THY1,TIMP1,SERPINE1,GREM1,LY6E,LEF1,PIK3R5,PCOLCE
GO:0016773	MF	phosphotransferase activity, alcohol group as acceptor	5.21E-06	1.65E-04	1.24E-03	5.60E-03	62	EPHB2,TRIO,PDGFRB,DGKH,MDFI,CHI3L1,F2R,ADCY3,NOD1,CAMK2N1,FCGR1A,AGT,PPP1R1B,CCL3,GPNMB,FGR,PLK1,IQGAP3,SFRP2,GDF15,FPR1,PKDCC,HKDC1,NOX4,STIL,APOE,MAPK15,SLC11A1,TPX2,PRKDC,CLSPN,IL6,PGM2L1,LRP8,NEK2,SPHK1,NRK,BUB1,BUB1B,KIF14,C5AR1,FOXK1,CAD,LCP2,STK31,ECT2,EDNRA,CCND2,PKMYT1,CCNF,THBS1,THY1,P2RX7,TREM2,DUSP10,GREM1,CDC6,CDC25B,AJUBA,PIK3R5,EPHA3,EPHB1
GO:0042802	MF	identical protein binding	2.99E-05	7.65E-04	5.78E-03	3.21E-02	76	EPHB2,PIK3AP1,CENPF,HJURP,DGKH,ACTN1,MDFI,MCM10,TRIM29,TRIP13,PGF,FAP,NOD1,FBN1,FCER1G,CCL3,ABCD1,C1QTNF6,ALDH1A3,PLEK,MMP9,PLK1,COL1A1,COL1A2,VIL1,COL7A1,FN1,MTHFD1L,GDF15,OLFML2B,MYOM3,CLDN4,CLDN3,CLDN7,STIL,APOE,AQP1,SLC11A1,STC2,POLQ,MYH10,HTRA1,INHBA,PIEZO1,BCAT1,BCL2A1,PTGS2,CD84,BMP1,SRPX2,APLN,GBP5,PTPRO,DNM1,SDS,NOTCH3,CAD,TYMP,ECT2,OLR1,CLDN2,CLDN1,HEYL,THBS1,HMCN1,P2RX7,ENTPD1,ROBO2,ILDR1,GREM1,PADI2,CDH3,CDH11,TOP2A,CDH13,CDH17
GO:0005524	MF	ATP binding	4.81E-04	9.75E-03	7.37E-02	5.17E-01	56	EPHB2,ABCA1,TRIO,PDGFRB,ATAD5,ABCA13,MCM2,MCM7,DGKH,TRIP13,ADCY3,NOD1,RECQL4,MKI67,ABCD1,FGR,PLK1,RAD54L,KIF23,MTHFD1L,PKDCC,HKDC1,XRCC2,CPS1,ATAD2,MAPK15,CHTF18,PRKDC,KIF18B,POLQ,KIF21B,MYH10,MYO7B,KIF4A,NE

								K2,SPHK1,NRK,BUB1,BUB1B,KIF14,ATP11A,KIF2C,CAD,KIF26B,UBE2C,STK31,ATP10A,PKMYT1,KIF20A,ORC1,P2RX7,ENTPD1,CDC6,TOP2A,EPHA3,EPHB1
GO:0060089	MF	molecular transducer activity	8.94E-04	1.48E-02	1.12E-01	9.61E-01	65	EPHB2,ABCA1,IGSF6,PDGFRB,CLEC7A,F2R,F2RL2,CAMK2N1,FCER1G,FCGR1A,FCGR3A,ANTXR1,CCR1,PLAU,PLK1,PLXNA1,SELE,ITGA11,FPR1,ICAM1,CLDN4,CLDN3,STIL,LGR5,CSF3R,IL2RA,DKK2,ITGAX,ITGB8,LRP8,PXDN,PTPRO,SPHK1,MRC2,C5AR1,STRA6,NOTCH1,NOTCH3,LILRB4,LILRB3,KRT17,GRIN2D,NFAM1,EDNRA,TNFRSF11B,CCND2,PKMYT1,CCNF,GPR161,CELSR3,HMCN1,P2RX7,PLXNC1,SERPINE1,TREM2,TREM1,ROBO2,GREM1,OSMR,LY6E,CDC6,LEF1,GPR176,EPHA3,EPHB1
GO:0016462	MF	pyrophosphatase activity	3.72E-03	4.26E-02	3.22E-01	1.00E+00	52	ABCA1,ATAD5,ABCA13,TRPM2,MCM2,MCM7,CHN1,F2R,TUBB3,RECQL4,CCL3,ABCD1,CCL18,IQGAP3,PLXNA1,RAD54L,KIF23,PLEKHG4,ICAM1,GINS4,XRCC2,ATAD2,CHTF18,KIF18B,POLQ,FGD6,DOCK4,KIF21B,MYH10,MYO7B,KIF4A,ARHGAP11A,GEM,RCC2,GBP5,KIF14,DNM1,KIF2C,RAB31,KIF26B,ARHGAP39,NCAPH,ECT2,RGS1,KIF20A,THY1,PLXNC1,ENTPD1,GNB4,AJUBA,TOP2A,EPHA3

Biological Process(BP), Cellular Component(CC) and Molecular Functions (MF)

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:0007586	BP	digestion	8.97E-20	4.55E-16	4.14E-15	4.55E-16	30	PGA5,PGC,HRH2,ASAH2,APOA1,APOA4,AQP5,SLC26A7,MUC6,CAPN9,CHIA,GHRL,VSIG1,PBLD,SST,PTGER3,AKR1C1,AKR1C2,CAPN8,KCNQ1,PGA3,PGA4,CCKAR,CCKBR,TFF1,TFF2,SLC9A4,GUCA2B,CD36,GKN1
GO:0006082	BP	organic acid metabolic process	1.13E-14	1.91E-11	1.74E-10	5.73E-11	73	HGD,ACADL,GGT6,ESRRB,CYP2S1,TST,ME1,ADH1C,CKB,ADH7,CKM,CKMT2,FBP1,HPGD,PLIN5,SMPD3,ELOVL6,ALDOB,ALDOC,ALDH6A1,ERO1B,FOLR1,HYAL1,UGT1A10

								,ASAH2,FA2H,UGT1A6,LIPF,PM20D1,APOA4,APOC3,SLC9A1,PTGR1,PRKAA2,AKR1C3,CYP4F12,CYB5A,CYP2C19,GALE,CYP2C8,CYP2C9,CYP2C18,CYP3A4,CYP3A5,INSIG1,ACSM1,GCKR,GNMT,AKR1C1,AKR1C2,BHMT,XYLT2,LDHD,ADHFE1,SULT1B1,SULT1C2,SULT2A1,MAMDC2,GLUL,NQO1,ANGPTL3,GPT2,SLC16A9,GPT,B3GNT7,ADTRP,GSTA1,SLC7A8,RGN,CD36,DHRS9,ENTPD5,HAS3
GO:0006629	BP	lipid metabolic process	7.00E-12	4.15E-09	3.78E-08	3.55E-08	75	AADAC,ACADL,CYP2S1,TM6SF2,KLF4,FOXA2,ME1,TTR,ADH1C,ADH7,TFCP2L1,PIK3C2G,LIPH,HPGD,PLIN5,SMPD3,ALDH1A1,ELOVL6,PSAPL1,NR0B2,ANG,CWH43,ASAH2,GDPD3,FA2H,LIPF,PM20D1,APOA1,APOA4,APOBEC1,APOC3,PTGR1,PRKAA2,AKR1C3,PLCXD3,CYP4F12,PRLR,CYB5A,ACER2,CYP2C19,CYP2C8,CYP2C9,CYP2C18,CYP3A4,CYP3A5,INSIG1,ACSM1,GATA6,GDPD2,GC,AKR1C1,AKR1C2,BMP5,SULT1B1,SULT2A1,PTPRN2,DHCR24,AKR1B10,ANGPTL3,SPTSSB,RDH12,ADTRP,LEPR,FAM135B,CCKBR,GSTA1,EEF1A2,RGN,ENHO,CD36,DHRS9,AKR1B15,TM7SF2,B4GALNT2,RORC
GO:0048878	BP	chemical homeostasis	5.50E-10	1.39E-07	1.27E-06	2.79E-06	66	ERBB4,CHGA,TM6SF2,FOXA1,FOXA2,FOXA3,F2RL1,CKB,CCL28,HPN,TMEM38A,SCNN1B,SCNN1G,SMPD3,HOMER2,ATP13A4,ERO1B,FA2H,KLF15,SLC26A9,APOA1,XK,APOA4,APOC3,SCGN,AQP4,MT1E,MT1F,MT1G,MT1H,MT1M,SLC9A1,SLC9A2,MT1X,SLC9A3,SCARA5,PRKAA2,CYP4F12,SLC4A4,ATP4A,ATP4B,GHRL,MYOC,INSIG1,ACSM1,GCKR,PTGER3,AKR1C1,PTPRN2,CXCL17,ANGPTL3,TESC,CA2,CA4,ATP13A5,FAM3B,LEPR,CCKAR,CCKBR,TFR2,SLC7A8,RGN,SLC9A4,OXCT1,CD36,LTF

GO:0055114	BP	oxidation-reduction process	9.89E-10	2.18E-07	1.99E-06	5.01E-06	62	HGD,MAOA,ACADL,ESRRB,CYP2S1,ME1,ADH1C,ADH7,FBP1,HPGD,PLIN5,PDIA2,ALDH1A1,ALDH3A1,ALDOB,ALDOC,ALDH6A1,FMO5,ERO1B,FA2H,LIPF,DUOX2,APOA1,PTGR1,DHRS7,PRKAA2,AKR7A3,AKR1C3,CYP4F12,PRDM16,CYB5A,CYP2C19,GALE,CYP2C8,CYP2C9,CYP2C18,CYP3A4,CYP3A5,ACSM1,GCKR,GNMT,AKR1C1,AKR1C2,LDHD,DUOX1,ADHFE1,DHCR24,AKR1B10,NQO1,SELENBP1,GPX3,RDH12,LEPR,GSTA1,RGN,CD36,DHRS9,ENTPD5,AKR1B15,TM7SF2,MRAP2,HBB
GO:1901135	BP	carbohydrate derivative metabolic process	2.45E-07	3.45E-05	3.14E-04	1.24E-03	58	ESRRB,B3GALT5,FOXA2,GCNT4,FBP1,SMPD3,ALDH1A1,ELOVL6,ALDOB,ALDOC,COL2A1,AMPD1,CWH43,HYAL1,FA2H,APOBEC1,APOC3,SLC9A1,GUCA1C,PRKAA2,FUT9,AKR1C3,B3GAT1,HS6ST3,MUC1,MUC6,ATP4B,ACER2,ST6GALNAC1,GALE,CHIA,ACSM1,FBP2,GCKR,GCNT1,GCNT2,GNMT,AKR1C1,AKR1C2,XYLT2,B3GNT6,LDHD,SULT1B1,SULT1C2,SULT2A1,MAMDC2,APOBEC2,AKR1B10,MUC5B,B3GNT7,GUCA2B,ENTPD5,B4GALNT2,A4GNT,GALNT6,GALNT5,HAS3,PDZD3
GO:0022610	BP	biological adhesion	8.56E-07	9.87E-05	8.99E-04	4.34E-03	63	LGALS9C,CLDN18,COL6A5,FOXA1,KLF4,FOXA2,CCL28,FGA,FGB,IGSF9,FGG,COL4A6,COL17A1,EPB41L4B,HYAL1,ID1,APLP1,APOA1,APOA4,GATA5,AQP4,HAPLN1,ARHGDIG,SLC9A1,IGFALS,IGFBP2,CSTA,SIGLEC11,MUC1,ATP4B,PRLR,CXADR,ACER2,SOX2,LGALS9B,CDHR2,MYOC,AZGP1,NCAM1,GCNT1,GCNT2,PTGER3,CADM2,BMP5,PTPRR,PTPRZ1,ANGPTL3,TESC,UNC5D,AMTN,DPT,RAP1GAP,DSC2,ADTRP,CLDN23,HHLA2,CD36,B4GALNT2,CNTN3,REG3A,LTF,HBB,CDH2
GO:0009719	BP	response to	2.12E-06	2.11E-04	1.92E-03	1.08E-02	71	ERBB4,ESRRB,ESRRG

		endogenous stimulus						,FOXA1,KLF4,ME1,KLF2,SCGB2A1,HPGD,HPN,TMEM38A,FGB,HRH2,SMPD3,ALDH3A1,ALDOB,NR0B2,COL2A1,COL4A6,HTR1E,ANG,FOLR1,HYAL1,SH3GL2,PAQR8,ID1,KLF15,SOSTDC1,APLP1,APOA1,APOBEC1,GATA5,APOC3,SLC5A5,SLC9A1,IGFBP2,PDGFD,PRKAA2,AKR1C3,PRDM16,PRLR,GABRB3,GHRL,GATA6,PBLD,GCNT1,GCNT2,SST,SSTR1,AKR1C1,AKR1C2,BMP5,DHCR24,NQO1,ANGPTL3,KCNQ1,CA2,CA9,RAP1GAP,VSTM2A,ADTRP,LEPR,CCKAR,TFF1,OXCT1,ENHO,CD36,REG3A,RORC,CLEC3B,TMEM100
GO:0046903	BP	secretion	4.23E-06	3.52E-04	3.20E-03	2.15E-02	70	LGALS9C,ERBB4,CHGA,FOXA2,F2RL1,TTR,F13A1,PLAC8,S100P,SERPINA4,FGA,FGB,HRH2,KRT20,SMPD3,FGG,ALDOC,NR0B2,METTL7A,ANG,SLC25A4,MYRIP,APOA1,SLC1A2,AQP5,STX19,SLC26A7,SCG3,RIMS4,SLPI,CYSTM1,RIMS1,SCIN,PRLR,CHIA,GHRL,LGALS9B,SYTL2,NCAM1,PTGER3,PTPRN2,IL1R2,GLUL,KCNQ1,RAB27A,RAB27B,CA2,CA9,TCN1,FAM3B,ADTRP,LEPR,CCKAR,CCKBR,TFF2,TFR2,SYT16,ORM1,ORM2,SLC9A4,OXCT1,ENHO,GUCA2B,SYTL5,CD36,RORC,CLEC3B,LTF,HBB,RAB37
GO:1901700	BP	response to oxygen-containing compound	4.56E-06	3.73E-04	3.40E-03	2.31E-02	70	CLDN18,FOXA1,KLF4,FOXA2,ME1,KLF2,ADH7,HPGD,HRH2,SMPD3,ALDH3A1,ALDOB,HOMER2,NR0B2,COL4A6,HTR1E,FOLR1,HYAL1,ID1,KLF15,DUOX2,APLP1,APOA4,APOBEC1,APOC3,AQP4,SLC1A2,SLC5A5,SLC9A1,IGFBP2,PDGFD,PRKAA2,SLPI,AKR1C3,ATP4B,PRLR,ACER2,SOX2,GHRL,INSIG1,NCAM1,GCKR,GCNT1,SST,SSTR1,PTGER3,AKR1C1,AKR1C2,DUOX1,PTPRN2,AKR1B10,GLUL,NQO1,KCNQ1,TESC,CA2,CA9,GPX3,RDH12,LEPR,TFF1,RGN,

								OXCT1,ENHO,CD36,PALM3,REG3A,RORC,LTF,HBB
GO:0140352	BP	export from cell	3.05E-05	1.64E-03	1.50E-02	1.55E-01	64	LGALS9C,CHGA,FOXA2,F2RL1,TTR,F13A1,PLAC8,S100P,SERPINA4,FGA,FGB,KRT20,SMPD3,FGG,ALDOC,NR0B2,METTL7A,ANG,SLC25A4,MYRIP,APOA1,SLC1A2,STX19,SLC9A1,SCG3,RIMS4,SLPI,CYSTM1,RIMS1,SCIN,ATP4A,ATP4B,CHIA,GHRL,LGALS9B,SYTL2,NCAM1,PTGER3,PTPRN2,IL1R2,GLUL,KCNQ1,RAB27A,RAB27B,KCNE2,TCN1,FAM3B,ADTRP,LEPR,CCKAR,CCKBR,TFR2,SYT16,ORM1,ORM2,OXCT1,ENHO,SYTL5,CD36,RORC,CLEC3B,LTF,HBB,RAB37
GO:0071495	BP	cellular response to endogenous stimulus	8.74E-05	3.59E-03	3.27E-02	4.43E-01	57	ERBB4,ESRRB,ESRRG,FOXA1,KLF4,KLF2,SCGB2A1,HPGD,TMEM38A,FGB,HRH2,SMPD3,NR0B2,COL2A1,COL4A6,HTR1E,FOLR1,HYAL1,SH3GL2,PAQR8,ID1,KLF15,SOSTDC1,APLP1,APOA1,APOBEC1,GATA5,SLC5A5,SLC9A1,IGFBP2,PDGFD,PRKAA2,AKR1C3,PRDM16,PRLR,GABRB3,GHRL,GATA6,PBLD,GCNT2,SST,SSTR1,AKR1C1,AKR1C2,BMP5,KCNQ1,CA2,RAP1GAP,VSTM2A,ADTRP,LEPR,CCKAR,ENHO,CD36,RORC,CLEC3B,TMEM100
GO:0045177	CC	apical part of cell	4.68E-09	2.26E-06	1.53E-05	2.26E-06	33	MAL,PROM2,HPN,UPK1B,SCNN1B,SCNN1G,HOMER2,DUOXA2,PAPPA2,EPB41L4B,FOLR1,MYRIP,SLC26A9,DUOX2,AQP5,SLC9A1,SLC9A3,IGFBP2,PRKAA2,CYP4F12,MUC1,ATP4A,CDHR2,DUOX1,RAB27A,RAB27B,CA2,CA4,AQP10,SLC9A4,CD36,PDZD3,CDH2
GO:0031012	CC	extracellular matrix	1.96E-07	2.37E-05	1.60E-04	9.49E-05	35	COL6A5,F13A1,FGA,FGB,FGG,COL2A1,COL4A6,ANG,COL17A1,APLP1,APOA1,APOA4,APOC3,HAPLN1,IGFALS,SLPI,MUC1,MUC6,MYOC,AZGP1,NCAM1,PTPRZ1,MAMDC2,SEMA3B,ADAMTS15,AMTN,DPT,ADAMTSL1,ENAM,ORM1,ORM2,CCBE1,CLEC3B,CDH2

								,SERPINA5
GO:0031226	CC	intrinsic component of plasma membrane	3.99E-06	3.21E-04	2.17E-03	1.93E-03	65	ERBB4,VSIG2,F2RL1,CLCNKA,PROM2,HPN,UPK1B,KIAA1324,SCNN1B,SCNN1G,HRH2,FXYD3,SHISA6,HTR1E,COL17A1,SLC25A4,FOLR1,ASAH2,SLC26A9,DUOX2,AQP4,SLC1A2,AQP5,SLC9A1,SLC15A1,SLC26A7,SCARA5,SLC4A4,MUC1,SLC2A12,ATP4A,ATP4B,CXADR,GABRB3,PRSS8,CDHR2,NCAM1,GPRC5C,SSTR1,PTGER3,DUOX1,PTPRN2,PTPRZ1,KCNJ15,KCNJ16,SEMA3B,KCNQ1,ENPP5,C6,CA4,KCNE2,AQP10,SLC16A9,GRIA4,LEPR,PRIMA1,CCKAR,TSPAN1,TFR2,SLC7A8,LIFR,CD36,SLC28A2,TM7SF2,TMPRSS2,HAS3,CDH2,SLC16A7,PTGDR2
GO:0009986	CC	cell surface	2.47E-04	9.93E-03	6.71E-02	1.19E-01	41	BTNL8,PROM2,HPN,SCNN1B,FGA,SCNN1G,FGB,FGG,FOLR1,SLC26A9,DUOX2,APOA1,APOA4,AQP4,SLC1A2,SLC9A1,SLC9A3,SCUBE2,SCARA5,SIGLEC11,MUC1,PRLR,AZGP1,NCAM1,PTGER3,DUOX1,ANGPTL3,ADAMTS15,UNC5D,CA4,KCNE2,ADTRP,LEPR,TFR2,LIFR,HHLA2,CD36,RORC,LTF,CDH2,SERPINA5
GO:0099503	CC	secretory vesicle	9.58E-04	2.01E-02	1.36E-01	4.63E-01	40	CHGA,CHGB,TTR,F13A1,PLAC8,S100P,SERPINA4,FGA,FGB,FGG,ALDOC,METTL7A,SH3GL2,MYRIP,APOA1,STX19,SCG3,SLPI,CYSTM1,CXADR,GHRL,KIF1A,SYTL2,PTPRN2,KCNQ1,RAB27A,RAB27B,CA4,KLK11,TCN1,ORM1,ORM2,SYTL5,CD36,CLEC3B,LTF,GKN1,HBB,RAB37,SERPINA5
GO:0005789	CC	endoplasmic reticulum membrane	1.17E-02	1.30E-01	8.77E-01	1.00E+00	36	AADAC,TMED6,ANO5,CYP2S1,TM6SF2,HPN,TMEM38A,ELOVL6,ALDOB,FXYD3,DUOXA2,ATP13A4,FMO5,ERO1B,FOLR1,UGT1A10,GDPD3,FA2H,UGT1A6,SLC9A1,B3GAT1,CYP4F12,CYB5A,CYP2C19,CYP2C8,CYP2C9,CYP2C18,CYP3A4,CYP3A5,INSIG1,DHCR24,SPTSSB,RDH12,DHRS9,TM7SF2,MRAP2

GO:0005794	CC	Golgi apparatus	2.04E-02			1.00E+00	49	MAL,TMED6,B3GALT5,GCNT4,F2RL1,PIK3C2G,KIAA1324,SMPD3,FOLR1,ASAH2,SH3GL2,PAQR8,ID1,CXCL14,APLP1,PDGFD,PRKAA2,FUT9,B3GAT1,MUC1,MUC6,ACER2,ST6GALNAC1,MYOC,INSIG1,NCAM1,GCNT1,GCNT2,CAPN8,XYLT2,B3GNT6,DEFB1,DHCR24,ANGPTL3,B4GALNT3,RAB27A,RAB27B,CA4,KLK11,KCNE2,RAP1GAP,GKN2,MUC5B,B3GNT7,CD36,B4GALNT2,A4GNT,GALNT6,GALNT5
GO:0030054	CC	cell junction	2.44E-01	5.70E-01	1.00E+00	1.00E+00	34	CLDN18,FOXA2,HPN,IGSF9,HOMER2,SHISA6,COL17A1,EPB41L4B,DUOX2,MYZAP,AQP4,SLC9A1,RIMS4,ANO7,RIMS1,SCIN,CXADR,GABRB3,CDHR2,NCAM1,FBP2,CADM2,PTPRN2,PTPRR,AMTN,DSC2,GRIA4,CLDN23,PRIMA1,TSPAN1,CGNL1,PDZD3,CDH2,C4orf19
GO:0045202	CC	synapse	2.46E-01	5.70E-01	1.00E+00	1.00E+00	37	ERBB4,FGA,FGB,IGSF9,FGG,ALDOC,HOMER2,SHISA6,SH3GL2,MYRIP,APOA4,BCAS1,SCGN,SLC1A2,HAPLN1,STX19,RIMS4,PLCXD3,RIMS1,CXADR,GABRB3,LYPD6B,GHRL,KIF1A,NCAM1,CADM2,ITPKA,PTPRN2,PTPRZ1,GLUL,RAB27B,GRIA4,PRIMA1,CCKAR,EEF1A2,CDH2,SLC16A7
GO:0043005	CC	neuron projection	2.63E-01	5.93E-01	1.00E+00	1.00E+00	40	CKB,HRH2,IGSF9,ALDOC,MLPH,HOMER2,SHISA6,HTR1E,ANG,SH3GL2,MYRIP,IRX3,SCGN,SLC1A2,GUCA1C,PRKAA2,CXADR,GABRB3,GHRL,KIF1A,MYOC,DNER,NCAM1,GC,PTGER3,CADM2,ITPKA,PTPRN2,PTPRZ1,GLUL,NQO1,RAB27A,RAB27B,CA2,RAP1GAP,GRIA4,CCKAR,GUCA2B,CDH2,SLC16A7
GO:0098805	CC	whole membrane	5.91E-01	8.62E-01	1.00E+00	1.00E+00	38	ERBB4,MAL,MAOA,FNDC5,CHGA,PROM2,KIAA1324,SLC25A4,FOLR1,ASAH2,SH3GL2,MYRIP,SCGN,AQP4,SLC9A1,SLC26A7,SCG3,CYSTM1,CXADR,CYB5A,PRSS8,MYOC,PTPRN2,PXMP2,KCNQ1,

								RAB27A,RAB27B,CA4,REP15,GRIA4,ADTRP,TSPAN1,EEF1A2,PLLP,CD36,RAB37,CDH2,SERPINA5
GO:0016491	MF	oxidoreductase activity	1.21E-09	1.33E-06	1.01E-05	1.33E-06	54	HGD,MAOA,ACADL,ESRRB,CYP2S1,ME1,ADH1C,ADH7,FBP1,HPGD,PDIA2,ALDH1A1,ALDH3A1,ALDOB,ALDOC,ALDH6A1,FMO5,ERO1B,FA2H,LIPF,DUOX2,PTGR1,DHRS7,PRKAA2,AKR7A3,AKR1C3,CYP4F12,CYB5A,CYP2C19,GALE,CYP2C8,CYP2C9,CYP2C18,CYP3A4,CYP3A5,GCKR,AKR1C1,AKR1C2,LDHD,DUOX1,ADHFE1,DHCR24,AKR1B10,NQO1,SELENBP1,GPX3,RDH12,GSTA1,RGN,DHRS9,ENTPD5,AKR1B15,TM7SF2,HBB
GO:0046914	MF	transition metal ion binding	2.54E-04	6.18E-03	4.68E-02	2.78E-01	44	ESRRB,ESRRG,CYP2S1,KLF4,ME1,ADH1C,ADH7,S100P,PAPPA2,ANG,ASAH2,FA2H,MYRIP,APLP1,CPA2,APOA4,APOBEC1,GATA5,MT1E,MT1F,MT1G,MT1H,MT1M,MT1X,CYP4F12,CYP2C19,CYP2C8,CYP2C9,CYP2C18,CYP3A4,CYP3A5,GATA6,ZNF385B,BHMT,XYLT2,GLUL,ADAMTS15,TRIM50,CA2,CA4,CA9,RGN,RORC,LTF
GO:0015318	MF	inorganic molecular entity transmembrane transporter activity	4.77E-04	9.94E-03	7.53E-02	5.23E-01	42	ANO5,CLCNKA,HPN,TMEM38A,SCNN1B,SCNN1G,FXYD3,SHISA6,ATP13A4,SLC26A9,AQP4,SLC1A2,AQP5,SLC5A5,SLC9A1,SLC9A2,SLC9A3,SLC15A1,SLC26A7,ANO7,SLC4A4,SLC2A12,ATP4A,ATP4B,CYB5A,GABRB3,PRSS8,KCNJ15,KCNJ16,KCNQ1,TESC,KCNE2,AQP10,SLC16A9,GRIA4,CLIC6,SGK2,SLC7A8,RGN,SLC9A4,SLC28A2,SLC16A7
GO:0042802	MF	identical protein binding	3.57E-03	3.66E-02	2.77E-01	1.00E+00	63	CLDN18,HGD,ERBB4,TTR,C16orf89,ADH7,S100P,FBP1,CLCNKA,HPGD,PLIN5,FGG,ALDOB,HOMER2,NR0B2,COL2A1,ANG,UGT1A10,UGT1A6,SH3GL2,ID1,APLP1,APOA1,APOA4,BCAS1,AQP4,AQP5,SCUBE2,AKR7A3,RASEF,DMRTA1,SLC4A4,CTSE,PRLR,CXADR,GABRB3,GALE,KIF1A,NCAM1,PBLD,FBP2,G

								NMT,DEFB1,APOBEC2,GLUL,NQO1,KCNQ1,TESC,TRIM50,KCNE2,RAP1GAP,VSTM2A,GRIA4,CLIC6,CLDN23,LEPR,SYT16,OXCT1,REG3A,HAS3,MRAP2,CDH2,TPD52L1
GO:0098772	MF	molecular function regulator	7.21E-03	5.85E-02	4.43E-01	1.00E+00	59	MAL,FNDC5,CHGB,KLF4,TTR,MTRNR2L2,ADH7,SERPINA4,CCL28,ALDH1A1,ARHGEF37,FXYD3,CXCL14,APOA1,APOA4,APOBEC1,DUSP19,APOC3,ARHGDIG,GUCA1C,RANBP3L,SLC15A1,PDGFD,SLPI,PKIB,CSTA,RIMS1,ATP4B,PRLR,SERPINB7,LYPD6B,PRSS8,GHRL,NRG4,GPRC5C,EPS8L1,GCKR,SST,SPINK13,MTRNR2L8,BMP5,CXCL17,SEMA3B,ANGPTL3,TESC,KCNE2,RAP1GAP,FAM3B,CCKBR,TFF1,SGK2,RGN,ENHO,GUCA2B,LTF,GKN1,MRAP2,PDZD3,SERPINA5
GO:0005102	MF	signaling receptor binding	9.67E-03	6.92E-02	5.25E-01	1.00E+00	56	ERBB4,BTNL8,FNDC5,CHGB,F2RL1,TTR,MTRNR2L2,ADH7,S100P,CCL28,EDARADD,FGA,FGB,FGG,HOMER2,NR0B2,SHISA6,COL2A1,ANG,CXCL14,APLP1,APOA1,APOC3,IGFALS,IGFBP2,PDGFD,OASL,CXADR,GHRL,NRG4,MYOC,SYTL2,DNER,GPRC5C,EPS8L1,SST,MTRNR2L8,DEFB1,BMP5,PTPRZ1,CXCL17,SEMA3B,ANGPTL3,PSCA,FAM3B,CLIC6,CCKBR,TFF1,TFF2,EEF1A2,LIFR,HHLA2,ENHO,CD36,GKN1,MRAP2
GO:0008324	MF	cationtransmembrane transporter activity	2.05E-02	1.08E-01	8.17E-01	1.00E+00	30	HPN,TMEM38A,SCNN1B,SCNN1G,FXYD3,SHISA6,ATP13A4,SLC1A2,SLC5A5,SLC9A1,SLC9A2,SLC9A3,SLC15A1,SLC4A4,SLC2A12,ATP4A,ATP4B,CYB5A,PRSS8,KCNJ15,KCNJ16,KCNQ1,TESC,KCNE2,GRIA4,SGK2,SLC7A8,RGN,SLC9A4,SLC28A2
GO:0030234	MF	enzyme regulator activity	7.96E-02	2.26E-01	1.00E+00	1.00E+00	32	MAL,KLF4,SERPINA4,ALDH1A1,APOA1,APOA4,APOBEC1,DUSP19,APOC3,ARHGDIG,GUCA1C,RANBP3L,SLPI,PKIB,CSTA,RIMS1,ATP4B,PRLR,SERPINB7,GHRL,GPRC5C,GCK

								R,SPINK13,ANGPTL3,TESC,RAP1GAP,CCKBR,RGN,GUCA2B,LTF,PDZD3,SERPINA5
GO:0008233	MF	peptidase activity	2.54E-01	4.22E-01	1.00E+00	1.00E+00	33	MAL,GGT6,KLF4,PGA5,PGC,CAPN13,SERPINA4,HPN,KIAA1324,PAPPA2,PM20D1,CPA2,SLPI,CSTA,CTSE,ACER2,CAPN9,SOX2,SERPINB7,PRSS8,ADAM28,SPINK13,CAPN8,RHBDL2,DHCR24,ADAMTS15,PGA3,KLK11,PGA4,ADAMTSL1,TMPRSS2,LTF,SERPINA5
GO:0016301	MF	kinase activity	5.59E-01	6.99E-01	1.00E+00	1.00E+00	36	ERBB4,ESRRB,STYK1,KLF4,FOXA2,CKB,CKM,CKMT2,FBP1,PIK3C2G,ALDH1A1,ALDOB,ALDOC,ANG,SOSTDC1,DUSP19,PDGFD,PRKAA2,PKIB,PRLR,GALE,GHRL,GPRC5C,GCKR,ITPKA,CXCL17,RPS6KA6,TESC,RIPK4,CCKBR,EEF1A2,SGK2,RGN,ENTPD5,LTF,TPD52L1

Biological Process(BP), Cellular Component(CC) and Molecular Functions (MF)

Table 7 Topology table for up and down regulated genes

Regulation	Node	Degree	Betweenness	Stress	Closeness	Clustering Coefficient
Down	SOX2	361	0.130645	91698482	0.314504	3.13E-05
Down	RIPK4	336	0.128603	98813078	0.314446	0
Down	FOXA1	290	0.103625	62359854	0.309195	3.87E-04
Down	EEF1A2	192	0.092037	39507690	0.326061	7.09E-04
Down	ANG	126	0.033985	31690134	0.29174	0
Down	FGB	119	0.043651	12625862	0.307262	0.004558
Down	PTGER3	113	0.038772	17588946	0.28297	3.16E-04
Down	CKB	111	0.036348	17987186	0.29959	0.002502
Down	FOXQ1	108	0.024413	25595054	0.265424	0
Down	ERBB4	101	0.039648	13011632	0.303684	0.00268
Down	PRKAA2	100	0.028743	15759608	0.279198	0
Down	APOA1	100	0.036853	10368028	0.293786	0.00451
Down	ESRRB	98	0.036893	21650562	0.308952	0.001052
Down	OXCT1	97	0.02688	16657230	0.275526	0
Down	ATP4A	92	0.038284	7433528	0.297688	2.50E-04
Down	F2RL1	90	0.02916	16825260	0.263862	0

Down	EYA2	88	0.023357	20081684	0.264175	0
Down	CDH2	83	0.025141	12416288	0.280608	0.001469
Down	SH3GL2	81	0.028376	10624252	0.281334	3.25E-04
Down	DUSP19	78	0.022667	8084684	0.289509	0.001053
Down	FAM189A2	78	0.023811	11453482	0.276839	9.99E-04
Down	ALDOC	75	0.024085	9254824	0.292324	0.004685
Down	SLC25A4	74	0.020138	14876712	0.282704	0
Down	HBB	72	0.024297	9837400	0.292358	0
Down	SELENBP1	69	0.020559	16033854	0.263576	0
Down	TTR	65	0.019611	8877534	0.281971	0.004608
Down	NR0B2	65	0.018911	9601392	0.285754	4.81E-04
Down	SLC15A1	65	0.022335	9413034	0.259481	0
Down	MRAP2	64	0.018209	14317820	0.246694	0
Down	APLP1	61	0.016887	7157580	0.275734	5.84E-04
Down	MIA2	61	0.023593	3857116	0.292911	0.003507
Down	MUC1	59	0.01901	8685324	0.297272	0.004386
Down	TMEM171	57	0.015929	7178790	0.265162	0
Down	VSIG1	57	0.015506	9968024	0.251724	0
Down	SLC2A12	56	0.014848	11274816	0.245344	0
Down	KIF1A	55	0.014262	10095312	0.273082	0
Down	LIPH	54	0.014461	5415600	0.258432	0
Down	FOXA3	53	0.011677	3197724	0.277576	0.007059
Down	FBP1	52	0.011778	5755732	0.259718	0.007347
Down	ID1	51	0.014356	8073662	0.260049	0
Down	GLUL	51	0.014074	7290628	0.273901	0
Down	LTF	51	0.015012	8074792	0.27279	0.001569
Down	SUSD4	50	0.014117	8153740	0.252171	0
Down	MYOC	49	0.012703	5520884	0.273784	0
Down	COL2A1	48	0.014506	2615324	0.251625	0
Down	CSTA	47	0.009908	5708660	0.266226	0
Down	PTPRR	46	0.012338	3050164	0.277425	0.008457
Down	ESRRG	46	0.01155	4874608	0.278438	0.001057
Down	SLC9A1	45	0.021666	3586826	0.290993	0.008081
Down	RORC	45	0.010968	7194834	0.26283	0
Down	FRMD1	45	0.01312	1673830	0.264627	0.005051
Down	NCAM1	44	0.011569	4653244	0.264476	0
Down	DHRS7	43	0.013463	2866004	0.265479	0.001107
Down	IL1R2	42	0.011437	5905866	0.234503	0
Down	CHGB	42	0.010047	5822946	0.266963	0
Down	BTNL8	42	0.011912	2086382	0.241256	0
Down	FBXL13	42	0.012583	5749328	0.240111	0
Down	FGA	41	0.010321	3281616	0.289247	0.062078
Down	SERPINA5	41	0.012219	1908132	0.278756	0.008097

Down	LDHD	40	0.011361	9207334	0.235747	0
Down	FGG	38	0.007185	2451080	0.281195	0.049206
Down	RPS6KA6	37	0.01036	3621900	0.266684	0.004505
Down	CYP2S1	37	0.009679	1915748	0.257936	0
Down	KLF4	36	0.008725	6243510	0.274829	0
Down	CA9	36	0.00838	3853714	0.278574	0
Down	DHCR24	36	0.006868	4428340	0.272965	0
Down	GALE	35	0.008601	4052878	0.272805	0
Down	GPRC5C	35	0.012273	2377340	0.271515	0.003361
Down	NQO1	34	0.008383	5150060	0.274136	0
Down	EPN3	34	0.010642	6541196	0.240269	0
Down	TMED6	34	0.008373	4030958	0.222818	0
Down	RAB27A	33	0.0091	2404172	0.26859	0.007576
Down	KRT20	33	0.007564	4522038	0.244323	0
Down	ALDOB	33	0.007577	5415906	0.25628	0
Down	AZGP1	33	0.007325	4722950	0.260102	0
Down	CYB5A	32	0.014497	2040568	0.281009	0.002016
Down	PTPRN2	32	0.006444	5188802	0.24512	0
Down	ME1	32	0.007918	3585304	0.249439	0
Down	LEPR	31	0.008148	2585854	0.250184	0
Down	S100P	31	0.00819	3141854	0.261794	0
Down	MAP7D2	31	0.006379	3776744	0.240393	0
Down	RIMS1	29	0.006836	2005214	0.262183	0.004926
Down	CD36	29	0.006605	3244170	0.25791	0
Down	VSIG2	29	0.005085	4523118	0.229594	0
Down	CKM	28	0.006486	1114366	0.26363	0.015385
Down	PTPRZ1	27	0.004562	2671328	0.243834	0
Down	PDIA2	27	0.011946	3842958	0.264791	0
Down	UGT1A10	27	0.00529	2201280	0.236884	0.02
Down	CMBL	27	0.005343	4698256	0.254001	0
Down	LGALS9C	27	0.006007	2789528	0.231267	0
Down	KLK11	27	0.005922	3556426	0.237026	0
Down	TFF1	26	0.00922	4457048	0.252932	0
Down	INSIG1	26	0.005325	1743502	0.245875	0
Down	RDH12	26	0.005489	2827404	0.239964	0
Down	GALNT6	26	0.009106	2128734	0.260779	0
Down	TPD52L1	25	0.004331	1988644	0.25113	0
Down	GC	25	0.00488	2756190	0.254786	0
Down	FOXA2	25	0.00442	692924	0.26162	0.027668
Down	RAP1GAP	25	0.005317	2730984	0.248493	0
Down	XYLT2	25	0.005125	3604190	0.230953	0
Down	PRLR	24	0.004513	2639920	0.241758	0
Down	SCNN1B	24	0.003266	1693310	0.233134	0.051948

Down	GNMT	24	0.003761	2292130	0.242538	0
Down	CA2	23	0.005398	1512836	0.267312	0
Down	CCKBR	23	0.004282	3289826	0.231162	0.009524
Down	DSC2	23	0.002627	1332696	0.243057	0
Down	SMPD3	23	0.00407	1526270	0.243462	0
Down	SOWAHA	23	0.005986	3656274	0.222304	0
Down	FBP2	22	0.00357	1236294	0.256075	0.047368
Down	SCGN	22	0.005448	2292384	0.224363	0
Down	CXADR	22	0.004966	1542936	0.256602	0
Down	SCGB2A1	22	0.00411	1974286	0.247626	0
Down	ALDH6A1	22	0.005212	3402338	0.242492	0
Down	PDGFD	22	0.004274	2794740	0.226934	0
Down	LIFR	21	0.004499	3194270	0.242423	0
Down	KCNQ1	21	0.004852	1329562	0.26667	0.005848
Down	PXMP2	21	0.009681	2045510	0.253585	0
Down	SCIN	21	0.004409	3432750	0.257481	0
Down	ALDH3A1	21	0.006292	975432	0.247662	0.011696
Down	STX19	20	0.005007	1935164	0.20909	0
Down	TCEAL2	20	0.003844	2368446	0.256576	0
Down	A4GNT	20	0.004387	1662140	0.225542	0
Down	CHIA	20	0.005062	3754078	0.241449	0
Down	GCNT1	20	0.004201	1845148	0.224926	0
Down	SCNN1G	19	0.001794	974542	0.233838	0.088235
Down	POU2AF1	19	0.005426	1886150	0.231267	0
Down	CLEC3B	19	0.003446	686120	0.253824	0.014706
Down	SGK2	19	0.003011	2291524	0.255806	0
Down	COL4A6	19	0.004108	2503680	0.231257	0
Down	GRIA4	18	0.004013	2094936	0.235172	0
Down	RAB27B	18	0.003176	889536	0.249147	0.013072
Down	F13A1	18	0.003111	636426	0.267886	0.05
Down	SYT16	18	0.003942	610066	0.237224	0
Down	GPT2	18	0.004219	2205028	0.24423	0
Down	CKMT2	18	0.003008	650282	0.255486	0.025
Down	ORM1	17	0.003066	2394818	0.233881	0.007353
Down	PDZD3	17	0.005754	836546	0.221188	0
Down	SPDEF	17	0.00438	1902948	0.247842	0
Down	SERPINA4	17	0.003389	1618954	0.242055	0
Down	CYP3A4	17	0.00331	1029374	0.24409	0.028571
Down	HOMER2	17	0.004213	2318450	0.2334	0
Down	GSTA1	17	0.003515	1770658	0.250711	0.038095
Down	CYP2C8	17	0.002329	1066708	0.23901	0
Down	MAL	17	0.003795	1666176	0.240382	0
Down	BPIFB1	17	0.002977	2398972	0.246159	0

Down	COL17A1	16	0.002553	1165170	0.246408	0
Down	EDARADD	16	0.002099	1184864	0.233166	0
Down	CYP2C9	16	0.002334	475378	0.234117	0.025
Down	EPB41L4B	16	0.003783	1719180	0.243196	0
Down	MUC5B	16	0.003656	1742484	0.254748	0.008333
Down	CGNL1	16	0.00242	1294404	0.24865	0
Down	AKR1C2	15	0.002609	727192	0.228844	0.025641
Down	SLPI	15	0.003639	1592814	0.245167	0
Down	AKR1B10	15	0.002313	855778	0.229543	0.009524
Down	TRIM50	15	0.003357	1937636	0.213465	0
Down	TST	15	0.002387	1686500	0.230797	0
Down	KLF15	15	0.002427	1312738	0.225164	0
Down	GABRB3	14	0.00218	943302	0.225941	0
Down	C6	14	0.002538	1748954	0.244323	0
Down	ASB11	14	0.002102	1319614	0.231351	0
Down	TMEM92	14	0.002742	768258	0.256538	0
Down	PTGR1	14	0.002181	1002112	0.221543	0
Down	CTSE	14	0.002273	897066	0.223471	0
Down	SYTL2	13	0.002043	537190	0.247338	0
Down	ARHGDIG	13	0.003657	1180020	0.219998	0
Down	SLC9A3	13	0.001716	783146	0.222324	0
Down	SULT1C2	13	0.002072	1077230	0.2131	0
Down	SLC1A2	13	0.001883	1174276	0.230433	0
Down	PBLD	13	0.002864	1604148	0.221707	0
Down	DEFB1	13	0.002672	969434	0.214874	0
Down	PLLP	13	0.002953	1704122	0.210528	0
Down	BHMT	12	0.001444	462034	0.200078	0
Down	GATA6	12	0.001888	766242	0.227925	0.015152
Down	SERPINB7	12	0.001574	903854	0.221697	0
Down	CHGA	12	0.002669	892042	0.237953	0
Down	SLC5A5	12	0.001844	1189896	0.214487	0
Down	CAPN13	12	0.002512	1267060	0.214649	0
Down	AKR7A3	11	0.002079	1092290	0.218905	0
Down	EPS8L1	11	0.00158	1034458	0.227337	0
Down	TFR2	11	0.002136	335802	0.241712	0
Down	KLF2	11	0.001827	864958	0.229162	0.036364
Down	SLC9A2	11	0.001361	674648	0.231749	0
Down	MAOA	11	0.001393	577172	0.229615	0
Down	AKR1C3	11	0.002239	398010	0.2158	0.054545
Down	REG3A	11	0.001394	775802	0.230807	0
Down	GHRL	11	0.003071	422262	0.230714	0
Down	DHRS9	11	0.002519	888628	0.20417	0
Down	AKR1B15	11	0.001364	380620	0.232964	0.018182

Down	SEMA3B	11	0.001852	912096	0.223676	0
Down	CYSTM1	11	0.002071	692870	0.215718	0
Down	AMTN	11	0.001781	621822	0.219159	0
Down	GKN1	11	8.02E-04	226994	0.217972	0
Down	AMPD1	11	8.02E-04	705838	0.229502	0
Down	MLPH	10	0.001483	571000	0.262331	0.088889
Down	TESC	10	0.001621	186720	0.23063	0.071429
Down	APOBEC1	10	0.002094	841430	0.200196	0
Down	AKR1C1	10	0.001725	316338	0.225492	0.071429
Down	RPRM	10	0.001932	971234	0.229646	0
Down	AQP5	10	0.001026	462940	0.220787	0
Down	GCNT2	10	0.002683	1431378	0.220463	0
Down	LIPF	10	0.002681	291688	0.235097	0
Down	ENTPD5	10	0.001423	576438	0.221966	0
Down	CYP2C18	10	0.00151	590472	0.218699	0.022222
Down	XK	10	0.00259	915288	0.211688	0
Down	UGT1A6	10	3.51E-04	63358	0.212075	0.25
Down	FOLR1	10	0.001826	786520	0.229811	0
Down	RASSF6	9	0.001679	758932	0.222314	0
Down	SLC4A4	9	8.25E-04	147548	0.228547	0
Down	HAPLN1	9	0.002127	937726	0.221514	0
Down	ALDH1A1	9	0.001071	502514	0.230225	0
Down	PAIP2B	9	0.001898	820018	0.212031	0
Down	FNDC5	9	0.00116	227236	0.234805	0
Down	OASL	9	0.001035	554244	0.235704	0
Down	CYP3A5	9	0.001621	242422	0.236227	0
Down	SCG3	9	0.00171	397816	0.234751	0
Down	ANGPTL3	9	0.001408	534524	0.201355	0
Down	CXCL14	9	0.001418	687382	0.225194	0
Down	FAM3B	9	0.002213	335698	0.2483	0
Down	RNASE1	8	8.75E-04	328862	0.22215	0
Down	BCAS1	8	7.11E-04	423002	0.24225	0
Down	HGD	8	0.001216	788412	0.213572	0
Down	C4orf19	8	0.001639	223746	0.256512	0.071429
Down	MYRIP	8	0.001238	430996	0.249634	0
Down	CIDEC	8	0.001237	380180	0.208885	0
Down	CA4	8	6.78E-04	175498	0.219715	0
Down	AQP4	8	7.48E-04	268154	0.211916	0
Down	IGFBP2	8	0.00149	766678	0.221294	0
Down	HTR1E	8	9.77E-04	621360	0.233262	0
Down	SULT2A1	8	7.70E-04	247322	0.211732	0
Down	C1orf116	8	7.46E-04	480606	0.241187	0
Down	FXYD3	8	0.001716	698152	0.219658	0

Down	TMEM38A	8	0.001989	673836	0.209975	0
Down	FUT9	8	0.001439	449312	0.206055	0
Down	FCGBP	8	5.65E-04	331640	0.230287	0
Down	PRDM16	8	6.15E-04	224982	0.23176	0
Down	ITPKA	8	6.95E-04	310188	0.215991	0
Down	BMP5	8	0.001564	204476	0.24629	0
Down	RGN	8	2.20E-04	146076	0.221064	0
Down	SOSTDC1	7	0.001188	367662	0.180492	0
Down	APOA4	7	4.08E-04	165970	0.21402	0
Down	ZBTB7C	7	0.001031	422450	0.227905	0
Down	METTL7A	7	4.95E-04	194766	0.227601	0
Down	ACADL	7	0.001679	791198	0.227946	0
Down	CYP4F12	7	9.87E-04	279876	0.220311	0
Down	PKIB	7	0.001587	460738	0.199914	0
Down	CCBE1	7	0.002002	326496	0.19495	0
Down	TFCP2L1	7	4.28E-04	250206	0.20633	0
Down	PALM3	7	0.00104	644144	0.248638	0
Down	HYAL1	7	0.002205	417022	0.238754	0
Down	ADAMTSL1	7	9.43E-04	207474	0.199906	0
Down	SYTL5	6	0.001222	233628	0.223393	0
Down	GSTA2	6	8.20E-04	333722	0.204948	0.133333
Down	DPT	6	4.89E-04	261260	0.232265	0
Down	MT1X	6	3.73E-04	229168	0.229285	0
Down	BEX5	6	7.89E-04	108852	0.200715	0
Down	ATP4B	6	0.002043	235970	0.235878	0
Down	PLIN5	6	0.001333	771154	0.195629	0
Down	CCL28	6	0.001575	487862	0.211872	0
Down	UPK1B	6	0.001572	934520	0.192781	0
Down	MAMDC2	6	0.001576	318360	0.213296	0
Down	SIGLEC11	6	5.99E-04	207770	0.228088	0
Down	PLAC8	6	3.02E-04	225896	0.228527	0
Down	RAB37	6	7.07E-04	123228	0.228967	0
Down	LGALS9B	6	3.47E-04	189584	0.218307	0
Down	ARL14	6	0.001956	1716690	0.182771	0
Down	SH3BGRL2	6	0.001142	565738	0.239863	0
Down	SST	6	0.002571	944178	0.209665	0.066667
Down	SLC16A7	6	0.00134	493152	0.193116	0
Down	FA2H	6	6.44E-04	190132	0.205889	0
Down	CPA2	6	8.69E-04	220104	0.204187	0
Down	DNER	6	5.68E-04	364110	0.227075	0
Down	GDPD3	6	2.89E-04	143022	0.209949	0
Down	KCNJ15	5	0.001063	395016	0.212383	0
Down	GCKR	5	8.07E-04	358596	0.212613	0

Down	HAS3	5	7.83E-04	180102	0.170839	0
Down	IGFALS	5	8.48E-04	200704	0.198178	0
Down	CCKAR	5	4.00E-08	2	0.18778	0.666667
Down	TFF2	5	4.28E-04	128148	0.208808	0
Down	SSTR1	5	8.16E-04	303142	0.175286	0.1
Down	GPX3	5	7.83E-04	182594	0.193995	0
Down	ORM2	5	1.57E-04	35318	0.220692	0.1
Down	APOC3	5	4.14E-04	47088	0.233667	0.2
Down	DDX60	5	8.81E-04	460534	0.218307	0
Down	HPN	5	7.26E-04	310120	0.230194	0
Down	GPT	5	8.29E-04	291602	0.206714	0
Down	ODAM	5	8.57E-04	403252	0.23236	0
Down	PAPPA2	5	8.40E-04	242380	0.196994	0
Down	FMO5	5	8.78E-04	467960	0.215254	0
Down	SLC16A9	5	8.61E-04	269782	0.220074	0
Down	TMEM220	5	5.22E-04	290922	0.220854	0
Down	GDPD2	5	0.001271	445450	0.207015	0
Down	VILL	5	8.06E-04	419916	0.21569	0
Down	ADH7	4	5.91E-05	29910	0.214631	0
Down	CLIC6	4	8.08E-04	292454	0.186417	0
Down	GALNT5	4	4.33E-04	155130	0.204366	0
Down	KCNJ16	4	8.03E-04	105342	0.195794	0
Down	CDHR2	4	0.001174	433218	0.180696	0
Down	KCNE2	4	5.03E-04	75192	0.235954	0.166667
Down	SULT1B1	4	4.79E-04	89616	0.204735	0
Down	VSTM2A	4	7.96E-04	681826	0.169553	0
Down	RASEF	4	6.42E-04	174228	0.220463	0
Down	GSTA3	4	5.10E-04	346118	0.238809	0.5
Down	ADH1C	4	1	2	1	0
Down	RIMS4	4	4.34E-04	216850	0.21482	0
Down	PGC	4	3.15E-04	58062	0.251142	0
Down	ENAM	4	1.68E-04	93264	0.210815	0
Down	FSIP2	4	8.09E-04	202852	0.206338	0
Down	SNORD22	4	3.76E-05	31698	0.209613	0
Down	TM7SF2	4	4.65E-04	146028	0.214496	0
Down	DMRTA1	4	9.92E-05	71054	0.21855	0
Down	SCUBE2	4	3.91E-04	94424	0.187498	0
Down	TMPRSS2	4	2.21E-05	4940	0.217944	0
Down	SCARA5	4	5.52E-04	205628	0.215645	0
Down	TMEM100	4	4.80E-04	116462	0.203253	0
Down	PTGDR2	4	1	12	1	0
Down	CAPN8	4	4.14E-04	137042	0.200597	0
Down	ZNF385B	4	7.92E-04	439412	0.235313	0

Down	RANBP3L	4	8.11E-04	270746	0.209966	0
Down	C6orf58	4	4.97E-04	152308	0.220055	0
Down	PLIN4	4	4.89E-05	42320	0.220444	0
Down	ACSM1	4	7.89E-04	357944	0.177842	0
Down	SLC7A8	3	7.83E-04	207170	0.191667	0
Down	CLCNKA	3	0	0	0.18787	0
Down	DUOX1	3	4.09E-04	206852	0.179214	0
Down	APOBEC2	3	0	0	0.166808	0
Down	ANXA10	3	4.21E-04	203664	0.234106	0
Down	MT1H	3	3.32E-04	64160	0.191459	0
Down	B4GALNT3	3	4.02E-04	211438	0.19202	0
Down	SOX21	3	3.00E-08	2	0.240767	0.666667
Down	NRG4	3	5.60E-04	49388	0.234267	0
Down	RHBDL2	3	4.08E-04	193280	0.180946	0
Down	GATA5	3	3.91E-04	70686	0.209613	0.333333
Down	ADTRP	3	2.92E-05	10622	0.192425	0
Down	PRSS8	3	4.57E-04	232278	0.22869	0
Down	STYK1	3	2.69E-05	15578	0.218494	0
Down	B3GAT1	3	0	0	0.18006	0
Down	PSCA	3	6.95E-04	79296	0.241335	0
Down	ADHFE1	3	8.07E-05	30016	0.199805	0
Down	CLDN18	3	4.17E-04	121720	0.197679	0
Down	LRRC66	3	1.72E-04	84034	0.221418	0
Down	RNASE4	3	0	0	0.192324	0
Down	KIAA0895	3	5.83E-05	24890	0.215581	0
Down	CYP2C19	2	0	0	0.200274	1
Down	FAM135B	2	1.11E-05	6158	0.192795	0
Down	SLC9A4	2	3.51E-06	1708	0.202689	0
Down	MT1G	2	9.97E-05	24412	0.172517	0
Down	C22orf23	2	3.91E-04	43196	0.16031	0
Down	DCAF12L1	2	1	2	1	0
Down	ANO5	2	1.16E-04	17930	0.21883	0
Down	TSPAN1	2	7.81E-06	4920	0.183381	0
Down	ARHGEF37	2	3.91E-04	89488	0.215282	0
Down	ELOVL6	2	3.91E-04	115044	0.204981	0
Down	GPR155	2	5.21E-05	24726	0.208979	0
Down	PM20D1	2	3.84E-06	2032	0.172669	0
Down	ST6GALNAC1	2	6.04E-05	4124	0.250171	0
Down	NWD1	2	3.91E-04	113138	0.197199	0
Down	IGSF9	2	5.44E-05	22396	0.216375	0
Down	SLC26A9	2	1.89E-04	21422	0.238342	0
Down	TCN1	2	3.66E-05	43932	0.218596	0
Down	ENTPD3	2	3.76E-05	15404	0.196516	0

Down	MSMB	2	9.51E-05	49854	0.214992	0
Down	CADM2	2	3.91E-04	72366	0.204858	0
Down	MT1M	2	3.91E-04	145464	0.190028	0
Down	MT1F	2	3.91E-04	224466	0.171194	0
Down	IRX3	2	1.13E-05	6548	0.207007	0
Down	FAM177B	2	1.06E-05	8836	0.198555	0
Down	ANKRD22	2	9.29E-06	1450	0.19975	0
Down	PROM2	2	5.53E-05	32190	0.222818	0
Down	C1orf115	2	1.47E-04	35652	0.214983	0
Down	CNTN3	2	0	0	0.236928	1
Down	CAPN9	2	1	2	1	0
Down	TTC39A	1	0	0	1	0
Down	DUOX2	1	0	0	0.172867	0
Down	MTRNR2L8	1	0	0	0.204965	0
Down	KIAA1324	1	0	0	0.224788	0
Down	UBE2QL1	1	0	0	0.179245	0
Down	MT1E	1	0	0	0.206689	0
Down	ADAMTS15	1	0	0	0.207486	0
Down	UNC5D	1	0	0	0.21045	0
Down	CWH43	1	0	0	0.167722	0
Down	B3GNT7	1	0	0	0.190987	0
Down	C16orf89	1	0	0	0.199244	0
Down	FER1L4	1	0	0	0.140277	0
Down	IL17REL	1	0	0	0.215263	0
Down	ENPP5	1	0	0	0.215263	0
Down	LYPD6B	1	0	0	0.178357	0
Down	SHISA6	1	0	0	0.185081	0
Down	FER1L6	1	0	0	0.203504	0
Down	COL6A5	1	0	0	0.204677	0
Down	AQP10	1	0	0	0.185733	0
Down	SEC14L5	1	0	0	0.236183	0
Down	HPGD	1	0	0	0.214766	0
Down	CNTD1	1	0	0	0.666667	0
Down	GGT6	1	0	0	0.666667	0
Down	PDILT	1	0	0	0.173137	0
Down	GKN2	1	0	0	0.20188	0
Down	CLDN23	1	0	0	0.198825	0
Down	HRH2	1	0	0	0.195128	0
Down	ADAM28	1	0	0	0.184706	0
Down	PRIMA1	1	0	0	1	0
Down	MUC6	1	0	0	0.20188	0
Down	IRX5	1	0	0	1	0
Down	GUCA2B	1	0	0	1	0

Down	ATP13A4	1	0	0	1	0
Down	SOX2	361	0.130645	91698482	0.314504	3.13E-05
Down	RIPK4	336	0.128603	98813078	0.314446	0
Down	FOXA1	290	0.103625	62359854	0.309195	3.87E-04
Down	EEF1A2	192	0.092037	39507690	0.326061	7.09E-04
Down	ANG	126	0.033985	31690134	0.29174	0
Down	FGB	119	0.043651	12625862	0.307262	0.004558
Down	PTGER3	113	0.038772	17588946	0.28297	3.16E-04
Down	CKB	111	0.036348	17987186	0.29959	0.002502
Down	FOXQ1	108	0.024413	25595054	0.265424	0
Down	ERBB4	101	0.039648	13011632	0.303684	0.00268
Down	PRKAA2	100	0.028743	15759608	0.279198	0
Down	APOA1	100	0.036853	10368028	0.293786	0.00451
Down	ESRRB	98	0.036893	21650562	0.308952	0.001052
Down	OXCT1	97	0.02688	16657230	0.275526	0
Down	ATP4A	92	0.038284	7433528	0.297688	2.50E-04
Down	F2RL1	90	0.02916	16825260	0.263862	0
Down	EYA2	88	0.023357	20081684	0.264175	0
Down	CDH2	83	0.025141	12416288	0.280608	0.001469
Down	SH3GL2	81	0.028376	10624252	0.281334	3.25E-04
Down	DUSP19	78	0.022667	8084684	0.289509	0.001053
Down	FAM189A2	78	0.023811	11453482	0.276839	9.99E-04
Down	ALDOC	75	0.024085	9254824	0.292324	0.004685
Down	SLC25A4	74	0.020138	14876712	0.282704	0
Down	HBB	72	0.024297	9837400	0.292358	0
Down	SELENBP1	69	0.020559	16033854	0.263576	0
Down	TTR	65	0.019611	8877534	0.281971	0.004608
Down	NR0B2	65	0.018911	9601392	0.285754	4.81E-04
Down	SLC15A1	65	0.022335	9413034	0.259481	0
Down	MRAP2	64	0.018209	14317820	0.246694	0
Down	APLP1	61	0.016887	7157580	0.275734	5.84E-04
Down	MIA2	61	0.023593	3857116	0.292911	0.003507
Down	MUC1	59	0.01901	8685324	0.297272	0.004386
Down	TMEM171	57	0.015929	7178790	0.265162	0
Down	VSIG1	57	0.015506	9968024	0.251724	0
Down	SLC2A12	56	0.014848	11274816	0.245344	0
Down	KIF1A	55	0.014262	10095312	0.273082	0
Down	LIPH	54	0.014461	5415600	0.258432	0
Down	FOXA3	53	0.011677	3197724	0.277576	0.007059
Down	FBP1	52	0.011778	5755732	0.259718	0.007347
Down	ID1	51	0.014356	8073662	0.260049	0
Down	GLUL	51	0.014074	7290628	0.273901	0
Down	LTF	51	0.015012	8074792	0.27279	0.001569

Down	SUSD4	50	0.014117	8153740	0.252171	0
Down	MYOC	49	0.012703	5520884	0.273784	0
Down	COL2A1	48	0.014506	2615324	0.251625	0
Down	CSTA	47	0.009908	5708660	0.266226	0
Down	PTPRR	46	0.012338	3050164	0.277425	0.008457
Down	ESRRG	46	0.01155	4874608	0.278438	0.001057
Down	SLC9A1	45	0.021666	3586826	0.290993	0.008081
Down	RORC	45	0.010968	7194834	0.26283	0
Down	FRMD1	45	0.01312	1673830	0.264627	0.005051
Down	NCAM1	44	0.011569	4653244	0.264476	0
Down	DHRS7	43	0.013463	2866004	0.265479	0.001107
Down	IL1R2	42	0.011437	5905866	0.234503	0
Down	CHGB	42	0.010047	5822946	0.266963	0
Down	BTNL8	42	0.011912	2086382	0.241256	0
Down	FBXL13	42	0.012583	5749328	0.240111	0
Down	FGA	41	0.010321	3281616	0.289247	0.062078
Down	SERPINA5	41	0.012219	1908132	0.278756	0.008097
Down	LDHD	40	0.011361	9207334	0.235747	0
Down	FGG	38	0.007185	2451080	0.281195	0.049206
Down	RPS6KA6	37	0.01036	3621900	0.266684	0.004505
Down	CYP2S1	37	0.009679	1915748	0.257936	0
Down	KLF4	36	0.008725	6243510	0.274829	0
Down	CA9	36	0.00838	3853714	0.278574	0
Down	DHCR24	36	0.006868	4428340	0.272965	0
Down	GALE	35	0.008601	4052878	0.272805	0
Down	GPRC5C	35	0.012273	2377340	0.271515	0.003361
Down	NQO1	34	0.008383	5150060	0.274136	0
Down	EPN3	34	0.010642	6541196	0.240269	0
Down	TMED6	34	0.008373	4030958	0.222818	0
Down	RAB27A	33	0.0091	2404172	0.26859	0.007576
Down	KRT20	33	0.007564	4522038	0.244323	0
Down	ALDOB	33	0.007577	5415906	0.25628	0
Down	AZGP1	33	0.007325	4722950	0.260102	0
Down	CYB5A	32	0.014497	2040568	0.281009	0.002016
Down	PTPRN2	32	0.006444	5188802	0.24512	0
Down	ME1	32	0.007918	3585304	0.249439	0
Down	LEPR	31	0.008148	2585854	0.250184	0
Down	S100P	31	0.00819	3141854	0.261794	0
Down	MAP7D2	31	0.006379	3776744	0.240393	0
Down	RIMS1	29	0.006836	2005214	0.262183	0.004926
Down	CD36	29	0.006605	3244170	0.25791	0
Down	VSIG2	29	0.005085	4523118	0.229594	0
Down	CKM	28	0.006486	1114366	0.26363	0.015385

Down	PTPRZ1	27	0.004562	2671328	0.243834	0
Down	PDIA2	27	0.011946	3842958	0.264791	0
Down	UGT1A10	27	0.00529	2201280	0.236884	0.02
Down	CMBL	27	0.005343	4698256	0.254001	0
Down	LGALS9C	27	0.006007	2789528	0.231267	0
Down	KLK11	27	0.005922	3556426	0.237026	0
Down	TFF1	26	0.00922	4457048	0.252932	0
Down	INSIG1	26	0.005325	1743502	0.245875	0
Down	RDH12	26	0.005489	2827404	0.239964	0
Down	GALNT6	26	0.009106	2128734	0.260779	0
Down	TPD52L1	25	0.004331	1988644	0.25113	0
Down	GC	25	0.00488	2756190	0.254786	0
Down	FOXA2	25	0.00442	692924	0.26162	0.027668
Down	RAP1GAP	25	0.005317	2730984	0.248493	0
Down	XYLT2	25	0.005125	3604190	0.230953	0
Down	PRLR	24	0.004513	2639920	0.241758	0
Down	SCNN1B	24	0.003266	1693310	0.233134	0.051948
Down	GNMT	24	0.003761	2292130	0.242538	0
Down	CA2	23	0.005398	1512836	0.267312	0
Down	CCKBR	23	0.004282	3289826	0.231162	0.009524
Down	DSC2	23	0.002627	1332696	0.243057	0
Down	SMPD3	23	0.00407	1526270	0.243462	0
Down	SOWAHA	23	0.005986	3656274	0.222304	0
Down	FBP2	22	0.00357	1236294	0.256075	0.047368
Down	SCGN	22	0.005448	2292384	0.224363	0
Down	CXADR	22	0.004966	1542936	0.256602	0
Down	SCGB2A1	22	0.00411	1974286	0.247626	0
Down	ALDH6A1	22	0.005212	3402338	0.242492	0
Down	PDGFD	22	0.004274	2794740	0.226934	0
Down	LIFR	21	0.004499	3194270	0.242423	0
Down	KCNQ1	21	0.004852	1329562	0.26667	0.005848
Down	PXMP2	21	0.009681	2045510	0.253585	0
Down	SCIN	21	0.004409	3432750	0.257481	0
Down	ALDH3A1	21	0.006292	975432	0.247662	0.011696
Down	STX19	20	0.005007	1935164	0.20909	0
Down	TCEAL2	20	0.003844	2368446	0.256576	0
Down	A4GNT	20	0.004387	1662140	0.225542	0
Down	CHIA	20	0.005062	3754078	0.241449	0
Down	GCNT1	20	0.004201	1845148	0.224926	0
Down	SCNN1G	19	0.001794	974542	0.233838	0.088235
Down	POU2AF1	19	0.005426	1886150	0.231267	0
Down	CLEC3B	19	0.003446	686120	0.253824	0.014706
Down	SGK2	19	0.003011	2291524	0.255806	0

Down	COL4A6	19	0.004108	2503680	0.231257	0
Down	GRIA4	18	0.004013	2094936	0.235172	0
Down	RAB27B	18	0.003176	889536	0.249147	0.013072
Down	F13A1	18	0.003111	636426	0.267886	0.05
Down	SYT16	18	0.003942	610066	0.237224	0
Down	GPT2	18	0.004219	2205028	0.24423	0
Down	CKMT2	18	0.003008	650282	0.255486	0.025
Down	ORM1	17	0.003066	2394818	0.233881	0.007353
Down	PDZD3	17	0.005754	836546	0.221188	0
Down	SPDEF	17	0.00438	1902948	0.247842	0
Down	SERPINA4	17	0.003389	1618954	0.242055	0
Down	CYP3A4	17	0.00331	1029374	0.24409	0.028571
Down	HOMER2	17	0.004213	2318450	0.2334	0
Down	GSTA1	17	0.003515	1770658	0.250711	0.038095
Down	CYP2C8	17	0.002329	1066708	0.23901	0
Down	MAL	17	0.003795	1666176	0.240382	0
Down	BPIFB1	17	0.002977	2398972	0.246159	0
Down	COL17A1	16	0.002553	1165170	0.246408	0
Down	EDARADD	16	0.002099	1184864	0.233166	0
Down	CYP2C9	16	0.002334	475378	0.234117	0.025
Down	EPB41L4B	16	0.003783	1719180	0.243196	0
Down	MUC5B	16	0.003656	1742484	0.254748	0.008333
Down	CGNL1	16	0.00242	1294404	0.24865	0
Down	AKR1C2	15	0.002609	727192	0.228844	0.025641
Down	SLPI	15	0.003639	1592814	0.245167	0
Down	AKR1B10	15	0.002313	855778	0.229543	0.009524
Down	TRIM50	15	0.003357	1937636	0.213465	0
Down	TST	15	0.002387	1686500	0.230797	0
Down	KLF15	15	0.002427	1312738	0.225164	0
Down	GABRB3	14	0.00218	943302	0.225941	0
Down	C6	14	0.002538	1748954	0.244323	0
Down	ASB11	14	0.002102	1319614	0.231351	0
Down	TMEM92	14	0.002742	768258	0.256538	0
Down	PTGR1	14	0.002181	1002112	0.221543	0
Down	CTSE	14	0.002273	897066	0.223471	0
Down	SYTL2	13	0.002043	537190	0.247338	0
Down	ARHGDIG	13	0.003657	1180020	0.219998	0
Down	SLC9A3	13	0.001716	783146	0.222324	0
Down	SULT1C2	13	0.002072	1077230	0.2131	0
Down	SLC1A2	13	0.001883	1174276	0.230433	0
Down	PBLD	13	0.002864	1604148	0.221707	0
Down	DEFB1	13	0.002672	969434	0.214874	0
Down	PLLP	13	0.002953	1704122	0.210528	0

Down	BHMT	12	0.001444	462034	0.200078	0
Down	GATA6	12	0.001888	766242	0.227925	0.015152
Down	SERPINB7	12	0.001574	903854	0.221697	0
Down	CHGA	12	0.002669	892042	0.237953	0
Down	SLC5A5	12	0.001844	1189896	0.214487	0
Down	CAPN13	12	0.002512	1267060	0.214649	0
Down	AKR7A3	11	0.002079	1092290	0.218905	0
Down	EPS8L1	11	0.00158	1034458	0.227337	0
Down	TFR2	11	0.002136	335802	0.241712	0
Down	KLF2	11	0.001827	864958	0.229162	0.036364
Down	SLC9A2	11	0.001361	674648	0.231749	0
Down	MAOA	11	0.001393	577172	0.229615	0
Down	AKR1C3	11	0.002239	398010	0.2158	0.054545
Down	REG3A	11	0.001394	775802	0.230807	0
Down	GHRL	11	0.003071	422262	0.230714	0
Down	DHRS9	11	0.002519	888628	0.20417	0
Down	AKR1B15	11	0.001364	380620	0.232964	0.018182
Down	SEMA3B	11	0.001852	912096	0.223676	0
Down	CYSTM1	11	0.002071	692870	0.215718	0
Down	AMTN	11	0.001781	621822	0.219159	0
Down	GKN1	11	8.02E-04	226994	0.217972	0
Down	AMPD1	11	8.02E-04	705838	0.229502	0
Down	MLPH	10	0.001483	571000	0.262331	0.088889
Down	TESC	10	0.001621	186720	0.23063	0.071429
Down	APOBEC1	10	0.002094	841430	0.200196	0
Down	AKR1C1	10	0.001725	316338	0.225492	0.071429
Down	RPRM	10	0.001932	971234	0.229646	0
Down	AQP5	10	0.001026	462940	0.220787	0
Down	GCNT2	10	0.002683	1431378	0.220463	0
Down	LIPF	10	0.002681	291688	0.235097	0
Down	ENTPD5	10	0.001423	576438	0.221966	0
Down	CYP2C18	10	0.00151	590472	0.218699	0.022222
Down	XK	10	0.00259	915288	0.211688	0
Down	UGT1A6	10	3.51E-04	63358	0.212075	0.25
Down	FOLR1	10	0.001826	786520	0.229811	0
Down	RASSF6	9	0.001679	758932	0.222314	0
Down	SLC4A4	9	8.25E-04	147548	0.228547	0
Down	HAPLN1	9	0.002127	937726	0.221514	0
Down	ALDH1A1	9	0.001071	502514	0.230225	0
Down	PAIP2B	9	0.001898	820018	0.212031	0
Down	FNDC5	9	0.00116	227236	0.234805	0
Down	OASL	9	0.001035	554244	0.235704	0
Down	CYP3A5	9	0.001621	242422	0.236227	0

Down	SCG3	9	0.00171	397816	0.234751	0
Down	ANGPTL3	9	0.001408	534524	0.201355	0
Down	CXCL14	9	0.001418	687382	0.225194	0
Down	FAM3B	9	0.002213	335698	0.2483	0
Down	RNASE1	8	8.75E-04	328862	0.22215	0
Down	BCAS1	8	7.11E-04	423002	0.24225	0
Down	HGD	8	0.001216	788412	0.213572	0
Down	C4orf19	8	0.001639	223746	0.256512	0.071429
Down	MYRIP	8	0.001238	430996	0.249634	0
Down	CIDEC	8	0.001237	380180	0.208885	0
Down	CA4	8	6.78E-04	175498	0.219715	0
Down	AQP4	8	7.48E-04	268154	0.211916	0
Down	IGFBP2	8	0.00149	766678	0.221294	0
Down	HTR1E	8	9.77E-04	621360	0.233262	0
Down	SULT2A1	8	7.70E-04	247322	0.211732	0
Down	C1orf116	8	7.46E-04	480606	0.241187	0
Down	FXYD3	8	0.001716	698152	0.219658	0
Down	TMEM38A	8	0.001989	673836	0.209975	0
Down	FUT9	8	0.001439	449312	0.206055	0
Down	FCGBP	8	5.65E-04	331640	0.230287	0
Down	PRDM16	8	6.15E-04	224982	0.23176	0
Down	ITPKA	8	6.95E-04	310188	0.215991	0
Down	BMP5	8	0.001564	204476	0.24629	0
Down	RGN	8	2.20E-04	146076	0.221064	0
Down	SOSTDC1	7	0.001188	367662	0.180492	0
Down	APOA4	7	4.08E-04	165970	0.21402	0
Down	ZBTB7C	7	0.001031	422450	0.227905	0
Down	METTL7A	7	4.95E-04	194766	0.227601	0
Down	ACADL	7	0.001679	791198	0.227946	0
Down	CYP4F12	7	9.87E-04	279876	0.220311	0
Down	PKIB	7	0.001587	460738	0.199914	0
Down	CCBE1	7	0.002002	326496	0.19495	0
Down	TFCP2L1	7	4.28E-04	250206	0.20633	0
Down	PALM3	7	0.00104	644144	0.248638	0
Down	HYAL1	7	0.002205	417022	0.238754	0
Down	ADAMTSL1	7	9.43E-04	207474	0.199906	0
Down	SYTL5	6	0.001222	233628	0.223393	0
Down	GSTA2	6	8.20E-04	333722	0.204948	0.133333
Down	DPT	6	4.89E-04	261260	0.232265	0
Down	MT1X	6	3.73E-04	229168	0.229285	0
Down	BEX5	6	7.89E-04	108852	0.200715	0
Down	ATP4B	6	0.002043	235970	0.235878	0
Down	PLIN5	6	0.001333	771154	0.195629	0

Down	CCL28	6	0.001575	487862	0.211872	0
Down	UPK1B	6	0.001572	934520	0.192781	0
Down	MAMDC2	6	0.001576	318360	0.213296	0
Down	SIGLEC11	6	5.99E-04	207770	0.228088	0
Down	PLAC8	6	3.02E-04	225896	0.228527	0
Down	RAB37	6	7.07E-04	123228	0.228967	0
Down	LGALS9B	6	3.47E-04	189584	0.218307	0
Down	ARL14	6	0.001956	1716690	0.182771	0
Down	SH3BGRL2	6	0.001142	565738	0.239863	0
Down	SST	6	0.002571	944178	0.209665	0.066667
Down	SLC16A7	6	0.00134	493152	0.193116	0
Down	FA2H	6	6.44E-04	190132	0.205889	0
Down	CPA2	6	8.69E-04	220104	0.204187	0
Down	DNER	6	5.68E-04	364110	0.227075	0
Down	GDPD3	6	2.89E-04	143022	0.209949	0
Down	KCNJ15	5	0.001063	395016	0.212383	0
Down	GCKR	5	8.07E-04	358596	0.212613	0
Down	HAS3	5	7.83E-04	180102	0.170839	0
Down	IGFALS	5	8.48E-04	200704	0.198178	0
Down	CCKAR	5	4.00E-08	2	0.18778	0.666667
Down	TFF2	5	4.28E-04	128148	0.208808	0
Down	SSTR1	5	8.16E-04	303142	0.175286	0.1
Down	GPX3	5	7.83E-04	182594	0.193995	0
Down	ORM2	5	1.57E-04	35318	0.220692	0.1
Down	APOC3	5	4.14E-04	47088	0.233667	0.2
Down	DDX60	5	8.81E-04	460534	0.218307	0
Down	HPN	5	7.26E-04	310120	0.230194	0
Down	GPT	5	8.29E-04	291602	0.206714	0
Down	ODAM	5	8.57E-04	403252	0.23236	0
Down	PAPPA2	5	8.40E-04	242380	0.196994	0
Down	FMO5	5	8.78E-04	467960	0.215254	0
Down	SLC16A9	5	8.61E-04	269782	0.220074	0
Down	TMEM220	5	5.22E-04	290922	0.220854	0
Down	GDPD2	5	0.001271	445450	0.207015	0
Down	VILL	5	8.06E-04	419916	0.21569	0
Down	ADH7	4	5.91E-05	29910	0.214631	0
Down	CLIC6	4	8.08E-04	292454	0.186417	0
Down	GALNT5	4	4.33E-04	155130	0.204366	0
Down	KCNJ16	4	8.03E-04	105342	0.195794	0
Down	CDHR2	4	0.001174	433218	0.180696	0
Down	KCNE2	4	5.03E-04	75192	0.235954	0.166667
Down	SULT1B1	4	4.79E-04	89616	0.204735	0
Down	VSTM2A	4	7.96E-04	681826	0.169553	0

Down	RASEF	4	6.42E-04	174228	0.220463	0
Down	GSTA3	4	5.10E-04	346118	0.238809	0.5
Down	ADH1C	4	1	2	1	0
Down	RIMS4	4	4.34E-04	216850	0.21482	0
Down	PGC	4	3.15E-04	58062	0.251142	0
Down	ENAM	4	1.68E-04	93264	0.210815	0
Down	FSIP2	4	8.09E-04	202852	0.206338	0
Down	SNORD22	4	3.76E-05	31698	0.209613	0
Down	TM7SF2	4	4.65E-04	146028	0.214496	0
Down	DMRTA1	4	9.92E-05	71054	0.21855	0
Down	SCUBE2	4	3.91E-04	94424	0.187498	0
Down	TMPRSS2	4	2.21E-05	4940	0.217944	0
Down	SCARA5	4	5.52E-04	205628	0.215645	0
Down	TMEM100	4	4.80E-04	116462	0.203253	0
Down	PTGDR2	4	1	12	1	0
Down	CAPN8	4	4.14E-04	137042	0.200597	0
Down	ZNF385B	4	7.92E-04	439412	0.235313	0
Down	RANBP3L	4	8.11E-04	270746	0.209966	0
Down	C6orf58	4	4.97E-04	152308	0.220055	0
Down	PLIN4	4	4.89E-05	42320	0.220444	0
Down	ACSM1	4	7.89E-04	357944	0.177842	0
Down	SLC7A8	3	7.83E-04	207170	0.191667	0
Down	CLCNKA	3	0	0	0.18787	0
Down	DUOX1	3	4.09E-04	206852	0.179214	0
Down	APOBEC2	3	0	0	0.166808	0
Down	ANXA10	3	4.21E-04	203664	0.234106	0
Down	MT1H	3	3.32E-04	64160	0.191459	0
Down	B4GALNT3	3	4.02E-04	211438	0.19202	0
Down	SOX21	3	3.00E-08	2	0.240767	0.666667
Down	NRG4	3	5.60E-04	49388	0.234267	0
Down	RHBDL2	3	4.08E-04	193280	0.180946	0
Down	GATA5	3	3.91E-04	70686	0.209613	0.333333
Down	ADTRP	3	2.92E-05	10622	0.192425	0
Down	PRSS8	3	4.57E-04	232278	0.22869	0
Down	STYK1	3	2.69E-05	15578	0.218494	0
Down	B3GAT1	3	0	0	0.18006	0
Down	PSCA	3	6.95E-04	79296	0.241335	0
Down	ADHFE1	3	8.07E-05	30016	0.199805	0
Down	CLDN18	3	4.17E-04	121720	0.197679	0
Down	LRRC66	3	1.72E-04	84034	0.221418	0
Down	RNASE4	3	0	0	0.192324	0
Down	KIAA0895	3	5.83E-05	24890	0.215581	0
Down	CYP2C19	2	0	0	0.200274	1

Down	FAM135B	2	1.11E-05	6158	0.192795	0
Down	SLC9A4	2	3.51E-06	1708	0.202689	0
Down	MT1G	2	9.97E-05	24412	0.172517	0
Down	C22orf23	2	3.91E-04	43196	0.16031	0
Down	DCAF12L1	2	1	2	1	0
Down	ANO5	2	1.16E-04	17930	0.21883	0
Down	TSPAN1	2	7.81E-06	4920	0.183381	0
Down	ARHGEF37	2	3.91E-04	89488	0.215282	0
Down	ELOVL6	2	3.91E-04	115044	0.204981	0
Down	GPR155	2	5.21E-05	24726	0.208979	0
Down	PM20D1	2	3.84E-06	2032	0.172669	0
Down	ST6GALNAC1	2	6.04E-05	4124	0.250171	0
Down	NWD1	2	3.91E-04	113138	0.197199	0
Down	IGSF9	2	5.44E-05	22396	0.216375	0
Down	SLC26A9	2	1.89E-04	21422	0.238342	0
Down	TCN1	2	3.66E-05	43932	0.218596	0
Down	ENTPD3	2	3.76E-05	15404	0.196516	0
Down	MSMB	2	9.51E-05	49854	0.214992	0
Down	CADM2	2	3.91E-04	72366	0.204858	0
Down	MT1M	2	3.91E-04	145464	0.190028	0
Down	MT1F	2	3.91E-04	224466	0.171194	0
Down	IRX3	2	1.13E-05	6548	0.207007	0

Table 8 miRNA - target gene interaction table

Regulation	Target Genes	Degree	MicroRNA	Regulation	Target Genes	Degree	MicroRNA
Up	MYB	24	hsa-mir-103a-3p	Down	GATA6	207	hsa-mir-4284
Up	SALL4	27	hsa-mir-107	Down	SULT1B1	131	hsa-mir-4643
Up	ARHGAP39	53	hsa-mir-1179	Down	GLUL	126	hsa-mir-4459
Up	CLDN4	73	hsa-mir-1200	Down	ENPP5	114	hsa-mir-8082
Up	CPS1	56	hsa-mir-1200	Down	KLF2	107	hsa-mir-5193
Up	OSMR	54	hsa-mir-1208	Down	GPR155	94	hsa-mir-3685
Up	IL2RA	50	hsa-mir-1248	Down	LDHD	91	hsa-mir-6077
Up	CDCA7	22	hsa-mir-1254	Down	INSIG1	85	hsa-mir-8073
Up	CDC25B	40	hsa-mir-1268a	Down	F2RL1	85	hsa-mir-3652
Up	BMP8A	38	hsa-mir-1273f	Down	B3GALT5	78	hsa-mir-4273
Up	ANKRD13B	42	hsa-mir-1275	Down	NWD1	75	hsa-mir-4532
Up	CAMK2N1	51	hsa-mir-1281	Down	SHISA6	71	hsa-mir-2278
Up	FGD6	41	hsa-mir-1289	Down	ANGPTL3	70	hsa-mir-1206
Up	ILDR1	29	hsa-mir-1303	Down	FOLR1	69	hsa-mir-4300
Up	COL4A1	42	hsa-mir-1305	Down	SLC16A9	69	hsa-mir-4500
Up	ITGA11	31	hsa-mir-1321	Down	ENTPD5	66	hsa-mir-4488
Up	TGFBI	22	hsa-mir-1322	Down	CADM2	66	hsa-mir-6074
Up	ITGBL1	18	hsa-mir-138-2-3p	Down	CCBE1	64	hsa-mir-4277
Up	PLXNA1	58	hsa-mir-1827	Down	CGNL1	61	hsa-mir-4293
Up	POLQ	86	hsa-mir-1912	Down	CMBL	60	hsa-mir-2052
Up	PTGS2	20	hsa-mir-199a-3p	Down	ACER2	59	hsa-mir-4280
Up	SPON2	23	hsa-mir-2110	Down	C1orf210	59	hsa-mir-4469
Up	BCAT1	50	hsa-mir-2113	Down	LIFR	55	hsa-mir-8060
Up	FPR1	94	hsa-mir-2117	Down	PRLR	54	hsa-mir-4719
Up	DOCK4	19	hsa-mir-23c	Down	METTL7A	54	hsa-mir-4432
Up	LY6E	26	hsa-mir-2861	Down	ALDH6A1	54	hsa-mir-5095
Up	SPSB1	45	hsa-mir-297	Down	FSIP2	53	hsa-mir-4641
Up	GREM1	18	hsa-mir-300	Down	GALNT6	52	hsa-mir-4770

Up	EMILIN2	31	hsa-mir-302f	Down	TSPAN1	51	hsa-mir-3662
Up	HAVCR2	30	hsa-mir-3122	Down	SLC5A5	51	hsa-mir-4421
Up	PLEKHS1	34	hsa-mir-3135b	Down	TMEM151A	50	hsa-mir-6069
Up	TRIP13	27	hsa-mir-3138	Down	FBXL13	49	hsa-mir-4435
Up	ADAMTS14	19	hsa-mir-3150a-3p	Down	SCIN	48	hsa-mir-5572
Up	SRPX2	40	hsa-mir-3178	Down	SLC1A2	47	hsa-mir-3122
Up	PIEZO1	17	hsa-mir-3191-3p	Down	B4GALNT3	47	hsa-mir-3910
Up	MARVELD1	47	hsa-mir-3202	Down	IL17REL	46	hsa-mir-4303
Up	MKI67	84	hsa-mir-3646	Down	ATP13A4	45	hsa-mir-4480
Up	ORC1	53	hsa-mir-3666	Down	PLCXD3	45	hsa-mir-1248
Up	PRRX1	17	hsa-mir-378j	Down	ANG	45	hsa-mir-5693
Up	PMEPA1	59	hsa-mir-3909	Down	DUSP19	45	hsa-mir-1303
Up	RCC2	135	hsa-mir-3911	Down	TMEM100	45	hsa-mir-4427
Up	ADAM12	23	hsa-mir-3915	Down	SLC26A9	44	hsa-mir-4306
Up	GEM	24	hsa-mir-3920	Down	DHCR24	43	hsa-mir-4496
Up	PLXDC2	58	hsa-mir-3924	Down	ACADL	42	hsa-mir-30c-2-3p
Up	PDPN	29	hsa-mir-3929	Down	FOXQ1	42	hsa-mir-3666
Up	INHBA	51	hsa-mir-3973	Down	PLLP	41	hsa-mir-3910
Up	CCND2	179	hsa-mir-3976	Down	ELOVL6	41	hsa-mir-5703
Up	SERPINE1	22	hsa-mir-3977	Down	APOC3	40	hsa-mir-7703
Up	ONECUT2	26	hsa-mir-4251	Down	RAB27A	40	hsa-mir-3170
Up	ITGB8	65	hsa-mir-4263	Down	PRKAA2	40	hsa-mir-3166
Up	FOXC1	106	hsa-mir-4269	Down	C1orf115	39	hsa-mir-4451
Up	E2F3	134	hsa-mir-4271	Down	CYB5A	39	hsa-mir-600
Up	MCM7	51	hsa-mir-4283	Down	PRSS8	38	hsa-mir-4441
Up	CTSB	26	hsa-mir-4291	Down	RIMS4	37	hsa-mir-1976
Up	IFITM1	38	hsa-mir-4295	Down	KIAA0895	37	hsa-mir-4307
Up	TNS4	41	hsa-mir-4300	Down	GPRC5C	36	hsa-mir-8089
Up	CELSR3	71	hsa-mir-4301	Down	EPB41L4B	36	hsa-mir-8077
Up	BUB1	67	hsa-mir-4302	Down	MTRNR2L8	34	hsa-mir-3159
Up	C1QTNF6	36	hsa-mir-4310	Down	CYP2C19	34	hsa-mir-5186
Up	FSTL3	39	hsa-mir-4314	Down	GABRB3	34	hsa-mir-298
Up	OLR1	81	hsa-mir-4316	Down	AKR1B10	34	hsa-mir-3611
Up	GINS4	46	hsa-mir-4318	Down	SEC14L5	33	hsa-mir-6131
Up	MMP16	28	hsa-mir-4318	Down	RPRM	32	hsa-mir-6090
Up	FSTL1	38	hsa-mir-4420	Down	SLC9A4	32	hsa-mir-8054
Up	FMNL3	78	hsa-mir-4421	Down	KIAA1324	32	hsa-mir-3135a
Up	COL1A2	30	hsa-mir-4424	Down	FOXA1	32	hsa-mir-4428
Up	CAD	64	hsa-mir-4426	Down	ASB11	31	hsa-mir-4803
Up	FSCN1	99	hsa-mir-4430	Down	SLC9A1	31	hsa-mir-644a
Up	COL5A1	31	hsa-mir-4434	Down	SOWAHA	30	hsa-mir-4999-3p
Up	GDF15	23	hsa-mir-4436a	Down	ASAH2	30	hsa-mir-4657
Up	THBS1	95	hsa-mir-4441	Down	PTGDR2	30	hsa-mir-5695
Up	GPR176	18	hsa-mir-4445-5p	Down	PAIP2B	30	hsa-mir-4287
Up	MEX3A	95	hsa-mir-4447	Down	NRG4	30	hsa-mir-4510
Up	DGKH	52	hsa-mir-4452	Down	PLAC8	30	hsa-mir-4481
Up	LIF	47	hsa-mir-4454	Down	TFCP2L1	29	hsa-mir-4468
Up	CLDN1	35	hsa-mir-4461	Down	HAS3	29	hsa-mir-520e
Up	SERPINH1	77	hsa-mir-4463	Down	LIPH	27	hsa-mir-6089
Up	TTYH3	56	hsa-mir-4468	Down	SSTR1	26	hsa-mir-4467
Up	XRCC2	65	hsa-mir-4469	Down	SLPI	26	hsa-mir-1827
Up	CYP2W1	56	hsa-mir-4472	Down	ECHDC3	26	hsa-mir-5697
Up	ELN	22	hsa-mir-4472	Down	KLF4	26	hsa-mir-663a
Up	ARHGAP11A	37	hsa-mir-4478	Down	GCNT4	25	hsa-mir-3689c
Up	TIMP1	22	hsa-mir-4481	Down	SERPINA4	25	hsa-mir-6073
Up	KIF2C	68	hsa-mir-4484	Down	RASSF6	25	hsa-mir-6778-3p
Up	LTBP2	33	hsa-mir-4487	Down	VSIG1	24	hsa-mir-3198
Up	CCNF	102	hsa-mir-4492	Down	RHBDL2	24	hsa-mir-6773-3p
Up	MYBL2	45	hsa-mir-4498	Down	CDH2	24	hsa-mir-1244
Up	ESPL1	34	hsa-mir-4500	Down	TM6SF2	23	hsa-mir-6081
Up	HIST3H2BB	35	hsa-mir-4507	Down	STYK1	23	hsa-mir-548u
Up	LOXL2	26	hsa-mir-4507	Down	TTR	23	hsa-mir-1273f
Up	KIF23	59	hsa-mir-4509	Down	VSIG2	23	hsa-mir-711
Up	IGSF6	48	hsa-mir-4514	Down	TMEM38A	23	hsa-mir-520b
Up	SLC37A2	30	hsa-mir-4514	Down	APOA1	22	hsa-mir-1305
Up	GFPT2	23	hsa-mir-4516	Down	HS6ST3	22	hsa-mir-147a
Up	IL6	22	hsa-mir-451a	Down	KCNJ15	22	hsa-mir-548ac
Up	MCM10	21	hsa-mir-4522	Down	MYZAP	22	hsa-mir-4801
Up	ALDH1A3	32	hsa-mir-4533	Down	FUT9	21	hsa-mir-664b-3p
Up	COL12A1	28	hsa-mir-4533	Down	PSAPL1	21	hsa-mir-550b-2-5p

Up	C3	118	hsa-mir-4537	Down	FGG	21	hsa-mir-5008-5p
Up	ODF2L	37	hsa-mir-4540	Down	MT1E	21	hsa-mir-138-2-3p
Up	F2RL2	62	hsa-mir-4635	Down	CLIC6	20	hsa-mir-8055
Up	IFFO2	51	hsa-mir-4641	Down	EDARADD	20	hsa-mir-103a-2-5p
Up	SLC2A3	47	hsa-mir-4654	Down	PTPRN2	20	hsa-mir-4311
Up	ICAM1	34	hsa-mir-466	Down	C4orf19	20	hsa-mir-4430
Up	COL1A1	97	hsa-mir-4660	Down	HRH2	20	hsa-mir-6129
Up	VCAN	24	hsa-mir-4666b	Down	CD36	20	hsa-mir-3190-5p
Up	ITGA5	27	hsa-mir-4667-3p	Down	SLC4A4	19	hsa-mir-6747-3p
Up	AHNAK2	16	hsa-mir-4670-3p	Down	SLC15A1	19	hsa-mir-4649-3p
Up	STC2	90	hsa-mir-4689	Down	IGSF9	19	hsa-mir-548x-3p
Up	SPARC	21	hsa-mir-4693-3p	Down	ANO7	19	hsa-mir-6852-5p
Up	THY1	32	hsa-mir-4706	Down	ALDOC	19	hsa-mir-2116-3p
Up	CLSPN	73	hsa-mir-4710	Down	GPT2	19	hsa-mir-3911
Up	WDR72	23	hsa-mir-4719	Down	SOX2	19	hsa-mir-1181
Up	THBS2	81	hsa-mir-4771	Down	SLC28A2	18	hsa-mir-4705
Up	MDFI	36	hsa-mir-4773	Down	LTF	18	hsa-mir-4768-5p
Up	PLA2G7	18	hsa-mir-4775	Down	C6	18	hsa-mir-6511a-3p
Up	RHBDF2	40	hsa-mir-4779	Down	FGB	18	hsa-mir-3155b
Up	PXDN	27	hsa-mir-4780	Down	HAPLN1	18	hsa-mir-548an
Up	CLSTN3	17	hsa-mir-4801	Down	SLC9A3	17	hsa-mir-4749-5p
Up	CBX2	80	hsa-mir-4803	Down	FAM174B	17	hsa-mir-5006-3p
Up	GNB4	27	hsa-mir-5001-3p	Down	CYP3A5	17	hsa-mir-599
Up	SLC11A1	19	hsa-mir-5006-3p	Down	PAQR8	17	hsa-mir-6881-3p
Up	LRP8	18	hsa-mir-5011-5p	Down	ADAMTSL1	17	hsa-mir-3689d
Up	PLK1	40	hsa-mir-5047	Down	PLIN5	17	hsa-mir-4418
Up	NCR3LG1	54	hsa-mir-5087	Down	HHLA2	16	hsa-mir-3133
Up	PLXDC1	20	hsa-mir-5091	Down	CAPN13	16	hsa-mir-549a
Up	HOXA10	83	hsa-mir-5093	Down	RASEF	16	hsa-mir-5700
Up	LIPG	89	hsa-mir-5096	Down	B3GNT7	15	hsa-mir-7975
Up	KIF18B	36	hsa-mir-5100	Down	TPD52L1	14	hsa-mir-8066
Up	HOXA13	111	hsa-mir-5190	Down	SLC2A12	14	hsa-mir-502-3p
Up	SLC43A3	60	hsa-mir-5191	Down	DUOX2	14	hsa-mir-6749-3p
Up	KRT80	65	hsa-mir-5192	Down	CIDEC	14	hsa-mir-548aw
Up	PGM2L1	117	hsa-mir-5193	Down	CTSE	14	hsa-mir-3650
Up	MFAP2	24	hsa-mir-520b	Down	NKX6-2	13	hsa-mir-6889-5p
Up	TOP2A	17	hsa-mir-520d-5p	Down	TMEM220	13	hsa-mir-7161-5p
Up	ATAD2	35	hsa-mir-520e	Down	C14orf180	13	hsa-mir-1255b-2-3p
Up	MMP9	21	hsa-mir-524-5p	Down	GCNT1	13	hsa-mir-2682-3p
Up	ATP11A	28	hsa-mir-526a	Down	FOXA2	13	hsa-mir-450a-1-3p
Up	DIO2	21	hsa-mir-544a	Down	SCNN1G	12	hsa-mir-433-3p
Up	CKAP2	17	hsa-mir-548ah-5p	Down	TTC39A	12	hsa-mir-1273g-3p
Up	RAB31	30	hsa-mir-548an	Down	SIGLEC11	12	hsa-mir-520h
Up	CDC6	28	hsa-mir-548ap-3p	Down	ESRRG	12	hsa-mir-4492
Up	EPHB1	18	hsa-mir-548aw	Down	UNC5D	12	hsa-mir-527
Up	CD84	33	hsa-mir-548s	Down	SLC16A7	12	hsa-mir-759
Up	WISP1	27	hsa-mir-557	Down	PBLD	12	hsa-mir-374a-5p
Up	GLI2	35	hsa-mir-5572	Down	PROM2	11	hsa-mir-6134
Up	COL8A1	39	hsa-mir-564	Down	TRNP1	11	hsa-mir-4793-3p
Up	NT5DC3	85	hsa-mir-5680	Down	PTGER3	11	hsa-mir-5003-3p
Up	FAM83D	40	hsa-mir-5691	Down	C1orf116	11	hsa-mir-581
Up	FOXK1	259	hsa-mir-5693	Down	ARHGEF37	11	hsa-mir-6780a-3p
Up	ST3GAL2	22	hsa-mir-5693	Down	ST6GALNAC1	11	hsa-mir-3155a
Up	GPX8	25	hsa-mir-5700	Down	SLC26A7	11	hsa-mir-4659b-3p
Up	APLN	30	hsa-mir-5708	Down	REG3A	11	hsa-mir-2277-3p
Up	TCOF1	28	hsa-mir-588	Down	RPS6KA6	11	hsa-mir-4687-3p
Up	SLC39A10	27	hsa-mir-591	Down	ADAM28	11	hsa-mir-23c
Up	GAS7	18	hsa-mir-599	Down	CKB	11	hsa-mir-551a
Up	ADAMTS9	24	hsa-mir-603	Down	SLC25A4	11	hsa-mir-7112-3p
Up	IGF2BP3	52	hsa-mir-6069	Down	FNDC5	10	hsa-mir-4659a-3p
Up	TNFAIP2	24	hsa-mir-6069	Down	AADAC	10	hsa-mir-1179
Up	IGSF9B	30	hsa-mir-607	Down	HOMER2	10	hsa-mir-922
Up	DUSP10	39	hsa-mir-6072	Down	RIPK4	10	hsa-mir-5003-5p
Up	ZNF703	115	hsa-mir-6074	Down	B3GNT6	9	hsa-mir-3909
Up	LPCAT1	29	hsa-mir-6077	Down	IRX2	9	hsa-mir-6808-3p
Up	PODXL	69	hsa-mir-6079	Down	BCAS1	9	hsa-mir-933
Up	ENTPD1	64	hsa-mir-6079	Down	PRIMA1	9	hsa-mir-5011-5p
Up	CYP2B6	43	hsa-mir-608	Down	TMEM92	9	hsa-mir-4713-5p
Up	CCDC80	135	hsa-mir-6083	Down	MUC1	9	hsa-mir-145-5p
Up	PLEKHG2	94	hsa-mir-6127	Down	ESRRB	9	hsa-mir-6769b-5p

Up	ABCA1	19	hsa-mir-613	Down	ERBB4	9	hsa-mir-221-3p
Up	VASH1	49	hsa-mir-6131	Down	KIF1A	9	hsa-mir-652-3p
Up	IFITM3	35	hsa-mir-6132	Down	EEF1A2	8	hsa-mir-663b
Up	NFAM1	40	hsa-mir-617	Down	RAB37	8	hsa-mir-4673
Up	NOTCH1	44	hsa-mir-623	Down	ID1	8	hsa-mir-100-5p
Up	KNTC1	27	hsa-mir-632	Down	XYLT2	8	hsa-mir-18a-5p
Up	CEP170	37	hsa-mir-633	Down	BMP5	7	hsa-mir-1266-3p
Up	F2R	37	hsa-mir-640	Down	ZBTB7C	7	hsa-mir-4650-5p
Up	GPR161	22	hsa-mir-6501-5p	Down	MTRNR2L2	7	hsa-mir-299-5p
Up	SNX10	20	hsa-mir-6507-5p	Down	PRDM16	7	hsa-mir-101-3p
Up	MTHFD1L	31	hsa-mir-6509-3p	Down	NCAM1	7	hsa-mir-200c-3p
Up	VGLL3	18	hsa-mir-6512-3p	Down	DSC2	7	hsa-mir-25-3p
Up	COL18A1	40	hsa-mir-661	Down	DPCR1	7	hsa-mir-24-1-5p
Up	KIF21B	23	hsa-mir-663b	Down	HPGD	7	hsa-mir-664a-3p
Up	FAR2	18	hsa-mir-6715b-3p	Down	ADAMTS15	6	hsa-mir-4540
Up	HJURP	24	hsa-mir-6720-3p	Down	XK	6	hsa-mir-31-3p
Up	TRIM29	20	hsa-mir-6746-5p	Down	CXCL14	5	hsa-mir-2276-3p
Up	IFI44L	19	hsa-mir-6809-3p	Down	ENAM	5	hsa-mir-15a-3p
Up	PADI2	24	hsa-mir-6826-3p	Down	GALNT5	5	hsa-mir-651-3p
Up	ANTXR1	21	hsa-mir-6837-3p	Down	FGA	5	hsa-mir-409-3p
Up	OMD	31	hsa-mir-6843-3p	Down	RORC	5	hsa-mir-1236-3p
Up	BICC1	18	hsa-mir-7110-3p	Down	MAOA	5	hsa-mir-5000-5p
Up	EPHB2	35	hsa-mir-7150	Down	POU2AF1	5	hsa-mir-210-3p
Up	NCAPH	31	hsa-mir-759	Down	CYSTM1	5	hsa-mir-183-3p
Up	P2RX7	39	hsa-mir-764	Down	UBE2QL1	4	hsa-mir-2909
Up	HEYL	83	hsa-mir-7641	Down	KLHDC7A	4	hsa-mir-4662a-3p
Up	CLEC7A	33	hsa-mir-7977	Down	FAM135B	4	hsa-mir-2114-3p
Up	SEMA6B	29	hsa-mir-8052	Down	GGT6	4	hsa-mir-501-5p
Up	PDE3A	84	hsa-mir-8066	Down	SLC7A8	4	hsa-mir-4644
Up	PKMYT1	39	hsa-mir-8078	Down	IGFBP2	4	hsa-mir-491-3p
Up	ATAD5	51	hsa-mir-8080	Down	SPTSSB	4	hsa-mir-3606-5p
Up	ADAMTS4	77	hsa-mir-8081	Down	CYP2C8	4	hsa-mir-1178-3p
Up	GDPD5	31	hsa-mir-922	Down	RAB27B	4	hsa-mir-193a-3p
Up	STIL	16	hsa-mir-4266	Down	OXCT1	4	hsa-mir-155-5p
Up	GRIN2D	16	hsa-mir-6804-5p	Down	GCNT2	4	hsa-mir-98-5p
Up	LRRC32	16	hsa-mir-378g	Down	CXADR	4	hsa-mir-342-3p
Up	MXRA8	16	hsa-mir-1295b-5p	Down	CA2	4	hsa-mir-99b-3p
Up	SCARF2	16	hsa-mir-6081	Down	SELENBP1	4	hsa-mir-20a-5p
Up	NOP2	15	hsa-mir-296-3p	Down	SPDEF	4	hsa-let-7c-5p
Up	KIF14	15	hsa-mir-4523	Down	LEPR	3	hsa-mir-200c-3p
Up	ANGPTL2	15	hsa-mir-548ac	Down	CYP2C9	3	hsa-mir-143-3p
Up	CDX2	15	hsa-mir-6747-3p	Down	OASL	3	hsa-mir-146a-5p
Up	TREM1	15	hsa-mir-421	Down	TFF1	3	hsa-mir-423-5p
Up	SERPINB5	14	hsa-mir-4762-5p	Down	PTPRZ1	3	hsa-mir-181a-5p
Up	SELE	14	hsa-mir-3065-5p	Down	CCKBR	3	hsa-mir-148a-3p
Up	FOXM1	14	hsa-mir-24-1-5p	Down	RNASE4	3	hsa-mir-215-5p
Up	PLEKHG4	14	hsa-mir-6502-5p	Down	MT1F	3	hsa-mir-219a-5p
Up	TDRD6	14	hsa-mir-5088-3p	Down	SH3GL2	3	hsa-mir-107
Up	PLEK	14	hsa-mir-3180-5p	Down	NR0B2	3	hsa-mir-141-3p
Up	CPXM2	14	hsa-mir-6877-3p	Down	S100P	3	hsa-mir-24-3p
Up	ECT2	13	hsa-mir-4255	Down	TST	3	hsa-mir-548b-3p
Up	ITGAX	13	hsa-mir-6087	Down	TM7SF2	2	hsa-mir-193b-3p
Up	CACNA1E	13	hsa-mir-541-3p	Down	APLP1	2	hsa-mir-484
Up	COL5A3	13	hsa-mir-642a-5p	Down	MIA2	2	hsa-mir-155-5p
Up	RELT	12	hsa-mir-6849-3p	Down	ALDOB	2	hsa-mir-378a-3p
Up	CENPF	12	hsa-mir-1226-3p	Down	PXMP2	2	hsa-mir-935
Up	COL4A2	12	hsa-mir-210-3p	Down	CLDN23	2	hsa-mir-222-3p
Up	PLXNC1	12	hsa-mir-7853-5p	Down	ALDH1A1	2	hsa-mir-140-5p
Up	BOC	12	hsa-mir-4659a-5p	Down	SULT1C2	2	hsa-mir-7-5p
Up	DPYSL3	12	hsa-mir-3667-3p	Down	ZNF385B	2	hsa-mir-215-5p
Up	PARVG	12	hsa-mir-6804-3p	Down	FAM189A2	2	hsa-mir-192-5p
Up	CRABP2	12	hsa-mir-3141	Down	RAP1GAP	2	hsa-mir-215-5p
Up	CLDN7	12	hsa-mir-3670	Down	MT1X	2	hsa-mir-1225-3p
Up	COL3A1	11	hsa-mir-455-3p	Down	ENTPD3	2	hsa-mir-192-5p
Up	KIF26B	11	hsa-mir-501-5p	Down	COL4A6	2	hsa-mir-29b-3p
Up	MMP14	11	hsa-mir-133b	Down	COL2A1	2	hsa-mir-106a-5p
Up	FBN1	11	hsa-mir-133a-3p	Down	AQP4	2	hsa-mir-320a
Up	NNMT	11	hsa-mir-6500-3p	Down	AKR1C3	2	hsa-mir-98-5p
Up	SULF2	11	hsa-mir-5585-3p	Down	DDX60	2	hsa-mir-1-3p
Up	LAMA5	11	hsa-mir-1909-3p	Down	HGD	2	hsa-mir-26b-5p

Up	TNC	11	hsa-mir-513a-3p	Down	CA9	2	hsa-mir-98-5p
Up	SLC24A3	11	hsa-mir-548aa	Down	SULT2A1	2	hsa-mir-24-3p
Up	BGN	11	hsa-mir-4311	Down	MT1M	2	hsa-mir-26b-5p
Up	UBE2C	10	hsa-mir-631	Down	PDGFD	2	hsa-mir-21-5p
Up	EGR2	10	hsa-mir-150-5p	Down	RNASE1	2	hsa-mir-19b-3p
Up	PDGFRB	10	hsa-mir-224-5p	Down	AMPD1	2	hsa-mir-10a-5p
Up	MCM2	10	hsa-mir-1296-5p	Down	IRX5	1	hsa-mir-4497
Up	ENC1	10	hsa-mir-5584-5p	Down	CLDN18	1	hsa-mir-1303
Up	RTKN2	10	hsa-mir-6876-5p	Down	ATP4A	1	hsa-mir-1289
Up	CDH13	10	hsa-mir-3074-5p	Down	PTGR1	1	hsa-mir-522-3p
Up	CD109	10	hsa-mir-103a-2-5p	Down	ITPKA	1	hsa-mir-193b-3p
Up	SH3PXD2B	10	hsa-mir-6749-3p	Down	AKR1C2	1	hsa-mir-193b-3p
Up	HMCN1	10	hsa-mir-1299	Down	GRIA4	1	hsa-mir-484
Up	TMEM158	10	hsa-mir-548z	Down	PLIN4	1	hsa-mir-335-5p
Up	ZNF469	10	hsa-mir-151b	Down	MUC5B	1	hsa-mir-335-5p
Up	FANCD2	9	hsa-mir-618	Down	LGALS9C	1	hsa-mir-335-5p
Up	LAPTM5	9	hsa-mir-4680-3p	Down	STX19	1	hsa-mir-335-5p
Up	NOTCH3	9	hsa-mir-206	Down	FMO6P	1	hsa-mir-335-5p
Up	FCGR3B	9	hsa-mir-6740-3p	Down	ENHO	1	hsa-mir-335-5p
Up	KIAA1755	9	hsa-mir-4756-3p	Down	C6orf58	1	hsa-mir-335-5p
Up	C2CD4A	8	hsa-mir-4659b-3p	Down	BEX5	1	hsa-mir-335-5p
Up	FADS2	8	hsa-mir-500a-3p	Down	SCARA5	1	hsa-mir-335-5p
Up	CTHRC1	8	hsa-mir-630	Down	LGALS9B	1	hsa-mir-335-5p
Up	MYH10	8	hsa-mir-106b-3p	Down	COL6A5	1	hsa-mir-335-5p
Up	FN1	8	hsa-mir-200c-3p	Down	GATA5	1	hsa-mir-335-5p
Up	MYBBP1A	8	hsa-mir-3186-5p	Down	TRIM50	1	hsa-mir-335-5p
Up	ROBO2	8	hsa-mir-514a-3p	Down	ANKRD22	1	hsa-mir-335-5p
Up	WDR62	8	hsa-mir-149-5p	Down	ACSM1	1	hsa-mir-335-5p
Up	C1R	8	hsa-mir-518c-5p	Down	AQP10	1	hsa-mir-335-5p
Up	TRIO	7	hsa-mir-92b-3p	Down	FRMD1	1	hsa-mir-335-5p
Up	TUBB3	7	hsa-mir-340-5p	Down	CDHR2	1	hsa-mir-335-5p
Up	PDLIM7	7	hsa-mir-30a-5p	Down	FAM3B	1	hsa-mir-335-5p
Up	PLAU	7	hsa-mir-23b-3p	Down	VILL	1	hsa-mir-335-5p
Up	COL5A2	7	hsa-mir-29c-3p	Down	SCG3	1	hsa-mir-335-5p
Up	CD248	7	hsa-mir-758-3p	Down	GNMT	1	hsa-mir-335-5p
Up	TGM2	7	hsa-mir-155-5p	Down	SOSTDC1	1	hsa-mir-335-5p
Up	NEK2	7	hsa-mir-4668-5p	Down	KLK11	1	hsa-mir-335-5p
Up	MMP7	7	hsa-mir-203a-5p	Down	FBP2	1	hsa-mir-335-5p
Up	FBXO32	7	hsa-mir-608	Down	SEMA3B	1	hsa-mir-335-5p
Up	MSR1	7	hsa-mir-410-5p	Down	CLEC3B	1	hsa-mir-335-5p
Up	FCGR2A	7	hsa-mir-29b-2-5p	Down	TFF2	1	hsa-mir-335-5p
Up	ESM1	7	hsa-mir-1260a	Down	MUC6	1	hsa-mir-335-5p
Up	ASPM	6	hsa-mir-193b-3p	Down	FOXA3	1	hsa-mir-335-5p
Up	ACTN1	6	hsa-mir-16-5p	Down	GUCA2B	1	hsa-mir-335-5p
Up	HTRA1	6	hsa-mir-6774-5p	Down	GC	1	hsa-mir-335-5p
Up	RAI14	6	hsa-mir-21-5p	Down	AQP5	1	hsa-mir-335-5p
Up	PRR5L	6	hsa-mir-502-5p	Down	ADH7	1	hsa-mir-335-5p
Up	DKK2	6	hsa-mir-221-3p	Down	CCL28	1	hsa-mir-148b-3p
Up	IL11	6	sa-mir-211-5p	Down	KCNJ16	1	hsa-mir-148b-3p
Up	HIST1H3G	6	hsa-mir-7856-5p	Down	DPT	1	hsa-mir-148b-3p
Up	LEF1	6	hsa-mir-449a	Down	KLF15	1	hsa-mir-376a-3p
Up	SPP1	6	hsa-mir-299-5p	Down	CHGB	1	hsa-mir-375
Up	LGR5	6	hsa-mir-142-3p	Down	SH3BGRL2	1	hsa-mir-195-5p
Up	TFEC	6	hsa-mir-769-5p	Down	ARL14	1	hsa-mir-186-5p
Up	CDCA2	6	hsa-mir-3613-3p	Down	PTPRR	1	hsa-mir-186-5p
Up	FKBP10	5	hsa-mir-132-3p	Down	ALDH3A1	1	hsa-mir-186-5p
Up	CALD1	5	hsa-mir-15a-5p	Down	KCNQ1	1	hsa-mir-133a-3p
Up	KIF20A	5	hsa-mir-124-3p	Down	B3GAT1	1	hsa-mir-132-3p
Up	CSGALNACT2	5	hsa-mir-377-3p	Down	AZGP1	1	hsa-mir-128-3p
Up	COL10A1	5	hsa-mir-29b-3p	Down	UGT1A10	1	hsa-mir-124-3p
Up	NOX4	5	hsa-mir-9-5p	Down	COL17A1	1	hsa-mir-124-3p
Up	ANLN	5	hsa-mir-497-5p	Down	CYP3A4	1	hsa-mir-27b-3p
Up	ZNF462	5	hsa-mir-330-5p	Down	SYTL2	1	hsa-mir-1-3p
Up	NTM	5	hsa-mir-340-5p	Down	RGN	1	hsa-mir-1-3p
Up	MMP1	5	hsa-mir-526b-3p	Down	LYPD6B	1	hsa-mir-218-5p
Up	SPHK1	5	hsa-mir-125b-5p	Down	SUSD4	1	hsa-mir-218-5p
Up	PLBD2	5	hsa-mir-3607-3p	Down	MYOC	1	hsa-mir-204-5p
Up	HEPH	5	hsa-mir-548c-3p	Down	ME1	1	hsa-mir-34a-5p
Up	RRP12	4	hsa-mir-24-3p	Down	CYP2S1	1	hsa-mir-147a
Up	TNFRSF11B	4	hsa-mir-181b-5p	Down	HPN	1	hsa-mir-197-3p

Up	BUB1B	4	hsa-mir-22-3p	Down	MAMDC2	1	hsa-mir-196a-5p
Up	ABCD1	4	hsa-mir-615-3p	Down	CHGA	1	hsa-mir-107
Up	COL15A1	4	hsa-mir-29b-3p	Down	HBB	1	hsa-mir-92a-3p
Up	SFRP4	4	hsa-mir-103a-3p	Down	GPX3	1	hsa-mir-92a-3p
Up	KIF4A	4	hsa-mir-222-3p	Down	EYA2	1	hsa-mir-30a-5p
Up	SERPINB9	4	hsa-mir-127-3p	Down	GKN1	1	hsa-mir-30a-5p
Up	PIK3AP1	4	hsa-mir-32-5p	Down	SMPD3	1	hsa-mir-26b-5p
Up	BMP1	4	hsa-mir-218-5p	Down	ODAM	1	hsa-mir-26b-5p
Up	MMP11	4	hsa-mir-135a-5p	Down	CAPN9	1	hsa-mir-26b-5p
Up	EDNRA	4	hsa-mir-200c-3p	Down	IL1R2	1	hsa-mir-26b-5p
Up	CDH11	4	hsa-mir-27b-3p	Down	TCN1	1	hsa-mir-26b-5p
Up	ADCY3	4	hsa-mir-1296-5p	Down	GSTA1	1	hsa-mir-26b-5p
Up	VIL1	4	hsa-mir-2054	Down	HYAL1	1	hsa-mir-25-3p
Up	TNFAIP6	4	hsa-mir-19b-1-5p	Down	MRAP2	1	hsa-mir-21-5p
Up	NID2	3	hsa-mir-181d-5p	Down	SLC9A2	1	hsa-mir-16-5p
Up	SERPINE2	3	hsa-mir-30e-3p	Down	MAP7D2	1	hsa-mir-505-5p
Up	MRC2	3	hsa-mir-10a-5p	Down	ANO5	1	hsa-mir-432-5p
Up	PTPRO	3	hsa-mir-20a-5p				
Up	CDCA5	3	hsa-mir-18b-5p				
Up	CXCL9	3	hsa-mir-34a-5p				
Up	CXCL6	3	hsa-mir-140-3p				
Up	ASPN	3	hsa-mir-124-3p				
Up	MMP3	3	hsa-mir-138-5p				
Up	TEAD4	3	hsa-mir-512-5p				
Up	APOE	3	hsa-mir-199a-3p				
Up	AJUBA	3	hsa-mir-196b-5p				
Up	BCL2A1	3	hsa-mir-146a-5p				
Up	CXCL1	3	hsa-mir-1-3p				
Up	ANGPT2	3	hsa-mir-542-3p				
Up	CDH3	3	hsa-mir-9-5p				
Up	EXO1	3	hsa-mir-375				
Up	CHTF18	3	hsa-mir-378a-5p				
Up	LILRB4	2	hsa-mir-193b-3p				
Up	CCR1	2	hsa-mir-21-5p				
Up	MSLN	2	hsa-mir-335-5p				
Up	CCL3	2	hsa-mir-223-3p				
Up	PKDCC	2	hsa-mir-25-3p				
Up	C5AR1	2	hsa-mir-26b-5p				
Up	MGP	2	hsa-mir-335-5p				
Up	GPNMB	2	hsa-mir-508-5p				
Up	ADAMTS12	2	hsa-mir-26b-5p				
Up	SFRP2	2	hsa-mir-29a-3p				
Up	CHN1	2	hsa-mir-1301-3p				
Up	COL7A1	2	hsa-mir-29b-3p				
Up	HOXB9	2	hsa-mir-215-5p				
Up	UPP1	2	hsa-mir-192-5p				
Up	WNT2	2	hsa-mir-199a-5p				
Up	NOD1	2	hsa-mir-1250-3p				
Up	LZTS1	2	hsa-mir-214-3p				
Up	PRKDC	2	hsa-mir-101-5p				
Up	ABCA13	2	hsa-mir-148b-3p				
Up	IGFBP7	2	hsa-mir-124-3p				
Up	SULF1	2	hsa-mir-516a-3p				
Up	HTRA3	2	hsa-mir-335-5p				
Up	P4HA3	2	hsa-mir-124-3p				
Up	AMIGO2	2	hsa-mir-155-5p				
Up	MEST	2	hsa-mir-145-5p				
Up	CLEC5A	2	hsa-mir-877-3p				
Up	BOP1	2	hsa-mir-296-3p				
Up	MAP1A	2	hsa-mir-338-3p				
Up	GGT5	2	hsa-mir-346				
Up	FNDC1	2	hsa-mir-1207-3p				
Up	RECQL4	2	hsa-mir-193b-3p				
Up	NEIL2	2	hsa-mir-3160-5p				
Up	KLK6	1	hsa-let-7f-5p				
Up	CLDN2	1	hsa-mir-16-5p				
Up	AGT	1	hsa-mir-26b-5p				
Up	ETV4	1	hsa-mir-26b-5p				
Up	RAD54L	1	hsa-mir-26b-5p				
Up	TYMP	1	hsa-mir-92a-3p				

Up	RCN3	1	hsa-mir-92a-3p
Up	LRFN4	1	hsa-mir-98-5p
Up	COL6A3	1	hsa-mir-29b-3p
Up	TREM2	1	hsa-mir-34a-5p
Up	ACAN	1	hsa-mir-181a-5p
Up	COL16A1	1	hsa-mir-181a-5p
Up	IQGAP3	1	hsa-mir-1-3p
Up	OLFML2B	1	hsa-mir-30b-5p
Up	NCF2	1	hsa-mir-124-3p
Up	SLC1A3	1	hsa-mir-124-3p
Up	HKDC1	1	hsa-mir-124-3p
Up	THBS4	1	hsa-mir-142-3p
Up	IDO1	1	hsa-mir-153-3p
Up	LGI2	1	hsa-mir-149-5p
Up	GUCY1B3	1	hsa-mir-186-5p
Up	PVT1	1	hsa-mir-186-5p
Up	AQP1	1	hsa-mir-320a
Up	RGS1	1	hsa-mir-374a-5p
Up	APOC1	1	hsa-mir-335-5p
Up	COL11A1	1	hsa-mir-335-5p
Up	CST1	1	hsa-mir-335-5p
Up	CHRDL2	1	hsa-mir-335-5p
Up	ATP10A	1	hsa-mir-335-5p
Up	GAL3ST4	1	hsa-mir-335-5p
Up	NRK	1	hsa-mir-335-5p
Up	TRPM2	1	hsa-mir-423-3p
Up	GUCY1A3	1	hsa-mir-412-3p
Up	RFTN1	1	hsa-mir-484
Up	TPX2	1	hsa-mir-193b-3p
Up	EPPK1	1	hsa-mir-193b-3p
Up	DNM1	1	hsa-mir-615-3p
Up	KLHL29	1	hsa-mir-127-5p
Up	ADAMTS2	1	hsa-mir-106b-3p
Up	CTSK	1	hsa-mir-296-3p
Up	FCER1G	1	hsa-mir-1225-3p
Up	CPZ	1	hsa-mir-1909-5p

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	SOX2	247	ABCA13	Down	TP63	177	DNER
Up	MYC	215	ACTN1	Down	STAT3	169	CKB
Up	EGR1	202	ABCD1	Down	HNF4A	165	PKIB
Up	SPI1	202	ADAMTS14	Down	AR	164	RAB27B
Up	NANOG	194	ADAMTS4	Down	SUZ12	150	IRX3
Up	TP63	189	ABCA1	Down	EGR1	149	GHRL
Up	TP53	182	ACAN	Down	SMAD4	133	CAPN8
Up	POU5F1	180	ADAM12	Down	SPI1	131	APOBEC1
Up	AR	179	ADAMTS12	Down	NANOG	131	EPB41L4B
Up	STAT3	179	ADAMTS9	Down	MYC	129	ASAH2
Up	SUZ12	175	ADAMTS2	Down	TP53	120	C6
Up	RUNX1	170	ADCY3	Down	POU5F1	113	GSTA3
Up	HNF4A	165	AGT	Down	MTF2	112	HRH2
Up	FLI1	155	AMIGO2	Down	REST	108	DSC2
Up	MITF	149	AEBP1	Down	MITF	103	KCNJ16
Up	SMAD4	137	ANGPT2	Down	RUNX1	102	CA9
Up	E2F1	131	APLN	Down	GATA2	101	NCAM1
Up	PPARG	129	ALDH1A3	Down	GATA1	96	GATA5
Up	GATA2	129	APOE	Down	TCF4	95	TMEM92
Up	KLF4	123	AJUBA	Down	PPARG	87	SERPINB7
Up	MTF2	121	ANKRD13B	Down	FLI1	86	MAMDC2
Up	GATA1	120	ANLN	Down	ESR1	84	SCNN1B
Up	PPARD	119	AHNAK2	Down	SRY	84	SLC25A4
Up	REST	117	ARHGAP11A	Down	RUNX2	84	SLC5A5
Up	SETDB1	114	ARMC9	Down	TFAP2C	83	ARHGDIG

Up	SRY	107	APOC1	Down	SIN3B	83	IGFALS
Up	SMAD3	106	ANGPTL2	Down	E2F1	77	BTNL8
Up	SOX9	105	ANTXR1	Down	SETDB1	77	MRAP2
Up	ESR1	105	ATP10A	Down	TCF3	76	GABRB3
Up	RUNX2	104	AQP9	Down	PPARD	72	DNMBP-AS1
Up	TCF3	102	ASPM	Down	EZH2	72	KCNQ1
Up	TRIM28	102	ATAD2	Down	SALL4	72	STYK1
Up	EP300	100	ANXA13	Down	RNF2	71	DUOXA2
Up	TCF4	97	ARHGAP39	Down	SMARCA4	71	OXCT1
Up	TET1	97	ATP11A	Down	SOX9	68	SCARA5
Up	SMARCA4	97	BCAT1	Down	SMAD3	67	AKR1C2
Up	KDM5B	95	ATAD5	Down	TRIM28	67	DHCR24
Up	TFAP2C	95	BGN	Down	EP300	65	MUC1
Up	EZH2	92	BICC1	Down	BMI1	63	MAL
Up	SIN3B	91	CACNA1E	Down	JARID2	61	CDHR2
Up	TAL1	84	AQP1	Down	TET1	59	RANBP3L
Up	CREM	84	BUB1	Down	RCOR3	58	SLC26A7
Up	YAP1	84	CCND2	Down	YAP1	57	ALDH3A1
Up	E2F4	83	BUB1B	Down	PBX1	57	CCL28
Up	RCOR3	83	C1R	Down	RAD21	53	HPN
Up	WT1	80	BOC	Down	FOXP1	53	ID1
Up	RNF2	79	BMP1	Down	CREM	53	PTGDR2
Up	CREB1	79	BOP1	Down	TAL1	51	PAIP2B
Up	ASH2L	79	CBX2	Down	OLIG2	51	TMEM100
Up	EOMES	78	C1QTNF6	Down	EOMES	50	RASEF
Up	FOXP1	78	C2CD4A	Down	POU3F2	50	SLC2A12
Up	ATF3	77	CCDC80	Down	ZNF217	48	B4GALNT2
Up	ZNF281	74	CAMK2N1	Down	BACH1	48	GDPD2
Up	PRDM14	74	CD109	Down	CREB1	47	EEF1A2
Up	CUX1	72	CAD	Down	ASH2L	47	PM20D1
Up	RELA	71	BCL2A1	Down	CUX1	45	GCNT2
Up	SMAD2	71	CALD1	Down	ERG	44	GPRC5C
Up	FOXA2	70	C3	Down	NR3C1	43	PRIMA1
Up	BACH1	70	CENPF	Down	CTNNB1	42	AADAC
Up	SCLY	66	C5AR1	Down	PRDM14	42	EYA2
Up	JARID2	63	CDH11	Down	CEBPB	42	GCNT4
Up	SOX17	62	CDC6	Down	KDM5B	42	IRX5
Up	ERG	60	CD248	Down	SOX17	42	ORM1
Up	DMRT1	58	CDH13	Down	ARNT	42	SLC1A2
Up	NR3C1	58	CDH17	Down	ZNF281	41	C1orf210
Up	STAT4	57	CCNF	Down	ATF3	41	TM7SF2
Up	NR0B1	57	CDH3	Down	TFAP2A	40	CCKBR
Up	ZNF217	57	CLDN4	Down	NR0B1	40	NWD1
Up	RAD21	57	CLSPN	Down	DMRT1	39	TM6SF2
Up	NFE2L2	55	CEP170	Down	NFE2L2	37	HAPLN1
Up	JUN	55	CLDN1	Down	E2F4	36	EDARADD
Up	LMO2	53	BMP8A	Down	STAT5A	36	XK
Up	MECOM	53	CCL3	Down	LMO2	35	CTSE
Up	BMI1	53	CDX2	Down	SCLY	35	INSIG1
Up	TBX5	52	CDCA7	Down	TEAD4	35	SH3BGRL2
Up	EWSR1	51	CCL18	Down	SMAD2	34	GKN1
Up	CEBPB	51	CDC25B	Down	RCOR1	34	RASSF6
Up	MYCN	50	COL12A1	Down	WT1	34	TPD52L1
Up	OLIG2	49	CD300LF	Down	JUN	33	CAPN9
Up	TFAP2A	49	CDCA5	Down	YY1	33	CYP3A4
Up	RBPJ	49	COL16A1	Down	KLF1	31	CYB5A
Up	FOXP2	48	CELSR3	Down	TBX5	31	DUSP19
Up	PBX1	45	CKAP2	Down	EWSR1	31	GKN2
Up	EED	45	COL4A1	Down	RBPJ	30	FMO6P
Up	ZFX	44	CTSB	Down	RELA	30	TFF1
Up	GATA4	44	DYSF	Down	CDX2	29	APOA4
Up	TCF7	43	CHRDL2	Down	EED	28	TMEM229A
Up	KLF1	42	COL5A2	Down	CTCF	26	IGSF9
Up	CTNNB1	41	CHI3L1	Down	PHC1	26	NKX6-2
Up	GFI1B	41	CLEC5A	Down	ZFX	26	SH3GL2
Up	TFCP2L1	41	CRISPLD1	Down	AHR	26	VSTM2A
Up	FOXO3	41	CSF3R	Down	MYCN	25	ESRRG
Up	YY1	39	CHN1	Down	MYBL2	24	CNTD1
Up	CCND1	39	CHTF18	Down	FOXP2	24	DHRS9
Up	PAX3	39	DKK2	Down	FOXO3	24	F2RL1

Up	ESRRB	37	COL18A1	Down	TBX3	24	OASL
Up	CTCF	37	DNM1	Down	PAX3	23	ANXA10
Up	TBX3	37	EGR2	Down	MEIS1	23	ARHGEF37
Up	POU3F2	36	CD84	Down	ESR2	23	MAOA
Up	CNOT3	36	CLDN3	Down	MECOM	23	PTGER3
Up	SOX11	36	CTHRC1	Down	GATA4	23	PXMP2
Up	NR1I2	34	COL5A3	Down	DNAJC2	23	VSIG2
Up	PHC1	34	COMP	Down	SIN3A	22	C16ORF89
Up	NR1H3	33	COL4A2	Down	TCF7	21	AMPD1
Up	NACC1	33	ENC1	Down	PAX6	21	ATP4B
Up	ELK1	33	EPPK1	Down	TAF7L	20	C11ORF86
Up	HOXB4	33	F2RL2	Down	NR1I2	20	CYP2C18
Up	RCOR1	32	COL10A1	Down	HTT	20	CYP2C8
Up	ZFP42	31	COL1A2	Down	CNOT3	19	CHGB
Up	ELF5	31	CRABP2	Down	GFI1B	19	CTAGE5
Up	VDR	31	DUSP10	Down	NACC1	19	KLF2
Up	DNAJC2	30	COL7A1	Down	STAT4	18	RAB37
Up	LYL1	29	COL5A1	Down	ELF5	17	CAPN13
Up	ARNT	29	CPXM2	Down	PRDM5	17	CKMT2
Up	HOXC9	28	CLSTN3	Down	STAT1	17	LIFR
Up	MEIS1	27	BACH1	Down	ELK1	17	MYRIP
Up	DACH1	27	CSGALNACT2	Down	GATA3	17	UNC5D
Up	TTF2	27	E2F3	Down	TCF7L2	16	FCGBP
Up	IRF8	27	ENTPD1	Down	CEBPA	16	GC
Up	SMAD1	27	F2R	Down	TTF2	16	POU2AF1
Up	RARG	26	DPYSL3	Down	MYB	16	SLPI
Up	XRN2	26	EXO1	Down	NR1H3	15	ALDOC
Up	HSF1	25	DNM3OS	Down	PADI4	15	CHIA
Up	PHF8	25	FAM83D	Down	HOXB4	15	METTL7A
Up	GATA3	25	GDF15	Down	SREBF2	15	REP15
Up	ELF1	24	CPXM1	Down	HOXC9	14	ELOVL6
Up	FOXP3	23	ECT2	Down	HSF1	14	GGT6
Up	STAT5A	23	GBP5	Down	CCND1	14	GLUL
Up	DROSHA	22	COL15A1	Down	SMAD1	14	PAQR8
Up	MEF2A	22	HMCN1	Down	LYL1	14	SCGN
Up	PAX6	20	ASH2L	Down	DROSHA	14	SHISA6
Up	SIN3A	20	COL8A1	Down	FOXO1	13	AZGP1
Up	PRDM5	20	CYP2W1	Down	SOX11	13	C1ORF115
Up	CLOCK	20	DIO2	Down	MEF2A	13	CDH2
Up	TCF7L2	20	EPHB1	Down	NFIB	13	SCUBE2
Up	KDM5A	20	ESPL1	Down	ELF1	12	AQP10
Up	AHR	20	FN1	Down	TBP	12	GALE
Up	STAT1	20	IER5L	Down	SRF	12	GPT2
Up	PADI4	19	CPS1	Down	ZFP42	12	HYAL1
Up	SRF	18	EPHA3	Down	IRF8	12	TMEM151A
Up	CRX	18	FCGR1A	Down	SREBF1	11	ALDOB
Up	STAT6	18	HAPLN3	Down	VDR	11	GALNT5
Up	RCOR2	16	DGKH	Down	IRF1	11	HHLA2
Up	SREBF2	16	GEM	Down	XRN2	11	SOX21
Up	SREBF1	15	FLRT2	Down	CLOCK	10	AQP4
Up	ESR2	15	H19	Down	CEBPD	9	PAPPA2
Up	CEBPD	15	MMP16	Down	HIF1A	9	UPK1B
Up	NUCKS1	14	DOCK4	Down	DACH1	8	FOXQ1
Up	THAP11	13	FGD6	Down	DCP1A	8	MT1E
Up	TAF7L	13	FKBP10	Down	STAT6	8	PLLP
Up	ZIC3	12	FBXO32	Down	RARG	8	PRSS8
Up	DCP1A	12	FSCN1	Down	CRX	7	HOMER2
Up	ETS1	12	GRIN2D	Down	GBX2	7	SLC16A7
Up	GBX2	12	LCP2	Down	PDX1	7	SLC7A8
Up	IRF1	12	LEF1	Down	THAP11	7	SLC9A1
Up	CEBPA	11	CYP2B6	Down	PHF8	7	XYLT2
Up	KDM6A	11	FANCD2	Down	KDM5A	6	ALDH6A1
Up	HOXD13	11	FBN1	Down	FOXP3	6	FOXA3
Up	NFIB	11	HTRA1	Down	TFEB	6	KLF15
Up	CHD1	11	IGF2BP3	Down	BCL3	6	RORC
Up	TFEB	10	FOXM1	Down	CHD1	6	SOX2
Up	PDX1	10	KIF20A	Down	RCOR2	5	HAS3
Up	HTT	9	IFI44L	Down	ZIC3	5	LIPH
Up	HIF1A	9	INHBA	Down	HOXD13	5	RHBDL2
Up	ASXL1	9	KIF21B	Down	ZNF274	5	SSTR1

Up	TBP	9	MMP14	Down	GLI1	4	ADAMTSL1
Up	E2F7	8	MCM7	Down	TCF21	4	AKR7A3
Up	NR4A2	7	LILRB3	Down	ZNF263	4	ITPKA
Up	BCL3	6	CXCL1	Down	ETS2	4	PRDM16
Up	ZNF274	6	KIF26B	Down	CHD7	3	APOA1
Up	PRDM16	6	MCM10	Down	NR4A2	3	CYP3A5
Up	AP1S2	6	PGM2L1	Down	SALL1	3	GRIA4
Up	THRA	5	IFITM1	Down	KLF5	3	KLF4
Up	FOXO1	5	NEIL2	Down	HCFC1	3	SCG3
Up	TCF21	5	NID2	Down	ZNF652	3	SPDEF
Up	IKZF1	5	PDGFRB	Down	THRA	3	TMED6
Up	ZNF322	5	PLXNC1	Down	MYBL1	2	FBP1
Up	ETS2	4	FOXK1	Down	NUCKS1	2	FGA
Up	CHD7	4	HOXA10	Down	IKZF1	2	GPX3
Up	HCFC1	4	KIF2C	Down	ASXL1	2	KIAA0895
Up	GLI1	4	RAI14	Down	ZNF322	2	RIMS1
Up	KLF2	3	HOXB9	Down	NOTCH1	2	SOWAHA
Up	BP1	3	IL2RA	Down	ETS1	1	SMPD3
Up	KLF5	3	NOTCH3				
Up	SALL1	3	OMD				
Up	CDKN2AIP	3	SPOCK1				
Up	ZNF263	2	LAMA5				
Up	MYBL1	2	NEK2				
Up	ZNF652	2	PLXDC2				
Up	HOXA2	1	KIAA1755				
Up	CIITA	1	PARVG				

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

Figures

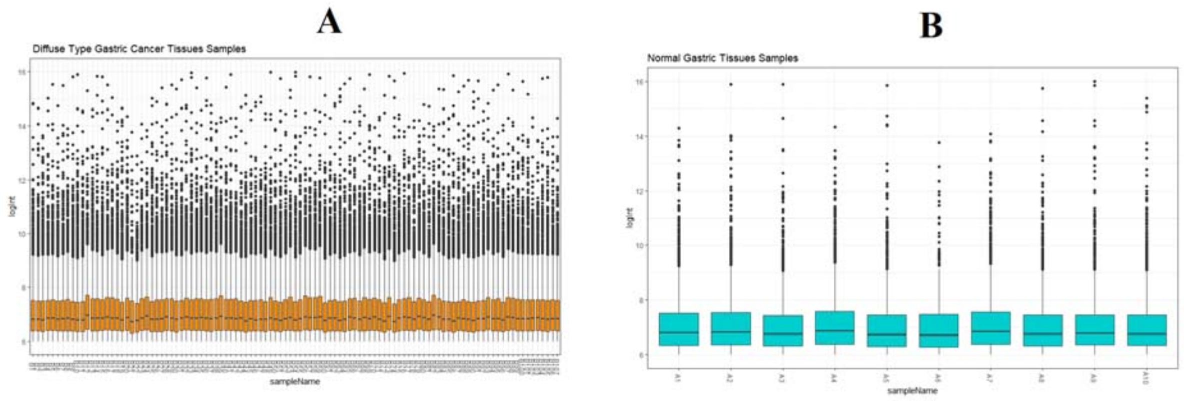

Fig. 1. Box plots of the normalized RNA-seq data. (A) 107 GC samples (B) 10 normal gastric tissue samples. Horizontal axis represents the sample symbol and the vertical axis represents the gene expression values. The black line in the box plot represents the median value of gene expression. (A1 – A10 = Normal gastric tissue samples (blue color box); B1 – B107 = GC samples (brown color box))

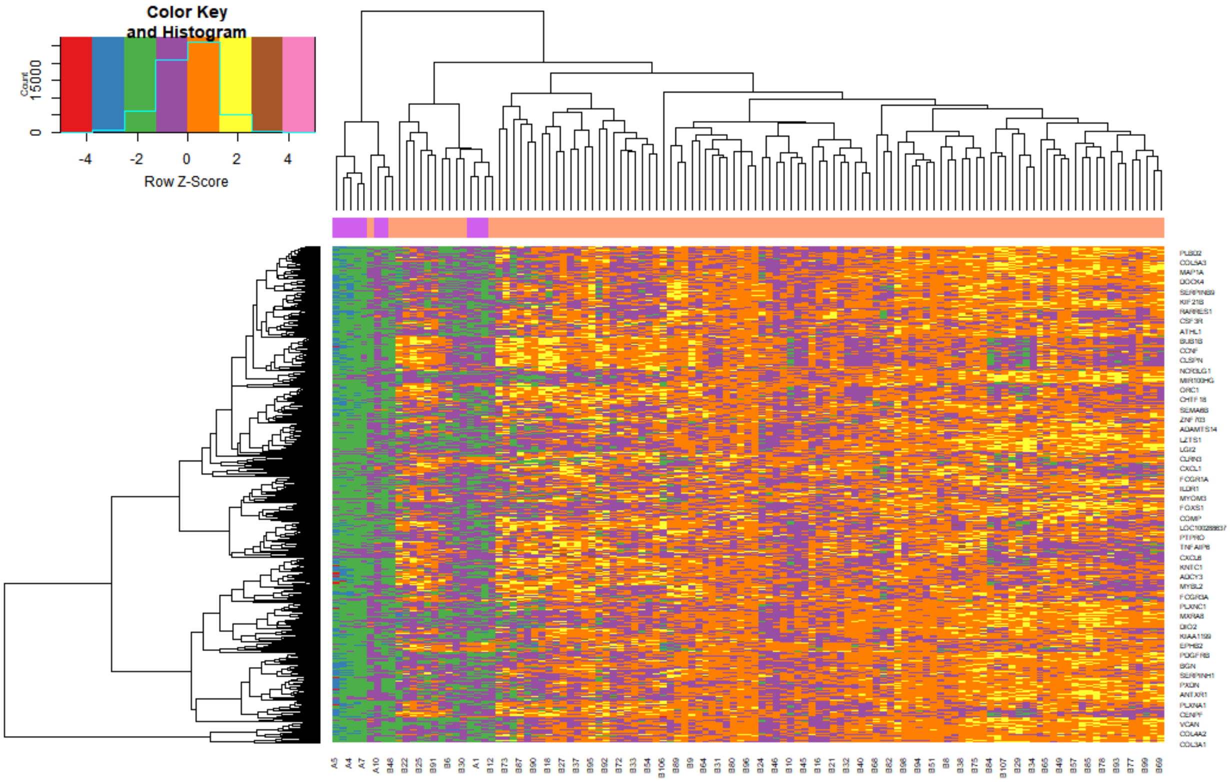

Fig. 2. Heat map of up regulated differentially expressed genes. Legend on the top left indicate log fold change of genes. (A1 – A10 = Normal gastric tissue samples; B1 – B107 = GC samples)

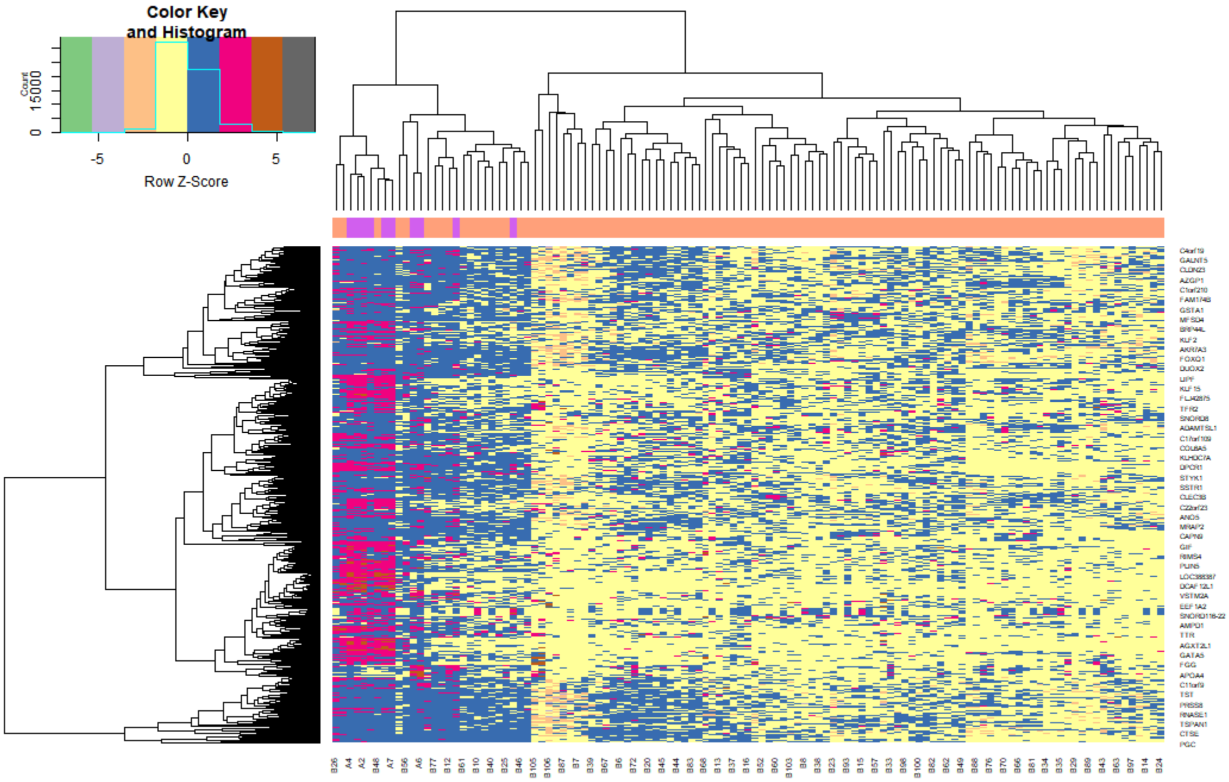

Fig. 3. Heat map of down regulated differentially expressed genes. Legend on the top left indicate log fold change of genes. (A1 – A10 = Normal gastric tissue samples; B1 – B107 = GC samples)

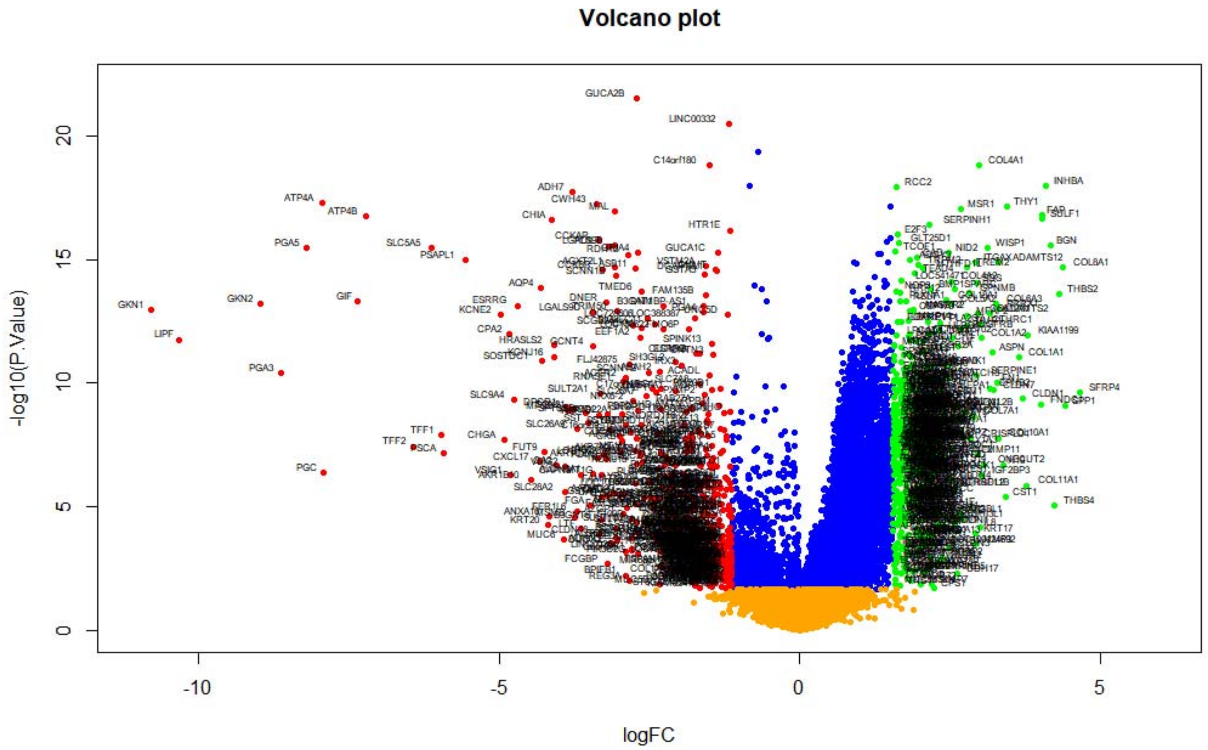

Fig. 4. Volcano plot of differentially expressed genes. Genes with a significant change of more than two-fold were selected.

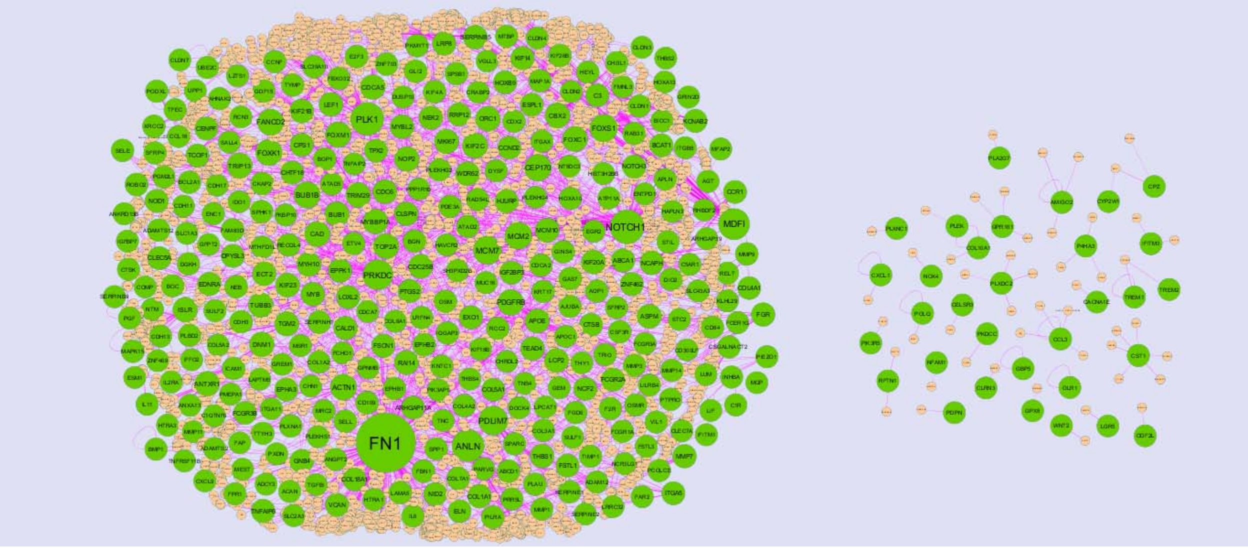

Fig. 5. Protein–protein interaction network of up regulated genes. Green nodes denotes up regulated genes.

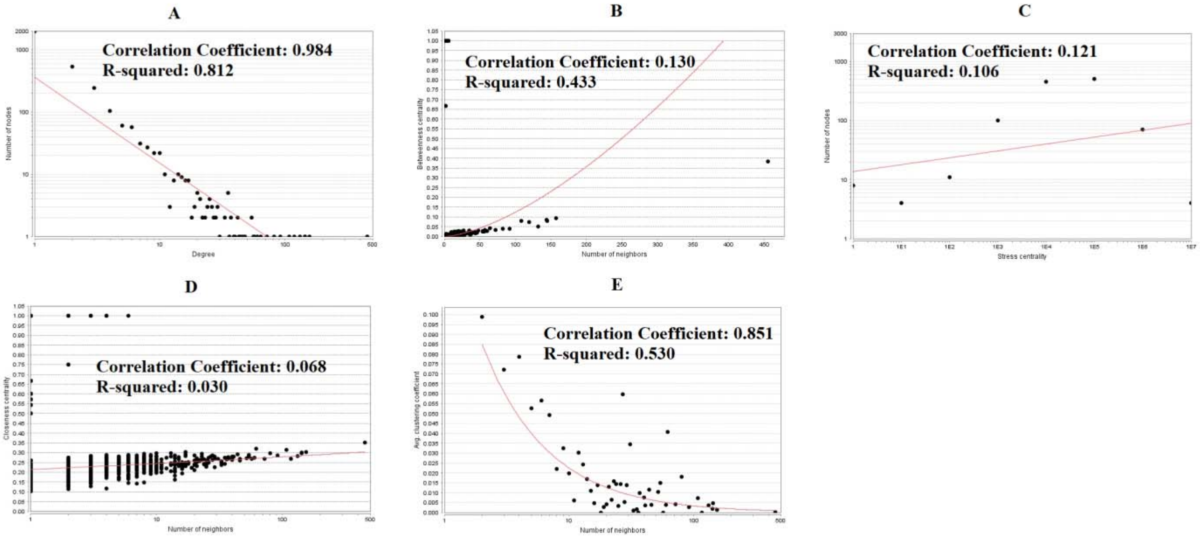

Fig. 6. Scatter plot for up regulated genes. (A- Node degree; B- Betweenness centrality; C- Stress centrality ; D- Closeness centrality; E- Clustering coefficient)

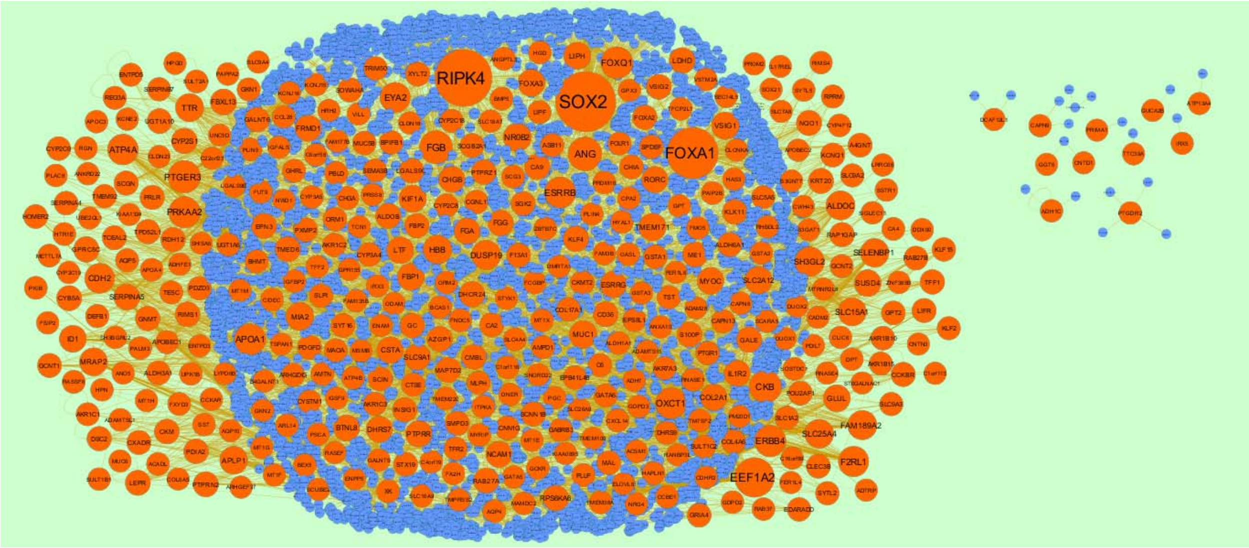

Fig. 7. Protein–protein interaction network of down regulated genes. Red nodes denotes down regulated genes.

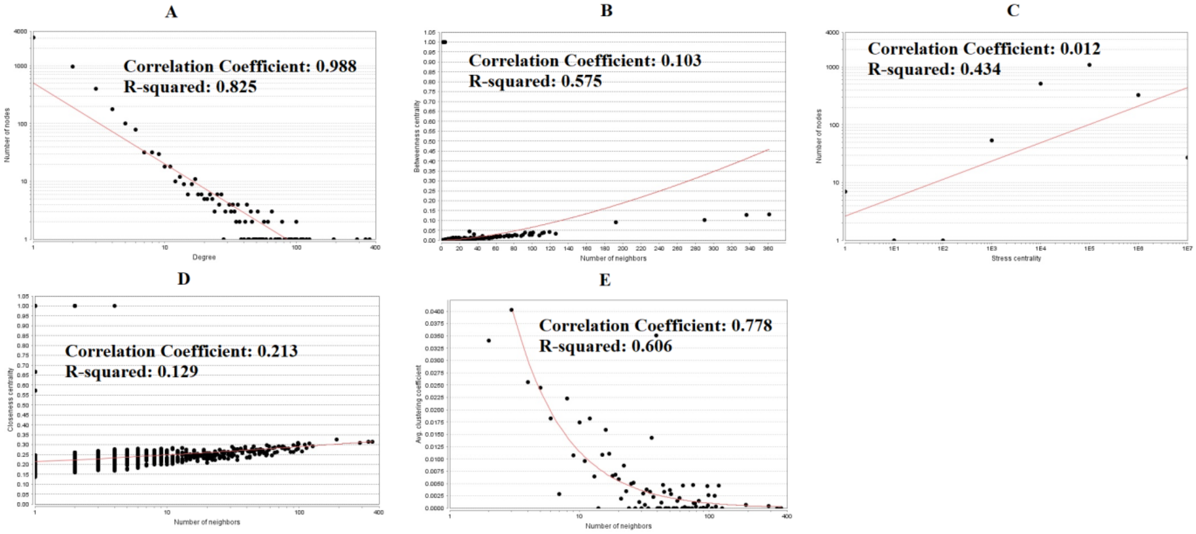

Fig. 8. Scatter plot for down regulated genes. (A- Node degree; B- Betweenness centrality; C- Stress centrality ; D- Closeness centrality; E- Clustering coefficient)

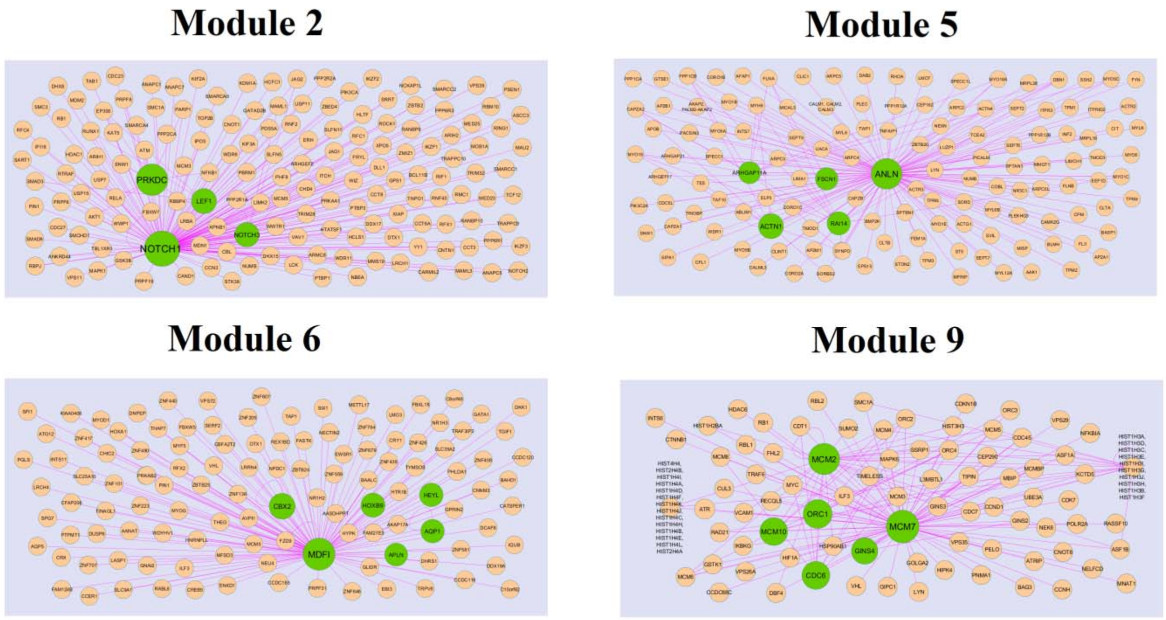

Fig. 9. Modules in PPI network. The green nodes denote the up regulated genes

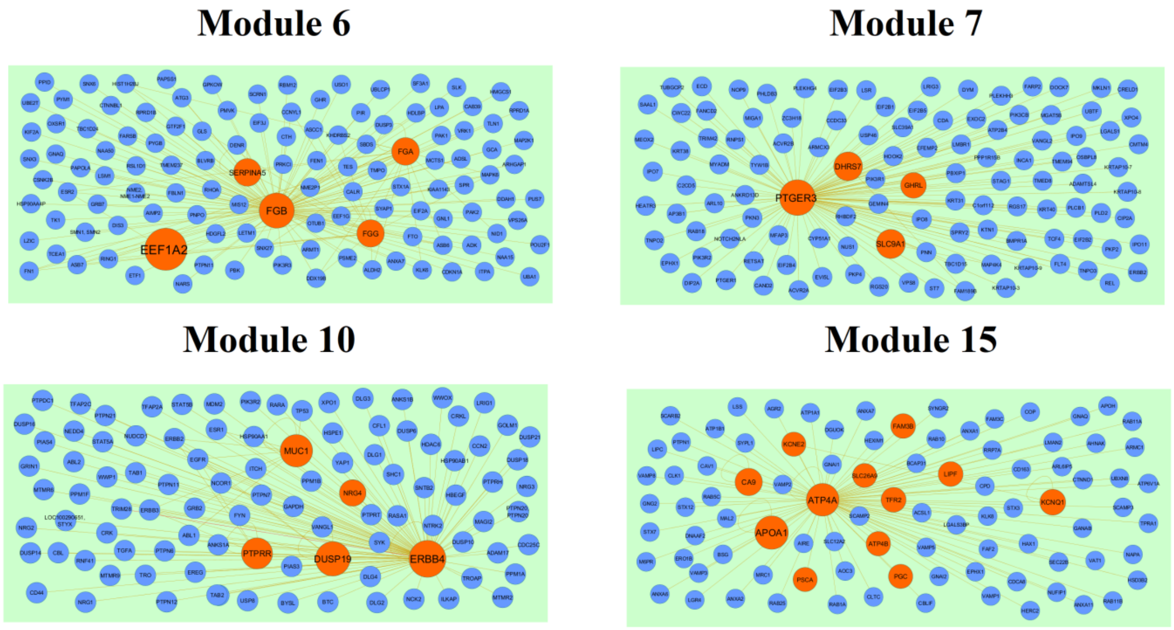

Fig. 10. Modules in PPI network. The red nodes denote the down regulated genes

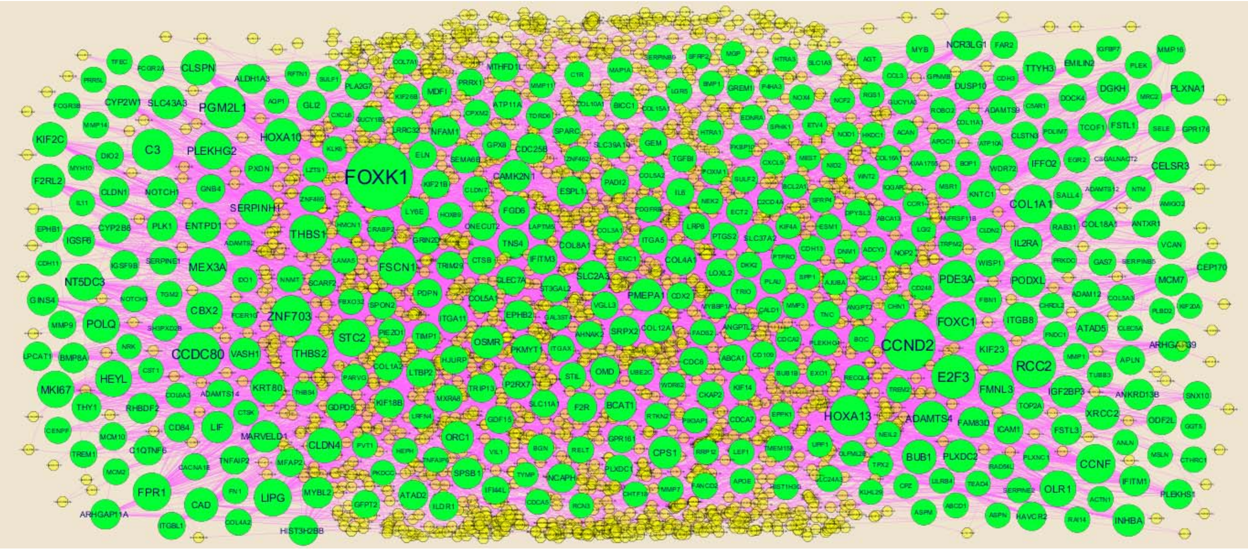

Fig. 11. The network of up regulated genes and their related miRNAs. The green circles nodes are the up regulated genes, and yellow diamond nodes are the miRNAs

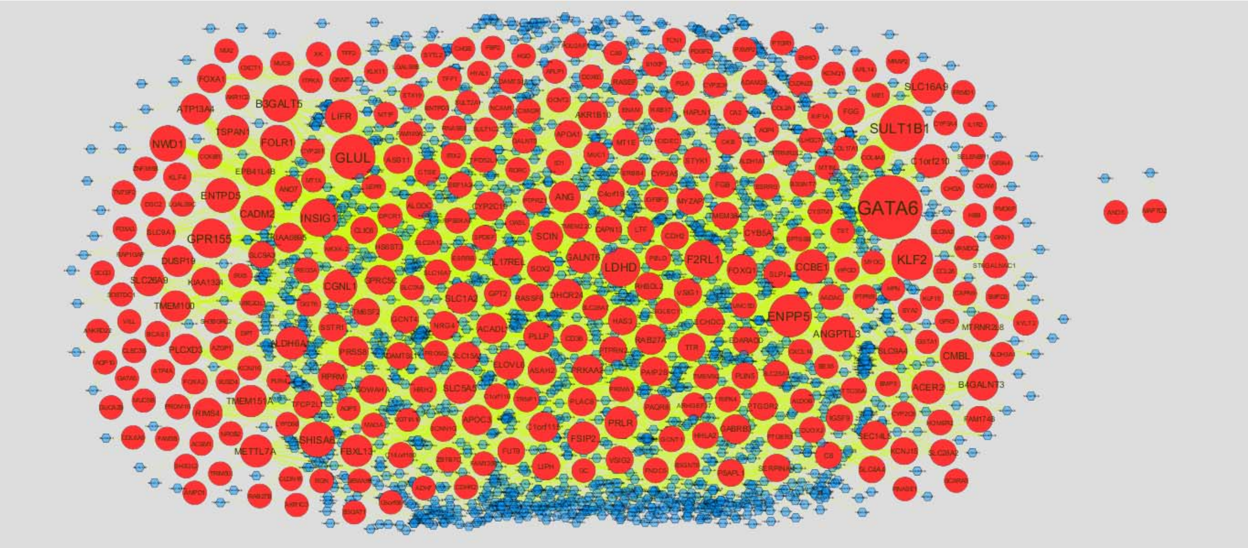

Fig. 12. The network of down regulated genes and their related miRNAs. The red circles nodes are the down regulated genes, and blue diamond nodes are the miRNAs

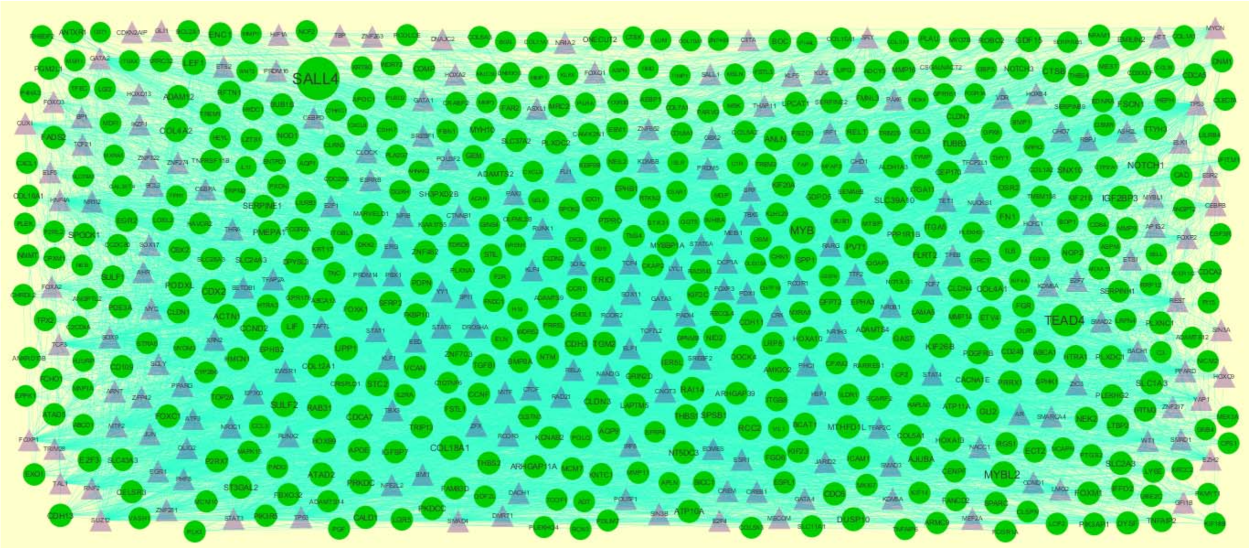

Fig. 13. The network of up regulated genes and their related TFs. The green circles nodes are the up regulated genes, and purple triangle nodes are the TFs

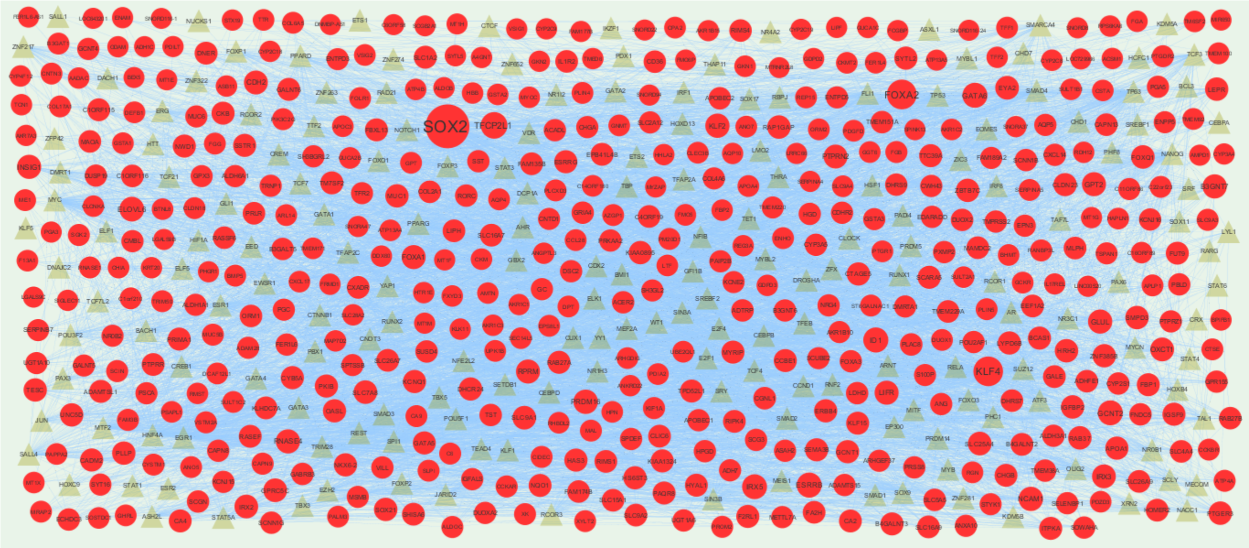

Fig. 14. The network of down regulated genes and their related TFs. The green circles nodes are the down regulated genes, and yellow triangle nodes are the TFs.

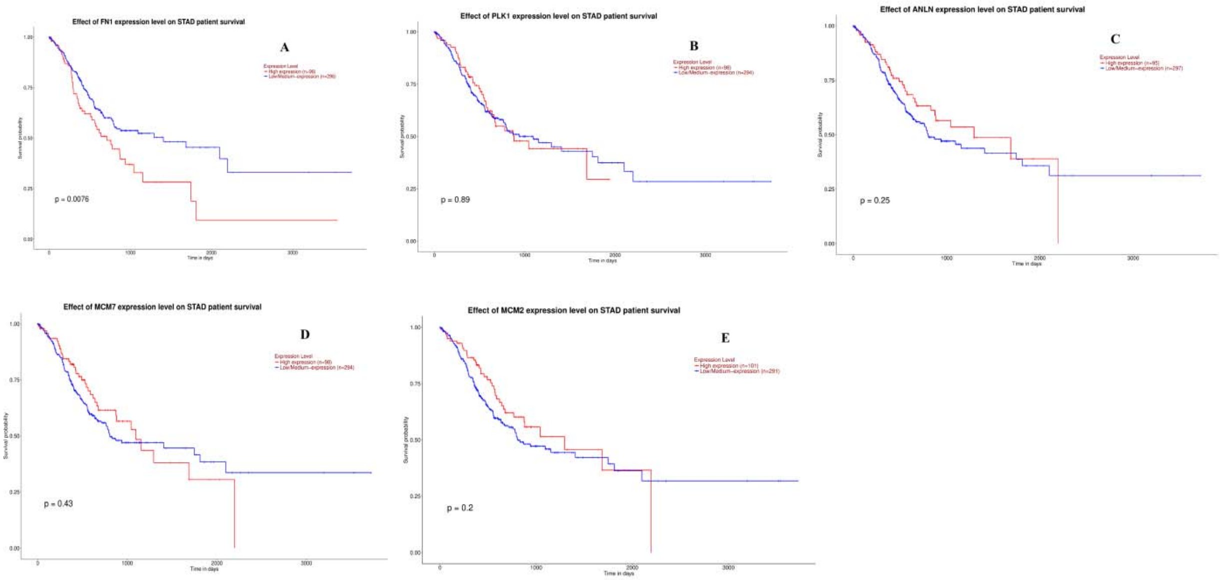

Fig. 15. Survival analysis of up regulated hub genes. Survival analyses were performed using the UALCAN online platform. Red line denotes - high expression; Blue line denotes – low expression. A) FN1 B) PLK1 C) ANLN D) MCM7 E) MCM2

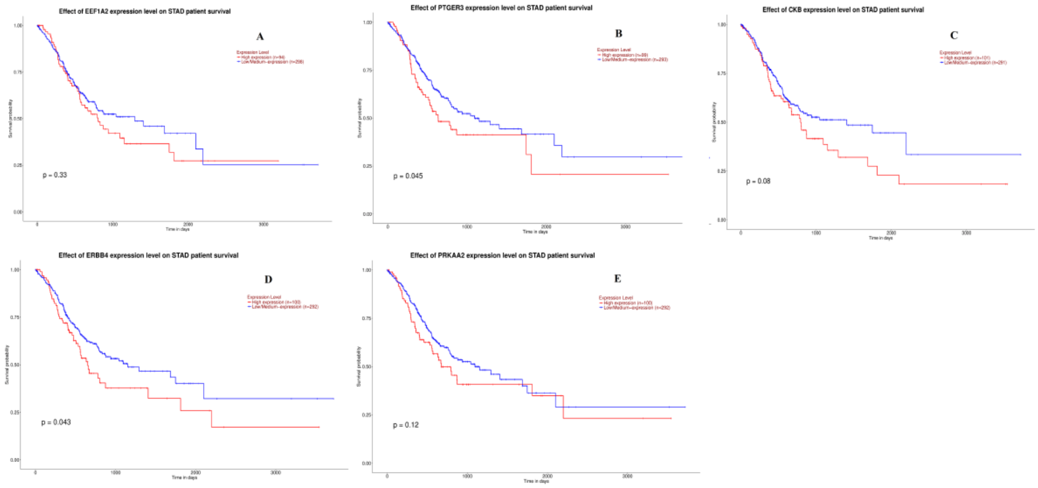

Fig. 16. Survival analysis of down regulated hub genes. Survival analyses were performed using the UALCAN online platform. Red line denotes - high expression; Blue line denotes – low expression. A) EEF1A2 B) PTGER3 C) CKB D) ERBB4 E) PRKAA2

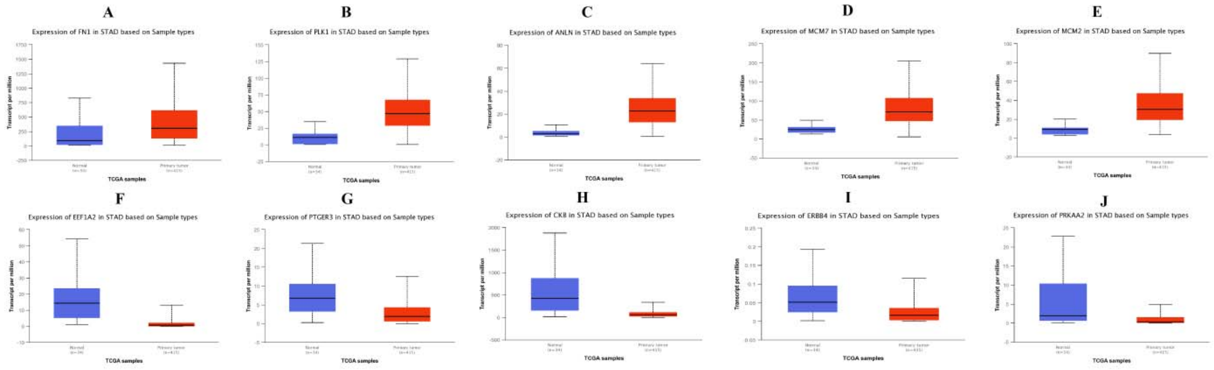

Fig. 17. Box plots (expression analysis) hub genes (up and down regulated) were produced using the UALCAN platform. A) FN1 B) PLK1 C) ANLN D) MCM7 E) MCM2 F) EEF1A2 G) PTGER3 H) CKB I) ERBB4 J) PRKAA2

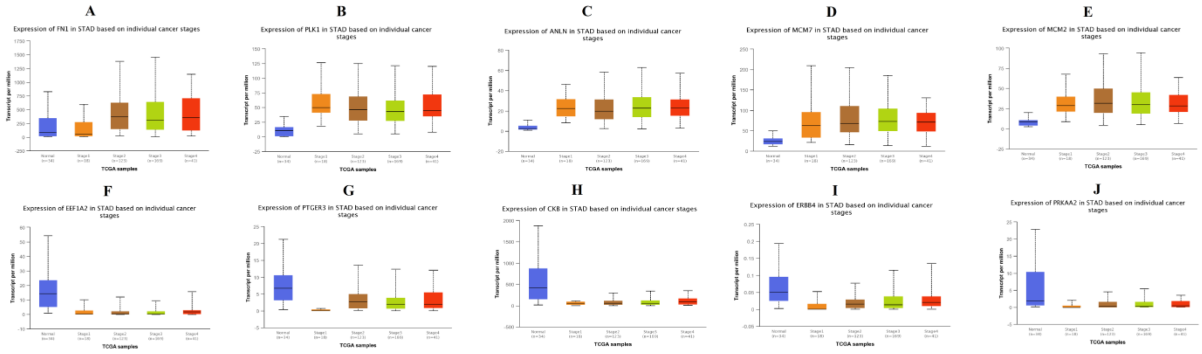

Fig. 18. Box plots (stage analysis) of hub genes (up and down regulated) were produced using the UALCAN platform. A) FN1 B) PLK1 C) ANLN D) MCM7 E) MCM2 F) EEF1A2 G) PTGER3 H) CKB I) ERBB4 J) PRKAA2

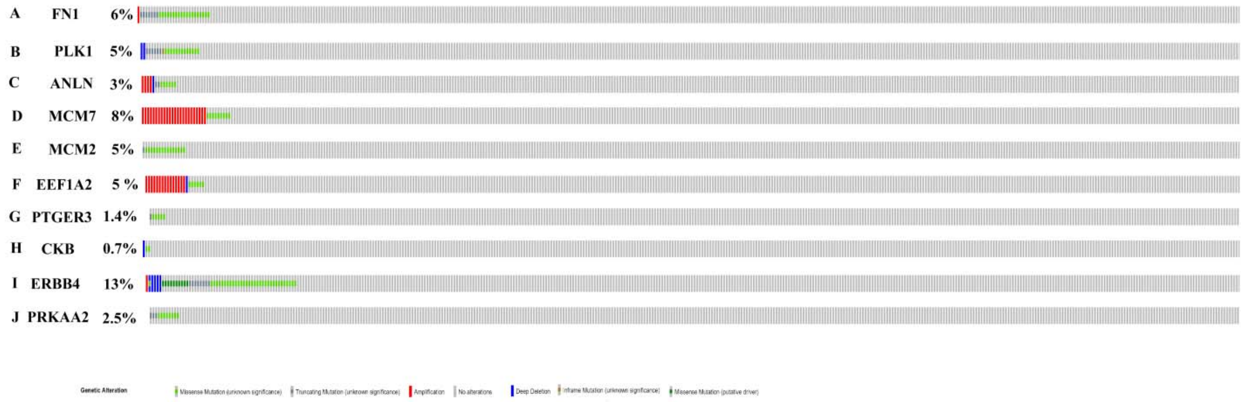

Fig. 19. Mutation analyses of hub genes were produced using the CbioPortal online platform. A) FN1 B) PLK1 C) ANLN D) MCM7 E) MCM2 F) EEF1A2 G) PTGER3 H) CKB I) ERBB4 J) PRKAA2

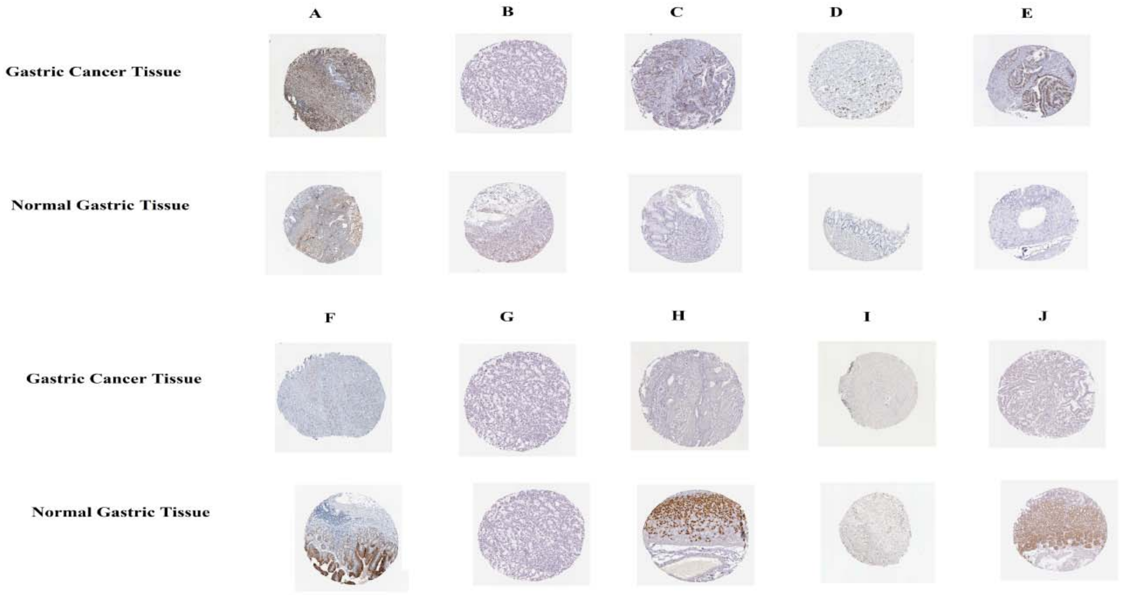

Fig. 20. Immunohisto chemical (IHC) analyses of hub genes were produced using the human protein atlas (HPA) online platform. A) FN1 B) PLK1 C) ANLN D) MCM7 E) MCM2 F) EEF1A2 G) PTGER3 H) CKB I) ERBB4 J) PRKAA2

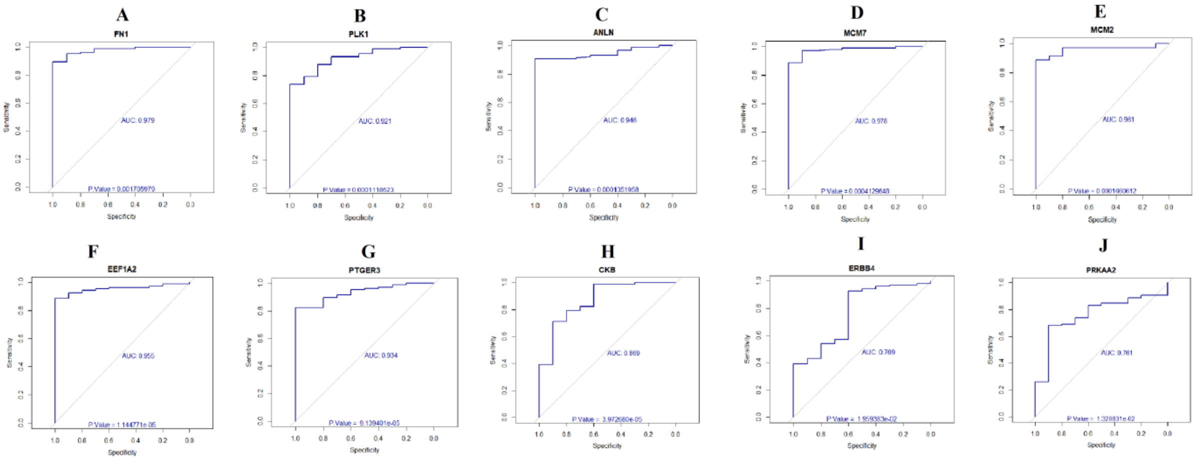

Fig. 21. ROC curve validated the sensitivity, specificity of hub genes as a predictive biomarker for hepatoblastoma prognosis. A) FN1 B) PLK1 C) ANLN D) MCM7 E) MCM2 F) EEF1A2 G) PTGER3 H) CKB I) ERBB4 J) PRKAA2

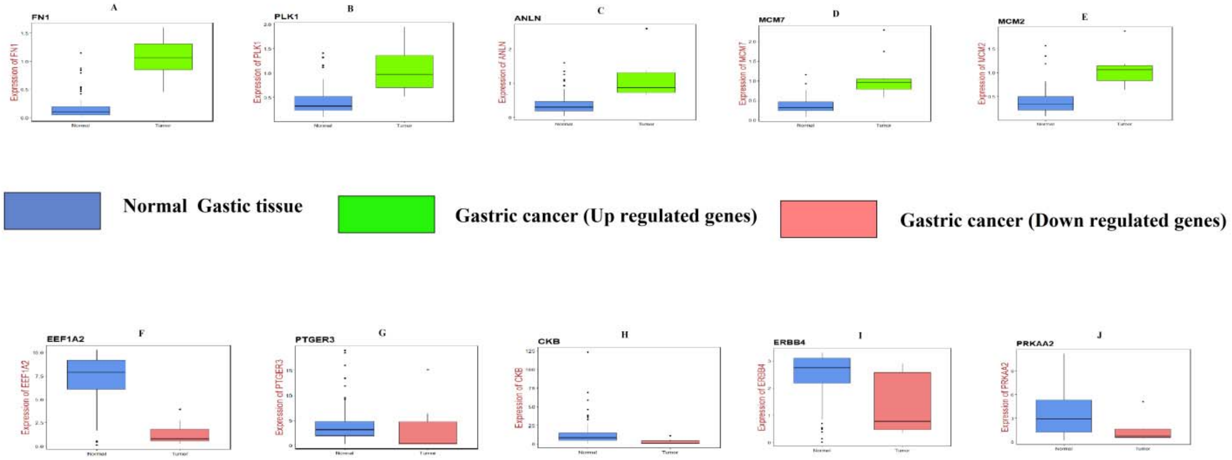

Fig. 22. Validation of hub genes (up and down regulated) by RT- PCR. A) FN1 B) PLK1 C) ANLN D) MCM7 E) MCM2 F) EEF1A2 G) PTGER3 H) CKB I) ERBB4 J) PRKAA2

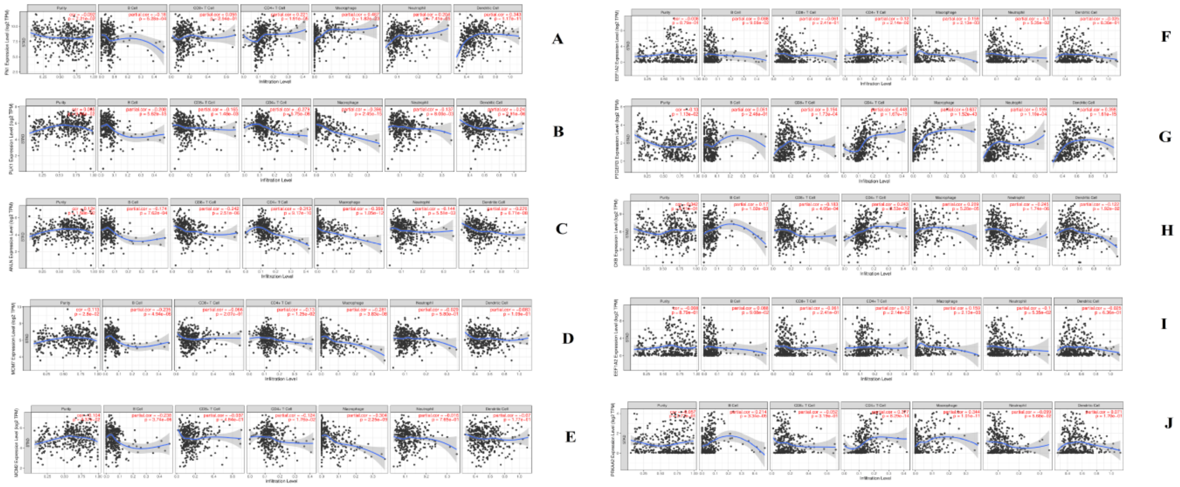

Fig. 23. Scatter plot for immune infiltration for hub genes (up and down regulated). A) FN1 B) PLK1 C) ANLN D) MCM7 E) MCM2 F) EEF1A2 G) PTGER3 H) CKB I) ERBB4 J) PRKAA2