Identification of key genes and associated pathways in neuroendocrine tumors through bioinformatics analysis and predictions of small drug molecules

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Abstract

Neuroendocrine tumor (NET) is one of malignant cancer and is identified with high morbidity and mortality rates around the world. With indigent clinical outcomes, potential biomarkers for diagnosis, prognosis and drug target are crucial to explore. The aim of this study is to examine the gene expression module of NET and to identify potential diagnostic and prognostic biomarkers as well as to find out new drug target. The differentially expressed genes (DEGs) identified from GSE65286 dataset was used for pathway enrichment analyses and gene ontology (GO) enrichment analyses and protein - protein interaction (PPI) analysis and module analysis. Moreover, miRNAs and transcription factors (TFs) that regulated the up and down regulated genes were predicted. Furthermore, validation of hub genes was performed. Finally, molecular docking studies were performed. DEGs were identified, including 453 down regulated and 459 up regulated genes. Pathway and GO enrichment analysis revealed that DEGs were enriched in sucrose degradation, creatine biosynthesis, anion transport and modulation of chemical synaptic transmission. Important hub genes and target genes were identified through PPI network, modules, target gene - miRNA network and target gene - TF network. Finally, survival analyses, receiver operating characteristic (ROC) curve and RT-PCR validated the significant difference of ATP1A1, LGALS3, LDHA, SYK, VDR, OBSL1, KRT40, WWOX, NINL and PPP2R2B between metastatic NET and normal controls. In conclusion, the DEGs and hub genes with their regulatory elements identified in this study will help us understand the molecular mechanisms underlying NET and provide candidate targets for future research.

Keywords: differentially expressed genes; neuroendocrine tumor; bioinformatics; hub gene; protein–protein interaction

Introduction

A small intestine neuroendocrine tumors (NET) is common cancer of small bowel [1]. The absence of early diagnostic and biomarkers are the main reasons for death caused by NET. The 5-year survival rate across all stages of NET is only 70-100% [2]. In the past several decades, numerous attempts have been taken to disclose the molecular pathogenesis of NET, and to advance the patient prognosis through many therapeutic strategies. However, narrow progress has been made to lengthen the survival and to diminish the mortality. For patients, surgery, trans arterial embolisation and chemotherapy offer only limited options for NET treatment [3-4]. However, due to surgical therapy limitations, progressive tumors can reappear even after complete surgical resection; maximum patients with NET are not suitable for surgical resection and fewer than 23.8% of patients respond to conventional chemotherapy [5]. In addition, the clinical success of NET always compromised due to initial metastasis and chemo resistance. Consequently, extensive investigations of potential diagnosis biomarkers and identification of new therapeutic targets for NET patients are urgently needed.

Recently, the gene expression profile chip, a high throughput and efficient technique, has been extensively used in an array of disease research fields to explain the association between disease and genes and pathways, and provide the important clues for the progression of the NET [6]. For example, alteration in CDKN1B was linked with development of NET [7]. Genes such as NAP1L1, MAGE-D2, MTA1, MIB-1, p53, and bcl-2 were responsible for pathogenesis of NET [8-9]. High expression of CDX-2 was liable for development of NET [10]. Loss of tumor suppressor gene TCEB3C was linked with development of NET [11]. Pathways such as mTOR signaling pathway [12], notch signaling [13], phosphatidylinositol 3-kinase/Akt signaling [14], sonic hedgehog-gli1 signaling pathway [15] and GPCR pathways [16] were responsible for pathogenesis of NET. Thus, more work is needed to discover the underlying molecular mechanisms in NET.

In this study, we diagnosed important genes in NET by combining bioinformatics analyses. In this study, we diagnosed important genes in NET by combining bioinformatics analyses. Differentially expressed genes (DEGs), pathways, and gene ontology (GO) terms associated with NET were investigated. Subsequently, the identification of hub genes from protein-protein interactions (PPIs) network, modules analysis, construction of target gene - miRNA network and target gene - TF network. Furthermore, survival analyses, receiver operating characteristic (ROC) curve and RT-PCR were

carried out for validation of hub genes. Finally, molecular docking studies was performed. We investigated the potential candidate biomarkers for their utility in diagnosis, prognosis, and drug targeting in NET.

Materials and methods

Microarray data

Gene expression profile GSE65286 was downloaded from the National Center for Biotechnology Information Gene Expression Omnibus (GEO, <http://www.ncbi.nlm.nih.gov/geo>) [17] database. GSE65286 included 33 patients with metastatic NET and on 10 normal controls. The expression profile was provided on GPL4133 Agilent-014850 Whole Human Genome Microarray 4x44K G4112F (Feature Number version).

DEG screening

The original txt files were downloaded and classified as patients with metastatic NET and normal controls. The limma package of Bioconductor (<http://www.bioconductor.org/>) [18] was used for data standardization and transforming raw data into expression values. The significance analysis of the empirical Bayes methods within limma package was applied to diagnose DEGs between patients with metastatic NET and on normal controls. The genes with the following cutoff criteria were considered as the significant DEGs: $p < 0.05$, and $|\log FC| > 3.01$ for up regulated genes and $|\log FC| > -2.75$ for down regulated genes.

Pathway enrichment analysis

Pathway enrichment analysis was used to diagnose the potential functional and metabolic pathways associated with DEGs. BIOCYC (<https://biocyc.org/>) [19], Kyoto Encyclopedia of Genes and Genomes (KEGG) (<http://www.genome.jp/kegg/pathway.html>) [20], Pathway Interaction Database (PID) (<https://wiki.nci.nih.gov/pages/viewpage.action?pageId=315491760>) [21], REACTOME (<https://reactome.org/>) [22], GenMAPP (<http://www.genmapp.org/>) [23], MSigDB C2 BIOCARTEA (v6.0) (<http://software.broadinstitute.org/gsea/msigdb/collections.jsp>) [24], PantherDB (<http://www.pantherdb.org/>) [25], Pathway Ontology (<http://www.obofoundry.org/ontology/pw.html>) [26] and Small Molecule Pathway Database (SMPDB)

(<http://smpdb.ca/>) [27] were a collection of databases that store a large number of information about genomes, biological pathways, diseases, chemical substances, and drugs. We performed pathway enrichment analysis by ToppCluster (<https://toppcluster.cchmc.org/>) [28]. ToppCluster is a commonly used online biological information database that provides comprehensive pathway interpretations. $p < 0.05$ was considered statistically significant.

Gene ontology (GO) enrichment analysis

The GO (<http://www.geneontology.org>) [29] database associated three categories such as biological process (BP), cellular component (CC), and molecular function (MF). ToppCluster (<https://toppcluster.cchmc.org/>) [28] provides a set of functional annotation tools to analyze the biological roles of genes. In this study, GO terms were analyzed using the DAVID online tool with the enrichment threshold of $P < 0.05$.

Protein–protein interaction (PPI) network construction and module analysis

Human Integrated Protein-Protein Interaction rEference (HIPPIE) (<http://cbdm.uni-mainz.de/hippie/>) [30] was used to construct the PPI network which integrates different PPI databases such as IntAct (<https://www.ebi.ac.uk/intact/>) [31], BioGRID (<https://thebiogrid.org/>) [32], HPRD (<http://www.hprd.org/>) [33], MINT (<https://mint.bio.uniroma2.it/>) [34], BIND (<http://download.baderlab.org/BINDTranslation/>) [35], MIPS (<http://mips.helmholtz-muenchen.de/proj/ppi/>) [36] and DIP (<http://dip.doe-mbi.ucla.edu/dip/Main.cgi>) [37]. The interactions with a combined score > 0.4 were considered significant. The PPI network was visualized through the Cytoscape software (<http://www.cytoscape.org/>) [38]. Five topological properties such as node degree (number of interactions with author genes) [39], betweenness (fraction of shortest paths between node pairs in a network) [40], stress (node is a node traversed by a high number of shortest paths) [41], closeness (inverse of the average length of the shortest paths to/from all the other nodes) [42] and clustering coefficient (measure of degree to which nodes in a graph tend to cluster together) [43] were implemented for PPI network analysis. PEWCC1 plug-in of the Cytoscape software was applied to screen significant modules from the PPI network [44]. The degree cutoff = 10, node score cutoff = 0.2, k-core = 2, and max. depth = 100 were used as selection criterion.

Construction of the target gene - miRNA network

NetworkAnalyst (<https://www.networkanalyst.ca/>) [45] was identify microRNAs (miRNAs) around which significant changes occur at the transcriptional level, we employed the comprehensive human post-transcriptional regulatory network consisting of the experimentally verified target gene - miRNA network from TarBase (<http://diana.imis.athena-innovation.gr/DianaTools/index.php?r=tarbase/index>) [46] and miRTarBase (<http://mirtarbase.mbc.nctu.edu.tw/php/download.php>) [47] databases. The target gene - miRNA network was visualized using Cytoscape software (<http://www.cytoscape.org/>) [38].

Construction of the target gene - TF network

NetworkAnalyst (<https://www.networkanalyst.ca/>) [45] was identify transcription factors (TFs) around which significant changes occur at the transcriptional level, we employed the comprehensive human transcriptional regulatory network consisting of the experimentally verified target gene - TF network from ChEA (<http://amp.pharm.mssm.edu/lib/chea.jsp>) [48] database. The target gene - TF network was visualized using Cytoscape software (<http://www.cytoscape.org/>) [38].

Validations of hub genes

PROGgeneV2 (<http://genomics.jefferson.edu/proggene/>) [49] was used to perform a survival analysis of the core genes. The hazard ratio (HR) with 95% confidence intervals and log-rank P value were calculated and displayed on the plot. The data of PROGgeneV2 are based on GEO and the Cancer Genome Atlas database. The receiver operating characteristic (ROC) curve was plotted and the area under the curve (AUC) was calculated by using the generalized linear model (GLM) in machine learning algorithms with R package“pROC” to evaluate the capability of genetic markers in distinguishing metastatic NET and normal controls using GEO database [50]. Finally, reverse transcription polymerase chain reaction (RT-PCR) was carried out for validation of hub genes. Total RNA from in vitro cultured cells of NET (ATCC® CRL-3254) and normal (ATCC® CRL-7869) was isolated with TRI Reagent® (Sigma, USA) according to the manufacturer's protocol. According protocol for cDNA synthesis was reverse transcription at 42°C for 75 min and at 98°C for 5 min by using Reverse transcription cDNA kit (Thermo Fisher Scientific, Waltham, MA, USA). PCR amplification was performed using the QuantStudio 7 Flex real-time PCR system (Thermo Fisher Scientific, Waltham, MA, USA). The RT -PCR thermocycling conditions were as follows: initial denaturation at 95°C for 30 sec and 40 cycles of 95°C for 5 sec and 60°C for 34 sec. The relative expression level was determined as targeting genes divided by β -actin. Relative miRNA expression

was generated with $2^{-\Delta\Delta C_t}$ method [51]. Primers used in this study are shown in Table 1. All experiments were performed independently in triplicate.

Molecular docking studies

The Surflex-Docking docking studies were conducted using the perpetual software module SYBYL-X 2.0 for the built molecules. The molecules were sketched using ChemDraw Tools, imported and saved into sdf. format using free Open Babel software. The co-crystallised protein structures of CFTR, EZR, ATP1A1, TUBA1C and LGALS3 and their co-crystallized PDB code of 4WZ6, 4RM8, 3KDP, 3E22 and 6FOF respectively were selected for docking and were extracted from Protein Data Bank [52-55]. Optimization of the designed molecules were performed by converting 3D concord structure, applying TRIPOS force field and adding Gasteiger Huckel (GH) charges, In addition, MMFF94s and MMFF94 algorithm processes have been used or energy minimization. After the introduction of protein, protein processing was accomplished. The co-crystallized ligand and all water molecules were expelled from the crystal structure; more hydrogen was added and the side chain was refined. The TRIPOS force field was used to reduce structure complexity and the interaction efficiency of the compounds with the receptor was represented in kcal/mol units by the Surflex-Dock score. The best spot between the protein and the ligand was inserted into the molecular region. The visualisation of ligand interaction with receptor is done by using discovery studio visualizer.

Results

DEG screening

In the current study, DEGs and their significant biological characteristics were diagnosed based on GEO data set by integrated bioinformatics analysis of NET. The NET expression microarray data set GSE65286 was first selected and [downloaded](#). There were a total of 43 samples including 33 patients with metastatic NET and 10 normal controls. After gene expression data processing and normalizing (Fig 1A and Fig 1B), we screened DEGs among GEO data set using the limma package with corrected $p < 0.05$, and $|\log FC| > 3.01$ for up regulated genes and $|\log FC| > -2.75$ for down regulated genes (Table 2). There were 912 DEGs including 459 up regulated and 453 down regulated genes. The volcano plots of DEGs is shown in Fig. 2. A heat map demonstrated the significant differential distribution of the DEGs (up and down regulated genes) using data profile GSE65286 as a reference (Fig. 3A and Fig. 3B).

Pathway enrichment analysis

To further analyze the biological function of the DEGs we processed pathway enrichment analysis with ToppCluster. As we conducted the pathway enrichment analysis, we found that these up and down regulated genes were mainly enriched in sucrose degradation, glutathione-mediated detoxification, chemical carcinogenesis, carbohydrate digestion and absorption, FOXA2 and FOXA3 transcription factor networks, a6b1 and a6b4 integrin signaling, transmembrane transport of small molecules, glutathione conjugation, Blood group glycolipid biosynthesis lact series, glycerolipid metabolism, genes encoding proteins affiliated structurally or functionally to extracellular matrix proteins, mechanism of gene regulation by peroxisome proliferators via PPARa (alpha), aginine biosynthesis, 2-arachidonoylglycerol biosynthesis, lipoprotein metabolic, renin-angiotensin system signaling, gluconeogenesis, arginine and proline metabolism, creatine biosynthesis, S-adenosyl-L-methionine biosynthesis, insulin secretion, complement and coagulation cascades, FOXA2 and FOXA3 transcription factor networks, FOXA transcription factor networks, platelet degranulation, cardiac conduction, urea cycle and metabolism of amino groups, extrinsic prothrombin activation pathway, acute myocardial infarction, blood coagulation, ionotropic glutamate receptor, insulin secretion pathway, coagulation cascade, lidocaine (antiarrhythmic) pathway and tranexamic acid pathway The pathways with p value <0.05 are shown in Table 3 and Table 4.

Gene ontology (GO) enrichment analysis

The significant enrichment result of DEGs in BP, CC and MF are shown in Table 5 and Table 6. Up regulated genes were enriched in anion transport, cellular response to xenobiotic stimulus, cluster of actin-based cell projections, membrane region, transmembrane transporter activity and carbohydrate binding. Meanwhile, down regulated genes were enriched in modulation of chemical synaptic transmission, anterograde trans-synaptic signaling, secretory granule, vesicle membrane, cytoskeletal protein binding and metal ion transmembrane transporter activity.

Protein–protein interaction (PPI) network construction and module analysis

The constructed PPI network of up regulated gene is shown in Fig. 4A. In total, 4933 nodes and 8183 interacting protein pairs were contained in the PPI network. The up regulated hub genes were ranked by node degree distribution, betweenness centrality, stress centrality, closeness centrality and clustering coefficient. CFTR, EZR, ATP1A1, TUBA1C, LGALS3,

C15orf48, LDHA, G6PC, ACOT11, PLA2G12B, HSD17B2 and DHDH were considered as up regulated hub genes in NET are listed in Table 7. These up regulated hub genes enriched in pancreatic secretion, cystic fibrosis transmembrane conductance regulator and beta 2 adrenergic receptor pathway, carbohydrate digestion and absorption, genes encoding proteins affiliated structurally or functionally to extracellular matrix proteins, metabolic pathways, carbohydrate digestion and absorption, metabolism of lipids and lipoproteins, lipid metabolic process, steroid hormone biosynthesis and oxidoreductase activity. Meanwhile, constructed PPI network of down regulated gene is shown in Fig. 4B. In total, 5307 nodes and 9099 interacting protein pairs were contained in the PPI network. The down regulated hub genes were ranked by node degree distribution, betweenness centrality, stress centrality, closeness centrality and clustering coefficient. KRT40, FOXA1, WWOX, OBSL1, ALB, PPP2R2B, CBX1, PHLDB2, HIPK2, SLC18A1, PNMA2 and ABCA3 are listed in Table 7. These down regulated hub genes enriched in developmental biology, FOXA2 and FOXA3 transcription factor networks, neuron projection morphogenesis, thyroid hormone synthesis, dopaminergic synapse, cell junction, cardiac conduction, adrenaline and noradrenaline biosynthesis and secretory granule.

A total of 748 modules were obtained from PPI network of up regulated genes. The four most significant modules (module 1, module 3, module 5 and module 6) were obtained using PEWCC1 in Cytoscape (Fig. 5A). Module 1 had 59 nodes and 119 edges, module 3 had 24 nodes and 55 edges, module 5 had 23 nodes and 50 edges and module 6 had 21 nodes and 43 edges. Hub genes in these modules are enriched in pancreatic secretion, cystic fibrosis transmembrane conductance regulator and beta 2 adrenergic receptor pathway, anion transport, metabolic pathways, gamma-glutamyl cycle, oxoacid metabolic process, PI3K-Akt signaling pathway, EPHA forward signaling, antigen binding to B cell receptors activates protein tyrosine kinases, such as the Src family, which ultimate activate MAP kinases, genes encoding proteins affiliated structurally or functionally to extracellular matrix proteins and carbohydrate digestion and absorption. Meanwhile, total of 889 modules were extracted from PPI network of down regulated genes. The four most significant modules (module 1, module 2, module 4 and module 6) were obtained using PEWCC1 in Cytoscape (Fig. 5B). Module 1 had 23 nodes and 49 edges, module 2 had 22 nodes and 51 edges, module 4 had 18 nodes and 36 edges and module 6 had 14 nodes and 27 edges. Hub genes in these modules are enriched in cell projection morphogenesis, neuroactive ligand-receptor interaction, thyroid hormone synthesis, hormone transport, secretory granule, insulin secretion, modulation of chemical synaptic transmission and Synaptic vesicle trafficking.

Construction of the target gene - miRNA network

Prediction of miRNAs was aimed to further understand which miRNAs and no of miRNAs controls the up and down regulated genes (Fig. 6A and Fig. 6B). Top five up regulated targeted genes such as VAV3 interacts with 164 miRNAs, SULT1B1 interacts with 131 miRNAs, MACC1 interacts with 97 miRNAs, E2F2 interacts with 78 miRNAs and SLC28A1 interacts with 75 miRNAs are listed in Table 8. These target genes in this network were enriched in EPHA forward signaling, biological oxidations and transmembrane transport of small molecules. Meanwhile, top five down regulated targeted genes such as SVOP interacts with 107 miRNAs, KCNJ6 interacts with 90 miRNAs, SORCS2 interacts with 88 miRNAs, HEYL interacts with 83 miRNAs and SMOC1 interacts with 80 miRNAs are listed in Table 8. These target genes in this network were enriched in vesicle membrane, dopaminergic synapse, neuron differentiation and calcium ion binding.

Construction of the target gene - TF network

TFs play a key role in the control of gene expression, so the TFs that controlled up and down regulated genes were also predicted (Fig. 7A and Fig. 7B). Top 5 up regulated targeted genes such as CYBRD1 interacts with 158 TFs, MUC13 interacts with 152 TFs, UGT1A6 interacts with 128 TFs, ATP1A1 interacts with 119 TFs and YIF1B interacts with 114 TFs are listed in Table 9. These target genes in this network were enriched in transmembrane transport of small molecules, O-linked glycosylation of mucins, chemical carcinogenesis, carbohydrate digestion and absorption. Meanwhile, Top 5 down regulated targeted genes such as TBXAS1 interacts with 186 TFs, HS6ST3 interacts with 165 TFs, RUNX1T1 interacts with 156 TFs, ATP1B2 interacts with 138 TFs and RFX6 interacts with 125 TFs are listed in Table 9. These target genes in this network were enriched in aspirin blocks signaling pathway involved in platelet activation, transcriptional misregulation in cancer, cardiac conduction and regulation of beta-cell development.

Validations of hub genes

The prognostic effects of the 10 hub genes (up and down regulated genes) in the PPI network were evaluated in PROGgeneV2. It showed that higher mRNA expressions of ATP1A1 (HR: 0.48 [0.35–0.67] (Fig. 8IA), $P = 1.37e-05$), LGALS3 (HR: 0.77 [0.62–0.77] (Fig. 8IB), $P = 0.024321$), SYK (HR: 0.65 [0.57–0.75], $P = 0$) (Fig. 8IC), VDR (HR: 0.77 [0.69–0.87], $P = 1.45e-05$) (Fig. 8ID), OBSL1 (HR: 0.56 [0.38–0.84], $P = 0.00487$) (Fig. 8IE), KRT40 (HR: 0.66 [0.58–

0.76], $P = 0$) (Fig. 8IF), NINL (HR: 0.52 [0.36–0.74], $P = 0.00034$) (Fig. 8IG) and PPP2R2B (HR: 0.75 [0.64–0.89], $P = 0.000777$) (Fig. 8IH) were associated with better overall survival in NET patients), whereas higher expression of LDHA (HR: 2.52 [2.05–3.1], $P = 0$) (Fig. 8IIA) and WWOX (HR: 4.87 [3.48–6.82], $P = 0$) (Fig. 8IIB) were related to poor overall survival in NET patients. ROC curve analysis was used to assess the ability of the expression levels of ATP1A1, LGALS3, SYK, VDR, LDHA, OBSL1, KRT40, NINL, PPP2R2B and WWOX to distinguish between metastatic NET and normal control. The results suggested that AUC values of ATP1A1, LGALS3, SYK, VDR, LDHA, OBSL1, KRT40, NINL, PPP2R2B and WWOX were 0.973, 0.991, 0.955, 0.976, 0.994, 0.042, 0.930, 0.921, 0.939 and 0.942 (Fig. 9I). These results had significant potential to distinguish between metastatic NET and normal control. However, the AUCs in the current investigations are relatively high and may be sufficient for each molecule on its own to predict recurrence. The expression levels of certain central genes identified, including ATP1A1, LGALS3, SYK, VDR, LDHA, OBSL1, KRT40, NINL, PPP2R2B and WWOX, were further examined by RT-qPCR. In the metastatic NET, genes such as ATP1A1, LGALS3, SYK, VDR and LDHA were significantly up regulated as compared with normal control (Fig. 9IIA – 9IIE), while in metastatic NET, genes such as OBSL1, KRT40, NINL, PPP2R2B and WWOX were significantly down regulated as compared with normal control (Fig. 9IIF – 9IIJ). The results indicated that, consistent with the micro array results.

Molecular docking studies

The docking simulation was performed in the current study to identify the active site conformation and major interactions responsible for complex stability with the binding sites receptor. Docking experiments on designed molecules containing purine heterocyclic ring were performed using Sybyl X 2.1 software. Molecules containing the heterocyclic ring of purine were constructed based on the nucleotide structure and are most widely used alone or in conjunction with other antineoplastic drug. Most neuroendocrine tumors occur in the lungs, appendix, small intestine, rectum and pancreas. When neuroendocrine cells develop changes (mutations) in their DNA, neuroendocrine tumours arise. There are instructions in the DNA within a cell that tell the cell what to do. The modifications suggest that the neuroendocrine cells replicate rapidly and form a tumour. The over expressed genes in neuroendocrine tumours and their X-RAY crystallographic structure of one protein from each over-expressed genes such as CFTR (Cystic fibrosis transmembrane conductance regulator), EZR (Ezrin), ATP1A1 (ATPase Na⁺/K⁺ transporting subunit alpha 1), TUBA1C (Tubulin alpha 1c) and LGALS3 (Galectin 3) and their co-crystallized PDB code of 4WZ6, 4RM8, 3KDP, 3E22 and 6FOF respectively were selected for docking. In order to

identify the possible molecule, an analysis of the designed molecules was carried out. The key molecules that have been designed have obtained a C-score greater than 5 and above are said to be active. A total of 28 molecules were designed shown in Fig. 10 and performed docking studies, few molecules obtained excellent binding energy (C-score) greater than 8 and few molecules obtained optimum binding score 4-4.9, only one molecule with one protein obtained less binding score 2.0-3.0 respectively. The molecules obtained good binding score more than 5-8 and are I26, I28, I24, Cl4, Br16, I23, Br20, Br18, Br15, Br21, F9, Br19, Cl1, Cl2, I25, F14, F8, Br17, Cl7 with 4WZ6 the molecules Br19, F14, Br16, Br21, Cl7, I28, Br18, I22, F12, Br16, Cl1, Br20, Br15, F8, I27, I25, Cl4, F9, Cl1, Cl5, Cl6, I23, F13, Cl3 with 4RM8, the molecules F14, Cl6, F10, F8, Br15, I28, Cl7, F11, F12, F13, I27, Cl3 with 3KDP, the molecules F12, I27, F10, F13, Br21, F9, Br20, Cl4, I24, Cl2, Cl6, F11, Cl1, I26, Br16, Br19, Cl5, F14, I25, Cl7, I28, Cl3, F8 with 3E22 and the molecules F11, I25, F14, I24, Cl1, Cl3, F10, Cl7, Br17, Cl2, I23, Br19, I26, Br21, F9, F12, I28, F13, Cl4, F8, I27, Br16, Cl5, Br15, Br20, Cl6 with 6FOF respectively. The molecules obtained optimum binding score less than 5 (3.0-4.9) are Cl4, F9, I23, Br21, Br18, I25, Cl4, I24, Cl2, I22, I26 with 3KDP, the molecules Br18, Br15, Cl7, I22, I23 with 3E22 and the molecules Br18, I22 with 6FOF respectively. One molecule Br19 obtained very less binding score of 2 with protein 3KDP respectively the values are depicted in Table 1. With all proteins the molecule Cl4, Cl6, F14, F8, Cl7, F11, F12, F13, I27, Cl3, F10 and I28 obtained good binding score. The hydrogen bonding interactions and other bonding interactions with amino acids with protein code 4RM8 of molecule Br17 are depicted by 3D and 2D (Fig.11 and Fig. 12).

Discussion

Various molecular methods have been used in the attempt to illuminate the heterogeneous nature of NET, resolve the mechanisms behind its progression, and introduce novel therapeutic and prognostic targets [56]. Microarray analysis or genome scale analysis has proven to be strong in numerous experimental settings and has the possible to feature the dynamic molecular diversity encountered during cancer development [57]. Since studies investigating gene expression changes during development of NET are lacking, this study sought to identify DEGs in NET that may be exploited as specific prognostic and therapeutic targets.

In the present study, a total of 459 up regulated and 453 down regulated genes were identified between patients with metastatic NET and on normal (controls). Genes such as TIAM2 [58] and SCIN (scinderin) [59] were associated with invasion of various types cancer cells, but these genes might be involves in invasion of NET cells. Polymorphic genes such as SLC6A4 [60] and SLC23A1 [61] were responsible for pathogenesis of various cancer types, but these polymorphic genes might be linked with development of NET. Increased expression of APOBEC1 was important for pathogenesis of colon cancer [62], but elevated expression of this gene may be identified with growth of NET. TTR (transthyretin) was responsible for progression of NET [63]. Methylation inactivation of tumor suppressor genes such as OGDHL (oxoglutarate dehydrogenase like) [64], CAMK2B [65] and RPRML (reprimin like) [66] were associated with progression of various cancer types, but loss of these genes might be liable for development of NET. Loss of tumor suppressor SRCIN1 was diagnosed with growth of gastric cancer [67], but loss of this gene might be linked with development of NET.

In pathway enrichment analysis for DEGs was performed. Genes such as ALDOB (aldolase, fructose-bisphosphate B) [68], KHK (ketohexokinase) [69], CHRNA7 [70], GSTA3 [71], APOA1 [72], CEBPA (CCAAT enhancer binding protein alpha) [73], PCK1 [74], ATP1A1 [75], CLCA1 [76], EMB (embigin) [77], SLC22A18 [78], FUT5 [79] and ITLN1 [80] were linked with progression of various cancer types, but these genes might be identified with growth of NET. Polymorphic genes such as GSTA1 [81], GSTA2 [82], MGST1 [83], NAT2 [84], SULT1A2 [85], SULT2A1 [86], UGT1A6 [87], UGT2B15 [88], UGT2B17 [89], ABCC2 [90], FUT2 [91] and APOB (apolipoprotein B) [92] were liable for progression of various cancer types, but these polymorphic genes might be diagnosed with growth of NET. Genes such as G6PC [93] and SGK1 [94] were associated with proliferation of various cancer cells types, but these gene might be linked with proliferation of NET cells. Increased expression of genes such as SLC2A2 [95], ABCG5 [96], SLC39A4 [97], SLC3A1 [98], SLC7A7 [99], LGALS3 [100], MUC13 [101], MUC17 [102], MUC2 [103], REG1A [104], REG3A [105], REG3G [106] and SEMA6A [107] were responsible for advancement of various cancer types, but high expression of these genes might be liable for growth of NET. Genes such as ABCB1 [108], ABCG2 [109] and SLC26A3 [110] were linked with drug resistance in various cancer types, but these genes might be associated with chemo resistance in NET. CFTR (cystic fibrosis transmembrane conductance regulator) was responsible for progression of NET [111]. Methylation inactivation of tumor suppressor genes such as MYO5B [112], FUT3 [113], CPS1 [114] and FBP1 [115] were identified with progression of various cancer types, but loss of these genes might be important for progression of NET. Genes such as SLC2A5 [116] and FUT6 [117] were associated with invasion of various cancer types, but these genes might be responsible

for invasion of NET cells. Stimulation of PCK2 was associated with development of lung cancer [118], but activation of this gene might be linked with progression of NET. Polymorphic genes such as ATP1B2 [119] and F5 (coagulation factor V) [120] were responsible for progression of breast cancer, but these polymorphic genes might be linked with pathogenesis of NET. Genes such as FXD2 [121], RAB3A [122], ALB (albumin) [123], A1BG [124], AHSB (alpha 2-HS glycoprotein) [125], FGG (fibrinogen gamma chain) [126], SCG3 [127], TF (transferrin) [128], CKB (creatine kinase B) [129] and F7 (coagulation factor VII) [130] were linked with pathogenesis of various cancer types, but high expression of these genes might be liable for progression of NET. Genes such as FOXA1 [131] and FOXA2 [132] were linked with development of NET. Genes such as ECM1 [133] and KCNH2 [134] were involved in invasion of various cancer cells types, but these genes might be involved in invasion of NET cells.

In GO enrichment analysis for DEGs was performed. Polymeric genes such as ACE (angiotensin I converting enzyme) [133], CD36 [136], FABP2 [137], MFSD2A [138], SLC52A3 [139] and LCT (lactase) [140] were responsible for advancement of various cancer types, but these polymorphic genes might be involved in development of NET. Genes such as ACE2 [141], CA13 [142], SLC10A2 [143] and KCNQ1 [144] were liable for progression of various cancer types, but these genes might be linked with development of NET. Increase expression of genes such as ACSL5 [145], FABP1 [146], FABP6 [147], P2RY2 [148], PDZK1 [149], EZR (ezrin) [150] and SI (sucrase-isomaltase) [151] were diagnosed with growth of various cancer types, but high expression of these genes might be identified with progression of NET. Methylation inactivation of tumor suppressor genes such as SYK (spleen associated tyrosine kinase) [152] and TNFRSF11A [153] were associated with pathogenesis of various cancer types, but loss of these genes might be diagnosed with growth of NET. Genes such as CPLX2 [154], CHGA (chromogranin A) [155], CHGB (chromogranin B) [155] and CPE (carboxypeptidase E) [156] were responsible for progression of NET. Polymorphic gene CTNND2 was linked with development of prostate cancer [157], but this gene might be involves in growth of NET. Methylation inactivation of tumor suppressor genes such as JPH3 [158], LZTS1 [159] and TAC1 [160] were important for progression of various cancer types, but loss of these genes might be linked with development of NET. Alteration in SLC18A1 was diagnosed with growth of colorectal cancer [161], but modification in this gene might be liable for advancement of NET. Decrease expression of genes such as SLC8A2 [162], ABCA3 [163], PCSK1 [164], APC2 [165], CRMP1 [166] and RCAN3 [167] were identified with progression of various cancer types, but low expression of these genes might be liable for progression of NET. Genes such as PTPRN2 [168] and DCX (doublecortin) [169] were liable for invasion of various cancers cells

types, but these genes might be linked with invasion of NET cells. Genes such as FGF13 [170], MTSS1 [171] and NRCAM (neuronal cell adhesion molecule) [172] were identified with pathogenesis of various cancer types, but these genes might be responsible for advancement of NET.

PPI network was constructed and analyzed. LDHA was associated with invasion of hepatic cancer cells [173], but this gene might be responsible for invasion of NET cells. Polymorphic gene HSD17B2 was liable for progression of breast cancer [174], but this polymorphic gene might be associated with development of NET. Methylation inactivation of tumor suppressor genes such as WWOX [175] and PPP2R2B [176] were identified with growth of various cancer types, but loss of these genes might be liable for pathogenesis of NET. CBX1 was liable of advancement of hepatocellular carcinoma [177], but this gene might be linked with development of NET. PHLDB2 was responsible for invasion of colon cancer cells [178], but this gene might be linked with invasion of NET cells. Decrease expression of HIPK2 was identified with growth of colorectal cancer [179], but low expression was this gene might be important for pathogenesis of NET. TUBA1C, C15orf48, ACOT11, PLA2G12B, DHDH (dihydrodiol dehydrogenase), KRT40 and PNMA2 might be the novel biomarkers for NET.

Modules were isolated from PPI network and analyzed. Increased expression of genes such as CNDP2 [180] and VAV3 [181] were important for pathogenesis of various cancer types, but high expression of these genes might be associated with development of NET. PEPD, BLNK, GPRASP2, GPRASP1 and CEP126 might be the novel biomarkers for NET.

Target gene - miRNA network was constructed and analyzed. MACC1 was linked with invasion of colon cancer cells [182], but this gene might be associated with invasion of NET cells. E2F2 was responsible for proliferation of colon cancer cells [183], but this gene might be important for proliferation of NET cells. Methylation inactivation of tumor suppressor genes such as HEYL [184] and SMOC1 [185] were diagnosed with growth of various cancer types, but loss of these genes might be important for advancement of NET. SULT1B1, SVOP, KCNJ6 and SORCS2 might be the novel biomarkers for NET.

Target gene - TF network was constructed and analyzed.. Target genes such as TBXAS1 [186], HS6ST3 [187] and RFX6 [188] were liable for progression of various cancer types of cancer, but these genes might be linked with progression

of NET. RUNX1T1 was associated with pathogenesis of pancreatic endocrine tumors [189], but this may be identified with growth of NET. YIF1B might be the novel biomarker for NET.

Conclusion

In the current investigation, bioinformatics analyses were used to screen for DEGs between metastatic NET and normal control. Among the 10 hub genes, ATP1A1, LGALS3, LDHA, SYK, VDR, OBSL1, KRT40, WWOX, NINL and PPP2R2B were indicated to be correlated with one another, and those genes were indicated to be able to help predict the prognosis of NET. The results of the current investigation may prove valuable from the perspectives of basic research and clinical treatment for NET. However, even though the current results might contribute to the understanding of the molecular pathogenesis of NET, further investigation are needed to verify genes linked with NET.

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Basavaraj Vastrad - Writing original draft, and review and editing

Anandkumar Tengli - Writing original draft and investigation

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Availability of data and materials

The datasets supporting the conclusions of this article are available in the GEO (<http://www.ncbi.nlm.nih.gov/geo>) repository. [(GSE65286) (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE65286>)]

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

Conflict of interest

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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.

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Figures

Figure 1. Box plots of the gene expression data before and after normalization. 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 control; B1-, B33 = metastatic NETs)

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

Figure 3. Heat map of (A) up regulated differentially expressed genes (B) down regulated differentially expressed genes. Legend on the top left indicate log fold change of genes. (A1-A10= normal control; B1-, B33 = metastatic NETs)

Figure 4. Protein–protein interaction network of (A) up regulated differentially expressed genes (B) down regulated differentially expressed genes. Green nodes denotes up regulated genes and red nodes denotes down regulated genes.

Figure 5. Modules in PPI network. (A) Green nodes denote the up regulated genes (B) Red nodes denote the down regulated genes

Figure 6. (A) The network of up regulated genes and their related miRNAs. The green circles nodes are the up regulated DEGs and purple diamond nodes are the miRNAs (B) The network of down regulated genes and their related miRNAs. The red circle nodes are the down regulated DEGs and blue diamond nodes are the miRNAs

Figure 7. (A) The network of up regulated genes and their related TFs. (Blue triangle - TFs and green circles- target up regulated genes) (B) The network of down regulated genes and their related TFs. (Blue triangle - TFs and red circles - target down regulated genes)

Figure 8. (I) Kaplan-Meier survival curves using GSE62564 data validate the prognostic value of genes have favorable overall survival in NETs. (Green – Low expression; Red- high expression) (A = ATP1A1; B = LGALS3; C = SYK; D = VDR; E = OBSL1; F = KRT40; G = NINL ;H = PPP2R2B) (II) Kaplan-Meier survival curves using GSE62564 data validate the prognostic value of genes have worse overall survival in NETs. (Green – Low expression; Red- high expression) (A = LDHA; B = WWOX)

Figure 9. (I) ROC curve validated the sensitivity, specificity of hub genes as a predictive biomarker for NET prognosis. A) ATP1A1 B) LGALS3 C) SYK D) VDR E) LDHA F) OBSL1 G) KRT40 H) NINL I) PPP2R2B J) WWOX (II) Validation of hub genes (up and down regulated) by RT- PCR. A) ATP1A1 B) LGALS3 C) SYK D) VDR E) LDHA F) OBSL1 G) KRT40 H) NINL I) PPP2R2B J) WWOX

Figure 10. Structures of Designed Molecules

Figure 11. 3D Binding of Molecule Br17with 4RM8

Figure 12. 2D Binding of Molecule Br17with 4RM8

Tables

Table 1. Primers used for quantitative PCR

Primer sequence (5'→3')

Gene	Forward	Reverse
ATP1A1	ACAGACTTGAGCCGGGGATTA	TCCATTTCAGGAGTAGTGGGAG
LGALS3	ATGGCAGACAATTTTTCGCTCC	GCCTGTCCAGGATAAGCCC
LDHA	ATGGCAACTCTAAAGGATCAGC	CCAACCCCAACAACCTGTAATCT
SYK	CATGGAAAAATCTCTCGGGAAGA	GTCGATGCGATAGTGCAGCA
VDR	GTGGACATCGGCATGATGAAG	GGTCGTAGGTCTTATGGTGGG
OBSL1	ATTCCGGCGTCTACGTGTG	CCAGTGCCATTCGATCTCGG
KRT40	TCCGTGGAAACAGCTTGTCTC	GCAGGGACTATTACAACTCCCA
WWOX	CTCCCAGGGATGTTTTGTGC	CACGCCAACCAGGTTTTTACT
NINL	AACGACCATTTCGCCAGGG	ACCATTTCACATACTTTGGAGGGA
PPP2R2B	CCACACGGGAGAATTACTAGCG	TGTATTCACCCCTACGATGAACC

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

Agilent Id	Gene Symbol	logFC	Adj p value	tvalue	Regulation	GeneName
A_24_P53778	ITLN2	6.318979	9.18E-28	25.47633	Up	intelectin 2
A_23_P391711	FABP2	5.039241	1.01E-23	20.20289	Up	fatty acid binding protein 2
A_24_P634768	C3orf85	6.374158	2.01E-22	18.71603	Up	chromosome 3 open reading frame 85
A_23_P38388	TMEM92	4.960821	2.47E-22	18.61745	Up	transmembrane protein 92
A_23_P28246	SLC23A3	4.263623	4.21E-22	18.36201	Up	solute carrier family 23 member 3
A_24_P68814	DQX1	3.559075	4.9E-22	18.28934	Up	DEAQ-box RNA dependent ATPase 1
A_32_P65628	REG3G	4.087376	5.58E-22	18.2279	Up	regenerating family member 3 gamma

A_24_P934704	#N/A	3.773127	8.93E-22	18.00665	Up	NA
A_23_P383258	GDA	4.316697	2.41E-21	17.54569	Up	guanine deaminase
A_23_P156826	ADTRP	5.063599	6.99E-21	17.06288	Up	androgen dependent TFPI regulating protein
A_24_P303454	TIAM2	3.917379	8.51E-21	16.97408	Up	T cell lymphoma invasion and metastasis 2
A_23_P152995	SLC6A4	5.828263	8.92E-21	16.95339	Up	solute carrier family 6 member 4
A_23_P21990	SLC23A1	4.785825	9.68E-21	16.9166	Up	solute carrier family 23 member 1
A_23_P157136	SCIN	4.992711	1.04E-20	16.88629	Up	scinderin
A_24_P169503	#N/A	3.581108	1.09E-20	16.86392	Up	NA
A_23_P14019	APOBEC1	5.074526	1.18E-20	16.82809	Up	apolipoprotein B mRNA editing enzyme catalytic subunit 1
A_23_P48816	SLC28A2	6.248742	1.78E-20	16.6459	Up	solute carrier family 28 member 2
A_32_P524904	C11orf86	7.059253	2.11E-20	16.57202	Up	chromosome 11 open reading frame 86
A_23_P128609	SLC15A1	3.444994	2.16E-20	16.56169	Up	solute carrier family 15 member 1
A_23_P12928	SLC5A12	5.01333	3.13E-20	16.39863	Up	solute carrier family 5 member 12
A_23_P217498	GDPD2	4.575899	4.41E-20	16.24928	Up	glycerophosphodiesterphosphodiesterase domain containing 2
A_24_P278603	MOGAT2	3.618233	4.59E-20	16.23132	Up	monoacylglycerol O-acyltransferase 2
A_23_P17438	EDN3	4.577677	4.66E-20	16.22561	Up	endothelin 3
A_23_P57110	SLC52A3	3.858095	5.42E-20	16.15999	Up	solute carrier family 52 member 3
A_23_P66311	DNASE1	4.975338	6.63E-20	16.07299	Up	deoxyribonuclease 1
A_32_P133395	EGFR-AS1	4.030842	6.67E-20	16.07005	Up	EGFR antisense RNA 1
A_23_P112162	DGAT1	4.207489	6.85E-20	16.05898	Up	diacylglycerol O-acyltransferase 1
A_24_P375322	GGT8P	3.661912	7.03E-20	16.04769	Up	gamma-glutamyltransferase 8 pseudogene
A_24_P472055	RNF125	4.815173	7.36E-20	16.02813	Up	ring finger protein 125
A_23_P7412	BTNL8	7.385338	7.56E-20	16.01653	Up	butyrophilin like 8
A_24_P828496	LINC01133	5.444864	1.11E-19	15.85033	Up	long intergenic non-protein coding RNA 1133
A_23_P203698	MOGAT2	5.479532	1.3E-19	15.78415	Up	monoacylglycerol O-acyltransferase 2
A_23_P162660	GPD1	3.629549	1.51E-19	15.72256	Up	glycerol-3-phosphate dehydrogenase 1
A_23_P56978	PTK6	4.721567	1.56E-19	15.70874	Up	protein tyrosine kinase 6
A_24_P34865	BTNL3	5.153638	1.75E-19	15.65926	Up	butyrophilin like 3
A_24_P392151	#N/A	4.925567	2.1E-19	15.58282	Up	NA
A_23_P23980	PLEKHS1	3.685659	2.41E-19	15.52377	Up	pleckstrin homology domain containing S1
A_32_P112263	AL365226.2	4.34772	2.85E-19	15.45344	Up	novel transcript
A_32_P66843	ERICH4	6.822291	3.06E-19	15.42386	Up	glutamate rich 4
A_23_P25475	SOAT2	4.737242	3.36E-19	15.38566	Up	sterol O-acyltransferase 2

A_23_P78353	MEP1B	5.801353	3.79E-19	15.3354	Up	meprin A subunit beta
A_23_P430839	HAPLN4	3.787223	3.88E-19	15.32498	Up	hyaluronan and proteoglycan link protein 4
A_23_P430842	HAPLN4	3.097128	3.96E-19	15.31659	Up	hyaluronan and proteoglycan link protein 4
A_23_P212061	MME	5.21812	4.2E-19	15.29216	Up	membrane metalloendopeptidase
A_23_P55828	CCL25	6.114546	4.23E-19	15.28886	Up	C-C motif chemokine ligand 25
A_23_P146444	CORO2A	4.163076	4.36E-19	15.27683	Up	coronin 2A
A_24_P851254	#N/A	5.168386	4.43E-19	15.2702	Up	NA
A_23_P253783	MFSD2A	4.220675	4.65E-19	15.24971	Up	major facilitator superfamily domain containing 2A
A_23_P135061	CORO2A	3.562223	5.78E-19	15.15966	Up	coronin 2A
A_24_P169507	MUC17	3.327118	6.12E-19	15.13668	Up	mucin 17, cell surface associated
A_23_P80491	RBP2	7.365791	7.36E-19	15.06047	Up	retinol binding protein 2
A_23_P105012	HRASLS2	5.630781	7.41E-19	15.05736	Up	HRAS like suppressor 2
A_23_P364625	LRRC19	5.724745	8.15E-19	15.01873	Up	leucine rich repeat containing 19
A_24_P152845	AKR1B10P1	5.437257	8.43E-19	15.00444	Up	aldo-ketoreductase family 1 member B10 pseudogene 1
A_32_P424761	MYRFL	5.200225	8.6E-19	14.99662	Up	myelin regulatory factor like
A_23_P368805	HHLA2	3.209019	8.63E-19	14.9949	Up	HERV-H LTR-associating 2
A_23_P24083	PNLIPRP2	7.320396	1.04E-18	14.91744	Up	pancreatic lipase related protein 2 (gene/pseudogene)
A_23_P212379	SLC6A20	5.504551	1.05E-18	14.91398	Up	solute carrier family 6 member 20
A_24_P740620	CASP16P	3.725988	1.07E-18	14.90848	Up	caspase 16, pseudogene
A_23_P119936	REG3A	7.163396	1.14E-18	14.88114	Up	regenerating family member 3 alpha
A_24_P260101	MME	6.332023	1.15E-18	14.87645	Up	membrane metalloendopeptidase
A_23_P56659	DQX1	5.853356	1.51E-18	14.767	Up	DEAQ-box RNA dependent ATPase 1
A_23_P17130	C2orf88	4.287287	1.61E-18	14.74031	Up	chromosome 2 open reading frame 88
A_32_P538017	TBX10	3.473968	1.73E-18	14.71198	Up	T-box 10
A_32_P515920	TMEM238L	5.316265	1.83E-18	14.68879	Up	transmembrane protein 238 like
A_23_P343719	PLCB3	3.159763	2.05E-18	14.64269	Up	phospholipase C beta 3
A_24_P211106	TNFRSF11A	3.608124	2.06E-18	14.64143	Up	TNF receptor superfamily member 11a
A_23_P123228	SLC26A3	6.155654	4.24E-18	14.35189	Up	solute carrier family 26 member 3
A_23_P98092	OAT	3.884099	4.63E-18	14.31743	Up	ornithine aminotransferase
A_23_P114008	TM4SF20	4.23777	4.94E-18	14.29158	Up	transmembrane 4 L six family member 20
A_23_P128050	BCL2L14	5.113146	5.72E-18	14.23341	Up	BCL2 like 14
A_24_P201360	ACSL5	4.417298	7.47E-18	14.12771	Up	acyl-CoA synthetase long chain family member 5
A_23_P58788	CDX1	4.487919	7.68E-18	14.11711	Up	caudal type homeobox 1

A_23_P42897	MGAM	6.025511	8.53E-18	14.07549	Up	maltase-glucoamylase
A_23_P63032	GUCA2B	5.830655	8.94E-18	14.05732	Up	guanylatecyclase activator 2B
A_23_P251421	CDCA7	3.717182	9.05E-18	14.05248	Up	cell division cycle associated 7
A_23_P202810	OVOL1	4.709832	9.69E-18	14.02552	Up	ovo like transcriptional repressor 1
A_32_P47027	TMEM229A	4.763353	9.96E-18	14.01495	Up	transmembrane protein 229A
A_23_P24903	P2RY2	3.759322	1.17E-17	13.95247	Up	purinergic receptor P2Y2
A_23_P313278	#N/A	3.062367	1.26E-17	13.92405	Up	NA
A_24_P695306	TMEM229A	4.894552	1.32E-17	13.9034	Up	transmembrane protein 229A
A_24_P938236	#N/A	3.49729	1.36E-17	13.89212	Up	NA
A_24_P363711	DEFA6	8.34463	1.38E-17	13.88719	Up	defensin alpha 6
A_24_P286951	PLEKHS1	4.491879	1.53E-17	13.84749	Up	pleckstrin homology domain containing S1 phosphoenolpyruvatecarboxykinase 2, mitochondrial
A_23_P128817	PCK2	4.10767	1.57E-17	13.83686	Up	
A_23_P90743	REG1A	8.779252	1.58E-17	13.83513	Up	regenerating family member 1 alpha ornithine aminotransferase (gyrate atrophy) (OAT) pseudogene
A_24_P508946	AL606490.2	3.376274	1.62E-17	13.82469	Up	
A_24_P126741	GLRXP3	3.125366	1.66E-17	13.81537	Up	glutaredoxinpseudogene 3
A_23_P337658	ALPI	4.595671	1.98E-17	13.74735	Up	alkaline phosphatase, intestinal
A_23_P15692	SLC52A1	5.119832	2.08E-17	13.72865	Up	solute carrier family 52 member 1
A_23_P32707	ESPL1	3.787032	2.18E-17	13.71021	Up	extra spindle pole bodies like 1, separase
A_23_P1043	INAVA	5.041385	2.21E-17	13.70454	Up	innate immunity activator
A_23_P5092	FUT6	3.312031	2.28E-17	13.69313	Up	fucosyltransferase 6
A_23_P152428	MARVELD3	3.203286	2.42E-17	13.67007	Up	MARVEL domain containing 3
A_23_P140009	SLC10A2	5.831536	2.56E-17	13.6486	Up	solute carrier family 10 member 2
A_23_P83659	XPNPEP2	6.099055	2.62E-17	13.63853	Up	X-prolylaminopeptidase 2
A_24_P636882	#N/A	3.299638	2.92E-17	13.59686	Up	NA
A_23_P47102	ACY3	3.43036	3.18E-17	13.56467	Up	aminoacylase 3
A_23_P204736	GPD1	3.53086	3.24E-17	13.55761	Up	glycerol-3-phosphate dehydrogenase 1
A_23_P82886	DEFA6	8.211332	3.59E-17	13.5176	Up	defensin alpha 6
A_23_P252981	ACE2	7.624092	3.62E-17	13.51442	Up	angiotensin I converting enzyme 2 cell death inducing DFFA like effector c pseudogene 1
A_24_P484797	CIDECPI	3.882541	3.81E-17	13.49584	Up	
A_23_P349463	CHP2	9.31251	4.21E-17	13.45759	Up	calcineurin like EF-hand protein 2
A_23_P371835	GATA5	3.815847	4.45E-17	13.43568	Up	GATA binding protein 5
A_23_P92025	CIDEC	4.347494	4.59E-17	13.42461	Up	cell death inducing DFFA like effector c
A_32_P2730	AL365181.3	4.048659	4.6E-17	13.42342	Up	novel transcript, antisense to BCAN

A_23_P43820	MFSD2A	4.023319	4.61E-17	13.42263	Up	major facilitator superfamily domain containing 2A
A_23_P121622	SULT1B1	4.326724	4.66E-17	13.41816	Up	sulfotransferase family 1B member 1
A_23_P86623	ENTPD7	3.108314	4.84E-17	13.40364	Up	ectonucleoside triphosphate diphosphohydrolase 7
A_24_P364263	HRASLS2	4.436682	5E-17	13.39161	Up	HRAS like suppressor 2
A_23_P112086	DEFA5	8.107209	5.55E-17	13.35202	Up	defensin alpha 5
A_24_P13790	CES2	4.198137	5.61E-17	13.34813	Up	carboxylesterase 2
A_24_P319374	GPA33	7.287644	6.6E-17	13.28618	Up	glycoprotein A33
A_23_P27005	DHRS11	4.108083	6.94E-17	13.26725	Up	dehydrogenase/reductase 11
A_23_P36129	TKFC	3.146426	6.95E-17	13.26643	Up	triokinase and FMN cyclase
A_23_P158297	BTNL3	7.756238	7.08E-17	13.25962	Up	butyrophilin like 3
A_23_P127608	TMPRSS4	5.718163	7.09E-17	13.25902	Up	transmembrane serine protease 4
A_32_P217140	ISX	5.670975	9.25E-17	13.15854	Up	intestine specific homeobox
A_23_P83436	PEPD	3.204264	1.01E-16	13.12721	Up	peptidase D
A_24_P599496	ANKRD9	3.317328	1.05E-16	13.11133	Up	ankyrin repeat domain 9
A_23_P95851	TUBAL3	5.269194	1.08E-16	13.09918	Up	tubulin alpha like 3
A_23_P99642	SLC7A7	4.082303	1.09E-16	13.09775	Up	solute carrier family 7 member 7
A_24_P256219	MAF	3.352493	1.29E-16	13.03256	Up	MAF bZIP transcription factor
A_23_P87036	APOA4	10.07826	1.31E-16	13.02884	Up	apolipoprotein A4
A_23_P37914	SLC5A11	5.306536	1.33E-16	13.02346	Up	solute carrier family 5 member 11
A_23_P54968	ST6GALNAC1	4.861272	1.42E-16	12.99708	Up	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 1
A_23_P312752	KCNJ13	6.020755	1.52E-16	12.97211	Up	potassium voltage-gated channel subfamily J member 13
A_23_P96556	GK	3.483533	1.59E-16	12.95523	Up	glycerol kinase
A_23_P140207	PCK2	3.617594	1.61E-16	12.95067	Up	phosphoenolpyruvatecarboxykinase 2, mitochondrial
A_23_P360316	FUT3	5.181279	1.63E-16	12.94567	Up	fucosyltransferase 3 (Lewis blood group)
A_23_P142239	YIF1B	3.094282	1.79E-16	12.91096	Up	Yip1 interacting factor homolog B, membrane trafficking protein
A_24_P360674	CDKN2B	3.728171	1.8E-16	12.90915	Up	cyclin dependent kinase inhibitor 2B
A_24_P64344	BLNK	3.236215	2.08E-16	12.85542	Up	B cell linker
A_23_P16252	KLK1	3.697596	2.13E-16	12.84641	Up	kallikrein 1
A_24_P942969	FUT2	3.48298	2.22E-16	12.8312	Up	fucosyltransferase 2
A_32_P158272	MACC1	3.264326	2.37E-16	12.80747	Up	MET transcriptional regulator MACC1
A_23_P349147	#N/A	6.661886	2.69E-16	12.76093	Up	NA
A_24_P131173	C1orf115	3.01193	2.71E-16	12.75705	Up	chromosome 1 open reading frame 115

A_23_P79587	ALPP	4.201716	2.94E-16	12.72693	Up	alkaline phosphatase, placental
A_23_P160433	C1orf115	3.180276	2.99E-16	12.72082	Up	chromosome 1 open reading frame 115
A_23_P404536	ENPP3	4.226246	3.13E-16	12.70398	Up	ectonucleotidetriphosphatase/phosphodiesterase 3
A_23_P68786	PRODH	3.152676	3.69E-16	12.64381	Up	proline dehydrogenase 1
A_24_P59062	GGTLC2	3.136229	3.69E-16	12.64377	Up	gamma-glutamyltransferase light chain 2
A_24_P252934	APOA4	5.790923	3.92E-16	12.62198	Up	apolipoprotein A4
A_23_P213050	HPGD	3.737686	4E-16	12.61434	Up	15-hydroxyprostaglandin dehydrogenase
A_23_P106773	SULT1A2	3.12074	4.25E-16	12.59168	Up	sulfotransferase family 1A member 2
A_24_P129341	AKR1B10	7.405056	4.39E-16	12.57997	Up	aldo-ketoreductase family 1 member B10
A_23_P31073	MYB	3.373053	4.48E-16	12.57286	Up	MYB proto-oncogene, transcription factor
A_23_P39202	C19orf33	4.57156	5.09E-16	12.52602	Up	chromosome 19 open reading frame 33
A_24_P345451	CYBRD1	3.981195	5.11E-16	12.5246	Up	cytochrome b reductase 1
A_23_P66854	KRT20	7.422756	5.16E-16	12.52051	Up	keratin 20
A_23_P52451	HKDC1	4.614568	5.77E-16	12.47999	Up	hexokinase domain containing 1
A_32_P25065	#N/A	3.647888	5.97E-16	12.46741	Up	NA
A_23_P381714	CA13	3.261059	6.05E-16	12.46286	Up	carbonic anhydrase 13
A_23_P101193	MYO5B	3.790436	6.09E-16	12.46047	Up	myosin VB
A_23_P102551	MALL	3.246603	6.42E-16	12.44102	Up	mal, T cell differentiation protein like
A_23_P15394	CD68	3.011316	6.57E-16	12.43284	Up	CD68 molecule
A_23_P93641	AKR1B10	7.531675	7.15E-16	12.4018	Up	aldo-ketoreductase family 1 member B10
A_23_P335388	C17orf78	6.925141	7.73E-16	12.37361	Up	chromosome 17 open reading frame 78
A_23_P40919	ADGRG7	4.745108	7.98E-16	12.36196	Up	adhesion G protein-coupled receptor G7
A_23_P214554	TRIM15	3.498853	8.78E-16	12.32712	Up	tripartite motif containing 15
A_23_P306610	MUC17	7.717103	9.26E-16	12.30807	Up	mucin 17, cell surface associated
A_23_P51217	CLCA1	6.464977	1.11E-15	12.2415	Up	chloride channel accessory 1
A_23_P57868	ACY1	3.812716	1.19E-15	12.21663	Up	aminoacylase 1
A_23_P333605	ENPEP	4.395963	1.22E-15	12.20847	Up	glutamylaminopeptidase
A_24_P20292	B3GNT7	3.164471	1.23E-15	12.20654	Up	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7
A_23_P19590	EZR	3.129165	1.24E-15	12.20272	Up	ezrin
A_23_P49192	CES2	4.542435	1.33E-15	12.17719	Up	carboxylesterase 2
A_24_P385732	SLC51A	5.389699	1.38E-15	12.16391	Up	solute carrier family 51 alpha subunit
A_23_P501010	COL17A1	5.724274	1.38E-15	12.16341	Up	collagen type XVII alpha 1 chain
A_23_P14667	SLC28A1	3.21644	1.51E-15	12.13122	Up	solute carrier family 28 member 1

A_32_P154911	PRR15	5.035633	1.56E-15	12.11979	Up	proline rich 15
A_23_P86599	DMBT1	7.476327	1.66E-15	12.09831	Up	deleted in malignant brain tumors 1
A_32_P218355	C6orf132	4.248888	1.69E-15	12.09071	Up	chromosome 6 open reading frame 132
A_23_P101759	FUT5	4.514325	1.8E-15	12.06792	Up	fucosyltransferase 5
A_23_P144384	GALNT7	3.732934	1.85E-15	12.05963	Up	polypeptide N-acetylgalactosaminyltransferase 7
A_24_P211709	XPNPEP2	3.837817	1.89E-15	12.0514	Up	X-prolylaminopeptidase 2
A_32_P101264	SLC35G1	3.488597	2.08E-15	12.01662	Up	solute carrier family 35 member G1
A_23_P69908	GLRX	3.233422	2.22E-15	11.99355	Up	glutaredoxin
A_23_P40761	SLC51A	5.495765	2.23E-15	11.99141	Up	solute carrier family 51 alpha subunit
A_23_P68487	BMP7	3.053498	2.27E-15	11.98597	Up	bone morphogenetic protein 7
A_24_P403561	LRP4	3.193611	2.42E-15	11.96267	Up	LDL receptor related protein 4
A_23_P4069	TMEM220	3.141049	2.47E-15	11.95492	Up	transmembrane protein 220
A_32_P35969	CHRNA7	3.610772	2.97E-15	11.8898	Up	cholinergic receptor nicotinic alpha 7 subunit
A_23_P17826	SLC5A1	7.053345	3.07E-15	11.87838	Up	solute carrier family 5 member 1
A_23_P207905	SECTM1	3.07523	3.22E-15	11.8617	Up	secreted and transmembrane 1
A_23_P12405	ESPN	3.155501	3.27E-15	11.85611	Up	espin
A_32_P302205	SI	6.517195	3.61E-15	11.82118	Up	sucrase-isomaltase
A_32_P44568	LDHA	3.096237	4.76E-15	11.72301	Up	lactate dehydrogenase A
A_24_P679796	#N/A	3.11566	4.92E-15	11.71167	Up	NA
A_23_P360329	CRYBG2	4.002211	5.08E-15	11.70024	Up	crystallin beta-gamma domain containing 2
A_24_P938614	CDS1	3.562049	5.38E-15	11.68018	Up	CDP-diacylglycerol synthase 1
A_23_P49145	ZG16	7.387701	5.45E-15	11.67512	Up	zymogen granule protein 16
A_23_P18713	ABCG2	4.819942	5.52E-15	11.6711	Up	ATP binding cassette subfamily G member 2 (Junior blood group)
A_23_P52668	NAALADL1	3.769799	5.52E-15	11.67072	Up	N-acetylated alpha-linked acidic dipeptidase like 1
A_24_P76267	GGT1	3.266678	6.35E-15	11.62194	Up	gamma-glutamyltransferase 1
A_23_P110569	TRIM36	3.430467	6.59E-15	11.60877	Up	tripartite motif containing 36
A_23_P41145	FAM3D	6.613591	6.96E-15	11.5893	Up	family with sequence similarity 3 member D
A_23_P9255	SYK	3.17526	7.04E-15	11.58568	Up	spleen associated tyrosine kinase
A_23_P209944	RETSAT	3.42411	7.14E-15	11.58064	Up	retinol saturase
A_23_P31798	NAT2	3.013459	7.36E-15	11.56978	Up	N-acetyltransferase 2
A_23_P166207	ABCC13	3.276044	7.86E-15	11.54711	Up	ATP binding cassette subfamily C member 13 (pseudogene)
A_32_P218707	AC244205.1	5.747872	8.95E-15	11.50138	Up	novel transcript
A_23_P500886	CLDN15	3.136413	9.89E-15	11.46662	Up	claudin 15

A_24_P100387	GK	3.816375	1.03E-14	11.45108	Up	glycerol kinase
A_23_P84219	LIPH	3.357691	1.05E-14	11.44437	Up	lipase H
A_23_P142395	#N/A	4.291339	1.1E-14	11.42956	Up	NA
A_23_P256312	MST1R	3.425711	1.12E-14	11.42291	Up	macrophage stimulating 1 receptor
A_23_P47282	ST14	3.808322	1.13E-14	11.41945	Up	suppression of tumorigenicity 14
A_23_P151506	PLEK2	3.78203	1.31E-14	11.36966	Up	pleckstrin 2
A_23_P88626	ANPEP	7.100124	1.31E-14	11.36902	Up	alanylaminopeptidase, membrane
A_23_P307525	ANKRD9	3.025586	1.57E-14	11.30586	Up	ankyrin repeat domain 9
A_23_P388150	PLA2G12B	3.573453	1.77E-14	11.26434	Up	phospholipase A2 group XIIB
A_23_P312150	EDN2	4.441691	1.82E-14	11.25473	Up	endothelin 2
A_23_P5845	KHK	3.911853	2.02E-14	11.21963	Up	ketohehexokinase
A_23_P15226	#N/A	5.814535	2.06E-14	11.21294	Up	NA
A_32_P319200	GGTLC2	3.437896	2.1E-14	11.20649	Up	gamma-glutamyltransferase light chain 2
A_23_P83857	MAOA	4.165966	2.1E-14	11.20584	Up	monoamine oxidase A
A_24_P246891	NEU4	3.123468	2.18E-14	11.19321	Up	neuraminidase 4
A_23_P214281	PAQR8	3.014102	2.48E-14	11.14865	Up	progesterone and adipoQ receptor family member 8 transient receptor potential cation channel subfamily M member 6
A_23_P216712	TRPM6	4.46031	2.5E-14	11.14612	Up	NA
A_32_P135906	#N/A	3.595057	2.52E-14	11.14322	Up	NA
A_23_P67971	GALM	3.17129	2.86E-14	11.10029	Up	galactosemutarotase
A_32_P110390	TMEM171	3.141528	2.99E-14	11.08458	Up	transmembrane protein 171
A_23_P202427	HKDC1	6.103293	3.01E-14	11.08223	Up	hexokinase domain containing 1 anterior gradient 3, protein disulphide isomerase family member
A_23_P42811	AGR3	4.478036	3.11E-14	11.07076	Up	C1q and TNF related 12
A_32_P75792	C1QTNF12	4.052825	3.15E-14	11.06644	Up	mal, T cell differentiation protein like
A_24_P80204	MALL	5.685475	3.45E-14	11.03506	Up	gamma-glutamyltransferase 3 pseudogene
A_24_P42066	GGT3P	3.195548	3.59E-14	11.02184	Up	solute carrier family 9 member A3
A_24_P419300	SLC9A3	3.11499	3.6E-14	11.02064	Up	ATP binding cassette subfamily B member 1
A_23_P82523	ABCB1	3.660805	3.77E-14	11.00484	Up	iodotyrosinedeiodinase
A_32_P110472	IYD	3.896566	3.8E-14	11.00267	Up	embiginpseudogene 1
A_32_P206541	EMBP1	3.289144	3.81E-14	11.00202	Up	regenerating family member 1 beta
A_23_P389500	REG1B	6.133995	4.14E-14	10.97339	Up	cytochrome P450 family 2 subfamily S member 1 cytochrome P450 family 4 subfamily F member 12
A_23_P101374	CYP2S1	4.262088	4.22E-14	10.96644	Up	
A_23_P108280	CYP4F12	3.28873	4.46E-14	10.94806	Up	
A_32_P144599	MACC1	3.880216	5.01E-14	10.90855	Up	MET transcriptional regulator MACC1

A_23_P13822	STYK1	3.225249	5.25E-14	10.89229	Up	serine/threonine/tyrosine kinase 1
A_23_P67799	TMEM37	4.38394	5.28E-14	10.89074	Up	transmembrane protein 37
A_24_P308506	NAT8B	4.385856	5.46E-14	10.87942	Up	N-acetyltransferase 8B (putative, gene/pseudogene)
A_32_P169353	#N/A	3.40296	6.08E-14	10.84289	Up	NA
A_24_P307626	ATP1A4	3.485652	6.39E-14	10.82571	Up	ATPase Na+/K+ transporting subunit alpha 4
A_23_P67042	MOCOS	3.612307	6.55E-14	10.81721	Up	molybdenum cofactor sulfurase
A_23_P160177	ATP1A4	3.411386	6.73E-14	10.80808	Up	ATPase Na+/K+ transporting subunit alpha 4
A_23_P89780	LAMA3	3.708626	7.21E-14	10.7849	Up	laminin subunit alpha 3
A_23_P256470	NPY	3.130204	1.02E-13	10.66764	Up	neuropeptide Y
A_23_P218626	NEU4	4.134634	1.1E-13	10.64118	Up	neuraminidase 4
A_23_P397376	MAF	3.940391	1.13E-13	10.63437	Up	MAF bZIP transcription factor
A_23_P11968	GUCA2A	5.865596	1.15E-13	10.62639	Up	guanylatecyclase activator 2A
A_24_P151084	CNDP2	3.172479	1.17E-13	10.62132	Up	carnosinedipeptidase 2
A_23_P131060	CYP4F8	3.662035	1.37E-13	10.56967	Up	cytochrome P450 family 4 subfamily F member 8
A_32_P119949	#N/A	3.510942	1.49E-13	10.54055	Up	NA
A_24_P181254	OLFM4	7.046668	1.56E-13	10.52563	Up	olfactomedin 4
A_24_P217234	SLC3A1	6.004246	1.72E-13	10.4936	Up	solute carrier family 3 member 1
A_23_P213171	MTTP	6.938614	1.82E-13	10.47485	Up	microsomal triglyceride transfer protein
A_23_P61426	MSRA	3.106542	1.91E-13	10.45788	Up	methionine sulfoxidereductase A
A_23_P254664	GCG	4.044968	1.97E-13	10.44705	Up	glucagon
A_23_P20502	SLC39A4	3.094611	2.02E-13	10.43973	Up	solute carrier family 39 member 4
A_24_P393571	GDA	6.065937	2.48E-13	10.37102	Up	guanine deaminase
A_23_P27472	ATP1A3	3.419286	2.49E-13	10.3695	Up	ATPase Na+/K+ transporting subunit alpha 3
A_24_P153713	MARVELD3	3.364359	2.5E-13	10.3684	Up	MARVEL domain containing 3
A_23_P166269	FAM3B	4.043351	2.66E-13	10.34789	Up	family with sequence similarity 3 member B
A_23_P154986	GGT1	3.040297	2.85E-13	10.32487	Up	gamma-glutamyltransferase 1
A_24_P684186	EMB	3.484968	2.95E-13	10.31333	Up	embigin
A_23_P211909	PLS1	3.757666	3.11E-13	10.29575	Up	plastin 1
A_24_P48204	SECTM1	4.518752	3.29E-13	10.27739	Up	secreted and transmembrane 1
A_23_P135257	PRSS3	4.731796	3.54E-13	10.25347	Up	serine protease 3
A_23_P14986	HSD11B2	4.200761	4.11E-13	10.20403	Up	hydroxysteroid 11-beta dehydrogenase 2
A_24_P10233	DAPK2	3.503674	4.18E-13	10.19844	Up	death associated protein kinase 2
A_23_P124619	S100A14	4.681617	4.62E-13	10.16532	Up	S100 calcium binding protein A14

A_23_P21495	FCGBP	5.480471	4.64E-13	10.16357	Up	Fc fragment of IgG binding protein
A_23_P214300	GSTA2	5.288637	4.71E-13	10.15928	Up	glutathione S-transferase alpha 2
A_23_P111766	#N/A	5.28519	4.8E-13	10.15291	Up	NA
A_32_P94444	PRSS2	4.991386	5E-13	10.13909	Up	serine protease 2
A_23_P1072	ATP1A1	3.457298	5.2E-13	10.12661	Up	ATPase Na ⁺ /K ⁺ transporting subunit alpha 1
A_23_P52480	CYP2C18	4.647031	6.33E-13	10.06174	Up	cytochrome P450 family 2 subfamily C member 18
A_23_P208788	C19orf33	4.729597	6.55E-13	10.05066	Up	chromosome 19 open reading frame 33
A_23_P62857	#N/A	4.585728	7.32E-13	10.01424	Up	NA
A_23_P408955	E2F2	3.393043	7.33E-13	10.01371	Up	E2F transcription factor 2
A_23_P149517	PIGR	4.144128	7.69E-13	9.998308	Up	polymeric immunoglobulin receptor
A_24_P913828	MUC3A	3.707162	7.81E-13	9.993152	Up	mucin 3A, cell surface associated
A_24_P700562	#N/A	4.537481	8.02E-13	9.984236	Up	NA
A_23_P49448	FA2H	3.419506	9.11E-13	9.942731	Up	fatty acid 2-hydroxylase
A_24_P150803	PRSS8	3.543592	9.16E-13	9.940963	Up	serine protease 8
A_24_P795662	#N/A	4.993505	9.35E-13	9.934228	Up	NA
A_23_P92161	ARL14	4.690178	9.44E-13	9.931298	Up	ADP ribosylation factor like GTPase 14
A_23_P202275	PRAP1	5.92312	1.19E-12	9.856105	Up	proline rich acidic protein 1
A_23_P329198	NABP1	3.102249	1.25E-12	9.840396	Up	nucleic acid binding protein 1
A_23_P78980	B3GNT3	4.966323	1.3E-12	9.826786	Up	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3
A_23_P101642	PTPRH	3.116765	1.44E-12	9.79293	Up	protein tyrosine phosphatase, receptor type H
A_23_P86012	LAMB3	5.587031	1.49E-12	9.782308	Up	laminin subunit beta 3
A_32_P200697	RFLNA	4.75605	1.77E-12	9.72749	Up	refilin A
A_32_P228341	#N/A	3.741656	1.81E-12	9.719085	Up	NA
A_23_P418234	PHLPP2	3.011853	1.98E-12	9.690156	Up	PH domain and leucine rich repeat protein phosphatase 2
A_24_P154868	MEP1A	5.896661	2.09E-12	9.672672	Up	meprin A subunit alpha
A_23_P216468	SLC1A1	4.230013	2.16E-12	9.662745	Up	solute carrier family 1 member 1
A_23_P144668	CMBL	3.042062	2.26E-12	9.648016	Up	carboxymethylenebutenolidase homolog
A_23_P420209	GCNT3	3.584778	2.28E-12	9.645569	Up	glucosaminyl (N-acetyl) transferase 3, mucin type
A_24_P395415	IGH	4.525345	2.59E-12	9.604477	Up	immunoglobulin heavy locus
A_23_P36882	NTS	4.590283	2.7E-12	9.591231	Up	neurotensin
A_23_P257355	OTC	4.893846	2.76E-12	9.584264	Up	ornithine carbamoyltransferase
A_23_P421483	CEACAM6	4.604236	3.05E-12	9.551841	Up	carcinoembryonic antigen related cell adhesion molecule 6
A_23_P417415	ACOT11	3.447322	3.67E-12	9.492342	Up	acyl-CoA thioesterase 11

A_23_P397999	FZD5	3.278061	4.45E-12	9.4308	Up	frizzled class receptor 5
A_23_P102864	TMPRSS15	3.479534	5.28E-12	9.376269	Up	transmembrane serine protease 15
A_23_P310274	PRSS2	5.176845	5.83E-12	9.344559	Up	serine protease 2
A_24_P639671	SNHG18	3.056954	5.89E-12	9.341498	Up	small nucleolar RNA host gene 18
A_23_P164436	ASPA	3.150679	5.99E-12	9.336151	Up	aspartoacylase
A_23_P93122	MEP1A	6.296252	6.42E-12	9.313644	Up	meprin A subunit alpha
A_24_P610945	KRT17P1	3.738314	6.5E-12	9.310142	Up	keratin 17 pseudogene 1
A_23_P36531	TSPAN8	6.704126	7.08E-12	9.282548	Up	tetraspanin 8
A_23_P253495	GSTA3	5.099532	7.55E-12	9.262411	Up	glutathione S-transferase alpha 3
A_23_P120809	GGTLC2	3.018005	7.88E-12	9.248563	Up	gamma-glutamyltransferase light chain 2
A_23_P103486	CYP2J2	5.283212	8.23E-12	9.2348	Up	cytochrome P450 family 2 subfamily J member 2
A_23_P131935	FERMT1	3.053181	8.54E-12	9.223221	Up	fermitin family member 1
A_23_P108082	CREB3L3	6.559723	1.06E-11	9.154169	Up	cAMP responsive element binding protein 3 like 3
A_23_P35977	PDZD3	4.002163	1.15E-11	9.130012	Up	PDZ domain containing 3
A_23_P133338	CDHR2	3.231795	1.21E-11	9.114198	Up	cadherin related family member 2
A_23_P71880	SPINK4	5.563491	1.22E-11	9.110463	Up	serine peptidase inhibitor, Kazal type 4
A_32_P32739	NAGS	3.121402	1.3E-11	9.090556	Up	N-acetylglutamate synthase
A_23_P162589	VDR	3.890347	1.31E-11	9.088556	Up	vitamin D receptor
A_23_P429977	KCNQ1	3.267476	1.61E-11	9.023193	Up	potassium voltage-gated channel subfamily Q member 1
A_23_P135417	GSTA1	6.024144	1.62E-11	9.02179	Up	glutathione S-transferase alpha 1
A_23_P56703	TRABD2A	3.102412	1.86E-11	8.977065	Up	TraB domain containing 2A
A_24_P188071	TUBA1C	3.065493	1.89E-11	8.972726	Up	tubulin alpha 1c
A_23_P109785	NR1I2	3.500402	2.08E-11	8.942589	Up	nuclear receptor subfamily 1 group I member 2
A_23_P1682	TMEM45B	5.315439	2.1E-11	8.939935	Up	transmembrane protein 45B
A_23_P436284	SLC51B	5.070399	2.26E-11	8.916289	Up	solute carrier family 51 beta subunit
A_23_P128919	LGALS3	4.651313	2.46E-11	8.890393	Up	galectin 3
A_23_P406187	NAGS	3.14552	2.47E-11	8.887902	Up	N-acetylglutamate synthase
A_32_P171793	TLR3	3.208549	2.75E-11	8.854788	Up	toll like receptor 3
A_24_P273647	BICDL2	4.151245	2.85E-11	8.844171	Up	BICD family like cargo adaptor 2
A_23_P252817	SST	3.227999	2.87E-11	8.841345	Up	somatostatin
A_23_P39067	SPIB	3.329966	2.88E-11	8.840059	Up	Spi-B transcription factor
A_23_P407695	FAM151A	5.266972	3.1E-11	8.817862	Up	family with sequence similarity 151 member A
A_23_P147326	SERINC2	3.230589	3.21E-11	8.806597	Up	serine incorporator 2

A_23_P256425	ADAMDEC1	4.319962	3.32E-11	8.795585	Up	ADAM like decysin 1
A_24_P313210	AMN	3.196696	3.7E-11	8.762359	Up	amnion associated transmembrane protein
A_23_P159076	SLC17A8	3.99934	4.06E-11	8.733415	Up	solute carrier family 17 member 8
A_23_P66355	ITGB4	3.536657	4.3E-11	8.715179	Up	integrin subunit beta 4
A_23_P42909	TMEM139	3.136199	4.6E-11	8.694371	Up	transmembrane protein 139
A_24_P97104	DPP4	3.318123	4.82E-11	8.679647	Up	dipeptidyl peptidase 4
A_23_P149613	FMO1	3.117996	5.59E-11	8.633708	Up	flavin containing monooxygenase 1
A_23_P202978	CASP1	3.136895	5.78E-11	8.623265	Up	caspase 1
A_23_P218442	CEACAM6	3.550603	5.81E-11	8.621914	Up	carcinoembryonic antigen related cell adhesion molecule 6
A_24_P399980	HEPH	3.528254	6.01E-11	8.611241	Up	hephaestin
A_23_P44569	ABCC2	3.799303	6.21E-11	8.601045	Up	ATP binding cassette subfamily C member 2
A_23_P158976	ABCC2	3.873807	6.72E-11	8.576443	Up	ATP binding cassette subfamily C member 2
A_23_P45821	#N/A	4.427235	7.28E-11	8.551825	Up	NA
A_23_P93349	SLC44A4	3.239696	7.58E-11	8.539178	Up	solute carrier family 44 member 4
A_23_P138541	AKR1C3	3.424674	9E-11	8.486066	Up	aldo-ketoreductase family 1 member C3
A_23_P57199	GGTLC1	3.490756	9.59E-11	8.466747	Up	gamma-glutamyltransferase light chain 1
A_24_P192727	KAZALD1	3.438688	1.23E-10	8.389652	Up	Kazal type serine peptidase inhibitor domain 1
A_24_P935147	#N/A	4.357137	1.27E-10	8.379134	Up	NA
A_23_P66347	#N/A	3.829394	1.27E-10	8.378864	Up	NA
A_23_P93141	GSTA5	6.479348	1.38E-10	8.354931	Up	glutathione S-transferase alpha 5
A_23_P102364	NGEF	4.846338	1.46E-10	8.336244	Up	neuronal guanine nucleotide exchange factor
A_23_P204133	GALNT6	3.018017	1.49E-10	8.330936	Up	polypeptide N-acetylgalactosaminyltransferase 6
A_23_P67367	DHDH	3.169689	1.57E-10	8.314347	Up	dihydrodiol dehydrogenase
A_23_P69586	FAT1	3.278498	1.77E-10	8.27726	Up	FAT atypical cadherin 1
A_24_P844984	PIGR	7.242045	1.88E-10	8.259237	Up	polymeric immunoglobulin receptor
A_23_P139260	SLC22A18	3.024902	2.32E-10	8.195445	Up	solute carrier family 22 member 18
A_23_P160159	SLC2A5	3.625022	3.1E-10	8.106496	Up	solute carrier family 2 member 5
A_23_P201636	LAMC2	3.22236	3.14E-10	8.102332	Up	laminin subunit gamma 2
A_23_P32143	ALDOB	7.475593	3.32E-10	8.08552	Up	aldolase, fructose-bisphosphate B
A_23_P256784	MUC2	4.233307	3.48E-10	8.070638	Up	mucin 2, oligomeric mucus/gel-forming
A_23_P134854	CLDN23	3.097362	3.56E-10	8.063791	Up	claudin 23
A_23_P385126	DEPDC7	3.259734	3.66E-10	8.055589	Up	DEP domain containing 7
A_23_P201551	VAV3	3.08238	3.8E-10	8.04429	Up	vav guanine nucleotide exchange factor 3

A_23_P2789	OLFM4	3.492536	3.89E-10	8.037279	Up	olfactomedin 4
A_24_P300394	GSTA2	6.81717	3.97E-10	8.031008	Up	glutathione S-transferase alpha 2
A_23_P15146	IL32	3.969719	4.39E-10	8.000387	Up	interleukin 32
A_23_P257111	FBP1	3.832134	4.99E-10	7.961347	Up	fructose-bisphosphatase 1 potassium voltage-gated channel modifier subfamily G member 1
A_23_P210581	KCNG1	3.325464	5.21E-10	7.948113	Up	angiotensin I converting enzyme
A_24_P365129	ACE	3.019418	5.52E-10	7.930473	Up	sushi domain containing 2
A_23_P314101	SUSD2	3.756631	7.17E-10	7.851184	Up	phospholipase B1
A_24_P379616	PLB1	3.11158	9.95E-10	7.751829	Up	inositol-trisphosphate 3-kinase A
A_23_P65918	ITPKA	4.406016	1.01E-09	7.747137	Up	carboxypeptidase O
A_23_P102172	CPO	5.012128	1.08E-09	7.727867	Up	adipogenesis regulatory factor
A_23_P161439	ADIRF	3.463609	1.1E-09	7.721698	Up	cadherin related family member 1
A_23_P149946	CDHR1	3.158461	1.47E-09	7.63476	Up	granzyme A
A_23_P133445	GZMA	3.108351	1.79E-09	7.574	Up	solute carrier family 7 member 9
A_23_P142250	SLC7A9	3.377014	2.15E-09	7.51919	Up	intelectin 1
A_23_P95790	ITLN1	4.473514	2.17E-09	7.516039	Up	syndecan binding protein 2
A_23_P131899	SDCBP2	3.137512	2.2E-09	7.511939	Up	hydroxysteroid 17-beta dehydrogenase 2
A_23_P118065	HSD17B2	5.360428	2.35E-09	7.491863	Up	vanin 1
A_23_P255345	VNN1	3.204107	2.5E-09	7.474256	Up	keratin 19
A_23_P66798	KRT19	4.255264	2.54E-09	7.46923	Up	mucin 13, cell surface associated
A_23_P155236	MUC13	4.327154	2.85E-09	7.434048	Up	phospholipase A2 group IIA
A_23_P321949	PLA2G2A	3.157816	3.19E-09	7.400907	Up	semaphorin 6A
A_23_P7752	SEMA6A	3.362002	3.25E-09	7.394952	Up	NA
A_32_P234405	#N/A	4.333751	3.32E-09	7.38835	Up	immunoglobulin heavy constant mu
A_24_P417352	IGHM	3.929729	3.78E-09	7.349224	Up	tripartite motif containing 15
A_23_P500300	TRIM15	4.16502	3.8E-09	7.348202	Up	POU class 2 associating factor 1
A_23_P312920	POU2AF1	3.633266	3.91E-09	7.339446	Up	NA
A_24_P725998	#N/A	3.744943	4.09E-09	7.325814	Up	dipeptidase 1
A_23_P152262	DPEP1	4.020226	4.13E-09	7.323146	Up	UDP glucuronosyltransferase family 2 member B17
A_23_P501624	UGT2B17	6.148132	4.37E-09	7.30632	Up	serum/glucocorticoid regulated kinase 1
A_23_P19673	SGK1	3.433283	5.13E-09	7.257807	Up	vanin 1
A_24_P337700	VNN1	3.390276	5.37E-09	7.244196	Up	CCAAT enhancer binding protein alpha
A_24_P224727	CEBPA	3.18922	6.13E-09	7.20477	Up	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1
A_23_P97173	HSD3B1	3.289675	7.02E-09	7.164055	Up	

A_23_P100711	PMP22	3.646706	7.5E-09	7.144422	Up	peripheral myelin protein 22
A_23_P52121	PDZK1	3.354471	8.06E-09	7.12292	Up	PDZ domain containing 1
A_23_P375494	CEBPA	3.112783	8.49E-09	7.10721	Up	CCAAT enhancer binding protein alpha
A_23_P151915	GCNT3	5.008318	8.76E-09	7.098162	Up	glucosaminyl (N-acetyl) transferase 3, mucin type
A_23_P67381	SULT2A1	4.024219	1.01E-08	7.056258	Up	sulfotransferase family 2A member 1
A_23_P111583	CD36	3.108409	1.2E-08	7.004335	Up	CD36 molecule
A_23_P79217	LCT	5.289419	1.21E-08	7.001845	Up	lactase
A_23_P209564	CYBRD1	3.163658	1.25E-08	6.9931	Up	cytochrome b reductase 1
A_32_P9368	EFNA2	3.138328	1.28E-08	6.984986	Up	ephrin A2
A_23_P22526	HEPH	3.222488	1.66E-08	6.907184	Up	hephaestin
A_23_P85015	MAOB	3.077571	1.92E-08	6.864496	Up	monoamine oxidase B
A_23_P29248	TST	4.295838	1.98E-08	6.854286	Up	thiosulfate sulfurtransferase
A_23_P43846	FABP6	7.038364	2.08E-08	6.840264	Up	fatty acid binding protein 6
A_24_P222872	UGT1A6	3.374833	2.4E-08	6.79725	Up	UDP glucuronosyltransferase family 1 member A6
A_23_P27013	HOXB9	3.513645	2.49E-08	6.787217	Up	homeobox B9
A_23_P56356	PLB1	3.789584	2.66E-08	6.767113	Up	phospholipase B1
A_32_P351968	HLA-DMB	3.111137	2.87E-08	6.744543	Up	major histocompatibility complex, class II, DM beta
A_23_P79591	APOB	5.178208	4.04E-08	6.642937	Up	apolipoprotein B
A_24_P234768	HTR4	3.489102	4.25E-08	6.627796	Up	5-hydroxytryptamine receptor 4
A_23_P79562	FABP1	6.969704	5.14E-08	6.571104	Up	fatty acid binding protein 1
A_32_P43664	JCHAIN	3.028678	7.27E-08	6.468355	Up	joining chain of multimeric IgA and IgM
A_23_P5300	CPS1	3.378841	7.32E-08	6.466193	Up	carbamoyl-phosphate synthase 1
A_23_P132285	MPST	3.989152	8.67E-08	6.416062	Up	mercaptopyruvatesulfurtransferase
A_24_P334208	#N/A	6.246553	1.03E-07	6.365668	Up	NA
A_23_P26024	C15orf48	4.319538	1.09E-07	6.347337	Up	chromosome 15 open reading frame 48
A_23_P80570	AADAC	4.301339	1.26E-07	6.30447	Up	arylacetamidedeacetylase
A_23_P160800	NR0B2	3.528035	1.69E-07	6.217371	Up	nuclear receptor subfamily 0 group B member 2
A_23_P132569	SLC2A2	3.603128	1.71E-07	6.215175	Up	solute carrier family 2 member 2
A_23_P430670	CHST5	3.296281	1.75E-07	6.207493	Up	carbohydrate sulfotransferase 5
A_23_P61042	IGHA2	3.902505	1.8E-07	6.199508	Up	immunoglobulin heavy constant alpha 2 (A2m marker)
A_23_P325562	SLC1A7	3.334617	2.06E-07	6.158795	Up	solute carrier family 1 member 7
A_23_P415974	ALDOB	6.509246	2.22E-07	6.136526	Up	aldolase, fructose-bisphosphate B
A_23_P94319	KBTBD11	3.102518	2.43E-07	6.109857	Up	kelch repeat and BTB domain containing 11

A_23_P10291	CTSE	3.319066	2.71E-07	6.077715	Up	cathepsin E
A_23_P71570	OSR2	3.498268	1.03E-06	5.680229	Up	odd-skipped related transcription factor 2
A_23_P408249	PCK1	4.709463	1.29E-06	5.613194	Up	phosphoenolpyruvatecarboxykinase 1
A_23_P136026	IGHA1	3.337144	1.66E-06	5.537527	Up	immunoglobulin heavy constant alpha 1
A_24_P405705	SLC2A2	3.387046	1.82E-06	5.510307	Up	solute carrier family 2 member 2
A_32_P37903	RNU1-70P	3.89463	1.89E-06	5.499043	Up	RNA, U1 small nuclear 70, pseudogene
A_23_P85008	MAOB	3.16043	2E-06	5.482423	Up	monoamine oxidase B
A_23_P203183	APOC3	4.801197	2.06E-06	5.47272	Up	apolipoprotein C3
A_24_P17691	UGT2B17	3.638378	2.21E-06	5.452183	Up	UDP glucuronosyltransferase family 2 member B17
A_23_P362694	FDCSP	3.131336	2.31E-06	5.439132	Up	follicular dendritic cell secreted protein
A_23_P60599	UGT1A6	4.089838	2.58E-06	5.40549	Up	UDP glucuronosyltransferase family 1 member A6
A_23_P203191	APOA1	4.926868	4.5E-06	5.238701	Up	apolipoprotein A1
A_23_P385017	G6PC	3.811582	6.46E-06	5.129322	Up	glucose-6-phosphatase catalytic subunit
A_23_P58407	UGT2B15	4.147012	6.95E-06	5.107137	Up	UDP glucuronosyltransferase family 2 member B15
A_23_P213745	CXCL14	4.066335	7.62E-06	5.079162	Up	C-X-C motif chemokine ligand 14
A_23_P167168	JCHAIN	3.647952	9.62E-06	5.008556	Up	joining chain of multimeric IgA and IgM
A_23_P36658	MGST1	3.452666	9.91E-06	4.999395	Up	microsomal glutathione S-transferase 1
A_23_P154379	NAT8	3.092889	1.78E-05	4.821375	Up	N-acetyltransferase 8 (putative)
A_23_P119763	ABCG5	3.122978	1.86E-05	4.80657	Up	ATP binding cassette subfamily G member 5
A_24_P169873	IGHA2	3.637602	3.11E-05	4.64929	Up	immunoglobulin heavy constant alpha 2 (A2m marker)
A_23_P126613	AQP10	3.470442	7.49E-05	4.37467	Up	aquaporin 10
A_23_P214079	SPINK1	3.874093	9.04E-05	4.315295	Up	serine peptidase inhibitor, Kazal type 1
A_23_P215720	CFTR	3.212191	0.00023	4.01602	Up	cystic fibrosis transmembrane conductance regulator
A_23_P68759	TFF1	3.195472	0.000546	3.732886	Up	trefoil factor 1
A_32_P187704	SNTG1	-7.91599	6.87E-38	-44.4872	Down	syntrophin gamma 1
A_23_P165201	PRODH2	-8.48125	2.28E-31	-31.1558	Down	proline dehydrogenase 2
A_23_P118722	ASGR1	-7.20906	1.82E-29	-28.0309	Down	asialoglycoprotein receptor 1
A_23_P130333	TTR	-8.72652	9.07E-29	-26.9586	Down	transthyretin
A_23_P90722	PTPRN	-5.39769	8.29E-28	-25.5401	Down	protein tyrosine phosphatase, receptor type N
A_32_P212258	#N/A	-4.39334	9.44E-25	-21.4507	Down	NA
A_23_P148568	NXF2	-5.4686	1.48E-24	-21.2104	Down	nuclear RNA export factor 2
A_23_P114353	NXF5	-5.411	3.08E-24	-20.8218	Down	nuclear RNA export factor 5

A_23_P161297	OGDHL	-4.92012	3.54E-24	-20.7476	Down	oxoglutarate dehydrogenase like
A_23_P5131	ISYNA1	-3.27789	4.98E-24	-20.5695	Down	inositol-3-phosphate synthase 1
A_23_P213508	PCSK1	-6.89448	1.04E-23	-20.1913	Down	proproteinconvertasesubtilisin/kexin type 1
A_23_P43679	ZNF618	-3.47711	2.56E-23	-19.7322	Down	zinc finger protein 618
A_23_P44794	RAB3C	-5.29257	2.84E-23	-19.6788	Down	RAB3C, member RAS oncogene family
A_24_P57977	SRCIN1	-5.34211	5.01E-23	-19.396	Down	SRC kinase signaling inhibitor 1
A_23_P42882	CAMK2B	-6.23545	5.2E-23	-19.3776	Down	calcium/calmodulin dependent protein kinase II beta
A_24_P928830	#N/A	-5.44257	5.28E-23	-19.3696	Down	NA
A_23_P160377	DNALI1	-3.87979	6.46E-23	-19.2704	Down	dynein axonemal light intermediate chain 1
A_24_P418744	AC133963.1	-2.88268	6.7E-23	-19.2524	Down	inositol-3-phosphate synthase 1 (ISYNA1) pseudogene
A_23_P169007	NPM2	-3.63505	9.19E-23	-19.0965	Down	nucleophosmin/nucleoplasmin 2
A_23_P165457	CRYBA2	-6.03321	1.69E-22	-18.7985	Down	crystallin beta A2
A_23_P418785	STXBP5L	-6.91021	4.49E-22	-18.3314	Down	syntaxin binding protein 5 like
A_32_P3476	RPRML	-6.55656	8.19E-22	-18.0473	Down	reprimin like
A_23_P57658	HRASLS	-6.72027	1.16E-21	-17.8844	Down	HRAS like suppressor
A_23_P87752	P3H3	-2.94788	1.42E-21	-17.7904	Down	prolyl 3-hydroxylase 3
A_32_P205624	SHC2	-3.97404	1.85E-21	-17.6684	Down	SHC adaptor protein 2
A_23_P170667	ASPHD1	-5.34133	2.01E-21	-17.6291	Down	aspartate beta-hydroxylase domain containing 1
A_23_P118122	RGS11	-3.85362	2.18E-21	-17.5926	Down	regulator of G protein signaling 11
A_32_P194423	#N/A	-3.85748	2.44E-21	-17.5402	Down	NA
A_23_P108143	GAMT	-4.09947	1.33E-20	-16.7745	Down	guanidinoacetate N-methyltransferase
A_32_P71675	SMIM1	-4.30117	1.41E-20	-16.7481	Down	small integral membrane protein 1 (Vel blood group)
A_23_P315836	BAIAP2	-3.82316	1.47E-20	-16.7299	Down	BAI1 associated protein 2
A_23_P17354	GDAP1L1	-4.48337	1.86E-20	-16.6258	Down	ganglioside induced differentiation associated protein 1 like 1
A_23_P400378	GPBAR1	-3.19125	2.41E-20	-16.5121	Down	G protein-coupled bile acid receptor 1
A_23_P33168	SLC18A1	-7.02722	2.46E-20	-16.503	Down	solute carrier family 18 member A1
A_32_P202502	MICU3	-2.98742	3.2E-20	-16.389	Down	mitochondrial calcium uptake family member 3
A_32_P134968	SPTB	-3.41419	5.24E-20	-16.1743	Down	spectrin beta, erythrocytic
A_32_P59277	RF00406	-3.41134	8.4E-20	-15.9712	Down	NA
A_24_P743802	ZNF618	-2.87497	8.51E-20	-15.9657	Down	zinc finger protein 618
A_23_P45955	TEKT2	-3.8055	9.39E-20	-15.9234	Down	tektin 2
A_23_P390984	KCNH6	-4.89531	1.01E-19	-15.8923	Down	potassium voltage-gated channel subfamily H member 6

A_32_P164593	ZMAT4	-5.12404	2.04E-19	-15.5947	Down	zinc finger matrin-type 4
A_23_P57155	CHGB	-7.25118	2.14E-19	-15.5742	Down	chromogranin B
A_23_P3483	CACNA1H	-3.0054	2.55E-19	-15.5013	Down	calcium voltage-gated channel subunit alpha1 H
A_23_P335695	OBSL1	-3.11844	2.98E-19	-15.4355	Down	obscurin like 1
A_23_P104692	PELI3	-3.17923	3.25E-19	-15.3987	Down	pellino E3 ubiquitin protein ligase family member 3
A_32_P36143	#N/A	-2.75881	3.69E-19	-15.3461	Down	NA
A_23_P66017	PRRT2	-3.99644	3.95E-19	-15.3175	Down	proline rich transmembrane protein 2
A_23_P365494	UNC13A	-4.20559	4.84E-19	-15.2336	Down	unc-13 homolog A
A_23_P431305	DIPK1B	-2.75605	5.25E-19	-15.1995	Down	divergent protein kinase domain 1B
A_23_P2223	MYL6B	-2.79391	6.15E-19	-15.1346	Down	myosin light chain 6B
A_24_P37355	AMER3	-5.35712	7.5E-19	-15.0526	Down	APC membrane recruitment protein 3
A_24_P32986	FAM95A	-2.91485	7.56E-19	-15.0493	Down	family with sequence similarity 95 member A
A_23_P17242	ABHD1	-3.62027	7.82E-19	-15.0353	Down	abhydrolase domain containing 1
A_23_P326931	CFAP70	-3.76041	8.66E-19	-14.9936	Down	cilia and flagella associated protein 70
A_24_P693986	TRNP1	-4.5439	9.54E-19	-14.9541	Down	TMF1-regulated nuclear protein 1
A_23_P132138	C21orf58	-3.99442	1.24E-18	-14.8462	Down	chromosome 21 open reading frame 58
A_23_P73150	TTC25	-3.64101	1.28E-18	-14.8335	Down	tetratricopeptide repeat domain 25
A_23_P373031	CACNA1C	-3.00524	1.69E-18	-14.7206	Down	calcium voltage-gated channel subunit alpha1 C
A_23_P67127	TMEM145	-4.93596	1.88E-18	-14.6775	Down	transmembrane protein 145
A_23_P20443	LZTS1	-3.30762	2.61E-18	-14.5458	Down	leucine zipper tumor suppressor 1
A_23_P120103	KCNS3	-4.11934	2.83E-18	-14.5134	Down	potassium voltage-gated channel modifier subfamily S member 3
A_23_P19182	REEP2	-4.26343	4.03E-18	-14.3719	Down	receptor accessory protein 2
A_23_P381954	EPOR	-4.22213	5.36E-18	-14.2588	Down	erythropoietin receptor
A_23_P146134	DUSP26	-5.54869	6.12E-18	-14.2064	Down	dual specificity phosphatase 26
A_32_P117846	#N/A	-2.95805	6.89E-18	-14.1594	Down	NA
A_23_P326893	CCDC151	-2.96294	7.26E-18	-14.1393	Down	coiled-coil domain containing 151
A_23_P210756	SNAP25	-3.6154	8.08E-18	-14.097	Down	synaptosome associated protein 25
A_23_P83558	KCNH6	-4.47246	8.33E-18	-14.0851	Down	potassium voltage-gated channel subfamily H member 6
A_23_P101480	MAST1	-3.71837	9.22E-18	-14.0452	Down	microtubule associated serine/threonine kinase 1
A_23_P143374	NINL	-3.0819	9.34E-18	-14.0402	Down	ninein like
A_23_P103011	RAB36	-3.39498	1.23E-17	-13.9336	Down	RAB36, member RAS oncogene family
A_23_P206413	WWOX	-3.21207	1.44E-17	-13.8712	Down	WW domain containing oxidoreductase
A_23_P99661	ARHGEF40	-2.99725	1.85E-17	-13.773	Down	Rho guanine nucleotide exchange factor 40

A_23_P85140	TCEAL2	-4.9494	1.89E-17	-13.7648	Down	transcription elongation factor A like 2
A_32_P185317	MNX1-AS1	-3.78122	1.9E-17	-13.7634	Down	MNX1 antisense RNA 1 (head to head)
A_23_P332713	ZFR2	-5.83473	2.27E-17	-13.6944	Down	zinc finger RNA binding protein 2
A_23_P141893	PPM1N	-3.84164	2.39E-17	-13.674	Down	protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent 1N (putative)
A_23_P89270	SERPINF2	-3.67214	2.48E-17	-13.6607	Down	serpin family F member 2
A_23_P140876	ABCA3	-3.09835	2.64E-17	-13.6358	Down	ATP binding cassette subfamily A member 3
A_23_P104741	KIRREL3	-5.71808	2.87E-17	-13.6045	Down	kirre like nephrin family adhesion molecule 3
A_23_P333029	ERICH5	-5.03878	2.87E-17	-13.6035	Down	glutamate rich 5
A_23_P145889	CDK14	-3.26648	3.41E-17	-13.5376	Down	cyclin dependent kinase 14
A_23_P112982	SVOP	-5.15992	3.43E-17	-13.5359	Down	SV2 related protein
A_23_P127220	DNAJC12	-3.96075	3.9E-17	-13.4865	Down	DnaJ heat shock protein family (Hsp40) member C12
A_24_P91094	RUNDC3A	-3.81498	4.45E-17	-13.4357	Down	RUN domain containing 3A
A_23_P200260	PCNX2	-3.32002	4.52E-17	-13.4304	Down	pecanex 2
A_23_P29124	SEPT5	-4.97434	4.73E-17	-13.4125	Down	septin 5
A_24_P310864	CCDC24	-2.9841	5.78E-17	-13.3363	Down	coiled-coil domain containing 24
A_23_P170541	KCNH6	-4.46123	6.53E-17	-13.2905	Down	potassium voltage-gated channel subfamily H member 6
A_23_P163711	FAM57B	-3.50535	1.16E-16	-13.0723	Down	family with sequence similarity 57 member B
A_23_P382607	WNT4	-3.26964	1.19E-16	-13.0648	Down	Wnt family member 4
A_23_P50786	CLIP3	-3.38167	1.19E-16	-13.0643	Down	CAP-Gly domain containing linker protein 3
A_23_P93938	NACAD	-3.71679	1.34E-16	-13.0202	Down	NAC alpha domain containing
A_23_P211727	FGF12	-4.98593	1.45E-16	-12.9892	Down	fibroblast growth factor 12
A_32_P212471	RIIAD1	-4.09285	1.48E-16	-12.9823	Down	regulatory subunit of type II PKA R-subunit (RIIa) domain containing 1
A_23_P159952	BEX1	-4.91188	1.7E-16	-12.9302	Down	brain expressed X-linked 1
A_23_P350249	GLIS3	-3.26219	1.75E-16	-12.9188	Down	GLIS family zinc finger 3
A_23_P22487	PCSK1N	-5.29913	1.79E-16	-12.9113	Down	proproteinconvertasesubtilisin/kexin type 1 inhibitor
A_23_P337849	CELF3	-5.63009	1.95E-16	-12.8788	Down	CUGBP Elav-like family member 3
A_24_P756657	FAM229B	-2.76707	2.12E-16	-12.8492	Down	family with sequence similarity 229 member B
A_23_P386356	KIF12	-3.03034	2.71E-16	-12.757	Down	kinesin family member 12
A_23_P368996	LRRC56	-2.7905	2.76E-16	-12.7508	Down	leucine rich repeat containing 56
A_23_P253622	ANKRD36B	-3.09948	2.9E-16	-12.7325	Down	ankyrin repeat domain 36B
A_32_P226205	ZFHX2	-3.30166	2.95E-16	-12.7264	Down	zinc finger homeobox 2
A_23_P107903	RGL3	-4.64248	3.36E-16	-12.6781	Down	ral guanine nucleotide dissociation stimulator like 3

A_23_P331700	SRRM3	-3.04629	3.82E-16	-12.6307	Down	serine/arginine repetitive matrix 3
A_23_P217228	TRO	-4.55863	3.84E-16	-12.6293	Down	trophinin
A_24_P226541	STX1A	-3.16855	4.12E-16	-12.603	Down	syntaxin 1A
A_23_P1833	B3GAT1	-4.87119	4.52E-16	-12.5693	Down	beta-1,3-glucuronyltransferase 1
A_23_P110624	CTNND2	-4.32754	4.57E-16	-12.5654	Down	catenin delta 2
A_23_P53247	DTX3	-3.11575	5.3E-16	-12.5112	Down	deltex E3 ubiquitin ligase 3
A_23_P347632	MTSS1	-3.31895	5.35E-16	-12.5078	Down	MTSS1, I-BAR domain containing
A_24_P128741	#N/A	-2.91614	5.91E-16	-12.4711	Down	NA
A_32_P27046	CHGA	-6.42459	6.73E-16	-12.424	Down	chromogranin A
A_23_P5460	FEV	-4.77057	1.01E-15	-12.2783	Down	FEV, ETS transcription factor
A_32_P69849	BEX5	-3.8995	1.1E-15	-12.2469	Down	brain expressed X-linked 5
A_32_P154872	#N/A	-3.88163	1.14E-15	-12.2322	Down	NA
A_23_P48585	SALL2	-2.97516	1.29E-15	-12.1875	Down	spalt like transcription factor 2
A_23_P210319	DTNB	-3.07328	1.98E-15	-12.0337	Down	dystrobrevin beta
A_23_P329271	MC1R	-2.97155	2.13E-15	-12.0086	Down	melanocortin 1 receptor
A_24_P14731	PCSK1N	-3.07735	2.58E-15	-11.9395	Down	proproteinconvertasesubtilisin/kexin type 1 inhibitor
A_23_P11787	WNT4	-4.23842	2.65E-15	-11.93	Down	Wnt family member 4
A_32_P47641	#N/A	-4.78361	3.15E-15	-11.8692	Down	NA
A_23_P91552	FTCD	-6.30941	3.19E-15	-11.8645	Down	formimidoyltransferasecyclodeaminase
A_24_P391868	CPLX2	-4.7865	3.23E-15	-11.8607	Down	complexin 2
A_24_P709844	#N/A	-6.50634	3.42E-15	-11.8401	Down	NA
A_32_P156851	RCAN2	-3.40973	3.6E-15	-11.8221	Down	regulator of calcineurin 2
A_23_P147786	RIMS2	-3.82774	3.88E-15	-11.7953	Down	regulating synaptic membrane exocytosis 2
A_23_P163306	CGNL1	-2.78544	3.88E-15	-11.7951	Down	cingulin like 1
A_32_P110485	#N/A	-3.3303	3.97E-15	-11.7872	Down	NA
A_32_P17145	#N/A	-3.34903	4.05E-15	-11.7796	Down	NA
A_23_P33093	ST6GALNAC5	-3.96783	4.46E-15	-11.7458	Down	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 5
A_23_P353667	MIR7-3HG	-5.44645	4.64E-15	-11.7317	Down	MIR7-3 host gene
A_24_P551067	AC092683.1	-2.77204	5.06E-15	-11.7012	Down	novel transcript
A_32_P223747	#N/A	-3.44533	5.24E-15	-11.6891	Down	NA
A_23_P16283	CPT1C	-4.62425	5.43E-15	-11.6766	Down	carnitinepalmitoyltransferase 1C
A_24_P38290	TAC1	-5.41757	6.12E-15	-11.6348	Down	tachykinin precursor 1
A_24_P933704	PAM	-3.14117	6.41E-15	-11.6185	Down	peptidylglycine alpha-amidatingmonooxygenase

A_24_P745883	DNM1P30	-3.01469	8.75E-15	-11.5096	Down	dynamain 1 pseudogene 30
A_32_P203878	#N/A	-3.04811	1.07E-14	-11.4407	Down	NA
A_32_P140475	CEP126	-3.99456	1.14E-14	-11.4181	Down	centrosomal protein 126
A_24_P31627	KCNB1	-4.27103	1.18E-14	-11.4059	Down	potassium voltage-gated channel subfamily B member 1
A_23_P326319	C16orf45	-2.79702	1.42E-14	-11.3404	Down	chromosome 16 open reading frame 45
A_32_P220463	FBLL1	-3.98423	1.44E-14	-11.337	Down	fibrillarin like 1
A_23_P77304	AP3B2	-3.57178	1.46E-14	-11.3307	Down	adaptor related protein complex 3 subunit beta 2
A_23_P156907	SOBP	-3.36326	1.69E-14	-11.281	Down	sine oculis binding protein homolog
A_32_P115382	KCNB1	-3.93819	1.76E-14	-11.2673	Down	potassium voltage-gated channel subfamily B member 1
A_24_P289260	DACT2	-4.50702	1.84E-14	-11.2511	Down	dishevelled binding antagonist of beta catenin 2
A_32_P66804	PTPRN2	-3.32557	2.02E-14	-11.2193	Down	protein tyrosine phosphatase, receptor type N2
A_23_P348253	CDHR3	-5.19487	2.04E-14	-11.2151	Down	cadherin related family member 3
A_23_P327462	RFX6	-4.34288	2.17E-14	-11.1951	Down	regulatory factor X6
A_23_P367899	EPOR	-3.71302	2.76E-14	-11.1119	Down	erythropoietin receptor
A_23_P315451	KIRREL2	-5.02204	3.38E-14	-11.0423	Down	kirre like nephrin family adhesion molecule 2
A_23_P86561	CALY	-4.33385	3.91E-14	-10.993	Down	calcyon neuron specific vesicular protein
A_23_P391275	RCAN3	-2.95062	4.18E-14	-10.9702	Down	RCAN family member 3
A_23_P83339	RNF183	-3.97056	4.2E-14	-10.9683	Down	ring finger protein 183
A_23_P45524	BEX3	-3.21265	4.34E-14	-10.957	Down	brain expressed X-linked 3
A_24_P938403	JPH3	-2.94036	4.4E-14	-10.9528	Down	junctophilin 3
A_23_P148768	F5	-4.55687	4.4E-14	-10.9528	Down	coagulation factor V
A_23_P215283	TAC1	-5.44757	5.2E-14	-10.8955	Down	tachykinin precursor 1
A_23_P109427	GSTT2	-2.94372	5.99E-14	-10.8479	Down	glutathione S-transferase theta 2 (gene/pseudogene)
A_23_P104804	ZBTB16	-2.90496	6.14E-14	-10.8391	Down	zinc finger and BTB domain containing 16
A_24_P293114	SPTBN4	-4.2389	6.99E-14	-10.7954	Down	spectrin beta, non-erythrocytic 4
A_23_P351837	KLHL35	-3.04621	7.32E-14	-10.78	Down	kelch like family member 35
A_23_P47867	PPFIBP1	-3.68552	8.34E-14	-10.7359	Down	PPFIA binding protein 1
A_23_P377957	KCTD12	-3.25006	8.65E-14	-10.7236	Down	potassium channel tetramerization domain containing 12
A_23_P423074	FAM169A	-3.28262	9.07E-14	-10.7075	Down	family with sequence similarity 169 member A
A_23_P258088	PACSL1	-4.41439	1.06E-13	-10.6555	Down	protein kinase C and casein kinase substrate in neurons 1
A_32_P126222	LRRC47	-3.27606	1.33E-13	-10.5785	Down	leucine rich repeat containing 47
A_23_P214011	CDH6	-2.89166	1.35E-13	-10.5726	Down	cadherin 6

A_24_P95154	TUSC3	-2.86798	1.45E-13	-10.5494	Down	tumor suppressor candidate 3
A_24_P326344	FAM135B	-3.36209	1.58E-13	-10.521	Down	family with sequence similarity 135 member B
A_32_P453321	ARMH1	-3.32502	1.65E-13	-10.507	Down	armadillo-like helical domain containing 1
A_32_P134764	CDH6	-3.51516	1.68E-13	-10.5015	Down	cadherin 6
A_23_P408167	GPRASP2	-3.03245	1.79E-13	-10.4798	Down	G protein-coupled receptor associated sorting protein 2
A_23_P117298	F7	-2.79906	1.84E-13	-10.4706	Down	coagulation factor VII
A_32_P95462	STXBP5L	-4.29821	2.21E-13	-10.4094	Down	syntaxin binding protein 5 like
A_23_P382584	CHGB	-6.69493	2.34E-13	-10.39	Down	chromogranin B
A_23_P156390	JAKMIP2	-3.12175	2.6E-13	-10.3558	Down	janus kinase and microtubule interacting protein 2
A_23_P378450	MBD3L2	-6.19045	2.6E-13	-10.3557	Down	methyl-CpG binding domain protein 3 like 2
A_23_P29735	BSN	-4.11698	2.71E-13	-10.3415	Down	bassoon presynaptic cytomatrix protein
A_23_P146572	NPDC1	-2.97553	2.74E-13	-10.3375	Down	neural proliferation, differentiation and control 1
A_23_P502274	MAPK11	-3.09152	3.03E-13	-10.3048	Down	mitogen-activated protein kinase 11
A_24_P240166	PHLDB2	-2.95449	3.15E-13	-10.292	Down	pleckstrin homology like domain family B member 2
A_23_P35444	INA	-3.52886	3.44E-13	-10.2623	Down	internexin neuronal intermediate filament protein alpha
A_23_P250102	CAND2	-2.9429	3.6E-13	-10.2471	Down	cullin associated and neddylation dissociated 2 (putative)
A_23_P161659	SYT13	-5.74473	3.74E-13	-10.2347	Down	synaptotagmin 13
A_23_P430658	HEYL	-3.80068	4.02E-13	-10.2114	Down	hes related family bHLH transcription factor with YRPW motif-like
A_23_P22735	BEX2	-4.57662	4.08E-13	-10.2062	Down	brain expressed X-linked 2
A_32_P204239	AC004836.1	-5.80176	4.15E-13	-10.2008	Down	NA
A_23_P128759	SERPINA10	-3.55335	4.22E-13	-10.195	Down	serpin family A member 10
A_32_P213948	#N/A	-3.18001	4.28E-13	-10.1908	Down	NA
A_24_P31275	ATP1B2	-3.06776	4.29E-13	-10.1895	Down	ATPase Na+/K+ transporting subunit beta 2
A_24_P203964	GUSBP1	-2.86755	4.41E-13	-10.1808	Down	glucuronidase, beta pseudogene 1
A_23_P83579	ARNT2	-3.59516	5.03E-13	-10.1373	Down	aryl hydrocarbon receptor nuclear translocator 2
A_23_P434442	TCEAL3	-3.01492	5.03E-13	-10.137	Down	transcription elongation factor A like 3
A_23_P357724	KCNK3	-3.90689	5.47E-13	-10.1097	Down	potassium two pore domain channel subfamily K member 3
A_32_P94	LHFPL4	-5.10403	6.11E-13	-10.0734	Down	LHFPL tetraspan subfamily member 4
A_23_P168556	STX1A	-3.89698	6.95E-13	-10.0311	Down	syntaxin 1A
A_23_P209360	KLHL29	-2.84223	7.23E-13	-10.0183	Down	kelch like family member 29
A_23_P468	CCDC181	-2.81201	7.38E-13	-10.0118	Down	coiled-coil domain containing 181
A_32_P174258	#N/A	-3.02691	8.93E-13	-9.94937	Down	NA

A_24_P548966	RAB3B	-5.26087	9.98E-13	-9.91292	Down	RAB3B, member RAS oncogene family
A_23_P422212	SLC35F3	-4.3341	1.06E-12	-9.89465	Down	solute carrier family 35 member F3
A_32_P113472	CDC42EP3	-3.63128	1.07E-12	-9.89063	Down	CDC42 effector protein 3
A_32_P45844	SLC8A2	-3.87534	1.26E-12	-9.83649	Down	solute carrier family 8 member A2
A_24_P84822	GUSBP2	-3.07478	1.29E-12	-9.8305	Down	glucuronidase, beta pseudogene 2
A_24_P149266	PACSN1	-3.60111	1.31E-12	-9.82427	Down	protein kinase C and casein kinase substrate in neurons 1
A_23_P82420	STX1A	-3.98668	1.41E-12	-9.8008	Down	syntaxin 1A
A_24_P508103	FAR2P2	-4.0095	1.47E-12	-9.78714	Down	fatty acyl-CoA reductase 2 pseudogene 2
A_23_P357571	GSTT2	-3.28402	1.6E-12	-9.76015	Down	glutathione S-transferase theta 2 (gene/pseudogene)
A_23_P165927	STMN3	-3.34039	1.63E-12	-9.75397	Down	stathmin 3
A_23_P54709	RAB26	-3.38568	1.74E-12	-9.7328	Down	RAB26, member RAS oncogene family
A_24_P734953	TRNP1	-3.06393	1.8E-12	-9.72088	Down	TMF1-regulated nuclear protein 1
A_32_P41604	F5	-4.13507	1.95E-12	-9.69524	Down	coagulation factor V
A_24_P192485	TNFRSF11B	-4.11607	2.05E-12	-9.67888	Down	TNF receptor superfamily member 11b
A_23_P50389	NAT14	-3.02013	2.16E-12	-9.66327	Down	N-acetyltransferase 14 (putative)
A_32_P212958	#N/A	-3.09467	2.22E-12	-9.65379	Down	NA
A_23_P401718	CCDC74B	-3.48502	2.44E-12	-9.6234	Down	coiled-coil domain containing 74B
A_24_P327181	WNK4	-3.92621	2.44E-12	-9.62308	Down	WNK lysine deficient protein kinase 4
A_23_P49546	GRIN2C	-6.03447	2.59E-12	-9.60401	Down	glutamate ionotropic receptor NMDA type subunit 2C
A_23_P253451	SLC7A14	-3.89471	3.03E-12	-9.55337	Down	solute carrier family 7 member 14
A_23_P150595	TPH1	-3.34769	3.04E-12	-9.55255	Down	tryptophan hydroxylase 1
A_23_P109122	EBF4	-2.84489	3.19E-12	-9.53688	Down	EBF family member 4
A_32_P192545	TCEAL6	-2.96468	3.23E-12	-9.53296	Down	transcription elongation factor A like 6
A_23_P69326	CADPS	-4.83305	3.35E-12	-9.52144	Down	calcium dependent secretion activator
A_23_P108200	RAB3A	-3.25304	3.95E-12	-9.46856	Down	RAB3A, member RAS oncogene family
A_24_P174793	PCSK1	-6.94233	4.09E-12	-9.4579	Down	proproteinconvertasesubtilisin/kexin type 1
A_23_P101806	HPN	-4.64581	4.52E-12	-9.42556	Down	hepsin
A_23_P38334	WNK4	-3.60009	4.55E-12	-9.42366	Down	WNK lysine deficient protein kinase 4
A_23_P31858	ST18	-3.89172	5.73E-12	-9.34998	Down	ST18, C2H2C-type zinc finger
A_23_P33326	ADRA1B	-2.80956	6.33E-12	-9.31853	Down	adrenoceptor alpha 1B
A_32_P77831	RAB3C	-5.14847	6.43E-12	-9.31338	Down	RAB3C, member RAS oncogene family
A_24_P827096	AP000525.1	-3.16973	7.09E-12	-9.28249	Down	novel transcript, sense intronic to novel transcript
A_23_P42768	#N/A	-4.1409	7.17E-12	-9.27856	Down	NA

A_23_P20697	ADAMTSL2	-3.22327	7.48E-12	-9.26515	Down	ADAMTS like 2
A_23_P5679	CFC1	-3.58854	7.71E-12	-9.25584	Down	cripto, FRL-1, cryptic family 1
A_24_P380196	CTNND2	-3.07123	7.74E-12	-9.25438	Down	catenin delta 2
A_23_P13232	#N/A	-3.67493	8.41E-12	-9.22818	Down	NA
A_32_P36404	PTPRT	-4.7787	8.96E-12	-9.20811	Down	protein tyrosine phosphatase, receptor type T
A_23_P107351	NLRP1	-3.17499	1.15E-11	-9.12887	Down	NLR family pyrin domain containing 1
A_23_P110882	TSPYL4	-2.79233	1.2E-11	-9.11591	Down	TSPY like 4
A_23_P79803	VSTM2L	-4.03403	1.32E-11	-9.08657	Down	V-set and transmembrane domain containing 2 like
A_32_P212886	TBXAS1	-2.99263	1.34E-11	-9.08126	Down	thromboxane A synthase 1
A_23_P216307	RUNX1T1	-3.05533	1.49E-11	-9.04812	Down	RUNX1 translocation partner 1
A_23_P169756	HIPK2	-2.79317	1.52E-11	-9.041	Down	homeodomain interacting protein kinase 2
A_23_P312901	ADGRG4	-4.0626	1.59E-11	-9.02692	Down	adhesion G protein-coupled receptor G4
A_32_P125163	#N/A	-4.73828	1.63E-11	-9.01856	Down	NA
A_32_P109755	TMEM179	-4.58876	1.69E-11	-9.00697	Down	transmembrane protein 179
A_24_P280333	KRT40	-3.84475	2.01E-11	-8.9525	Down	keratin 40
A_24_P162226	RIMBP2	-4.87104	2.13E-11	-8.93523	Down	RIMS binding protein 2
A_23_P211141	DSCAM	-3.73627	2.15E-11	-8.93264	Down	DS cell adhesion molecule
A_24_P416961	ARVCF	-3.27155	2.3E-11	-8.91144	Down	ARVCF, delta catenin family member
A_32_P172339	GRIA2	-4.76653	2.45E-11	-8.89142	Down	glutamate ionotropic receptor AMPA type subunit 2
A_23_P163697	SYT17	-3.04252	2.57E-11	-8.87629	Down	synaptotagmin 17
A_23_P315273	MT3	-4.0394	2.78E-11	-8.85203	Down	metallothionein 3
A_23_P168403	KCNH2	-4.14327	3.66E-11	-8.76519	Down	potassium voltage-gated channel subfamily H member 2
A_32_P39394	GLIS3	-2.75912	3.68E-11	-8.76391	Down	GLIS family zinc finger 3
A_23_P101671	ATCAY	-4.39749	3.72E-11	-8.76068	Down	ATCAY, caytaxin
A_23_P406385	FBXL16	-3.89134	3.82E-11	-8.75208	Down	F-box and leucine rich repeat protein 16
A_23_P304489	FAM19A5	-3.20379	4.25E-11	-8.71931	Down	family with sequence similarity 19 member A5, C-C motif chemokine like
A_23_P92093	CELSR3	-3.45239	4.65E-11	-8.69128	Down	cadherin EGF LAG seven-pass G-type receptor 3
A_23_P501831	FAXDC2	-3.14788	4.87E-11	-8.67665	Down	fatty acid hydroxylase domain containing 2
A_24_P322908	USP27X	-3.00875	4.95E-11	-8.67124	Down	ubiquitin specific peptidase 27 X-linked
A_23_P381102	CCDC74B	-2.84544	5.19E-11	-8.65676	Down	coiled-coil domain containing 74B
A_32_P196263	ADAMTS9	-3.16376	5.3E-11	-8.65039	Down	ADAM metalloproteinase with thrombospondin type 1 motif 9
A_23_P216108	ANK1	-4.75878	5.41E-11	-8.64418	Down	ankyrin 1

A_32_P58614	CEP126	-3.44373	5.42E-11	-8.64317	Down	centrosomal protein 126
A_32_P201897	FMN2	-4.59682	6.76E-11	-8.57488	Down	formin 2
A_23_P13493	OR51E1	-3.89446	6.89E-11	-8.56908	Down	olfactory receptor family 51 subfamily E member 1
A_23_P52727	NAV2	-2.79282	7.12E-11	-8.5587	Down	neuron navigator 2
A_32_P171386	#N/A	-2.87423	7.59E-11	-8.539	Down	NA
A_23_P61810	BAIAP2	-2.88369	8.09E-11	-8.51936	Down	BAI1 associated protein 2
A_23_P38630	SSTR2	-3.45136	9.2E-11	-8.47932	Down	somatostatin receptor 2
A_32_P6015	MNX1	-3.99468	9.26E-11	-8.47752	Down	motor neuron and pancreas homeobox 1
A_23_P213620	PPP2R2B	-2.85989	9.62E-11	-8.46557	Down	protein phosphatase 2 regulatory subunit Bbeta
A_32_P29551	AC009135.2	-5.67259	1.02E-10	-8.44898	Down	TEC
A_23_P132889	CRMP1	-3.71766	1.04E-10	-8.44188	Down	collapsin response mediator protein 1
A_23_P391228	MANEAL	-3.17094	1.14E-10	-8.41261	Down	mannosidaseendo-alpha like
A_23_P78479	ZIM2	-3.61509	1.17E-10	-8.40568	Down	zinc finger imprinted 2
A_23_P366366	SCRN1	-2.80136	1.21E-10	-8.39526	Down	secernin 1
A_24_P711496	#N/A	-3.09354	1.35E-10	-8.36157	Down	NA
A_23_P132619	OXTR	-3.28787	1.41E-10	-8.34791	Down	oxytocin receptor
A_24_P298174	CBX1	-2.7792	1.56E-10	-8.31733	Down	chromobox 1
A_23_P500328	DCX	-3.9424	1.67E-10	-8.29505	Down	doublecortin
A_32_P14721	DNAH12	-4.03353	1.69E-10	-8.29156	Down	dynein axonemal heavy chain 12
A_23_P79968	PCSK2	-4.6487	1.72E-10	-8.28616	Down	proproteinconvertasesubtilisin/kexin type 2
A_32_P83049	EFR3B	-3.35446	1.79E-10	-8.27422	Down	EFR3 homolog B
A_23_P251412	SCGN	-4.41972	1.81E-10	-8.2713	Down	secretagogin, EF-hand calcium binding protein
A_23_P210835	MYT1	-3.4	2.03E-10	-8.23646	Down	myelin transcription factor 1
A_23_P160559	ECM1	-5.26597	2.16E-10	-8.21727	Down	extracellular matrix protein 1
A_23_P421843	#N/A	-2.76955	2.33E-10	-8.19413	Down	NA
A_23_P406782	HPN	-3.86984	2.45E-10	-8.17826	Down	hepsin
A_23_P41390	SH3TC1	-2.76561	2.53E-10	-8.16824	Down	SH3 domain and tetratricopeptide repeats 1
A_23_P62081	SCG5	-5.26867	2.63E-10	-8.15691	Down	secretogranin V
A_32_P79434	PTPRN2	-3.40174	2.77E-10	-8.14068	Down	protein tyrosine phosphatase, receptor type N2
A_24_P150466	SMOC1	-3.79543	3.12E-10	-8.10385	Down	SPARC related modular calcium binding 1
A_23_P67896	SCN3A	-2.89214	3.18E-10	-8.09881	Down	sodium voltage-gated channel alpha subunit 3
A_23_P71530	TNFRSF11B	-3.47066	3.19E-10	-8.09776	Down	TNF receptor superfamily member 11b
A_23_P96590	GPRASP1	-2.87531	3.78E-10	-8.04556	Down	G protein-coupled receptor associated sorting protein 1

A_24_P710730	GUSBP1	-3.17925	3.93E-10	-8.03419	Down	glucuronidase, beta pseudogene 1
A_23_P19134	ADGRV1	-3.27824	4.2E-10	-8.01371	Down	adhesion G protein-coupled receptor V1
A_32_P227216	LINC00643	-4.53763	4.46E-10	-7.99555	Down	long intergenic non-protein coding RNA 643
A_32_P206344	#N/A	-2.84457	4.7E-10	-7.97913	Down	NA
A_23_P502078	MAPK8IP2	-2.8463	5.26E-10	-7.94487	Down	mitogen-activated protein kinase 8 interacting protein 2
A_23_P54267	SCG3	-4.40101	6.8E-10	-7.86697	Down	secretogranin III
A_32_P183367	CELF4	-2.91802	7.59E-10	-7.83361	Down	CUGBP Elav-like family member 4
A_32_P82895	C2CD4C	-3.4786	8.13E-10	-7.81297	Down	C2 calcium dependent domain containing 4C
A_23_P10194	SEZ6L2	-3.56656	8.58E-10	-7.79649	Down	seizure related 6 homolog like 2
A_23_P345183	NMNAT2	-2.86167	8.79E-10	-7.7893	Down	nicotinamide nucleotide adenyltransferase 2
A_32_P82111	LRFN2	-3.96431	8.92E-10	-7.7849	Down	leucine rich repeat and fibronectin type III domain containing 2
A_23_P254507	HOPX	-4.29153	9E-10	-7.78224	Down	HOP homeobox
A_32_P154021	ST8SIA3	-3.74118	9.44E-10	-7.76751	Down	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3
A_23_P200737	RGS4	-2.90296	9.81E-10	-7.75584	Down	regulator of G protein signaling 4
A_24_P334300	FGF12	-3.10311	9.95E-10	-7.75176	Down	fibroblast growth factor 12
A_23_P113777	ITGBL1	-2.78447	9.98E-10	-7.75075	Down	integrin subunit beta like 1
A_23_P385199	EPHA10	-3.22137	1.03E-09	-7.74084	Down	EPH receptor A10
A_23_P56494	SLC38A11	-4.08304	1.06E-09	-7.73275	Down	solute carrier family 38 member 11
A_23_P127584	NNMT	-3.18398	1.07E-09	-7.73089	Down	nicotinamide N-methyltransferase
A_24_P389415	PNMA2	-3.23771	1.09E-09	-7.72501	Down	PNMA family member 2
A_32_P93736	#N/A	-3.08902	1.13E-09	-7.71347	Down	NA
A_23_P158675	KCNMB2	-3.01215	1.19E-09	-7.69676	Down	potassium calcium-activated channel subfamily M regulatory beta subunit 2
A_32_P111394	#N/A	-4.02605	1.2E-09	-7.69579	Down	NA
A_24_P733308	#N/A	-2.98331	1.23E-09	-7.68782	Down	NA
A_23_P134914	LY6H	-4.30096	1.27E-09	-7.677	Down	lymphocyte antigen 6 family member H
A_23_P47728	MAP6	-3.20565	1.34E-09	-7.66272	Down	microtubule associated protein 6
A_24_P817863	UNC80	-3.65123	1.39E-09	-7.64963	Down	unc-80 homolog, NALCN channel complex subunit
A_24_P329795	DEPP1	-2.76804	1.7E-09	-7.59059	Down	DEPP1, autophagy regulator
A_24_P933319	RAB3B	-4.53847	1.82E-09	-7.5697	Down	RAB3B, member RAS oncogene family
A_23_P14892	IGFALS	-2.88781	1.9E-09	-7.55695	Down	insulin like growth factor binding protein acid labile subunit
A_24_P840042	LINC00643	-4.90938	2.02E-09	-7.5385	Down	long intergenic non-protein coding RNA 643
A_24_P913146	HOPX	-3.25199	2.23E-09	-7.50774	Down	HOP homeobox

A_24_P347431	FOXA1	-3.12824	2.42E-09	-7.48313	Down	forkhead box A1
A_23_P25674	CKB	-3.05866	2.46E-09	-7.47801	Down	creatine kinase B
A_23_P149153	PDE4DIP	-3.00285	3.12E-09	-7.40679	Down	phosphodiesterase 4D interacting protein
A_23_P167367	PITX2	-3.5805	3.2E-09	-7.39994	Down	paired like homeodomain 2
A_23_P80068	BTG3	-2.80473	3.29E-09	-7.39154	Down	BTG anti-proliferation factor 3
A_23_P163492	BAIAP3	-3.14508	4.07E-09	-7.32717	Down	BAI1 associated protein 3
A_23_P37127	FOXA1	-2.83689	4.48E-09	-7.2988	Down	forkhead box A1
A_23_P121545	GPM6A	-4.03459	4.85E-09	-7.27472	Down	glycoprotein M6A
A_24_P871940	#N/A	-2.80377	6.04E-09	-7.20905	Down	NA
A_23_P107507	CBX1	-2.7898	6.46E-09	-7.18925	Down	chromobox 1
A_23_P416581	GNAZ	-3.31435	7.11E-09	-7.16055	Down	G protein subunit alpha z
A_32_P179998	DMRTC1	-3.20032	8.31E-09	-7.11382	Down	DMRT like family C1 downregulated RNA in cancer, inhibitor of cell invasion and migration
A_32_P46594	DRAIC	-3.1544	1.26E-08	-6.99057	Down	NA
A_32_P160615	#N/A	-2.89515	1.3E-08	-6.98073	Down	NA
A_23_P110212	ACSL1	-3.38508	1.31E-08	-6.97809	Down	acyl-CoA synthetase long chain family member 1
A_32_P18470	TCEAL5	-3.13902	1.53E-08	-6.93082	Down	transcription elongation factor A like 5
A_23_P78099	VTN	-3.36782	1.63E-08	-6.91318	Down	vitronectin
A_32_P23731	#N/A	-3.17925	1.69E-08	-6.90155	Down	NA
A_24_P568190	GUSBP1	-2.86661	1.79E-08	-6.88528	Down	glucuronidase, beta pseudogene 1
A_23_P17522	NKX2-2	-3.26277	1.94E-08	-6.86161	Down	NK2 homeobox 2
A_24_P16337	AL773545.3	-3.35684	1.96E-08	-6.85714	Down	NA
A_32_P130999	ASB4	-3.60889	1.99E-08	-6.85398	Down	ankyrin repeat and SOCS box containing 4 glutamate ionotropic receptor AMPA type subunit 3
A_32_P177897	GRIA3	-3.39794	2E-08	-6.85149	Down	membrane associated ring-CH-type finger 4
A_23_P333228	MARCH4	-3.28701	2.05E-08	-6.84501	Down	kinesin family member 1A potassium voltage-gated channel subfamily B member 1
A_23_P395460	KIF1A	-3.19612	2.06E-08	-6.84281	Down	retbindin
A_32_P19966	KCNB1	-3.42456	2.21E-08	-6.82178	Down	immunoglobulin-like and fibronectin type III domain containing 1
A_23_P130653	RTBDN	-2.75098	2.43E-08	-6.79414	Down	kelch like family member 1
A_32_P425998	IGFN1	-3.28838	2.53E-08	-6.78141	Down	early growth response 4
A_23_P2825	KLHL1	-3.44834	2.6E-08	-6.77406	Down	claudin 1
A_23_P380318	EGR4	-3.3526	2.66E-08	-6.76703	Down	ARFGEF family member 3
A_23_P57784	CLDN1	-2.82501	2.86E-08	-6.74576	Down	ras related dexamethasone induced 1
A_32_P65473	ARFGEF3	-3.06751	3.49E-08	-6.68597	Down	
A_23_P118392	RASD1	-3.37717	3.76E-08	-6.66376	Down	

A_32_P88262	SLC7A14	-3.62152	3.95E-08	-6.64952	Down	solute carrier family 7 member 14
A_23_P356731	ZDHHC8P1	-2.94386	3.98E-08	-6.64705	Down	zinc finger DHHC-type containing 8 pseudogene 1
A_23_P40096	PROC	-3.57425	4.18E-08	-6.63255	Down	protein C, inactivator of coagulation factors Va and VIIIa
A_23_P109184	INSM1	-2.92003	4.27E-08	-6.62608	Down	INSM transcriptional repressor 1
A_23_P342869	FMN2	-3.43826	4.58E-08	-6.60543	Down	formin 2
A_32_P25243	#N/A	-3.43588	4.72E-08	-6.59671	Down	NA
A_23_P202245	RET	-4.13508	4.85E-08	-6.58832	Down	ret proto-oncogene
A_32_P217797	#N/A	-4.08381	4.89E-08	-6.58586	Down	NA
A_24_P85009	FGF13	-2.81815	4.9E-08	-6.58518	Down	fibroblast growth factor 13
A_23_P56787	CNTNAP5	-3.9037	5.62E-08	-6.54477	Down	contactin associated protein like 5
A_23_P354908	NMNAT2	-3.18182	5.92E-08	-6.52933	Down	nicotinamide nucleotide adenyltransferase 2
A_23_P371966	FAM171B	-2.90129	6.2E-08	-6.5155	Down	family with sequence similarity 171 member B
A_23_P105651	PDZRN4	-3.22265	7.41E-08	-6.46245	Down	PDZ domain containing ring finger 4
A_32_P203688	KCNJ6	-3.74256	7.97E-08	-6.44111	Down	potassium voltage-gated channel subfamily J member 6
A_32_P119033	PLCXD3	-2.94566	8.05E-08	-6.43801	Down	phosphatidylinositol specific phospholipase C X domain containing 3
A_23_P209484	NEUROD1	-3.58331	8.14E-08	-6.43454	Down	neuronal differentiation 1
A_24_P323787	#N/A	-3.43261	8.74E-08	-6.41369	Down	NA
A_32_P154473	KIF5C	-3.50398	9.82E-08	-6.3791	Down	kinesin family member 5C
A_32_P190303	LONRF2	-2.75973	1.01E-07	-6.37148	Down	LON peptidase N-terminal domain and ring finger 2
A_24_P85888	SCN3A	-2.92209	1.1E-07	-6.34605	Down	sodium voltage-gated channel alpha subunit 3
A_24_P252364	NRCAM	-2.96367	1.19E-07	-6.32147	Down	neuronal cell adhesion molecule
A_23_P259442	CPE	-3.06643	1.44E-07	-6.26471	Down	carboxypeptidase E
A_23_P78248	KRT23	-3.2481	1.48E-07	-6.25789	Down	keratin 23
A_32_P42224	CLSTN2	-2.77778	1.61E-07	-6.23271	Down	calsynenin 2
A_23_P377299	ECE2	-3.30956	1.94E-07	-6.17649	Down	endothelin converting enzyme 2
A_23_P140748	NDRG4	-2.81446	2.15E-07	-6.14577	Down	NDRG family member 4
A_23_P140858	RBFOX1	-3.21039	2.18E-07	-6.14274	Down	RNA binding fox-1 homolog 1
A_23_P213678	PAM	-3.30341	2.23E-07	-6.13537	Down	peptidylglycine alpha-amidatingmonooxygenase
A_23_P13725	SLC6A15	-2.9719	2.25E-07	-6.13315	Down	solute carrier family 6 member 15
A_23_P68167	CNGA3	-3.90818	2.42E-07	-6.11097	Down	cyclic nucleotide gated channel alpha 3
A_32_P224157	LDLRAD4	-2.84792	2.6E-07	-6.08975	Down	low density lipoprotein receptor class A domain containing 4
A_24_P716405	#N/A	-2.85315	2.64E-07	-6.08561	Down	NA

A_32_P119830	#N/A	-3.82961	2.89E-07	-6.05871	Down	NA
A_32_P18668	RAB3B	-3.41206	2.99E-07	-6.04801	Down	RAB3B, member RAS oncogene family
A_23_P161769	FXVD2	-4.7247	3.66E-07	-5.98868	Down	FXVD domain containing ion transport regulator 2
A_23_P18223	ITIH1	-3.95845	3.84E-07	-5.97445	Down	inter-alpha-trypsin inhibitor heavy chain 1
A_24_P71468	QPCT	-3.09102	3.95E-07	-5.96557	Down	glutaminy-peptide cyclotransferase
A_23_P37088	RDH12	-3.27221	4.18E-07	-5.94924	Down	retinol dehydrogenase 12
A_23_P500936	FOXA2	-2.88432	4.48E-07	-5.92858	Down	forkhead box A2
A_32_P114483	C6orf141	-2.81472	4.98E-07	-5.89661	Down	chromosome 6 open reading frame 141
A_23_P134484	CALCR	-3.76923	5.29E-07	-5.87873	Down	calcitonin receptor
A_32_P153773	#N/A	-2.95477	6.42E-07	-5.82113	Down	NA
A_24_P116587	SEZ6L2	-2.92327	6.83E-07	-5.80273	Down	seizure related 6 homolog like 2
A_23_P29719	CASR	-3.14195	7.4E-07	-5.77884	Down	calcium sensing receptor
A_24_P944714	#N/A	-5.05926	7.55E-07	-5.77298	Down	NA
A_23_P112698	PNMA2	-2.75795	8.33E-07	-5.74365	Down	PNMA family member 2
A_23_P417646	SV2C	-3.71983	9.26E-07	-5.71223	Down	synaptic vesicle glycoprotein 2C
A_24_P196562	FXVD2	-4.16344	1.06E-06	-5.67161	Down	FXVD domain containing ion transport regulator 2
A_23_P386398	C6orf141	-3.40292	1.06E-06	-5.67124	Down	chromosome 6 open reading frame 141
A_23_P388168	RAB3B	-3.23944	1.08E-06	-5.66532	Down	RAB3B, member RAS oncogene family
A_23_P422911	HS6ST3	-3.1699	1.12E-06	-5.65449	Down	heparansulfate 6-O-sulfotransferase 3
A_32_P218823	#N/A	-3.13456	1.16E-06	-5.64511	Down	NA
A_23_P46639	C8A	-3.9753	1.22E-06	-5.62931	Down	complement C8 alpha chain
A_24_P97703	PAM	-2.99568	1.25E-06	-5.62363	Down	peptidylglycine alpha-amidatingmonooxygenase
A_23_P258612	ATP8A2	-3.7238	1.25E-06	-5.62341	Down	ATPase phospholipid transporting 8A2
A_32_P229618	DLG2	-3.06768	1.47E-06	-5.57348	Down	discs large MAGUK scaffold protein 2
A_23_P121665	SORCS2	-2.77779	1.75E-06	-5.52221	Down	sortilin related VPS10 domain containing receptor 2
A_24_P825874	POTEE	-3.09212	1.76E-06	-5.52052	Down	POTE ankyrin domain family member E
A_24_P298224	NCKAP5	-2.90026	2.54E-06	-5.40998	Down	NCK associated protein 5
A_24_P296808	PNMA8A	-3.54319	2.58E-06	-5.40598	Down	PNMA family member 8A
A_23_P130113	ASGR2	-3.68107	2.99E-06	-5.36127	Down	asialoglycoprotein receptor 2
A_23_P29057	KCNJ6	-3.22518	3.74E-06	-5.29455	Down	potassium voltage-gated channel subfamily J member 6
A_23_P38816	A1BG	-2.92595	4.16E-06	-5.26216	Down	alpha-1-B glycoprotein
A_23_P94879	F2	-3.84779	4.56E-06	-5.23436	Down	coagulation factor II, thrombin
A_24_P914411	HOXA10	-3.83124	5.1E-06	-5.20046	Down	homeobox A10

A_32_P464135	DACH2	-2.88655	6.54E-06	-5.1256	Down	dachshund family transcription factor 2
A_24_P933580	NAV2	-2.82716	8.38E-06	-5.05022	Down	neuron navigator 2
A_32_P33576	OPRK1	-3.15037	8.41E-06	-5.0492	Down	opioid receptor kappa 1
A_23_P11629	TMEM61	-2.78842	9.45E-06	-5.01379	Down	transmembrane protein 61
A_23_P43197	CALB1	-4.00419	9.79E-06	-5.00299	Down	calbindin 1
A_32_P379467	ISLR2	-3.34995	1.22E-05	-4.93702	Down	immunoglobulin superfamily containing leucine rich repeat 2
A_32_P16323	#N/A	-2.97898	1.25E-05	-4.92908	Down	NA
A_23_P40184	CDH22	-3.10473	2.19E-05	-4.75701	Down	cadherin 22
A_23_P23996	MAT1A	-3.64068	3.89E-05	-4.57951	Down	methionine adenosyltransferase 1A
A_23_P257834	ALB	-5.85562	6.87E-05	-4.40171	Down	albumin
A_23_P256504	AMBP	-3.42093	7.59E-05	-4.37054	Down	alpha-1-microglobulin/bikunin precursor
A_23_P208030	SYT4	-2.99727	7.71E-05	-4.36565	Down	synaptotagmin 4
A_23_P120125	COLEC11	-3.20396	8.66E-05	-4.32881	Down	collectin subfamily member 11
A_23_P24774	ABCC8	-3.02446	0.00023	-4.01699	Down	ATP binding cassette subfamily C member 8
A_23_P101905	APC2	-2.82505	0.000399	-3.83639	Down	APC2, WNT signaling pathway regulator
A_23_P206760	HP	-4.7008	0.001458	-3.39904	Down	haptoglobin
A_23_P38244	APOH	-3.16108	0.002297	-3.23961	Down	apolipoprotein H
A_23_P146855	MPPED1	-2.78685	0.00372	-3.06621	Down	metallophosphoesterase domain containing 1
A_23_P212500	TF	-2.82941	0.004844	-2.9692	Down	transferrin
A_23_P148088	FGG	-3.02109	0.008309	-2.76553	Down	fibrinogen gamma chain
A_23_P155509	AHSG	-3.19568	0.010427	-2.6774	Down	alpha 2-HS glycoprotein
A_23_P321892	HRG	-3.19492	0.010875	-2.66092	Down	histidine rich glycoprotein
A_23_P421493	HPR	-2.75872	0.015608	-2.51683	Down	haptoglobin-related protein

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

BIOCYC

Pathway ID	Pathway Name	LogP	Gene Count	Genes
545347	sucrose degradation	5.440631958	04	ALDOB,GALM,KHK,TKF C
142435	glutathione-mediated detoxification	3.128828706	04	ANPEP,GSTA1,GSTA5,M GST1

142324	dopamine degradation	2.826858567	02	MAOA,MAOB
1108786	mucin core 1 and core 2 O-glycosylation	2.661178182	04	B3GNT3,GALNT6,GALNT7,GCNT3
703096	4-hydroxy-2-nonenal detoxification	2.532406779	02	GSTA1,GSTA5
142426	urea cycle	2.532406779	02	CPS1,OTC
545352	acetone degradation I (to methylglyoxal)	1.889290581	02	AKR1B10,CYP2S1
142419	phospholipases	1.573239126	03	PLA2G2A,PLB1,PLCB3
545345	ascorbate recycling (cytosolic)	1.351760358	01	GLRX
142226	gamma-glutamyl cycle	1.351760358	01	CNDP2

KEGG

673221	Chemical carcinogenesis	10	13	CHRNA7,CYP2C18,GSTA1,GSTA2,GSTA3,GSTA5, MGST1,NAT2,SULT1A2, SULT2A1,UGT1A6,UGT2B15,UGT2B17
170720	Carbohydrate digestion and absorption	10	10	ATP1A1,ATP1A3,ATP1A4,G6PC,HKDC1,LCT,MGAM,SLC2A2,SLC2A5,SLC5A1
132956	Metabolic pathways	10	64	ACSL5,ACY1,AKR1B10, AKR1C3,ALDOB,ALPI,ALPP,ANPEP,ASPA,B3GNT3,CDS1,CMBL,CNDP2,CPS1,CYP2C18,CYP2J2,CYP2S1,CYP4F8,DGAT1,ENPP3,FBP1,FUT2,FUT3,FUT5,FUT6,G6PC,GALM,GALNT6,GALNT7,GCNT3, GDA,GGT1,GK,HKDC1,HS17B2,HSD3B1,ITPKA, KHK,LAMA3,LCT,LDHA, MAOA,MAOB,MGAM,MGST1,NAGS,NAT2,OAT,OTC,PCK1,PCK2,PLA2G12B,PLA2G2A,PLB1,PLCB3,PNLIPRP2,PRODH,SI,ST

				6GALNAC1,TKFC,TST,UGT1A6,UGT2B15,UGT2B17
199556	Vitamin digestion and absorption	10	07	APOA1,APOA4,APOB,PLB1,RBP2,SLC23A1,SLC52A3
169306	Pancreatic secretion	10	13	ATP1A1,ATP1A3,ATP1A4,CFTR,CLCA1,KCNQ1,PLA2G12B,PLA2G2A,PLCB3,PNLIPRP2,PRSS2,PRSS3,SLC26A3
172847	Protein digestion and absorption	10	20	ACE2,ATP1A1,ATP1A3,ATP1A4,COL17A1,DPP4,KCNJ13,KCNQ1,MEP1A,MEP1B,MME,PRSS2,PRSS3,SLC15A1,SLC1A1,SLC3A1,SLC7A7,SLC7A9,SLC9A3,XPNPEP2
193146	Bile secretion	10	15	ABCB1,ABCC2,ABCG2,ABCG5,ATP1A1,ATP1A3,ATP1A4,CFTR,NR0B2,SLC10A2,SLC51A,SLC51B,SLC5A1,SLC9A3,SULT2A1
83075	Renin-angiotensin system	5.047158184	06	ACE,ACE2,ANPEP,ENPEP,KLK1,MME
82940	Steroid hormone biosynthesis	3.516610683	07	AKR1C3,HSD11B2,HSD17B2,HSD3B1,UGT1A6,UGT2B15,UGT2B17
692234	PI3K-Akt signaling pathway	1.340091285	13	CREB3L3,EFNA2,G6PC,ITGB4,LAMA3,LAMB3,LAMC2,MYB,PCK1,PCK2,PHLPP2,SGK1,SYK
Pathway Interaction Database				
137911	FOXA2 and FOXA3 transcription factor networks	3.374605622	06	ALDOB,APOA1,CEBPA,G6PC,PCK1,SLC2A2
138008	a6b1 and a6b4 Integrin signaling	2.311285384	04	COL17A1,ITGB4,MST1R,PMP22

137979	FOXA1 transcription factor network	1.808793655	04	APOB,CYP2C18,GCG,TF F1
137958	Endothelins	1.508697694	04	EDN2,EDN3,PLCB3,SLC9 A3
138041	EPHA forward signaling	1.497457782	03	EFNA2,NGEF,VAV3
REACTOME				
1269903	Transmembrane transport of small molecules	10	38	ABCB1,ABCC2,ABCG2,A BCG5,APOA1,AQP10,AT P1A1,ATP1A3,ATP1A4,C FTR,CLCA1,CYBRD1,EM B,G6PC,HEPH,MYO5B,S GK1,SLC15A1,SLC17A8, SLC1A1,SLC1A7,SLC22A 18,SLC26A3,SLC28A1,SL C28A2,SLC2A2,SLC2A5, SLC39A4,SLC3A1,SLC44 A4,SLC5A1,SLC5A11,SL C5A12,SLC6A20,SLC7A7, SLC7A9,SLC9A3,TRPM6
1270213	Glutathione conjugation	10	09	CNDP2,GGT1,GGT3P,GG TLC2,GSTA1,GSTA2,GST A3,GSTA5,MGST1
1270001	Metabolism of lipids and lipoproteins	10	44	ABCG5,ACOT11,ACSL5, AKR1C3,ALPI,AMN,APO A1,APOA4,APOB,APOC3, CD36,CDS1,CIDEA,CREB 3L3,CYP2J2,CYP4F8,DG AT1,DPEP1,FA2H,FABP1, FABP2,FABP6,GGT1,GG TLC2,GK,GPD1,HPGD,H RASLS2,HSD11B2,HSD17 B2,HSD3B1,LIPH,MFSD2 A,MOGAT2,MTTP,NEU4, PLA2G2A,PLB1,PNLIPRP 2,SLC10A2,SLC44A4,SO AT2,SULT2A1,TIAM2
1270002	Lipid digestion, mobilization, and transport	10	15	ABCG5,AMN,APOA1,AP OA4,APOB,APOC3,CIDE C,CREB3L3,FABP1,FABP 2,FABP6,LIPH,MTTP,PNL

				IPRP2,SOAT2
1270189	Biological oxidations	10	30	AADAC,ACY1,ACY3,CE S2,CMBL,CNDP2,CYP2C 18,CYP2J2,CYP2S1,CYP4 F12,CYP4F8,DPEP1,FMO 1,GGT1,GGT3P,GGTLC2, GSTA1,GSTA2,GSTA3,G STA5,MAOA,MAOB,MG ST1,NAT2,SULT1A2,SUL T1B1,SULT2A1,UGT1A6, UGT2B15,UGT2B17
1269907	SLC-mediated transmembrane transport	10	23	EMB,G6PC,HEPH,SLC15 A1,SLC17A8,SLC1A1,SL C1A7,SLC22A18,SLC26A 3,SLC28A1,SLC28A2,SLC 2A2,SLC2A5,SLC39A4,SL C3A1,SLC44A4,SLC5A1, SLC5A11,SLC5A12,SLC6 A20,SLC7A7,SLC7A9,SL C9A3
1270220	Aflatoxin activation and detoxification	10	07	ACY1,ACY3,DPEP1,GGT 1,GGT3P,GGTLC2,MGST 1
1270207	Phase II conjugation	10	16	CNDP2,GGT1,GGT3P,GG TLC2,GSTA1,GSTA2,GST A3,GSTA5,MGST1,NAT2, SULT1A2,SULT1B1,SUL T2A1,UGT1A6,UGT2B15, UGT2B17
1268736	O-linked glycosylation of mucins	4.752926495	09	B3GNT3,B3GNT7,GALN T6,GALNT7,GCNT3,MUC 13,MUC17,MUC2,MUC3 A
1457776	Miscellaneous digestion events	4.353789253	03	ALPI,GUCA2A,GUCA2B
GenMAPP				
MAP00601	Blood group glycolipid biosynthesis lact series	5.440631958	04	FUT2,FUT3,FUT5,FUT6
MAP00561	Glycerolipid metabolism	4.104632268	07	ALPI,ALPP,DGAT1,GK,G

				PD1,PLA2G2A,PNLIPRP2
MAP00361	gamma Hexachlorocyclohexane degradation	3.373285759	05	ALPI,ALPP,CYP2C18,CYP2J2,CYP4F8
MAP00220	Urea cycle and metabolism of amino groups	3.325237326	04	ACY1,CPS1,OAT,OTC
MAP00150	Androgen and estrogen metabolism	3.325237326	04	HSD11B2,HSD17B2,HSD3B1,UGT2B15
MAP00500	Starch and sucrose metabolism	1.898584881	03	G6PC,MGAM,UGT2B15
MAP00480	Glutathione metabolism	1.898584881	03	GGT1,GSTA2,MGST1
MAP00052	Galactose metabolism	1.794195726	03	G6PC,LCT,MGAM
MAP00051	Fructose and mannose metabolism	1.794195726	03	ALDOB,FBP1,KHK
MAP00272	Cysteine metabolism	1.786588127	02	LDHA,MPST
MSigDB C2 BIOCARTA (v6.0)				
M5880	Genes encoding proteins affiliated structurally or functionally to extracellular matrix proteins	3.313407628	12	ITLN1,ITLN2,LGALS3,MUC13,MUC17,MUC2,MUC3A,REG1A,REG1B,REG3A,REG3G,SEMA6A
M2404	Mechanism of Gene Regulation by Peroxisome Proliferators via PPARa(alpha)	2.016360037	05	APOA1,CD36,FABP1,FAT1,NR0B2
M17200	Antigen binding to B cell receptors activates protein tyrosine kinases, such as the Src family, which ultimate activate MAP kinases.	1.794195726	03	BLNK,SYK,VAV3
M3061	Feeder Pathways for Glycolysis	1.786588127	02	KHK,LCT
M5374	The SARS-coronavirus Life Cycle	1.696107885	02	ANPEP,LDHA
M4170	Interferon gamma pathway.	1.696107885	02	PLA2G2A,REG1A
M12399	Cystic Fibrosis Transmembrane Conductance Regulator And Beta 2 Adrenergic Receptor Pathway	1.542599118	02	CFTR,EZR

M5885	Ensemble of genes encoding ECM-associated proteins including ECM-affiliated proteins, ECM regulators and secreted factors	1.483729086	25	ADAMDEC1,BMP7,CCL25,CTSE,CXCL14,ITLN1,ITLN2,KAZALD1,LGALS3,MEP1A,MEP1B,MUC13,MUC17,MUC2,MUC3A,PRSS2,PRSS3,REG1A,REG1B,REG3A,REG3G,S100A14,SEMA6A,ST14,TMPRSS15
M12950	Angiotensin-converting enzyme 2 regulates heart function	1.476441258	02	ACE,ACE2
M16393	Nuclear Receptors in Lipid Metabolism and Toxicity	1.360094946	02	ABCB1,NR0B2
PantherDB				
P02728	Arginine biosynthesis	3.433720499	03	CPS1,NAGS,OTC
P05726	2-arachidonoylglycerol biosynthesis	2.147436745	02	LIPH,PLCB3
P02744	Fructose galactose metabolism	2.007775097	02	ALDOB,KHK
P00001	Adrenaline and noradrenaline biosynthesis	1.613560784	03	MAOA,MAOB,SLC6A20
Pathway Ontology				
PW:0000482	lipoprotein metabolic	5.210190254	05	APOA1,APOA4,APOB,APOBEC1,APOC3
PW:0000492	renin-angiotensin system signaling	4.858291194	05	ACE,ACE2,ANPEP,ENPEP,MME
PW:0000641	gluconeogenesis pathway	4.560358066	05	ALDOB,FBP1,G6PC,PCK1,PCK2
PW:0000529	angiotensin (1-7) signaling	3.963207752	03	ACE,ACE2,MME
PW:0000373	glutathione conjugation	3.06805765	03	GSTA1,GSTA2,GSTA3
PW:0000134	glutathione metabolic	2.789369229	03	ANPEP,GGT1,GSTA2
PW:0000729	statin pharmacokinetics pathway	2.564970949	03	ABCB1,ABCC2,ABCG2

PW:0000025	glycolysis/gluconeogenesis	2.41817363	04	FBP1,G6PC,LDHA,PCK1
PW:0000153	glycerolipid metabolic	2.363657524	04	ALPI,DGAT1,PLA2G2A,P NLIPRP2
PW:0000485	eicosanoids metabolic	2.145712709	03	GGT1,MGST1,PLA2G2A
SMPDB				
SMP00128	Gluconeogenesis	4.302449166	05	FBP1,G6PC,GALM,PCK1, PCK2
SMP00020	Arginine and Proline Metabolism	3.223794804	04	CPS1,OAT,OTC,PRODH
SMP00392	Benzocaine Pathway	2.920417845	03	ATP1A1,ATP1A3,ATP1A 4
SMP00207	Prolidase Deficiency(PD)	2.217697329	03	CPS1,OAT,PRODH
SMP00058	Starch and Sucrose Metabolism	2.078267374	03	G6PC,MGAM,SI
SMP00328	Lidocaine (Antiarrhythmic) Pathway	2.034900164	04	ATP1A1,ATP1A3,ATP1A 4,KCNQ1
SMP00085	Ketoprofen Pathway	2.007775097	02	AKR1C3,PLA2G2A
SMP00039	Glycerolipid Metabolism	1.542599118	02	GK,GPD1
SMP00043	Galactose Metabolism	1.476441258	02	G6PC,LCT
SMP00064	Fructose and Mannose Degradation	1.360094946	02	FBP1,KHK

Kyoto Encyclopedia of Genes and Genomes (KEGG), GenMAPP(MAP) and Pathway Ontology (PW)

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

Pathway ID	Pathway Name	LogP	Gene Count	Genes
142292	creatine biosynthesis	1.780451609	01	GAMT
142208	S-adenosyl-L-methionine biosynthesis	1.317617614	01	MAT1A
142372	methionine degradation	1.317617614	01	MAT1A

KEGG

777534	Insulin secretion	5.9393066	10	ABCC8,ATP1B2,CACNA1C,CAMK2B,FXVD2,KCNMB2,RAB3A,RIMS2,SNAP25,STX1A
83073	Complement and coagulation cascades	4.375441485	08	C8A,F2,F5,F7,FGG,PROC,SERPINF2,VTN
469199	Dopaminergic synapse	4.285164445	10	CACNA1C,CALY,CAMK2B,GRIA2,GRIA3,KCNJ6,KIF5C,MAPK11,PPP2R2B,SLC18A1
83096	Maturity onset diabetes of the young	4.262809353	05	FOXA2,MNX1,NEUROD1,NKX2-2,RFX6
547607	Amphetamine addiction	3.937736608	07	CACNA1C,CAMK2B,GRIA2,GRIA3,GRIN2C,SLC18A1,STX1A
698773	Circadian entrainment	3.771907968	08	CACNA1C,CACNA1H,CAMK2B,GRIA2,GRIA3,GRIN2C,KCNJ6,RASD1
373900	Synaptic vesicle cycle	3.261733327	06	CPLX2,RAB3A,SLC18A1,SNAP25,STX1A,UNC13A
835410	Thyroid hormone synthesis	2.890411466	06	ALB,ASGR1,ASGR2,ATP1B2,FXVD2,TTR
523016	Transcriptional misregulation in cancer	2.028833011	08	ARNT2,BAIAP3,CDK14,FEV,GRIA3,HOXA10,RUNX1T1,ZBTB16
83053	Neuroactive ligand-receptor interaction	1.799997742	10	ADRA1B,CALCR,F2,GRIA2,GRIA3,GRIN2C,MC1R,OPRK1,OXTR,SSTR2

Pathway Interaction Database

137911	FOXA2 and FOXA3 transcription factor networks	5.197340755	07	ABCC8,ALB,CPT1C,F2,FOXA1,FOXA2,TTR
138065	FOXA transcription factor networks	3.104996365	02	FOXA1,FOXA2

137979	FOXA1 transcription factor network	2.288033527	04	DSCAM,FOXA1,FOXA2,VT N
138028	Effects of Botulinum toxin	2.053927332	02	SNAP25,STX1A
REACTOME				
1269367	Platelet degranulation	4.990258663	11	A1BG,AHSG,ALB,APOH,EC M1,F5,FGG,HRG,SCG3,SER PINF2,TF
1339115	Cardiac conduction	4.689528084	11	ATP1B2,CACNA1C,CAMK2 B,FGF12,FGF13,FXVD2,HIP K2,KCNH2,KCNK3,SCN3A, SLC8A2
1268763	Neuronal System	4.208590822	17	ABCC8,CAMK2B,DLG2,GRI A2,GRIA3,GRIN2C,KCNB1, KCNH2,KCNH6,KCNJ6,KC NK3,KCNMB2,KCNS3,LRF N2,RAB3A,SNAP25,STX1A
1269868	Muscle contraction	3.889439519	12	ATP1B2,CACNA1C,CAMK2 B,FGF12,FGF13,FXVD2,HIP K2,KCNH2,KCNK3,MYL6B, SCN3A,SLC8A2
1270337	Regulation of beta-cell development	3.745792947	05	FOXA2,INSM1,NEUROD1,N KX2-2,RFX6
1470928	RAB geranylgeranylation	2.358353703	05	RAB26,RAB36,RAB3A,RAB 3B,RAB3C
1270323	L1CAM interactions	2.191642555	06	ANK1,DCX,NRCAM,SCN3A ,SPTB,SPTBN4
1269340	Hemostasis	2.072347482	19	A1BG,AHSG,ALB,APOH,AT P1B2,ECM1,F2,F5,F7,FGG,H RG,KCNMB2,KIF12,KIF1A, PROC,SCG3,SERPINF2,SLC 8A2,TF
1270303	Axon guidance	1.424816334	15	ANK1,CACNA1C,CACNA1 H,CAMK2B,CRMP1,DCX,E PHA10,FGG,GRIN2C,NRCA M,RET,SCN3A,SHC2,SPTB, SPTBN4

1270302	Developmental Biology	1.326193493	25	ANK1,CACNA1C,CACNA1H,CAMK2B,CFC1,CRMP1,DCX,EPHA10,FGG,FOXA2,GRIN2C,INSM1,KRT23,KRT40,MAPK11,NEUROD1,NKX2-2,NRCAM,RET,RFX6,SCN3A,SHC2,SPTB,SPTBN4,STX1A
GenMAPP				
MAP00220	Urea cycle and metabolism of amino groups	1.513771719	02	CKB,GAMT
MSigDB C2 BIOCARTA (v6.0)				
M4470	Extrinsic Prothrombin Activation Pathway	5.896313193	05	F2,F5,F7,FGG,PROC
M15394	Acute Myocardial Infarction	3.567232197	04	F2,F7,FGG,PROC
M15997	Intrinsic Prothrombin Activation Pathway	3.32197078	04	F2,F5,FGG,PROC
M3468	Genes encoding enzymes and their regulators involved in the remodeling of the extracellular matrix	2.245476478	10	ADAMTS9,ADAMTSL2,AMB,FB,F7,HRG,ITIH1,P3H3,SERPINA10,SERPINF2
M2842	Fibrinolysis Pathway	1.804638393	02	F2,FGG
M16518	Wnt/Ca2+/cyclic GMP signaling.	1.382357835	02	CAMK2B,TF
M8731	Aspirin Blocks Signaling Pathway Involved in Platelet Activation	1.306668013	02	F2,TBXAS1
PantherDB				
P00011	Blood coagulation	4.374734794	06	F2,F7,FGG,PROC,SERPINA10,SERPINF2
P00037	Ionotropic glutamate receptor pathway	3.058687754	05	CAMK2B,GRIA2,GRIA3,GRIN2C,SNAP25
P00001	Adrenaline and noradrenaline biosynthesis	2.985600904	04	NNMT,SLC18A1,SLC6A15,SNAP25

P04375	5HT3 type receptor mediated signaling pathway	2.689310353	03	KCNK3,SLC18A1,SNAP25
P00039	Metabotropic glutamate receptor group III pathway	2.415980373	05	GRIA2,GRIA3,GRIN2C,SNA P25,STX1A
P05734	Synaptic vesicle trafficking	2.225682871	03	RAB3A,RIMS2,STX1A
P04395	Vasopressin synthesis	1.87917507	02	CPE,PAM
P04376	5HT4 type receptor mediated signaling pathway	1.862522052	03	KCNK3,SLC18A1,SNAP25
P04374	5HT2 type receptor mediated signaling pathway	1.713393583	04	CACNA1C,KCNK3,SLC18A 1,SNAP25
P00003	Alzheimer disease-amyloid secretase pathway	1.668612706	04	CACNA1C,MAPK11,PCSK1, PCSK2
Pathway Ontology				
PW:0000674	insulin secretion pathway	10	07	ABCC8,CACNA1C,KCNB1, RAB3A,SNAP25,STX1A,UN C13A
PW:0000474	coagulation cascade	5.090952402	04	APOH,F2,F5,F7
PW:0000365	melanocortin system	4.874681254	04	CPE,PAM,PCSK1,PCSK2
PW:0000480	protein C anticoagulant	4.084114566	03	F2,F5,PROC
PW:0000048	methionine cycle/metabolic	2.122536726	03	GAMT,MAT1A,NNMT
PW:0000076	pathway of urea cycle and metabolism of amino groups	1.736726011	02	CKB,GAMT
PW:0000229	G protein signaling via Galphaq family	1.674411209	02	ADRA1B,OXTR
PW:0000398	homocysteine metabolic	1.467225843	02	GAMT,NNMT
PW:0000050	arginine and proline metabolic	1.343479628	02	CKB,GAMT
PW:0000198	p38 MAPK signaling	1.306668013	02	MAPK11,MAPK8IP2
SMPDB				
SMP00328	Lidocaine (Antiarrhythmic) Pathway	3.504730143	05	ABCC8,ATP1B2,CACNA1H,

				FXVD2,KCNH2
SMP00287	Tranexamic Acid Pathway	2.689310353	03	F2,F7,FGG
SMP00048	Nicotinate and Nicotinamide Metabolism	1.804638393	02	NMNAT2,NNMT
SMP00188	GuanidinoacetateMethyltransferase Deficiency (GAMT Deficiency)	1.780451609	01	GAMT
SMP00232	Cimetidine Pathway	1.513771719	02	SNAP25,STX1A
SMP00381	Nisoldipine Pathway	1.467225843	02	ABCC8,CACNA1H
SMP00233	Nizatidine Pathway	1.467225843	02	SNAP25,STX1A
SMP00382	Nitrendipine Pathway	1.467225843	02	ABCC8,CACNA1H
SMP00377	Felodipine Pathway	1.467225843	02	ABCC8,CACNA1H
SMP00228	Pantoprazole Pathway	1.467225843	02	SNAP25,STX1A

Kyoto Encyclopedia of Genes and Genomes (KEGG), GenMAPP(MAP) and Pathway Ontology (PW)

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

GO ID	CATEGORY	GO Name	logP	Gene Count	Genes
GO:0006820	BP	anion transport		43	ABCC2,ACE,ACE2,ACSL5,AP OA1,APOA4,APOC3,CA13,CD 36,CFTR,CLCA1,EMB,ENPP3, FABP1,FABP2,FABP6,LGALS3 ,MAOB,MFSD2A,MTTP,P2RY 2,PDZK1,SERINC2,SLC10A2,S LC15A1,SLC17A8,SLC1A1,SL C1A7,SLC22A18,SLC23A1,SL C26A3,SLC2A2,SLC3A1,SLC5 1A,SLC51B,SLC52A1,SLC52A 3,SLC5A12,SLC6A20,SLC7A7, SLC7A9,SYK,TNFRSF11A
			10		
GO:0071466	BP	cellular response to xenobiotic stimulus		18	AADAC,ACY1,ACY3,CES2,C MBL,CYP2C18,CYP2J2,DPEP1 ,FMO1,GGT1,MGST1,NAT2,N
			10		

					R112,SULT1A2,SULT1B1,UGT1A6,UGT2B15,UGT2B17
GO:0055085	BP	transmembrane transport	10	54	ABCB1,ABCC13,ABCC2,ABCG2,ABCG5,ACE,ACSL5,APOA1,APOC3,AQP10,ATP1A1,ATP1A3,ATP1A4,CFTR,CHRNA7,CLCA1,EDN3,EMB,GCG,GLRX,KCNG1,KCNJ13,KCNQ1,LGALS3,MFSD2A,PDZK1,SGK1,SLC10A2,SLC15A1,SLC17A8,SLC1A1,SLC1A7,SLC22A18,SLC23A1,SLC23A3,SLC26A3,SLC28A1,SLC28A2,SLC2A2,SLC2A5,SLC39A4,SLC3A1,SLC44A4,SLC5A1,SLC5A11,SLC5A12,SLC6A20,SLC6A4,SLC7A7,SLC7A9,SLC9A3,SPINK1,TMEM37,TRPM6
GO:0015711	BP	organic anion transport	10	38	ABCC2,ACE,ACE2,ACSL5,APOA1,APOA4,APOC3,CA13,CD36,CFTR,EMB,FABP1,FABP2,FABP6,MFSD2A,MTTP,P2RY2,PDZK1,SERINC2,SLC10A2,SLC15A1,SLC17A8,SLC1A1,SLC1A7,SLC23A1,SLC26A3,SLC2A2,SLC3A1,SLC51A,SLC51B,SLC52A1,SLC52A3,SLC5A12,SLC6A20,SLC7A7,SLC7A9,SYK,TNFRSF11A
GO:0007586	BP	digestion		38	ABCG5,ACE,ACE2,AKR1B10,APOA1,APOA4,CD36,CTSE,DGAT1,ENPEP,EZR,FABP1,FABP2,GCNT3,ISX,KCNQ1,LCT,LIPH,MEP1A,MEP1B,MGAM,MOGAT2,MUC13,MUC2,NPY,PLS1,PNLIPRP2,PRSS2,PRSS3,SGK1,SLC15A1,SLC5A1,SOAT2,SST,SULT2A1,TFF1,VDR
GO:0006575	BP	cellular modified amino acid metabolic process	10	21	CNDP2,CPS1,DPEP1,GGT1,GGT3P,GGTLC1,GGTLC2,GSTA1,GSTA2,GSTA3,GSTA5,IYD,MGST1,MPST,NAT8,OTC,PLA2G2A,PRODH,SERINC2,SULT1

					B1,VNN1
GO:0006629	BP	lipid metabolic process	10	67	AADAC,ACOT11,ACSL5,AKR1B10,AKR1C3,APOA1,APOA4,APOB,APOBEC1,APOC3,ATP1A1,CD36,CDS1,CEBPA,CFTR,CPS1,CYP2C18,CYP2J2,CYP4F12,CYP4F8,DGAT1,DPEP1,EDN2,FA2H,FABP1,FABP2,FABP6,G6PC,GDPD2,GGT1,GGT3P,GGTLC1,GGTLC2,GK,GPD1,HPGD,HASLS2,HSD11B2,HSD17B2,HSD3B1,ISX,LIPH,MOGAT2,MTTP,NEU4,NR0B2,NR1H2,PCK1,PLA2G12B,PLA2G2A,PLB1,PLCB3,PNLIPRP2,RBP2,RETSAT,SERINC2,SLC44A4,SOAT2,ST6GALNAC1,SULT1A2,SULT1B1,SULT2A1,SYK,UGT1A6,UGT2B15,UGT2B17,VA3,VDR
GO:0043436	BP	oxoacid metabolic process	10	58	ACOT11,ACSL5,ACY1,AKR1C3,ALDOB,APOA1,APOA4,APOC3,ASPA,B3GNT3,B3GNT7,CD36,CHST5,CNDP2,CPS1,CYP2C18,CYP2J2,CYP4F12,CYP4F8,DGAT1,DPEP1,EDN2,FA2H,FABP1,FABP2,FABP6,FBP1,GGT1,GGT3P,GGTLC1,GGTLC2,GK,GPD1,HKDC1,HPGD,KHK,LDHA,MPST,MSRA,NAGS,OTAT,OTC,PCK1,PCK2,PEPD,PRODH,SLC23A1,SLC3A1,SLC7A7,SULT1A2,SULT1B1,SULT2A1,SYK,TKFC,UGT1A6,UGT2B15,UGT2B17,VNN1
GO:0008202	BP	steroid metabolic process	10	23	AKR1B10,AKR1C3,APOA1,APOA4,APOB,ATP1A1,CEBPA,CFTR,FABP6,G6PC,HSD11B2,HSD17B2,HSD3B1,MTTP,NR0B2,NR1H2,SOAT2,SULT1A2,SULT1B1,SULT2A1,UGT2B15,UGT2B17,VDR
GO:0048870	BP	cell motility	1.502667027	37	ACE,APOA1,APOB,ATP1A4,CCCL25,CEACAM6,CHRNA7,CX

					CL14,DAPK2,DPEP1,DPP4,EDN2,EDN3,ENPEP,FAT1,FERMT1,HOXB9,ITGB4,LAMA3,LGALS3,MARVELD3,MUC2,OLFM4,P2RY2,PRSS3,PTK6,S100A14,SEMA6A,SGK1,SLC7A7,SLC7A9,SST,ST14,STYK1,SYK,TNFRSF11A,VAV3
GO:0098862	CC	cluster of actin-based cell projections	10	31	ABCB1,ACE,CD36,CDHR2,CORO2A,CYBRD1,ENPEP,ESPN,EZR,ITLN1,LCT,MME,MTTP,MYO5B,PDZD3,PDZK1,PLB1,PLS1,SCIN,SLC15A1,SLC23A1,SLC26A3,SLC2A2,SLC3A1,SLC5A1,SLC7A9,SLC9A3,SOAT2,TMPRSS15,TRPM6
GO:0098589	CC	membrane region	10	63	ABCB1,ABCC2,ABCG2,ABCG5,ACE,ACE2,ACY3,AMN,ATP1A1,CD36,CDHR1,CDHR2,CFTCR,CHRNA7,CYBRD1,CYP4F12,DPEP1,DPP4,ENPEP,EZR,FERMT1,HEPH,HPGD,ITGB4,ITLN1,KCNQ1,LCT,LRP4,MALL,MGAM,MTTP,MUC13,MUC17,NAALADL1,P2RY2,PDZK1,PHLPP2,PLB1,PLEK2,PRSS8,REG1A,SLC10A2,SLC1A1,SLC22A18,SLC23A1,SLC26A3,SLC28A1,SLC2A2,SLC2A5,SLC39A4,SLC3A1,SLC52A3,SLC5A1,SLC5A12,SLC6A20,SLC6A4,SLC7A7,SLC7A9,SLC9A3,ST14,TRPM6,VDR
GO:0005615	CC	extracellular space	10	56	ACE,ACE2,AMN,ANPEP,APOA1,APOA4,APOB,APOC3,BMP7,C1QTNF12,CCL25,CD36,CEACAM6,CES2,CLCA1,CPO,CXCL14,DEFA5,DEFA6,DMBT1,DPEP1,EDN2,EDN3,EZR,FAM3B,GGC,GGT1,IGHA1,IGHA2,IGHM,IL32,JCHAIN,LAMC2,LGALS3,LIPH,MEP1A,MEP1B,MUC13,NAT8B,NPY,OLFM4,PIGR,PLA2G2A,PNLIPRP2,PRSS2,P

					RSS3,PRSS8,REG1A,REG3A,SECTM1,SPINK1,SST,ST14,TFF1,TST,VNN1
GO:0016324	CC	apical plasma membrane	10	40	ABCC2,ABCG2,ABCG5,ACY3,AMN,ATP1A1,CD36,CDHR2,CFTR,CHRNA7,CYP4F12,DPEP1,DPP4,ENPEP,EZR,LCT,MGAM,MUC13,MUC17,NAALADL1,P2RY2,PDZK1,PLB1,SLC10A2,SLC1A1,SLC22A18,SLC23A1,SLC26A3,SLC28A1,SLC2A2,SLC2A5,SLC39A4,SLC52A3,SLC5A1,SLC5A12,SLC6A20,SLC7A9,SLC9A3,TRPM6
GO:0045177	CC	apical part of cell	10	46	ABCB1,ABCC2,ABCG2,ABCG5,ACY3,AMN,ATP1A1,CD36,CDHR2,CFTR,CHRNA7,CYP4F12,DPEP1,DPP4,ENPEP,EZR,FABP1,FABP2,LCT,MGAM,MGST1,MUC13,MUC17,MYO5B,NAALADL1,P2RY2,PDZD3,PDZK1,PLB1,REG3A,SLC10A2,SLC1A1,SLC22A18,SLC23A1,SLC26A3,SLC28A1,SLC2A2,SLC2A5,SLC39A4,SLC52A3,SLC5A1,SLC5A12,SLC6A20,SLC7A9,SLC9A3,TRPM6
GO:0098590	CC	plasma membrane region	10	59	ABCB1,ABCC2,ABCG2,ABCG5,ACE,ACY3,AMN,ATP1A1,CD36,CDHR1,CDHR2,CFTR,CHRNA7,CYBRD1,CYP4F12,DPEP1,DPP4,ENPEP,EZR,FERMT1,HEPH,HPGD,ITGB4,ITLN1,KCNQ1,LCT,LRP4,MGAM,MTTP,MUC13,MUC17,NAALADL1,P2RY2,PDZK1,PHLPP2,PLB1,PLEK2,REG1A,SLC10A2,SLC1A1,SLC22A18,SLC23A1,SLC26A3,SLC28A1,SLC2A2,SLC2A5,SLC39A4,SLC3A1,SLC52A3,SLC5A1,SLC5A12,SLC6A20,SLC7A7,SLC7A9,SLC9A3,ST14,TRPM6,VDR

GO:0031253	CC	cell projection membrane	10	25	ABCB1,ACE,CD36,CDHR1,CDHR2,CHRNA7,CYBRD1,DPEP1,DPP4,EZR,FERMT1,ITLN1,MTTP,PDZK1,PHLPP2,PLB1,PLEK2,REG1A,SLC26A3,SLC2A2,SLC3A1,SLC5A1,SLC7A9,SLC9A3,TRPM6
GO:0005789	CC	endoplasmic reticulum membrane	3.292636218	34	AADAC,ACSL5,ALDOB,APOB,CDS1,CFTR,CREB3L3,CYP2C18,CYP2J2,CYP2S1,CYP4F12,CYP4F8,DGAT1,FA2H,FMO1,G6PC,HSD11B2,HSD17B2,HSD3B1,MFSD2A,MGST1,MOGAT2,NAT8,NAT8B,PLA2G2A,RETSAT,SGK1,SLC35G1,SLC51A,SOAT2,TLR3,UGT1A6,UGT2B15,UGT2B17
GO:0044463	CC	cell projection part	3.120948922	37	ABCB1,ACE,ATP1A1,ATP1A3,CD36,CDHR1,CDHR2,CHRNA7,CYBRD1,DPEP1,DPP4,ESPN,EZR,FERMT1,ITLN1,ITPKA,LDDHA,MME,MTTP,MYO5B,NGEF,NPY,NTS,PDZK1,PHLPP2,PLB1,PLEK2,REG1A,SLC17A8,SLC26A3,SLC2A2,SLC3A1,SLC5A1,SLC7A9,SLC9A3,TIAM2,TRPM6
GO:0005773	CC	vacuole	1.665121979	33	ACE,AKR1B10,ALDOB,AMN,ANPEP,APOA1,APOA4,APOB,APOC3,ATP1A1,CD68,CFTR,CITSE,DAPK2,DPP4,ENPEP,EZR,FZD5,HLA-DMB,HTR4,KCNQ1,MST1R,MYO5B,NEU4,OLFM4,P2RY2,PIGR,SLC17A8,SLC2A2,SLC39A4,SLC3A1,SLC6A4,TLR3
GO:0022857	MF	transmembrane transporter activity	10	43	ABCB1,ABCC13,ABCC2,ABCG2,ABCG5,AQP10,ATP1A1,ATP1A3,ATP1A4,CFTR,CHRNA7,CLCA1,EMB,KCNG1,KCNJ13,KCNQ1,MFSD2A,SERINC2,SLC10A2,SLC15A1,SLC17A8,SLC1A1,SLC1A7,SLC22A18,SLC23A1,SLC26A3,SLC28A1,SLC2

					8A2,SLC2A2,SLC2A5,SLC39A4,SLC3A1,SLC44A4,SLC5A1,SLC5A11,SLC5A12,SLC6A20,SLC6A4,SLC7A7,SLC7A9,SLC9A3,TMEM37,TRPM6
GO:0030246	MF	carbohydrate binding	10	20	ALDOB,CRYBG2,ENPP3,FBP1,GALM,GALNT6,GALNT7,HKDC1,ITLN1,ITLN2,LGALS3,MGAM,REG1A,REG1B,REG3A,REG3G,SI,SLC2A5,SUSD2,ZG16
GO:0008238	MF	exopeptidase activity	10	14	ACE,ACE2,ANPEP,CNDP2,CPO,DPEP1,DPP4,ENPEP,GGT1,GGT3P,MME,NAALADL1,PEPD,XPNPEP2
GO:0015291	MF	secondary active transmembrane transporter activity	10	19	MFSD2A,SLC10A2,SLC15A1,SLC17A8,SLC1A1,SLC1A7,SLC22A18,SLC23A1,SLC26A3,SLC28A1,SLC28A2,SLC5A1,SLC5A11,SLC5A12,SLC6A20,SLC6A4,SLC7A7,SLC7A9,SLC9A3
GO:0005215	MF	transporter activity	10	57	ABCB1,ABCC13,ABCC2,ABCG2,ABCG5,APOA1,APOA4,APOB,AQP10,ATP1A1,ATP1A3,ATP1A4,CFTR,CHRNA7,CLCA1,EMB,FABP1,FABP2,FABP6,KCNG1,KCNJ13,KCNQ1,MFSD2A,MTTP,PDZK1,RBP2,SERINC2,SLC10A2,SLC15A1,SLC17A8,SLC1A1,SLC1A7,SLC22A18,SLC23A1,SLC23A3,SLC26A3,SLC28A1,SLC28A2,SLC2A2,SLC2A5,SLC39A4,SLC3A1,SLC44A4,SLC51A,SLC51B,SLC52A1,SLC52A3,SLC5A1,SLC5A11,SLC5A12,SLC6A20,SLC6A4,SLC7A7,SLC7A9,SLC9A3,TMEM37,TRPM6
GO:0016491	MF	oxidoreductase activity	3.003448195	27	AKR1B10,AKR1C3,CYBRD1,CYP2C18,CYP2J2,CYP2S1,CYP4F12,CYP4F8,DHSDH,DHRS11,FA2H,FMO1,GLRX,GPD1,HEPH,HPGD,HSD11B2,HSD17B2,HS

					D3B1,IYD,LDHA,MAOA,MAOB,MGST1,MSRA,PRODH,RET SAT
GO:0042802	MF	identical protein binding	2.488609723	40	ABCG2,ACY3,ALDOB,ALPP,APOA1,APOA4,CEBPA,CHRNA7,CLDN15,CLDN23,CREB3L3,CTSE,DAPK2,DPP4,FBP1,GALM,GCG,GPD1,GZMA,HPGD,JCHAIN,KCNQ1,LDHA,LRP4,MAF,MAOB,MGST1,MPST,MUC13,NR0B2,OAT,OLFM4,PTK6,REG1A,REG3A,SDCBP2,SLC51A,SLC6A4,TLR3,UGT1A6
GO:0042803	MF	protein homodimerization activity	2.130384645	26	ABCG2,ALPP,APOA4,CEBPA,CHRNA7,CREB3L3,CTSE,DPP4,GALM,GPD1,GZMA,HPGD,JCHAIN,KCNQ1,LRP4,MAF,MAOB,MGST1,MUC13,NR0B2,OLFM4,REG1A,SDCBP2,SLC51A,SLC6A4,UGT1A6
GO:0016788	MF	hydrolase activity, acting on ester bonds	1.368915128	22	AADAC,ACOT11,ACY3,ALPI,ALPP,ASPA,ATP1A1,CES2,CMBL,DNASE1,ENPP3,FBP1,G6PC,GDPD2,LIPH,PHLPP2,PLA2G12B,PLA2G2A,PLB1,PLCB3,PNLIPRP2,PTPRH
GO:0016705	MF	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	1.31964782	07	AKR1C3,CYP2C18,CYP2J2,CYP2S1,CYP4F12,CYP4F8,FMO1

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	logP	Gene Count	Genes
GO:0050804	BP	modulation of chemical synaptic	10	23	BAIAP2,CALB1,CAMK2B,C ELF4,CLSTN2,CPLX2,CTN

		transmission			ND2,GRIA2,JPH3,KCNB1,LZTS1,MAPK8IP2,OXTR,RAB3A,RAB3B,RIMS2,SEPT5,SLC18A1,SLC8A2,SNAP25,STX1A,TAC1,UNC13A
GO:0098916	BP	anterograde trans-synaptic signaling	10	42	BAIAP2,BAIAP3,BSN,C2CD4C,CACNA1C,CADPS,CALB1,CAMK2B,CELF4,CLSTN2,CPLX2,CTNND2,DLG2,FGF12,GRIA2,GRIA3,GRIN2C,JPH3,KCNB1,KCNK3,KCNMB2,LRFN2,LZTS1,MAPK8IP2,OPRK1,OXTR,PTPRN2,RAB3A,RAB3B,RIMS2,SEPT5,SLC18A1,SLC8A2,SNAP25,SSTR2,STX1A,SV2C,SYT13,SYT17,SYT4,TAC1,UNC13A
GO:0051046	BP	regulation of secretion	10	39	ABCC8,C2CD4C,CACNA1C,CACNA1H,CADPS,CASR,CHGA,CPLX2,FGG,FOXA2,KCNB1,KCNS3,MAPK11,MYT1,NEUROD1,NLRP1,OPRK1,OXTR,PAM,RAB26,RAB3A,RAB3B,RAB3C,RFX6,RIMS2,SCG5,SEPT5,SERPINA10,SLC18A1,SNAP25,SRIN1,STX1A,STXBPL,SYT13,SYT17,SYT4,TAC1,UNC13A,WNK4
GO:0048812	BP	neuron projection morphogenesis	10	31	ATP8A2,BAIAP2,CAMK2B,CELSR3,CRMP1,CTNND2,DCX,DSCAM,FGF13,GPM6A,ISLR2,KIF5C,KIRREL3,LRFN2,LZTS1,MAP6,MAPK8IP2,MNX1,MT3,NRCAM,OBSL1,PACSIN1,RAB3A,RET,RIMS2,SPTB,SPTBN4,SRIN1,SYT17,SYT4,UNC13A
GO:0045055	BP	regulated exocytosis	10	29	A1BG,AHSG,ALB,APOH,C2CD4C,CACNA1C,CACNA1H,CADPS,CHGA,CPLX2,ECM1,F5,FGG,HRG,KCNB1,RAB26,RAB3A,RIMS2,SCG3,

					SEPT5,SERPINA10,SERPINF2,SNAP25,STX1A,SYT13,SYT17,SYT4,TF,UNC13A
GO:0030182	BP			50	ADGRV1,ATCAY,ATP8A2,BAIAP2,CAMK2B,CELSR3,CNGA3,CRMP1,CTNND2,DCX,DLG2,DSCAM,EPOR,FGF13,FOXA1,FOXA2,GPM6A,HEYLA,HIPK2,INSM1,ISLR2,KIF5C,KIRREL3,KLHL1,LRFN2,LZTS1,MAP6,MAPK8IP2,MNX1,MT3,NDRG4,NEUROD1,NKX2-2,NRCAM,OBSL1,PACSIN1,PITX2,RAB3A,RET,RIMS2,SNAP25,SPTB,SPTBN4,SRCN1,STMN3,SYT17,SYT4,UNC13A,WNT4
		neuron differentiation	5.60062407		
GO:0031175	BP			37	ATCAY,ATP8A2,BAIAP2,CAMK2B,CELSR3,CRMP1,CTNND2,DCX,DSCAM,EPOR,FGF13,GPM6A,ISLR2,KIF5C,KIRREL3,KLHL1,LRFN2,LZTS1,MAP6,MAPK8IP2,MNX1,MT3,NDRG4,NRCAM,OBSL1,PACSIN1,RAB3A,RET,RIMS2,SNAP25,SPTB,SPTBN4,SRCN1,STMN3,SYT17,SYT4,UNC13A
		neuron projection development	5.005906998		
GO:0007610	BP	behavior	4.863920376	29	ADRA1B,ALB,ATP8A2,CACNA1C,CALB1,CASR,CTNND2,DSCAM,FGF12,FGF13,FOXA2,HIPK2,JPH3,KIRREL3,KLHL1,MAPK8IP2,MC1R,NAV2,NDRG4,OPRK1,OXR,RCAN2,SEZ6L2,SLC8A2,SNAP25,SOBP,SPTBN4,TAC1,ZFHX2
GO:0009914	BP	hormone transport	4.851085746	20	ABCC8,CACNA1C,CASR,FGG,FOXA2,KCNB1,KCNS3,MYT1,NEUROD1,OPRK1,PTPRN,PTPRN2,RFX6,RIMS2,SCG5,SNAP25,STX1A,STX

					BP5L,TAC1,TTR
GO:0048858	BP			34	ATP8A2,BAIAP2,CAMK2B,CCDC151,CELSR3,CEP126,CRMP1,CTNND2,DCX,DSCAM,FGF13,GPM6A,ISLR2,KIF5C,KIRREL3,LRFN2,LZTS1,MAP6,MAPK8IP2,MNX1,MT3,NRCAM,OBSL1,PACSI N1,RAB3A,RET,RIMS2,SPTB,SPTBN4,SRCIN1,SYT17,SYT4,TEKT2,UNC13A
		cell projection morphogenesis	4.358560461		
GO:0030141	CC	secretory granule	10	31	A1BG,ABCA3,AHSG,ALB,APOH,BAIAP2,CALCR,CHGA,CHGB,CPE,ECM1,F5,FGG,HRG,PAM,PCSK1,PCSK1N,PCSK2,PTPRN,PTPRN2,RAB26,RAB3A,RAB3B,SCG3,SCG5,SERPINF2,STX1A,STXBP5L,SYT4,TF
GO:0012506	CC	vesicle membrane	10	28	ABCA3,ABCC8,AP3B2,ARFGEF3,CADPS,CALY,CAMK2B,CHGA,CPE,ECE2,FMN2,GRIA2,GRIA3,PACSIN1,PAM,PTPRN,PTPRN2,RAB26,RAB3A,SCG3,SCGN,SLC18A1,STX1A,SV2C,SVOP,SYT4,TF,WNT4
GO:0030425	CC		10	32	ATCAY,BAIAP2,BSN,CACNA1C,CACNA1H,CALB1,CAMK2B,CNGA3,CPE,CPLX2,CPT1C,CRMP1,CTNND2,DCX,DLG2,FGF13,GNAZ,GPM6A,GRIA2,GRIA3,KCNB1,KCNJ6,KIRREL3,KLHL1,LZTS1,MT3,OPRK1,PCSK2,RET,RGS11,SLC8A2,SRCIN1
		dendrite			
GO:0044463	CC		10	46	ADGRV1,ANK1,AP3B2,APC2,BAIAP2,BSN,CACNA1C,CALB1,CAMK2B,CASR,CCDC151,CEP126,CLSTN2,CNGA3,CPLX2,DLG2,DNAH12,DNALI1,DSCAM,FGF13,GPM6A,GRIA2,GRIA3,KCNB1,
		cell projection part			

					KIF1A,KIF5C,KIRREL3,LZTS1,MAPK8IP2,MT3,NDRG4,NRCAM,OPRK1,PACSIN1,PTPRN,PTPRN2,RAB3A,RGS11,SEPT5,SLC8A2,SNAP25,SNTG1,SPTBN4,SRIN1,STMN3,UNC13A
GO:0044433	CC		10	40	A1BG,ABCA3,ABCC8,AHSG,ALB,AP3B2,APOH,ARFGEF3,CADPS,CALY,CAMK2B,CHGA,CPE,ECE2,ECM1,F5,FGG,FMN2,GRIA2,GRIA3,HP,HRG,PACSIN1,PAM,PCSK1,PCSK2,PTPRN,PTPRN2,RAB26,RAB3A,SCG3,SCGN,SERPINF2,SLC18A1,STX1A,SV2C,SVOP,SYT4,TF,WNT4
		cytoplasmic vesicle part			
GO:0045202	CC		10	54	ABCC8,ADGRV1,ANK1,ATCAY,BAIAP2,BAIAP3,BSN,CACNA1C,CADPS,CALB1,CAMK2B,CLSTN2,CPE,CPLX2,CPT1C,CTNND2,DLG2,DSCAM,DTNB,GPM6A,GRIA2,GRIA3,GRIN2C,KCNB1,KCTD12,LRFN2,LZTS1,MAPK8IP2,MT3,NMNAT2,NRCAM,OPRK1,PACSIN1,PRRT2,PTPRN,PTPRN2,RAB3A,RAB3B,RAB3C,RIMBP2,RIMS2,SCGN,SEPT5,SLC18A1,SLC8A2,SNAP25,SRIN1,STX1A,SV2C,SVOP,SYT13,SYT17,SYT4,UNC13A
		synapse			
GO:0030054	CC		4.252036651	41	ADRA1B,ATCAY,BSN,CADPS,CGNL1,CLDN1,CPT1C,CTNND2,DLG2,DSCAM,FGF13,FOXA2,GRIA2,GRIA3,GRIN2C,HPN,KCNB1,KCTD12,KIRREL2,LRFN2,LZTS1,MTSS1,OBSL1,OXTR,PACSIN1,PHLDB2,PFIBP1,PRRT2,PTPRN,PTPRN2,RIMBP2,RIMS2,SNAP25,SPTBN4,SRIN1,STX1A,SV2C,SVOP,S
		cell junction			

				YT4,UNC13A,WNK4
GO:0098590	CC	2.665460607	32	ADGRV1,ANK1,APC2,ATP1B2,CACNA1C,CACNA1H,CASR,CLDN1,CLSTN2,CNGA3,CPE,DLG2,FXSD2,GRIA2,GRIA3,GRIN2C,HPN,KCNB1,KCTD12,LRFN2,LZTS1,NDRG4,OXTR,PACSIN1,RDH12,RIMS2,SLC8A2,SNAP25,SNTG1,SRIN1,TF,UNC13A
				plasma membrane region
GO:0044431	CC	2.284856735	28	AP3B2,ATP8A2,B3GAT1,BSN,CLIP3,CLSTN2,ECE2,F2,F5,F7,FAM57B,FTCD,MANEAL,MARCH4,NMNAT2,PACSIN1,PAM,PCSK1N,PROC,RAB26,RAB36,RBFOX1,SNAP25,ST6GALNAC5,ST8SIA3,SYT17,VTN,WNT4
				Golgi apparatus part
GO:0005615	CC	1.924944983	38	A1BG,ABCA3,ADAMTS9,AHSG,ALB,AMBP,APOH,C8A,CHGA,CKB,CPE,ECM1,F2,F5,F7,FGF12,FGG,HP,HPR,HRG,IGFALS,INA,ITIH1,MT3,PAM,PCSK1,PCSK1N,PCSK2,POTEE,PROC,SERPINA10,SERPINF2,TAC1,TF,TNFRSF11B,TTR,VTN,WNT4
				extracellular space
GO:0008092	MF		39	ADGRV1,ANK1,APC2,ATCAY,BAIAP2,CACNA1C,CAMK2B,CDC42EP3,CLIP3,CRMP1,DCX,FGF13,FMN2,FTCD,JAKMIP2,KIF12,KIF1A,KIF5C,KLHL1,LZTS1,MAP6,MAPK8IP2,MTSS1,NRCAM,OBSL1,PACSIN1,PTPRN,PTPRT,RAB3A,RAB3B,RAB3C,RCAN3,SNAP25,SNTG1,SPTB,SPTBN4,STMN3,STX1A,UNC13A
				cytoskeletal protein binding
		10		
GO:0046873	MF		22	ABCC8,ATP1B2,CACNA1C,CACNA1H,CNGA3,FXSD2,GPM6A,HPN,JPH3,KCNB1,KCNH2,KCNH6,KCNJ6,KC
				metal ion transmembrane transporter activity
		4.941741441		

					NK3,KCNMB2,KCNS3,SCN3A,SLC6A15,SLC8A2,SNAP25,TF,TUSC3
GO:0050699	MF	WW domain binding	3.52865194	05	ATCAY,TCEAL2,TCEAL3,TCEAL5,TCEAL6
GO:008017	MF	microtubule binding	3.258023065	12	APC2,CLIP3,DCX,FGF13,FMN2,FTCD,JAKMIP2,KIF12,KIF1A,KIF5C,LZTS1,MAP6
GO:0019904	MF	protein domain specific binding	3.081915788	26	ATCAY,BAIAP2,CACNA1C,CPE,DLG2,FOXA1,FOXA2,GRIA2,GRIA3,GRIN2C,HEYL,KCNH2,KIRREL3,NLRP1,RIMS2,SNAP25,SRIN1,SSTR2,STMN3,STX1A,TCEAL2,TCEAL3,TCEAL5,TCEAL6,UNC13A,ZBTB16
GO:0005509	MF	calcium ion binding	2.595409931	24	ADGRV1,C2CD4C,CADPS,CALB1,CASR,CDH22,CDH6,CDHR3,CELSR3,CLSTN2,F2,F7,ITIH1,MICU3,MYL6B,NINL,PAM,PROC,RET,SCGN,SMOC1,SYT13,SYT17,SYT4
GO:0022857	MF	transmembrane transporter activity	2.502531496	31	ABCA3,ABCC8,ATP1B2,CACNA1C,CACNA1H,CNGA3,FXYP2,GPM6A,GRIA2,GRIA3,GRIN2C,HPN,JPH3,KCNB1,KCNH2,KCNH6,KCNJ6,KCNK3,KCNMB2,KCNS3,SCN3A,SLC18A1,SLC38A11,SLC6A15,SLC7A14,SLC8A2,SNAP25,SV2C,SVOP,TF,TUSC3
GO:0098772	MF	molecular function regulator	2.394945834	40	AHSG,AMBP,APOH,ARFGEF3,ARHGEF40,ATP1B2,BEX3,CAMK2B,CDC42EP3,FGF12,FGF13,FXYP2,GRIN2C,HARG,ITIH1,KCNMB2,KCNS3,MAPK8IP2,MT3,NLRP1,PCSKIN,PPP2R2B,RAB3A,RCAN2,RCAN3,RET,RGL3,RGS11,RGS4,RUNDC3A,SCG5,SERPINA10,SERPINF2,SHC2,S

					PTB,SPTBN4,STX1A,STXBP5L,WNK4,WNT4
GO:0033613	MF	activating transcription factor binding	2.308627574	05	BEX1,DUSP26,HIPK2,NEUROD1,PITX2
GO:0005215	MF			34	ABCA3,ABCC8,AP3B2,ATP1B2,ATP8A2,CACNA1C,CACNA1H,CALCR,CNGA3,FXR,YD2,GPM6A,GRIA2,GRIA3,GRIN2C,HPN,JPH3,KCNB1,KCNH2,KCNH6,KCNJ6,KCNK3,KCNMB2,KCNS3,SCN3A,SLC18A1,SLC38A11,SLC6A15,SLC7A14,SLC8A2,SNAP25,SV2C,SVOP,TF,TUSC3
		transporter activity	1.728615907		

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
Up	CFTR	800	0.337235	1.45E+08	0.392074	5.13E-04
Up	EZR	349	0.126854	34965820	0.361082	0.002027
Up	ATP1A1	274	0.094222	46791492	0.345467	0.002112
Up	TUBA1C	263	0.072768	47179314	0.331775	0.001521
Up	LGALS3	212	0.08454	16465044	0.355499	0.002233
Up	LDHA	193	0.053376	22674450	0.34324	0.003803
Up	SYK	150	0.053587	15517378	0.32379	0.00524
Up	C15orf48	124	0.033441	28877652	0.277891	0
Up	MME	122	0.039535	26177876	0.30894	1.40E-04
Up	CEBPA	117	0.037697	16708358	0.304502	0.004119
Up	VDR	115	0.030132	14887176	0.302135	0.004267
Up	SGK1	111	0.029622	10995114	0.31383	0.001529
Up	ATP1A3	107	0.032375	7841018	0.306733	0.00335
Up	SLC39A4	102	0.029866	16234750	0.264231	0
Up	APOA1	100	0.032611	6131354	0.307485	0.007732

Up	IGHA1	98	0.02602	6148446	0.306426	0.005143
Up	MYB	82	0.019764	12482362	0.285956	0.001807
Up	APOB	78	0.019406	10010588	0.297708	0.002105
Up	PCK1	77	0.014006	6246062	0.307369	0.002523
Up	KRT19	75	0.017829	15330732	0.290468	0
Up	OAT	70	0.012398	4627170	0.307678	0.006146
Up	CASP1	68	0.016772	6320288	0.293409	0.002797
Up	NR0B2	65	0.016429	6079986	0.291696	0.009615
Up	PDZK1	65	0.023918	3173138	0.317307	0.00625
Up	SLC15A1	65	0.016501	11586520	0.260423	0
Up	CDX1	64	0.02066	4802286	0.262489	0
Up	CPS1	62	0.014201	4810928	0.301558	0.005817
Up	DEFA5	62	0.018314	4653506	0.269911	0
Up	CDKN2B	61	0.014774	7835636	0.284676	0
Up	ITGB4	59	0.015686	3698572	0.322553	0.008182
Up	TMEM171	57	0.01519	8369774	0.264631	0
Up	DPEP1	56	0.013124	8597320	0.247311	0
Up	CNDP2	54	0.011201	3331272	0.294256	0.021116
Up	PLS1	54	0.01501	3421152	0.301855	0.008386
Up	LIPH	54	0.015285	3190118	0.266301	6.99E-04
Up	HOXB9	53	0.012568	4397654	0.27581	0
Up	FBP1	52	0.011561	6182572	0.280133	0
Up	IGHM	52	0.010415	3635462	0.296124	0.011905
Up	GK	52	0.01714	4346954	0.257873	0
Up	MYO5B	50	0.010242	7050886	0.27698	0
Up	ABCC2	49	0.012097	5021856	0.282802	8.50E-04
Up	SDCBP2	49	0.012927	4614160	0.254959	0
Up	BMP7	47	0.012261	2622618	0.27379	0
Up	NR1I2	47	0.007648	3629024	0.291818	0.012121
Up	FAT1	47	0.019271	2429964	0.309252	0.002775
Up	PEPD	47	0.009287	2272078	0.293128	0.036364
Up	PCK2	46	0.014132	3554922	0.303615	0.002899
Up	INAVA	45	0.009883	9611672	0.258008	0

Up	BLNK	43	0.006729	2524002	0.287012	0.0299
Up	TLR3	43	0.009769	2353776	0.269703	0.009756
Up	ESPL1	42	0.00964	6154014	0.267158	0
Up	TRIM15	42	0.00762	3054792	0.284544	0.008974
Up	BTNL8	42	0.012508	2064298	0.260645	0
Up	GDA	41	0.008491	6780708	0.266199	0.008537
Up	SLC1A1	38	0.011405	3933480	0.291142	0
Up	OLFM4	38	0.011718	2953482	0.269926	0
Up	PRSS3	37	0.006314	2598386	0.29283	0.007508
Up	CYP2S1	37	0.009537	2793704	0.271392	0
Up	PTK6	36	0.006833	4448616	0.288194	0
Up	CORO2A	36	0.006165	3928330	0.270777	0
Up	PIGR	36	0.005258	1063636	0.283555	0
Up	MST1R	35	0.005176	3915532	0.27797	0
Up	DPP4	35	0.010462	2507724	0.266547	0.003788
Up	PLA2G2A	35	0.007051	4468226	0.263975	0
Up	KRT20	33	0.005563	3702134	0.260659	0
Up	ALDOB	33	0.005853	2636566	0.283851	0
Up	PTPRH	33	0.006883	3455408	0.265607	0
Up	MAF	31	0.007292	1443322	0.287096	0.03202
Up	PHLPP2	30	0.005704	1554578	0.288568	0.016092
Up	ALPP	30	0.005396	2666888	0.276401	0.004598
Up	RNF125	30	0.00725	2864040	0.263833	0
Up	PLCB3	30	0.006291	1737252	0.293251	0.013793
Up	ACY1	30	0.005877	2916288	0.271137	0
Up	LAMB3	30	0.007202	1107190	0.30591	0.027586
Up	GALNT7	30	0.008985	1595066	0.279429	0.004598
Up	VAV3	29	0.004039	1943432	0.278065	0.024631
Up	CD36	29	0.00463	1796558	0.27567	0
Up	IGHA2	29	0.003678	772100	0.256993	0
Up	E2F2	28	0.005109	1528176	0.271107	0.005291
Up	LRP4	28	0.008354	1968528	0.246725	0
Up	SLC22A18	28	0.009513	1210786	0.270627	0

Up	MOCOS	27	0.007485	1343242	0.277718	0
Up	CMBL	27	0.003993	3409522	0.25954	0
Up	RETSAT	27	0.009185	2077104	0.246651	0
Up	TUBAL3	27	0.002362	2067286	0.271392	0
Up	TFF1	26	0.007463	1959490	0.278428	0
Up	LAMA3	26	0.006013	1246148	0.279957	0.009231
Up	TKFC	26	0.004887	3159590	0.252527	0
Up	GALNT6	26	0.006453	2256640	0.264374	0
Up	CREB3L3	24	0.004301	1202464	0.254548	0
Up	KHK	24	0.005176	2034326	0.239497	0
Up	ALPI	24	0.003831	1743574	0.274757	0.007246
Up	GLRX	24	0.006194	4094144	0.253415	0
Up	JCHAIN	24	0.003384	638116	0.28308	0.014493
Up	S100A14	24	0.004232	2312790	0.27892	0
Up	NGEF	23	0.005906	1469564	0.25014	0
Up	NAT2	23	0.006037	3161322	0.26783	0
Up	ENTPD7	23	0.005123	1816294	0.231515	0
Up	MEP1A	23	0.005682	1256968	0.255865	0.033333
Up	CYBRD1	22	0.002777	1907726	0.263975	0
Up	B3GNT3	22	0.004684	1304208	0.256508	0.004329
Up	ABCB1	22	0.004149	812176	0.286592	0
Up	KCNQ1	21	0.002735	1722856	0.271678	0
Up	SPIB	21	0.002833	797762	0.25884	0.011696
Up	ST14	21	0.003441	2186960	0.256253	0
Up	SCIN	21	0.002994	1757300	0.264932	0
Up	DMBT1	20	0.001957	602578	0.269451	0
Up	GZMA	20	0.003214	1482956	0.263577	0
Up	HTR4	20	0.00501	1553870	0.244471	0
Up	SEMA6A	20	0.003562	1239734	0.26352	0
Up	MPST	20	0.004058	2865974	0.247161	0
Up	TNFRSF11A	19	0.001836	609874	0.262546	0.017544
Up	POU2AF1	19	0.005132	803526	0.259101	0
Up	IL32	19	0.004046	631432	0.269777	0.007353

Up	NABP1	19	0.004459	2061856	0.254416	0
Up	TRIM36	19	0.005131	2253212	0.244911	0
Up	NPY	18	0.004855	787246	0.238762	0.013072
Up	NEU4	18	0.003706	1210438	0.247273	0
Up	BCL2L14	18	0.004341	1470846	0.238378	0
Up	FZD5	18	0.004544	1080252	0.251826	0
Up	FERMT1	18	0.00321	1478780	0.25241	0
Up	PDZD3	17	0.005367	1979004	0.288228	0
Up	GSTA1	17	0.004191	2423636	0.254244	0.038095
Up	ACY3	17	0.002972	912628	0.240155	0
Up	PRSS2	17	0.003706	1513068	0.269258	0
Up	COL17A1	16	0.001221	417876	0.273102	0.032967
Up	GCG	16	0.003025	414046	0.241327	0.021978
Up	MEP1B	16	0.001905	480452	0.259995	0.076923
Up	SLC23A1	16	0.002253	1014062	0.241517	0
Up	DEFA6	16	0.004482	1839192	0.26052	0
Up	PMP22	15	0.002488	1069508	0.262335	0
Up	CDS1	15	0.003438	804204	0.266301	0
Up	AKR1B10	15	0.00368	1668902	0.23773	0
Up	OTC	15	0.003311	428194	0.25675	0
Up	CD68	15	0.001831	395168	0.270478	0.009524
Up	TST	15	0.001422	910420	0.250588	0
Up	FUT3	15	0.001565	361244	0.226881	0
Up	ITLN1	14	0.003009	1148284	0.239532	0.015152
Up	YIF1B	14	0.001214	609094	0.256737	0
Up	DGAT1	14	0.004526	770454	0.26591	0.030303
Up	MGST1	14	0.001007	575984	0.274157	0
Up	SLC6A4	14	0.001345	870594	0.26311	0
Up	TMEM92	14	0.002316	1835366	0.24644	0
Up	AGR3	14	0.002315	853538	0.269377	0
Up	DQX1	14	0.003521	632600	0.232074	0
Up	CTSE	14	0.004046	973114	0.23497	0
Up	DAPK2	13	0.002512	629624	0.259581	0

Up	SLC9A3	13	0.003201	786034	0.254469	0.036364
Up	LAMC2	13	0.00171	309654	0.257249	0.064103
Up	PLB1	13	0.002808	869066	0.238193	0
Up	EMB	13	0.00353	388650	0.272783	0
Up	TM4SF20	13	0.003116	1599200	0.242594	0
Up	ATP1A4	13	0.001495	955306	0.252905	0
Up	MUC13	13	0.00265	562262	0.294415	0.038462
Up	ABCG2	12	9.37E-04	457756	0.241042	0
Up	C2orf88	12	0.002921	663448	0.252228	0
Up	SLC2A5	12	0.002447	567722	0.246019	0
Up	MAOA	11	0.001204	320798	0.260742	0
Up	AKR1C3	11	0.00193	583766	0.206773	0
Up	REG3A	11	9.14E-04	374400	0.256952	0
Up	GGT1	11	0.002101	623688	0.240935	0
Up	GPD1	11	0.002761	434422	0.252358	0
Up	DEPDC7	11	0.00134	483812	0.255545	0
Up	MUC2	11	0.002233	604140	0.297618	0.055556
Up	TIAM2	11	9.32E-04	492674	0.237017	0
Up	APOBEC1	10	0.001758	490246	0.225647	0
Up	ACE	10	0.001784	930240	0.253652	0
Up	MALL	10	0.001736	842716	0.23524	0
Up	CYP2C18	10	0.002131	523900	0.244386	0
Up	ACE2	10	0.001465	410120	0.244948	0
Up	GCNT3	10	0.002162	498298	0.239158	0
Up	UGT1A6	10	0.002857	746830	0.170319	0
Up	NTS	9	0.001559	270952	0.226545	0
Up	CEACAM6	9	0.002097	501902	0.256441	0
Up	EFNA2	9	0.001761	409026	0.235535	0
Up	SERINC2	9	0.002662	322276	0.266055	0
Up	ACSL5	9	7.04E-04	233130	0.241398	0
Up	P2RY2	9	0.001616	562524	0.269718	0
Up	FAM3B	9	0.00234	516058	0.242847	0
Up	CXCL14	9	7.83E-04	328100	0.260271	0

Up	CHRNA7	8	7.73E-04	284446	0.255651	0
Up	CIDEC	8	2.94E-04	56020	0.247448	0
Up	SULT2A1	8	5.07E-04	280534	0.22373	0
Up	FCGBP	8	8.65E-04	120196	0.274342	0
Up	SULT1A2	8	0.001712	370540	0.215698	0
Up	ITPKA	8	3.40E-04	152284	0.248415	0
Up	SLC6A20	8	1.08E-04	67436	0.20693	0
Up	BTNL3	8	0.002464	510786	0.236194	0
Up	RBP2	8	0.001734	688052	0.236399	0
Up	APOA4	7	4.23E-04	102270	0.233558	0
Up	ASPA	7	5.82E-04	99922	0.209901	0
Up	MTTP	7	8.28E-04	124768	0.261886	0.095238
Up	SLC2A2	7	0.001733	246526	0.26379	0
Up	FABP1	7	7.59E-04	224536	0.233368	0
Up	CDCA7	7	4.12E-04	179658	0.26263	0
Up	PRAP1	7	9.42E-04	163794	0.259169	0
Up	IYD	7	0.001013	235034	0.233993	0
Up	CYP4F12	7	0.001265	440686	0.236171	0
Up	PRODH	7	7.81E-04	229406	0.254126	0
Up	MSRA	7	0.001267	428902	0.244985	0
Up	SPINK4	7	0.001042	113078	0.228075	0
Up	GSTA2	6	0.001225	1030988	0.202783	0.133333
Up	MAOB	6	4.83E-04	47718	0.222207	0
Up	GALM	6	0.001643	429332	0.221664	0
Up	HSD11B2	6	5.51E-04	231476	0.242042	0
Up	ARL14	6	0.00157	459078	0.207817	0
Up	KCNG1	6	0.001274	410378	0.24805	0
Up	SLC51A	6	7.26E-04	239708	0.232416	0
Up	SST	6	0.001642	183390	0.19581	0
Up	HKDC1	6	0.00138	184786	0.210063	0
Up	TMEM37	6	0.001176	146386	0.229239	0
Up	FA2H	6	2.35E-04	139998	0.240414	0
Up	ENPEP	6	4.41E-04	282938	0.207237	0

Up	SOAT2	6	4.49E-04	178370	0.251839	0
Up	DNASE1	5	5.08E-05	26748	0.248895	0
Up	CHP2	5	8.59E-04	188378	0.228352	0
Up	ANPEP	5	9.38E-05	51116	0.232637	0
Up	REG1A	5	7.94E-04	130752	0.243499	0
Up	CCL25	5	0.001633	284204	0.173714	0
Up	ACOT11	5	1	6	1	0
Up	ZG16	5	1.64E-04	47082	0.206511	0
Up	APOC3	5	4.36E-04	69572	0.241851	0.2
Up	EDN3	5	8.58E-04	238392	0.191844	0
Up	OVOL1	5	4.34E-04	147796	0.246489	0
Up	TMEM220	5	4.74E-04	125106	0.2318	0
Up	TMPRSS4	5	5.18E-04	160574	0.234767	0
Up	SLC7A9	5	1.10E-04	86068	0.239779	0
Up	GDPD2	5	0.00132	279976	0.219301	0
Up	SPINK1	5	8.88E-04	173028	0.237465	0
Up	DHRS11	5	0.001633	570244	0.223363	0
Up	ABCG5	4	8.19E-04	284038	0.22254	0
Up	SLC26A3	4	6.26E-04	347922	0.236707	0
Up	CDHR2	4	8.22E-04	178854	0.178002	0
Up	SULT1B1	4	4.61E-04	102090	0.224912	0
Up	LCT	4	8.67E-05	65136	0.262644	0
Up	GSTA3	4	7.03E-04	558834	0.253875	0.5
Up	TMEM139	4	8.45E-04	142780	0.211424	0
Up	REG1B	4	4.47E-04	61468	0.215784	0
Up	TRPM6	4	4.67E-05	18606	0.23657	0
Up	ENPP3	4	6.48E-04	211732	0.238042	0
Up	OSR2	4	5.12E-04	124196	0.243172	0
Up	G6PC	4	1	12	1	0
Up	CDHR1	4	8.17E-04	397562	0.222804	0
Up	PNLIPRP2	4	0.001225	231078	0.184904	0
Up	KLK1	3	8.17E-04	160214	0.169323	0
Up	SLC5A1	3	1.18E-05	13140	0.249987	0

Up	PLEKHS1	3	5.27E-04	130624	0.223495	0
Up	SUSD2	3	4.09E-04	92026	0.226242	0
Up	FABP2	3	1.25E-04	80830	0.225897	0
Up	ITLN2	3	4.08E-04	154834	0.193275	0.333333
Up	PLA2G12B	3	1	6	1	0
Up	CYP2J2	3	5.35E-04	153486	0.222814	0
Up	SLC5A11	3	8.17E-04	235582	0.225543	0
Up	CLCA1	3	4.08E-04	113728	0.283933	0.333333
Up	TMPRSS15	3	5.89E-05	5524	0.219813	0
Up	C19orf33	3	5.68E-04	125876	0.237074	0
Up	GATA5	3	4.10E-04	158858	0.221885	0
Up	ADTRP	3	4.30E-04	129188	0.223179	0
Up	NAT8	3	1.39E-04	59608	0.234609	0
Up	RFLNA	3	4.11E-04	91142	0.22254	0
Up	PRSS8	3	4.16E-04	124214	0.246031	0
Up	TMEM45B	3	4.94E-04	84124	0.19073	0
Up	HSD3B1	3	6.93E-04	184720	0.220268	0
Up	STYK1	3	3.48E-05	28866	0.247661	0
Up	ADGRG7	3	4.58E-05	36714	0.237672	0
Up	SI	3	1.91E-04	60786	0.233669	0
Up	EDN2	3	9.29E-04	606870	0.236353	0
Up	PLEK2	3	8.17E-04	202562	0.184084	0
Up	SLC7A7	2	7.08E-06	812	0.219577	0
Up	CYP4F8	2	4.20E-07	10	0.227524	0
Up	GPA33	2	2.20E-05	10356	0.230664	0
Up	SECTM1	2	4.08E-04	93950	0.230111	0
Up	HSD17B2	2	1	2	1	0
Up	FAM3D	2	7.25E-06	3146	0.243257	0
Up	MOGAT2	2	4.08E-04	347922	0.173763	0
Up	ANKRD9	2	4.08E-04	108178	0.222996	0
Up	ESPN	2	4.08E-04	213846	0.218929	0
Up	SLC23A3	2	1.76E-05	582	0.212129	0
Up	SLC3A1	2	4.08E-04	108730	0.246266	0

Up	MACC1	2	2.19E-06	542	0.234172	0
Up	SLC44A4	2	4.08E-04	60686	0.209533	0
Up	GGTLC1	2	1.43E-06	66	0.21888	0
Up	MUC3A	2	3.52E-06	2442	0.217712	0
Up	ST6GALNAC1	2	4.08E-04	84508	0.160457	0
Up	DHDH	2	1	2	1	0
Up	CES2	2	6.29E-05	28026	0.238378	0
Up	NAALADL1	2	8.17E-04	406740	0.174482	0
Up	ADIRF	2	4.58E-05	15000	0.209794	0
Up	SLC1A7	2	4.08E-04	130768	0.18985	0
Up	ISX	2	3.10E-07	562	0.242342	0
Up	PRR15	2	1.09E-05	13756	0.243196	0
Up	C1orf115	2	8.59E-05	57840	0.244191	0
Up	C6orf132	2	0	0	0.269169	1
Up	GSTA5	1	0	0	0.1686	0
Up	GUCA2A	1	0	0	0.195107	0
Up	SLC10A2	1	0	0	1	0
Up	IGH	1	0	0	0.190426	0
Up	BICDL2	1	0	0	0.198067	0
Up	MFSD2A	1	0	0	0.211762	0
Up	CIDECP1	1	0	0	0.218909	0
Up	MGAM	1	0	0	1	0
Up	B3GNT7	1	0	0	0.196896	0
Up	TRABD2A	1	0	0	0.216557	0
Up	HEPH	1	0	0	0.229949	0
Up	AMN	1	0	0	1	0
Up	SLC35G1	1	0	0	0.223017	0
Up	XPNPEP2	1	0	0	0.129359	0
Up	AQP10	1	0	0	0.228778	0
Up	NAGS	1	0	0	1	0
Up	UGT2B15	1	0	0	1	0
Up	FMO1	1	0	0	0.187316	0
Up	ABCC13	1	0	0	0.195208	0

Up	CLDN15	1	0	0	1	0
Up	FUT2	1	0	0	0.187819	0
Up	SLC5A12	1	0	0	0.219794	0
Up	FAM151A	1	0	0	0.236707	0
Up	HPGD	1	0	0	0.236707	0
Up	TBX10	1	0	0	0.221004	0
Up	NAT8B	1	0	0	0.191424	0
Up	CLDN23	1	0	0	0.224211	0
Up	GUCA2B	1	0	0	1	0
Up	SLC17A8	1	0	0	0.219794	0
Up	FABP6	1	0	0	1	0
Down	OBSL1	632	0.22585	166189424	0.367261	3.58E-04
Down	KRT40	322	0.10228	35746980	0.322477	2.60E-04
Down	FOXA1	290	0.072223	82474260	0.310802	1.69E-04
Down	WWOX	269	0.074496	68514600	0.331913	3.88E-04
Down	ALB	233	0.091274	25854652	0.350261	0.003903
Down	NINL	220	0.066445	27438942	0.31789	1.68E-04
Down	PPP2R2B	199	0.048785	36528806	0.327825	8.12E-04
Down	PDE4DIP	152	0.039093	23273202	0.304285	2.68E-04
Down	CBX1	147	0.043849	9984612	0.328517	0.003065
Down	VTN	142	0.036692	20961438	0.315485	6.17E-04
Down	ZBTB16	132	0.039671	15803384	0.318885	0.001789
Down	STX1A	120	0.035584	9430820	0.315824	0.003187
Down	CRMP1	111	0.029042	12792938	0.310766	1.80E-04
Down	CKB	111	0.027054	8414642	0.317776	0.002002
Down	CEP126	103	0.025046	10912824	0.308521	0.002856
Down	MAPK8IP2	97	0.026885	6179474	0.303483	8.96E-04
Down	PTPRN	94	0.027103	8349732	0.293788	0.001911
Down	BAIAP2	90	0.024158	10448514	0.321381	0.003135
Down	GPRASP2	83	0.020114	6629478	0.307572	0.009403
Down	PHLDB2	80	0.016878	11828612	0.28788	0
Down	HIPK2	77	0.017893	9957538	0.300283	0
Down	TF	76	0.020636	6837338	0.313543	0.009369

Down	C6orf141	74	0.017011	6517270	0.285537	3.70E-04
Down	RUNX1T1	70	0.01385	5565976	0.291156	0.004829
Down	UNC13A	70	0.014838	10456886	0.284311	4.14E-04
Down	ARNT2	69	0.017469	4321320	0.299452	0.002261
Down	RET	67	0.015376	6321036	0.292976	0
Down	TTR	65	0.01652	4264850	0.308665	0.010241
Down	GNAZ	61	0.016566	7386950	0.290836	0
Down	CAMK2B	58	0.018935	5204944	0.29802	0.001299
Down	KCTD12	58	0.01106	6182096	0.276924	0
Down	LRRC47	57	0.010757	6845830	0.290119	0
Down	GPRASP1	55	0.013829	3218786	0.292587	0.014141
Down	KIF1A	55	0.013129	5897858	0.295971	0
Down	SLC18A1	55	0.015629	9692346	0.251806	0
Down	RAB3A	54	0.012852	3656924	0.29541	0.015837
Down	CADPS	54	0.012341	3396630	0.291942	0.001508
Down	EPOR	52	0.010684	5143738	0.272872	0
Down	PNMA2	52	0.010457	9247944	0.270725	0
Down	HP	51	0.009829	3675352	0.302064	0.007059
Down	LDLRAD4	51	0.013051	3950394	0.282703	0.001569
Down	MAPK11	50	0.011271	3184788	0.310948	0.005319
Down	INA	50	0.011835	3108450	0.312029	0.004082
Down	PACSIN1	49	0.009781	5386162	0.28025	0
Down	DTNB	49	0.012033	3055320	0.292814	0.0037
Down	DCX	48	0.01334	3903000	0.307447	0.001932
Down	DLG2	47	0.010711	7623202	0.271099	0
Down	MAST1	47	0.010432	4332122	0.294638	0.00555
Down	ASGR2	47	0.009164	5969666	0.259314	0.006061
Down	SNAP25	46	0.012157	3743182	0.29957	0.020085
Down	F2	46	0.00927	1858036	0.271488	0.014799
Down	DTX3	45	0.010905	4581310	0.244959	0
Down	RUNDC3A	45	0.009226	3251682	0.27362	0
Down	ISYNA1	44	0.00897	7504244	0.280933	0
Down	KIF5C	42	0.00764	4861700	0.283793	0

Down	CHGB	42	0.007489	4169980	0.2839	0
Down	PPFIBP1	41	0.006845	4747722	0.294098	0
Down	POTEE	40	0.00868	5686572	0.271252	0
Down	FGG	38	0.007095	1603386	0.283884	0.003175
Down	CAND2	38	0.010368	3187512	0.262983	0
Down	GRIA2	37	0.008198	7098760	0.256178	0.010511
Down	SALL2	36	0.007154	2810564	0.257348	0
Down	GPM6A	36	0.009292	4870712	0.272143	0
Down	BEX2	36	0.006106	1890772	0.271168	0.004762
Down	ECM1	36	0.008908	5034202	0.277402	0
Down	SLC6A15	36	0.007485	5226242	0.246395	0
Down	BEX3	35	0.005084	2987926	0.262839	0
Down	CELSR3	35	0.007773	2065118	0.272129	0.001783
Down	KCNS3	35	0.009833	3894790	0.248103	0.001681
Down	RAB3B	34	0.006275	1775830	0.266811	0.024955
Down	SPTB	34	0.007337	2591972	0.280235	0.005348
Down	KCNH2	34	0.005956	3482068	0.286805	0
Down	AHSG	34	0.006575	2648590	0.296021	0.01426
Down	MYL6B	34	0.004001	2506244	0.278907	0
Down	ANK1	33	0.006769	2076124	0.272018	0.005682
Down	PITX2	33	0.006003	3881170	0.275226	0
Down	NPDC1	33	0.006904	4313480	0.249541	0
Down	MC1R	33	0.007929	1691372	0.275972	0.001894
Down	WNT4	32	0.008121	6219598	0.272901	0
Down	PTPRN2	32	0.007052	1956882	0.288508	0.016092
Down	CDK14	31	0.005023	3253754	0.276288	0
Down	CCDC151	30	0.004898	3115670	0.253384	0
Down	CPE	30	0.00769	3419552	0.266529	0
Down	CTNND2	29	0.005029	2210800	0.271349	0
Down	DUSP26	28	0.005965	1633144	0.269828	0
Down	ABCA3	28	0.006746	7983044	0.219592	0
Down	CNGA3	28	0.007042	2826170	0.24062	0
Down	ASB4	27	0.004756	3877736	0.259848	0

Down	TRO	27	0.004787	1130718	0.26976	0
Down	RFX6	27	0.006321	1022480	0.275727	0.005698
Down	NAT14	27	0.006699	4579710	0.249776	0
Down	GRIA3	26	0.005092	1627720	0.245459	0.021538
Down	SPTBN4	26	0.007255	1329004	0.283429	0.012308
Down	NLRP1	26	0.004945	4162560	0.256439	0
Down	MPPED1	26	0.004919	1745920	0.254175	0
Down	HOXA10	26	0.004041	2525396	0.26118	0
Down	RDH12	26	0.006691	3548314	0.248196	0
Down	ADGRV1	26	0.007026	2379056	0.259593	0
Down	SMOC1	26	0.004639	3373564	0.260641	0
Down	F7	25	0.003953	1007924	0.288492	0.023715
Down	APC2	25	0.004295	2664566	0.257824	0
Down	FOXA2	25	0.005179	790178	0.255906	0.027668
Down	QPCT	25	0.004284	3054088	0.257862	0
Down	CACNA1C	24	0.004509	2788798	0.280859	0
Down	RCAN2	24	0.004391	2105240	0.242259	0
Down	CCDC74B	24	0.006323	2665894	0.247466	0
Down	TUSC3	24	0.006652	3323652	0.27078	0
Down	PAM	23	0.005616	4164992	0.232804	0
Down	ASGR1	23	0.005671	3227068	0.276332	0.023715
Down	APOH	22	0.002609	1681762	0.265022	0
Down	NEUROD1	22	0.003355	1777730	0.25481	0
Down	PROC	22	0.003569	1045992	0.251675	0.042105
Down	SCGN	22	0.0044	4260562	0.240161	0
Down	HEYL	22	0.005356	2219666	0.276	0
Down	ARFGEF3	22	0.003868	2168556	0.278043	0
Down	A1BG	22	0.004881	2399462	0.256737	0
Down	TSPYL4	22	0.003994	853630	0.275656	0.008658
Down	SERPINF2	21	0.002977	1759450	0.236115	0
Down	ARVCF	21	0.004141	2216118	0.258013	0
Down	F5	21	0.002292	1593624	0.254725	0.017544
Down	SYT17	21	0.006058	1242820	0.290104	0

Down	ERICH5	21	0.003116	2181290	0.232355	0
Down	C16orf45	21	0.00529	2494406	0.24174	0
Down	KLHL29	21	0.00455	2257966	0.269966	0
Down	OXTR	21	0.004043	814612	0.2514	0
Down	KCNB1	20	0.006113	911192	0.27797	0.013072
Down	WNK4	20	0.003939	2572260	0.266181	0.005263
Down	CASR	20	0.003328	1755122	0.252527	0
Down	TCEAL2	20	0.003172	1772030	0.272901	0
Down	TTC25	20	0.003608	749938	0.270863	0.005263
Down	P3H3	20	0.004776	1993538	0.258453	0
Down	FGF12	19	0.003527	844020	0.276707	0.011696
Down	TEKT2	19	0.0046	1768450	0.254065	0
Down	DNALI1	19	0.003156	1128570	0.266087	0
Down	SCRN1	19	0.003063	923998	0.250307	0
Down	MANEAL	19	0.003709	1760250	0.201277	0
Down	RIMS2	18	0.002859	743202	0.261103	0.039216
Down	BEX1	18	0.002175	1062514	0.246923	0
Down	HRG	18	0.003121	1205902	0.230294	0
Down	NAV2	18	0.003064	1108740	0.26158	0
Down	AMBP	17	0.002967	712112	0.283732	0.038095
Down	TAC1	17	0.002737	1518818	0.244937	0
Down	ADRA1B	17	0.003063	643770	0.280279	0.009524
Down	KCNJ6	17	0.003039	1142350	0.228221	0
Down	DNAJC12	17	0.003883	910444	0.261735	0.007353
Down	NACAD	17	0.002	1056536	0.254761	0
Down	MTSS1	16	0.001919	1309340	0.255302	0
Down	CALCR	16	0.003711	551518	0.266355	0.008333
Down	CLDN1	16	0.00248	1233640	0.23869	0.010989
Down	JAKMIP2	16	0.001133	907522	0.24344	0
Down	FMN2	16	0.00369	3336364	0.24247	0
Down	ZMAT4	16	0.003263	1894480	0.260782	0
Down	CGNL1	16	0.002796	887190	0.27403	0
Down	ACSL1	16	0.003705	1730574	0.261852	0

Down	RGS4	15	0.002719	952772	0.2462	0
Down	PELI3	15	0.003039	1329108	0.257762	0
Down	SRCIN1	15	0.001846	1068822	0.283338	0.028571
Down	ECE2	15	0.003548	2105654	0.242171	0
Down	SHC2	14	0.002782	1375182	0.267215	0
Down	CDC42EP3	14	0.001155	623666	0.257824	0
Down	SYT4	14	0.001891	362224	0.261387	0.030303
Down	MAT1A	14	0.002752	1597958	0.238324	0
Down	AP3B2	14	0.002329	849250	0.258151	0
Down	RCAN3	14	0.003261	615194	0.289059	0
Down	BTG3	14	0.003132	1176242	0.233225	0
Down	NRCAM	14	0.001971	819068	0.247697	0
Down	ST8SIA3	14	0.002377	743666	0.24153	0
Down	FAM171B	14	0.002464	1102938	0.235653	0
Down	OPRK1	13	0.001838	516502	0.247848	0.012821
Down	PTPRT	13	0.002143	562478	0.259975	0
Down	NDRG4	13	0.002908	1836170	0.247906	0
Down	ZNF618	13	0.001415	923972	0.269773	0
Down	RNF183	13	0.001924	1045818	0.253481	0
Down	HOPX	13	0.002829	936234	0.247489	0
Down	ATP1B2	13	0.002471	1886836	0.236759	0
Down	RASD1	12	0.00104	644012	0.246728	0
Down	CLIP3	12	0.002088	864382	0.230194	0
Down	COLEC11	12	0.00227	1565416	0.228093	0
Down	CPLX2	12	0.002052	411836	0.269993	0.015152
Down	CHGA	12	0.001764	584984	0.248406	0
Down	SSTR2	11	0.001988	923516	0.261671	0
Down	KCNK3	11	0.001145	979168	0.2472	0
Down	FGF13	11	0.001681	420024	0.279496	0.027778
Down	CACNA1H	11	0.002274	931046	0.261813	0.018182
Down	SNTG1	11	0.001484	278182	0.246992	0.018182
Down	LONRF2	11	0.003088	970504	0.222619	0
Down	TPH1	11	0.001535	595914	0.27146	0.018182

Down	SEZ6L2	11	0.003572	1041366	0.262488	0
Down	KLHL1	11	0.001665	662204	0.24851	0.018182
Down	FBXL16	11	7.58E-04	367982	0.247188	0
Down	SCN3A	11	0.001089	702818	0.245243	0
Down	INSM1	10	0.001262	392624	0.252527	0
Down	KIRREL2	10	0.001195	242394	0.246017	0
Down	PRRT2	10	0.002441	323082	0.238432	0
Down	CELF3	10	0.001058	265010	0.247454	0
Down	PCSK1	10	0.002576	924116	0.2237	0
Down	NXF5	10	9.09E-04	772210	0.251818	0
Down	MBD3L2	10	9.87E-04	614694	0.246258	0
Down	NPM2	9	8.82E-04	584884	0.231928	0
Down	ABCC8	9	0.002071	799078	0.253603	0
Down	MYT1	9	4.98E-04	285914	0.265367	0
Down	GLIS3	9	2.53E-04	156006	0.232672	0
Down	OGDHL	9	6.95E-04	301014	0.246613	0
Down	EFR3B	9	5.08E-04	305838	0.208379	0
Down	RTBDN	9	0.001944	703420	0.206045	0
Down	SLC8A2	9	0.001315	1087398	0.240663	0
Down	SCG5	9	0.001515	679398	0.231017	0
Down	SCG3	9	8.99E-04	479130	0.245141	0
Down	ZIM2	9	8.42E-04	309160	0.239337	0
Down	ARHGEF40	9	0.002138	518274	0.266074	0
Down	TNFRSF11B	8	0.001684	505802	0.248639	0
Down	RAB3C	8	4.89E-04	220910	0.238346	0.035714
Down	NCKAP5	8	5.69E-04	321532	0.236907	0
Down	ATCAY	8	8.28E-04	407674	0.25629	0
Down	CALB1	8	8.39E-04	291652	0.228181	0
Down	BSN	8	6.64E-04	127018	0.249835	0.071429
Down	KIRREL3	8	0.001558	1272598	0.225827	0
Down	PCSK1N	8	0.0021	199746	0.202168	0
Down	DEPPI	8	8.65E-04	574450	0.216806	0
Down	GAMT	8	9.46E-04	526730	0.230736	0

Down	UNC80	8	0.00129	739434	0.240652	0
Down	CDH6	8	0.001887	931890	0.217286	0
Down	SERPINA10	8	8.70E-04	340962	0.235067	0
Down	DACH2	8	0.001925	536558	0.199774	0
Down	GRIN2C	7	8.12E-04	490510	0.194072	0
Down	RGS11	7	6.44E-04	323234	0.241905	0
Down	PNMA8A	7	9.71E-04	473862	0.251496	0
Down	SOBP	7	6.29E-04	207670	0.264071	0
Down	JPH3	7	0.001059	499176	0.250461	0
Down	RAB26	7	0.001229	470478	0.250083	0
Down	CCDC24	7	4.11E-04	160904	0.223022	0
Down	SV2C	7	0.001906	453466	0.200788	0
Down	FBLL1	7	6.42E-04	321868	0.252418	0
Down	NNMT	7	0.001739	684950	0.251364	0
Down	REEP2	7	0.001227	610582	0.203903	0
Down	LZTS1	6	1.37E-04	87676	0.251126	0
Down	STMN3	6	8.13E-04	397800	0.221326	0
Down	CALY	6	4.83E-04	203224	0.222582	0
Down	CRYBA2	6	0.001167	450920	0.203348	0
Down	BEX5	6	4.01E-04	212922	0.204699	0
Down	ITIH1	6	9.01E-04	156324	0.262319	0.066667
Down	PCSK2	6	4.57E-04	103040	0.19701	0
Down	SORCS2	6	9.45E-04	656558	0.234132	0
Down	GUSBP1	6	1.76E-04	78946	0.255142	0
Down	KLHL35	6	1.77E-04	61504	0.207815	0
Down	DIPK1B	6	7.34E-04	388716	0.221382	0
Down	LRRC56	6	4.67E-04	264228	0.228536	0
Down	MAP6	6	8.77E-04	486404	0.213108	0
Down	IGFALS	5	4.00E-04	231118	0.212637	0
Down	USP27X	5	4.77E-04	193846	0.208215	0
Down	KIF12	5	4.66E-04	288194	0.232488	0
Down	SVOP	5	8.06E-04	277988	0.207563	0
Down	HPN	5	3.70E-04	179372	0.26444	0.1

Down	FTCD	5	0.001159	336186	0.22218	0
Down	VSTM2L	5	8.38E-04	415274	0.246958	0
Down	FAM169A	5	4.39E-04	236728	0.237427	0
Down	MNX1	5	2.90E-04	234742	0.239597	0
Down	EPHA10	5	1.72E-04	71850	0.212663	0
Down	DACT2	5	5.23E-04	287378	0.228063	0
Down	BAIAP3	4	5.89E-05	26110	0.246797	0
Down	AMER3	4	4.86E-04	160924	0.220883	0
Down	SYT13	4	3.18E-05	6862	0.215045	0
Down	C8A	4	1	12	1	0
Down	TCEAL5	4	4.92E-04	102328	0.216134	0
Down	STXBP5L	4	4.66E-04	203498	0.249764	0
Down	HPR	4	7.56E-04	232714	0.216646	0
Down	ATP8A2	4	4.47E-04	136424	0.215816	0
Down	LHFPL4	4	4.11E-04	186902	0.21685	0
Down	C21orf58	4	1.00E-04	88064	0.227056	0
Down	ANKRD36B	4	3.94E-04	187876	0.228595	0
Down	MICU3	4	5.11E-04	168570	0.225779	0
Down	MT3	3	2.78E-04	33880	0.247767	0
Down	RIMBP2	3	4.12E-04	195876	0.241563	0
Down	ST6GALNAC5	3	1.57E-05	8366	0.192401	0
Down	CCDC181	3	1.04E-05	4434	0.238937	0
Down	PDZRN4	3	1.92E-04	38884	0.263441	0
Down	EBF4	3	4.32E-04	167168	0.249623	0
Down	LY6H	3	4.09E-04	173608	0.224383	0
Down	NMNAT2	3	4.45E-04	270394	0.26369	0
Down	ZFR2	3	5.58E-05	29480	0.23129	0
Down	KRT23	3	5.92E-05	21168	0.230645	0
Down	B3GAT1	3	0	0	1	0
Down	EGR4	3	7.55E-04	133914	0.202795	0
Down	FAM135B	2	5.99E-06	2358	0.225789	0
Down	SH3TC1	2	1.76E-04	88462	0.244982	0
Down	IGFN1	2	3.78E-04	69778	0.201277	0

Down	ARMH1	2	3.69E-05	26682	0.216841	0
Down	ADAMTS9	2	3.78E-04	104194	0.219383	0
Down	CELF4	2	3.78E-04	127008	0.247917	0
Down	TBXAS1	2	1.57E-06	2528	0.22116	0
Down	ASPHD1	2	1.79E-05	5712	0.206205	0
Down	ZFHX2	2	1.38E-05	33604	0.253191	0
Down	RAB36	2	9.43E-06	4142	0.217482	0
Down	DSCAM	2	5.05E-06	2548	0.197252	0
Down	ADGRG4	2	5.82E-06	2854	0.206503	0
Down	ADAMTSL2	2	1.14E-05	7290	0.208158	0
Down	RBFOX1	2	3.01E-05	15668	0.223776	0
Down	LRFN2	2	2.79E-05	40318	0.250473	0
Down	ST18	2	1.45E-05	6812	0.210057	0
Down	KCNMB2	2	1.63E-05	5282	0.248138	0
Down	SRRM3	1	0	0	0.216257	0
Down	RGL3	1	0	0	0.226097	0
Down	ABHD1	1	0	0	0.153844	0
Down	FAXDC2	1	0	0	0.219328	0
Down	ISLR2	1	0	0	0.223154	0
Down	PCNX2	1	0	0	0.244835	0
Down	CNTNAP5	1	0	0	1	0
Down	SLC7A14	1	0	0	0.238894	0
Down	HRASLS	1	0	0	0.247894	0
Down	FXYD2	1	0	0	0.19948	0
Down	TCEAL6	1	0	0	0.199113	0
Down	C2CD4C	1	0	0	0.178314	0
Down	TCEAL3	1	0	0	0.197878	0

Table 8 miRNA - target gene interaction table

Regulation	Target Genes	Degree	MicroRNA	Regulation	Target Genes	Degree	MicroRNA
Up	VAV3	164	hsa-mir-1250-3p	Down	SVOP	107	hsa-mir-4776-3p
Up	SULT1B1	131	hsa-mir-4764-5p	Down	KCNJ6	90	hsa-mir-7850-5p
Up	MACC1	97	hsa-mir-3653-5p	Down	SORCS2	88	hsa-mir-520e
Up	E2F2	78	hsa-mir-6742-3p	Down	HEYL	83	hsa-mir-892c-3p
Up	SLC28A1	75	hsa-mir-7851-3p	Down	SMOC1	80	hsa-mir-1260b
Up	SPIB	67	hsa-mir-5698	Down	CPE	80	hsa-mir-7515
Up	PIGR	66	hsa-mir-4649-5p	Down	HOXA10	75	hsa-mir-4666b
Up	SLC6A4	64	hsa-mir-6890-3p	Down	SRCIN1	73	hsa-mir-3180-5p
Up	CES2	64	hsa-mir-660-3p	Down	CELSR3	71	hsa-mir-548ac
Up	CMBL	60	hsa-mir-3170	Down	LONRF2	70	hsa-mir-4326
Up	CPS1	57	hsa-mir-548l	Down	MANEA L	68	hsa-mir-4757-5p
Up	ENTPD7	55	hsa-mir-6806-3p	Down	KCNB1	67	hsa-mir-6871-5p
Up	PHLPP2	55	hsa-mir-6838-5p	Down	NAV2	64	hsa-mir-3120-5p
Up	SGK1	55	hsa-mir-548g-5p	Down	LRRC47	60	hsa-mir-1273e
Up	SLC35G1	55	hsa-mir-4777-5p	Down	RAB3B	58	hsa-mir-410-3p
Up	G6PC	53	hsa-mir-4311	Down	UNC13A	58	hsa-mir-147a
Up	IYD	51	hsa-mir-4755-3p	Down	PACSIN1	53	hsa-mir-4459
Up	MFSD2A	48	hsa-mir-7107-5p	Down	RAB36	52	hsa-mir-4722-5p
Up	C6orf132	48	hsa-mir-2392	Down	PNMA2	52	hsa-mir-3135b
Up	FZD5	47	hsa-mir-4693-3p	Down	RUNX1T 1	51	hsa-mir-3688-3p
Up	FUT2	46	hsa-mir-6780a-5p	Down	PRRT2	50	hsa-mir-4669
Up	SLC5A12	45	hsa-mir-7110-3p	Down	BTG3	50	hsa-mir-3163

Up	VDR	43	hsa-mir-2861	Down	CDH6	48	hsa-mir-216a-3p
Up	LDHA	43	hsa-mir-3913-3p	Down	MARCH4	48	hsa-mir-6833-3p
Up	CYBRD1	42	hsa-mir-4698	Down	KCNK3	46	hsa-mir-3656
Up	ANKRD9	42	hsa-mir-4430	Down	ANK1	46	hsa-mir-5698
Up	PTK6	39	hsa-mir-6849-3p	Down	SLC7A14	46	hsa-mir-5701
Up	SLC2A5	38	hsa-mir-4790-3p	Down	F2	46	hsa-mir-378g
Up	APOC3	37	hsa-mir-6895-3p	Down	PLCXD3	44	hsa-mir-5088-3p
Up	RNF125	36	hsa-mir-759	Down	MAT1A	43	hsa-mir-4510
Up	GALNT6	36	hsa-mir-6504-3p	Down	ZBTB16	43	hsa-mir-1976
Up	CORO2A	35	hsa-mir-3120-5p	Down	ATCAY	42	hsa-mir-588
Up	SCIN	35	hsa-mir-5582-3p	Down	CACNA1C	42	hsa-mir-6857-5p
Up	ESPL1	34	hsa-mir-2467-5p	Down	STMN3	42	hsa-mir-663a
Up	AKR1B10	34	hsa-mir-4676-3p	Down	APOH	42	hsa-mir-520g-3p
Up	GALNT7	34	hsa-mir-4801	Down	TSPYL4	40	hsa-mir-4311
Up	SLC1A1	33	hsa-mir-1255b-5p	Down	ASGR2	40	hsa-mir-1910-3p
Up	SYK	33	hsa-mir-6852-5p	Down	ZMAT4	39	hsa-mir-7977
Up	PLS1	31	hsa-mir-1178-3p	Down	RAB3C	38	hsa-mir-4731-3p
Up	MUC17	30	hsa-mir-6881-3p	Down	SSTR2	35	hsa-mir-4295
Up	SLC23A1	30	hsa-mir-1185-5p	Down	CDK14	35	hsa-mir-6783-5p
Up	EMB	29	hsa-mir-5089-5p	Down	CBX1	35	hsa-mir-2052
Up	TM4SF20	29	hsa-mir-371b-5p	Down	WNT4	35	hsa-mir-1238-3p
Up	ABCG2	28	hsa-mir-7158-3p	Down	KCTD12	35	hsa-mir-3179
Up	ALPI	28	hsa-mir-6795-5p	Down	FBXL16	34	hsa-mir-7159-5p
Up	TRPM6	27	hsa-mir-5011-5p	Down	CLDN1	33	hsa-mir-5100

Up	OVOL1	26	hsa-mir-3190-3p	Down	PDE4DIP	33	hsa-mir-4434
Up	PCK1	25	hsa-mir-4482-3p	Down	TMEM145	32	hsa-mir-7160-5p
Up	ATP1A1	24	hsa-mir-3124-3p	Down	PTPRT	32	hsa-mir-6747-3p
Up	GLRX	24	hsa-mir-219a-1-3p	Down	RCAN2	31	hsa-mir-6511b-3p
Up	BTNL3	24	hsa-mir-6820-3p	Down	DCX	31	hsa-mir-4419a
Up	EZR	23	hsa-mir-3677-5p	Down	SOBP	31	hsa-mir-599
Up	SEMA6A	23	hsa-mir-147a	Down	NMNAT2	31	hsa-mir-6795-5p
Up	RETSAT	23	hsa-mir-6507-3p	Down	RCAN3	30	hsa-mir-5583-3p
Up	GALM	23	hsa-mir-1305	Down	C8A	29	hsa-mir-3127-3p
Up	STYK1	23	hsa-mir-2116-5p	Down	C16orf45	26	hsa-mir-3666
Up	BMP7	22	hsa-mir-4700-5p	Down	PCSK2	25	hsa-mir-6754-5p
Up	CDCA7	22	hsa-mir-4720-3p	Down	RTBDN	24	hsa-mir-5787
Up	MYB	22	hsa-mir-200a-3p	Down	CNTNAP5	24	hsa-mir-4789-3p
Up	MOCOS	22	hsa-mir-6879-3p	Down	SNAP25	24	hsa-mir-3157-5p
Up	TMEM37	22	hsa-mir-5480-3p	Down	ADAMTS9	24	hsa-mir-5688
Up	DGAT1	21	hsa-mir-548q	Down	TTR	23	hsa-mir-590-3p
Up	EDN2	21	hsa-mir-1281	Down	AP3B2	23	hsa-mir-4701-5p
Up	ACY1	21	hsa-mir-6764-5p	Down	PCSK1	23	hsa-mir-520c-5p
Up	KBTBD11	21	hsa-mir-6727-3p	Down	SALL2	23	hsa-mir-6722-3p
Up	C1orf115	20	hsa-mir-4520-3p	Down	MAPK8IP2	22	hsa-mir-4728-3p
Up	CD36	19	hsa-mir-6872-3p	Down	C6orf141	22	hsa-mir-6884-5p
Up	MAF	19	hsa-mir-6514-5p	Down	HS6ST3	22	hsa-mir-6767-3p

Up	SLC15A1	19	hsa-mir-6893-5p	Down	ST8SIA3	21	hsa-mir-6847-5p
Up	TRIM36	18	hsa-mir-4699-3p	Down	FGG	21	hsa-mir-769-5p
Up	CD68	18	hsa-mir-6833-3p	Down	GDAP1L1	20	hsa-mir-6864-3p
Up	TNFRSF11A	17	hsa-mir-548f-5p	Down	BSN	20	hsa-mir-3944-5p
Up	MGAM	17	hsa-mir-2114-5p	Down	PTPRN2	20	hsa-mir-6809-3p
Up	SLC9A3	17	hsa-mir-2277-3p	Down	A1BG	20	hsa-mir-6736-5p
Up	P2RY2	16	hsa-mir-4433b-3p	Down	NKX2-2	20	hsa-mir-6766-5p
Up	HHLA2	16	hsa-mir-520d-5p	Down	KIF5C	20	hsa-mir-610
Up	TMPRSS4	16	hsa-mir-1299	Down	ISLR2	19	hsa-mir-3689d
Up	CDKN2B	15	hsa-mir-4726-5p	Down	GLIS3	19	hsa-mir-3609
Up	APOA1	15	hsa-mir-3659	Down	PPFIBP1	19	hsa-mir-548x-5p
Up	B3GNT7	15	hsa-mir-5588-3p	Down	REEP2	19	hsa-mir-6734-3p
Up	EDN3	15	hsa-mir-3606-3p	Down	ITGBL1	18	hsa-mir-664b-3p
Up	ZG16	15	hsa-mir-4768-5p	Down	STXBP5L	17	hsa-mir-6749-3p
Up	SLC23A3	14	hsa-mir-5001-3p	Down	SV2C	17	hsa-mir-522-5p
Up	CIDEC	14	hsa-mir-4717-3p	Down	LY6H	17	hsa-mir-4730
Up	CTSE	14	hsa-mir-297	Down	NEUROD1	17	hsa-mir-299-5p
Up	TLR3	14	hsa-mir-548e-5p	Down	APC2	16	hsa-mir-6785-3p
Up	ATP1A3	14	hsa-mir-362-3p	Down	CRMP1	16	hsa-mir-151b
Up	GPD1	13	hsa-mir-5088-3p	Down	ASGR1	16	hsa-mir-4668-3p
Up	DAPK2	13	hsa-mir-548u	Down	NAT14	16	hsa-mir-6887-3p
Up	TMEM45B	13	hsa-mir-5193	Down	MPPED1	15	hsa-mir-6852-5p
Up	VNN1	13	hsa-mir-4294	Down	HOPX	15	hsa-mir-516b-3p

Up	TMEM220	13	hsa-mir-3646	Down	RASD1	15	hsa-mir-4488
Up	PMP22	12	hsa-mir-4769-5p	Down	SYT4	15	hsa-mir-548m
Up	SLC7A7	12	hsa-mir-5701	Down	MTSS1	15	hsa-mir-5193
Up	C15orf48	11	hsa-mir-3692-3p	Down	MNX1	15	hsa-mir-6720-5p
Up	ST6GALN AC1	11	hsa-mir-3155a	Down	ZNF618	15	hsa-mir-3926
Up	SLC1A7	11	hsa-mir-4660	Down	SCRN1	15	hsa-mir-4426
Up	ASPA	10	hsa-mir-4713-5p	Down	RBFOX1	15	hsa-mir-1305
Up	MALL	10	hsa-mir-3178	Down	FOXA1	15	hsa-mir-4715-3p
Up	PRR15	10	hsa-mir-6792-3p	Down	PPP2R2B	14	hsa-mir-6804-5p
Up	PAQR8	10	hsa-mir-3679-3p	Down	EPOR	14	hsa-mir-5580-3p
Up	AADAC	10	hsa-mir-5585-3p	Down	C21orf58	14	hsa-mir-664a-5p
Up	APOB	10	hsa-mir-1911-5p	Down	PDZRN4	13	hsa-mir-4719
Up	BCL2L14	10	hsa-mir-8069	Down	SERPINF 2	13	hsa-mir-4685-3p
Up	PLCB3	9	hsa-mir-4709-3p	Down	SYT17	12	hsa-mir-520h
Up	CNDP2	9	hsa-mir-580-3p	Down	JAKMIP2	12	hsa-mir-6818-5p
Up	TUBA1C	9	hsa-mir-221-3p	Down	SNTG1	12	hsa-mir-23c
Up	LAMC2	9	hsa-mir-29b-3p	Down	JPH3	11	hsa-mir-1470
Up	HSD3B1	9	hsa-mir-5696	Down	FTCD	11	hsa-mir-6727-3p
Up	CFTR	9	hsa-mir-433-3p	Down	UNC80	11	hsa-mir-888-5p
Up	FUT6	9	hsa-mir-526b-5p	Down	NNMT	11	hsa-mir-6500-3p
Up	SECTM1	9	hsa-mir-6778-3p	Down	HIPK2	11	hsa-mir-296-3p
Up	TMPRSS15	9	hsa-mir-3920	Down	FAM169 A	10	hsa-mir-3133
Up	TMEM92	8	hsa-mir-2116-3p	Down	HPR	10	hsa-mir-5699-3p

Up	KCNJ13	8	hsa-mir-4668-3p	Down	ZFHX2	10	hsa-mir-586
Up	CDX1	8	hsa-mir-3928-5p	Down	PITX2	10	hsa-mir-369-3p
Up	CASP1	8	hsa-mir-6515-3p	Down	GNAZ	10	hsa-mir-4469
Up	SLC28A2	8	hsa-mir-208a-5p	Down	CALCR	10	hsa-mir-4760-3p
Up	FAM3D	8	hsa-mir-6833-3p	Down	RET	10	hsa-mir-15a-5p
Up	ANPEP	7	hsa-mir-155-5p	Down	ACSL1	10	hsa-mir-205-5p
Up	CEBPA	7	hsa-mir-1226-3p	Down	KCNH6	9	hsa-mir-4722-3p
Up	SUSD2	7	hsa-mir-3934-3p	Down	RIMBP2	9	hsa-mir-514b-5p
Up	MAOB	7	hsa-mir-4647	Down	CCDC74 B	9	hsa-mir-380-3p
Up	ABCG5	7	hsa-mir-3191-5p	Down	DNALI1	9	hsa-mir-548t-3p
Up	SLC6A20	7	hsa-mir-1228-3p	Down	NCKAP5	9	hsa-mir-3925-3p
Up	ITGB4	6	hsa-mir-16-5p	Down	KIF1A	9	hsa-mir-423-3p
Up	MYO5B	6	hsa-mir-103a-3p	Down	CKB	9	hsa-mir-346
Up	HPGD	6	hsa-mir-4289	Down	RGS11	8	hsa-mir-935
Up	EFNA2	6	hsa-mir-548n	Down	EBF4	8	hsa-mir-4753-3p
Up	TUBAL3	6	hsa-mir-4301	Down	PELI3	8	hsa-mir-6778-3p
Up	XPNPEP2	6	hsa-mir-4502	Down	FXVD2	8	hsa-mir-4999-5p
Up	POU2AF1	5	hsa-mir-15b-5p	Down	QPCT	7	hsa-mir-6851-5p
Up	CA13	5	hsa-mir-9-5p	Down	NDRG4	7	hsa-mir-3941
Up	ABCB1	5	hsa-mir-296-5p	Down	CGNL1	7	hsa-mir-192-5p
Up	HEPH	5	hsa-mir-449b-3p	Down	CADPS	6	hsa-mir-5096
Up	FABP2	5	hsa-mir-520f-5p	Down	GPM6A	6	hsa-mir-548e-5p
Up	OAT	4	hsa-mir-99b-5p	Down	SCN3A	6	hsa-let-7c-3p
Up	NR1I2	4	hsa-let-7a-5p	Down	RIMS2	6	hsa-mir-376a-3p

Up	KAZALD1	4	hsa-mir-6887-3p	Down	TMEM17 9	5	hsa-mir-7109-3p
Up	FERMT1	4	hsa-mir-125a-5p	Down	SEPT5	5	hsa-mir-1825
Up	FAT1	4	hsa-mir-222-3p	Down	CPLX2	5	hsa-mir-3622a-3p
Up	PRAP1	4	hsa-mir-23b-3p	Down	ASB4	5	hsa-mir-4420
Up	NAGS	4	hsa-mir-7106-3p	Down	SYT13	5	hsa-mir-6798-5p
Up	MME	3	hsa-mir-1-1	Down	RGS4	5	hsa-mir-6867-5p
Up	TST	3	hsa-let-7d-5p	Down	ZFR2	5	hsa-mir-1911-3p
Up	OLFM4	3	hsa-let-7c-5p	Down	INA	5	hsa-mir-101-3p
Up	LAMB3	3	hsa-mir-218-5p	Down	CLSTN2	5	hsa-mir-3180-5p
Up	PCK2	3	hsa-mir-24-3p	Down	ABCA3	5	hsa-mir-20a-5p
Up	YIF1B	3	hsa-mir-103a-3p	Down	PHLDB2	5	hsa-mir-16-5p
Up	NR0B2	3	hsa-mir-141-3p	Down	BAIAP3	4	hsa-mir-4462
Up	LRP4	3	hsa-mir-197-3p	Down	FAM135 B	4	hsa-mir-6823-3p
Up	IL32	3	hsa-mir-205-5p	Down	FMN2	4	hsa-mir-374c-3p
Up	SLC26A3	3	hsa-mir-7-5p	Down	ST6GAL NAC5	4	hsa-mir-3688-3p
Up	TFF1	3	hsa-mir-504-5p	Down	USP27X	4	hsa-mir-302c-5p
Up	CDS1	3	hsa-mir-324-5p	Down	F5	4	hsa-mir-5585-5p
Up	ST14	3	hsa-mir-27b-3p	Down	TAC1	4	hsa-mir-206
Up	ACSL5	3	hsa-mir-128-3p	Down	KCNH2	4	hsa-mir-133b
Up	MUC13	3	hsa-mir-132-3p	Down	PAM	4	hsa-mir-125b-5p
Up	SOAT2	3	hsa-mir-6086	Down	KCNS3	4	hsa-mir-215-5p
Up	SPINK1	2	hsa-mir-1-3p	Down	FAM171 B	4	hsa-mir-99a-5p

Up	S100A14	2	hsa-mir-193b-3p	Down	TUSC3	4	hsa-mir-1229-3p
Up	SULT2A1	2	hsa-mir-24-3p	Down	EFR3B	4	hsa-mir-33a-3p
Up	DHRS11	2	hsa-mir-296-3p	Down	FGF12	4	hsa-mir-590-5p
Up	HSD17B2	2	hsa-mir-124-3p	Down	PPM1N	3	hsa-mir-1587
Up	KHK	2	hsa-mir-375	Down	CNGA3	3	hsa-mir-3611
Up	LAMA3	2	hsa-mir-181a-5p	Down	FOXA2	3	hsa-mir-1185-1-3p
Up	CEACAM6	2	hsa-mir-29a-3p	Down	CDC42EP3	3	hsa-mir-122-5p
Up	MGST1	2	hsa-mir-652-3p	Down	SLC35F3	3	hsa-mir-124-3p
Up	AKR1C3	2	hsa-mir-155-5p	Down	LHFPL4	3	hsa-mir-10a-5p
Up	HOXB9	2	hsa-mir-215-5p	Down	STX1A	3	hsa-mir-34a-5p
Up	MTTP	2	hsa-mir-30e-5p	Down	ST18	3	hsa-mir-451b
Up	C17orf78	2	hsa-mir-7-5p	Down	ANKRD36B	3	hsa-mir-615-3p
Up	HLA-DMB	2	hsa-mir-9-5p	Down	BEX1	3	hsa-mir-15b-5p
Up	GK	2	hsa-mir-10b-5p	Down	SLC6A15	3	hsa-mir-23a-3p
Up	CLDN23	2	hsa-mir-222-3p	Down	TNFRSF11B	3	hsa-mir-181a-5p
Up	ALDOB	2	hsa-mir-378a-3p	Down	MAPK11	3	hsa-let-7a-5p
Up	GDA	2	hsa-mir-492	Down	GPRASP1	2	hsa-mir-2681-5p
Up	ENPEP	2	hsa-mir-320a	Down	NRCAM	2	hsa-mir-708-5p
Up	PLEK2	2	hsa-mir-138-5p	Down	TBXAS1	2	hsa-mir-34b-3p
Up	SLC7A9	2	hsa-mir-142-3p	Down	RAB26	2	hsa-mir-421
Up	UGT2B17	2	hsa-mir-335-5p	Down	OGDHL	2	hsa-mir-130b-5p
Up	MPST	2	hsa-mir-191-5p	Down	SPTB	2	hsa-mir-331-3p

Up	PDZK1	2	hsa-mir-148b-3p	Down	MAST1	2	hsa-mir-148b-3p
Up	SLC3A1	2	hsa-mir-548e-5p	Down	DLG2	2	hsa-mir-335-5p
Up	PNLIPRP2	2	hsa-mir-148b-3p	Down	DUSP26	2	hsa-mir-544a
Up	KRT19	2	hsa-mir-193b-3p	Down	ABCC8	2	hsa-mir-136-5p
Up	LGALS3	2	hsa-mir-744-5p	Down	B3GAT1	2	hsa-mir-106b-5p
Up	GCG	2	hsa-mir-3611	Down	DACT2	2	hsa-mir-128-3p
Up	CYP2J2	1	hsa-let-7b-5p	Down	LZTS1	2	hsa-mir-135b-5p
Up	MAOA	1	hsa-mir-22-3p	Down	BEX2	2	hsa-mir-204-5p
Up	ACE2	1	hsa-mir-26b-5p	Down	GRIA2	2	hsa-mir-181b-5p
Up	BLNK	1	hsa-mir-26b-5p	Down	ISYNA1	2	hsa-mir-197-3p
Up	CYP4F8	1	hsa-mir-26b-5p	Down	ARHGEF40	2	hsa-mir-192-5p
Up	GSTA1	1	hsa-mir-26b-5p	Down	CASR	2	hsa-mir-31-5p
Up	MEP1A	1	hsa-mir-26b-5p	Down	VTN	2	hsa-mir-26b-5p
Up	OTC	1	hsa-mir-26b-5p	Down	SHC2	2	hsa-mir-26a-5p
Up	SI	1	hsa-mir-26b-5p	Down	TF	2	hsa-mir-19a-3p
Up	CDHR1	1	hsa-mir-93-5p	Down	ATP8A2	2	hsa-mir-30a-5p
Up	CYP2S1	1	hsa-mir-147a	Down	DTNB	2	hsa-let-7e-5p
Up	DEFA5	1	hsa-mir-7-5p	Down	ARNT2	2	hsa-mir-26b-5p
Up	CHST5	1	hsa-mir-218-5p	Down	RFX6	2	hsa-mir-30c-5p
Up	ACOT11	1	hsa-mir-124-3p	Down	OXTR	2	hsa-mir-1-1
Up	COL17A1	1	hsa-mir-124-3p	Down	GPRASP2	1	hsa-mir-744-5p
Up	HKDC1	1	hsa-mir-124-3p	Down	BAIAP2	1	hsa-mir-455-3p
Up	MSRA	1	hsa-mir-124-3p	Down	KLHL29	1	hsa-mir-127-5p

Up	NEU4	1	hsa-mir-124-3p	Down	CPT1C	1	hsa-mir-615-3p
Up	C2orf88	1	hsa-mir-125b-5p	Down	PTPRN	1	hsa-mir-18a-3p
Up	DEPDC7	1	hsa-mir-132-3p	Down	CDH22	1	hsa-mir-412-3p
Up	KCNQ1	1	hsa-mir-133a-3p	Down	MIR7-3HG	1	hsa-mir-335-5p
Up	ARL14	1	hsa-mir-186-5p	Down	VSTM2L	1	hsa-mir-335-5p
Up	FMO1	1	hsa-mir-320a	Down	SRRM3	1	hsa-mir-335-5p
Up	SLC52A3	1	hsa-mir-106b-5p	Down	SCG3	1	hsa-mir-335-5p
Up	MEP1B	1	hsa-mir-148b-3p	Down	RNF183	1	hsa-mir-335-5p
Up	KCNG1	1	hsa-mir-324-5p	Down	RIIAD1	1	hsa-mir-335-5p
Up	ACE	1	hsa-mir-335-5p	Down	NLRP1	1	hsa-mir-335-5p
Up	AGR3	1	hsa-mir-335-5p	Down	NINL	1	hsa-mir-335-5p
Up	AQP10	1	hsa-mir-335-5p	Down	KLHL35	1	hsa-mir-335-5p
Up	B3GNT3	1	hsa-mir-335-5p	Down	KLHL1	1	hsa-mir-335-5p
Up	CCL25	1	hsa-mir-335-5p	Down	ITIH1	1	hsa-mir-335-5p
Up	CDHR2	1	hsa-mir-335-5p	Down	GPBAR1	1	hsa-mir-335-5p
Up	CHRNA7	1	hsa-mir-335-5p	Down	CRYBA2	1	hsa-mir-335-5p
Up	CPO	1	hsa-mir-335-5p	Down	CLIP3	1	hsa-mir-335-5p
Up	FABP1	1	hsa-mir-335-5p	Down	CELF4	1	hsa-mir-335-5p
Up	FABP6	1	hsa-mir-335-5p	Down	BEX5	1	hsa-mir-335-5p
Up	FAM151A	1	hsa-mir-335-5p	Down	ATP1B2	1	hsa-mir-335-5p
Up	FAM3B	1	hsa-mir-335-5p	Down	CDHR3	1	hsa-mir-331-3p
Up	GATA5	1	hsa-mir-335-5p	Down	CHGB	1	hsa-mir-375
Up	GCNT3	1	hsa-mir-335-5p	Down	WNK4	1	hsa-mir-296-5p
Up	GUCA2B	1	hsa-mir-335-5p	Down	OPRK1	1	hsa-mir-106b-5p

Up	LRRC19	1	hsa-mir-335-5p	Down	DTX3	1	hsa-mir-320a
Up	MUC3A	1	hsa-mir-335-5p	Down	CAMK2B	1	hsa-mir-186-5p
Up	NPY	1	hsa-mir-335-5p	Down	OBSL1	1	hsa-mir-149-5p
Up	PRSS8	1	hsa-mir-335-5p	Down	KIRREL2	1	hsa-mir-124-3p
Up	PTPRH	1	hsa-mir-335-5p	Down	IGFN1	1	hsa-mir-124-3p
Up	SERINC2	1	hsa-mir-335-5p	Down	GRIA3	1	hsa-mir-124-3p
Up	SLC22A18	1	hsa-mir-335-5p	Down	ECE2	1	hsa-mir-124-3p
Up	SLC52A1	1	hsa-mir-335-5p	Down	KIRREL3	1	hsa-mir-218-5p
Up	SLC5A1	1	hsa-mir-335-5p	Down	TRO	1	hsa-mir-183-5p
Up	PEPD	1	hsa-mir-423-3p	Down	ADRA1B	1	hsa-mir-10b-5p
Up	ITPKA	1	hsa-mir-193b-3p	Down	CCDC151	1	hsa-mir-10b-5p
Up	LCT	1	hsa-mir-671-5p	Down	HPN	1	hsa-mir-197-3p
Up	PRODH	1	hsa-mir-23b-5p	Down	PCSK1N	1	hsa-mir-31-5p
Up	ISX	1	hsa-mir-3928-3p	Down	MYT1	1	hsa-mir-27a-3p
				Down	RAB3A	1	hsa-mir-26b-5p
				Down	POTEE	1	hsa-mir-26b-5p
				Down	GSTT2	1	hsa-mir-26b-5p
				Down	DNAJC12	1	hsa-mir-26b-5p
				Down	CAND2	1	hsa-let-7a-5p
				Down	TCEAL5	1	hsa-mir-2115-3p
				Down	TCEAL3	1	hsa-mir-2115-3p

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

Table 9 TF - target gene interaction table

Regulation	TF	Degree	Target Gene	Regulation	TF	Degree	Target Gene
Up	SOX2	158	CYBRD1	Down	SUZ12	186	TBXAS1
Up	HNF4A	152	MUC13	Down	SOX2	165	HS6ST3
Up	TP63	128	UGT1A6	Down	REST	156	RUNX1T1
Up	EGR1	119	ATP1A1	Down	EGR1	138	ATP1B2
Up	AR	114	YIF1B	Down	AR	125	RFX6
Up	MYC	113	MSRA	Down	STAT3	122	SVOP
Up	SPI1	113	GLRX	Down	NANOG	122	STMN3
Up	STAT3	106	ENPP3	Down	HNF4A	120	TF
Up	NANOG	103	APOBEC1	Down	MYC	112	MYT1
Up	POU5F1	95	RNF125	Down	TP63	110	TTR
Up	SUZ12	93	NPY	Down	TP53	109	NPM2
Up	RUNX1	91	TUBA1C	Down	MTF2	108	WNT4
Up	GATA2	88	GATA5	Down	POU5F1	107	CBX1
Up	TP53	78	OAT	Down	SMAD4	104	ATP8A2
Up	GATA1	78	VAV3	Down	SIN3B	96	CPLX2
Up	SMAD4	76	GGTLC1	Down	RUNX1	95	UNC13A
Up	MITF	76	PLB1	Down	TCF4	95	CDK14
Up	TCF4	74	PEPD	Down	MITF	94	RAB26
Up	FLI1	74	ACY3	Down	SPI1	89	WWOX
Up	KLF4	74	MALL	Down	GATA1	84	BSN
Up	REST	74	LGALS3	Down	RCOR3	81	VTN

Up	MTF2	68	MARVELD3	Down	FLI1	80	RUNDC3A
Up	PPARG	66	APOA1	Down	RUNX2	76	SYT4
Up	SOX9	60	LAMA3	Down	TET1	73	HEYL
Up	TRIM28	59	PRSS8	Down	SRY	73	ECE2
Up	TET1	57	CREB3L3	Down	TCF3	71	MAP6
Up	RUNX2	57	B3GNT7	Down	EZH2	71	FOXA1
Up	SETDB1	55	FABP6	Down	GATA2	68	VSTM2L
Up	ESR1	54	TFF1	Down	PPARD	67	HPR
Up	FOXA2	53	GGT1	Down	E2F1	66	ZIM2
Up	E2F1	51	SUSD2	Down	KLF4	66	FEV
Up	PPARD	51	GCG	Down	SOX9	65	GDAP1L1
Up	SRY	51	FAM3B	Down	TRIM28	64	NNMT
Up	SALL4	51	CDCA7	Down	FOXP1	62	RASD1
Up	SMARCA4	50	APOB	Down	SETDB1	62	FGG
Up	SIN3B	49	EFNA2	Down	TFAP2C	60	RGL3
Up	PBX1	49	MTTP	Down	RNF2	60	INA
Up	TCF3	48	FUT2	Down	CREB1	59	NACAD
Up	EOMES	48	DHRS11	Down	CREM	58	RIMBP2
Up	EZH2	48	HAPLN4	Down	SMARCA4	58	NAV2
Up	TFAP2C	47	KAZALD1	Down	PPARG	56	ARHGEF40
Up	NR0B1	46	CXCL14	Down	SMAD3	55	PITX2
Up	SMAD3	44	KRT19	Down	JARID2	55	FOXA2
Up	BACH1	44	CDKN2B	Down	ZNF281	55	EPHA10
Up	ASH2L	43	OSR2	Down	ESR1	54	PPFIBP1

Up	FOXP1	43	SLC39A4	Down	NR3C1	52	ASB4
Up	YAP1	42	SLC10A2	Down	BMI1	50	CALY
Up	RCOR3	41	SLC52A3	Down	BACH1	49	KCNJ6
Up	CDX2	41	SLC35G1	Down	SALL4	47	TEKT2
Up	RNF2	40	GALNT6	Down	TEAD4	47	ST6GALNAC5
Up	NR3C1	39	SI	Down	YAP1	46	KIRREL3
Up	CREB1	38	FZD5	Down	KDM5B	42	LZTS1
Up	ZNF281	38	KRT19	Down	EP300	40	MAPK11
Up	RAD21	38	TMPRSS15	Down	OLIG2	38	GRIA3
Up	BMI1	38	HOXB9	Down	RAD21	38	CKB
Up	EP300	36	CNDP2	Down	TAL1	38	CDC42EP3
Up	KLF1	36	E2F2	Down	SCLY	37	SHC2
Up	JARID2	35	DQX1	Down	EOMES	37	DACT2
Up	CEBPB	35	SOAT2	Down	PBX1	36	MAPK8IP2
Up	TAL1	34	SYK	Down	WT1	36	LY6H
Up	CREM	32	ACE	Down	DMRT1	36	ABCA3
Up	KDM5B	32	CCL25	Down	TFAP2A	35	TRO
Up	CUX1	32	SLC2A2	Down	PRDM14	34	RBFOX1
Up	CTNNB1	32	KRT20	Down	ERG	34	LRRC56
Up	RELA	32	IL32	Down	JUN	34	FAM135B
Up	ERG	30	HRASLS2	Down	EWSR1	33	KIF12
Up	OLIG2	30	MAOB	Down	POU3F2	32	TAC1
Up	RBPJ	30	MST1R	Down	YY1	32	MNX1
Up	PRDM14	29	BMP7	Down	TCF7	31	RET

Up	TFCP2L1	29	FA2H	Down	CTNNB1	31	MC1R
Up	ATF3	29	SDCBP2	Down	NR0B1	30	FXVD2
Up	POU3F2	29	ADAMDEC1	Down	TFCP2L1	30	EGR4
Up	SMAD2	28	SPINK1	Down	MYCN	29	MT3
Up	STAT5A	28	TSPAN8	Down	TBX5	29	ARVCF
Up	ZNF217	27	KCNQ1	Down	FOXP2	28	JPH3
Up	TFAP2A	27	MOCOS	Down	PAX3	28	ITGBL1
Up	E2F4	26	LGALS3	Down	ZNF217	28	DTNB
Up	FOXO3	26	DEFA6	Down	TTF2	27	PAM
Up	SOX17	26	SECTM1	Down	CEBPB	27	F7
Up	TEAD4	26	FAT1	Down	GFI1B	26	RAB36
Up	SCLY	26	TBX10	Down	EED	26	NKX2-2
Up	JUN	26	REG3A	Down	SIN3A	26	NEUROD1
Up	YY1	24	VDR	Down	SMAD2	26	BAIAP2
Up	DNAJC2	24	ANPEP	Down	NFE2L2	25	RGS4
Up	ESRRB	23	CDX1	Down	KLF1	25	ISYNA1
Up	EWSR1	23	GSTA2	Down	CUX1	25	AMBP
Up	CNOT3	22	MYO5B	Down	MYBL2	24	ZFHX2
Up	MECOM	22	CTSE	Down	RCOR1	24	PCSK1N
Up	FOXP2	22	DMBT1	Down	ESRRB	24	NDRG4
Up	TBX3	22	ISX	Down	RBPJ	24	KRT23
Up	NFE2L2	21	TM4SF20	Down	ARNT	24	ADAMTS9
Up	ZFX	21	CA13	Down	E2F4	23	MANEAL
Up	MYCN	21	C2ORF88	Down	ASH2L	23	GLIS3

Up	TBX5	21	CMBL	Down	PHC1	22	ST8SIA3
Up	LMO2	21	RBP2	Down	HOXC9	22	MIR7-3HG
Up	WT1	20	GPD1	Down	NR1I2	22	HP
Up	CTCF	20	GDA	Down	ZFP42	21	TSPYL4
Up	IRF8	20	NAT2	Down	SOX11	21	RCAN2
Up	ARNT	19	MYB	Down	SOX17	21	ISLR2
Up	TTF2	19	POU2AF1	Down	RCOR2	21	FBLL1
Up	STAT4	19	TRPM6	Down	ZFX	20	NINL
Up	RCOR1	19	HSD3B1	Down	ATF3	20	MYL6B
Up	PAX3	18	GK	Down	CTCF	20	CRYBA2
Up	EED	17	TNFRSF11A	Down	CNOT3	19	SSTR2
Up	GATA3	17	EMB	Down	GATA4	19	TTC25
Up	ELK1	16	SST	Down	TBX3	19	PTPRT
Up	GF11B	16	NEU4	Down	RELA	19	OXTR
Up	TCF7	16	PEPD	Down	DNAJC2	19	TCEAL6
Up	SOX11	16	ABCG2	Down	DROSHA	19	RTBDN
Up	DMRT1	15	PNLIPRP2	Down	MEF2A	18	KCNH2
Up	MYBL2	15	ZG16	Down	ELF1	18	TMEM61
Up	NACC1	15	DPP4	Down	LMO2	17	F5
Up	SMAD1	15	XPNPEP2	Down	HTT	17	NXF2
Up	PRDM5	15	AGR3	Down	AHR	16	HS6ST3
Up	ELF1	15	TST	Down	ELK1	16	RPRML
Up	HTT	15	AADAC	Down	CDX2	16	PDE4DIP
Up	GATA4	14	KHK	Down	PAX6	16	REEP2

Up	PHC1	14	MFSD2A	Down	CCND1	15	GAMT
Up	SREBF2	14	CDHR2	Down	XRN2	14	CLIP3
Up	STAT1	14	HLA-DMB	Down	MECOM	14	RDH12
Up	AHR	13	PLEK2	Down	CRX	14	PPP2R2B
Up	DACH1	13	CES2	Down	VDR	13	CACNA1C
Up	ELF5	13	ST6GALNAC1	Down	MEIS1	13	GPBAR1
Up	XRN2	12	RETSAT	Down	SREBF2	13	PROC
Up	CCND1	12	LRP4	Down	GATA3	13	ST18
Up	ZFP42	12	TUBAL3	Down	TBP	12	RAB3A
Up	MEIS1	12	MAF	Down	CEBPA	12	AHSG
Up	PAX6	12	MME	Down	PDX1	12	STXBP5L
Up	IRF1	12	HPGD	Down	ESR2	12	C6ORF141
Up	SIN3A	11	HSD11B2	Down	GBX2	12	JAKMIP2
Up	TAF7L	11	MGST1	Down	NACC1	11	MANEAL
Up	SREBF1	10	NAT8B	Down	SMAD1	11	INSM1
Up	NR1H3	10	ANPEP	Down	DACH1	10	NPDC1
Up	HOXB4	9	CTSE	Down	FOXO3	10	RASD1
Up	TCF7L2	9	FCGBP	Down	ELF5	10	ZNF618
Up	PADI4	9	BLNK	Down	PADI4	10	QPCT
Up	HIF1A	9	TMEM45B	Down	STAT1	10	DLG2
Up	DROSHA	9	MUC2	Down	KDM5A	9	PRRT2
Up	MEF2A	8	DPEP1	Down	NR4A2	9	FGF12
Up	SRF	8	AKR1B10	Down	LYL1	8	MBD3L2
Up	LYL1	8	ITLN1	Down	NFIB	8	BTG3

Up	ASXL1	8	TNFRSF11A	Down	CEBPD	7	A1BG
Up	CLOCK	8	FMO1	Down	ETS1	7	CPT1C
Up	ESR2	8	SGK1	Down	HOXB4	7	ECE2
Up	IKZF1	8	GUCA2A	Down	SRF	7	MTSS1
Up	CEBPD	7	TRPM6	Down	MYB	7	CDC42EP3
Up	HOXC9	7	NR0B2	Down	TCF7L2	7	SHC2
Up	HSF1	7	ALPI	Down	STAT4	6	RTBDN
Up	DCP1A	7	SEMA6A	Down	HSF1	6	DACT2
Up	PDX1	7	TST	Down	IRF1	6	RIIAD1
Up	FOXO1	7	FABP1	Down	CLOCK	6	BEX1
Up	FOXP3	6	CES2	Down	THAP11	6	KIF5C
Up	NUCKS1	6	FZD5	Down	SREBF1	6	SEZ6L2
Up	ZIC3	6	LIPH	Down	NR1H3	6	ECM1
Up	TFEB	6	CLCA1	Down	STAT6	6	HIPK2
Up	CRX	6	ISX	Down	FOXO1	6	C8A
Up	NFIB	6	ALDOB	Down	ETS2	6	DTX3
Up	KDM5A	5	PRODH	Down	FOXP3	5	NLRP1
Up	PHF8	5	SLC35G1	Down	NUCKS1	5	BAIAP2
Up	CHD1	5	MPST	Down	STAT5A	5	RCAN3
Up	STAT6	5	PRSS2	Down	TFEB	5	CCDC151
Up	PRDM16	5	PIGR	Down	RARG	5	TNFRSF11B
Up	KLF2	4	MFSD2A	Down	HOXD13	5	SCGN
Up	KLF5	4	HOXB9	Down	THRA	5	TF
Up	ETS1	4	DGAT1	Down	CHD1	4	ABHD1

Up	TBP	4	CD68	Down	ZIC3	4	NKX2-2
Up	BCL3	4	ZG16	Down	TAF7L	4	ARHGEF40
Up	RCOR2	4	PRSS3	Down	PRDM5	4	TSPYL4
Up	RARG	4	PRSS8	Down	IRF8	4	GNAZ
Up	ETS2	4	KRT19	Down	CDKN2AIP	4	DSCAM
Up	ZNF263	4	ITGB4	Down	ZNF322	4	PPP2R2B
Up	THAP11	3	ESPL1	Down	IKZF1	4	ADAMTS9
Up	FOXM1	3	TUBA1C	Down	PHF8	3	SMOC1
Up	THRA	3	APOA1	Down	DCP1A	3	LRRC56
Up	NR4A2	3	HAPLN4	Down	ZNF274	3	ZIM2
Up	SALL1	3	CDCA7	Down	TCF21	3	F7
Up	CHD7	3	CFTR	Down	HCFC1	2	CBX1
Up	ZNF274	3	CYP2S1	Down	HIF1A	2	PTPRN
Up	TCF21	3	KLK1	Down	FOXM1	2	SPTB
Up	AP1S2	2	LDHA	Down	ZNF652	2	RUNDC3A
Up	KDM6A	2	PEPD	Down	KLF2	1	DTNB
Up	E2F7	2	E2F2	Down	KLF5	1	DTNB
Up	GLI1	2	SLC10A2	Down	AP1S2	1	MYL6B
Up	CIITA	2	IGHA1	Down	BCL3	1	GSTT2
Up	GBX2	1	CFTR	Down	ASXL1	1	PPFIBP1
Up	MYBL1	1	FBP1	Down	KDM6A	1	INA
Up	CDKN2AIP	1	ATP1A3	Down	NOTCH1	1	CPE
Up	BCL11B	1	MOCOS	Down	CHD7	1	HOXA10
				Down	ZNF263	1	FOXA1

Down BCL11B 1 FMN2
Down GLI1 1 CDK14
Down HOXA2 1 ASB4

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

Table 10. Docking results of Designed Molecules on Over expressed Proteins

Sl. No/ Code	CFTR			EZR			ATP1A1			TUBA1C			LGALS3		
	PDB: 4WZ6			PDB: 4RM8			PDB: 3KDP			PDB: 3E22			PDB: 6FOF		
	Total Score	Crash (-Ve)	Polar	Total Score	Crash (-Ve)	Polar	Total Score	Crash (-Ve)	Polar	Total Score	Crash (-Ve)	Polar	Total Score	Crash (-Ve)	Polar
C11	7.171	-1.223	5.487	6.670	-1.488	4.211	4.695	-0.715	1.055	5.644	-1.055	2.977	6.757	-1.687	2.133
C12	6.310	-1.086	4.378	6.246	-1.809	3.687	4.691	-1.243	1.155	5.084	-1.023	2.758	6.653	-1.651	2.095
C13	8.037	-1.128	4.805	6.710	-0.628	3.692	4.523	-0.850	1.098	6.166	-1.266	1.026	5.486	-1.030	2.152
C14	7.153	-1.772	5.756	5.968	-2.552	3.359	4.320	-1.011	1.124	5.765	-1.111	2.771	6.436	-1.471	2.852
C15	7.933	-1.053	4.653	6.385	-1.767	3.847	3.981	-1.358	1.360	5.364	-0.682	2.426	5.206	-0.780	2.132
C16	6.482	-0.973	2.695	6.380	-1.279	1.886	5.360	-1.204	0.817	5.746	-1.726	1.948	5.139	-1.209	2.798
C17	7.026	-1.320	7.144	8.238	-1.444	5.024	4.481	-0.675	2.776	5.206	-1.908	2.272	6.505	-1.149	4.761
F8	7.091	-1.597	2.900	6.850	-1.441	4.435	5.304	-0.577	2.081	5.820	-0.908	0.658	5.374	-1.292	1.690
F9	6.260	-0.885	3.597	5.952	-1.066	2.346	5.307	-1.179	1.751	6.651	-1.565	1.748	6.510	-1.503	1.995
F10	6.703	-1.546	3.828	6.937	-0.708	3.254	4.876	-0.928	1.304	5.678	-1.550	1.014	7.298	-1.686	2.146
F11	7.295	-1.256	5.196	6.683	-0.816	3.540	4.715	-1.033	1.153	6.261	-1.188	1.069	5.795	-1.580	1.338
F12	6.606	-2.244	3.598	7.387	-1.238	4.398	4.539	-0.999	1.641	6.825	-1.994	2.048	5.744	-1.020	4.521
F13	6.494	-0.853	3.721	6.292	-1.197	3.422	4.184	-1.896	1.105	6.494	-1.392	2.073	5.541	-1.048	1.070
F14	7.104	-1.311	4.998	8.703	-1.508	5.554	5.746	-1.013	1.217	5.225	-1.046	1.886	6.908	-0.815	1.677
Br15	7.479	-1.218	4.434	6.905	-1.561	4.293	5.042	-1.019	2.081	4.607	-0.814	2.185	5.195	-2.079	0.686
Br16	7.080	-1.923	5.685	5.339	-1.974	2.944	3.796	-1.698	1.337	4.598	-1.298	1.099	6.468	-1.532	1.756

Br17	7.599	-1.197	4.893	7.627	-1.362	3.623	4.568	-1.149	1.019	4.764	-1.452	0.941	4.946	-1.767	1.769
Br18	7.965	-1.363	5.391	7.181	-1.346	3.488	3.893	-1.206	2.144	5.468	-1.144	0.003	5.330	-1.221	1.207
Br19	7.269	-1.301	4.579	8.714	-1.335	4.904	2.855	-0.820	0.000	5.411	-2.184	1.918	6.007	-1.067	4.471
Br20	7.697	-1.807	4.287	6.934	-1.952	4.541	3.995	-0.956	0.995	6.171	-1.394	1.126	5.177	-0.966	0.002
Br21	7.302	-0.822	6.105	8.350	-1.532	4.990	4.568	-0.942	1.141	6.484	-1.103	4.032	5.924	-2.313	4.091
I22	6.716	-1.394	5.265	7.618	-1.435	4.361	4.171	-0.854	3.112	4.548	-1.140	2.198	4.876	-0.822	1.751
I23	8.275	-1.377	5.175	5.800	-2.758	3.584	4.426	-1.216	1.022	6.113	-1.246	1.417	6.781	-1.630	1.952
I24	7.117	-1.111	3.228	6.712	-1.188	3.789	4.553	-1.074	3.004	5.211	-1.319	0.872	7.218	-1.529	1.926
I25	7.864	-0.784	4.261	6.367	-2.423	3.620	4.671	-0.871	1.037	4.479	-0.725	0.662	6.107	-1.498	2.081
I26	8.358	-1.964	6.127	8.446	-1.653	5.643	4.038	-0.860	2.104	5.616	-2.016	2.062	5.975	-1.103	4.700
I27	6.364	-1.308	5.194	6.820	-1.109	3.885	4.641	-1.042	3.222	6.673	-1.266	2.744	5.339	-1.069	2.169
I28	8.309	-2.505	2.928	8.015	-1.418	5.152	5.820	-0.650	2.808	5.152	-1.565	2.391	5.707	-1.811	1.911