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Identification of Differentially Expressed Genes and Enriched Pathways in SARS-CoV-2/ COVID-19 using Bioinformatics Analysis

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Research article

Keywords: biological markers, computational biology, COVID-19, enrichment analysis, protein –protein interaction

Posted Date: December 11th, 2020

DOI: https://doi.org/10.21203/rs.3.rs-122015/v1

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Abstract

Background

The exact molecular mechanisms of the progression of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection remain unclear. The current investigation strived to understand and functionally analyze the differentially expressed genes (DEGs) between SARS-CoV-2 infection and mock samples applying extensive bioinformatics analyses.

Methods

GSE148729 dataset was downloaded from the Gene Expression Omnibus (GEO) and investigated utilising the limma package in R software to identify DEGs. Pathway and gene ontology (GO) enrichment analysis of the up and down-regulated genes were performed in ToppGene. The HIPPIE database was applied to estimate the interactions of up and down-regulated genes and to construct a protein-protein interaction (PPI) network using Cytoscape software. Receiver operating characteristic (ROC) was utilized for validation.

Results

A total of 928 DEGs (461 up-regulated genes and 467 down-regulated genes) were identified between SARS-CoV-2 infection and mock samples. The up and down-regulated genes were significantly enriched in cytokine-cytokine receptor interaction, and ascorbate and aldarate metabolism. Several significant GO terms, including the response to biotic stimulus and oxoacid metabolic process, were identified. The top hub genes and target genes included JUN, FBXO6, PCLAF, CFTR, TXNIP, PMAIP1, BRI3BP, FAHD1, PROX1, CXCL11, SERHL2 and CFI. ROC curve analysis showed that messenger RNA levels of these ten genes (DDX58, IFITM2, IRF1, PML, SAMHD1, ACSS1, CYP2U1, DDC, PNMT and UGT2A3) exhibited better diagnostic efficiency between SARS-CoV-2 infection and mock.

Conclusions

The current investigation distinguished vital genes and pathways that may be implicated in the progression of SARS-CoV-2 infection, providing a new understanding of the underlying molecular mechanisms of SARS-CoV-2 infection.

Background

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is a key cause of respiratory disease in the pandemic form [1] and named as COVID-19. As of October 2020, more than 1,000,000 people have died of SARS-CoV-2 complications globally. Restriction of the spread of SARS-CoV-2 virus has been difficult, and the transmission of this virus develops through close contact with large-particle aerosols [2]. SARS-CoV-2 infections in humans cause severe pneumonia that is disastrous in about 11% of infected individuals [3].

An intensive investigation has been achieved on the virulence and evolution of the SARS-CoV-2 virus [4]. However, very little is known about the influence of specific genes or biomarkers in humans that add to the susceptibility to SARS-CoV-2 infections. Consequently, it requires more extra effort to elucidate the molecular mechanism underlying SARS-CoV-2 infections advancement and progression, holding hope for discovering potential drug targets and diagnostic biomarkers of SARS-CoV-2 infections.

Expression profiling by microarray technology-based high throughput sequencing analysis can detect changes in gene expression of thousands of genes on the mRNA level concurrently. Gene expression profiling analysis has revealed many differentially expressed genes with a key role in SARS-CoV-2 infection initiation and development and could be possible diagnostic markers and molecular targets. ACE2 and TMPRSS2 could function as a key mediator of SARS-CoV-2 infections by means of gene expression analysis [5]. In the present investigation, we identified SARS-CoV-2 infection linked with differential expressed genes (DEGs) between SARS-CoV-2 infected samples and mock samples, and successively performed pathway and GO term enrichment analysis, PPI network analysis, modules analysis, target gene - miRNA regulatory network and target gene - TF regulatory network analysis to discover the hub and target genes and pathways closely related to SARS-CoV-2 infections. Finally, hub genes were validated by receiver operating characteristic (ROC) curve analysis.

Materials And Methods

Microarray data

GSE148729 dataset was downloaded from the Gene Expression Omnibus database [6] and was based on the GPL18573 IlluminaNextSeq 500 (Homo sapiens) array. The GSE148729 dataset, which is expression profiling by high throughput sequencing dataset, contains 22 samples, including 14 SARS-CoV-2 infections samples and 8 mock samples.

Data preprocessing and identification of DEG

Limma package in R Bioconductor was used for the preprocessing for GSE148729 dataset, which included background correcting, normalizing and calculating expression [7]. The DEGs in SARS-CoV-2 infections samples compared with mock samples were determined using the limma package. DEGs were screened with an adjusted P-value corrected $P<0.05$ and |log fold-change (FC)|>1. The adjusted P-Value for up and down-regulated genes corrected $P<0.05$ and | log FC|>1 were used as the screening thresholds.

Pathway enrichment analysis of DEGs

The route of gene cluster and related functions was determined using the BIOCYC [8], Kyoto Encyclopedia of Genes and Genomes (KEGG) [9], Pathway Interaction Database (PID) [10], REACTOME [11], GenMAPP [12], MSigDB C2 BIOCARTA [13], PantherDB [14], Pathway Ontology [15] and Small Molecule Pathway Database (SMPDB) [16]. This investigation used the ToppGene (ToppFun) [17] to perform the pathway enrichment analysis. A P-value <0.05 was considered to be statistically significant.

Gene ontology (GO) enrichment analysis

GO enrichment analysis defines an approach used to characterize gene function and relationships [18]. It classifies functions such as biological process (BP), cellular component (CC) and molecular function (MF). ToppGene (ToppFun) was used to classify significant DEGs by their BP, CC and MF through GO and the Functional Annotation clustering tool was used to identify the significant transcripts (Benjamini–Hochberg false discovery rate <0.05).

Protein-protein interaction network construction and module analysis

The online Human Integrated Protein-Protein Interaction rEference (HIPPIE) [19] database was used to identify potential interaction among the up and down-regulated genes and associated with various PPI databases such as IntAct [20], BioGRID [21], HPRD [22], MINT [23], BIND [24], MIPS [25] and DIP [26]. Cytoscape 3.8.0 [27] was used to visualize the results from the PPI network. The Network Analyzer Cytoscape plugin was used to explore hub genes were generated using highest node degree [28], betweenness centrality [29], stress centrality [30], closeness centrality [31] and lowest clustering coefficient [Wang et al. 2012] methods and hub genes were further analyzed for pathway and GO enrichment analysis. Module analysis on the PPI network results was performed using the PEWCC1 (http://apps.cytoscape.org/apps/PEWCC1) [33] clustering algorithm that comes with Cytoscape. Module analysis was applied to analyze more connected gene groups. Besides, the module analysis results were further analyzed for pathway and GO enrichment analysis.

Construction of target genes - miRNA regulatory network

miRNet database [34] is a bioinformatics platform for predicting target genes (up and down-regulated genes) and miRNA pairs. In the current investigation, the targets genes were predicted using ten databases: TarBase [35], miRTarBase [36], miRecords [37], miR2Disease [38], HMDD [39], PhenomiR [40], SM2miR [41], PharmacomiR [42], EpimiR [43] and starBase [Li et al. 2014]. The screening criterion was that the miRNA target exists in the ten miRNA databases concurrently. The target genes - miRNA regulatory network was depicted and visualized using Cytoscape software.

Construction of target genes - TF regulatory network

NetworkAnalyst database [45] is a bioinformatics platform for predicting target genes (up and down-regulated genes) and TF pairs. In the current investigation, the targets genes were predicted using JASPAR [46]. The screening criterion was that the TF target exists in the TF database concurrently. The target genes - TF regulatory network was depicted and visualized using Cytoscape software.

ROC analysis

Receiver operating characteristic (ROC) curve analysis was implemented to calculate the sensitivity and specificity of the up and down-regulated genes for SARS-CoV-2 infections diagnosis using the R “pROC” package [47]. An area under the curve (AUC) value was determined and used to label the ROC effect.

Results

Data preprocessing and identification of DEG

After quality detection of microarray raw data, microarray-based on GPL18573 platform, including 14 SARS-CoV-2 infections samples and 8 mock samples, Limma in R package was used for preprocessing and gene differential expression analysis of microarray data (Fig. 1A and Fig. 1B). Total of 928 DEGs (fold change >1, Fig. 2) consisting of 461 significantly up-regulated genes and 467 significantly down-regulated genes, for the subsequent bioinformatics analysis. The hierarchical clustering heat map of up and down-regulated genes showed the differences between SARS-CoV-2 infections and mock samples (Fig. 3 and Fig. 4).

Pathway enrichment analysis of DEGs

Pathway analysis revealed that the up regulated genes were mainly enriched in superpathway of steroid hormone biosynthesis, aspirin triggered resolvin E biosynthesis, cytokine-cytokine receptor interaction, TNF signaling pathway, calcineurin-regulated NFAT-dependent transcription in lymphocytes, ATF-2 transcription factor network, cytokine signaling in immune system, interferon signaling, steroid hormone metabolism, androgen and estrogen metabolism, genes encoding secreted soluble factors, cytokines and inflammatory response, toll receptor signaling pathway, interleukin signaling pathway, nuclear factor kappa B signaling, c-Jun N-terminal kinases MAPK signaling, 17-beta hydroxysteroid dehydrogenase III deficiency and adrenal hyperplasia type 3 or congenital adrenal hyperplasia due to 21-hydroxylase deficiency, listed in Table 2, while down regulated genes were mainly enriched in catecholamine biosynthesis, noradrenaline and adrenaline degradation, ascorbate and aldarate metabolism, steroid hormone biosynthesis, signaling mediated by p38-gamma and p38-delta, aurora A signaling, biological oxidations, the citric acid (TCA) cycle and respiratory electron transport, bile acid biosynthesis, valineleucine and isoleucine degradation, angiotensin-converting enzyme 2 regulates heart function, apoptotic DNA fragmentation and tissue homeostasis, nicotine degradation, serine glycine biosynthesis, renin-angiotensin system signaling, histidine metabolic, fatty Acid elongation in mitochondria and gluconeogenesis, listed in Table 3.

Gene ontology (GO) enrichment analysis

GO term enrichment analysis results varied from GO classification and the expression change of up and down-regulated genes, listed in Table 4 and Table 5. As to BP, the up-regulated genes significantly enriched in response to biotic stimulus and defense response, and the down-regulated genes significantly enriched in oxoacid metabolic process, and monocarboxylic acid metabolic process. For CC, the up-regulated genes significantly enriched in cell surface and synapse, and the down-regulated genes significantly enriched in mitochondrion and polymeric cytoskeletal fiber. About MF, the up-regulated genes significantly enriched in cytokine activity and signalling receptor binding and the down-regulated genes significantly enriched in cofactor binding and oxidoreductase activity.

Protein-protein interaction network construction and module analysis

PPI network of up-regulated genes, consisting of 5698 nodes and 11384 edges, was constructed by Cytoscape software, based on HIPPIE database (Fig. 5). The up and down-regulated genes with highest node degree, betweenness centrality, stress centrality, closeness centrality and lowest clustering coefficient were selected as the hub genes of SARS-CoV-2 infections and are listed in Table 6. The scatter plots of node degree, betweenness centrality, stress centrality, closeness centrality and clustering coefficient for up-regulated genes are shown in Fig. 6. The up-regulated hub genes (JUN, FBXO6, CYLD, IFI16, ADRB2, PML, ZC3HAV1, SYNPR, CH25H, LSMEM1, CRTAM and RAET1L) in this PPI network were significantly enriched in TNF signalling pathway, RIG-I/MDA5 mediated induction of IFN-alpha/beta pathways, NOD-like receptor signalling pathway, cAMPsignalling pathway, influenza A, response to biotic stimulus, IL-17 signalling pathway, cytokine-cytokine receptor interaction, positive regulation of RNA metabolic process, transition metal ion binding and response to endogenous stimulus. Similarly, the PPI network of down-regulated genes consisted of 5712 nodes and 11002 edges (Fig. 7). The scatter plots of node degree, betweenness centrality, stress centrality, closeness centrality and clustering coefficient for down-regulated genes are shown in Fig. 8. The down-regulated hub genes (PCLAF, CFTR, TUBA1A, AURKA, ARRB1, KPNA2, PRDX2, PGK1, GALM, ACYP2, HSD17B2, CEACAM7 and SEMA3E) in this PPI network were significantly enriched in microtubule cytoskeleton, peptidase activity, metabolism of proteins, aurora A signalling, morphine addiction, regulation of cytoplasmic and nuclear SMAD2/3 signalling, oxidation-reduction process, metabolic pathways, protein homodimerization activity, identical protein binding, steroid hormone biosynthesis and genes encoding proteins affiliated structurally or functionally to extracellular matrix proteins.

PEWCC1 was used to identify the total 1503 modules in the PPI network of up-regulated genes, and the four significant modules were selected (Fig. 9). Pathway and GO enrichment analysis, module 25 (nodes 92 and edges 173), module 33 (nodes 75 and edges 153), module 37 (nodes 63 and edges 109) and module 70 (nodes 20 and edges 41) revealed that the four significant modules were mainly enriched in cytokine-cytokine receptor interaction, influenza A, Jak-STAT signalling pathway, inflammation mediated by chemokine and cytokine signalling pathway, response to cytokine, response to biotic stimulus, response to virus and response to endogenous stimulus. Similarly, PEWCC1 was used to identify the total 1405 modules in the PPI network of down-regulated genes, and the four significant modules were selected (Fig. 10). Pathway and GO enrichment analysis, module 14 (nodes 111 and edges 135), module 15 (nodes 107 and edges 121), module 27 (nodes 81 and edges 97) and module 45 (nodes 54 and edges 75) revealed that the four significant modules were mainly enriched in hedgehog signalling events mediated by Gli proteins, metabolism of proteins, metabolism of lipids and lipoproteins, the citric acid (TCA) cycle and respiratory electron transport, mitochondrion, growth, intrinsic component of plasma membrane and cellular lipid metabolic process.

Construction of target genes - miRNA regulatory network

To further understand the regulatory network between miRNA and target genes, various miRNA databases such as TarBase, miRTarBase, miRecords, miR2Disease, HMDD, PhenomiR, SM2miR, PharmacomiR, EpimiR and starBase through miRNet were constructed by Cytoscape. As shown in Fig. 11, the target genes - miRNA regulatory network for up-regulated genes with 5667 edges and 2144 nodes was obtained for target genes. Different up-regulated target genes regulated by miRNA are shown in Table 7, of which top five miRNAs such as hsa-mir-4511, hsa-mir-3924, hsa-mir-4478, hsa-mir-3650 and hsa-mir-4252 had been predicted to regulate target genes such as TXNIP, PMAIP1, APOL6, CHAC1 and KLF2. Pathway and GO enrichment analysis revealed that target genes in this network were mainly involved in NOD-like receptor signalling pathway, Direct p53 effectors, signalling receptor binding and response to cytokine. Similarly, as shown in Fig. 12, the target genes - miRNA regulatory network for down-regulated genes with 6679 edges and 2236 nodes was obtained for target genes. Different down-regulated target genes regulated by miRNA are shown in Table 7, of which top five miRNAs such ashsa-mir-4312, hsa-mir-4527, hsa-mir-4673, hsa-mir-4496 and hsa-mir-3153 had been predicted to regulate target genes such as BRI3BP, FAHD1, CPM, HOXA13 and TMBIM6. Pathway and GO enrichment analysis revealed that target genes in this network were mainly involved in the mitochondrion, metabolic pathways, metabolism of proteins and ion transport.

Construction of target genes - TF regulatory network

To further understand the regulatory network between TFs and target genes, JASPAR through NetworkAnalyst were constructed by Cytoscape. As shown in Fig. 13, the target genes - TF regulatory network for up-regulated genes with 2844 edges and 439 nodes was obtained for target genes. Different up-regulated target genes regulated by TF are shown in Table 8, of which top five TFs such as FOXC1, GATA2, YY1, FOXL1 and NFKB1 had been predicted to regulate target genes such as PROX1, CXCL11, C4A, JAK2 and IL15RA. Pathway and GO enrichment analysis revealed that target genes in this network were mainly involved in viral genome replication, cytokine-cytokine receptor interaction, innate immune system, influenza A and Jak-STAT signalling pathway. Similarly, as shown in Fig.14, the target genes - TF regulatory network for down-regulated genes with 3191 edges and 505 nodes was obtained for target genes. Different down-regulated target genes regulated by TF are shown in Table 8, of which top five TFs such as FOXC1, GATA2, YY1, NFIC and FOXL1 had been predicted to regulate target genes such as SERHL2, CFI, TCN1, PGP and PGK1. Pathway and GO enrichment analysis revealed that target genes in this network were mainly involved in the mitochondrion, peptidase activity, drug metabolic process, metabolic pathways and carbon metabolism.

ROC analysis

As these five up and five down-regulated genes are prominently expressed in SARS-CoV-2 infection, we performed a ROC curve analysis to evaluate their sensitivity and specificity for the diagnosis of SARS-CoV-2 infection. As shown in Fig. 15, DDX58, IFITM2, IRF1, PML, SAMHD1, ACSS1, CYP2U1, DDC, PNMT

and UGT2A3 achieved an AUC value of 0.777, 0.857, 0.929, 0.804, 0.759, 0.714, 0.728, 0. 754, 0.714 and 0.763, respectively, demonstrating that these genes have high sensitivity and specificity for SARS-CoV-2 infection diagnosis. The results suggested that DDX58, IFITM2, IRF1, PML, SAMHD1, ACSS1, CYP2U1, DDC, PNMT and UGT2A3 can be used as biomarkers for the diagnosis of SARS-CoV-2 infection.

Discussion

SARS-CoV-2 infection transmits worldwide, and its mortality rate has increased in recent times. This research represents a comprehensive study of genes linked with SARS-CoV-2 virus infection, using bioinformatics analysis. The probable biomarkers for diagnosis and treatment with high competence are crucially required as the underlying molecular mechanisms of SARS-CoV-2 are poorly understood. Microarray technology is a plausible approach to diagnose novel biomarkers in SARS-CoV-2 infection.

In the current investigation, expression profiling by high throughput sequencing dataset was analyzed to obtain DEGs between SARS-CoV-2 infections samples and mock samples. A total of 928 DEGs were identified, including 461 up-regulated genes and 467 down-regulated genes. Genes such as SOCS3 [48] and IL1A [49] were liable for progression of influenza virus infection, but these genes may be linked with the progress of SARS-CoV-2 infection as well. Genes such as KLF6 [50], DUSP1 [51] and OLFM4 [52] were associated with the development of respiratory syncytial virus infection, but these genes may be responsible for the advancement of SARS-CoV-2 infection. IL6 was involved in the progression of SARS-CoV-2 infection [53]. Genes such as MAGT1 [54], CD24 [55] and UGT1A7 [56] were involved in the progression of various viral infections, but these genes may be associated with the development of SARS-CoV-2 infection as well. AQP1 was linked with the development of porcine reproductive and respiratory syndrome virus infection [57], but this gene may be responsible for the progression of SARS-CoV-2 infection.

In the pathway enrichment analysis, many up and down-regulated genes may play a very key role in the progression of SARS-CoV-2 infection. Enriched genes such as CXCL9 [58], CX3CL1 [59], IFNB1 [60], IL7 [61], TNFSF10 [62], IFNL3 [63], EGR1 [64], USP18 [65], DDX58 [66], UBA7 [67], IFI35 [68], IFIT2 [69], IFIT1 [70], TRIM5 [71], RSAD2 [72], XAF1 [73], MX2 [74], GBP1 [75], TRIM21 [76], FGF19 [77], PELI1 [78], OAS1 [79], DUSP10 [80], TLR6 [81], TICAM1 [82], DDC (dopa decarboxylase) [83], UGT1A1 [84], STMN1 [85], CYP27A1 [86] and ACE (angiotensin I converting enzyme) [87] were linked with advancement of various viral infections, but these genes may be responsible for progression of SARS-CoV-2 infection as well. Enriched genes such as CCL2 [88], FLT3 [89], CXCL8 [90], IL11 [91], CXCL10 [92], TNF (tumor necrosis factor) [93], EGR2 [94], TRIM22 [95], PML (promyelocyticleukemia) [96], ICAM1 [97], IFITM1 [98], IFITM2 [99], ISG15 [100], SOCS1 [101], IRF1 [102], IRF7 [103], ISG20 [104], STAT2 [105], OAS2 [106], HERC5 [107] and TNFAIP3 [108] were associated with the advancement of influenza virus infection; however, these genes may be liable for the development of SARS-CoV-2 infection. Enriched genes such as CCL20 [109], TSLP (thymic stromal lymphopoietin) [110], IL7R [111], IFIT3 [112] and OASL (2'-5'-oligoadenylate synthetase like) [113] were involved in the development of respiratory syncytial virus infection, but these genes may be associated with the development of SARS-CoV-2 infection. SAMHD1 was involved in the progression of porcine reproductive and respiratory syndrome virus infection [114], but this gene may be liable for the progression of SARS-CoV-2 infection. Enriched genes such as JAK2 [115] and ACE2 [116] were responsible for the progression of SARS-CoV-2 infection. As seen in the pathway enrichment analysis for up and down regulated genes, HSD17B3, CYP21A2, TNFRSF4, CXCL11, FLT3LG, CSF2, TNFSF13B, IL12A, IL15RA, INHBA (inhibin subunit beta A), IL17C, IL22RA1, BMP2, CXCL2, CXCL3, LTB (lymphotoxin beta), IFNL2, IFNL1, FOS (Fos proto-oncogene, AP-1 transcription factor subunit), GATA3, PTGS2, JUN (Jun proto-oncogene, AP-1 transcription factor subunit), EGR3, EGR4, UBE2L6, HLA-F, SPTBN5, RASGRP3, TRIM38, KLB (klotho beta), MAP3K8, MT2A, PSMB9, FGF18, DUSP8, RELB (RELB proto-oncogene, NF-kB subunit), LGALS9, RASGRP1, FST (follistatin), WIF1, NFKBIA (NFKB inhibitor alpha), PNMT (phenylethanolamine N-methyltransferase), ALDH2, UGT1A10, UGT1A8, UGT1A6, UGT1A5, UGT1A9, UGT1A4, UGT1A3, UGT2A3, SNTA1, EPHX1, ADH6, FDX1, ACSS1, GSTO2, GGT1, NR1H4, GLYATL2, GSTA4, CYP2U1, CYP4F3, HADHB (hydroxyacyl-CoA dehydrogenase trifunctionalmultienzyme complex subunit beta), AGT (angiotensinogen), MME (membrane metalloendopeptidase), PPT1 and PRDX3are novel biomarkers for SARS-CoV-2 infection.

Similarly, GO enrichment analysis, many up and down-regulated genes may play a very key role in the progression of SARS-CoV-2 infection. Enriched genes such as IFNL4 [117], ZFP36 [118], CD274 [119], MIR21 [120], CYP1A1 [121], CMPK2 [122], C4A [123], SERPINE1 [124], CCRL2 [125], CD69 [126], FAH (fumarylacetoacetate hydrolase) [127], ERFE (erythroferrone) [128], SERINC5 [129], ADI1 [130], AP2M1 [131], PRIMPOL (primase and DNA directed polymerase) [132], BIRC5 [133] and TF (transferrin) [134] were responsible for the advancement of various viral infections, but these genes may be involved in the progression of SARS-CoV-2 infection. Enriched genes such as APOBEC3G [135], NLRC5 [136], PTX3 [137], FAP (fibroblast activation protein alpha) [138] and CAT (catalase) [139] were linked with the development of influenza viral infection, but these genes may be associated with progression of SARS-CoV-2 infection as well. Enriched genes such as IFI16 [140], TAP1 [141] and PIN1 [142] were involved in the development of porcine reproductive and respiratory syndrome virus infection; however, these genes may be associated with the progression of SARS-CoV-2 infection. NLRP3 was key for the advancement of SARS-CoV-2 infection [143]. PDK1 was liable for the development of SARS coronavirus infection [144], but this gene may belinked with the advancement ofSARS-CoV-2 infection. As given in the GO enrichment analysis for up and down regulated genes, PDE2A, PDE4B, NT5C3A, PGLYRP2, DTX3L, PLAC8, NOCT (nocturnin), PMAIP1, ZC3H12A, DHX58, TENT5A, IFI44, BATF2, TXNIP (thioredoxin interacting protein), SH2D1B, MIR181B1, RAET1L, STX11, ZC3HAV1, CYLD (CYLD lysine 63 deubiquitinase), TAGAP (T cell activation RhoGTPase activating protein), BCL3, PTGER4, RTP4, GFI1, IFIH1, CLEC4A, GLI2, C4B, GPER1, CRTAM (cytotoxic and regulatory T cell molecule), PCK1, acetylcholinesterase (Cartwright blood group), TRPC4, DSCAML1, HEG1, PLAUR (plasminogen activator, urokinase receptor), SLITRK6, ACKR4, LAYN (layilin), GRIA2, MMP25, EPHA4, SECTM1, VSTM1, RIMKLA (ribosomal modification protein rimK like family member A), ACO1, ETFB (electron transfer flavoprotein subunit beta), ETFDH (electron transfer flavoprotein dehydrogenase), MDH1, HNMT (histamine N-methyltransferase), PGK1, FABP6, ACSM3, FBP1, HOGA1, SCP2, ECI2, ALDH6A1, PCYOX1, MPC2, HACD3, FOLR1, SHMT1, ACSF2, SLC3A1, CRYM (crystallin mu), CSPG5, PPA2, AKR1C3, DHFRP1, SPR (sepiapterinreductase), BDH2, GATM (glycine amidinotransferase), BCKDHB (branched chain keto acid dehydrogenase E1 subunit beta), PSMD10, ITIH2, PHGDH (phosphoglycerate dehydrogenase), BTD (biotinidase), SLC25A21, OAT (ornithine aminotransferase), OAZ1, HACD2, ECH1, BCO2, BNIPL (BCL2 interacting protein like), PAH (phenylalanine hydroxylase), LTC4S, DSEL (dermatansulfateepimerase like), ATPSCKMT (ATP synthase c subunit lysine N-methyltransferase), COX16, ACYP2, TRMT2B, TSTD1, ASB9, UCP2, AK4, CEBPZOS (CEBPZ opposite strand), SERHL2, HSPE1, SLC25A27, COA3, AGR2, MACROD1, COX11, NUBPL (nucleotide binding protein like), CRLS1,

BRI3BP, DNLZ (DNL-type zinc finger), CYBA (cytochrome b-245 alpha chain), KLK6, NDUFS7, PSAP (prosaposin), NDUFAF8, ACOT13, SRI (sorcin), TOMM20, NDUFA2, SGPP1, TMEM160, HEBP1, AKR1B10, DPYSL2, ATP5IF1, NRGN (neurogranin), DTYMK (deoxythymidylate kinase), NTHL1, PRDX2, TMBIM6, GSR (glutathione-disulfidereductase), TFRC (transferrin receptor), ANXA10, SAMD13, FAHD1, ENDOG (endonuclease G), COX14, FMO5, CRYZ (crystallin zeta), ACBD7, KCNAB1, CREG2 and TCN1 are novel biomarkers for SARS-CoV-2 infection.

PPI network was constructed and modules extracted to explore the molecular mechanism SARS-CoV-2 infection. In this investigation, the expression of hub genes in SARS-CoV-2 infection was done. Hub gene CH25H was liable for progression of porcine reproductive and respiratory syndrome virus infection [145], but this gene may be involved in the advancement of SARS-CoV-2 infection. Hub genes such as TRAF1 [146], IFIT5 [147], CFTR (CF transmembrane conductance regulator) [148] and SMARCA2 [149] were key for progression of influenza viral infection; however, these genes may be linked with the progression of SARS-CoV-2 infection. Hub gene SAP30 was responsible for the advancement of Rift Valley fever virus infection [150], but this gene may be vital for the advancement of SARS-CoV-2 infection. Hub gene APOE (apolipoprotein E) was responsible for the development of SARS-CoV-2 infection [151]. As given in the PPI network and module analysis for up and down-regulated genes, FBXO6, ADRB2, SYNPR (synaptoporin), LSMEM1, ARRDC3, ACTA1, LMO2, ATF3, KLF4, PCLAF (PCNA clamp associated factor), TUBA1A, AURKA (aurora kinase A), ARRB1, KPNA2, GALM (galactosemutarotase), HSD17B2, CEACAM7, SEMA3E, EPN3, ROM1, SORL1 and PDCD4 are novel biomarkers for SARS-CoV-2 infection.

Target gene - miRNA regulatory network and target gene - TF regulatory network analysis (up and down-regulated genes) can be regarded as key to the understanding of SARS-CoV-2 infection and might also lead to new therapeutic approaches. Hub genes such as PROX1 [152] and HOXA13 [153] were responsible for the development of hepatitis B virus infection, but these genes may also be essential for the advancement of for SARS-CoV-2 infection. As given in the target gene - miRNA regulatory network and target gene - TF regulatory network for up and down-regulated genes, APOL6, CHAC1, KLF2, CPM (carboxypeptidase M), CFI (complement factor I) and PGP (phosphoglycolate phosphatase) are novel biomarkers for SARS-CoV-2 infection.

Conclusion

In conclusion, the current investigation provided comprehensive bioinformatics analysis of up and down-regulated genes in SARS-CoV-2 infection. Analysis of these genes delivered information regarding the molecular mechanisms of SARS-CoV-2 infection and key biomarkers or targets for the diagnosis and treatment of SARS-CoV-2/COVID-19 disease. However, further molecular biological experiments are required to confirm the action of the up and down-regulated genes and pathways in different types of SARS-CoV-2 infections.

Abbreviations

JUN - Jun proto-oncogene, AP-1 transcription factor subunit

FBXO6 - F-box protein 6

PCLAF - PCNA clamp associated factor

CFTR - CF transmembrane conductance regulator

TXNIP - thioredoxin interacting protein

PMAIP1 - phorbol-12-myristate-13-acetate-induced protein 1

BRI3BP - BRI3 binding protein

PROX1 - prosperohomeobox 1

CXCL11 - C-X-C motif chemokine ligand 11

SERHL2 - serine hydrolase like 2

DDX58 - DExD/H-box helicase 58

IFITM2 - interferon induced transmembrane protein 2

PML - promyelocyticleukemia

SAMHD1 - SAM and HD domain containing deoxynucleoside triphosphate triphosphohydrolase 1

ACSS1 - acyl-CoA synthetase short chain family member 1

CYP2U1 - cytochrome P450 family 2 subfamily U member 1

DDC - dopa decarboxylase

PNMT - phenylethanolamine N-methyltransferase

UGT2A3 - UDP glucuronosyltransferase family 2 member A3

Declarations

Ethics approval and consent to participate

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.

Availability of data and materials

The datasets supporting the conclusions of this article are available in the GEO (Gene Expression Omnibus) (https://www.ncbi.nlm.nih.gov/geo/) repository. [(GSE148729) https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE148729)]

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

Funding

This study was supported by grants from Deanship of Scientific Research, Najran University, Najran, Saudi Arabia (grant no. NU/MID/18/018).

Author Contributions

A.M.A associated with project administration, methodology and review and editing.

I.A.S participated in writing original draft and investigation.

C.V performed software, supervision, formal analysis and validation.

B.V made substantial contributions to acquisition of resources, formal analysis and validation.

Acknowledgements

We also thank Emanuel Wyler, Max Delbrück Center for Molecular Medicine, Berlin Institute for Medical Systems Biology, Robert Roessle Str 10, Berlin, Germany., very much, the author who deposited their microarray dataset, GSE148729, into the public GEO database.

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Tables

Table 1 The statistical metrics for key differentially expressed genes (DEGs)

Gene Symbol	logFC	pValue	adj.P.Val	tvalue	Regulation	Gene Name
SOCS3	1.029557	1.21E-08	1.21E-08	7.082396	Up	suppressor of cytokine signaling 3
ETS2	1.162876	5.82E-06	5.82E-06	5.197414	Up	ETS proto-oncogene 2, transcription factor
ERICD	1.138842	8.01E-06	8.01E-06	5.099039	Up	E2F1-regulated inhibitor of cell death
SPRY2	1.289333	4.96E-05	4.96E-05	4.529091	Up	sprouty RTK signaling antagonist 2
PLEKHG5	1.103153	4.14E-05	4.14E-05	4.58625	Up	pleckstrin homology and RhoGEF domain containing G5
KLF6	1.219624	8.62E-05	8.62E-05	4.353553	Up	Kruppel like factor 6
RPL39P5	1.198859	8.25E-05	8.25E-05	4.367571	Up	ribosomal protein L39 pseudogene 5
IL1A	2.500916	0.00011	0.00011	4.274553	Up	interleukin 1 alpha
IL6	3.463376	0.00013	0.00013	4.220788	Up	interleukin 6
EPC1	1.17429	0.000193	0.000193	4.092739	Up	enhancer of polycomb homolog 1
CSF2	2.591821	6.26E-05	6.26E-05	4.455695	Up	colony stimulating factor 2
ADRB2	1.050404	0.000226	0.000226	4.040984	Up	adrenoceptor beta 2
TIPARP	1.646696	0.000261	0.000261	3.994215	Up	TCDD inducible poly(ADP-ribose) polymerase
COL4A1	2.492335	7.79E-05	7.79E-05	4.385885	Up	collagen type IV alpha 1 chain
DUSP1	1.950421	0.000352	0.000352	3.895466	Up	dual specificity phosphatase 1
G0S2	1.056752	0.000353	0.000353	3.8946	Up	G0/G1 switch 2
CD274	2.559212	0.000383	0.000383	3.86675	Up	CD274 molecule
GADD45B	1.037288	0.000586	0.000586	3.724348	Up	growth arrest and DNA damage inducible beta
MB21D2	1.524927	0.0006	0.0006	3.716393	Up	Mab-21 domain containing 2
CD69	2.028046	0.000315	0.000315	3.931994	Up	CD69 molecule
CSRNP1	1.686588	0.000721	0.000721	3.653985	Up	cysteine and serine rich nuclear protein 1
AMOTL2	1.044122	0.000665	0.000665	3.68167	Up	angiomotin like 2
SPTBN5	1.059205	0.000531	0.000531	3.757737	Up	spectrin beta, non-erythrocytic 5
FOSB	1.736709	0.000792	0.000792	3.622197	Up	FosB proto-oncogene, AP-1 transcription factor subunit
OGFR	1.070808	0.000713	0.000713	3.657808	Up	opioid growth factor receptor
IL11	1.198667	0.000741	0.000741	3.644948	Up	interleukin 11
CXCL3	1.515004	0.000888	0.000888	3.583149	Up	C-X-C motif chemokine ligand 3
TRIM21	1.165551	0.000906	0.000906	3.576125	Up	tripartite motif containing 21
DUSP10	0.977857	0.000964	0.000964	3.554731	Up	dual specificity phosphatase 10
GATA3	1.361589	0.001006	0.001006	3.539994	Up	GATA binding protein 3
MIR6881	1.053893	0.00036	0.00036	3.888052	Up	microRNA 6881
ZNF627	1.049596	0.001161	0.001161	3.490391	Up	zinc finger protein 627
KIF26B	1.165483	0.000853	0.000853	3.596631	Up	kinesin family member 26B
JUN	1.811995	0.000955	0.000955	3.557814	Up	Jun proto-oncogene, AP-1 transcription factor subunit
HDX	1.111154	0.001164	0.001164	3.489549	Up	highly divergent homeobox
IL22RA1	1.710662	0.000832	0.000832	3.605157	Up	interleukin 22 receptor subunit alpha 1
SLC25A28	1.117785	0.001208	0.001208	3.476763	Up	solute carrier family 25 member 28
AHRR	1.976907	0.000703	0.000703	3.662819	Up	aryl-hydrocarbon receptor repressor
CYP1A1	2.582763	0.001264	0.001264	3.460967	Up	cytochrome P450 family 1 subfamily A member 1
TXNIP	1.117427	0.001073	0.001073	3.51763	Up	thioredoxin interacting protein
COL8A1	0.990515	0.000985	0.000985	3.54749	Up	collagen type VIII alpha 1 chain
EGR3	1.828393	0.000966	0.000966	3.554019	Up	early growth response 3
TCIM	1.199207	0.001273	0.001273	3.458447	Up	transcriptional and immune response regulator

TICAM1	0.991094	0.001568	0.001568	3.385469	Up	toll like receptor adaptor molecule 1
CXCL9	4.005381	0.000334	0.000334	3.91269	Up	C-X-C motif chemokine ligand 9
TNFAIP3	3.039604	0.001664	0.001664	3.364687	Up	TNF alpha induced protein 3
STX11	2.198163	0.000686	0.000686	3.670822	Up	syntaxin 11
IL12A	1.796495	0.001351	0.001351	3.437811	Up	interleukin 12A
PLAUR	1.307972	0.001622	0.001622	3.373573	Up	plasminogen activator, urokinase receptor
EGR2	2.487318	0.001533	0.001533	3.393528	Up	early growth response 2
THEMIS2	1.896802	0.001812	0.001812	3.33449	Up	thymocyte selection associated family member 2
ATF3	3.358037	0.001895	0.001895	3.318661	Up	activating transcription factor 3
ZFP36	1.66189	0.001798	0.001798	3.337269	Up	ZFP36 ring finger protein
NFKBIZ	1.40522	0.001728	0.001728	3.351401	Up	NFKB inhibitor zeta
CHAC1	1.209221	0.00171	0.00171	3.354989	Up	ChaC glutathione specific gamma-glutamylcyclotransferase 1
PGAM1P7	0.975288	0.001809	0.001809	3.335094	Up	phosphoglyceratemutase 1 pseudogene 7
NUAK2	2.320463	0.002327	0.002327	3.245474	Up	NUAK family kinase 2
CXCL2	2.091483	0.00237	0.00237	3.238994	Up	C-X-C motif chemokine ligand 2
SERPINE1	1.345573	0.001394	0.001394	3.426875	Up	serpin family E member 1
USP8P1	1.178748	0.001238	0.001238	3.468297	Up	ubiquitin specific peptidase 8 pseudogene 1
CXCL8	0.970987	0.001888	0.001888	3.319985	Up	C-X-C motif chemokine ligand 8
CPEB2	1.287266	0.002709	0.002709	3.190899	Up	cytoplasmic polyadenylation element binding protein 2
MIR4658	1.214578	0.000988	0.000988	3.546126	Up	microRNA 4658
PCK1	2.332999	0.000686	0.000686	3.671182	Up	phosphoenolpyruvatecarboxykinase 1
PTGS2	1.166879	0.002825	0.002825	3.175745	Up	prostaglandin-endoperoxide synthase 2
PYY2	1.951724	0.0009	0.0009	3.578458	Up	peptide YY 2 (pseudogene)
MIR155HG	2.607755	0.003291	0.003291	3.120187	Up	MIR155 host gene
FST	1.002466	0.003484	0.003484	3.099328	Up	follistatin
NT5C3AP1	1.382344	0.003652	0.003652	3.082118	Up	5'-nucleotidase, cytosolic IIIA pseudogene 1
S1PR3	1.016866	0.003129	0.003129	3.138595	Up	sphingosine-1-phosphate receptor 3
SH2D1B	1.950662	0.001057	0.001057	3.522935	Up	SH2 domain containing 1B
IL15RA	1.031885	0.003663	0.003663	3.081023	Up	interleukin 15 receptor subunit alpha
MIR6858	1.530612	0.000995	0.000995	3.543749	Up	microRNA 6858
PELI1	1.01622	0.003845	0.003845	3.063173	Up	pellino E3 ubiquitin protein ligase 1
RASGRP3	2.152879	0.004317	0.004317	3.020408	Up	RAS guanyl releasing protein 3
RND1	1.676447	0.00431	0.00431	3.021007	Up	Rho family GTPase 1
RAET1L	2.341954	0.003051	0.003051	3.147777	Up	retinoic acid early transcript 1L
PMAIP1	1.579452	0.00395	0.00395	3.053234	Up	phorbol-12-myristate-13-acetate-induced protein 1
LINC00702	1.692421	0.001703	0.001703	3.356428	Up	long intergenic non-protein coding RNA 702
ARRDC3	2.112019	0.003983	0.003983	3.050118	Up	arrestin domain containing 3
NFKBIA	2.468374	0.003893	0.003893	3.058548	Up	NFKB inhibitor alpha
FLRT3	1.128602	0.004664	0.004664	2.991615	Up	fibronectinleucine rich transmembrane protein 3
PTX3	2.370746	0.004751	0.004751	2.984718	Up	pentraxin 3
RASGRP1	1.171393	0.004796	0.004796	2.98127	Up	RAS guanyl releasing protein 1
SNPH	1.448459	0.004712	0.004712	2.987847	Up	syntaphilin
FAM110B	1.109894	0.004934	0.004934	2.970648	Up	family with sequence similarity 110 member B
IRF1	2.300085	0.004348	0.004348	3.017739	Up	interferon regulatory factor 1

SSTR2	1.261819	0.004685	0.004685	2.989962	Up	somatostatin receptor 2
INHBA	1.646008	0.004556	0.004556	3.000373	Up	inhibin subunit beta A
MEG9	2.535238	0.00317	0.00317	3.133856	Up	maternally expressed 9
MT2A	1.780429	0.005458	0.005458	2.932775	Up	metallothionein 2A
PCF11-AS1	0.986792	0.00518	0.00518	2.95242	Up	PCF11 antisense RNA 1
FILIP1L	1.100385	0.005771	0.005771	2.911785	Up	filamin A interacting protein 1 like
SNORD99	1.243138	0.004039	0.004039	3.045008	Up	small nucleolar RNA, C/D box 99
PTBP1P	1.255259	0.002482	0.002482	3.222381	Up	polypyrimidine tract binding protein 1 pseudogene
ZNF433	0.986216	0.005996	0.005996	2.897283	Up	zinc finger protein 433
ISG20	1.625812	0.005233	0.005233	2.948589	Up	interferon stimulated exonuclease gene 20
NPIPB12	1.304191	0.004596	0.004596	2.997106	Up	nuclear pore complex interacting protein family member B12
RNU6-42P	1.985584	0.002162	0.002162	3.271766	Up	RNA, U6 small nuclear 42, pseudogene
EPHA4	1.317026	0.006338	0.006338	2.876247	Up	EPH receptor A4
PHF11	1.023572	0.00619	0.00619	2.885234	Up	PHD finger protein 11
TMEM140	1.901798	0.006549	0.006549	2.863836	Up	transmembrane protein 140
GJB7	2.091619	0.002468	0.002468	3.224359	Up	gap junction protein beta 7
DRD1	1.203743	0.004927	0.004927	2.971207	Up	dopamine receptor D1
NKX3-1	1.66839	0.006759	0.006759	2.85177	Up	NK3 homeobox 1
HSH2D	1.388184	0.00634	0.00634	2.876122	Up	hematopoietic SH2 domain containing
CCDC116	1.816182	0.003193	0.003193	3.131229	Up	coiled-coil domain containing 116
LMO2	2.357774	0.006131	0.006131	2.888866	Up	LIM domain only 2
TCAF2P1	1.39396	0.002514	0.002514	3.217777	Up	TRPM8 channel associated factor 2 pseudogene 1
STX19	1.228144	0.007424	0.007424	2.815858	Up	syntaxin 19
NEURL3	1.180071	0.006801	0.006801	2.849388	Up	neuralized E3 ubiquitin protein ligase 3
PIM3	0.971536	0.006055	0.006055	2.893626	Up	Pim-3 proto-oncogene, serine/threonine kinase
TRIM5	1.060149	0.006461	0.006461	2.868977	Up	tripartite motif containing 5
PPP1R15A	2.652991	0.005578	0.005578	2.924601	Up	protein phosphatase 1 regulatory subunit 15A
SUSD3	1.860803	0.004923	0.004923	2.971514	Up	sushi domain containing 3
FBXO6	1.003573	0.007611	0.007611	2.806265	Up	F-box protein 6
VXN	1.394123	0.004571	0.004571	2.999171	Up	vexin
HIVEP1	1.001707	0.007557	0.007557	2.809016	Up	HIVEP zinc finger 1
IRF7	1.729251	0.006649	0.006649	2.858056	Up	interferon regulatory factor 7
TTLL11-IT1	1.253247	0.004223	0.004223	3.028542	Up	TTLL11 intronic transcript 1
BATF2	2.429025	0.008237	0.008237	2.775774	Up	basic leucine zipper ATF-like transcription factor 2
LSMEM1	1.091776	0.008071	0.008071	2.78367	Up	leucine rich single-pass membrane protein 1
PRKD2	1.113189	0.006541	0.006541	2.86427	Up	protein kinase D2
KLF4	1.96856	0.007874	0.007874	2.793199	Up	Kruppel like factor 4
IL7	1.224412	0.007628	0.007628	2.805444	Up	interleukin 7
SOCS1	1.705696	0.008894	0.008894	2.746003	Up	suppressor of cytokine signaling 1
ZC3H12A	1.050079	0.007753	0.007753	2.799153	Up	zinc finger CCCH-type containing 12A
CPEB3	1.400172	0.009168	0.009168	2.734169	Up	cytoplasmic polyadenylation element binding protein 3
CCL2	1.791533	0.0096	0.0096	2.716167	Up	C-C motif chemokine ligand 2
RNU6-118P	1.59562	0.004039	0.004039	3.044986	Up	RNA, U6 small nuclear 118, pseudogene
RTP4	2.084552	0.009589	0.009589	2.716614	Up	receptor transporter protein 4

NPFFR2	1.282538	0.009832	0.009832	2.706821	Up	neuropeptide FF receptor 2
FGF18	2.351473	0.006955	0.006955	2.840835	Up	fibroblast growth factor 18
HLA-F	1.391048	0.008852	0.008852	2.747861	Up	major histocompatibility complex, class I, F
PTCH2	1.044968	0.00774	0.00774	2.799821	Up	patched 2
FLT3LG	1.069156	0.010147	0.010147	2.694435	Up	fms related tyrosine kinase 3 ligand
IFIT5	1.67296	0.00902	0.00902	2.740526	Up	interferon induced protein with tetratricopeptide repeats 5
PDE2A	1.188121	0.008243	0.008243	2.775493	Up	phosphodiesterase 2A
STAT2	1.407434	0.008501	0.008501	2.763565	Up	signal transducer and activator of transcription 2
HM13-IT1	1.090514	0.008136	0.008136	2.780538	Up	HM13 intronic transcript 1
REC8	1.021857	0.010947	0.010947	2.664519	Up	REC8 meiotic recombination protein
CAVIN2	2.285666	0.006243	0.006243	2.882018	Up	caveolae associated protein 2
HSPB9	1.950222	0.005864	0.005864	2.905719	Up	heat shock protein family B (small) member 9
SYT1	1.240353	0.00991	0.00991	2.70374	Up	synaptotagmin 1
PPP4R1-AS1	1.416349	0.00527	0.00527	2.94595	Up	PPP4R1 antisense RNA 1
TNF	4.476993	0.010253	0.010253	2.690364	Up	tumor necrosis factor
NLRP3	1.161308	0.009898	0.009898	2.704187	Up	NLR family pyrin domain containing 3
MT2P1	1.653905	0.01201	0.01201	2.627752	Up	metallothionein 2 pseudogene 1
CCDC65	1.167987	0.008399	0.008399	2.768226	Up	coiled-coil domain containing 65
TDRD7	1.057286	0.010386	0.010386	2.685272	Up	tudor domain containing 7
MAP3K8	1.80803	0.011453	0.011453	2.646607	Up	mitogen-activated protein kinase kinasekinase 8
SNORD45A	1.256796	0.006181	0.006181	2.885782	Up	small nucleolar RNA, C/D box 45A
EYA1	1.132006	0.012143	0.012143	2.623339	Up	EYA transcriptional coactivator and phosphatase 1
GRM8	2.154	0.006504	0.006504	2.866431	Up	glutamate metabotropic receptor 8
CRTAM	1.58508	0.006252	0.006252	2.881438	Up	cytotoxic and regulatory T cell molecule
USP18	2.34472	0.012652	0.012652	2.606962	Up	ubiquitin specific peptidase 18
C4A	1.451882	0.012813	0.012813	2.601887	Up	complement C4A (Rodgers blood group)
EGR1	1.66146	0.010871	0.010871	2.66728	Up	early growth response 1
SEC16B	1.346299	0.013593	0.013593	2.578155	Up	SEC16 homolog B, endoplasmic reticulum export factor
TLR6	1.035853	0.011756	0.011756	2.636266	Up	toll like receptor 6
RRAD	1.434268	0.013182	0.013182	2.590506	Up	RRAD, Ras related glycolysis inhibitor and calcium channel regulator
SNORD43	1.013019	0.006974	0.006974	2.839796	Up	small nucleolar RNA, C/D box 43
NT5C3A	1.362242	0.009792	0.009792	2.708416	Up	5'-nucleotidase, cytosolic IIIA
PSMB8-AS1	1.488965	0.013918	0.013918	2.568645	Up	PSMB8 antisense RNA 1 (head to head)
SNORA75	1.356852	0.008426	0.008426	2.766984	Up	small nucleolar RNA, H/ACA box 75
DDX58	1.510966	0.010341	0.010341	2.686996	Up	DExD/H-box helicase 58
EXOC3L1	2.466537	0.009826	0.009826	2.707084	Up	exocyst complex component 3 like 1
TNFSF10	1.557624	0.011108	0.011108	2.658763	Up	TNF superfamily member 10
KLB	1.220487	0.009959	0.009959	2.701796	Up	klotho beta
PPM1K	1.467005	0.013458	0.013458	2.582188	Up	protein phosphatase, Mg2+/Mn2+ dependent 1K
ADAM20P1	1.21742	0.010682	0.010682	2.674194	Up	ADAM metallopeptidase domain 20 pseudogene 1
TRIM69	1.112992	0.012995	0.012995	2.596233	Up	tripartite motif containing 69
ICAM1	1.198605	0.011427	0.011427	2.647528	Up	intercellular adhesion molecule 1
KLF2	0.992225	0.015396	0.015396	2.527762	Up	Kruppel like factor 2
LINC00379	1.280167	0.007885	0.007885	2.792652	Up	long intergenic non-protein coding RNA 379

HLA-V	2.062224	0.014819	0.014819	2.543277	Up	major histocompatibility complex, class I, V (pseudogene)
MT1E	1.34699	0.015352	0.015352	2.528933	Up	metallothionein 1E
BDKRB2	2.347703	0.011723	0.011723	2.637358	Up	bradykinin receptor B2
PML	1.231562	0.01112	0.01112	2.658331	Up	promyelocyticleukemia
TSLP	1.139512	0.013131	0.013131	2.592064	Up	thymic stromal lymphopoietin
CCL20	1.320712	0.013951	0.013951	2.567674	Up	C-C motif chemokine ligand 20
MXD1	1.07566	0.01356	0.01356	2.579134	Up	MAX dimerization protein 1
MAGI2-AS3	1.279478	0.012211	0.012211	2.621132	Up	MAGI2 antisense RNA 3
MIR6755	1.162425	0.009661	0.009661	2.713702	Up	microRNA 6755
NOCT	1.603703	0.015388	0.015388	2.527964	Up	nocturnin
UQCRBP1	1.075448	0.011354	0.011354	2.650073	Up	ubiquinol-cytochrome c reductase binding protein pseudogene 1
JAK2	1.311816	0.015691	0.015691	2.520035	Up	Janus kinase 2
CMPK2	2.70339	0.015326	0.015326	2.529601	Up	cytidine/uridine monophosphate kinase 2
CX3CL1	1.925664	0.015426	0.015426	2.526979	Up	C-X3-C motif chemokine ligand 1
SLC5A5	2.242138	0.010518	0.010518	2.680321	Up	solute carrier family 5 member 5
PARP12	1.175203	0.012789	0.012789	2.60264	Up	poly(ADP-ribose) polymerase family member 12
DDR2	0.978944	0.013894	0.013894	2.569329	Up	discoidin domain receptor tyrosine kinase 2
OASL	2.738979	0.014331	0.014331	2.556821	Up	2'-5'-oligoadenylate synthetase like
PDE4B	2.095245	0.016787	0.016787	2.492428	Up	phosphodiesterase 4B
IFI16	1.597567	0.014307	0.014307	2.557501	Up	interferon gamma inducible protein 16
HELZ2	1.994702	0.011455	0.011455	2.646565	Up	helicase with zinc finger 2
TRAF1	2.20676	0.018458	0.018458	2.453351	Up	TNF receptor associated factor 1
ADGRL3	1.033359	0.01695	0.01695	2.488459	Up	adhesion G protein-coupled receptor L3
RPL32P33	1.257833	0.010268	0.010268	2.689796	Up	ribosomal protein L32 pseudogene 33
NPM1P25	1.008455	0.013652	0.013652	2.576406	Up	nucleophosmin 1 pseudogene 25
GPER1	1.116291	0.015696	0.015696	2.519906	Up	G protein-coupled estrogen receptor 1
FOS	1.706227	0.017598	0.017598	2.473045	Up	Fos proto-oncogene, AP-1 transcription factor subunit
DUSP8	1.371125	0.016284	0.016284	2.504892	Up	dual specificity phosphatase 8
LINC01776	1.165105	0.011202	0.011202	2.655405	Up	long intergenic non-protein coding RNA 1776
ZNF300P1	2.24229	0.013533	0.013533	2.579942	Up	zinc finger protein 300 pseudogene 1
ACHE	1.544797	0.019349	0.019349	2.433815	Up	acetylcholinesterase (Cartwright blood group)
MIR181B1	1.160878	0.011121	0.011121	2.658298	Up	microRNA 181b-1
CRYZL2P-SEC16B	1.027383	0.019339	0.019339	2.434045	Up	CRYZL2P-SEC16B readthrough
TTBK1	1.503124	0.013633	0.013633	2.576986	Up	tau tubulin kinase 1
GLCCI1	1.148217	0.019112	0.019112	2.438929	Up	glucocorticoid induced 1
IFNL4	4.46189	0.01501	0.01501	2.538078	Up	interferon lambda 4 (gene/pseudogene)
DSCAML1	1.460424	0.012937	0.012937	2.598035	Up	DS cell adhesion molecule like 1
FAP	2.823863	0.018119	0.018119	2.461027	Up	fibroblast activation protein alpha
SNORA23	1.063009	0.013827	0.013827	2.571278	Up	small nucleolar RNA, H/ACA box 23
RPL23AP67	1.335781	0.012478	0.012478	2.612487	Up	ribosomal protein L23a pseudogene 67
MIR6732	1.251011	0.017038	0.017038	2.486355	Up	microRNA 6732
LINC00944	1.508372	0.021096	0.021096	2.397768	Up	long intergenic non-protein coding RNA 944
MXRA5	1.934851	0.017135	0.017135	2.484009	Up	matrix remodeling associated 5
KRT8P41	1.187927	0.012931	0.012931	2.598206	Up	keratin 8 pseudogene 41

TENT5A	1.884328	0.017779	0.017779	2.468826	Up	terminal nucleotidyltransferase 5A
PGLYRP2	2.929254	0.015156	0.015156	2.534141	Up	peptidoglycan recognition protein 2
RPS3P2	1.464118	0.013958	0.013958	2.567496	Up	ribosomal protein S3 pseudogene 2
EGR4	1.730147	0.020773	0.020773	2.404222	Up	early growth response 4
DACT1	1.295892	0.0146	0.0146	2.54931	Up	dishevelled binding antagonist of beta catenin 1
CCRL2	1.058009	0.018202	0.018202	2.459137	Up	C-C motif chemokine receptor like 2
PTPN20CP	1.200421	0.013809	0.013809	2.571804	Up	protein tyrosine phosphatase non-receptor type 20C, pseudogene
UBE2FP1	0.976314	0.018618	0.018618	2.449779	Up	UBE2F pseudogene 1
EPSTI1	1.998154	0.020865	0.020865	2.402374	Up	epithelial stromal interaction 1
C17orf82	1.121734	0.013795	0.013795	2.572217	Up	chromosome 17 open reading frame 82
LINC00921	1.081181	0.019125	0.019125	2.438646	Up	long intergenic non-protein coding RNA 921
RELB	1.134588	0.017791	0.017791	2.468551	Up	RELB proto-oncogene, NF-kB subunit
OTOG	1.246961	0.014307	0.014307	2.557504	Up	otogelin
SNED1	1.126954	0.018021	0.018021	2.463255	Up	sushi, nidogen and EGF like domains 1
KRT8P9	1.127192	0.017976	0.017976	2.464283	Up	keratin 8 pseudogene 9
RSAD2	2.968518	0.017912	0.017912	2.465764	Up	radical S-adenosyl methionine domain containing 2
FABP5P7	1.183973	0.018952	0.018952	2.442416	Up	fatty acid binding protein 5 pseudogene 7
RPL3P3	1.040919	0.01776	0.01776	2.469267	Up	ribosomal protein L3 pseudogene 3
HUS1B	1.176098	0.014771	0.014771	2.544578	Up	HUS1 checkpoint clamp component B
PTGER4	1.166411	0.017949	0.017949	2.464901	Up	prostaglandin E receptor 4
NRIR	2.534489	0.016852	0.016852	2.490855	Up	negative regulator of interferon response
BAHCC1	2.310362	0.018059	0.018059	2.46238	Up	BAH domain and coiled-coil containing 1
POU5F1P4	1.205331	0.015216	0.015216	2.53253	Up	POU class 5 homeobox 1 pseudogene 4
TRIM38	1.011581	0.016894	0.016894	2.489823	Up	tripartite motif containing 38
HEG1	1.405079	0.019606	0.019606	2.428325	Up	heart development protein with EGF like domains 1
IBA57-DT	1.270711	0.015518	0.015518	2.524546	Up	IBA57 divergent transcript
GFI1	1.038605	0.019788	0.019788	2.424484	Up	growth factor independent 1 transcriptional repressor
IFI44	1.333776	0.016286	0.016286	2.504844	Up	interferon induced protein 44
HCG27	1.170291	0.023867	0.023867	2.345765	Up	HLA complex group 27
SLFN5	1.280898	0.016339	0.016339	2.503512	Up	schlafen family member 5
SNORD51	1.151033	0.017661	0.017661	2.471574	Up	small nucleolar RNA, C/D box 51
HIVEP2	1.293468	0.018322	0.018322	2.456407	Up	HIVEP zinc finger 2
ZNFX1	1.627282	0.014175	0.014175	2.561264	Up	zinc finger NFX1-type containing 1
IFIT1	2.561105	0.016495	0.016495	2.499621	Up	interferon induced protein with tetratricopeptide repeats 1
IFIT3	3.218305	0.01961	0.01961	2.428246	Up	interferon induced protein with tetratricopeptide repeats 3
CLEC4A	1.189563	0.018783	0.018783	2.446145	Up	C-type lectin domain family 4 member A
GBP1	2.03415	0.020119	0.020119	2.417586	Up	guanylate binding protein 1
NCKAP5	0.996077	0.023759	0.023759	2.347681	Up	NCK associated protein 5
NTNG2	1.601333	0.017227	0.017227	2.481819	Up	netrin G2
NCOA7	1.441337	0.019458	0.019458	2.431477	Up	nuclear receptor coactivator 7
SIX2	1.120981	0.020052	0.020052	2.418961	Up	SIX homeobox 2
SLC30A3	2.133137	0.018958	0.018958	2.442283	Up	solute carrier family 30 member 3
C1QTNF1	1.067021	0.026362	0.026362	2.303386	Up	C1q and TNF related 1
MIR4746	1.276655	0.017879	0.017879	2.466522	Up	microRNA 4746

TRIM40	1.454307	0.017735	0.017735	2.469864	Up	tripartite motif containing 40
RPL7P4	1.136645	0.017474	0.017474	2.475968	Up	ribosomal protein L7 pseudogene 4
PDZD2	1.653125	0.026708	0.026708	2.297798	Up	PDZ domain containing 2
BBC3	1.867442	0.02492	0.02492	2.327414	Up	BCL2 binding component 3
SLC25A2	1.698735	0.018696	0.018696	2.448053	Up	solute carrier family 25 member 2
RBM11	1.06029	0.027123	0.027123	2.291171	Up	RNA binding motif protein 11
TAP1	1.637892	0.016736	0.016736	2.493673	Up	transporter 1, ATP binding cassette subfamily B member
GTF2IP5	1.205973	0.020502	0.020502	2.409704	Up	general transcription factor IIipseudogene 5
HSD17B14	1.721928	0.026856	0.026856	2.295424	Up	hydroxysteroid 17-beta dehydrogenase 14
TGIF2P1	1.308314	0.01858	0.01858	2.450639	Up	TGFB induced factor homeobox 2 pseudogene 1
IFIT2	3.561866	0.019495	0.019495	2.430687	Up	interferon induced protein with tetratricopeptide repeats 2
LINC01828	0.980615	0.023596	0.023596	2.350603	Up	long intergenic non-protein coding RNA 1828
CYP21A2	1.608816	0.020828	0.020828	2.403107	Up	cytochrome P450 family 21 subfamily A member 2
ID4	1.517486	0.023666	0.023666	2.349345	Up	inhibitor of DNA binding 4, HLH protein
LTB	1.280863	0.027193	0.027193	2.290071	Up	lymphotoxin beta
BCL3	1.233657	0.023166	0.023166	2.358376	Up	BCL3 transcription coactivator
LINC00365	1.462171	0.019292	0.019292	2.435048	Up	long intergenic non-protein coding RNA 365
LINC01842	1.02113	0.022746	0.022746	2.366107	Up	long intergenic non-protein coding RNA 1842
RPS29P5	0.981563	0.018987	0.018987	2.441648	Up	ribosomal protein S29 pseudogene 5
OR52K3P	3.103385	0.024559	0.024559	2.333614	Up	olfactory receptor family 52 subfamily K member 3 pseudogene
PPP4R4	1.863424	0.028674	0.028674	2.267217	Up	protein phosphatase 4 regulatory subunit 4
UNC93B3	1.117507	0.022747	0.022747	2.36608	Up	unc-93 homolog B3, pseudogene
MMP25	0.973873	0.026311	0.026311	2.304209	Up	matrix metallopeptidase 25
LINC01270	1.195411	0.023609	0.023609	2.350372	Up	long intergenic non-protein coding RNA 1270
CPO	1.34441	0.020348	0.020348	2.412851	Up	carboxypeptidase O
KRT18P23	1.092607	0.02103	0.02103	2.399081	Up	keratin 18 pseudogene 23
HSD17B3	0.986893	0.021642	0.021642	2.387047	Up	hydroxysteroid 17-beta dehydrogenase 3
KRT8P51	1.056055	0.021823	0.021823	2.383542	Up	keratin 8 pseudogene 51
GRIP2	2.364844	0.022972	0.022972	2.361941	Up	glutamate receptor interacting protein 2
NPTX1	1.892145	0.027887	0.027887	2.279222	Up	neuronal pentraxin 1
HIF1A-AS2	1.125575	0.024679	0.024679	2.33154	Up	HIF1A antisense RNA 2
CYLD	1.094273	0.023034	0.023034	2.360798	Up	CYLD lysine 63 deubiquitinase
MX2	2.681049	0.024951	0.024951	2.326879	Up	MX dynamin like GTPase 2
MIR3149	1.183791	0.021476	0.021476	2.390278	Up	microRNA 3149
ACTBP13	1.061712	0.027204	0.027204	2.289892	Up	ACTB pseudogene 13
GFPT2	1.751351	0.024276	0.024276	2.33854	Up	glutamine-fructose-6-phosphate transaminase 2
IFNL2	7.294253	0.026645	0.026645	2.298816	Up	interferon lambda 2
LINC00592	1.216015	0.021953	0.021953	2.381058	Up	long intergenic non-protein coding RNA 592
SECTM1	1.759868	0.03083	0.03083	2.235763	Up	secreted and transmembrane 1
C11orf96	1.785984	0.030349	0.030349	2.242603	Up	chromosome 11 open reading frame 96
ESRRAP1	1.147711	0.026589	0.026589	2.299719	Up	estrogen-related receptor alpha pseudogene 1
HMGN2P17	1.106579	0.02261	0.02261	2.368634	Up	high mobility group nucleosomal binding domain 2 pseudogene 17
DHX58	2.060659	0.028206	0.028206	2.274327	Up	DExH-box helicase 58
NPR3	1.143846	0.031319	0.031319	2.228904	Up	natriuretic peptide receptor 3

ENO4	1.324046	0.02347	0.02347	2.352871	Up	enolase 4
DNAJB4	1.195125	0.025158	0.025158	2.323368	Up	DnaJ heat shock protein family (Hsp40) member B4
AGAP7P	1.197694	0.024391	0.024391	2.336542	Up	ArfGAP with GTPase domain, ankyrin repeat and PH domain 7, pseudogene
WIF1	1.801026	0.027444	0.027444	2.286126	Up	WNT inhibitory factor 1
GIMAP2	1.450887	0.033618	0.033618	2.197865	Up	GTPase, IMAP family member 2
SNCA-AS1	1.30856	0.024784	0.024784	2.329738	Up	SNCA antisense RNA 1
IGHEP2	1.730187	0.025917	0.025917	2.310664	Up	immunoglobulin heavy constant epsilon P2 (pseudogene)
NKAIN4	1.079188	0.030231	0.030231	2.244293	Up	sodium/potassium transporting ATPase interacting 4
IFNL3	6.960425	0.030292	0.030292	2.243419	Up	interferon lambda 3
APOL6	1.972526	0.023754	0.023754	2.347772	Up	apolipoprotein L6
HLA-K	1.398083	0.031612	0.031612	2.224833	Up	major histocompatibility complex, class I, K (pseudogene)
APOBEC3G	1.393513	0.034315	0.034315	2.188823	Up	apolipoprotein B mRNA editing enzyme catalytic subunit 3G
MIR6783	1.146925	0.026554	0.026554	2.300273	Up	microRNA 6783
FAXDC2	1.31946	0.025905	0.025905	2.310869	Up	fatty acid hydroxylase domain containing 2
GRIN3B	1.025113	0.025676	0.025676	2.314671	Up	glutamate ionotropic receptor NMDA type subunit 3B
NR4A3	2.456563	0.032207	0.032207	2.216678	Up	nuclear receptor subfamily 4 group A member 3
GSN-AS1	1.34287	0.02662	0.02662	2.299211	Up	GSN antisense RNA 1
HSPA8P4	1.110122	0.028288	0.028288	2.273064	Up	heat shock protein family A (Hsp70) member 8 pseudogene 4
RPL5P27	1.029437	0.028985	0.028985	2.262557	Up	ribosomal protein L5 pseudogene 27
HCRTR1	1.356253	0.026783	0.026783	2.296597	Up	hypocretin receptor 1
DTX3L	1.241553	0.022503	0.022503	2.370634	Up	deltex E3 ubiquitin ligase 3L
PLAC8	1.12988	0.036412	0.036412	2.162594	Up	placenta associated 8
FAM153B	1.109809	0.027683	0.027683	2.282391	Up	family with sequence similarity 153 member B
KRT18P65	1.153395	0.027995	0.027995	2.277555	Up	keratin 18 pseudogene 65
GMPR	1.58705	0.037047	0.037047	2.154903	Up	guanosine monophosphate reductase
TAGAP	1.952626	0.031513	0.031513	2.226205	Up	T cell activation RhoGTPase activating protein
TSACC	0.983953	0.031583	0.031583	2.22523	Up	TSSK6 activating cochaperone
RNVU1-3	1.057849	0.028659	0.028659	2.267445	Up	RNA, variant U1 small nuclear 3
FAR1-IT1	1.242995	0.031536	0.031536	2.22589	Up	FAR1 intronic transcript 1
LAYN	1.01366	0.034792	0.034792	2.182737	Up	layilin
PRRX2	1.066129	0.029118	0.029118	2.260562	Up	paired related homeobox 2
OAS1	1.597942	0.02226	0.02226	2.375201	Up	2'-5'-oligoadenylate synthetase 1
LGALS9DP	1.229939	0.037564	0.037564	2.148731	Up	galectin 9D, pseudogene
LYL1	1.02326	0.030923	0.030923	2.234445	Up	LYL1 basic helix-loop-helix family member
TRPC4	2.46787	0.033183	0.033183	2.203595	Up	transient receptor potential cation channel subfamily C member 4
TRANK1	2.363383	0.03259	0.03259	2.211501	Up	tetratricopeptide repeat and ankyrin repeat containing 1
DNAH17	2.326232	0.039601	0.039601	2.125132	Up	dynein axonemal heavy chain 17
DUSP26	1.054625	0.03446	0.03446	2.186973	Up	dual specificity phosphatase 26
EGOT	1.086133	0.039665	0.039665	2.124413	Up	eosinophil granule ontogeny transcript
PRDX3P1	1.083736	0.031075	0.031075	2.232304	Up	peroxiredoxin 3 pseudogene 1
SLC6A13	1.501002	0.036308	0.036308	2.163859	Up	solute carrier family 6 member 13
TNFSF13B	2.065925	0.040316	0.040316	2.117106	Up	TNF superfamily member 13b
ETV7	2.824932	0.039935	0.039935	2.121369	Up	ETS variant transcription factor 7

CXCL11	3.746603	0.039022	0.039022	2.131729	Up	C-X-C motif chemokine ligand 11
IL7R	1.798366	0.039173	0.039173	2.129999	Up	interleukin 7 receptor
MIR561	1.447165	0.031861	0.031861	2.221401	Up	microRNA 561
RPS15AP36	1.015597	0.032121	0.032121	2.217845	Up	ribosomal protein S15a pseudogene 36
RAB19	1.058422	0.04094	0.04094	2.1102	Up	RAB19, member RAS oncogene family
NPM1P8	1.170906	0.03213	0.03213	2.217726	Up	nucleophosmin 1 pseudogene 8
CFAP57	1.463252	0.041154	0.041154	2.107843	Up	cilia and flagella associated protein 57
RNU6-9	1.245936	0.032744	0.032744	2.209429	Up	RNA, U6 small nuclear 9
DNAH3	1.414655	0.038431	0.038431	2.13856	Up	dynein axonemal heavy chain 3
HERC5	2.161167	0.030697	0.030697	2.237641	Up	HECT and RLD domain containing E3 ubiquitin protein ligase 5
GJC3	1.038149	0.033576	0.033576	2.198413	Up	gap junction protein gamma 3
CLPSL1	1.039994	0.033025	0.033025	2.205691	Up	colipase like 1
NANOS3	0.973953	0.039476	0.039476	2.126556	Up	nanos C2HC-type zinc finger 3
HLX	0.980112	0.040761	0.040761	2.112168	Up	H2.0 like homeobox
PPEF1	1.701957	0.034682	0.034682	2.184142	Up	protein phosphatase with EF-hand domain 1
BNIP3P5	1.033777	0.034589	0.034589	2.185322	Up	BCL2 interacting protein 3 pseudogene 5
RNU6-2	1.318645	0.034433	0.034433	2.187314	Up	RNA, U6 small nuclear 2
FGF19	1.848509	0.037723	0.037723	2.14686	Up	fibroblast growth factor 19
GRIA2	1.275124	0.034497	0.034497	2.18649	Up	glutamate ionotropic receptor AMPA type subunit 2
SAMD9L	2.208484	0.028313	0.028313	2.272692	Up	sterile alpha motif domain containing 9 like
SOGA3	1.273369	0.039684	0.039684	2.124196	Up	SOGA family member 3
VSTM1	1.437544	0.036407	0.036407	2.162649	Up	V-set and transmembrane domain containing 1
MIR21	0.99124	0.03483	0.03483	2.182251	Up	microRNA 21
SNCAIP	1.309269	0.036092	0.036092	2.166507	Up	synuclein alpha interacting protein
GLI2	1.229791	0.042829	0.042829	2.089831	Up	GLI family zinc finger 2
ATP5MFP5	0.981783	0.035159	0.035159	2.178105	Up	ATP synthase membrane subunit f pseudogene 5
NLRC5	2.313605	0.039075	0.039075	2.131125	Up	NLR family CARD domain containing 5
MOGAT3	1.263134	0.035615	0.035615	2.172396	Up	monoacylglycerol O-acyltransferase 3
IFNL1	6.558198	0.042365	0.042365	2.094759	Up	interferon lambda 1
RNU6-36P	1.000687	0.035366	0.035366	2.175511	Up	RNA, U6 small nuclear 36, pseudogene
BARX1	1.219153	0.035867	0.035867	2.169275	Up	BARX homeobox 1
NEURL1	1.252787	0.036034	0.036034	2.167215	Up	neuralized E3 ubiquitin protein ligase 1
UBE2L6	1.187087	0.028313	0.028313	2.27269	Up	ubiquitin conjugating enzyme E2 L6
RPL7P16	1.000687	0.035979	0.035979	2.167896	Up	ribosomal protein L7 pseudogene 16
CAPN9	1.164853	0.036313	0.036313	2.1638	Up	calpain 9
SCARNA21	1.112307	0.036345	0.036345	2.163406	Up	small Cajal body-specific RNA 21
CREB5	1.271347	0.033318	0.033318	2.2018	Up	cAMP responsive element binding protein 5
TTC9B	1.702168	0.042771	0.042771	2.090449	Up	tetratricopeptide repeat domain 9B
PLA2G4C	1.765984	0.044372	0.044372	2.073774	Up	phospholipase A2 group IVC
OR52K1	1.334067	0.037334	0.037334	2.151468	Up	olfactory receptor family 52 subfamily K member 1
EEF1B2P1	0.984321	0.036822	0.036822	2.15762	Up	eukaryotic translation elongation factor 1 beta 2 pseudogene 1
RGS16	0.995551	0.045839	0.045839	2.058957	Up	regulator of G protein signaling 16
RPS4XP6	0.985811	0.038419	0.038419	2.13869	Up	ribosomal protein S4X pseudogene 6
C12orf74	1.430087	0.046128	0.046128	2.056088	Up	chromosome 12 open reading frame 74

IL17C	1.502953	0.0387	0.0387	2.135437	Up	interleukin 17C
ST7-AS2	1.093846	0.038488	0.038488	2.137896	Up	ST7 antisense RNA 2
RPL15P14	1.086068	0.038276	0.038276	2.140367	Up	ribosomal protein L15 pseudogene 14
MKRN4P	1.066528	0.040566	0.040566	2.114323	Up	makorin ring finger protein 4, pseudogene
RNU6-112P	1.316138	0.039026	0.039026	2.131687	Up	RNA, U6 small nuclear 112, pseudogene
C4B	1.325091	0.047086	0.047086	2.046681	Up	complement C4B (Chido blood group)
XRN1	1.118066	0.0286	0.0286	2.268334	Up	5'-3' exoribonuclease 1
TENT5C	1.355371	0.047524	0.047524	2.042439	Up	terminal nucleotidyltransferase 5C
CH25H	4.536363	0.044758	0.044758	2.069841	Up	cholesterol 25-hydroxylase
CXCL10	4.060103	0.045354	0.045354	2.06381	Up	C-X-C motif chemokine ligand 10
ICAM5	1.09693	0.047503	0.047503	2.042646	Up	intercellular adhesion molecule 5
KRT8P21	1.050895	0.039864	0.039864	2.122164	Up	keratin 8 pseudogene 21
DRP2	1.00278	0.045983	0.045983	2.057525	Up	dystrophin related protein 2
IQUB	0.998389	0.044762	0.044762	2.069799	Up	IQ motif and ubiquitin domain containing
IFNB1	7.886233	0.046451	0.046451	2.052901	Up	interferon beta 1
MIR1260B	1.000687	0.040129	0.040129	2.119193	Up	microRNA 1260b
ACKR4	1.676381	0.049108	0.049108	2.027371	Up	atypical chemokine receptor 4
LINC00896	1.002351	0.046506	0.046506	2.052355	Up	long intergenic non-protein coding RNA 896
KRT18P32	1.040177	0.040846	0.040846	2.111227	Up	keratin 18 pseudogene 32
RASD1	1.869128	0.043244	0.043244	2.085464	Up	ras related dexamethasone induced 1
RANBP20P	1.025185	0.047951	0.047951	2.038334	Up	RAN binding protein 20 pseudogene
IFITM2	1.503363	0.040572	0.040572	2.114262	Up	interferon induced transmembrane protein 2
UBA7	1.433698	0.039971	0.039971	2.120967	Up	ubiquitin like modifier activating enzyme 7
RPL21P39	1.092851	0.042334	0.042334	2.095097	Up	ribosomal protein L21 pseudogene 39
LRIT3	1.088965	0.044742	0.044742	2.069999	Up	leucine rich repeat, Ig-like and transmembrane domains 3
RNVU1-6	1.013387	0.042786	0.042786	2.090292	Up	RNA, variant U1 small nuclear 6
RPL7P48	1.05168	0.042941	0.042941	2.088652	Up	ribosomal protein L7 pseudogene 48
GAPDHP14	1.025312	0.045953	0.045953	2.057821	Up	glyceraldehyde-3-phosphate dehydrogenase pseudogene 14
CFAP126	1.018579	0.043708	0.043708	2.080627	Up	cilia and flagella associated protein 126
SLITRK6	0.985385	0.04893	0.04893	2.029046	Up	SLIT and NTRK like family member 6
SLC39A2	0.99807	0.043863	0.043863	2.079022	Up	solute carrier family 39 member 2
BMP2	1.088449	0.043048	0.043048	2.087522	Up	bone morphogenetic protein 2
PROX1	2.157738	0.046523	0.046523	2.052189	Up	prosperohomeobox 1
LINC02208	1.163731	0.044216	0.044216	2.075374	Up	long intergenic non-protein coding RNA 2208
KRT8P13	1.061892	0.047377	0.047377	2.043857	Up	keratin 8 pseudogene 13
FAM71A	1.384372	0.044806	0.044806	2.069348	Up	family with sequence similarity 71 member A
KRT18P39	1.055271	0.044327	0.044327	2.074238	Up	keratin 18 pseudogene 39
TNFRSF4	1.161419	0.045014	0.045014	2.067238	Up	TNF receptor superfamily member 4
LINC02158	1.71431	0.04625	0.04625	2.054877	Up	long intergenic non-protein coding RNA 2158
SYNPR	1.148755	0.048624	0.048624	2.031935	Up	synaptoporin
MIR378D2HG	0.981368	0.047575	0.047575	2.041953	Up	MIR378D2 host gene
MIR616	1.253841	0.04747	0.04747	2.042961	Up	microRNA 616
SPINK9	0.983536	0.0458	0.0458	2.059351	Up	serine peptidase inhibitor, Kazal type 9
ZC3HAV1	1.663924	0.02955	0.02955	2.254194	Up	zinc finger CCCH-type containing, antiviral 1

WASIR1	1.008143	0.046413	0.046413	2.053269	Up	WASH and IL9R antisense RNA 1
NYAP2	1.229121	0.046708	0.046708	2.050375	Up	neuronal tyrosine-phosphorylated phosphoinositide-3-kinase adaptor 2
FBLN2	1.398336	0.047561	0.047561	2.042085	Up	fibulin 2
IFNA22P	1.191131	0.047354	0.047354	2.044079	Up	interferon alpha 22, pseudogene
IFIH1	2.02643	0.031036	0.031036	2.232862	Up	interferon induced with helicase C domain 1
DDX60L	1.599206	0.03412	0.03412	2.191341	Up	DExD/H-box 60 like
ACTA1	1.277548	0.049708	0.049708	2.021775	Up	actin alpha 1, skeletal muscle
HCG4B	1.366816	0.048693	0.048693	2.031275	Up	HLA complex group 4B
RAB44	0.976113	0.048958	0.048958	2.02878	Up	RAB44, member RAS oncogene family
FLT3	1.052002	0.049512	0.049512	2.023598	Up	fms related tyrosine kinase 3
MYLPF	1.062085	0.049819	0.049819	2.020748	Up	myosin light chain, phosphorylatable, fast skeletal muscle
ISG15	1.263658	0.030733	0.030733	2.237127	Up	ISG15 ubiquitin like modifier
PARP10	1.234323	0.030263	0.030263	2.243842	Up	poly(ADP-ribose) polymerase family member 10
TRIM22	2.76806	0.047353	0.047353	2.044093	Up	tripartite motif containing 22
IFI35	1.186849	0.035784	0.035784	2.17031	Up	interferon induced protein 35
XAF1	2.277595	0.048717	0.048717	2.031053	Up	XIAP associated factor 1
SP110	1.220132	0.037857	0.037857	2.145278	Up	SP110 nuclear body protein
IFITM1	1.532486	0.046551	0.046551	2.051918	Up	interferon induced transmembrane protein 1
SAMD9	1.587525	0.030596	0.030596	2.239074	Up	sterile alpha motif domain containing 9
SAMHD1	1.302206	0.035925	0.035925	2.16856	Up	SAM and HD domain containing deoxynucleoside triphosphate triphosphohydrolase 1
OAS2	2.244301	0.040811	0.040811	2.111617	Up	2'-5'-oligoadenylate synthetase 2
LGALS9	1.196441	0.048775	0.048775	2.030501	Up	galectin 9
PSMB9	1.080296	0.049952	0.049952	2.019517	Up	proteasome 20S subunit beta 9
MAGT1	-0.46678	1.09E-06	1.09E-06	-5.70983	Down	magnesium transporter 1
CFI	-0.93098	1.33E-05	1.33E-05	-4.94224	Down	complement factor I
SGPP1	-0.42842	3.03E-05	3.03E-05	-4.68502	Down	sphingosine-1-phosphate phosphatase 1
ITM2A	-0.79568	3.34E-05	3.34E-05	-4.65404	Down	integral membrane protein 2A
PSAP	-0.50092	2.89E-05	2.89E-05	-4.69931	Down	prosaposin
LYZ	-0.58944	3.85E-05	3.85E-05	-4.60915	Down	lysozyme
CTSH	-0.59789	5.02E-05	5.02E-05	-4.52551	Down	cathepsin H
SLC44A4	-0.73935	6.46E-05	6.46E-05	-4.44558	Down	solute carrier family 44 member 4
SSPN	-0.72555	6.75E-05	6.75E-05	-4.43157	Down	sarcospan
TSPAN8	-0.68203	8.56E-05	8.56E-05	-4.35561	Down	tetraspanin 8
VWA1	-0.55974	0.00012	0.00012	-4.24652	Down	von Willebrand factor A domain containing 1
OLFM4	-0.80311	0.000122	0.000122	-4.2421	Down	olfactomedin 4
TM4SF4	-0.64526	0.000109	0.000109	-4.2794	Down	transmembrane 4 L six family member 4
PLS1	-0.43719	0.000122	0.000122	-4.24199	Down	plastin 1
ANXA13	-1.66049	7.64E-05	7.64E-05	-4.39178	Down	annexin A13
METRN	-0.55327	0.000146	0.000146	-4.18407	Down	meteorin, glial cell differentiation regulator
GJB1	-0.81958	0.00016	0.00016	-4.15427	Down	gap junction protein beta 1
TMBIM6	-0.51036	0.000131	0.000131	-4.21891	Down	transmembrane BAX inhibitor motif containing 6
CD24	-0.51865	0.000151	0.000151	-4.17251	Down	CD24 molecule
SCGN	-0.99086	0.000181	0.000181	-4.11456	Down	secretagogin, EF-hand calcium binding protein
SIAE	-0.52037	0.000271	0.000271	-3.98215	Down	sialic acid acetylesterase

UGT1A7	-0.45953	0.000307	0.000307	-3.93991	Down	UDP glucuronosyltransferase family 1 member A7
UGT1A9	-0.46823	0.000326	0.000326	-3.92013	Down	UDP glucuronosyltransferase family 1 member A9
UGT1A3	-0.46877	0.000343	0.000343	-3.90325	Down	UDP glucuronosyltransferase family 1 member A3
UGT1A8	-0.46698	0.00035	0.00035	-3.89726	Down	UDP glucuronosyltransferase family 1 member A8
HOGA1	-0.79131	0.000329	0.000329	-3.91705	Down	4-hydroxy-2-oxoglutarate aldolase 1
SHMT1	-0.4209	0.00036	0.00036	-3.8875	Down	serine hydroxymethyltransferase 1
UGT1A5	-0.46515	0.000369	0.000369	-3.87933	Down	UDP glucuronosyltransferase family 1 member A5
SAC3D1	-0.43211	0.000393	0.000393	-3.8582	Down	SAC3 domain containing 1
GNG12	-0.41783	0.000359	0.000359	-3.88813	Down	G protein subunit gamma 12
GALM	-0.5502	0.00041	0.00041	-3.84468	Down	galactosemutarotase
UGT1A4	-0.45879	0.000415	0.000415	-3.83988	Down	UDP glucuronosyltransferase family 1 member A4
DNAJC22	-0.6406	0.000451	0.000451	-3.81275	Down	DnaJ heat shock protein family (Hsp40) member C22
AQP1	-1.17011	0.000306	0.000306	-3.94147	Down	aquaporin 1 (Colton blood group)
TRNP1	-0.38875	0.000407	0.000407	-3.84671	Down	TMF1 regulated nuclear protein 1
RARRES1	-0.56345	0.00045	0.00045	-3.81304	Down	retinoic acid receptor responder 1
ADORA1	-0.9796	0.000419	0.000419	-3.83685	Down	adenosine A1 receptor
UGT1A6	-0.44678	0.000557	0.000557	-3.74143	Down	UDP glucuronosyltransferase family 1 member A6
FDX1	-0.41547	0.000595	0.000595	-3.71951	Down	ferredoxin 1
PGRMC1	-0.45097	0.000529	0.000529	-3.75906	Down	progesterone receptor membrane component 1
PROM2	-0.67421	0.000627	0.000627	-3.70129	Down	prominin 2
PIGN	-0.41433	0.000617	0.000617	-3.7068	Down	phosphatidylinositol glycan anchor biosynthesis class N
SLC38A4	-0.79405	0.000539	0.000539	-3.75265	Down	solute carrier family 38 member 4
PIGK	-0.4078	0.00063	0.00063	-3.70002	Down	phosphatidylinositol glycan anchor biosynthesis class K
CEBPZOS	-0.4198	0.000649	0.000649	-3.68965	Down	CEBPZ opposite strand
DPYSL2	-0.49063	0.000742	0.000742	-3.6445	Down	dihydropyrimidinase like 2
OAT	-0.46474	0.000772	0.000772	-3.63064	Down	ornithine aminotransferase
ALDH2	-0.41385	0.000807	0.000807	-3.61555	Down	aldehyde dehydrogenase 2 family member
VTCN1	-0.97713	0.000891	0.000891	-3.5817	Down	V-set domain containing T cell activation inhibitor 1
SPDEF	-0.78179	0.000878	0.000878	-3.58696	Down	SAM pointed domain containing ETS transcription factor
ALCAM	-0.44456	0.00071	0.00071	-3.65946	Down	activated leukocyte cell adhesion molecule
SCP2	-0.41269	0.000896	0.000896	-3.58005	Down	sterol carrier protein 2
ALDH6A1	-0.46343	0.001038	0.001038	-3.52913	Down	aldehyde dehydrogenase 6 family member A1
TRMT2B	-0.37714	0.001062	0.001062	-3.5214	Down	tRNAmethyltransferase 2 homolog B
AIF1L	-0.47647	0.001086	0.001086	-3.51375	Down	allograft inflammatory factor 1 like
FAHD1	-0.41952	0.001089	0.001089	-3.51274	Down	fumarylacetoacetate hydrolase domain containing 1
MME	-0.88764	0.001092	0.001092	-3.51173	Down	membrane metalloendopeptidase
NR2F2-AS1	-0.5503	0.001173	0.001173	-3.48692	Down	NR2F2 antisense RNA 1
CRYZ	-0.57692	0.001065	0.001065	-3.52039	Down	crystallin zeta
GLYATL2	-1.13178	0.000661	0.000661	-3.68389	Down	glycine-N-acyltransferase like 2
TMPRSS4	-0.39083	0.001257	0.001257	-3.46293	Down	transmembrane serine protease 4
TSPAN6	-0.40619	0.00115	0.00115	-3.49376	Down	tetraspanin 6
RBPMS-AS1	-0.57454	0.001256	0.001256	-3.46318	Down	RBPMS antisense RNA 1
NOSTRIN	-0.61474	0.001355	0.001355	-3.43683	Down	nitric oxide synthase trafficking
SPP1	-0.60713	0.000845	0.000845	-3.59982	Down	secreted phosphoprotein 1

EPHX1	-0.48783	0.001396	0.001396	-3.42625	Down	epoxide hydrolase 1
SOSTDC1	-1.15425	0.001117	0.001117	-3.50403	Down	sclerostin domain containing 1
COX11	-0.45161	0.00153	0.00153	-3.39417	Down	cytochrome c oxidase copper chaperone COX11
PPT1	-0.41882	0.001477	0.001477	-3.40658	Down	palmitoyl-protein thioesterase 1
CRP	-1.25615	0.0007	0.0007	-3.66439	Down	C-reactive protein
TAGLN2P1	-0.39463	0.001718	0.001718	-3.35342	Down	transgelin 2 pseudogene 1
HMGB3	-0.49836	0.001534	0.001534	-3.39324	Down	high mobility group box 3
UGT1A10	-0.4502	0.001601	0.001601	-3.3783	Down	UDP glucuronosyltransferase family 1 member A10
PRSS33	-0.87938	0.001838	0.001838	-3.32957	Down	serine protease 33
TCN1	-0.60793	0.001673	0.001673	-3.36276	Down	transcobalamin 1
REPS2	-0.50784	0.00205	0.00205	-3.29076	Down	RALBP1 associated Eps domain containing 2
PCSK1N	-0.43131	0.002065	0.002065	-3.28814	Down	proproteinconvertasesubtilisin/kexin type 1 inhibitor
C4orf48	-0.69782	0.002204	0.002204	-3.26498	Down	chromosome 4 open reading frame 48
FAM171A2	-0.63443	0.002233	0.002233	-3.26026	Down	family with sequence similarity 171 member A2
DSEL	-0.48713	0.0021	0.0021	-3.2822	Down	dermatansulfateepimerase like
LINC02532	-0.65328	0.002475	0.002475	-3.22341	Down	long intergenic non-protein coding RNA 2532
ASAH1	-0.39025	0.002045	0.002045	-3.29169	Down	N-acylsphingosineamidohydrolase 1
FCGRT	-0.47015	0.00225	0.00225	-3.25754	Down	Fc fragment of IgG receptor and transporter
SLC12A2	-0.58534	0.001699	0.001699	-3.35729	Down	solute carrier family 12 member 2
CLDN16	-0.6794	0.002464	0.002464	-3.22505	Down	claudin 16
BCKDHB	-0.41787	0.002668	0.002668	-3.19641	Down	branched chain keto acid dehydrogenase E1 subunit beta
SEMA3E	-0.49497	0.002604	0.002604	-3.20514	Down	semaphorin 3E
EPN3	-0.418	0.002657	0.002657	-3.19777	Down	epsin 3
SRD5A3	-0.45001	0.002722	0.002722	-3.1891	Down	steroid 5 alpha-reductase 3
LOX	-0.62134	0.002832	0.002832	-3.17481	Down	lysyl oxidase
HSD17B2	-0.81698	0.002767	0.002767	-3.18318	Down	hydroxysteroid 17-beta dehydrogenase 2
BCAS1	-0.89748	0.002871	0.002871	-3.16989	Down	breast carcinoma amplified sequence 1
SLC3A1	-0.71911	0.002936	0.002936	-3.16178	Down	solute carrier family 3 member 1
ACSS1	-0.5491	0.002948	0.002948	-3.1603	Down	acyl-CoA synthetase short chain family member 1
GATM	-0.52222	0.003064	0.003064	-3.14624	Down	glycine amidinotransferase
CENPV	-0.42391	0.002958	0.002958	-3.15897	Down	centromere protein V
HACD2	-0.38233	0.002543	0.002543	-3.21358	Down	3-hydroxyacyl-CoA dehydratase 2
APOE	-0.61083	0.003182	0.003182	-3.13244	Down	apolipoprotein E
CUEDC2	-0.45942	0.003069	0.003069	-3.14562	Down	CUE domain containing 2
GSTO2	-0.38908	0.003242	0.003242	-3.12564	Down	glutathione S-transferase omega 2
SERINC5	-0.46221	0.003037	0.003037	-3.14946	Down	serine incorporator 5
LYPLAL1	-0.45829	0.003363	0.003363	-3.11227	Down	lysophospholipase like 1
NAALADL2	-0.42755	0.003273	0.003273	-3.12222	Down	N-acetylated alpha-linked acidic dipeptidase like 2
EFCAB11	-0.45221	0.003521	0.003521	-3.09545	Down	EF-hand calcium binding domain 11
PSMD10	-0.47396	0.003093	0.003093	-3.14275	Down	proteasome 26S subunit, non-ATPase 10
GALNT12	-0.42917	0.003351	0.003351	-3.11365	Down	polypeptide N-acetylgalactosaminyltransferase 12
GSR	-0.37832	0.002831	0.002831	-3.17493	Down	glutathione-disulfidereductase
SORBS2	-0.60397	0.003636	0.003636	-3.08374	Down	sorbin and SH3 domain containing 2
DDC	-0.58323	0.003891	0.003891	-3.05882	Down	dopa decarboxylase

ADI1	-0.44463	0.003574	0.003574	-3.09002	Down	acireductonedioxygenase 1
RIMKLA	-0.88904	0.004092	0.004092	-3.04021	Down	ribosomal modification protein rimK like family member A
UGT1A1	-0.40946	0.004137	0.004137	-3.03618	Down	UDP glucuronosyltransferase family 1 member A1
SORT1	-0.38343	0.003756	0.003756	-3.07174	Down	sortilin 1
CRLS1	-0.44641	0.004474	0.004474	-3.00715	Down	cardiolipin synthase 1
PDZK1IP1	-0.62981	0.004227	0.004227	-3.02818	Down	PDZK1 interacting protein 1
SPR	-0.38089	0.003973	0.003973	-3.05107	Down	sepiapterinreductase
SMIM10	-0.72072	0.004574	0.004574	-2.99892	Down	small integral membrane protein 10
EHMT2-AS1	-0.88579	0.003647	0.003647	-3.08256	Down	EHMT2 and SLC44A4 antisense RNA 1
FOLR1	-1.1431	0.003475	0.003475	-3.10031	Down	folate receptor alpha
CLGN	-0.69988	0.004551	0.004551	-3.00081	Down	calmegin
KPNA2	-0.39084	0.00366	0.00366	-3.08129	Down	karyopherin subunit alpha 2
FAH	-0.39607	0.005027	0.005027	-2.9637	Down	fumarylacetoacetate hydrolase
TMEM59	-0.45581	0.003928	0.003928	-3.0553	Down	transmembrane protein 59
VEPH1	-0.45193	0.005337	0.005337	-2.94121	Down	ventricular zone expressed PH domain containing 1
HACD3	-0.40154	0.004028	0.004028	-3.04599	Down	3-hydroxyacyl-CoA dehydratase 3
DNLZ	-0.44578	0.00577	0.00577	-2.91183	Down	DNL-type zinc finger
ST6GALNAC1	-0.42569	0.005622	0.005622	-2.92163	Down	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 1
KLK6	-0.43792	0.004702	0.004702	-2.98858	Down	kallikrein related peptidase 6
SLC16A10	-0.76258	0.005818	0.005818	-2.9087	Down	solute carrier family 16 member 10
MAGIX	-0.48625	0.005931	0.005931	-2.90146	Down	MAGI family member, X-linked
BCO2	-0.56805	0.005875	0.005875	-2.90499	Down	beta-carotene oxygenase 2
COLCA2	-0.94948	0.005228	0.005228	-2.94895	Down	colorectal cancer associated 2
STMN1	-0.47077	0.004392	0.004392	-3.01395	Down	stathmin 1
HSPE1P4	-0.44058	0.006225	0.006225	-2.88309	Down	heat shock protein family E (Hsp10) member 1 pseudogene 4
CA12	-0.70373	0.006024	0.006024	-2.89552	Down	carbonic anhydrase 12
LTC4S	-1.08462	0.004673	0.004673	-2.99093	Down	leukotriene C4 synthase
NXNL2	-1.0576	0.004797	0.004797	-2.98117	Down	nucleoredoxin like 2
RHBDL2	-0.53298	0.006307	0.006307	-2.87813	Down	rhomboid like 2
AK4	-0.40547	0.005472	0.005472	-2.9318	Down	adenylate kinase 4
MLEC	-0.47988	0.00421	0.00421	-3.02967	Down	malectin
HNMT	-0.46823	0.005469	0.005469	-2.93206	Down	histamine N-methyltransferase
MAGEE1	-0.62146	0.006249	0.006249	-2.88166	Down	MAGE family member E1
PXMP4	-0.42775	0.006079	0.006079	-2.8921	Down	peroxisomal membrane protein 4
CPM	-0.65192	0.006535	0.006535	-2.86463	Down	carboxypeptidase M
NRGN	-0.4896	0.006741	0.006741	-2.85278	Down	neurogranin
FAM89B	-0.40528	0.006177	0.006177	-2.88603	Down	family with sequence similarity 89 member B
TSPAN10	-0.41969	0.006773	0.006773	-2.85097	Down	tetraspanin 10
CCDC115	-0.50597	0.005926	0.005926	-2.90175	Down	coiled-coil domain containing 115
FBP1	-0.879	0.006778	0.006778	-2.85072	Down	fructose-bisphosphatase 1
PAIP2B	-0.64669	0.006785	0.006785	-2.8503	Down	poly(A) binding protein interacting protein 2B
RAD9B	-0.72362	0.005904	0.005904	-2.90315	Down	RAD9 checkpoint clamp component B
CDNF	-0.89269	0.006191	0.006191	-2.8852	Down	cerebral dopamine neurotrophic factor
RNF128	-0.46498	0.005244	0.005244	-2.94785	Down	ring finger protein 128

KCNE3	-0.79151	0.00661	0.00661	-2.8603	Down	potassium voltage-gated channel subfamily E regulatory subunit 3
TMEM238	-0.68002	0.006346	0.006346	-2.87578	Down	transmembrane protein 238
PCLAF	-0.4371	0.005788	0.005788	-2.91068	Down	PCNA clamp associated factor
PDK1	-0.56719	0.00672	0.00672	-2.85398	Down	pyruvate dehydrogenase kinase 1
CALB1	-0.92397	0.005871	0.005871	-2.90531	Down	calbindin 1
MDH1	-0.52824	0.005101	0.005101	-2.95815	Down	malate dehydrogenase 1
PLEKHB1	-0.50145	0.005556	0.005556	-2.92608	Down	pleckstrin homology domain containing B1
WDR72	-0.54895	0.00751	0.00751	-2.81143	Down	WD repeat domain 72
ARRB1	-0.41675	0.007438	0.007438	-2.81512	Down	arrestin beta 1
ENSAP2	-0.51177	0.007766	0.007766	-2.79852	Down	endosulfine alpha pseudogene 2
NUBPL	-0.38896	0.007529	0.007529	-2.81046	Down	nucleotide binding protein like
HAGLR	-0.66013	0.007606	0.007606	-2.80653	Down	HOXD antisense growth-associated long non-coding RNA
HADHB	-0.38803	0.006429	0.006429	-2.87086	Down	hydroxyacyl-CoA dehydrogenase trifunctionalmultienzyme complex subunit beta
VSIG1	-0.5897	0.008626	0.008626	-2.75789	Down	V-set and immunoglobulin domain containing 1
ANKS4B	-0.67874	0.008683	0.008683	-2.75533	Down	ankyrin repeat and sterile alpha motif domain containing 4B
SLC38A11	-0.73576	0.008043	0.008043	-2.78498	Down	solute carrier family 38 member 11
CTHRC1	-0.72027	0.006805	0.006805	-2.84917	Down	collagen triple helix repeat containing 1
FGFR3	-0.45158	0.007536	0.007536	-2.81007	Down	fibroblast growth factor receptor 3
ANXA10	-0.3914	0.008207	0.008207	-2.77718	Down	annexin A10
METTL7A	-0.88534	0.009349	0.009349	-2.72656	Down	methyltransferase like 7A
DNAH10OS	-0.74962	0.008914	0.008914	-2.74511	Down	dynein axonemal heavy chain 10 opposite strand
CYBRD1	-0.55088	0.009524	0.009524	-2.71927	Down	cytochrome b reductase 1
ACE2	-0.54396	0.009168	0.009168	-2.73419	Down	angiotensin I converting enzyme 2
AKR1C3	-0.56373	0.007238	0.007238	-2.82556	Down	aldo-ketoreductase family 1 member C3
GGT1	-0.56919	0.009572	0.009572	-2.71733	Down	gamma-glutamyltransferase 1
NME5	-0.68514	0.00963	0.00963	-2.71495	Down	NME/NM23 family member 5
ARL6IP5	-0.50567	0.006894	0.006894	-2.84423	Down	ADP ribosylation factor like GTPase 6 interacting protein 5
IL20RA	-0.39063	0.010033	0.010033	-2.69889	Down	interleukin 20 receptor subunit alpha
MMP7	-0.61709	0.007045	0.007045	-2.83592	Down	matrix metallopeptidase 7
EFHC2	-0.85121	0.009534	0.009534	-2.7189	Down	EF-hand domain containing 2
PBXIP1	-0.54253	0.008054	0.008054	-2.78446	Down	PBX homeobox interacting protein 1
C14orf132	-0.58628	0.010324	0.010324	-2.68764	Down	chromosome 14 open reading frame 132
SLC25A27	-0.79693	0.010075	0.010075	-2.69724	Down	solute carrier family 25 member 27
ACE	-0.73381	0.010202	0.010202	-2.69231	Down	angiotensin I converting enzyme
AGR2	-0.48548	0.008277	0.008277	-2.77392	Down	anterior gradient 2, protein disulphide isomerase family member
BNIPL	-0.8267	0.009771	0.009771	-2.70927	Down	BCL2 interacting protein like
ITIH2	-0.60334	0.0109	0.0109	-2.66621	Down	inter-alpha-trypsin inhibitor heavy chain 2
ZNF710-AS1	-0.78809	0.010799	0.010799	-2.66991	Down	ZNF710 antisense RNA 1
PDGFD	-0.64209	0.00994	0.00994	-2.70254	Down	platelet derived growth factor D
COA3	-0.51134	0.009145	0.009145	-2.73515	Down	cytochrome c oxidase assembly factor 3
CFAP73	-0.69749	0.011536	0.011536	-2.64374	Down	cilia and flagella associated protein 73
CARD9	-0.3925	0.011319	0.011319	-2.65128	Down	caspase recruitment domain family member 9
SAP30	-0.4749	0.011229	0.011229	-2.65445	Down	Sin3A associated protein 30

PGP	-0.386	0.008842	0.008842	-2.7483	Down	phosphoglycolate phosphatase
ARL6IP1P2	-0.60694	0.011909	0.011909	-2.63111	Down	ADP ribosylation factor like GTPase 6 interacting protein 1 pseudogene 2
LINC00327	-0.73999	0.010373	0.010373	-2.68579	Down	long intergenic non-protein coding RNA 327
ATPSCKMT	-0.50355	0.011256	0.011256	-2.65352	Down	ATP synthase c subunit lysine N-methyltransferase
SRI	-0.59821	0.00904	0.00904	-2.73967	Down	sorcin
TRAPPC6A	-0.75773	0.010859	0.010859	-2.66771	Down	trafficking protein particle complex 6A
KLK7	-0.76267	0.01241	0.01241	-2.61468	Down	kallikrein related peptidase 7
YBX1P10	-0.51753	0.011825	0.011825	-2.63393	Down	Y-box binding protein 1 pseudogene 10
RTL8B	-0.47752	0.012688	0.012688	-2.60582	Down	retrotransposon Gag like 8B
MATN2	-0.39339	0.011846	0.011846	-2.63322	Down	matrilin 2
WFDC2	-0.46122	0.011833	0.011833	-2.63365	Down	WAP four-disulfide core domain 2
NBDY	-0.42997	0.01082	0.01082	-2.66914	Down	negative regulator of P-body association
SPCS2	-0.42304	0.010306	0.010306	-2.68832	Down	signal peptidase complex subunit 2
MAD2L1	-0.38095	0.01034	0.01034	-2.68704	Down	mitotic arrest deficient 2 like 1
SORL1	-1.11637	0.012575	0.012575	-2.60938	Down	sortilin related receptor 1
PDE1A	-0.95681	0.011193	0.011193	-2.65574	Down	phosphodiesterase 1A
SNRPEP4	-0.4078	0.013229	0.013229	-2.58907	Down	small nuclear ribonucleoprotein polypeptide E pseudogene 4
QPCT	-0.37767	0.012069	0.012069	-2.6258	Down	glutaminyl-peptide cyclotransferase
TMEM160	-0.68435	0.01114	0.01114	-2.65761	Down	transmembrane protein 160
PHGDH	-0.40806	0.010445	0.010445	-2.68304	Down	phosphoglycerate dehydrogenase
BCAS3	-0.41895	0.013851	0.013851	-2.57059	Down	BCAS3 microtubule associated cell migration factor
SDHCP3	-0.79104	0.011573	0.011573	-2.64247	Down	succinate dehydrogenase complex subunit C pseudogene 3
SCNN1A	-0.53791	0.013115	0.013115	-2.59256	Down	sodium channel epithelial 1 alpha subunit
IGSF10	-0.55537	0.014548	0.014548	-2.55074	Down	immunoglobulin superfamily member 10
PLEKHS1	-0.60046	0.014768	0.014768	-2.54466	Down	pleckstrin homology domain containing S1
ST6GALNAC2	-0.39995	0.014331	0.014331	-2.55684	Down	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 2
IGFBP2	-0.51385	0.013486	0.013486	-2.58134	Down	insulin like growth factor binding protein 2
SPAG16	-0.53058	0.012976	0.012976	-2.59684	Down	sperm associated antigen 16
HOXA11	-0.67787	0.014618	0.014618	-2.54881	Down	homeobox A11
CYS1	-0.80385	0.014782	0.014782	-2.54429	Down	cystin 1
CRYM	-1.04724	0.015367	0.015367	-2.52853	Down	crystallin mu
GNG11	-0.64022	0.015309	0.015309	-2.53007	Down	G protein subunit gamma 11
PCAT7	-0.59417	0.015373	0.015373	-2.52836	Down	prostate cancer associated transcript 7
MYO3B	-0.51317	0.015446	0.015446	-2.52644	Down	myosin IIIB
AP2M1	-0.41089	0.007714	0.007714	-2.80109	Down	adaptor related protein complex 2 subunit mu 1
NRTN	-0.42622	0.015239	0.015239	-2.53193	Down	neurturin
GPSM2	-0.47617	0.013424	0.013424	-2.58321	Down	G protein signaling modulator 2
ASB9	-0.41316	0.014282	0.014282	-2.55821	Down	ankyrin repeat and SOCS box containing 9
SUN2	-0.46432	0.011837	0.011837	-2.63351	Down	Sad1 and UNC84 domain containing 2
TOMM20	-0.38473	0.010534	0.010534	-2.67969	Down	translocase of outer mitochondrial membrane 20
KCNMB4	-0.48697	0.015023	0.015023	-2.53772	Down	potassium calcium-activated channel subfamily M regulatory beta subunit 4
ATP5PDP2	-0.6462	0.015744	0.015744	-2.51867	Down	ATP synthase peripheral stalk subunit d pseudogene 2
CCDC74B	-1.0029	0.013756	0.013756	-2.57335	Down	coiled-coil domain containing 74B

ECH1	-0.44958	0.010791	0.010791	-2.67019	Down	enoyl-CoA hydratase 1
AZGP1	-0.5984	0.016589	0.016589	-2.49729	Down	alpha-2-glycoprotein 1, zinc-binding
KLHDC2	-0.40843	0.0139	0.0139	-2.56916	Down	kelch domain containing 2
PRIMPOL	-0.39892	0.01558	0.01558	-2.52293	Down	primase and DNA directed polymerase
TMEM45B	-0.37827	0.014624	0.014624	-2.54865	Down	transmembrane protein 45B
SLAIN1	-0.38153	0.016643	0.016643	-2.49596	Down	SLAIN motif family member 1
DNAJC9-AS1	-1.20338	0.014086	0.014086	-2.5638	Down	DNAJC9 antisense RNA 1
ARHGAP19	-0.43004	0.0163	0.0163	-2.5045	Down	Rho GTPase activating protein 19
SERPINA4	-0.5724	0.015509	0.015509	-2.52478	Down	serpin family A member 4
LEPR	-0.4178	0.01657	0.01657	-2.49777	Down	leptin receptor
PSMG3-AS1	-0.52351	0.016953	0.016953	-2.48839	Down	PSMG3 antisense RNA 1 (head to head)
SYT12	-0.68091	0.015883	0.015883	-2.51507	Down	synaptotagmin 12
RERG	-0.70304	0.016596	0.016596	-2.49712	Down	RAS like estrogen regulated growth inhibitor
BTBD16	-0.88899	0.015431	0.015431	-2.52684	Down	BTB domain containing 16
ETFB	-0.54425	0.012714	0.012714	-2.60498	Down	electron transfer flavoprotein subunit beta
NTRK2	-0.51677	0.018348	0.018348	-2.45582	Down	neurotrophic receptor tyrosine kinase 2
GNG7	-0.85502	0.018223	0.018223	-2.45867	Down	G protein subunit gamma 7
ERP27	-0.7466	0.018084	0.018084	-2.46182	Down	endoplasmic reticulum protein 27
FABP6	-0.89891	0.01736	0.01736	-2.47864	Down	fatty acid binding protein 6
TRMT9B	-0.87192	0.019079	0.019079	-2.43965	Down	tRNAmethyltransferase 9B (putative)
TMEM37	-0.84092	0.018022	0.018022	-2.46324	Down	transmembrane protein 37
DHRS4L2	-0.38409	0.018843	0.018843	-2.44481	Down	dehydrogenase/reductase 4 like 2
DBP	-0.55009	0.019461	0.019461	-2.43143	Down	D-box binding PAR bZIP transcription factor
PDCD4	-0.57081	0.01663	0.01663	-2.49627	Down	programmed cell death 4
ABCC4	-0.37804	0.017031	0.017031	-2.48652	Down	ATP binding cassette subfamily C member 4
RSPH1	-0.67924	0.019742	0.019742	-2.42546	Down	radial spoke head component 1
RARRES2	-1.09616	0.020292	0.020292	-2.41401	Down	retinoic acid receptor responder 2
GACAT2	-0.89674	0.01931	0.01931	-2.43465	Down	gastric cancer associated transcript 2
CD302	-0.37696	0.01816	0.01816	-2.46009	Down	CD302 molecule
MIR193BHG	-0.60372	0.020887	0.020887	-2.40193	Down	MIR193B host gene
TTR	-0.87179	0.020496	0.020496	-2.40982	Down	transthyretin
PRDX3	-0.38219	0.013342	0.013342	-2.58566	Down	peroxiredoxin 3
AKR1B10	-0.6267	0.017481	0.017481	-2.47579	Down	aldo-ketoreductase family 1 member B10
NDUFAF8	-0.69456	0.016805	0.016805	-2.49199	Down	NADH:ubiquinoneoxidoreductase complex assembly factor 8
ANXA9	-0.53242	0.018233	0.018233	-2.45843	Down	annexin A9
FGFBP2	-0.39128	0.021826	0.021826	-2.38349	Down	fibroblast growth factor binding protein 2
TUBA1A	-0.92382	0.017846	0.017846	-2.46729	Down	tubulin alpha 1a
HMGB1P1	-0.4657	0.02233	0.02233	-2.37388	Down	high mobility group box 1 pseudogene 1
ACYP2	-0.44182	0.020861	0.020861	-2.40245	Down	acylphosphatase 2
CREG2	-0.88476	0.022642	0.022642	-2.36804	Down	cellular repressor of E1A stimulated genes 2
IQCD	-0.57327	0.022704	0.022704	-2.36689	Down	IQ motif containing D
SHH	-0.90573	0.021091	0.021091	-2.39787	Down	sonic hedgehog signaling molecule
SEMA5A	-0.80779	0.022709	0.022709	-2.3668	Down	semaphorin 5A
CNGA1	-0.64756	0.022769	0.022769	-2.36569	Down	cyclic nucleotide gated channel subunit alpha 1

PAH	-0.45883	0.021426	0.021426	-2.39125	Down	phenylalanine hydroxylase
TGFB2-OT1	-0.46945	0.02296	0.02296	-2.36215	Down	TGFB2 overlapping transcript 1
OAZ1	-0.44222	0.011684	0.011684	-2.63871	Down	ornithine decarboxylase antizyme 1
TPBGL	-0.97153	0.020877	0.020877	-2.40212	Down	trophoblast glycoprotein like
MMEL1	-0.77541	0.023608	0.023608	-2.35039	Down	membrane metalloendopeptidase like 1
MIR4700	-0.43809	0.02378	0.02378	-2.34731	Down	microRNA 4700
FFAR4	-0.66314	0.023876	0.023876	-2.3456	Down	free fatty acid receptor 4
SYNPR-AS1	-0.8959	0.020945	0.020945	-2.40077	Down	SYNPR antisense RNA 1
SLC45A1	-0.70304	0.02189	0.02189	-2.38226	Down	solute carrier family 45 member 1
HMGN1P37	-0.99803	0.020556	0.020556	-2.40862	Down	high mobility group nucleosome binding domain 1 pseudogene 37
WDR54	-0.50089	0.019586	0.019586	-2.42876	Down	WD repeat domain 54
GLTPD2	-0.64725	0.024625	0.024625	-2.33247	Down	glycolipid transfer protein domain containing 2
AGT	-0.6792	0.022722	0.022722	-2.36655	Down	angiotensinogen
CFTR	-0.50874	0.013227	0.013227	-2.58914	Down	CF transmembrane conductance regulator
ENTPD8	-0.95426	0.024739	0.024739	-2.33051	Down	ectonucleoside triphosphate diphosphohydrolase 8
CTSV	-0.5691	0.018821	0.018821	-2.4453	Down	cathepsin V
PRDX2	-0.39558	0.017233	0.017233	-2.48167	Down	peroxiredoxin 2
CLDN10	-0.72557	0.020262	0.020262	-2.41462	Down	claudin 10
RAD51B	-0.4762	0.024911	0.024911	-2.32756	Down	RAD51 paralog B
USH1C	-0.56735	0.021763	0.021763	-2.38472	Down	USH1 protein network component harmonin
BTD	-0.39756	0.023376	0.023376	-2.35456	Down	biotinidase
SRP9	-0.39062	0.015471	0.015471	-2.52577	Down	signal recognition particle 9
CASR	-0.47076	0.022072	0.022072	-2.37877	Down	calcium sensing receptor
KRT14	-0.49366	0.026133	0.026133	-2.30712	Down	keratin 14
PROM1	-0.38007	0.018214	0.018214	-2.45885	Down	prominin 1
MCM3AP-AS1	-0.43448	0.024968	0.024968	-2.3266	Down	MCM3AP antisense RNA 1
SELENOP	-0.76553	0.026822	0.026822	-2.29598	Down	selenoprotein P
ARL3	-0.54734	0.021613	0.021613	-2.38761	Down	ADP ribosylation factor like GTPase 3
VWA2	-0.58649	0.024577	0.024577	-2.33331	Down	von Willebrand factor A domain containing 2
BDH2	-0.57138	0.025317	0.025317	-2.32068	Down	3-hydroxybutyrate dehydrogenase 2
C2orf81	-0.53116	0.02751	0.02751	-2.28509	Down	chromosome 2 open reading frame 81
UGT2A3	-0.95168	0.027478	0.027478	-2.28559	Down	UDP glucuronosyltransferase family 2 member A3
HOXA13	-0.62887	0.027794	0.027794	-2.28066	Down	homeobox A13
NEURL1B	-0.92354	0.026681	0.026681	-2.29822	Down	neuralized E3 ubiquitin protein ligase 1B
BPIFB1	-0.6748	0.027931	0.027931	-2.27855	Down	BPI fold containing family B member 1
IDH1-AS1	-1.11143	0.02736	0.02736	-2.28743	Down	IDH1 antisense RNA 1
ACBD7	-0.41044	0.025703	0.025703	-2.31422	Down	acyl-CoA binding domain containing 7
CNTNAP3B	-0.43225	0.027004	0.027004	-2.29306	Down	contactin associated protein like 3B
BRI3BP	-0.42394	0.017079	0.017079	-2.48536	Down	BRI3 binding protein
LINC02614	-0.62293	0.028476	0.028476	-2.2702	Down	long intergenic non-protein coding RNA 2614
RAB26	-0.77343	0.028123	0.028123	-2.27559	Down	RAB26, member RAS oncogene family
HHLA2	-0.78119	0.028325	0.028325	-2.27251	Down	HERV-H LTR-associating 2
HEBP1	-0.43462	0.024886	0.024886	-2.32799	Down	heme binding protein 1
LRP3	-0.91184	0.026645	0.026645	-2.29881	Down	LDL receptor related protein 3

SYNGR1	-0.42523	0.023971	0.023971	-2.34392	Down	synaptogyrin 1
LINC00674	-0.45812	0.029015	0.029015	-2.26211	Down	long intergenic non-protein coding RNA 674
TSTD1	-0.68327	0.02279	0.02279	-2.36528	Down	thiosulfate sulfurtransferase like domain containing 1
DHFRP1	-0.45653	0.027573	0.027573	-2.2841	Down	dihydrofolatereductasepseudogene 1
SYT5	-0.87394	0.029569	0.029569	-2.25391	Down	synaptotagmin 5
DTYMK	-0.40092	0.02003	0.02003	-2.41943	Down	deoxythymidylate kinase
PLA2R1	-0.46134	0.027744	0.027744	-2.28145	Down	phospholipase A2 receptor 1
TBC1D3B	-1.36297	0.027582	0.027582	-2.28397	Down	TBC1 domain family member 3B
SEMA4G	-0.40369	0.0259	0.0259	-2.31095	Down	semaphorin 4G
ACSF2	-0.44736	0.021153	0.021153	-2.39664	Down	acyl-CoA synthetase family member 2
HAGLROS	-0.60327	0.031068	0.031068	-2.23241	Down	HAGLR opposite strand lncRNA
HNRNPA1P10	-0.9639	0.026827	0.026827	-2.29589	Down	heterogeneous nuclear ribonucleoprotein A1 pseudogene 10
STRA6	-1.1921	0.030582	0.030582	-2.23927	Down	stimulated by retinoic acid 6
SNAP25	-0.63923	0.031465	0.031465	-2.22687	Down	synaptosome associated protein 25
SRPX	-0.58717	0.031004	0.031004	-2.2333	Down	sushi repeat containing protein X-linked
LINC01088	-0.91401	0.026947	0.026947	-2.29397	Down	long intergenic non-protein coding RNA 1088
LRRC26	-0.75526	0.029946	0.029946	-2.24841	Down	leucine rich repeat containing 26
LHPP	-0.48928	0.029307	0.029307	-2.25776	Down	phospholysinephosphohistidine inorganic pyrophosphate phosphatase
PCDHB12	-0.39614	0.031053	0.031053	-2.23262	Down	protocadherin beta 12
CRISP3	-0.826	0.032084	0.032084	-2.21835	Down	cysteine rich secretory protein 3
UBL7-AS1	-0.37631	0.031851	0.031851	-2.22154	Down	UBL7 antisense RNA 1 (head to head)
TMEM121	-0.82997	0.032905	0.032905	-2.20729	Down	transmembrane protein 121
COX16	-0.4738	0.023986	0.023986	-2.34365	Down	cytochrome c oxidase assembly factor COX16
CAB39L	-0.38299	0.030748	0.030748	-2.23692	Down	calcium binding protein 39 like
SLPI	-0.46993	0.024416	0.024416	-2.3361	Down	secretory leukocyte peptidase inhibitor
SAMD13	-0.67194	0.033129	0.033129	-2.2043	Down	sterile alpha motif domain containing 13
FMO5	-0.58649	0.034026	0.034026	-2.19256	Down	flavin containing dimethylanilinemonoxygenase 5
ACOT13	-0.40429	0.021379	0.021379	-2.39218	Down	acyl-CoA thioesterase 13
ATP5IF1	-0.4335	0.02333	0.02333	-2.3554	Down	ATP synthase inhibitory factor subunit 1
LRRC66	-0.97614	0.030714	0.030714	-2.2374	Down	leucine rich repeat containing 66
MIR302CHG	-1.06942	0.029988	0.029988	-2.2478	Down	miR-302/367 cluster host gene
RPS23P1	-0.71376	0.032422	0.032422	-2.21376	Down	ribosomal protein S23 pseudogene 1
EML6	-0.61006	0.035838	0.035838	-2.16963	Down	EMAP like 6
REX1BD	-0.41782	0.027441	0.027441	-2.28616	Down	required for excision 1-B domain containing
KCNIP3	-0.85669	0.035692	0.035692	-2.17145	Down	potassium voltage-gated channel interacting protein 3
CP	-0.80531	0.036806	0.036806	-2.15781	Down	ceruloplasmin
SERHL2	-0.8673	0.03571	0.03571	-2.17122	Down	serine hydrolase like 2
CNIH4	-0.45142	0.023086	0.023086	-2.35984	Down	cornichon family AMPA receptor auxiliary protein 4
SUMF1	-0.56581	0.0255	0.0255	-2.3176	Down	sulfatase modifying factor 1
ALG1L	-0.64935	0.037374	0.037374	-2.151	Down	ALG1 chitobiosyldiphosphodolichol beta-mannosyltransferase like
TF	-0.92745	0.037547	0.037547	-2.14894	Down	transferrin
SLC25A21	-0.60073	0.036986	0.036986	-2.15563	Down	solute carrier family 25 member 21
SMARCA2	-0.39335	0.026967	0.026967	-2.29366	Down	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2

CD1D	-0.89907	0.037042	0.037042	-2.15497	Down	CD1d molecule
ATRAID	-0.43058	0.02409	0.02409	-2.34181	Down	all-trans retinoic acid induced differentiation factor
MRPL3P1	-0.40656	0.036626	0.036626	-2.15999	Down	mitochondrial ribosomal protein L3 pseudogene 1
SERPINA5	-0.49498	0.02753	0.02753	-2.28477	Down	serpin family A member 5
TUBB4A	-0.51838	0.036336	0.036336	-2.16352	Down	tubulin beta 4A class IVa
UBBP4	-0.85535	0.038969	0.038969	-2.13234	Down	ubiquitin B pseudogene 4
CDC42EP5	-0.4214	0.033788	0.033788	-2.19564	Down	CDC42 effector protein 5
PCYOX1	-0.42124	0.025382	0.025382	-2.31958	Down	prenylcysteine oxidase 1
TRAF3IP2-AS1	-0.47913	0.038122	0.038122	-2.14216	Down	TRAF3IP2 antisense RNA 1
ENDOG	-0.40418	0.031482	0.031482	-2.22663	Down	endonuclease G
IL6STP1	-0.87497	0.03963	0.03963	-2.1248	Down	interleukin 6 signal transducer pseudogene 1
TFRC	-0.42836	0.016049	0.016049	-2.51082	Down	transferrin receptor
SATB1-AS1	-0.58765	0.041362	0.041362	-2.10558	Down	SATB1 antisense RNA 1
LEFTY1	-0.8092	0.039291	0.039291	-2.12865	Down	left-right determination factor 1
PPA2	-0.4066	0.025658	0.025658	-2.31496	Down	inorganic pyrophosphatase 2
ROS1	-0.63081	0.036999	0.036999	-2.15548	Down	ROS proto-oncogene 1, receptor tyrosine kinase
CYP4F3	-0.38185	0.036494	0.036494	-2.16159	Down	cytochrome P450 family 4 subfamily F member 3
HELLPAR	-0.91996	0.038353	0.038353	-2.13947	Down	HELLP associated long non-coding RNA
TPGS1	-0.39445	0.034648	0.034648	-2.18456	Down	tubulin polyglutamylase complex subunit 1
CSPG5	-0.40082	0.036829	0.036829	-2.15753	Down	chondroitin sulfate proteoglycan 5
NACA2	-0.46287	0.03896	0.03896	-2.13244	Down	nascent polypeptide associated complex subunit alpha 2
TCTEX1D2	-0.47264	0.036612	0.036612	-2.16015	Down	Tctex1 domain containing 2
MPC2	-0.53298	0.025348	0.025348	-2.32016	Down	mitochondrial pyruvate carrier 2
CUTC	-0.45828	0.035413	0.035413	-2.17492	Down	cutC copper transporter
ADH6	-1.01999	0.042081	0.042081	-2.0978	Down	alcohol dehydrogenase 6 (class V)
KCNAB1	-0.66091	0.043852	0.043852	-2.07913	Down	potassium voltage-gated channel subfamily A member regulatory beta subunit 1
LINC00992	-0.48054	0.037478	0.037478	-2.14976	Down	long intergenic non-protein coding RNA 992
TEX15	-0.77015	0.038871	0.038871	-2.13347	Down	testis expressed 15, meiosis and synapsis associated
SLC39A10	-0.49705	0.025646	0.025646	-2.31517	Down	solute carrier family 39 member 10
FLYWCH2	-0.48889	0.037002	0.037002	-2.15545	Down	FLYWCH family member 2
HOXA2	-0.60382	0.044354	0.044354	-2.07396	Down	homeobox A2
POLR2J2	-0.78702	0.042476	0.042476	-2.09358	Down	RNA polymerase II subunit J2
LCT	-1.02104	0.044215	0.044215	-2.07539	Down	lactase
PRR15L	-0.37843	0.033995	0.033995	-2.19296	Down	proline rich 15 like
LINC02280	-0.77481	0.044602	0.044602	-2.07142	Down	long intergenic non-protein coding RNA 2280
ERFE	-0.55162	0.044822	0.044822	-2.06919	Down	erythroferrone
PIN1	-0.37801	0.029635	0.029635	-2.25294	Down	peptidylprolylcis/trans isomerase, NIMA-interacting 1
UCP2	-0.52664	0.042065	0.042065	-2.09798	Down	uncoupling protein 2
NR1H4	-0.54069	0.04192	0.04192	-2.09953	Down	nuclear receptor subfamily 1 group H member 4
SPATA17	-0.60205	0.046598	0.046598	-2.05145	Down	spermatogenesis associated 17
CYP27A1	-0.45434	0.042177	0.042177	-2.09677	Down	cytochrome P450 family 27 subfamily A member 1
GSTA4	-0.75811	0.047635	0.047635	-2.04137	Down	glutathione S-transferase alpha 4
LRRC24	-0.489	0.04585	0.04585	-2.05885	Down	leucine rich repeat containing 24

C21orf62-AS1	-0.68584	0.046413	0.046413	-2.05328	Down	C21orf62 antisense RNA 1
COX14	-0.52304	0.036246	0.036246	-2.16461	Down	cytochrome c oxidase assembly factor COX14
ENTPD3	-0.49339	0.044557	0.044557	-2.07189	Down	ectonucleoside triphosphate diphosphohydrolase 3
ACO1	-0.66228	0.030729	0.030729	-2.23718	Down	aconitase 1
CEACAM7	-1.00983	0.046012	0.046012	-2.05724	Down	CEA cell adhesion molecule 7
TCEA3	-0.47798	0.044834	0.044834	-2.06907	Down	transcription elongation factor A3
ROM1	-0.51692	0.046146	0.046146	-2.05591	Down	retinal outer segment membrane protein 1
PNMT	-0.76002	0.044521	0.044521	-2.07225	Down	phenylethanolamine N-methyltransferase
ECI2	-0.48523	0.036372	0.036372	-2.16308	Down	enoyl-CoA delta isomerase 2
NLGN1	-0.62362	0.048973	0.048973	-2.02864	Down	neuroligin 1
ADGRB3	-1.04491	0.047637	0.047637	-2.04135	Down	adhesion G protein-coupled receptor B3
KY	-1.21803	0.04789	0.04789	-2.03892	Down	kyphoscoliosis peptidase
RAMP1	-0.70566	0.042311	0.042311	-2.09534	Down	receptor activity modifying protein 1
SNTA1	-0.39759	0.039898	0.039898	-2.12179	Down	syntrophin alpha 1
LINP1	-0.4422	0.034289	0.034289	-2.18916	Down	lncRNA in non-homologous end joining pathway 1
TMEM61	-0.86021	0.049938	0.049938	-2.01964	Down	transmembrane protein 61
LEMD1	-1.18622	0.048602	0.048602	-2.03213	Down	LEM domain containing 1
NDUFA2	-0.59611	0.029824	0.029824	-2.25019	Down	NADH:ubiquinoneoxidoreductase subunit A2
ETFDH	-0.39296	0.039509	0.039509	-2.12617	Down	electron transfer flavoprotein dehydrogenase
HNRNPA1P55	-0.71507	0.049042	0.049042	-2.02799	Down	heterogeneous nuclear ribonucleoprotein A1 pseudogene 55
DNAAF4	-0.52146	0.047654	0.047654	-2.04118	Down	dynein axonemal assembly factor 4
DNPH1	-0.51715	0.032033	0.032033	-2.21905	Down	2'-deoxynucleoside 5'-phosphate N-hydrolase 1
METTL7B	-0.45392	0.036093	0.036093	-2.16649	Down	methyltransferase like 7B
RPL39L	-0.44192	0.038025	0.038025	-2.1433	Down	ribosomal protein L39 like
C2orf74	-0.42087	0.042728	0.042728	-2.09091	Down	chromosome 2 open reading frame 74
ARHGDIB	-0.50007	0.04157	0.04157	-2.10331	Down	Rho GDP dissociation inhibitor beta
ORAI3	-0.37956	0.045819	0.045819	-2.05915	Down	ORAI calcium release-activated calcium modulator 3
MOGAT1	-0.51635	0.048438	0.048438	-2.0337	Down	monoacylglycerol O-acyltransferase 1
SYNJ2BP-COX16	-0.40553	0.035524	0.035524	-2.17354	Down	SYNJ2BP-COX16 readthrough
DNAAF3	-0.50277	0.04716	0.04716	-2.04596	Down	dynein axonemal assembly factor 3
CYP2U1	-0.40096	0.046549	0.046549	-2.05193	Down	cytochrome P450 family 2 subfamily U member 1
COMMD8	-0.38216	0.039433	0.039433	-2.12704	Down	COMM domain containing 8
REEP6	-0.48009	0.044376	0.044376	-2.07373	Down	receptor accessory protein 6
NDUFS7	-0.41664	0.036942	0.036942	-2.15617	Down	NADH:ubiquinoneoxidoreductase core subunit S7
NEK2	-0.47265	0.039647	0.039647	-2.12461	Down	NIMA related kinase 2
NTHL1	-0.37869	0.040831	0.040831	-2.1114	Down	nth like DNA glycosylase 1
AURKA	-0.39942	0.03637	0.03637	-2.1631	Down	aurora kinase A
DEPDC1	-0.37937	0.039012	0.039012	-2.13185	Down	DEP domain containing 1
ACSM3	-0.4022	0.046823	0.046823	-2.04925	Down	acyl-CoA synthetase medium chain family member 3
CAT	-0.40749	0.035942	0.035942	-2.16835	Down	catalase
FKBP3	-0.38463	0.035718	0.035718	-2.17112	Down	FKBP prolylisomerase 3
MACROD1	-0.43096	0.043535	0.043535	-2.08242	Down	mono-ADP ribosylhydrolase 1
CARHSP1	-0.43046	0.03964	0.03964	-2.12469	Down	calcium regulated heat stable protein 1
STC1	-0.50342	0.048514	0.048514	-2.03297	Down	stanniocalcin 1

BIRC5	-0.42876	0.043263	0.043263	-2.08526	Down	baculoviral IAP repeat containing 5
HMGN3	-0.37648	0.040553	0.040553	-2.11447	Down	high mobility group nucleosomal binding domain 3
HSPE1	-0.42594	0.035991	0.035991	-2.16774	Down	heat shock protein family E (Hsp10) member 1
DPY30	-0.39353	0.045246	0.045246	-2.0649	Down	dpy-30 histone methyltransferase complex regulatory subunit
ODAM	-0.39798	0.043536	0.043536	-2.08241	Down	odontogenic, ameloblast associated
UPK1B	-0.543	0.049733	0.049733	-2.02155	Down	uroplakin 1B
PGK1	-0.44301	0.02891	0.02891	-2.26367	Down	phosphoglycerate kinase 1
LSM3	-0.41046	0.04787	0.04787	-2.03911	Down	LSM3 homolog, U6 small nuclear RNA and mRNA degradation associated
TOP2A	-0.45633	0.032147	0.032147	-2.21749	Down	DNA topoisomerase II alpha
CYBA	-0.49932	0.046118	0.046118	-2.05618	Down	cytochrome b-245 alpha chain

Table 2 The enriched pathway terms of the up regulated differentially expressed genes

BIOCYC							
Pathway ID	Pathway Name	P-value	FDR B&H	FDR B&Y	Bonferroni	Gene Count	Gene
907943	superpathway of steroid hormone biosynthesis	2.34E-02	1.98E-01	7.11E-01	4.68E-01	2	HSD17B3,CYP21A2
782386	aspirin triggered resolvin E biosynthesis	3.99E-02	1.98E-01	7.11E-01	7.99E-01	1	PTGS2
142304	UDP-N-acetyl-D-glucosamine biosynthesis II	9.68E-02	2.42E-01	8.71E-01	1.00E+00	1	GFPT2
1208955	protein ubiquitylation	1.15E-01	2.56E-01	9.22E-01	1.00E+00	2	UBE2L6,UBA7
142279	adenosine nucleotides degradation	1.50E-01	2.73E-01	9.84E-01	1.00E+00	1	NT5C3A
782393	CMP phosphorylation	1.84E-01	2.84E-01	1.00E+00	1.00E+00	1	CMPK2
142242	triacylglycerol biosynthesis	3.99E-01	4.20E-01	1.00E+00	1.00E+00	1	MOGAT3
142419	phospholipases	4.46E-01	4.46E-01	1.00E+00	1.00E+00	1	PLA2G4C
83051	Cytokine-cytokine receptor interaction	5.49E-17	1.12E-14	6.61E-14	1.12E-14	33	TNFRSF4,CXCL9,CCL2,CCL20,CXCL11,CX3CL1,FLT3,F TNFSF13B,IL1A,TSLP,IL6,IL7,IL7R,CXCL8,IL11,IL12A,IL INHBA,CXCL10,IL17C,IL22RA1,BMP2,CXCL2,CXCL3,LT
812256	TNF signaling pathway	3.49E-14	3.56E-12	2.10E-11	7.13E-12	20	TRAF1,CCL2,CCL20,CX3CL1,MAP3K8,FOS,ICAM1,CRE BCL3,PTGS2,JUN,NFKBIA,SOCS3,CXCL2,CXCL3,TNF,T
217173	Influenza A	7.40E-14	5.04E-12	2.97E-11	1.51E-11	24	DDX58,CCL2,PML,ICAM1,IFNB1,RSAD2,IL1A,IL6,CXCL CXCL10,TICAM1,IRF7,STAT2,JAK2,IFIH1,JUN,NFKBIA,S
377873	Herpes simplex infection	1.97E-11	1.01E-09	5.93E-09	4.02E-09	22	TRAF1,DDX58,HLA-F,CCL2,PML,FOS,IFIT1,IFNB1,IL6,IL STAT2,JAK2,IFIH1,JUN,NFKBIA,TAP1,SOCS3,OAS1,OA
1474301	IL-17 signaling pathway	4.41E-11	1.80E-09	1.06E-08	9.00E-09	16	CCL2,CCL20,FOS,FOSB,CSF2,IL6,CXCL8,CXCL10,IL17C NFKBIA,CXCL2,CXCL3,TNF,TNFAIP3
122191	NOD-like receptor signaling pathway	1.42E-09	4.83E-08	2.85E-07	2.90E-07	19	CCL2,IFI16,IFNB1,TXNIP,IL6,CXCL8,TICAM1,GBP1,IRF7 NFKBIA,OAS1,OAS2,CXCL2,CXCL3,NLRP3,TNF,TNFAIP
83077	Jak-STAT signaling pathway	1.57E-08	3.21E-07	1.89E-06	3.21E-06	17	IFNB1,CSF2,SOCS1,TSLP,IL6,IL7,IL7R,IL11,IL12A,IL15R STAT2,JAK2,SOCS3,IFNL2,IFNL3,IFNL1
213306	Measles	7.85E-08	1.23E-06	7.27E-06	1.60E-05	15	DDX58,IFNB1,IL1A,BBC3,IL6,IL12A,TNFSF10,IRF7,STA IFIH1,NFKBIA,OAS1,OAS2,TNFAIP3
83048	MAPK signalingpathway	2.07E-04	1.84E-03	1.08E-02	4.23E-02	15	RASGRP3,MAP3K8,FOS,PLA2G4C,IL1A,GADD45B,FGF DUSP1,DUSP8,RELB,RASGRP1,TNF,DUSP10
373901	HTLV-I infection	2.16E-04	1.84E-03	1.08E-02	4.41E-02	15	HLA-F,ETS2,FOS,ICAM1,ZFP36,CSF2,ATF3,IL6,IL15RA, NFKBIA,RELB,EGR1,EGR2,TNF
1017634	cAMPsignaling pathway	6.89E-03	3.70E-02	2.18E-01	1.00E+00	10	PDE4B,ADRB2,FOS,CREB5,SSTR2,JUN,NFKBIA,GRIN3E
Pathway Interaction Database							
137993	Calcineurin-regulated NFAT-dependent transcription in lymphocytes	2.10E-09	2.25E-07	1.18E-06	2.25E-07	11	FOS,CSF2,CXCL8,GATA3,PTGS2,JUN,EGR1,EGR2,EGR3
138006	ATF-2 transcription factor network	1.22E-07	6.54E-06	3.44E-05	1.31E-05	10	ACHE,FOS,ATF3,IL6,CXCL8,JUN,DUSP1,DUSP8,SOCS3
138000	IL23-mediated signaling events	7.65E-06	2.73E-04	1.43E-03	8.18E-04	7	CXCL9,CCL2,IL6,JAK2,NFKBIA,SOCS3,TNF

137929	IL27-mediated signaling events	1.04E-05	2.78E-04	1.46E-03	1.11E-03	6	IL6,IL12A,GATA3,STAT2,JAK2,TNF
138014	Glucocorticoid receptor regulatory network	3.88E-05	8.29E-04	4.36E-03	4.15E-03	9	FOS,ICAM1,CSF2,IL6,CXCL8,GATA3,IRF1,JUN,EGR1
137932	IL6-mediated signaling events	2.06E-04	3.28E-03	1.73E-02	2.21E-02	6	FOS,IL6,IRF1,JAK2,JUN,SOCS3
137922	IL12-mediated signaling events	2.15E-04	3.28E-03	1.73E-02	2.30E-02	7	HLX,FOS,SOCS1,GADD45B,IL12A,JAK2,RELB
137939	Direct p53 effectors	3.36E-04	4.04E-03	2.12E-02	3.59E-02	10	CX3CL1,PMAIP1,PML,ATF3,BBC3,BDKRB2,JUN,TAP1,D
137989	FGF signaling pathway	3.40E-04	4.04E-03	2.12E-02	3.64E-02	6	SPRY2,PLAUR,KLB,FOS,JUN,FGF19
138018	Downstream signaling in naive CD8+ T cells	4.78E-04	5.12E-03	2.69E-02	5.12E-02	6	TNFRSF4,FOS,JUN,EGR1,EGR4,TNF
REACTOME							
1269310	Cytokine Signaling in Immune system	6.11E-35	3.85E-32	2.70E-31	3.85E-32	78	USP18,UBE2L6,DDX58,HLA-F,TRIM22,TNFRSF4,SPTBN CCL2,CCL20,TRIM38,PML,KLB,FLT3,FLT3LG,MAP3K8,I IFITM1,SAMHD1,IFITM2,IFI35,IFIT2,IFIT1,IFIT3,TRIM5,I MT2A,RSAD2,CSF2,ISG15,TNFSF13B,OASL,SOCS1,XA IL6,IL7,IL7R,CXCL8,MX2,IL11,IL12A,IL15RA,CXCL10,IL1 GATA3,PSMB9,GBP1,IRF1,TRIM21,IRF7,ISG20,IL22RA1 FGF18,STAT2,JAK2,FGF19,DUSP1,DUSP8,SOCS3,PELI OAS2,RELB,CXCL2,LGALS9,RASGRP1,EGR1,LTB,TNF,D HERC5,IFNL2,IFNL3,IFNL1
1269311	Interferon Signaling	3.09E-25	9.72E-23	6.82E-22	1.94E-22	37	USP18,UBE2L6,DDX58,HLA-F,TRIM22,UBA7,TRIM38,PM ICAM1,IFITM1,SAMHD1,IFITM2,IFI35,IFIT2,IFIT1,IFIT3, TRIM5,IFNB1,MT2A,RSAD2,ISG15,OASL,SOCS1,XAF1,I GBP1,IRF1,TRIM21,IRF7,ISG20,STAT2,JAK2,SOCS3,OA OAS2,EGR1,HERC5
1269312	Interferon alpha/beta signaling	6.94E-24	1.46E-21	1.02E-20	4.36E-21	24	USP18,HLA-F,IFITM1,SAMHD1,IFITM2,IFI35,IFIT2,IFIT1 IFIT3,IFNB1,RSAD2,ISG15,OASL,SOCS1,XAF1,MX2,IRF IRF7,ISG20,STAT2,SOCS3,OAS1,OAS2,EGR1
1269318	Signaling by Interleukins	8.36E-14	1.32E-11	9.23E-11	5.26E-11	41	SPTBN5,RASGRP3,CCL2,CCL20,KLB,FLT3,FLT3LG, MAP3K8,FOS,ICAM1,CSF2,SOCS1,IL1A,IL6,IL7,IL7R, CXCL8,IL11,IL12A,IL15RA,CXCL10,IL17C,GATA3,PSMB IL22RA1,PTGS2,FGF18,JAK2,FGF19,DUSP1,DUSP8,SC CXCL2,LGALS9,RASGRP1,TNF,DUSP10,IFNL2,IFNL3,IF
1269314	Interferon gamma signaling	4.61E-12	5.80E-10	4.07E-09	2.90E-09	17	HLA-F,TRIM22,TRIM38,PML,ICAM1,TRIM5,MT2A,OASL GBP1,IRF1,TRIM21,IRF7,JAK2,SOCS3,OAS1,OAS2
1269259	RIG-I/MDA5 mediated induction of IFN-alpha/beta pathways	1.15E-09	1.04E-07	7.28E-07	7.26E-07	14	UBE2L6,DDX58,UBA7,NLRC5,DHX58,IFNB1,ISG15,CYL NFKBIA,TNFAIP3,HERC5
1269545	Class A/1 (Rhodopsin-like receptors)	2.85E-05	1.50E-03	1.05E-02	1.80E-02	19	ADRB2,CXCL9,CCL20,CXCL11,CX3CL1,ACKR4,CXCL8,(SSTR2,PTGER4,BDKRB2,NPFFR2,DRD1,GPER1,CCRL2
1269203	Innate Immune System	6.17E-05	2.98E-03	2.10E-02	3.88E-02	47	UBE2L6,DDX58,PGLYRP2,TLR6,PLAC8,SPTBN5,UBA7,I NLRC5,PLAUR,KLB,DHX58,MAP3K8,FOS,IFI16,IFNB1,T ISG15,SOCS1,CYLD,TICAM1,PSMB9,IRF1,TRIM21,IRF7 JAK2,IFIH1,JUN,CLEC4A,PTX3,NFKBIA,C4A,C4B,FGF19 DUSP8,PELI1,RELB,RAB44,NLRP3,MMP25,RASGRP1,D

1269544	GPCR ligand binding	3.59E-04	1.13E-02	7.92E-02	2.26E-01	21	ADRB2,CXCL9,CCL20,CXCL11,CX3CL1,ACKR4,PTCH2,(CXCL10,SSTR2,PTGER4,BDKRB2,NPFFR2,DRD1,GPER GRM8,CXCL2,CXCL3,S1PR3,HCRTR1
1269501	MAPK family signaling cascades	2.50E-03	4.50E-02	3.16E-01	1.00E+00	14	SPTBN5,RASGRP3,KLB,CSF2,IL6,PSMB9,FGF18,JAK2, DUSP1,DUSP8,RASGRP1,DUSP10
Gen MAPP							
MAP00140	C21 Steroid hormone metabolism	1.84E-01	6.17E-01	1.00E+00	1.00E+00	1	CYP21A2
MAP00150	M Androgen and estrogen metabolism	2.93E-01	6.17E-01	1.00E+00	1.00E+00	1	HSD17B3
MAP00020	Citrate cycle TCA cycle	3.07E-01	6.17E-01	1.00E+00	1.00E+00	1	PCK1
MAP00860	Porphyrin and chlorophyll metabolism	3.07E-01	6.17E-01	1.00E+00	1.00E+00	1	CPO
MAP00590	Prostaglandin and leukotriene metabolism	3.21E-01	6.17E-01	1.00E+00	1.00E+00	1	PTGS2
MAP00361	gamma Hexachlorocyclohexane degradation	4.46E-01	6.17E-01	1.00E+00	1.00E+00	1	CYP1A1
MAP00620	Pyruvate metabolism	4.69E-01	6.17E-01	1.00E+00	1.00E+00	1	PCK1
MAP00230	Purine metabolism	5.08E-01	6.17E-01	1.00E+00	1.00E+00	2	PDE4B,GMPR
MAP00380	Tryptophan metabolism	6.09E-01	6.17E-01	1.00E+00	1.00E+00	1	CYP1A1
MAP00561	Glycerolipid metabolism	6.17E-01	6.17E-01	1.00E+00	1.00E+00	1	ACHE
MSigDB C2 BIOCARTA (v6.0)							
M5883	Genes encoding secreted soluble factors	3.08E-10	4.78E-08	2.69E-07	4.78E-08	28	CXCL9,CCL2,CCL20,FST,CXCL11,CX3CL1,FLT3LG,IFNB CSF2,TNFSF13B,IL1A,IL6,IL7,CXCL8,IL11,IL12A,TNFSF INHBA,CXCL10,IL17C,FGF18,BMP2,FGF19,CXCL2,CXC
M6910	Cytokines and Inflammatory Response	3.36E-09	2.60E-07	1.46E-06	5.21E-07	9	IFNB1,CSF2,IL1A,IL6,IL7,CXCL8,IL11,IL12A,TNF
M17406	Cytokine Network	2.66E-06	1.38E-04	7.74E-04	4.13E-04	6	IFNB1,IL1A,IL6,CXCL8,IL12A,TNF
M5298	Regulation of hematopoiesis by cytokines	8.15E-06	2.53E-04	1.42E-03	1.26E-03	5	CSF2,IL6,IL7,CXCL8,IL11
M3952	Cells and Molecules involved in local acute inflammatory response	1.62E-05	4.20E-04	2.36E-03	2.52E-03	5	ICAM1,IL1A,IL6,CXCL8,TNF
M5885	Ensemble of genes encoding ECM-associated proteins including ECM-affilaited proteins, ECM regulators and secreted factors	2.03E-05	4.50E-04	2.53E-03	3.15E-03	33	CXCL9,CCL2,C1QTNF1,CCL20,FST,CXCL11,CX3CL1, FLT3LG,IFNB1,CSF2,TNFSF13B,IL1A,IL6,IL7,CXCL8,IL1 IL12A,TNFSF10,INHBA,CXCL10,IL17C,FGF18,BMP2, CL CXCL2,CXCL3,LGALS9,MMP25,WIF1, SERPINE1,LTB,TI
M5889	Ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins	3.98E-05	7.64E-04	4.30E-03	6.16E-03	40	FBLN2,CXCL9,CCL2,C1QTNF1,CCL20,FST,CXCL11, CX3CL1,COL4A1,COL8A1,FLT3LG,MXRA5,IFNB1,SNED TNFSF13B,IL1A,IL6,IL7,CXCL8,IL11,IL12A, TNFSF10,INHBA,CXCL10,IL17C,FGF18,BMP2,NTNG2, CLEC4A,FGF19,CXCL2,CXCL3,LGALS9,MMP25,WIF1, S
M2579	Differentiation Pathway in PC12 Cells; this is a specific case of PAC1 Receptor Pathway.	2.67E-04	3.18E-03	1.79E-02	4.13E-02	6	CREB5,JUN,EGR1,EGR2,EGR3,EGR4
M6778	IL-10 Anti-inflammatory Signaling Pathway	3.12E-04	3.46E-03	1.94E-02	4.84E-02	4	IL1A,IL6,STAT2,TNF
M10082	TNFR2 Signaling Pathway	3.95E-04	4.08E-03	2.30E-02	6.12E-02	4	TRAF1,NFKBIA,DUSP1,TNFAIP3

Panther DB							
P00054	Toll receptor signaling pathway	6.30E-06	3.28E-04	1.49E-03	3.28E-04	8	TLR6,MAP3K8,IFNB1,TICAM1,PTGS2,JUN,NFKBIA,TNF
P00036	Interleukin signaling pathway	9.64E-05	2.51E-03	1.14E-02	5.02E-03	9	FOS,IL1A,IL6,IL7,CXCL8,IL11,IL12A,IL15RA,STAT2
P00006	Apoptosis signaling pathway	1.05E-03	1.82E-02	8.24E-02	5.44E-02	8	FOS,ATF3,TNFSF10,JUN,NFKBIA,RELB,LTB,TNF
P00046	Oxidative stress response	2.24E-03	2.91E-02	1.32E-01	1.16E-01	5	DUSP26,JUN,DUSP1,DUSP8,DUSP10
P00027	Heterotrimeric G-protein signaling pathway-Gq alpha and Go alpha mediated pathway	7.16E-03	7.44E-02	3.38E-01	3.72E-01	7	RASGRP3,SSTR2,BDKRB2,DRD1,GRM8,RGS16,RASGR
P00031	Inflammation mediated by chemokine and cytokine signaling pathway	1.54E-02	1.34E-01	6.06E-01	8.01E-01	9	ACTA1,CCL2,CCL20,CX3CL1,CXCL8,CXCL10,JAK2,JUN
P00038	JAK/STAT signaling pathway	4.03E-02	2.93E-01	1.00E+00	1.00E+00	2	SOCS1,JAK2
P00050	Plasminogen activating cascade	4.51E-02	2.93E-01	1.00E+00	1.00E+00	2	PLAUR,SERPINE1
P00037	Ionotropic glutamate receptor pathway	6.52E-02	3.52E-01	1.00E+00	1.00E+00	3	STX19,STX11,GRIA2
P02757	O-antigen biosynthesis	7.83E-02	3.52E-01	1.00E+00	1.00E+00	1	GFPT2
Pathway Ontology							
PW:0000499	Nuclear Factor Kappa B signaling	1.99E-03	7.44E-02	3.27E-01	8.97E-02	3	NFKBIA,RELB,TNF
PW:0000313	c-Jun N-terminal kinases MAPK signaling	3.31E-03	7.44E-02	3.27E-01	1.49E-01	4	DUSP1,DUSP8,TNF,DUSP10
PW:0000060	long term potentiation	1.33E-02	1.03E-01	4.52E-01	5.97E-01	2	DRD1,EGR1
PW:0000244	Angiotensin II signaling	1.64E-02	1.03E-01	4.52E-01	7.37E-01	2	CCL2,JAK2
PW:0000209	JAK-STAT signaling	2.01E-02	1.03E-01	4.52E-01	9.05E-01	3	STAT2,JAK2,SOCS3
PW:0000356	oxygen homeostasis	2.06E-02	1.03E-01	4.52E-01	9.26E-01	1	SERPINE1
PW:0000585	orexin/hypocretinsignaling through the orexin/hypocretin receptor 1	3.99E-02	1.38E-01	6.07E-01	1.00E+00	1	HCRTR1
PW:0000031	purine metabolic	5.54E-02	1.78E-01	7.82E-01	1.00E+00	3	PDE2A,PDE4B,GMPR
PW:0000104	intrinsic apoptotic	1.15E-01	2.16E-01	9.50E-01	1.00E+00	2	PMAIP1,BBC3
PW:0000201	canonical Wntsignaling	6.09E-01	6.09E-01	1.00E+00	1.00E+00	1	WIF1
SMPDB							
SMP00356	17-Beta Hydroxysteroid Dehydrogenase III Deficiency	2.06E-02	2.61E-01	1.00E+00	6.79E-01	1	HSD17B3
SMP00373	Adrenal Hyperplasia Type 3 or Congenital Adrenal Hyperplasia due to 21-hydroxylase Deficiency	2.06E-02	2.61E-01	1.00E+00	6.79E-01	1	CYP21A2
SMP00321	Intracellular Signalling Through Adenosine Receptor A2b and Adenosine	3.06E-02	2.61E-01	1.00E+00	1.00E+00	3	CXCL8,JUN,NFKBIA
SMP00094	Sulindac Pathway	1.33E-01	2.61E-01	1.00E+00	1.00E+00	1	PTGS2

SMP00320	Intracellular Signalling Through Adenosine Receptor A2a and Adenosine	1.43E-01	2.61E-01	1.00E+00	1.00E+00	2	JUN,NFKBIA
SMP00063	Tryptophan Metabolism	2.93E-01	3.56E-01	1.00E+00	1.00E+00	1	CYP1A1
SMP00035	Bile Acid Biosynthesis	2.93E-01	3.56E-01	1.00E+00	1.00E+00	1	CH25H
SMP00196	Leigh Syndrome	3.07E-01	3.56E-01	1.00E+00	1.00E+00	1	PCK1
SMP00025	Phospholipid Biosynthesis	3.99E-01	3.99E-01	1.00E+00	1.00E+00	1	ACHE
SMP00046	Pyrimidine Metabolism	3.99E-01	3.99E-01	1.00E+00	1.00E+00	1	CMPK2

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

BIOCYC							
Pathway ID	Pathway Name	P-value	FDR B&H	FDR B&Y	Bonferroni	Gene Count	Gene
142238	catecholamine biosynthesis	5.58E-04	3.89E-02	1.97E-01	4.85E-02	2	PNMT,DDC
545354	noradrenaline and adrenaline degradation	9.56E-04	3.89E-02	1.97E-01	8.32E-02	3	ADH6,ALDH2,PNMT
142437	nicotine degradation IV	1.34E-03	3.89E-02	1.97E-01	1.17E-01	3	FMO5,UGT1A4,CYP2U1
545351	sphingosine and sphingosine-1-phosphate metabolism	1.76E-02	1.53E-01	7.72E-01	1.00E+00	2	ASAH1,SGPP1
142224	glutathione redox reactions II	2.39E-02	1.83E-01	9.22E-01	1.00E+00	1	GSR
782379	pyrimidine deoxyribonucleotide phosphorylation	2.61E-02	1.83E-01	9.22E-01	1.00E+00	2	NME5,DTYMK
142387	valine degradation	3.08E-02	1.83E-01	9.22E-01	1.00E+00	2	ALDH6A1,BCKDHB
545316	bile acid biosynthesis, neutral pathway	3.08E-02	1.83E-01	9.22E-01	1.00E+00	2	SCP2,CYP27A1
545306	dolichol and dolichyl phosphate biosynthesis	4.62E-02	1.83E-01	9.22E-01	1.00E+00	1	SRD5A3
142152	glycine/serine biosynthesis	4.62E-02	1.83E-01	9.22E-01	1.00E+00	1	SHMT1
KEGG							
82932	Ascorbate and aldarate metabolism	8.82E-12	1.88E-09	1.12E-08	1.88E-09	11	ALDH2,UGT1A10,UGT1A8,UGT1A7,UGT1A6,UGT1A5,UGT1A9 UGT1A4,UGT1A1,UGT1A3,UGT2A3
82940	Steroid hormone biosynthesis	5.86E-10	2.71E-08	1.61E-07	1.25E-07	13	HSD17B2,UGT1A10,UGT1A8,UGT1A7,UGT1A6,UGT1A5,UGT1 UGT1A4,UGT1A1,UGT1A3,AKR1C3,SRD5A3,UGT2A3
83032	Drug metabolism - cytochrome P450	6.35E-10	2.71E-08	1.61E-07	1.35E-07	14	ADH6,FMO5,UGT1A10,UGT1A8,UGT1A7,UGT1A6,UGT1A5, UGT1A9,UGT1A4,UGT1A1,UGT1A3,GSTO2,GSTA4,UGT2A3
673221	Chemical carcinogenesis	5.62E-09	1.50E-07	8.89E-07	1.20E-06	14	EPHX1,ADH6,UGT1A10,UGT1A8,UGT1A7,UGT1A6,UGT1A5, UGT1A9,UGT1A4,UGT1A1,UGT1A3,GSTO2,GSTA4,UGT2A3
132956	Metabolic pathways	1.27E-08	3.00E-07	1.78E-06	2.70E-06	62	PIGN,RIMKLA,ACO1,MDH1,PGK1,ADH6,FAH,ACSM3,FBP1,HO SCP2,AK4,ALDH2,PGP,HSD17B2,ALDH6A1,PNMT,UGT1A10,U UGT1A7,DHRS4L2,UGT1A6,UGT1A5,SHMT1,UGT1A9,COX11, UGT1A1,UGT1A3,CRLS1,PPT1,ASAH1,AKR1C3,ST6GALNAC1 GALM,SPR,ACSS1,CYP27A1,BDH2,GATM,BCKDHB,NDUFA2,D GGT1,BTD,AKR1B10,PIGK,DTYMK,OAT,GALNT12,LCT,UGT2A3 POLR2J2,CYP2U1,CYP4F3,ADI1,LTC4S,HADHB,FAHD1
814926	Carbon metabolism	3.33E-04	5.46E-03	3.24E-02	7.10E-02	10	ACO1,MDH1,PGK1,FBP1,PGP,ALDH6A1,SHMT1,ACSS1,PHGD
83075	Renin-angiotensin system	1.82E-03	2.59E-02	1.54E-01	3.88E-01	4	AGT,MME,ACE,ACE2
82934	Fatty acid elongation	2.51E-03	3.34E-02	1.99E-01	5.35E-01	4	HACD3,PPT1,HACD2,HADHB
552665	Morphine addiction	1.97E-02	1.75E-01	1.00E+00	1.00E+00	6	PDE1A,ADORA1,ARRB1,GNG12,GNG7,GNG11
99052	Lysosome	2.53E-02	1.93E-01	1.00E+00	1.00E+00	7	SORT1,PPT1,ASAH1,CTSH,CTSV,PSAP,SUMF1

Pathway Interaction Database							
138043	Signaling mediated by p38-gamma and p38-delta	2.61E-02	7.67E-01	1.00E+00	1.00E+00	2	SNTA1,STMN1
137925	Aurora A signaling	3.51E-02	7.67E-01	1.00E+00	1.00E+00	3	BIRC5,AURKA,OAZ1
138045	HIF-1-alpha transcription factor network	6.53E-02	7.67E-01	1.00E+00	1.00E+00	4	PGK1,CP,TF,TFRC
137911	FOXA2 and FOXA3 transcription factor networks	8.31E-02	7.75E-01	1.00E+00	1.00E+00	3	TTR,UCP2,TFRC
137912	Hedgehog signaling events mediated by Gli proteins	2.75E-01	8.18E-01	1.00E+00	1.00E+00	2	SHH,SAP30
137975	RXR and RAR heterodimerization with other nuclear receptor	2.82E-01	8.18E-01	1.00E+00	1.00E+00	1	NR1H4
138027	Regulation of Androgen receptor activity	3.27E-01	8.18E-01	1.00E+00	1.00E+00	2	SPDEF,SMARCA2
137927	Arf1 pathway	3.47E-01	8.18E-01	1.00E+00	1.00E+00	1	AP2M1
138015	Regulation of cytoplasmic and nuclear SMAD2/3 signaling	3.62E-01	8.18E-01	1.00E+00	1.00E+00	1	KPNA2
138002	E-cadherin signaling in keratinocytes	3.62E-01	8.18E-01	1.00E+00	1.00E+00	1	CASR
REACTOME							
1270189	Biological oxidations	1.96E-08	7.24E-06	5.20E-05	1.45E-05	22	EPHX1,ADH6,FDX1,ALDH2,UGT1A8,UGT1A7,UGT1A6, UGT1A5,UGT1A9,UGT1A4,UGT1A1,UGT1A3,ACSS1,CYP27A1 GSTO2,GGT1,NR1H4,GLYATL2,GSTA4,UGT2A3,CYP2U1,CYP4
1270121	The citric acid (TCA) cycle and respiratory electron transport	6.84E-04	6.81E-02	4.89E-01	5.05E-01	12	COX16,PDK1,ETFB,ETFDH,UCP2,SLC25A27,MPC2,COX11, NUBPL,NDUFS7,NDUFA2,COX14
1268749	Metabolism of Angiotensinogen to Angiotensins	6.91E-04	6.81E-02	4.89E-01	5.10E-01	4	AGT,MME,ACE,ACE2
1270001	Metabolism of lipids and lipoproteins	7.29E-04	6.81E-02	4.89E-01	5.38E-01	34	FABP6,AP2M1,ACSM3,FDX1,AGT,SCP2,ECI2,HSD17B2, HACD3,UGT1A9,APOE,ACSF2,PLA2R1,CRLS1,PPT1,ASAH1,A AKR1C3,PSAP,MOGAT1,ACOT13,CYP27A1,BDH2,GGT1,SGPP SUMF1,NR1H4,SRD5A3,HACD2,SLC44A4,CYP2U1,CYP4F3,LT
1270127	Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins.	7.38E-04	6.81E-02	4.89E-01	5.45E-01	10	COX16,ETFB,ETFDH,UCP2,SLC25A27,COX11,NUBPL,NDUFS7
1270158	Metabolism of amino acids and derivatives	1.02E-03	8.40E-02	6.03E-01	7.56E-01	19	RPL39L,HNMT,FAH,ALDH6A1,PNMT,SHMT1,CRYM,GATM,BCI PSMD10,DDC,PHGDH,SLC25A21,OAT,OAZ1,GSR,PAH,SERINC
1270011	Triglyceride Biosynthesis	3.02E-03	1.30E-01	9.32E-01	1.00E+00	7	HACD3,ACSF2,PPT1,ACBD7,MOGAT1,ACOT13,HACD2
1269624	Retinoid metabolism and transport	3.47E-03	1.35E-01	9.69E-01	1.00E+00	5	TTR,APOE,AKR1C3,AKR1B10,BCO2
1309221	Histidine, lysine, phenylalanine,	3.83E-03	1.41E-01	1.00E+00	1.00E+00	5	HNMT,FAH,CRYM,SLC25A21,PAH

	tyrosine, proline and tryptophan catabolism						
1268677	Metabolism of proteins	1.72E-01	6.24E-01	1.00E+00	1.00E+00	44	PIGN,CFTR,ETFB,CEACAM7,MAGT1,RPL39L,TTR,TUBB4A,AG MME,RAB26,TRAPPC6A,FOLR1,BIRC5,CPM,ST6GALNAC2,AR IGFBP2,CTSH,SORL1,ST6GALNAC1,MLEC,SPCS2,SRP9,TOM PSMD10,ACE,FFAR4,AURKA,GNG12,TUBA1A,ODAM,SUMF1, RNF128,GNG7,GNG11,CALB1,SRD5A3,PIGK,SEMA5A,GALNT ACE2,LYZ,TOP2A
Gen MAPP							
MAP00120_	Bile acid biosynthesis	1.82E-03	4.54E-02	1.97E-01	7.84E-02	4	ADH6,ALDH2,CYP27A1,HADHB
MAP00280	Valineleucine and isoleucine degradation	2.91E-03	4.54E-02	1.97E-01	1.25E-01	4	ALDH2,ALDH6A1,BCKDHB,HADHB
MAP00460	Cyanoamino acid metabolism	3.17E-03	4.54E-02	1.97E-01	1.36E-01	2	SHMT1,GGT1
MAP00350	Tyrosine metabolism	4.96E-03	4.86E-02	2.11E-01	2.13E-01	4	ADH6,FAH,PNMT,DDC
MAP00710	Carbon fixation	5.65E-03	4.86E-02	2.11E-01	2.43E-01	3	MDH1,PGK1,FBP1
MAP00590	Prostaglandin and leukotriene metabolism	7.17E-02	1.90E-01	8.25E-01	1.00E+00	2	GGT1,CYP4F3
MAP03020	RNA polymerase	3.31E-01	4.19E-01	1.00E+00	1.00E+00	1	POLR2J2
MAP00220	Urea cycle and metabolism of amino groups	3.31E-01	4.19E-01	1.00E+00	1.00E+00	1	OAT
MAP00251	Glutamate metabolism	3.77E-01	4.50E-01	1.00E+00	1.00E+00	1	GSR
MAP00910	Nitrogen metabolism	3.92E-01	4.55E-01	1.00E+00	1.00E+00	1	CA12
MSigDB C2 BIOCARTA (v6.0)							
M12950	Angiotensin-converting enzyme 2 regulates heart function	3.04E-03	1.73E-01	8.01E-01	1.73E-01	3	AGT,ACE,ACE2
M7239	Apoptotic DNA fragmentation and tissue homeostasis	2.17E-02	3.09E-01	1.00E+00	1.00E+00	2	ENDOG,TOP2A
M17370	Role of Ran in mitotic spindle regulation	2.17E-02	3.09E-01	1.00E+00	1.00E+00	2	AURKA,KPNA2
M7772	fl-arrestins in GPCR Desensitization	2.17E-02	3.09E-01	1.00E+00	1.00E+00	2	AP2M1,ARRB1
M3468	Genes encoding enzymes and their regulators involved in the remodeling of the extracellular matrix	5.32E-02	5.80E-01	1.00E+00	1.00E+00	10	SERPINA4,AGT,MMP7,SLPI,CTSH,CTSV,ITIH2,KY,LOX,SERPIN
M3008	Genes encoding structural ECM glycoproteins	8.93E-02	5.80E-01	1.00E+00	1.00E+00	8	MATN2,CTHRC1,SRPX,VWA1,IGFBP2,SPP1,IGSF10,VWA2
M5880	Genes encoding proteins affiliated structurally or functionally to extracellular matrix proteins	1.06E-01	5.80E-01	1.00E+00	1.00E+00	7	ANXA9,ANXA13,SEMA4G,CSPG5,SEMA3E,SEMA5A,ANXA10
M5889	Ensemble of genes encoding	1.21E-01	5.80E-01	1.00E+00	1.00E+00	30	MATN2,SERPINA4,AGT,CTHRC1,SRPX,MMP7,ANXA9,ANXA13

	extracellular matrix and extracellular matrix-associated proteins						SHH,VWA1,SEMA4G,LEFTY1,IGFBP2,CSPG5,PDGFD,SLPI,CTS CTSV,SEMA3E,SPP1,ITIH2,IGSF10,VWA2,NRTN,SEMA5A,KY,L FGFBP2,ANXA10,SERPINA5
M5885	Ensemble of genes encoding ECM-associated proteins including ECM-affilaited proteins, ECM regulators and secreted factors	1.65E-01	5.80E-01	1.00E+00	1.00E+00	22	SERPINA4,AGT,MMP7,ANXA9,ANXA13,SHH,SEMA4G,LEFTY1 CSPG5,PDGFD,SLPI,CTSH,CTSV,SEMA3E,ITIH2,NRTN,SEMA5 KY,LOX,FGFBP2,ANXA10,SERPINA5
M5884	Ensemble of genes encoding core extracellular matrix including ECM glycoproteins, collagens and proteoglycans	3.15E-01	5.80E-01	1.00E+00	1.00E+00	8	MATN2,CTHRC1,SRPX,VWA1,IGFBP2,SPP1,IGSF10,VWA2
Panther DB							
P05914	Nicotine degradation	3.80E-11	2.36E-09	1.11E-08	2.36E-09	9	UGT1A10,UGT1A8,UGT1A7,UGT1A6,UGT1A5,UGT1A9,UGT1A
P02776	Serine glycine biosynthesis	5.20E-03	1.61E-01	7.59E-01	3.22E-01	2	SHMT1,PHGDH
P05911	Angiotensin II-stimulated signaling through G proteins and beta-arrestin	8.66E-03	1.79E-01	8.43E-01	5.37E-01	4	AGT,ARRB1,GNG7,GNG11
P04396	Vitamin D metabolism and pathway	1.76E-02	1.82E-01	8.55E-01	1.00E+00	2	FDX1,CYP27A1
P04373	5HT1 type receptor mediated signaling pathway	1.77E-02	1.82E-01	8.55E-01	1.00E+00	4	SNAP25,GNG12,GNG7,GNG11
P02771	Pyrimidine Metabolism	2.17E-02	1.82E-01	8.55E-01	1.00E+00	2	ALDH6A1,DPYSL2
P02754	Methylcitrate cycle	4.62E-02	1.97E-01	9.30E-01	1.00E+00	1	ACO1
P05734	Synaptic vesicle trafficking	9.99E-02	2.66E-01	1.00E+00	1.00E+00	2	SYT12,SYT5
P00016	Cytoskeletal regulation by Rho GTPase	2.18E-01	3.87E-01	1.00E+00	1.00E+00	3	TUBB4A,MYO3B,STMN1
P00047	PDGF signaling pathway	8.01E-01	8.87E-01	1.00E+00	1.00E+00	2	RERG,SPDEF
Pathway Ontology							
PW:0000492	renin-angiotensin system signaling	3.26E-04	1.35E-02	6.76E-02	2.70E-02	4	AGT,MME,ACE,ACE2
PW:0000051	histidine metabolic	2.38E-03	4.93E-02	2.47E-01	1.97E-01	3	HNMT,ALDH2,DDC
PW:0000047	glycine, serine and threonine metabolic	3.80E-03	6.31E-02	3.16E-01	3.15E-01	3	SHMT1,GATM,PHGDH
PW:0000054	tryptophan metabolic	1.58E-02	1.48E-01	7.38E-01	1.00E+00	3	ALDH2,DDC,CAT
PW:0000373	glutathione conjugation	1.76E-02	1.48E-01	7.38E-01	1.00E+00	2	GSTO2,GSTA4
PW:0000729	statin pharmacokinetics pathway	3.58E-02	1.48E-01	7.38E-01	1.00E+00	2	UGT1A1,UGT1A3
PW:0000057	carbon fixation	3.58E-02	1.48E-01	7.38E-01	1.00E+00	2	MDH1,FBP1
PW:0000485	eicosanoids metabolic	6.51E-02	1.67E-01	8.36E-01	1.00E+00	2	GGT1,LTC4S
PW:0000398	homocysteine	6.51E-	1.67E-	8.36E-01	1.00E+00	2	HNMT,PNMT

	metabolic	02	01				
PW:0000021	hypertension	9.03E-02	1.74E-01	8.72E-01	1.00E+00	1	LOX
SMPDB							
SMP00054	Fatty Acid Elongation In Mitochondria	4.13E-04	5.27E-02	2.95E-01	6.19E-02	3	PPT1,PRDX3,HADHB
SMP00128	Gluconeogenesis	8.59E-04	5.27E-02	2.95E-01	1.29E-01	4	MDH1,PGK1,FBP1,GALM
SMP00075	Arachidonic Acid Metabolism	1.05E-03	5.27E-02	2.95E-01	1.58E-01	4	AKR1C3,CYP2U1,CYP4F3,LTC4S
SMP00006	Tyrosine Metabolism	2.15E-03	7.53E-02	4.21E-01	3.22E-01	4	FAH,PNMT,CYBA,DDC
SMP00004	Glycine, Serine and Threonine Metabolism	2.51E-03	7.53E-02	4.21E-01	3.77E-01	4	ALDH2,SHMT1,GATM,PHGDH
SMP00016	Propanoate Metabolism	3.08E-02	2.42E-01	1.00E+00	1.00E+00	2	ALDH6A1,ACSS1
SMP00032	Valine, Leucine and Isoleucine Degradation	3.22E-02	2.42E-01	1.00E+00	1.00E+00	3	ALDH2,ALDH6A1,BCKDHB
SMP00020	Arginine and Proline Metabolism	6.51E-02	3.32E-01	1.00E+00	1.00E+00	2	GATM,OAT
SMP00066	Biotin Metabolism	6.85E-02	3.32E-01	1.00E+00	1.00E+00	1	BTD
SMP00199	Maple Syrup Urine Disease	6.85E-02	3.32E-01	1.00E+00	1.00E+00	1	BCKDHB

Table 4 The enriched GO terms of the up regulated differentially expressed genes

GO ID	CATEGORY	GO Name	P Value	FDR B&H	FDR B&Y	Bonferroni	Gene Count	Gene
GO:0009607	BP	response to biotic stimulus	4.21E-43	4.21E-43	4.21E-43	2.47E-39	117	USP18,PDE2A,PDE4B,DDX58,NT5C3A,IFNL4,HLA-F,A DTX3L,TLR6,TRIM22,PLAC8,CXCL9,NLRC5,CCL2,NC CCL20,CXCL11,CX3CL1,TRIM38,PMAIP1,PML,FLT3, ZC3H12A,DHX58,FOS,TENT5A,ICAM1,IFI44,IFITM1, SAMHD1,IFITM2,IFI16,BATF2,IFI35,IFIT2,IFIT1,IFIT3, TRIM5,IFNB1,TXNIP,MT2A,RSAD2,CSF2,SH2D1B,ISG MIR181B1,OASL,CD274,MIR21,SOCS1,RAET1L,XAF1 TSLP,IL6,CXCL8,MX2,ZC3HAV1,CYLD,CYP1A1,IL12A CXCL10,TICAM1,GATA3,PSMB9,CMPK2,GBP1,IFIT5, TRIM21,IRF7,ISG20,BCL3,PTGER4,IL22RA1,RTP4,PT GFI1,STAT2,JAK2,IFIH1,BMP2,JUN,CLEC4A,PTX3,GL C4B,TAP1,FGF19,GPER1,SOCS3,PELI1,OAS1,OAS2,R NLRP3,LGALS9,RASGRP1,EGR1,CRTAM,SERPINE1,T PCK1,HERC5,IFNL2,IFNL3,IFNL1
GO:0006952	BP	defense response	3.55E-39	5.21E-36	4.82E-35	2.08E-35	119	USP18,PDE2A,DDX58,NT5C3A,IFNL4,HLA-F,APOBEC DTX3L,TLR6,KLF4,TRIM22,PLAC8,TNFRSF4,ADRB2, NLRC5,CCL2,CCL20,CXCL11,CX3CL1,TRIM38,PMAIF THEMIS2,ZC3H12A,DHX58,FOS,ICAM1,IFITM1,SAMI IFITM2,IFI16,BATF2,IFI35,IFIT2,IFIT1,IFIT3,ZFP36,TR MT2A,RSAD2,PLA2G4C,SH2D1B,ISG15,MIR181B1,O SOCS1,RAET1L,XAF1,IL1A,STX11,TSLP,IL6,CXCL8,M CYLD,IL12A,INHBA,TAGAP,CXCL10,TICAM1,IL17C,GA GBP1,IFIT5,IRF1,TRIM21,IRF7,ISG20,BCL3,PTGER4,I RTP4,PTGS2,BDKRB2,GFI1,STAT2,JAK2,IFIH1,BMP2 CLEC4A,PTX3,NFKBIA,C4A,C4B,TAP1,DRD1,GPER1,S CCRL2,OAS1,OAS2,NFKBIZ,RELB,CXCL2,CXCL3,S1P LGALS9,MMP25,RASGRP1,EGR1,CRTAM,SERPINE1, TNFAIP3,HERC5,IFNL2,IFNL3,IFNL1
GO:0034097	BP	response to cytokine	1.86E-38	2.18E-35	2.02E-34	1.09E-34	99	USP18,SPRY2,TRAF1,PDE2A,DDX58,HLA-F,KLF4,TRI TNFRSF4,CXCL9,NLRC5,CCL2,CCL20,CXCL11,CX3CI PML,FLT3,FLT3LG,ZC3H12A,KLF6,MAP3K8,FOS,ICAI SAMHD1,IFITM2,ACKR4,IFI16,IFI35,IFIT2,IFIT1,IFIT3, TRIM5,IFNB1,MT2A,RSAD2,CSF2,ISG15,MIR181B1,T OASL,CD274,MIR21,SOCS1,XAF1,IL1A,STX11,TSLP,I IL7R,CXCL8,MX2,CYLD,IL11,IL12A,IL15RA,CXCL10,IL GATA3,PSMB9,GBP1,IRF1,TRIM21,IRF7,ISG20,IL22R GFI1,STAT2,JAK2,IFIH1,JUN,NFKBIA,NKX3-1,GFPT2, DUSP1,SOCS3,PELI1,CCRL2,OAS1,OAS2,RELB,CXCL LGALS9,EGR1,SERPINE1,LTB,TNF,TNFAIP3,PCK1,IFN
GO:0009615	BP	response to virus	7.96E-38	7.78E-35	7.20E-34	4.67E-34	56	DDX58,NT5C3A,IFNL4,APOBEC3G,DTX3L,TRIM22,C TRIM38,PMAIP1,PML,FLT3,ZC3H12A,DHX58,IFI44,IF IFITM2,IFI16,IFIT2,IFIT1,IFIT3,TRIM5,IFNB1,RSAD2,IS OASL,IL6,MX2,ZC3HAV1,CYP1A1,IL12A,TAGAP,CXCL GATA3,GBP1,IFIT5,IRF1,IRF7,ISG20,BCL3,RTP4,STAT

								GLI2,OAS1,OAS2,NLRP3,LGALS9,TNF,TNFAIP3,HERC
GO:0071345	BP	cellular response to cytokine stimulus	2.30E-37	2.30E-37	2.30E-37	1.35E-33	94	USP18,SPRY2,TRAF1,PDE2A,HLA-F,KLF4,TRIM22,KL CXCL9,NLRC5,CCL2,CCL20,CXCL11,CX3CL1,TRIM38 FLT3LG,ZC3H12A,KLF6,MAP3K8,FOS,ICAM1,IFITM1 IFITM2,ACKR4,IFI16,IFI35,IFIT2,IFIT1,IFIT3,ZFP36,TR IFNB1,MT2A,RSAD2,CSF2,ISG15,MIR181B1,TNFSF1 MIR21,SOCS1,XAF1,IL1A,STX11,TSLP,IL6,IL7,IL7R,C MX2,CYLD,IL11,IL12A,IL15RA,CXCL10,IL17C,GATA3, GBP1,IRF1,TRIM21,IRF7,ISG20,IL22RA1,PTGS2,GFI1 JAK2,NFKBIA,NKX3-1,GFPT2,GPER1,DUSP1,SOCS3, OAS1,OAS2,CXCL2,CXCL3,LGALS9,EGR1,SERPINE1, TNFAIP3,PCK1,IFNL2,IFNL3,IFNL1
GO:0051607	BP	defense response to virus	3.34E-34	1.96E-31	1.82E-30	1.96E-30	47	DDX58,NT5C3A,IFNL4,APOBEC3G,DTX3L,TRIM22,C TRIM38,PMAIP1,PML,ZC3H12A,DHX58,IFITM1,SAM IFI16,IFIT2,IFIT1,IFIT3,TRIM5,IFNB1,RSAD2,ISG15,OA MX2,ZC3HAV1,TAGAP,CXCL10,TICAM1,GBP1,IFIT5,I ISG20,RTP4,STAT2,IFIH1,OAS1,OAS2,NLRP3,TNFAIP
GO:0045087	BP	innate immune response	9.78E-30	5.22E-27	4.83E-26	5.74E-26	79	USP18,DDX58,IFNL4,HLA-F,APOBEC3G,PGLYRP2,DT NLRC5,CCL2,CCL20,CX3CL1,TRIM38,PML,DHX58,IC SAMHD1,IFITM2,IFI16,IFI35,IFIT2,IFIT1,IFIT3,TRIM5, MT2A,RSAD2,SH2D1B,ISG15,MIR181B1,OASL,MIR2 RAET1L,XAF1,STX11,MX2,ZC3HAV1,CYLD,IL12A,TIC PSMB9,GBP1,IFIT5,IRF1,TRIM21,IRF7,ISG20,GFI1,ST IFIH1,CLEC4A,PTX3,NFKBIA,C4A,C4B,TAP1,GPER1,S OAS1,OAS2,RELB,NLRP3,LGALS9,RASGRP1,EGR1,C TNFAIP3,HERC5,IFNL2,IFNL3,IFNL1
GO:0002682	BP	regulation of immune system process	1.14E-25	5.12E-23	4.74E-22	6.66E-22	97	USP18,PDE4B,DDX58,IFNL4,HLA-F,HLX,APOBEC3G, PGLYRP2,DTX3L,TLR6,TNFRSF4,NLRC5,CCL2,CCL2 TRIM38,PML,THEMIS2,PRKD2,FLT3,FLT3LG,ZC3H12 MAP3K8,FOS,ICAM1,IFITM1,SAMHD1,IFI16,IFIT1,ZF TRIM5,IFNB1,RSAD2,CSF2,SH2D1B,ISG15,MIR181B TNFSF13B,CD274,MIR21,SOCS1,RAET1L,IL1A,TSLP, ZC3HAV1,CYLD,IL11,IL12A,IL15RA,INHBA,CXCL10,T PSMB9,GBP1,IRF1,IRF7,PTGER4,GFI1,JAK2,IFIH1,JU GLI2,NFKBIA,C4A,C4B,TAP1,GPER1,DUSP1,SOCS3,P RELB,NLRP3,LGALS9,RASGRP1,LMO2,EGR3,ICAM5, DUSP10,TNFAIP3,HERC5,IFNL2,IFNL3,IFNL1
GO:0001816	BP	cytokine production	1.15E-24	4.82E-22	4.46E-21	6.75E-21	66	PDE4B,UBE2L6,DDX58,HLA-F,PGLYRP2,TLR6,KLF4,K HEG1,UBA7,NLRC5,CCL2,CCL20,CX3CL1,TRIM38,PM ZC3H12A,DHX58,IFI16,ZFP36,IFNB1,RSAD2,CSF2,IS SOCS1,IL1A,TSLP,IL6,IL7,ZC3HAV1,CYLD,IL12A,INHE GATA3,GBP1,IRF1,TRIM21,IRF7,BCL3,PTGER4,PTGS PELI1,NR4A3,RELB,S1PR3,NLRP3,LGALS9,RASGRP1 LTB,TNF,TNFAIP3,HERC5,IFNL1
GO:0019079	BP	viral genome replication	3.31E-15	3.66E-13	3.39E-12	1.94E-11	21	APOBEC3G,CCL2,TRIM38,ZC3H12A,IFITM1,IFITM2,I

								RSAD2,ISG15,OASL,CXCL8,PROX1,ZC3HAV1,IFIT5,IS
GO:0019058	BP	viral life cycle	1.14E-11	6.49E-10	6.01E-09	6.68E-08	28	APOBEC3G,TNFRSF4,CCL2,TRIM38,PML,ZC3H12A,I IFI16,IFIT1,TRIM5,IFNB1,RSAD2,ISG15,OASL,CXCL8, IFIT5,TRIM21,ISG20,PTX3,OAS1,LGALS9,PARP10,TN
GO:0019220	BP	regulation of phosphate metabolic process	1.81E-11	9.65E-10	8.93E-09	1.06E-07	76	SPRY2,PDE2A,PPP1R15A,TLR6,KLF4,TNFRSF4,DAC ADRB2,NLRC5,CCL2,C1QTNF1,PLAUR,CCL20,TSACC FLT3,FLT3LG,ZC3H12A,MAP3K8,ICAM1,TRIM5,PPP4 MIR21,SOCS1,ATF3,IL1A,TSLP,IL6,IL7,PROX1,CYLD,I INHBA,CXCL10,TCIM,GBP1,IRF1,PTGER4,PTGS2,BDI NPFFR2,BMP2,JUN,TTBK1,NKX3-1,FGF19,DRD1,GPI SOCS3,LGALS9,RASGRP1,EGR1,NEURL1,TNF,DUSP1 HERC5,EPHA4,IFNL1
GO:0016032	BP	viral process	7.54E-11	3.48E-09	3.22E-08	4.42E-07	44	DDX58,APOBEC3G,TRIM22,TNFRSF4,CCL2,TRIM38, DHX58,ICAM1,IFITM1,IFITM2,IFI16,SP110,IFIT1,ZFP RSAD2,ISG15,OASL,RAET1L,CXCL8,PROX1,ZC3HAV IFIT5,TRIM21,IRF7,ISG20,GFI1,STAT2,IFIH1,JUN,PTX OAS1,LGALS9,PARP10,TNF,IFNL3
GO:0051254	BP	positive regulation of RNA metabolic process	1.16E-10	5.19E-09	4.80E-08	6.83E-07	70	HIVEP1,HIVEP2,DDX58,ETS2,DTX3L,EYA1,PPP1R15. CSRNP1,AHRR,ADRB2,NLRC5,CX3CL1,CAVIN2,PRRX ZC3H12A,KLF6,FOS,FOSB,CPEB3,ID4,IFI16,ZFP36,CI ATF3,IL1A,SIX2,IL6,PROX1,ZC3HAV1,IL11,INHBA,CX(BCL3,GFI1,STAT2,JAK2,BMP2,JUN,GLI2,NFKBIA,NKX RELB,NLRP3,LMO2,EGR1,EGR2,EGR3,EGR4,SERPINE LYL1,PCK1,IFNL1
GO:0009719	BP	response to endogenous stimulus	3.16E-08	8.94E-07	8.28E-06	1.85E-04	64	SPRY2,PDE2A,PDE4B,HIVEP1,ACTA1,TLR6,KLF4,LRI CCL2,FLRT3,FST,PML,KLB,COL4A1,PRKD2,FLT3,MXI CPEB3,ZFP36,SLC5A5,IFNB1,TXNIP,MIR21,SOCS1,IL TICAM1,GATA3,IRF1,SSTR2,PTGER4,PTGS2,FGF18,S JUN,NKX3-1,FGF19,CPEB2,DRD1,GPER1,DUSP1,SOC EGR1,EGR2,EGR3,NEURL1,SERPINE1,TNF,PCK1,EPH.
GO:0009986	CC	cell surface	3.98E-04	4.86E-02	3.29E-01	1.95E-01	33	ACHE,TRPC4,HLA-F,DSCAML1,TNFRSF4,FAP,HEG1,C CX3CL1,FLT3,FLT3LG,ICAM1,ACKR4,CD274,RAET1L, IL15RA,LAYN,CXCL10,RTP4,BMP2,CCRL2,GRIA2,MM
GO:0045202	CC	synapse	1.18E-02	1.92E-01	1.00E+00	1.00E+00	37	PDE2A,PDE4B,ACHE,PLEKHG5,DSCAML1,SYNPR,DA FLRT3,CX3CL1,CPEB3,STX19,SNCAIP,STX11,PDZD2 JAK2,NTNG2,SYT1,C4A,C4B,GRIN3B,ADGRL3,CPEB2 GRIA2,GRM8,NEURL1,GRIP2,EPHA4
GO:0031226	CC	intrinsic component of plasma membrane	1.97E-02	2.41E-01	1.00E+00	1.00E+00	42	TRPC4,TLR6,TNFRSF4,ADRB2,RASGRP3,C1QTNF1,F FLT3,FLT3LG,SLC39A2,ICAM1,ACKR4,SLC6A13,IL6,T BDKRB2,NPFFR2,BMP2,NTNG2,CLEC4A,CPO,GRIN3I GPER1,DDR2,CCRL2,GRIA2,GRM8,S1PR3,ICAM5,CRT EPHA4,IFNL1
GO:0030054	CC	cell junction	2.26E-02	2.59E-01	1.00E+00	1.00E+00	33	DDX58,ACHE,TRPC4,PLEKHG5,DSCAML1,SYNPR,DA PLAUR,FLRT3,AMOTL2,ICAM1,CPEB3,PDZD2,SNPH, RND1,SYT1,C4A,C4B,GJB7,GRIN3B,ADGRL3,DRP2,G

								NEURL1,GJC3,EPHA4
GO:0000790	CC	nuclear chromatin	3.70E-02	2.92E-01	1.00E+00	1.00E+00	43	ZNF627,HIVEP1,HIVEP2,HDX,ETS2,HLX,KLF4,KLF2,C PRRX2,KLF6,FOS,FOSB,ETV7,ID4,IFI16,BATF2,SP11(PROX1,GATA3,IRF1,IRF7,GFI1,STAT2,JUN,GLI2,NKX3 ZNFX1,RELB,LMO2,EGR1,EGR2,EGR3,EGR4,LYL1,MX
GO:0043005	CC	neuron projection	5.95E-02	3.48E-01	1.00E+00	1.00E+00	36	PDE2A,PDE4B,ACHE,LRIT3,DSCAML1,SYNPR,SPTBI FLRT3,CX3CL1,FOS,CPEB3,SLC6A13,PDZD2,SNPH,S NTNG2,SYT1,C4A,C4B,GRIN3B,ADGRL3,CPEB2,DRD GRIA2,GRM8,NEURL1,GRIP2,EPHA4
GO:0005789	CC	endoplasmic reticulum membrane	7.98E-02	3.61E-01	1.00E+00	1.00E+00	25	RAB19,HLA-F,PPP1R15A,LRIT3,PLAUR,FLRT3,HSD17 RSAD2,PLA2G4C,MOGAT3,CYP1A1,IL15RA,CYP21A2 SEC16B,DRD1,GPER1,CH25H,GRIA2,RASGRP1,CRYZ
GO:0005768	CC	endosome	1.96E-01	5.45E-01	1.00E+00	1.00E+00	20	HLA-F,DTX3L,SAMD9L,ADRB2,ARRDC3,AMOTL2,PM IL12A,IL15RA,TICAM1,IRF7,SLC30A3,BDKRB2,JAK2,
GO:0098805	CC	whole membrane	2.97E-01	6.86E-01	1.00E+00	1.00E+00	33	PDE2A,TRPC4,HLA-F,DTX3L,PPP1R15A,TLR6,SYNPI CAVIN2,PMAIP1,PML,ICAM1,RSAD2,CD274,IL7R,TIC PTGS2,JAK2,SYT1,TAP1,SEC16B,DRD1,GRIA2,RAB4 CRYZL2P-SEC16B,TNF,EPHA4
GO:0005739	CC	mitochondrion	6.47E-01	9.41E-01	1.00E+00	1.00E+00	30	PDE2A,HIVEP1,NT5C3A,PPP1R15A,DUSP26,PMAIP1 IFIT3,TXNIP,RSAD2,XAF1,BBC3,MX2,CYP1A1,SNPH,T NPTX1,GPER1,OAS1,TDRD7,SLC25A2,HSH2D,SLC25
GO:0005125	MF	cytokine activity	7.41E-19	6.55E-16	4.82E-15	6.55E-16	31	IFNL4,CXCL9,CCL2,CCL20,CXCL11,CX3CL1,SECTM1 TNFSF13B,IL1A,TSLP,IL6,IL7,CXCL8,IL11,IL12A,TNFS IL17C,BMP2,VSTM1,CXCL2,CXCL3,LTB,TNF,IFNL2,IF
GO:0005102	MF	signaling receptor binding	3.29E-13	1.45E-10	1.07E-09	2.90E-10	77	TRAF1,IFNL4,HLA-F,PYY2,ETS2,TLR6,FAP,ADRB2,CX(ARRDC3,CCL20,FST,CXCL11,CX3CL1,CHAC1,KLB,SE IFNB1,SNED1,CSF2,ISG15,TNFSF13B,OASL,PTCH2,S IL6,IL7,CXCL8,PROX1,IL11,IL12A,TNFSF10,INHBA,CX RTP4,BDKRB2,FGF18,JAK2,NPFFR2,BMP2,RND1,SY VSTM1,DRD1,CCRL2,NR4A3,CXCL2,CXCL3,S1PR3,L(SERPINE1,NCOA7,LTB,TNF,GRIP2,EPHA4,IFNL2,IFNL
GO:0030545	MF	receptor regulator activity	1.45E-11	2.14E-09	1.57E-08	1.28E-08	36	IFNL4,PYY2,CXCL9,CCL2,FLRT3,CCL20,FST,CXCL11, IFNB1,CSF2,TNFSF13B,IL1A,TSLP,IL6,IL7,CXCL8,IL1 INHBA,CXCL10,IL17C,FGF18,BMP2,FGF19,VSTM1,C IFNL2,IFNL3,IFNL1
GO:0098772	MF	molecular function regulator	8.57E-08	1.08E-05	7.96E-05	7.57E-05	66	SPRY2,IFNL4,PYY2,DTX3L,RRAD,PPP1R15A,TLR6,K RASGRP3,CXCL9,CCL2,FLRT3,CCL20,FST,TSACC,CX SECTM1,FLT3LG,SPINK9,PPP4R4,IFNB1,TXNIP,CSF2 TSLP,IL6,IL7,CXCL8,IL11,IL12A,TNFSF10,INHBA,TAG BMP2,JUN,C4A,C4B,NKX3-1,FGF19,VSTM1,CPEB2,S CXCL3,RGS16,LGALS9,MMP25,RASGRP1,SERPINE1 IFNL2,IFNL3,IFNL1
GO:0046914	MF	transition metal ion binding	5.07E-05	2.04E-03	1.50E-02	4.48E-02	39	TRAF1,PDE2A,HIVEP1,DDX58,APOBEC3G,PGLYRP2, PML,DHX58,SAMHD1,PPEF1,TRIM5,MT1E,MT2A,XA CYP1A1,TNFSF10,CYP21A2,GATA3,FAXDC2,TRIM21

								CH25H,NR4A3,ZNFX1,MMP25,RASGRP1,EGR1,NAN(
GO:0000977	MF	RNA polymerase II regulatory region sequence-specific DNA binding	5.93E-05	2.04E-03	1.50E-02	5.24E-02	32	HIVEP1,HIVEP2,ETS2,KLF4,NLRC5,PRRX2,KLF6,FOS BATF2,ATF3,SIX2,PROX1,GATA3,IRF1,IRF7,STAT2,JU NR4A3,RELB,LMO2,EGR1,EGR2,EGR3,EGR4,LYL1,MX
GO:0016772	MF	transferase activity, transferring phosphorus-containing groups	6.00E-05	2.04E-03	1.50E-02	5.30E-02	56	SPRY2,NT5C3A,APOBEC3G,TLR6,KLF4,TNFRSF4,DU XRN1,NLRC5,CCL2,TSACC,PML,PRKD2,FLT3,MAP3K OASL,MIR21,SOCS1,IL6,CXCL8,PROX1,GADD45B,CX TENT5C,FGF18,JAK2,ENO4,NPFFR2,BMP2,JUN,TTB DUSP8,SOCS3,OAS1,OAS2,NUAK2,LGALS9,RASGRP DUSP10,TNFAIP3,PCK1,HERC5,EPHA4
GO:0044212	MF	transcription regulatory region DNA binding	8.84E-05	2.69E-03	1.98E-02	7.80E-02	36	HIVEP1,HIVEP2,ETS2,KLF4,NLRC5,PRRX2,KLF6,FOS TIPARP,ATF3,SIX2,PROX1,GATA3,IRF1,IRF7,GFI1,STA BARX1,NR4A3,RELB,LGALS9,LMO2,EGR1,EGR2,EGR
GO:0004672	MF	protein kinase activity	6.23E-04	1.28E-02	9.42E-02	5.51E-01	40	SPRY2,TLR6,TNFRSF4,DUSP26,HEG1,ADRB2,CCL2, PIM3,MIR21,SOCS1,IL6,PROX1,GADD45B,CXCL10,T(BMP2,JUN,TTBK1,DRD1,DUSP1,DDR2,DUSP8,SOCS EGR1,NEURL1,TNF,DUSP10,TNFAIP3,HERC5,EPHA4
GO:0042802	MF	identical protein binding	7.96E-03	7.03E-02	5.17E-01	1.00E+00	50	TRAF1,PDE2A,DDX58,ACHE,APOBEC3G,TLR6,DSCAI AMOTL2,PML,FLT3,FLT3LG,SAMHD1,IFIT3,TRIM5,SI TNFSF10,INHBA,GIMAP2,TICAM1,GBP1,TRIM21,PT(BMP2,JUN,PTX3,NFKBIA,SYT1,TAP1,RBM11,NPR3,G RASGRP1,CRTAM,CD69,TNF,TNFAIP3,GJC3,HSD17B

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

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

GO ID	CATEGORY	GO Name	P Value	FDR B&H	FDR B&Y	Bonferroni	Gene Count	Gene
GO:0043436	BP	oxoacid metabolic process	9.03E-16	1.67E-12	1.53E-11	5.00E-12	71	RIMKLA,PDK1,ACO1,ETFB,ETFDH,MDH1,HNMT,F ACSM3,FBP1,HOGA1,AGT,SCP2,ECI2,ALDH6A1,F FOLR1,UGT1A10,UGT1A8,UGT1A7,UGT1A6,UGT ACSF2,SLC3A1,UGT1A4,UGT1A1,UGT1A3,CRYM DHFRP1,SPR,ACSS1,CYP27A1,BDH2,GATM,BCK ITIH2,PHGDH,GGT1,ERFE,BTD,NR1H4,SLC25A21 ECH1,BCO2,BNIPL,UGT2A3,PAH,CYP2U1,CYP4F3
GO:0032787	BP	monocarboxylic acid metabolic process	2.51E-12	1.78E-09	1.64E-08	1.39E-08	46	PDK1,ETFB,ETFDH,PGK1,FABP6,ADH6,FAH,ACSL SCP2,ECI2,MPC2,HACD3,UGT1A10,UGT1A8,UGT UGT1A9,ACSF2,UGT1A4,UGT1A1,UGT1A3,CSPG BDH2,GATM,PHGDH,GGT1,ERFE,BTD,NR1H4,GLY UGT2A3,CYP2U1,CYP4F3,LTC4S,HADHB,DSEL
GO:0010817	BP	regulation of hormone levels	1.04E-10	4.79E-08	4.40E-07	5.75E-07	40	CFTR,TTR,HMGN3,ADH6,ADORA1,FDX1,AGT,UCH MPC2,UGT1A8,UGT1A7,SHH,UGT1A9,BIRC5,AQP ARRB1,AKR1C3,SNAP25,SLC16A10,KLK6,SPP1,C AKR1B10,PCSK1N,NR1H4,SRD5A3,CASR,SLC44A
GO:0055114	BP	oxidation-reduction process	2.33E-09	9.92E-07	9.12E-06	1.29E-05	58	ABCC4,CYBRD1,ACO1,ETFB,ETFDH,MDH1,PGK1 AGT,SCP2,ECI2,ALDH2,HSD17B2,ALDH6A1,PCYC COX11,CP,APOE,CRYM,CRYZ,AKR1C3,CYBA,NDU CYP27A1,BDH2,BCKDHB,NDUFA2,GSTO2,PHGD KCNAB1,SRD5A3,CAT,PRDX2,ECH1,LEPR,GSR,BC ADI1,LTC4S,HADHB,NOSTRIN,FAHD1
GO:0017144	BP	drug metabolic process	5.53E-09	2.19E-06	2.01E-05	3.06E-05	42	ATPSCKMT,ACO1,PGK1,ADH6,FAH,AGT,SCP2,AK SHMT1,CRP,UGT1A1,CSPG5,AKR1C3,CTSH,CYB ACSS1,CYP27A1,BDH2,GATM,NDUFA2,ACE,DDC AKR1B10,TCN1,OAT,CAT,PRDX2,SLC44A4,PAH,C
GO:0051186	BP	cofactor metabolic process	1.14E-08	3.95E-06	3.64E-05	6.33E-05	32	PDK1,ACSM3,SCP2,MPC2,FOLR1,SHMT1,ACSF2 PPT1,AKR1C3,CYBA,DHFRP1,SPR,ACOT13,ACSS HEBP1,PRDX3,AKR1B10,ATP5IF1,TCN1,CAT,HAC
GO:0044283	BP	small molecule biosynthetic process	1.87E-08	6.00E-06	5.52E-05	1.04E-04	41	EPHX1,PDE1A,RIMKLA,CFTR,MDH1,PGK1,ACSM SCP2,PGP,HACD3,SHMT1,APOE,DNPH1,ASAH1,C ACSS1,CYP27A1,BDH2,GATM,PHGDH,GGT1,NR1 OAT,HACD2,LEPR,ENTPD3,PAH,SERINC5,ADI1,LT
GO:0044255	BP	cellular lipid metabolic process	6.57E-08	1.73E-05	1.59E-04	3.64E-04	51	PIGN,PDK1,ETFB,ETFDH,TTR,FABP6,ADH6,ACSM PGP,HACD3,UGT1A8,UGT1A7,UGT1A9,APOE,ACS PPT1,ASAH1,AKR1C3,SORL1,PSAP,MOGAT1,ACS SUMF1,AKR1B10,STRA6,NR1H4,SRD5A3,RARRE SLC44A4,ECH1,BCO2,CYP2U1,CYP4F3,SERINC5,
GO:0006629	BP	lipid metabolic process	4.88E-07	1.01E-04	9.29E-04	2.70E-03	59	PIGN,PDK1,CFTR,ETFB,ETFDH,TTR,FABP6,ADH6 SCP2,FGFR3,ECI2,PGP,HSD17B2,HACD3,UGT1A8 APOE,ACSF2,UGT1A1,UGT1A3,CRLS1,PPT1,ASA MOGAT1,SPP1,ACSS1,CYP27A1,BDH2,GGT1,SG STRA6,NR1H4,SRD5A3,RARRES2,PIGK,GLYATL2

								LEPR,BCO2,CYP2U1,CYP4F3,SERINC5,LTC4S,HA
GO:0006811	BP	ion transport	1.77E-05	2.08E-03	1.91E-02	9.78E-02	67	ATPSCKMT,ABCC4,RAMP1,CFTR,MAGT1,KCNIP3 SCNN1A,SCP2,AK4,GLTPD2,CNGA1,PCYOX1,SLC CP,NLGN1,APOE,AQP1,SLC3A1,PLA2R1,SLC12A2 SLC45A1,SNTA1,SLC16A10,CYBA,NDUFS7,PSAP ERFE,LRRC26,KCNAB1,SYT5,KCNMB4,SLC38A1 SLC25A21,KCNE3,TCN1,SLC38A4,NTRK2,CASR,S TF,CLDN10,TFRC,CUTC,ACE2,ORAI3,ROS1
GO:0040007	BP	growth	2.16E-05	2.48E-03	2.29E-02	1.19E-01	46	RERG,MATN2,HOXA11,FBP1,PIN1,AGT,FGFR3,AL SORBS2,AGR2,SHH,TMPRSS4,VWA1,APOE,DNP SLC12A2,PPT1,CSPG5,SMARCA2,SEMA3E,CYBA AZGP1,PSMD10,HAGLR,STC1,IGSF10,AURKA,ST SEMA5A,SLC44A4,LEPR,TFRC,BNIPL,TM4SF4,R
GO:0046903	BP	secretion	3.29E-04	2.30E-02	2.11E-01	1.00E+00	59	ABCC4,CFTR,CRISP3,MAGT1,TTR,HMGN3,ADOR UCP2,QPCT,MME,MMP7,RAB26,METTL7A,SELEI BIRC5,NLGN1,APOE,AQP1,CRP,PLA2R1,ARRB1,PI SNAP25,CTSH,SLC16A10,CYBA,PSAP,MLEC,SYT FFAR4,STC1,SYT5,KCNMB4,NR1H4,DPYSL2,RAI CASR,CAT,SLC44A4,TMBIM6,TF,LEPR,SYNGR1,L
GO:0005739	CC	mitochondrion	1.47E-13	8.98E-11	6.28E-10	8.98E-11	86	ATPSCKMT,COX16,PDK1,ACO1,ETFB,ETFDH,MD AP2M1,ACSM3,ASB9,HOGA1,PIN1,FDX1,UCP2,S CEBPZOS,ALDH6A1,PRIMPOL,SERHL2,HSPE1,S AGR2,MACROD1,OLFM4,SHMT1,COX11,ACSF2,I BRI3BP,DNLZ,PPA2,CYBA,KLK6,NDUFS7,DHFRP ACSS1,CYP27A1,SRI,BDH2,GATM,TOMM20,BCK BTD,HEBP1,PRDX3,AKR1B10,DPYSL2,SLC25A2 GLYATL2,OAT,CAT,PRDX2,TMBIM6,ECH1,GSR,TF HADHB,FAHD1,ENDOG,COX14
GO:0099513	CC	polymeric cytoskeletal fiber	4.18E-05	2.56E-03	1.79E-02	2.56E-02	48	CYBRD1,CFTR,TUBB4A,CYS1,PROM2,MYO3B,NM BIRC5,NLGN1,APOE,AQP1,SLC3A1,CRP,EFHC2,AI CYBA,BCAS3,EML6,AIF1L,ANKS4B,ACE,AURKA,P TUBA1A,CD302,SPAG16,TCTEX1D2,DPYSL2,KR LCT,USH1C,ACE2,PBXIP1
GO:0036477	CC	somatodendritic compartment	1.98E-04	5.77E-03	4.04E-02	1.21E-01	40	PDE1A,CFTR,KCNIP3,SORT1,ADORA1,TUBB4A,A PNMT,SHH,NLGN1,APOE,MAGEE1,SCGN,AQP1,A CYBA,NDUFS7,SYT12,SRI,PGRMC1,DDC,AURKA, CALB1,NRGN,NTRK2,TPGS1,CASR,ENDOG
GO:0098805	CC	whole membrane	1.14E-03	2.20E-02	1.54E-01	6.97E-01	54	PXMP4,ABCC4,CYBRD1,CFTR,MAGT1,PGK1,SOR SUN2,SCP2,MME,RAB26,FOLR1,TMEM59,SHH,C SLC3A1,ARRB1,BRI3BP,PPT1,CSPG5,CD24,SNAP SYT12,SRI,TOMM20,PGRMC1,TUBA1A,REEP6,S TFRC,ACE2,CD1D,SYNGR1,LTC4S,HADHB,NOST
GO:0031226	CC	intrinsic component of plasma membrane	1.66E-03	2.74E-02	1.92E-01	1.00E+00	54	RAMP1,CFTR,MAGT1,KCNIP3,ADORA1,PROM2,U MME,CNGA1,RAB26,FOLR1,CP,NLGN1,AQP1,SEM CSPG5,CD24,SNAP25,SEMA3E,SORL1,SLC16A1

								FFAR4,PROM1,LRRC26,KCNAB1,KCNMB4,STRA CASR,SLC39A10,TMBIM6,LCT,LEPR,TFRC,CD1D, ROM1,ROS1
GO:0015629	CC	actin cytoskeleton	4.05E-03	4.76E-02	3.33E-01	1.00E+00	28	CYBRD1,CFTR,PROM2,MYO3B,SCNN1A,MME,PL AQP1,SLC3A1,CRP,CD24,SNAP25,CTSV,CYBA,AI GNG12,CD302,CALB1,LCT,USH1C,ACE2
GO:0098552	CC	side of membrane	4.13E-03	4.76E-02	3.33E-01	1.00E+00	24	FCGRT,SCNN1A,FGFR3,ALCAM,FOLR1,NLGN1,A ACE,GNG12,KCNAB1,GNG7,GNG11,VTCN1,TF,LE
GO:0043005	CC	neuron projection	4.46E-03	4.78E-02	3.34E-01	1.00E+00	48	CFTR,KCNIP3,HNMT,PLEKHB1,SORT1, ADORA1, MME,CNGA1,SORBS2,PNMT,SHH, NLGN1,APOE, ARRB1,PPT1,SNAP25,CTSV,CYBA, NDUFS7,SYT PROM1,REEP6,KCNAB1,SYT5, DPYSL2,KCNE3,C TPGS1,CASR,STMN1,USH1C, ROM1
GO:0030659	CC	cytoplasmic vesicle membrane	6.15E-03	5.61E-02	3.92E-01	1.00E+00	27	ABCC4,CFTR,MAGT1,SORT1,AP2M1,MME,RAB2 ARRB1,SNAP25,CYBA,PSAP,MLEC,SYT12,SRI,PG TF,TFRC,SYNGR1,NOSTRIN,SERPINA5
GO:0015630	CC	microtubule cytoskeleton	2.66E-01	4.56E-01	1.00E+00	1.00E+00	31	TUBB4A,CYS1,NME5,SCNN1A,GPSM2, SAC3D1, CTSH,PCLAF,BCAS3,ACOT13, EML6,ACE,AURKA, TCTEX1D2,DPYSL2,CFAP73, DNAAF4,TPGS1,ST
GO:0005794	CC	Golgi apparatus	3.14E-01	5.04E-01	1.00E+00	1.00E+00	36	ACO1,KCNIP3,PLEKHB1,SORT1,FGFR3, MME,ITM TMEM59,SHH,NLGN1,APOE, ST6GALNAC2,ARL3 PDGFD,SNAP25,SORL1,CYBA, ST6GALNAC1,SP CREG2,RNF128,NTRK2, GALNT12,CAT,SERINC5,
GO:0048037	MF	cofactor binding	5.36E-10	6.15E-07	4.69E-06	6.15E-07	37	ACO1,ETFDH,MDH1,FDX1,SCP2,ECI2,ALDH2,ALD NUBPL,CRYM,CRYZ,ACBD7,CYBA,NDUFS7,DHFR PHGDH,HEBP1,KCNAB1,CREG2,TCN1,NTHL1,OA CYP4F3,LTC4S,HADHB
GO:0016491	MF	oxidoreductase activity	9.75E-09	2.24E-06	1.70E-05	1.12E-05	50	ABCC4,CYBRD1,ETFB,ETFDH,MDH1,PGK1,ADH6 HSD17B2,ALDH6A1,PCYOX1,TRMT9B,FMO5,DH CRYM,CRYZ,AKR1C3,CYBA,NDUFS7,DHFRP1,SP NDUFA2,GSTO2,PHGDH,SUMF1,PRDX3,AKR1B1 PRDX2,GSR,BCO2,LOX,PAH,CYP2U1,CYP4F3,AD
GO:0042803	MF	protein homodimerization activity	1.44E-05	1.57E-03	1.19E-02	1.65E-02	43	PDK1,KCNIP3,PLEKHB1,HOGA1,SCP2,MME,ANX UGT1A7,UGT1A6,AGR2,OLFM4,SHMT1,UGT1A9, CRP,UGT1A4,UGT1A1,UGT1A3,CRYM,PSAP,GALM DPY30,SUMF1,ATP5IF1,NTRK2,CASR,CAT,GSR,T
GO:0042802	MF	identical protein binding	5.34E-04	2.33E-02	1.78E-01	6.13E-01	64	PDK1,ACYP2,KCNIP3,PLEKHB1,TTR,FBP1,HOGA ALCAM,MME,ALDH2,ANXA9,UGT1A10,UGT1A8,U SHMT1,UGT1A9,BIRC5,VWA1,BCAS1,APOE,DNP UGT1A3,CRYM,CLDN16,PSAP,GALM,SPR,SRI,LH DPY30,SUMF1,PRDX3,VWA2,DPYSL2,ATP5IF1,N GSR,TFRC,GSTA4,BNIPL,PAH,LTC4S,LYZ,TOP2A,
GO:0008233	MF	peptidase activity	1.14E-02	1.27E-01	9.64E-01	1.00E+00	40	CFTR,SERPINA4,WFDC2,AGT,MME,MMP7,HSPE TMPRSS4,BIRC5,PRSS33,CPM,CFI,AQP1,ARRB1, SORL1,KLK7,KLK6,SPCS2,TOMM20,PSMD10,AC

								PRDX3,PCSK1N,RNF128,RARRES1,PIGK,ACE2,K
GO:0098772	MF	molecular function regulator	2.54E-02	1.43E-01	1.00E+00	1.00E+00	53	CFTR,KCNIP3,TTR,SERPINA4,METRN,WFDC2,AG UGT1A7,SHH,BIRC5,DEPDC1,APOE,TBC1D3B,SE ARHGDIB,ARRB1,CSPG5,PDGFD,SLPI,CD24,CTS SPP1,BCAS3,SRI,ADGRB3,ITIH2,STC1,ERFE,PRD KCNMB4,ATP5IF1,KCNE3,RARRES1,NRTN,SEMA SERPINA5,ARHGAP19
GO:0005102	MF	signaling receptor binding	3.50E-02	1.65E-01	1.00E+00	1.00E+00	50	RERG,TTR,HMGN3,ADORA1,AP2M1,METRN,AGT AGR2,SHH,NLGN1,APOE,AQP1,SEMA4G,CRP,LEF ASAH1,CSPG5,PDGFD,CTSH,SEMA3E,PSAP,SPP PCSK1N,NR1H4,RARRES2,NRTN,DNAAF4,NTRK2 TF,ACE2,HHLA2,CD1D,LOX,TSPAN8
GO:0015318	MF	inorganic molecular entity transmembrane transporter activity	4.02E-02	1.65E-01	1.00E+00	1.00E+00	32	ATPSCKMT,ABCC4,CFTR,MAGT1,KCNIP3,SCNN1 NLGN1,AQP1,SLC3A1,SLC12A2,CLDN16,TMEM3 SLC16A10,SRI,LRRC26,KCNAB1,KCNMB4,SLC38 SLC38A4,SLC39A10,TF,TFRC,ORAI3
GO:0030234	MF	enzyme regulator activity	9.38E-02	2.43E-01	1.00E+00	1.00E+00	30	SERPINA4,WFDC2,AGT,GPSM2,HACD3,UGT1A8, TBC1D3B,UGT1A1,ARHGDIB,ARRB1,SLPI,CD24, ITIH2,PRDX3,PCSK1N,ATP5IF1,RARRES1,OAZ1, ARHGAP19
GO:0016818	MF	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	1.01E-01	2.48E-01	1.00E+00	1.00E+00	39	ATPSCKMT,RERG,ABCC4,CFTR,ACYP2,TUBB4A, GPSM2,RAB26,TRAPPC6A,PCYOX1,HACD3,DEP ARL3,ARRB1,PPA2,SMARCA2,BCAS3,ADGRB3,LH GNG7,GNG11,RAD51B,ATP5IF1,CFAP73,NTRK2, ENTPD8,ARHGAP19
GO:0046914	MF	transition metal ion binding	1.18E-01	2.75E-01	1.00E+00	1.00E+00	30	ADH6,FDX1,QPCT,MME,MMP7,PRIMPOL,SHH,SH CRYZ,MMEL1,DNLZ,CYP27A1,ACE,SUMF1,NR1H CUTC,ACE2,LOX,PAH,CYP2U1,CYP4F3,ADI1

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

Table 6 Topology table for up and down regulated genes

Regulation	Node	Degree	Betweenness	Stress	Closeness	Clustering Coefficient
Up	JUN	1463	0.391453	1.016E+09	0.415898	2.86E-04
Up	FBXO6	621	0.12966	493715688	0.353842	5.75E-05
Up	CYLD	608	0.103943	382426264	0.359075	7.80E-04
Up	IFI16	432	0.074647	147288646	0.349575	0.001063
Up	ADRB2	307	0.065447	120555780	0.338941	4.13E-04
Up	TRAF1	264	0.063246	72422838	0.337611	0.001467
Up	TNF	259	0.03929	76146724	0.344238	0.004256
Up	PML	234	0.056839	32809074	0.374284	0.004516
Up	ISG15	198	0.033378	48463634	0.341138	0.003846
Up	ICAM1	172	0.020484	54377736	0.31907	8.16E-04
Up	NFKBIA	171	0.026417	48434352	0.328288	0.002352
Up	ZC3HAV1	157	0.022112	12840580	0.362234	0.011922
Up	LMO2	155	0.032438	32263182	0.314392	4.36E-04
Up	ACTA1	148	0.027304	30357948	0.328193	8.50E-04
Up	FOS	132	0.014696	19098404	0.322621	0.007871
Up	PPP1R15A	130	0.015717	52057574	0.305846	0
Up	SPRY2	128	0.024553	23663296	0.310628	0.002839
Up	STX11	110	0.022909	25856594	0.305533	0
Up	JAK2	109	0.018338	18613612	0.321526	0.009346
Up	RELB	104	0.009702	17452368	0.316176	0.006139
Up	TRIM21	103	0.019363	9498044	0.339934	0.005347
Up	PLAUR	96	0.024508	28704600	0.297799	2.19E-04
Up	MIR21	96	0.006608	34185424	0.292104	0
Up	TNFAIP3	93	0.014225	10441280	0.329735	0.018315
Up	UBE2L6	91	0.01148	13366068	0.319914	0.00293
Up	XRN1	91	0.017619	6441514	0.350222	0.013675
Up	AMOTL2	89	0.015533	27398694	0.29877	0
Up	SAMHD1	86	0.010242	19438896	0.308118	0
Up	SOCS3	77	0.014788	9258178	0.322804	0.011962
Up	IFIT3	76	0.005604	8632792	0.311342	0.028508
Up	LGALS9	74	0.015887	21471046	0.280482	0
Up	PCK1	74	0.005113	16092358	0.298315	0
Up	CYP1A1	70	0.011023	20286860	0.2879	0
Up	PSMB9	64	0.007914	24671042	0.287682	0.001586
Up	ATF3	63	0.006767	2850414	0.344176	0.029508
Up	DDX58	62	0.007815	3885286	0.333177	0.015819
Up	SOCS1	62	0.007568	4945796	0.310696	0.023268
Up	TENT5A	62	0.011895	11622694	0.29122	0
Up	ZFP36	62	0.009922	5629422	0.318712	0.010048
Up	NLRP3	57	0.007142	11376526	0.291789	0
Up	CD274	56	0.011395	7918474	0.287115	0
Up	CREB5	56	0.009697	3368448	0.336831	0.031447
Up	DNAJB4	54	0.011227	2848256	0.34196	0.014675

Up	HIVEP1	53	0.008651	7583710	0.299921	0
Up	ARRDC3	52	0.009286	4496646	0.311428	0.008296
Up	PRKD2	52	0.008496	8986048	0.297285	0
Up	EPHA4	51	0.009698	7488664	0.298393	0
Up	TNFSF13B	51	0.010004	14670962	0.273765	0
Up	FAM110B	51	0.012282	5854450	0.287391	0
Up	GJB7	51	0.01113	6654884	0.280247	0
Up	IFIT1	50	0.003257	3831088	0.307817	0.048163
Up	GATA3	50	0.007535	4224572	0.309696	0.005714
Up	TRIM5	49	0.004714	4647006	0.302927	0.004625
Up	PPEF1	49	0.002709	10148694	0.282518	0
Up	SYT1	48	0.010026	11473940	0.284712	0
Up	STAT2	47	0.008114	3894220	0.31474	0.006061
Up	TXNIP	47	0.006288	7234358	0.30968	0
Up	IFIT2	47	0.002695	2415382	0.316828	0.053654
Up	BCL3	46	0.005598	3853674	0.350741	0.04058
Up	IRF7	46	0.005525	2722200	0.308335	0.028541
Up	PTGER4	46	0.008846	8712240	0.285973	0
Up	HERC5	46	0.00626	1999072	0.339508	0.02029
Up	DUSP1	43	0.007404	9881246	0.285729	0
Up	IFIH1	43	0.005107	4427676	0.295676	0.002439
Up	DTX3L	43	0.004014	2749452	0.307717	0.006098
Up	MAP3K8	42	0.002033	5606884	0.297316	0
Up	EGR1	42	0.005365	10758488	0.288984	0
Up	DUSP8	40	0.007103	9679710	0.275464	0
Up	TAP1	39	0.005951	5400094	0.284128	0.004505
Up	TICAM1	38	0.00429	1735214	0.304632	0.039683
Up	EPC1	37	0.005568	10528994	0.28026	0
Up	TRIM69	37	0.008196	1832444	0.296555	0.001681
Up	NPTX1	37	0.010108	2709042	0.306803	0
Up	ETS2	36	0.004578	1417696	0.336891	0.044563
Up	PPM1K	36	0.006375	7409146	0.28366	0
Up	GRIA2	35	0.008317	5355686	0.277063	0.001681
Up	PTGS2	35	0.003066	5240048	0.300524	0
Up	MXD1	34	0.00566	6501490	0.280219	0
Up	BDKRB2	33	0.006217	6153240	0.279998	0
Up	KLF4	32	0.002673	3840432	0.292751	0.004032
Up	IRF1	32	0.001962	3474450	0.294755	0
Up	IFIT5	32	0.002218	1820152	0.309208	0.032258
Up	FLT3	31	0.004016	1494250	0.30156	0.027094
Up	ZNFX1	31	0.004309	6508432	0.283632	0
Up	C4A	30	0.007292	3247912	0.285614	0.002299
Up	TRIM38	30	0.002344	2355780	0.292389	0.005291
Up	NOCT	29	0.006399	2073096	0.275504	0.002463

Up	SNCAIP	28	0.003401	3245970	0.286002	0
Up	DACT1	28	0.003146	3928826	0.291744	0
Up	MT2A	27	0.003912	4760352	0.275544	0
Up	USP18	27	0.003059	1225134	0.300381	0.005698
Up	ZC3H12A	27	0.00213	2801102	0.289662	0
Up	GADD45B	25	0.003888	3366314	0.272767	0
Up	PELI1	25	0.00249	2957160	0.277265	0
Up	DUSP26	25	0.004535	2941596	0.278488	0
Up	PROX1	24	0.004285	16107194	0.271437	0
Up	COL8A1	24	0.003169	2213366	0.284015	0.032609
Up	CPEB2	24	0.004295	4467186	0.274241	0
Up	EYA1	23	0.002153	2128522	0.275973	0
Up	IQUB	23	0.002391	1203500	0.263202	0
Up	BMP2	22	0.004312	18691536	0.221641	0
Up	DUSP10	22	0.002204	2864262	0.280288	0
Up	GBP1	22	0.002595	1000546	0.297971	0.010526
Up	COL4A1	22	0.002863	2607454	0.271101	0
Up	FAP	22	0.005548	3870386	0.269698	0
Up	OGFR	22	0.002205	2655202	0.281301	0
Up	SUSD3	22	0.004704	4071688	0.256165	0
Up	SIX2	21	0.003571	8412618	0.276712	0
Up	SERPINE1	21	0.002642	2835100	0.274426	0
Up	TNFSF10	21	0.001951	568660	0.293325	0.035088
Up	SH2D1B	21	0.002804	2711936	0.275705	0
Up	GFI1	20	0.001671	2287272	0.280745	0
Up	CCL2	20	0.003651	13213044	0.254365	0
Up	STX19	20	0.002016	4118520	0.263629	0
Up	GFPT2	20	0.003471	3336484	0.262581	0
Up	EPSTI1	20	0.00325	3249910	0.280981	0
Up	ID4	19	0.002629	4326290	0.272335	0
Up	GLI2	19	0.001432	1621152	0.289573	0
Up	KIF26B	19	0.002895	7592782	0.272845	0
Up	HSD17B14	19	0.002848	2576328	0.267943	0
Up	NT5C3A	19	0.003246	2228448	0.27052	0
Up	SP110	19	0.003311	10407810	0.270224	0
Up	PARP12	19	0.001835	1556266	0.289219	0
Up	FBLN2	17	0.002375	4342946	0.24669	0
Up	CXCL8	17	0.003104	5807616	0.261602	0
Up	BATF2	17	0.001488	673498	0.316846	0.066176
Up	NUAK2	17	0.001431	1869996	0.28655	0
Up	DHX58	17	7.56E-04	378214	0.283547	0.022059
Up	EGR2	17	0.001365	1236754	0.273094	0
Up	HSH2D	16	0.002763	4324164	0.251717	0
Up	ICAM5	16	0.003076	975228	0.287944	0.008333

Up	BAHCC1	16	0.0028	2723838	0.269009	0
Up	HLX	16	0.002307	11160974	0.260989	0
Up	KLF6	15	0.001547	970324	0.277414	0.019048
Up	PMAIP1	15	0.001884	1642980	0.27736	0
Up	PTX3	15	0.002898	9388846	0.228184	0
Up	FST	15	0.004416	4435932	0.262097	0
Up	DDR2	15	0.001744	1518680	0.292209	0
Up	HELZ2	15	0.001613	443664	0.303672	0.028571
Up	CAVIN2	15	0.001682	2412720	0.268133	0
Up	PLEKHG5	15	0.001572	1701170	0.276053	0
Up	CSF2	14	0.00116	1889870	0.269852	0
Up	RGS16	14	0.001861	718520	0.287667	0
Up	TRPC4	14	0.002828	1943444	0.264009	0
Up	RBM11	14	0.001878	1828290	0.272871	0
Up	FAM153B	14	0.002653	3477710	0.257874	0
Up	RND1	13	0.002239	1185570	0.258885	0
Up	TDRD7	13	0.001582	1442486	0.260846	0
Up	HSPB9	13	0.00286	5829338	0.236701	0
Up	CCDC116	13	0.002082	461686	0.278516	0
Up	PDE4B	13	9.28E-04	990686	0.276739	0
Up	MB21D2	13	0.002789	3445016	0.299699	0.012821
Up	BBC3	12	0.001158	1273498	0.274918	0
Up	RRAD	12	0.001005	1216160	0.275558	0
Up	XAF1	12	8.16E-04	854676	0.271399	0
Up	HIVEP2	12	5.59E-04	1066810	0.27808	0
Up	RASD1	12	0.001236	1637624	0.263605	0
Up	GRIP2	12	0.001639	459476	0.270959	0.015152
Up	WIF1	12	0.001258	1533126	0.248752	0
Up	HSD17B3	12	0.00121	960490	0.266448	0
Up	CLPSL1	12	0.002625	4984078	0.238569	0
Up	TRIM22	12	0.001699	3885096	0.261988	0
Up	CX3CL1	11	8.21E-04	5602570	0.221167	0
Up	IL7R	11	6.04E-04	214668	0.279173	0.054545
Up	IL15RA	11	8.68E-04	439258	0.257104	0
Up	NCOA7	11	0.001109	1176472	0.271528	0
Up	TLR6	11	0.001923	546340	0.255762	0
Up	IL1A	10	7.77E-04	3293906	0.239706	0
Up	PDZD2	10	9.97E-04	1491868	0.267514	0
Up	DRD1	10	0.001536	1383092	0.255371	0
Up	ADGRL3	10	0.001968	1838502	0.24909	0.022222
Up	ISG20	10	0.001009	739652	0.238719	0
Up	IL12A	9	0.001778	5075032	0.223481	0
Up	INHBA	9	0.001875	1683324	0.208155	0
Up	KLF2	9	0.00115	2979256	0.269711	0

Up	SLC30A3	9	0.001761	2282282	0.252219	0
Up	LYL1	9	7.29E-04	325024	0.27736	0.083333
Up	PARP10	9	8.53E-04	831780	0.279777	0
Up	RASGRP3	9	0.001478	1136680	0.261121	0
Up	ETV7	9	0.001819	3573824	0.236582	0
Up	TENT5C	9	7.10E-04	1401768	0.266648	0
Up	OASL	9	0.001171	1046730	0.232716	0
Up	TRIM40	9	1.64E-04	65598	0.273173	0.083333
Up	MXRA5	9	8.23E-04	1006366	0.262618	0
Up	SLC5A5	9	0.001806	2393436	0.248155	0
Up	FOSB	8	1.57E-04	163366	0.305813	0.285714
Up	IFI35	8	7.73E-04	252820	0.275584	0.035714
Up	UBA7	8	0.001825	1905274	0.260165	0
Up	ACHE	8	7.17E-04	660488	0.260129	0
Up	CXCL9	8	0.001775	584820	0.193694	0
Up	HUS1B	8	0.001773	914094	0.22299	0
Up	NCKAP5	8	8.91E-05	92984	0.271243	0
Up	TTBK1	8	3.65E-04	856610	0.259464	0
Up	OAS1	8	6.22E-04	760138	0.25976	0
Up	CCRL2	8	0.001801	7031454	0.228901	0
Up	CD69	8	0.001176	2347246	0.235689	0
Up	C17orf82	8	9.12E-04	1038246	0.261638	0
Up	GLCCI1	8	0.001077	2135006	0.261277	0
Up	CCDC65	8	5.11E-04	860378	0.253763	0
Up	APOL6	8	8.59E-04	1253550	0.255061	0
Up	SSTR2	7	0.001449	2000906	0.262934	0
Up	TNFRSF4	7	4.65E-04	227678	0.266999	0.142857
Up	IL22RA1	7	0.002111	2414238	0.247592	0
Up	KLB	7	4.75E-04	631206	0.255394	0
Up	RSAD2	7	0.001763	1461322	0.248839	0
Up	ZNF627	7	0.002111	4319562	0.227471	0
Up	CSRNP1	7	3.95E-04	377470	0.271931	0
Up	CXCL2	7	0.001037	1235666	0.254913	0
Up	C1QTNF1	7	5.31E-04	528034	0.261928	0
Up	NYAP2	7	0.001115	4594960	0.221029	0
Up	GIMAP2	7	0.001056	6411806	0.216177	0
Up	SOGA3	7	0.001422	1398048	0.235954	0
Up	PHF11	7	8.65E-04	1177296	0.246326	0
Up	SAMD9	7	5.62E-04	1172518	0.244356	0
Up	DNAH3	7	3.73E-04	1306158	0.26246	0
Up	SLFN5	7	1.09E-04	132916	0.265254	0
Up	HDX	7	4.07E-04	93906	0.292059	0.047619
Up	MYLPF	7	0.001061	1102698	0.238569	0
Up	ZNF433	7	1.90E-05	18816	0.239444	0

Up	PDE2A	6	4.57E-05	44722	0.245708	0
Up	DRP2	6	7.14E-04	620154	0.261843	0
Up	CXCL11	6	8.04E-04	968686	0.247248	0
Up	MX2	6	1.86E-05	16086	0.238299	0
Up	REC8	6	7.19E-04	1880208	0.245284	0
Up	FLRT3	6	6.90E-04	524162	0.253085	0.066667
Up	PLAC8	6	6.37E-04	133872	0.290833	0
Up	IFITM1	6	0.001056	2302398	0.20584	0
Up	BARX1	6	0.001759	652470	0.196324	0
Up	NEURL1	6	4.14E-04	729676	0.262824	0
Up	TTC9B	6	7.39E-04	1226806	0.252052	0
Up	RPL39P5	6	9.53E-05	127766	0.251918	0
Up	CCL20	5	8.10E-04	1464858	0.25241	0
Up	NFKBIZ	5	1.20E-04	92196	0.259464	0
Up	IL6	5	4.44E-05	25698	0.236248	0
Up	PPP4R4	5	4.06E-04	411532	0.26492	0
Up	NPR3	5	8.05E-04	1437156	0.250485	0
Up	HEG1	5	4.36E-04	420686	0.258015	0
Up	AHRR	5	3.61E-04	911582	0.245676	0
Up	NLRC5	5	5.05E-05	36762	0.280787	0
Up	CPEB3	5	7.21E-04	1354408	0.25798	0
Up	DDX60L	5	5.58E-04	106390	0.285757	0
Up	TSLP	5	5.41E-05	56036	0.269481	0
Up	C12orf74	5	0.001408	2101516	0.239555	0
Up	DSCAML1	5	7.23E-04	404406	0.235046	0
Up	NR4A3	4	3.74E-04	281622	0.258461	0
Up	IL11	4	7.69E-04	970820	0.247992	0
Up	FLT3LG	4	3.52E-04	441898	0.186687	0
Up	PTCH2	4	3.59E-04	239450	0.261289	0
Up	GRM8	4	4.88E-05	60636	0.251016	0
Up	SLC25A28	4	7.17E-04	314688	0.199173	0
Up	IFI44	4	3.54E-04	793396	0.238359	0
Up	FILIP1L	4	6.95E-06	17990	0.245836	0
Up	OAS2	4	7.09E-04	2206848	0.213955	0
Up	SAMD9L	4	2.02E-04	178878	0.252601	0
Up	IL7	3	8.89E-06	5468	0.244188	0
Up	CRTAM	3	0	0	1	0
Up	C4B	3	3.67E-04	760652	0.233856	0
Up	IFNB1	3	0	0	0.200508	0
Up	IFNL1	3	7.04E-04	286726	0.181847	0
Up	RASGRP1	3	3.53E-04	1636020	0.240132	0
Up	GMPR	3	0	0	0.202034	0
Up	GRIN3B	3	7.04E-04	419778	0.178343	0
Up	NTNG2	3	4.15E-04	778996	0.234997	0

Up	THEMIS2	3	3.57E-04	195936	0.225199	0
Up	TSACC	3	7.04E-04	1012770	0.237046	0
Up	TRANK1	3	2.83E-05	25900	0.234725	0
Up	PIM3	3	2.63E-06	7676	0.267036	0
Up	NANOS3	3	3.86E-04	598848	0.235309	0
Up	SNPH	3	7.04E-04	752350	0.181481	0
Up	CFAP57	3	9.67E-06	10884	0.244545	0
Up	TCIM	3	3.56E-04	282420	0.26812	0
Up	IFITM2	3	6.26E-06	2138	0.243685	0
Up	SNED1	3	3.61E-04	312294	0.235484	0
Up	SLC39A2	3	7.04E-04	419778	0.178343	0
Up	DNAH17	3	2.64E-06	7226	0.242076	0
Up	TMEM140	3	2.65E-04	109188	0.252567	0
Up	LTB	2	1.38E-06	880	0.222283	0
Up	CXCL10	2	3.52E-06	5504	0.181319	0
Up	SEC16B	2	9.98E-06	1564	0.207085	0
Up	S1PR3	2	3.52E-04	125910	0.193246	0
Up	SECTM1	2	7.60E-07	1940	0.213184	0
Up	SYNPR	2	1	2	1	0
Up	ACKR4	2	3.52E-04	105848	0.226086	0
Up	CXCL3	2	2.00E-08	2	0.176017	0
Up	HCRTR1	2	5.90E-07	2934	0.240712	0
Up	IFNL3	2	1.47E-05	1654	0.260022	0
Up	TIPARP	2	1.60E-07	966	0.242107	0
Up	AGAP7P	2	1.52E-06	1108	0.237601	0
Up	SLC25A2	2	1.30E-05	15088	0.202596	0
Up	G0S2	2	3.52E-04	538416	0.240101	0
Up	CH25H	2	1	2	1	0
Up	CYP21A2	2	1.40E-07	304	0.253491	0
Up	RAB19	2	1.30E-05	22056	0.227946	0
Up	SPTBN5	2	5.75E-06	2802	0.205156	0
Up	LSMEM1	2	1	2	1	0
Up	RAET1L	1	0	0	1	0
Up	FGF19	1	0	0	0.190818	0
Up	CHAC1	1	0	0	0.183444	0
Up	PLA2G4C	1	0	0	0.203904	0
Up	MMP25	1	0	0	0.223718	0
Up	PRRX2	1	0	0	0.187494	0
Up	FAXDC2	1	0	0	0.251483	0
Up	MKRN4P	1	0	0	0.205691	0
Up	FGF18	1	0	0	0.232051	0
Up	RTP4	1	0	0	0.203103	0
Up	MT2P1	1	0	0	1	0
Up	NEURL3	1	0	0	0.227362	0

Up	CLEC4A	1	0	0	0.251483	0
Up	VSTM1	1	0	0	0.251483	0
Up	SLC6A13	1	0	0	0.207934	0
Up	SLITRK6	1	0	0	0.194803	0
Up	IFNL2	1	0	0	0.153871	0
Up	MT1E	1	0	0	0.226068	0
Down	PCLAF	812	0.218172	359294224	0.374432	4.31E-04
Down	CFTR	793	0.234611	322168046	0.383841	4.83E-04
Down	TUBA1A	295	0.073386	95262602	0.34024	5.53E-04
Down	AURKA	288	0.066175	95293564	0.335004	4.94E-04
Down	ARRB1	278	0.063576	117688160	0.330445	7.91E-05
Down	AP2M1	240	0.051023	53956278	0.334984	0.001395
Down	PIN1	233	0.05541	61425008	0.322878	8.96E-04
Down	PPT1	214	0.025145	56590318	0.326664	0.001229
Down	KPNA2	210	0.048841	31690140	0.359711	0.003298
Down	ECH1	171	0.037362	32902382	0.320981	0.004128
Down	SORT1	140	0.033936	24033152	0.310662	6.35E-04
Down	NDUFAF8	138	0.025397	14258978	0.304976	0.00817
Down	TOP2A	116	0.022369	13840310	0.337511	0.005247
Down	SMARCA2	110	0.021051	15613416	0.315526	0.004003
Down	PHGDH	106	0.015868	17099330	0.339224	0.002516
Down	PRDX2	104	0.018527	11194300	0.352394	0.016752
Down	HADHB	100	0.014925	23497982	0.311752	0
Down	PRDX3	98	0.012844	11624744	0.335122	0.010526
Down	MME	98	0.019032	19636640	0.306291	0
Down	NDUFS7	95	0.020867	10021646	0.309713	0.007246
Down	TFRC	92	0.015457	20619840	0.317483	7.49E-04
Down	SPP1	91	0.017414	22929672	0.295261	0
Down	PGK1	85	0.013136	10869004	0.351413	0.013165
Down	HSPE1	84	0.016392	8167734	0.343656	0.005737
Down	CARD9	83	0.017033	17706614	0.273081	0
Down	MAD2L1	82	0.013467	11228100	0.302331	0.003481
Down	APOE	82	0.015722	8495082	0.309359	0.004747
Down	ECI2	81	0.017144	6745260	0.334058	0.020772
Down	PSMD10	80	0.011633	18967998	0.292947	0.006013
Down	HACD3	76	0.011455	8537096	0.329334	0.00386
Down	DPY30	69	0.012998	3608682	0.323761	0.007689
Down	KRT14	68	0.007328	6921514	0.312215	0.004662
Down	PGRMC1	67	0.011618	7275690	0.331893	0.002261
Down	TTR	62	0.011258	3849642	0.30946	0.00452
Down	PDK1	62	0.015109	5811968	0.302862	0.001695
Down	TF	62	0.013173	4442358	0.327097	0.013115
Down	LSM3	60	0.010618	3544932	0.319411	0.007345
Down	SORBS2	60	0.007529	12616146	0.290046	0

Down	SUN2	60	0.010092	10654138	0.297316	0
Down	AQP1	59	0.010857	15194568	0.266273	0
Down	FCGRT	58	0.011796	10166374	0.274506	0
Down	SAP30	57	0.010382	4967848	0.286536	0.005013
Down	BIRC5	57	0.010055	4138496	0.302298	0.005387
Down	FGFR3	57	0.010393	14039520	0.28944	0
Down	VSIG1	57	0.01306	15695216	0.270636	0
Down	PBXIP1	54	0.010614	10304456	0.304632	0
Down	SIAE	54	0.013244	12796284	0.265675	0
Down	PDCD4	53	0.006391	5609270	0.304453	0.002353
Down	COA3	53	0.008434	4984146	0.285916	0.015239
Down	ARL6IP5	52	0.009516	10225900	0.285772	0
Down	SORL1	52	0.013461	3187416	0.320926	0.003017
Down	CRP	52	0.010286	12871524	0.266473	0
Down	LYZ	52	0.009492	4965110	0.333843	0.00905
Down	NEK2	51	0.007854	5234492	0.286333	0.007979
Down	DPYSL2	50	0.007286	7448216	0.298377	0
Down	KLHDC2	50	0.008897	5250882	0.28447	0.001633
Down	OAT	50	0.003591	5772930	0.300619	0
Down	MATN2	47	0.004801	8947738	0.275011	0
Down	EFHC2	46	0.00998	7644676	0.283533	0
Down	TOMM20	45	0.005817	6307430	0.296045	0
Down	ALDH2	45	0.005548	3285442	0.300143	0.014396
Down	PLS1	45	0.009691	9306744	0.293962	0
Down	SHMT1	45	0.007636	6740640	0.289632	0
Down	COMMD8	43	0.010139	10786064	0.272244	0
Down	CAT	40	0.004514	2013782	0.317253	0.009009
Down	PSAP	38	0.006296	1613534	0.318212	0.011111
Down	SNTA1	36	0.007213	4632886	0.271788	0
Down	IL20RA	36	0.007017	3724834	0.261061	0
Down	FKBP3	36	0.003137	5467580	0.286709	0
Down	REEP6	36	0.006396	5434122	0.27975	0
Down	OLFM4	36	0.009929	9248612	0.246518	0
Down	FBP1	35	0.005939	7368466	0.270006	0
Down	ASB9	35	0.003272	2351460	0.290446	0.001681
Down	MACROD1	35	0.003592	4507598	0.287857	0
Down	ETFB	34	0.003651	3852208	0.289543	0
Down	NTRK2	34	0.005945	2603946	0.291385	0.004032
Down	STMN1	34	0.003516	4643746	0.294526	0
Down	BCAS3	34	0.006118	4646608	0.287303	0.001783
Down	SPCS2	34	0.006974	5087150	0.287682	0
Down	SNAP25	33	0.006639	6543728	0.268945	0
Down	NDUFA2	33	0.003053	2154888	0.278598	0.022727
Down	OAZ1	33	0.006126	5396496	0.283278	0

Down	EPN3	33	0.00504	1915204	0.29334	0.003788
Down	MDH1	33	0.002594	4817858	0.297347	0
Down	ASAH1	33	0.00488	3587898	0.28242	0
Down	SRI	32	0.005105	1488768	0.311138	0.009195
Down	LOX	32	0.006177	4646592	0.2841	0
Down	AZGP1	32	0.005468	1872944	0.316475	0.006897
Down	SERPINA5	31	0.005857	7511304	0.251639	0
Down	ARL3	30	0.006232	13687072	0.262061	0
Down	USH1C	30	0.005617	5497520	0.252063	0
Down	CENPV	30	0.003211	1920008	0.291849	0.004598
Down	MAGT1	30	0.004602	2336808	0.300143	0.006897
Down	PPA2	30	0.003801	2369172	0.283222	0.002299
Down	LEPR	29	0.005342	1235306	0.287115	0.008547
Down	GSR	29	0.003256	4520096	0.286276	0
Down	TMBIM6	28	0.006617	3930572	0.266049	0
Down	MAGIX	28	0.003725	4110518	0.252601	0
Down	TCTEX1D2	27	0.004965	3306670	0.276712	0
Down	SLC12A2	27	0.003475	3319408	0.2914	0
Down	HMGB3	27	0.003782	4552850	0.274599	0
Down	SCNN1A	26	0.003296	2605722	0.275131	0
Down	UGT1A10	26	0.003889	2182702	0.249857	0.076087
Down	SGPP1	26	0.005535	2937084	0.260022	0
Down	AGR2	26	0.002769	2106576	0.273055	0
Down	FLYWCH2	26	0.005095	4034146	0.282771	0
Down	MMP7	25	0.003941	5161756	0.24307	0
Down	KLK7	25	0.00322	1404854	0.274665	0
Down	QPCT	25	0.003988	1675088	0.322859	0.003333
Down	KCNIP3	24	0.002929	2031928	0.270933	0
Down	HACD2	24	0.00282	4108012	0.268996	0
Down	WDR54	24	0.004613	1636010	0.262085	0
Down	CCDC74B	24	6.32E-04	823160	0.25976	0.068841
Down	GALNT12	24	0.003388	3320846	0.243674	0
Down	BRI3BP	24	0.002911	3155498	0.295537	0
Down	REPS2	23	0.002298	943312	0.293704	0.031621
Down	GNG12	23	0.002502	2644352	0.28318	0
Down	ATP5IF1	23	0.001796	1882604	0.278352	0
Down	EPHX1	23	0.003835	3846898	0.270365	0
Down	CTSV	23	0.003354	3298694	0.270997	0
Down	KLK6	23	0.003994	4351866	0.255256	0
Down	NR1H4	22	0.002702	2827702	0.280814	0
Down	SCGN	22	0.004697	2842038	0.257722	0
Down	ENDOG	22	0.002925	4844118	0.262618	0
Down	UCP2	22	0.003189	5093696	0.267615	0
Down	CYBRD1	22	0.001991	2583536	0.267413	0

Down	FAM171A2	22	0.005194	6237368	0.256524	0
Down	SLC39A10	22	0.003962	2959034	0.281065	0
Down	ACO1	22	0.002762	3211908	0.27399	0
Down	TRAPPC6A	21	0.00429	2846052	0.233558	0
Down	CLGN	21	0.003204	2561754	0.274135	0.009524
Down	TMEM160	21	0.003642	2914984	0.265663	0
Down	MLEC	21	0.00103	1483940	0.293461	0
Down	CUTC	21	0.002901	2747214	0.264784	0
Down	ITIH2	21	0.00462	2122054	0.311223	0.004762
Down	CPM	21	0.001225	2025788	0.267716	0
Down	SCP2	20	0.00205	1341952	0.279406	0
Down	CARHSP1	20	0.002367	900588	0.286941	0.031579
Down	TSPAN6	20	0.003276	2297122	0.253073	0
Down	MPC2	20	0.002196	1540396	0.286492	0.010526
Down	ALCAM	19	0.002306	1806346	0.285169	0
Down	GPSM2	19	0.003277	2315670	0.267817	0
Down	CTSH	19	0.001797	2514428	0.262679	0
Down	CUEDC2	19	0.001548	798944	0.28263	0.011696
Down	DNLZ	19	0.003085	3592482	0.257255	0
Down	NTHL1	19	0.00223	3396078	0.265526	0
Down	ABCC4	19	0.001862	786850	0.313853	0.040936
Down	HMGN3	19	0.002456	3109514	0.259784	0
Down	SLAIN1	19	0.002817	3056466	0.269545	0
Down	PDGFD	19	0.003428	1205058	0.264895	0.005848
Down	CCDC115	18	0.002826	2285326	0.261458	0
Down	PCYOX1	18	0.003583	8446758	0.23677	0
Down	CRYZ	18	0.001913	2068000	0.273462	0
Down	CYBA	17	0.002951	3808914	0.261229	0
Down	CASR	17	0.001909	1723524	0.264784	0
Down	NAALADL2	17	0.003907	2420506	0.266986	0
Down	BPIFB1	17	0.003539	1290834	0.296555	0
Down	RAD51B	16	0.002526	1468392	0.256988	0
Down	BNIPL	16	0.002098	1205590	0.25391	0
Down	BCKDHB	16	0.001908	899240	0.284242	0.016667
Down	CA12	16	0.001737	1527784	0.266086	0
Down	ARHGDIB	16	0.001954	1503958	0.263997	0
Down	SPDEF	16	0.003703	2566442	0.257092	0
Down	ACSF2	16	0.002256	917996	0.264193	0.008333
Down	ITM2A	16	0.002542	3570696	0.246829	0
Down	SYT12	16	0.00219	2456732	0.258885	0
Down	AGT	15	0.00203	1399880	0.271217	0
Down	SERPINA4	15	0.002918	2511994	0.257933	0
Down	MAGEE1	15	0.002044	517062	0.264291	0.012821
Down	COX11	15	0.001329	551426	0.283293	0.038095

Down	PIGN	15	0.001677	1802516	0.258484	0
Down	AK4	15	0.002243	1781206	0.28655	0
Down	GNG7	14	8.07E-04	1203444	0.240691	0
Down	DNAAF4	14	0.001692	1344800	0.265043	0
Down	RNF128	14	0.001893	1616230	0.261109	0
Down	PRIMPOL	14	0.002412	743698	0.264414	0.021978
Down	FAHD1	14	0.002795	644508	0.288148	0
Down	VWA1	14	0.002625	3346112	0.239222	0
Down	DEPDC1	14	0.003306	1204126	0.251694	0
Down	PIGK	13	0.001895	1583670	0.275906	0
Down	ADORA1	13	0.002795	7921574	0.247841	0
Down	UGT1A9	13	0.001153	582216	0.24655	0.381818
Down	AKR1B10	13	9.64E-04	612592	0.25931	0
Down	CP	13	3.16E-04	334300	0.254319	0
Down	CNIH4	13	9.08E-04	657858	0.272153	0
Down	SUMF1	13	0.00365	5382188	0.215244	0
Down	BTD	13	0.002291	4692120	0.244093	0
Down	HOGA1	13	4.42E-04	139224	0.269378	0.109091
Down	SLC16A10	13	0.002765	2327152	0.248404	0
Down	ACOT13	12	5.34E-04	685904	0.266485	0
Down	TMEM59	12	0.00124	1195426	0.283194	0
Down	ALDH6A1	12	0.002667	1929240	0.298268	0.015152
Down	WFDC2	12	0.002312	3710300	0.24253	0
Down	UGT1A1	12	4.90E-04	234312	0.233146	0.488889
Down	ARHGAP19	12	0.001764	1175714	0.249791	0
Down	SHH	11	0.001553	1344250	0.229892	0
Down	GNG11	11	6.29E-04	446072	0.231531	0
Down	DBP	11	0.002147	1263390	0.228248	0
Down	AKR1C3	11	0.001585	1883162	0.23225	0
Down	TRMT2B	11	0.001231	364378	0.270842	0.018182
Down	BDH2	11	0.001938	2940122	0.227708	0
Down	ACBD7	11	0.001913	2665132	0.212745	0
Down	KCNAB1	10	0.001578	1441876	0.262715	0
Down	SLPI	10	6.87E-04	730598	0.272531	0
Down	UGT1A7	10	1.48E-04	147666	0.232917	0.75
Down	NRGN	10	0.001198	804138	0.243278	0
Down	DTYMK	10	4.07E-04	477472	0.270816	0
Down	UGT1A4	10	3.52E-04	360614	0.207236	0.75
Down	UGT1A6	10	2.57E-05	29130	0.217302	0.785714
Down	KCNE3	10	0.001543	1658534	0.256015	0
Down	NLGN1	9	0.001779	757946	0.219036	0
Down	CAB39L	9	0.001094	1068850	0.262885	0
Down	HOXA13	9	0.001512	1290038	0.226799	0
Down	PAIP2B	9	0.001063	1289582	0.251305	0

Down	ADI1	9	8.03E-04	780520	0.275411	0
Down	SYT5	9	7.92E-04	785402	0.239182	0
Down	GSTO2	9	0.002108	2906418	0.224479	0
Down	UGT1A3	9	0	0	0.207229	1
Down	ADH6	9	0.001175	245930	0.276308	0
Down	UGT1A8	9	0	0	0.207229	1
Down	ROS1	8	6.06E-04	472030	0.266074	0
Down	BCAS1	8	6.06E-04	363330	0.268209	0
Down	FDX1	8	0.001103	578096	0.262254	0
Down	RTL8B	8	0.001779	672198	0.213144	0
Down	PLEKHB1	8	0.001437	1463156	0.205572	0
Down	ACSS1	8	5.15E-04	157658	0.275011	0.107143
Down	TEX15	8	4.88E-04	386702	0.254114	0
Down	SEMA4G	8	3.65E-04	316380	0.239071	0
Down	COX16	8	0.001217	335052	0.23265	0.035714
Down	TPGS1	8	0.001772	1501030	0.252972	0
Down	AIF1L	8	5.96E-04	573374	0.269596	0
Down	REX1BD	7	4.37E-04	306602	0.249287	0
Down	GSTA4	7	5.87E-04	389590	0.23207	0
Down	CALB1	7	0.001079	789700	0.242831	0
Down	PCSK1N	7	0.001089	438704	0.209043	0
Down	ANXA13	7	0.001413	2971764	0.231145	0
Down	SLC25A21	7	0.001078	835750	0.256872	0
Down	METTL7A	7	7.06E-04	226918	0.266136	0
Down	SPR	7	1.04E-04	183356	0.267754	0
Down	VWA2	7	8.79E-04	427782	0.264033	0
Down	HMGB1P1	7	1.51E-04	188006	0.261001	0
Down	NOSTRIN	6	7.25E-04	1004432	0.234619	0
Down	HOXA2	6	5.68E-04	782382	0.239524	0
Down	GJB1	6	4.17E-04	275550	0.256872	0
Down	SRPX	6	3.79E-04	352136	0.245793	0
Down	HOXA11	6	8.52E-04	787204	0.243455	0
Down	CSPG5	6	7.25E-04	995570	0.226501	0
Down	DDC	6	3.64E-04	211502	0.244777	0
Down	CRYM	6	7.21E-04	929406	0.244766	0
Down	DNPH1	6	3.57E-04	308250	0.232089	0
Down	RAB26	6	0.001431	550126	0.190658	0
Down	GGT1	6	0.001081	2176244	0.23106	0
Down	TSPAN10	6	4.57E-04	332150	0.269162	0
Down	ACE2	6	3.97E-04	78710	0.242014	0
Down	CLDN10	6	8.18E-04	719788	0.246572	0
Down	DHRS4L2	6	5.66E-04	410300	0.233385	0
Down	NUBPL	6	8.67E-05	104668	0.261085	0
Down	SYNGR1	6	6.16E-04	562506	0.243978	0

Down	METTL7B	6	8.00E-04	664448	0.24189	0
Down	SPAG16	6	0.001417	796754	0.231691	0
Down	PROM1	6	7.49E-04	715970	0.244819	0
Down	PGP	6	3.25E-04	560276	0.239737	0
Down	FAH	6	8.20E-04	1577596	0.251305	0
Down	ETFDH	6	4.51E-05	84272	0.258944	0
Down	MYO3B	6	9.94E-05	140794	0.271178	0
Down	SERHL2	6	9.93E-04	2370162	0.227216	0
Down	TMEM37	6	0.00107	444308	0.215407	0
Down	FOLR1	6	7.19E-04	594236	0.247539	0
Down	CD1D	5	4.28E-04	610068	0.239262	0
Down	RAMP1	5	7.04E-04	585402	0.240183	0
Down	PAH	5	3.52E-04	1027734	0.215627	0
Down	ACE	5	9.01E-05	31416	0.259003	0
Down	COX14	5	2.27E-04	74032	0.255222	0.2
Down	IGFBP2	5	5.79E-04	830356	0.247269	0
Down	TRMT9B	5	4.62E-04	393934	0.242158	0
Down	NME5	5	3.76E-04	219046	0.236386	0
Down	ANXA9	5	8.13E-04	1078698	0.223807	0
Down	UPK1B	5	9.32E-04	986068	0.23896	0
Down	CD302	5	1.28E-04	102000	0.236888	0
Down	PRSS33	5	7.92E-04	563640	0.199859	0
Down	ERP27	5	3.90E-04	715786	0.231814	0
Down	TMPRSS4	5	9.29E-04	1170718	0.23875	0
Down	HEBP1	5	5.34E-05	32076	0.247463	0.1
Down	FMO5	5	0.001061	1626188	0.205825	0
Down	METRN	5	2.65E-04	228024	0.249156	0
Down	SOSTDC1	4	7.98E-04	1232612	0.212929	0
Down	LTC4S	4	3.52E-04	362426	0.175176	0
Down	PDZK1IP1	4	5.32E-05	29312	0.232051	0
Down	CD24	4	7.09E-04	1206718	0.228938	0
Down	ORAI3	4	0.001056	973290	0.18522	0
Down	NACA2	4	7.21E-05	102110	0.256895	0
Down	ANKS4B	4	4.70E-04	198792	0.246443	0
Down	ACYP2	4	1	2	1	0
Down	ATRAID	4	7.25E-04	1034828	0.232974	0
Down	RAD9B	4	7.10E-04	847910	0.17993	0
Down	HNMT	4	7.05E-04	602900	0.227489	0
Down	LCT	4	1.30E-04	202466	0.265961	0
Down	SELENOP	4	3.89E-04	783822	0.255934	0
Down	ODAM	4	7.05E-04	1023430	0.233885	0
Down	GATM	4	3.92E-04	330478	0.241008	0
Down	UGT2A3	4	7.09E-04	285884	0.22072	0
Down	CFI	3	3.54E-04	506448	0.230162	0

Down	NRTN	3	7.04E-04	492878	0.191687	0
Down	PLEKHS1	3	3.96E-04	274568	0.237027	0
Down	PNMT	3	2.73E-05	47234	0.240569	0
Down	ANXA10	3	4.81E-05	62170	0.246326	0
Down	LRP3	3	7.47E-06	2116	0.220883	0
Down	C4orf48	3	9.20E-06	4274	0.194051	0
Down	CDNF	3	3.52E-04	361602	0.199208	0
Down	RIMKLA	3	7.04E-04	128342	0.182871	0
Down	GALM	3	1	6	1	0
Down	DNAAF3	3	1.94E-05	5614	0.240071	0
Down	ROM1	3	3.55E-04	173536	0.253355	0
Down	PLA2R1	3	3.61E-04	497398	0.229873	0
Down	TM4SF4	3	6.82E-05	63168	0.213032	0
Down	LRRC66	3	4.86E-05	34828	0.238991	0
Down	VEPH1	3	3.53E-04	283260	0.211754	0
Down	DSEL	3	2.01E-04	30300	0.263923	0
Down	CTHRC1	3	4.56E-05	36850	0.228239	0
Down	TMEM45B	3	7.04E-04	204542	0.207706	0
Down	SERINC5	3	6.14E-05	120978	0.25832	0
Down	LEFTY1	3	3.56E-04	256664	0.235719	0
Down	PDE1A	3	3.56E-04	306882	0.248328	0
Down	ADGRB3	3	7.04E-04	556450	0.195567	0
Down	IQCD	3	9.81E-06	13826	0.244083	0
Down	UBBP4	3	3.25E-06	3318	0.241654	0
Down	PCDHB12	3	4.19E-05	32484	0.219509	0
Down	EML6	3	3.62E-04	1079642	0.249879	0
Down	EFCAB11	3	9.02E-05	51112	0.236661	0
Down	PXMP4	2	6.51E-06	3138	0.239333	0
Down	SAMD13	2	1.66E-05	4492	0.242935	0
Down	CRISP3	2	3.52E-04	153340	0.213473	0
Down	HSD17B2	2	1	2	1	0
Down	ERFE	2	9.90E-07	460	0.208223	0
Down	ACSM3	2	3.52E-04	227006	0.237343	0
Down	RPL39L	2	3.52E-04	552058	0.221305	0
Down	CRLS1	2	3.64E-06	1822	0.206708	0
Down	CEACAM7	2	1	2	1	0
Down	RHBDL2	2	3.52E-04	192488	0.229279	0
Down	KY	2	3.56E-06	7364	0.234029	0
Down	SLC3A1	2	3.52E-04	690930	0.246187	0
Down	SLC25A27	2	6.70E-07	408	0.210211	0
Down	LHPP	2	3.52E-04	292702	0.240162	0
Down	SSPN	2	1.96E-06	2908	0.229279	0
Down	VTCN1	2	3.52E-04	98318	0.2071	0
Down	ST6GALNAC1	2	4.10E-07	1210	0.226573	0

Down	SAC3D1	2	3.20E-05	1612	0.190633	0
Down	TCEA3	2	1.60E-05	6450	0.155975	0
Down	SLC44A4	2	7.40E-07	1704	0.238619	0
Down	STRA6	2	3.03E-06	5772	0.239565	0
Down	ENTPD3	2	1.13E-04	257856	0.238689	0
Down	LRRC24	2	3.52E-04	410756	0.220309	0
Down	IGSF10	2	4.19E-06	11938	0.248839	0
Down	CDC42EP5	1	0	0	0.210017	0
Down	SEMA3E	1	0	0	1	0
Down	CNGA1	1	0	0	1	0
Down	SPATA17	1	0	0	1	0
Down	CLDN16	1	0	0	1	0
Down	BTBD16	1	0	0	0.204168	0
Down	CYP27A1	1	0	0	0.224071	0
Down	GACAT2	1	0	0	0.236829	0
Down	CYP2U1	1	0	0	0.237343	0
Down	POLR2J2	1	0	0	0.240142	0
Down	SLC45A1	1	0	0	0.225119	0
Down	CYP4F3	1	0	0	1	0
Down	ATPSCKMT	1	0	0	0.236829	0
Down	RERG	1	0	0	1	0
Down	LYPLAL1	1	0	0	0.222214	0
Down	PROM2	1	0	0	0.240142	0
Down	FAM89B	1	0	0	0.234503	0
Down	ST6GALNAC2	1	0	0	0.207995	0
Down	GLTPD2	1	0	0	0.224071	0
Down	CREG2	1	0	0	0.236829	0
Down	CYS1	1	0	0	0.246166	0
Down	TCN1	1	0	0	0.215121	0
Down	CFAP73	1	0	0	0.231145	0
Down	LEMD1	1	0	0	0.226663	0
Down	LRRC26	1	0	0	1	0
Down	RSPH1	1	0	0	1	0
Down	FGFBP2	1	0	0	0.214447	0
Down	C2orf74	1	0	0	0.219934	0
Down	MMEL1	1	0	0	0.215211	0

Table 7 miRNA - target gene interaction table

Regulation	Target Genes	Degree	MicroRNA	Regulation	Target Genes	Degree	MicroRNA
Up	TXNIP	228	hsa-mir-4511	Down	BRI3BP	123	hsa-mir-4312
Up	PMAIP1	147	hsa-mir-3924	Down	FAHD1	113	hsa-mir-4527
Up	APOL6	127	hsa-mir-4478	Down	CPM	111	hsa-mir-4673
Up	CHAC1	118	hsa-mir-3650	Down	HOXA13	111	hsa-mir-4496
Up	KLF2	107	hsa-mir-4252	Down	TMBIM6	104	hsa-mir-3153
Up	DNAJB4	102	hsa-mir-4438	Down	GSR	104	hsa-mir-4438
Up	ID4	91	hsa-mir-4265	Down	SHMT1	97	hsa-mir-3174
Up	TRAF1	90	hsa-mir-6077	Down	TMEM59	88	hsa-mir-1200
Up	AMOTL2	89	hsa-mir-4284	Down	MLEC	88	hsa-mir-4475
Up	EPHA4	74	hsa-mir-3609	Down	DSEL	85	hsa-mir-8055
Up	BBC3	73	hsa-mir-4770	Down	PXMP4	83	hsa-mir-4432
Up	PPM1K	72	hsa-mir-4459	Down	KPNA2	83	hsa-mir-5688
Up	TNFAIP3	70	hsa-mir-5700	Down	TSPAN6	81	hsa-mir-4464
Up	NPTX1	69	hsa-mir-4295	Down	PDCD4	78	hsa-mir-4748
Up	CYLD	69	hsa-mir-3941	Down	BIRC5	78	hsa-mir-2053
Up	DDR2	68	hsa-mir-2053	Down	TOMM20	77	hsa-mir-4523
Up	STAT2	63	hsa-mir-3929	Down	EFCAB11	75	hsa-mir-5702
Up	RRAD	62	hsa-mir-4450	Down	ANKS4B	74	hsa-mir-4507
Up	KLF6	62	hsa-mir-4305	Down	AURKA	73	hsa-mir-3611
Up	FGF19	62	hsa-mir-4721	Down	HACD2	69	hsa-mir-1827
Up	ZNFX1	61	hsa-mir-8067	Down	FOLR1	69	hsa-mir-4643
Up	FOS	58	hsa-mir-8081	Down	AP2M1	69	hsa-mir-6133
Up	MXD1	57	hsa-mir-5690	Down	TFRC	67	hsa-mir-1299
Up	SSTR2	57	hsa-mir-6131	Down	SYNGR1	64	hsa-mir-3169
Up	SP110	55	hsa-mir-3674	Down	PGK1	64	hsa-mir-5683
Up	PLEKHG5	54	hsa-mir-3612	Down	DNAH10OS	63	hsa-mir-3689c
Up	CPEB3	53	hsa-mir-5047	Down	LEFTY1	63	hsa-mir-4251
Up	ZFP36	53	hsa-mir-6126	Down	STMN1	62	hsa-mir-4459
Up	DTX3L	51	hsa-mir-7703	Down	PCLAF	62	hsa-mir-4705
Up	SLC5A5	51	hsa-mir-4257	Down	SLC16A10	61	hsa-mir-3149
Up	DNAH17	51	hsa-mir-2278	Down	SEMA3E	60	hsa-mir-4294
Up	INHBA	51	hsa-mir-5688	Down	LSM3	60	hsa-mir-5095
Up	CD274	47	hsa-mir-3977	Down	MOGAT1	59	hsa-mir-4660
Up	SOGA3	46	hsa-mir-1297	Down	TRMT2B	57	hsa-mir-3672
Up	PIM3	46	hsa-mir-4494	Down	GNG12	57	hsa-mir-4426
Up	CPEB2	44	hsa-mir-4643	Down	FLYWCH2	56	hsa-mir-4430
Up	PSMB9	44	hsa-mir-3658	Down	PIN1	56	hsa-mir-4472
Up	GMPR	43	hsa-mir-661	Down	METTL7A	54	hsa-mir-4692
Up	SOCS1	42	hsa-mir-4500	Down	ACBD7	54	hsa-mir-4421
Up	COL4A1	42	hsa-mir-8070	Down	ALDH6A1	54	hsa-mir-4284
Up	PPP1R15A	40	hsa-mir-6165	Down	DPYSL2	54	hsa-mir-3666
Up	COL8A1	39	hsa-mir-4266	Down	GJB1	53	hsa-mir-6085
Up	RAB19	39	hsa-mir-4451	Down	CARHSP1	51	hsa-mir-4255

Up	DUSP10	39	hsa-mir-4791	Down	GATM	49	hsa-mir-4460
Up	JUN	38	hsa-mir-4480	Down	SRP9	48	hsa-mir-3714
Up	IFITM1	38	hsa-mir-644a	Down	DEPDC1	48	hsa-mir-1305
Up	CREB5	38	hsa-mir-3911	Down	CLDN16	47	hsa-mir-548w
Up	GJB7	38	hsa-mir-4272	Down	AK4	45	hsa-mir-4280
Up	BMP2	37	hsa-mir-4463	Down	NRGN	44	hsa-mir-3141
Up	CXCL8	36	hsa-mir-4662b	Down	DNAAF3	43	hsa-mir-3155a
Up	BCL3	36	hsa-mir-3132	Down	MAGT1	43	hsa-mir-1273f
Up	DUSP8	36	hsa-mir-4475	Down	BTD	42	hsa-mir-5100
Up	SAMD9L	35	hsa-mir-2110	Down	NEURL1B	42	hsa-mir-2117
Up	TRIM38	35	hsa-mir-4705	Down	CYBRD1	42	hsa-mir-3199
Up	GLI2	35	hsa-mir-4651	Down	DNLZ	41	hsa-mir-4510
Up	SLFN5	35	hsa-mir-4635	Down	TUBB4A	41	hsa-mir-3974
Up	FAM153B	35	hsa-mir-1200	Down	UBBP4	39	hsa-mir-6132
Up	ICAM1	34	hsa-mir-3975	Down	CD1D	39	hsa-mir-548ac
Up	RASGRP3	33	hsa-mir-4264	Down	PSAP	39	hsa-mir-3689d
Up	PCK1	33	hsa-mir-548aa	Down	LHPP	38	hsa-mir-3929
Up	PROX1	33	hsa-mir-548u	Down	SRD5A3	38	hsa-mir-4481
Up	SOCS3	32	hsa-mir-4473	Down	LYZ	38	hsa-mir-4486
Up	MB21D2	32	hsa-mir-4517	Down	ARRB1	38	hsa-mir-1470
Up	IRF1	32	hsa-mir-6073	Down	TPGS1	37	hsa-mir-7703
Up	CXCL10	31	hsa-mir-1231	Down	PCYOX1	37	hsa-mir-4775
Up	ETS2	31	hsa-mir-3662	Down	NUBPL	36	hsa-mir-6088
Up	NCOA7	31	hsa-mir-5680	Down	HADHB	36	hsa-mir-4493
Up	DUSP1	30	hsa-mir-940	Down	FFAR4	35	hsa-mir-640
Up	PLAC8	30	hsa-mir-1261	Down	SEMA4G	34	hsa-mir-8085
Up	GLCCI1	29	hsa-mir-4443	Down	SUN2	34	hsa-mir-4310
Up	NR4A3	29	hsa-mir-6079	Down	PLEKHS1	34	hsa-mir-3652
Up	PRKD2	28	hsa-mir-378h	Down	AKR1B10	34	hsa-mir-548ax
Up	S1PR3	28	hsa-mir-3199	Down	CCDC115	34	hsa-mir-4471
Up	IFIT3	27	hsa-mir-3926	Down	TMPRSS4	33	hsa-mir-298
Up	KLF4	26	hsa-mir-663a	Down	GSTO2	33	hsa-mir-8057
Up	SAMHD1	26	hsa-mir-1976	Down	GPSM2	33	hsa-mir-3135b
Up	KLB	26	hsa-mir-7641	Down	KCNIP3	32	hsa-mir-7974
Up	HIVEP2	25	hsa-mir-520e	Down	LRP3	32	hsa-mir-4306
Up	CYP1A1	25	hsa-mir-632	Down	ETFDH	31	hsa-mir-4270
Up	NEURL1	25	hsa-mir-4505	Down	VWA1	30	hsa-mir-592
Up	ACTA1	24	hsa-mir-1252-3p	Down	PAIP2B	30	hsa-mir-1273e
Up	ATF3	24	hsa-mir-5000-5p	Down	CRLS1	30	hsa-mir-23c
Up	RGS16	24	hsa-mir-548aw	Down	PLS1	30	hsa-mir-577
Up	ARRDC3	23	hsa-mir-5193	Down	HMGB3	30	hsa-mir-759
Up	SLC25A28	23	hsa-mir-2392	Down	PGRMC1	30	hsa-mir-3194-5p
Up	TLR6	23	hsa-mir-1245a	Down	SSPN	29	hsa-mir-4719
Up	GFPT2	23	hsa-mir-5703	Down	PRDX3	29	hsa-mir-8063

Up	ETV7	23	hsa-mir-6087	Down	PDK1	29	hsa-mir-138-1-3p
Up	FBLN2	23	hsa-mir-548ac	Down	HOXA11	28	hsa-mir-4441
Up	IL6	22	hsa-mir-107	Down	SEMA5A	28	hsa-mir-8077
Up	ZC3HAV1	22	hsa-mir-612	Down	CREG2	27	hsa-mir-7158-3p
Up	NLRC5	22	hsa-mir-4794	Down	SLC39A10	27	hsa-mir-7106-3p
Up	IL7R	22	hsa-mir-8052	Down	SLPI	26	hsa-mir-151b
Up	SERPINE1	22	hsa-mir-204-5p	Down	GALM	26	hsa-mir-4444
Up	NUAK2	22	hsa-mir-4464	Down	CTSV	26	hsa-mir-302f
Up	ENO4	22	hsa-mir-6088	Down	SERPINA4	25	hsa-mir-544a
Up	SYT1	21	hsa-mir-711	Down	QPCT	25	hsa-mir-4419a
Up	MT1E	21	hsa-mir-4302	Down	SNAP25	25	hsa-mir-641
Up	NYAP2	21	hsa-mir-4780	Down	VSIG1	24	hsa-mir-4309
Up	EGR3	20	hsa-mir-3978	Down	RHBDL2	24	hsa-mir-1307-3p
Up	PTGS2	20	hsa-mir-558	Down	LOX	24	hsa-mir-5583-3p
Up	TNFSF10	20	hsa-mir-5697	Down	HACD3	24	hsa-mir-3920
Up	SLC30A3	20	hsa-mir-548ap-3p	Down	TCEA3	24	hsa-mir-4433a-3p
Up	HLX	20	hsa-mir-5572	Down	CYP2U1	24	hsa-mir-500a-5p
Up	OAS2	19	hsa-mir-4531	Down	CA12	24	hsa-mir-548m
Up	MX2	19	hsa-mir-630	Down	DNAJC22	23	hsa-mir-4772-3p
Up	RASGRP1	18	hsa-mir-599	Down	TTR	23	hsa-mir-6890-5p
Up	HIVEP1	18	hsa-mir-595	Down	WDR72	23	hsa-mir-181d-5p
Up	TIPARP	18	hsa-mir-4799-5p	Down	FDX1	23	hsa-mir-548x-3p
Up	MOGAT3	18	hsa-mir-3689d	Down	TMEM37	22	hsa-mir-4709-5p
Up	TRIM5	16	hsa-mir-3689e	Down	KY	22	hsa-mir-6799-3p
Up	RTP4	16	hsa-mir-892c-3p	Down	KCNMB4	22	hsa-mir-190b
Up	IFIT1	16	hsa-mir-2054	Down	CDNF	21	hsa-mir-1273g-3p
Up	CCRL2	16	hsa-mir-1306-5p	Down	RAD51B	21	hsa-mir-6780a-5p
Up	SNED1	16	hsa-mir-4666b	Down	ACO1	20	hsa-mir-6858-3p
Up	PELI1	15	hsa-mir-4639-3p	Down	ABCC4	20	hsa-let-7f-1-3p
Up	CCDC65	15	hsa-mir-4433b-3p	Down	ARL3	20	hsa-mir-4429
Up	RASD1	15	hsa-mir-4488	Down	UCP2	20	hsa-mir-4739
Up	TSLP	15	hsa-mir-4270	Down	KCNE3	19	hsa-mir-6842-5p
Up	XRN1	14	hsa-mir-5011-5p	Down	SHH	19	hsa-mir-6882-3p
Up	JAK2	14	hsa-mir-5692a	Down	NDUFA2	19	hsa-mir-6755-5p
Up	IL1A	14	hsa-mir-92a-1-5p	Down	CYP4F3	18	hsa-mir-6849-3p
Up	LRIT3	14	hsa-mir-4758-5p	Down	STC1	17	hsa-mir-2276-5p
Up	IFNB1	13	hsa-mir-607	Down	BCAS3	17	hsa-mir-378g
Up	BDKRB2	13	hsa-mir-4659a-3p	Down	PHGDH	17	hsa-mir-107
Up	NT5C3A	12	hsa-mir-582-5p	Down	MAD2L1	17	hsa-mir-376a-3p
Up	CLPSL1	12	hsa-mir-2278	Down	TOP2A	17	hsa-mir-7-1-3p
Up	EPC1	11	hsa-mir-4742-3p	Down	SIAE	16	hsa-mir-6511a-5p
Up	HEG1	11	hsa-mir-507	Down	HHLA2	16	hsa-mir-548n
Up	KIF26B	11	hsa-mir-6795-3p	Down	SLC38A4	16	hsa-mir-3150b-3p
Up	MT2A	11	hsa-let-7a-2-3p	Down	RNF128	16	hsa-mir-629-3p

Up	IL7	11	hsa-mir-376b-3p	Down	LYPLAL1	16	hsa-mir-7-2-3p
Up	FBXO6	11	hsa-mir-7151-3p	Down	HMGN3	15	hsa-mir-5011-5p
Up	NFKBIA	10	hsa-mir-891a-5p	Down	ITM2A	15	hsa-mir-411-5p
Up	SPTBN5	10	hsa-mir-4747-5p	Down	SLC12A2	15	hsa-mir-5580-3p
Up	MAP3K8	10	hsa-mir-589-5p	Down	SORBS2	14	hsa-mir-6791-3p
Up	EGR2	10	hsa-mir-142-3p	Down	EML6	14	hsa-mir-5582-3p
Up	PTGER4	10	hsa-mir-519d-3p	Down	SCP2	14	hsa-mir-622
Up	TNF	10	hsa-mir-130a-3p	Down	TMEM45B	13	hsa-mir-5193
Up	SPRY2	10	hsa-mir-24-2-5p	Down	SPAG16	13	hsa-mir-1260a
Up	CCL2	10	hsa-mir-518a-5p	Down	PROM1	13	hsa-mir-514b-5p
Up	CX3CL1	10	hsa-mir-5093	Down	ACSF2	13	hsa-mir-6858-5p
Up	HDX	10	hsa-mir-6888-5p	Down	OAZ1	12	hsa-mir-6070
Up	PDZD2	10	hsa-mir-8055	Down	CRYZ	12	hsa-mir-6849-5p
Up	OTOG	10	hsa-mir-3074-5p	Down	REPS2	12	hsa-mir-6817-5p
Up	LAYN	10	hsa-mir-6501-5p	Down	ARHGAP19	12	hsa-mir-4762-5p
Up	PTCH2	10	hsa-mir-6074	Down	PROM2	11	hsa-mir-6851-5p
Up	PPEF1	10	hsa-mir-6809-3p	Down	TRNP1	11	hsa-mir-6720-5p
Up	TRIM21	10	hsa-mir-6780b-5p	Down	ST6GALNAC1	11	hsa-mir-4743-3p
Up	NCKAP5	9	hsa-mir-6892-5p	Down	SLC25A27	11	hsa-mir-5692c
Up	TNFSF13B	9	hsa-mir-5681b	Down	PDE1A	11	hsa-mir-1264
Up	SECTM1	9	hsa-mir-1281	Down	SRI	11	hsa-let-7f-1-3p
Up	BARX1	9	hsa-mir-1268a	Down	SYT5	11	hsa-mir-4691-3p
Up	SLC25A2	9	hsa-mir-6771-3p	Down	SAP30	11	hsa-mir-125b-2-3p
Up	RAB44	8	hsa-mir-711	Down	METRN	11	hsa-mir-8081
Up	RAET1L	8	hsa-mir-448	Down	CD302	11	hsa-mir-4690-3p
Up	CXCL11	8	hsa-mir-548b-3p	Down	SMARCA2	11	hsa-mir-19a-3p
Up	EGR1	8	hsa-mir-487a-3p	Down	PPT1	11	hsa-mir-339-5p
Up	ZC3H12A	8	hsa-mir-3194-5p	Down	ALDH2	11	hsa-mir-8079
Up	GPER1	8	hsa-mir-4750-3p	Down	PIGN	11	hsa-mir-3617-5p
Up	GATA3	7	hsa-mir-132-3p	Down	SORT1	10	hsa-mir-1185-5p
Up	C1QTNF1	7	hsa-mir-6815-5p	Down	NDUFS7	10	hsa-mir-5588-3p
Up	DNAH3	7	hsa-mir-519e-5p	Down	FGFR3	10	hsa-mir-8064
Up	SLC39A2	7	hsa-mir-4747-3p	Down	CFAP73	9	hsa-mir-99a-5p
Up	SYNPR	6	hsa-mir-877-3p	Down	BCAS1	9	hsa-mir-4756-3p
Up	PLAUR	6	hsa-mir-622	Down	CCDC74B	9	hsa-mir-411-3p
Up	OGFR	6	hsa-mir-505-3p	Down	RIMKLA	9	hsa-mir-6791-5p
Up	GRM8	6	sa-mir-7111-3p	Down	CFTR	9	hsa-mir-509-3p
Up	IFI16	6	hsa-mir-136-5p	Down	PBXIP1	9	hsa-mir-296-3p
Up	PDE2A	6	hsa-mir-3619-3p	Down	SERINC5	9	hsa-mir-548an
Up	IL11	6	hsa-mir-211-5p	Down	TUBA1A	9	hsa-mir-10a-5p
Up	C17orf82	6	hsa-mir-6802-3p	Down	C21orf62-AS1	8	hsa-mir-548as-3p
Up	PDE4B	5	hsa-mir-374a-5p	Down	EFHC2	8	hsa-mir-4455
Up	NKX3-1	5	hsa-mir-215-5p	Down	NLGN1	8	hsa-mir-1251-3p
Up	CXCL2	5	hsa-mir-223-3p	Down	KCNAB1	8	hsa-mir-513a-3p

Up	NFKBIZ	5	hsa-mir-193b-3p	Down	CLDN10	8	hsa-mir-6810-3p
Up	FST	5	hsa-mir-3680-3p	Down	ATRAID	8	hsa-mir-548az-5p
Up	CXCL3	5	hsa-mir-100-3p	Down	ACOT13	8	hsa-mir-10b-5p
Up	IFIT2	5	hsa-mir-645	Down	ALCAM	8	hsa-mir-323a-5p
Up	STX11	5	hsa-mir-5188	Down	ADI1	8	hsa-mir-711
Up	DRP2	5	hsa-mir-7641	Down	CNIH4	8	hsa-mir-301b-3p
Up	IFIT5	4	hsa-mir-146a-5p	Down	SPCS2	8	hsa-mir-4789-5p
Up	NPR3	4	hsa-mir-30a-5p	Down	CTHRC1	8	hsa-mir-148b-3p
Up	AHRR	4	hsa-mir-18a-5p	Down	CRP	7	hsa-mir-509-3-5p
Up	ICAM5	4	hsa-mir-4707-5p	Down	SLC25A21	7	hsa-mir-4666a-3p
Up	TRPC4	4	hsa-mir-33a-5p	Down	SLC44A4	7	hsa-mir-6728-5p
Up	USP18	4	hsa-mir-221-3p	Down	VWA2	7	hsa-mir-4749-3p
Up	IFIH1	4	hsa-mir-424-5p	Down	SMIM10	7	hsa-mir-431-5p
Up	CD69	4	hsa-mir-32-5p	Down	PRR15L	7	hsa-mir-4446-5p
Up	NTNG2	4	hsa-mir-3613-5p	Down	IGSF10	7	hsa-mir-518a-5p
Up	WIF1	4	hsa-mir-374a-5p	Down	PRDX2	7	hsa-mir-339-5p
Up	BAHCC1	3	hsa-let-7e-5p	Down	MMP7	7	hsa-mir-543
Up	IL12A	3	hsa-mir-10a-5p	Down	NACA2	7	hsa-mir-513c-3p
Up	PTX3	3	hsa-mir-9-5p	Down	HOGA1	7	hsa-mir-6771-3p
Up	CXCL9	3	hsa-mir-34a-5p	Down	NEK2	7	hsa-mir-4778-5p
Up	TRIM22	3	hsa-mir-146a-5p	Down	SGPP1	7	hsa-mir-32-5p
Up	IFI44	3	hsa-mir-26b-5p	Down	ECH1	7	hsa-mir-378a-3p
Up	NLRP3	3	hsa-mir-223-3p	Down	PSMD10	6	hsa-mir-605-5p
Up	GFI1	3	hsa-mir-142-3p	Down	SPP1	6	hsa-mir-299-5p
Up	PLA2G4C	3	hsa-mir-181a-5p	Down	CAB39L	6	hsa-mir-27a-3p
Up	FAM110B	3	hsa-mir-7109-3p	Down	NTRK2	6	hsa-mir-204-5p
Up	OASL	3	hsa-mir-1-3p	Down	SLAIN1	6	hsa-mir-302a-3p
Up	BATF2	3	hsa-mir-122-5p	Down	MCM3AP-AS1	6	hsa-mir-15b-5p
Up	PARP10	3	hsa-mir-421	Down	PLEKHB1	5	hsa-mir-9-5p
Up	PML	3	hsa-mir-378a-3p	Down	TRAPPC6A	5	hsa-mir-4461
Up	TDRD7	2	hsa-let-7e-5p	Down	CUEDC2	4	hsa-mir-186-5p
Up	NOCT	2	hsa-mir-296-3p	Down	ERP27	4	hsa-mir-210-3p
Up	MMP25	2	hsa-mir-181c-3p	Down	IGFBP2	4	hsa-mir-491-3p
Up	CCL20	2	hsa-mir-21-5p	Down	GNG7	4	hsa-mir-4311
Up	TAP1	2	hsa-mir-346	Down	CAT	4	hsa-mir-30b-5p
Up	FAXDC2	2	hsa-mir-124-3p	Down	ACSS1	4	hsa-mir-191-5p
Up	FILIP1L	2	hsa-mir-335-5p	Down	FAH	4	hsa-mir-375
Up	LGALS9	2	hsa-mir-22-3p	Down	BDH2	4	hsa-mir-21-5p
Up	SNPH	2	hsa-mir-375	Down	KLHDC2	4	hsa-mir-19b-3p
Up	TRANK1	2	hsa-mir-26b-5p	Down	NTHL1	4	hsa-mir-93-5p
Up	CRTAM	2	hsa-mir-335-5p	Down	PRIMPOL	4	hsa-mir-16-5p
Up	RSAD2	2	hsa-mir-146a-5p	Down	SPDEF	4	hsa-mir-510-5p
Up	ZNF627	2	hsa-mir-27a-3p	Down	OLFM4	4	hsa-mir-103a-3p
Up	HLA-F	2	hsa-mir-93-5p	Down	FAM171A2	4	hsa-mir-106b-5p

Up	EYA1	2	hsa-mir-562	Down	PAH	3	hsa-mir-590-3p
Up	THEMIS2	2	hsa-mir-197-3p	Down	LEPR	3	hsa-mir-877-5p
Up	RND1	2	hsa-mir-199a-5p	Down	ARL6IP5	3	hsa-mir-31-3p
Up	LYL1	2	hsa-mir-10b-5p	Down	SUMF1	3	hsa-mir-148b-3p
Up	DDX58	2	hsa-mir-218-5p	Down	DTYMK	3	hsa-mir-183-5p
Up	HSD17B3	2	hsa-mir-181a-5p	Down	APOE	3	hsa-mir-199a-3p
Up	GRIA2	2	hsa-mir-181b-5p	Down	OAT	3	hsa-mir-1-3p
Up	ACHE	2	hsa-mir-212-3p	Down	GALNT12	3	hsa-mir-215-5p
Up	TICAM1	2	hsa-mir-193b-3p	Down	FKBP3	3	hsa-mir-98-5p
Up	FOSB	2	hsa-mir-663a	Down	CASR	3	hsa-mir-135b-5p
Up	ISG20	2	hsa-mir-1-3p	Down	CSPG5	3	hsa-mir-3691-5p
Up	ISG15	2	hsa-mir-146a-5p	Down	ROS1	3	hsa-mir-300
Up	HERC5	2	hsa-mir-3529-3p	Down	MDH1	3	hsa-mir-186-5p
Up	DACT1	2	hsa-mir-124-3p	Down	CFI	3	hsa-mir-181a-5p
Up	IRF7	2	hsa-mir-762	Down	ECI2	3	hsa-mir-877-3p
Up	EPSTI1	2	hsa-mir-654-5p	Down	SORL1	2	hsa-mir-127-5p
Up	FLT3	2	hsa-mir-150-5p	Down	RAD9B	2	hsa-mir-187-5p
Up	DUSP26	2	hsa-mir-544a	Down	RAB26	2	hsa-mir-421
Up	DRD1	2	hsa-mir-382-5p	Down	SLC3A1	2	hsa-mir-548e-5p
Up	GIMAP2	2	hsa-mir-193b-3p	Down	SYT12	2	hsa-mir-146a-5p
Up	HELZ2	2	hsa-mir-6793-3p	Down	AIF1L	2	hsa-mir-1229-3p
Up	SLC6A13	2	hsa-mir-4709-5p	Down	KRT14	2	hsa-mir-122-5p
Up	C11orf96	1	hsa-mir-19b-3p	Down	CYBA	2	hsa-mir-320a
Up	ADGRL3	1	hsa-mir-20a-5p	Down	MYO3B	2	hsa-mir-1-3p
Up	RELB	1	hsa-mir-26b-5p	Down	SAC3D1	2	hsa-mir-423-3p
Up	CH25H	1	hsa-mir-26b-5p	Down	PPA2	2	hsa-mir-193b-3p
Up	CAPN9	1	hsa-mir-26b-5p	Down	CD24	2	hsa-mir-373-3p
Up	HSD17B14	1	hsa-mir-26b-5p	Down	FAM89B	2	hsa-mir-7-5p
Up	IL22RA1	1	hsa-mir-26b-5p	Down	AGR2	2	hsa-mir-4419a
Up	SAMD9	1	hsa-mir-30a-5p	Down	ERFE	2	hsa-mir-192-5p
Up	PARP12	1	hsa-mir-98-5p	Down	ENTPD3	2	hsa-mir-335-5p
Up	CMPK2	1	hsa-mir-192-5p	Down	AKR1C3	2	hsa-mir-98-5p
Up	SIX2	1	hsa-mir-181b-5p	Down	TMEM160	2	hsa-mir-185-5p
Up	LMO2	1	hsa-mir-223-3p	Down	NR1H4	2	hsa-mir-192-3p
Up	CAVIN2	1	hsa-mir-1-3p	Down	ASAH1	2	hsa-mir-92a-3p
Up	GBP1	1	hsa-mir-124-3p	Down	NME5	2	hsa-mir-148b-3p
Up	PRRX2	1	hsa-mir-124-3p	Down	ROM1	2	hsa-mir-124-3p
Up	DSCAML1	1	hsa-mir-124-3p	Down	MME	2	hsa-mir-26b-5p
Up	SH2D1B	1	hsa-mir-124-3p	Down	HSD17B2	2	hsa-mir-124-3p
Up	OR52K1	1	hsa-mir-106b-5p	Down	EPHX1	2	hsa-mir-193b-3p
Up	TAGAP	1	hsa-mir-374a-5p	Down	DHFRP1	2	hsa-mir-24-3p
Up	CYP21A2	1	hsa-mir-335-5p	Down	PDGFD	2	hsa-mir-21-5p
Up	HCRTR1	1	hsa-mir-335-5p	Down	TF	2	hsa-mir-19a-3p
Up	OAS1	1	hsa-mir-335-5p	Down	ORAI3	2	hsa-mir-18a-5p

Up	MYLPF	1	hsa-mir-335-5p	Down	TEX15	2	hsa-mir-186-5p
Up	XAF1	1	hsa-mir-335-5p	Down	C2orf74	2	hsa-mir-15a-5p
Up	TMEM140	1	hsa-mir-335-5p	Down	CENPV	2	hsa-mir-28-5p
Up	GRIP2	1	hsa-mir-335-5p	Down	COX14	2	hsa-let-7e-5p
Up	HSH2D	1	hsa-mir-335-5p	Down	SPATA17	1	hsa-mir-6818-3p
Up	SEC16B	1	hsa-mir-335-5p	Down	CRISP3	1	hsa-mir-1229-3p
Up	NEURL3	1	hsa-mir-335-5p	Down	TSTD1	1	hsa-mir-335-5p
Up	CPO	1	hsa-mir-335-5p	Down	CNTNAP3B	1	hsa-mir-335-5p
Up	TRIM40	1	hsa-mir-335-5p	Down	C2orf81	1	hsa-mir-335-5p
Up	TRIM69	1	hsa-mir-335-5p	Down	GLTPD2	1	hsa-mir-335-5p
Up	SUSD3	1	hsa-mir-335-5p	Down	NXNL2	1	hsa-mir-335-5p
Up	LSMEM1	1	hsa-mir-335-5p	Down	RERG	1	hsa-mir-335-5p
Up	STX19	1	hsa-mir-335-5p	Down	VTCN1	1	hsa-mir-335-5p
Up	UBA7	1	hsa-mir-455-5p	Down	MMEL1	1	hsa-mir-335-5p
				Down	SLC45A1	1	hsa-mir-335-5p
				Down	SOSTDC1	1	hsa-mir-335-5p
				Down	USH1C	1	hsa-mir-335-5p
				Down	RARRES2	1	hsa-mir-335-5p
				Down	KLK7	1	hsa-mir-335-5p
				Down	LTC4S	1	hsa-mir-335-5p
				Down	HOXA2	1	hsa-mir-335-5p
				Down	FCGRT	1	hsa-mir-335-5p
				Down	FABP6	1	hsa-mir-335-5p
				Down	ACE	1	hsa-mir-335-5p
				Down	ADGRB3	1	hsa-mir-335-5p
				Down	ADH6	1	hsa-mir-335-5p
				Down	AQP1	1	hsa-mir-320a
				Down	GSTA4	1	hsa-mir-185-5p
				Down	DDC	1	hsa-mir-145-5p
				Down	TCTEX1D2	1	hsa-mir-133a-3p
				Down	AZGP1	1	hsa-mir-128-3p
				Down	SCNN1A	1	hsa-mir-125b-5p
				Down	TMEM121	1	hsa-mir-124-3p
				Down	UGT1A10	1	hsa-mir-124-3p
				Down	SNTA1	1	hsa-mir-124-3p
				Down	NRTN	1	hsa-mir-124-3p
				Down	CTSH	1	hsa-mir-124-3p
				Down	WDR54	1	hsa-mir-23b-3p
				Down	IQCD	1	hsa-mir-1-3p
				Down	DPY30	1	hsa-mir-1-3p
				Down	MACROD1	1	hsa-mir-1-3p
				Down	BCKDHB	1	hsa-mir-1-3p
				Down	COMMD8	1	hsa-mir-183-5p
				Down	ARHGDIB	1	hsa-mir-34a-5p

	Down	SAMD13	1	hsa-mir-192-5p
	Down	RPL39L	1	hsa-mir-100-5p
	Down	PGP	1	hsa-mir-93-5p
	Down	DNPH1	1	hsa-mir-93-5p
	Down	PCSK1N	1	hsa-mir-31-5p
	Down	MAGIX	1	hsa-mir-26b-5p
	Down	ACE2	1	hsa-mir-26b-5p
	Down	ODAM	1	hsa-mir-26b-5p
	Down	IL20RA	1	hsa-mir-26b-5p
	Down	MPC2	1	hsa-mir-26b-5p
	Down	SRPX	1	hsa-mir-26b-5p
	Down	TCN1	1	hsa-mir-26b-5p
	Down	PNMT	1	hsa-mir-26b-5p
	Down	ENDOG	1	hsa-mir-26b-5p
	Down	AGT	1	hsa-mir-26b-5p
	Down	KLK6	1	hsa-let-7f-5p
	Down	COX16	1	hsa-let-7e-5p
	Down	SPR	1	hsa-let-7b-5p

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

Table 8 TF - target gene interaction table

Regulation	TF	Degree	Target Gene	Regulation	TF	Degree	Target Gene
Up	FOXC1	202	PROX1	Down	FOXC1	261	SERHL2
Up	GATA2	175	CXCL11	Down	GATA2	183	CFI
Up	YY1	122	C4A	Down	YY1	131	TCN1
Up	FOXL1	93	JAK2	Down	NFIC	104	PGP
Up	NFKB1	88	IL15RA	Down	FOXL1	102	PGK1
Up	E2F1	82	FOS	Down	E2F1	88	PDK1
Up	RELA	77	FAM110B	Down	SRF	87	CSPG5
Up	USF2	74	FLT3LG	Down	USF2	87	UGT1A4
Up	NFIC	72	SPTBN5	Down	STAT3	83	ROS1
Up	CREB1	67	OAS2	Down	NFKB1	81	CEACAM7
Up	HINFP	66	EGR4	Down	PPARG	79	CCDC74B
Up	PPARG	63	HSD17B14	Down	MEF2A	74	VWA2
Up	TFAP2A	60	C1QTNF1	Down	NFYA	72	UGT1A8
Up	TP53	59	DHX58	Down	CREB1	70	TFRC
Up	MEF2A	57	SDPR	Down	JUN	69	PTPLB
Up	POU2F2	57	SLC6A13	Down	POU2F2	69	KIAA0101
Up	STAT3	56	CD274	Down	HINFP	64	RAD9B
Up	SRF	53	C4B	Down	TFAP2A	58	DNAJC22
Up	HOXA5	48	CYP1A1	Down	TP53	58	PPT1
Up	SREBF1	45	SYNPR	Down	GATA3	57	BNIPL
Up	RUNX2	42	TIPARP	Down	ELK1	50	PRR15L
Up	MAX	41	HLX	Down	HNF4A	49	KIAA1456
Up	HNF4A	38	ATF3	Down	SREBF1	49	KLK7
Up	USF1	38	GRIN3B	Down	PRDM1	47	SLPI
Up	TEAD1	37	IL6	Down	HOXA5	45	NEURL1B
Up	NFYA	37	PTGER4	Down	ARID3A	43	CRLS1
Up	ELK1	35	SYT1	Down	RELA	42	SEMA5A
Up	ZNF354C	33	AMOTL2	Down	ESR1	42	CNGA1
Up	JUND	33	FAP	Down	STAT1	40	SHH
Up	FOXA1	33	PPEF1	Down	JUND	39	SLAIN1
Up	CEBPB	32	DACT1	Down	ELK4	38	NXNL2
Up	STAT1	30	CCL2	Down	TFAP2C	37	ACE
Up	BRCA1	30	CPO	Down	FOXA1	37	PLEKHS1
Up	PRDM1	29	FST	Down	RUNX2	36	SLC44A4
Up	ESR1	28	RND1	Down	BRCA1	35	TTR
Up	E2F6	28	SNCAIP	Down	NR3C1	35	AKR1C3
Up	TP63	27	CPEB3	Down	MAX	33	SEMA4G
Up	NR3C1	27	IFIT1	Down	PRRX2	31	LHPP
Up	TFAP2C	27	PLEKHG5	Down	FOS	31	ALCAM
Up	SREBF2	27	THEMIS2	Down	TEAD1	31	TF
Up	SP1	26	BBC3	Down	IRF2	30	PTPLAD1
Up	ELK4	26	WIF1	Down	PAX2	30	SORT1
Up	KLF5	25	VSTM1	Down	SP1	29	HEBP1

Up	IRF2	24	GRM8	Down	SREBF2	29	GNG7
Up	ARID3A	24	PPM1K	Down	E2F6	28	DPYSL2
Up	FOXF2	22	LRIT3	Down	CEBPB	27	TRMT2B
Up	SPIB	18	EGR2	Down	TP63	27	ANXA10
Up	PAX2	18	ID4	Down	USF1	26	FMO5
Up	NR2F1	16	NCKAP5	Down	NRF1	26	LYPLAL1
Up	NKX3-2	14	ACTA1	Down	KLF5	25	REPS2
Up	EN1	14	SOCS1	Down	NR2F1	21	KCNAB1
Up	PDX1	13	TTC9B	Down	ZNF354C	20	HOXA11
Up	SOX5	12	PELI1	Down	FOXF2	19	TSPAN10
Up	SOX10	9	FBXO6	Down	NKX3-2	17	RIMKLA
Up	NRF1	7	FOSB	Down	EN1	17	BTD
Up	NKX2-5	7	SP110	Down	SOX5	14	MOGAT1
Up	REL	7	TAP1	Down	SOX10	14	NDUFA2
Up	FOXI1	6	EPSTI1	Down	SRY	11	EFHC2
Up	SOX17	6	FGF18	Down	EGR1	11	CAT
Up	FOXD1	6	NANOS3	Down	ELF5	11	LTC4S
Up	NR4A2	5	CSF2	Down	PDX1	10	ENTPD3
Up	FOXO3	5	CYP21A2	Down	SOX17	10	ARL6IP5
Up	FEV	5	GIMAP2	Down	SPIB	8	IL20RA
Up	SRY	5	HIVEP1	Down	NKX2-5	6	COX14
Up	ELF5	5	IRF1	Down	E2F4	6	CASR
Up	MYB	5	TLR6	Down	NFATC2	6	TMPRSS4
Up	NFATC2	4	CCL20	Down	GATA1	6	RHBDL2
Up	NFIL3	4	EYA1	Down	HNF1B	5	RNF128
Up	ESR2	4	SSTR2	Down	MYB	5	ACE2
Up	HLF	4	TNF	Down	FOXI1	4	WDR54
Up	HNF1B	3	CD69	Down	NR2E3	4	ITM2A
Up	RREB1	3	CYP21A2	Down	NFYB	3	TOP2A
Up	NHLH1	3	CYP21A2	Down	NKX3-1	2	AKR1B10
Up	PBX1	3	CYP21A2	Down	REL	2	TOMM20
Up	PLAG1	3	TNF	Down	NOBOX	2	ECH1
Up	INSM1	3	TNF	Down	ARNT	2	PCYOX1
Up	SOX9	3	TNF	Down	ZFX	2	SEPP1
Up	REST	3	TRIM40	Down	KLF4	2	TSTD1
Up	PAX6	3	TRIM40	Down	ESR2	1	CCDC115
Up	CTCF	3	TRIM40	Down	FEV	1	HHLA2
Up	NR2E3	2	ISG15	Down	NR2C2	1	APOE
Up	NR2C2	2	MAP3K8	Down	ESRRB	1	SHMT1
Up	NOBOX	1	LMO2	Down	MYCN	1	RARRES2
Up	ESRRB	1	NLRC5	Down	MYC	1	RARRES2
Up	ARNT	1	PDE2A	Down	RUNX1	1	DPY30
Up	E2F4	1	PHF11				
Up	TFCP2L1	1	CCRN4L				

Up	MYC	1	PDE2A
Up	RUNX1	1	IL22RA1

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

Figures

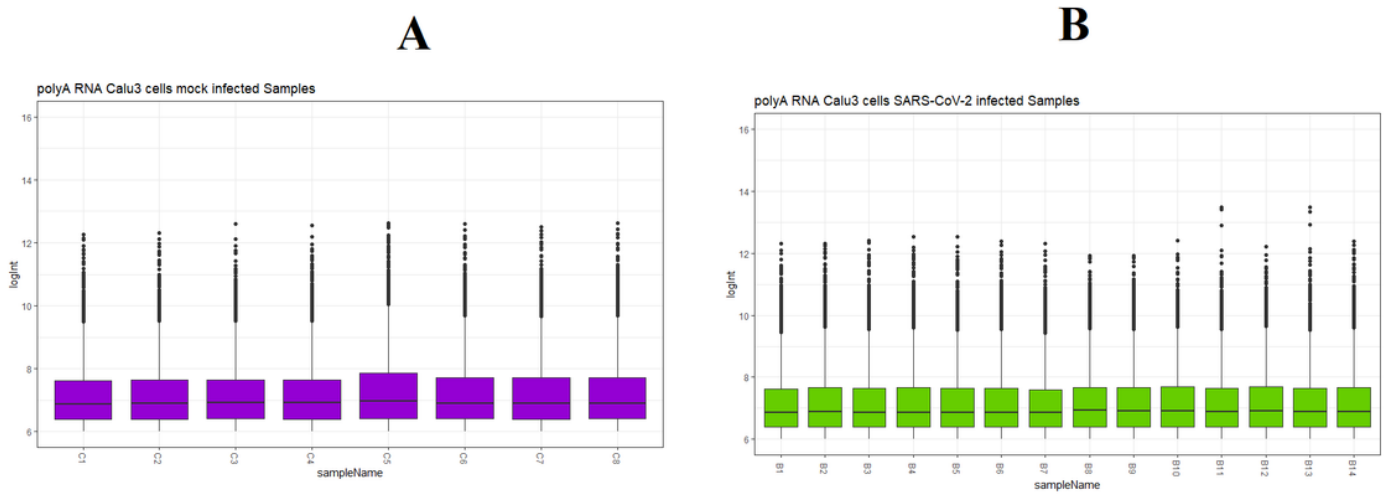
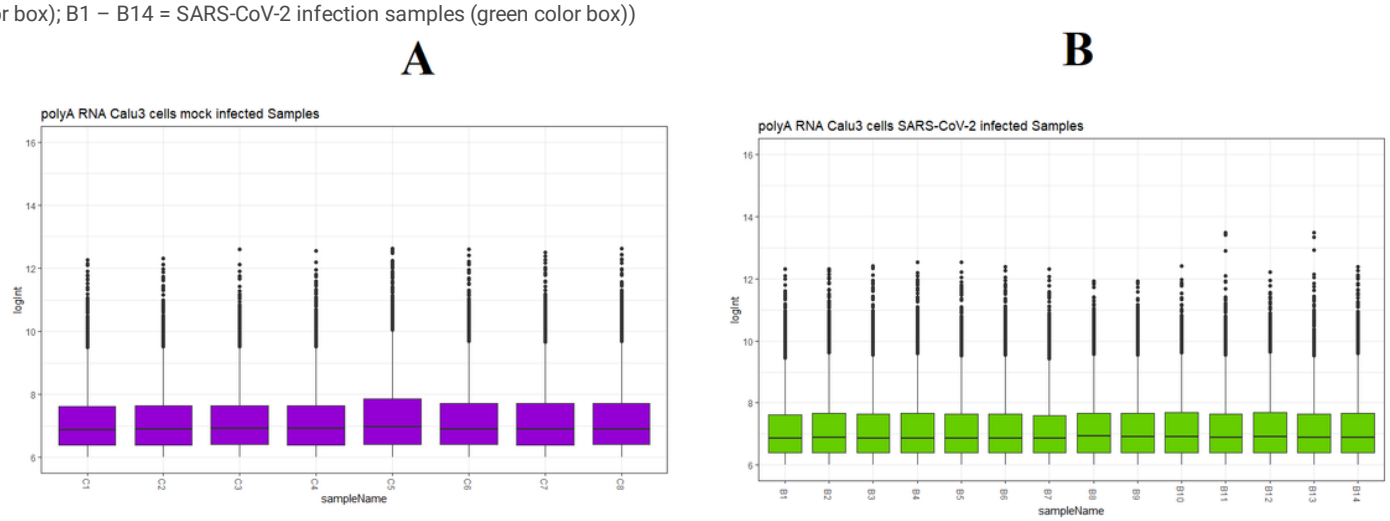


Figure 1

Box plots of the normalized data. (A) 8 Mock samples (B) 12 SARS-CoV-2 infection samples. Horizontal axis represents the sample symbol and the vertical axis represents the gene expression values. The black line in the box plot represents the median value of gene expression. (A1 – A8 = Mock samples (lavender color box); B1 – B14 = SARS-CoV-2 infection samples (green color box))



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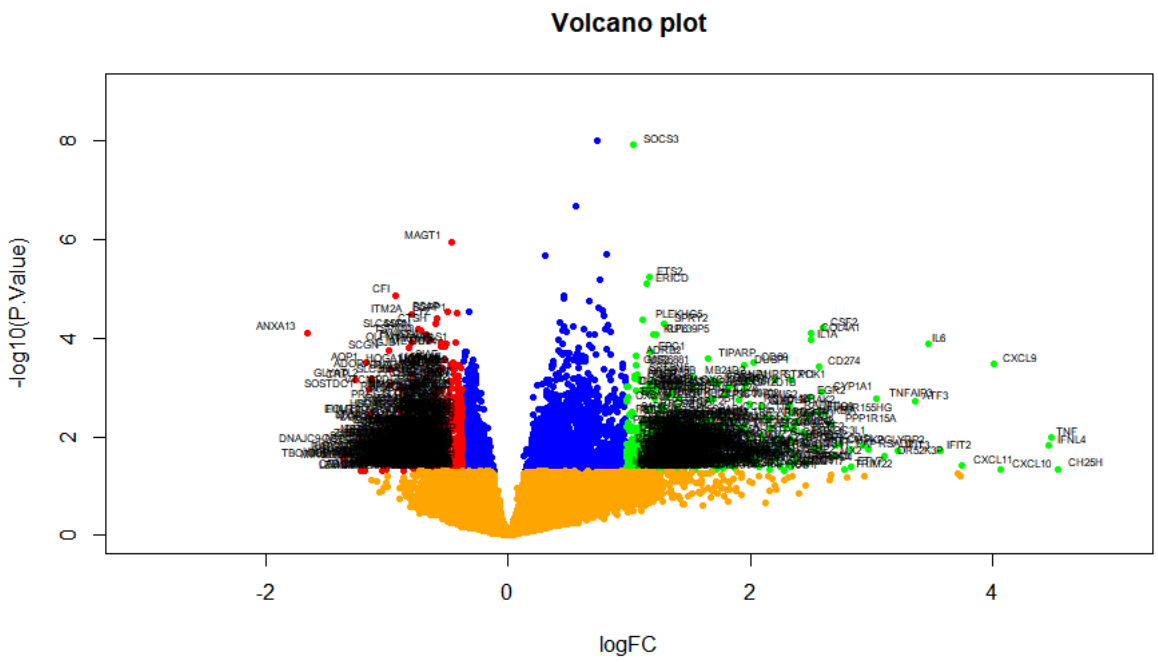
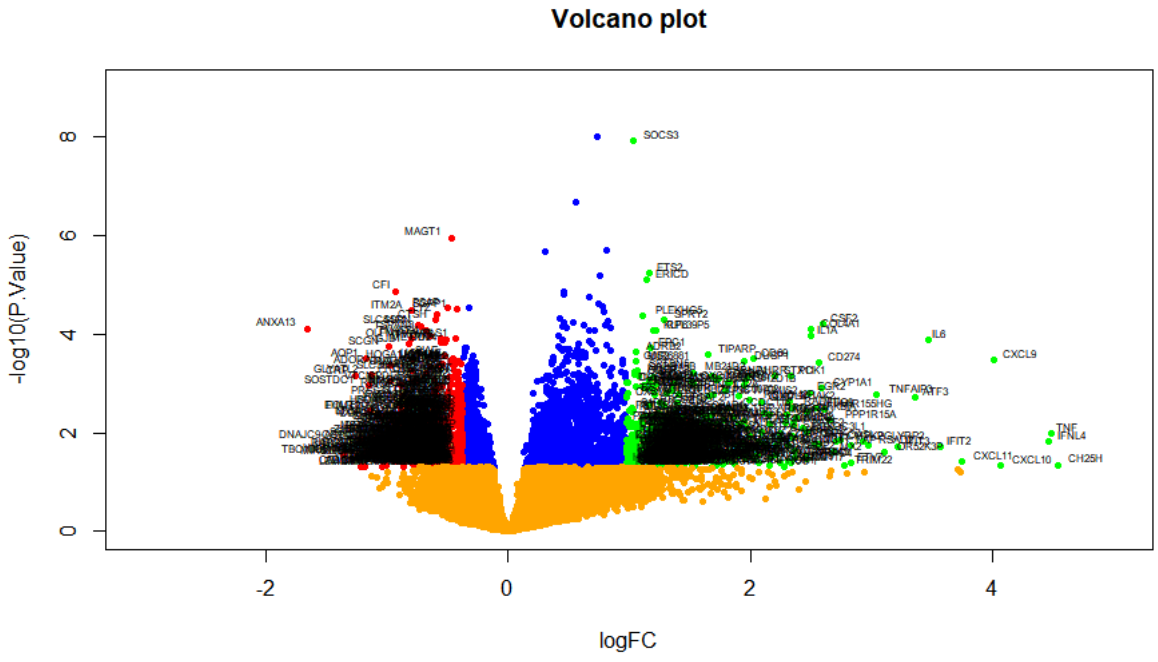


Figure 2

Volcano plot of differentially expressed genes. Genes with a significant change of more than two-fold were selected. Green dot represented up regulated significant genes and red dot represented down regulated significant genes.



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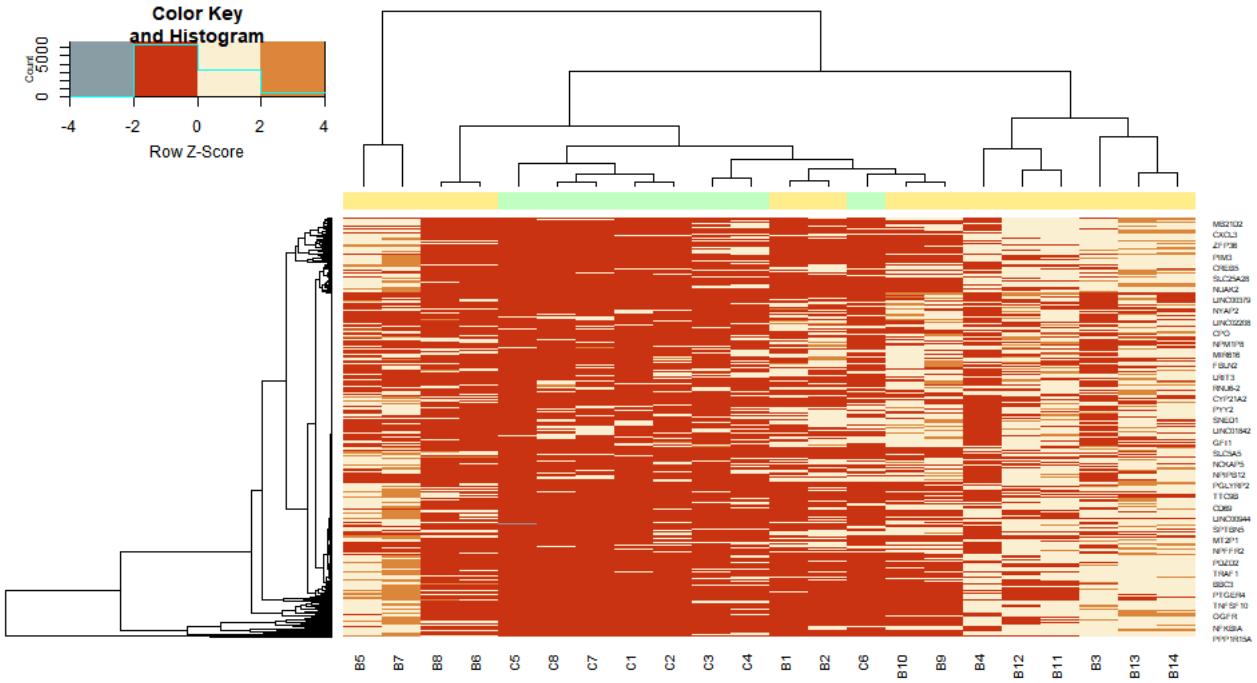
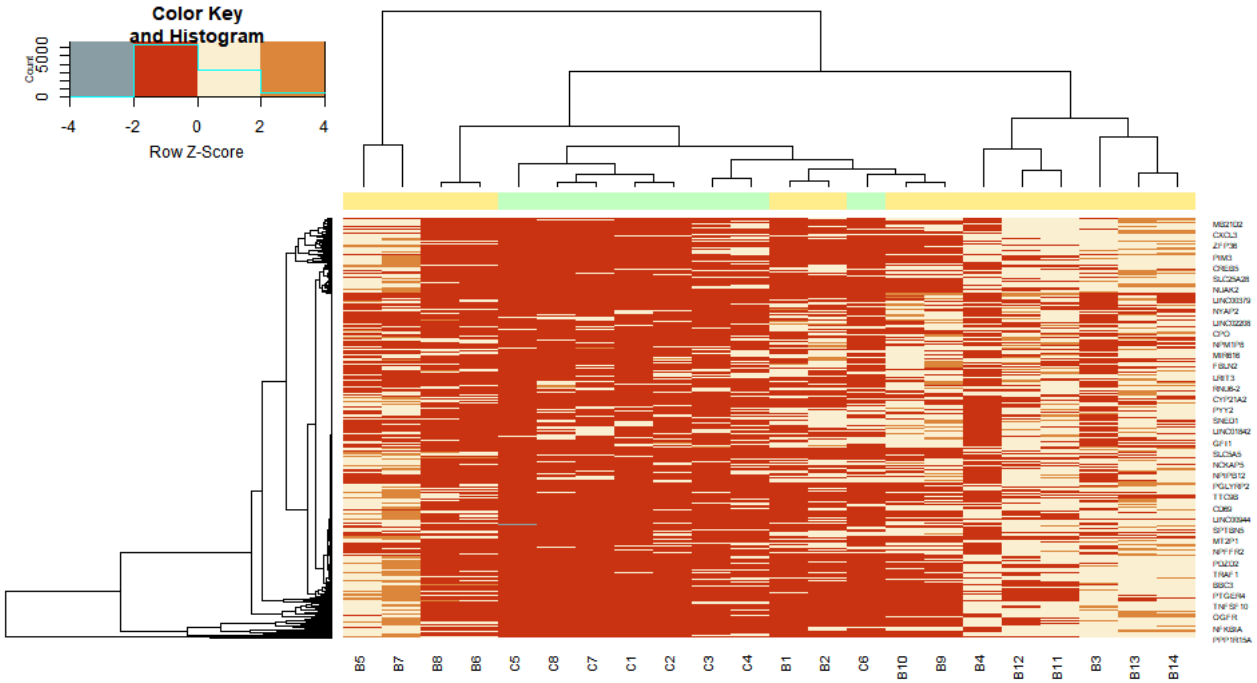


Figure 3

Heat map of up regulated differentially expressed genes. Legend on the top left indicate log fold change of genes. (A1 – A8 = Mock samples; B1 – B14 = SARS-CoV-2 infection samples)



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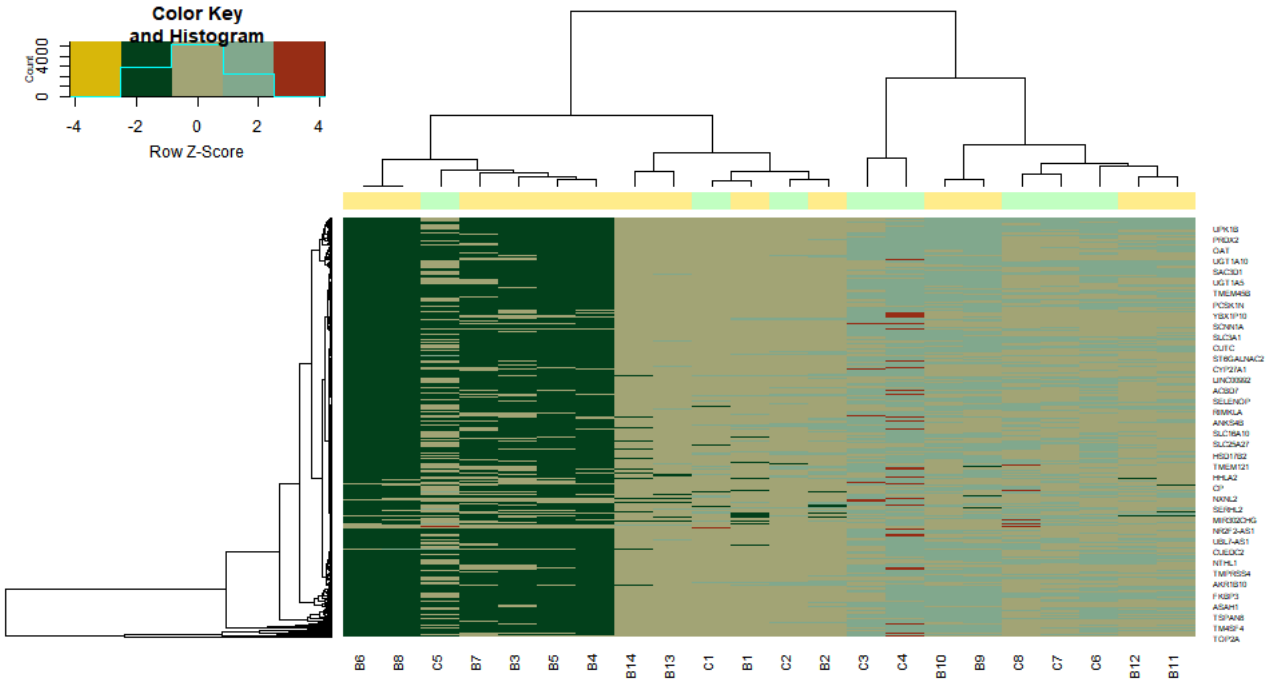
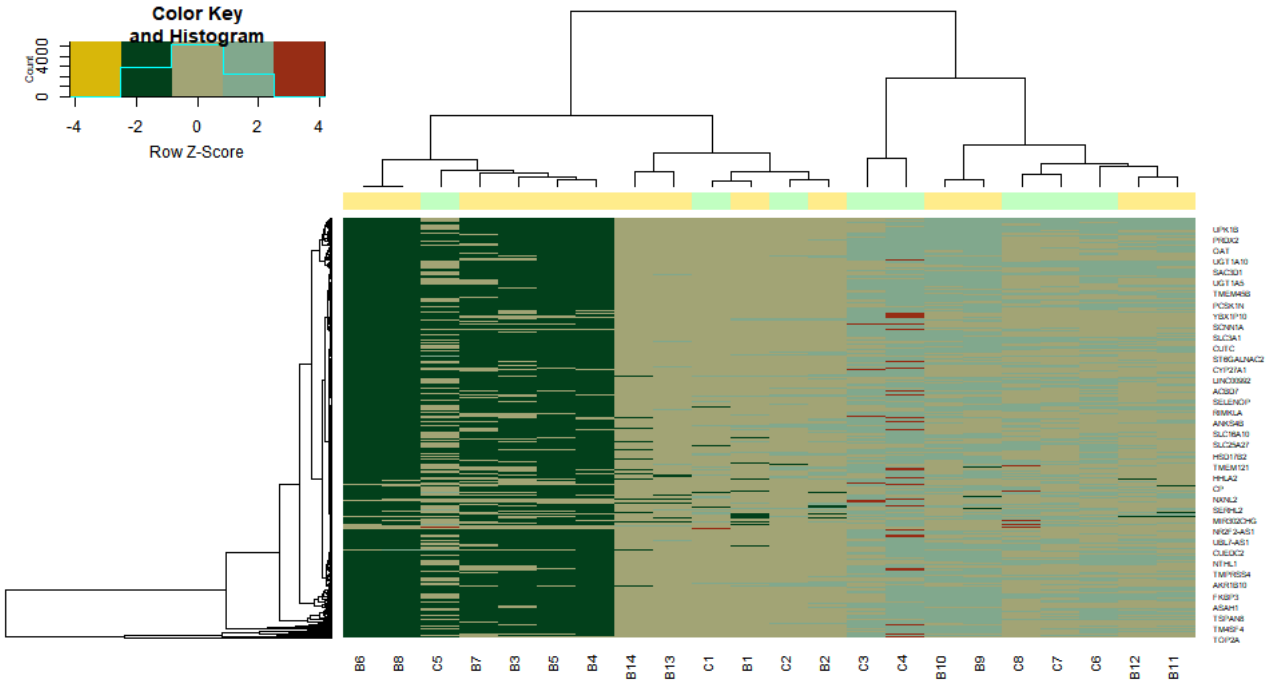


Figure 4

Heat map of downp regulated differentially expressed genes. Legend on the top left indicate log fold change of genes. (A1 – A8 = Mock samples; B1 – B14 = SARS-CoV-2 infection samples)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and Histogram
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4000
0
-4
-2
0
2
4
Row Z-Score
B6
B8
C5
B7
B3
B5
B4
B14
B13
C1
B1
C2
B2
C3
C4
B10
B9
C8
C7
C6
B12
B11

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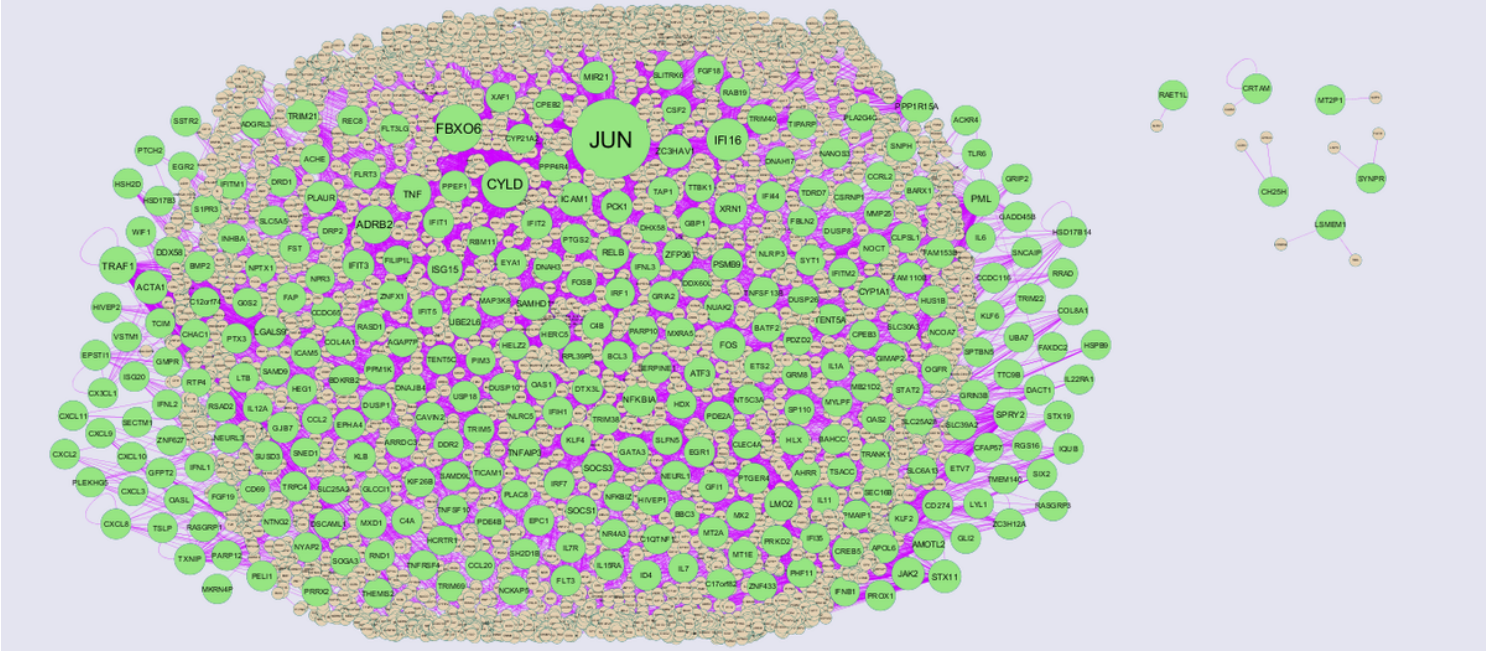
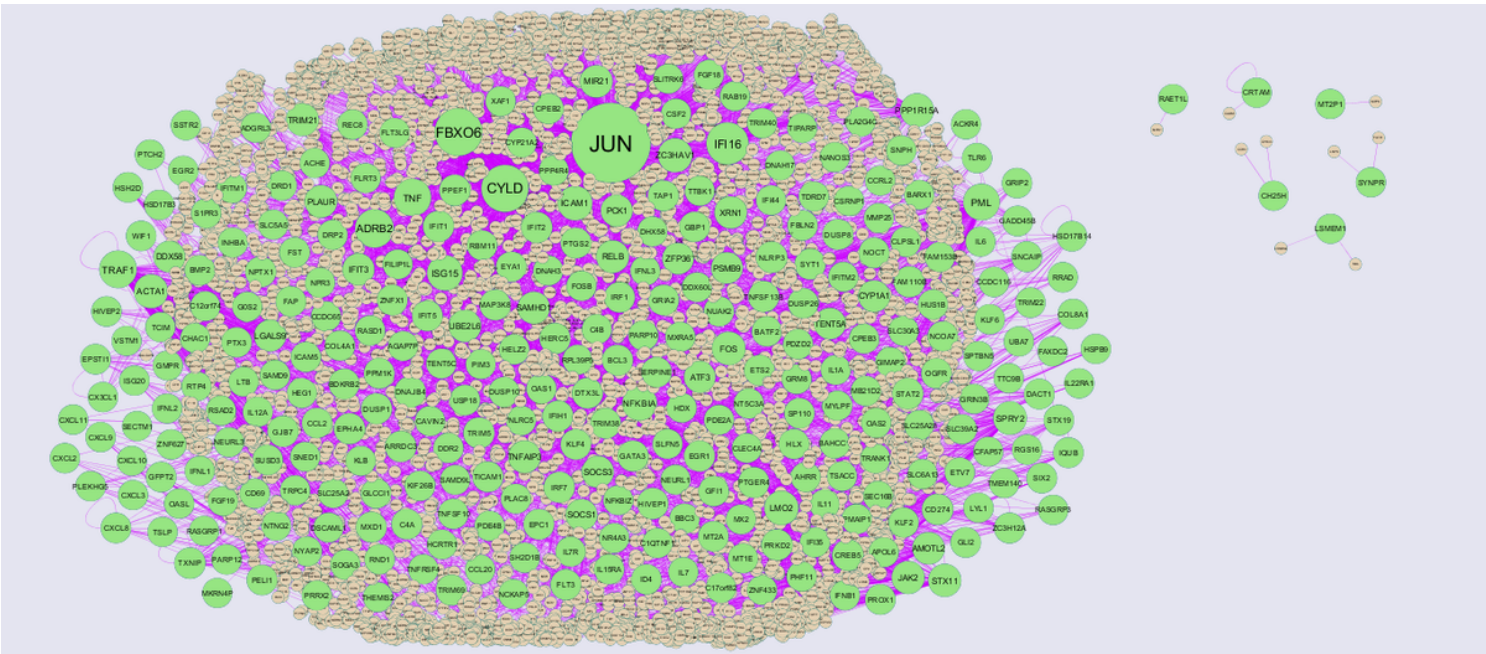


Figure 5

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



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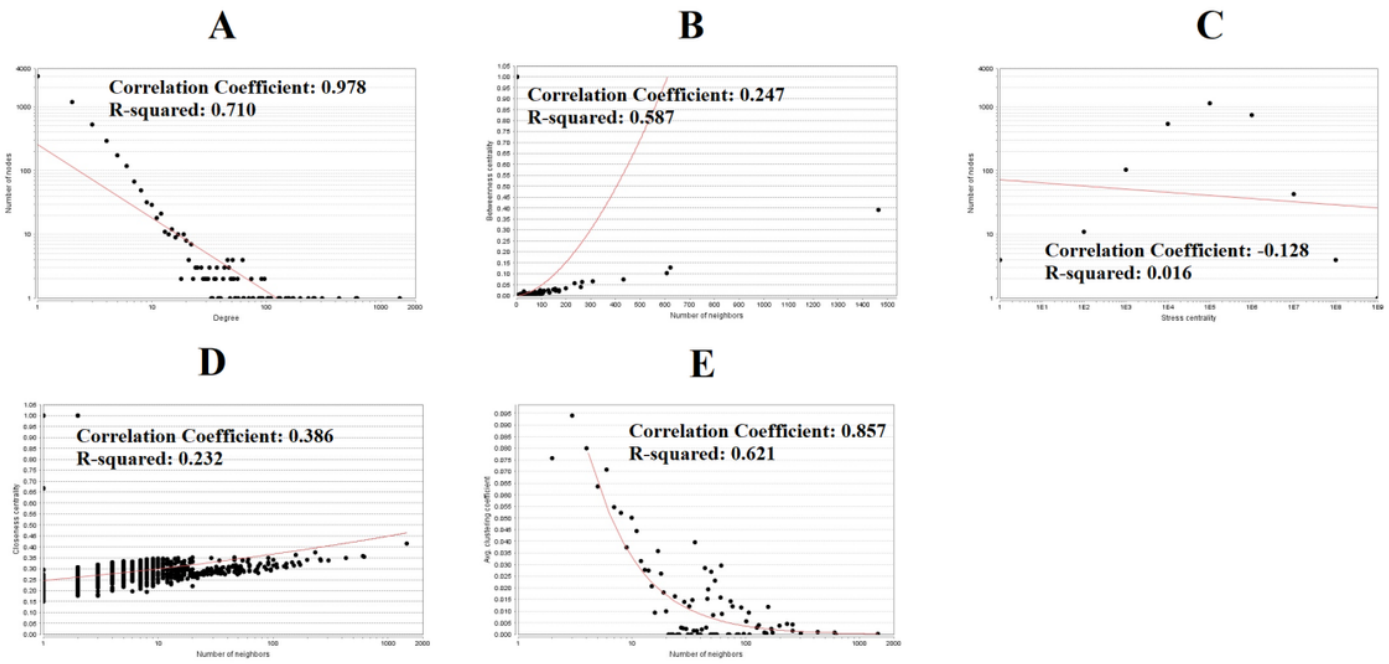
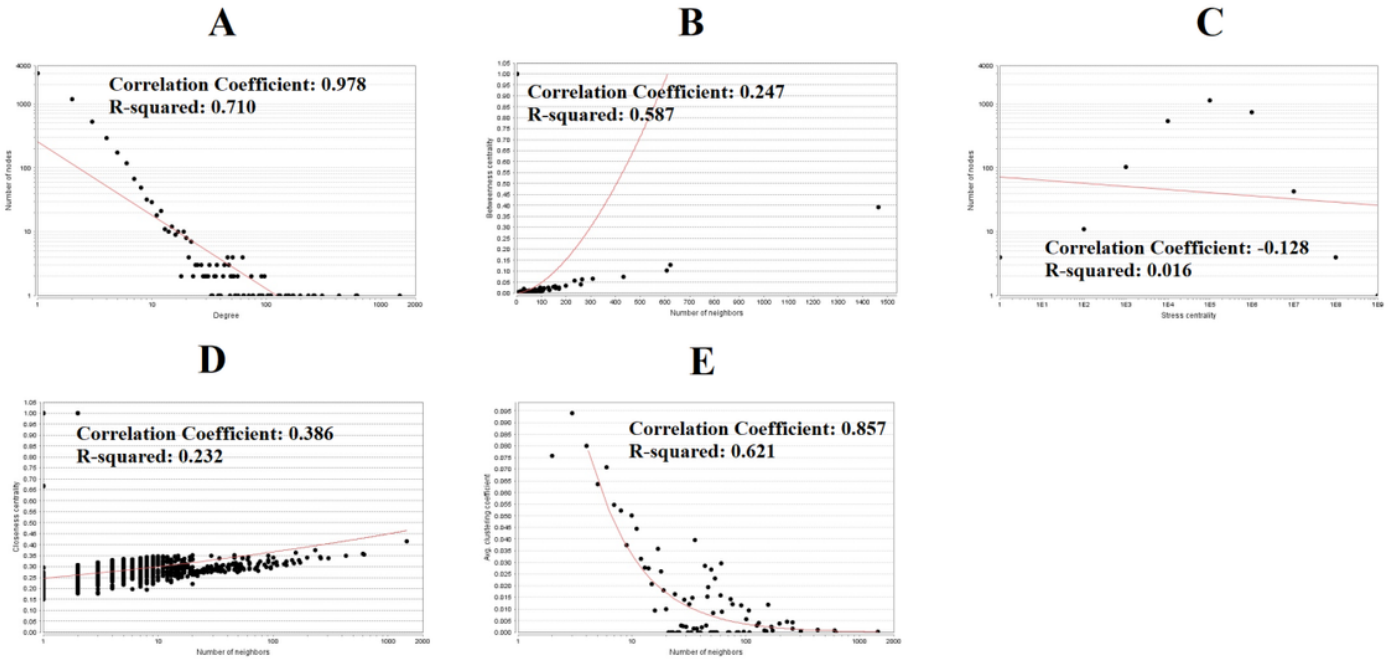


Figure 6

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



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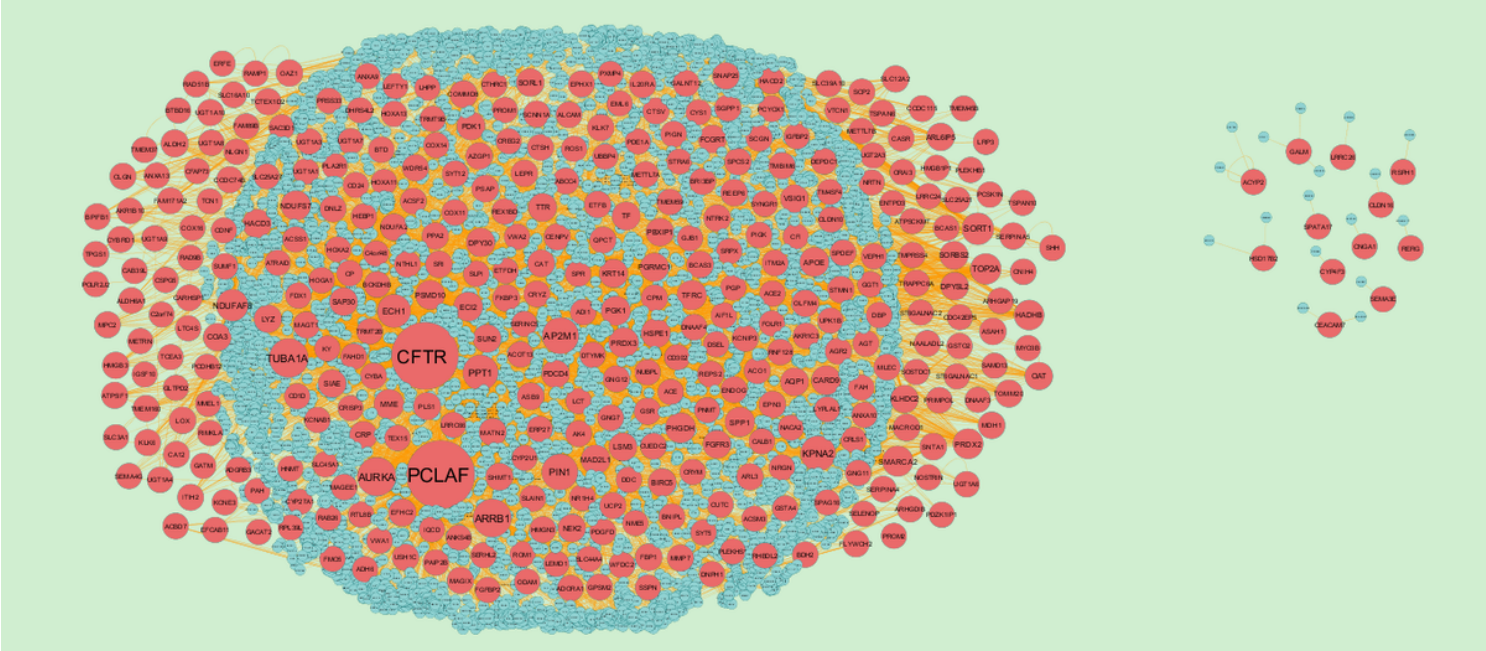


Figure 7

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

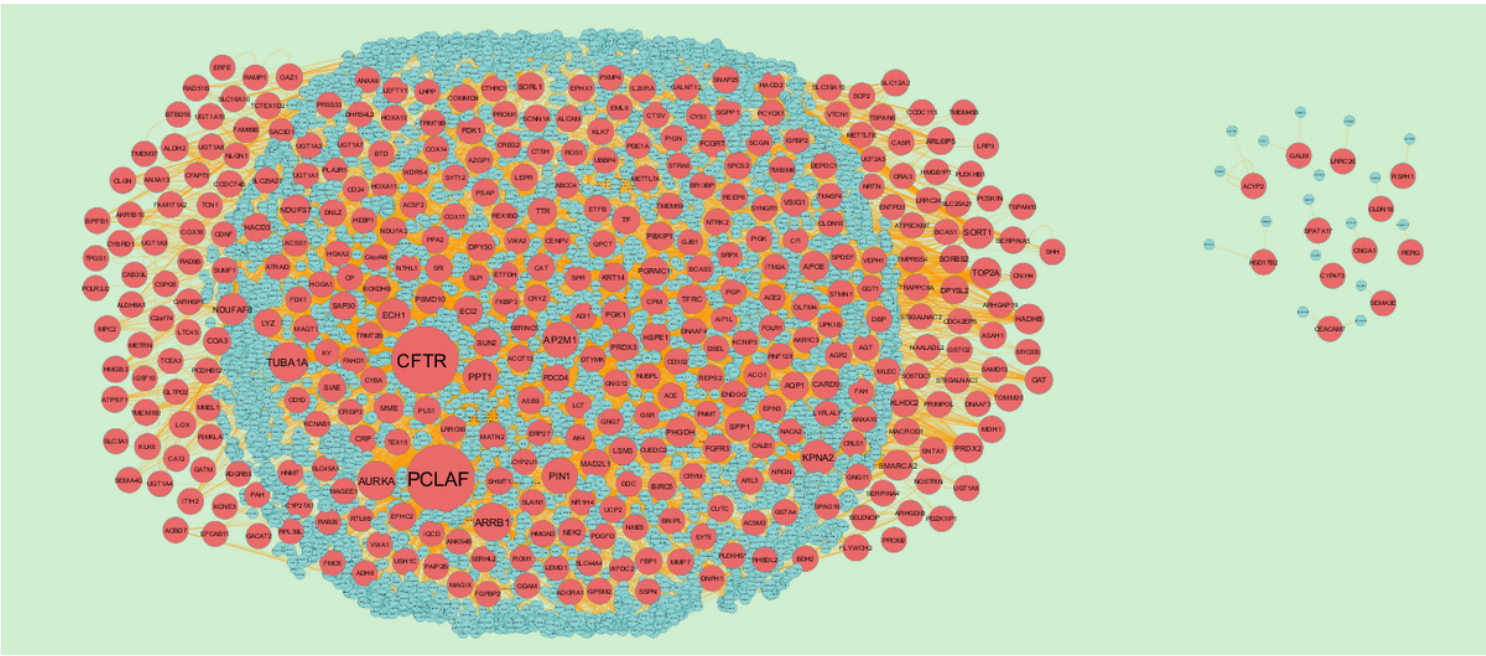


Figure 7

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

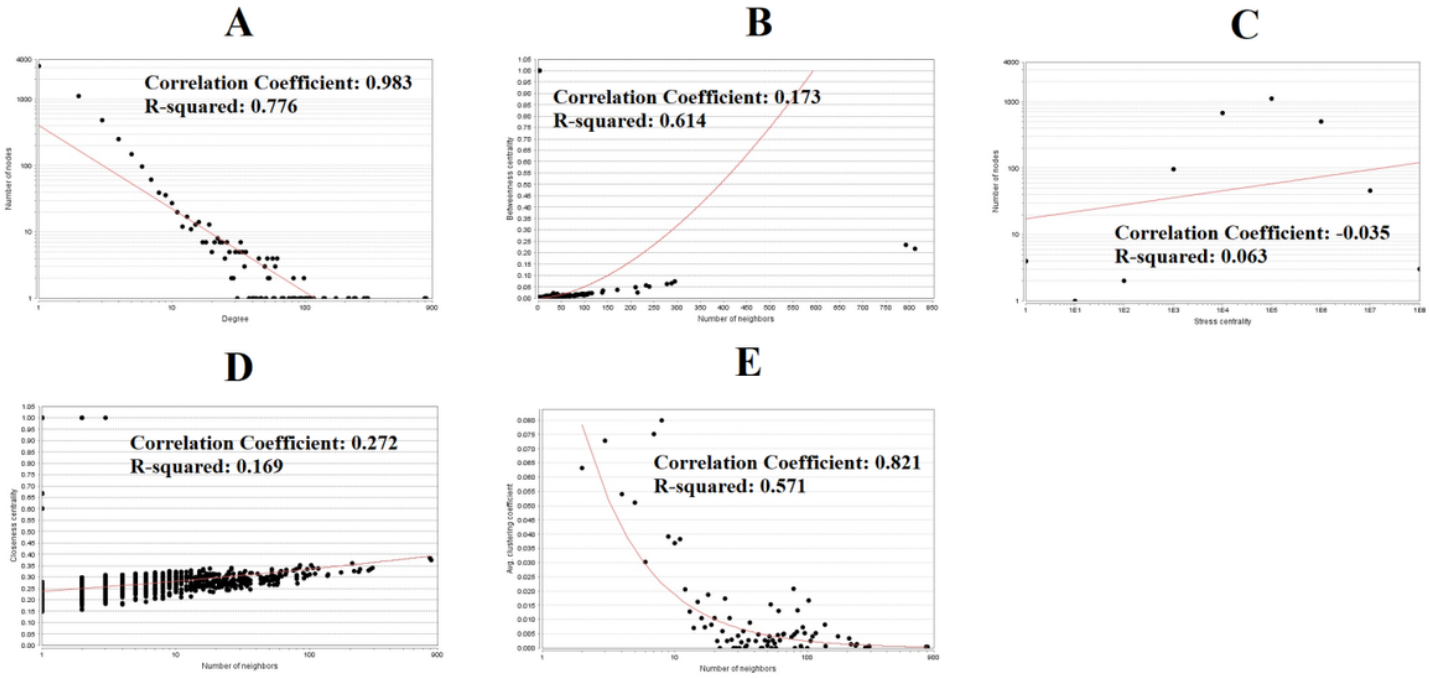
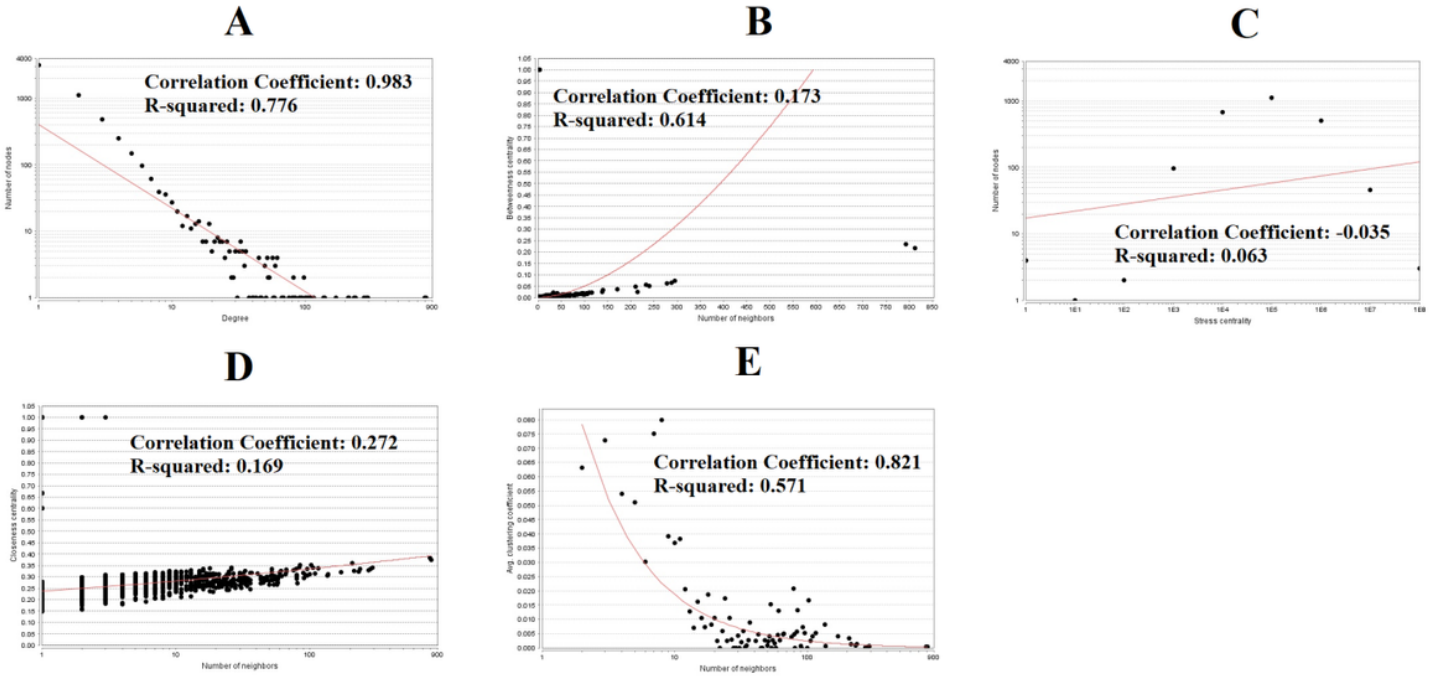


Figure 8

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



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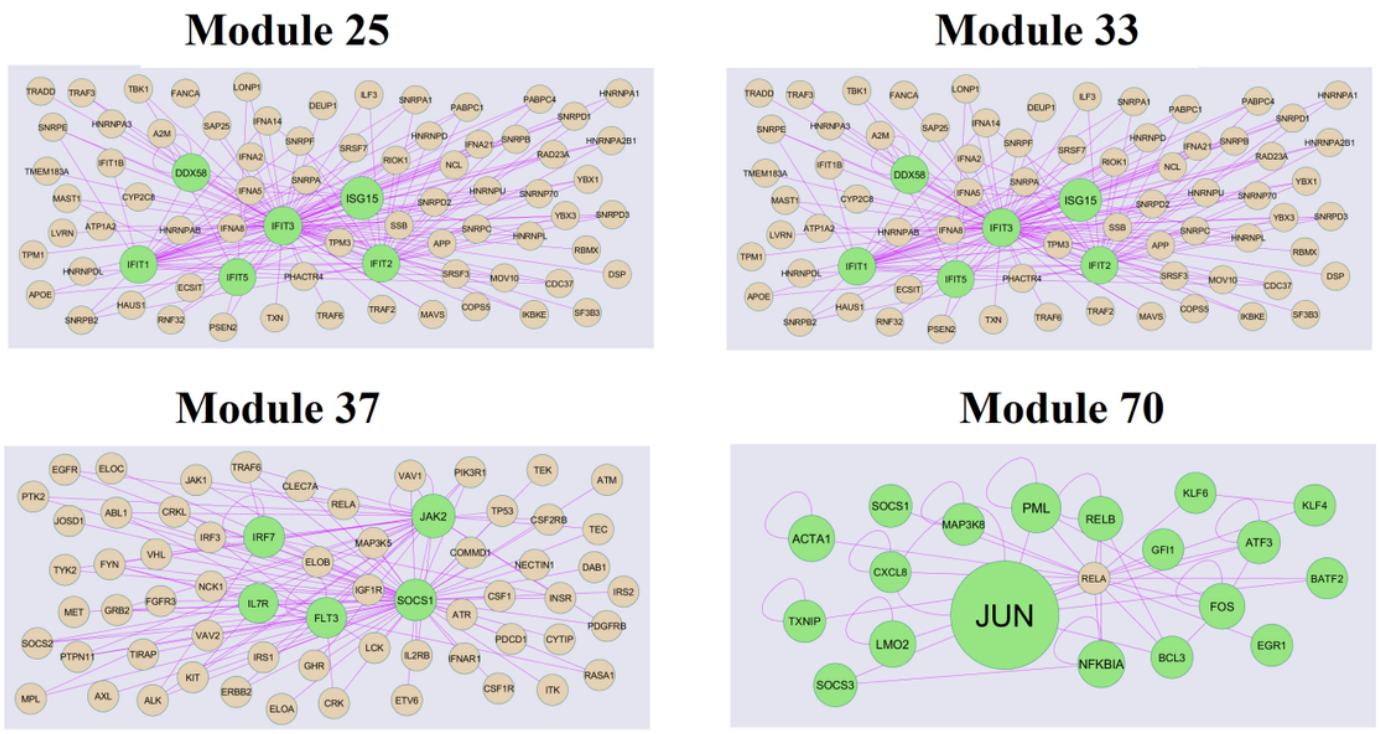
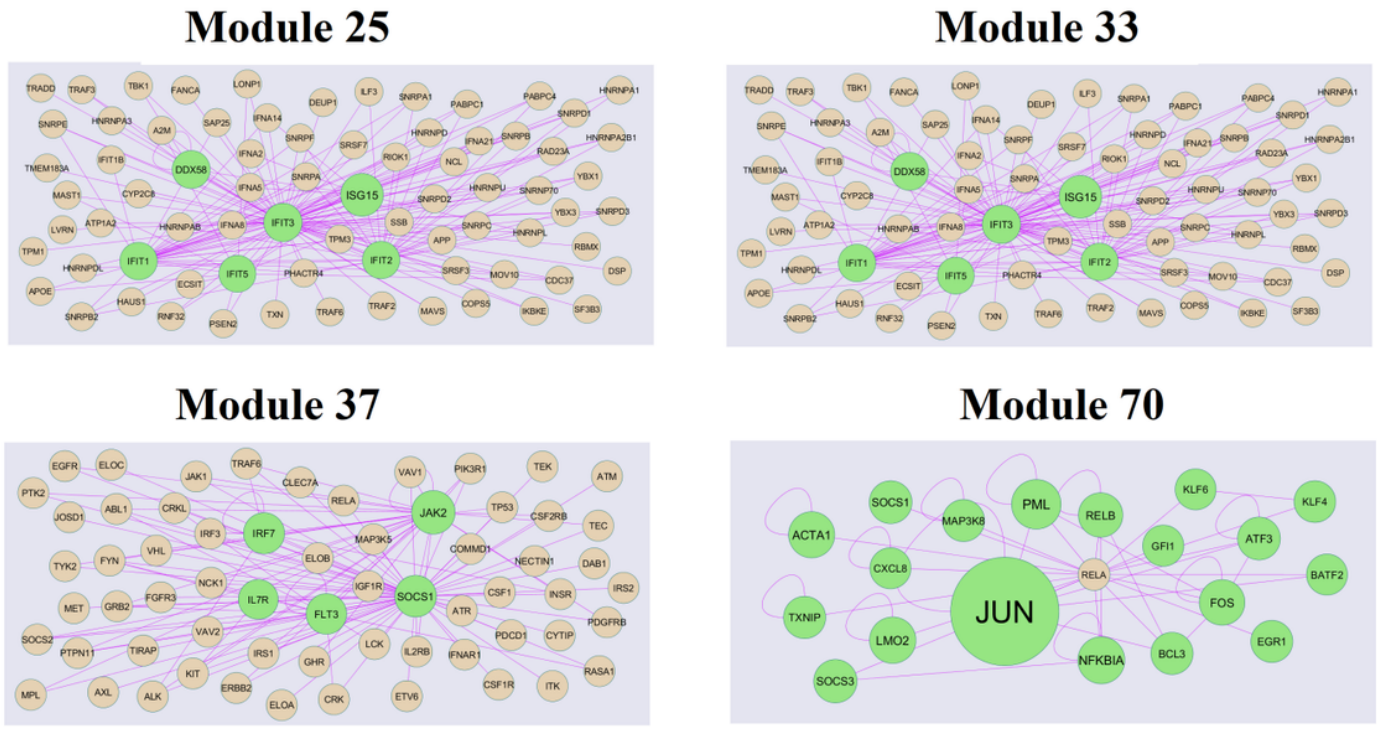


Figure 9

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


Module 25
Module 33
Module 37
Module 70
ISG15
IFIT3
IFIT1
IFIT2
IFIT5
DDX58
JAK2
IRF7
IL7R
FLT3
SOCS1
JUN
FOS
PML
RELB
RELA
NFKBIA
MAP3K8
SOCS3
LMO2
TXNIP
CXCL8
ACTA1
GFI1
ATF3
BATF2
BCL3
EGR1
KLF6
KLF4

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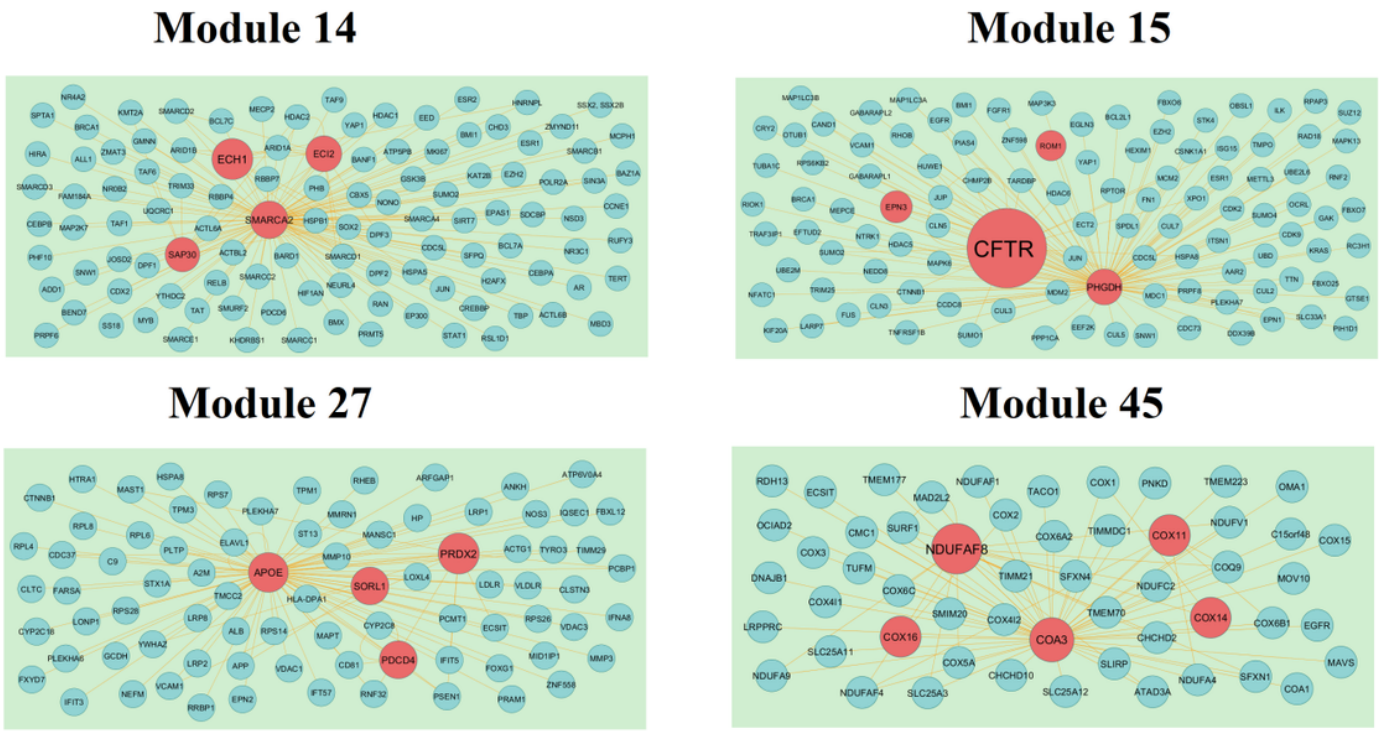


Figure 10

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

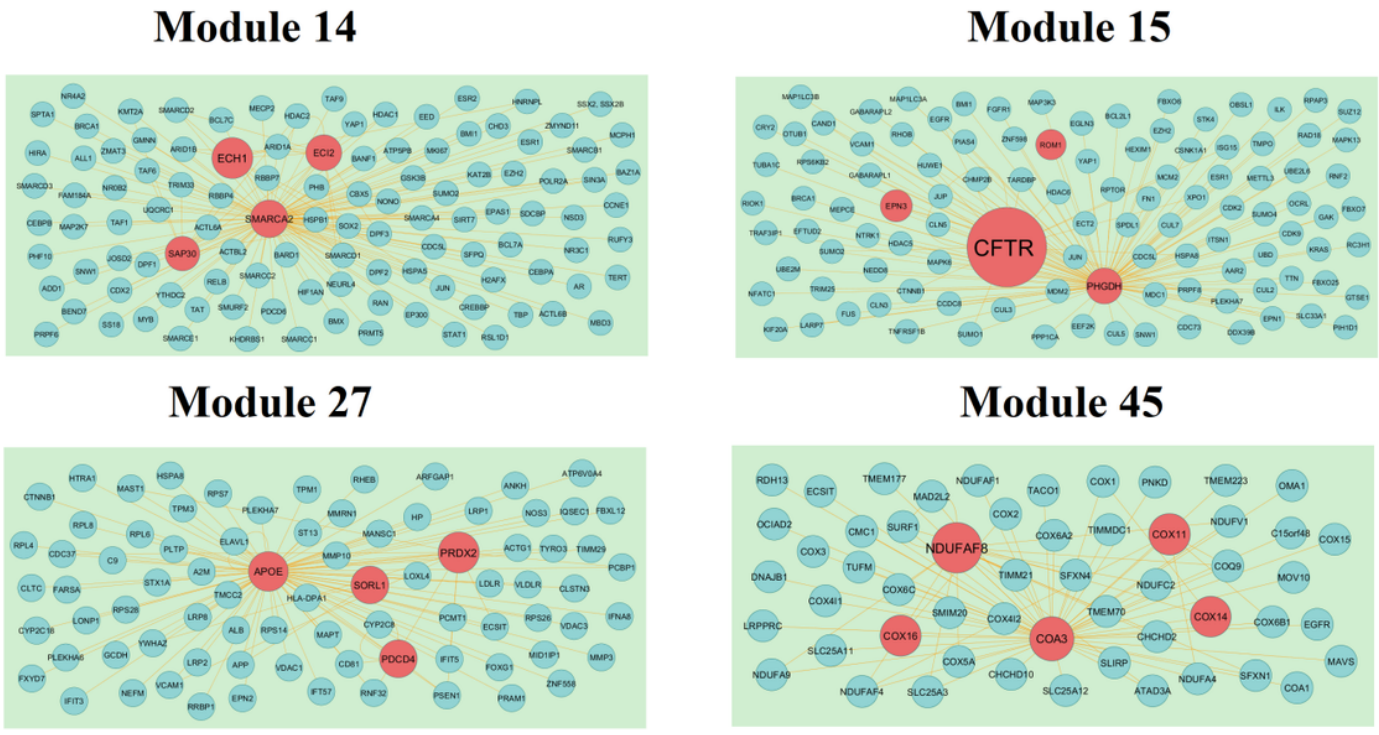


Figure 10

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

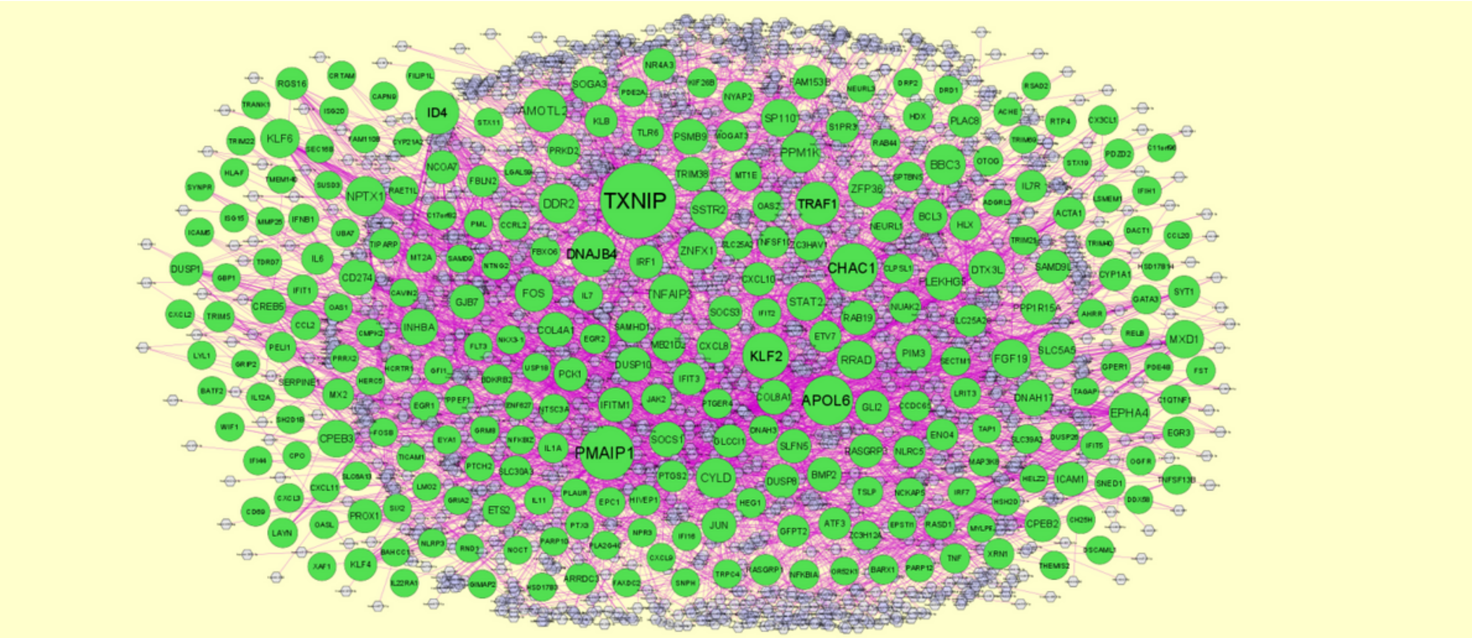
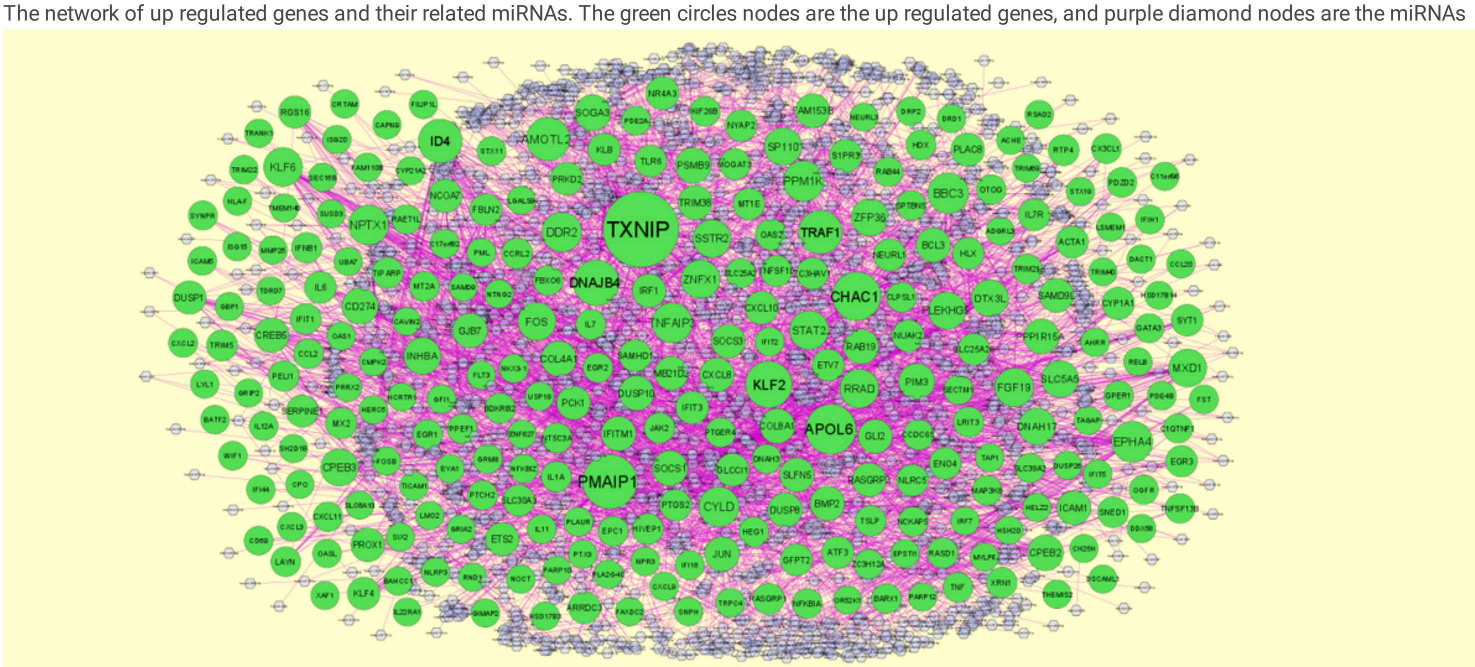


Figure 11

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



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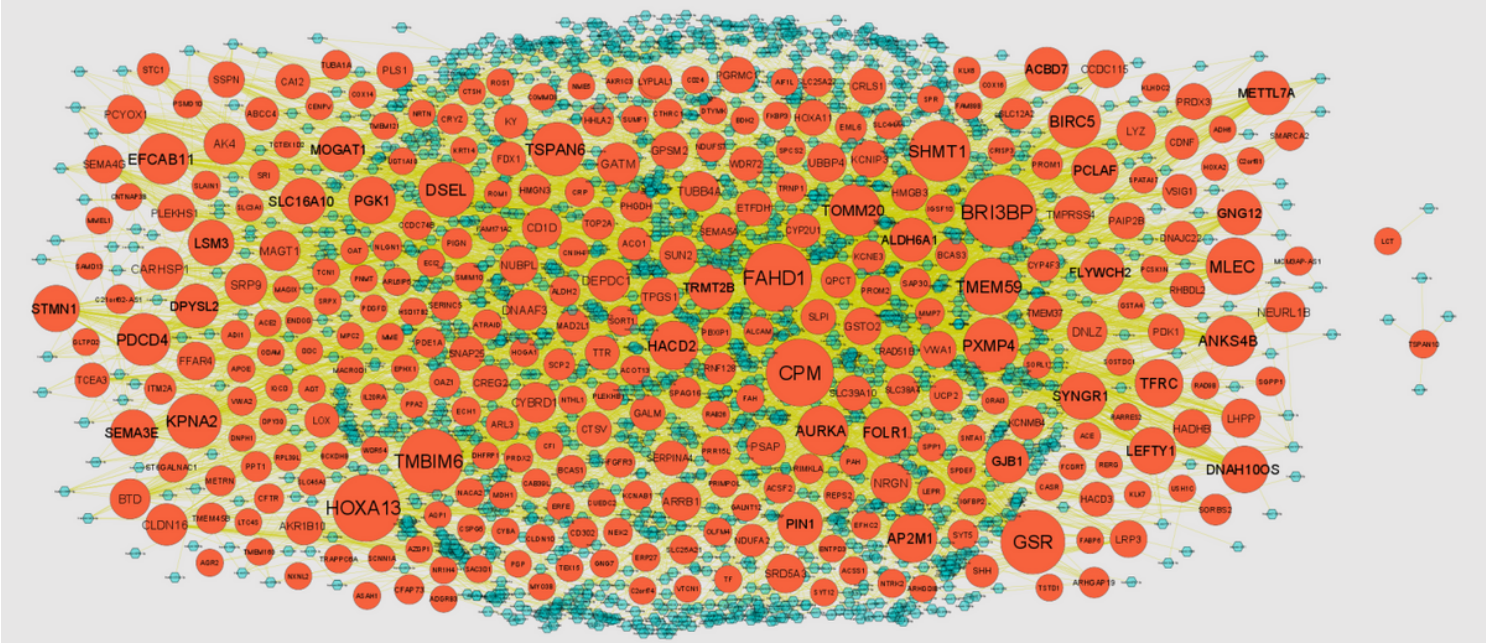


Figure 12

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

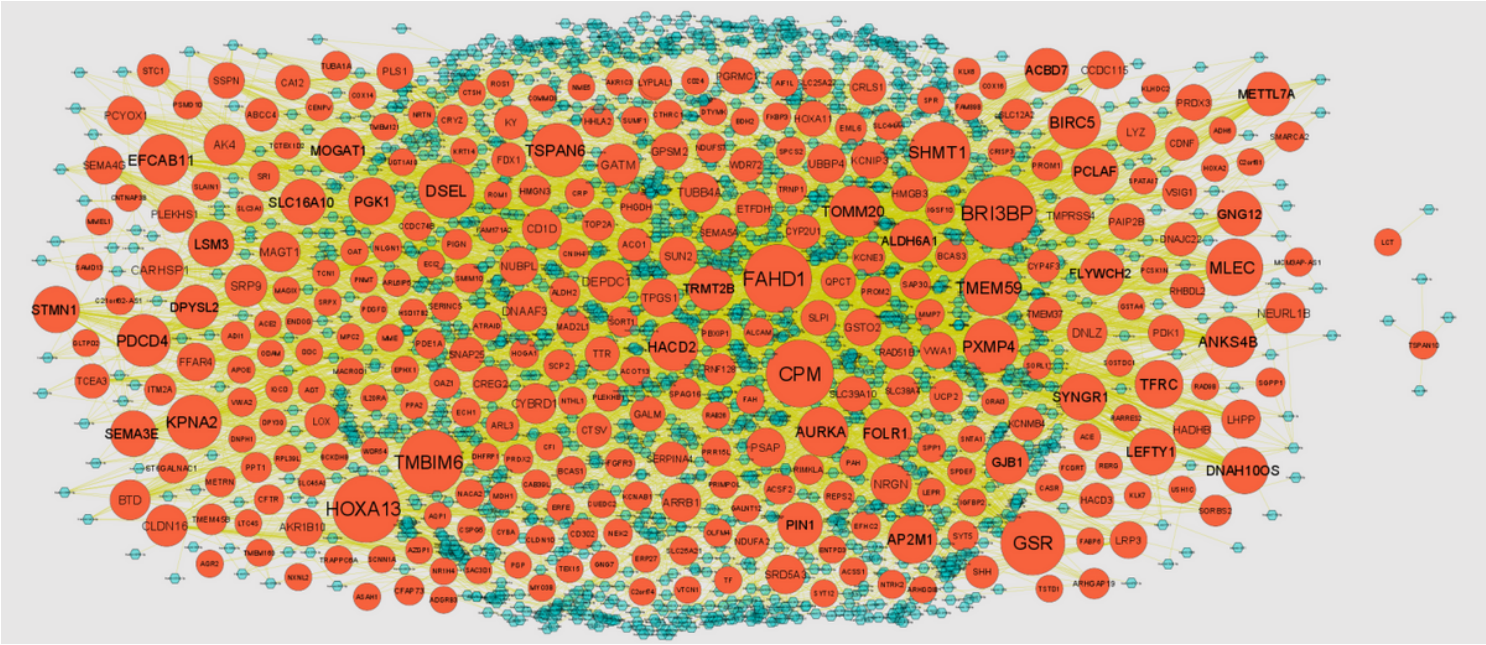


Figure 12

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

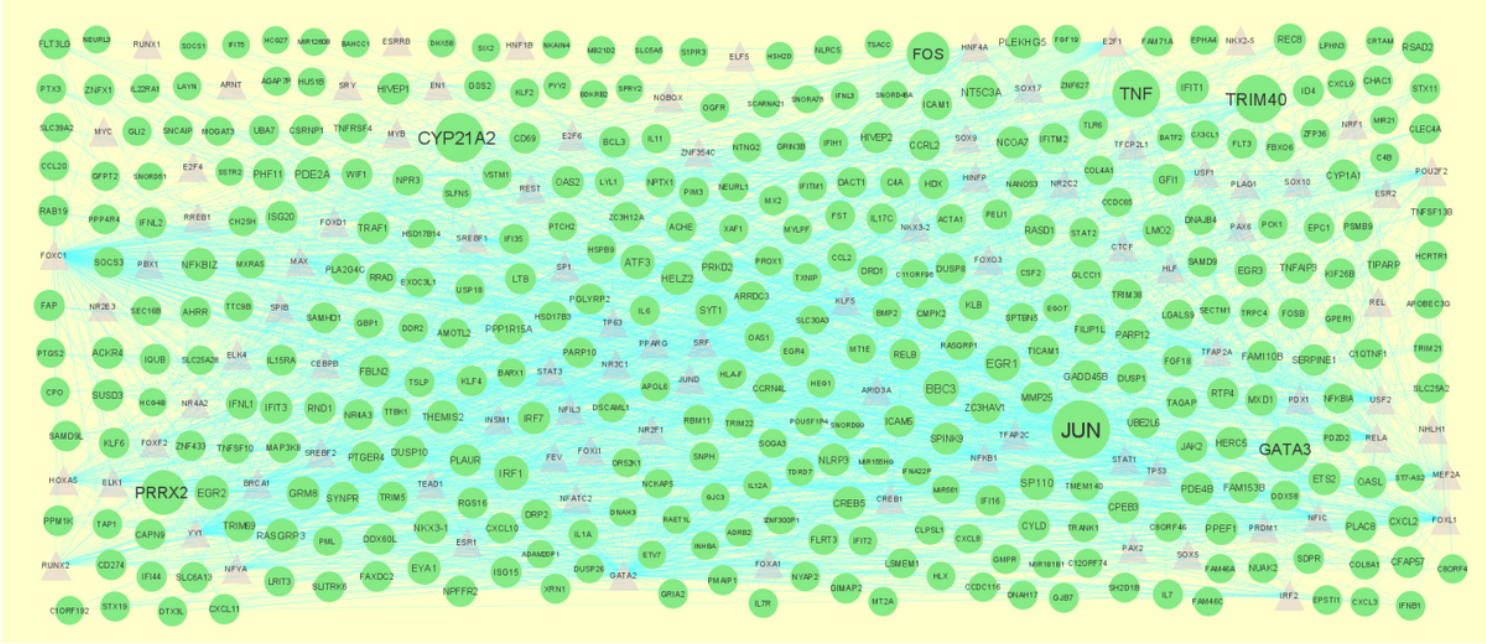
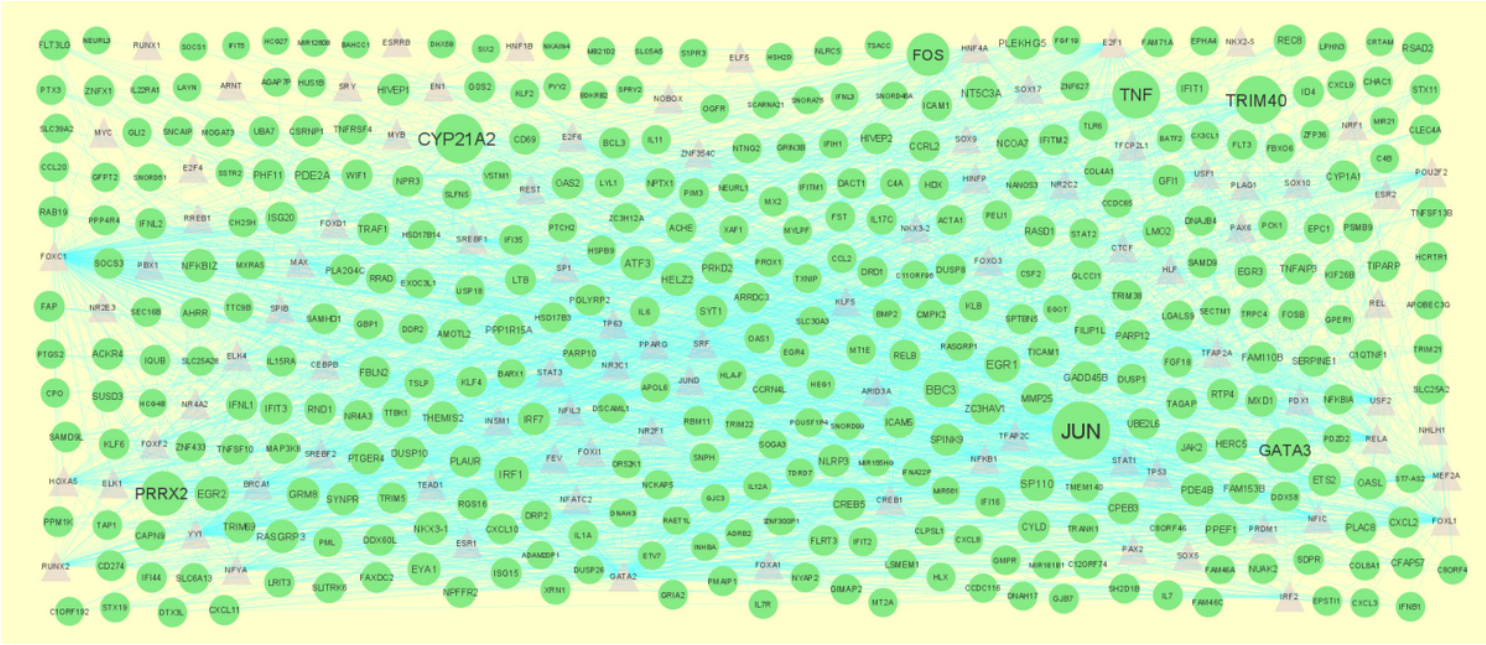


Figure 13

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



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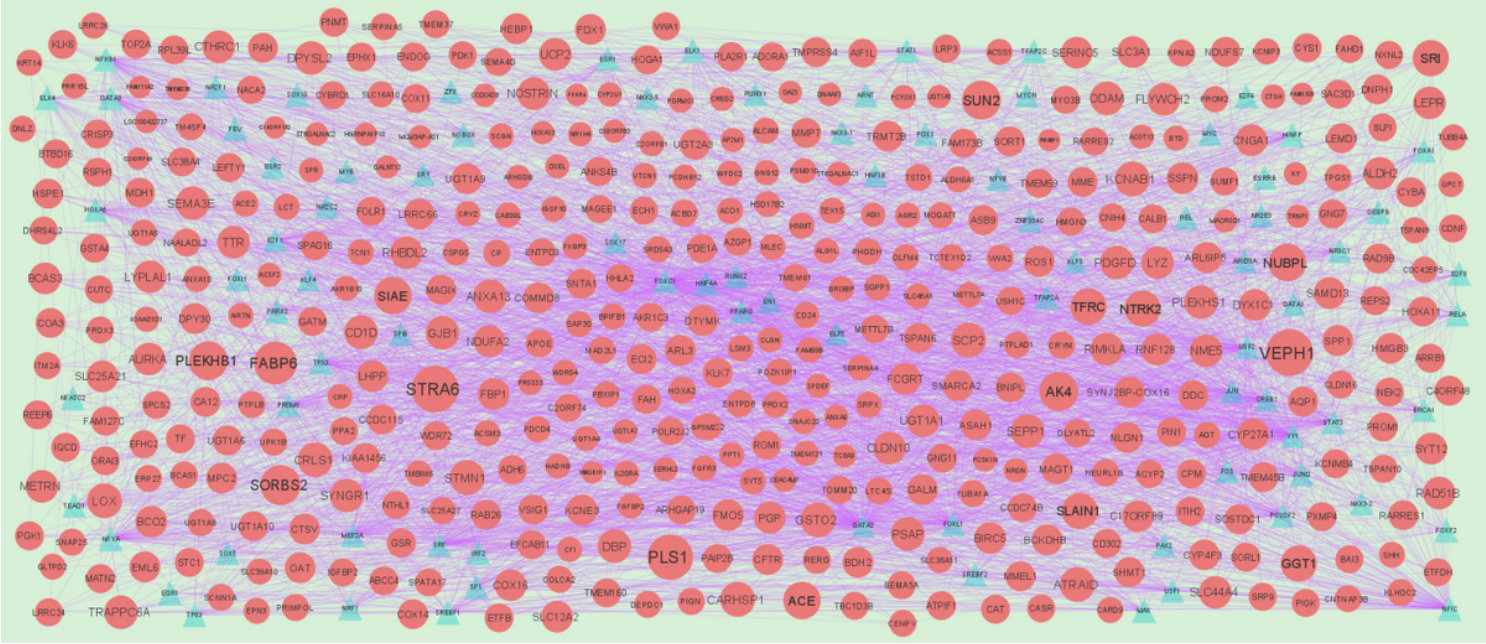


Figure 14

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

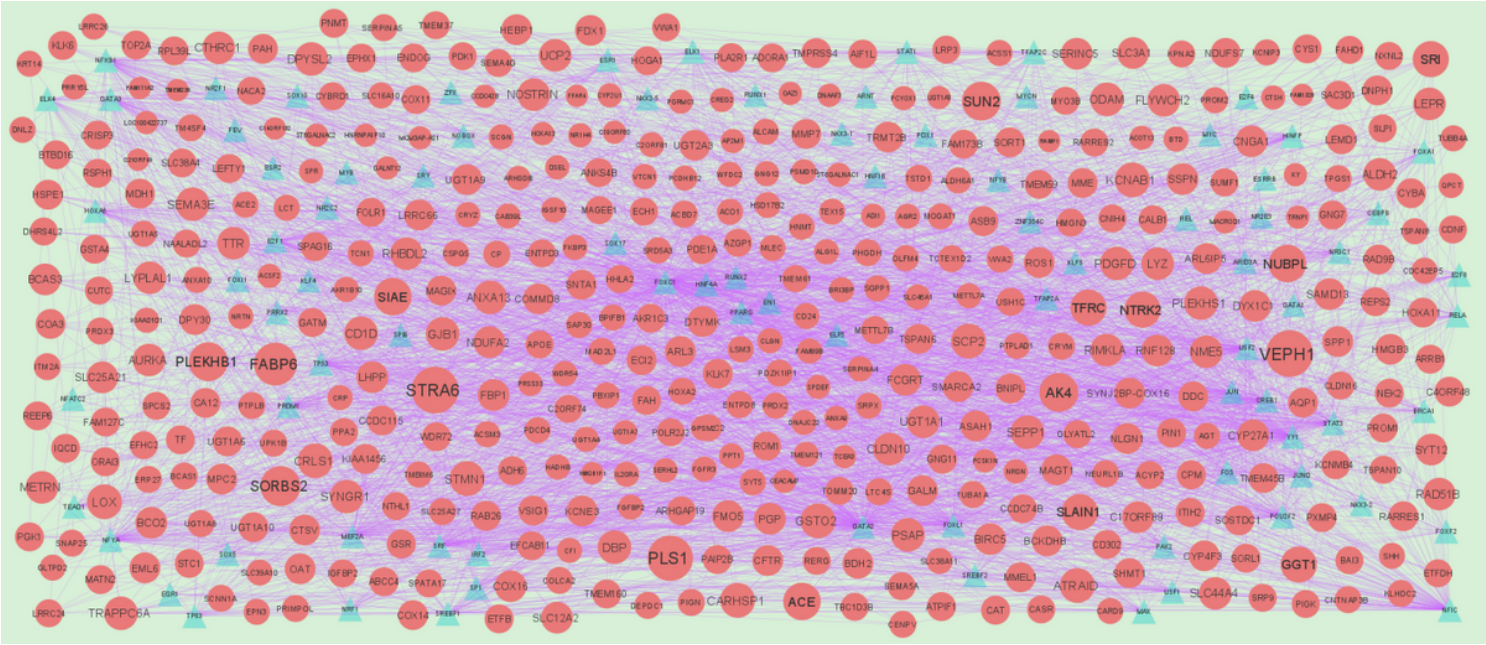


Figure 14

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

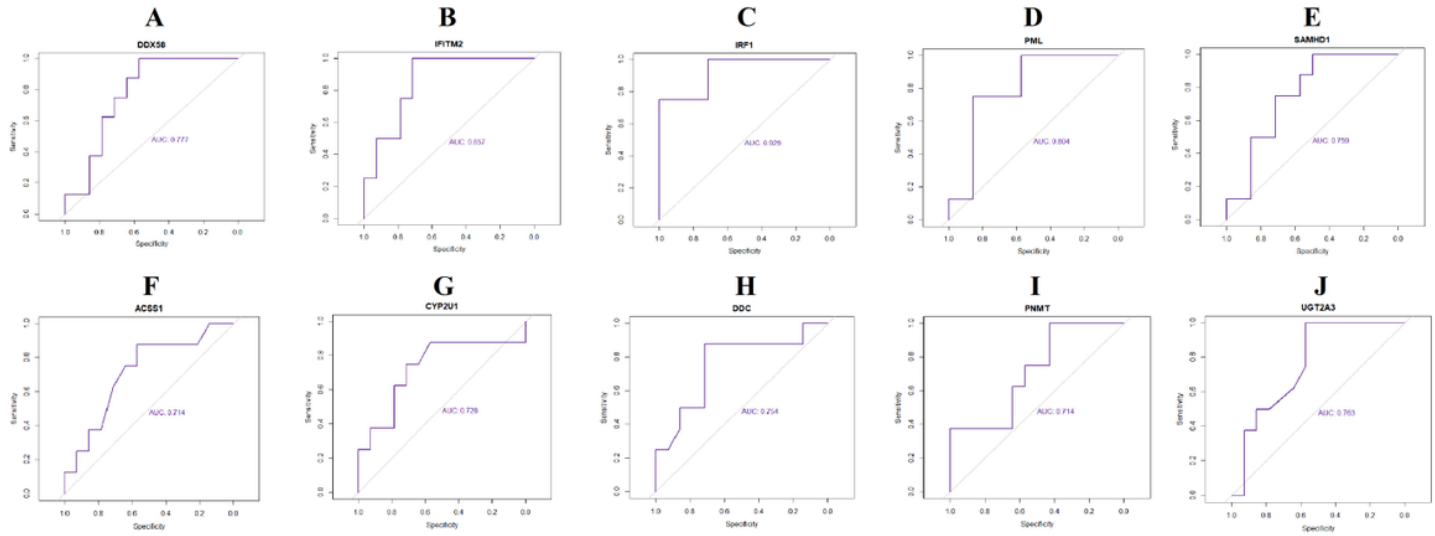
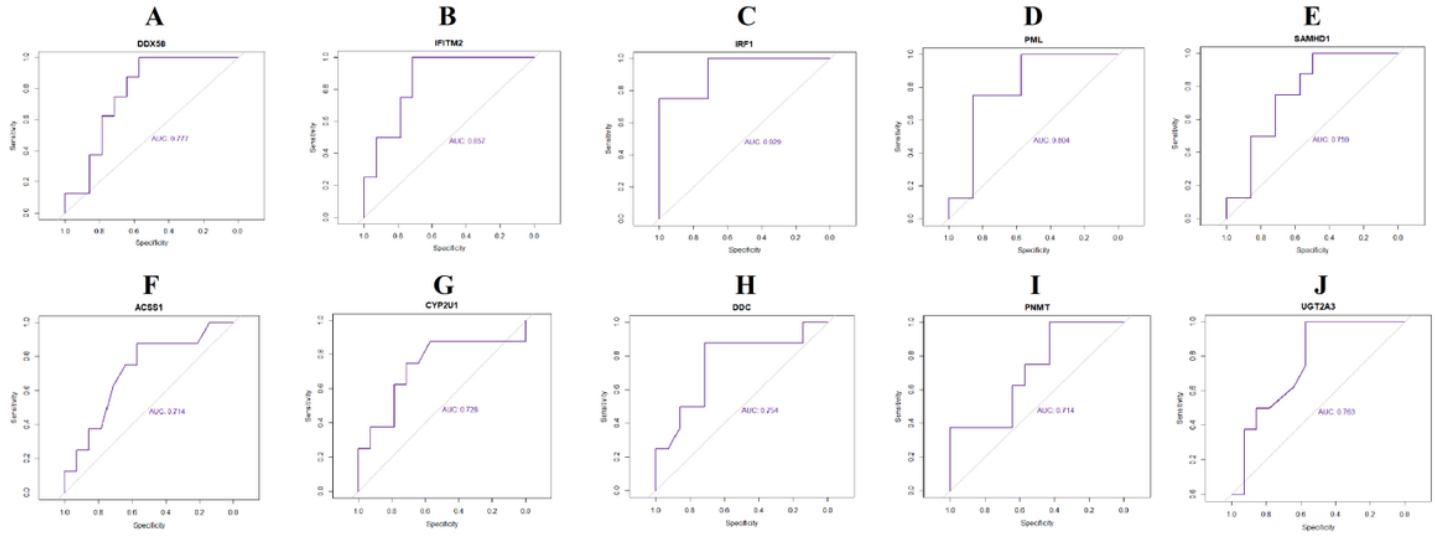


Figure 15

ROC curve validated the sensitivity, specificity of hub genes as a predictive biomarker for SARS-CoV-2 infection. A) DDX58 B) IFITM2 C) IRF1 D) PML E) SAMHD1 F) ACSS1 G) CYP2U1 H) DDC I) PNMT J) UGT2A3



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