Identification of candidate biomarkers and therapeutic agents for heart failure by bioinformatics analysis

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Abstract

Heart failure (HF) is a heterogeneous clinical syndrome and affects millions of people all over the world. HF occurs when the cardiac overload and injury, which is a worldwide complaint. The aim of this study was to screen and verify hub genes involved in developmental HF as well as to explore active drug molecules. The expression profiling by high throughput sequencing of GSE141910 dataset was downloaded from the Gene Expression Omnibus (GEO) database, which contained 366 samples, including 200 heart failure samples and 166 non heart failure samples. The raw data was integrated to find differentially expressed genes (DEGs) and were further analyzed with bioinformatics analysis. Gene ontology (GO) and REACTOME enrichment analyses were performed via ToppGene; protein-protein interaction (PPI) networks of the DEGs was constructed based on data from the HiPPIE interactome database; modules analysis was performed; target gene - miRNA regulatory network and target gene - TF regulatory network were constructed and analyzed; hub genes were validated; molecular docking studies was performed. A total of 881 DEGs, including 442 up regulated genes and 439 down regulated genes were observed. Most of the DEGs were significantly enriched in biological adhesion, extracellular matrix, signaling receptor binding, secretion, intrinsic component of plasma membrane, signaling receptor activity, extracellular matrix organization and neutrophil degranulation. The top hub genes ESR1, PYHIN1, PPP2R2B, LCK, TP63, PCLAF, CFTR, TK1, ECT2 and FKBP5 were identified from the PPI network. Module analysis revealed that HF was associated with adaptive immune system and neutrophil degranulation. The target genes, miRNAs and TFs were identified from the target gene - miRNA regulatory network and target gene - TF regulatory network. Furthermore, receiver operating characteristic (ROC) curve analysis and RT-PCR analysis revealed that ESR1, PYHIN1, PPP2R2B, LCK, TP63, PCLAF, CFTR, TK1, ECT2 and FKBP5 might serve as prognostic, diagnostic biomarkers and therapeutic target for HF. The predicted targets of these active molecules were then confirmed. The current investigation identified a series of key genes and pathways that might be involved in the progression of HF, providing a new understanding of the underlying molecular mechanisms of HF.

Keywords: heart failure; differentially expressed genes; molecular docking; enrichment analysis; prognosis

Introduction

Heart failure (HF) is a cardiovascular disease characterized by tachycardia, tachypnoea, pulmonary rales, pleural effusion, raised jugular venous pressure, peripheral oedema and hepatomegaly [1]. Morbidity and mortality linked with HF is a prevalent worldwide health problem holding a universal position as the leading cause of death [2]. The numbers of cases of HF are rising globally and it has become a key health issue. According to a survey, the prevalence HF is expected to exceed 50% of the global population [3]. Research suggests that modification in multiple genes and signaling pathways are associated in controlling the advancement of HF. However, a lack of investigation on the precise molecular mechanisms of HF development limits the treatment efficacy of the disease at present.

Previous study showed that HF was related to the expression of MECP2 [4] and RBM20 [5]. Toll-Like receptor signaling pathway [6] and activin type II receptor signaling pathway [7] were liable for progression of HF. More investigations are required to focus on treatments that enhance the outcome of patients with HF, to strictly make the diagnosis of the disease based on screening of biomarkers. These investigations can upgrade prognosis of patients by lowering the risk of advancement of HF and related complications. So it is essential to recognize the mechanism and find biomarkers with a good specificity and sensitivity.

The recent high-throughput RNA sequencing data has been widely employed to screen the differentially expressed genes (DEGs) between normal samples and HF samples in human beings, which makes it accessible for us to further explore the entire molecular alterations in HF at multiple levels involving DNA, RNA, proteins, epigenetic alterations, and metabolism [8]. However, there still exist obstacles to put these RNA seq data in application in clinic for the reason that the number of DEGs found by expression profiling by high throughput sequencing were massive and the statistical analyses were also too sophisticated [9-10]

In this study, first, we had chosen dataset GSE141910 from Gene Expression Omnibus (GEO) ([http:// www.ncbi.nlm.nih.gov/geo/](http://www.ncbi.nlm.nih.gov/geo/)) [11]. Second, we applied for

limma tool in R software to obtain the differentially expressed genes (DEGs) in this dataset. Third, the ToppGene was used to analyze these DEGs including molecular function (MF), cellular component (CC), biological process (BP) and REACTOME pathways. Fourth, we established protein-protein interaction (PPI) network and then applied Cytotype PEWCC1 for module analysis of the DEGs which would identify some hub genes. Fifth, we established target gene - miRNA regulatory network and target gene - TF regulatory network. In addition, we further validated the hub genes by receiver operating characteristic (ROC) curve analysis and RT-PCR analysis. Finally, we performed molecular docking studies for over expressed hub genes. Results from the present investigation might provide new vision into potential prognostic and therapeutic targets for HF.

Materials and Methods

Data resource

Expression profiling by high throughput sequencing with series number GSE141910 based on platform GPL16791 was downloaded from the GEO database. The dataset of GSE141910 contained 200 heart failure samples and 166 non heart failure samples. It was downloaded from the GEO database in NCBI based on the platform of GPL16791 Illumina HiSeq 2500 (Homo sapiens).

Identification of DEGs in HF

DEGs of dataset GSE141910 between HF groups and non heart failure groups were respectively analyzed using the limma package in R [12]. Fold changes (FCs) in the expression of individual genes were calculated and DEGs with $P < 0.05$, $|\log FC| > 1.158$ for up regulated genes and $|\log FC| < -0.83$ for down regulated genes were considered to be significant. Hierarchical clustering and visualization were used by Heat-map package of R.

Functional enrichment analysis

Gene Ontology (GO) analysis and REACTOME pathway analysis were performed to determine the functions of DEGs using the ToppGene (ToppFun) (<https://toppgene.cchmc.org/enrichment.jsp>) [13] GO terms (<http://geneontology.org/>) [14] included biological processes (BP), cellular components (CC) and molecular functions (MF) of genomic products.

REACTOME (<https://reactome.org/>) [15] analyzes pathways of important gene products. ToppGene is a bioinformatics database for analyzing the functional interpretation of lists of proteins and genes. The cutoff value was set to $P < 0.05$.

Protein–protein interaction network construction and module screening

PPI networks are used to establish all protein coding genes into a massive biological network that serves an advance compassionate of the functional system of the proteome [16]. The HiPPIE interactome (<https://cbdm.uni-mainz.de/hippie/>) [17] database furnish information regarding predicted and experimental interactions of proteins. In the current investigation, the DEGs were mapped into the HiPPIE interactome database to find significant protein pairs with a combined score of >0.4 . The PPI network was subsequently constructed using Cytoscape software, version 3.8.2 (www.cytoscape.org) [18]. The nodes with a higher node degree [19], higher betweenness centrality [20], higher stress centrality [21] and higher closeness centrality [22] were considered as hub genes. Additionally, cluster analysis for identifying significant function modules with a degree cutoff >2 in the PPI network was performed using the PEWCC1 (<http://apps.cytoscape.org/apps/PEWCC1>) [23] in Cytoscape.

Target gene - miRNA regulatory network construction

The miRNet database (<https://www.mirnet.ca/>) [24] contains information on miRNA and the regulated genes. Using information collected from the miRNet database, hub genes were matched with their associated miRNA. The target gene - miRNA regulatory network then was constructed using Cytoscape software.

Target gene - TF regulatory network construction

The NetworkAnalyst database (<https://www.networkanalyst.ca/>) [25] contains information on TF and the regulated genes. Using information collected from the NetworkAnalyst database, hub genes were matched with their associated TF. The target gene - TF regulatory network then was constructed using Cytoscape software.

Receiver operating characteristic (ROC) curve analysis

Then ROC curve analysis was implemented to classify the sensitivity and specificity of the hub genes for HF diagnosis and we investigated how large the area under the curve (AUC) was by using the statistical package pROC in R software [26].

RT-PCR analysis

Total RNA was isolated from H9c2 (ATCC® CRL-1446) and VH2 (ATCC® CCL-140) using the TRI Reagent® (Sigma, USA). cDNA was synthesized using 2.0 µg of total RNA with the Reverse transcription cDNA kit (Thermo Fisher Scientific, Waltham, MA, USA). The 7 Flex real-time PCR system (Thermo Fisher Scientific, Waltham, MA, USA) was employed to detect the relative mRNA expression. The relative expression levels were determined by the $2^{-\Delta\Delta C_t}$ method and normalized to internal control beta-actin [27]. All RT-PCR reactions were performed in triplicate. The primers used to explore mRNA expression of ten hub genes were listed in Table 1.

Identification of Candidate Small Molecules

SYBYL-X 2.0 perpetual drug design software has been used for surflex-docking studies of the designed novel molecules and the standard on over expressed genes of PDB protein. Using ChemDraw Software, all designed molecules and standards were sketched, imported and saved using open babel free software in sdf. template. The protein of over expressed genes of ESR1, LCK, PPP2R2B, TP63 and their co-crystallised protein of PDB code 4PXM, 1KSW, 2HV7, 3VD8 and 6RU6 were extracted from Protein Data Bank [28-31]. Optimizations of the designed molecules were performed by standard process by applying Gasteiger Huckel (GH) charges together with the TRIPOS force field. In addition, energy minimization was achieved using MMFF94s and MMFF94 algorithm methods. The preparation of the protein was done after protein incorporation. The co-crystallized ligand and all water molecules have been eliminated from the crystal structure; more hydrogen's were added and the side chain was set, TRIPOS force field was used for the minimization of structure. The interaction efficiency of the compounds with the receptor was expressed in kcal / mol units by the Surflex-Dock score. The best location was integrated into the molecular region by the interaction between the protein and the ligand. Using Discovery Studio Visualizer, the visualisation of ligand interaction with receptor is performed.

Results

Identification of DEGs in HF

We identified 881 DEGs in the GSE141910 dataset using the limma package in R. Based on the limma analysis, using the adj P val < 0.05 , $|\log FC| > 1.158$ for up regulated genes and $|\log FC| < -0.83$ for down regulated genes criteria, a total of 881 DEGs were identified, consisting of 442 genes were up regulated and 439 genes were down regulated. The DEGs are listed in Table 2. The volcano plot for DEGs is illustrated in Fig. 1. Fig. 2 is the hierarchical clustering heat-map.

Functional enrichment analysis

Results of GO analysis showed that the up regulated genes were significantly enriched in BP, CC, and MF, including biological adhesion, regulation of immune system process, extracellular matrix, cell surface, signaling receptor binding and molecular function regulator (Table 3); the down regulated genes were significantly enriched in BP, CC, and MF, including secretion, defense response, intrinsic component of plasma membrane, whole membrane, signaling receptor activity and molecular transducer activity (Table 3). Pathway analysis showed that the up regulated genes were significantly enriched in extracellular matrix organization and immunoregulatory interactions between a lymphoid and a non-lymphoid cell (Table 4); the down regulated genes were significantly enriched in neutrophil degranulation and SLC-mediated transmembrane transport (Table 4).

Protein-protein interaction (PPI) network and module analysis

Based on the HiPPIE interactome database, the PPI network for the DEGs (including 6541 nodes and 13909 edges) was constructed (Fig. 3A). Up regulated gene with higher node degree, higher betweenness centrality, higher stress centrality and higher closeness centrality were as follows: ESR1, PYHIN1, PPP2R2B, LCK, TP63 and so on. Down regulated genes had higher node degree, higher betweenness centrality, higher stress centrality and higher closeness centrality were as follows PCLAF, CFTR, TK1, ECT2, FKBP5 and so on. The node degree, betweenness centrality, stress centrality and closeness centrality are listed in Table 5.

Additionally, two significant modules, including module 1 (10 nodes and 24 edges) and module 2 (5 nodes and 10 edges) (Fig. 3B) and module 3 (55 nodes and 115 edges), were acquired by PEWCC1 plug-in (Fig. 3C). Furthermore, GO terms and REACTOME pathways were significantly enriched by module 1, including adaptive immune system, immunoregulatory interactions between a lymphoid and a non-lymphoid cell, hemostasis, biological adhesion and regulation of immune system process. Meanwhile, the nodes in module 2 were significantly enriched in GO terms and REACTOME pathways, including neutrophil degranulation and secretion.

Target gene - miRNA regulatory network construction

Associations between 2063 miRNAs and their 319 target genes were collected from the target gene - miRNA regulatory network (Fig. 4). MiRNAs of hsa-mir-4533, hsa-mir-548ac, hsa-mir-548i, hsa-mir-5585-3p, hsa-mir-6750-3p, hsa-mir-200c-3p, hsa-mir-1273g-3p, hsa-mir-1244, hsa-mir-4789-3p and hsa-mir-766-3p, which exhibited a high degree of interaction, were selected from this network. Furthermore, the results also showed that FSCN1 was the target of hsa-mir-4533, ESR1 was the target of hsa-mir-548ac, TMEM30B was the target of hsa-mir-548i, SCN2B was the target of hsa-mir-5585-3p, CENPA was the target of hsa-mir-6750-3p, FKBP5 was the target of hsa-mir-200c-3p, PCLAF was the target of hsa-mir-1273g-3p, CEP55 was the target of hsa-mir-1244, ATP2A2 was the target of hsa-mir-4789-3p and TK1 was the target of hsa-mir-766-3p, and are listed in Table 6.

Target gene - TF regulatory network construction

Associations between 330 TFs and their 247 target genes were collected from the target gene - TF regulatory network (Fig. 5). TFs of ESRRA, RERE, HMG20B, THRAP3, ATF1, MXD3, ARID4B, CBFB, TAF7 and CREM, which exhibited a high degree of interaction, were selected from this network. Furthermore, the results also showed that FSCN1 was the target of ESRRA, APOA1 was the target of RERE, COL1A1 was the target of HMG20B, HBB was the target of THRAP3, LCK was the target of ATF1, SOCS3 was the target of MXD3, BCL6 was the target of ARID4B, FKBP5 was the target of CBFB, ANLN was the target of TAF7 and ATP2A2 was the target of CREM, and are listed in Table 6.

Receiver operating characteristic (ROC) curve analysis

First of all, we performed the ROC curve analysis among 10 hub genes based on the GSE141910. The results showed that ESR1, PYHIN1, PPP2R2B, LCK, TP63, PCLAF, CFTR, TK1, ECT2 and FKBP5 achieved an AUC value of $\square > \square 0.7$, demonstrating that these ten genes have high sensitivity and specificity for HF, suggesting they can be served as biomarkers for the diagnosis of HF (Fig. 6).

RT-PCR analysis

RT-PCR was used to validate the hub genes between normal and HF cell lines. The results suggested that the mRNA expression level of ESR1, PYHIN1, PPP2R2B, LCK and TP63 were significantly increased in HF compared with that in normal, while PCLAF, CFTR, TK1, ECT2 and FKBP5 were significantly decreased in HF compared with that in normal and are shown in Fig. 7.

Identification of Candidate Small Molecules

In the present study docking simulations are performed to spot the active site and foremost interactions accountable for complex stability with the receptor binding sites. In heart failure recognized over expressed genes and their proteins of x-ray crystallographic structure are chosen from PDB for docking studies. Most generally, medications containing benzothiadiazine ring hydrochlorothiazide are used in heart failure either alone or in conjunction with other drugs, based on this the molecules containing heterocyclic ring of benzothiadiazine are designed and hydrochlorothiazide is uses as a reference standard. Docking experiments using Sybyl-X 2.1.1. drug design perpetual software were used on the designed molecules. Docking studies were performed in order to understand the biding interaction of standard hydrochlorothiazide and designed molecules on over expressed protein. The X- RAY crystallographic structure of one proteins from each over expressed genes of ESR1, LCK, PPP2R2B, PYHIN1, TP63 and their co-crystallised protein of PDB code 4PXM, 1KSW, 2HV7, 3VD8 and 6RU6 respectively were selected for the docking studies to identify and predict the potential molecule based on the binding score with the protein and successful in heart failure. For the docking tests, a total of 34 molecules were built and the molecule with binding score greater than 5 is believed to be good. The designed molecules obtained docking score of 5 to 7 were HIM10, HTZ5, HIM6, HTZ31,

HIM3, HIM14, HIM1, HIM7 and HIM11, HIM16, HTZ9, HIM17, HIM12, HTZ12, HIM6, HTZ7, HIM10, HTZ3 and HIM8, HTZ9, HIM6, HIM4, HIM13, HTZ16, HIM9, HIM7, HTZ5, HIM16, HTZ7, HIM10, HIM5, HIM12, HIM15, HTZ12, HIM3, HIM14 and HIM14, HIM6, HIM17, HTZ7, HIM10, HIM1, HTZ9, HIM3, HIM16, HIM15, HIM8, HIM9, HIM7, HTZ10, HTZ3, HTZ5, HTZ1, HIM13, HTZ4, HIM11, HTZ12, HTZ14, HIM2 and HIM7, HTZ13, HTZ5, HIM15, HIM12, HIM6, HTZ11, HIM14, HTZ9, HIM11, HIM13, HIM9, HIM8, HIM10, HIM1, HIM5, HIM4, HTZ12, HIM2, HIM17, HIM3, HTZ1, HTZ8, HIM3, HTZ14, HTZ3 with proteins 4PXM and, 1KSW and 2HV7 and 3VD8 and 6RUR respectively (Fig. 8). The molecules obtained binding score of less than 5 were HTZ13, HTZ12, HTZ10, HIM3, HIM15, HIM16, HIM13, HIM8, HTZ16, HIM2, HIM4, HIM17, HTZ17, HIM11, HTZ5, HTZ3, HIM9, HTZ15, HTZ5, HTZ9, HTZ11, HIM5, HTZ8 and HTZ14, HIM14, HTZ13, HIM13, HTZ16, HIM2, HIM3, HTZ10, HIM7, HIM1, HTZ1, HTZ4, HIM8, HIM5, HTZ2, HIM9, HTZ5, HTZ15, HTZ3, HIM4, HIM15, HTZ17, HTZ8, HTZ11 and HTZ14, HIM2, HIM1, HTZ11, HIM17, HTZ13, HTZ4, HTZ2, HIM3, HTZ15, HTZ8, HTZ17, HTZ1, HTZ3 and HTZ8, HIM4, HTZ16, HTZ15, HIM5, HTZ11, HTZ13, HIM3, HTZ17, HTZ2 and HTZ7, HTZ4, HTZ2, HTZ17, HTZ15 with proteins 4PXM and, 1KSW and 2HV7 and 3VD8 and 6RUR respectively. The molecules obtained very less binding score are HTZ1, HIM12, HTZ2, HTZ4 with protein 4PXM and the standard hydrochlorothiazide (HTZ) obtained less binding score with all proteins, the values are depicted in Table 7.

Discussion

HF is the most prevalent form of cardiovascular disease among the elderly. A complete studies of HF, comprising pathogenic factors, pathological processes, clinical manifestations, early clinical diagnosis, clinical prevention, and drug therapy targets urgency to be consistently analyzed. In the present investigation, bioinformatics analysis was engaged to explore HF biomarkers and the pathological processes in myocardial tissues, acquired from HF groups and non heart failure groups. We analyzed GSE141910 expression profiling by high throughput sequencing obtained 881 different genes between HF groups and non heart failure groups, 442 up regulated and 439 down regulated genes. HBA2 and HBA1 have a key role in hypertension [32], but these genes might be linked with

development HF. SFRP4 was linked with progression of myocardial ischemia [33]. Emmens et al. [34] and Broch et al. [35] found that PENK (proenkephalin) and IL1RL1 were up regulated in HF. ALOX15B has lipid accumulation and inflammation activity and is highly expressed in atherosclerosis [36]. Studies have shown that expression of MYH6 was associated with hypertrophic cardiomyopathy [37].

In functional enrichment analysis, some genes involved with regulation of cardiovascular system processes were enriched in HF. Liu et al. [38], Kosugi et al. [39], McMacken et al. [40], Pan and Zhang [41], Li et al. [42] and Jiang et al. [43] presented that expression of HLA-DQA1, KDM5D, UCHL1, SAA1, ARG1 and LYVE1 were associated with progression of cardiomyopathy. Hou et al. [44] and Olesen et al. [45] demonstrated that DACT2 and KCND3 were found to be substantially related to atrial fibrillation. Ge and Concannon [46], Ferjeni et al. [47], Anquetil et al. [48], Glawe et al. [49], Kawabata et al. [50], Li et al. [51], Buraczynska et al. [52], Amini et al. [53], Yang et al. [54], Du Toit et al. [55], Hirose et al. [56], Zhang et al. [57], Griffin et al. [58], Zouidi et al. [59], Trombetta et al. [60], Alharbi et al. [61], Ikarashi et al. [62], Dharmadhikari et al. [63], Sutton et al. [64] and Deng et al. [65] reported that UBASH3A, ZAP70, IDO1, ITGAL (integrin subunit alpha L), ITGB7, RASGRP1, CNR1, SLC2A1, SLC11A1, GPR84, SSTR5, KCNB1, GLUL (glutamate-ammonia ligase), BANK1, CACNA1E, LGR5, AQP3, SIGLEC7, SSTR2 and DNER (delta/notch like EGF repeat containing) could be an index for diabetes, but these genes might be responsible for progression of HF. Experiments show that expression of FAP (fibroblast activation protein alpha) [66], THBS4 [67], CD27 [68], LEF1 [69], CTHRC1 [70], ESR1 [71], CXCL9 [72], SERPINA3 [73], TRPC4 [74], F13A1 [75], PIK3C2A [76], KCNIP2 [77] and GPR4 [78] contributed to myocardial infarction. MFAP4 [79], ALOX15 [80], COL1A1 [81], APOA1 [82], PDE5A [83], CX3CR1 [84], THY1 [85], GREM1 [86], FMOD (fibromodulin) [87], NPPA (natriuretic peptide A) [88], LTBP2 [89], LUM (lumican) [90], IL34 [91], NRG1 [92], CXCL14 [93], CXCL10 [94], ACE (angiotensin I converting enzyme) [95], CFTR (cystic fibrosis transmembrane conductance regulator) [96], S100A8 [97], S100A9 [97], HP (haptoglobin) [98], AGTR1 [99], ATP2A2 [100], IL10 [101], EDN1 [102], TLR2 [103], MCEMP1 [104], TPO (thyroid peroxidase) [105], CD163 [106], IL18R1 [107], KCNA7 [108] and CALCRL (calcitonin receptor like

receptor) [109] have an important role in HF. Li et al [110], Deckx et al [111], Ichihara et al [112] and Paik et al [113] showed that the SERPINE2, OGN (osteoglycin), AGTR2 and WNT10B promoted cardiac interstitial fibrosis. Cai et al [114], Mo et al [115], Sun et al [116], Martinelli et al [117], Zhao et al [118], Assimes et al [119] and Piechota et al [120] showed that CCR7, FCN1, ESM1, F8 (coagulation factor VIII), C1QTNF1, ALOX5 and MSR1 were an important target gene for coronary artery disease. STAB2 have been suggested to be associated with venous thromboembolic disease [121]. Genes such as COMP (cartilage oligomeric matrix protein) [122], CHI3L1 [123], PLA2G2A [124], P2RY12 [125], CR1 [126], HPSE (heparanase) [127], PTX3 [128] and SERPINE1 [129] were related to atherosclerosis. CCDC80 [130], CMA1 [131], MDK (midkine) [132], GNA14 [133], SCG2 [134], NPPB (natriuretic peptide B) [135], FGF10 [136], ARNTL (aryl hydrocarbon receptor nuclear translocator like) [137], WNK3 [138], EDNRB (endothelin receptor type B) [139], THBS1 [140], SELE (selectin E) [141], SLC4A7 [142], AQP4 [143] and KCNK3 [144] are thought to be responsible for progression of hypertension, but these genes might to be associated with progression of HF. CNTNAP2 [145], GLI2 [146], DPT (dermatopontin) [147], AEBP1 [148], ITIH5 [149], CXCL11 [150], GDNF (glial cell derived neurotrophic factor) [151], MCHR1 [152], FLT3 [153], ELANE (elastase, neutrophil expressed) [154], OSMR (oncostatin M receptor) [155] and IL15RA [156] are involved in development of obesity, but these genes might be key for progression of HF. CTSG (cathepsin G) is a protein coding gene plays important roles in aortic aneurysms [157]. Evidence from Safa et al. [158], Chen et al. [159], Zhou et al. [160], Hu et al. [161], Lou et al. [162], Zhang et al. [163] and Chen et al. [164] study indicated that the expression of CCL22, CCR1, FPR1, KNG1, CRISPLD2, CD38 and GPRC5A were linked with progression of ischemic heart disease. Li et al. [165] showed that STEAP3 expression can be associated with cardiac hypertrophy progression.

The HiPPIE interactome database was used to construct the PPI network, and modules analysis was performed. We finally screened out up regulated hub genes and down regulated hub genes, including ESR1, PYHIN1, PPP2R2B, LCK, TP63, PCLAF, CD247, CD2, CD5, CD48, CFTR, TK1, ECT2, FKBP5, S100A9 and S100A8 from the PPI network and its modules. TP63 might serve as a potential prognostic factor in cardiomyopathy [166]. The expression of FKBP5 is

related to the progression of coronary artery disease [167]. CD247 plays a central role in hypertension [168], but this gene might be involved in the HF. PYHIN1, PPP2R2B, LCK (LCK proto-oncogene, Src family tyrosine kinase), PCLAF (PCNA clamp associated factor), TK1, ECT2, CD2, CD5 and CD48 might be the novel biomarker for HF.

The miRNet database and NetworkAnalyst database were used to construct the target gene - miRNA regulatory network and target gene - TF regulatory network. We finally screened out target genes, miRNA, TFs, including FSCN1, ESR1, TMEM30B, SCN2B, CENPA, FKBP5, PCLAF, CEP55, ATP2A2, TK1, APOA1, COL1A1, HBB, LCK, SOCS3, BCL6, ANLN, hsa-mir-4533, hsa-mir-548ac, hsa-mir-548i, hsa-mir-5585-3p, hsa-mir-6750-3p, hsa-mir-200c-3p, hsa-mir-1273g-3p, hsa-mir-1244, hsa-mir-4789-3p, hsa-mir-766-3p, ESRRA, RERE, HMG20B, THRAP3, ATF1, MXD3, ARID4B, CBFB, TAF7 and CREM from the target gene - miRNA regulatory network and target gene - TF regulatory network. SCN2B [169] and SOCS3 [170] are considered as a markers for HF and might be a new therapeutic target. BCL6 levels are correlated with disease severity in patients with atherosclerosis [171]. A previous study showed that hsa-mir-1273g-3p [172], hsa-mir-4789-3p [173] and ATF1 [174] could involved in hypertension, but these markers might be responsible for progression of HF. hsa-miR-518f, was demonstrated to be associated with cardiomyopathy [175]. An evidence demonstrating a role for ESRRA (estrogen related receptor alpha) [176] and THRAP3 [177] in diabetes, but these genes might be liable for development of HF. FSCN1, TMEM30B, CENPA (centromere protein A), CEP55, HBB (hemoglobin subunit beta), ANLN (anillin actin binding protein), hsa-mir-4533, hsa-mir-548ac, hsa-mir-548i, hsa-mir-5585-3p, hsa-mir-6750-3p, hsa-mir-200c-3p, hsa-mir-1244, RERE(arginine-glutamic acid dipeptide repeats), HMG20B, MXD3, ARID4B, CBFB (core-binding factor subunit beta), TAF7 and CREM (cAMP response element modulator) might be the novel biomarker for HF.

The molecules HIM6, HIM10 obtained good binding score of more 5 to 6.999 with all proteins and the molecules HIM11, HIM12, HIM14, HTZ9, HTZ10 and HTZ12 obtained binding score above 5 and less than 9 with PDB protein code of 2HV7, 3VD8 and 6RUR respectively. The molecule HIM11 obtained highest binding score of 8.678 with 2HV7 and its interaction with amino acids are molecule HIM11 (Fig. 9) has obtained with a high binding score with PDB protein

2HV7, the interactions of molecule is the C6 side chain acyl carbonyl C=O formed hydrogen bond interaction with amino acid GLN-207 with bond length 1.92 Å and 3' N-H group of imidazole ring formed hydrogen bond interaction with VAL-305 with bond length 2.36 Å respectively. It also formed other interactions of carbon hydrogen bond of -CH₃ group of carboxylate at C6 with PRO-304 and amide- π stacked and π - π stacked interaction of electrons of aromatic ring A with ALA-204 and ring C with HIS-155 and HIS-308. Molecule formed π -alkyl interaction of ring B with PRO-304 and all interactions with amino acids and bond length are depicted by 3D and 2D figures (Fig.10 and Fig.11).

Conclusions

The present study provided an extensive bioinformatics analysis of DEGs and revealed a series of targets and pathways, which may affect the progression of HF, for future investigation. And many of them, such as ESR1, PYHIN1, PPP2R2B, LCK, TP63, PCLAF, CFTR, TK1, ECT2 and FKBP5, might be key genes related to HF. The current investigation identified active molecules that might represent novel treatments for HF and may reduce the range of potential drugs for treating HF. These findings add to significant insights into the diagnosis and treatment of HF.

Acknowledgement

I thank Michael Patrick Morley, Perelman School of Medicine at the University of Pennsylvania, Penn Cardiovascular Institute, Philadelphia, USA, very much, the author who deposited their profiling by high throughput sequencing dataset GSE141910, into the public GEO database.

Conflict of interest

The authors declare that they have no conflict of interest.

Ethical approval

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

Informed consent

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

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. [(GSE141910) (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE141910>)]

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

Author Contributions

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

A. T - Formal analysis and validation

C. V - Software and investigation

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Figures

Fig. 1. 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.

Figure 2 consists of three panels (A, B, and C) showing network visualizations of gene expression data. Panel A is a large, dense network of nodes (circles) colored by cluster (red, green, purple) and sized by degree. Panel B shows a sub-network with highlighted nodes like CD247, CD2, CD5, CD48, LCK, and PTK. Panel C shows another sub-network with highlighted nodes like PCLAF, S100A8, and S100A9.

Fig. 3. PPI network and the most significant modules of DEGs. (A) The PPI network of DEGs was constructed using Cytoscape (B) The most significant module was obtained from PPI network with 4 nodes and 6 edges for up regulated genes (C) The most significant module was obtained from PPI network with 6 nodes and 10 edges for down regulated genes. Up regulated genes are marked in green; down regulated genes are marked in red

Fig. 4. Target gene - miRNA regulatory network between target genes. The light orange color diamond nodes represent the key miRNAs; up regulated genes are marked in green; down regulated genes are marked in red.

Fig. 5. Target gene - TF regulatory network between target genes. The sky blue color triangle nodes represent the key TFs; up regulated genes are marked in green; down regulated genes are marked in red.

Fig. 6. ROC curve analyses of hub genes. A) ESR1 B) PYHIN1 C) PPP2R2B D) LCK E) TP63 F) PCLAF G) CFTR H) TK1 I) ECT2 J) FKBP5

Fig. 7. RT-PCR analyses of hub genes. A) ESR1 B) PYHIN1 C) PPP2R2B D) LCK E) TP63 F) PCLAF G) CFTR H) TK1 I) ECT2 J) FKBP5

Fig. 8. Structures of Designed Molecules

Fig. 9 Structure of active designed molecule of HIM11

Fig.10. 3D Binding of Molecule HIM11 with 2HV7

Fig.11. 2D Binding of Molecule HIM11 with 2HV7

Table 1 The sequences of primers for quantitative RT-PCR

Genes	Forward Primers	Reverse Primers
ESR1	CCCACTCAACAGCGTGTCTC	CGTCGATTATCTGAATTTGGCCT
PYHIN1	CCAAGCAACCGTCTCACAG	GCCGAGTCTGCTCTTTGGA
PPP2R2B	CCACACGGGAGAATTACTAGCG	TGTATTACCCCTACGATGAACC
LCK	TGCCATTATCCCATAGTCCCA	GAGCCTTCGTAGGTAACCAGT
TP63	GGACCAGCAGATTCAGAACGG	AGGACACGTCGAAACTGTGC
PCLAF	GACCAATATAAACTGTGGCGGG	CCAGGGTAAACAAGGAGACGTT
CFTR	AAAAGGCCAGCGTTGTCTCC	AAACATCGCCGAAGGGCATT
TK1	GGGCAGATCCAGGTGATTCTC	TGTAGCGAGTGTCTTTGGCATA
ECT2	ACTACTGGGAGGACTAGCTTG	CACCTCTGTTTCAATCTGAGGCA
FKBP5	AATGGTGAGGAAACGCCGATG	TCGAGGGAATTTTAGGGAGACT

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

GeneSymbol	logFC	pValue	adj.P.Val	tvalue	Regulation	Gene Name
SEZ6L	3.540921	3.57E-88	1.24E-84	26.74214	Up	seizure related 6 homolog like
HBA2	3.52441	2.69E-34	1.06E-32	13.57556	Up	hemoglobin subunit alpha 2
FHAD1-AS1	3.514827	9.64E-90	4.01E-86	27.14088	Up	FHAD1 antisense RNA 1
COL22A1	3.442684	3.27E-74	4E-71	23.26846	Up	collagen type XXII alpha 1 chain
SFRP4	3.439595	3.23E-87	9.58E-84	26.49986	Up	secreted frizzled related protein 4
HBB	3.311845	4.49E-46	4.34E-44	16.48352	Up	hemoglobin subunit beta
PENK	3.292908	1.23E-69	8.22E-67	22.15479	Up	proenkephalin
HBA1	3.239241	7.91E-35	3.22E-33	13.71027	Up	hemoglobin subunit alpha 1
APCDD1L	3.102854	1.43E-70	9.91E-68	22.38121	Up	APC down-regulated 1 like
FNDC1	2.952	8.2E-99	8.53E-95	29.4879	Up	fibronectin type III domain containing 1
SLC1A7	2.935446	3.45E-58	9.31E-56	19.39718	Up	solute carrier family 1 member 7
LYPD1	2.786956	1.94E-49	2.57E-47	17.29603	Up	LY6/PLAUR domain containing 1
FCER1A	2.775152	5.58E-63	2.11E-60	20.5475	Up	Fc fragment of IgE receptor 1a
HAPLN1	2.766834	6.66E-48	7.6E-46	16.92589	Up	hyaluronan and proteoglycan link protein 1
LEFTY2	2.748568	3.27E-71	2.52E-68	22.53707	Up	left-right determination factor 2
CAPN6	2.718519	3.14E-44	2.57E-42	16.03574	Up	calpain 6
UNC80	2.706223	6.44E-53	1.21E-50	18.13271	Up	unc-80 homolog, NALCN channel complex subunit
CHRNA3	2.691289	3.77E-48	4.53E-46	16.98549	Up	cholinergic receptor nicotinic alpha 3 subunit
ARMS2	2.677012	7.71E-60	2.39E-57	19.79325	Up	age-related maculopathy susceptibility 2
MXRA5	2.665146	7.01E-66	3.31E-63	21.24615	Up	matrix remodeling associated 5
CXCL10	2.648986	1.88E-39	1.06E-37	14.8648	Up	C-X-C motif chemokine ligand 10
LAMP5	2.634422	1.79E-67	8.84E-65	21.63104	Up	lysosomal associated membrane protein family member 5
GZMH	2.585101	1.39E-52	2.54E-50	18.05238	Up	granzyme H
COL10A1	2.58157	3.89E-42	2.71E-40	15.52492	Up	collagen type X alpha 1 chain
TNMD	2.561494	2.35E-41	1.55E-39	15.3336	Up	tenomodulin
CRISPLD1	2.551697	1.75E-57	4.48E-55	19.22821	Up	cysteine rich secretory protein LCCL domain containing 1
MKRN2OS	2.518052	1.81E-31	5.81E-30	12.85257	Up	MKRN2 opposite strand
CMA1	2.49186	2.56E-41	1.68E-39	15.32454	Up	chymase 1

CRACD	2.409728	7.61E-35	3.1E-33	13.71447	Up	capping protein inhibiting regulator of actin dynamics
LOC339260	2.40851	9.48E-72	8.21E-69	22.66783	Up	uncharacterized LOC339260
CENPA	2.378802	2.87E-29	7.86E-28	12.27893	Up	centromere protein A
LINC02593	2.357621	6.61E-52	1.09E-49	17.8899	Up	long intergenic non-protein coding RNA 2593
LRRC55	2.35454	4.34E-43	3.3E-41	15.75782	Up	leucine rich repeat containing 55
AGTR2	2.346789	3.04E-39	1.69E-37	14.81336	Up	angiotensin II receptor type 2
GLIS1	2.270732	1.08E-41	7.24E-40	15.41668	Up	GLIS family zinc finger 1
AQP10	2.238434	5.77E-60	1.82E-57	19.82339	Up	aquaporin 10
TMEM130	2.225534	1.08E-32	3.78E-31	13.16693	Up	transmembrane protein 130
CXCL11	2.22214	3.56E-30	1.03E-28	12.51639	Up	C-X-C motif chemokine ligand 11
NKG7	2.203903	2.69E-41	1.75E-39	15.3192	Up	natural killer cell granule protein 7
ESM1	2.203875	1.56E-35	6.67E-34	13.88776	Up	endothelial cell specific molecule 1
NPPA	2.194101	5.13E-29	1.38E-27	12.21264	Up	natriuretic peptide A
FRZB	2.175346	4.1E-91	2.13E-87	27.49106	Up	frizzled related protein signal peptide, CUB domain and EGF like domain containing 2
SCUBE2	2.170552	1.48E-78	2.8E-75	24.33596	Up	
TGFB2-AS1	2.167994	1.32E-41	8.84E-40	15.39479	Up	TGFB2 antisense RNA 1 (head to head)
ANKRD34C	2.159555	2.72E-45	2.48E-43	16.29382	Up	ankyrin repeat domain 34C
ZNF365	2.146095	9.54E-49	1.2E-46	17.1295	Up	zinc finger protein 365
KCNIP1	2.140052	9.06E-50	1.24E-47	17.37589	Up	potassium voltage-gated channel interacting protein 1
CD1C	2.134028	3.98E-44	3.25E-42	16.01054	Up	CD1c molecule
ASPN	2.117196	3.21E-68	1.71E-65	21.8113	Up	asporin
PPP2R2B	2.092908	2.1E-59	6.14E-57	19.68888	Up	protein phosphatase 2 regulatory subunit Bbeta
NPPB	2.091998	1.57E-18	1.74E-17	9.274014	Up	natriuretic peptide B
HRK	2.091711	4.32E-44	3.5E-42	16.00206	Up	harakiri, BCL2 interacting protein
LOC101928834	2.091398	4.58E-47	4.96E-45	16.72358	Up	uncharacterized LOC101928834
GZMB	2.085361	2.05E-40	1.25E-38	15.10213	Up	granzyme B
RTL3	2.083673	1.52E-53	3.09E-51	18.28344	Up	retrotransposon Gag like 3
CX3CR1	2.069035	3.8E-45	3.42E-43	16.25861	Up	C-X3-C motif chemokine receptor 1
COMP	2.051651	1.51E-19	1.82E-18	9.579662	Up	cartilage oligomeric matrix protein
CTSG	2.049972	5.94E-37	2.83E-35	14.24398	Up	cathepsin G
FAM180B	2.034044	4.11E-41	2.64E-39	15.27385	Up	family with sequence similarity 180 member B
MDK	2.023427	5.33E-46	5.08E-44	16.46554	Up	midkine
NFIA-AS2	2.011983	1.41E-51	2.25E-49	17.81082	Up	NFIA antisense RNA 2
FATE1	2.011836	5.31E-38	2.71E-36	14.50539	Up	fetal and adult testis expressed 1
PRKAG3	2.002215	4.44E-48	5.27E-46	16.96846	Up	protein kinase AMP-activated non-catalytic subunit gamma 3
COL9A1	2.001739	5.6E-52	9.31E-50	17.90721	Up	collagen type IX alpha 1 chain
SSC5D	1.998905	6.1E-72	5.51E-69	22.71447	Up	scavenger receptor cysteine rich family member with 5 domains
ACE	1.99576	1.54E-53	3.12E-51	18.28159	Up	angiotensin I converting enzyme
GDF6	1.994884	6.98E-50	9.74E-48	17.40311	Up	growth differentiation factor 6
SHISA2	1.989108	1.04E-43	8.27E-42	15.90886	Up	shisa family member 2
XG	1.986441	2.84E-34	1.11E-32	13.56967	Up	Xg glycoprotein (Xg blood group)
LUM	1.96673	4.91E-75	6.81E-72	23.47008	Up	lumican

RGS4	1.958569	2.81E-47	3.09E-45	16.77466	Up	regulator of G protein signaling 4
FCGR3B	1.945296	1.19E-31	3.87E-30	12.89978	Up	Fc fragment of IgG receptor IIIb
HSH2D	1.94243	6.51E-46	6.15E-44	16.44441	Up	hematopoietic SH2 domain containing
WNT9A	1.941347	4.74E-36	2.09E-34	14.018	Up	Wnt family member 9A
SAMD11	1.937898	2.66E-28	6.76E-27	12.02359	Up	sterile alpha motif domain containing 11
LTB	1.919135	1.96E-30	5.77E-29	12.5841	Up	lymphotoxin beta
CTSW	1.916821	3.18E-37	1.55E-35	14.31185	Up	cathepsin W
ARMC4	1.913783	2.91E-50	4.17E-48	17.49459	Up	armadillo repeat containing 4
ATP1B4	1.909761	8.05E-19	9.12E-18	9.36208	Up	ATPase Na ⁺ /K ⁺ transporting family member beta 4
TNNI1	1.901808	5.89E-21	8.11E-20	9.993524	Up	troponin I1, slow skeletal type
CYP4F3	1.901148	4.61E-32	1.55E-30	13.0053	Up	cytochrome P450 family 4 subfamily F member 3
RYR3	1.890853	2.04E-46	2.07E-44	16.56646	Up	ryanodine receptor 3
NDP	1.884805	7.22E-39	3.91E-37	14.72038	Up	norrincystine knot growth factor NDP
SLAMF7	1.880253	9.55E-37	4.48E-35	14.1924	Up	SLAM family member 7
PI16	1.873783	2.52E-45	2.31E-43	16.30173	Up	peptidase inhibitor 16
OGN	1.873487	6.47E-51	9.81E-49	17.65171	Up	osteoglycin
BIRC7	1.867331	1.22E-20	1.61E-19	9.901493	Up	baculoviral IAP repeat containing 7
APLNR	1.85994	8.58E-53	1.59E-50	18.10284	Up	apelin receptor
ADAM18	1.857904	1.11E-25	2.24E-24	11.31964	Up	ADAM metallopeptidase domain 18
OASL	1.857886	9.34E-50	1.27E-47	17.3727	Up	2'-5'-oligoadenylate synthetase like
CREG2	1.844542	3.04E-37	1.49E-35	14.31649	Up	cellular repressor of E1A stimulated genes 2
SIGLEC17P	1.840393	6.23E-38	3.17E-36	14.48798	Up	sialic acid binding Ig like lectin 17, pseudogene
LINC00861	1.837563	1.09E-39	6.29E-38	14.92381	Up	long intergenic non-protein coding RNA 861
GPR68	1.834869	2.31E-32	7.86E-31	13.0825	Up	G protein-coupled receptor 68
ISLR	1.831354	1.03E-49	1.39E-47	17.36275	Up	immunoglobulin superfamily containing leucine rich repeat
AK5	1.822757	3.92E-60	1.25E-57	19.8637	Up	adenylate kinase 5
FREM1	1.822486	3.96E-86	1.03E-82	26.22491	Up	FRAS1 related extracellular matrix 1
SYTL5	1.818907	5.97E-20	7.48E-19	9.698984	Up	synaptotagmin like 5
STAT4	1.815386	1.94E-40	1.18E-38	15.10812	Up	signal transducer and activator of transcription 4
SMOC2	1.808707	3.5E-105	7.3E-101	31.18302	Up	SPARC related modular calcium binding 2
SAMD3	1.804067	4.45E-45	3.97E-43	16.2419	Up	sterile alpha motif domain containing 3
VGLL2	1.802895	5.36E-18	5.67E-17	9.111967	Up	vestigial like family member 2
LINC01563	1.792042	1.87E-40	1.15E-38	15.11196	Up	long intergenic non-protein coding RNA 1563
KCNK17	1.791993	4.93E-29	1.32E-27	12.21731	Up	potassium two pore domain channel subfamily K member 17
TMEM119	1.786136	3.08E-34	1.2E-32	13.5608	Up	transmembrane protein 119
SLC16A9	1.78355	4.41E-59	1.24E-56	19.61146	Up	solute carrier family 16 member 9
GZMA	1.780273	7.61E-43	5.69E-41	15.69824	Up	granzyme A
OGDHL	1.772273	6.58E-45	5.8E-43	16.20069	Up	oxoglutarate dehydrogenase like
ATP1A4	1.772266	1.92E-44	1.6E-42	16.08796	Up	ATPase Na ⁺ /K ⁺ transporting subunit alpha 4
GAP43	1.770722	1.3E-26	2.84E-25	11.57199	Up	growth associated protein 43
RASEF	1.767816	9.28E-35	3.77E-33	13.69272	Up	RAS and EF-hand domain containing
CHD5	1.767757	3.25E-36	1.46E-34	14.05911	Up	chromodomain helicase DNA binding protein 5

PRF1	1.765387	2.68E-42	1.88E-40	15.56459	Up	perforin 1
OXER1	1.757588	1.14E-51	1.86E-49	17.8326	Up	oxoeicosanoid receptor 1
LSP1	1.755261	7.18E-55	1.57E-52	18.6014	Up	lymphocyte specific protein 1
NRXN2	1.753031	1.35E-39	7.71E-38	14.90069	Up	neurexin 2
CXCL9	1.752192	1.37E-20	1.81E-19	9.886423	Up	C-X-C motif chemokine ligand 9
MYL1	1.741306	3.26E-23	5.46E-22	10.6376	Up	myosin light chain 1
DBH-AS1	1.740319	2.27E-43	1.76E-41	15.82628	Up	DBH antisense RNA 1
CERS1	1.737417	7.6E-28	1.84E-26	11.90259	Up	ceramide synthase 1
OPCML	1.7359	8.75E-40	5.11E-38	14.94691	Up	opioid binding protein/cell adhesion molecule like
APOA1	1.735578	1.38E-27	3.24E-26	11.83363	Up	apolipoprotein A1
STAB2	1.73447	1.05E-26	2.31E-25	11.5969	Up	stabilin 2
C16orf89	1.731539	1.26E-40	7.83E-39	15.15416	Up	chromosome 16 open reading frame 89
LRRC15	1.731261	5.75E-30	1.65E-28	12.46207	Up	leucine rich repeat containing 15
C1QTNF7	1.725627	7.28E-71	5.4E-68	22.45257	Up	C1q and TNF related 7
TMEM200A	1.7209	4.9E-25	9.41E-24	11.14357	Up	transmembrane protein 200A
LHCGR	1.716273	2.18E-22	3.38E-21	10.40422	Up	luteinizing hormone/choriogonadotropin receptor
PRSS35	1.713597	7.99E-34	3.01E-32	13.45573	Up	serine protease 35
S1PR5	1.710201	5.13E-30	1.48E-28	12.47513	Up	sphingosine-1-phosphate receptor 5
NTM	1.707182	4.2E-65	1.94E-62	21.05873	Up	neurotrimin
FCRL3	1.703236	3.65E-29	9.88E-28	12.25172	Up	Fc receptor like 3
KLHDC8A	1.697472	3.11E-36	1.4E-34	14.06389	Up	kelch domain containing 8A
MELTF-AS1	1.696996	1.04E-54	2.24E-52	18.56314	Up	MELTF antisense RNA 1
C1QTNF2	1.695983	1.18E-66	5.71E-64	21.4328	Up	C1q and TNF related 2
CYS1	1.688006	6.01E-69	3.57E-66	21.9875	Up	cystin 1
SLC6A4	1.687739	1.34E-23	2.31E-22	10.74587	Up	solute carrier family 6 member 4
LINC00670	1.682454	2.21E-52	3.9E-50	18.00406	Up	long intergenic non-protein coding RNA 670
COL14A1	1.681527	8.37E-50	1.15E-47	17.38423	Up	collagen type XIV alpha 1 chain
AEBP1	1.678926	2.77E-45	2.51E-43	16.29209	Up	AE binding protein 1
TLL2	1.670045	4.29E-69	2.7E-66	22.023	Up	tolloid like 2
LOC107986163	1.669682	3.03E-33	1.1E-31	13.30833	Up	uncharacterized LOC107986163
NRK	1.665994	9.57E-60	2.88E-57	19.7707	Up	Nik related kinase
EXOC3L4	1.657167	1.47E-23	2.52E-22	10.73476	Up	exocyst complex component 3 like 4
HTR2A	1.656339	9.15E-27	2.03E-25	11.61333	Up	5-hydroxytryptamine receptor 2A
HDC	1.653783	5.15E-36	2.25E-34	14.00907	Up	histidine decarboxylase
GSTM5	1.650191	4.21E-45	3.77E-43	16.24794	Up	glutathione S-transferase mu 5
CD3D	1.641321	1.18E-31	3.86E-30	12.90043	Up	CD3d molecule
ECRG4	1.632088	1.01E-46	1.06E-44	16.64023	Up	ECRG4 augurin precursor
FAP	1.627064	6.1E-37	2.9E-35	14.24099	Up	fibroblast activation protein alpha
BPI	1.624603	2.16E-31	6.91E-30	12.83272	Up	bactericidal permeability increasing protein
CYP11A1	1.621266	4.82E-52	8.15E-50	17.92274	Up	cytochrome P450 family 11 subfamily A member 1
LCN12	1.619771	4.59E-32	1.55E-30	13.00586	Up	lipocalin 12
MFAP4	1.616857	5.78E-73	5.46E-70	22.96383	Up	microfibril associated protein 4
MYOC	1.605119	1.96E-31	6.3E-30	12.84334	Up	myocilin

THY1	1.604584	1.17E-22	1.87E-21	10.48087	Up	Thy-1 cell surface antigen
ITGAL	1.604327	4.27E-46	4.14E-44	16.48893	Up	integrin subunit alpha L
KIAA1755	1.603838	2.97E-55	6.63E-53	18.69335	Up	KIAA1755
FMOD	1.601342	5.22E-42	3.61E-40	15.49365	Up	fibromodulin
GFRA3	1.59901	1.15E-35	4.93E-34	13.9215	Up	GDNF family receptor alpha 3
PHLDA1	1.593007	1.25E-63	4.89E-61	20.70408	Up	pleckstrin homology like domain family A member 1
SH2D1B	1.592988	1.23E-30	3.7E-29	12.63695	Up	SH2 domain containing 1B
IL34	1.590541	4.65E-46	4.48E-44	16.4798	Up	interleukin 34
ADAMTS14	1.590348	1.8E-36	8.26E-35	14.12324	Up	ADAM metalloproteinase with thrombospondin type 1 motif 14
APCDD1L-DT	1.585375	8.02E-32	2.64E-30	12.94358	Up	APCDD1L divergent transcript
CMTM2	1.584966	3.97E-22	5.98E-21	10.33056	Up	CKLF like MARVEL transmembrane domain containing 2
PROM1	1.584399	1.37E-53	2.85E-51	18.29382	Up	prominin 1
TENM4	1.57826	2.99E-46	2.97E-44	16.52634	Up	teneurin transmembrane protein 4
CD3E	1.577059	1.44E-34	5.75E-33	13.64473	Up	CD3e molecule
TMEM30B	1.573717	8.62E-43	6.39E-41	15.68505	Up	transmembrane protein 30B
SARDH	1.564223	1.52E-43	1.2E-41	15.86877	Up	sarcosine dehydrogenase
KLRB1	1.5636	2.78E-31	8.82E-30	12.80414	Up	killer cell lectin like receptor B1
NAPSB	1.559889	6.93E-30	1.98E-28	12.44091	Up	napsin B aspartic peptidase, pseudogene
SLCO4C1	1.559829	6.69E-31	2.06E-29	12.70541	Up	solute carrier organic anion transporter family member 4C1
GABRD	1.559743	8.36E-25	1.58E-23	11.07971	Up	gamma-aminobutyric acid type A receptor delta subunit
CD6	1.558091	6.44E-31	1.99E-29	12.70964	Up	CD6 molecule
LINC02028	1.556023	2.42E-42	1.71E-40	15.57541	Up	long intergenic non-protein coding RNA 2028
RASL11B	1.554174	6E-53	1.14E-50	18.14009	Up	RAS like family 11 member B
TBX21	1.552213	4.5E-31	1.4E-29	12.74998	Up	T-box transcription factor 21
IL2RB	1.546229	1.51E-39	8.57E-38	14.88881	Up	interleukin 2 receptor subunit beta
HAAO	1.54259	2.21E-46	2.23E-44	16.55819	Up	3-hydroxyanthranilate 3,4-dioxygenase
MS4A1	1.541164	1.65E-21	2.37E-20	10.15294	Up	membrane spanning 4-domains A1
LRRC17	1.539065	4.14E-53	8.04E-51	18.17887	Up	leucine rich repeat containing 17
CCL24	1.538643	5.69E-20	7.15E-19	9.70512	Up	C-C motif chemokine ligand 24
LINC00906	1.535912	2.36E-23	4E-22	10.67709	Up	long intergenic non-protein coding RNA 906
LMF1	1.535428	1.04E-41	6.99E-40	15.42078	Up	lipase maturation factor 1
TNFRSF4	1.535	8.46E-14	6.01E-13	7.761017	Up	TNF receptor superfamily member 4
P3H2	1.532878	2.18E-36	9.95E-35	14.10244	Up	prolyl 3-hydroxylase 2
LOC101926964	1.529325	1.15E-28	2.98E-27	12.12071	Up	uncharacterized LOC101926964
PTN	1.528239	1.59E-62	5.8E-60	20.43819	Up	pleiotrophin
EIF1AY	1.527175	0.003828	0.007083	2.910526	Up	eukaryotic translation initiation factor 1A Y-linked
DNAH8	1.526078	7.16E-28	1.73E-26	11.90949	Up	dynein axonemal heavy chain 8
GREM1	1.524172	2E-13	1.37E-12	7.633388	Up	gremlin 1, DAN family BMP antagonist
CEACAM3	1.522791	2.87E-23	4.85E-22	10.65294	Up	CEA cell adhesion molecule 3
ATRNL1	1.52238	1.39E-22	2.19E-21	10.45995	Up	atractin like 1
FCN1	1.522239	4.41E-25	8.52E-24	11.15616	Up	ficolin 1
AMHR2	1.519307	1.07E-26	2.35E-25	11.59475	Up	anti-Mullerian hormone receptor type 2

CRHBP	1.517324	7.94E-50	1.1E-47	17.38973	Up	corticotropin releasing hormone binding protein
NME8	1.515954	5.23E-28	1.29E-26	11.94592	Up	NME/NM23 family member 8
ZAP70	1.514658	7.62E-33	2.68E-31	13.2059	Up	zeta chain of T cell receptor associated protein kinase 70
RPS4Y1	1.513872	0.003664	0.006805	2.924581	Up	ribosomal protein S4 Y-linked 1
LIPH	1.512512	7.39E-38	3.72E-36	14.46955	Up	lipase H
FAM181B	1.509658	1.41E-29	3.94E-28	12.36002	Up	family with sequence similarity 181 member B
LY9	1.506257	1.04E-25	2.1E-24	11.32764	Up	lymphocyte antigen 9
CCR7	1.505912	4.46E-24	7.96E-23	10.87865	Up	C-C motif chemokine receptor 7
FBXL16	1.500323	7.88E-30	2.24E-28	12.42638	Up	F-box and leucine rich repeat protein 16
IL17D	1.492141	1.85E-48	2.26E-46	17.0602	Up	interleukin 17D
FBLN7	1.490721	2.97E-38	1.54E-36	14.56812	Up	fibulin 7
CTD-3080P12.3	1.489908	3.27E-15	2.65E-14	8.231737	Up	uncharacterized LOC101928857
DIO2	1.489605	1.7E-50	2.45E-48	17.55098	Up	iodothyroninedeiodinase 2
ZBP1	1.487429	3.84E-33	1.37E-31	13.28194	Up	Z-DNA binding protein 1
SFTA1P	1.486617	1.26E-25	2.52E-24	11.30493	Up	surfactant associated 1, pseudogene
CD2	1.485796	9.06E-31	2.76E-29	12.6712	Up	CD2 molecule
FCRL6	1.48399	2.5E-24	4.54E-23	10.94834	Up	Fc receptor like 6
FZD10-AS1	1.483735	3.65E-33	1.31E-31	13.28767	Up	FZD10 antisense divergent transcript
CD1E	1.483648	4.01E-21	5.57E-20	10.04196	Up	CD1e molecule
COL16A1	1.481494	1.07E-46	1.11E-44	16.63474	Up	collagen type XVI alpha 1 chain
EFCC1	1.476925	1.03E-45	9.65E-44	16.3961	Up	EF-hand and coiled-coil domain containing 1
ETV4	1.475328	1.73E-37	8.55E-36	14.37775	Up	ETS variant transcription factor 4
DLGAP1	1.473619	2.54E-25	4.99E-24	11.22147	Up	DLG associated protein 1
HYAL4	1.472457	1.68E-28	4.29E-27	12.07691	Up	hyaluronidase 4
MCHR1	1.471883	1.03E-24	1.94E-23	11.05502	Up	melanin concentrating hormone receptor 1
LOC101928731	1.467565	8.57E-36	3.7E-34	13.95348	Up	uncharacterized LOC101928731
TIGIT	1.467506	9.66E-26	1.95E-24	11.33618	Up	T cell immunoreceptor with Ig and ITIM domains
PRRT2	1.467191	4.38E-51	6.84E-49	17.69245	Up	proline rich transmembrane protein 2
CA3	1.462163	2.97E-20	3.81E-19	9.788456	Up	carbonic anhydrase 3
GADL1	1.461411	5.68E-20	7.14E-19	9.705276	Up	glutamate decarboxylase like 1
CD3G	1.458347	4.25E-26	8.92E-25	11.4331	Up	CD3g molecule
SPNS3	1.457263	4.56E-22	6.83E-21	10.31312	Up	sphingolipid transporter 3 (putative)
FERMT1	1.456951	1.48E-33	5.45E-32	13.38789	Up	fermitin family member 1
GRIK4	1.454408	2.49E-31	7.95E-30	12.81649	Up	glutamate ionotropic receptor kainate type subunit 4
SDSL	1.453371	8.03E-31	2.46E-29	12.68483	Up	serine dehydratase like
NRG1	1.452944	9.93E-21	1.33E-19	9.927464	Up	neuregulin 1
TARP	1.452369	1.3E-25	2.6E-24	11.30092	Up	TCR gamma alternate reading frame protein
SCG2	1.450549	1.85E-16	1.69E-15	8.633202	Up	secretogranin II
EGR2	1.448114	5.93E-26	1.22E-24	11.39379	Up	early growth response 2
GSG1L	1.445137	1.2E-11	6.83E-11	7.00315	Up	GSG1 like
SCARA3	1.444259	5.52E-63	2.11E-60	20.54857	Up	scavenger receptor class A member 3
UBASH3A	1.439792	5.08E-25	9.75E-24	11.1393	Up	ubiquitin associated and SH3 domain containing A
DMC1	1.439293	5.98E-61	2.04E-58	20.05974	Up	DNA meiotic recombinase 1

NGEF	1.439001	1.44E-19	1.75E-18	9.585604	Up	neuronal guanine nucleotide exchange factor
DNAJC22	1.437657	3.51E-29	9.52E-28	12.25626	Up	DnaJ heat shock protein family (Hsp40) member C22
SMPD3	1.436276	7.03E-22	1.04E-20	10.25951	Up	sphingomyelinphosphodiesterase 3
CCDC168	1.436207	4.17E-29	1.12E-27	12.23649	Up	coiled-coil domain containing 168
CRABP2	1.432348	7.38E-30	2.1E-28	12.43378	Up	cellular retinoic acid binding protein 2
PRPH	1.430396	4.69E-28	1.16E-26	11.95832	Up	peripherin
PALM3	1.430275	4.36E-28	1.08E-26	11.9668	Up	paralemmin 3
FOXS1	1.429428	2.74E-19	3.24E-18	9.502675	Up	forkhead box S1
ITIH5	1.429207	3.76E-74	4.34E-71	23.25374	Up	inter-alpha-trypsin inhibitor heavy chain 5
SKAP1	1.428481	2.6E-28	6.61E-27	12.02632	Up	src kinase associated phosphoprotein 1
ITGBL1	1.42419	1.72E-33	6.3E-32	13.37084	Up	integrin subunit beta like 1
COL8A2	1.424064	2.12E-45	1.95E-43	16.32026	Up	collagen type VIII alpha 2 chain
KIRREL3	1.420945	8.98E-32	2.95E-30	12.93087	Up	kirre like nephrin family adhesion molecule 3
BEX1	1.420178	1.54E-22	2.41E-21	10.44694	Up	brain expressed X-linked 1
FCER2	1.416596	3.81E-22	5.76E-21	10.33555	Up	Fc fragment of IgE receptor II
SLC24A2	1.415998	6.97E-21	9.53E-20	9.972135	Up	solute carrier family 24 member 2
TBC1D10C	1.415564	3.36E-24	6.04E-23	10.91276	Up	TBC1 domain family member 10C
ESR1	1.415141	6.38E-59	1.77E-56	19.57293	Up	estrogen receptor 1
SCN2B	1.414446	3.55E-55	7.84E-53	18.67482	Up	sodium voltage-gated channel beta subunit 2
PADI4	1.413441	5.7E-17	5.47E-16	8.793997	Up	peptidyl arginine deiminase 4
OMG	1.411113	2.11E-29	5.84E-28	12.31411	Up	oligodendrocyte myelin glycoprotein
CTHRC1	1.410717	9.47E-28	2.26E-26	11.87721	Up	collagen triple helix repeat containing 1
LEF1	1.409598	1.53E-33	5.64E-32	13.38369	Up	lymphoid enhancer binding factor 1
SYTL1	1.405901	3.05E-23	5.12E-22	10.64567	Up	synaptotagmin like 1
CCL22	1.404475	2.6E-17	2.58E-16	8.900267	Up	C-C motif chemokine ligand 22
CLEC4F	1.403759	3.69E-20	4.71E-19	9.760544	Up	C-type lectin domain family 4 member F
P2RX6	1.403444	3.73E-27	8.5E-26	11.71788	Up	purinergic receptor P2X 6
TGFB2	1.399181	2.8E-29	7.65E-28	12.2821	Up	transforming growth factor beta 2
LINC00484	1.397493	1.11E-28	2.89E-27	12.12447	Up	long intergenic non-protein coding RNA 484
GALNT5	1.396805	7.38E-23	1.2E-21	10.53766	Up	polypeptide N-acetylgalactosaminyltransferase 5
LOC101929705	1.396659	2.98E-48	3.62E-46	17.01031	Up	uncharacterized LOC101929705
DACT2	1.393311	2.7E-16	2.43E-15	8.580885	Up	dishevelled binding antagonist of beta catenin 2
WNT10B	1.388628	1.31E-24	2.44E-23	11.02636	Up	Wnt family member 10B
MATN2	1.387237	1.33E-71	1.06E-68	22.63224	Up	matrilin 2
AZIN2	1.38529	1.78E-64	7.56E-62	20.90748	Up	antizyme inhibitor 2
B3GALT5	1.381072	1.64E-19	1.98E-18	9.568734	Up	beta-1,3-galactosyltransferase 5
LINC00968	1.380375	2.74E-31	8.72E-30	12.80576	Up	long intergenic non-protein coding RNA 968
RIMS4	1.378732	2.96E-24	5.34E-23	10.92819	Up	regulating synaptic membrane exocytosis 4
RASGRP1	1.37836	2.81E-28	7.1E-27	12.01751	Up	RAS guanyl releasing protein 1
CPXM2	1.376429	6.43E-39	3.5E-37	14.73275	Up	carboxypeptidase X, M14 family member 2
FMO1	1.375361	2.26E-21	3.2E-20	10.11404	Up	flavin containing dimethylanilinemonooxygenase 1
CD83	1.374802	5.06E-51	7.79E-49	17.67736	Up	CD83 molecule
SYT17	1.374273	3.68E-62	1.32E-59	20.3506	Up	synaptotagmin 17

ABCG2	1.373113	9.52E-47	1E-44	16.64667	Up	ATP binding cassette subfamily G member 2 (Junior blood group)
FAM133A	1.369938	1.35E-18	1.5E-17	9.294288	Up	family with sequence similarity 133 member A
FEZF1-AS1	1.36779	8.24E-23	1.34E-21	10.52416	Up	FEZF1 antisense RNA 1
DNAAF3	1.367564	6.54E-30	1.87E-28	12.44747	Up	dynein axonemal assembly factor 3
IGFN1	1.364677	5.51E-21	7.61E-20	10.00175	Up	immunoglobulin like and fibronectin type III domain containing 1
SH2D1A	1.363761	7.86E-21	1.07E-19	9.957054	Up	SH2 domain containing 1A
SRGAP3-AS4	1.363047	1.3E-18	1.45E-17	9.298963	Up	SRGAP3 antisense RNA 4
COL9A2	1.362168	4.17E-34	1.61E-32	13.52748	Up	collagen type IX alpha 2 chain
SIT1	1.359564	7.31E-23	1.19E-21	10.5389	Up	signaling threshold regulating transmembrane adaptor 1
CHRD1	1.359548	1.08E-18	1.21E-17	9.323916	Up	chordin like 1
RGS17	1.359486	6.69E-25	1.28E-23	11.10644	Up	regulator of G protein signaling 17
ACKR4	1.358827	1.17E-40	7.32E-39	15.16203	Up	atypical chemokine receptor 4
COL1A1	1.358302	1.03E-23	1.79E-22	10.77798	Up	collagen type I alpha 1 chain
CD5	1.356328	1.97E-22	3.06E-21	10.41671	Up	CD5 molecule
SOX8	1.353422	1.7E-41	1.13E-39	15.36824	Up	SRY-box transcription factor 8
LRRRC77P	1.351962	3.85E-39	2.11E-37	14.78807	Up	leucine rich repeat containing 77, pseudogene
UNC5B-AS1	1.351117	1.06E-12	6.71E-12	7.381669	Up	UNC5B antisense RNA 1
SCG5	1.350517	2.08E-24	3.81E-23	10.97082	Up	secretogranin V
LINC01267	1.348563	1.11E-18	1.25E-17	9.319702	Up	long intergenic non-protein coding RNA 1267
RXRG	1.346393	4.44E-37	2.14E-35	14.2756	Up	retinoid X receptor gamma
CD27	1.345829	1.13E-16	1.06E-15	8.700302	Up	CD27 molecule
GLYATL2	1.342594	9.82E-35	3.98E-33	13.68647	Up	glycine-N-acyltransferase like 2
ANKRD24	1.342518	1.54E-25	3.07E-24	11.28066	Up	ankyrin repeat domain 24
INKA1	1.340521	8.59E-22	1.26E-20	10.23452	Up	inka box actin regulator 1
IFI44L	1.338481	1E-44	8.57E-43	16.15631	Up	interferon induced protein 44 like
MS4A2	1.33714	2.29E-16	2.08E-15	8.603622	Up	membrane spanning 4-domains A2
RHCG	1.336804	4.25E-12	2.55E-11	7.166944	Up	Rh family C glycoprotein
METTL21EP	1.332538	1.34E-27	3.17E-26	11.83678	Up	methyltransferase like 21E, pseudogene
CEMIP	1.332429	4.08E-15	3.29E-14	8.200242	Up	cell migration inducing hyaluronidase 1
CD247	1.330672	4.07E-38	2.09E-36	14.53411	Up	CD247 molecule
F2RL2	1.33014	1.01E-24	1.91E-23	11.05693	Up	coagulation factor II thrombin receptor like 2
IL31RA	1.327493	7.49E-14	5.34E-13	7.779083	Up	interleukin 31 receptor A
USP9Y	1.322424	0.009551	0.016327	2.605368	Up	ubiquitin specific peptidase 9 Y-linked
BRINP1	1.317235	1.88E-21	2.68E-20	10.13695	Up	BMP/retinoic acid inducible neural specific 1
MOXD1	1.313654	3.61E-40	2.16E-38	15.04169	Up	monooxygenase DBH like 1
MED12L	1.312022	6.18E-28	1.5E-26	11.92652	Up	mediator complex subunit 12L
LOC101927811	1.310553	1.22E-27	2.89E-26	11.84779	Up	uncharacterized LOC101927811
DNAJC27-AS1	1.309638	3.13E-32	1.06E-30	13.04877	Up	DNAJC27 antisense RNA 1
FAM225B	1.309169	1.21E-25	2.43E-24	11.30969	Up	family with sequence similarity 225 member B
SERPINE2	1.30842	1.21E-34	4.89E-33	13.66314	Up	serpin family E member 2
C1QTNF9	1.308078	6.34E-32	2.1E-30	12.96982	Up	C1q and TNF related 9
LMX1A	1.305166	2.75E-22	4.22E-21	10.37562	Up	LIM homeobox transcription factor 1 alpha

MIR181A2HG	1.303865	6.57E-32	2.17E-30	12.96582	Up	MIR181A2 host gene
THBS4	1.302766	3.46E-33	1.24E-31	13.2937	Up	thrombospondin 4
ROBO2	1.302226	4.74E-19	5.49E-18	9.431255	Up	roundabout guidance receptor 2
LOC105373878	1.300436	9.52E-38	4.77E-36	14.4422	Up	uncharacterized LOC105373878
ATP1B2	1.30027	1.37E-57	3.57E-55	19.25327	Up	ATPase Na ⁺ /K ⁺ transporting subunit beta 2
FHAD1	1.29999	3.37E-26	7.14E-25	11.46057	Up	forkhead associated phosphopeptide binding domain 1
LCK	1.297893	2.03E-30	5.98E-29	12.57993	Up	LCK proto-oncogene, Src family tyrosine kinase
TMEM156	1.294685	1.97E-22	3.06E-21	10.41685	Up	transmembrane protein 156
LINC00211	1.293649	1.35E-30	4.05E-29	12.62631	Up	long intergenic non-protein coding RNA 211
PLEKHH2	1.29203	2.39E-30	7E-29	12.56159	Up	pleckstrin homology, MyTH4 and FERM domain containing H2
LINC01426	1.289853	9.64E-23	1.55E-21	10.50485	Up	long intergenic non-protein coding RNA 1426
ZMYND15	1.289009	7.84E-39	4.22E-37	14.71153	Up	zinc finger MYND-type containing 15
UCHL1	1.288567	6E-25	1.15E-23	11.11939	Up	ubiquitin C-terminal hydrolase L1
MYOZ1	1.288488	2.05E-25	4.04E-24	11.24716	Up	myozenin 1
MAP3K7CL	1.288168	8.27E-21	1.12E-19	9.950544	Up	MAP3K7 C-terminal like
PLCH2	1.287447	1.12E-18	1.26E-17	9.318392	Up	phospholipase C eta 2
MRC2	1.286807	6.94E-34	2.63E-32	13.47131	Up	mannose receptor C type 2
ADAMTSL1	1.286675	1.51E-31	4.89E-30	12.87241	Up	ADAMTS like 1
PDE4C	1.285231	2.27E-38	1.19E-36	14.59704	Up	phosphodiesterase 4C
CXCL14	1.281807	6.76E-16	5.83E-15	8.453562	Up	C-X-C motif chemokine ligand 14
GDNF	1.280842	2.33E-24	4.25E-23	10.95683	Up	glial cell derived neurotrophic factor
ASB18	1.280174	5.71E-37	2.73E-35	14.24819	Up	ankyrin repeat and SOCS box containing 18
HHIP	1.278593	7.98E-19	9.06E-18	9.363129	Up	hedgehog interacting protein
KDM5D	1.277307	0.011648	0.019535	2.535361	Up	lysine demethylase 5D
MIR3142HG	1.277276	1.35E-26	2.93E-25	11.5679	Up	MIR3142 host gene
LTBP2	1.274413	1.1E-34	4.45E-33	13.67374	Up	latent transforming growth factor beta binding protein 2
IRX6	1.271621	1.65E-28	4.22E-27	12.079	Up	iroquoishomeobox 6
CLEC11A	1.271266	1.43E-22	2.25E-21	10.45611	Up	C-type lectin domain containing 11A
IDO1	1.270315	2.09E-16	1.91E-15	8.615828	Up	indoleamine 2,3-dioxygenase 1
C1QTNF9B	1.268225	7.19E-17	6.84E-16	8.76235	Up	C1q and TNF related 9B
CRYM	1.266414	1.15E-47	1.3E-45	16.86886	Up	crystallin mu
EFCAB1	1.265871	4.84E-24	8.61E-23	10.86895	Up	EF-hand calcium binding domain 1
DDX3Y	1.264424	0.013065	0.021716	2.494173	Up	DEAD-box helicase 3 Y-linked
CHIT1	1.264407	4.27E-10	2.05E-09	6.417928	Up	chitinase 1
GNG8	1.2627	8.4E-11	4.37E-10	6.689199	Up	G protein subunit gamma 8
NT5E	1.261748	1.1E-52	2.02E-50	18.07717	Up	5'-nucleotidase ecto
HCG20	1.261078	2.49E-24	4.52E-23	10.94906	Up	HLA complex group 20
NEURL1	1.260771	1.31E-24	2.45E-23	11.0258	Up	neuralized E3 ubiquitin protein ligase 1
EYS	1.260064	7.24E-19	8.26E-18	9.375881	Up	eyes shut homolog
GLI2	1.255414	6.95E-43	5.21E-41	15.70783	Up	GLI family zinc finger 2
LINC01133	1.254973	2.04E-14	1.54E-13	7.969277	Up	long intergenic non-protein coding RNA 1133
LOC105371795	1.253649	3.74E-17	3.66E-16	8.851004	Up	uncharacterized LOC105371795

DPT	1.250345	5.78E-42	3.96E-40	15.48293	Up	dermatopontin
PRR15	1.249204	2.22E-21	3.15E-20	10.11632	Up	proline rich 15
CTNNA2	1.248053	6.25E-22	9.25E-21	10.2742	Up	catenin alpha 2
HMCN2	1.24733	1.65E-24	3.05E-23	10.99834	Up	hemicentin 2
ITGB2-AS1	1.247241	6.45E-29	1.72E-27	12.18654	Up	ITGB2 antisense RNA 1
TLR7	1.246342	4.37E-26	9.15E-25	11.42984	Up	toll like receptor 7
HLA-DQA1	1.244186	3.69E-21	5.15E-20	10.05236	Up	major histocompatibility complex, class II, DQ alpha 1
TAC4	1.24286	1.46E-20	1.91E-19	9.878964	Up	tachykinin precursor 4
LRRC52-AS1	1.241509	7.78E-13	5.01E-12	7.428482	Up	LRRC52 antisense RNA 1
PPM1K-DT	1.240771	1.97E-10	9.85E-10	6.547691	Up	PPM1K divergent transcript
PIEZO2	1.240568	7.72E-16	6.63E-15	8.434952	Up	piezo type mechanosensitive ion channel component 2
CCDC80	1.239608	1.42E-30	4.24E-29	12.62065	Up	coiled-coil domain containing 80
DUSP15	1.239063	4.11E-35	1.7E-33	13.78207	Up	dual specificity phosphatase 15
GNLY	1.238419	1.78E-27	4.16E-26	11.80405	Up	granulysin
CNTNAP2	1.235959	5.04E-18	5.34E-17	9.11997	Up	contactin associated protein like 2
PRRX2	1.235523	3.93E-12	2.36E-11	7.178965	Up	paired related homeobox 2
DUOX2	1.23448	5.79E-28	1.41E-26	11.93408	Up	dual oxidase 2
GNA14	1.233753	1.61E-50	2.34E-48	17.55626	Up	G protein subunit alpha 14
PMP2	1.233661	5.07E-20	6.39E-19	9.719945	Up	peripheral myelin protein 2
FOXO6-AS1	1.231713	1.06E-20	1.42E-19	9.918623	Up	FOXO6 antisense RNA 1
MALRD1	1.231194	3.34E-18	3.59E-17	9.174723	Up	MAM and LDL receptor class A domain containing 1
PHF21B	1.227657	1.22E-30	3.69E-29	12.63719	Up	PHD finger protein 21B
OLFML1	1.224413	5.26E-65	2.38E-62	21.03513	Up	olfactomedin like 1
TRIM17	1.221292	5.11E-26	1.06E-24	11.41147	Up	tripartite motif containing 17
TSPAN10	1.220763	5.54E-31	1.72E-29	12.72652	Up	tetraspanin 10
IER3	1.220245	1.19E-22	1.9E-21	10.4788	Up	immediate early response 3
NUP62CL	1.219897	2.88E-34	1.12E-32	13.56819	Up	nucleoporin 62 C-terminal like
GPA33	1.219144	1.29E-23	2.22E-22	10.75057	Up	glycoprotein A33
CLEC9A	1.21506	1.84E-16	1.69E-15	8.633518	Up	C-type lectin domain containing 9A
HMGA2-AS1	1.214586	5.25E-21	7.26E-20	10.00787	Up	HMGA2 antisense RNA 1
LUARIS	1.213922	1.79E-17	1.81E-16	8.950795	Up	lncRNAupregulator of antiviral response interferon signaling
KCNN3	1.211097	5.05E-50	7.1E-48	17.43693	Up	potassium calcium-activated channel subfamily N member 3
MSS51	1.211068	4.05E-43	3.1E-41	15.76499	Up	MSS51 mitochondrial translational activator
LOC286178	1.203156	3.35E-17	3.28E-16	8.866208	Up	uncharacterized LOC286178
BCL11B	1.200808	5E-21	6.92E-20	10.01416	Up	BAF chromatin remodeling complex subunit BCL11B
FSCN1	1.200742	5.5E-22	8.18E-21	10.29007	Up	fascin actin-bundling protein 1
ARSI	1.199759	1.81E-14	1.37E-13	7.986748	Up	arylsulfatase family member I
TP63	1.199611	1.25E-32	4.34E-31	13.15108	Up	tumor protein p63
APOA1-AS	1.198437	1.23E-11	6.96E-11	6.999998	Up	APOA1 antisense RNA
LINC01531	1.197352	5.61E-13	3.67E-12	7.478264	Up	long intergenic non-protein coding RNA 1531
CD40LG	1.196777	8.21E-16	7.01E-15	8.42641	Up	CD40 ligand
CAMK4	1.196139	1.86E-19	2.23E-18	9.552711	Up	calcium/calmodulin dependent protein kinase IV

TM6SF2	1.194983	2.63E-30	7.66E-29	12.55083	Up	transmembrane 6 superfamily member 2
TRAF3IP3	1.193405	4.01E-36	1.79E-34	14.03636	Up	TRAF3 interacting protein 3
SIGLEC8	1.192	1.1E-18	1.23E-17	9.321523	Up	sialic acid binding Ig like lectin 8
WDR66	1.191782	5.11E-49	6.63E-47	17.19495	Up	WD repeat domain 66
ALOX15	1.189497	2.11E-14	1.59E-13	7.96447	Up	arachidonate 15-lipoxygenase
KLHL35	1.186728	4.84E-19	5.59E-18	9.428585	Up	kelch like family member 35
ITGB7	1.184564	1.14E-39	6.55E-38	14.91886	Up	integrin subunit beta 7
SEC14L6	1.18353	2.24E-18	2.45E-17	9.227693	Up	SEC14 like lipid binding 6
PDIA2	1.181381	8.1E-21	1.1E-19	9.953216	Up	protein disulfideisomerase family A member 2
LGI1	1.180437	1.29E-19	1.57E-18	9.600238	Up	leucine rich glioma inactivated 1
PPDPF	1.180084	2.23E-16	2.03E-15	8.60702	Up	pancreatic progenitor cell differentiation and proliferation factor
SYTL2	1.179465	1.01E-34	4.07E-33	13.68374	Up	synaptotagmin like 2
ADAMTSL2	1.179365	2.6E-22	4E-21	10.38261	Up	ADAMTS like 2
FZD2	1.178996	1.82E-18	2E-17	9.255263	Up	frizzled class receptor 2
LAMB4	1.17768	7.69E-18	8.02E-17	9.063817	Up	laminin subunit beta 4
NRIP2	1.176935	9.58E-49	1.2E-46	17.12912	Up	nuclear receptor interacting protein 2
SULF1	1.175739	2.88E-38	1.49E-36	14.57145	Up	sulfatase 1
ETV7	1.175707	8.16E-17	7.74E-16	8.745045	Up	ETS variant transcription factor 7
ANKRD36BP2	1.171138	3.75E-18	4.02E-17	9.159248	Up	ankyrin repeat domain 36B pseudogene 2
COLQ	1.170037	5.17E-28	1.27E-26	11.94726	Up	collagen like tail subunit of asymmetric acetylcholinesterase
PODXL2	1.169919	8.66E-47	9.23E-45	16.65665	Up	podocalyxin like 2
LINC00501	1.169906	9.77E-31	2.97E-29	12.6627	Up	long intergenic non-protein coding RNA 501
CARD11	1.169111	1.27E-22	2.01E-21	10.47111	Up	caspase recruitment domain family member 11
ANO9	1.168436	6.51E-16	5.62E-15	8.458675	Up	anoctamin 9
SERTAD4	1.167618	5.18E-28	1.28E-26	11.94687	Up	SERTA domain containing 4
PYHIN1	1.16663	1.63E-21	2.34E-20	10.15473	Up	pyrin and HIN domain family member 1
CD48	1.165664	5.88E-26	1.21E-24	11.39481	Up	CD48 molecule
C12orf75	1.164765	1.52E-28	3.92E-27	12.08817	Up	chromosome 12 open reading frame 75
HTR2B	1.161887	2.28E-18	2.49E-17	9.225086	Up	5-hydroxytryptamine receptor 2B
ECM2	1.161863	9.81E-31	2.97E-29	12.66225	Up	extracellular matrix protein 2
PDE5A	1.160025	1.39E-39	7.94E-38	14.89735	Up	phosphodiesterase 5A
GZMK	1.159035	4.82E-19	5.58E-18	9.429051	Up	granzyme K
TEX41	1.15826	7.5E-23	1.22E-21	10.53572	Up	testis expressed 41
IL1RL1	-4.16665	1.16E-92	8.03E-89	-27.8886	Down	interleukin 1 receptor like 1
RNASE2	-3.13727	1.02E-71	8.46E-69	-22.6604	Down	ribonuclease A family member 2
ALOX15B	-3.04933	8.54E-42	5.82E-40	-15.4414	Down	arachidonate 15-lipoxygenase type B
LCN10	-3.01762	7.59E-61	2.5E-58	-20.0349	Down	lipocalin 10
TUBA3E	-2.99401	5.3E-73	5.25E-70	-22.973	Down	tubulin alpha 3e
TUBA3D	-2.93212	1.14E-70	8.14E-68	-22.4056	Down	tubulin alpha 3d
MYH6	-2.7545	1.4E-76	2.23E-73	-23.8495	Down	myosin heavy chain 6
PI15	-2.74552	3.93E-40	2.34E-38	-15.0328	Down	peptidase inhibitor 15
TUBA3C	-2.74348	1.64E-56	4E-54	-18.9952	Down	tubulin alpha 3c

CYP4B1	-2.71576	9.65E-56	2.23E-53	-18.8104	Down	cytochrome P450 family 4 subfamily B member 1
NPTX2	-2.59581	1.15E-68	6.46E-66	-21.9193	Down	neuronal pentraxin 2
AOX1	-2.57613	8.34E-69	4.81E-66	-21.953	Down	aldehyde oxidase 1
PLA2G2A	-2.55621	2.06E-43	1.6E-41	-15.8368	Down	phospholipase A2 group IIA
LCN6	-2.54437	7.91E-59	2.16E-56	-19.5506	Down	lipocalin 6
CD163	-2.50965	1.12E-85	2.6E-82	-26.1108	Down	CD163 molecule
GNMT	-2.50909	2.21E-57	5.61E-55	-19.2036	Down	glycine N-methyltransferase
AQP4	-2.50556	1.63E-36	7.51E-35	-14.1345	Down	aquaporin 4
SCGN	-2.48857	7.7E-44	6.13E-42	-15.9409	Down	secretagoin, EF-hand calcium binding protein
FCN3	-2.48214	5.69E-69	3.48E-66	-21.9932	Down	ficolin 3
SLCO4A1	-2.41668	4.74E-68	2.46E-65	-21.7703	Down	solute carrier organic anion transporter family member 4A1
PPEF1	-2.40843	4.16E-51	6.54E-49	-17.6979	Down	protein phosphatase with EF-hand domain 1
SGPP2	-2.38709	1.41E-45	1.31E-43	-16.3629	Down	sphingosine-1-phosphate phosphatase 2
SAA1	-2.36387	6.15E-14	4.41E-13	-7.80794	Down	serum amyloid A1
IL1R2	-2.33348	8.84E-47	9.38E-45	-16.6544	Down	interleukin 1 receptor type 2
OLAH	-2.32381	1.23E-49	1.65E-47	-17.3439	Down	oleoyl-ACP hydrolase
LCN15	-2.30949	1.71E-34	6.83E-33	-13.6252	Down	lipocalin 15
CYP4Z1	-2.2978	4.89E-54	1.03E-51	-18.4015	Down	cytochrome P450 family 4 subfamily Z member 1
OVOS2	-2.29611	2.76E-28	6.99E-27	-12.0196	Down	alpha-2-macroglobulin like 1 pseudogene
IL10	-2.26244	1.07E-46	1.11E-44	-16.6348	Down	interleukin 10
CD177	-2.24129	1.27E-25	2.55E-24	-11.3037	Down	CD177 molecule
GALNT15	-2.23547	2.82E-69	1.83E-66	-22.067	Down	polypeptide N-acetylgalactosaminyltransferase 15
FKBP5	-2.20125	1.02E-64	4.52E-62	-20.9657	Down	FKBP prolylisomerase 5
HOPX	-2.19678	2.33E-39	1.3E-37	-14.842	Down	HOP homeobox
MCEMP1	-2.16877	7.4E-33	2.6E-31	-13.2092	Down	mast cell expressed membrane protein 1
SYN2	-2.13215	4.46E-44	3.61E-42	-15.9986	Down	synapsin II
SERPINA3	-2.12094	2.93E-28	7.39E-27	-12.0128	Down	serpin family A member 3
TCF24	-2.09501	6.7E-26	1.37E-24	-11.3795	Down	transcription factor 24
CFTR	-2.08432	2.72E-36	1.23E-34	-14.0784	Down	CF transmembrane conductance regulator
RARRES1	-2.08128	1.7E-44	1.43E-42	-16.1007	Down	retinoic acid receptor responder 1
EREG	-2.0761	5.3E-22	7.89E-21	-10.2947	Down	epiregulin
LBP	-2.0676	1.07E-20	1.43E-19	-9.91761	Down	lipopolysaccharide binding protein
C4orf54	-2.05065	8.08E-20	9.99E-19	-9.66017	Down	chromosome 4 open reading frame 54
LGI3	-2.04234	5.28E-32	1.77E-30	-12.9903	Down	leucine rich repeat LGI family member 3
BLM	-2.03762	5.04E-74	5.51E-71	-23.2226	Down	BLM RecQ like helicase
SULT1B1	-2.03126	2.66E-49	3.5E-47	-17.263	Down	sulfotransferase family 1B member 1
C1orf105	-2.02075	2.12E-41	1.4E-39	-15.3444	Down	chromosome 1 open reading frame 105
ADAMTS4	-2.01588	5.48E-45	4.87E-43	-16.2199	Down	ADAM metalloproteinase with thrombospondin type 1 motif 4
HMGCS2	-2.00935	9.11E-18	9.44E-17	-9.04123	Down	3-hydroxy-3-methylglutaryl-CoA synthase 2
VSIG4	-1.98626	3.18E-76	4.71E-73	-23.7619	Down	V-set and immunoglobulin domain containing 4
STAC2	-1.96935	2.46E-34	9.76E-33	-13.5853	Down	SH3 and cysteine rich domain 2
FGF10	-1.92961	4.3E-26	9.02E-25	-11.4317	Down	fibroblast growth factor 10

LYVE1	-1.92131	1.57E-62	5.8E-60	-20.4397	Down	lymphatic vessel endothelial hyaluronan receptor 1
LAD1	-1.91982	9.62E-41	6.02E-39	-15.1832	Down	ladinin 1
WNK3	-1.9035	3.09E-61	1.09E-58	-20.1286	Down	WNK lysine deficient protein kinase 3
DHRS7C	-1.88942	1.04E-19	1.28E-18	-9.62709	Down	dehydrogenase/reductase 7C
NMRAL2P	-1.86141	1.01E-41	6.86E-40	-15.4235	Down	NmrA like redox sensor 2, pseudogene
GMNC	-1.83731	6.65E-29	1.76E-27	-12.1831	Down	geminin coiled-coil domain containing
METTL7B	-1.83099	2.07E-40	1.25E-38	-15.1014	Down	methyltransferase like 7B
PLA2G4F	-1.81396	4.24E-24	7.58E-23	-10.8848	Down	phospholipase A2 group IVF
SLC11A1	-1.8014	5.26E-44	4.24E-42	-15.9811	Down	solute carrier family 11 member 1
LINC00964	-1.77887	1.45E-36	6.73E-35	-14.1472	Down	long intergenic non-protein coding RNA 964
LINC02207	-1.76058	3.51E-29	9.52E-28	-12.2562	Down	long intergenic non-protein coding RNA 2207
OVCH1	-1.75228	1.32E-37	6.59E-36	-14.4065	Down	ovochoymase 1
RHBDL3	-1.74833	8.3E-31	2.54E-29	-12.681	Down	rhomboid like 3
MGST1	-1.73713	2.06E-39	1.16E-37	-14.8552	Down	microsomal glutathione S-transferase 1
MARCO	-1.7321	5.53E-16	4.82E-15	-8.48151	Down	macrophage receptor with collagenous structure
SLC25A18	-1.69891	5.06E-39	2.77E-37	-14.7586	Down	solute carrier family 25 member 18
MANCR	-1.6978	1.89E-40	1.15E-38	-15.1112	Down	mitotically associated long non coding RNA
TBC1D29P	-1.6943	1.92E-27	4.46E-26	-11.7954	Down	TBC1 domain family member 29, pseudogene
IL17RB	-1.68748	5.8E-43	4.39E-41	-15.727	Down	interleukin 17 receptor B
C5orf64	-1.66664	9.16E-29	2.4E-27	-12.1463	Down	chromosome 5 open reading frame 64
TDRD9	-1.65083	3.47E-52	5.96E-50	-17.9571	Down	tudor domain containing 9
CNTN3	-1.65075	1.17E-29	3.28E-28	-12.3817	Down	contactin 3
SSTR5	-1.64589	1.42E-10	7.2E-10	-6.60229	Down	somatostatin receptor 5
FAM155B	-1.64483	3.91E-31	1.22E-29	-12.7659	Down	family with sequence similarity 155 member B
TMEFF2	-1.63641	9.72E-21	1.3E-19	-9.9302	Down	transmembrane protein with EGF like and two follistatin like domains 2
SIGLEC9	-1.61765	9.97E-57	2.47E-54	-19.0468	Down	sialic acid binding Ig like lectin 9
IL18R1	-1.61068	2.84E-55	6.41E-53	-18.698	Down	interleukin 18 receptor 1
AQP3	-1.59794	1.16E-48	1.44E-46	-17.1093	Down	aquaporin 3 (Gill blood group)
SLC38A8	-1.59297	8.76E-15	6.82E-14	-8.09114	Down	solute carrier family 38 member 8
TMIGD3	-1.59103	1.26E-42	9.18E-41	-15.6445	Down	transmembrane and immunoglobulin domain containing 3
MT1A	-1.58793	1.47E-13	1.02E-12	-7.67924	Down	metallothionein 1A
CA14	-1.58283	5.77E-28	1.41E-26	-11.9346	Down	carbonic anhydrase 14
CPM	-1.5817	1.23E-50	1.8E-48	-17.5848	Down	carboxypeptidase M
ETNPPL	-1.55969	1.83E-29	5.09E-28	-12.3302	Down	ethanolamine-phosphate phospho-lyase
SLC66A1L	-1.54109	1.16E-43	9.14E-42	-15.8978	Down	solute carrier family 66 member 1 like
GPR84	-1.5373	1.18E-21	1.71E-20	-10.1951	Down	G protein-coupled receptor 84
HOOK1	-1.53589	2.71E-43	2.09E-41	-15.8079	Down	hook microtubule tethering protein 1
CHDH	-1.52384	2.82E-55	6.41E-53	-18.6987	Down	choline dehydrogenase
SERTM1	-1.52131	7.14E-21	9.74E-20	-9.96917	Down	serine rich and transmembrane domain containing 1
SHISA3	-1.51927	2.09E-36	9.56E-35	-14.107	Down	shisa family member 3
PCSK1	-1.50962	2.47E-21	3.49E-20	-10.1028	Down	proproteinconvertasesubtilisin/kexin type 1
ADH1B	-1.49531	3.76E-35	1.57E-33	-13.7917	Down	alcohol dehydrogenase 1B (class I), beta polypeptide

CATSPERB	-1.48402	3.22E-35	1.35E-33	-13.8089	Down	cation channel sperm associated auxiliary subunit beta
CD38	-1.48372	1.86E-52	3.3E-50	-18.0222	Down	CD38 molecule
POM121L9P	-1.47176	1.12E-54	2.41E-52	-18.5546	Down	POM121 transmembranenucleoporin like 9, pseudogene
LINC01166	-1.47139	3.94E-20	5E-19	-9.75233	Down	long intergenic non-protein coding RNA 1166
RDH10-AS1	-1.47137	1.52E-36	7.04E-35	-14.142	Down	RDH10 antisense RNA 1
CACNA1E	-1.46899	4.75E-19	5.5E-18	-9.43103	Down	calcium voltage-gated channel subunit alpha1 E
PAQR5	-1.45849	2.86E-37	1.4E-35	-14.323	Down	progesterin and adipoQ receptor family member 5
LINC02388	-1.45595	2.84E-15	2.32E-14	-8.25187	Down	long intergenic non-protein coding RNA 2388
LINC01134	-1.44716	4.56E-31	1.42E-29	-12.7486	Down	long intergenic non-protein coding RNA 1134
HPCAL4	-1.44324	1.12E-20	1.49E-19	-9.91235	Down	hippocalcin like 4
BMP7	-1.43955	1.41E-20	1.85E-19	-9.88326	Down	bone morphogenetic protein 7
SERPINE1	-1.43704	5.19E-17	5.01E-16	-8.80674	Down	serpin family E member 1
KNG1	-1.43341	1.09E-20	1.45E-19	-9.916	Down	kininogen 1
MCM10	-1.42685	7.91E-27	1.76E-25	-11.6304	Down	minichromosome maintenance 10 replication initiation factor
SLC22A16	-1.41592	1.05E-21	1.52E-20	-10.2097	Down	solute carrier family 22 member 16
LOC105378909	-1.41396	3.53E-27	8.05E-26	-11.7245	Down	uncharacterized LOC105378909
TMEM151B	-1.41097	3.2E-11	1.74E-10	-6.84623	Down	transmembrane protein 151B
WNT9B	-1.40828	2.89E-27	6.65E-26	-11.7476	Down	Wnt family member 9B
ST6GALNAC3	-1.4044	8.83E-77	1.53E-73	-23.8986	Down	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 3
ZBTB16	-1.40189	1.08E-26	2.37E-25	-11.594	Down	zinc finger and BTB domain containing 16
LINC01088	-1.39856	2.94E-29	8.01E-28	-12.2765	Down	long intergenic non-protein coding RNA 1088
ANPEP	-1.39173	1.79E-35	7.6E-34	-13.8727	Down	alanylaminopeptidase, membrane
CHST9	-1.39105	2.86E-17	2.83E-16	-8.88726	Down	carbohydrate sulfotransferase 9
CHAC2	-1.39049	4.46E-51	6.91E-49	-17.6907	Down	ChaCcation transport regulator homolog 2
ANKRD2	-1.38594	1.02E-21	1.49E-20	-10.2128	Down	ankyrin repeat domain 2
EDNRB	-1.37805	1.43E-45	1.32E-43	-16.3619	Down	endothelin receptor type B
TMEM132B	-1.37526	5.39E-29	1.44E-27	-12.207	Down	transmembrane protein 132B
SSTR2	-1.36986	6.6E-38	3.34E-36	-14.4818	Down	somatostatin receptor 2
TFCP2L1	-1.36492	1.52E-30	4.54E-29	-12.6127	Down	transcription factor CP2 like 1
LMAN1L	-1.35734	9.77E-15	7.57E-14	-8.07551	Down	lectin, mannose binding 1 like
NSG1	-1.35624	1.61E-34	6.43E-33	-13.6323	Down	neuronal vesicle trafficking associated 1
SCGB1D2	-1.34714	1.13E-14	8.67E-14	-8.05497	Down	secretoglobulin family 1D member 2
S1PR3	-1.33974	6.86E-68	3.48E-65	-21.7316	Down	sphingosine-1-phosphate receptor 3
HP	-1.33891	2.46E-11	1.36E-10	-6.88868	Down	haptoglobin
TMTC1	-1.33154	7.96E-61	2.58E-58	-20.0299	Down	transmembrane O-mannosyltransferase targeting cadherins 1
TOGARAM2	-1.33092	1.63E-16	1.49E-15	-8.65076	Down	TOG array regulator of axonemal microtubules 2
SDR16C5	-1.32851	1.79E-22	2.78E-21	-10.4291	Down	short chain dehydrogenase/reductase family 16C member 5
RGR	-1.3272	3.63E-16	3.22E-15	-8.54004	Down	retinal G protein coupled receptor
S100A9	-1.32587	2.6E-19	3.08E-18	-9.50952	Down	S100 calcium binding protein A9
FCGR3A	-1.32476	1.14E-35	4.89E-34	-13.9225	Down	Fc fragment of IgG receptor IIIa
KRT7	-1.3219	3.25E-11	1.77E-10	-6.84385	Down	keratin 7
HS6ST2	-1.31832	5.38E-20	6.76E-19	-9.71245	Down	heparansulfate 6-O-sulfotransferase 2

SERPINA5	-1.3169	3.35E-31	1.06E-29	-12.7831	Down	serpin family A member 5
SRARP	-1.31534	3.97E-17	3.86E-16	-8.84306	Down	steroid receptor associated and regulated protein
CEP55	-1.3114	5.49E-18	5.79E-17	-9.10864	Down	centrosomal protein 55
SLC7A11	-1.30737	3.72E-21	5.19E-20	-10.0514	Down	solute carrier family 7 member 11
ELANE	-1.30624	1.4E-12	8.75E-12	-7.33899	Down	elastase, neutrophil expressed
LOC100419170	-1.30099	6.81E-16	5.87E-15	-8.4525	Down	toll like receptor 2 pseudogene
TENT5B	-1.29835	4.23E-30	1.22E-28	-12.4969	Down	terminal nucleotidyltransferase 5B
KCNB1	-1.29075	8.19E-36	3.55E-34	-13.9585	Down	potassium voltage-gated channel subfamily B member 1
GPRC5A	-1.29031	7.12E-23	1.16E-21	-10.5421	Down	G protein-coupled receptor class C group 5 member A
FGF5	-1.28935	1.24E-16	1.16E-15	-8.68752	Down	fibroblast growth factor 5
CFAP77	-1.28763	5.19E-34	1.99E-32	-13.5033	Down	cilia and flagella associated protein 77
PDE11A	-1.28742	1.21E-22	1.92E-21	-10.4774	Down	phosphodiesterase 11A
TMEM178B	-1.28381	1.72E-36	7.93E-35	-14.1282	Down	transmembrane protein 178B
MATN3	-1.28258	9.51E-31	2.89E-29	-12.6658	Down	matrilin 3
SBK3	-1.28125	1.17E-16	1.09E-15	-8.69549	Down	SH3 domain binding kinase family member 3
GRIP1	-1.27293	3.11E-18	3.36E-17	-9.18402	Down	glutamate receptor interacting protein 1
PART1	-1.27148	6.39E-23	1.05E-21	-10.5554	Down	prostate androgen-regulated transcript 1
TIMP4	-1.26931	2.11E-35	8.86E-34	-13.8552	Down	TIMP metalloproteinase inhibitor 4
EHD4-AS1	-1.26754	9.1E-30	2.58E-28	-12.4099	Down	EHD4 antisense RNA 1
VSTM2L	-1.26748	8.09E-16	6.92E-15	-8.4284	Down	V-set and transmembrane domain containing 2 like
RHAG	-1.26165	7.36E-20	9.13E-19	-9.67218	Down	Rh associated glycoprotein
PLIN2	-1.25946	1.41E-53	2.89E-51	-18.2914	Down	perilipin 2
MYOT	-1.25393	2.67E-30	7.78E-29	-12.549	Down	myotilin
LOC100287036	-1.24828	4.78E-16	4.2E-15	-8.50169	Down	uncharacterized LOC100287036
MEI4	-1.24458	8.2E-20	1.01E-18	-9.65827	Down	meiotic double-stranded break formation protein 4
NPPC	-1.24339	4.79E-13	3.16E-12	-7.50207	Down	natriuretic peptide C
FMO5	-1.24005	7.97E-24	1.4E-22	-10.8086	Down	flavin containing dimethylanilinemonooxygenase 5
KCNK1	-1.23892	1.6E-40	9.84E-39	-15.1288	Down	potassium two pore domain channel subfamily K member 1
SYT13	-1.23357	1.52E-22	2.38E-21	-10.4493	Down	synaptotagmin 13
PRODH	-1.22635	1.2E-21	1.74E-20	-10.1925	Down	proline dehydrogenase 1
FMN1	-1.22607	2.26E-31	7.21E-30	-12.8276	Down	formin 1
LINC02248	-1.22281	5.24E-10	2.49E-09	-6.38341	Down	long intergenic non-protein coding RNA 2248
DEPDC1B	-1.22028	5.87E-20	7.36E-19	-9.70121	Down	DEP domain containing 1B
DCXR-DT	-1.21729	4.05E-22	6.09E-21	-10.3281	Down	DCXR divergent transcript
CPAMD8	-1.21453	4.03E-42	2.79E-40	-15.5212	Down	C3 and PZP like alpha-2-macroglobulin domain containing 8
FPR1	-1.21425	9.03E-25	1.71E-23	-11.0706	Down	formyl peptide receptor 1
NQO1	-1.21175	9.69E-37	4.54E-35	-14.1908	Down	NAD(P)H quinone dehydrogenase 1
MT1X	-1.21115	1.52E-17	1.54E-16	-8.97267	Down	metallothionein 1X
GCOM1	-1.20921	2.46E-17	2.45E-16	-8.90776	Down	GRINL1A complex locus 1
SIGLEC10	-1.20658	4.38E-23	7.28E-22	-10.6014	Down	sialic acid binding Ig like lectin 10
REELD1	-1.20551	4.1E-20	5.2E-19	-9.74706	Down	reeler domain containing 1
TMEM63C	-1.20356	1.46E-12	9.14E-12	-7.33185	Down	transmembrane protein 63C

CHL1	-1.19884	8.63E-22	1.26E-20	-10.2341	Down	cell adhesion molecule L1 like
FOSL1	-1.19066	2.83E-11	1.55E-10	-6.86606	Down	FOS like 1, AP-1 transcription factor subunit
KIAA1549	-1.18909	1.17E-44	9.94E-43	-16.1398	Down	KIAA1549
ADAMTS9	-1.18748	1.39E-47	1.55E-45	-16.8488	Down	ADAM metalloproteinase with thrombospondin type 1 motif 9
F13A1	-1.17752	1.45E-30	4.33E-29	-12.6184	Down	coagulation factor XIII A chain
AASS	-1.177	7.57E-23	1.23E-21	-10.5345	Down	aminoadipate-semialdehyde synthase
LUCAT1	-1.17537	2.09E-19	2.5E-18	-9.5374	Down	lung cancer associated transcript 1
CDH16	-1.17513	1.51E-15	1.26E-14	-8.34112	Down	cadherin 16
ADAMTS5	-1.17106	2.15E-29	5.93E-28	-12.3122	Down	ADAM metalloproteinase with thrombospondin type 1 motif 5
KCNIP2	-1.17026	9.89E-23	1.59E-21	-10.5018	Down	potassium voltage-gated channel interacting protein 2
WWC1	-1.1615	2.31E-15	1.9E-14	-8.28103	Down	WW and C2 domain containing 1
S100A3	-1.15808	2.16E-13	1.48E-12	-7.62156	Down	S100 calcium binding protein A3
AGTR1	-1.15766	3.66E-28	9.17E-27	-11.987	Down	angiotensin II receptor type 1
SERPINF2	-1.15346	1.27E-22	2.01E-21	-10.4714	Down	serpin family F member 2
PRRG4	-1.14332	5.89E-24	1.04E-22	-10.8453	Down	proline rich and Gla domain 4
TC2N	-1.14268	2.27E-26	4.85E-25	-11.5069	Down	tandem C2 domains, nuclear
TPO	-1.13971	1.9E-43	1.48E-41	-15.8455	Down	thyroid peroxidase
GCKR	-1.13956	2.58E-13	1.75E-12	-7.59508	Down	glucokinase regulator
GPR82	-1.13898	3.09E-16	2.77E-15	-8.56224	Down	G protein-coupled receptor 82
CDC45	-1.13722	7.61E-19	8.64E-18	-9.36946	Down	cell division cycle 45
HERC2P3	-1.13576	2.68E-10	1.32E-09	-6.49664	Down	hect domain and RLD 2 pseudogene 3
ANGPTL4	-1.13308	3.75E-09	1.63E-08	-6.04163	Down	angiopoietin like 4
KCNA7	-1.13228	3.56E-12	2.15E-11	-7.1944	Down	potassium voltage-gated channel subfamily A member 7
ESRP2	-1.12695	3.32E-22	5.04E-21	-10.3527	Down	epithelial splicing regulatory protein 2
ART3	-1.12533	1.64E-43	1.28E-41	-15.861	Down	ADP-ribosyltransferase 3
IL20RA	-1.12045	3.43E-18	3.69E-17	-9.17123	Down	interleukin 20 receptor subunit alpha
KCNS2	-1.12023	9.08E-15	7.05E-14	-8.08602	Down	potassium voltage-gated channel modifier subfamily S member 2
MBNL3	-1.11831	3.63E-17	3.54E-16	-8.85536	Down	muscleblind like splicing regulator 3
GRB14	-1.11785	4.49E-48	5.3E-46	-16.9673	Down	growth factor receptor bound protein 14
MELK	-1.11646	6.76E-13	4.38E-12	-7.44996	Down	maternal embryonic leucine zipper kinase
NAMPT	-1.11563	4.32E-36	1.92E-34	-14.0282	Down	nicotinamidephosphoribosyltransferase
TLR2	-1.11382	1.37E-33	5.06E-32	-13.3964	Down	toll like receptor 2
ADGRF4	-1.1107	7.39E-09	3.09E-08	-5.92035	Down	adhesion G protein-coupled receptor F4
TTLL6	-1.10862	3.1E-17	3.06E-16	-8.87646	Down	tubulin tyrosine ligase like 6
KCND3	-1.10777	6.54E-58	1.74E-55	-19.3306	Down	potassium voltage-gated channel subfamily D member 3
GPSM2	-1.09924	5.94E-32	1.98E-30	-12.9771	Down	G protein signaling modulator 2
CAMSAP3	-1.0914	2.63E-11	1.44E-10	-6.87822	Down	calmodulin regulated spectrin associated protein family member 3
NID1	-1.08953	2E-53	3.99E-51	-18.2549	Down	nidogen 1
MOG	-1.08574	8.19E-13	5.26E-12	-7.42074	Down	myelin oligodendrocyte glycoprotein
PALLD	-1.08474	2.46E-46	2.47E-44	-16.5468	Down	palladin, cytoskeletal associated protein
MPP3	-1.08422	7.46E-37	3.52E-35	-14.2192	Down	membrane palmitoylated protein 3
THBS1	-1.08344	2.37E-19	2.82E-18	-9.52148	Down	thrombospondin 1

SLCO2A1	-1.0825	3.32E-35	1.39E-33	-13.8055	Down	solute carrier organic anion transporter family member 2A1
SPOCK3	-1.07804	2.78E-08	1.09E-07	-5.67797	Down	SPARC (osteonectin), cwcv and kazal like domains proteoglycan 3
CR1	-1.07745	6.04E-16	5.23E-15	-8.46919	Down	complement C3b/C4b receptor 1 (Knops blood group)
TUBB4A	-1.07702	7.72E-19	8.77E-18	-9.36749	Down	tubulin beta 4A class IVa
F8	-1.07543	1.03E-33	3.85E-32	-13.4275	Down	coagulation factor VIII
ZNF366	-1.07245	1.55E-09	6.99E-09	-6.19713	Down	zinc finger protein 366
ADGRD1	-1.07197	3.68E-56	8.89E-54	-18.9109	Down	adhesion G protein-coupled receptor D1
LINC01844	-1.06936	1.81E-20	2.35E-19	-9.85152	Down	long intergenic non-protein coding RNA 1844
SLA	-1.06836	1.06E-25	2.14E-24	-11.3249	Down	Src like adaptor
DNER	-1.06766	5.57E-16	4.85E-15	-8.48051	Down	delta/notch like EGF repeat containing
C20orf197	-1.06693	7.83E-15	6.13E-14	-8.1072	Down	chromosome 20 open reading frame 197
FAM83F	-1.06644	1.85E-29	5.14E-28	-12.3289	Down	family with sequence similarity 83 member F
SSTR5-AS1	-1.06089	8.95E-06	2.52E-05	-4.50452	Down	SSTR5 antisense RNA 1
VIT	-1.0607	1.39E-32	4.82E-31	-13.139	Down	vitron
LRRC8E	-1.06061	2.76E-19	3.26E-18	-9.50137	Down	leucine rich repeat containing 8 VRAC subunit E
STOX1	-1.05648	1.79E-20	2.33E-19	-9.85271	Down	storkhead box 1
PKHD1L1	-1.05526	2.52E-10	1.24E-09	-6.50688	Down	PKHD1 like 1
ALOX5	-1.05509	5.75E-39	3.14E-37	-14.7448	Down	arachidonate 5-lipoxygenase
SMTNL2	-1.05192	4.46E-31	1.39E-29	-12.7511	Down	smoothelin like 2
SPC24	-1.05123	1.24E-28	3.22E-27	-12.1119	Down	SPC24 component of NDC80 kinetochore complex
OSMR	-1.04998	3.8E-35	1.58E-33	-13.7905	Down	oncostatin M receptor
PPM1E	-1.04982	1.48E-07	5.31E-07	-5.35894	Down	protein phosphatase, Mg2+/Mn2+ dependent 1E SAM domain, SH3 domain and nuclear localization signals 1
SAMSN1	-1.04852	2.33E-19	2.78E-18	-9.52335	Down	CD109 molecule
CD109	-1.04808	1.53E-42	1.1E-40	-15.6243	Down	cystathionine beta-synthase
CBS	-1.04794	1.09E-28	2.84E-27	-12.1267	Down	G protein-coupled receptor 12
GPR12	-1.04772	2E-14	1.51E-13	-7.97205	Down	synapsin III
SYN3	-1.04745	2.11E-24	3.86E-23	-10.969	Down	C-C motif chemokine receptor 1
CCR1	-1.04606	5.34E-27	1.2E-25	-11.6762	Down	growth factor receptor bound protein 7
GRB7	-1.04361	2.79E-19	3.29E-18	-9.50014	Down	periplakin
PPL	-1.04306	6.42E-43	4.83E-41	-15.7162	Down	uncharacterized LOC100507516
LOC100507516	-1.04141	1.94E-20	2.52E-19	-9.84253	Down	G protein-coupled receptor 183
GPR183	-1.04045	2.19E-20	2.83E-19	-9.827	Down	TLC domain containing 2
TLCD2	-1.04031	3.05E-23	5.12E-22	-10.6458	Down	pentraxin 3
PTX3	-1.0381	9.31E-10	4.3E-09	-6.28492	Down	kelch like family member 32
KLHL32	-1.03311	1.69E-18	1.87E-17	-9.26454	Down	zinc finger DHHC-type containing 20
ZDHHC20	-1.03268	6.12E-07	2.03E-06	-5.07664	Down	cannabinoid receptor 1
CNR1	-1.03125	3.36E-14	2.48E-13	-7.89646	Down	retinitis pigmentosaGTPase regulator
RPGR	-1.03109	2.64E-38	1.38E-36	-14.5809	Down	transcription factor EC
TFEC	-1.02784	2.48E-18	2.7E-17	-9.21407	Down	macrophage scavenger receptor 1
MSR1	-1.02631	2.77E-23	4.69E-22	-10.6573	Down	CMT1A duplicated region transcript 1
CDRT1	-1.02519	1.15E-19	1.4E-18	-9.6148	Down	FRAS1 related extracellular matrix 2
FREM2	-1.02482	1.96E-09	8.73E-09	-6.15591	Down	

F5	-1.02393	6.87E-10	3.22E-09	-6.3371	Down	coagulation factor V
SMIM9	-1.01786	2.38E-19	2.83E-18	-9.52073	Down	small integral membrane protein 9
NECTIN1	-1.01749	6.29E-46	5.97E-44	-16.4481	Down	nectin cell adhesion molecule 1
ZFP57	-1.01535	0.0101	0.017165	-2.5858	Down	ZFP57 zinc finger protein
LINC02289	-1.01329	1.62E-28	4.16E-27	-12.0808	Down	long intergenic non-protein coding RNA 2289
CDKL5	-1.01252	9.24E-06	2.6E-05	-4.49752	Down	cyclin dependent kinase like 5
EIF4EBP1	-1.01195	8.78E-18	9.12E-17	-9.04606	Down	eukaryotic translation initiation factor 4E binding protein 1
LOC100129434	-1.0107	1.39E-21	2.01E-20	-10.1743	Down	uncharacterized LOC100129434
ITPKA	-1.01004	8.87E-11	4.6E-10	-6.68031	Down	inositol-trisphosphate 3-kinase A
HAS2	-1.00952	1.03E-17	1.07E-16	-9.02455	Down	hyaluronan synthase 2
PCNT	-1.00784	4.48E-52	7.63E-50	-17.9305	Down	pericentrin
NUDT4	-1.00756	4.52E-36	2E-34	-14.0233	Down	nudix hydrolase 4
ELF3	-1.00732	1.12E-10	5.76E-10	-6.6416	Down	E74 like ETS transcription factor 3
B3GALT1	-1.00415	1.6E-17	1.62E-16	-8.96561	Down	beta-1,3-galactosyltransferase 1
SIGLEC14	-1.0039	5.59E-10	2.65E-09	-6.37216	Down	sialic acid binding Ig like lectin 14
NUDT4B	-0.99985	5.54E-10	2.63E-09	-6.37373	Down	nudix hydrolase 4B
CLEC7A	-0.99973	9.85E-23	1.58E-21	-10.5023	Down	C-type lectin domain containing 7A
RNF157	-0.99959	1.36E-31	4.4E-30	-12.8846	Down	ring finger protein 157
STEAP4	-0.99897	2.2E-31	7.03E-30	-12.8307	Down	STEAP4 metalloproteinase
KCNK3	-0.99891	2.34E-20	3.03E-19	-9.8184	Down	potassium two pore domain channel subfamily K member 3
SAMHD1	-0.99873	6.11E-53	1.15E-50	-18.1382	Down	SAM and HD domain containing deoxynucleoside triphosphate triphosphohydrolase 1
INSYN1	-0.99843	1.37E-27	3.22E-26	-11.8347	Down	inhibitory synaptic factor 1
INKA2	-0.99831	6.14E-61	2.06E-58	-20.057	Down	inka box actin regulator 2
BCAT1	-0.99623	1.02E-28	2.68E-27	-12.1336	Down	branched chain amino acid transaminase 1
SLC5A1	-0.99614	1.53E-30	4.56E-29	-12.6121	Down	solute carrier family 5 member 1
SLC38A4	-0.99485	9.56E-11	4.94E-10	-6.6679	Down	solute carrier family 38 member 4
CSDC2	-0.99426	2.67E-21	3.77E-20	-10.0929	Down	cold shock domain containing C2
ETNK2	-0.99114	1.11E-30	3.37E-29	-12.6479	Down	ethanolamine kinase 2
PHACTR3	-0.98446	3.47E-12	2.1E-11	-7.19855	Down	phosphatase and actin regulator 3
INKA2-AS1	-0.98382	1.85E-30	5.48E-29	-12.5904	Down	INKA2 antisense RNA 1
LGR5	-0.98318	2.63E-11	1.45E-10	-6.8778	Down	leucine rich repeat containing G protein-coupled receptor 5
LGR6	-0.98193	2.9E-23	4.89E-22	-10.6518	Down	leucine rich repeat containing G protein-coupled receptor 6
ADGRF5	-0.98027	7.74E-38	3.89E-36	-14.4646	Down	adhesion G protein-coupled receptor F5
LOC105370401	-0.9795	2.07E-07	7.27E-07	-5.29359	Down	uncharacterized LOC105370401
ADAMTS15	-0.97867	3.08E-41	1.99E-39	-15.3047	Down	ADAM metalloproteinase with thrombospondin type 1 motif 15
C1QTNF1	-0.97823	6.59E-19	7.53E-18	-9.38821	Down	C1q and TNF related 1
SIGLEC7	-0.97434	1.41E-21	2.03E-20	-10.1729	Down	sialic acid binding Ig like lectin 7
TRHDE	-0.97406	2.27E-09	1E-08	-6.13046	Down	thyrotropin releasing hormone degrading enzyme
LILRA6	-0.97359	2.41E-21	3.41E-20	-10.106	Down	leukocyte immunoglobulin like receptor A6
SERPINB8	-0.97086	2.03E-34	8.05E-33	-13.6069	Down	serpin family B member 8
LRRN3	-0.97031	2.16E-14	1.62E-13	-7.96079	Down	leucine rich repeat neuronal 3
MT1M	-0.96838	6.61E-09	2.79E-08	-5.94048	Down	metallothionein 1M

WDR86-AS1	-0.9683	3.6E-10	1.74E-09	-6.44704	Down	WDR86 antisense RNA 1
PCK1	-0.96425	0.00069	0.001457	-3.42273	Down	phosphoenolpyruvatecarboxykinase 1
EDN1	-0.96378	1.44E-25	2.87E-24	-11.289	Down	endothelin 1
KLF10	-0.96307	1.82E-29	5.05E-28	-12.3313	Down	Kruppel like factor 10
MANEA	-0.96278	5.36E-17	5.16E-16	-8.80226	Down	mannosidaseendo-alpha
TUBAL3	-0.96258	6.11E-13	3.98E-12	-7.46512	Down	tubulin alpha like 3
PMFBP1	-0.96247	6.09E-12	3.59E-11	-7.11034	Down	polyamine modulated factor 1 binding protein 1
DAAM2-AS1	-0.96155	1.13E-30	3.41E-29	-12.6465	Down	DAAM2 antisense RNA 1
ABCB1	-0.96049	1.45E-23	2.49E-22	-10.7363	Down	ATP binding cassette subfamily B member 1
ELL2	-0.95986	1.16E-29	3.25E-28	-12.3828	Down	elongation factor for RNA polymerase II 2
HIF3A	-0.95866	2.09E-33	7.63E-32	-13.3492	Down	hypoxia inducible factor 3 subunit alpha
ZBED6	-0.95784	0.000413	0.000904	-3.56438	Down	zinc finger BED-type containing 6
GFI1B	-0.95657	2.87E-12	1.75E-11	-7.22798	Down	growth factor independent 1B transcriptional repressor
HMOX2	-0.95588	9.44E-45	8.14E-43	-16.1626	Down	hemeoxygenase 2
TK1	-0.95442	7.38E-13	4.77E-12	-7.43647	Down	thymidine kinase 1
SLC36A4	-0.95143	6.25E-49	8.02E-47	-17.1738	Down	solute carrier family 36 member 4
TMEM132C	-0.95116	3.19E-18	3.45E-17	-9.18058	Down	transmembrane protein 132C
STEAP3	-0.95098	3.34E-49	4.37E-47	-17.2393	Down	STEAP3 metalloredutase
PCLAF	-0.9505	3.17E-10	1.54E-09	-6.46829	Down	PCNA clamp associated factor
ALOX5AP	-0.94867	2.9E-25	5.66E-24	-11.2059	Down	arachidonate 5-lipoxygenase activating protein
SLC1A1	-0.94735	1.64E-32	5.67E-31	-13.1204	Down	solute carrier family 1 member 1
EHF	-0.94691	3.32E-10	1.62E-09	-6.4604	Down	ETS homologous factor
CCDC68	-0.94642	4.3E-18	4.58E-17	-9.14123	Down	coiled-coil domain containing 68
BCL6	-0.94633	5.81E-61	2.01E-58	-20.0628	Down	BCL6 transcription repressor
SLC31A2	-0.94625	2.68E-53	5.31E-51	-18.224	Down	solute carrier family 31 member 2
TXNRD1	-0.94184	6.66E-33	2.35E-31	-13.2209	Down	thioredoxinreductase 1
GGT5	-0.93863	5.73E-17	5.5E-16	-8.79326	Down	gamma-glutamyltransferase 5
GRAP2	-0.93849	7.28E-23	1.19E-21	-10.5394	Down	GRB2 related adaptor protein 2
IGSF22	-0.9363	5.2E-23	8.57E-22	-10.5805	Down	immunoglobulin superfamily member 22
MARVELD2	-0.93616	4.75E-29	1.28E-27	-12.2216	Down	MARVEL domain containing 2
SLC19A2	-0.93586	3.58E-19	4.2E-18	-9.46764	Down	solute carrier family 19 member 2
SELE	-0.93559	3.88E-06	1.15E-05	-4.68889	Down	selectin E
LINC01235	-0.93519	2.15E-08	8.55E-08	-5.7253	Down	long intergenic non-protein coding RNA 1235
RAB39A	-0.93499	3E-11	1.64E-10	-6.85672	Down	RAB39A, member RAS oncogene family
ANLN	-0.93394	6.42E-10	3.02E-09	-6.3487	Down	anillin actin binding protein
CLSPN	-0.93196	9.75E-13	6.21E-12	-7.39409	Down	claspin
ACPP	-0.93112	4.27E-15	3.43E-14	-8.19383	Down	acid phosphatase, prostate
LRGUK	-0.92812	1.91E-12	1.18E-11	-7.29067	Down	leucine rich repeats and guanylate kinase domain containing
ARG1	-0.9274	1.06E-06	3.42E-06	-4.96388	Down	arginase 1
P2RY12	-0.92637	1.78E-10	8.9E-10	-6.56544	Down	purinergic receptor P2Y12
ARNTL	-0.92612	7.2E-18	7.53E-17	-9.07262	Down	aryl hydrocarbon receptor nuclear translocator like
LINC01684	-0.92272	1.34E-13	9.32E-13	-7.69327	Down	long intergenic non-protein coding RNA 1684

C1orf162	-0.92206	1.85E-35	7.8E-34	-13.8696	Down	chromosome 1 open reading frame 162
TRPC4	-0.92014	2.7E-18	2.94E-17	-9.20265	Down	transient receptor potential cation channel subfamily C member 4
AIF1L	-0.91594	1.75E-52	3.13E-50	-18.0287	Down	allograft inflammatory factor 1 like
KIF18B	-0.91286	4.17E-10	2.01E-09	-6.42185	Down	kinesin family member 18B
CRISPLD2	-0.9128	1.26E-38	6.7E-37	-14.66	Down	cysteine rich secretory protein LCCL domain containing 2
AMD1	-0.91169	1.46E-48	1.79E-46	-17.0851	Down	adenosylmethionine decarboxylase 1
FLT3	-0.91165	2.93E-14	2.17E-13	-7.91632	Down	fms related tyrosine kinase 3
ARRDC4	-0.91072	3.74E-26	7.89E-25	-11.4482	Down	arrestin domain containing 4
SLC4A7	-0.91068	3.18E-13	2.13E-12	-7.56366	Down	solute carrier family 4 member 7
TOP2A	-0.9091	2.87E-09	1.26E-08	-6.08903	Down	DNA topoisomerase II alpha
CENPM	-0.90902	4.38E-08	1.68E-07	-5.59272	Down	centromere protein M
S100A8	-0.90893	7.54E-10	3.51E-09	-6.32114	Down	S100 calcium binding protein A8
SIRPB2	-0.90766	3.38E-19	3.98E-18	-9.47503	Down	signal regulatory protein beta 2
MEDAG	-0.90694	8.83E-23	1.43E-21	-10.5157	Down	mesenteric estrogen dependent adipogenesis
SLC2A1	-0.90689	9.89E-45	8.49E-43	-16.1578	Down	solute carrier family 2 member 1
SLC52A3	-0.90653	5.43E-32	1.82E-30	-12.9872	Down	solute carrier family 52 member 3
SOCS3	-0.90502	2.05E-10	1.02E-09	-6.54144	Down	suppressor of cytokine signaling 3
PDK4	-0.90267	1.31E-10	6.69E-10	-6.61548	Down	pyruvate dehydrogenase kinase 4
GLUL	-0.90223	8.16E-46	7.67E-44	-16.4208	Down	glutamate-ammonia ligase
HPSE	-0.90161	2.07E-23	3.53E-22	-10.6928	Down	heparanase
GABRR2	-0.90116	2.86E-06	8.66E-06	-4.75471	Down	gamma-aminobutyric acid type A receptor rho2 subunit
FAM111B	-0.90086	1.25E-08	5.12E-08	-5.82455	Down	family with sequence similarity 111 member B
SNORD101	-0.90003	2.16E-11	1.19E-10	-6.90987	Down	small nucleolar RNA, C/D box 101
WASF1	-0.89554	6.06E-27	1.36E-25	-11.6614	Down	WASP family member 1
KIF5C	-0.89536	4.84E-25	9.31E-24	-11.145	Down	kinesin family member 5C
MARK3	-0.89489	6.12E-82	1.27E-78	-25.1753	Down	microtubule affinity regulating kinase 3
SLC30A10	-0.89439	1.02E-12	6.49E-12	-7.38702	Down	solute carrier family 30 member 10
TGFBR3	-0.89378	5.11E-39	2.79E-37	-14.7576	Down	transforming growth factor beta receptor 3
FCER1G	-0.89232	1.4E-26	3.05E-25	-11.5633	Down	Fc fragment of IgE receptor Ig
KLHL41	-0.89223	5.91E-33	2.09E-31	-13.2341	Down	kelch like family member 41
EDN2	-0.89167	6.37E-09	2.69E-08	-5.94703	Down	endothelin 2
CHI3L1	-0.89162	3.32E-05	8.66E-05	-4.20254	Down	chitinase 3 like 1
SFRP5	-0.89029	1.32E-07	4.77E-07	-5.38124	Down	secreted frizzled related protein 5
LAPTM5	-0.88976	1.02E-22	1.64E-21	-10.4975	Down	lysosomal protein transmembrane 5
SLC9A7	-0.88906	6.45E-22	9.53E-21	-10.2702	Down	solute carrier family 9 member A7
C8orf88	-0.88787	7.65E-51	1.14E-48	-17.6342	Down	chromosome 8 open reading frame 88
CLEC4G	-0.88685	7.21E-07	2.37E-06	-5.04324	Down	C-type lectin domain family 4 member G
GPAT2	-0.88402	1.9E-17	1.91E-16	-8.94253	Down	glycerol-3-phosphate acyltransferase 2, mitochondrial
SCN3A	-0.88292	8.31E-14	5.91E-13	-7.76375	Down	sodium voltage-gated channel alpha subunit 3
BANK1	-0.88095	1E-10	5.18E-10	-6.66001	Down	B cell scaffold protein with ankyrin repeats 1
SEC14L2	-0.88054	1.42E-15	1.19E-14	-8.34963	Down	SEC14 like lipid binding 2
LANCL3	-0.87923	1.15E-10	5.92E-10	-6.63674	Down	LanC like 3

E2F2	-0.87786	2.5E-09	1.1E-08	-6.11349	Down	E2F transcription factor 2
IL15RA	-0.87627	2.9E-47	3.17E-45	-16.7715	Down	interleukin 15 receptor subunit alpha
ACR	-0.87563	6.53E-15	5.15E-14	-8.13328	Down	acrosin
ATP2A2	-0.8755	1.39E-30	4.18E-29	-12.6227	Down	ATPase sarcoplasmic/endoplasmic reticulum Ca2+ transporting 2
MAMDC2	-0.87509	9.15E-18	9.49E-17	-9.04054	Down	MAM domain containing 2
MYZAP	-0.87372	3.64E-05	9.46E-05	-4.18075	Down	myocardial zonulaadherens protein
EBLN2	-0.87327	3.93E-06	1.17E-05	-4.68593	Down	endogenous Bornavirus like nucleoprotein 2
USP31	-0.87252	1.22E-40	7.61E-39	-15.1575	Down	ubiquitin specific peptidase 31
LRMDA	-0.87106	1.27E-21	1.83E-20	-10.1859	Down	leucine rich melanocyte differentiation associated
GPR4	-0.87078	8.84E-33	3.09E-31	-13.1895	Down	G protein-coupled receptor 4
OPN4	-0.87003	1.81E-11	1.01E-10	-6.9378	Down	opsin 4
PIIP5K2	-0.86979	1.84E-24	3.38E-23	-10.9854	Down	diphosphoinositolpentakisphosphate kinase 2
SNAI3	-0.86358	4.07E-11	2.19E-10	-6.8073	Down	snail family transcriptional repressor 3
CDCP1	-0.86318	2.13E-16	1.94E-15	-8.6134	Down	CUB domain containing protein 1
PAPSS2	-0.86311	1.62E-26	3.51E-25	-11.5461	Down	3'-phosphoadenosine 5'-phosphosulfate synthase 2
KIF14	-0.86236	6.12E-09	2.59E-08	-5.95432	Down	kinesin family member 14
LNCOG	-0.86037	2.38E-07	8.3E-07	-5.2659	Down	lncRNAosteogenesis associated
FAM107A	-0.85818	2.59E-40	1.57E-38	-15.0771	Down	family with sequence similarity 107 member A
ANKRD7	-0.85782	2.72E-14	2.02E-13	-7.92723	Down	ankyrin repeat domain 7
AKR1C1	-0.85714	6.87E-23	1.12E-21	-10.5464	Down	aldo-ketoreductase family 1 member C1
LINC02177	-0.85669	7.6E-08	2.83E-07	-5.48796	Down	long intergenic non-protein coding RNA 2177
LSAMP	-0.85556	9.78E-14	6.9E-13	-7.73966	Down	limbic system associated membrane protein
DOCK9	-0.8547	6.23E-22	9.22E-21	-10.2746	Down	dedicator of cytokinesis 9
MS4A4A	-0.85425	1.02E-21	1.48E-20	-10.2137	Down	membrane spanning 4-domains A4A
LINC01128	-0.85327	5.03E-32	1.69E-30	-12.9958	Down	long intergenic non-protein coding RNA 1128
HK3	-0.85159	2.75E-16	2.48E-15	-8.57828	Down	hexokinase 3
SNTG2	-0.84977	2.78E-16	2.5E-15	-8.57682	Down	syntrophin gamma 2
EPB41L4B	-0.84874	8.53E-24	1.49E-22	-10.8005	Down	erythrocyte membrane protein band 4.1 like 4B
LOC105378721	-0.84723	1.25E-26	2.73E-25	-11.577	Down	uncharacterized LOC105378721
CALCRL	-0.84699	2.1E-13	1.43E-12	-7.62605	Down	calcitonin receptor like receptor
CTH	-0.84525	2.34E-27	5.43E-26	-11.7723	Down	cystathionine gamma-lyase
ANXA3	-0.84508	2.77E-39	1.55E-37	-14.8233	Down	annexin A3
NCEH1	-0.84422	1.43E-27	3.35E-26	-11.8296	Down	neutral cholesterol ester hydrolase 1
RASD1	-0.84259	3.42E-06	1.03E-05	-4.71643	Down	ras related dexamethasone induced 1
MERTK	-0.84249	1.24E-28	3.23E-27	-12.1114	Down	MER proto-oncogene, tyrosine kinase
TCHH	-0.84214	3.38E-11	1.83E-10	-6.83748	Down	trichohyalin
APOB	-0.84165	1.21E-17	1.24E-16	-9.00323	Down	apolipoprotein B
EPN3	-0.84144	2.21E-12	1.36E-11	-7.26849	Down	epsin 3
LOC101927858	-0.84129	3.29E-13	2.2E-12	-7.55892	Down	uncharacterized LOC101927858
ECT2	-0.83943	2.39E-17	2.39E-16	-8.91154	Down	epithelial cell transforming 2
TMEM100	-0.83941	2.92E-15	2.38E-14	-8.24789	Down	transmembrane protein 100
MYBL2	-0.83919	1.2E-07	4.34E-07	-5.40031	Down	MYB proto-oncogene like 2

AFF2	-0.83824	1.98E-10	9.87E-10	-6.54735	Down	AF4/FMR2 family member 2
VEPH1	-0.83738	2.57E-11	1.41E-10	-6.8819	Down	ventricular zone expressed PH domain containing 1
RAET1E	-0.83675	8.68E-17	8.2E-16	-8.73659	Down	retinoic acid early transcript 1E
IRAK3	-0.8363	1.24E-19	1.51E-18	-9.60519	Down	interleukin 1 receptor associated kinase 3
ARMC12	-0.83589	1.42E-15	1.19E-14	-8.34925	Down	armadillo repeat containing 12
HPR	-0.83392	6.8E-11	3.58E-10	-6.72376	Down	haptoglobin-related protein
MT1JP	-0.83257	1.41E-06	4.47E-06	-4.9042	Down	metallothionein 1J, pseudogene
PIK3C2A	-0.83111	7.57E-15	5.93E-14	-8.11208	Down	phosphatidylinositol-4-phosphate 3-kinase catalytic subunit type 2 alpha
FGR	-0.8308	1.35E-26	2.94E-25	-11.5676	Down	FGR proto-oncogene, Src family tyrosine kinase
NHLRC2	-0.83012	1.09E-13	7.65E-13	-7.72382	Down	NHL repeat containing 2

Table 3 The enriched GO terms of the up and down regulated differentially expressed genes

GO ID	CATEGORY	GO Name	P Value	FDR B&H	FDR B&Y	Bonferroni	Gene Count	Gene
Up regulated genes								
GO:0022610	BP	biological adhesion	1.32E-13	3.37E-10	3.08E-09	6.75E-10	72	HLA-DQA1,DACT2,CD83,MDK,UBASH3A,ITGBL1,FAP,MFAP4,SERPINE2,NRXN2,COL14A1,CCR7,ALOX15,COL1A1,LAMB4,COL8A2,STAB2,COL16A1,COMP,TBX21,FERMT1,XG,CDC80,APOA1,PODXL2,ZAP70,HAPLN1,TENM4,SKAP1,CNTNAP2,PDE5A,CARD11,CTNNA2,SLAMF7,ATP1B2,CX3CR1,LRRRC15,IDO1,MYOC,SIGLEC8,ISLR,SMOC2,ITGAL,ITGB7,FREM1,PTN,KIRREL3,NTM,GLI2,FBXN7,DPT,NTSE,ECM2,LCK,OMG,OPCML,TGFB2,RASGRP1,CD2,CD3E,THBS4,CD5,CD6,THY1,TIGIT,CD27,CD40LG,ROBO2,GREM1,LY9,HBB,LEF1
GO:0002682	BP	regulation of immune system process	2.20E-10	2.25E-07	2.05E-06	1.12E-06	72	IL34,HLA-DQA1,ESR1,TLR7,CD83,IL17D,MDK,UBASH3A,TNFRSF4,PTYHIN1,ZBP1,FCER1A,MS4A2,FCER2,FCN1,CCR7,SMPD3,CCL24,SCARA3,ALOX15,COL1A1,IL31RA,TBX21,XG,CXCL14,APOA1,ZAP70,SH2D1B,SKAP1,PDE5A,CARD11,SLAMF7,CTSG,CX3CR1,IDO1,CXCL10,ITGAL,ACE,SIT1,ITGB7,PT

								N,TBC1D10C,FCRL3,BPI,GLI2,KLRB1,NPPA,CAMK4,LCK,TGFB2,RASGRP1,CD1C,CD1E,CD2,CD3D,CD3E,THBS4,CD3G,CD247,CD5,CD6,THY1,TIGIT,MS4A1,CD27,GPR68,CD40LG,CD48,GREM1,SH2D1A,LEF1,LRR
GO:0031012	CC	extracellular matrix	1.09E-20	2.77E-18	1.89E-17	5.54E-18	52	C17, MATN2, COL22A1, MDK, COLQ, MFAP4, SERPINE2, HMCN2, AEBP1, FCN1, CMA1, CTHRC1, COL14A1, SCARA3, COL1A1, LAMB4, COL8A2, COL9A1, COL9A2, COL10A1, MXRA5, FMO2, COL16A1, COMP, CCDC80, APOA1, HAPLN1, CTSG, ADAMTSL2, LRRC15, ASPN, MYOC, NDP, SMO2, FREM1, PTN, SSC5D, SULF1, DPT, NPPA, ADAMTSL1, ECM2, OGN, ITIH5, TGFBR2, LEFTY2, EYS, THBS4, P3H2, LTBP2, GREM1, LUM, LRRC17
GO:0009986	CC	cell surface	5.07E-17	8.61E-15	5.86E-14	2.58E-14	63	HYAL4, NRG1, HLA-DQA1, CD83, TNFRSF4, ITGBL1, FAP, SERPINE2, FCER1A, MS4A2, FCER2, FCN1, CXCL9, CCR7, IL31RA, SFRP4, STAB2, DUOX2, APOA1, ACKR4, FCRL6, SCUBE2, CNTNAP2, SLAMF7, CTSG, IL2RB, CX3CR1, LRRC15, CXCL10, NDP, ITGAL, ACE, ITGB7, GFRA3, PTN, PROM1, SSC5D, FCRL3, SULF1, MRC2, NTM, CLEC9A, NTSE, TGFBR2, LHCGR, CD1C, HHIP, CD1E, CD2, CD3D, CD3E, CD3G, CD5, CD6, THY1, TIGIT, MS4A1, CD27, CD40LG, CD48, ROBO2, GREM1, LY9
GO:0005102	MF	signaling receptor binding	1.36E-09	5.99E-07	4.41E-06	1.20E-06	73	IL34, NRG1, HLA-DQA1, ESR1, GDF6, PENK, TAC4, KDM5D, IL17D, MDK, ITGBL1, FAP, SERPINE2, FCER2, NRXN2, FCN1, CLEC11A, UCHL1, AGTR2, CXCL9, NGEF, CTHRC1, C1QTNF2, CCL22, CCL24, CXCL11, COL16A1, COMP, WNT10B, WNT9A,

GO:0098772	MF	molecular function regulator	3.79E-04	1.59E-02	1.17E-01	3.34E-01	58	CXCL14,APOA1,FC RL6,GNA14,OASL, RASL11B,LRRC15, CXCL10,ADAM18, MYOC,SYTL2,NDP, ACE,GDNF,ITGB7, GFRA3,PTN,LYPD1 ,SCG2,NPPA,NPPB, MCHR1,ECM2,CMT M2,ESM1,LCK,OGN ,TGFB2,LEFTY2,CD 2,CD3E,THBS4,CD3 G,THY1,TIGIT,MS4 A1,C1QTNF9,CD40 LG,LTB,GREM1,SY TL1,LEF1,LGI1 IL34,NRG1,ESR1,G DF6,PENK,TAC4,IL 17D,MDK,KCNIP1,S ERPINE2,MYOZ1,N RXN2,CLEC11A,SC N2B,AGTR2,CXCL9 ,NGEF,CCL22,CCL2 4,CXCL11,HTR2B,P I16,SCG5,WNT10B, WNT9A,CXCL14,A POA1,LRRC55,PPP2 R2B,ATP1B2,CXCL 10,NDP,BIRC7,GDN F,PTN,TBC1D10C,L YPD1,SCG2,NPPA, NPPB,AZIN2,CMT M2,OGN,RGS4,ITIH 5,TGFB2,LEFTY2,R ASGRP1,THBS4,TH Y1,CD27,C1QTNF9, CD40LG,RGS17,LT B,GREM1,LEF1,INK A1
Down regulated genes								
GO:0046903	BP	secretion	1.07E-11	5.64E-08	5.16E-07	5.64E-08	78	SERPINA3,HK3,SY N3,ACP3,TRPC4,CF TR,CD109,HMOX2, CHI3L1,F5,F8,F13A 1,S100A8,S100A9,S AA1,FCER1G,MGS T1,PIK3C2A,HP,AG TR1,PLA2G2A,CCR 1,FGF10,C1QTNF1, PLA2G4F,FGR,MER TK,SERPINF2,ALO X5,SYT13,IL17RB,C NR1,ALOX15B,FLT 3,ANPEP,P2RY12,A NXA3,FPR1,CR1,SL C1A1,SLC2A1,ARG 1,ARNTL,SLC11A1, SLC22A16,LGI3,NS G1,ATP2A2,IL10,SI GLEC9,GPR84,NHL RC2,SSTR5,HPSE,K CNB1,IL1R2,PTX3, GLUL,SYN2,BANK 1,WNK3,KNG1,CRI SPLD2,CACNA1E,C D177,SIGLEC14,ED N1,EDN2,EDNRB,T HBS1,RNASE2,CD3 8,TLR2,SERPINE1,E LANE,STEAP3,IL1R

GO:0006952	BP	defense response	1.04E-06	1.63E-04	1.49E-03	5.50E-03	65	L1,MCEMP1 SERPINA3,EREG,V SIG4,TMIGD3,CLE C7A,RAET1E,CHI3 L1,F8,CD163,S100A 8,S100A9,SAA1,FCE R1G,HP,HPR,AGTR 1,PLA2G2A,CCR1,F GR,SERPINF2,ALO X5,ALOX5AP,IL17 RB,CNR1,SELE,AD AMTS4,ANXA3,FP R1,APOB,SAMHD1, CR1,FCN3,AQP4,A RG1,SLC11A1,MAR CO,IL10,BCL6,IL18 R1,GGT5,IL1R2,PT X3,SIGLEC10,KNG 1,CACNA1E,CD177, SOCS3,SIGLEC14,A DAMTS5,LBP,S1PR 3,EDN1,EDNRB,FO SL1,THBS1,RNASE 2,NAMPT,TLR2,SE RPINE1,ELANE,IR AK3,ELF3,IL1RL1,C ALCRL,OSMR
GO:0031226	CC	intrinsic component of plasma membrane	1.74E-10	4.55E-08	3.11E-07	9.10E-08	74	TPO,EREG,OPN4,T RPC4,CFTR,TMIGD 3,KCNIP2,CD163,FC ER1G,SCN3A,AGT R1,CCR1,C1QTNF1, MERTK,SYT13,IL17 RB,CNR1,TRHDE,S ELE,LRRC8E,FLT3, SLC4A7,P2RY12,SL C31A2,CR1,LGR5,A QP3,AQP4,SLC1A1, SLC2A1,SLC5A1,M SR1,SLC11A1,SIGL EC7,ART3,SLCO2A 1,ATP2A2,MARCO, GABRR2,SIGLEC9, SLCO4A1,GPR84,SS TR2,SSTR5,IL18R1, LAPTM5,GGT5,SLC 52A3,LYVE1,KCNA 7,KCNB1,KCND3,N ECTIN1,KCNK1,KC NK3,KCNS2,ADGR D1,CACNA1E,GPR4 ,GPR12,SLC38A4,G PR183,GPRC5A,RG R,S1PR3,RHAG,ED NRB,TGFBR3,TLR2 ,LGR6,CALCRL,OS MR,HAS2,CDH16
GO:0098805	CC	whole membrane	1.91E-03	4.99E-02	3.41E-01	9.97E-01	51	EREG,SYN3,ACP3, TRPC4,CFTR,CD10 9,HMOX2,CD163,F CER1G,MGST1,PLA 2G4F,GPAT2,MOG, CNR1,SELE,ANPEP, P2RY12,ANXA3,FP R1,APOB,SCGN,CR 1,AQP4,SLC1A1,SL C2A1,ARG1,MSR1, SLC11A1,NSG1,RA B39A,MARCO,SIGL EC9,GPR84,HPSE,L

GO:0038023	MF	signaling receptor activity	2.36E-04	1.97E-02	1.49E-01	2.53E-01	55	APTM5,KCND3,SY N2,SLC9A7,WASF1, CD177,SIGLEC14,G RB14,STEAP4,EDN RB,GRIP1,CD38,TL R2,STEAP3,HAS2,S ERPINA5,MCEMP1 EREG,OPN4,CLEC7 A,FCER1G,FCGR3A ,AGTR1,CCR1,ADG RF5,ADGRF4,MER TK,IL17RB,CNR1,S ELE,FLT3,MYOT,A NPEP,P2RY12,ANX A3,FPR1,CR1,LGR5, SIGLEC7,MARCO,P ALLD,IL10,GABRR 2,IL15RA,GPR82,D NER,PAQR5,GPR84, IL20RA,SSTR2,SST R5,IL18R1,LYVE1,I L1R2,NECTIN1,AD GRD1,GPR4,GPR12, NPTX2,GPR183,GP RC5A,PKHD1L1,RG R,S1PR3,EDNRB,T GFBR3,TLR2,SERPI NE1,IL1RL1,LGR6, CALCRL,OSMR
GO:0060089	MF	molecular transducer activity	4.71E-04	2.10E-02	1.59E-01	5.04E-01	58	EREG,OPN4,CLEC7 A,FCER1G,FCGR3A ,AGTR1,CCR1,ADG RF5,ADGRF4,MER TK,IL17RB,CNR1,S ELE,FLT3,MYOT,A NPEP,P2RY12,ANX A3,FPR1,CR1,LGR5, SIGLEC7,MARCO,P ALLD,IL10,GABRR 2,IL15RA,GPR82,D NER,PAQR5,GPR84, IL20RA,STOX1,SST R2,SSTR5,IL18R1,B LM,CDKL5,LYVE1, IL1R2,NECTIN1,AD GRD1,GPR4,GPR12, NPTX2,GPR183,GP RC5A,PKHD1L1,RG R,S1PR3,EDNRB,T GFBR3,TLR2,SERPI NE1,IL1RL1,LGR6, CALCRL,OSMR

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

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

Pathway ID	Pathway Name	P-value	FDR B&H	FDR B&Y	Bonferroni	Gene Count	Gene
Up regulated genes							
1270244	Extracellular matrix organization	3.33E-08	1.80E-05	1.23E-04	1.80E-05	24	COL22A1,MFAP4,CMA1, COL14A1,COL1A1,COL8 A2,COL9A1,COL9A2,CO L10A1,FMOD,COL16A1, COMP,HAPLN1,ADAMT S14,CTSG,ASPN,ITGAL,I TGB7,CAPN6,TGFB2,P3 H2,TLL2,LTBP2,LUM
1269201	Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell	8.13E-06	7.31E-04	5.03E-03	4.39E-03	13	SH2D1B,SLAMF7,SIGLE C8,ITGAL,ITGB7,KLRB1 ,CD1C,CD3D,CD3E,CD3 G,CD247,CD40LG,SH2D1 A
1269544	GPCR ligand binding	3.92E-04	1.51E-02	1.04E-01	2.12E-01	22	GNG8,PENK,F2RL2,AGT R2,APLNR,CXCL9,CCR7, CXCL11,OXER1,HTR2A, HTR2B,WNT10B,WNT9A ,ACKR4,CRHBP,S1PR5,F ZD2,CX3CR1,CXCL10,M CHR1,LHCGR,GPR68
1268749	Metabolism of Angiotensinogen to Angiotensins	5.26E-04	1.85E-02	1.27E-01	2.84E-01	4	CMA1,CTSG,ACE,GZMH
1269868	Muscle contraction	3.44E-02	4.03E-01	1.00E+00	1.00E+00	9	KCNIP1,RYR3,SCN2B,A TP1A4,ATP1B2,MYL1,K CNK17,NPPA,TNNI1
1269340	Hemostasis	6.57E-02	5.21E-01	1.00E+00	1.00E+00	20	GNG8,CEACAM3,F2RL2, SERPINE2,APOA1,GNA1 4,PDE5A,ATP1B2,IL2RB, CTSW,ISLR,ITGAL,LCK, TGFB2,LEFTY2,RASGRP 1,CD2,P2RX6,CD48,HBB
1269171	Adaptive Immune System	1.32E-01	6.87E-01	1.00E+00	1.00E+00	23	NRG1,HLA-DQA1,ZAP70,SH2D1B,C ARD11,SLAMF7,SIGLEC 8,ITGAL,ITGB7,ASB18,I ER3,MRC2,KLRB1,LCK, RASGRP1,CD1C,CD3D,C D3E,CD3G,CD247,FBXL 16,CD40LG,SH2D1A
Down regulated genes							
1457780	Neutrophil degranulation	4.82E-06	3.14E-03	2.22E-02	3.14E-03	28	SERPINA3,HK3,ACP3,H MOX2,CHI3L1,S100A8,S 100A9,FCER1G,MGST1, HP,FGR,ALOX5,ANPEP, FPR1,CR1,ARG1,SLC11A 1,SIGLEC9,GPR84,HPSE, PTX3,CRISPLD2,CD177, SIGLEC14,RNASE2,TLR 2,ELANE,MCEMP1
1269907	SLC-mediated transmembrane transport	6.91E-04	4.74E-02	3.35E-01	4.51E-01	16	HK3,SLC7A11,SLC4A7,S LC1A1,SLC2A1,SLC5A1, SLC11A1,SLC22A16,SLC O2A1,SLCO4A1,GCKR,L CN15,SLC9A7,SLC25A18 ,SLC38A4,RHAG
1269545	Class A/1 (Rhodopsin-like receptors)	8.72E-04	4.74E-02	3.35E-01	5.69E-01	17	OPN4,SAA1,AGTR1,CCR 1,CNR1,P2RY12,FPR1,SS TR2,SSTR5,KNG1,GPR4, GPR183,RGR,S1PR3,EDN 1,EDN2,EDNRB
1269340	Hemostasis	2.18E-03	7.11E-02	5.02E-01	1.00E+00	26	SERPINA3,CD109,SLC7A

							11,F5,F8,F13A1,SERPINB8,FCER1G,FGR,MERTK,SERPINF2,SELE,P2RY12,APOB,KIF18B,ATP2A2,NHLRC2,KNG1,PDE11A,CD177,DOCK9,GRB7,GRB14,THBS1,SERPINE1,SERPINA5
1269903	Transmembrane transport of small molecules	4.89E-03	1.28E-01	9.01E-01	1.00E+00	26	HK3,TRPC4,CFTR,HMOX2,SLC7A11,ABCB1,SLC4A7,AQP3,AQP4,SLC1A1,SLC2A1,SLC5A1,SLC11A1,SLC22A16,SLCO2A1,ATP2A2,GABRR2,SLCO4A1,GCKR,LCN15,SLC9A7,WNK3,SLC25A18,SLC38A4,RHAG,STEAP3
1269203	Innate Immune System	9.62E-03	1.96E-01	1.00E+00	1.00E+00	42	SERPINA3,EREG,HK3,MARK3,ACP3,CLEC7A,HMOX2,CHI3L1,S100A8,S100A9,SAA1,FCER1G,MGST1,FCGR3A,HP,GRAP2,PLA2G2A,FGF5,FGF10,FGR,ALOX5,ANPEP,FPR1,APOB,CR1,FCN3,ARG1,SLC11A1,SIGLEC9,GPR84,HPSE,PTX3,WASF1,CRISPLD2,CD177,SIGLEC14,LBP,RNASE2,TLR2,ELANE,IRAK3,MCEMP1
1269310	Cytokine Signaling in Immune system	8.42E-02	4.76E-01	1.00E+00	1.00E+00	23	EREG,MARK3,F13A1,SAI1,FGF5,CCR1,FGF10,ALOX5,IL17RB,FLT3,FPR1,SAMHD1,IL10,IL15RA,IL20RA,BCL6,IL18R1,IL1R2,SOC3,LBP,IRAK3,IL1RL1,OSMR

Table 5 Topology table for up and down regulated genes.

Regulation	Node	Degree	Betweenness	Stress	Closeness
Up	ESR1	1094	0.250896	7.4E+08	0.392769
Up	PYHIN1	342	0.054258	1.1E+08	0.339882
Up	PPP2R2B	199	0.023115	35268762	0.346839
Up	LCK	162	0.033618	18589354	0.353915
Up	TP63	142	0.018577	39426608	0.319664
Up	CD247	129	0.013832	18625274	0.317784
Up	PTN	105	0.016638	36892166	0.300662
Up	APLN	103	0.016611	40715208	0.288093
Up	APOA1	100	0.018834	13935332	0.315866
Up	CENPA	98	0.009846	31131318	0.301786
Up	SKAP1	97	0.01599	10109482	0.313338
Up	FSCN1	88	0.010226	9387016	0.335367
Up	SCN2B	86	0.01089	24233242	0.284756
Up	TMEM30B	79	0.016411	10490230	0.270807
Up	FOXS1	79	0.009408	26398078	0.293247
Up	COL1A1	76	0.010472	9315670	0.308098
Up	ZAP70	75	0.007096	5315196	0.317614
Up	UCHL1	74	0.009753	9381024	0.331525
Up	HBB	72	0.009984	14209592	0.304767
Up	NRG1	70	0.01151	13449066	0.29526
Up	LEF1	61	0.007998	18260094	0.290744
Up	NT5E	60	0.009599	11470634	0.301563
Up	MDK	59	0.006889	7533352	0.305822
Up	ISLR	58	0.010139	9992806	0.294012
Up	FATE1	57	0.011609	9248788	0.281581
Up	LRRC15	56	0.010069	4772792	0.299094
Up	MATN2	54	0.004491	9580600	0.286792

Up	LIPH	54	0.008197	6873658	0.282347
Up	MYOC	49	0.005138	12313276	0.291029
Up	SCARA3	49	0.006492	11494220	0.290151
Up	NPPA	46	0.009502	4868574	0.307143
Up	CD83	43	0.005149	5484906	0.272841
Up	COL14A1	41	0.006129	5699128	0.292893
Up	CTSG	40	0.003821	1913996	0.296155
Up	SFRP4	40	0.004006	7876966	0.282518
Up	TRAF3IP3	38	0.006447	4263002	0.290602
Up	CLEC11A	38	0.005085	3520012	0.283596
Up	ATP1B4	38	0.005722	2476482	0.245939
Up	CD3E	37	0.003892	1537326	0.297624
Up	SH2D1A	37	0.003969	2117220	0.308113
Up	DDX3Y	37	0.003754	1632916	0.32095
Up	PRPH	37	0.001871	1994266	0.301494
Up	BIRC7	35	0.004835	2567254	0.28549
Up	CARD11	35	0.002249	2510852	0.292173
Up	RXRG	35	0.002394	7134478	0.26225
Up	CCL22	34	0.005706	3916024	0.281423
Up	CD27	33	0.003915	2076446	0.294263
Up	GZMB	32	0.003277	6141522	0.285602
Up	THY1	32	0.003561	1793684	0.291509
Up	CHRNA3	32	0.004247	3415720	0.236631
Up	LSP1	32	0.003371	5734010	0.281836
Up	IL2RB	31	0.002351	1938172	0.305808
Up	HTR2B	30	0.004018	2165998	0.27434
Up	DLGAP1	29	0.003816	6072882	0.277754
Up	TRIM17	29	0.002943	5543810	0.275137
Up	CTNNA2	29	0.003554	3511510	0.30254
Up	SERPINE2	28	0.002577	3031536	0.27426
Up	CD1E	28	0.003282	3419392	0.255229
Up	MRC2	28	0.003395	2950548	0.296276
Up	C1QTNF2	28	0.003203	2505388	0.270147
Up	SH2D1B	27	0.001864	1043570	0.29028
Up	BRINP1	27	0.001516	4402948	0.27726
Up	PDIA2	27	0.001967	2895182	0.286453
Up	CHD5	27	0.001918	5223636	0.286503
Up	FAP	27	0.003531	5820086	0.268583
Up	IL31RA	26	0.002073	1606954	0.263603
Up	GAP43	25	0.002745	2793268	0.279858
Up	CD5	25	0.001695	655904	0.295861
Up	UBASH3A	25	0.001652	1347264	0.290951
Up	ROBO2	25	0.002959	3726616	0.267048
Up	ITGB7	24	0.002686	3351660	0.276124
Up	HTR2A	24	0.002571	2472010	0.275833
Up	MOXD1	24	0.002391	2492756	0.259926
Up	ASB18	24	9.77E-04	3202162	0.273001
Up	CD2	23	0.002221	926408	0.287954
Up	BCL11B	23	8.18E-04	1888298	0.28836
Up	STAT4	23	0.001786	2435506	0.277166
Up	NGEF	23	0.001809	1548206	0.277636
Up	SMPD3	23	0.002518	2175774	0.281
Up	FZD2	22	0.003673	3239390	0.250335
Up	DUSP15	22	0.001253	2474532	0.284472
Up	CD3D	21	0.001725	1111132	0.288589
Up	SYT17	21	0.002549	2482574	0.285802
Up	FCGR3B	21	0.002748	1492022	0.282286
Up	EGR2	21	0.002934	3438856	0.266406
Up	ZBP1	21	0.001876	2664938	0.26006
Up	CAMK4	21	0.001773	3472134	0.272716
Up	DMC1	20	0.002511	4659098	0.254277
Up	GDNF	20	0.002515	3274958	0.244751
Up	FCN1	20	0.002571	1243380	0.236742
Up	LUM	20	0.002276	1515870	0.283903
Up	GZMA	20	0.001051	3258230	0.276498
Up	TGFB2	20	0.002259	1632566	0.277119
Up	SLAMF7	20	0.00211	1035482	0.271708
Up	MS4A1	20	0.002857	1169078	0.288398
Up	ETV4	20	0.001747	1674080	0.301883
Up	GLI2	20	0.001398	2977194	0.285902

Up	PHLDA1	19	4.37E-04	818256	0.298194
Up	COL8A2	19	0.00147	1089762	0.273835
Up	GABRD	19	0.002826	2629544	0.25748
Up	LMF1	19	0.004342	2024228	0.265132
Up	F2RL2	19	0.001554	790338	0.282933
Up	LYPD1	19	0.003123	3995458	0.266276
Up	CAPN6	19	0.001415	3046736	0.267802
Up	SOX8	19	0.003361	2763024	0.251306
Up	IER3	18	0.001921	3613164	0.282982
Up	BEX1	18	0.001034	1286206	0.273606
Up	COLQ	18	0.001173	1414826	0.261234
Up	NTM	18	0.00284	2486684	0.275102
Up	RPS4Y1	18	0.001013	1200768	0.287713
Up	FERMT1	18	0.001713	4279868	0.270315
Up	RGS17	18	0.002928	3868106	0.249895
Up	TNNI1	17	0.001349	1550004	0.266765
Up	MYOZ1	17	0.00128	2111156	0.283203
Up	KLHDC8A	17	0.001147	7007508	0.251036
Up	MYL1	17	7.90E-04	1213666	0.289945
Up	DIO2	16	0.001161	1959228	0.279416
Up	ITGAL	16	0.001182	1521116	0.271527
Up	CRABP2	16	4.13E-04	675182	0.272171
Up	HS2D	16	0.001425	889856	0.26034
Up	CD48	3	0	0	0.265422
Up	CD3G	2	0	0	0.23833
Up	LY9	2	0	0	0.240141
Up	SIT1	2	0	0	0.264221
Up	ATP1A4	2	1.16E-04	79140	0.235049
Up	FMOD	2	3.96E-05	20526	0.240707
Up	CCDC80	2	3.58E-05	499704	0.288908
Up	CCR7	2	0	0	0.244312
Up	KCNIP1	1	0	0	0.219995
Up	CD6	1	0	0	0.22832
Up	FCRL3	1	0	0	0.241062
Up	SERTAD4	1	0	0	0.257531
Up	PRF1	1	0	0	0.222162
Up	C1QTNF9	1	0	0	0.226548
Up	OPCML	1	0	0	0.215756
Up	ESM1	1	0	0	0.213551
Up	CD40LG	1	0	0	0.240053
Up	S1PR5	1	0	0	0.24224
Up	AGTR2	1	0	0	0.259256
Up	NPPB	1	0	0	0.211726
Up	SCG5	1	0	0	0.238721
Up	PDE5A	1	0	0	0.243548
Up	RYR3	1	0	0	0.274755
Up	RASEF	1	0	0	0.274755
Up	PODXL2	1	0	0	0.213106
Up	OGN	1	0	0	0.226548
Up	PLCH2	1	0	0	0.238721
Up	SCG2	1	0	0	0.267704
Up	P3H2	1	0	0	0.207132
Up	C12orf75	1	0	0	0.217608
Up	ACE	1	0	0	0.241159
Up	GNA14	1	0	0	0.217608
Up	HDC	1	0	0	0.216614
Up	CMA1	1	0	0	0.226713
Up	CEACAM3	1	0	0	0.265519
Down	PCLAF	817	0.135529	4.95E+08	0.365547
Down	CFTR	800	0.168404	4.5E+08	0.378823
Down	TK1	188	0.034997	43663230	0.331089
Down	ECT2	164	0.020509	39431940	0.325989
Down	FKBP5	157	0.028064	15963868	0.346288
Down	ANLN	153	0.021564	38168832	0.325066
Down	ATP2A2	148	0.027131	19656040	0.363859
Down	BCL6	142	0.022279	29419916	0.314181
Down	TOP2A	132	0.018571	16838266	0.361426
Down	ZBTB16	132	0.025165	14500206	0.349976
Down	S100A9	124	0.01355	11186464	0.352219
Down	CEP55	123	0.019583	21505878	0.316891

Down	BLM	108	0.014259	18458556	0.321945
Down	AGTR1	100	0.019518	14083216	0.313564
Down	SAMHD1	94	0.011463	12340270	0.337357
Down	S100A8	88	0.011637	8662548	0.361486
Down	GRAP2	86	0.011721	16819438	0.305936
Down	CBS	83	0.011248	20466334	0.301591
Down	SOCS3	83	0.011071	9067820	0.324888
Down	GFI1B	80	0.011791	21469034	0.299012
Down	APOB	78	0.014102	9290092	0.319133
Down	PCK1	77	0.004102	12732476	0.305408
Down	MARK3	76	0.008497	19265788	0.304512
Down	HMOX2	75	0.011098	15258770	0.312053
Down	PCNT	74	0.011297	9190430	0.312261
Down	PIK3C2A	69	0.005568	8768122	0.313053
Down	KIF14	69	0.01035	12506564	0.304668
Down	WASF1	67	0.009478	18219554	0.29633
Down	ARNTL	65	0.00974	19494854	0.295526
Down	ALOX5	65	0.010921	7343824	0.306424
Down	MCM10	64	0.006773	8807396	0.306438
Down	THBS1	64	0.008915	6203038	0.312694
Down	VSIG4	64	0.010353	10534518	0.302037
Down	WWC1	64	0.007241	14604594	0.301647
Down	MELK	63	0.008554	18629232	0.283953
Down	P2RY12	63	0.008962	9063088	0.286641
Down	PPL	62	0.007851	16137388	0.297313
Down	MYBL2	59	0.006189	16766208	0.291964
Down	FAM107A	59	0.006172	12510302	0.289688
Down	GRIP1	58	0.008069	3384760	0.320055
Down	ELF3	56	0.004945	7205142	0.309118
Down	PALLD	55	0.00509	15467012	0.293274
Down	CTH	54	0.007754	5179060	0.296908
Down	EIF4EBP1	53	0.005367	9748852	0.303946
Down	KNG1	53	0.007017	4204766	0.304243
Down	GLUL	51	0.00728	10616752	0.30116
Down	SLC2A1	51	0.004557	8307646	0.303974
Down	HP	51	0.006741	3398298	0.314741
Down	RPGR	50	0.004441	10097488	0.29384
Down	TLR2	50	0.00754	8322330	0.294595
Down	GRB7	49	0.004147	4832846	0.308113
Down	PPEF1	49	0.001983	3327232	0.298276
Down	TXNRD1	49	0.00627	2860122	0.328561
Down	NAMPT	48	0.005035	10420710	0.290538
Down	BMP7	47	0.007622	4442306	0.286981
Down	CA14	47	0.005218	4884858	0.279189
Down	CCR1	46	0.008305	11217842	0.27812
Down	CDC45	45	0.004479	3231162	0.30618
Down	ARG1	45	0.004931	2347856	0.32381
Down	SPC24	43	0.005356	6589710	0.294834
Down	FGR	43	0.003434	3020950	0.303452
Down	KIF5C	42	0.004876	2365086	0.319586
Down	IL1R2	42	0.006825	9489620	0.289265
Down	SERPINA3	42	0.005518	4047110	0.293168
Down	DEPDC1B	42	0.002978	9632346	0.260838
Down	SLC4A7	41	0.006314	2752106	0.316232
Down	SERPINA5	41	0.003604	13750404	0.273206
Down	MPP3	40	0.008262	9328402	0.297003
Down	NCEH1	40	0.009405	3554728	0.304214
Down	SLC1A1	38	0.008678	2278154	0.320573
Down	CLSPN	38	0.003668	3801300	0.294343
Down	BCAT1	38	0.0052	9066238	0.269657
Down	MYH6	38	0.005049	1731786	0.308578
Down	IL20RA	37	0.005252	8769348	0.267901
Down	HOOK1	37	0.005558	7195380	0.279177
Down	FLT3	37	0.002948	1938440	0.292408
Down	ADAMTS4	37	0.005524	2338476	0.307519
Down	CAMSAP3	36	0.003339	4795892	0.29578
Down	PLA2G2A	35	0.003637	1686594	0.300565
Down	FOSL1	34	0.004151	10955318	0.269402
Down	NQO1	34	0.001945	5351260	0.289201
Down	ELANE	34	0.005024	2289646	0.302834

Down	KCND3	34	0.002555	9153178	0.28203
Down	EPN3	34	0.005073	7423282	0.280302
Down	GPR183	34	0.003642	4243792	0.256783
Down	CD109	34	0.006381	3655940	0.303565
Down	TUBA3E	34	0.003459	6711886	0.289048
Down	TGFBR3	33	0.005143	1983082	0.267386
Down	NID1	33	0.004536	1702236	0.311503
Down	STEAP3	33	0.004665	2788716	0.285365
Down	AMD1	32	0.005714	3154782	0.29099
Down	EDNRB	31	0.003092	7273156	0.265368
Down	IL17RB	31	0.004227	6381040	0.261527
Down	SLC19A2	30	0.004653	2505974	0.281302
Down	SLC22A16	30	0.004545	3831872	0.240618
Down	PHACTR3	29	0.002193	6417862	0.280976
Down	LAPTM5	29	0.003298	2735158	0.274317
Down	ANGPTL4	29	0.003467	1447446	0.325163
Down	PPM1E	29	0.002894	5733032	0.270427
Down	E2F2	28	0.002816	5508320	0.28041
Down	SERPINE1	28	0.001474	2497574	0.271302
Down	ACPP	28	0.003084	2749550	0.291223
Down	KRT7	28	0.002861	1288592	0.315774
Down	SERPINB8	28	0.002944	3167812	0.28186
Down	FREM2	28	0.003954	3395758	0.276661
Down	RNF157	28	0.002172	6196626	0.265551
Down	PPIP5K2	28	0.003886	8572108	0.270014
Down	F8	27	0.002839	4879016	0.274836
Down	TUBAL3	27	0.002055	1052840	0.318915
Down	ELL2	26	0.003971	6281508	0.255859
Down	GRB14	25	0.002326	3092024	0.28378
Down	IRAK3	25	0.00257	6900170	0.265897
Down	MANEA	25	0.004508	5075608	0.263869
Down	CLEC7A	25	0.004246	4293212	0.277095
Down	KLF10	24	0.001607	3013994	0.281339
Down	GNMT	24	0.00165	3015768	0.269136
Down	ART3	24	0.002904	2401360	0.255748
Down	LRRC8E	24	0.003739	4188308	0.288665
Down	SLA	23	0.001714	1003510	0.289329
Down	CLEC4G	23	0.002667	2376260	0.277495
Down	TUBB4A	5	1.28E-04	181440	0.250652
Down	CD38	4	0	0	0.268176
Down	FCGR3A	4	1.01E-04	73756	0.268385
Down	F5	3	8.10E-07	708	0.248641
Down	EHF	2	7.11E-06	4180	0.254842
Down	KIAA1549	2	4.16E-04	193604	0.261391
Down	S100A3	2	1.84E-05	45822	0.254376
Down	ADH1B	2	3.40E-05	28184	0.233546
Down	PAPSS2	2	1.05E-05	8726	0.251868
Down	PTX3	1	0	0	0.19143
Down	IL15RA	1	0	0	0.234199
Down	EDN1	1	0	0	0.209723
Down	SERPINF2	1	0	0	0.232451
Down	ZNF366	1	0	0	0.282018
Down	ACR	1	0	0	0.214588
Down	MATN3	1	0	0	0.222881
Down	CNR1	1	0	0	0.216205
Down	LBP	1	0	0	0.240053
Down	ALOX5AP	1	0	0	0.23456
Down	SCGN	1	0	0	0.23353
Down	MAMDC2	1	0	0	0.248745
Down	CDKL5	1	0	0	0.219891
Down	CENPM	1	0	0	0.231833
Down	KCNIP2	1	0	0	0.219995
Down	CPM	1	0	0	0.24533
Down	GPSM2	1	0	0	0.245855
Down	LSAMP	1	0	0	0.215756
Down	KCNK3	1	0	0	0.219353
Down	ALOX15B	1	0	0	0.234981
Down	ST6GALNAC3	1	0	0	0.233263
Down	GPRC5A	1	0	0	0.274755
Down	SLC31A2	1	0	0	0.215287

Down	MARVELD2	1	0	0	0.218671
Down	SNTG2	1	0	0	0.229
Down	TRHDE	1	0	0	0.208786
Down	SIGLEC7	1	0	0	0.245229
Down	SMTNL2	1	0	0	0.265519
Down	ANXA3	1	0	0	0.274755
Down	F13A1	1	0	0	0.248745
Down	ANKRD7	1	0	0	0.233438
Down	KCNS2	1	0	0	0.219721
Down	SIGLEC9	1	0	0	0.227565
Down	SIGLEC10	1	0	0	0.282018
Down	C20orf197	1	0	0	0.282018
Down	SCGB1D2	1	0	0	0.226548
Down	IL1RL1	1	0	0	0.21698
Down	PLIN2	1	0	0	0.241935
Down	CD163	1	0	0	0.239403
Down	HPR	1	0	0	0.240053

Table 6 miRNA - target gene and TF - target gene interaction

Regulation	Target Genes	Degree	MicroRNA	Regulation	Target Genes	Degree	TF
Up	FSCN1	99	hsa-mir-4533	Up	FSCN1	62	ESRRA
Up	ESR1	72	hsa-mir-548ac	Up	APOA1	48	RERE
Up	TMEM30B	64	hsa-mir-548i	Up	COL1A1	21	HMG20B
Up	SCN2B	46	hsa-mir-5585-3p	Up	HBB	16	THRAP3
Up	CENPA	35	hsa-mir-6750-3p	Up	LCK	15	ATF1
Up	APOA1	22	hsa-mir-6722-5p	Up	FOXS1	14	YBX1
Up	PPP2R2B	14	hsa-mir-149-3p	Up	CENPA	10	SAP30
Up	TP63	12	hsa-mir-1178-3p	Up	SCN2B	5	RCOR2
Up	PYHIN1	5	hsa-mir-205-3p	Up	TMEM30B	5	ZNF24
Up	APLNR	2	hsa-mir-10b-5p	Up	APLNR	4	FOXJ2
Up	PTN	1	hsa-mir-155-5p	Up	NRG1	2	SUZ12
Up	LCK	1	hsa-mir-335-5p	Up	PTN	2	L3MBTL2
Up	CD247	1	hsa-mir-346	Up	UCHL1	2	MAZ
Down	FKBP5	88	hsa-mir-200c-3p	Up	ESR1	1	EZH2
Down	PCLAF	62	hsa-mir-1273g-3p	Up	ZAP70	1	ZFX
Down	CEP55	57	hsa-mir-1244	Down	SOC3	48	MXD3
Down	ATP2A2	55	hsa-mir-4789-3p	Down	BCL6	44	ARID4B
Down	TK1	45	hsa-mir-766-3p	Down	FKBP5	43	CBFB
Down	ZBTB16	43	hsa-mir-1976	Down	ANLN	38	TAF7
Down	SAMHD1	26	hsa-mir-3124-3p	Down	ATP2A2	35	CREM
Down	TOP2A	17	hsa-mir-186-5p	Down	CBS	31	IKZF1
Down	BCL6	13	hsa-mir-339-5p	Down	BLM	19	ZNF501
Down	ECT2	13	hsa-mir-132-3p	Down	ECT2	15	KLF16
Down	CFTR	9	hsa-mir-145-5p	Down	CEP55	10	FOSL2
Down	S100A9	7	hsa-mir-4679	Down	GRAP2	10	CEBPD
Down	AGTR1	5	hsa-mir-410-3p	Down	ZBTB16	4	TRIM28
Down	ANLN	5	hsa-mir-503-5p	Down	S100A8	3	STAT3
Down	BLM	3	hsa-mir-193b-3p	Down	S100A9	2	CEBPG
				Down	AGTR1	1	EZH2

Table 7 Docking results of Designed Molecules on Over Expressed Proteins

Sl. No/ Code	Over expressed gene: ESR1			Over expressed gene: LCK			Over expressed gene: PPP2R2B			Over expressed gene: PYHIN 1			Over expressed gene: TP63		
	PDB: 4PXM			PDB: 1KSW			PDB: 2HV7			PDB: 3VD8			PDB: 6RU6		
	Total Score	Crash (-Ve)	Polar	Total Score	Crash (-Ve)	Polar	Total Score	Crash (-Ve)	Polar	Total Score	Crash (-Ve)	Polar	Total Score	Crash (-Ve)	Polar
HIM1	5.097	-4.375	0.114	4.258	-1.555	1.784	4.904	-0.870	0.004	5.794	-0.514	3.828	5.770	-1.440	2.231
HIM2	4.057	-6.172	0.039	4.624	-0.997	1.959	4.906	-0.468	1.517	5.052	-0.780	3.415	5.414	-1.529	2.444
HIM3	5.353	-5.309	0.161	4.578	-1.492	1.790	5.042	-1.845	1.073	5.680	-0.804	3.956	5.350	-1.170	2.316
HIM4	3.976	-5.132	0.167	3.839	-1.635	1.196	6.328	-1.172	1.128	4.966	-0.666	1.818	5.627	-1.416	2.320
HIM5	2.707	-7.759	0.179	4.067	-0.997	1.987	5.254	-0.674	1.618	4.563	-1.068	2.935	5.698	-1.240	2.485
HIM6	5.948	-3.902	1.796	5.229	-0.707	3.656	6.766	-1.424	1.858	6.670	-0.941	5.519	6.218	-1.468	2.578

HIM7	5.019	-7.055	0.203	4.382	-2.443	3.329	6.028	-0.629	1.660	5.374	-1.876	0.670	6.627	-1.484	2.579
HIM8	4.429	-3.983	0.344	4.150	-4.382	4.210	6.794	-1.279	1.129	5.468	-0.769	3.444	5.842	-2.088	2.272
HIM9	3.722	-5.956	0.197	4.051	-2.006	0.002	6.116	-0.597	1.717	5.407	-0.565	1.370	5.877	-2.054	0.792
HIM10	6.771	-3.977	1.836	5.176	-3.512	4.023	5.332	-1.378	3.349	6.071	-0.923	3.854	5.825	-0.966	3.672
HIM11	3.775	-6.079	0.898	6.998	-2.086	3.842	8.678	-1.065	2.876	5.087	-0.881	1.854	5.948	-1.015	1.202
HIM12	0.190	-8.149	0.022	5.302	-2.305	3.475	5.227	-1.636	0.710	7.322	-1.128	4.099	6.237	-2.562	2.171
HIM13	4.523	-4.537	0.014	4.840	-0.664	3.305	6.181	-2.966	3.523	5.281	-0.503	3.981	5.905	-1.136	2.218
HIM14	5.247	-3.183	0.000	4.888	-1.296	2.563	5.037	-0.377	1.647	7.057	-0.799	4.256	6.116	-1.366	2.438
HIM15	4.633	-4.173	0.180	3.756	-0.710	2.072	5.188	-1.559	1.143	5.570	-1.125	3.718	6.238	-1.708	2.443
HIM16	4.588	-2.883	0.000	6.027	-1.099	3.903	5.606	-0.987	4.197	5.661	-0.926	2.751	7.263	-1.533	4.212
HIM17	3.944	-4.806	0.236	5.329	-0.590	2.798	4.830	-1.682	1.617	6.234	-0.830	3.912	5.366	-1.257	3.022
HTZ1	0.593	-7.518	0	4.221	-0.692	1.975	3.993	-0.539	0.003	5.284	-0.566	1.432	5.227	-1.045	0.903
HTZ2	-1.770	-8.477	0.000	4.055	-1.438	2.877	4.388	-1.665	1.170	4.100	-0.546	3.017	4.563	-0.976	1.266
HTZ3	4.649	-5.870	0.148	5.104	-0.861	3.922	4.243	-1.539	1.933	5.304	-1.370	1.398	5.138	-1.217	1.930
HTZ4	-3.169	-	0.482	4.173	-1.898	1.864	4.654	-1.627	1.128	5.163	-0.745	1.304	5.084	-1.143	1.018
		12.002													
HTZ5	4.021	-	0.246	3.215	-1.481	4.232	3.256	-6.374	2.317	2.382	-5.263	1.238	4.623	-0.951	1.280
		12.325													
HTZ6	6.605	-3.866	1.6487	4.004	-1.104	2.851	5.834	-1.310	3.111	5.286	-1.530	1.436	6.336	-2.326	3.781
HTZ7	4.977	-5.434	0.655	5.197	-2.040	3.250	5.352	-1.371	1.172	6.138	-1.734	1.627	4.908	-1.057	1.335
HTZ8	1.025	-8.223	0.000	3.549	-1.310	2.403	4.024	-3.825	2.440	4.980	-0.593	1.474	5.164	-1.291	0.999
HTZ9	3.386	-7.041	0.194	5.567	-1.622	3.057	6.792	-2.581	1.088	5.794	-0.683	1.774	6.053	-1.408	1.037
HTZ10	4.744	-5.463	0.837	4.520	-2.469	3	7.758	-1.518	3.765	5.345	-1.133	3.661	7.507	-2.080	4.086
HTZ11	2.991	-6.177	0	3.453	-0.721	1.266	4.841	-1.738	0.045	4.368	-0.805	1.074	6.176	-1.380	1.511
HTZ12	4.810	-6.157	0.275	5.296	-2.814	3.605	5.138	-1.840	2.189	5.083	-0.870	1.536	5.592	-1.321	1.525
HTZ13	4.868	-3.837	0	4.863	-0.535	2.405	4.656	-0.681	3.152	4.246	-2.335	0.529	6.404	-0.975	2.954
HTZ14	5.646	-3.473	0	4.948	-0.801	2.324	4.953	-1.672	1.066	5.058	-1.174	1.121	5.114	-1.299	1.296
HTZ15	3.428	-4.957	0.348	3.949	-0.614	1.873	4.049	-0.787	1.224	4.796	-1.066	1.489	3.510	-0.607	0.461
HTZ16	4.227	-4.787	0.298	4.654	-1.534	2.096	6.143	-1.204	2.879	4.854	-0.994	1.564	7.102	-0.917	3.001
HTZ17	3.784	-5.018	0.380	3.661	-0.897	1.676	4.016	-1.179	1.384	4.039	-0.569	2.706	4.256	-1.040	1.236
HTZ STD	4.722	-1.084	1.063	3.319	-0.890	3.033	3.564	-0.272	2.367	3.394	-0.882	1.169	4.237	-0.801	1.855