Identification of novel key genes and signaling pathways in hypertrophic cardiomyopathy: evidence from bioinformatics and next generation sequencing data analysis

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Abstract

Hypertrophic cardiomyopathy (HCM) is a global health problem characterized by left ventricle become thick and stiff with effect of indication including chest pain, fluttering, fainting and shortness of breath. In this investigation, we aimed to identify diagnostic markers and analyzed the therapeutic potential of essential genes. Next generation sequencing (NGS) dataset GSE180313 was obtained from the Gene Expression Omnibus (GEO) database and used to identify differentially expressed genes (DEGs) in HCM. DEGs were screened using the DESeq2 Rbioconductor tool. Then, Gene Ontology (GO) and REACTOME pathway enrichment analyses were performed. Moreover, a protein-protein interaction (PPI) network of the DEGs was constructed, and module analysis was performed. Next, miRNA-hub gene regulatory network and TF-hub gene regulatory network were constructed and analyzed. Finally, diagnostic values of hub genes were assessed by by receiver operating characteristic (ROC) curve analysis. By performing DEGs analysis, total 958 DEGs (479 up regulated genes and 479 down regulated genes) were successfully identified from GSE180313, respectively. GO and REACTOME pathway enrichment analyses revealed that GO functions and signaling pathways were significantly enriched including response to stimulus, multicellular organismal process, metabolism and extracellular matrix organization. The hub genes of FN1, SOX2, TUBA4A, RPS2, TUBA1C, ESR1, SNCA, LCK, PAK1 and APLNR might be associated with HCM. The hub gens of FN1 and TPM3, together with corresponding predicted miRNAs (e.g., hsa-mir-374a-5p and hsa-miR-8052), and SH3KBP1 and ESR1 together with corresponding predicted TFs (e.g PRRX2 and STAT3) were found to be significantly correlated with HCM. This investigation could serve as a basis for further understanding the molecular pathogenesis and potential therapeutic targets of HCM.

Keywords: hypertrophic cardiomyopathy; bioinformatics; differentially expressed genes; protein-protein interaction; next generation sequencing

Introduction

Hypertrophic cardiomyopathy (HCM) is a prevalent heritable cardiovascular disease [1], which affects around 1:500 (0.2%) of the world's population [2]. HCM is primarily characterized by left ventricle become thick and stiff [3]. The clinical incidence of HCM is high, and its main features include chest pain, fluttering, fainting and shortness of breath [4]. Studies have revealed that the progression of HCM is related to genetic factors [5]. Complications of HCM can include atrial fibrillation [6], blocked blood flow [7], mitral valve disease [8], dilated cardiomyopathy [9], heart failure [10], cardiac death [11], myocardial infarction [12], myocardial ischemia [13], coronary artery disease [14], cardiac arrest [15], atherosclerosis [16], cardiac fibrosis [17], hypercholesterolemia [18], inflammation [19], hypertension [20], obesity [21] and diabetes mellitus [22]. Medications (beta blockers, calcium channel blockers, mavacamten, amiodarone and Warfarin) [23-27] and Surgeries or other procedures (septal myectomy, septal ablation, implantable cardioverter-defibrillator, cardiac resynchronization therapy, ventricular assist device and heart transplant) [28-32] are the current feasible treatment of HCM patients. Despite advancement in diagnosis and treatment, the prognosis of HCM patient's remains destitute, this has become an effective topic of clinical and fundamental investigation. Hence, dynamic novel diagnosis biomarkers thoughtful the damage of heart muscles is engaging for the timely diagnoses and therapies of HCM.

The recent next generation sequencing (NGS) analysis of specimens from sufferers and normal individuals enables us to investigate various diseases [33-34]. Genetic mutations, epigenetic alterations and aberrant molecular signaling pathways are associated in the HCM [35-37]. Recently, numerous specific genes have been identified to participate in the advancement of HCM. For instance, it was reported that the expression level of ACTN2 [38], MYBPC3 [39], MYOZ2 [40], ACTC [41] and NEXN [42] were considerably higher in damaged heart muscles from HCM sufferers in contrast to normal heart muscles. RAS signaling pathway [43], Hippo/YAP signaling pathway [44], Akt/GSK-3β signaling pathway [45], alcineurin-NFAT signaling pathway [46] and mTOR signaling pathway [47] reveals that the treatment manipulation of such signaling pathways can offer novel enlightenment for the treatment of HCM. These finding suggested the key roles of

few function genes in HCM development. However, the diagnostic value of many genes has not been studied in HCM.

NGS technology and bioinformatics analysis have been broadly applied to screen for genetic modification at the genomic level. Our main determination is to explore the connection between HCM and its complications. First, we download the GSE180313 [48] dataset file in the NCBI-Gene Expression Omnibus database (NCBI-GEO) (https://www.ncbi.nlm.nih.gov/geo) [49] database for analysis, then use DESeq2 [Love et al. 2014] to draw the differentially expressed genes (DEGs) distribution map of the HCM and normal control samples in the dataset. Immediately after, we performed gene ontology (GO) and REACTOME pathway enrichment analysis on these DEGs. By constructing protein-protein interaction (PPI) network, we screened for the highest scoring modules and hub genes. Immediately afterward miRNA-hub gene regulatory network and TF-hub gene regulatory network were built by Cytoscape to predict the underlying microRNAs (miRNAs) and transcription factors (TFs) linked with hub genes. To validate that these hub genes can serve as biomarkers of HCM, we determined diagnostic value of hub gene by receiver operating characteristic (ROC) curve analysis. This investigation will develop our perceptive of the molecular mechanisms of HCM and supply genomic-targeted therapy preference for HCM.

Materials and Methods

Next generation sequencing (NGS) data source

The publicly accessible NGS data were all obtained from the NCBI-GEO. NGS dataset deposited by Ranjbarvaziri et al. [48], accession no. GSE180313, containing 20 samples (13 HCM samples and 7 normal control samples) were employed in the current investigation. The GSE180313 dataset generated using the GPL24676 platform (Illumina NovaSeq 6000 (Homo sapiens)).

Identification of DEGs

Determining DEGs between HCM and normal blood samples was performed using DESeq2 [50]. DESeq2 is an R bioconductor tool that allows users to determine DEGs for various experimental situations. The adjusted P-values (adj. P) and Benjamini and Hochberg false discovery rate were used to find statistically

significant genes [51]. The screening criteria of DEGs were set as false discovery rate (FDR) ≤ 0.05, and |log2 fold change (FC)| > 0.828 for up regulated genes and |log2 fold change (FC)| < -1.219 for down regulated genes. The volcano plot and heatmap were generated using the "ggplot2" and "gplot" packages in the R bioconductor software.

GO and pathway enrichment analyses of DEGs

Online biological information can be establish in the g:Profiler (http://biit.cs.ut.ee/gprofiler/) [52] program. A essential bioinformatics tool for annotating genes and examining their biological processes is the GO (http://www.geneontology.org) [53]. GO enrichment analysis includes biological processes (BP), cellular components (CC), and molecular functions (MF). The REACTOME pathway (https://reactome.org/) [54] is a database tool for analyzing large-scale molecular data sets produced by high-throughput experimental techniques to superior understand high-level biological processes and systems. P < 0.05 was considered statistically significant.

Construction of the PPI network and module analysis

The Cytoscape software (version 3.10.2) (http://www.cytoscape.org/) [55] and HIPPIE (Human Integrated Protein-Protein Interaction rEference) (https://cbdm-01.zdv.uni-mainz.de/~mschaefer/hippie/) [56] interactome database were used to establish the PPI analysis of the DEGs. First, the HIPPIE PPI database was used to construct the PPI network. The PPI network was visualized using Cytoscape (version 3.10.2). Subsequently, genes with the top interaction scores were screened as hub genes using the node degree [57], betweenness [58], stress [59] and closeness [60] algorithms of the Network Analyzer plugin in Cytoscape software. And PEWCC algorithm [61] was used for identifying significant modules.

Construction of the miRNA-hub gene regulatory network

miRNet (https://www.mirnet.ca/) [62] is a bioinformatics platform for predicting hub genes and miRNA- hub gene pairs. In the current investigation, the targets of the hub gene were predicted using eight databases: TarBase, miRTarBase, miRecords, miRanda, miR2Disease, HMDD, PhenomiR, SM2miR, PharmacomiR,

EpimiR, starBase, TransmiR, ADmiRE, and TAM 2.0. The miRNA-hub gene regulatory network was depicted and visualized using Cytoscape software [55].

Construction of the TF-hub gene regulatory network

NetworkAnalyst (https://www.networkanalyst.ca/) [63] is a bioinformatics platform for predicting hub genes and TF- hub gene pairs. In the current investigation, the targets of the hub gene were predicted using Jasper database. The TF-hub gene regulatory network was depicted and visualized using Cytoscape software [55].

Receiver operating characteristic curve (ROC) analysis

To determine the sensitivity and specificity of the selected hub genes for HCM diagnosis, the visualization tool "pROC" package in R software [64] was used to construct a receiver operating characteristic (ROC) curve. The area under the curve (AUC) was calculated for each dataset, and hub genes with an AUC exceptional 0.7 were classified as holding a strong inequitable capacity for HCM.

Results

Identification of DEGs

We selected GSE180313 NGS dataset to analyze and identify the DEGs. A total of 958 DEGs were identified, which include 479 up regulated DEGs and 479 down regulated DEGs (Table 1). The volcano plot and heatmap are shown in Fig. 1 and Fig. 2.

GO and pathway enrichment analyses of DEGs

The GO enrichment analysis revealed the following most GO significant enrichment terms: (1) BP: response to stimulus, multicellular organism development, multicellular organismal process and cell communication; (2) CC: cell periphery, membrane, plasma membrane and cellular anatomical entity; and (3) MF: oxidoreductase activity, transporter activity, signaling receptor binding and molecular function regulator activity (Table 2). The REACTOME pathway enrichment analysis revealed that the DEGs were particularly enriched in metabolism, cardiac conduction, extracellular matrix organization and GPCR ligand binding (Table 3).

Construction of the PPI network and module analysis

The visual PPI network of 958 DEGs was constructed using Cytoscape software. The PPI network was composed of 5887 nodes and 10291 edges (Fig. 3). Among the 5887 nodes, 958 hub genes with the highest nodes degree, betweenness, stress and closeness were screened based on the Cytoscape software analysis results. The results were as follows: FN1, SOX2, TUBA4A, RPS2, TUBA1C, ESR1, SNCA, LCK, PAK1 and APLNR (Table 4). The two significant modules with the highest degree were screened, and GO and pathway enrichment of genes in these two modules was analyzed using g:Profiler online tools. The key modules were obtained using PEWCC. Module 1 contained 53 nodes and 66 edges (Fig. 4A), mainly involved in response to stimulus, multicellular organism development and cell periphery. Module 2 was comprised of 19 nodes and 59 edges (Fig. 4B), which were associated with multicellular organismal process, cell communication and cytokine signaling in immune system.

Construction of the miRNA -hub gene regulatory network

The related miRNA-hub gene regulatory network was shown in Fig. 5. In the miRNA-hub gene regulatory network, FN1 was regulated by 439 miRNAs including hsa-mir-374a-5p; TFRC was regulated by 422 miRNAs including hsa-miR-520d-5p; FKBP5 was regulated by 305 miRNAs including hsa-miR-34a-5p; FHL2 was regulated by 291 miRNAs including hsa-mir-4646-5p; RPLP0 was regulated by 232 miRNAs including hsa-mir-548aw; TPM3 was regulated by 456 miRNAs including hsa-miR-8052; ESR1 was regulated by 266 miRNAs including hsa-mir-302b-3p; CHRM3 was regulated by 226 miRNAs including hsa-miR-194-5p; TMEM30B was regulated by 203 miRNAs including hsa-mir-548i; PAK1 was regulated by 162 miRNAs including hsa-miR-524-5p (Table 5).

Construction of the TF-hub gene regulatory network

The related TF-hub gene regulatory network was shown in Fig. 6. In the TF-hub gene regulatory network, SH3KBP1 was regulated by 20 TFs including PRRX2; FHL2 was regulated by 19 TFs including SRY; FKBP5 was regulated by 17 TFs including USF2; TFRC was regulated by 15 TFs including BRCA1; FN1 was regulated by 14 TFs including STAT1; ESR1 was regulated by 26 TFs including STAT3; TP63 was regulated by 21 TFs including FOS; PTPRR was regulated by

16 TFs including MEF2A; TPM3 was regulated by 13 TFs including MEF2A; SNCA was regulated by 11 TFs including GATA2 (Table 5).

Receiver operating characteristic curve (ROC) analysis

The ROC curve was utilized to assess the diagnostic efficacy of hub genes in predicting HCM occurrence and advancement. A greater AUC value demonstrate better predictive efficacy. The AUC values of the hub genes were FN1-AUC:0.934, SOX2-AUC:0.919, TUBA4A-AUC:0.923, RPS2-AUC:0.891, TUBA1C-AUC:0.908, ESR1-AUC:0.927, SNCA-AUC:0.900, LCK-AUC:0.938, PAK1-AUC:0.895 and APLNR-AUC:0.897 suggesting that these hub genes all display remarkable predictive ability for obesity occurrence and development (Fig. 7).

Discussion

HCM is a cardiovascular disorder with high rates of pervasiveness and mortality [65]. Therefore, sensitive and specific biomarkers of HCM are urgently needed to be detected. In the current investigations, bioinformatics and NGS methods are promising methods to analyze the key genes and signaling pathways, which might contribute new indication for diagnosis, therapy, and prognosis of HCM.

In this investigation, we analyzed the HCM NGS data GSE146638 screened from the GEO database. It includes 7 normal control samples and 13 HCM samples. We identified 958 DEGs, including 479 up-regulated genes and 479 down-regulated genes. SAA1 [66], MYH6 [67] and MSTN (myostatin) [68] are mainly associated with HCM. SAA1 [66], MYH6 [69] and MSTN (myostatin) [70] plays a role in diagnosis of dilated cardiomyopathy. SAA1 [71], SERPINA3 [72], MYH6 [73], ESM1 [74] and MSTN (myostatin) [75] served as a biomarkers for heart failure diagnosis and prognosis. SAA1 [76], SERPINA3 [77], ESM1 [74] and MSTN (myostatin) [78] have been known to be involved in myocardial infarction progression. SAA1 [79], SERPINA3 [80], IL1RL1 [81], ESM1 [82] and MSTN (myostatin) [83] have a significant prognostic potential in coronary artery disease. SAA1 [84] and MSTN (myostatin) [85] are molecular markers for the diagnosis and prognosis of atherosclerosis. Studies had shown that SAA1 [71] and MSTN (myostatin) [86] were associated with cardiac fibrosis. Studies have found

that SAA1 [87], RNASE2 [88], SERPINA3 [89], IL1RL1 [90], ESM1 [91] and MSTN (myostatin) [92] are altered expressed in inflammation. The altered expression of SAA1 [93], IL1RL1 [90], ESM1 [94] and MSTN (myostatin) [95] might indicate increased risk of obesity. SAA1 [96], PTPRN (protein tyrosine phosphatase receptor type N) [97], MYH6 [98], ESM1 [99] and MSTN (myostatin) [95] plays an indispensable role in diabetes mellitus. MYH6 [100] and CUX2 [101] could be an early detection markers for atrial fibrillation. MYH6 [69] plays a significant role in cardiac death. Study suggested that MYH6 [102] as potential diagnostic biomarker for cardiac arrest. Recently, mounting investigation has revealed that ESM1 [103] was vital for the onset and developmental process of mitral valve disease. MSTN (myostatin) [104] has been demonstrated to be involved in myocardial ischemia. These findings suggest that significant DEGs can serve as candidate diagnostic biomarkers or drug targets for the clinical treatment of HCM.

g:Profiler online tool was used to predict the significantly enriched GO and REACTOME pathways. It has been confirmed that the pathogenesis of HCM is related to signaling pathways include metabolism [105], cardiac conduction [106], muscle contraction [107], neutrophil degranulation [108], metabolism of lipids [109], extracellular matrix organization [110], GPCR ligand binding [111], signaling by receptor tyrosine kinases [112] and signal transduction [113]. The expression of CD177 [114], ALOX15B [115], EREG (epiregulin) [116], FCN3 [117], SSTR5 [118], SFRP5 [119], SLAMF1 [120], CD163 [121], AQP4 [122], PCK1 [123], VDR (vitamin D receptor) [124], SERPINE1 [125], AZGP1 [126], VSIG4 [127], ELANE (elastase, neutrophil expressed) [128], FKBP5 [129], MFSD2A [130], RBP4 [131], HMGCS2 [132], MOG (myelin oligodendrocyte glycoprotein) [133], C3 [134], FGFR4 [135], ITLN1 [136], IL18R1 [137], TIMP4 [138], LYVE1 [139], GRIP1 [140], IL20RA [141], HCRTR1 [142], LGR6 [143], SOX2 [144], TWIST2 [145], NPPC (natriuretic peptide C) [146], SPP1 [147], CD109 [148], S1PR3 [149], BMP7 [150], SLC7A11 [151], MLXIPL (MLX interacting protein like) [152], AGTR1 [153], PTX3 [154], EPHB2 [155], SLC2A1 [156], TGM2 [157], FHL2 [158], CD38 [159], FGF7 [160]. OSR1 [161], STXBP2 [162], CRLF1 [163], POMC (proopiomelanocortin) [164], APOB (apolipoprotein B) [165], OLFM4 [166], BMAL1 [167], HEY2 [168], ARG2 [169], LPCAT3 [170], IL15RA [171], FABP4 [172], PTGS1 [173], C1QTNF1 [174], LMCD1

[175], TPO (thyroid peroxidase) [176], LOX (lysyl oxidase) [177], ADAMTS5 [178], CD63 [179], HAS2 [180], NQO1 [181], SIGLEC1 [182], NGFR (nerve growth factor receptor) [183], PRDX6 [184], DHCR24 [185], PDPN (podoplanin) [186], AKR1C1 [187], CTSB (cathepsin B) [188], GLRX2 [189], PRKCD (protein kinase C delta) [190], RAMP1 [191], LGALS3 [192], SLAMF8 [193], FTH1 [194], HMOX1 [195], BCL6 [196], MPST (mercaptopyruvate sulfurtransferase) [197], GAREM1 [198], RNASE6 [199], PMVK (phosphomevalonate kinase) [200], FIBCD1 [201], SLCO4A1 [202], SYN2 [203], TRPC4 [204], IGFBP2 [205], ELN (elastin) [206], NALCN (sodium leak channel, non-selective) [207], NINJ2 [208], ADAMTS15 [209], LAMB3 [210], MMP19 [211], SLCO2A1 [212], STEAP4 [213], GPSM1 [214], CYP4B1 [215], LDHA (lactate dehydrogenase A) [216], GNMT (glycine N-methyltransferase) [217], PTDSS1 [218], B3GNT7 [219], RPSA (ribosomal protein SA) [220], BCAT1 [221], RPS5 [222], SFRP4 [223], CD1C [224], TRPM8 [225], CST1 [226], UCMA (upper zone of growth plate and cartilage matrix associated) [227], RSPO2 [228], ARMS2 [229], ALOX15 [230], CTLA4 [231], PENK (proenkephalin) [232], IL1B [233], SCUBE2 [234], CTSG (cathepsin G) [235], CX3CR1 [236], CX3CR1 [237], FRZB (frizzled related protein) [238], ZNF365 [239], CMA1 [240], E2F7 [241], RGS4 [242], THBS4 [243], GDF6 [244], ENPP2 [245], GDF15 [246], TGFB2 [247], C1QTNF3 [248], MYOC (myocilin) [249], CXCL10 [250], MME (membrane metalloendopeptidase) [251], BDNF (brain derived neurotrophic factor) [252], EGR3 [253], PTN (pleiotrophin) [254], OLR1 [255], THY1 [256], MDK (midkine) [257], ANGPTL7 [258], TNFRSF11B [259], DIO2 [260], TAGLN3 [261], SMOC2 [262], PLAC8 [263], HTR2B [264], UCHL1 [265], LUM (lumican) [266], TP73 [267], TRPV3 [268], PRF1 [269], PROS1 [270], CD7 [271], ARID5A [272], FREM1 [273], SLC26A4 [274], ESR1 [375], NOS2 [276], SNCA (synuclein alpha) [277], EPHA3 [278], ACE (angiotensin I converting enzyme) [279], NT5E [280], PDE5A [281], PLCE1 [282], PAK1 [283], SOX8 [284], APOE (apolipoprotein E) [285], P2RX1 [286], BCL6B [287], EGR2 [288], GLI1 [289], PRDM1 [290], SCT (secretin) [291], HLA-DPA1 [292], FCN1 [293], EGR1 [294], TFPI2 [295], DUSP6 [296], IL34 [297], IER3 [298], RUNX1 [299], LTB (lymphotoxin beta) [300], SCN8A [301], TPM3 [302], LAMP5 [303], RHCG (Rh family C glycoprotein) [304], GZMB (granzyme B) [305], CXCL9 [306], MMP25 [307], PALM3 [308], PRSS8 [309], SELL (selectin L) [310], GZMA (granzyme A) [311], KCNN3 [312], FSCN1 [313], HAS3 [314], SYTL2 [315],

SV2A [316], PTPRH (protein tyrosine phosphatase receptor type H) [317], LSP1 [318], TREH (trehalase) [319], CXCL11 [320], CXCL3 [321], CXCL2 [322], CXCL14 [323], ADAMTS8 [324], ANGPTL8 [325] and FMOD (fibromodulin) [326] have been observed to be altered in inflammation. HOPX (HOP homeobox) [327], EREG (epiregulin) [328], KCNIP2 [329], AQP4 [330], CCN5 [331], VDR (vitamin D receptor) [332], KCNK3 [333], RBP4 [334], FGFR4 [335], TIMP4 [336], LYVE1 [337], LGR6 [338], SOX2 [339], NPPC (natriuretic peptide C) [340], SLC7A11 [341], TFEC (transcription factor EC) [342], AGTR1 [343], ITGA7 [344], FHL2 [345], CD38 [346], HCN4 [347], POMC (proopiomelanocortin) [348], APOB (apolipoprotein B) [349], BMAL1 [350], HEY2 [351], RAP1GAP [352], IGFBP2 [353], FABP4 [354], C1QTNF1 [355], LMCD1 [356], LOX (lysyl oxidase) [357], DMPK (DM1 protein kinase) [356], EDN1 [359], CTSB (cathepsin B) [360], KCNH2 [361], HMOX1 [362], CORIN (corin, serine peptidase) [363], CA14 [364], TRPC4 [365], ELN (elastin) [366], ADAMTS2 [367], LDHA (lactate dehydrogenase A) [368], LEF1 [369], IRX2 [370], CX3CR1 [371], RGS4 [372], THBS4 [373], GDF15 [374], KIT (KIT proto-oncogene, receptor tyrosine kinase) [375], ABCG2 [376], MDK (midkine) [377], DIO2 [378], PCDH17 [379], UCHL1 [380], LUM (lumican) [381], TRPV3 [382], SLC26A4 [383], ACE (angiotensin I converting enzyme) [384], PDE5A [385], PAK1 [386], APOE (apolipoprotein E) [387], EGR1 [388], RUNX1 [389], KIF1A [390], ATRNL1 [391] and ANGPTL8 [392] plays a vital role in the development of HCM. HOPX (HOP homeobox) [393], FCN3 [394], SFRP5 [395], CD163 [396], TFRC (transferrin receptor) [397], AQP4 [398], CCN5 [399], VDR (vitamin D receptor) [400], SERPINE1 [401], AZGP1 [402], VSIG4 [403], FGF12 [404], RBP4 [395], HMGCS2 [405], FGFR4 [406], TIMP4 [407], SOX2 [408], NPPC (natriuretic peptide C) [340], PRODH (proline dehydrogenase 1) [409], BMP7 [410], SLC7A11 [411], AGTR1 [412], PTX3 [413], GPD1L [414], ITGA7 [344], ATP2A2 [415], HCN4 [416], POMC (proopiomelanocortin) [417], APOB (apolipoprotein B) [418], BMAL1 [419], HEY2 [420], IGFBP2 [421], FABP4 [422], LOX (lysyl oxidase) [423], ADAMTS5 [424], HAS2 [425], NQO1 [426], PRDX6 [427], EDN1 [428], HSPB7 [429], CTSB (cathepsin B) [360], RAMP1 [430], LGALS3 [431], KCNH2 [432], F8 [433], CD276 [434], CORIN (corin, serine peptidase) [435], ELN (elastin) [436], SLC6A6 [437], PALLD (palladin, cytoskeletal associated protein) [438], DHRS7C [439], TKT (transketolase) [440], SFRP4 [441], IRX1 [442], ALOX15 [443], CTLA4 [444], PENK (proenkephalin)

[445], RGS4 [446], THBS4 [447], CX3CR1 [448], CRISPLD1 [449], GDF15 [450], CXCL10 [451], BDNF (brain derived neurotrophic factor) [452], THY1 [453], ABCG2 [376], ANGPTL7 [454], SMOC2 [455], UCHL1 [456], LUM (lumican) [457], NOS2 [458], ACE (angiotensin I converting enzyme) [459], PDE5A [460], PAK1 [461], SSC5D [462], IL34 [463], BOC (BOC cell adhesion associated, oncogene regulated) [464], RUNX1 [465], GZMB (granzyme B) [466], KCNN3 [467], CXCL14 [468], ADAMTS8 [469] and FMOD (fibromodulin) [470] expression were significantly higher in patients with heart failure. The expression levels of ALOX15B [471], SFRP5 [472], F5 [473], CD163 [474], PLA2G2A [475], VDR (vitamin D receptor) [476], SERPINE1 [477], AZGP1 [402], FKBP5 [478], RBP4 [479], C3 [480], ITLN1 [481], TIMP4 [482], LYVE1 [483], NPPC (natriuretic peptide C) [484], MLXIPL (MLX interacting protein like) [485], AGTR1 [486], PTX3 [487], GPD1L [488], FN1 [489], CMTM5 [490], APOB (apolipoprotein B) [491], IGFBP2 [492], FABP4 [493], C1QTNF1 [494], LOX (lysyl oxidase) [495], ADAMTS5 [496], CD63 [497], NQO1 [498], PROCR (protein C receptor) [499], SIGLEC1 [500], EDN1 [501], LGALS3 [502], F8 [433], HMOX1 [503], CORIN (corin, serine peptidase) [504], NINJ2 [505], SFRP4 [506], ALOX15 [507], IL1B [508], CX3CR1 [509], FRZB (frizzled related protein) [510], CRISPLD1 [511], GDF15 [512], APLNR (apelin receptor) [513], CXCL10 [514], BDNF (brain derived neurotrophic factor) [515], EGR3 [516], OLR1 [517], ABCG2 [518], S1PR5 [519], ESR1 [520], CUBN (cubilin) [521], ACE (angiotensin I converting enzyme) [522], PDE5A [523], GNB3 [524], APOE (apolipoprotein E) [525], F2RL3 [526], F2R [527], TNNT1 [528], FCN1 [529], EGR1 [530], TFPI2 [531], IL34 [532], RUNX1 [533], GZMB (granzyme B) [466], TREH (trehalase) [534], CXCL2 [535], CXCL14 [536] and ANGPTL8 [537] have been proved to be altered in coronary artery disease. The study showed that ALOX15B [115], EREG (epiregulin) [538], SFRP5 [539], CD163 [540], PLA2G2A [541], VDR (vitamin D receptor) [542], SERPINE1 [477], AZGP1 [402], ELANE (elastase, neutrophil expressed) [543], RBP4 [544], C3 [545], FGFR4 [546], TIMP4 [547], NPPC (natriuretic peptide C) [548], SPP1 [549], BMP7 [550], SLC7A11 [551], CFD (complement factor D) [552], AGTR1 [553], PTX3 [554], EPHB2 [555], SLC2A1 [556], FHL2 [557], CD38 [558], FGF7 [559], C1QA [560], CRLF1 [561], POMC (proopiomelanocortin) [562], APOB (apolipoprotein B) [563], BMAL1 [564], IGFBP2 [565], ARG2 [566], FABP4 [567], C1QTNF1 [568], LOX (lysyl oxidase) [569], ADAMTS5 [570], CD63

[571], HAS2 [572], NQO1 [573], SIGLEC1 [574], PRDX6 [575], EDN1 [576], CTSB (cathepsin B) [577], LGALS3 [578], HMOX1 [579], BCL6 [580], RNASE6 [581], EPN1 [582], CORIN (corin, serine peptidase) [583], ELN (elastin) [584], PRIMA1 [585], NINJ2 [586], PALLD (palladin, cytoskeletal associated protein) [587], GNMT (glycine N-methyltransferase) [588], BCAT1 [589], SFRP4 [590], RSPO2 [591], CTLA4 [592], CTSG (cathepsin G) [593], CX3CR1 [594], ENPP2 [245], GDF15 [595], CXCL10 [596], BDNF (brain derived neurotrophic factor) [597], PTN (pleiotrophin) [598], OLR1 [599], MDK (midkine) [600], TNFRSF11B [601], LUM (lumican) [602], TP73 [603], ACE (angiotensin I converting enzyme) [604], PAK1 [605], GNB3 [606], APOE (apolipoprotein E) [607], EGR1 [608], TFPI2 [609], IL34 [610], TNFSF13B [611], LTB (lymphotoxin beta) [612], RSAD2 [613], ITGAX (integrin subunit alpha X) [614], GZMB (granzyme B) [615], CXCL9 [616], TREH (trehalase) [617], CXCL2 [618], CXCL14 [619], ADAMTS8 [324] and ANGPTL8 [620] were related to atherosclerosis. Altered expression of EREG (epiregulin) [328], FCN3 [621], CD163 [622], CCN5 [331], VDR (vitamin D receptor) [623], SERPINE1 [624], VSIG4 [625], TIMP4 [626], LYVE1 [337], BMP7 [627], SLC7A11 [411], PTX3 [628], EPHB2 [629], TGM2 [630], FHL2 [631], CRLF1 [632], BMAL1 [633], GPD1 [634], FABP4 [635], LOX (lysyl oxidase) [423], CTSB (cathepsin B) [360], PRKCD (protein kinase C delta) [636], LGALS3 [637], CORIN (corin, serine peptidase) [638], SMOC1 [639], ELN (elastin) [640], LDHA (lactate dehydrogenase A) [641], RPS5 [642], SFRP4 [643], ALOX15 [644], IRX2 [645], CYTL1 [646], RGS4 [647], GDF15 [648], CXCL10 [649], BDNF (brain derived neurotrophic factor) [650], SULF1 [651], SMOC2 [652], HTR2B [653], UCHL1 [654], LUM (lumican) [655], TRPV3 [656], ACE (angiotensin I converting enzyme) [657], APOE (apolipoprotein E) [658], GLI1 [659], EGR1 [660], DKK2 [661], RUNX1 [662], GZMB (granzyme B) [663], CXCL9 [664] and ADAMTS8 [665] have been observed to be associated with cardiac fibrosis. EREG (epiregulin) [666], SFRP5 [667], SPINK1 [668], CD163 [669], PLA2G2A [670], TFRC (transferrin receptor) [671], CCN5 [672], PCK1 [673], VDR (vitamin D receptor) [674], SERPINE1 [675], KCNK3 [676], ELANE (elastase, neutrophil expressed) [677], FKBP5 [678], RBP4 [679], CPNE5 [680], MOG (myelin oligodendrocyte glycoprotein) [681], C3 [682], FGFR4 [683], ITLN1 [684], TIMP4 [685], LYVE1 [686], NPPC (natriuretic peptide C) [340], SPP1 [687], BMP7 [688], SLC7A11 [689], CFD (complement factor D) [690], AGTR1 [691], PTX3 [692], EPHB2

[693], GPD1L [694], FHL2 [695], CD38 [696], OSR1 [697], POMC (proopiomelanocortin) [164], APOB (apolipoprotein B) [698], BMAL1 [699], IGFBP2 [700], ARG2 [701], IL15RA [702], GPD1 [703], FABP4 [704], PTGS1 [173], LOX (lysyl oxidase) [177], NQO1 [705], EDN1 [706], CTSB (cathepsin B) [707], PRKCD (protein kinase C delta) [708], RAMP1 [709], TSKU (tsukushi, small leucine rich proteoglycan) [710], LGALS3 [711], NID1 [712], ACACB (acetyl-CoA carboxylase beta) [713], BCL6 [714], MPST (mercaptopyruvate sulfurtransferase) [715], CD276 [716], HIF3A [717], ADH1B [718], ELN (elastin) [719], AIF1L [720], LAMB3 [721], MMP19 [722], SLC6A6 [723], STEAP4 [724], GPSM1 [725], CHDH (choline dehydrogenase) [726], RETSAT (retinol saturase) [727], PNMT (phenylethanolamine N-methyltransferase) [728], RPLP0 [729], TKT (transketolase) [730], TNMD (tenomodulin) [731], SFRP4 [732], TRPM8 [733], ALOX15 [734], CTLA4 [735], IL1B [736], CX3CR1 [737], RGS4 [738], ENPP2 [739], GDF15 [740], C1QTNF3 [741], APLNR (apelin receptor) [742], CXCL10 [743], BDNF (brain derived neurotrophic factor) [744], OLR1 [745], THY1 [746], CHRNA3 [747], ABCG2 [748], ANGPTL7 [749], DIO2 [750], PLAC8 [751], PHOSPHO1 [752], HTR2B [753], LUM (lumican) [754], TRPV3 [755], ESR1 [756], NOS2 [757], EPHA3 [758], ACE (angiotensin I converting enzyme) [759], GNB3 [760], APOE (apolipoprotein E) [761], GDF9 [762], SCT (secretin) [763], EGR1 [764], IL34 [765], RUNX1 [766], GZMB (granzyme B) [767], CXCL9 [768], TREH (trehalase) [769], CXCL11 [320], IGSF1 [770], CXCL2 [771], CXCL14 [772], ANGPTL8 [773], C1QTNF12 [774] and INHBE (inhibin subunit beta E) [775] might serve as therapeutic targets for obesity. The altered expression of FCN3 [776], SFRP5 [777], CD163 [778], TFRC (transferrin receptor) [779], AQP4 [780], VDR (vitamin D receptor) [781], KCNK3 [333], FGF12 [782], RBP4 [783], HMGCS2 [784], MOG (myelin oligodendrocyte glycoprotein) [785], C3 [786], FGFR4 [787], TIMP4 [788], GRIP1 [789], SOX2 [790], NPPC (natriuretic peptide C) [340], EIF4EBP1 [791], SPP1 [792], BMP7 [793], KCNK2 [794], PPP1R1A [795], CFD (complement factor D) [796], AGTR1 [797], PTX3 [413], SEPTIN4 [798], EPHB2 [799], ATP2A2 [800], FHL2 [801], CD38 [802], FGF7 [803], OSR1 [804], POMC (proopiomelanocortin) [805], APOB (apolipoprotein B) [806], BMAL1 [807], IGFBP2 [808], CHGB (chromogranin B) [809], FABP4 [810], SDK1 [811], LOX (lysyl oxidase) [812], HAS2 [813], NQO1 [814], CAMK1D [815], NGFR (nerve growth factor receptor) [816], PRDX6 [817], EDN1 [818], PRKCD (protein kinase

C delta) [819], RAMP1 [820], LGALS3 [821], KCNK1 [794], HMOX1 [362], BCL6 [822], HIF3A [823], CORIN (corin, serine peptidase) [363], ADH1B [824], TRPC4 [825], ELN (elastin) [584], LDHA (lactate dehydrogenase A) [826] PNMT (phenylethanolamine N-methyltransferase) [827], TRPM8 [828], CTLA4 [829], IL1B [830], RXFP2 [831], CX3CR1 [832], THBS4 [833], GDF15 [834], APLNR (apelin receptor) [835], CXCL10 [836], BDNF (brain derived neurotrophic factor) [837], LEFTY2 [838], OLR1 [839], CHRNA3 [840], MDK (midkine) [841], DIO2 [842], CHRM3 [843], HTR2B [844], UCHL1 [845], SLC26A4 [846], ESR1 [847], NOS2 [848], ACE (angiotensin I converting enzyme) [849], PDE5A [850], PLCE1 [851], SCG2 [852], KCNA5 [853], GNB3 [854], APOE (apolipoprotein E) [855], F2RL3 [856], F2R [527], GLI1 [857], PRDM1 [858], SCT (secretin) [859], EGR1 [860], RUNX1 [861], TNFRSF4 [862], TPM3 [863], DLGAP1 [864], GZMB (granzyme B) [865], CXCL9 [866], SLC16A9 [867], KCNN3 [868], TREH (trehalase) [869], ADAMTS8 [870], ANGPTL8 [871] and FMOD (fibromodulin) [872] were observed to be associated with the progression of hypertension. FCN3 [873], SSTR5 [874], SFRP5 [777], SLAMF1 [875], SPINK1 [876], CD163 [877], PLA2G2A [541], AQP4 [878], CCN5 [672], PCK1 [879], VDR (vitamin D receptor) [880], SERPINE1 [881], ACVR1C [882], GRB14 [883], FKBP5 [884], RBP4 [479], HMGCS2 [885], C3 [682], FGFR4 [683], ITLN1 [684], TIMP4 [886], LYVE1 [686], SOX2 [887], NPPC (natriuretic peptide C) [888], SPP1 [889], BMP7 [688], SLC7A11 [890], MLXIPL (MLX interacting protein like) [891], AGTR1 [892], PTX3 [893], EPHB2 [894], SLC2A1 [156], TGM2 [895], FHL2 [896], CD38 [897], FGF7 [898], OSR1 [899], HCN4 [900], POMC (proopiomelanocortin) [164], APOB (apolipoprotein B) [901], BMAL1 [902], IGFBP2 [700], CHGB (chromogranin B) [903], FCGR3A [904], IL15RA [905], GPD1 [703], FABP4 [906], TPO (thyroid peroxidase) [907], NQO1 [908], SIGLEC1 [909], CAMK1D [815], PRDX6 [910], EDN1 [911], CTSB (cathepsin B) [912], TSKU (tsukushi, small leucine rich proteoglycan) [913], LGALS3 [914], NID1 [915], HMOX1 [916], AKR1B1 [917], ACACB (acetyl-CoA carboxylase beta) [918], HIF3A [919], CORIN (corin, serine peptidase) [920], ADH1B [824], TRPC4 [921], NINJ2 [922], STEAP4 [923], GPSM1 [924], LDHA (lactate dehydrogenase A) [925], ETNPPL (ethanolamine-phosphate phospho-lyase) [926], HK3 [927], BCAT1 [928], NMRAL1 [929], SFRP4 [732], FOXA1 [930], ALOX15 [931], CTLA4 [932], PENK (proenkephalin) [933], IL1B [934], HBB (hemoglobin subunit beta) [935], SCUBE2 [936], CX3CR1 [937], RGS4 [938],

ENPP2 [739], GDF15 [939], TGFB2 [940], CXCL10 [941], BDNF (brain derived neurotrophic factor) [597], LRRN1 [942], LEFTY2 [838], ABCG2 [943], ANGPTL7 [944], TNFRSF11B [945], DIO2 [946], CHRM3 [947], PLAC8 [948], PHOSPHO1 [752], HTR2B [753], UCHL1 [949], LUM (lumican) [754], ESR1 [950], NOS2 [951], CUBN (cubilin) [952], ACE (angiotensin I converting enzyme) [953], PAK1 [954], GNB3 [955], APOE (apolipoprotein E) [956], EGR2 [957], OAS3 [958], SCT (secretin) [959], HLA-DPA1 [960], FCN1 [961], EGR1 [962], TFPI2 [963], IL34 [765], RUNX1 [533], KIF1A [964], KCNJ15 [965], GZMB (granzyme B) [767], GRIA3 [966], COLEC12 [967], GPR27 [968], TREH (trehalase) [769], KCNIP1 [969], CXCL11 [320], CXCL14 [772], ANGPTL8 [620], C1QTNF12 [774], INHBE (inhibin subunit beta E) [970] and FMOD (fibromodulin) [971] are the main regulators of diabetes mellitus. SFRP5 [972], F5 [973], CD163 [974], AQP4 [975], CCN5 [976], VDR (vitamin D receptor) [476], SERPINE1 [977], AZGP1 [402], VSIG4 [625], RBP4 [978], C3 [979], TIMP4 [980], SPP1 [981], BMP7 [982], SLC7A11 [983], TFEC (transcription factor EC) [984], CFD (complement factor D) [985], AGTR1 [486], PTX3 [628], EPHB2 [986], FGF7 [987], FN1 [988], HCN4 [989], STXBP2 [990], POMC (proopiomelanocortin) [991], APOB (apolipoprotein B) [992], BMAL1 [993], RAP1GAP [994], FABP4 [995], LOX (lysyl oxidase) [996], ADAMTS5 [997], CD63 [998], EDN1 [999], DHCR24 [1000], PDPN (podoplanin) [1001], CTSB (cathepsin B) [360], FCER1G [1002], LGALS3 [1003], KCNH2 [1004], HMOX1 [1005], CORIN (corin, serine peptidase) [1006], TRPC4 [1007], ELN (elastin) [1008], ADAMTS2 [1009], QSOX1 [1010], BCAT1 [1011], TRPM8 [1012], LEF1 [1013], CTLA4 [1014], PENK (proenkephalin) [1015], IL1B [1016], CX3CR1 [1017], F2RL2 [1018], GDF15 [1019], BDNF (brain derived neurotrophic factor) [1020], OLR1 [1021], ABCG2 [1022], MDK (midkine) [1023], HTR2B [1024], UCHL1 [456], ESR1 [1025], NOS2 [1026], CUBN (cubilin) [1027], ACE (angiotensin I converting enzyme) [657], PDE5A [281], PAK1 [1028], GNB3 [1029], APOE (apolipoprotein E) [1030], F2RL3 [1031], F2R [1032], EGR2 [288], GLI1 [659], EGR1 [660], TFPI2 [963], DUSP6 [1033], IL34 [1034], GZMB (granzyme B) [1035], CXCL9 [664], TREH (trehalase) [1036], CXCL2 [1037], RUNX1 [662] and ADAMTS8 [1038] are associated to the risk of myocardial infarction. SFRP5 [1039], CD163 [1040], AQP4 [1041], TIMP4 [1042], SOX2 [1043], NPPC (natriuretic peptide C) [1044], SPP1 [1045], SLC7A11 [1046], TGFA (transforming growth factor alpha) [1047],

PTX3 [1048], EPHB2 [1049], GPD1L [414], FHL2 [1050], CD38 [1051], FN1 [1052], HCN4 [1053], APOB (apolipoprotein B) [1054], BMAL1 [1055], LOX (lysyl oxidase) [1056], PRDX6 [1057], CTSB (cathepsin B) [1058], PRKCD (protein kinase C delta) [1059], LGALS3 [1060], HMOX1 [1061], CORIN (corin, serine peptidase) [1062], ELN (elastin) [640], CACNA2D3 [1063], STEAP4 [1064], BCAT1 [1065], SFRP4 [1066], TRPM8 [1067], ALOX15 [1068], IL1B [1069], GDF15 [1019], APLNR (apelin receptor) [1070], CXCL10 [1071], BDNF (brain derived neurotrophic factor) [1072], PTN (pleiotrophin) [1073], MDK (midkine) [1074], UCHL1 [1075], ESR1 [1076], ACE (angiotensin I converting enzyme) [1077], PLCE1 [282], PAK1 [1028], APOE (apolipoprotein E) [1030], EGR1 [1078], TFPI2 [1079], DUSP6 [1080], IL34 [1081], RUNX1 [1082], GZMB (granzyme B) [1083], EDA2R [1084], FSCN1 [1085], HAS3 [1086], TREH (trehalase) [1087] and CXCL14 [1088] are found to be associated with myocardial ischemia. Studies show that CD163 [1089], PLA2G2A [1090], GPD1L [1091], GSTM3 [1092], APOB (apolipoprotein B) [1093], HEY2 [1094], FABP4 [1095], CTSB (cathepsin B) [1096], LGALS3 [1097], GDF15 [1098], CUBN (cubilin) [1027], ACE (angiotensin I converting enzyme) [1099], GNB3 [1100], EGR1 [1101], KCNN3 [1102] and TREH (trehalase) [1103] are involved in the cardiac death. CD163 [1104], PLA2G2A [1105], AQP4 [1106], FGF12 [1107], IL18R1 [1108], PTX3 [1109], GPD1L [414], KCNH2 [1110], ELN (elastin) [1111], GDF15 [1112], BDNF (brain derived neurotrophic factor) [1113], PTN (pleiotrophin) [1114], UCHL1 [1115], KCNA5 [1116] and APOE (apolipoprotein E) [1117] plays an essential role in facilitating cardiac arrest. Altered expression of TFRC (transferrin receptor) [1118], CCN5 [672], FKBP5 [1119], RBP4 [1120], HMGCS2 [405], XRCC4 [1121], NPPC (natriuretic peptide C) [1044], BMP7 [627], SLC7A11 [1122], HMOX2 [1123], GPD1L [1091], DIRAS3 [1124], ITGA7 [1125], FHL2 [1126], CD38 [1127], HCN4 [1128], APOB (apolipoprotein B) [1129], BMAL1 [1130], HEY2 [1131], IGFBP2 [1132], LPCAT3 [1133], LOX (lysyl oxidase) [1134], DMPK (DM1 protein kinase) [1135], NQO1 [1136], EDN1 [1137], DHCR24 [1138], HSPB7 [1139], CTSB (cathepsin B) [1140], LGALS3 [1141], KCNH2 [1142], HMOX1 [1143], HIF3A [1144], CORIN (corin, serine peptidase) [1145], ADAMTS2 [1146], SLC6A6 [1147], PALLD (palladin, cytoskeletal associated protein) [1148], SERINC2 [1149], NMRAL1 [929], CTLA4 [1150], CX3CR1 [1151], GDF15 [1152], CXCL10 [1153], BDNF (brain derived neurotrophic factor) [1154], DIO2 [1155],

MYOZ1 [1156], TP63 [1157], ACE (angiotensin I converting enzyme) [1158], PAK1 [1159], GNB3 [1160], APOE (apolipoprotein E) [1161], CACNG8 [1162], TNNT1 [1163], HLA-DPA1 [1164], IL34 [1165], IER3 [1166], GZMB (granzyme B) [466], CXCL9 [1167], KCNN3 [1162], HAS3 [1168] and TREH (trehalase) [1169] have been reported to be associated with dilated cardiomyopathy. VDR (vitamin D receptor) [1170], PTX3 [1171], FN1 [489], APOB (apolipoprotein B) [1172], ADAMTS5 [1173], CX3CR1 [1174], ABCG2 [1175], MDK (midkine) [1176], ACE (angiotensin I converting enzyme) [1177], GNB3 [1178], APOE (apolipoprotein E) [1169] and CXCL3 [1170] have been revealed to be associated with hypercholesterolemia. VSIG4 [1181], FKBP5 [1182], C3 [1183], TIMP4 [626], SPP1 [1184], BMP7 [1185], CFD (complement factor D) [1186], AGTR1 [1187], PTX3 [1188], FN1 [1189], HCN4 [1190], APOB (apolipoprotein B) [1191], BMAL1 [1192], C1QC [1193], FABP4 [1194], LOX (lysyl oxidase) [1195], CD63 [1196], NQO1 [1197], KCNH2 [1198], CORIN (corin, serine peptidase) [1199], CDHR3 [1200], ELN (elastin) [640], RGS4 [446], GDF15 [1201], CXCL10 [1202], BDNF (brain derived neurotrophic factor) [1203], ABCG2 [1204], SMOC2 [1205], UCHL1 [1206], ESR1 [1207], MYOZ1 [1208], ACE (angiotensin I converting enzyme) [1209], PAK1 [1210], KCNA5 [1211], GNB3 [1212], APOE (apolipoprotein E) [1213], IL34 [1214], KCNN3 [467], KCNIP1 [1215] and FMOD (fibromodulin) [872] have been identified as a targets for atrial fibrillation. AGTR1 [1216], PTX3 [1217], LOX (lysyl oxidase) [1218], TGFB2 [1219], ACE (angiotensin I converting enzyme) [1220] and GLIS1 [1221] are correlates positively with the incidence of mitral valve disease. The results suggest that enriched genes might affect the disease progression of HCM and its associated complications include inflammation, heart failure, coronary artery disease, atherosclerosis, cardiac fibrosis, obesity, hypertension, diabetes mellitus, myocardial infarction, myocardial ischemia, cardiac death, cardiac arrest, dilated cardiomyopathy, hypercholesterolemia, atrial fibrillation and mitral valve disease.

The PPI network was constructed using the HIPPIE database, and the analysis of significant modules was performed. Finally, we identified hub genes form PPI network and modules. FN1 [489], ESR1 [520], APLNR (apelin receptor) [513], LOX (lysyl oxidase) [495] and APOE (apolipoprotein E) [525] can be used as an important therapeutic targets for coronary artery disease. FN1 [489] and APOE (apolipoprotein E) [1179] have become a potential biomarkers for

hypercholesterolemia. Altered expression of FN1 [988], ESR1 [1025], PAK1 [1028], LOX (lysyl oxidase) [996] and APOE (apolipoprotein E) [1030] were associated with prognosis in myocardial infarction. FN1 [1052], SOX2 [1043], ESR1 [1076], PAK1 [1028], APLNR (apelin receptor) [1070], LOX (lysyl oxidase) [1056] and APOE (apolipoprotein E) [1030] expression was shown to be regulated in myocardial ischemia. FN1 [1189], ESR1 [1207], PAK1 [1210], LOX (lysyl oxidase) [1195] and APOE (apolipoprotein E) [1213] are implicated in atrial fibrillation. In many clinical studies, SOX2 [144], ESR1 [275], SNCA (synuclein alpha) [277], PAK1 [283], TGM2 [157], LOX (lysyl oxidase) [177], APOE (apolipoprotein E) [285] and HLA-DPA1 [292] have been linked to the start of inflammation. Previous study confirmed that SOX2 [339], PAK1 [386], LOX (lysyl oxidase) [357] and APOE (apolipoprotein E) [387] are strongly associated with HCM. The altered expression of SOX2 [408], PAK1 [461] and LOX (lysyl oxidase) [423] are related to prognosis in heart failure. SOX2 [790], ESR1 [847], APLNR (apelin receptor) [835], LOX (lysyl oxidase) [812] and APOE (apolipoprotein E) [855] played an important role in hypertension. SOX2 [887], ESR1 [950], PAK1 [954], TGM2 [895], APOE (apolipoprotein E) [956] and HLA-DPA1 [960] were involved in regulating the occurrence of diabetes mellitus. Previous studies have been reported that altered expression of ESR1 [756], APLNR (apelin receptor) [742], LOX (lysyl oxidase) [177] and APOE (apolipoprotein E) [761] increased the risk of obesity. PAK1 [605], LOX (lysyl oxidase) [569] and APOE (apolipoprotein E) [607] have been found to have a strong association with atherosclerosis. PAK1 [1159], LOX (lysyl oxidase) [1134], APOE (apolipoprotein E) [1161] and HLA-DPA1 [1164] expression has been reported with dilated cardiomyopathy progression. TGM2 [630], LOX (lysyl oxidase) [423] and APOE (apolipoprotein E) [658] are important in the successful progression of cardiac fibrosis. Altered expression and activity of LOX (lysyl oxidase) [1218] has been demonstrated in mitral valve disease. Recent studies have proposed that APOE (apolipoprotein E) [1117] is associated with the development and progression of cardiac arrest. Our studies have shown that novel biomarkers such as TUBA4A, RPS2 and LCK (LCK proto-oncogene, Src family tyrosine kinase) are involved in the regulation of HCM. We assumed that these hub genes might play a essential role in the pathogenesis of HCM; however, this hypothesis needs to be verified in future investigation.

It is evident that miRNA-hub gene regulatory network and TF-hub gene regulatory network play a key part in the development of HCM. In this way, it increases the knowledge of HCM identification and contributes to targeted therapeutic management strategies and HCM prediction. FN1 [489], FKBP5 [478], ESR1 [275], hsa-miR-34a-5p [1222], BRCA1 [1223], STAT1 [1224], STAT3 [1225], MEF2A [1226] and GATA2 [1227] participates in the regulation of the pathophysiological process in coronary artery disease. Studies have demonstrated that the altered expression of FN1 [489] in patients with hypercholesterolemia. Recent studies have demonstrated that the FN1 [988], ESR1 [1025], PAK1 [1028], hsa-miR-34a-5p [1228], PRRX2 [1229], BRCA1 [1230], STAT1 [1231], STAT3 [1232], MEF2A [1233] and GATA2 [1234] are associated with myocardial infarction. FN1 [1052], FHL2 [1050], ESR1 [1076], PAK1 [1028], SRY (sex determining region Y) [1235], STAT1 [1236] and STAT3 [1237] are important in the development of myocardial ischemia. Recent studies have proposed that the FN1 [1189], FKBP5 [1182], ESR1 [1207], PAK1 [1210], STAT1 [1238] and STAT3 [1239] are associated with in atrial fibrillation. TFRC (transferrin receptor) [397], PAK1 [461], BRCA1 [1240], STAT1 [1241] and STAT3 [1242] are associated with progression of heart failure. TFRC (transferrin receptor) [671], FKBP5 [678], FHL2 [695], RPLP0 [729], ESR1 [756], BRCA1 [1243], STAT1 [1244], STAT3 [1245] and GATA2 [1246] are involved in the progression of obesity. The abnormal expression of TFRC (transferrin receptor) [779], FHL2 [801], TPM3 [863], ESR1 [847], CHRM3 [843], BRCA1 [1247], STAT1 [1248], STAT3 [1249], FOS (Fos proto-oncogene, AP-1 transcription factor subunit) [1250] and GATA2 [1251] have been reported in hypertension. TFRC (transferrin receptor) [1118], FKBP5 [1119], FHL2 [1126], PAK1 [1159], TP63 [1157], hsa-miR-34a-5p [1252], hsa-miR-194-5p [1253], BRCA1 [1254], STAT3 [1255] and MEF2A [1256] are the risk factors of dilated cardiomyopathy. FKBP5 [129], FHL2 [158], TPM3 [302]. ESR1 [275], PAK1 [283], SNCA (synuclein alpha) [277], hsa-mir-374a-5p [1257], hsa-miR-34a-5p [1258], BRCA1 [1259], STAT1 [1260], STAT3 [1261], FOS (Fos proto-oncogene, AP-1 transcription factor subunit) [1262], MEF2A [1263] and GATA2 [1264] might be involved in the process of inflammation. Studies have also confirmed that FKBP5 [884], FHL2 [896], ESR1 [950], CHRM3 [947], PAK1 [954], STAT1 [1265] and STAT3 [1266] participates in diabetes mellitus. FHL2 [345], PAK1 [386], STAT1 [1267], STAT3 [1268] and MEF2A [1269] have been reported to be correlated with HCM.

FHL2 [557], PAK1 [605], hsa-miR-34a-5p [1222], hsa-miR-524-5p [1270], SRY (sex determining region Y) [1271], BRCA1 [1272], STAT1 [1273], STAT3 [1274], MEF2A [1275] and GATA2 [1276] have been reported to be associated with atherosclerosis. FHL2 [631], PRRX2 [1229], BRCA1 [1277], STAT1 [1278], STAT3 [1279], MEF2A [1280] and GATA2 [1281] are a pivotal regulator of cardiac fibrosis. STAT3 [1282] is associated with the progression of cardiac arrest. MEF2A [1283] serves a vital role in cardiac death. SH3KBP1, TMEM30B, PTPRR (protein tyrosine phosphatase receptor type R), hsa-miR-520d-5p, hsa-mir-4646-5p, hsa-mir-548aw, hsa-miR-8052, hsa-mir-302b-3p, hsa-mir-548i, USF2 and EN1 might be a novel biomarkers associated with HCM and might be involved in the development of HCM. The results therefore were in accordance with previous studies and suggested that the hub genes, miRNAs and TFs served significant roles in the development of HCM and its associated complications.

In conclusion, via bioinformatics analysis of NGS data from HCM human models, we identified and selected several essential DEGs that are associated in the development of HCM and its associated complication. Furthermore, our results indicate that the identified DEGs not only are linked with numerous GO terms and functions, and signaling pathways, but also could construct complex PPI, miRNA-hub gene regulatory network and TF-hub gene regulatory network. In addition, a lot of DEGs with distinct GO functions and signaling pathways could form significant modules. Our investigation provides novel insight on HCM advancement not only in the gene level, but also in the GO functions, signaling pathways and module levels. The identified DEGs, associated GO functions, signaling pathways, and modules could serve as potentially diagnostic and therapeutic targets for HCM. In addition, our investigations have some limitations. For example, the identified DEGs, associated GO functions, signaling pathways, and modules were only generated from bioinformatics analysis. These analyzed data still need to be further confirmed in clinical specimens in future investigations. Despite these limitations, the results of our investigations for further examining the roles and associated molecular mechanisms mediated by identified key genes, associated GO functions, signaling pathways, and modules in HCM.

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Conflict of interest

The authors declare that they have no conflict of interest.

Ethical approval

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

Informed consent

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

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. [(GSE180313) https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE180313]

Consent for publication

Not applicable.

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C. V. - Software and investigation

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Tables

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

Gene Symbol	logFC	pValue	adj.P.Val	tvalue	Regulation	Gene Name
SAA1	6.031613	2.13E-10	1.68E-08	6.351559	Up	serum amyloid A1
FAM83B	4.969281	1.95E-05	0.000289	4.270947	Up	family with sequence similarity 83 member B
RNASE2	4.798281	2.26E-07	6.89E-06	5.17659	Up	ribonuclease A family member 2
C4orf54	4.538191	2.81E-11	2.89E-09	6.656158	Up	chromosome 4 open reading frame 54
SERPINA3	4.195281	4.19E-24	8.26E-21	10.12704	Up	serpin family A member 3
GAL	4.185174	0.001648	0.011064	3.147232	Up	galanin and GMAP prepropeptide
IL1RL1	4.180414	1.35E-14	3.56E-12	7.700874	Up	interleukin 1 receptor like 1
PTPRN	4.153073	0.002187	0.013764	3.063522	Up	protein tyrosine phosphatase receptor type N
MYH6	4.120238	1.40E-30	7.60E-27	11.49477	Up	myosin heavy chain 6
CACNA1E	4.096019	0.000246	0.002361	3.666371	Up	calcium voltage-gated channel subunit alpha1 E
CD177	4.009335	1.89E-05	0.000283	4.277493	Up	CD177 molecule
C5orf64	3.67539	1.43E-07	4.70E-06	5.261721	Up	chromosome 5 putative open reading frame 64
HOXA3	3.509383	1.85E-06	4.09E-05	4.769131	Up	homeobox A3
HOPX	3.456612	7.77E-09	3.76E-07	5.773391	Up	HOP homeobox
ALOX15B	3.450149	0.0002	0.001986	3.719364	Up	arachidonate 15-lipoxygenase type B
EREG	3.412855	2.77E-05	0.00039	4.191497	Up	epiregulin

LAD1	3.398614	6.99E-13	1.16E-10	7.179535	Up	ladinin 1
FCN3	3.396068	1.78E-47	3.85E-43	14.47368	Up	ficolin 3
KCNIP2	3.384064	1.04E-13	2.13E-11	7.435594	Up	potassium voltage-gated channel interacting protein 2
TUBA3E	3.372706	5.56E-15	1.65E-12	7.813598	Up	tubulin alpha 3e
C11orf87	3.331745	0.000898	0.006737	3.320598	Up	chromosome 11 open reading frame 87
VWA5B1	3.322015	0.002885	0.017172	2.979712	Up	von Willebrand factor A domain containing 5B1
SSTR5	3.295726	5.79E-10	3.92E-08	6.196053	Up	somatostatin receptor 5
GNMT	3.276271	1.18E-10	1.00E-08	6.441684	Up	glycine N-methyltransferase
DHRS7C	3.265833	2.65E-05	0.000376	4.201242	Up	dehydrogenase/reductase 7C
SFRP5	3.232748	2.96E-07	8.68E-06	5.126214	Up	secreted frizzled related protein 5
F5	3.180002	2.90E-08	1.19E-06	5.547488	Up	coagulation factor V
SCGN	3.177912	4.58E-13	8.08E-11	7.237135	Up	secretagogin, EF-hand calcium binding protein
TUBA3D	3.173975	9.68E-15	2.66E-12	7.74337	Up	tubulin alpha 3d
KCNK12	3.15564	2.13E-05	0.000312	4.251153	Up	potassium two pore domain channel subfamily K member 12
CHRDL2	3.055243	8.61E-07	2.16E-05	4.920902	Up	chordin like 2
PRSS46P	3.03459	0.003993	0.022108	2.878705	Up	serine protease 46, pseudogene
FIBCD1	3.023088	6.44E-06	0.000115	4.511252	Up	fibrinogen C domain containing 1
SLAMF1	2.976309	3.53E-06	7.02E-05	4.637009	Up	signaling lymphocytic activation molecule family member 1
SRARP	2.948856	2.28E-05	0.00033	4.235736	Up	steroid receptor associated and regulated protein
CHRNA4	2.945108	0.003704	0.020899	2.902298	Up	cholinergic receptor nicotinic alpha 4 subunit
IGSF23	2.938618	0.001862	0.012139	3.11139	Up	immunoglobulin superfamily member 23
CFAP95	2.850166	0.004287	0.023368	2.856206	Up	cilia and flagella associated protein 95
NPTX2	2.784862	1.74E-11	1.91E-09	6.726445	Up	neuronal pentraxin 2
FREM3	2.783224	0.002881	0.017164	2.980186	Up	FRAS1 related extracellular matrix 3
SERTM1	2.759568	2.95E-05	0.000411	4.176975	Up	serine rich and transmembrane domain containing 1
CORIN	2.758089	1.59E-06	3.63E-05	4.79956	Up	corin, serine peptidase
VWFP1	2.754115	0.000206	0.002036	3.711714	Up	von Willebrand factor pseudogene 1
CATSPERB	2.744954	0.000778	0.006013	3.360575	Up	cation channel sperm associated auxiliary subunit beta
LCN10	2.735136	5.73E-11	5.38E-09	6.550626	Up	lipocalin 10
TCF24	2.703249	4.20E-08	1.63E-06	5.482258	Up	transcription factor 24
VSTM2L	2.696383	6.12E-08	2.29E-06	5.415172	Up	V-set and transmembrane domain containing 2 like
SLCO4A1	2.669599	3.13E-07	9.09E-06	5.115195	Up	solute carrier organic anion transporter family member 4A1
MARCO	2.636418	0.00213	0.013513	3.071543	Up	macrophage receptor with collagenous structure
DNER	2.625999	0.000494	0.004189	3.4842	Up	delta/notch like EGF repeat containing
METTL7B	2.621637	1.21E-21	1.38E-18	9.557516	Up	methyltransferase like 7B
RAB39A	2.61413	0.00738	0.035813	2.679179	Up	RAB39A, member RAS oncogene family
SPINK1	2.61372	4.74E-05	0.000606	4.067848	Up	serine peptidase inhibitor Kazal type 1
MGST1	2.58199	1.56E-12	2.24E-10	7.069297	Up	microsomal glutathione S-transferase 1
CD163	2.579336	7.76E-07	1.98E-05	4.941246	Up	CD163 molecule
DHRS9	2.535486	3.23E-06	6.51E-05	4.655469	Up	dehydrogenase/reductase 9
RGR	2.529393	0.000226	0.002199	3.68834	Up	retinal G protein coupled receptor

LGI3	2.491519	8.98E-08	3.14E-06	5.34634	Up	leucine rich repeat LGI family member 3
FAM209B	2.453806	0.005707	0.029182	2.764161	Up	family with sequence similarity 209 member B
PLA2G2A	2.414458	4.19E-09	2.15E-07	5.876674	Up	phospholipase A2 group IIA
TSPEAR	2.407365	0.00671	0.033246	2.710896	Up	thrombospondin type laminin G domain and EAR repeats
HERC2P6	2.396583	0.000678	0.005384	3.398187	Up	HERC2 pseudogene 6
LRRN3	2.393736	4.63E-12	5.93E-10	6.916573	Up	leucine rich repeat neuronal 3
C1QL1	2.366777	5.35E-14	1.20E-11	7.523069	Up	complement C1q like 1
TFRC	2.364549	4.43E-19	3.20E-16	8.925597	Up	transferrin receptor
SCN1A	2.357664	0.000575	0.004714	3.44292	Up	sodium voltage-gated channel alpha subunit 1
CPNE4	2.355728	5.79E-12	7.05E-10	6.884698	Up	copine 4
CHDH	2.354191	5.13E-14	1.16E-11	7.528474	Up	choline dehydrogenase
AQP4	2.338792	0.000241	0.002322	3.671965	Up	aquaporin 4
STAC2	2.336075	0.001251	0.008879	3.227079	Up	SH3 and cysteine rich domain 2
CCN5	2.316564	1.29E-08	5.86E-07	5.687418	Up	cellular communication network factor 5
FER1L6	2.296165	1.61E-06	3.66E-05	4.797352	Up	fer-1 like family member 6
PCK1	2.293413	0.00613	0.030979	2.740763	Up	phosphoenolpyruvate carboxykinase 1
CYP4B1	2.292144	9.74E-06	0.000162	4.422873	Up	cytochrome P450 family 4 subfamily B member 1
PKHD1L1	2.25476	0.004295	0.023393	2.855616	Up	PKHD1 like 1
LMO1	2.236756	2.84E-05	0.000398	4.186313	Up	LIM domain only 1
ETNK2	2.218528	3.19E-07	9.21E-06	5.111714	Up	ethanolamine kinase 2
GMNC	2.215772	0.000474	0.004058	3.494925	Up	geminin coiled-coil domain containing
VDR	2.214893	6.04E-07	1.60E-05	4.990041	Up	vitamin D receptor
HOTAIRM1	2.213629	0.000721	0.005651	3.381503	Up	HOXA transcript antisense RNA, myeloid-specific 1
BEX5	2.207165	2.14E-09	1.21E-07	5.986586	Up	brain expressed X-linked 5
SERPINE1	2.204094	0.000237	0.002291	3.67617	Up	serpin family E member 1
ACVR1C	2.203855	0.004589	0.024635	2.834533	Up	activin A receptor type 1C
AZGP1	2.186441	2.54E-08	1.05E-06	5.570279	Up	alpha-2-glycoprotein 1, zinc-binding
CHST9	2.182094	0.00011	0.001217	3.867736	Up	carbohydrate sulfotransferase 9
KCNK13	2.133648	0.004945	0.026113	2.810601	Up	potassium two pore domain channel subfamily K member 13
RPL32P18	2.126084	0.004111	0.022625	2.869482	Up	ribosomal protein L32 pseudogene 18
RPSAP15	2.112454	3.06E-05	0.000423	4.168666	Up	ribosomal protein SA pseudogene 15
AOX1	2.085457	3.02E-05	0.000417	4.17225	Up	aldehyde oxidase 1
VSIG4	2.075866	8.44E-07	2.12E-05	4.924826	Up	V-set and immunoglobulin domain containing 4
TOGARAM2	2.064907	1.97E-06	4.31E-05	4.75623	Up	TOG array regulator of axonemal microtubules 2
KCNK3	2.061094	0.000232	0.002254	3.680895	Up	potassium two pore domain channel subfamily K member 3
CAMSAP3	2.058358	3.56E-06	7.04E-05	4.635555	Up	calmodulin regulated spectrin associated protein family member 3
GALNT15	2.05654	1.80E-07	5.74E-06	5.21883	Up	polypeptide N-acetylgalactosaminyltransferase 15
FGF12	2.0558	2.15E-05	0.000315	4.24866	Up	fibroblast growth factor 12
AGBL4	2.034061	0.001544	0.010496	3.166241	Up	AGBL carboxypeptidase 4
ELANE	2.033617	5.82E-05	0.000715	4.020024	Up	elastase, neutrophil expressed
CYP4Z2P	2.020532	0.000492	0.004178	3.485125	Up	cytochrome P450 family 4 subfamily Z member 2, pseudogene

GRB14	2.010488	4.47E-14	1.03E-11	7.54662	Up	growth factor receptor bound protein 14
SPOCK1	1.995971	5.51E-13	9.40E-11	7.212127	Up	SPARC (osteonectin), cwcv and kazal like domains proteoglycan 1
FREM2	1.989507	0.000113	0.001241	3.861473	Up	FRAS1 related extracellular matrix 2
RHBDL3	1.989046	4.66E-07	1.28E-05	5.039858	Up	rhomboid like 3
RPLP0P6	1.986754	2.83E-07	8.37E-06	5.134191	Up	ribosomal protein lateral stalk subunit P0 pseudogene 6
HRCT1	1.98584	3.63E-10	2.67E-08	6.269122	Up	histidine rich carboxyl terminus 1
SMTNL2	1.98551	1.40E-11	1.58E-09	6.757964	Up	smoothelin like 2
SGPP2	1.982841	5.97E-06	0.000108	4.527278	Up	sphingosine-1-phosphate phosphatase 2
SVOP	1.979575	0.001764	0.011655	3.127318	Up	SV2 related protein
ART1	1.96356	0.002438	0.015021	3.030955	Up	ADP-ribosyltransferase 1
LCN6	1.93873	4.73E-05	0.000604	4.068736	Up	lipocalin 6
CA14	1.924287	4.87E-07	1.33E-05	5.031417	Up	carbonic anhydrase 14
HS3ST2	1.922263	2.53E-05	0.000361	4.211721	Up	heparan sulfate-glucosamine 3-sulfotransferase 2
TMIGD3	1.902402	3.38E-06	6.76E-05	4.646078	Up	transmembrane and immunoglobulin domain containing 3
FKBP5	1.901118	4.08E-12	5.33E-10	6.934417	Up	FKBP prolyl isomerase 5
SLC38A4	1.893644	0.000521	0.004344	3.469704	Up	solute carrier family 38 member 4
ADAM11	1.891191	0.000146	0.001536	3.797347	Up	ADAM metallopeptidase domain 11
RPSAP19	1.886048	0.000125	0.00135	3.835333	Up	ribosomal protein SA pseudogene 19
RPP38-DT	1.881637	0.002616	0.015905	3.009611	Up	RPP38 divergent transcript
MFSD2A	1.87639	0.000124	0.001335	3.838767	Up	major facilitator superfamily domain containing 2A
SYN2	1.87252	1.16E-10	9.90E-09	6.445008	Up	synapsin II
LCN15	1.864478	0.010978	0.048132	2.543393	Up	lipocalin 15
RBP4	1.859611	0.003464	0.0198	2.923271	Up	retinol binding protein 4
BLM	1.840844	5.74E-07	1.53E-05	4.999611	Up	BLM RecQ like helicase
EXPH5	1.83947	9.39E-06	0.000157	4.430751	Up	exophilin 5
ADH1B	1.8341	2.16E-05	0.000317	4.247487	Up	alcohol dehydrogenase 1B (class I), beta polypeptide
CDHR3	1.830924	2.20E-05	0.000321	4.243662	Up	cadherin related family member 3
TOX-DT	1.818291	0.00427	0.023283	2.857511	Up	TOX divergent transcript
RPL21P75	1.812596	0.000343	0.003106	3.580104	Up	ribosomal protein L21 pseudogene 75
HMGCS2	1.806869	0.004875	0.025832	2.81515	Up	3-hydroxy-3-methylglutaryl-CoA synthase 2
CFAP77	1.802833	5.31E-13	9.17E-11	7.217048	Up	cilia and flagella associated protein 77
NSG1	1.798957	2.12E-07	6.50E-06	5.188255	Up	neuronal vesicle trafficking associated 1
HOGA1	1.787234	1.88E-10	1.51E-08	6.370605	Up	4-hydroxy-2-oxoglutarate aldolase 1
CPNE5	1.785599	0.00012	0.001304	3.845404	Up	copine 5
SLC66A1L	1.784132	1.36E-05	0.000215	4.349609	Up	solute carrier family 66 member 1 like
MELTF	1.761017	0.000166	0.001703	3.766101	Up	melanotransferrin
SERPINA5	1.752584	4.11E-06	7.96E-05	4.605762	Up	serpin family A member 5
CENPM	1.747165	0.00505	0.026532	2.803806	Up	centromere protein M
MOG	1.746616	0.001201	0.008579	3.238605	Up	myelin oligodendrocyte glycoprotein
PHACTR3	1.739966	8.93E-09	4.26E-07	5.749978	Up	phosphatase and actin regulator 3
C3	1.738464	0.000104	0.001165	3.881342	Up	complement C3
SMOC1	1.731692	0.001156	0.008319	3.249611	Up	SPARC related modular calcium binding 1

FGFR4	1.730972	3.92E-05	0.000522	4.111986	Up	fibroblast growth factor receptor 4
TENT5B	1.723607	6.57E-07	1.71E-05	4.973586	Up	terminal nucleotidyltransferase 5B
ITLN1	1.723243	0.004945	0.026113	2.810576	Up	intelectin 1
TMEM52	1.714257	5.20E-05	0.000652	4.046544	Up	transmembrane protein 52
XRCC4	1.711157	7.09E-06	0.000125	4.490822	Up	X-ray repair cross complementing 4
VIT	1.705363	3.63E-09	1.90E-07	5.90033	Up	vitrin
IL18R1	1.702701	5.12E-12	6.49E-10	6.902136	Up	interleukin 18 receptor 1
HOXB4	1.699565	0.000393	0.003474	3.545069	Up	homeobox B4
RTN4RL1	1.697085	1.50E-09	8.91E-08	6.043944	Up	reticulon 4 receptor like 1
CHI3L2	1.686869	0.005644	0.028933	2.767789	Up	chitinase 3 like 2
RPS7P11	1.683155	0.000945	0.007037	3.306483	Up	ribosomal protein S7 pseudogene 11
SUSD4	1.675462	6.28E-07	1.65E-05	4.98242	Up	sushi domain containing 4
TRPC4	1.673984	4.69E-07	1.29E-05	5.038718	Up	transient receptor potential cation channel subfamily C member 4
TIMP4	1.66936	9.16E-13	1.41E-10	7.142555	Up	TIMP metallopeptidase inhibitor 4
LYVE1	1.668893	0.003164	0.018463	2.951387	Up	lymphatic vessel endothelial hyaluronan receptor 1
GRIP1	1.663007	4.18E-05	0.000551	4.097207	Up	glutamate receptor interacting protein 1
FAM81A	1.650419	3.46E-06	6.90E-05	4.641533	Up	family with sequence similarity 81 member A
IL20RA	1.648921	0.000109	0.00121	3.869482	Up	interleukin 20 receptor subunit alpha
RNF157	1.643614	4.04E-09	2.10E-07	5.882667	Up	ring finger protein 157
ELN	1.641958	2.19E-06	4.69E-05	4.73492	Up	elastin
PTDSS1	1.63835	3.63E-15	1.19E-12	7.86706	Up	phosphatidylserine synthase 1
C1orf105	1.630831	3.60E-06	7.10E-05	4.632948	Up	chromosome 1 open reading frame 105
HCRTR1	1.6267	7.58E-05	0.000894	3.957173	Up	hypocretin receptor 1
MEI4	1.626425	0.000846	0.006422	3.337132	Up	meiotic double-stranded break formation protein 4
AQP7P2	1.623511	3.60E-06	7.10E-05	4.633281	Up	aquaporin 7 pseudogene 2
TRIM16L	1.613155	1.09E-10	9.47E-09	6.453605	Up	tripartite motif containing 16 like
PLA2G4F	1.609339	5.19E-05	0.000652	4.046998	Up	phospholipase A2 group IVF
QSOX1	1.605862	5.02E-17	2.31E-14	8.386309	Up	quiescin sulfhydryl oxidase 1
TUBB4B	1.600347	6.94E-10	4.62E-08	6.167423	Up	tubulin beta 4B class IVb
ELAPOR1	1.593174	0.001152	0.008299	3.250388	Up	endosome-lysosome associated apoptosis and autophagy regulator 1
LGR6	1.591446	6.86E-06	0.000122	4.498057	Up	leucine rich repeat containing G protein-coupled receptor 6
NALF2	1.578852	0.005585	0.028723	2.771179	Up	NALCN channel auxiliary factor 2
ETNPPL	1.55998	0.000416	0.003648	3.52951	Up	ethanolamine-phosphate phospho-lyase
OPN4	1.541755	5.88E-06	0.000107	4.530618	Up	opsin 4
LRMDA	1.534761	3.08E-18	1.82E-15	8.708553	Up	leucine rich melanocyte differentiation associated
SOX2	1.533322	0.007561	0.036518	2.67107	Up	SRY-box transcription factor 2
PEBP4	1.532286	1.17E-11	1.33E-09	6.783862	Up	phosphatidylethanolamine binding protein 4
SHC4	1.529956	9.49E-06	0.000159	4.428562	Up	SHC adaptor protein 4
SNX22	1.525498	4.06E-09	2.10E-07	5.881619	Up	sorting nexin 22
SLPI	1.522099	0.011038	0.048315	2.541503	Up	secretory leukocyte peptidase inhibitor
TDRD9	1.515953	3.21E-05	0.00044	4.157847	Up	tudor domain containing 9
SPATA17	1.515858	0.002332	0.014486	3.044359	Up	spermatogenesis associated 17

RPL17P6	1.512249	0.001399	0.009691	3.19487	Up	ribosomal protein L17 pseudogene 6
KIF26B	1.502642	8.13E-06	0.00014	4.461654	Up	kinesin family member 26B
CPM	1.500298	3.34E-07	9.57E-06	5.103399	Up	carboxypeptidase M
TWIST2	1.498116	8.99E-06	0.000152	4.440057	Up	twist family bHLH transcription factor 2
TC2N	1.492669	4.79E-05	0.000611	4.065515	Up	tandem C2 domains, nuclear
NPPC	1.490897	0.003386	0.019466	2.93037	Up	natriuretic peptide C
FAM222A	1.489774	1.46E-09	8.75E-08	6.048962	Up	family with sequence similarity 222 member A
ITPKA	1.47904	4.44E-06	8.45E-05	4.589828	Up	inositol-trisphosphate 3-kinase A
RPL17P7	1.478262	0.000699	0.005517	3.389982	Up	ribosomal protein L17 pseudogene 7
PITX3	1.477826	0.001651	0.01108	3.14674	Up	paired like homeodomain 3
TUBA1C	1.469249	1.09E-08	5.07E-07	5.715972	Up	tubulin alpha 1c
PLP2	1.458759	3.53E-12	4.63E-10	6.954951	Up	proteolipid protein 2
EIF4EBP1	1.449352	6.78E-19	4.74E-16	8.878408	Up	eukaryotic translation initiation factor 4E binding protein 1
ADAMTS2	1.439063	8.74E-06	0.000148	4.446312	Up	ADAM metallopeptidase with thrombospondin type 1 motif 2
TUBB4A	1.435769	0.000194	0.001944	3.726333	Up	tubulin beta 4A class IVa
CHST7	1.434918	9.88E-11	8.70E-09	6.468814	Up	carbohydrate sulfotransferase 7
SPP1	1.43243	0.001553	0.010547	3.164652	Up	secreted phosphoprotein 1
GOLGA7B	1.430581	0.002337	0.014508	3.043735	Up	golgin A7 family member B
CHL1	1.426267	1.14E-06	2.74E-05	4.865155	Up	cell adhesion molecule L1 like
CD109	1.4197	3.02E-12	4.04E-10	6.976662	Up	CD109 molecule
HOOK1	1.41943	8.21E-06	0.000141	4.459537	Up	hook microtubule tethering protein 1
S1PR3	1.419048	4.51E-15	1.42E-12	7.840012	Up	sphingosine-1-phosphate receptor 3
TUBA1B	1.417921	3.17E-09	1.68E-07	5.922605	Up	tubulin alpha 1b
RPL3P4	1.413749	0.004254	0.023227	2.858679	Up	ribosomal protein L3 pseudogene 4
C1QB	1.412486	5.63E-05	0.000695	4.027896	Up	complement C1q B chain
SBK3	1.407809	5.77E-06	0.000105	4.534672	Up	SH3 domain binding kinase family member 3
TOX	1.403341	0.00603	0.030537	2.746165	Up	thymocyte selection associated high mobility group box
PRODH	1.401838	1.08E-06	2.62E-05	4.876221	Up	proline dehydrogenase 1
BMP7	1.393887	0.002671	0.016181	3.003262	Up	bone morphogenetic protein 7
NECTIN1	1.391515	4.01E-15	1.28E-12	7.854709	Up	nectin cell adhesion molecule 1
B3GNT7	1.389318	1.95E-07	6.06E-06	5.20426	Up	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7
BEAN1	1.387958	2.40E-07	7.27E-06	5.165117	Up	brain expressed associated with NEDD4 1
NUDT4B	1.382654	0.001907	0.01239	3.10428	Up	nudix hydrolase 4B
RPS3AP5	1.381306	0.005146	0.026928	2.797773	Up	RPS3A pseudogene 5
UBXN10	1.37313	0.000314	0.002888	3.603763	Up	UBX domain protein 10
PNMT	1.372447	2.49E-09	1.38E-07	5.962366	Up	phenylethanolamine N-methyltransferase
CPAMD8	1.369517	2.24E-13	4.26E-11	7.333651	Up	C3 and PZP like alpha-2-macroglobulin domain containing 8
RPL18AP3	1.369129	0.000558	0.004588	3.451358	Up	ribosomal protein L18a pseudogene 3
SLC7A11	1.368236	0.010985	0.048151	2.543185	Up	solute carrier family 7 member 11
TGFA	1.367493	0.000948	0.007054	3.305611	Up	transforming growth factor alpha
KCNA7	1.364725	0.00639	0.032069	2.727064	Up	potassium voltage-gated channel subfamily A member 7

TMEM132B	1.362351	0.001091	0.007934	3.265897	Up	transmembrane protein 132B
KCNK2	1.359505	0.008815	0.040872	2.61914	Up	potassium two pore domain channel subfamily K member 2
PPP1R1A	1.352253	9.19E-14	1.90E-11	7.452092	Up	protein phosphatase 1 regulatory inhibitor subunit 1A
PRIMA1	1.351041	8.39E-10	5.41E-08	6.137349	Up	proline rich membrane anchor 1
CHAC2	1.340836	4.77E-06	8.97E-05	4.574465	Up	ChaC glutathione specific gamma-glutamylcyclotransferase 2
RPL36AP37	1.338159	0.00221	0.01388	3.060472	Up	ribosomal protein L36a pseudogene 37
ADGRD1	1.335981	2.59E-15	9.05E-13	7.909311	Up	adhesion G protein-coupled receptor D1
MYOT	1.322671	0.001174	0.008418	3.245228	Up	myotilin
FAM83F	1.321399	0.000459	0.003957	3.50374	Up	family with sequence similarity 83 member F
C1QL3	1.321367	0.002232	0.013986	3.057515	Up	complement C1q like 3
SHISA4	1.320009	7.26E-11	6.62E-09	6.515113	Up	shisa family member 4
MS4A4A	1.319705	0.000254	0.002418	3.65851	Up	membrane spanning 4-domains A4A
LDHA	1.319198	1.75E-14	4.26E-12	7.667693	Up	lactate dehydrogenase A
FTH1P2	1.314132	0.000213	0.002098	3.702674	Up	ferritin heavy chain 1 pseudogene 2
TIGD3	1.31189	0.006823	0.033711	2.705378	Up	tigger transposable element derived 3
POM121L9P	1.310379	0.000491	0.004173	3.485638	Up	POM121 transmembrane nucleoporin like 9, pseudogene
SBK2	1.306647	0.000882	0.006631	3.325717	Up	SH3 domain binding kinase family member 2
PARVB	1.299971	4.06E-18	2.26E-15	8.677024	Up	parvin beta
TFEC	1.290984	0.003987	0.022087	2.879178	Up	transcription factor EC
CFD	1.290434	0.001032	0.007574	3.281788	Up	complement factor D
RPL21P16	1.270344	9.10E-05	0.00104	3.91353	Up	ribosomal protein L21 pseudogene 16
MLXIPL	1.266584	0.011385	0.049444	2.530661	Up	MLX interacting protein like
INSYN1	1.265971	5.33E-13	9.17E-11	7.216608	Up	inhibitory synaptic factor 1
AGTR1	1.258908	6.28E-05	0.000763	4.002152	Up	angiotensin II receptor type 1
PTX3	1.256277	0.002341	0.01453	3.043203	Up	pentraxin 3
SEPTIN4	1.249344	2.05E-14	4.93E-12	7.647556	Up	septin 4
HMOX2	1.249238	2.96E-24	7.14E-21	10.16091	Up	heme oxygenase 2
PLEKHH1	1.241406	3.44E-15	1.15E-12	7.873793	Up	pleckstrin homology, MyTH4 and FERM domain containing H1
RPL7P1	1.235145	0.005675	0.029042	2.765985	Up	ribosomal protein L7 pseudogene 1
EPHB2	1.23419	0.00136	0.009458	3.202918	Up	EPH receptor B2
GPD1L	1.232928	2.72E-20	2.26E-17	9.229634	Up	glycerol-3-phosphate dehydrogenase 1 like
DIRAS3	1.230333	6.12E-05	0.000746	4.008307	Up	DIRAS family GTPase 3
CACNA2D3	1.22902	3.49E-06	6.94E-05	4.639829	Up	calcium voltage-gated channel auxiliary subunit alpha2delta 3
DPY19L2P2	1.225901	3.08E-06	6.26E-05	4.665498	Up	DPY19L2 pseudogene 2
ALDH1L1	1.225133	5.71E-10	3.89E-08	6.198363	Up	aldehyde dehydrogenase 1 family member L1
CLIC3	1.224084	0.001764	0.011655	3.127297	Up	chloride intracellular channel 3
ZNF703	1.218854	1.66E-06	3.74E-05	4.791401	Up	zinc finger protein 703
CSDC2	1.2118	1.59E-14	3.96E-12	7.680143	Up	cold shock domain containing C2
DIRAS1	1.21122	5.17E-16	2.00E-13	8.10746	Up	DIRAS family GTPase 1
ZNG1E	1.211123	3.79E-07	1.08E-05	5.079399	Up	Zn regulated GTPase metalloprotein activator 1E
SLC2A1	1.209496	1.16E-08	5.38E-07	5.705373	Up	solute carrier family 2 member 1

ITGA7	1.209088	1.68E-11	1.85E-09	6.731784	Up	integrin subunit alpha 7
NALCN	1.209044	2.41E-10	1.86E-08	6.33278	Up	sodium leak channel, non-selective
SOX2-OT	1.205553	0.00815	0.038565	2.645775	Up	SOX2 overlapping transcript
SLC44A3	1.202879	6.51E-07	1.70E-05	4.975584	Up	solute carrier family 44 member 3
ATP2A2	1.198046	2.98E-10	2.25E-08	6.299574	Up	ATPase sarcoplasmic/endoplasmic reticulum Ca2+ transporting 2
GSTM3	1.191904	1.49E-09	8.87E-08	6.045888	Up	glutathione S-transferase mu 3
TENT5C	1.189239	2.06E-09	1.18E-07	5.992639	Up	terminal nucleotidyltransferase 5C
TGM2	1.185645	5.09E-07	1.38E-05	5.022934	Up	transglutaminase 2
FHL2	1.185418	9.96E-09	4.72E-07	5.731397	Up	four and a half LIM domains 2
RPLP0	1.181906	3.61E-13	6.41E-11	7.269473	Up	ribosomal protein lateral stalk subunit P0
RPS27AP16	1.17739	0.00281	0.01686	2.987836	Up	RPS27A pseudogene 16
CD38	1.172194	0.000242	0.002335	3.670346	Up	CD38 molecule
FAM78B	1.169715	1.09E-07	3.67E-06	5.311728	Up	family with sequence similarity 78 member B
SLC7A1	1.166618	6.00E-07	1.59E-05	4.991196	Up	solute carrier family 7 member 1
SIRPB2	1.16641	0.008251	0.038947	2.641626	Up	signal regulatory protein beta 2
MEGF9	1.163082	2.15E-09	1.21E-07	5.985764	Up	multiple EGF like domains 9
WNK3	1.159488	0.000164	0.001691	3.768555	Up	WNK lysine deficient protein kinase 3
RPL27AP6	1.158505	0.003534	0.020133	2.917006	Up	ribosomal protein L27a pseudogene 6
KLHL3	1.153267	1.87E-16	7.82E-14	8.229829	Up	kelch like family member 3
GRIN2A	1.146594	0.003412	0.019589	2.92799	Up	glutamate ionotropic receptor NMDA type subunit 2A
FGF7	1.145308	6.17E-09	3.04E-07	5.812029	Up	fibroblast growth factor 7
FN1	1.143925	0.001799	0.011823	3.121478	Up	fibronectin 1
PCARE	1.143335	0.000323	0.002952	3.596493	Up	photoreceptor cilium actin regulator
SERINC2	1.14253	9.22E-05	0.001052	3.910156	Up	serine incorporator 2
SMYD1	1.141773	3.58E-20	2.88E-17	9.19986	Up	SET and MYND domain containing 1
ART5	1.139887	0.003215	0.018711	2.946434	Up	ADP-ribosyltransferase 5
MARVELD2	1.138619	0.000119	0.001293	3.848363	Up	MARVEL domain containing 2
EPN3	1.137555	1.50E-06	3.45E-05	4.811194	Up	epsin 3
PRSS36	1.13463	8.07E-05	0.00094	3.942252	Up	serine protease 36
HAGHL	1.133864	2.45E-05	0.000351	4.219735	Up	hydroxyacylglutathione hydrolase like
RPL13AP25	1.13331	0.009892	0.04455	2.579581	Up	ribosomal protein L13a pseudogene 25
MATN3	1.133234	0.000255	0.002426	3.657502	Up	matrilin 3
ENTPD6	1.132651	1.09E-12	1.63E-10	7.119162	Up	ectonucleoside triphosphate diphosphohydrolase 6
OSR1	1.13203	0.000349	0.003143	3.57622	Up	odd-skipped related transcription factor 1
CMTM5	1.131771	0.000851	0.006444	3.335612	Up	CKLF like MARVEL transmembrane domain containing 5
PPP1R14B	1.12904	5.33E-07	1.44E-05	5.01393	Up	protein phosphatase 1 regulatory inhibitor subunit 14B
HCN4	1.127776	2.19E-05	0.000321	4.244177	Up	hyperpolarization activated cyclic nucleotide gated potassium channel 4
PRRG4	1.123978	0.002825	0.016926	2.98615	Up	proline rich and Gla domain 4
SLC4A3	1.120213	5.21E-18	2.75E-15	8.648687	Up	solute carrier family 4 member 3
LRRC7	1.118524	0.007755	0.037196	2.662571	Up	leucine rich repeat containing 7
STXBP2	1.11251	0.000429	0.003737	3.521722	Up	syntaxin binding protein 2
SLC5A1	1.109955	2.57E-07	7.68E-06	5.152881	Up	solute carrier family 5 member 1

RPL13AP5	1.109672	5.20E-05	0.000652	4.046556	Up	ribosomal protein L13a pseudogene 5
C1QA	1.104959	0.000125	0.00135	3.835175	Up	complement C1q A chain
MRO	1.104795	0.008506	0.039821	2.631305	Up	maestro
CRLF1	1.102263	0.001947	0.012603	3.09818	Up	cytokine receptor like factor 1
POMC	1.100485	0.002162	0.013648	3.067084	Up	proopiomelanocortin
APOB	1.100355	8.30E-08	2.95E-06	5.360571	Up	apolipoprotein B
TMEM178B	1.098754	2.40E-08	1.00E-06	5.580264	Up	transmembrane protein 178B
OLFM4	1.098597	0.006843	0.033781	2.704386	Up	olfactomedin 4
RPS15P4	1.098371	0.002499	0.015346	3.023443	Up	ribosomal protein S15 pseudogene 4
MYO7B	1.098014	2.59E-07	7.73E-06	5.151425	Up	myosin VIIB
TMEM26	1.097008	0.003543	0.020178	2.916229	Up	transmembrane protein 26
CHADL	1.096481	1.95E-06	4.27E-05	4.758547	Up	chondroadherin like
BMAL1	1.096161	0.000125	0.001346	3.836442	Up	basic helix-loop-helix ARNT like 1
HEY2	1.092581	4.13E-06	7.98E-05	4.604788	Up	hes related family bHLH transcription factor with YRPW motif 2
C1QC	1.088725	0.001456	0.009997	3.183325	Up	complement C1q C chain
RAP1GAP	1.087453	3.89E-07	1.10E-05	5.074213	Up	RAP1 GTPase activating protein
IGFBP2	1.087314	0.00067	0.005337	3.401769	Up	insulin like growth factor binding protein 2
SERF1A	1.085241	0.000866	0.006537	3.330766	Up	small EDRK-rich factor 1A
ANKRD2	1.084717	0.008452	0.039628	2.633472	Up	ankyrin repeat domain 2
NINJ2	1.083521	7.06E-05	0.000843	3.974187	Up	ninjurin 2
CHGB	1.082407	0.000154	0.0016	3.785001	Up	chromogranin B
MZT2A	1.081823	3.37E-08	1.34E-06	5.52093	Up	mitotic spindle organizing protein 2A
ARG2	1.077937	0.007269	0.035376	2.684263	Up	arginase 2
ORMDL2	1.076301	1.29E-07	4.27E-06	5.280896	Up	ORMDL sphingolipid biosynthesis regulator 2
S100A10	1.076148	1.02E-08	4.81E-07	5.726995	Up	S100 calcium binding protein A10
FCGR3A	1.076127	0.00255	0.01557	3.017393	Up	Fc gamma receptor IIIa
TMTC1	1.073139	8.28E-15	2.39E-12	7.763155	Up	transmembrane O-mannosyltransferase targeting cadherins 1
GPSM2	1.063368	0.000784	0.006048	3.358294	Up	G protein signaling modulator 2
GGH	1.061541	0.000593	0.004829	3.434894	Up	gamma-glutamyl hydrolase
LPCAT3	1.061072	6.23E-13	1.05E-10	7.195297	Up	lysophosphatidylcholine acyltransferase 3
IL15RA	1.060951	4.54E-05	0.000584	4.078377	Up	interleukin 15 receptor subunit alpha
REPS2	1.059318	0.001048	0.007675	3.27738	Up	RALBP1 associated Eps domain containing 2
MLF1	1.05351	4.29E-09	2.20E-07	5.872576	Up	myeloid leukemia factor 1
RORB	1.052267	0.000424	0.003709	3.524428	Up	RAR related orphan receptor B
CHPF	1.052013	2.50E-07	7.51E-06	5.158054	Up	chondroitin polymerizing factor
GPD1	1.050149	7.41E-05	0.000877	3.962715	Up	glycerol-3-phosphate dehydrogenase 1
FABP4	1.043675	5.24E-05	0.000656	4.04446	Up	fatty acid binding protein 4
AIF1L	1.041639	2.52E-14	5.94E-12	7.620837	Up	allograft inflammatory factor 1 like
PTGS1	1.041087	0.000484	0.004125	3.489678	Up	prostaglandin-endoperoxide synthase 1
BHMT2	1.038158	8.03E-05	0.000936	3.943548	Up	betaine--homocysteine S-methyltransferase 2
QRFPR	1.03293	0.003967	0.022011	2.880748	Up	pyroglutamylated RFamide peptide receptor
C1QTNF1	1.032803	1.79E-06	4.00E-05	4.775687	Up	C1q and TNF related 1

LMCD1	1.030855	3.82E-07	1.08E-05	5.077748	Up	LIM and cysteine rich domains 1
CASKIN1	1.030294	6.58E-06	0.000117	4.50697	Up	CASK interacting protein 1
LRRC73	1.022236	4.19E-05	0.000551	4.096888	Up	leucine rich repeat containing 73
HK3	1.020868	0.003316	0.019156	2.936838	Up	hexokinase 3
VGLL3	1.020075	0.000109	0.001208	3.870325	Up	vestigial like family member 3
SDK1	1.019941	0.000306	0.002827	3.610504	Up	sidekick cell adhesion molecule 1
TPO	1.019432	5.94E-06	0.000108	4.52863	Up	thyroid peroxidase
PPIL1	1.018639	3.22E-08	1.29E-06	5.528843	Up	peptidylprolyl isomerase like 1
LRP4	1.01809	8.82E-09	4.22E-07	5.751897	Up	LDL receptor related protein 4
PLEKHN1	1.016341	0.004033	0.022273	2.875558	Up	pleckstrin homology domain containing N1
NFXL1	1.009298	9.69E-05	0.001098	3.898277	Up	nuclear transcription factor, X-box binding like 1
LOX	1.009253	0.000343	0.003104	3.580584	Up	lysyl oxidase
ADAMTS5	1.008298	0.00761	0.036683	2.668882	Up	ADAM metallopeptidase with thrombospondin type 1 motif 5
CD63	1.006901	5.17E-10	3.63E-08	6.213778	Up	CD63 molecule
ADAMTS15	1.005903	9.34E-05	0.001065	3.907072	Up	ADAM metallopeptidase with thrombospondin type 1 motif 15
CES4A	1.005567	5.51E-07	1.48E-05	5.007697	Up	carboxylesterase 4A
RPSA	1.002379	3.31E-17	1.59E-14	8.435149	Up	ribosomal protein SA
TSPAN2	1.002265	0.000227	0.002206	3.687257	Up	tetraspanin 2
HMBS	1.00194	8.33E-08	2.96E-06	5.359936	Up	hydroxymethylbilane synthase
ECE2	1.001266	0.000939	0.006999	3.308094	Up	endothelin converting enzyme 2
HAS2	0.999359	0.00706	0.034578	2.693979	Up	hyaluronan synthase 2
DMPK	0.998563	1.02E-08	4.80E-07	5.727498	Up	DM1 protein kinase
ALDOC	0.998201	5.63E-12	6.94E-10	6.888681	Up	aldolase, fructose-bisphosphate C
RPL15P3	0.997813	0.003199	0.018635	2.947937	Up	ribosomal protein L15 pseudogene 3
NQO1	0.996485	1.36E-05	0.000215	4.349613	Up	NAD(P)H quinone dehydrogenase 1
KLHL31	0.994088	1.34E-12	1.94E-10	7.090551	Up	kelch like family member 31
STXBP6	0.991408	0.00022	0.002151	3.695079	Up	syntaxin binding protein 6
TMEM37	0.984351	0.00046	0.003965	3.503017	Up	transmembrane protein 37
SLC17A9	0.98239	0.001532	0.010428	3.168583	Up	solute carrier family 17 member 9
LAMB3	0.98046	2.50E-06	5.21E-05	4.708423	Up	laminin subunit beta 3
RGS9BP	0.979373	3.56E-05	0.00048	4.134215	Up	regulator of G protein signaling 9 binding protein
PROCR	0.97865	5.56E-07	1.49E-05	5.005796	Up	protein C receptor
BCAT1	0.978293	0.011136	0.048687	2.538395	Up	branched chain amino acid transaminase 1
PTGDR	0.978039	0.002081	0.013271	3.07841	Up	prostaglandin D2 receptor
SIGLEC1	0.97573	0.002692	0.016278	3.000931	Up	sialic acid binding Ig like lectin 1
ZNG1C	0.974481	0.005358	0.027846	2.784673	Up	Zn regulated GTPase metalloprotein activator 1C
CAMK1D	0.973523	0.000188	0.001894	3.734622	Up	calcium/calmodulin dependent protein kinase ID
DDN	0.972604	0.0005	0.004216	3.480607	Up	dendrin
RPS6KA2	0.972468	9.24E-11	8.21E-09	6.478861	Up	ribosomal protein S6 kinase A2
PPIP5K2	0.969162	1.26E-13	2.43E-11	7.41053	Up	diphosphoinositol pentakisphosphate kinase 2
SLC29A2	0.969079	1.66E-07	5.36E-06	5.23419	Up	solute carrier family 29 member 2
NMRAL1	0.969006	7.72E-05	0.000906	3.953031	Up	NmrA like redox sensor 1

RALGPS2	0.966538	7.79E-08	2.80E-06	5.371814	Up	Ral GEF with PH domain and SH3 binding motif 2
NGFR	0.960061	0.002514	0.015414	3.021686	Up	nerve growth factor receptor
RPS2	0.956895	2.35E-12	3.22E-10	7.011857	Up	ribosomal protein S2
CENPV	0.953979	1.71E-05	0.00026	4.300079	Up	centromere protein V
RPS3AP26	0.952969	0.009264	0.042507	2.602158	Up	RPS3A pseudogene 26
PSMD8	0.950822	1.75E-12	2.49E-10	7.053132	Up	proteasome 26S subunit, non-ATPase 8
PRDX6	0.950566	1.02E-18	6.89E-16	8.833171	Up	peroxiredoxin 6
EDN1	0.950283	0.003236	0.018789	2.944399	Up	endothelin 1
EBP	0.948459	2.56E-11	2.71E-09	6.66991	Up	EBP cholestenol delta-isomerase
DHCR24	0.948293	0.004586	0.024627	2.834793	Up	24-dehydrocholesterol reductase
PDPN	0.944024	8.37E-05	0.000968	3.933428	Up	podoplanin
AKR1C1	0.933987	0.000125	0.001349	3.835698	Up	aldo-keto reductase family 1 member C1
CCDC184	0.933487	0.000802	0.006152	3.352086	Up	coiled-coil domain containing 184
HSPB7	0.931877	1.08E-12	1.63E-10	7.119389	Up	heat shock protein family B (small) member 7
SLC25A34	0.931047	3.52E-05	0.000475	4.136694	Up	solute carrier family 25 member 34
RASSF7	0.930056	0.0005	0.004216	3.48068	Up	Ras association domain family member 7
MMP19	0.92655	0.000932	0.006946	3.310437	Up	matrix metallopeptidase 19
CTSB	0.925437	1.04E-23	1.73E-20	10.03797	Up	cathepsin B
GLRX2	0.924516	1.67E-06	3.77E-05	4.789786	Up	glutaredoxin 2
LRRC32	0.921878	2.97E-08	1.21E-06	5.543104	Up	leucine rich repeat containing 32
MYL3	0.921472	7.10E-13	1.17E-10	7.177425	Up	myosin light chain 3
SMCO4	0.919571	3.46E-11	3.44E-09	6.625366	Up	single-pass membrane protein with coiled-coil domains 4
ITGA11	0.919375	2.16E-06	4.65E-05	4.73767	Up	integrin subunit alpha 11
PRKCD	0.917729	9.41E-06	0.000157	4.430357	Up	protein kinase C delta
FCER1G	0.917263	0.000329	0.002999	3.591448	Up	Fc epsilon receptor Ig
RPL27	0.916013	1.28E-10	1.07E-08	6.42969	Up	ribosomal protein L27
EFL1	0.915911	5.35E-07	1.44E-05	5.01316	Up	elongation factor like GTPase 1
SLCO2A1	0.914237	1.88E-05	0.000282	4.2786	Up	solute carrier organic anion transporter family member 2A1
SLC6A6	0.914068	1.92E-05	0.000286	4.273802	Up	solute carrier family 6 member 6
SLC9A7	0.913523	0.000357	0.003211	3.570057	Up	solute carrier family 9 member A7
RAMP1	0.912441	2.63E-07	7.85E-06	5.14836	Up	receptor activity modifying protein 1
TIFA	0.907331	0.000617	0.004992	3.424241	Up	TRAF interacting protein with forkhead associated domain
TSKU	0.907142	3.71E-08	1.47E-06	5.504114	Up	tsukushi, small leucine rich proteoglycan
SASH3	0.906894	0.005187	0.027114	2.795157	Up	SAM and SH3 domain containing 3
LGALS3	0.906007	7.66E-10	5.00E-08	6.151733	Up	galectin 3
NSDHL	0.903134	1.19E-13	2.36E-11	7.418028	Up	NAD(P) dependent steroid dehydrogenase-like
STEAP4	0.901749	0.000127	0.001361	3.832772	Up	STEAP4 metalloreductase
RPS5	0.901556	1.11E-09	6.91E-08	6.092253	Up	ribosomal protein S5
ABCG4	0.899377	0.000241	0.002322	3.672119	Up	ATP binding cassette subfamily G member 4
VIPR1	0.899325	5.47E-05	0.000679	4.034777	Up	vasoactive intestinal peptide receptor 1
KCNH2	0.898831	5.33E-11	5.05E-09	6.561335	Up	potassium voltage-gated channel subfamily H member 2
C8orf88	0.897743	3.23E-07	9.30E-06	5.109543	Up	chromosome 8 open reading frame 88

GPSM1	0.897483	6.74E-13	1.12E-10	7.184681	Up	G protein signaling modulator 1
LPCAT4	0.892491	1.34E-06	3.12E-05	4.833832	Up	lysophosphatidylcholine acyltransferase 4
COMTD1	0.890247	3.76E-07	1.07E-05	5.080717	Up	catechol-O-methyltransferase domain containing 1
ANKRD37	0.88827	3.93E-05	0.000522	4.111719	Up	ankyrin repeat domain 37
NACAD	0.888089	0.00255	0.01557	3.01735	Up	NAC alpha domain containing
TUBA4A	0.885552	0.000567	0.004652	3.446919	Up	tubulin alpha 4a
EPB41L4B	0.885224	0.002067	0.013216	3.080452	Up	erythrocyte membrane protein band 4.1 like 4B
SLAMF8	0.884149	0.003872	0.021624	2.888428	Up	SLAM family member 8
ZDHHC23	0.884111	0.00036	0.003234	3.567794	Up	zinc finger DHHC-type palmitoyltransferase 23
KCNK1	0.882224	0.000994	0.007341	3.292139	Up	potassium two pore domain channel subfamily K member 1
FTH1	0.880517	2.72E-09	1.47E-07	5.947709	Up	ferritin heavy chain 1
GGT5	0.879595	4.46E-06	8.46E-05	4.588919	Up	gamma-glutamyltransferase 5
NID1	0.878325	3.41E-05	0.000462	4.144327	Up	nidogen 1
IMPA2	0.87685	1.44E-10	1.19E-08	6.41118	Up	inositol monophosphatase 2
CREB3L1	0.875323	1.01E-07	3.47E-06	5.324906	Up	cAMP responsive element binding protein 3 like 1
FRK	0.874037	5.76E-06	0.000105	4.535166	Up	fyn related Src family tyrosine kinase
F8	0.873081	9.95E-07	2.44E-05	4.892682	Up	coagulation factor VIII
SRRM3	0.872029	0.006155	0.03108	2.739386	Up	serine/arginine repetitive matrix 3
NOCT	0.871412	4.66E-07	1.28E-05	5.039942	Up	nocturnin
SNAI3	0.869649	0.001987	0.012804	3.09214	Up	snail family transcriptional repressor 3
HMOX1	0.869394	0.001014	0.007474	3.286495	Up	heme oxygenase 1
AKR1B1	0.868698	1.85E-05	0.000278	4.282764	Up	aldo-keto reductase family 1 member B
ZDHHC9	0.867612	1.29E-06	3.03E-05	4.84134	Up	zinc finger DHHC-type palmitoyltransferase 9
RPL6P27	0.865558	0.00444	0.023969	2.845103	Up	ribosomal protein L6 pseudogene 27
ACACB	0.862721	2.42E-19	1.88E-16	8.992222	Up	acetyl-CoA carboxylase beta
NUDT4	0.861292	7.95E-10	5.17E-08	6.145934	Up	nudix hydrolase 4
ALPL	0.861175	1.86E-07	5.87E-06	5.212504	Up	alkaline phosphatase, biomineralization associated
SLC25A19	0.861029	4.20E-07	1.18E-05	5.059868	Up	solute carrier family 25 member 19
SH3KBP1	0.860753	6.01E-06	0.000109	4.525954	Up	SH3 domain containing kinase binding protein 1
BCL6	0.860165	1.43E-11	1.60E-09	6.754946	Up	BCL6 transcription repressor
MPST	0.859653	5.21E-12	6.52E-10	6.899819	Up	mercaptopyruvate sulfurtransferase
GAREM1	0.857939	2.74E-09	1.47E-07	5.946406	Up	GRB2 associated regulator of MAPK1 subtype 1
PALLD	0.855494	1.79E-10	1.45E-08	6.378635	Up	palladin, cytoskeletal associated protein
CD276	0.851975	1.92E-07	6.00E-06	5.207066	Up	CD276 molecule
KIF24	0.850893	0.003482	0.019881	2.921673	Up	kinesin family member 24
NQO2	0.850874	0.001582	0.010699	3.159217	Up	N-ribosyldihydronicotinamide:quinone reductase 2
CABP1	0.847902	2.51E-05	0.000358	4.213805	Up	calcium binding protein 1
MCRIP2	0.847354	2.40E-08	1.00E-06	5.580226	Up	MAPK regulated corepressor interacting protein 2
FAM86DP	0.846945	0.00029	0.00271	3.62384	Up	family with sequence similarity 86 member D, pseudogene
HIF3A	0.845481	1.87E-06	4.12E-05	4.767027	Up	hypoxia inducible factor 3 subunit alpha
TUBG1	0.841452	2.98E-07	8.71E-06	5.124896	Up	tubulin gamma 1
NRAV	0.837301	8.06E-06	0.000139	4.463559	Up	negative regulator of antiviral response

RETSAT	0.835155	2.51E-08	1.04E-06	5.572753	Up	retinol saturase
RNASE6	0.833596	0.010755	0.047383	2.550565	Up	ribonuclease A family member k6
TKT	0.830832	2.24E-05	0.000326	4.239435	Up	transketolase
PMVK	0.830181	6.77E-12	8.15E-10	6.862402	Up	phosphomevalonate kinase
EPN1	0.828162	8.02E-10	5.21E-08	6.144462	Up	epsin 1
RFPL4A	-6.08612	6.11E-06	0.00011	-4.52272	Down	ret finger protein like 4A
EDN3	-5.81897	2.27E-09	1.27E-07	-5.9774	Down	endothelin 3
CST2	-5.75383	5.07E-08	1.93E-06	-5.44897	Down	cystatin SA
SEZ6L	-5.57904	7.11E-39	7.71E-35	-13.0414	Down	seizure related 6 homolog like
CUX2	-5.56999	8.47E-10	5.43E-08	-6.1358	Down	cut like homeobox 2
ESM1	-5.53143	1.29E-10	1.08E-08	-6.42835	Down	endothelial cell specific molecule 1
SIGLEC17P	-5.52859	1.48E-09	8.85E-08	-6.04672	Down	sialic acid binding Ig like lectin 17, pseudogene
GSG1L	-5.08812	8.54E-15	2.40E-12	-7.75928	Down	GSG1 like
VGLL2	-4.82825	2.64E-14	6.15E-12	-7.61497	Down	vestigial like family member 2
MSTN	-4.80687	3.20E-08	1.29E-06	-5.53016	Down	myostatin
LYPD1	-4.72384	1.12E-05	0.000181	-4.39289	Down	LY6/PLAUR domain containing 1
TNMD	-4.65997	2.90E-09	1.55E-07	-5.9374	Down	tenomodulin
IL31RA	-4.45949	1.93E-08	8.29E-07	-5.61815	Down	interleukin 31 receptor A
PRND	-4.24837	0.000294	0.00274	-3.62066	Down	prion like protein doppel
CA3	-4.24797	7.57E-10	4.97E-08	-6.15363	Down	carbonic anhydrase 3
RFPL4AL1	-4.06067	0.002819	0.016892	-2.98684	Down	ret finger protein like 4A like 1
HBA1	-3.93318	7.06E-05	0.000843	-3.97425	Down	hemoglobin subunit alpha 1
SFRP4	-3.90669	8.49E-25	2.63E-21	-10.2821	Down	secreted frizzled related protein 4
SHISA2	-3.88696	1.74E-09	1.01E-07	-6.02032	Down	shisa family member 2
COL22A1	-3.88282	6.44E-08	2.39E-06	-5.40611	Down	collagen type XXII alpha 1 chain
LAMP5	-3.88196	5.26E-05	0.000657	-4.04397	Down	lysosomal associated membrane protein family member 5
CYP21A2	-3.86616	6.67E-05	0.000804	-3.98787	Down	cytochrome P450 family 21 subfamily A member 2
CENPA	-3.78995	6.66E-08	2.46E-06	-5.40011	Down	centromere protein A
CXCL11	-3.77668	0.000238	0.002305	-3.67431	Down	C-X-C motif chemokine ligand 11
CBLN4	-3.75516	0.000492	0.004178	-3.48504	Down	cerebellin 4 precursor
CD1C	-3.74245	1.12E-07	3.74E-06	-5.30645	Down	CD1c molecule
IRX1	-3.67142	1.38E-24	3.75E-21	-10.2349	Down	iroquois homeobox 1
KCNK10	-3.64322	0.000246	0.002361	-3.66631	Down	potassium two pore domain channel subfamily K member 10
CYP4F3	-3.63956	0.000769	0.005958	-3.36384	Down	cytochrome P450 family 4 subfamily F member 3
TRPM8	-3.62602	0.010099	0.045275	-2.57243	Down	transient receptor potential cation channel subfamily M member 8
SYTL5	-3.60488	1.91E-10	1.52E-08	-6.3687	Down	synaptotagmin like 5
HBA2	-3.59683	1.49E-09	8.87E-08	-6.04504	Down	hemoglobin subunit alpha 2
ZSCAN4	-3.58877	0.000508	0.004267	-3.47649	Down	zinc finger and SCAN domain containing 4
CST1	-3.54945	0.003149	0.018407	-2.95282	Down	cystatin SN
PIPSL	-3.51637	1.35E-05	0.000213	-4.35172	Down	PIP5K1A and PSMD4 like (pseudogene)
P3H2	-3.50657	4.00E-15	1.28E-12	-7.85484	Down	prolyl 3-hydroxylase 2
L1TD1	-3.48386	0.001653	0.011091	-3.14636	Down	LINE1 type transposase domain containing 1

UCMA	-3.48194	0.001171	0.008408	-3.24585	Down	upper zone of growth plate and cartilage matrix associated
FOXA1	-3.45448	0.00224	0.014029	-3.05646	Down	forkhead box A1
IL22RA2	-3.4501	0.001113	0.008053	-3.26037	Down	interleukin 22 receptor subunit alpha 2
APOBEC3A	-3.4404	0.001068	0.007806	-3.27194	Down	apolipoprotein B mRNA editing enzyme catalytic subunit 3A
RSPO2	-3.4195	0.000263	0.002489	-3.64925	Down	R-spondin 2
ARMS2	-3.40932	0.000232	0.002247	-3.68188	Down	age-related maculopathy susceptibility 2
LEF1	-3.39897	5.91E-09	2.92E-07	-5.81916	Down	lymphoid enhancer binding factor 1
ALOX15	-3.39735	0.003337	0.019255	-2.93482	Down	arachidonate 15-lipoxygenase
KLHDC8A	-3.39219	0.000412	0.003618	-3.53199	Down	kelch domain containing 8A
CTLA4	-3.38635	0.001687	0.011269	-3.14042	Down	cytotoxic T-lymphocyte associated protein 4
SLITRK4	-3.37805	2.08E-12	2.93E-10	-7.02874	Down	SLIT and NTRK like family member 4
SLC4A8	-3.35749	4.88E-08	1.87E-06	-5.4555	Down	solute carrier family 4 member 8
MAP3K7CL	-3.33799	2.17E-12	3.03E-10	-7.02312	Down	MAP3K7 C-terminal like
TMEM114	-3.3051	0.00107	0.007816	-3.27147	Down	transmembrane protein 114
ZNF497	-3.28471	1.06E-06	2.57E-05	-4.88079	Down	zinc finger protein 497
MYH2	-3.26621	0.00069	0.005454	-3.39364	Down	myosin heavy chain 2
PCDH15	-3.23631	1.20E-08	5.52E-07	-5.70003	Down	protocadherin related 15
MATN4	-3.21706	0.005603	0.028785	-2.77014	Down	matrilin 4
FBN3	-3.20371	0.000762	0.005914	-3.36612	Down	fibrillin 3
PENK	-3.20157	1.42E-08	6.38E-07	-5.67074	Down	proenkephalin
OIT3	-3.18648	0.001047	0.007669	-3.27769	Down	oncoprotein induced transcript 3
FCGR3B	-3.18466	3.45E-05	0.000467	-4.14164	Down	Fc gamma receptor IIIb
IL1B	-3.15644	0.004337	0.023551	-2.85253	Down	interleukin 1 beta
PPP2R2B	-3.1265	5.41E-10	3.73E-08	-6.20685	Down	protein phosphatase 2 regulatory subunit Bbeta
FCER1A	-3.11477	1.80E-12	2.54E-10	-7.04952	Down	Fc epsilon receptor Ia
TINCR	-3.02355	0.002331	0.014486	-3.04444	Down	TINCR ubiquitin domain containing
HBB	-3.01782	4.64E-06	8.74E-05	-4.58031	Down	hemoglobin subunit beta
RXFP2	-3.00027	7.07E-05	0.000843	-3.97379	Down	relaxin family peptide receptor 2
SLC16A6	-2.99211	5.09E-06	9.45E-05	-4.56122	Down	solute carrier family 16 member 6
ANKRD18B	-2.9787	0.00653	0.0326	-2.71989	Down	ankyrin repeat domain 18B
ATP1A4	-2.97464	6.55E-08	2.43E-06	-5.40298	Down	ATPase Na+/K+ transporting subunit alpha 4
IRX2	-2.97222	2.20E-21	2.39E-18	-9.49489	Down	iroquois homeobox 2
AARSD1P1	-2.97018	0.002885	0.017172	-2.97972	Down	AARSD1 pseudogene 1
COL10A1	-2.95457	6.10E-07	1.61E-05	-4.98814	Down	collagen type X alpha 1 chain
FNDC1	-2.94983	9.88E-17	4.37E-14	-8.30623	Down	fibronectin type III domain containing 1
DPYSL5	-2.94034	0.004785	0.025452	-2.82118	Down	dihydropyrimidinase like 5
CDH8	-2.93542	3.82E-07	1.08E-05	-5.0777	Down	cadherin 8
DUXAP8	-2.92529	2.28E-08	9.60E-07	-5.58952	Down	double homeobox A pseudogene 8
SCUBE2	-2.91312	5.58E-23	8.07E-20	-9.87061	Down	signal peptide, CUB domain and EGF like domain containing 2
PCSK1N	-2.91045	8.48E-09	4.08E-07	-5.75856	Down	proprotein convertase subtilisin/kexin type 1 inhibitor
DLGAP1	-2.9102	3.34E-10	2.50E-08	-6.28233	Down	DLG associated protein 1
KCNJ15	-2.88108	0.007867	0.037565	-2.65773	Down	potassium inwardly rectifying channel subfamily J member 15

ECEL1	-2.87494	0.005376	0.027904	-2.7836	Down	endothelin converting enzyme like 1
CTSG	-2.86227	3.46E-06	6.90E-05	-4.64134	Down	cathepsin G
RPS4XP5	-2.86191	1.18E-05	0.000191	-4.38147	Down	ribosomal protein S4X pseudogene 5
AQP10	-2.84503	2.45E-06	5.15E-05	-4.71239	Down	aquaporin 10
MUC13	-2.84396	0.003438	0.019707	-2.92563	Down	mucin 13, cell surface associated
C2CD4D	-2.83404	0.000836	0.006351	-3.34073	Down	C2 calcium dependent domain containing 4D
CX3CR1	-2.83102	5.17E-10	3.63E-08	-6.21387	Down	C-X3-C motif chemokine receptor 1
CRACD	-2.81495	1.48E-07	4.84E-06	-5.25561	Down	capping protein inhibiting regulator of actin dynamics
HS3ST5	-2.80116	0.000915	0.006843	-3.31547	Down	heparan sulfate-glucosamine 3-sulfotransferase 5
TMEM262	-2.79837	0.007145	0.034919	-2.69003	Down	transmembrane protein 262
UNC80	-2.79241	1.25E-06	2.97E-05	-4.84703	Down	unc-80 homolog, NALCN channel complex subunit
DUXAP9	-2.78798	1.14E-06	2.74E-05	-4.86569	Down	double homeobox A pseudogene 9
SFTA1P	-2.77093	0.002232	0.013986	-3.05754	Down	surfactant associated 1, lncRNA
PLD4	-2.77083	4.28E-05	0.00056	-4.09205	Down	phospholipase D family member 4
TAS2R18P	-2.76001	0.001362	0.009463	-3.20265	Down	taste 2 receptor member 18 pseudogene
APCDD1L-DT	-2.75889	8.68E-05	0.000999	-3.92493	Down	APCDD1L divergent transcript
GZMM	-2.74069	0.006992	0.034342	-2.69725	Down	granzyme M
RHCG	-2.73901	7.18E-05	0.000853	-3.97033	Down	Rh family C glycoprotein
APCDD1L	-2.73757	3.29E-15	1.11E-12	-7.87949	Down	APC down-regulated 1 like
SUPT20HL2	-2.71694	0.008404	0.039459	-2.63541	Down	SUPT20H like 2
UGT8	-2.71408	0.011227	0.048973	-2.53555	Down	UDP glycosyltransferase 8
RASEF	-2.71297	5.46E-05	0.000679	-4.03484	Down	RAS and EF-hand domain containing
MTCO2P11	-2.70143	0.009939	0.044724	-2.57795	Down	MT-CO2 pseudogene 11
ITPRID1	-2.69273	0.005594	0.028754	-2.77068	Down	ITPR interacting domain containing 1
ANKRD34C	-2.67122	4.83E-15	1.47E-12	-7.83126	Down	ankyrin repeat domain 34C
WNT9A	-2.66476	1.23E-07	4.09E-06	-5.28946	Down	Wnt family member 9A
FRZB	-2.66108	1.91E-20	1.65E-17	-9.26745	Down	frizzled related protein
ATP1B4	-2.65405	1.37E-09	8.36E-08	-6.05903	Down	ATPase Na+/K+ transporting family member beta 4
TMEM30B	-2.61461	1.15E-12	1.73E-10	-7.11066	Down	transmembrane protein 30B
MKRN2OS	-2.60614	3.69E-06	7.26E-05	-4.62816	Down	MKRN2 opposite strand
FMN2	-2.60154	0.011006	0.048226	-2.5425	Down	formin 2
TM6SF2	-2.59953	0.004838	0.025678	-2.81763	Down	transmembrane 6 superfamily member 2
ZNF365	-2.59706	2.50E-09	1.38E-07	-5.9613	Down	zinc finger protein 365
STK4-DT	-2.59357	0.004025	0.022253	-2.87617	Down	STK4 divergent transcript
GZMB	-2.59298	0.003346	0.019292	-2.93399	Down	granzyme B
DOCK11P1	-2.56323	0.007399	0.035881	-2.67832	Down	dedicator of cytokinesis 11 pseudogene 1
CACNA1B	-2.56238	9.28E-08	3.23E-06	-5.34025	Down	calcium voltage-gated channel subunit alpha1 B
BCL2A1	-2.55969	0.005986	0.030365	-2.74853	Down	BCL2 related protein A1
HYAL4	-2.55492	0.011543	0.049923	-2.52581	Down	hyaluronidase 4
HLA-DRB6	-2.53952	0.005389	0.027961	-2.78279	Down	major histocompatibility complex, class II, DR beta 6 (pseudogene)
CMA1	-2.53309	0.003571	0.020307	-2.91375	Down	chymase 1
GNLY	-2.52776	5.74E-07	1.53E-05	-4.99987	Down	granulysin

E2F7	-2.51473	0.00724	0.035267	-2.68561	Down	E2F transcription factor 7
HCCAT5	-2.51024	0.010079	0.045196	-2.5731	Down	hepatocellular carcinoma associated transcript 5
IL6ST-DT	-2.50982	0.009757	0.044144	-2.58432	Down	IL6ST divergent transcript
CYTL1	-2.49129	3.38E-06	6.76E-05	-4.6463	Down	cytokine like 1
RGS4	-2.47243	3.34E-18	1.91E-15	-8.69914	Down	regulator of G protein signaling 4
MXRA5	-2.47011	3.93E-08	1.53E-06	-5.49408	Down	matrix remodeling associated 5
FMOD	-2.45729	1.09E-09	6.81E-08	-6.09513	Down	fibromodulin
THBS4	-2.45021	1.20E-13	2.37E-11	-7.41632	Down	thrombospondin 4
CRISPLD1	-2.44475	6.56E-14	1.39E-11	-7.49642	Down	cysteine rich secretory protein LCCL domain containing 1
SLC7A5P1	-2.44044	0.011106	0.048586	-2.53933	Down	solute carrier family 7 member 5 pseudogene 1
HSH2D	-2.4346	0.00559	0.028739	-2.77092	Down	hematopoietic SH2 domain containing
ATRNL1	-2.42686	1.02E-07	3.48E-06	-5.32359	Down	attractin like 1
LAMB4	-2.42586	0.005571	0.028662	-2.77202	Down	laminin subunit beta 4
COL9A1	-2.41734	1.01E-09	6.33E-08	-6.10827	Down	collagen type IX alpha 1 chain
DEGS2	-2.39719	0.007633	0.03675	-2.6679	Down	delta 4-desaturase, sphingolipid 2
PHF21B	-2.38857	2.48E-05	0.000354	-4.21669	Down	PHD finger protein 21B
XG	-2.38566	4.33E-08	1.67E-06	-5.477	Down	Xg glycoprotein (Xg blood group)
HDC	-2.38328	0.002285	0.014238	-3.0505	Down	histidine decarboxylase
ELFN2	-2.37429	0.006887	0.033926	-2.70227	Down	extracellular leucine rich repeat and fibronectin type III domain containing 2
F2RL2	-2.37276	5.66E-10	3.87E-08	-6.19958	Down	coagulation factor II thrombin receptor like 2
CXCL9	-2.36714	2.96E-07	8.68E-06	-5.12612	Down	C-X-C motif chemokine ligand 9
GDF6	-2.36071	7.63E-10	5.00E-08	-6.15245	Down	growth differentiation factor 6
IGFALS	-2.35613	0.000438	0.003805	-3.5163	Down	insulin like growth factor binding protein acid labile subunit
KIF5A	-2.34574	0.001438	0.009898	-3.18701	Down	kinesin family member 5A
GABRD	-2.34318	0.000712	0.005599	-3.38487	Down	gamma-aminobutyric acid type A receptor subunit delta
ENPP2	-2.335	4.36E-08	1.68E-06	-5.47568	Down	ectonucleotide pyrophosphatase/phosphodiesterase 2
GDF15	-2.31502	7.65E-08	2.75E-06	-5.37521	Down	growth differentiation factor 15
TGFB2	-2.31242	1.31E-16	5.68E-14	-8.27273	Down	transforming growth factor beta 2
MED12L	-2.30972	2.36E-10	1.83E-08	-6.33587	Down	mediator complex subunit 12L
IGSF1	-2.30639	7.56E-07	1.94E-05	-4.9463	Down	immunoglobulin superfamily member 1
LRRC9	-2.30007	0.007113	0.034795	-2.69152	Down	leucine rich repeat containing 9
C1QTNF3	-2.29553	2.32E-08	9.76E-07	-5.58636	Down	C1q and TNF related 3
FAM133A	-2.27467	0.000104	0.001166	-3.8808	Down	family with sequence similarity 133 member A
HCG20	-2.25055	0.000473	0.004052	-3.49583	Down	HLA complex group 20
COL17A1	-2.24285	0.000785	0.006052	-3.35788	Down	collagen type XVII alpha 1 chain
ODF3	-2.2393	0.005735	0.029307	-2.76254	Down	outer dense fiber of sperm tails 3
SCG5	-2.23254	0.009418	0.042998	-2.59648	Down	secretogranin V
CHRDL1	-2.23168	1.75E-07	5.62E-06	-5.22427	Down	chordin like 1
AEBP1	-2.22447	7.36E-12	8.81E-10	-6.85056	Down	AE binding protein 1
SYNPR	-2.21286	0.005472	0.028262	-2.77784	Down	synaptoporin
EDA2R	-2.2116	4.38E-06	8.36E-05	-4.59238	Down	ectodysplasin A2 receptor
CCDC63	-2.2071	4.39E-09	2.24E-07	-5.86896	Down	coiled-coil domain containing 63

LYPD2	-2.20064	0.00069	0.005454	-3.39363	Down	LY6/PLAUR domain containing 2
CAPN12	-2.19325	1.87E-05	0.000281	-4.27947	Down	calpain 12
SLC5A7	-2.18407	0.003921	0.021839	-2.88442	Down	solute carrier family 5 member 7
NALF1	-2.17655	9.77E-06	0.000162	-4.42226	Down	NALCN channel auxiliary factor 1
KIT	-2.16548	2.89E-13	5.32E-11	-7.2992	Down	KIT proto-oncogene, receptor tyrosine kinase
SV2C	-2.16317	0.002041	0.01309	-3.08417	Down	synaptic vesicle glycoprotein 2C
APLNR	-2.16156	2.06E-07	6.36E-06	-5.19353	Down	apelin receptor
CH25H	-2.15932	0.000573	0.004696	-3.44415	Down	cholesterol 25-hydroxylase
MCF2L2	-2.15848	1.13E-06	2.72E-05	-4.86736	Down	MCF.2 cell line derived transforming sequence-like 2
NELL2	-2.14059	0.006995	0.034345	-2.69706	Down	neural EGFL like 2
ANKRD24	-2.14048	5.27E-05	0.000658	-4.0432	Down	ankyrin repeat domain 24
ODAD2	-2.13575	0.000399	0.003522	-3.54074	Down	outer dynein arm docking complex subunit 2
TMEM163	-2.12774	4.65E-06	8.74E-05	-4.58001	Down	transmembrane protein 163
AKR7A3	-2.12635	0.001277	0.00903	-3.22115	Down	aldo-keto reductase family 7 member A3
FAT3	-2.12241	0.002811	0.01686	-2.98769	Down	FAT atypical cadherin 3
CERS1	-2.11356	0.000377	0.003356	-3.55591	Down	ceramide synthase 1
DUXAP10	-2.10055	0.001321	0.009265	-3.21144	Down	double homeobox A pseudogene 10
CXCL3	-2.09566	0.000229	0.00223	-3.68434	Down	C-X-C motif chemokine ligand 3
MYOC	-2.09045	1.77E-05	0.000268	-4.29226	Down	myocilin
PHB1P9	-2.07929	0.006579	0.032763	-2.71741	Down	PHB1 pseudogene 9
CXCL10	-2.07443	0.000302	0.002801	-3.61373	Down	C-X-C motif chemokine ligand 10
MME	-2.06139	1.22E-11	1.38E-09	-6.77822	Down	membrane metalloendopeptidase
BDNF	-2.05823	1.43E-08	6.40E-07	-5.66955	Down	brain derived neurotrophic factor
RIPOR2	-2.05701	1.80E-11	1.96E-09	-6.72111	Down	RHO family interacting cell polarization regulator 2
NGEF	-2.05378	0.003916	0.021824	-2.88488	Down	neuronal guanine nucleotide exchange factor
DBIL5P	-2.05223	0.000881	0.006624	-3.32611	Down	diazepam binding inhibitor-like 5, pseudogene
NR4A1AS	-2.03655	0.006884	0.033926	-2.7024	Down	NR4A1 antisense RNA
LAMC3	-2.02991	6.45E-06	0.000115	-4.51123	Down	laminin subunit gamma 3
EGR3	-2.0234	0.001794	0.011799	-3.12243	Down	early growth response 3
TSPAN10	-2.0188	0.001949	0.012611	-3.0979	Down	tetraspanin 10
C14orf132	-2.01582	8.69E-13	1.36E-10	-7.1498	Down	chromosome 14 open reading frame 132
CCDC62	-1.99899	0.000848	0.006434	-3.33651	Down	coiled-coil domain containing 62
PTGER3	-1.99827	2.35E-05	0.00034	-4.22875	Down	prostaglandin E receptor 3
CFAP92	-1.99623	0.003973	0.022037	-2.88026	Down	cilia and flagella associated protein 92 (putative)
LRRN1	-1.99182	0.008313	0.039113	-2.63909	Down	leucine rich repeat neuronal 1
SULF1	-1.98704	8.37E-14	1.76E-11	-7.46439	Down	sulfatase 1
LEFTY2	-1.97634	1.41E-07	4.65E-06	-5.26416	Down	left-right determination factor 2
PTN	-1.97623	1.09E-11	1.26E-09	-6.79383	Down	pleiotrophin
CACNB4	-1.97556	9.12E-05	0.001042	-3.91295	Down	calcium voltage-gated channel auxiliary subunit beta 4
LRRC55	-1.97183	6.31E-05	0.000766	-4.00087	Down	leucine rich repeat containing 55
CHD5	-1.95394	7.09E-05	0.000845	-3.97314	Down	chromodomain helicase DNA binding protein 5
LMX1A	-1.94888	0.004546	0.024459	-2.83755	Down	LIM homeobox transcription factor 1 alpha

OLR1	-1.94809	0.003801	0.021316	-2.89424	Down	oxidized low density lipoprotein receptor 1
MYCN	-1.94117	9.47E-05	0.001077	-3.90377	Down	MYCN proto-oncogene, bHLH transcription factor
SLC16A9	-1.94029	1.36E-16	5.78E-14	-8.26816	Down	solute carrier family 16 member 9
THY1	-1.94016	0.000502	0.004226	-3.47947	Down	Thy-1 cell surface antigen
CHRNA3	-1.93888	1.56E-06	3.56E-05	-4.80378	Down	cholinergic receptor nicotinic alpha 3 subunit
LOXHD1	-1.93501	1.18E-08	5.45E-07	-5.70283	Down	lipoxygenase homology PLAT domains 1
FATE1	-1.93408	0.001437	0.009898	-3.18711	Down	fetal and adult testis expressed 1
ABCG2	-1.93274	1.14E-10	9.77E-09	-6.44768	Down	ATP binding cassette subfamily G member 2 (Junior blood group)
NTNG2	-1.92239	3.67E-10	2.68E-08	-6.26748	Down	netrin G2
CXCL2	-1.91931	0.000362	0.003245	-3.56643	Down	C-X-C motif chemokine ligand 2
MMP25	-1.90316	0.000271	0.002553	-3.64195	Down	matrix metallopeptidase 25
MDK	-1.89822	9.34E-22	1.12E-18	-9.58401	Down	midkine
KIAA1549L	-1.89026	0.001342	0.009368	-3.20686	Down	KIAA1549 like
CATSPER1	-1.88726	0.000914	0.006841	-3.31563	Down	cation channel sperm associated 1
PALM3	-1.88587	9.83E-05	0.001111	-3.89485	Down	paralemmin 3
CCDC27	-1.87998	0.001315	0.009234	-3.21277	Down	coiled-coil domain containing 27
ANGPTL7	-1.86726	2.67E-08	1.10E-06	-5.56178	Down	angiopoietin like 7
IQCN	-1.85833	4.81E-10	3.42E-08	-6.22512	Down	IQ motif containing N
SP5	-1.85737	0.006355	0.031924	-2.72888	Down	Sp5 transcription factor
DNAH5	-1.84947	0.007085	0.034674	-2.69283	Down	dynein axonemal heavy chain 5
ASB18	-1.84755	3.53E-13	6.32E-11	-7.27259	Down	ankyrin repeat and SOCS box containing 18
RPL9P16	-1.83375	0.007491	0.036238	-2.67418	Down	ribosomal protein L9 pseudogene 16
TLL2	-1.83353	4.85E-14	1.11E-11	-7.53585	Down	tolloid like 2
RASSF10	-1.83297	0.000106	0.001181	-3.87681	Down	Ras association domain family member 10
PRSS8	-1.8269	0.005429	0.02813	-2.78044	Down	serine protease 8
PTCH2	-1.82443	2.91E-05	0.000407	-4.18003	Down	patched 2
TNFRSF11B	-1.82131	4.33E-11	4.17E-09	-6.59247	Down	TNF receptor superfamily member 11b
DIO2	-1.81759	5.88E-22	7.50E-19	-9.63162	Down	iodothyronine deiodinase 2
CEROX1	-1.81659	2.23E-10	1.75E-08	-6.34479	Down	cytoplasmic endogenous regulator of oxidative phosphorylation 1
PRSS35	-1.81634	0.000182	0.001838	-3.74346	Down	serine protease 35
PLEKHH2	-1.81491	1.07E-13	2.16E-11	-7.43216	Down	pleckstrin homology, MyTH4 and FERM domain containing H2
CYS1	-1.81286	8.90E-27	3.86E-23	-10.7124	Down	cystin 1
TAGLN3	-1.80646	0.01052	0.046693	-2.55825	Down	transgelin 3
PTPRR	-1.79996	8.65E-05	0.000997	-3.92569	Down	protein tyrosine phosphatase receptor type R
DNAAF3	-1.79833	2.66E-11	2.78E-09	-6.66454	Down	dynein axonemal assembly factor 3
PCDH17	-1.79354	3.06E-08	1.24E-06	-5.53817	Down	protocadherin 17
KLHL4	-1.79317	4.36E-08	1.68E-06	-5.47555	Down	kelch like family member 4
INHBA	-1.79264	1.41E-14	3.60E-12	-7.69542	Down	inhibin subunit beta A
PMAIP1	-1.7905	0.003407	0.019568	-2.92841	Down	phorbol-12-myristate-13-acetate-induced protein 1
COL14A1	-1.78358	7.72E-13	1.25E-10	-7.16599	Down	collagen type XIV alpha 1 chain
COL24A1	-1.77738	2.18E-06	4.67E-05	-4.73622	Down	collagen type XXIV alpha 1 chain
SYT17	-1.77529	8.98E-08	3.14E-06	-5.34619	Down	synaptotagmin 17

PRG4	-1.77474	1.01E-07	3.47E-06	-5.32461	Down	proteoglycan 4
CHRM3	-1.77434	0.003553	0.02022	-2.91533	Down	cholinergic receptor muscarinic 3
SMOC2	-1.77092	6.19E-14	1.33E-11	-7.50404	Down	SPARC related modular calcium binding 2
PLAC8	-1.76299	0.010898	0.047887	-2.54595	Down	placenta associated 8
GPR173	-1.76164	9.15E-13	1.41E-10	-7.14269	Down	G protein-coupled receptor 173
EFCC1	-1.75798	1.25E-18	8.23E-16	-8.80985	Down	EF-hand and coiled-coil domain containing 1
PHOSPHO1	-1.75375	6.52E-07	1.70E-05	-4.975	Down	phosphoethanolamine/phosphocholine phosphatase 1
GATM	-1.75104	1.66E-11	1.85E-09	-6.73306	Down	glycine amidinotransferase
NDP	-1.75011	0.000373	0.003331	-3.55837	Down	norrin cystine knot growth factor NDP
LYPD3	-1.74918	0.002402	0.014856	-3.03539	Down	LY6/PLAUR domain containing 3
MPIG6B	-1.74658	7.97E-06	0.000137	-4.46603	Down	megakaryocyte and platelet inhibitory receptor G6b
TTLL7	-1.74424	8.43E-15	2.40E-12	-7.76101	Down	tubulin tyrosine ligase like 7
EIF4EBP3	-1.73862	0.004056	0.02237	-2.87377	Down	eukaryotic translation initiation factor 4E binding protein 3
HTR2B	-1.73026	1.74E-05	0.000263	-4.29648	Down	5-hydroxytryptamine receptor 2B
UCHL1	-1.72923	9.65E-06	0.000161	-4.42476	Down	ubiquitin C-terminal hydrolase L1
LUM	-1.72714	6.51E-16	2.48E-13	-8.07929	Down	lumican
ARSJ	-1.72266	5.73E-08	2.16E-06	-5.42709	Down	arylsulfatase family member J
HNRNPH1P1	-1.72097	0.009472	0.04315	-2.59452	Down	heterogeneous nuclear ribonucleoprotein H1 pseudogene 1
MID1	-1.71622	1.41E-10	1.17E-08	-6.4145	Down	midline 1
CFAP251	-1.71099	2.62E-09	1.43E-07	-5.95377	Down	cilia and flagella associated protein 251
ANKLE1	-1.71053	0.006382	0.032035	-2.7275	Down	ankyrin repeat and LEM domain containing 1
SLC6A12	-1.70743	0.000772	0.005975	-3.36271	Down	solute carrier family 6 member 12
CREG2	-1.7072	0.001721	0.011437	-3.13465	Down	cellular repressor of E1A stimulated genes 2
MTUS1-DT	-1.70266	0.002272	0.014188	-3.05217	Down	MTUS1 divergent transcript
CSPG5	-1.69814	0.000304	0.002816	-3.61167	Down	chondroitin sulfate proteoglycan 5
GADL1	-1.69603	5.32E-06	9.81E-05	-4.55181	Down	glutamate decarboxylase like 1
IFI44L	-1.69463	1.13E-08	5.26E-07	-5.70945	Down	interferon induced protein 44 like
LRRC3B	-1.69378	0.010166	0.045512	-2.57012	Down	leucine rich repeat containing 3B
OPCML	-1.69359	5.62E-05	0.000695	-4.02812	Down	opioid binding protein/cell adhesion molecule like
IRX6	-1.68864	3.63E-11	3.57E-09	-6.61857	Down	iroquois homeobox 6
SELL	-1.68599	0.001064	0.007777	-3.27309	Down	selectin L
S1PR5	-1.68547	0.007911	0.037706	-2.65583	Down	sphingosine-1-phosphate receptor 5
CCDC168	-1.67966	6.56E-05	0.000792	-3.9918	Down	coiled-coil domain containing 168
METTL21EP	-1.67946	2.25E-08	9.49E-07	-5.59188	Down	methyltransferase like 21E, pseudogene
ITIH5	-1.67495	1.90E-32	1.37E-28	-11.8606	Down	inter-alpha-trypsin inhibitor heavy chain 5
B3GNT5	-1.67159	2.32E-10	1.81E-08	-6.33821	Down	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5
RTL3	-1.66681	2.59E-05	0.000369	-4.20655	Down	retrotransposon Gag like 3
NXPH4	-1.66465	7.42E-07	1.91E-05	-4.95008	Down	neurexophilin 4
TP73	-1.65689	6.54E-05	0.000791	-3.99229	Down	tumor protein p73
RHBDL2	-1.65396	0.000742	0.005792	-3.37339	Down	rhomboid like 2
TRPV3	-1.65149	2.07E-06	4.48E-05	-4.74648	Down	transient receptor potential cation channel subfamily V member 3

SLC6A17	-1.64997	0.002246	0.014052	-3.05566	Down	solute carrier family 6 member 17
ECT2L	-1.64828	4.20E-06	8.05E-05	-4.60146	Down	epithelial cell transforming 2 like
PRF1	-1.64536	0.000367	0.003289	-3.56251	Down	perforin 1
PROS1	-1.64427	1.05E-20	9.87E-18	-9.33116	Down	protein S
FAM181B	-1.6414	3.94E-05	0.000523	-4.11108	Down	family with sequence similarity 181 member B
RFX8	-1.63571	0.003768	0.021159	-2.89697	Down	regulatory factor X8
C10orf67	-1.63283	6.90E-05	0.000826	-3.97984	Down	chromosome 10 open reading frame 67
CD7	-1.62592	0.009309	0.042632	-2.6005	Down	CD7 molecule
CRHBP	-1.62003	7.58E-07	1.94E-05	-4.94577	Down	corticotropin releasing hormone binding protein
SLC44A5	-1.61944	0.008639	0.040253	-2.62602	Down	solute carrier family 44 member 5
BRSK1	-1.618	8.19E-10	5.30E-08	-6.14117	Down	BR serine/threonine kinase 1
SLC24A5	-1.60402	0.003222	0.018742	-2.94568	Down	solute carrier family 24 member 5
PHLDA1	-1.59329	3.41E-09	1.80E-07	-5.91037	Down	pleckstrin homology like domain family A member 1
IPCEF1	-1.59282	2.78E-06	5.72E-05	-4.68664	Down	interaction protein for cytohesin exchange factors 1
ARID5A	-1.59249	2.40E-11	2.55E-09	-6.67909	Down	AT-rich interaction domain 5A
PRRX2	-1.59197	9.03E-06	0.000153	-4.43925	Down	paired related homeobox 2
HAUS7	-1.59073	0.000147	0.001542	-3.79586	Down	HAUS augmin like complex subunit 7
SLC22A7	-1.59053	0.004924	0.02605	-2.81198	Down	solute carrier family 22 member 7
YIPF7	-1.59033	0.009801	0.04427	-2.58277	Down	Yip1 domain family member 7
FREM1	-1.58947	6.12E-12	7.41E-10	-6.87679	Down	FRAS1 related extracellular matrix 1
SLC26A4	-1.58555	4.82E-07	1.32E-05	-5.0333	Down	solute carrier family 26 member 4
ESR1	-1.58555	6.67E-10	4.46E-08	-6.17376	Down	estrogen receptor 1
SAMD11	-1.58368	1.32E-06	3.09E-05	-4.83676	Down	sterile alpha motif domain containing 11
P2RY8	-1.58181	1.20E-15	4.41E-13	-8.00436	Down	P2Y receptor family member 8
ANKRD33B	-1.5746	1.50E-07	4.90E-06	-5.25286	Down	ankyrin repeat domain 33B
ZMYND15	-1.56869	0.004639	0.024847	-2.83109	Down	zinc finger MYND-type containing 15
MYL1	-1.56818	0.002005	0.012902	-3.08954	Down	myosin light chain 1
NOS2	-1.56717	0.001336	0.009332	-3.20811	Down	nitric oxide synthase 2
EPHX3	-1.56568	0.009698	0.04393	-2.58643	Down	epoxide hydrolase 3
CPXM2	-1.56566	2.84E-05	0.000398	-4.18631	Down	carboxypeptidase X, M14 family member 2
MYOZ1	-1.56414	8.37E-05	0.000968	-3.93352	Down	myozenin 1
SNCA	-1.56009	1.13E-11	1.30E-09	-6.78896	Down	synuclein alpha
CDHR5	-1.55895	1.14E-06	2.74E-05	-4.86505	Down	cadherin related family member 5
APOL4	-1.55836	6.86E-07	1.78E-05	-4.96526	Down	apolipoprotein L4
CXCL14	-1.55448	0.000319	0.002924	-3.59965	Down	C-X-C motif chemokine ligand 14
GZMA	-1.55144	0.008555	0.039964	-2.62935	Down	granzyme A
FOXI2	-1.55128	0.002803	0.01684	-2.9885	Down	forkhead box I2
TP63	-1.54935	3.57E-06	7.04E-05	-4.63508	Down	tumor protein p63
LRRC77P	-1.54742	4.01E-08	1.56E-06	-5.49056	Down	leucine rich repeat containing 77, pseudogene
KCNN3	-1.54203	6.45E-11	5.92E-09	-6.53291	Down	potassium calcium-activated channel subfamily N member 3
PLXDC1	-1.5404	4.27E-21	4.41E-18	-9.42571	Down	plexin domain containing 1
FSCN1	-1.53751	1.67E-14	4.11E-12	-7.67392	Down	fascin actin-bundling protein 1

TAC4	-1.53747	0.010288	0.045922	-2.566	Down	tachykinin precursor 4
SHANK2	-1.53095	0.002729	0.016491	-2.99671	Down	SH3 and multiple ankyrin repeat domains 2
CUBN	-1.52536	1.90E-05	0.000284	-4.27577	Down	cubilin
ENPP6	-1.52098	0.010521	0.046693	-2.55821	Down	ectonucleotide pyrophosphatase/phosphodiesterase 6
COL9A2	-1.51864	1.63E-06	3.69E-05	-4.79442	Down	collagen type IX alpha 2 chain
SEMA3D	-1.51514	0.000238	0.002304	-3.67449	Down	semaphorin 3D
CLIC6	-1.51495	7.63E-05	0.000897	-3.95577	Down	chloride intracellular channel 6
HAS3	-1.51252	8.53E-06	0.000146	-4.45153	Down	hyaluronan synthase 3
GABRE	-1.51238	1.40E-14	3.60E-12	-7.69647	Down	gamma-aminobutyric acid type A receptor subunit epsilon
GFRA3	-1.50943	0.001296	0.009141	-3.21689	Down	GDNF family receptor alpha 3
EPHA3	-1.5088	1.36E-14	3.56E-12	-7.69964	Down	EPH receptor A3
BRINP1	-1.50667	1.38E-06	3.22E-05	-4.82727	Down	BMP/retinoic acid inducible neural specific 1
COL8A2	-1.50558	3.64E-10	2.67E-08	-6.26873	Down	collagen type VIII alpha 2 chain
FAM216B	-1.5017	0.010594	0.046925	-2.55582	Down	family with sequence similarity 216 member B
EXOC3L4	-1.49629	0.009788	0.044239	-2.58322	Down	exocyst complex component 3 like 4
EXTL1	-1.4958	1.42E-09	8.62E-08	-6.0527	Down	exostosin like glycosyltransferase 1
DLEU2	-1.48588	1.20E-05	0.000193	-4.37796	Down	deleted in lymphocytic leukemia 2
PDE6A	-1.4837	3.22E-06	6.51E-05	-4.65596	Down	phosphodiesterase 6A
SYTL2	-1.48205	1.25E-13	2.43E-11	-7.4113	Down	synaptotagmin like 2
HSD17B14	-1.48189	6.84E-08	2.50E-06	-5.39539	Down	hydroxysteroid 17-beta dehydrogenase 14
LRRTM3	-1.47765	0.008089	0.038399	-2.64834	Down	leucine rich repeat transmembrane neuronal 3
TMEM45B	-1.47762	0.007825	0.037436	-2.65951	Down	transmembrane protein 45B
ACE	-1.4731	1.73E-07	5.58E-06	-5.22604	Down	angiotensin I converting enzyme
SLC9C1	-1.47254	7.34E-05	0.00087	-3.96501	Down	solute carrier family 9 member C1
OGDHL	-1.47099	0.003474	0.019849	-2.92233	Down	oxoglutarate dehydrogenase L
NT5E	-1.47026	4.40E-10	3.17E-08	-6.23918	Down	5'-nucleotidase ecto
PDE5A	-1.46609	4.15E-22	5.62E-19	-9.66743	Down	phosphodiesterase 5A
PTGFR	-1.46562	0.000137	0.001453	-3.8133	Down	prostaglandin F receptor
GLIS1	-1.4642	0.001922	0.012462	-3.10208	Down	GLIS family zinc finger 1
CACNA1C-AS4	-1.46312	0.000304	0.002811	-3.61218	Down	CACNA1C antisense RNA 4
GRIA3	-1.46008	0.001304	0.009187	-3.21508	Down	glutamate ionotropic receptor AMPA type subunit 3
SSPOP	-1.45895	3.82E-06	7.48E-05	-4.62102	Down	SCO-spondin, pseudogene
PLCE1	-1.45784	3.28E-12	4.33E-10	-6.96521	Down	phospholipase C epsilon 1
SCG2	-1.45495	0.003119	0.018261	-2.95578	Down	secretogranin II
AMPH	-1.4535	1.54E-08	6.80E-07	-5.65759	Down	amphiphysin
PAK1	-1.45013	9.13E-08	3.19E-06	-5.34328	Down	p21 (RAC1) activated kinase 1
KCNA5	-1.44658	8.54E-12	1.01E-09	-6.82911	Down	potassium voltage-gated channel subfamily A member 5
CAPN3	-1.44627	1.08E-05	0.000176	-4.40028	Down	calpain 3
GNB3	-1.44437	7.60E-08	2.74E-06	-5.37631	Down	G protein subunit beta 3
SOX8	-1.43922	2.05E-05	0.000302	-4.25946	Down	SRY-box transcription factor 8
APOE	-1.43161	0.000627	0.005059	-3.41961	Down	apolipoprotein E
SV2B	-1.43052	1.80E-06	4.01E-05	-4.77462	Down	synaptic vesicle glycoprotein 2B

SDSL	-1.42997	3.99E-16	1.57E-13	-8.13902	Down	serine dehydratase like
TMEM233	-1.42801	0.001266	0.008971	-3.22348	Down	transmembrane protein 233
MOXD1	-1.42647	2.48E-08	1.03E-06	-5.57494	Down	monooxygenase DBH like 1
GDF9	-1.42458	0.001954	0.012639	-3.09706	Down	growth differentiation factor 9
ADAMTS8	-1.4226	3.03E-06	6.17E-05	-4.66877	Down	ADAM metallopeptidase with thrombospondin type 1 motif 8
F2RL3	-1.42044	0.01049	0.046612	-2.55926	Down	F2R like thrombin or trypsin receptor 3
P2RX1	-1.40797	0.002581	0.015724	-3.01367	Down	purinergic receptor P2X 1
BCL6B	-1.40443	1.54E-08	6.80E-07	-5.65742	Down	BCL6B transcription repressor
F2R	-1.40364	1.95E-10	1.56E-08	-6.36491	Down	coagulation factor II thrombin receptor
SOX15	-1.40199	1.92E-07	6.00E-06	-5.20716	Down	SRY-box transcription factor 15
GUCA1C	-1.40145	0.011022	0.048254	-2.54201	Down	guanylate cyclase activator 1C
SETBP1-DT	-1.40135	0.000141	0.00149	-3.80624	Down	SETBP1 divergent transcript
ANKS1B	-1.39718	0.000183	0.001854	-3.74091	Down	ankyrin repeat and sterile alpha motif domain containing 1B
SV2A	-1.39678	8.15E-08	2.90E-06	-5.36388	Down	synaptic vesicle glycoprotein 2A
SEZ6L2	-1.39483	5.12E-06	9.51E-05	-4.55972	Down	seizure related 6 homolog like 2
IQCA1	-1.39455	0.001308	0.009204	-3.21428	Down	IQ motif containing with AAA domain 1
EGR2	-1.39417	0.000136	0.001446	-3.81474	Down	early growth response 2
SYT12	-1.38866	0.002916	0.0173	-2.97642	Down	synaptotagmin 12
RASL11B	-1.3879	2.25E-07	6.86E-06	-5.17768	Down	RAS like family 11 member B
COLEC12	-1.38753	2.24E-12	3.11E-10	-7.01842	Down	collectin subfamily member 12
FAM107B	-1.38688	8.10E-13	1.29E-10	-7.15947	Down	family with sequence similarity 107 member B
GLI1	-1.38443	0.00011	0.00122	-3.86639	Down	GLI family zinc finger 1
KIAA1755	-1.3831	3.75E-10	2.73E-08	-6.26401	Down	KIAA1755
SNCAIP	-1.38061	2.72E-06	5.63E-05	-4.69078	Down	synuclein alpha interacting protein
NRK	-1.38057	1.49E-08	6.62E-07	-5.66294	Down	Nik related kinase
SAMD12	-1.37912	3.54E-09	1.86E-07	-5.90419	Down	sterile alpha motif domain containing 12
SRRM4	-1.37811	1.85E-07	5.85E-06	-5.21358	Down	serine/arginine repetitive matrix 4
NTM	-1.37328	2.19E-06	4.69E-05	-4.73483	Down	neurotrimin
CACNG8	-1.37083	0.00628	0.031618	-2.73282	Down	calcium voltage-gated channel auxiliary subunit gamma 8
PRDM1	-1.36772	7.21E-06	0.000126	-4.48748	Down	PR/SET domain 1
PTPRH	-1.36528	5.71E-06	0.000104	-4.53697	Down	protein tyrosine phosphatase receptor type H
TNNT1	-1.36382	1.24E-12	1.82E-10	-7.10135	Down	troponin T1, slow skeletal type
CSPG4P13	-1.36315	5.70E-08	2.15E-06	-5.42794	Down	chondroitin sulfate proteoglycan 4 pseudogene 13
DCLK3	-1.36216	0.00213	0.013513	-3.07151	Down	doublecortin like kinase 3
MSH4	-1.3613	0.010965	0.048082	-2.54383	Down	mutS homolog 4
RPLP0P2	-1.35449	0.00171	0.011381	-3.13654	Down	ribosomal protein lateral stalk subunit P0 pseudogene 2
OAS3	-1.3536	4.90E-11	4.68E-09	-6.57383	Down	2'-5'-oligoadenylate synthetase 3
SCT	-1.35259	0.005881	0.029933	-2.75432	Down	secretin
SSC5D	-1.35241	2.25E-12	3.11E-10	-7.01809	Down	scavenger receptor cysteine rich family member with 5 domains
ANGPTL8	-1.35235	0.003603	0.020443	-2.91101	Down	angiopoietin like 8
NRIP3	-1.35169	3.10E-08	1.25E-06	-5.53585	Down	nuclear receptor interacting protein 3
C1QTNF12	-1.35165	0.000817	0.006244	-3.34681	Down	C1q and TNF related 12

HLA-DPA1	-1.35043	1.73E-09	1.01E-07	-6.02145	Down	major histocompatibility complex, class II, DP alpha 1
FCN1	-1.34983	0.002116	0.013442	-3.07339	Down	ficolin 1
DMC1	-1.34937	4.92E-06	9.19E-05	-4.56808	Down	DNA meiotic recombinase 1
APOLD1	-1.34638	0.006941	0.034147	-2.69967	Down	apolipoprotein L domain containing 1
HMCN2	-1.34618	2.51E-09	1.39E-07	-5.96055	Down	hemicentin 2
EGR1	-1.34558	0.001977	0.012753	-3.09369	Down	early growth response 1
CCDC13	-1.34266	0.003103	0.018203	-2.95735	Down	coiled-coil domain containing 13
QPCT	-1.33864	5.30E-05	0.00066	-4.0421	Down	glutaminyl-peptide cyclotransferase
MYO5B	-1.33625	1.12E-05	0.000182	-4.39205	Down	myosin VB
TFPI2	-1.33386	0.000598	0.004862	-3.43272	Down	tissue factor pathway inhibitor 2
MUC20	-1.33085	0.002154	0.013625	-3.0681	Down	mucin 20, cell surface associated
LSP1	-1.33079	1.67E-18	1.06E-15	-8.77761	Down	lymphocyte specific protein 1
ISLR	-1.32932	1.43E-14	3.60E-12	-7.69384	Down	immunoglobulin superfamily containing leucine rich repeat
CASP4LP	-1.32568	4.26E-05	0.000558	-4.09311	Down	caspase 4 like, pseudogene
PLPPR4	-1.32424	0.000822	0.00627	-3.34518	Down	phospholipid phosphatase related 4
ZNF541	-1.32309	7.86E-05	0.00092	-3.94852	Down	zinc finger protein 541
CRABP2	-1.3219	0.000447	0.003867	-3.51094	Down	cellular retinoic acid binding protein 2
ATCAY	-1.32126	0.002025	0.013001	-3.08648	Down	ATCAY kinesin light chain interacting caytaxin
PRR22	-1.31968	0.006208	0.031322	-2.7366	Down	proline rich 22
P2RX6	-1.3193	4.56E-05	0.000586	-4.07718	Down	purinergic receptor P2X 6
PSD	-1.31315	0.000373	0.003333	-3.55816	Down	pleckstrin and Sec7 domain containing
SLC1A7	-1.30464	0.000968	0.007175	-3.2997	Down	solute carrier family 1 member 7
DUSP6	-1.30463	4.15E-11	4.03E-09	-6.59872	Down	dual specificity phosphatase 6
SLC6A1	-1.29776	2.73E-09	1.47E-07	-5.94701	Down	solute carrier family 6 member 1
DKK2	-1.29423	0.003532	0.020128	-2.91717	Down	dickkopf WNT signaling pathway inhibitor 2
RAB39B	-1.29287	0.009304	0.042619	-2.60068	Down	RAB39B, member RAS oncogene family
IL34	-1.29173	1.08E-06	2.61E-05	-4.87712	Down	interleukin 34
TNFSF13B	-1.29043	0.00066	0.005275	-3.40581	Down	TNF superfamily member 13b
PRR16	-1.28945	8.28E-15	2.39E-12	-7.76316	Down	proline rich 16
ALMS1-IT1	-1.28494	0.005781	0.029491	-2.75995	Down	ALMS1 intronic transcript 1
BOC	-1.2768	8.55E-12	1.01E-09	-6.82893	Down	BOC cell adhesion associated, oncogene regulated
INHBE	-1.27612	0.007857	0.03753	-2.65815	Down	inhibin subunit beta E
IER3	-1.27428	9.84E-07	2.42E-05	-4.89478	Down	immediate early response 3
GPR27	-1.27393	1.34E-06	3.13E-05	-4.83326	Down	G protein-coupled receptor 27
GJC2	-1.27176	1.10E-07	3.72E-06	-5.30856	Down	gap junction protein gamma 2
MDGA1	-1.2713	2.68E-11	2.79E-09	-6.66331	Down	MAM domain containing glycosylphosphatidylinositol anchor 1
LCK	-1.2706	0.004089	0.022515	-2.87124	Down	LCK proto-oncogene, Src family tyrosine kinase
RUNX1	-1.27016	8.73E-07	2.18E-05	-4.91839	Down	RUNX family transcription factor 1
LTB	-1.26913	0.007803	0.037364	-2.66046	Down	lymphotoxin beta
ZC3H12B	-1.26901	3.56E-06	7.04E-05	-4.6358	Down	zinc finger CCCH-type containing 12B
NUP62CL	-1.2637	4.79E-05	0.000611	-4.06559	Down	nucleoporin 62 C-terminal like
RSAD2	-1.26293	4.92E-06	9.19E-05	-4.56836	Down	radical S-adenosyl methionine domain containing 2

NRXN2	-1.26176	0.000147	0.001544	-3.79546	Down	neurexin 2
REC8	-1.25896	3.31E-08	1.32E-06	-5.52402	Down	REC8 meiotic recombination protein
CYP11A1	-1.25322	0.000315	0.0029	-3.60239	Down	cytochrome P450 family 11 subfamily A member 1
TNFRSF4	-1.25287	0.000251	0.002402	-3.66084	Down	TNF receptor superfamily member 4
ACHE	-1.25085	4.88E-05	0.000619	-4.06124	Down	acetylcholinesterase (Cartwright blood group)
SCN8A	-1.25013	0.001178	0.008443	-3.24426	Down	sodium voltage-gated channel alpha subunit 8
KIF1A	-1.24594	0.006481	0.032436	-2.7224	Down	kinesin family member 1A
TREH	-1.24543	0.003648	0.020645	-2.90711	Down	trehalase
UNC13D	-1.24488	1.43E-05	0.000223	-4.33899	Down	unc-13 homolog D
CPEB1	-1.24447	0.009503	0.043222	-2.59339	Down	cytoplasmic polyadenylation element binding protein 1
KCNIP1	-1.24326	3.45E-05	0.000467	-4.14123	Down	potassium voltage-gated channel interacting protein 1
PICART1	-1.24198	0.003929	0.021862	-2.88377	Down	p53 inducible cancer associated RNA transcript 1
TPM3	-1.24075	0.004269	0.023283	-2.85754	Down	tropomyosin 3
TENM1	-1.23996	0.001112	0.008051	-3.26063	Down	teneurin transmembrane protein 1
SCARA3	-1.23987	5.35E-10	3.71E-08	-6.20844	Down	scavenger receptor class A member 3
MEST	-1.23709	2.10E-07	6.43E-06	-5.19065	Down	mesoderm specific transcript
STX1B	-1.23163	0.000902	0.006762	-3.31939	Down	syntaxin 1B
MYCBPAP	-1.22985	0.001407	0.009725	-3.19323	Down	MYCBP associated protein
MX2	-1.22635	1.33E-09	8.14E-08	-6.06419	Down	MX dynamin like GTPase 2
GABRP	-1.22572	0.007743	0.037185	-2.66308	Down	gamma-aminobutyric acid type A receptor subunit pi
COL12A1	-1.22564	4.75E-09	2.41E-07	-5.8558	Down	collagen type XII alpha 1 chain
C9orf131	-1.22552	0.001146	0.008257	-3.25204	Down	chromosome 9 open reading frame 131
ITGAX	-1.21952	0.006853	0.033812	-2.70393	Down	integrin subunit alpha X

Table 2 The enriched GO terms of the up and down regulated differentially expressed genes

GO ID	CATEGORY	GO Name	adjusted_p_value	negative_log10_of_adjusted_p_value	Gene Count	Gene
				Up regulated genes		
GO:0050896	BP	response to stimulus	8.83E-08	7.053914375	232	SAA1,FAM83B,RNASE2,SERPINA3,GAL,IL1RL1,PTPRN,MYH6,CD177,HOPX,ALOX15B,EREG,FCN3,KCNIP2,SSTR5,SFRP5,F5,CHRDL2,SLAMF1,SRARP,CHRNA4,MARCO,DNER,RAB39A,SPINK1,MGST1,CD163,RGR,PLA2G2A,TSPEAR,TFRC,SCN1A,CPNE4,AQP4,CCN5,FER1L6,PCK1,PKHD1L1,VDR,BEX5,SERPINE1,ACVR1C,AZGP1,AOX1,VSIG4,KCNK3,CAMSAP3,FGF12,AGBL4,ELANE,GRB14,TMIGD3,FKBP5,ADAM11,MFSD2A,RBP4,BLM,HMGCS2,NSG1,CPNE5,MOG,C3,FGFR4,ITLN1,XRCC4,IL18R1,RTN4RL1,SUSD4,TIMP4,LYVE1,GRIP1,IL20RA,HCRTR1,PLA2G4F,TU

						BB4B,ELAPOR1,LGR6,OPN4,SOX2,SHC4,SLPI,TWIST2,NPPC,ITPKA,PITX3,PLP2,EIF4EBP1,SPP1,CHL1,CD109,S1PR3,TUBA1B,PRODH,BMP7,NECTIN1,SLC7A11,TGFA,KCNK2,PPP1R1A,ADGRD1,FAM83F,SBK2,TFEC,CFD,MLXIPL,INSYN1,AGTR1,PTX3,SEPTIN4,HMOX2,EPHB2,GPD1L,DIRAS3,CLIC3,ZNF703,DIRAS1,SLC2A1,ITGA7,ATP2A2,GSTM3,TGM2,FHL2,CD38,WNK3,GRIN2A,FGF7,FN1,PCARE,ENTPD6,OSR1,CMTM5,PPP1R14B,HCN4,STXBP2,SLC5A1,C1QA,CRLF1,POMC,APOB,OLFM4,BMAL1,HEY2,C1QC,RAP1GAP,IGFBP2,CHGB,ARG2,S100A10,FCGR3A,GPSM2,LPCAT3,IL15RA,REPS2,MLF1,RORB,GPD1,FABP4,PTGS1,QRFPR,C1QTNF1,LMCD1,CASKIN1,SDK1,TPO,LRP4,PLEKHN1,LOX,ADAMTS5,CD63,TSPAN2,ECE2,HAS2,DMPK,NQO1,KLHL31,RGS9BP,PROCR,PTGDR,SIGLEC1,CAMK1D,RPS6KA2,RALGPS2,NGFR,PRDX6,EDN1,DHCR24,PDPN,AKR1C1,HSPB7,RASSF7,CTSB,GLRX2,LRRC32,ITGA11,PRKCD,FCER1G,RPL27,RAMP1,TIFA,TSKU,SASH3,LGALS3,NSDHL,ABCG4,VIPR1,KCNH2,EPB41L4B,SLAMF8,KCNK1,FTH1,GGT5,NID1,IMPA2,CREB3L1,FRK,F8,NOCT,HMOX1,AKR1B1,ZDHHC9,ACACB,NUDT4,ALPL,BCL6,MPST,GAREM1,CD276,CABP1,HIF3A,RNASE6,PMVK,EPN1
GO:0007275	BP	multicellular organism development	6.45987E-06	5.189776108	135	GAL,PTPRN,MYH6,HOXA3,HOPX,ALOX15B,EREG,KCNIP2,SFRP5,CHRDL2,DNER,LRRN3,C1QL1,TFRC,SCN1A,PCK1,ETNK2,VDR,SERPINE1,ACVR1C,CAMSAP3,FGF12,AGBL4,SPOCK1,FREM2,MFSD2A,RBP4,HMGCS2,CPNE5,SERPINA5,MOG,C3,SMOC1,FGFR4,XRCC4,VIT,HOXB4,RTN4RL1,TRPC4,GRIP1,RNF157,ELN,LGR6,OPN4,SOX2,KIF26B,NPPC,ITPKA,PITX3,ADAMTS2,SPP1,CHL1,CD109,S1PR3,TOX,BMP7,NECTIN1,CPAMD8,SLC7A11,TGFA,KCNK2,MYOT,C1QL3,AGTR1,PTX3,SEPTIN4,EPHB2,SLC2A1,ITGA7,GSTM3,TENT5C,TGM2,FHL2,CD38,KLHL3,GRIN2A,FGF7,FN1,PCARE,SMYD1,MATN3,OSR1,HCN4,C1QA,CRLF1,APOB,CHADL,BMAL1,HEY2,C1QC,RAP1GAP,NINJ2,ARG2,S100A10,IL15RA,RORB,SDK1,TPO,PPIL1,LRP4,LOX,ADAMTS5,TSPAN2,HAS2,LAMB3,PTGDR,CAMK1D,RPS6KA2,

						NGFR,EDN1,EBP,DHCR24,PDPN,HSPB7,SLC25A34,MMP19,MYL3,RAMP1,TSKU,SASH3,NSDHL,GPSM1,SLAMF8,NID1,CREB3L1,NOCT,HMOX1,AKR1B1,ACACB,ALPL,BCL6,MPST,PALLD,HIF3A,EPN1
GO:0071944	CC	cell periphery	2.36E-14	13.62695566	200	SERPINA3,IL1RL1,PTPRN,CACNA1E,CD177,ALOX15B,EREG,LAD1,FCN3,KCNIP2,SSTR5,F5,FIBCD1,SLAMF1,CHRNA4,IGSF23,CFAP95,FREM3,CORIN,CATSPERB,SLCO4A1,MARCO,DNER,RAB39A,MGST1,CD163,RGR,PLA2G2A,TSPEAR,LRRN3,TFRC,SCN1A,CPNE4,AQP4,STAC2,CCN5,PKHD1L1,SERPINE1,ACVR1C,AZGP1,KCNK13,KCNK3,ELANE,GRB14,FREM2,SVOP,ART1,CA14,TMIGD3,SLC38A4,ADAM11,MFSD2A,SYN2,ADH1B,CDHR3,NSG1,CPNE5,MELTF,SERPINA5,MOG,C3,SMOC1,FGFR4,ITLN1,VIT,IL18R1,RTN4RL1,TRPC4,TIMP4,LYVE1,GRIP1,IL20RA,ELN,HCRTR1,PLA2G4F,ELAPOR1,LGR6,NALF2,OPN4,SHC4,SLPI,CPM,PLP2,ADAMTS2,GOLGA7B,CHL1,CD109,S1PR3,BMP7,NECTIN1,CPAMD8,SLC7A11,TGFA,KCNA7,KCNK2,PRIMA1,ADGRD1,MYOT,MS4A4A,PARVB,AGTR1,PTX3,SEPTIN4,HMOX2,EPHB2,GPD1L,DIRAS3,CACNA2D3,DIRAS1,SLC2A1,ITGA7,NALCN,SLC44A3,ATP2A2,TGM2,CD38,SLC7A1,SIRPB2,MEGF9,GRIN2A,FN1,MARVELD2,EPN3,MATN3,ENTPD6,OSR1,HCN4,PRRG4,SLC4A3,LRRC7,STXBP2,SLC5A1,C1QA,CRLF1,APOB,OLFM4,CHADL,C1QC,IGFBP2,NINJ2,S100A10,FCGR3A,GPSM2,IL15RA,REPS2,AIF1L,QRFPR,C1QTNF1,SDK1,TPO,LRP4,PLEKHN1,LOX,ADAMTS5,CD63,ADAMTS15,RPSA,TSPAN2,ECE2,HAS2,DMPK,LAMB3,PROCR,PTGDR,SIGLEC1,DDN,SLC29A2,RALGPS2,NGFR,PDPN,MMP19,CTSB,LRRC32,ITGA11,PRKCD,FCER1G,SLCO2A1,SLC6A6,SLC9A7,RAMP1,LGALS3,STEAP4,ABCG4,VIPR1,KCNH2,GPSM1,EPB41L4B,KCNK1,GGT5,NID1,FRK,F8,ALPL,SH3KBP1,GAREM1,PALLD,CD276,CABP1,HIF3A,EPN1
GO:0016020	CC	membrane	3.58E-08	7.445873461	252	FAM83B,IL1RL1,PTPRN,CACNA1E,CD177,ALOX15B,EREG,FCN3,KCNIP2,C11ORF87,SSTR5,DHRS7C,F5,SCGN,KCNK12,FIBCD1,SLAMF1,CHRNA4,IGSF23,CFAP95,FREM3,SERTM1,CORIN,CATSPERB,S

						LCO4A1,MARCO,DNER,RAB39A,MGST1,CD163,DHRS9,RGR,FAM209B,PLA2G2A,TSPEAR,LRRN3,TFRC,SCN1A,CPNE4,CHDH,AQP4,STAC2,FER1L6,CYP4B1,PKHD1L1,SERPINE1,ACVR1C,AZGP1,CHST9,KCNK13,VSIG4,KCNK3,GALNT15,GRB14,FREM2,RHBDL3,HRCT1,SGPP2,SVOP,ART1,CA14,HS3ST2,TMIGD3,FKBP5,SLC38A4,ADAM11,MFSD2A,SYN2,ADH1B,CDHR3,NSG1,HOGA1,CPNE5,MELTF,SERPINA5,MOG,C3,FGFR4,ITLN1,TMEM52,IL18R1,RTN4RL1,SUSD4,TRPC4,LYVE1,GRIP1,IL20RA,PTDSS1,HCRTR1,PLA2G4F,QSOX1,ELAPOR1,LGR6,NALF2,OPN4,PEBP4,SHC4,SNX22,CPM,PLP2,CHST7,GOLGA7B,CHL1,CD109,HOOK1,S1PR3,C1QB,PRODH,NECTIN1,B3GNT7,BEAN1,CPAMD8,SLC7A11,TGFA,KCNA7,TMEM132B,KCNK2,PRIMA1,ADGRD1,MYOT,SHISA4,MS4A4A,LDHA,PARVB,AGTR1,SEPTIN4,HMOX2,EPHB2,GPD1L,DIRAS3,CACNA2D3,CLIC3,DIRAS1,SLC2A1,ITGA7,NALCN,SLC44A3,ATP2A2,TGM2,RPLP0,CD38,SLC7A1,SIRPB2,MEGF9,GRIN2A,FN1,SERINC2,MARVELD2,EPN3,ENTPD6,CMTM5,HCN4,PRRG4,SLC4A3,LRRC7,STXBP2,SLC5A1,CRLF1,APOB,TMEM178B,OLFM4,TMEM26,RAP1GAP,IGFBP2,NINJ2,ORMDL2,S100A10,FCGR3A,TMTC1,GPSM2,LPCAT3,IL15RA,REPS2,CHPF,AIF1L,PTGS1,QRFPR,C1QTNF1,SDK1,TPO,LRP4,PLEKHN1,NFXL1,CD63,RPSA,TSPAN2,ECE2,HAS2,DMPK,STXBP6,TMEM37,SLC17A9,RGS9BP,PROCR,PTGDR,SIGLEC1,DDN,SLC29A2,RALGPS2,NGFR,RPS2,CENPV,PRDX6,EBP,DHCR24,PDPN,SLC25A34,CTSB,LRRC32,SMCO4,ITGA11,PRKCD,FCER1G,RPL27,SLCO2A1,SLC6A6,SLC9A7,RAMP1,LGALS3,NSDHL,STEAP4,RPS5,ABCG4,VIPR1,KCNH2,GPSM1,LPCAT4,COMTD1,EPB41L4B,SLAMF8,ZDHHC23,KCNK1,FTH1,GGT5,CREB3L1,FRK,F8,HMOX1,ZDHHC9,ACACB,ALPL,SLC25A19,SH3KBP1,GAREM1,PALLD,CD276,CABP1,HIF3A,RETSAT,TKT,PMVK,EPN1
GO:0016491	MF	oxidoreductase activity	0.011001055	1.958565663	31	ALOX15B,DHRS7C,MGST1,DHRS9,CHDH,CYP4B1,AOX1,ADH1B,QSOX1,PRODH,LDHA,HMOX2,GPD1L,ALDH1L1,GPD1,PTGS1,TPO,LOX,NQO1,PRDX6,DHCR24,AKR1

						C1,GLRX2,NSDHL,STEAP4,FTH1,F8,HMOX1,AKR1B1,NQO2,RETSAT
GO:0005215	MF	transporter activity	0.023061571	1.637111108	43	CACNA1E,KCNIP2,KCNK12,CHRNA4,SLCO4A1,SCN1A,AQP4,AZGP1,KCNK13,KCNK3,SVOP,SLC38A4,MFSD2A,RBP4,TRPC4,NALF2,PLP2,SLC7A11,KCNA7,KCNK2,CACNA2D3,CLIC3,SLC2A1,NALCN,SLC44A3,ATP2A2,SLC7A1,GRIN2A,HCN4,SLC4A3,SLC5A1,APOB,FABP4,TMEM37,SLC17A9,SLC29A2,SLCO2A1,SLC6A6,SLC9A7,ABCG4,KCNH2,KCNK1,SLC25A19
				Down regulated genes		
GO:0032501	BP	multicellular organismal process	1.37E-18	17.86328493	241	EDN3,CST2,SEZ6L,CUX2,ESM1,MSTN,LYPD1,TNMD,IL31RA,SFRP4,CBLN4,CD1C,IRX1,KCNK10,TRPM8,CST1,UCMA,FOXA1,RSPO2,ARMS2,LEF1,ALOX15,CTLA4,SLITRK4,SLC4A8,MYH2,PCDH15,PENK,OIT3,IL1B,FCER1A,HBB,RXFP2,ATP1A4,IRX2,COL10A1,DPYSL5,SCUBE2,PCSK1N,ECEL1,CTSG,MUC13,CX3CR1,CRACD,HS3ST5,PLD4,UGT8,WNT9A,FRZB,FMN2,ZNF365,CMA1,E2F7,CYTL1,RGS4,THBS4,CRISPLD1,F2RL2,GDF6,KIF5A,ENPP2,GDF15,TGFB2,C1QTNF3,ODF3,CHRDL1,CCDC63,SLC5A7,KIT,APLNR,NELL2,ANKRD24,ODAD2,TMEM163,FAT3,MYOC,CXCL10,MME,BDNF,RIPOR2,NGEF,LAMC3,EGR3,CCDC62,PTGER3,LRRN1,SULF1,LEFTY2,PTN,CHD5,LMX1A,OLR1,THY1,CHRNA3,LOXHD1,ABCG2,NTNG2,MDK,CATSPER1,ANGPTL7,IQCN,SP5,DNAH5,TLL2,RASSF10,PTCH2,TNFRSF11B,DIO2,TAGLN3,PTPRR,DNAAF3,PCDH17,INHBA,PMAIP1,COL14A1,SYT17,CHRM3,SMOC2,PLAC8,GPR173,PHOSPHO1,GATM,NDP,MPIG6B,TTLL7,HTR2B,UCHL1,LUM,MID1,CSPG5,OPCML,IRX6,S1PR5,B3GNT5,TP73,TRPV3,SLC6A17,PRF1,PROS1,RFX8,CD7,CRHBP,BRSK1,ARID5A,FREM1,SLC26A4,ESR1,ZMYND15,MYL1,NOS2,MYOZ1,SNCA,TP63,PLXDC1,TAC4,SHANK2,CUBN,COL9A2,SEMA3D,GFRA3,EPHA3,BRINP1,COL8A2,EXTL1,PDE6A,LRRTM3,ACE,SLC9C1,NT5E,PDE5A,PTGFR,GLIS1,PLCE1,SCG2,PAK1,KCNA5,CAPN3,GNB3,SOX8,APOE,GDF9,F2RL3,P2RX1,BCL6B,F2R,SOX15,GUCA1C,SEZ6L2,EGR2,GLI1,KIAA1755,SRRM4,NTM,C

						ACNG8,PRDM1,TNNT1,MSH4,OAS3,SCT,SSC5D,HLA-DPA1,FCN1,DMC1,APOLD1,HMCN2,EGR1,MYO5B,TFPI2,PLPPR4,ZNF541,CRABP2,ATCAY,P2RX6,PSD,SLC1A7,DUSP6,SLC6A1,DKK2,IL34,TNFSF13B,BOC,IER3,GJC2,MDGA1,LCK,RUNX1,LTB,RSAD2,NRXN2,REC8,TNFRSF4,ACHE,SCN8A,KIF1A,UNC13D,TPM3,TENM1,STX1B,MYCBPAP,COL12A1,ITGAX
GO:0007154	BP	cell communication	4.11E-10	9.386286619	192	RFPL4A,EDN3,SEZ6L,CUX2,ESM1,MSTN,LYPD1,IL31RA,RFPL4AL1,SFRP4,SHISA2,CXCL11,KCNK10,TRPM8,UCMA,FOXA1,IL22RA2,RSPO2,LEF1,ALOX15,CTLA4,SLC4A8,PENK,FCGR3B,IL1B,FCER1A,RXFP2,ATP1A4,DPYSL5,CDH8,SCUBE2,PCSK1N,DLGAP1,ECEL1,CTSG,CX3CR1,APCDD1L,WNT9A,FRZB,FMN2,GZMB,CACNA1B,BCL2A1,E2F7,CYTL1,RGS4,FMOD,THBS4,HSH2D,ATRNL1,F2RL2,CXCL9,GDF6,IGFALS,KIF5A,GABRD,GDF15,TGFB2,IGSF1,C1QTNF3,SCG5,CHRDL1,EDA2R,SLC5A7,KIT,SV2C,APLNR,CXCL3,MYOC,CXCL10,MME,BDNF,RIPOR2,NGEF,EGR3,PTGER3,SULF1,LEFTY2,PTN,CHD5,THY1,CHRNA3,NTNG2,CXCL2,MDK,PALM3,ASB18,RASSF10,PTCH2,TNFRSF11B,PTPRR,PCDH17,INHBA,PMAIP1,SYT17,CHRM3,SMOC2,GPR173,NDP,MPIG6B,HTR2B,UCHL1,MID1,CSPG5,S1PR5,NXPH4,TP73,PRF1,RFX8,CD7,CRHBP,BRSK1,FREM1,ESR1,NOS2,MYOZ1,SNCA,CXCL14,GZMA,TP63,TAC4,SHANK2,SEMA3D,GABRE,GFRA3,EPHA3,PDE6A,ACE,PDE5A,PTGFR,GRIA3,PLCE1,SCG2,AMPH,PAK1,KCNA5,CAPN3,GNB3,SOX8,APOE,SV2B,GDF9,F2RL3,P2RX1,F2R,GUCA1C,ANKS1B,SV2A,SEZ6L2,EGR2,SYT12,RASL11B,COLEC12,GLI1,SNCAIP,SAMD12,CACNG8,DCLK3,OAS3,SCT,ANGPTL8,C1QTNF12,FCN1,EGR1,MUC20,LSP1,PLPPR4,CRABP2,P2RX6,PSD,SLC1A7,DUSP6,SLC6A1,DKK2,RAB39B,IL34,TNFSF13B,INHBE,IER3,GPR27,GJC2,LCK,LTB,RSAD2,NRXN2,TNFRSF4,ACHE,SCN8A,TENM1,STX1B,MYCBPAP,ITGAX
GO:0005886	CC	plasma membrane	2.22E-13	12.65296711	182	GSG1L,LYPD1,IL31RA,PRND,LAMP5,CD1C,KCNK10,TRPM8,SYTL5,ALOX15,CTLA4,SLITRK4,SLC4A8,TMEM114,PCDH15,PENK,FCG

						R3B,FCER1A,RXFP2,SLC16A6,ATP1A4,CDH8,DLGAP1,KCNJ15,ECEL1,CTSG,AQP10,MUC13,CX3CR1,TMEM262,UNC80,RHCG,APCDD1L,UGT8,ATP1B4,TMEM30B,FMN2,GZMB,CACNA1B,RGS4,XG,F2RL2,CXCL9,GABRD,ENPP2,COL17A1,CHRDL1,EDA2R,LYPD2,SLC5A7,NALF1,KIT,SV2C,APLNR,ANKRD24,TMEM163,FAT3,CXCL10,MME,RIPOR2,PTGER3,SULF1,PTN,LRRC55,OLR1,SLC16A9,THY1,CHRNA3,ABCG2,NTNG2,MMP25,CATSPER1,PALM3,PRSS8,PTCH2,TNFRSF11B,DIO2,PLEKHH2,CYS1,PTPRR,PCDH17,SYT17,CHRM3,GPR173,LYPD3,MPIG6B,HTR2B,UCHL1,SLC6A12,CSPG5,OPCML,SELL,S1PR5,RHBDL2,TRPV3,SLC6A17,PRF1,PROS1,CD7,SLC44A5,IPCEF1,HAUS7,SLC22A7,SLC26A4,ESR1,NOS2,SNCA,CDHR5,GZMA,KCNN3,PLXDC1,FSCN1,SHANK2,CUBN,ENPP6,CLIC6,HAS3,GABRE,GFRA3,EPHA3,PDE6A,SYTL2,LRRTM3,ACE,SLC9C1,NT5E,PTGFR,GRIA3,PLCE1,AMPH,PAK1,KCNA5,CAPN3,GNB3,APOE,SV2B,TMEM233,F2RL3,P2RX1,F2R,ANKS1B,SV2A,SEZ6L2,SYT12,COLEC12,KIAA1755,SNCAIP,SAMD12,NTM,CACNG8,PTPRH,OAS3,HLA-DPA1,FCN1,APOLD1,HMCN2,MUC20,LSP1,PLPPR4,P2RX6,PSD,SLC1A7,SLC6A1,RAB39B,TNFSF13B,BOC,GPR27,GJC2,MDGA1,LCK,LTB,NRXN2,TNFRSF4,ACHE,SCN8A,TREH,KCNIP1,TENM1,STX1B,MYCBPAP,GABRP,ITGAX
GO:0110165	CC	cellular anatomical entity	0.000389829	3.409125795	417	RFPL4A,EDN3,CST2,SEZ6L,CUX2,ESM1,GSG1L,VGLL2,MSTN,LYPD1,TNMD,IL31RA,PRND,CA3,RFPL4AL1,SFRP4,SHISA2,COL22A1,LAMP5,CYP21A2,CENPA,CXCL11,CBLN4,CD1C,IRX1,KCNK10,CYP4F3,TRPM8,SYTL5,ZSCAN4,CST1,P3H2,L1TD1,UCMA,FOXA1,IL22RA2,APOBEC3A,RSPO2,ARMS2,LEF1,ALOX15,CTLA4,SLITRK4,SLC4A8,MAP3K7CL,TMEM114,ZNF497,MYH2,PCDH15,MATN4,FBN3,PENK,OIT3,FCGR3B,IL1B,PPP2R2B,FCER1A,HBB,RXFP2,SLC16A6,ATP1A4,IRX2,COL10A1,FNDC1,DPYSL5,CDH8,SCUBE2,PCSK1N,DLGAP1,KCNJ15,ECEL1,CTSG,AQP10,MUC13,CX3CR1,CRACD,HS3ST5,TMEM262,UNC80,PLD4,GZMM,RHCG,APCDD1L,SUPT20HL2,UGT8,RASEF,ANKRD34C,WNT9A,FRZB,

ATP1B4,TMEM30B,FMN2,TM6SF2
,ZNF365,GZMB,CACNA1B,BCL2A
1,HYAL4,CMA1,GNLY,E2F7,CYT
L1,RGS4,MXRA5,FMOD,THBS4,C
RISPLD1,HSH2D,ATRNL1,LAMB4
,COL9A1,DEGS2,XG,HDC,F2RL2,
CXCL9,GDF6,IGFALS,KIF5A,GAB
RD,ENPP2,GDF15,TGFB2,MED12L
,IGSF1,LRRC9,C1QTNF3,COL17A1
,ODF3,SCG5,CHRDL1,AEBP1,SYN
PR,EDA2R,CCDC63,LYPD2,CAPN
12,SLC5A7,NALF1,KIT,SV2C,APL
NR,CH25H,MCF2L2,NELL2,ANKR
D24,ODAD2,TMEM163,AKR7A3,F
AT3,CERS1,CXCL3,MYOC,CXCL1
0,MME,BDNF,RIPOR2,NGEF,LAM
C3,EGR3,TSPAN10,C14ORF132,CC
DC62,PTGER3,LRRN1,SULF1,LEF
TY2,PTN,LRRC55,CHD5,LMX1A,
OLR1,MYCN,SLC16A9,THY1,CHR
NA3,LOXHD1,FATE1,ABCG2,NTN
G2,CXCL2,MMP25,MDK,KIAA154
9L,CATSPER1,PALM3,ANGPTL7,I
QCN,SP5,DNAH5,ASB18,TLL2,RA
SSF10,PRSS8,PTCH2,TNFRSF11B,
DIO2,PRSS35,PLEKHH2,CYS1,TA
GLN3,PTPRR,DNAAF3,PCDH17,K
LHL4,INHBA,PMAIP1,COL14A1,C
OL24A1,SYT17,PRG4,CHRM3,SM
OC2,PLAC8,GPR173,PHOSPHO1,G
ATM,NDP,LYPD3,MPIG6B,TTLL7,
EIF4EBP3,HTR2B,UCHL1,LUM,A
RSJ,MID1,CFAP251,ANKLE1,SLC6
A12,CREG2,CSPG5,GADL1,IFI44L,
LRRC3B,OPCML,IRX6,SELL,S1PR
5,CCDC168,ITIH5,B3GNT5,RTL3,
NXPH4,TP73,RHBDL2,TRPV3,SLC
6A17,PRF1,PROS1,RFX8,C10ORF6
7,CD7,CRHBP,SLC44A5,BRSK1,SL
C24A5,PHLDA1,IPCEF1,ARID5A,P
RRX2,HAUS7,SLC22A7,YIPF7,FR
EM1,SLC26A4,ESR1,SAMD11,ZM
YND15,MYL1,NOS2,EPHX3,CPX
M2,MYOZ1,SNCA,CDHR5,APOL4,
CXCL14,GZMA,FOXI2,TP63,KCN
N3,PLXDC1,FSCN1,TAC4,SHANK
2,CUBN,ENPP6,COL9A2,SEMA3D,
CLIC6,HAS3,GABRE,GFRA3,EPH
A3,BRINP1,COL8A2,EXOC3L4,EX
TL1,PDE6A,SYTL2,HSD17B14,LR
RTM3,TMEM45B,ACE,SLC9C1,OG
DHL,NT5E,PDE5A,PTGFR,GLIS1,
GRIA3,PLCE1,SCG2,AMPH,PAK1,
KCNA5,CAPN3,GNB3,SOX8,APOE
,SV2B,SDSL,TMEM233,MOXD1,G
DF9,ADAMTS8,F2RL3,P2RX1,BCL
6B,F2R,SOX15,GUCA1C,ANKS1B,
SV2A,SEZ6L2,IQCA1,EGR2,SYT12
,COLEC12,GLI1,KIAA1755,SNCAI
P,NRK,SAMD12,SRRM4,NTM,CA
CNG8,PRDM1,PTPRH,TNNT1,DCL

						K3,MSH4,OAS3,SCT,SSC5D,ANGPTL8,C1QTNF12,HLA-DPA1,FCN1,DMC1,APOLD1,HMCN2,EGR1,CCDC13,QPCT,MYO5B,TFPI2,MUC20,LSP1,ISLR,PLPPR4,ZNF541,CRABP2,ATCAY,P2RX6,PSD,SLC1A7,DUSP6,SLC6A1,DKK2,RAB39B,IL34,TNFSF13B,BOC,INHBE,IER3,GPR27,GJC2,MDGA1,LCK,RUNX1,LTB,ZC3H12B,NUP62CL,RSAD2,NRXN2,REC8,CYP11A1,TNFRSF4,ACHE,SCN8A,KIF1A,TREH,UNC13D,CPEB1,KCNIP1,TPM3,TENM1,SCARA3,MEST,STX1B,MYCBPAP,MX2,GABRP,COL12A1,ITGAX
GO:0005102	MF	signaling receptor binding	1.93E-07	6.713939136	68	EDN3,ESM1,MSTN,LYPD1,CXCL11,SYTL5,RSPO2,PENK,IL1B,PCSK1N,CTSG,CX3CR1,ITPRID1,WNT9A,CYTL1,THBS4,ATRNL1,F2RL2,CXCL9,GDF6,GDF15,TGFB2,IGSF1,CXCL3,MYOC,CXCL10,BDNF,LEFTY2,PTN,THY1,CXCL2,MDK,PTCH2,TNFRSF11B,INHBA,NDP,UCHL1,CSPG5,NXPH4,CXCL14,TAC4,SHANK2,SEMA3D,CLIC6,GFRA3,SYTL2,ACE,SCG2,KCNA5,APOE,GDF9,ADAMTS8,F2R,ANKS1B,RASL11B,SCT,ANGPTL8,C1QTNF12,FCN1,DKK2,IL34,TNFSF13B,INHBE,LCK,LTB,NRXN2,STX1B,ITGAX
GO:0098772	MF	molecular function regulator activity	0.002101883	2.677391414	69	EDN3,CST2,MSTN,LYPD1,CXCL11,CST1,LEF1,PENK,IL1B,PPP2R2B,PCSK1N,CTSG,WNT9A,RGS4,THBS4,F2RL2,CXCL9,GDF6,GDF15,TGFB2,IGSF1,SCG5,MCF2L2,CXCL3,CXCL10,BDNF,NGEF,LEFTY2,PTN,LRRC55,THY1,CXCL2,MDK,TNFRSF11B,INHBA,NDP,HTR2B,CSPG5,ITIH5,ECT2L,PROS1,ESR1,MYOZ1,SNCA,CXCL14,TAC4,SEMA3D,PLCE1,SCG2,CAPN3,APOE,GDF9,GUCA1C,RASL11B,KIAA1755,CACNG8,SCT,ANGPTL8,C1QTNF12,TFPI2,PSD,DKK2,IL34,TNFSF13B,INHBE,LCK,LTB,NRXN2,KCNIP

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

Pathway ID	Pathway Name	adjusted_p_	negative_log10_of_adjust	Gene	Gene

		value	ed_p_value	Count	
			Up regulated genes		
REAC:R-HSA-1430728	Metabolism	0.000235364	3.62825969	84	CACNA1E,ALOX15B,GNMT,MGST1,PLA2G2A,CHDH,PCK1,CYP4B1,ETNK2,VDR,AOX1,SGPP2,CA14,HS3ST2,MFSD2A,RBP4,ADH1B,HMGCS2,HOGA1,LYVE1,PTDSS1,PLA2G4F,ETNPPL,ITPKA,CHST7,PRODH,B3GNT7,PNMT,CHAC2,LDHA,MLXIPL,HMOX2,GPD1L,ALDH1L1,SLC2A1,SLC44A3,GSTM3,FHL2,RPLP0,CD38,SERINC2,ENTPD6,POMC,APOB,BMAL1,ARG2,ORMDL2,LPCAT3,CHPF,GPD1,FABP4,PTGS1,BHMT2,HK3,TPO,RPSA,HMBS,HAS2,ALDOC,NQO1,BCAT1,PPIP5K2,NMRAL1,RPS2,PSMD8,EBP,DHCR24,AKR1C1,RPL27,NSDHL,RPS5,LPCAT4,GGT5,IMPA2,HMOX1,AKR1B1,ACACB,NUDT4,SLC25A19,MPST,NQO2,RETSAT,TKT,PMVK
REAC:R-HSA-5576891	Cardiac conduction	0.001413139	2.849815073	13	KCNIP2,KCNK12,CORIN,SCN1A,KCNK13,KCNK3,FGF12,NPPC,KCNK2,ATP2A2,DMPK,KCNH2,KCNK1
REAC:R-HSA-397014	Muscle contraction	0.006736679	2.171554137	15	MYH6,KCNIP2,KCNK12,CORIN,SCN1A,KCNK13,KCNK3,FGF12,NPPC,KCNK2,ATP2A2,DMPK,MYL3,KCNH2,KCNK1
REAC:R-HSA-6798695	Neutrophil degranulation	0.019351752	1.713279701	24	RNASE2,SERPINA3,CD177,MGST1,ELANE,C3,QSOX1,TUBB4B,SLPI,CFD,PTX3,HMOX2,OLFM4,GGH,HK3,CD63,ALDOC,PRDX6,CTSB,PRKCD,FCER1G,LGALS3,FTH1,FRK
REAC:R-HSA-112316	Neuronal System	0.023934563	1.620974495	21	CACNA1E,TUBA3E,TUBA3D,CHRNA4,KCNK13,KCNK3,SYN2,GRIP1,TUBB4B,TUBA1C,TUBB4A,TUBA1B,KCNA7,KCNK2,CACNA2D3,GRIN2A,HCN4,RPS6KA2,KCNH2,TUBA4A,KCNK1
REAC:R-HSA-556833	Metabolism of lipids	0.072411275	1.140193808	30	ALOX15B,PLA2G2A,CYP4B1,ETNK2,VDR,SGPP2,MFSD2A,HMGCS2,PTDSS1,PLA2G4F,ETNPPL,GPD1L,SLC44A3,FHL2,POMC,BMAL1,ORMDL2,LPCAT3,GPD1,FABP4,PTGS1,EBP,DHCR24,AKR1C1,NSDHL,LPCAT4,GGT5,AKR1B1,ACACB,P

					MVK
Down regulated genes					
REAC:R-HSA-1474244	Extracellular matrix organization	4.18982E-05	4.377804489	24	COL22A1,P3H2,MATN4,FBN3,COL10A1,CTSG,CMA1,FMOD,COL9A1,TGFB2,COL17A1,CAPN12,LAMC3,MMP25,TLL2,COL14A1,COL24A1,LUM,COL9A2,COL8A2,CAPN3,ADAMTS8,COL12A1,ITGAX
REAC:R-HSA-500792	GPCR ligand binding	0.006878481	2.162507445	24	EDN3,CXCL11,PENK,RXFP2,CX3CR1,WNT9A,F2RL2,CXCL9,APLNR,CXCL3,CXCL10,PTGER3,CXCL2,PTCH2,CHRM3,HTR2B,S1PR5,CRHBP,PTGFR,GNB3,F2RL3,F2R,SCT,PLPPR4
REAC:R-HSA-9006934	Signaling by Receptor Tyrosine Kinases	0.116865935	0.932312061	21	CMA1,THBS4,COL9A1,KIT,BDNF,LAMC3,EGR3,PTN,MYCN,MDK,COL24A1,ESR1,COL9A2,PAK1,APOE,EGR2,PRDM1,EGR1,MUC20,DUSP6,LCK
REAC:R-HSA-382551	Transport of small molecules	0.312352071	0.505355611	24	TRPM8,SLC4A8,HBB,ATP1A4,AQP10,UNC80,RHCG,SLC5A7,ABCG2,SLC6A12,TRPV3,SLC44A5,SLC24A5,SLC22A7,SLC26A4,CUBN,SLC9C1,GNB3,APOE,ANGPTL8,MYO5B,SLC1A7,SLC6A1,RUNX1
REAC:R-HSA-162582	Signal Transduction	0.312352071	0.505355611	70	EDN3,CENPA,CXCL11,FOXA1,RSPO2,LEF1,PENK,RXFP2,SCUBE2,MUC13,CX3CR1,WNT9A,ATP1B4,GZMB,CMA1,RGS4,THBS4,COL9A1,F2RL2,CXCL9,KIF5A,TGFB2,CHRDL1,KIT,APLNR,CXCL3,CXCL10,BDNF,NGEF,LAMC3,EGR3,PTGER3,PTN,MYCN,CXCL2,MDK,PTCH2,INHBA,COL24A1,CHRM3,HTR2B,S1PR5,CRHBP,ESR1,COL9A2,GFRA3,PDE6A,PDE5A,PTGFR,PAK1,GNB3,APOE,F2RL3,F2R,EGR2,GLI1,PRDM1,SCT,EGR1,MUC20,PLPPR4,CRABP2,DUSP6,DKK2,BOC,IER3,GPR27,LCK,RUNX1,TPM3
REAC:R-HSA-1280215	Cytokine Signaling in Immune system	0.312352071	0.505355611	24	IL31RA,IL22RA2,ALOX15,IL1B,CTSG,EDA2R,CXCL10,CXCL2,TNFRSF11B,MID1,NOS2,FSCN1,OAS3,HLA-DPA1,EGR1,DUSP6,IL34,TNFSF13B,LCK,LTB,RSAD2,TNFRSF4,MX2,ITGAX

Table 4 Topology table for up and down regulated genes

Regulation	Node	Degree	Betweenness	Stress	Closeness
Up	FN1	473	0.109116	2E+08	0.353245
Up	SOX2	365	0.067486	1.39E+08	0.335598
Up	TUBA4A	190	0.051172	31857448	0.338477
Up	RPS2	185	0.017276	9220676	0.352736
Up	TUBA1C	159	0.026635	11323556	0.368273
Up	RPLP0	135	0.011368	5958366	0.353606
Up	RPSA	127	0.010703	4989992	0.348574
Up	TFRC	119	0.023334	13206196	0.325219
Up	SH3KBP1	115	0.020202	15272296	0.312793
Up	FKBP5	114	0.024673	5207364	0.348905
Up	TUBG1	111	0.01699	14037244	0.323839
Up	FHL2	110	0.025894	5500746	0.352863
Up	LGALS3	105	0.037206	9288028	0.360636
Up	RPS5	104	0.004324	8076866	0.300174
Up	SLAMF1	93	0.02151	13052026	0.305176
Up	BCL6	87	0.016104	38882434	0.28111
Up	TUBB4B	83	0.009611	4892884	0.331211
Up	AGTR1	79	0.017946	13625904	0.298922
Up	RPL27	79	0.00269	4989026	0.296779
Up	CTSB	74	0.008072	8115280	0.303631
Up	PSMD8	67	0.011493	14491824	0.286494
Up	ATP2A2	66	0.01283	2892110	0.350988
Up	BLM	65	0.011026	4194338	0.338868
Up	PRKCD	65	0.009793	7186238	0.301652
Up	LDHA	63	0.009788	4456804	0.312743
Up	FTH1	61	0.0163	9590872	0.281702
Up	TKT	59	0.011703	3289292	0.316055
Up	COMTD1	58	0.01091	2782068	0.338536
Up	FGFR4	57	0.012763	5933936	0.296854
Up	SLC7A1	57	0.00955	7759190	0.278671
Up	MLF1	55	0.008756	6468492	0.287166
Up	TGM2	54	0.00675	3832120	0.304465
Up	TUBA1B	54	0.006453	2313722	0.352609
Up	VDR	50	0.003094	6670838	0.287082
Up	APOB	47	0.008005	8376134	0.28704
Up	VSIG4	44	0.008612	6686408	0.282596
Up	HMOX2	41	0.00664	5365262	0.285798
Up	S100A10	38	0.008222	1650734	0.332937
Up	CA14	38	0.005092	3736514	0.275872
Up	NGFR	36	0.006982	3780622	0.284099
Up	CMTM5	35	0.008279	14619696	0.260273
Up	BMP7	33	0.006033	1877220	0.276964
Up	HOOK1	33	0.005894	3437722	0.271163
Up	SLC2A1	32	0.005084	1174034	0.337758
Up	EPN1	31	0.006012	2893678	0.336482
Up	PRDX6	31	0.004018	2195578	0.337797
Up	EBP	31	0.00771	2319812	0.285589
Up	XRCC4	30	0.004505	4648986	0.272571
Up	GRIP1	29	0.006273	1116134	0.33095
Up	C3	29	0.006523	1748362	0.26456
Up	VIPR1	29	0.004782	4501030	0.270913
Up	RPS6KA2	28	0.003346	2787366	0.281486
Up	ZNF703	27	0.00574	3186288	0.279758
Up	PTPRN	27	0.003999	2599642	0.275445
Up	LRP4	26	0.00579	4196724	0.266963
Up	ITGA7	26	0.006226	1514106	0.282338
Up	CREB3L1	26	0.005421	6842918	0.257525
Up	CD109	26	0.004376	1446820	0.276742
Up	SERPINA5	25	0.005416	2316392	0.259652
Up	DHCR24	25	0.004356	1582028	0.335273
Up	HMOX1	24	0.004098	1062466	0.268807
Up	PALLD	23	0.00278	2890772	0.26946
Up	SCGN	23	0.00222	2783418	0.267925

Up	GGH	23	0.003317	1734178	0.277421
Up	CAMSAP3	23	0.003796	724928	0.329891
Up	LAMB3	23	0.002864	2744672	0.273459
Up	CENPV	22	0.0016	2181446	0.267681
Up	FAM83B	21	0.004065	855502	0.328417
Up	TSPAN2	21	0.002911	841734	0.276664
Up	RETSAT	20	0.005823	1206702	0.217301
Up	OLFM4	19	0.002721	2301970	0.257999
Up	LPCAT3	19	0.002441	856790	0.233876
Up	GRIN2A	18	0.002535	1487360	0.271551
Up	GSTM3	18	0.003353	2050812	0.315377
Up	LMO1	18	0.00188	2198674	0.260042
Up	SERPINA3	15	0.001793	1341152	0.250854
Up	SPP1	15	0.001261	1035292	0.266371
Up	QSOX1	15	0.003012	876874	0.275071
Up	PTX3	14	0.001544	296724	0.222079
Up	CD63	14	0.001771	454040	0.279439
Up	AZGP1	14	0.002473	516882	0.261733
Up	ALDOC	13	0.00214	775190	0.273268
Up	C1QB	13	0.001481	349616	0.291423
Up	CENPM	13	0.00215	1268210	0.232176
Up	C1QA	12	0.001147	273520	0.289828
Up	PPIL1	12	0.001228	953586	0.269683
Up	NSDHL	12	0.002668	931962	0.243345
Up	EIF4EBP1	11	0.001079	786496	0.245633
Up	EPB41L4B	11	8.48E-04	505270	0.261663
Up	IMPA2	11	0.002456	511818	0.265049
Up	TGFA	10	0.00206	953334	0.267925
Up	ITLN1	10	0.00138	607600	0.262247
Up	MGST1	9	7.89E-04	213342	0.277173
Up	PLEKHN1	9	0.001057	461348	0.260411
Up	SLC25A19	9	0.001733	567864	0.252926
Up	SLC7A11	8	3.26E-04	192724	0.265997
Up	INSYN1	8	0.001098	1061652	0.24508
Up	PTDSS1	8	0.002433	559240	0.327174
Up	NFXL1	7	3.61E-04	176314	0.241545
Up	NMRAL1	6	6.82E-04	316974	0.254514
Up	PLP2	6	3.64E-04	208280	0.201716
Up	ACACB	6	0.001026	231722	0.232304
Up	DIRAS3	6	0.001361	614158	0.242272
Up	AKR1B1	6	8.67E-04	350252	0.246158
Up	PCK1	6	0.001023	338526	0.259549
Up	FGF12	5	0.001051	717040	0.244784
Up	CRLF1	5	7.25E-04	192770	0.223345
Up	ZDHHC23	5	0.001021	1097504	0.180285
Up	CLIC3	5	0.001024	404550	0.229314
Up	FCER1G	4	0.001021	1301232	0.204502
Up	TENT5B	4	3.51E-04	94702	0.223864
Up	KCNK1	3	0	0	0.240193
Up	CHRNA4	3	6.80E-04	177662	0.228201
Up	LOX	3	1.47E-04	314464	0.275833
Up	CD177	3	3.41E-04	156616	0.246674
Up	MPST	3	1.73E-04	43716	0.238082
Up	AIF1L	3	3.08E-04	523656	0.320781
Up	C1QC	2	0	0	0.227521
Up	EPN3	2	4.90E-05	24322	0.254404
Up	SUSD4	2	9.57E-05	44366	0.256704
Up	C1QL1	2	4.16E-05	22008	0.226077
Up	NOCT	2	2.65E-05	9576	0.243456
Up	ZDHHC9	2	5.43E-05	42280	0.234595
Up	ELN	2	4.82E-04	181544	0.265684
Up	SMCO4	2	3.20E-06	1148	0.186077
Up	REPS2	1	0	0	0.251778
Up	HMBS	1	0	0	0.206188
Up	SDK1	1	0	0	0.265061
Up	GPD1L	1	0	0	0.223932
Up	FREM2	1	0	0	0.20518
Up	TUBB4A	1	0	0	0.223932
Up	RPLP0P6	1	0	0	0.237793
Up	RBP4	1	0	0	0.219796

Up	FCGR3A	1	0	0	0.24038
Up	CD38	1	0	0	0.24038
Up	KCNK3	1	0	0	0.249788
Up	DDN	1	0	0	0.238275
Up	ELANE	1	0	0	0.200553
Up	SHC4	1	0	0	0.228298
Up	EPHB2	1	0	0	0.219591
Up	ECE2	1	0	0	0.219664
Up	GPD1	1	0	0	0.222374
Up	SCN1A	1	0	0	0.196654
Up	CCDC184	1	0	0	0.235129
Up	NQO1	1	0	0	0.236349
Up	ADAMTS2	1	0	0	0.233829
Up	SMYD1	1	0	0	0.20349
Up	MZT2A	1	0	0	0.244631
Up	NID1	1	0	0	0.217454
Up	AKR1C1	1	0	0	0.261047
Up	FAM83F	1	0	0	0.230419
Up	TUBA3E	1	0	0	0.265002
Up	NACAD	1	0	0	0.23014
Up	HK3	1	0	0	0.217101
Up	ADAM11	1	0	0	0.199416
Up	CAMK1D	1	0	0	0.209323
Up	VGLL3	1	0	0	0.202007
Up	CPM	1	0	0	0.219796
Up	NINJ2	1	0	0	1
Up	CD276	1	0	0	0.224918
Up	PNMT	1	0	0	0.31193
Up	RASSF7	1	0	0	0.216135
Down	ESR1	1870	0.587746	6.06E+08	0.453305
Down	SNCA	152	0.028384	29984254	0.321395
Down	LCK	140	0.025956	37786260	0.31643
Down	PAK1	124	0.022263	7344224	0.360525
Down	APLNR	103	0.021058	18728968	0.298694
Down	MME	92	0.014314	26289176	0.299394
Down	PTN	83	0.015066	30315076	0.285951
Down	LYPD3	83	0.016511	11354608	0.294106
Down	TMEM30B	79	0.019648	8034502	0.290171
Down	KIT	78	0.012759	5349150	0.295823
Down	TPM3	78	0.016964	4732412	0.355145
Down	TP63	73	0.01026	6665850	0.312278
Down	PTPRR	68	0.005181	12706912	0.2892
Down	CHRM3	66	0.012005	6298970	0.307395
Down	PTGER3	63	0.009919	7717250	0.277933
Down	PPP2R2B	58	0.006908	17779292	0.283769
Down	CENPA	56	0.009147	18078458	0.276651
Down	RUNX1	54	0.008039	4243964	0.301823
Down	IQCN	52	0.01118	6561672	0.290042
Down	FOXI2	50	0.008496	8995428	0.27729
Down	TP73	47	0.007147	2794244	0.309482
Down	HAUS7	45	0.009874	4600502	0.280533
Down	TNFSF13B	44	0.006882	2305716	0.282135
Down	ISLR	43	0.008179	4354258	0.288533
Down	HBB	39	0.007697	4400028	0.287728
Down	MDK	38	0.004675	4525992	0.277867
Down	RASSF10	38	0.005534	5558018	0.275717
Down	APOE	37	0.005982	1520704	0.289756
Down	FOXA1	37	0.007923	1504684	0.329762
Down	UCHL1	37	0.003544	3457024	0.29477
Down	NT5E	37	0.007781	2437198	0.330968
Down	AMPH	36	0.005036	2073600	0.28204
Down	DUSP6	36	0.002327	4567326	0.28447
Down	GLI1	36	0.004917	5607508	0.277906
Down	MID1	35	0.008667	9261972	0.257965
Down	FATE1	35	0.008464	3280534	0.265528
Down	KCNA5	34	0.006666	4914932	0.271752
Down	COL14A1	34	0.005473	4954518	0.274724
Down	NELL2	34	0.008879	21199980	0.244733
Down	COLEC12	33	0.005923	2612196	0.287377
Down	CST1	33	0.007365	3245290	0.264727

Down	ENPP6	32	0.00448	6212680	0.260873
Down	SCARA3	32	0.005253	2452164	0.286285
Down	MYO5B	31	0.003969	3447796	0.27034
Down	EGR1	28	0.002804	4772834	0.272382
Down	KIF5A	27	0.005414	4625872	0.276469
Down	FSCN1	27	0.004427	1253374	0.305113
Down	GABRE	27	0.005457	2350010	0.259732
Down	LEF1	26	0.002478	1979092	0.275265
Down	P2RY8	25	0.002849	1315046	0.241149
Down	CATSPER1	25	0.005701	4329576	0.259721
Down	EPHA3	24	0.00493	2169906	0.281365
Down	ATP1B4	22	0.004574	1533138	0.260607
Down	UGT8	22	0.005283	1254082	0.283004
Down	TNNT1	21	0.00323	1407954	0.275704
Down	MED12L	21	0.001388	2429252	0.262188
Down	RAB39B	21	0.004034	3389366	0.262727
Down	PRDM1	20	0.001876	2288998	0.274301
Down	KIF1A	20	0.00528	1570854	0.329042
Down	CAPN3	19	0.002618	1884174	0.26107
Down	CHD5	19	8.17E-04	1303948	0.274647
Down	FAT3	19	0.003776	2357898	0.261547
Down	CPEB1	19	0.002605	2888188	0.256368
Down	LYPD1	19	0.003396	1385812	0.288533
Down	L1TD1	18	0.001788	3163346	0.254911
Down	SOX15	18	9.53E-04	2101480	0.257153
Down	GNB3	17	0.003936	1467014	0.241853
Down	QPCT	17	0.00147	1321274	0.271941
Down	GDF9	17	0.001887	959826	0.287222
Down	CTLA4	16	0.001925	478968	0.278591
Down	DPYSL5	16	0.002263	1645258	0.253986
Down	FMN2	16	0.004284	2094738	0.266988
Down	CST2	16	0.002433	1572406	0.247933
Down	FCGR3B	16	0.00239	1401182	0.27529
Down	SHANK2	15	0.00289	1349692	0.318125
Down	NOS2	15	0.001522	990244	0.275561
Down	FCN1	15	0.002371	785522	0.220712
Down	NGEF	15	0.002204	815484	0.268512
Down	OAS3	15	0.001036	1799246	0.259091
Down	MYCN	14	0.001515	1462590	0.269782
Down	COL8A2	14	0.003061	905588	0.286466
Down	GDF15	13	0.001439	431970	0.264334
Down	CTSG	13	0.002251	1851570	0.258135
Down	SFRP4	13	0.001516	1557424	0.255254
Down	CBLN4	13	0.001994	3439406	0.249078
Down	HSD17B14	13	0.00222	1544882	0.241307
Down	INHBE	12	0.002311	849116	0.273027
Down	MOXD1	12	5.38E-04	181788	0.246871
Down	ARID5A	12	0.00266	1286468	0.316942
Down	STX1B	11	0.001401	812102	0.257265
Down	CRABP2	11	0.001337	518600	0.246003
Down	PHLDA1	11	4.37E-04	258070	0.271953
Down	MYOC	9	0.001524	327962	0.284814
Down	MYOZ1	9	6.21E-04	406780	0.26462
Down	ECEL1	9	0.001398	792216	0.200635
Down	SYT17	8	0.001447	331592	0.232488
Down	PMAIP1	7	0.001718	1636374	0.198233
Down	OGDHL	7	0.001124	576564	0.255465
Down	THY1	7	4.94E-04	265200	0.256984
Down	CCDC13	7	0.001047	527720	0.24786
Down	FAM133A	7	0.001371	717144	0.253395
Down	PRF1	6	3.72E-04	107324	0.232774
Down	MYH2	6	5.71E-04	273698	0.258169
Down	PTPRH	5	3.56E-04	85552	0.278975
Down	SV2A	4	9.55E-05	66646	0.254404
Down	TSPAN10	4	0.001021	1532322	0.196267
Down	PIPSL	4	6.84E-04	821316	0.187508
Down	COL12A1	4	6.81E-04	3129376	0.209562
Down	IL1B	3	6.80E-04	325214	0.174111
Down	CXCL9	3	6.80E-04	333774	0.197129
Down	ATP1A4	3	1.88E-04	101716	0.238691

Down	PHOSPHO1	3	1	6	1
Down	P2RX6	3	6.80E-04	1359298	0.211302
Down	DLGAP1	2	2.82E-06	1266	0.248258
Down	SNCAIP	2	2.55E-04	157082	0.247131
Down	HLA-DPA1	2	6.31E-05	10974	0.230709
Down	ECT2L	2	0	0	0.312161
Down	PRSS8	2	2.81E-05	13536	0.314399
Down	BCL6B	1	0	0	0.219435
Down	ITGAX	1	0	0	0.209219
Down	GRIA3	1	0	0	0.248667
Down	GPR173	1	0	0	0.212103
Down	SEZ6L2	1	0	0	0.180811
Down	MUC20	1	0	0	0.252893
Down	IL31RA	1	0	0	0.265061
Down	CSPG5	1	0	0	0.223235
Down	CDHR5	1	0	0	0.178516
Down	PCDH17	1	0	0	0.224918
Down	PTGFR	1	0	0	0.23014
Down	DKK2	1	0	0	1
Down	SCT	1	0	0	0.213172
Down	HSH2D	1	0	0	0.228298
Down	IER3	1	0	0	0.260839
Down	GZMB	1	0	0	0.188827
Down	SYNPR	1	0	0	0.209824
Down	OIT3	1	0	0	0.158715
Down	CACNB4	1	0	0	0.222374
Down	PALM3	1	0	0	0.31193
Down	SCG5	1	0	0	0.23014
Down	MEST	1	0	0	0.31193
Down	S1PR5	1	0	0	0.237976
Down	E2F7	1	0	0	0.24038

Table 5 MiRNA - hub gene and TF – hub gene topology table

Regulation	Hub Genes	Degree	MicroRNA	Regulation	Hub Genes	Degree	TF
Up	FN1	439	hsa-mir-374a-5p	Up	SH3KBP1	20	PRRX2
Up	TFRC	422	hsa-miR-520d-5p	Up	FHL2	19	SRY
Up	FKBP5	305	hsa-miR-34a-5p	Up	FKBP5	17	USF2
Up	FHL2	291	hsa-mir-4646-5p	Up	TFRC	15	BRCA1
Up	RPLP0	232	hsa-mir-548aw	Up	FN1	14	STAT1
Up	TUBA1C	208	hsa-mir-603	Up	RPSA	10	PPARG
Up	TUBG1	170	hsa-miR-148a-3p	Up	SOX2	9	ARID3A
Up	SH3KBP1	159	hsa-miR-135b-5p	Up	TUBA4A	7	TFAP2C
Up	RPS2	141	hsa-mir-378a-3p	Up	TUBG1	6	NFIC
Up	RPS5	139	hsa-miR-182-3p	Up	RPLP0	6	FOXF2
Up	TUBA4A	105	hsa-mir-147a	Up	SLAMF1	6	YY1
Up	RPSA	98	hsa-miR-23a-3p	Up	TUBA1C	5	GATA3
Up	SOX2	96	hsa-miR-744-5p	Up	LGALS3	5	NFATC2
Up	SLAMF1	95	hsa-miR-106a-5p	Up	RPS5	5	RELA
Up	LGALS3	88	hsa-miR-4525	Up	RPS2	4	SOX17
Down	TPM3	456	hsa-miR-8052	Down	ESR1	26	STAT3
Down	ESR1	266	hsa-mir-302b-3p	Down	TP63	21	FOS
Down	CHRM3	226	hsa-miR-194-5p	Down	PTPRR	16	MEF2A
Down	TMEM30B	203	hsa-mir-548i	Down	TPM3	13	EN1
Down	PAK1	162	hsa-miR-524-5p	Down	SNCA	11	GATA2
Down	KIT	150	hsa-miR-23a-3p	Down	LCK	10	FOXL1
Down	PTPRR	127	hsa-mir-129-2-3p	Down	PTGER3	9	POU2F2
Down	MME	126	hsa-mir-181d-5p	Down	MME	9	NFYB
Down	LYPD3	115	hsa-mir-27a-3p	Down	KIT	8	FOXC1
Down	SNCA	84	hsa-miR-99b-5p	Down	PAK1	7	REL
Down	TP63	82	hsa-miR-1285-3p	Down	TMEM30B	7	PAX2
Down	PTN	66	hsa-miR-320b	Down	LYPD3	6	SRF

Down	APLNR	61	hsa-miR-146a-5p	Down	PTN	6	ELK4
Down	PTGER3	49	hsa-miR-5695	Down	APLNR	4	TP53
Down	LCK	37	hsa-miR-183-5p	Down	CHRM3	2	HOXA5

Figures

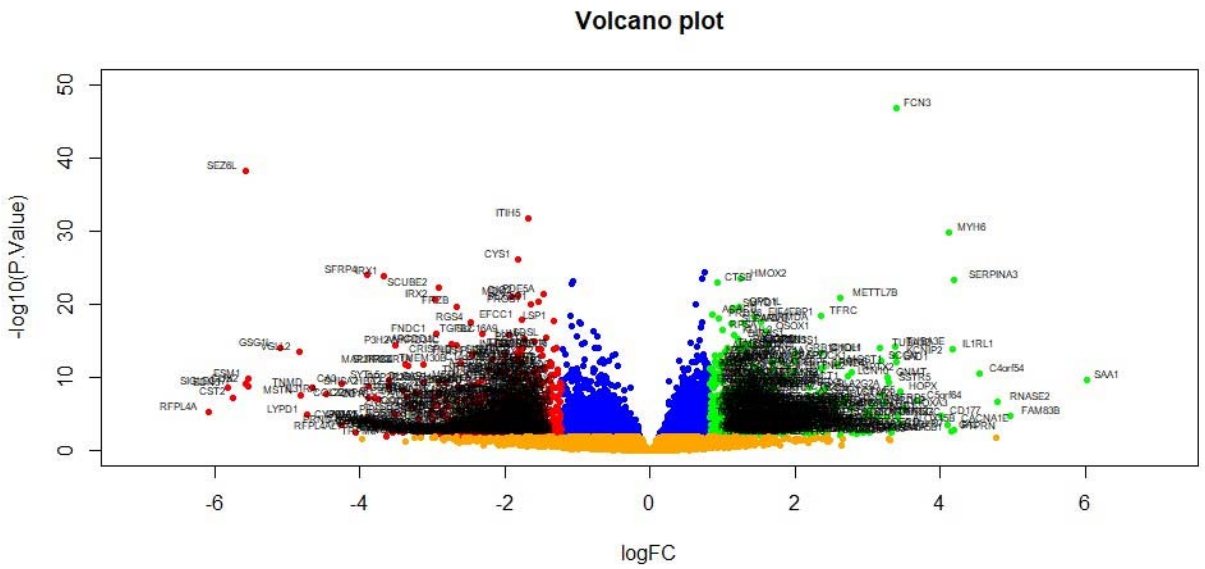

Fig. 1. Volcano plot of differentially expressed genes. Genes with a significant change of more than two-fold were selected. Green dot represented up regulated significant genes and red dot represented down regulated significant genes.

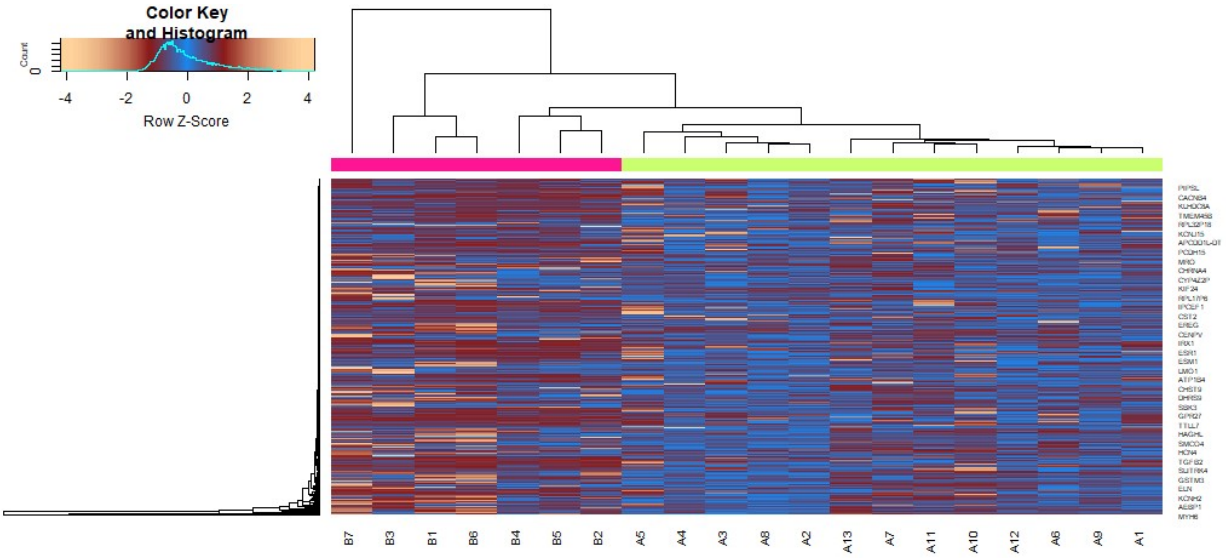

Fig. 2. Heat map of differentially expressed genes. Legend on the top left indicate log fold change of genes. (A1 – A106 = HD samples; B1 – B46 = Normal control samples)

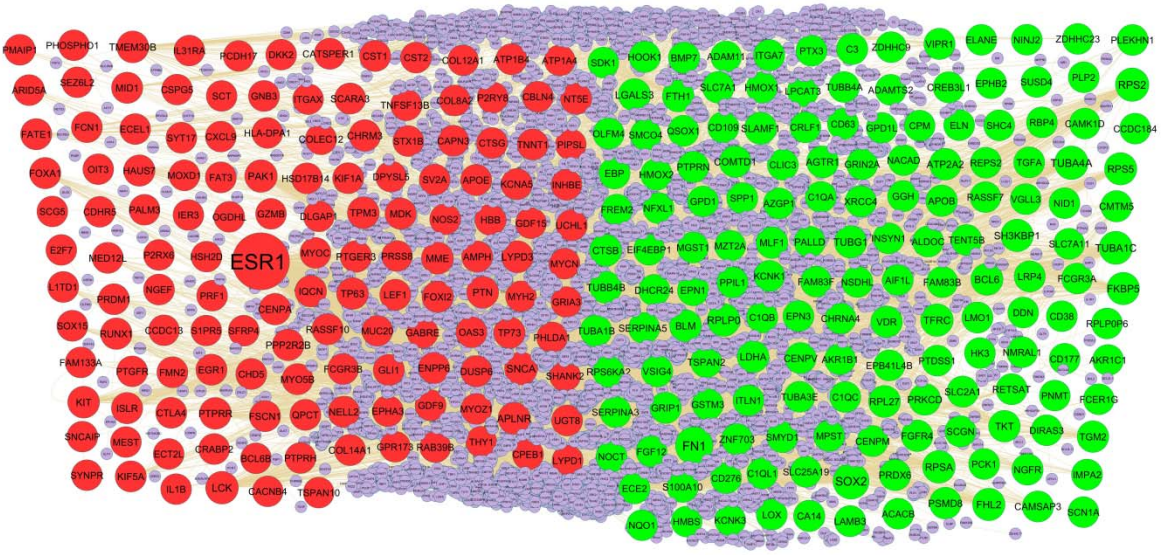

Fig. 3. PPI network of DEGs. Up regulated genes are marked in parrot green; down regulated genes are marked in red.

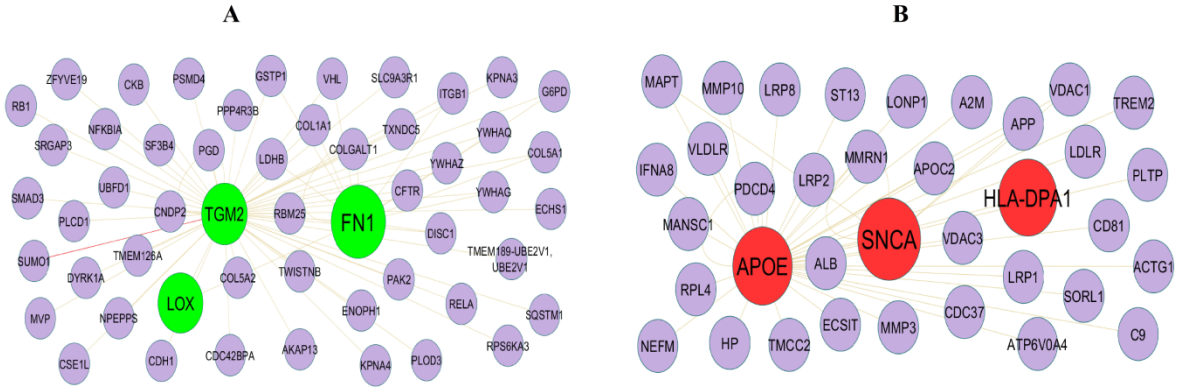

Fig. 4. Modules selected from the PPI network. (A) The most significant module was obtained from PPI network with 53 nodes and 66 edges for up regulated genes (B) The most significant module was obtained from PPI network with 19 nodes and 59 edges for down regulated genes. Up regulated genes are marked in parrot green; down regulated genes are marked in red.

Fig. 5. Hub gene - miRNA regulatory network. The light gray color diamond nodes represent the key miRNAs; up regulated genes are marked in green; down regulated genes are marked in red.

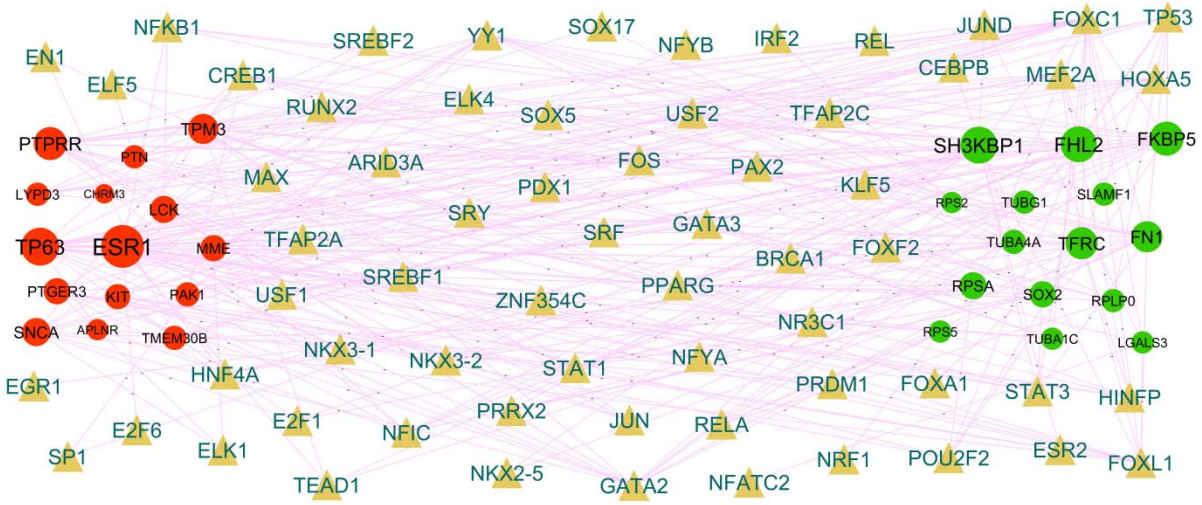

Fig. 6. Hub gene - TF regulatory network. The goldenrod color triangle nodes represent the key TFs; up regulated genes are marked in dark green; down regulated genes are marked in dark red.

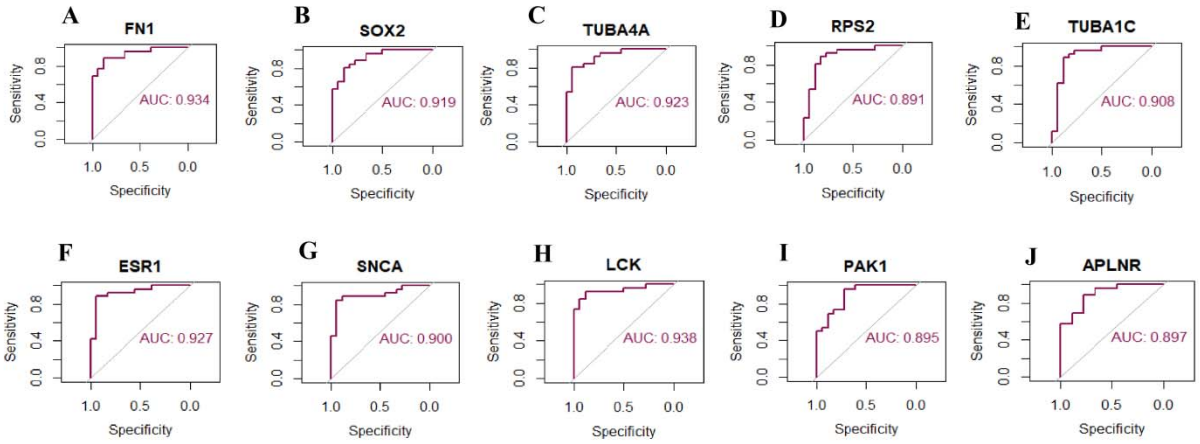

Fig. 7. ROC curve analyses of hub genes. A) FN1 B) SOX2 C) TUBA4A D) RPS2 E) TUBA1C F) ESR1G) SNCA H) LCK I) PAK1 J) APLNR