Bioinformatics analysis of differentially expressed genes in non alcoholic fatty liver disease using next generation sequencing data

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Abstract

Non alcoholic fatty liver disease (NAFLD) is the most common metabolic disease in humans, affecting the majority of individuals. In the current investigation, we aim to identify potential key genes linked with NAFLD through bioinformatics analyses of next generation sequencing (NGS) dataset. NGS dataset of GSE135251 from the Gene Expression Omnibus (GEO) database were retrieved. Differentially expressed genes (DEGs) were obtained by DESeq2 package. g:Profiler database was further used to identify the potential gene ontology (GO) and REACTOME pathways. Protein-protein interaction (PPI) network was constructed using the Hippie interactome database. miRNet and NetworkAnalyst databases were used to establish a miRNA-hub gene regulatory network and TF-hub gene regulatory network for the hub genes. Hub genes were verified based on receiver operating characteristic curve (ROC) analysis. Totally, 951 DEGs were identified including 476 up regulated genes and 475 down regulated genes screened in NAFLD and normal control. GO showed that DEGs were significantly enhanced for signaling and regulation of biological quality. REACTOME pathway analysis revealed that DEGs were enriched in signaling by interleukins and extracellular matrix organization. ESR2, JUN, PTN, PTGER3, CEBPB, IKBKG, HSPA8, SFN, CDKN1A and E2F1 were indicated as hub genes from PPI network, miRNA-hub gene regulatory network and TF-hub gene regulatory network. Furthermore, ROC analysis revealed that ESR2, JUN, PTN, PTGER3, CEBPB, IKBKG, HSPA8, SFN, CDKN1A and E2F1 might serve as diagnostic biomarkers in NAFLD. The current investigation provided insights into the molecular mechanism of NAFLD that might be useful in further investigations.

Keywords: non alcoholic fatty liver disease; bioinformatics analysis; differentially expressed genes; gene ontology; gene expression omnibus

Introduction

Non alcoholic fatty liver disease (NAFLD) has emerged as the main cause of metabolic disorder, but current treatments are still suboptimal [1]. NAFLD is a heterogeneous liver disorder that is characterized by hepatic steatosis to non-alcoholic steatohepatitis (NASH) and cirrhosis [2]. NAFLD are linked with progression of hepatocellular carcinoma [3], cardiovascular diseases [4], cerebrovascular diseases [5], diabetes mellitus [6], dietary rhythm [7], obesity [8], hypertension [9] and renal diseases [10]. Genetic factors can be used to show the pathogenesis of NAFLD [11]. Our understanding of the occurrence and advancement molecular mechanism of NAFLD has been greatly upgraded; however, the cause and potential molecular pathogenesis of NAFLD is still unclear [12]. Therefore, it is necessary to explore novel hub genes and signaling pathways for understanding the molecular mechanism and discovering key biomarkers for NAFLD.

At present, next generation sequencing (NGS) technology is widely used in molecular mechanism study and has a broad range of application in molecular biology [13]. It offers an efficient method for systematically screening NAFLD genes and signaling pathways, and identifying their regulatory mechanisms with bioinformatics [14]. Genes includes heme oxygenase-1 [15], odd-skipped related 1 (Osr1) [16], serine rich splicing factor 3 (SRSF3) [17], lipocalin-type prostaglandin D2 synthase (L-PGDS) [18] and β -Klotho (KLB) [19] are responsible for advancement of NAFLD. Signaling pathways includes LKB1/AMPK signaling pathway [20], Nrf2 signaling pathway [21], Sirt1/AMPK and NF- κ B signaling pathways [22], eIF2 α signaling pathway [23] and AMPK and LXR signaling pathways [24] are liable for progression of NAFLD. Therefore, a plenty of valuable clues could be explored for novel studies on the base of these data. Furthermore, many bioinformatics investigation on NAFLD have been produced in recent years [25], which proved that the integrated bioinformatics methods could help us to further investigation and better exploring the molecular mechanisms.

We downloaded NGS dataset GSE135251 [26-27] from Gene Expression Omnibus database (GEO) database (<http://www.ncbi.nlm.nih.gov/geo/>) [28], which contain expression profiling by high throughput sequencing data from NAFLD samples and normal control samples. We then performed deep bioinformatics

analysis, including identifying common DEGs, gene ontology (GO) and pathway enrichment analysis, protein-protein interaction (PPI) network analysis, module analysis, construction and analysis of miRNA-hub gene regulatory network and TF-hub gene regulatory network. The findings were further validated by receiver operating characteristic curve (ROC) analysis. The aim of this study was to identify DEGs and key signaling pathways, and to explore potential candidate biomarkers for the diagnosis and therapeutic targets in NAFLD.

Materials and methods

Data resources

Expression profiling by high throughput sequencing dataset GSE135251 [26-27] was downloaded from the GEO database. The data was produced using a GPL18573 Illumina NextSeq 500 (Homo sapiens). The GSE135251 dataset contained data from 216 samples, including 206 NAFLD samples and 10 normal control samples.

Identification of DEGs

To assess DEGs, using the “DESeq2” package of R software [29]. A moderated t-statistic and a log-odds of DEG was computed for each contrast for each gene. The Benjamini and Hochberg (BH) method was performed to adjust P value to reduce the false positive error [30]. DEGs between NAFLD samples and normal control samples were identified via DESeq2 package of R software with $|\log FC| \geq 1.295$ for up regulated genes, $|\log FC| \geq -1.368$ for down regulated genes and adjust P value ≤ 0.05 , which were visualized as volcano plots and heat map. “ggplot2” and “gplot” packages of R software was applied to generate volcano plots and heat map.

GO and pathway enrichment analyses of DEGs

g:Profiler (<http://biit.cs.ut.ee/gprofiler/>) [31] is an online functional annotation tool to provide a comprehensive understanding of biological information of genes and proteins. GO enrichment analysis (<http://www.geneontology.org>) [32] is a commonly used approach for defining genes and its RNA or protein product to identify unique biological properties of high-throughput genomic data. GO enrichment analysis including biological process (BP), cellular components (CC),

and molecular function (MF). REACTOME (<https://reactome.org/>) [33] pathway database is a collection of databases dealing with genomes, diseases, biological pathways, drugs, and chemical materials. P value ≤ 0.05 was considered as the threshold.

Construction of the PPI network and module analysis

The online Hippie interactome (<http://cbdm-01.zdv.uni-mainz.de/~mschaefer/hippie/>) [34] database was used to identify potential interaction among the common DEGs. Cytoscape software version 3.8.2 (<http://www.cytoscape.org/>) [35] was applied to establish the protein interaction network. The Network Analyzer plug-in was used to explore hub genes were generated using node degree [36], betweenness centrality [37], stress centrality [38] and closeness centrality [39]. The intersect function was used to identify the hub genes. Then, PEWCC1 plug-in [40] was performed to monitor PPI network modules with Cytoscape. The functional enhancement analysis of DEGs in the significant module were performed using g:Profiler.

MiRNA-hub gene regulatory network construction

miRNet database (<https://www.mirnet.ca/>) [41] is a bioinformatics platform for predicting miRNA- hub gene pairs. In the current investigation, the targets of the hub genes were predicted using fourteen databases: TarBase, miRTarBase, miRecords, miRanda (S mansoni only), miR2Disease, HMDD, PhenomiR, SM2miR, PharmacomiR, EpimiR, starBase, TransmiR, ADmiRE, and TAM 2.0. The screening criterion was that the miRNA target exists in the fourteen databases concurrently. The miRNA-hub gene regulatory network was depicted and visualized using Cytoscape software [35].

TF-hub gene regulatory network construction

NetworkAnalyst database (<https://www.networkanalyst.ca/>) [42] is a bioinformatics platform for predicting TF- hub gene pairs. In the current investigation, the targets of the hub genes were predicted using ChEA database. The screening criterion was that the TF target exists in the ChEA database concurrently. The TF-hub gene regulatory network was depicted and visualized using Cytoscape software [35].

Receiver operating characteristic curve (ROC) analysis

ROC curve analysis was accomplished to assess the sensitivity (true positive rate) and specificity (true negative rate) of the hub genes for NAFLD diagnosis and we studied how large the area under the curve (AUC) was by using the pROC package in R statistical software [43].

Results

Identification of DEGs

We obtained Expression profiling by high throughput sequencing from newly diagnosed patients with NAFLD and normal controls from the GSE135251 and analyzed DEGs using DESeq2 package of R software. Setting the cut-off criterion as adjust P value < 0.05 , $|\log FC| > 1.295$ for up regulated genes and $|\log FC| < -1.368$ for down regulated genes, we identified 951 DEGs from GSE135251. Total 951 DEGs, 476 were up regulated and 475 down regulated genes in NAFLD compared with normal control samples and are listed in Table 1. The heatmap and volcano plot are shown in Fig. 1 and Fig. 2, respectively.

GO and pathway enrichment analyses of DEGs

The online software g:Profiler was used to identify overrepresented GO categories and REACTOME pathways. The up regulated genes and all of the down regulated genes were uploaded to the gene list separately. GO enrichment analysis showed that the up regulated genes were significantly enriched in BP, including signaling and response to stimulus. The down regulated genes were also significantly enriched in BP, including regulation of biological quality and cell development. As for CC, the up regulated genes were enriched in chromatin and integral component of plasma membrane, and the down regulated genes were enriched in cell periphery and membrane. In addition, with regards to MF, the up regulated genes were enriched in DNA-binding transcription activator activity, RNA polymerase II-specific and signaling receptor binding, and the down regulated genes were enriched in calcium ion binding and structural molecule activity. The results are shown in full in Table 2. REACTOME pathway enrichment analysis found significantly enriched pathways. The up regulated genes were enriched in signaling by interleukins and signal transduction, while all of the down regulated genes were

enriched in extracellular matrix organization and biological oxidations. The results are shown in full in Table 3.

Construction of the PPI network and module analysis

All of the up regulated genes and the down regulated genes were uploaded to Hippie interactome database to draw the PPI network. A total of 3199 nodes and 5019 edges were analyzed in Cytoscape and is displayed in Fig. 3. The hub genes with high node degree, betweenness centrality, stress centrality and closeness centrality were selected as the hub genes of NAFLD. These hub genes were ESR2, JUN, PTN, PTGER3, CEBPB, IKBKG, HSPA8, SFN, CDKN1A and E2F1. All of the results are shown in Tables 4. The two significant modules are displayed in Fig. 4A and Fig. 4B. There are 38 nodes and 121 edges genes involved in module 1 and 45 nodes, and 96 edges genes involved in module 2. These modules were significantly enriched in signaling by interleukins, signaling, signal transduction, response to stimulus, signaling by receptor tyrosine kinases, chromatin, DNA-binding transcription activator activity, RNA polymerase II-specific, metabolism of lipids and regulation of biological quality.

MiRNA-hub gene regulatory network construction

To investigate the molecular mechanisms underlying the hub genes and miRNAs were searched by bioinformatics methods. The miRNAs of hub genes were predicted by miRNet database. The miRNA-hub gene regulatory network is consisted of 2546 nodes and 13598 edges, including 2204 miRNAs and 252 hub genes (Fig. 5). As shown in Table 5, miRNAs of hub genes were displayed. JUN might be the target of 118 miRNAs (ex; hsa-mir-199a-5p), FOXO1 might be the target of 63 miRNAs (ex; hsa-mir-33a-3p), FOXC1 might be the target of 62 miRNAs (ex; hsa-mir-561-3p), SOCS3 might be the target of 48 miRNAs (ex; hsa-mir-22-5p), CEBPB might be the target of 47 miRNAs (ex; hsa-mir-3613-3p), CDKN1A might be the target of 187 miRNAs (ex; hsa-mir-30b-3p), HSPA8 might be the target of 116 miRNAs (ex; hsa-mir-338-5p), FASN might be the target of 116 miRNAs (ex; hsa-mir-103a-3p), E2F1 might be the target of 74 miRNAs (ex; hsa-mir-150-5p) and CDT1 might be the target of 45 miRNAs (ex; hsa-mir-202-3p).

TF-hub gene regulatory network construction

To investigate the molecular mechanisms underlying the hub genes and TFs were searched by bioinformatics methods. The TFs of hub genes were predicted by NetworkAnalyst database. The TF-hub gene regulatory network is consisted of 441 nodes and 6738 edges, including 181 TFs and 260 hub genes (Fig. 6). As shown in Table 5, TFs of hub genes were displayed. JUN might be the target of 61 TFs (ex; GATA2), SOCS3 might be the target of 56 TFs (ex; RUNX1), TFAP2A might be the target of 55 TFs (ex; SUZ12), ATF3 might be the target of 48 TFs (ex; NUCKS1), CEBPB might be the target of 46 TFs (ex; FOXP2), CDKN1A might be the target of 57 TFs (ex; TP53), HSPA8 might be the target of 39 TFs (ex; KLF4), FASN might be the target of 39 TFs (ex; EGR1), ZWINT might be the target of 37 TFs (ex; AHR) and BCAR1 might be the target of 37 TFs (ex; TRIM28).

Receiver operating characteristic curve (ROC) analysis

ROC curve analysis using “pROC” in R statistical software packages was performed to calculate the capacity of ten hub genes to distinguish NAFLD samples from normal control samples. ESR2, JUN, PTN, PTGER3, CEBPB, IKBKG, HSPA8, SFN, CDKN1A and E2F1 all exhibited excellent diagnostic efficiency (AUC > 0.88) (Fig. 6).

Discussion

The NAFLD is a metabolic disease in light of molecular characteristics, distinct morphologies, metabolic pathways, therapeutic response and clinical outcomes. Therefore, it is important to explore the mechanisms of NAFLD progression to limit its advancement. The NGS platforms for detection of gene expression have been progressing briskly in diseases advancement, which provides the basis of novel targets discovery for diagnosis and therapy for NAFLD.

In the current investigation, NGS dataset, GSE135251 was extracted to identify the DEGs between NAFLD samples and normal control samples. The results showed that there are 476 up regulated and 475 down regulated genes between the NAFLD samples and normal control samples by using bioinformatics analysis. Altered expression of FOS (Fos proto-oncogene, AP-1 transcription factor subunit) [44], IGFBP1 [45], IL6 [46], RGS1 [47], NR4A3 [48] and SLC22A12 [49] occurs in hypertension, but these genes might be novel targets for

NAFLD. Pan et al. [50], McKee et al. [51], Simon et al. [52] and Shi et al. [53] proved that IGFBP1, AREG (amphiregulin), IL6 and AKR1B10 were involved in NAFLD progression. Ross et al. [54] and Lin et al. [55] further demonstrated that IGFBP1 and IL6 was involved in liver cirrhosis. IGFBP1 [56], AREG (amphiregulin) [57], IL6 [58], NR4A3 [59], EEF1A2 [60] and AKR1B10 [61] are implicated in the growth and metastasis of hepatocellular carcinoma. IGFBP1 [62], IL6 [63], RGS1 [64], NR4A3 [65], EEF1A2 [66] and MYH7 [67] acts in the progression of cardiovascular diseases, but these genes might be novel targets for NAFLD. IGFBP1 [68], IL6 [69], NR4A3 [70] and SLC22A12 [49] plays in the development of obesity, but these genes might be novel targets for NAFLD. Increasing evidence suggested that IGFBP1 [71] and IL6 [72] are involved in diabetes mellitus development and progression, but these genes might be novel targets for NAFLD. Recent studies found that AREG (amphiregulin) [73], IL6 [74] and RGS1 [75] plays an important role in the occurrence and development of cerebrovascular diseases, but these genes might be novel targets for NAFLD. IL6 [76] has been demonstrated to function in kidney disease, but this gene might be novel target for NAFLD.

Subsequently, GO annotation and REACTOME pathway enrichment analysis were performed to elucidate the significance of these identified altered expressed genes. Pathways and GO annotation include signal transduction [77], GPCR ligand binding [78], metabolism of lipids [79], fatty acid metabolism [80], signaling [81], chromatin [82], cell periphery [83] and membrane [84] were linked with progression of NAFLD. EGR1 [85], NR4A1 [86], DLK1 [87], SIK1 [88], CCN1 [89], SOCS2 [90], IRS2 [91], GADD45B [92], SOCS3 [93], MMP1 [94], CXCR4 [95], THBS1 [96], FST (follistatin) [97], KLF4 [98], CCL2 [99], OSM (oncostatin M) [100], MSTN (myostatin) [101], EPO (erythropoietin) [102], IL10 [103], JUN (Jun proto-oncogene, AP-1 transcription factor subunit) [104], FOXO1 [105], DKK1 [106], PTN (pleiotrophin) [107], ATF3 [108], SOCS1 [109], GPR183 [110], AKR1B10 [111], TREM2 [112], SCD (stearoyl-CoA desaturase) [113], GCK (glucokinase) [114], LPL (lipoprotein lipase) [115], ANGPTL8 [116], UGT1A1 [117], IL2RA [118], CDKN1A [119], GAS6 [120], ACE2 [121], NLRP6 [122], S1PR4 [123], FADS2 [124], FASN (fatty acid synthase) [125], TIMP3 [126], CHI3L1 [127], ADAMTSL2 [128], FNDC5 [129], MMP9 [130] and TMC4 [131] were involved in progression of NAFLD. EGR1 [132], NR4A2 [133],

DUSP1 [134], DLK1 [135], SIK1 [136], CCN1 [137], CEBPD (CCAAT enhancer binding protein delta) [138], SOCS2 [139], IRS2 [91], GADD45B [140], CXCL2 [141], ZFAND5 [142], EGR3 [143], PTGS2 [144], KL (klotho) [145], SOCS3 [146], MMP1 [147], CXCR4 [148], THBS1 [149], SLC7A11 [150], FAM83A [151], EGR2 [152], ZFP36 [153], NR0B2 [154], CCN2 [155], FST (follistatin) [156], PCK1 [157], CTLA4 [158], KLF4 [159], PRDM1 [160], CCL2 [161], OSM (oncostatin M) [162], ERBB4 [163], MSTN (myostatin) [164], ADAMTS1 [165], PDK4 [166], INHBB (inhibin subunit beta B) [167], EPO (erythropoietin) [168], TSPAN5 [169], RASSF10 [170], GATA3 [171], IL10 [172], ESR2 [173], VIP (vasoactive intestinal peptide) [174], CEBPB (CCAAT enhancer binding protein beta) [175], FOXC1 [176], FOXO1 [177], DKK1 [178], RNF152 [179], SOX17 [180], PTN (pleiotrophin) [181], GAS1 [182], PMAIP1 [183], CCL3 [184], FGF2 [185], ATF3 [186], FZD7 [187], ANGPT2 [188], SOCS1 [189], MAP3K8 [190], LPAR6 [191], EYA4 [192], FOSL1 [193] MAFF (MAF bZIP transcription factor F) [194], KLF6 [195], BASP1 [196], CTCFL (CCCTC-binding factor like) [197], AKR1B10 [198], S1PR2 [199], COMP (cartilage oligomeric matrix protein) [200], IGF2BP1 [201], ACHE (acetylcholinesterase) [202], TREM2 [203], SCD (stearoyl-CoA desaturase) [204], FOXP3 [205], SCIN (scinderin) [206], EPHB2 [207], ANGPTL8 [208], HSPA8 [209], KCNJ11 [210], PFKL (phosphofructokinase, liver type) [211], EYA2 [212], GLIS2 [213], CDKN1A [214], ITGB3 [215], GAS6 [216], PIEZO1 [217], SYT7 [218], AGRN (agrin) [219], DAB2IP [220], EXO1 [221], WNK2 [222], ACE2 [223], SPP1 [224], ANXA6 [225], E2F1 [226], CLDN3 [227], ALDH3A1 [228], ROS1 [229], FASN (fatty acid synthase) [230], NKD2 [231], TIMP3 [232], CHI3L1 [233], RAB25 [234], SUSD2 [235], LAMB3 [236], LYPD1 [237], ADAMTSL5 [238], FAT1 [239], GPBAR1 [240], FNDC5 [241], HLA-G [242], TRAF7 [243], MMP9 [244], TMC4 [245], TNFRSF12A [246], CABYR (calcium binding tyrosine phosphorylation regulated) [247], BMP10 [248] and LOXL4 [249] contributes to the progression of hepatocellular carcinoma. Previous studies have demonstrated that EGR1 [250], SIK1 [251], PTGS2 [252], RGS2 [253], KL (klotho) [254], SOCS3 [255], MMP1 [256], CXCR4 [257], THBS1 [258], CHRM3 [259], KLF4 [260], CACNA1A [261], CCL2 [262], AVPR1A [263], PDK4 [264], EPO (erythropoietin) [265], IL10 [266], ESR2 [267], VIP (vasoactive intestinal peptide) [268], FOXC1 [269], FOXO1 [270], S100B [271], FGF7 [272], SOX17 [273], FGF2 [274], ATF3 [275], IMPA1 [276], HPGDS (hematopoietic prostaglandin D

synthase) [277], F2RL3 [278], SCUBE1 [279], COMP (cartilage oligomeric matrix protein) [280], ADAMTS16 [281], ACHE (acetylcholinesterase) [282], SLC6A2 [283], TREM2 [284], GCK (glucokinase) [285], FOXP3 [286], CYP7A1 [287], CMA1 [288], SLC22A2 [289], LPL (lipoprotein lipase) [290], ANGPTL8 [291], HSPA8 [292], MB (myoglobin) [293], KCNJ11 [294], MUC6 [295], UGT1A1 [296], KCNJ5 [297], GDF2 [298], ARHGEF18 [299], ITGB3 [300], P2RY2 [301], PIEZO1 [302], PDGFA (platelet derived growth factor subunit A) [303], ACE2 [304], NLRP6 [305], ROS1 [306], FASN (fatty acid synthase) [307], TIMP3 [308], CHI3L1 [309], TREH (trehalase) [310], SLC6A19 [311], FNDC5 [312], HLA-G [313], MMP9 [314], SLC22A18 [315] and BMP10 [316] are an independent prognostic factors in hypertension, but these genes might be novel targets for NAFLD. EGR1 [317], NR4A1 [318], NR4A2 [319], DUSP1 [320], GADD45G [321], DLK1 [322], SOCS2 [323], GADD45B [324], CXCL2 [325], EGR3 [326], PTGS2 [327], RGS2 [328], KL (klotho) [329], SOCS3 [330], MMP1 [331], CXCR4 [332], THBS1 [333], SLC7A11 [334], EGR2 [335], ZFP36 [336], KCNE4 [337], CCN2 [338], FST (follistatin) [339], CLEC4E [340], OGN (osteoglycin) [341], CTLA4 [342], KLF4 [343], CYTL1 [344], IL1RL1 [345], HBEGF (heparin binding EGF like growth factor) [346], CCL2 [347], OSM (oncostatin M) [348], PRRX1 [349], ERBB4 [350], MSTN (myostatin) [351], ADAMTS1 [352], PDK4 [353], EPO (erythropoietin) [354], GATA3 [355], IL10 [356], ADTRP (androgen dependent TFPI regulating protein) [357], ESR2 [358], VIP (vasoactive intestinal peptide) [359], KCNIP1 [360], PLA2G2A [361], FOXC1 [362], FOXO1 [363], S100B [364], DKK1 [365], SOX17 [366], SLC6A4 [367], CCL3 [368], NPHP3 [369], ATF3 [370], ANGPT2 [371], SOCS1 [372], MYZAP (myocardial zonulaadherens protein) [373], EYA4 [374], F2RL3 [278], TFAP2A [375], MYH7 [376], SLC22A12 [377], SCUBE1 [378], S1PR2 [379], COMP (cartilage oligomeric matrix protein) [380], EDN2 [381], ACHE (acetylcholinesterase) [382], SLC6A2 [383], TREM2 [384], LMOD2 [385], GCK (glucokinase) [386], FOXP3 [387], CYP7A1 [388], LPL (lipoprotein lipase) [389], ANGPTL8 [390], HCN2 [391], HSPA8 [392], MB (myoglobin) [393], KCNJ11 [394], HRH2 [395], TNFSF13 [396], UGT1A1 [397], IL2RA [398], KCNJ5 [399], ITGB3 [400], P2RY2 [401], GAS6 [402], PIEZO1 [403], DAB2IP [404], ACE2 [405], KCNE1 [406], S1PR4 [407], E2F1 [408], ROS1 [409], FADS2 [410], TIMP3 [411], CHI3L1 [412], PHLDA3 [413], MMP17 [414], RASAL1 [415], SLC5A10 [416], SUSD2 [417], OLFM2 [418], LAMA3 [419], BCAR1 [420], TREH (trehalase)

[421], FNDC5 [422], HLA-G [313], MMP9 [423] and MYL7 [424] are an important members in the progress of cardiovascular diseases, but these genes might be novel targets for NAFLD. Previous studies have shown that EGR1 [425], NR4A1 [426], DUSP1 [427], DLK1 [428], SIK1 [429], SOCS2 [430], IRS2 [431], SOCS3 [432], CXCR4 [433], THBS1 [434], GPAT3 [435], ZFP36 [436], DUSP2 [437], CCN2 [438], FST (follistatin) [439], PCK1 [440], KLF4 [441], IL1RL1 [442], CCL2 [443], OSM (oncostatin M) [444], MSTN (myostatin) [445], PDK4 [446], EPO (erythropoietin) [447], IL10 [448], VIP (vasoactive intestinal peptide) [449], CEBPB (CCAAT enhancer binding protein beta) [450], FOXO1 [451], S100B [452], DKK1 [453], SLC6A4 [454], CCL3 [455], FGF2 [456], ATF3 [457], SOCS1 [109], IL1RAP [458], MAP3K8 [459], SIM1 [460], SCUBE1 [461], CIDEA (cell death inducing DFFA like effector a) [462], ACHE (acetylcholinesterase) [463], TREM2 [464], SCD (stearoyl-CoA desaturase) [465], GCK (glucokinase) [466], CYP7A1 [467], LPL (lipoprotein lipase) [468], ANGPTL8 [469], KCNJ11 [470], UGT1A1 [471], KCNJ5 [472], GAS6 [473], ACE2 [474], MCHR1 [475], SPP1 [476], E2F1 [477], FADS2 [478], FASN (fatty acid synthase) [479], TIMP3 [480], CHI3L1 [481], MFAP5 [482], LAMB3 [483], SERPINA12 [484], GPBAR1 [485], TREH (trehalase) [486], ANGPTL7 [487], FNDC5 [488], HLA-G [489] and MMP9 [490] are involved in the progression of obesity, but these genes might be novel targets for NAFLD. Studies indicated that EGR1 [491], NR4A1 [492], DLK1 [493], SOCS2 [494], IRS2 [495], PTGS2 [496], RGS2 [497], SOCS3 [498], MMP1 [499], CXCR4 [500], FST (follistatin) [439], PCK1 [501], CHRM3 [502], CTLA4 [503], CCL2 [504], OSM (oncostatin M) [505], EPO (erythropoietin) [506], GATA3 [507], IL10 [508], ESR2 [509], VIP (vasoactive intestinal peptide) [510], KCNIP1 [511], PLA2G2A [361], FOXO1 [451], S100B [512], DKK1 [513], FGF7 [514], RGS16 [515], SLC6A4 [516], CCL3 [517], FGF2 [518], ATF3 [519], SOCS1 [372], COMP (cartilage oligomeric matrix protein) [520], IGF2BP1 [521], ACHE (acetylcholinesterase) [522], TREM2 [523], SCD (stearoyl-CoA desaturase) [524], GCK (glucokinase) [525], EIF2S3B [526], PDX1 [527], FOXP3 [528], CYP7A1 [529], LPL (lipoprotein lipase) [530], ANGPTL8 [531], HSPA8 [532], MB (myoglobin) [533], KCNJ11 [534], UGT1A9 [535], IL2RA [536], CDKN1A [537], SLC29A4 [538], GAS6 [539], PIEZO1 [540], ACE2 [541], E2F1 [542], ALDH3A1 [543], FADS2 [544], FASN (fatty acid synthase) [545], CHI3L1 [546], VTCN1 [547], SERPINA12 [548], GPBAR1 [549], BCAR1 [550], TREH (trehalase) [551], CFB (complement

factor B) [552], ANGPTL7 [553], FNDC5 [554], HLA-G [313] and MMP9 [555] played important roles in promoting the diabetes mellitus, but these genes might be novel targets for NAFLD. Németh et al. [556], Westbrook et al. [557], Hu et al. [558], Hu et al. [559], Duitman et al. [560], Landau et al. [561], Jang et al. [562], Kaludjerovic et al. [563], Li et al. [564], Zhang et al. [565], Dwivedi et al. [566], Mehta et al. [567], Baek et al. [341], Grywalska et al. [568], Xu et al. [569], Yu et al. [570], Sakai et al. [571], Feng et al. [572], Elbjeirami et al. [573], Feng et al. [574], Li et al. [575], Bataille et al. [576], Schrimpf et al. [577], Mitra et al. [578], Sun et al. [579], Hanudel et al. [580], Peda et al. [581], Yamaguchi et al. [582], Wang and He [583], Neto et al. [584], Luna-Antonio et al. [585], Hoff et al. [586], Li et al. [587], Cheng and Lin, [588], Tsai et al. [589], Chen et al. [590], Niitsuma et al. [591], Atanasio et al. [592], Sanchez-Niño et al. [593], Shaw et al. [594], Ichida et al. [595], Mazumder et al. [596], Cao et al. [597], Niida et al. [598], Hishida et al. [599], Hirooka et al. [600], Sallinen et al. [289], Huang et al. [601], Ćwiklińska et al. [602], Zou et al. [603], Tsantoulas et al. [604], Oguri et al. [292], Lenglet et al. [605], Pietrzak-Nowacka et al. [606], Lu et al. [607], Zhong et al. [608], Iatrino et al. [609], Yanagita, [610], Yard et al. [611], Maksimowski et al. [612], Valiño-Rivas et al. [613], Guan et al. [614], Wang et al. [615], Hoste et al. [616], Mao, [617], Fabretti et al. [618], Xiao et al. [619], Atwood et al. [620], Lu et al. [621], Khidr [554], Hauer et al. [622], Laucyte-Cibulskiene et al. [623], Yang et al. [624] and Matejas et al. [625] showed that EGR1, NR4A1, SIK1, CCN1, CEBPD (CCAAT enhancer binding protein delta), SOCS2, RGS2, KL (klotho), SOCS3, MMP1, CXCR4, CCN2, FST (follistatin), OGN (osteoglycin), CTLA4, KLF4, PTGER3, HBEGF (heparin binding EGF like growth factor), CCL2, OSM (oncostatin M), ERBB4, TNFSF11, MSTN (myostatin), ADAMTS1, CALCR (calcitonin receptor), INHBB (inhibin subunit beta B), EPO (erythropoietin), IL10, CEBPB (CCAAT enhancer binding protein beta), FOXO1, DKK1, GAS1, NPHP3, FGF2, ATF3, ANGPT2, SOCS1, IL1RAP, C9ORF72, BASP1, AKR1B10, SLC22A12, ACHE (acetylcholinesterase), TREM2, SCD (stearoyl-CoA desaturase), GCK (glucokinase), FOXP3, SLC22A2, EPHB2, LPL (lipoprotein lipase), ANGPTL8, HCN2, HSPA8, MB (myoglobin), KCNJ11, GLIS2, TNFSF13, LSS (lanosterol synthase), GAS6, AGRN (agrin), ACE2, NLRP6, DPEP1, TIMP3, CHI3L1, RASAL1, FAT1, GPBAR1, TREH (trehalase), CFB (complement factor B), FNDC5, HLA-G, MMP9, C4A and LAMB2 were associated with kidney disease, but these genes might be novel targets for NAFLD.

Xu et al. [626], Moles et al. [627], Ogata et al. [628], Okamoto et al. [629], Liu et al. [630], Nakamura et al. [631], Liu et al. [632], Zhu et al. [633], Kovalenko et al. [634], Yang et al. [635], Li et al. [636], Znoyko et al. [637], Gong et al. [638], Diamantis et al. [639], Guo et al. [640], Lee et al. [641], Saleh et al. [642], Heinrichs et al. [643], Kurniawan et al. [644], She et al. [645], Mafanda et al. [646], Norman et al. [200], García-Ayllón et al. [647], Zhao et al. [648], Butler et al. [649], Urbánek et al. [650], Smirne et al. [651], Wu et al. [652], Yang et al. [653], Nishimura et al. [654], Han et al. [655] and Barascuk et al. [656] revealed that IRS2, CXCL2, SOCS3, MMP1, CXCR4, SLC7A11, CCN2, KLF4, CCL2, OSM (oncostatin M), PRRX1, ADAMTS1, IL10, VIP (vasoactive intestinal peptide), S100B, CCL3, FGF2, MSMP (microseminoprotein, prostate associated), SOCS1, COMP (cartilage oligomeric matrix protein), ACHE (acetylcholinesterase), FOXP3, EPHB2, UGT1A1, GAS6, ACE2, E2F1, CHI3L1, PHLDA3 and MMP9 are associated with liver cirrhosis. Altered expression of KL (klotho) [657], SOCS3 [658], MMP1 [659], CXCR4 [660], RASD1 [661], SLC7A11 [662], OGN (osteoglycin) [341], KLF4 [663], IL1RL1 [664], CCL2 [665], EPO (erythropoietin) [666], IL10 [667], ESR2 [668], VIP (vasoactive intestinal peptide) [669], FOXC1 [670], FOXO1 [671], S100B [672], DKK1 [673], SOCS1 [674], C9ORF72 [675], CTCFL (CCCTC-binding factor like) [676], S1PR2 [677], ACHE (acetylcholinesterase) [678], TREM2 [679], EPHB2 [680], LPL (lipoprotein lipase) [681], P2RY2 [682], ACE2 [683], CHI3L1 [684], HLA-G [685] and MMP9 [686] are found in cerebrovascular diseases, but these genes might be novel targets for NAFLD.

By analyzing the PPI network and modules, a number of hub genes were identified that may provide new approaches for therapeutic studies of NAFLD. Thus, IKBKG (inhibitor of nuclear factor kappa B kinase regulatory subunit gamma), SFN (stratifin), FOSB (FosB proto-oncogene, AP-1 transcription factor subunit), JUNB (JunB proto-oncogene, AP-1 transcription factor subunit) and JUND (JunD proto-oncogene, AP-1 transcription factor subunit) can be a novel molecular markers of NAFLD and provide new insight to improve therapeutic strategies for NAFLD complications.

A miRNA-hub gene regulatory network and TF-hub gene regulatory network were constructed with hub genes, and then miRNAs and TFs were identified. CDT1 [687], ZWINT (ZW10 interacting kinetochore protein) [688],

hsa-mir-3613-3p [689], GATA2 [690], RUNX1 [691], SUZ12 [692], NUCKS1 [693], FOXP2 [694], TP53 [695], AHR (aryl hydrocarbon receptor) [696] and TRIM28 [697] were revealed to be correlated with disease outcome in patients with hepatocellular carcinoma. Hsa-mir-199a-5p [698], hsa-mir-22-5p [699], hsa-mir-338-5p [700], GATA2 [701], RUNX1 [702], SUZ12 [703], TP53 [704] and AHR (aryl hydrocarbon receptor) [705] were revealed to be associated with cardiovascular diseases, but these molecular markers might be novel targets for NAFLD. Hsa-mir-199a-5p [698], GATA2 [706], FOXP2 [707] and AHR (aryl hydrocarbon receptor) [708] have been demonstrated to function in hypertension, but these genes might be novel targets for NAFLD. Previous studies have demonstrated that hsa-mir-22-5p [709], hsa-mir-150-5p [710], RUNX1 [711], TP53 [712], AHR (aryl hydrocarbon receptor) [713] and TRIM28 [714] are an independent prognostic factor in obesity and might be associated with obesity pathogenesis, but these genes might be novel targets for NAFLD. Wang et al. [715], Lu et al. [716], Shi et al. [717], Yu et al. [718], Zhang et al. [719] and Ren et al. [720] reported that altered expression of hsa-mir-3613-3p, hsa-mir-103a-3p, hsa-mir-150-5p, GATA2, RUNX1 and AHR (aryl hydrocarbon receptor) correlated in patients with kidney disease, but these genes might be novel targets for NAFLD. Previous reports have demonstrated that hsa-mir-150-5p [721] and RUNX1 [722] are associated with liver cirrhosis. Increasing evidence demonstrated that hsa-mir-150-5p [723] and TP53 [724] have a function in diabetes mellitus, but these genes might be novel targets for NAFLD. Bertran et al. [725], Yan et al. [726] and Zhu et al. [727] revealed that RUNX1, TP53 and AHR (aryl hydrocarbon receptor) may be the potential targets for NAFLD diagnosis and treatment. Thus, hsa-mir-33a-3p, hsa-mir-561-3p, hsa-mir-30b-3p and hsa-mir-202-3p can be novel molecular markers of NAFLD and provide new insight to improve therapeutic strategies for NAFLD complications.

In conclusion, the large-scale data analysis of the current investigation provides a comprehensive bioinformatics analysis of DEGs that might be associated in the progress of NAFLD. This investigation provides a set of important targets for future studies into the molecular mechanisms and molecular markers involved in NAFLD. The exploration of potential key genes of NAFLD might provide some potential help in further identification of novel molecular markers for the susceptibility of NAFLD and useful treatment targets. The real

function of key genes needs to be explored further to determine the clinical and biological mechanism of NAFLD.

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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. [(GSE135251) <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE135251>]

Consent for publication

Not applicable.

Competing interests

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Author Contributions

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

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Tables

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

GeneSymbol	logFC	pValue	adj.P.Val	tvalue	Regulation	GeneName
FOSB	7.509016	4.43E-56	1.09E-51	15.77765	Up	FosB proto-oncogene, AP-1 transcription factor subunit
MTND1P23	6.79767	2.13E-15	1.54E-13	7.933622	Up	MT-ND1 pseudogene 23
FOS	6.258907	1.45E-38	3.96E-35	12.98684	Up	Fos proto-oncogene, AP-1 transcription factor subunit
LRFN5	5.351826	2.24E-05	0.000156	4.239322	Up	leucine rich repeat and fibronectin type III domain containing 5
MTND4P24	5.321435	4.45E-06	3.72E-05	4.589004	Up	MT-ND4 pseudogene 24
IGFBP1	5.012589	1.29E-18	1.82E-16	8.806635	Up	insulin like growth factor binding protein 1
MTCO1P12	4.800342	4.28E-26	2.62E-23	10.5661	Up	MT-CO1 pseudogene 12
MTATP8P2	4.76102	1.76E-17	2.04E-15	8.508799	Up	MT-ATP8 pseudogene 2
MT1B	4.627883	0.000204	0.001083	3.714405	Up	metallothionein 1B
AREG	4.57058	6.70E-08	8.74E-07	5.399035	Up	amphiregulin
IL6	4.563953	1.22E-11	3.70E-10	6.777366	Up	interleukin 6
RNU4-62P	4.522144	6.60E-09	1.07E-07	5.80073	Up	RNA, U4 small nuclear 62, pseudogene
RGS1	4.489436	4.29E-52	5.26E-48	15.1873	Up	regulator of G protein signaling 1
NR4A3	4.369466	3.37E-25	1.80E-22	10.37078	Up	nuclear receptor subfamily 4 group A member 3
CA8	4.132752	9.87E-08	1.23E-06	5.329048	Up	carbonic anhydrase 8
C12orf56	4.068513	0.000151	0.000836	3.78956	Up	chromosome 12 open reading frame 56
MTATP6P2	3.982091	1.26E-11	3.79E-10	6.773653	Up	MT-ATP6 pseudogene 2
IGLV1-70	3.898277	0.000306	0.001547	3.61001	Up	immunoglobulin lambda variable (I)-70 (pseudogene)
EGR1	3.87839	3.24E-14	1.68E-12	7.588421	Up	early growth response 1
RGS7	3.861976	0.000784	0.003461	3.358377	Up	regulator of G protein signaling 7
PPP1R3G	3.777764	2.29E-28	1.81E-25	11.04614	Up	protein phosphatase 1 regulatory subunit 3G
MTCO1P53	3.760854	2.05E-07	2.36E-06	5.194552	Up	MT-CO1 pseudogene 53
NR4A1	3.697306	2.69E-38	6.59E-35	12.93971	Up	nuclear receptor subfamily 4 group A member 1
RPL17P18	3.568068	8.08E-16	6.43E-14	8.053015	Up	ribosomal protein L17 pseudogene 18
TBC1D3E	3.551988	0.000154	0.000851	3.783997	Up	TBC1 domain family member 3E
CPA4	3.533492	2.82E-12	9.90E-11	6.986471	Up	carboxypeptidase A4
LEMD1-AS1	3.489395	4.45E-10	9.51E-09	6.237295	Up	LEMD1 antisense RNA 1
FAM177B	3.394518	7.18E-08	9.27E-07	5.38665	Up	family with sequence similarity 177 member B
RPL17P39	3.39451	7.47E-16	6.04E-14	8.06266	Up	ribosomal protein L17 pseudogene 39
RPL10P6	3.368648	5.51E-07	5.72E-06	5.007802	Up	ribosomal protein L10 pseudogene 6
RPL3P7	3.25205	4.34E-22	1.29E-19	9.662755	Up	ribosomal protein L3 pseudogene 7
NR4A2	3.23937	3.08E-45	1.26E-41	14.11474	Up	nuclear receptor subfamily 4 group A member 2
APOL5	3.221593	6.35E-08	8.33E-07	5.408528	Up	apolipoprotein L5
SIK1B	3.211802	1.44E-14	8.24E-13	7.692873	Up	salt inducible kinase 1B (putative)
DUSP1	3.20409	7.62E-38	1.46E-34	12.85939	Up	dual specificity phosphatase 1

RPS8P10	3.176006	2.19E-05	0.000153	4.244817	Up	ribosomal protein S8 pseudogene 10
GADD45G	3.141297	1.55E-23	6.25E-21	9.998028	Up	growth arrest and DNA damage inducible gamma
NRK	3.095682	5.48E-06	4.47E-05	4.545684	Up	Nik related kinase
IGKV2-29	3.082976	0.008586	0.026623	2.628128	Up	immunoglobulin kappa variable 2- 29
RPL21P16	3.081713	1.17E-09	2.25E-08	6.084296	Up	ribosomal protein L21 pseudogene 16
RPL10P9	3.043306	1.79E-07	2.09E-06	5.220161	Up	ribosomal protein L10 pseudogene 9
DLK1	2.99651	0.00287	0.010537	2.981288	Up	delta like non-canonical Notch ligand 1
SIK1	2.959782	0.000172	0.000933	3.757288	Up	salt inducible kinase 1
ST8SIA6-AS1	2.951242	0.001784	0.007028	3.123985	Up	ST8SIA6 antisense RNA 1
IGKV1D-17	2.946644	0.005022	0.017005	2.805605	Up	immunoglobulin kappa variable 1D- 17
RPS7P3	2.934627	4.44E-09	7.47E-08	5.866903	Up	ribosomal protein S7 pseudogene 3
SYT4	2.82887	4.32E-05	0.000278	4.089632	Up	synaptotagmin 4
CCN1	2.827779	3.22E-21	7.80E-19	9.455473	Up	cellular communication network factor 1
FAM83A-AS1	2.771735	2.10E-11	6.09E-10	6.698917	Up	FAM83A antisense RNA 1
TUBA3E	2.764423	0.002742	0.010125	2.995272	Up	tubulin alpha 3e
SIM1	2.76156	1.66E-06	1.54E-05	4.790749	Up	SIM bHLH transcription factor 1
MTND4P12	2.760641	3.71E-15	2.48E-13	7.864314	Up	MT-ND4 pseudogene 12
APOLD1	2.751719	2.08E-43	7.28E-40	13.81474	Up	apolipoprotein L domain containing 1
MROH2B	2.737739	0.000161	0.000881	3.774058	Up	maestro heat like repeat family member 2B
RPS8P1	2.731071	1.23E-16	1.17E-14	8.279741	Up	ribosomal protein S8 pseudogene 1
LGALS17A	2.699805	6.49E-05	0.000398	3.994152	Up	galectin 14 pseudogene
CEBPD	2.684378	1.82E-33	2.35E-30	12.05516	Up	CCAAT enhancer binding protein delta
SOCS2	2.676608	5.13E-19	7.76E-17	8.909519	Up	suppressor of cytokine signaling 2
RPS3AP25	2.645136	3.68E-09	6.31E-08	5.897792	Up	RPS3A pseudogene 25
IRS2	2.642965	7.72E-38	1.46E-34	12.85831	Up	insulin receptor substrate 2
RPS3AP47	2.637009	1.87E-09	3.43E-08	6.009013	Up	RPS3A pseudogene 47
CH25H	2.602118	2.84E-08	4.02E-07	5.55077	Up	cholesterol 25-hydroxylase
TAT-AS1	2.594205	6.24E-06	5.01E-05	4.518183	Up	TAT antisense RNA 1
RPL17P7	2.590889	1.36E-18	1.89E-16	8.800982	Up	ribosomal protein L17 pseudogene 7
GADD45B	2.576253	4.72E-30	4.63E-27	11.38948	Up	growth arrest and DNA damage inducible beta
CTCFL	2.562592	6.48E-05	0.000398	3.99448	Up	CCCTC-binding factor like
ZAN	2.554624	0.002909	0.01067	2.977209	Up	zonadhesin
RPL26P6	2.543475	2.52E-15	1.78E-13	7.912631	Up	ribosomal protein L26 pseudogene 6
MIR3682	2.519782	1.18E-09	2.28E-08	6.082498	Up	microRNA 3682
CXCL2	2.502701	1.50E-19	2.61E-17	9.044824	Up	C-X-C motif chemokine ligand 2
ZFAND5	2.497585	2.43E-47	1.19E-43	14.4521	Up	zinc finger AN1-type containing 5
EGR3	2.496834	1.26E-11	3.81E-10	6.772787	Up	early growth response 3
PTGS2	2.476561	7.15E-17	7.10E-15	8.344464	Up	prostaglandin-endoperoxide synthase 2
TUBA3D	2.476513	5.74E-05	0.000358	4.023169	Up	tubulin alpha 3d
RPS15AP17	2.470538	0.000988	0.004218	3.293942	Up	ribosomal protein S15a pseudogene 17

RPL7AP50	2.468082	1.00E-15	7.73E-14	8.026603	Up	ribosomal protein L7a pseudogene 50
PET117	2.466199	4.45E-08	6.02E-07	5.472009	Up	PET117 cytochrome c oxidase chaperone
GABRG3	2.456083	0.000421	0.002033	3.526739	Up	gamma-aminobutyric acid type A receptor subunit gamma3
RPS15AP19	2.453508	1.34E-13	6.05E-12	7.401896	Up	ribosomal protein S15a pseudogene 19
RGS2	2.446243	4.80E-36	7.85E-33	12.53503	Up	regulator of G protein signaling 2
TCIM	2.44542	3.72E-50	2.28E-46	14.89189	Up	transcriptional and immune response regulator
SLC22A10	2.432567	1.21E-09	2.32E-08	6.079215	Up	solute carrier family 22 member 10
KL	2.410474	7.70E-07	7.72E-06	4.942877	Up	klotho
NPAS3	2.404282	2.09E-16	1.92E-14	8.21704	Up	neuronal PAS domain protein 3
ZNF804A	2.401022	3.92E-05	0.000255	4.11228	Up	zinc finger protein 804A
C3orf80	2.399839	2.20E-06	1.97E-05	4.733781	Up	chromosome 3 open reading frame 80
FOSL1	2.398478	5.20E-05	0.000327	4.046326	Up	FOS like 1, AP-1 transcription factor subunit
RPS15AP1	2.389314	4.76E-17	4.85E-15	8.392432	Up	ribosomal protein S15a pseudogene 1
SOCS3	2.363137	1.30E-11	3.91E-10	6.7682	Up	suppressor of cytokine signaling 3
ART5	2.362353	1.62E-05	0.000118	4.311213	Up	ADP-ribosyltransferase 5
RPL3P4	2.357828	1.06E-25	6.05E-23	10.48058	Up	ribosomal protein L3 pseudogene 4
PTCHD3	2.354559	0.002263	0.008608	3.053386	Up	patched domain containing 3
B3GALT1	2.327229	0.000514	0.002413	3.473165	Up	beta-1,3-galactosyltransferase 1
MMP1	2.320053	0.004845	0.016479	2.817184	Up	matrix metalloproteinase 1
RPL21P119	2.306992	9.38E-13	3.63E-11	7.139298	Up	ribosomal protein L21 pseudogene 119
RPL17P50	2.305436	2.21E-08	3.18E-07	5.594934	Up	ribosomal protein L17 pseudogene 50
AGAP1-IT1	2.300341	3.40E-07	3.72E-06	5.099901	Up	AGAP1 intronic transcript 1
TMSB4XP4	2.294475	1.75E-07	2.05E-06	5.223613	Up	TMSB4X pseudogene 4
ODF3L1	2.276254	0.00018	0.000971	3.746004	Up	outer dense fiber of sperm tails 3 like 1
CXCR4	2.267462	2.64E-20	5.31E-18	9.232643	Up	C-X-C motif chemokine receptor 4
RASD1	2.242336	4.69E-10	9.96E-09	6.229049	Up	ras related dexamethasone induced 1
RPL7P6	2.216399	8.62E-05	0.000511	3.926336	Up	ribosomal protein L7 pseudogene 6
NKAIN2	2.209145	0.000198	0.001053	3.722051	Up	sodium/potassium transporting ATPase interacting 2
SDR9C7	2.202416	0.000616	0.002826	3.424569	Up	short chain dehydrogenase/reductase family 9C member 7
THBS1	2.192697	2.35E-12	8.42E-11	7.011796	Up	thrombospondin 1
SLC7A11	2.184833	6.64E-06	5.29E-05	4.504792	Up	solute carrier family 7 member 11
FAM83A	2.175805	2.73E-05	0.000186	4.195017	Up	family with sequence similarity 83 member A
SNORA72	2.166943	2.70E-08	3.84E-07	5.559819	Up	small nucleolar RNA, H/ACA box 72
CCDC196	2.166171	6.65E-17	6.66E-15	8.353008	Up	coiled-coil domain containing 196
GPAT3	2.165337	3.20E-21	7.80E-19	9.456108	Up	glycerol-3-phosphate acyltransferase 3
MT1JP	2.163846	0.000391	0.001912	3.545784	Up	metallothionein 1J, pseudogene
TNR	2.158655	0.000978	0.00418	3.296878	Up	tenascin R
PCSK2	2.156702	0.000486	0.002293	3.488601	Up	proprotein convertase subtilisin/kexin type 2

GMPS1	2.155866	5.58E-06	4.54E-05	4.541867	Up	guanine monophosphate synthase pseudogene 1
LNCPRESS1	2.141163	0.006186	0.020181	2.737739	Up	lncRNA p53 regulated and ESC associated 1
TMEM233	2.139537	4.08E-08	5.55E-07	5.48752	Up	transmembrane protein 233
TUBB8	2.139495	0.004889	0.016615	2.814237	Up	tubulin beta 8 class VIII pleckstrin homology like domain family A member 1
PHLDA1	2.124507	6.68E-24	3.04E-21	10.08129	Up	ribosomal protein L10 pseudogene 15
RPL10P15	2.122853	1.19E-05	8.93E-05	4.379778	Up	
KRT27	2.113841	9.80E-07	9.58E-06	4.895642	Up	keratin 27
EGR2	2.101963	1.39E-10	3.31E-09	6.417418	Up	early growth response 2
ZFP36	2.098365	3.89E-32	4.54E-29	11.80029	Up	ZFP36 ring finger protein RNA, U6 small nuclear 925, pseudogene
RNU6-925P	2.09668	0.000372	0.001826	3.559347	Up	nuclear receptor subfamily 0 group B member 2
NR0B2	2.096677	1.40E-11	4.15E-10	6.758341	Up	
RSPH10B	2.069831	3.38E-05	0.000224	4.146435	Up	radial spoke head 10 homolog B UDP glucuronosyltransferase family 2 member A1 complex locus
UGT2A1	2.067302	2.11E-05	0.000148	4.252913	Up	
MAFF	2.061383	2.65E-15	1.86E-13	7.906445	Up	MAF bZIP transcription factor F NACA family member 3, pseudogene
NACA3P	2.058831	1.85E-11	5.43E-10	6.717409	Up	ribosomal protein L21 pseudogene 28
RPL21P28	2.049875	9.43E-09	1.47E-07	5.740738	Up	
CXCL3	2.039437	6.61E-08	8.63E-07	5.401447	Up	C-X-C motif chemokine ligand 3 cysteine and serine rich nuclear protein 1
CSRN1	2.037053	3.72E-39	1.14E-35	13.09076	Up	
RHOB	2.019831	5.27E-27	3.40E-24	10.76089	Up	ras homolog family member B
NRXN1	2.016855	0.000483	0.002284	3.489914	Up	neurexin 1
DUSP2	2.013612	5.28E-14	2.61E-12	7.524771	Up	dual specificity phosphatase 2
RPS15P4	2.000167	8.91E-11	2.24E-09	6.484331	Up	ribosomal protein S15 pseudogene 4
RPL6P27	1.98693	1.25E-17	1.50E-15	8.548251	Up	ribosomal protein L6 pseudogene 27
RPS18P2	1.984916	2.31E-07	2.61E-06	5.172765	Up	ribosomal protein S18 pseudogene 2
RPS7P1	1.982026	3.24E-21	7.80E-19	9.454582	Up	ribosomal protein S7 pseudogene 1
DIPK2A	1.974751	2.51E-15	1.78E-13	7.913013	Up	divergent protein kinase domain 2A potassium voltage-gated channel subfamily E regulatory subunit 4 small nucleolar RNA, H/ACA box 53
SNORA53	1.963291	0.001923	0.007492	3.101925	Up	
KLHDC8A	1.962945	0.001504	0.00606	3.173832	Up	kelch domain containing 8A
IFT74-AS1	1.96109	0.002183	0.008352	3.064192	Up	IFT74 antisense RNA 1
RPL15P3	1.957616	1.42E-14	8.18E-13	7.69415	Up	ribosomal protein L15 pseudogene 3 cellular communication network factor 2
CCN2	1.957222	7.39E-11	1.89E-09	6.512488	Up	ribosomal protein L13a pseudogene 25
RPL13AP25	1.957217	4.05E-07	4.35E-06	5.066623	Up	
FST	1.933931	1.42E-14	8.18E-13	7.694133	Up	follistatin
RPS27AP5	1.927614	8.92E-14	4.20E-12	7.455995	Up	ribosomal protein S27a pseudogene 5
CLEC4E	1.92307	3.48E-08	4.82E-07	5.515565	Up	C-type lectin domain family 4 member E
OGN	1.91717	0.00397	0.013914	2.880561	Up	osteoglycin
RNU6-1136P	1.912888	0.001005	0.004284	3.289068	Up	RNA, U6 small nuclear 1136, pseudogene
ANKRD45	1.911025	5.65E-05	0.000353	4.026814	Up	ankyrin repeat domain 45

NDUFB4P11	1.909743	0.001524	0.006128	3.170125	Up	NADH:ubiquinoneoxidoreductase subunit B4 pseudogene 11
CABCOCO1	1.905323	8.53E-05	0.000505	3.929085	Up	ciliary associated calcium binding coiled-coil 1
PCK1	1.903228	2.03E-07	2.34E-06	5.196364	Up	phosphoenolpyruvatecarboxykinase 1
B3GALT1-AS1	1.902615	3.53E-07	3.84E-06	5.092787	Up	B3GALT1 antisense RNA 1
RPL21P94	1.902553	0.014774	0.04179	2.437883	Up	ribosomal protein L21 pseudogene 94
RNY1	1.895286	0.008163	0.025526	2.645258	Up	RNA, Ro60-associated Y1 solute carrier organic anion transporter family member 1B7 (putative)
SLCO1B7	1.893336	1.63E-05	0.000118	4.310229	Up	proteoglycan 3, pro eosinophil major basic protein 2 pseudogene
SLED1	1.891885	2.40E-06	2.13E-05	4.716077	Up	neuronal growth regulator 1
NEGR1	1.889876	0.000808	0.00355	3.350059	Up	cholinergic receptor muscarinic 3
CHRM3	1.882762	0.000537	0.002507	3.461619	Up	ribosomal protein L36a pseudogene 37
RPL36AP37	1.879388	2.71E-16	2.43E-14	8.185357	Up	protein phosphatase 2 regulatory subunit B'gammapseudogene
PPP2R5CP	1.87835	4.06E-07	4.35E-06	5.066279	Up	cytotoxic T-lymphocyte associated protein 4
CTLA4	1.877365	2.30E-06	2.05E-05	4.724841	Up	pentraxin 3
PTX3	1.873603	1.30E-05	9.66E-05	4.359909	Up	chromosome 5 open reading frame 49
C5orf49	1.869027	1.50E-07	1.79E-06	5.252558	Up	keratin 18 pseudogene 10
KRT18P10	1.868467	0.000131	0.000739	3.824838	Up	ribosomal protein L26 pseudogene 4
RPL26P4	1.868368	1.41E-07	1.70E-06	5.26363	Up	Kruppel like factor 4
KLF4	1.867989	1.03E-21	2.80E-19	9.573951	Up	prostaglandin E receptor 3
PTGER3	1.867904	6.51E-06	5.21E-05	4.509082	Up	zinc finger protein 80
ZNF80	1.867497	0.001214	0.005047	3.235491	Up	cytokine like 1
CYTL1	1.861148	0.005892	0.019379	2.753754	Up	coiled-coil domain containing 177
CCDC177	1.860448	0.015727	0.043996	2.415179	Up	mohawkhomeobox
MKX	1.859697	4.23E-10	9.08E-09	6.245392	Up	ferritin heavy chain 1 pseudogene 10
FTH1P10	1.858724	1.96E-12	7.25E-11	7.037284	Up	ELMO domain containing 1
ELMOD1	1.85691	0.011405	0.033691	2.530048	Up	ribosomal protein S15a pseudogene 11
RPS15AP11	1.856289	4.57E-08	6.15E-07	5.467376	Up	KH domain containing 1
KHDC1	1.852479	0.003308	0.0119	2.937532	Up	SOCS2 antisense RNA 1
SOCS2-AS1	1.849462	1.75E-07	2.05E-06	5.224608	Up	activity regulated cytoskeleton associated protein
ARC	1.845826	0.00877	0.027081	2.620898	Up	peripheral myelin protein 2
PMP2	1.843023	0.00603	0.019754	2.746154	Up	calcium voltage-gated channel subunit alpha1 A
CACNA1A	1.83943	0.001526	0.006137	3.169604	Up	ADAM metalloproteinase with thrombospondin type 1 motif 4
ADAMTS4	1.833043	2.71E-11	7.64E-10	6.661573	Up	T-box transcription factor 18
TBX18	1.829962	7.22E-07	7.30E-06	4.955406	Up	interleukin 1 receptor like 1
IL1RL1	1.821031	1.08E-06	1.05E-05	4.876324	Up	cold shock domain containing C2
CSDC2	1.817497	0.005732	0.018963	2.762706	Up	ankyrin repeat and SOCS box containing 3
ASB3	1.816111	8.20E-11	2.08E-09	6.496898	Up	XK related 4
XKR4	1.804937	0.009181	0.028134	2.605256	Up	heparin binding EGF like growth factor
HBEGF	1.80474	6.43E-16	5.38E-14	8.080866	Up	

BEND6	1.803952	0.000229	0.001201	3.68458	Up	BEN domain containing 6
CCL4L2	1.802129	3.31E-06	2.84E-05	4.65038	Up	C-C motif chemokine ligand 4 like 2
RNF212	1.798307	2.01E-05	0.000142	4.263366	Up	ring finger protein 212
VGLL3	1.79515	5.98E-05	0.00037	4.013588	Up	vestigial like family member 3
PRDM1	1.794699	1.68E-19	2.86E-17	9.032239	Up	PR/SET domain 1
PSME2P6	1.794645	0.004039	0.014133	2.87509	Up	proteasome activator subunit 2 pseudogene 6
CCL2	1.787317	1.01E-10	2.51E-09	6.466196	Up	C-C motif chemokine ligand 2
KIR3DL2	1.786695	0.008617	0.026703	2.626891	Up	killer cell immunoglobulin like receptor, three Ig domains and long cytoplasmic tail 2
OSM	1.77864	0.000168	0.000917	3.762343	Up	oncostatin M
PELI2	1.774532	3.79E-16	3.31E-14	8.1451	Up	pellino E3 ubiquitin protein ligase family member 2
RPS23P8	1.773323	2.19E-13	9.52E-12	7.336716	Up	ribosomal protein S23 pseudogene 8
RPL21P51	1.771997	0.004584	0.015692	2.83487	Up	ribosomal protein L21 pseudogene 51
EDIL3	1.768903	0.001467	0.005929	3.181202	Up	EGF like repeats and discoidin domains 3
H4C11	1.759585	0.000275	0.001408	3.6379	Up	H4 clustered histone 11
PRRX1	1.759548	0.008856	0.027289	2.617567	Up	paired related homeobox 1
AADACP1	1.758315	4.90E-13	2.02E-11	7.228004	Up	arylacetamidedeacetylasepseudogen e 1
ERBB4	1.757092	0.00382	0.013463	2.892634	Up	erb-b2 receptor tyrosine kinase 4
NOTCH2NLA	1.752141	1.25E-06	1.19E-05	4.847961	Up	notch 2 N-terminal like A
SORD2P	1.751557	4.34E-12	1.46E-10	6.9255	Up	sorbitol dehydrogenase 2, pseudogene
ATP2B1-AS1	1.747586	1.54E-13	6.87E-12	7.384068	Up	ATP2B1 antisense RNA 1
GRIK1	1.735597	2.55E-06	2.24E-05	4.704272	Up	glutamate ionotropic receptor kainate type subunit 1
CBLN4	1.733543	1.59E-09	2.97E-08	6.034994	Up	cerebellin 4 precursor
TNFSF11	1.729199	3.89E-10	8.40E-09	6.258213	Up	TNF superfamily member 11
MSTN	1.723793	1.70E-05	0.000123	4.300462	Up	myostatin
PFN1P2	1.722251	7.64E-05	0.00046	3.955298	Up	profilin 1 pseudogene 2
MEIOB	1.720415	0.000456	0.002175	3.505626	Up	meiosis specific with OB-fold
PDXDC2P	1.720344	0.000265	0.001365	3.647073	Up	pyridoxal dependent decarboxylase domain containing 2, pseudogene
ATP8B5P	1.719646	0.000126	0.000713	3.834438	Up	ATPase phospholipid transporting 8B5, pseudogene
PDILT	1.717883	0.000262	0.001352	3.649979	Up	protein disulfideisomerase like, testis expressed
ADAMTS1	1.717205	3.97E-14	2.01E-12	7.562035	Up	ADAM metalloproteinase with thrombospondin type 1 motif 1
PCAT1	1.713874	1.42E-05	0.000105	4.339982	Up	prostate cancer associated transcript 1
AVPR1A	1.711915	4.13E-06	3.48E-05	4.604557	Up	arginine vasopressin receptor 1A
CXXC4	1.707905	3.74E-08	5.15E-07	5.502608	Up	CXXC finger protein 4
WDFY3-AS2	1.707075	8.09E-12	2.55E-10	6.837004	Up	WDFY3 antisense RNA 2
CALCR	1.707024	0.000785	0.003464	3.358004	Up	calcitonin receptor
NDUFAF2P1	1.706418	1.33E-06	1.26E-05	4.835401	Up	NDUFAF2 pseudogene 1
PDK4	1.705309	5.72E-14	2.81E-12	7.51428	Up	pyruvate dehydrogenase kinase 4
CPB2-AS1	1.704581	0.002092	0.008058	3.076862	Up	CPB2 antisense RNA 1
RPS3AP20	1.704152	6.19E-07	6.36E-06	4.985037	Up	RPS3A pseudogene 20

RPL32P18	1.703802	5.44E-11	1.44E-09	6.558387	Up	ribosomal protein L32 pseudogene 18
NT5C3AP1	1.701405	0.00044	0.002111	3.514799	Up	NT5C3A pseudogene 1
NUDT11	1.701216	0.005951	0.019544	2.750452	Up	nudix hydrolase 11
VN1R51P	1.699727	0.002377	0.008978	3.038631	Up	vomeroneural 1 receptor 51 pseudogene
RPLP0P2	1.696493	0.010436	0.031353	2.561047	Up	ribosomal protein lateral stalk subunit P0 pseudogene 2
RPS4XP6	1.695047	0.000357	0.001762	3.570007	Up	ribosomal protein S4X pseudogene 6
DEPP1	1.693129	5.96E-12	1.94E-10	6.880713	Up	DEPP1 autophagy regulator
NOX4	1.690982	3.21E-05	0.000214	4.15799	Up	NADPH oxidase 4
INHBB	1.687805	2.31E-09	4.17E-08	5.974173	Up	inhibin subunit beta B
MIR3671	1.687276	0.000118	0.000674	3.850576	Up	microRNA 3671
PGM5-AS1	1.684539	0.000406	0.001972	3.53597	Up	PGM5 antisense RNA 1
RPL34P27	1.683143	2.65E-06	2.33E-05	4.695857	Up	ribosomal protein L34 pseudogene 27
TDRD12	1.682348	0.009546	0.029069	2.591842	Up	tudor domain containing 12
EPO	1.678747	0.000107	0.000616	3.874877	Up	erythropoietin
PLP1	1.67764	0.014317	0.040728	2.449217	Up	proteolipid protein 1
CADM2	1.675113	7.65E-06	6.01E-05	4.474733	Up	cell adhesion molecule 2
MGARP	1.673807	0.004779	0.016275	2.821587	Up	mitochondria localized glutamic acid rich protein
CFHR2	1.673732	4.45E-05	0.000285	4.082771	Up	complement factor H related 2 family with sequence similarity 107 member A
FAM107A	1.671913	4.09E-11	1.11E-09	6.600638	Up	hypoxanthine phosphoribosyltransferase 1
HPRT1	1.670049	8.74E-22	2.43E-19	9.590864	Up	PTPRF interacting protein alpha 2
PPFIA2	1.66714	0.000739	0.003297	3.374616	Up	PTPRF interacting protein alpha 2
RPS2P29	1.666342	0.001156	0.004834	3.249621	Up	ribosomal protein S2 pseudogene 29
TWIST2	1.659778	0.000191	0.001023	3.730004	Up	twist family bHLH transcription factor 2
LRRIC19	1.658596	0.001867	0.007309	3.110546	Up	leucine rich repeat containing 19
TSPAN5	1.658119	6.93E-09	1.11E-07	5.792731	Up	tetraspanin 5
RASSF10	1.657867	0.013723	0.039341	2.46443	Up	Ras association domain family member 10
GATA3	1.6567	2.55E-12	9.04E-11	7.000656	Up	GATA binding protein 3
SOWAHA	1.655972	2.64E-15	1.86E-13	7.906717	Up	sosondowahankyrin repeat domain family member A
HPR	1.655467	1.63E-23	6.43E-21	9.993558	Up	haptoglobin-related protein
RETREG1	1.653676	4.03E-12	1.36E-10	6.936084	Up	reticulophagy regulator 1
ANKRD37	1.653229	1.35E-18	1.89E-16	8.801384	Up	ankyrin repeat domain 37
RNU4ATAC18P	1.652161	0.011504	0.033914	2.527009	Up	RNA, U4atac small nuclear 18, pseudogene
SLCO1B3	1.650672	8.06E-06	6.30E-05	4.463656	Up	solute carrier organic anion transporter family member 1B3
RPL13P12	1.649024	4.16E-08	5.65E-07	5.48412	Up	ribosomal protein L13 pseudogene 12
ITGA6-AS1	1.648396	8.93E-07	8.83E-06	4.913781	Up	ITGA6 antisense RNA 1
MSH4	1.646883	0.002222	0.00848	3.058855	Up	mutS homolog 4
B3GAT2	1.645964	5.83E-06	4.70E-05	4.532617	Up	beta-1,3-glucuronyltransferase 2
SPATA9	1.644539	3.59E-06	3.06E-05	4.633551	Up	spermatogenesis associated 9
IL10	1.643001	8.90E-07	8.80E-06	4.914459	Up	interleukin 10

ODAD2	1.640553	0.002537	0.009489	3.018837	Up	outer dynein arm docking complex subunit 2
ADTRP	1.638465	5.73E-07	5.94E-06	5.000017	Up	androgen dependent TFPI regulating protein
JUN	1.634479	2.85E-12	1.00E-10	6.984719	Up	Jun proto-oncogene, AP-1 transcription factor subunit
RPL13AP20	1.634355	0.0003	0.001522	3.615061	Up	ribosomal protein L13a pseudogene 20
ABCA11P	1.63226	5.63E-06	4.57E-05	4.539981	Up	ATP binding cassette subfamily A member 11, pseudogene
FGF14	1.630385	0.002576	0.009593	3.014286	Up	fibroblast growth factor 14
EEF1A1P24	1.627818	1.20E-05	9.01E-05	4.377373	Up	eukaryotic translation elongation factor 1 alpha 1 pseudogene 24
ZNF350-AS1	1.627791	0.001177	0.004911	3.244409	Up	ZNF350 antisense RNA 1
MAK	1.626412	0.011212	0.033226	2.536015	Up	male germ cell associated kinase
KBTBD12	1.626196	0.015176	0.042723	2.428143	Up	kelch repeat and BTB domain containing 12
WDR38	1.623695	0.012356	0.036003	2.501801	Up	WD repeat domain 38
ESR2	1.620495	0.000314	0.001578	3.603715	Up	estrogen receptor 2
TAS2R14	1.619489	1.92E-09	3.52E-08	6.004531	Up	taste 2 receptor member 14
VIP	1.618694	8.82E-07	8.73E-06	4.916321	Up	vasoactive intestinal peptide
ARRDC5	1.61767	0.01052	0.031536	2.558261	Up	arrestin domain containing 5
RPS15AP12	1.616767	2.11E-05	0.000148	4.252723	Up	ribosomal protein S15a pseudogene 12
MT1A	1.60812	8.30E-07	8.27E-06	4.928084	Up	metallothionein 1A
MT1M	1.607404	2.83E-05	0.000192	4.186825	Up	metallothionein 1M
CD69	1.606622	1.27E-09	2.43E-08	6.070742	Up	CD69 molecule
KCNIP1	1.606506	0.005638	0.018733	2.768133	Up	potassium voltage-gated channel interacting protein 1
CMAHP	1.602829	4.19E-15	2.74E-13	7.84913	Up	cytidinemonomophospho-N-acetylneuraminic acid hydroxylase, pseudogene
RPS18P5	1.601651	2.41E-13	1.04E-11	7.323906	Up	ribosomal protein S18 pseudogene 5
CHRD1	1.597591	0.004005	0.014026	2.87777	Up	chordin like 1
RPL7AP47	1.593485	0.000249	0.001292	3.663534	Up	ribosomal protein L7a pseudogene 47
CEBPB	1.591328	5.14E-18	6.63E-16	8.650327	Up	CCAAT enhancer binding protein beta
CLEC4D	1.591313	0.002141	0.008216	3.069939	Up	C-type lectin domain family 4 member D
TFAP2A	1.584838	0.000518	0.002429	3.47106	Up	transcription factor AP-2 alpha
GRM1	1.583142	0.003826	0.013479	2.892139	Up	glutamate metabotropic receptor 1
RPL7AP20	1.582155	0.006966	0.022325	2.698448	Up	ribosomal protein L7a pseudogene 20
MTATP8P1	1.581843	0.012717	0.036884	2.491586	Up	MT-ATP8 pseudogene 1
DUTP6	1.581115	0.002193	0.008384	3.062809	Up	deoxyuridinetriphosphatase pseudogene 6
ELOVL4	1.577086	0.001432	0.005807	3.188102	Up	ELOVL fatty acid elongase 4
DNAJC12	1.576596	1.77E-22	6.02E-20	9.754225	Up	DnaJ heat shock protein family (Hsp40) member C12
TMED6	1.576477	2.88E-06	2.51E-05	4.679043	Up	transmembrane p24 trafficking protein 6
HCG14	1.576421	5.74E-06	4.65E-05	4.535612	Up	HLA complex group 14
RPL21P69	1.574643	0.001443	0.005847	3.185972	Up	ribosomal protein L21 pseudogene 69
PDE6C	1.571067	0.000494	0.00233	3.483743	Up	phosphodiesterase 6C
PLA2G2A	1.564533	0.005164	0.017406	2.796591	Up	phospholipase A2 group IIA

LRRC70	1.563805	3.07E-06	2.66E-05	4.665845	Up	leucine rich repeat containing 70
GRIK2	1.56236	0.000604	0.00278	3.429763	Up	glutamate ionotropic receptor kainate type subunit 2
RPL37P6	1.56236	3.09E-05	0.000207	4.166692	Up	ribosomal protein L37 pseudogene 6
HSPE1	1.562285	2.11E-12	7.72E-11	7.027042	Up	heat shock protein family E (Hsp10) member 1
RPL19P6	1.562067	0.013422	0.03863	2.472381	Up	ribosomal protein L19 pseudogene 6
C6orf58	1.558405	0.017892	0.049039	2.367847	Up	chromosome 6 open reading frame 58
HAO2-IT1	1.555911	2.71E-05	0.000185	4.19618	Up	HAO2 intronic transcript 1
MT1F	1.549617	2.26E-05	0.000158	4.237384	Up	metallothionein 1F
FAM86GP	1.547081	0.005528	0.018433	2.774539	Up	family with sequence similarity 86, member A pseudogene
HAS2	1.544557	2.99E-05	0.000201	4.174251	Up	hyaluronan synthase 2
ZNF45-AS1	1.539852	0.001236	0.005123	3.230393	Up	ZNF45 antisense RNA 1
PRIMA1	1.539522	0.00018	0.000973	3.745191	Up	proline rich membrane anchor 1
C20orf202	1.538826	3.61E-05	0.000238	4.130809	Up	chromosome 20 open reading frame 202
RNU6-117P	1.53795	0.016843	0.046595	2.390124	Up	RNA, U6 small nuclear 117, pseudogene
FOXC1	1.535716	5.51E-05	0.000344	4.032925	Up	forkhead box C1
JUNB	1.531729	5.12E-09	8.50E-08	5.843294	Up	JunB proto-oncogene, AP-1 transcription factor subunit
LURAP1L	1.526815	1.04E-20	2.30E-18	9.331585	Up	leucine rich adaptor protein 1 like
CCL3L1	1.521988	0.000532	0.002486	3.464243	Up	C-C motif chemokine ligand 3 like 1
JUND	1.519835	2.10E-10	4.80E-09	6.353753	Up	JunD proto-oncogene, AP-1 transcription factor subunit
FMC1	1.519018	2.01E-10	4.62E-09	6.360298	Up	formation of mitochondrial complex V assembly factor 1 homolog
FOXO1	1.516945	3.27E-14	1.69E-12	7.587183	Up	forkhead box O1
KLHL14	1.51536	0.000292	0.001484	3.622606	Up	kelch like family member 14
KLHDC1	1.511863	1.56E-12	5.84E-11	7.068695	Up	kelch domain containing 1
RPL18AP6	1.509833	8.21E-06	6.40E-05	4.459717	Up	ribosomal protein L18a pseudogene 6
ZNF37CP	1.504191	0.005799	0.01913	2.758936	Up	zinc finger protein 37C, pseudogene
NACA2	1.503051	7.39E-10	1.50E-08	6.157478	Up	nascent polypeptide associated complex subunit alpha 2
GPM6B	1.500962	0.000102	0.000592	3.88589	Up	glycoprotein M6B
S100B	1.500523	0.001011	0.004304	3.287458	Up	S100 calcium binding protein B
TAAR3P	1.496998	1.24E-06	1.19E-05	4.848583	Up	trace amine associated receptor 3, pseudogene
RPL10AP6	1.495206	7.19E-12	2.29E-10	6.853915	Up	ribosomal protein L10a pseudogene 6
KLF6	1.494742	6.72E-18	8.41E-16	8.619521	Up	Kruppel like factor 6
POLR2J3	1.492582	1.08E-06	1.04E-05	4.876755	Up	RNA polymerase II subunit J3
MIR659	1.486835	0.003056	0.011137	2.962021	Up	microRNA 659
MICU3	1.484976	1.12E-09	2.17E-08	6.091098	Up	mitochondrial calcium uptake family member 3
KCNK1	1.481597	9.09E-12	2.82E-10	6.82028	Up	potassium two pore domain channel subfamily K member 1
DKK1	1.481425	0.010366	0.031187	2.563366	Up	dickkopf WNT signaling pathway inhibitor 1
CCDC26	1.479692	0.001046	0.004433	3.277941	Up	CCDC26 long non-coding RNA
RNF152	1.479196	1.03E-10	2.56E-09	6.462488	Up	ring finger protein 152
HTR4	1.476899	0.016493	0.045783	2.397815	Up	5-hydroxytryptamine receptor 4

MT1X	1.475089	1.46E-07	1.75E-06	5.257638	Up	metallothionein 1X
PTPRD-AS1	1.472749	3.68E-07	4.00E-06	5.08468	Up	PTPRD antisense RNA 1
SMIM26	1.470783	3.28E-22	1.03E-19	9.691483	Up	small integral membrane protein 26
SLC19A2	1.470255	1.74E-14	9.75E-13	7.668188	Up	solute carrier family 19 member 2
RPL5P12	1.468986	0.007436	0.023566	2.676649	Up	ribosomal protein L5 pseudogene 12
NNMT	1.468269	6.60E-05	0.000403	3.990419	Up	nicotinamide N-methyltransferase
FGF7	1.461635	0.000152	0.00084	3.788302	Up	fibroblast growth factor 7
MTND2P28	1.460417	0.000184	0.000989	3.73989	Up	MT-ND2 pseudogene 28
PCDHB10	1.458696	0.000117	0.000669	3.852343	Up	protocadherin beta 10
CPNE6	1.457575	0.006078	0.01989	2.743523	Up	copine 6
ID2	1.454669	1.69E-21	4.47E-19	9.522325	Up	inhibitor of DNA binding 2
FSIP2-AS2	1.452052	0.003773	0.013316	2.896543	Up	FSIP2 antisense RNA 2
RGS16	1.451916	0.000213	0.001126	3.703575	Up	regulator of G protein signaling 16
RPL24P8	1.451284	2.97E-10	6.59E-09	6.300558	Up	RPL24 pseudogene 8
GPR171	1.449495	2.08E-06	1.88E-05	4.745306	Up	G protein-coupled receptor 171
SOX17	1.449013	5.36E-07	5.59E-06	5.012883	Up	SRY-box transcription factor 17
TENM3	1.44662	0.006502	0.021052	2.721353	Up	teneurintransmembrane protein 3
SLC6A4	1.446287	0.014593	0.041374	2.442334	Up	solute carrier family 6 member 4
CRP	1.444104	0.001367	0.005583	3.201457	Up	C-reactive protein
PTN	1.443214	8.58E-17	8.39E-15	8.322899	Up	pleiotrophin
C1QTNF3	1.443103	1.34E-08	2.02E-07	5.681129	Up	C1q and TNF related 3 family with sequence similarity 89 member A
FAM89A	1.442638	8.10E-20	1.49E-17	9.1119	Up	
SLC38A2	1.441664	1.03E-08	1.59E-07	5.725883	Up	solute carrier family 38 member 2
ZNF426-DT	1.441459	2.43E-06	2.15E-05	4.714288	Up	ZNF426 divergent transcript
DPY19L2P3	1.439901	5.05E-05	0.000319	4.053422	Up	DPY19L2 pseudogene 3
PTPRR	1.435579	0.016663	0.046198	2.394061	Up	protein tyrosine phosphatase receptor type R
EEF1B2P3	1.433112	5.85E-15	3.71E-13	7.80709	Up	eukaryotic translation elongation factor 1 beta 2 pseudogene 3
MLANA	1.433016	0.000175	0.00095	3.752448	Up	melan-A
GAS1	1.432266	2.91E-08	4.10E-07	5.546503	Up	growth arrest specific 1
PRKG2	1.431247	0.007483	0.023684	2.674537	Up	protein kinase cGMP-dependent 2 phorbol-12-myristate-13-acetate-induced protein 1
PMAIP1	1.430917	2.42E-05	0.000168	4.221907	Up	brain abundant membrane attached signal protein 1
BASPI	1.429931	2.51E-10	5.64E-09	6.326489	Up	eukaryotic translation elongation factor 1 beta 2 pseudogene 2
EEF1B2P2	1.428523	0.000563	0.002613	3.448994	Up	
EBPL	1.427247	2.40E-23	9.20E-21	9.954863	Up	EBP like
SLC25A25	1.426012	3.56E-11	9.77E-10	6.621131	Up	solute carrier family 25 member 25
CEACAM20	1.425738	0.007332	0.02331	2.681391	Up	CEA cell adhesion molecule 20
PCBP2	1.418328	5.65E-25	2.89E-22	10.32122	Up	poly(rC) binding protein 2
RPL21P98	1.418022	0.000141	0.000786	3.807132	Up	ribosomal protein L21 pseudogene 98
RPL9P8	1.417734	2.24E-08	3.22E-07	5.592552	Up	ribosomal protein L9 pseudogene 8
GRIP1	1.416974	0.000109	0.000627	3.870455	Up	glutamate receptor interacting protein 1
GLIPR1L2	1.415322	6.06E-07	6.23E-06	4.989402	Up	GLIPR1 like 2

N4BP2L1	1.414653	1.79E-20	3.79E-18	9.274107	Up	NEDD4 binding protein 2 like 1
CCL3	1.413627	2.21E-10	5.03E-09	6.345713	Up	C-C motif chemokine ligand 3
ADAMTS9-AS1	1.413236	0.000984	0.004204	3.295044	Up	ADAMTS9 antisense RNA 1 methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2 like
MTHFD2L	1.412824	5.17E-13	2.11E-11	7.220853	Up	chaperonin containing TCP1 subunit 8 pseudogene 1
CCT8P1	1.411651	1.89E-14	1.04E-12	7.657639	Up	ribosomal protein L7a pseudogene 6
RPL7AP6	1.409258	2.96E-11	8.27E-10	6.648454	Up	nephrocystin 3
NPHP3	1.408328	1.42E-10	3.38E-09	6.413764	Up	fibroblast growth factor 2 transient receptor potential cation channel subfamily C member 6 ribosomal protein SA pseudogene 14
FGF2	1.404873	1.83E-06	1.67E-05	4.771575	Up	microseminoprotein, prostate associated
TRPC6	1.402152	0.00569	0.018865	2.765138	Up	SREK1 interacting protein 1
RPSAP14	1.401113	0.005598	0.018618	2.770445	Up	SUGT1 pseudogene 3 dynein axonemal intermediate chain 1
MSMP	1.400859	0.017712	0.048617	2.371577	Up	mitotic spindle organizing protein 1 ribosomal protein SA pseudogene 18
SREK1IP1	1.400074	1.06E-16	1.02E-14	8.297516	Up	pleckstrin and Sec7 domain containing 2
SUGT1P3	1.397258	3.87E-05	0.000252	4.115203	Up	RPS3A pseudogene 26
DNAI1	1.39644	9.31E-05	0.000547	3.907924	Up	ribosomal protein L7 pseudogene 9
MZT1	1.394299	6.25E-11	1.63E-09	6.537717	Up	activating transcription factor 3 RNA binding motif single stranded interacting protein 1
RPSAP18	1.39349	0.00136	0.005558	3.203019	Up	arginase 2
PSD2	1.393387	0.000104	0.000602	3.881068	Up	frizzled class receptor 7
RPS3AP26	1.392672	5.75E-13	2.33E-11	7.206341	Up	t-complex 10 like
RPL7P9	1.392587	2.17E-17	2.45E-15	8.484453	Up	transmembrane protein 256
ATF3	1.392572	2.88E-10	6.43E-09	6.304884	Up	angiopoietin 2
RBMS1	1.390154	2.30E-15	1.64E-13	7.924183	Up	homeobox A4
ARG2	1.390135	3.33E-05	0.000221	4.149873	Up	synaptotagmin 6
FZD7	1.389708	2.40E-06	2.13E-05	4.716466	Up	suppressor of cytokine signaling 1 RNA, U6 small nuclear 817, pseudogene
TCP10L	1.384988	5.24E-07	5.48E-06	5.017235	Up	family with sequence similarity 9 member B
TMEM256	1.384523	1.73E-09	3.20E-08	6.021429	Up	GULP PTB domain containing engulfment adaptor 1
ANGPT2	1.380617	1.31E-05	9.70E-05	4.358759	Up	G protein subunit gamma 11
HOXA4	1.379579	1.42E-05	0.000105	4.340036	Up	zinc and ring finger 2 6-phosphofructo-2-kinase/fructose- 2,6-biphosphatase 3
SYT6	1.378974	0.017414	0.047915	2.377856	Up	chromosome 8 open reading frame 76
SOCS1	1.378464	0.000147	0.000818	3.795832	Up	MAM domain containing 2
RNU6-817P	1.377636	0.008245	0.025732	2.641868	Up	syntabulin
FAM9B	1.374994	0.000399	0.001943	3.540692	Up	STX5 divergent transcript
GULP1	1.37394	0.000842	0.003684	3.338558	Up	
GNG11	1.373805	5.34E-13	2.17E-11	7.216268	Up	
ZNRF2	1.373446	3.38E-18	4.48E-16	8.697829	Up	
PFKFB3	1.37301	4.42E-09	7.46E-08	5.867653	Up	
C8orf76	1.372952	1.75E-09	3.24E-08	6.019534	Up	
MAMDC2	1.371873	0.000945	0.00406	3.306357	Up	
SYBU	1.369174	2.59E-08	3.69E-07	5.567278	Up	
STX5-DT	1.36826	0.001929	0.007511	3.10094	Up	

PKN2-AS1	1.366929	0.007645	0.024112	2.66735	Up	PKN2 antisense RNA 1
GPR183	1.365495	1.73E-08	2.55E-07	5.637522	Up	G protein-coupled receptor 183
MT1H	1.363788	0.001207	0.00502	3.237303	Up	metallothionein 1H
EIF3EP3	1.362319	4.63E-07	4.92E-06	5.041079	Up	eukaryotic translation initiation factor 3 subunit E pseudogene 3
MYZAP	1.358181	4.54E-08	6.13E-07	5.468401	Up	myocardial zonulaadherens protein
RASL10A	1.357934	0.000227	0.001192	3.687119	Up	RAS like family 10 member A
MEF2C-AS1	1.357618	2.87E-05	0.000194	4.183199	Up	MEF2C antisense RNA 1
SNX16	1.356849	4.92E-10	1.04E-08	6.221555	Up	sorting nexin 16
IMPA1	1.3563	1.49E-14	8.48E-13	7.68832	Up	inositol monophosphatase 1
IL1RAP	1.355745	2.47E-07	2.77E-06	5.160162	Up	interleukin 1 receptor accessory protein
MAP3K8	1.355588	1.55E-24	7.45E-22	10.22399	Up	mitogen-activated protein kinase kinasekinase 8
SLC26A7	1.354428	0.004269	0.014795	2.857554	Up	solute carrier family 26 member 7
ARL17A	1.354312	0.000465	0.002211	3.500322	Up	ADP ribosylation factor like GTPase 17A
KNDC1	1.353624	0.008177	0.025558	2.644673	Up	kinase non-catalytic C-lobe domain containing 1
FAM72D	1.352185	0.012849	0.037199	2.487938	Up	family with sequence similarity 72 member D
EEF1A1P25	1.347851	0.010037	0.030344	2.574559	Up	eukaryotic translation elongation factor 1 alpha 1 pseudogene 25
LPAR6	1.347429	6.45E-10	1.33E-08	6.179	Up	lysophosphatidic acid receptor 6
MPPED2	1.346314	7.62E-06	5.99E-05	4.475613	Up	metallophosphoesterase domain containing 2
NEXMIF	1.346009	0.00145	0.005875	3.18451	Up	neurite extension and migration factor
HPGDS	1.339982	0.000183	0.000986	3.741103	Up	hematopoietic prostaglandin D synthase
RPL21P11	1.338479	0.009216	0.028223	2.603952	Up	ribosomal protein L21 pseudogene 11
DYNLRB2	1.337711	1.09E-07	1.34E-06	5.311566	Up	dynein light chain roadblock-type 2
PNRC1	1.336584	5.74E-18	7.28E-16	8.637672	Up	proline rich nuclear receptor coactivator 1
SAXO2	1.335654	0.005859	0.019287	2.755574	Up	stabilizer of axonemal microtubules 2
BTG1	1.335214	2.16E-28	1.77E-25	11.05113	Up	BTG anti-proliferation factor 1
CTNNA1-AS1	1.329634	0.00255	0.009525	3.01738	Up	CTNNA1 antisense RNA 1
PDGFRL	1.328152	1.33E-07	1.61E-06	5.275247	Up	platelet derived growth factor receptor like
RPL7AP43	1.327426	0.000104	0.000602	3.881026	Up	ribosomal protein L7a pseudogene 43
SLC22A24	1.325345	0.000548	0.002552	3.456034	Up	solute carrier family 22 member 24
EYA4	1.325125	0.004051	0.014172	2.874125	Up	EYA transcriptional coactivator and phosphatase 4
C1orf167	1.323889	0.002562	0.009557	3.015932	Up	chromosome 1 open reading frame 167
KLRC1	1.322003	2.89E-05	0.000195	4.181868	Up	killer cell lectin like receptor C1
C9orf72	1.321966	1.16E-11	3.53E-10	6.785186	Up	C9orf72-SMCR8 complex subunit
ETFRF1	1.319712	1.33E-06	1.26E-05	4.835314	Up	electron transfer flavoprotein regulatory factor 1
RPS13P8	1.318783	0.010926	0.032516	2.545048	Up	ribosomal protein S13 pseudogene 8
SNORA33	1.318036	0.000371	0.001824	3.559773	Up	small nucleolar RNA, H/ACA box 33
F2RL3	1.317994	0.002317	0.008788	3.046282	Up	F2R like thrombin or trypsin receptor 3
TAFA2	1.317707	6.86E-10	1.40E-08	6.169349	Up	TAFA chemokine like family member 2

EEF1E1	1.31754	5.94E-05	0.000368	4.015177	Up	eukaryotic translation elongation factor 1 epsilon 1
DNAAF10	1.31446	1.24E-06	1.18E-05	4.849685	Up	dynein axonemal assembly factor 10
MT1E	1.314439	3.70E-06	3.15E-05	4.62736	Up	metallothionein 1E
ST3GAL6	1.312024	4.19E-15	2.74E-13	7.849	Up	ST3 beta-galactoside alpha-2,3-sialyltransferase 6
FILIP1L	1.311283	9.16E-07	9.03E-06	4.908804	Up	filamin A interacting protein 1 like
RPL7P32	1.310868	0.000356	0.00176	3.570631	Up	ribosomal protein L7 pseudogene 32
MTCO1P40	1.30979	4.49E-06	3.74E-05	4.587496	Up	MT-CO1 pseudogene 40
MPC1	1.304989	6.94E-21	1.56E-18	9.374673	Up	mitochondrial pyruvate carrier 1
ZNF503	1.303743	1.08E-12	4.17E-11	7.119445	Up	zinc finger protein 503
RPL14P3	1.303011	0.006861	0.022035	2.703494	Up	ribosomal protein L14 pseudogene 3
SGK3	1.300848	2.73E-25	1.49E-22	10.39078	Up	serum/glucocorticoid regulated kinase family member 3
BORCS7	1.298373	5.18E-08	6.90E-07	5.445177	Up	BLOC-1 related complex subunit 7
TRGC1	1.296444	9.25E-06	7.15E-05	4.434004	Up	T cell receptor gamma constant 1
EEF1A2	-6.78044	8.40E-12	2.65E-10	-6.83148	Down	eukaryotic translation elongation factor 1 alpha 2
AKR1B10	-5.14695	3.38E-16	2.98E-14	-8.15898	Down	aldo-ketoreductase family 1 member B10
MYL1	-4.90941	0.016073	0.044809	-2.40726	Down	myosin light chain 1
MYH7	-4.88067	0.006709	0.02164	-2.71096	Down	myosin heavy chain 7
CKM	-4.64741	0.001485	0.005993	-3.17768	Down	creatine kinase, M-type
NTN3	-4.51477	1.39E-09	2.64E-08	-6.05643	Down	netrin 3
CYP51A1	-4.50016	4.58E-19	7.02E-17	-8.92192	Down	cytochrome P450 family 51 subfamily A member 1
SLC22A12	-4.3699	1.93E-06	1.76E-05	-4.76075	Down	solute carrier family 22 member 12
AKR1B15	-4.3508	6.66E-05	0.000407	-3.98798	Down	aldo-ketoreductase family 1 member B15
CALML3	-4.29847	6.94E-08	9.01E-07	-5.3927	Down	calmodulin like 3
SCUBE1	-4.09318	7.09E-17	7.07E-15	-8.34548	Down	signal peptide, CUB domain and EGF like domain containing 1 extracellular leucine rich repeat and fibronectin type III domain containing 2
ELFN2	-4.00421	2.63E-07	2.94E-06	-5.14813	Down	
ULBP3	-3.992	1.47E-08	2.21E-07	-5.66456	Down	UL16 binding protein 3
PKP3	-3.98907	1.45E-05	0.000106	-4.33578	Down	plakophilin 3
MYBPC1	-3.94165	0.00018	0.000974	-3.74507	Down	myosin binding protein C1
SLC7A14	-3.87956	7.67E-08	9.84E-07	-5.37477	Down	solute carrier family 7 member 14
S1PR2	-3.83906	7.09E-10	1.45E-08	-6.1641	Down	sphingosine-1-phosphate receptor 2
C6orf223	-3.78181	0.000467	0.002221	-3.49891	Down	chromosome 6 open reading frame 223
COMP	-3.50732	0.000387	0.001895	-3.54854	Down	cartilage oligomeric matrix protein
PCDHA12	-3.50397	0.00024	0.001256	-3.67231	Down	protocadherin alpha 12
CDH15	-3.46323	3.62E-09	6.22E-08	-5.90067	Down	cadherin 15
ADAMTS16	-3.46228	1.44E-05	0.000106	-4.337	Down	ADAM metalloproteinase with thrombospondin type 1 motif 16
CIDEC	-3.44103	1.19E-08	1.83E-07	-5.7005	Down	cell death inducing DFFA like effector c
PLCH2	-3.41778	5.03E-09	8.36E-08	-5.84626	Down	phospholipase C eta 2
OVOL1-AS1	-3.40166	0.000284	0.001449	-3.6295	Down	OVOL1 antisense RNA 1
TPSG1	-3.39044	6.26E-05	0.000386	-4.00276	Down	tryptase gamma 1

FOXN4	-3.35637	1.18E-06	1.14E-05	-4.85858	Down	forkhead box N4
GUCY1B2	-3.29627	0.001015	0.004319	-3.28625	Down	guanylatecyclase 1 soluble subunit beta 2 (pseudogene)
CIDEA	-3.28659	0.003209	0.011613	-2.94701	Down	cell death inducing DFFA like effector a
PRAMEF10	-3.26836	5.96E-06	4.80E-05	-4.5279	Down	PRAME family member 10
MEOX1	-3.25061	0.000134	0.000753	-3.81953	Down	mesenchyme homeobox 1 polypeptide N-
GALNT4	-3.23735	1.73E-05	0.000124	-4.29693	Down	acetylglucosaminyltransferase 4
CPT1B	-3.22996	3.83E-05	0.00025	-4.11771	Down	carnitinepalmitoyltransferase 1B
PAGE4	-3.21736	0.002538	0.00949	-3.01873	Down	PAGE family member 4 chromosome 9 open reading frame 152
C9orf152	-3.18193	7.47E-11	1.91E-09	-6.51082	Down	ovo like transcriptional repressor 1
OVOL1	-3.17275	0.001632	0.006505	-3.15011	Down	troponin C2, fast skeletal type
TNNC2	-3.16826	2.83E-05	0.000192	-4.18659	Down	RAB43, member RAS oncogene family
RAB43	-3.15996	8.13E-09	1.29E-07	-5.76583	Down	basic helix-loop-helix family member a15
BHLHA15	-3.14837	3.22E-05	0.000214	-4.15766	Down	peptide deformylase, mitochondrial
PDF	-3.14555	3.51E-05	0.000232	-4.13746	Down	complement C1q like 1
C1QL1	-3.13075	0.000142	0.000794	-3.80388	Down	insulin like growth factor 2 mRNA binding protein 1
IGF2BP1	-3.12435	0.00357	0.012716	-2.91383	Down	PDE11A antisense RNA 1
PDE11A-AS1	-3.12333	0.001363	0.005568	-3.20238	Down	insulin like growth factor binding protein like 1
IGFBPL1	-3.1155	0.000197	0.001048	-3.7233	Down	C-C motif chemokine ligand 24
CCL24	-3.11512	1.45E-07	1.74E-06	-5.25891	Down	collagen type XI alpha 1 chain
COL11A1	-3.09707	0.000512	0.002402	-3.47465	Down	dipeptidase 1
DPEP1	-3.09044	0.002456	0.00924	-3.02866	Down	low density lipoprotein receptor class A domain containing 1
LDLRAD1	-3.08322	0.00056	0.002603	-3.45018	Down	tryptase delta 1
TPSD1	-2.99279	0.001747	0.006899	-3.13012	Down	aldehyde dehydrogenase 3 family member A1
ALDH3A1	-2.97765	1.63E-10	3.82E-09	-6.39253	Down	ROS proto-oncogene 1, receptor tyrosine kinase
ROS1	-2.93235	1.73E-07	2.03E-06	-5.22632	Down	kelch like family member 34 immunoglobulin like and fibronectin type III domain containing 1
KLHL34	-2.91949	9.41E-05	0.000552	-3.90522	Down	endothelin 2
IGFN1	-2.90623	0.002926	0.010719	-2.97544	Down	fatty acid desaturase 2
EDN2	-2.87592	9.31E-13	3.62E-11	-7.14035	Down	cell wall biogenesis 43 C-terminal homolog
FADS2	-2.85846	4.80E-23	1.73E-20	-9.88572	Down	glutathione S-transferase theta 2 (gene/pseudogene)
CWH43	-2.8486	7.84E-11	1.99E-09	-6.5037	Down	cadherin 16
GSTT2	-2.84694	0.004065	0.014209	-2.87309	Down	transmembrane protein 240
CDH16	-2.81836	0.003589	0.01277	-2.91219	Down	transmembrane protein 151A
TMEM240	-2.78828	0.000178	0.000964	-3.74784	Down	acetylcholinesterase (Cartwright blood group)
TMEM151A	-2.76275	0.00033	0.00165	-3.59039	Down	stratifin
ACHE	-2.75941	1.76E-07	2.06E-06	-5.22295	Down	T cell receptor beta variable 4-2
SFN	-2.75927	0.0016	0.006391	-3.15589	Down	keratin 8 pseudogene 45
TRBV4-2	-2.75397	0.002537	0.009489	-3.01885	Down	troponin T3, fast skeletal type
KRT8P45	-2.7474	5.78E-06	4.67E-05	-4.53427	Down	
TNNT3	-2.74632	0.016663	0.046198	-2.39405	Down	

COL10A1	-2.72786	0.001241	0.005141	-3.22923	Down	collagen type X alpha 1 chain
SLC6A2	-2.72128	2.78E-05	0.000189	-4.19076	Down	solute carrier family 6 member 2
H2AC7	-2.70804	0.000605	0.002781	-3.42954	Down	H2A clustered histone 7
R3HDM2-DT	-2.70252	5.57E-07	5.79E-06	-5.00541	Down	R3HDM2 divergent transcript
PRAMEF33	-2.68464	0.000179	0.000969	-3.7466	Down	PRAME family member 33
NMRAL2P	-2.67396	0.010828	0.032284	-2.54819	Down	NmrA like redox sensor 2, pseudogene
PLXNA4	-2.6335	3.34E-10	7.33E-09	-6.28189	Down	plexin A4
TTYT10	-2.62408	0.008172	0.025548	-2.64487	Down	testis-specific transcript, Y-linked 10
EDA2R	-2.59387	5.11E-07	5.37E-06	-5.02205	Down	ectodysplasin A2 receptor
KRT23	-2.58962	0.001287	0.005303	-3.21888	Down	keratin 23
MUC3A	-2.58818	3.97E-06	3.35E-05	-4.61317	Down	mucin 3A, cell surface associated
FASN	-2.58603	2.22E-15	1.58E-13	-7.92862	Down	fatty acid synthase
CDC45	-2.58591	5.37E-09	8.87E-08	-5.83542	Down	cell division cycle 45
STMN2	-2.58521	0.00115	0.004813	-3.2511	Down	stathmin 2
PKD1P4	-2.58251	1.35E-05	9.94E-05	-4.35259	Down	polycystin 1, transient receptor potential channel interacting pseudogene 4
DGCR6	-2.55256	6.10E-05	0.000377	-4.00892	Down	DiGeorge syndrome critical region gene 6
H2BC8	-2.54656	0.00025	0.001299	-3.662	Down	H2B clustered histone 8
TREM2	-2.53973	1.92E-08	2.82E-07	-5.61876	Down	triggering receptor expressed on myeloid cells 2
PHLDA2	-2.53806	0.001948	0.007579	-3.09807	Down	pleckstrin homology like domain family A member 2
PKD1P5	-2.53162	0.00088	0.003821	-3.32618	Down	polycystin 1, transient receptor potential channel interacting pseudogene 5
EHHADH-AS1	-2.5195	0.013976	0.039929	-2.45789	Down	EHHADH antisense RNA 1
ADAMTS16-DT	-2.49987	0.005731	0.018963	-2.76277	Down	ADAMTS16 divergent transcript
CABYR	-2.49835	0.001386	0.005648	-3.19756	Down	calcium binding tyrosine phosphorylation regulated
TCAP	-2.48704	5.92E-08	7.82E-07	-5.42115	Down	titin-cap
ACTA1	-2.48486	0.018099	0.049501	-2.36359	Down	actin alpha 1, skeletal muscle
OMP	-2.47707	0.000475	0.002252	-3.49434	Down	olfactory marker protein
PKD1P3	-2.47297	1.56E-05	0.000114	-4.32012	Down	polycystin 1, transient receptor potential channel interacting pseudogene 3
LMOD2	-2.46877	0.007129	0.022775	-2.69075	Down	leiomodulin 2
SCD	-2.46405	4.63E-15	2.99E-13	-7.8367	Down	stearoyl-CoA desaturase
RAB44	-2.46293	0.002773	0.010225	-2.99184	Down	RAB44, member RAS oncogene family
INSYN2B	-2.45996	0.007498	0.023729	-2.67386	Down	inhibitory synaptic factor family member 2B
NKD2	-2.44909	3.13E-06	2.70E-05	-4.66213	Down	NKD inhibitor of WNT signaling pathway 2
ANKRD1	-2.44285	0.012847	0.037197	-2.488	Down	ankyrin repeat domain 1
LLPH-DT	-2.44217	0.003016	0.011012	-2.96607	Down	LLPH divergent transcript
KRTAP5-AS1	-2.44143	0.004573	0.015661	-2.83564	Down	KRTAP5-1/KRTAP5-2 antisense RNA 1
COL19A1	-2.41154	0.010081	0.03046	-2.57303	Down	collagen type XIX alpha 1 chain
TMEM150B	-2.40791	2.36E-07	2.66E-06	-5.16875	Down	transmembrane protein 150B
UGT1A6	-2.40789	2.68E-22	8.65E-20	-9.71194	Down	UDP glucuronosyltransferase family

						1 member A6
GCK	-2.40669	1.42E-07	1.71E-06	-5.26273	Down	glucokinase
FAM111B	-2.40455	2.26E-08	3.25E-07	-5.59116	Down	FAM111 trypsin like peptidase B
MYEOV	-2.3967	0.000987	0.004214	-3.29426	Down	myeloma overexpressed
TUBB4A	-2.39535	0.000118	0.000673	-3.85112	Down	tubulin beta 4A class IVa polycystin 1, transient receptor potential channel interacting pseudogene 2
PKD1P2	-2.39027	0.006194	0.020202	-2.73731	Down	eukaryotic translation initiation factor 2 subunit gamma B
EIF2S3B	-2.38568	1.43E-05	0.000105	-4.33905	Down	small transmembrane regulator of ion transport 1
STRIT1	-2.38128	0.0045	0.015445	-2.84077	Down	pancreatic and duodenal homeobox 1
PDX1	-2.37668	0.000238	0.001246	-3.6746	Down	Lck interacting transmembrane adaptor 1
LIME1	-2.35784	3.89E-12	1.32E-10	-6.94125	Down	myosin light chain 7
MYL7	-2.35742	0.011953	0.034982	-2.51353	Down	retrotransposon Gag like 9
RTL9	-2.35506	5.18E-10	1.09E-08	-6.2137	Down	hedgehog acyltransferase like pleckstrin homology domain containing N1
HHATL	-2.35438	0.003409	0.012214	-2.92827	Down	reticulon 4 receptor
PLEKHN1	-2.34458	0.003293	0.011854	-2.93898	Down	dystrobrein alpha
RTN4R	-2.33641	4.55E-13	1.89E-11	-7.23797	Down	TRPM8 channel associated factor 1
DTNA	-2.33082	3.86E-08	5.30E-07	-5.49721	Down	pseudogene 1
TCAF1P1	-2.32258	2.42E-06	2.14E-05	-4.71487	Down	phenylethanolamine N-methyltransferase
PNMT	-2.32202	0.009936	0.030094	-2.57806	Down	keratin 8 pseudogene 39
KRT8P39	-2.30165	0.001833	0.007191	-3.1161	Down	MRGPRF antisense RNA 1
MRGPRF-AS1	-2.2924	6.17E-05	0.000381	-4.00608	Down	leucine rich repeat containing 36
LRRC36	-2.28354	0.008726	0.026963	-2.62261	Down	BCL2 binding component 3
BBC3	-2.28163	1.32E-15	9.88E-14	-7.99258	Down	ADAM metallopeptidase domain 21
ADAM21	-2.2735	0.00218	0.008344	-3.06458	Down	galectin 4
LGALS4	-2.27326	3.28E-12	1.14E-10	-6.96499	Down	transmembrane protein 52B
TMEM52B	-2.27065	0.007782	0.024499	-2.66139	Down	E2F transcription factor 8
E2F8	-2.26648	7.63E-05	0.000459	-3.95568	Down	neuropeptide W
NPW	-2.26236	4.41E-05	0.000283	-4.08492	Down	crystallin beta-gamma domain containing 2
CRYBG2	-2.26205	0.000762	0.00338	-3.36631	Down	TIMP metallopeptidase inhibitor 3
TIMP3	-2.26056	0.005479	0.018304	-2.77744	Down	starch binding domain 1
STBD1	-2.25931	3.37E-14	1.74E-12	-7.5833	Down	PDZK1 interacting protein 1
PDZK1IP1	-2.24994	5.19E-05	0.000326	-4.0471	Down	cytochrome b5 domain containing 1
CYB5D1	-2.24811	6.99E-13	2.78E-11	-7.17962	Down	cystathionine beta-synthase like
CBSL	-2.24619	0.000645	0.002937	-3.41198	Down	N-acetyltransferase 8 like
NAT8L	-2.24394	0.001899	0.007411	-3.10562	Down	LAMA5 antisense RNA 1
LAMA5-AS1	-2.23645	2.19E-09	3.97E-08	-5.98284	Down	archaelysin family metallopeptidase 1
AMZ1	-2.22745	0.000742	0.003309	-3.3735	Down	EPHA1 antisense RNA 1
EPHA1-AS1	-2.2252	0.001005	0.004282	-3.28921	Down	keratin 8 pseudogene 8
KRT8P8	-2.22281	0.007556	0.023875	-2.67128	Down	MAM domain containing 4
MAMDC4	-2.22149	4.39E-12	1.47E-10	-6.92418	Down	HECT, C2 and WW domain containing E3 ubiquitin protein
HECW1	-2.21946	0.000295	0.001498	-3.61977	Down	

							ligase 1
CHI3L1	-2.21774	1.76E-05	0.000126	-4.29346	Down		chitinase 3 like 1
GJD3	-2.21664	0.003787	0.013363	-2.89534	Down		gap junction protein delta 3
DOK7	-2.19662	2.87E-08	4.05E-07	-5.54889	Down		docking protein 7
FOXP3	-2.19545	2.85E-08	4.02E-07	-5.55031	Down		forkhead box P3 pleckstrin homology like domain
PHLDA3	-2.19391	1.33E-14	7.76E-13	-7.70265	Down		family A member 3 mevalonatediphosphate decarboxylase
MVD	-2.19189	7.42E-07	7.48E-06	-4.95002	Down		
MMP17	-2.18697	0.002363	0.008937	-3.04034	Down		matrix metalloproteinase 17
SV2B	-2.17442	4.14E-06	3.48E-05	-4.60429	Down		synaptic vesicle glycoprotein 2B
MTCYBP23	-2.17278	0.009478	0.028883	-2.59431	Down		MT-CYB pseudogene 23
PTCHD4	-2.1719	0.000331	0.001653	-3.58978	Down		patched domain containing 4 F-box and leucine rich repeat protein 18
FBXL18	-2.17022	6.54E-11	1.70E-09	-6.53093	Down		
RAVER1	-2.15777	1.35E-10	3.23E-09	-6.42123	Down		ribonucleoprotein, PTB binding 1
SEZ6	-2.15547	0.010856	0.032351	-2.5473	Down		seizure related 6 homolog
ANKRD65	-2.15338	2.01E-06	1.82E-05	-4.7528	Down		ankyrin repeat domain 65 hes family bHLH transcription factor 2
HES2	-2.14811	0.008433	0.026213	-2.63422	Down		matrix remodeling associated 5 Y- linked (pseudogene)
MXRA5Y	-2.14283	0.014544	0.041259	-2.44355	Down		
SLC51B	-2.13699	6.63E-05	0.000405	-3.98926	Down		solute carrier family 51 subunit beta dendrocyte expressed seven transmembrane protein
DCSTAMP	-2.12473	0.01316	0.037983	-2.47942	Down		
NOMO2	-2.12437	6.68E-16	5.51E-14	-8.07631	Down		NODAL modulator 2 cilia and flagella associated protein 74
CFAP74	-2.11687	0.002564	0.009563	-3.01565	Down		adenosine deaminase tRNA specific 3
ADAT3	-2.09883	0.008424	0.026191	-2.63457	Down		
MTFP1	-2.09741	0.00049	0.002311	-3.48617	Down		mitochondrial fission process 1
TRAV9-2	-2.09596	0.009964	0.030158	-2.57707	Down		T cell receptor alpha variable 9-2
LAMC3	-2.08766	1.52E-06	1.43E-05	-4.80846	Down		laminin subunit gamma 3
SATB2-AS1	-2.08699	0.006281	0.020449	-2.73274	Down		SATB2 antisense RNA 1 heterogeneous nuclear ribonucleoprotein A3 pseudogene 12
HNRNPA3P12	-2.08092	0.008072	0.025293	-2.64904	Down		
TBX20	-2.06136	0.010108	0.030513	-2.57212	Down		T-box transcription factor 20 cytochrome P450 family 7 subfamily A member 1
CYP7A1	-2.0509	1.04E-06	1.00E-05	-4.88469	Down		inhibitor of nuclear factor kappa B kinase regulatory subunit gamma
IKBKG	-2.05014	2.32E-25	1.29E-22	-10.4063	Down		
SNORD83A	-2.04769	0.005191	0.017484	-2.79492	Down		small nucleolar RNA, C/D box 83A
H4C5	-2.04703	0.010433	0.031348	-2.56115	Down		H4 clustered histone 5
SPTA1	-2.03607	0.015058	0.042462	-2.43098	Down		spectrin alpha, erythrocytic 1
RPS10P1	-2.03604	0.01396	0.039896	-2.4583	Down		ribosomal protein S10 pseudogene 1
CMA1	-2.02962	0.003695	0.013089	-2.90312	Down		chymase 1
TYMS	-2.02771	2.21E-16	2.01E-14	-8.21002	Down		thymidylate synthetase
NPAS1	-2.02649	0.0163	0.045333	-2.40214	Down		neuronal PAS domain protein 1
BMP10	-2.01966	2.92E-05	0.000197	-4.17949	Down		bone morphogenetic protein 10
TRAV8-3	-2.01825	0.014048	0.040084	-2.45604	Down		T cell receptor alpha variable 8-3
SLC22A2	-2.01758	0.003298	0.011869	-2.9385	Down		solute carrier family 22 member 2

TRBV7-9	-2.017	0.006792	0.021841	-2.70687	Down	T cell receptor beta variable 7-9
GALR3	-2.01254	0.007937	0.024924	-2.65474	Down	galanin receptor 3
CMTM1	-2.00815	0.004996	0.016926	-2.80729	Down	CKLF like MARVEL transmembrane domain containing 1
NOMO3	-2.00758	5.01E-07	5.27E-06	-5.02605	Down	NODAL modulator 3
SPOCD1	-2.00359	0.005509	0.018381	-2.77563	Down	SPOC domain containing 1 tubulin polyglutamylase complex subunit 1
TPGS1	-1.99673	1.01E-05	7.73E-05	-4.41477	Down	family with sequence similarity 83 member G
FAM83G	-1.99455	9.57E-20	1.75E-17	-9.09368	Down	ribosomal protein S15 pseudogene 2
RPS15P2	-1.99317	0.00329	0.011848	-2.93922	Down	RAS protein activator like 1
RASAL1	-1.99074	0.00474	0.016162	-2.82418	Down	synaptogyrin 4
SYNGR4	-1.989	0.008824	0.027208	-2.61879	Down	fatty acid desaturase 1
FADS1	-1.9853	2.56E-08	3.65E-07	-5.56933	Down	H4 clustered histone 8
H4C8	-1.98261	0.005974	0.019605	-2.74921	Down	phosphatidylinositol transfer protein membrane associated 1
PITPNM1	-1.97467	6.55E-22	1.89E-19	-9.62046	Down	APC regulator of WNT signaling pathway 2
APC2	-1.97401	0.014496	0.041144	-2.44472	Down	keratin 7
KRT7	-1.97382	6.45E-07	6.59E-06	-4.97725	Down	chitinase 1
CHIT1	-1.96831	0.005229	0.0176	-2.7926	Down	potassium voltage-gated channel subfamily H member 3
KCNH3	-1.96581	0.004241	0.014717	-2.85967	Down	ankyrin repeat domain 61
ANKRD61	-1.95117	0.011086	0.032931	-2.53998	Down	protocadherin gamma subfamily B, 2
PCDHGB2	-1.951	0.000111	0.000638	-3.86537	Down	scinderin
SCIN	-1.9459	0.005903	0.019408	-2.75314	Down	protocadherin gamma subfamily A, 4
PCDHGA4	-1.94343	0.000578	0.002673	-3.44184	Down	NACHT and WD repeat domain containing 1
NWD1	-1.9427	0.009632	0.02929	-2.58877	Down	EPH receptor B2
EPHB2	-1.93596	7.72E-09	1.23E-07	-5.77438	Down	solute carrier family 5 member 10
SLC5A10	-1.93018	0.000136	0.000767	-3.81447	Down	RNA, 7SL, cytoplasmic 521, pseudogene
RN7SL521P	-1.92852	0.014466	0.041073	-2.44547	Down	solute carrier family 26 member 1
SLC26A1	-1.92185	2.07E-16	1.91E-14	-8.21813	Down	lipoprotein lipase
LPL	-1.92086	0.000356	0.00176	-3.57069	Down	KRAB-A domain containing 2
KRBA2	-1.90982	0.01046	0.031398	-2.56026	Down	lysyl oxidase like 4
LOXL4	-1.90851	7.61E-06	5.99E-05	-4.47582	Down	regulator of telomere elongation helicase 1
RTEL1	-1.90377	0.007583	0.023944	-2.67009	Down	urothelial cancer associated 1
UCA1	-1.8968	0.002844	0.010451	-2.9841	Down	immunoglobulin superfamily member 1
IGSF1	-1.89524	2.07E-11	6.02E-10	-6.701	Down	melanocortin 2 receptor accessory protein
MRAP	-1.89426	4.92E-05	0.000312	-4.05951	Down	leucine rich repeat and fibronectin type III domain containing 4
LRFN4	-1.88679	9.91E-05	0.000577	-3.89282	Down	RAB25, member RAS oncogene family
RAB25	-1.88623	0.000516	0.002418	-3.47247	Down	zinc finger protein 385D
ZNF385D	-1.8862	0.004912	0.016683	-2.81275	Down	RIMS binding protein 3
RIMBP3	-1.88586	0.012858	0.037221	-2.48769	Down	solute carrier family 2 member 14
SLC2A14	-1.88566	2.95E-05	0.000199	-4.17709	Down	spermatogenesis associated 21
SPATA21	-1.88289	0.00243	0.009151	-3.03191	Down	

NPM2	-1.87861	1.58E-07	1.87E-06	-5.24296	Down	nucleophosmin/nucleoplasmin 2
VWCE	-1.87765	1.52E-07	1.81E-06	-5.25006	Down	von Willebrand factor C and EGF domains
DNM1P46	-1.87522	0.011745	0.034509	-2.51971	Down	dynamins 1 pseudogene 46
ANGPTL8	-1.87005	1.11E-10	2.73E-09	-6.45131	Down	angiopoietin like 8
TMPRSS9	-1.86919	3.35E-09	5.80E-08	-5.91322	Down	transmembrane serine protease 9
CNTN2	-1.86288	0.004247	0.014735	-2.85921	Down	contactin 2
LRRRC37A11P	-1.85905	0.0053	0.017799	-2.78824	Down	leucine rich repeat containing 37 member A11, pseudogene
MTHFS	-1.85429	1.73E-06	1.60E-05	-4.78224	Down	methenyltetrahydrofolatesynthetase
EVC	-1.85387	2.82E-07	3.13E-06	-5.13512	Down	EvCiliary complex subunit 1
ACAD11	-1.84871	9.74E-12	3.00E-10	-6.81026	Down	acyl-CoA dehydrogenase family member 11
EFNA2	-1.84533	9.87E-07	9.65E-06	-4.89413	Down	ephrin A2
HCN2	-1.84433	0.014685	0.041593	-2.44006	Down	hyperpolarization activated cyclic nucleotide gated potassium and sodium channel 2
VTCN1	-1.84363	6.14E-05	0.000379	-4.00741	Down	V-set domain containing T cell activation inhibitor 1
PRSS27	-1.84291	0.005462	0.018262	-2.77845	Down	serine protease 27
CENPM	-1.84236	7.80E-05	0.000468	-3.95033	Down	centromere protein M
SUPT16HP1	-1.84206	0.012271	0.035789	-2.50425	Down	SPT16 homolog, facilitates chromatin remodeling subunit pseudogene 1
SEC14L4	-1.84131	6.00E-10	1.24E-08	-6.19035	Down	SEC14 like lipid binding 4
SNORA47	-1.84081	0.015049	0.042451	-2.43121	Down	small nucleolar RNA, H/ACA box 47
BRICD5	-1.83271	1.59E-05	0.000116	-4.31587	Down	BRICHOS domain containing 5
HSPA8	-1.83246	6.21E-29	5.25E-26	-11.1627	Down	heat shock protein family A (Hsp70) member 8
MB	-1.81472	6.56E-05	0.000402	-3.99159	Down	myoglobin
RAB3B	-1.81341	0.012044	0.035207	-2.51085	Down	RAB3B, member RAS oncogene family
ZNF541	-1.81121	0.000973	0.004164	-3.29808	Down	zinc finger protein 541
TUT1	-1.8092	8.47E-05	0.000502	-3.93075	Down	terminal uridylyltransferase 1, U6 snRNA-specific
ADAMTSL2	-1.80698	4.82E-10	1.02E-08	-6.22491	Down	ADAMTS like 2
CCDC9B	-1.80681	6.13E-15	3.87E-13	-7.80124	Down	coiled-coil domain containing 9B
GPLD1	-1.80664	4.23E-16	3.66E-14	-8.13182	Down	glycosylphosphatidylinositol specific phospholipase D1
DUSP8	-1.80593	0.000106	0.00061	-3.87749	Down	dual specificity phosphatase 8
CDH24	-1.80493	3.77E-05	0.000247	-4.12117	Down	cadherin 24
MFAP5	-1.8011	0.014657	0.041536	-2.44075	Down	microfibril associated protein 5
HSPA8P1	-1.79979	0.002574	0.009587	-3.01455	Down	heat shock protein family A (Hsp70) member 8 pseudogene 1
KRT8P3	-1.79769	3.20E-06	2.75E-05	-4.65765	Down	keratin 8 pseudogene 3
ACKR1	-1.79742	0.000963	0.004126	-3.301	Down	atypical chemokine receptor 1 (Duffy blood group)
PPP1R3C	-1.79542	4.78E-11	1.28E-09	-6.57767	Down	protein phosphatase 1 regulatory subunit 3C
CFAP221	-1.79449	5.54E-06	4.51E-05	-4.54327	Down	cilia and flagella associated protein 221
KCNJ11	-1.78809	8.78E-05	0.000519	-3.92203	Down	potassium inwardly rectifying channel subfamily J member 11
TMEM102	-1.78704	2.82E-23	1.06E-20	-9.93882	Down	transmembrane protein 102
IL4I1	-1.78201	2.90E-05	0.000196	-4.1808	Down	interleukin 4 induced 1

BICDL2	-1.78032	0.010798	0.032215	-2.54918	Down	BICD family like cargo adaptor 2
EVPLL	-1.77727	6.69E-07	6.82E-06	-4.97004	Down	envoplakin like
HRH2	-1.76944	0.01824	0.049838	-2.3607	Down	histamine receptor H2
TRIM56	-1.76909	1.56E-10	3.69E-09	-6.39893	Down	tripartite motif containing 56
SLC1A7	-1.76866	1.51E-05	0.000111	-4.32667	Down	solute carrier family 1 member 7 fibroblast growth factor 7
FGF7P6	-1.76858	9.43E-05	0.000552	-3.90477	Down	pseudogene 6
RDM1	-1.76832	0.014804	0.041851	-2.43715	Down	RAD52 motif containing 1
SLC49A3	-1.76337	5.13E-09	8.52E-08	-5.84283	Down	solute carrier family 49 member 3
DAGLA	-1.76033	1.32E-06	1.26E-05	-4.83672	Down	diacylglycerol lipase alpha eukaryotic translation initiation factor 3 subunit C
EIF3C	-1.74634	2.79E-15	1.94E-13	-7.89974	Down	
TMEM125	-1.74542	0.001928	0.00751	-3.10109	Down	transmembrane protein 125
PITPNM2-AS1	-1.745	0.004537	0.015557	-2.83817	Down	PITPNM2 antisense RNA 1
SUSD2	-1.73294	7.12E-08	9.19E-07	-5.38822	Down	sushi domain containing 2 adaptor related protein complex 1 subunit mu 2
AP1M2	-1.72709	0.000661	0.002999	-3.40508	Down	UDP-GlcNAc:betaGal beta-1,3-N- acetylglucosaminyltransferase 8
B3GNT8	-1.72507	8.48E-06	6.60E-05	-4.45281	Down	
SUSD3	-1.72163	1.07E-13	4.92E-12	-7.43242	Down	sushi domain containing 3
CPSF1P1	-1.71878	0.000514	0.002411	-3.47348	Down	CPSF1 pseudogene 1
PCDHAC2	-1.71866	0.00181	0.007113	-3.11974	Down	protocadherin alpha subfamily C, 2 WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 1
WFIKKN1	-1.71846	0.000874	0.003796	-3.3283	Down	
LAMB3	-1.71487	2.67E-14	1.41E-12	-7.61352	Down	laminin subunit beta 3
LYPD1	-1.7147	0.003196	0.011573	-2.94825	Down	LY6/PLAUR domain containing 1 apical junction component 1
AJM1	-1.70693	4.60E-09	7.70E-08	-5.86107	Down	homolog
MUC6	-1.70437	0.003179	0.011525	-2.94986	Down	mucin 6, oligomeric mucus/gel- forming
RRAD	-1.70259	0.000131	0.000738	-3.82521	Down	RRAD, Ras related glycolysis inhibitor and calcium channel regulator
PFKL	-1.70107	4.19E-28	3.11E-25	-10.9917	Down	phosphofructokinase, liver type
EYA2	-1.70045	0.0002	0.001065	-3.71889	Down	EYA transcriptional coactivator and phosphatase 2
GLIS2	-1.70003	2.17E-05	0.000152	-4.24691	Down	GLIS family zinc finger 2
TNFSF13	-1.69837	2.41E-16	2.18E-14	-8.19993	Down	TNF superfamily member 13 acyl-CoA binding domain containing 7
ACBD7	-1.69527	0.014274	0.040636	-2.45028	Down	protocadherin gamma subfamily B, 4
PCDHGB4	-1.6939	4.67E-06	3.88E-05	-4.5792	Down	
RPS6KL1	-1.68923	4.24E-09	7.20E-08	-5.87439	Down	ribosomal protein S6 kinase like 1
TMEM121	-1.68534	0.000135	0.00076	-3.81706	Down	transmembrane protein 121
UGT1A1	-1.68471	2.81E-07	3.13E-06	-5.13559	Down	UDP glucuronosyltransferase family 1 member A1
ZBED6	-1.68083	1.19E-06	1.15E-05	-4.85701	Down	zinc finger BED-type containing 6 UDP glucuronosyltransferase family 1 member A9
UGT1A9	-1.67922	4.82E-12	1.60E-10	-6.91076	Down	
SORCS2	-1.66714	2.34E-07	2.64E-06	-5.16988	Down	sortilin related VPS10 domain containing receptor 2
PCDHGC3	-1.66632	1.26E-06	1.20E-05	-4.8463	Down	protocadherin gamma subfamily C, 3
IL2RA	-1.66589	0.002347	0.008884	-3.04236	Down	interleukin 2 receptor subunit alpha

LYPD2	-1.65839	0.002565	0.009565	-3.01556	Down	LY6/PLAUR domain containing 2
ANXA13	-1.65595	1.06E-06	1.03E-05	-4.88004	Down	annexin A13
LSS	-1.65413	2.97E-10	6.59E-09	-6.3004	Down	lanosterol synthase
POLD1	-1.65394	1.27E-15	9.63E-14	-7.99722	Down	DNA polymerase delta 1, catalytic subunit
SERPINA12	-1.65324	0.001067	0.004513	-3.27214	Down	serpin family A member 12
KCNJ5	-1.65101	4.90E-05	0.000311	-4.06013	Down	potassium inwardly rectifying channel subfamily J member 5
GTF2I	-1.64959	2.94E-14	1.53E-12	-7.60113	Down	general transcription factor Iii
RHBDD3	-1.64454	4.94E-13	2.03E-11	-7.2269	Down	rhomboid domain containing 3
LURAP1	-1.64186	0.017058	0.047128	-2.38546	Down	leucine rich adaptor protein 1
WDR62	-1.64152	2.14E-06	1.92E-05	-4.73976	Down	WD repeat domain 62
VWA7	-1.64039	1.45E-10	3.45E-09	-6.41027	Down	von Willebrand factor A domain containing 7
MICAL3	-1.63658	3.69E-15	2.48E-13	-7.86489	Down	microtubule associated monooxygenase, calponin and LIM domain containing 3
ZNF366	-1.63564	2.63E-05	0.00018	-4.2036	Down	zinc finger protein 366
EPPK1	-1.63507	2.08E-05	0.000147	-4.25573	Down	epiplakin 1
GLTPD2	-1.63359	4.63E-11	1.24E-09	-6.58233	Down	glycolipid transfer protein domain containing 2
TEDC1	-1.63335	1.51E-06	1.42E-05	-4.81018	Down	tubulin epsilon and delta complex 1
GDF2	-1.63192	5.37E-11	1.42E-09	-6.56029	Down	growth differentiation factor 2
SMCR8	-1.62642	2.77E-09	4.88E-08	-5.94494	Down	SMCR8-C9orf72 complex subunit family with sequence similarity 83 member F
FAM83F	-1.62156	0.000171	0.000927	-3.75894	Down	kelch domain containing 7A
KLHDC7A	-1.6109	6.51E-21	1.48E-18	-9.38139	Down	sodium leak channel, non-selective
NALCN	-1.60845	2.95E-05	0.000199	-4.17696	Down	zinc finger protein 837
ZNF837	-1.60702	7.89E-06	6.18E-05	-4.46822	Down	ribosomal protein L13 pseudogene 5
RPL13P5	-1.60016	0.000136	0.000764	-3.81558	Down	hemicentin 2
HMCN2	-1.59972	2.54E-05	0.000174	-4.21145	Down	CIRBP antisense RNA 1
CIRBP-AS1	-1.59552	0.004394	0.015161	-2.84838	Down	small nucleolar RNA host gene 21
SNHG21	-1.59391	0.005454	0.018242	-2.77889	Down	ST14 transmembrane serine protease matriptase
ST14	-1.58972	1.26E-10	3.03E-09	-6.43219	Down	chromatin licensing and DNA replication factor 1
CDT1	-1.58932	6.92E-05	0.000421	-3.979	Down	keratin 8 pseudogene 36
KRT8P36	-1.58925	0.01384	0.039625	-2.46139	Down	Rho/Rac guanine nucleotide exchange factor 18
ARHGEF18	-1.58881	1.30E-09	2.48E-08	-6.06754	Down	MAS related GPR family member F
MRGPRF	-1.5883	6.75E-08	8.79E-07	-5.39783	Down	SH2 domain containing 6
SH2D6	-1.58642	0.001777	0.007002	-3.12524	Down	BICD family like cargo adaptor 1
BICDL1	-1.58413	2.12E-07	2.42E-06	-5.18889	Down	apolipoprotein B mRNA editing enzyme catalytic subunit 3B
APOBEC3B	-1.58111	0.000589	0.002718	-3.43664	Down	farnesyltransferase synthase
FDPS	-1.58085	4.21E-08	5.72E-07	-5.48169	Down	fucosyltransferase 7
FUT7	-1.58062	0.015048	0.042451	-2.43123	Down	ectonucleoside triphosphate diphosphohydrolase 8
ENTPD8	-1.58033	9.13E-18	1.12E-15	-8.58437	Down	olfactomedin 2
OLFM2	-1.58018	2.14E-06	1.93E-05	-4.73927	Down	mitogen-activated protein kinase 8
MAPK8IP2	-1.57887	0.000569	0.002638	-3.44617	Down	interacting protein 2

FAM151A	-1.57694	0.00016	0.000878	-3.77511	Down	family with sequence similarity 151 member A
CDKN1A	-1.57674	1.35E-11	4.03E-10	-6.76316	Down	cyclin dependent kinase inhibitor 1A
CDCA2	-1.57528	0.0021	0.008081	-3.0757	Down	cell division cycle associated 2
DISP2	-1.57517	0.000159	0.000875	-3.77601	Down	dispatched RND transporter family member 2
C6orf132	-1.57305	0.003376	0.012107	-2.93123	Down	chromosome 6 open reading frame 132
ITGB3	-1.5724	3.63E-08	5.02E-07	-5.50775	Down	integrin subunit beta 3
NHEJ1	-1.57198	6.79E-05	0.000414	-3.98357	Down	non-homologous end joining factor 1
NDOR1	-1.57159	5.23E-10	1.10E-08	-6.21199	Down	NADPH dependent diflavinoxidoreductase 1
ATP13A2	-1.57094	1.94E-12	7.20E-11	-7.03851	Down	ATPase cation transporting 13A2
RNASE7	-1.56631	0.0109	0.032449	-2.5459	Down	ribonuclease A family member 7
P2RY2	-1.56617	1.52E-16	1.42E-14	-8.25489	Down	purinergic receptor P2Y2
ABCA2	-1.56221	3.04E-15	2.08E-13	-7.88916	Down	ATP binding cassette subfamily A member 2
INAVA	-1.55839	0.008878	0.027347	-2.61672	Down	innate immunity activator
SLC29A4	-1.55707	0.000531	0.002485	-3.46453	Down	solute carrier family 29 member 4
MFAP3	-1.55685	2.37E-07	2.67E-06	-5.16794	Down	microfibril associated protein 3
ERICH5	-1.55679	6.77E-10	1.39E-08	-6.17129	Down	glutamate rich 5
GLI4	-1.55566	4.68E-07	4.97E-06	-5.03889	Down	GLI family zinc finger 4
TRPV6	-1.55553	0.002255	0.008582	-3.05443	Down	transient receptor potential cation channel subfamily V member 6
DNMT3L-AS1	-1.55519	0.000235	0.001229	-3.6784	Down	DNMT3L antisense RNA 1
MAP1S	-1.54851	1.26E-08	1.92E-07	-5.69138	Down	microtubule associated protein 1S
PAQR4	-1.54304	1.08E-07	1.34E-06	-5.31261	Down	progestin and adipoQ receptor family member 4
TP53I3	-1.54121	2.56E-10	5.75E-09	-6.32341	Down	tumor protein p53 inducible protein 3
NYNRIN	-1.54115	1.23E-05	9.21E-05	-4.37165	Down	NYN domain and retroviral integrase containing
ADAMTSL5	-1.54062	1.17E-07	1.43E-06	-5.29829	Down	ADAMTS like 5
PCDHGB7	-1.53857	3.67E-05	0.000241	-4.1274	Down	protocadherin gamma subfamily B, 7
LAMA3	-1.5374	6.89E-10	1.41E-08	-6.16851	Down	laminin subunit alpha 3
GAS6	-1.53657	8.94E-15	5.43E-13	-7.75348	Down	growth arrest specific 6
HUNK	-1.53575	4.93E-06	4.07E-05	-4.5679	Down	hormonally up-regulated Neu-associated kinase
CCL25	-1.53573	0.014441	0.04102	-2.4461	Down	C-C motif chemokine ligand 25
HYAL3	-1.5357	1.21E-11	3.66E-10	-6.77917	Down	hyaluronidase 3
RHEX	-1.52735	9.31E-07	9.15E-06	-4.9056	Down	regulator of hemoglobinization and erythroid cell expansion
PIEZO1	-1.52717	2.70E-14	1.42E-12	-7.61171	Down	piezo type mechanosensitive ion channel component 1
SYT7	-1.52583	8.06E-14	3.84E-12	-7.46936	Down	synaptotagmin 7
KIF4A	-1.52226	0.000312	0.00157	-3.60518	Down	kinesin family member 4A
ME1	-1.52127	1.01E-06	9.79E-06	-4.89052	Down	malic enzyme 1
AGRN	-1.51923	2.38E-09	4.27E-08	-5.96956	Down	agrin
INHBC	-1.51753	8.42E-13	3.30E-11	-7.15416	Down	inhibin subunit beta C
INTS1	-1.51656	5.92E-12	1.93E-10	-6.88154	Down	integrator complex subunit 1
MIB2	-1.51608	3.06E-07	3.37E-06	-5.11998	Down	MIB E3 ubiquitin protein ligase 2

DISC1FP1	-1.51175	0.000391	0.001912	-3.54585	Down	DISC1 fusion partner 1
FAT1	-1.51083	2.84E-08	4.01E-07	-5.55101	Down	FAT atypical cadherin 1
KRT8P33	-1.51013	7.77E-05	0.000467	-3.95124	Down	keratin 8 pseudogene 33
FDXR	-1.50998	3.74E-17	3.97E-15	-8.42087	Down	ferredoxin reductase
CLCN7	-1.50141	1.38E-13	6.21E-12	-7.39827	Down	chloride voltage-gated channel 7
GPBAR1	-1.49988	1.26E-05	9.38E-05	-4.36688	Down	G protein-coupled bile acid receptor 1
DAB2IP	-1.49841	1.48E-22	5.11E-20	-9.77244	Down	DAB2 interacting protein
PPP6R1	-1.49691	1.15E-14	6.84E-13	-7.72164	Down	protein phosphatase 6 regulatory subunit 1
PDGFA	-1.49561	3.71E-06	3.16E-05	-4.62682	Down	platelet derived growth factor subunit A
B3GNT3	-1.4955	0.003621	0.012878	-2.90941	Down	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3
TMEM104	-1.49501	9.13E-22	2.52E-19	-9.58631	Down	transmembrane protein 104
LRRC24	-1.49291	0.000462	0.002201	-3.50176	Down	leucine rich repeat containing 24
CDC42EP1	-1.49167	1.71E-10	3.98E-09	-6.38578	Down	CDC42 effector protein 1
AGAP12P	-1.4889	0.014062	0.040116	-2.45567	Down	ArfGAP with GTPase domain, ankyrin repeat and PH domain 12, pseudogene
BEGAIN	-1.48824	0.001042	0.00442	-3.27881	Down	brain enriched guanylate kinase associated
PARP10	-1.48799	7.56E-12	2.40E-10	-6.84662	Down	poly(ADP-ribose) polymerase family member 10
EXO1	-1.48757	0.001001	0.004268	-3.29026	Down	exonuclease 1
BCAR1	-1.48638	2.88E-10	6.43E-09	-6.30488	Down	BCAR1 scaffold protein, Cas family member
OPLAH	-1.48562	6.10E-11	1.59E-09	-6.5413	Down	5-oxoprolinase, ATP-hydrolysing
WDR24	-1.48372	1.12E-15	8.58E-14	-8.01259	Down	WD repeat domain 24
CORO1B	-1.4816	7.92E-19	1.14E-16	-8.86116	Down	coronin 1B
TYMSOS	-1.48114	1.56E-05	0.000114	-4.3198	Down	TYMS opposite strand RNA
ASL	-1.48091	1.40E-21	3.74E-19	-9.54196	Down	argininosuccinatelyase
SPINT1	-1.47726	0.000231	0.001211	-3.68241	Down	serine peptidase inhibitor, Kunitz type 1
LRRC55	-1.47721	0.000378	0.001856	-3.5547	Down	leucine rich repeat containing 55
C1orf116	-1.47582	0.001644	0.006549	-3.14794	Down	chromosome 1 open reading frame 116
IGSF3	-1.47565	4.23E-06	3.55E-05	-4.59955	Down	immunoglobulin superfamily member 3
TREH	-1.47495	1.35E-07	1.63E-06	-5.27221	Down	trehalase
WNK2	-1.47236	0.002633	0.009775	-3.00757	Down	WNK lysine deficient protein kinase 2
ERV3-1	-1.47098	6.85E-07	6.96E-06	-4.9656	Down	endogenous retrovirus group 3 member 1, envelope
CEP170B	-1.46663	8.04E-10	1.62E-08	-6.14416	Down	centrosomal protein 170B
ACE2	-1.46473	4.52E-09	7.60E-08	-5.8638	Down	angiotensin converting enzyme 2
ENTPD7	-1.46291	9.47E-10	1.87E-08	-6.11811	Down	ectonucleoside triphosphate diphosphohydrolase 7
CFB	-1.46278	2.49E-11	7.07E-10	-6.67406	Down	complement factor B
CCNP	-1.46241	0.000664	0.003008	-3.40411	Down	cyclin P
COL7A1	-1.46198	0.004458	0.015324	-2.84378	Down	collagen type VII alpha 1 chain
UGT1A4	-1.46036	2.82E-09	4.97E-08	-5.94169	Down	UDP glucuronosyltransferase family 1 member A4
CCDC117	-1.45695	5.95E-07	6.14E-06	-4.99298	Down	coiled-coil domain containing 117
RASEF	-1.456	4.66E-05	0.000297	-4.07181	Down	RAS and EF-hand domain

						containing
LIPH	-1.45546	0.001237	0.005127	-3.23013	Down	lipase H
ST6GALNAC1	-1.4544	0.00031	0.001563	-3.60674	Down	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 1
AP5B1	-1.45435	6.05E-16	5.10E-14	-8.08827	Down	adaptor related protein complex 5 subunit beta 1
INHBE	-1.45366	1.18E-14	7.01E-13	-7.71814	Down	inhibin subunit beta E
OXT	-1.45103	0.008113	0.025392	-2.64733	Down	oxytocin/neurophysin I prepropeptide
MCHR1	-1.44683	6.42E-14	3.12E-12	-7.49923	Down	melanin concentrating hormone receptor 1
KCNAB2	-1.4463	5.48E-06	4.47E-05	-4.54542	Down	potassium voltage-gated channel subfamily A regulatory beta subunit 2
NLRP6	-1.44096	4.68E-06	3.89E-05	-4.57847	Down	NLR family pyrin domain containing 6
TECTB	-1.44095	0.002955	0.010814	-2.97236	Down	tectorin beta
TBC1D16	-1.43965	2.28E-35	3.49E-32	-12.4111	Down	TBC1 domain family member 16
SLC6A19	-1.43862	0.002749	0.010149	-2.9945	Down	solute carrier family 6 member 19
FCAMR	-1.43846	3.53E-07	3.85E-06	-5.09264	Down	Fc fragment of IgA and IgM receptor
MXD4	-1.43771	3.48E-22	1.07E-19	-9.68525	Down	MAX dimerization protein 4
EVI5L	-1.43741	1.25E-11	3.78E-10	-6.7741	Down	ecotropic viral integration site 5 like 2-oxoglutarate and iron dependent oxygenase domain containing 2
OGFOD2	-1.43511	3.33E-06	2.85E-05	-4.64912	Down	secreted phosphoprotein 1
SPP1	-1.43113	0.000765	0.003394	-3.36501	Down	secreted phosphoprotein 1
ANGPTL7	-1.42894	0.008476	0.026327	-2.63248	Down	angiopoietin like 7
DBNDD1	-1.42809	2.50E-07	2.80E-06	-5.15741	Down	dysbindin domain containing 1
PWWP2B	-1.42585	7.47E-08	9.61E-07	-5.37949	Down	PWWP domain containing 2B
KRT8	-1.42514	2.41E-20	4.92E-18	-9.2425	Down	keratin 8
KCNE1	-1.42511	0.002386	0.009005	-3.03749	Down	potassium voltage-gated channel subfamily E regulatory subunit 1
ZFPM1	-1.42295	4.75E-06	3.94E-05	-4.57534	Down	zinc finger protein, FOG family member 1
FNDC5	-1.42289	4.63E-11	1.24E-09	-6.58242	Down	fibronectin type III domain containing 5
HLA-G	-1.42099	0.000337	0.001678	-3.58543	Down	major histocompatibility complex, class I, G
PCNX3	-1.42041	1.23E-20	2.67E-18	-9.31422	Down	pecanex 3
TFCP2L1	-1.41931	0.000788	0.003475	-3.35698	Down	transcription factor CP2 like 1
TRAF7	-1.41725	5.58E-29	4.89E-26	-11.1721	Down	TNF receptor associated factor 7
ANXA6	-1.41587	1.24E-19	2.20E-17	-9.0658	Down	annexin A6
DERL3	-1.41532	9.90E-05	0.000577	-3.89302	Down	derlin 3
S1PR4	-1.41477	8.81E-05	0.00052	-3.9212	Down	sphingosine-1-phosphate receptor 4
ABCB8	-1.41349	5.76E-18	7.28E-16	-8.63717	Down	ATP binding cassette subfamily B member 8
MMP9	-1.41229	0.004448	0.015304	-2.84451	Down	matrix metalloproteinase 9
C4A	-1.41037	9.16E-08	1.15E-06	-5.34273	Down	complement C4A (Rodgers blood group)
C1QTNF12	-1.40872	0.016276	0.045294	-2.40266	Down	C1q and TNF related 12
LAMB2	-1.40483	4.32E-25	2.25E-22	-10.347	Down	laminin subunit beta 2
C19orf25	-1.40382	5.25E-19	7.90E-17	-8.90678	Down	chromosome 19 open reading frame 25
IER5L	-1.40367	5.95E-05	0.000369	-4.01481	Down	immediate early response 5 like
SLC22A18	-1.40245	6.44E-10	1.32E-08	-6.17938	Down	solute carrier family 22 member 18

MKI67	-1.40185	2.32E-05	0.000161	-4.23188	Down	marker of proliferation Ki-67
PRR36	-1.40098	0.015139	0.04265	-2.42904	Down	proline rich 36
DUS3L	-1.38897	7.17E-14	3.45E-12	-7.48465	Down	dihydrouridine synthase 3 like
CCDC134	-1.38829	5.02E-10	1.06E-08	-6.2186	Down	coiled-coil domain containing 134
MED16	-1.38544	5.12E-10	1.08E-08	-6.21536	Down	mediator complex subunit 16
E2F1	-1.38532	3.65E-05	0.00024	-4.12847	Down	E2F transcription factor 1
MCM5	-1.38379	2.25E-11	6.45E-10	-6.68897	Down	minichromosome maintenance complex component 5
UNC119B	-1.38359	6.01E-35	8.67E-32	-12.3331	Down	unc-119 lipid binding chaperone B
FBXW5	-1.38275	1.63E-15	1.19E-13	-7.96643	Down	F-box and WD repeat domain containing 5
TMEM63A	-1.38259	2.01E-20	4.18E-18	-9.26169	Down	transmembrane protein 63A
TUBB2B	-1.38134	9.45E-06	7.28E-05	-4.42944	Down	tubulin beta 2B class IIb
TMC4	-1.37914	0.014715	0.041648	-2.43933	Down	transmembrane channel like 4
LAMA5	-1.37896	9.23E-05	0.000542	-3.90998	Down	laminin subunit alpha 5
ZWINT	-1.37634	3.59E-08	4.96E-07	-5.51012	Down	ZW10 interacting kinetochore protein
EXTL3	-1.37621	1.07E-34	1.45E-31	-12.2868	Down	exostosin like glycosyltransferase 3
GOLGA6B	-1.37545	0.000455	0.002172	-3.50617	Down	golgin A6 family member B
ITGA7	-1.37454	0.000336	0.001677	-3.58562	Down	integrin subunit alpha 7
TBL3	-1.37429	2.93E-15	2.02E-13	-7.89384	Down	transducin beta like 3
CLDN3	-1.3729	2.17E-06	1.94E-05	-4.73723	Down	claudin 3
FMO1	-1.37057	0.001259	0.005204	-3.22523	Down	flavin containing dimethylanilinemonooxygenase 1
SPHK2	-1.3695	1.62E-11	4.78E-10	-6.73701	Down	sphingosine kinase 2
KIAA0100	-1.36898	2.50E-27	1.75E-24	-10.8293	Down	KIAA0100
MID1IP1	-1.36897	1.19E-13	5.43E-12	-7.41829	Down	MID1 interacting protein 1
TNFRSF12A	-1.36817	0.00015	0.000831	-3.7912	Down	TNF receptor superfamily member 12A

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:0023052	BP	signaling	1.05E-07	6.977588081	163	FOS,IGFBP1,AREG,IL6, RGS1,NR4A3,CA8,EGR1,RGS7,NR4A1,NR4A2, SIK1B,DUSP1,GADD45 G,NRK,DLK1,SIK1,SYT

4,CCN1,MROH2B,CEBP
D,SOCS2,IRS2,GADD45
B,CXCL2,ZFAND5,EGR
3,PTGS2,GABRG3,RGS
2,TCIM,KL,SOCS3,MM
P1,CXCR4,RASD1,THB
S1,SLC7A11,FAM83A,G
PAT3,TNR,EGR2,ZFP36
,NR0B2,CXCL3,CSRNP
1,RHOB,NRXN1,DUSP2
,DIPK2A,KCNE4,CCN2,
FST,CLEC4E,OGN,PCK
1,CHRM3,CTLA4,KLF4,
PTGER3,CYTL1,ARC,C
ACNA1A,TBX18,IL1RL
1,ASB3,HBEGF,BEND6,
CCL4L2,PRDM1,CCL2,
OSM,PELI2,H4C11,PRR
X1,ERBB4,NOTCH2NL
A,GRIK1,TNFSF11,MST
N,ADAMTS1,AVPR1A,
CALCR,PDK4,INHBB,E
PO,PLP1,FAM107A,PPF
IA2,LRRC19,TSPAN5,R
ASSF10,GATA3,IL10,A
DTRP,JUN,FGF14,MAK
,ESR2,TAS2R14,VIP,KC
NIP1,CHRD1,CEBPB,
CLEC4D,GRM1,PDE6C,
PLA2G2A,GRIK2,FOXC
1,JUNB,LURAP1L,CCL
3L1,FOXO1,S100B,KCN
K1,DKK1,RNF152,HTR
4,FGF7,PCDHB10,CPNE
6,RGS16,GPR171,SOX1
7,TENM3,SLC6A4,PTN,
C1QTNF3,PTPRR,GAS1
,PRKG2,PMAIP1,GRIP1,
CCL3,NPHP3,FGF2,MS
MP,DNAI1,PSD2,ATF3,
FZD7,ANGPT2,SYT6,S
OCS1,GNG11,SYBU,GP
R183,MYZAP,RASL10A
,IMPA1,IL1RAP,MAP3K

						8,KNDC1,LPAR6,HPGD S,PDGFRL,EYA4,KLRC 1,C9ORF72,F2RL3,TAF A2,EEF1E1
GO:0050896	BP	response to stimulus	5.80E-07	6.236824 38	199	FOSB,FOS,LRFN5,IGFB P1,MT1B,AREG,IL6,RG S1,NR4A3,CA8,EGR1,R GS7,NR4A1,NR4A2,SIK 1B,DUSP1,GADD45G,N RK,DLK1,SIK1,IGKV1D - 17,SYT4,CCN1,APOLD1 ,MROH2B,CEBPD,SOC S2,IRS2,CH25H,GADD4 5B,CXCL2,ZFAND5,EG R3,PTGS2,GABRG3,RG S2,TCIM,KL,FOSL1,SO CS3,MMP1,CXCR4,RAS D1,THBS1,SLC7A11,FA M83A,GPAT3,TNR,EGR 2,ZFP36,NR0B2,UGT2A 1,MAFF,CXCL3,CSRNP 1,RHOB,NRXN1,DUSP2 ,DIPK2A,CCN2,FST,CL EC4E,OGN,PCK1,CHR M3,CTLA4,PTX3,KLF4, PTGER3,CYTL1,ARC,C ACNA1A,TBX18,IL1RL 1,ASB3,HBEGF,BEND6, CCL4L2,PRDM1,CCL2, KIR3DL2,OSM,PELI2,H 4C11,PRRX1,ERBB4,N OTCH2NLA,GRIK1,TN FSF11,MSTN,MEIOB,A DAMTS1,AVPR1A,CAL CR,PDK4,NOX4,INHBB ,EPO,PLP1,MGARP,CF HR2,FAM107A,HPRT1, LRRC19,TSPAN5,RASS F10,GATA3,HPR,MSH4, IL10,ADTRP,JUN,FGF1 4,MAK,ESR2,TAS2R14, VIP,MT1A,MT1M,CHR

						DL1,CEBPB,CLEC4D,T FAP2A,GRM1,ELOVL4, PDE6C,PLA2G2A,LRRC 70,GRIK2,HSPE1,MT1F, HAS2,FOXC1,JUNB,LU RAP1L,CCL3L1,JUND,F OXO1,S100B,KCNK1,D KK1,RNF152,HTR4,MT 1X,NNMT,FGF7,CPNE6 ,ID2,RGS16,GPR171,SO X17,TENM3,SLC6A4,C RP,PTN,C1QTNF3,SLC3 8A2,PTPRR,GAS1,PRK G2,PMAIP1,SLC25A25, PCBP2,GRIP1,CCL3,NP HP3,FGF2,TRPC6,MSM P,DNAI1,PSD2,ATF3,A RG2,FZD7,ANGPT2,SY T6,SOCS1,GNG11,SYB U,GPR183,MT1H,MYZ AP,RASL10A,IMPA1,IL 1RAP,MAP3K8,KNDC1, LPAR6,HPGDS,BTG1,P DGFR1,EYA4,KLRC1,C 9ORF72,F2RL3,TAF4A, EEF1E1,MT1E,ST3GAL
						6
GO:0000785	CC	chromatin	0.122802 411	0.910793 105	35	FOSB,FOS,NR4A3,EGR 1,NR4A1,NR4A2,SIM1, CEBPD,EGR3,NPAS3,F OSL1,EGR2,NR0B2,MA FF,CSRNP1,KLF4,MKX, TBX18,H4C11,PRRX1,G ATA3,JUN,ESR2,CEBP B,TFAP2A,FOXC1,JUN B,JUND,FOXO1,KLF6,I D2,SOX17,BASP1,ATF3 ,HOXA4
GO:0005887	CC	integral component of plasma membrane	0.233885 989	0.630995 795	41	LRFN5,IL6,GABRG3,K L,NRXN1,KCNE4,CHR M3,CTLA4,PTGER3,HB EGF,KIR3DL2,ERBB4,G RIK1,TNFSF11,AVPR1

						A,CALCR,NOX4,PLP1, TSPAN5,SLCO1B3,CD6 9,KCNIP1,GRM1,LRRC 70,GRIK2,HAS2,KCNK1 ,HTR4,PCDHB10,TENM 3,SLC6A4,SLC38A2,ML ANA,TRPC6,SYT6,GPR 183,IL1RAP,SLC26A7,L PAR6,KLRC1,F2RL3
GO:0001228	MF	DNA- binding transcriptio n activator activity, RNA polymerase II-specific	5.29244E -06	5.276343 964	26	FOSB,FOS,NR4A3,EGR 1,NR4A1,NR4A2,CEBP D,CTCFL,EGR3,FOSL1, EGR2,MAFF,CSRNP1,K LF4,PRRX1,GATA3,JU N,CEBPB,TFAP2A,FOX C1,JUNB,JUND,FOXO1, KLF6,SOX17,ATF3
GO:0005102	MF	signaling receptor binding	0.000106 287	3.973518 903	50	IGFBP1,AREG,IL6,CCN 1,SOCS2,IRS2,CXCL2,T CIM,KL,THBS1,TNR,N R0B2,CXCL3,NRXN1,C CN2,FST,OGN,CYTL1, HBEGF,CCL4L2,CCL2, KIR3DL2,OSM,EDIL3,E RBB4,NOTCH2NLA,TN FSF11,MSTN,AVPR1A,I NHBB,EPO,GATA3,IL1 0,FGF14,ESR2,VIP,CCL 3L1,S100B,DKK1,FGF7, CRP,PTN,CCL3,FGF2,M SMP,FZD7,ANGPT2,SO CS1,IL1RAP,TAF2
Down regulated genes						
GO:0065008	BP	regulation of biological quality	0.172987 3	0.761985 781	110	AKR1B10,MYH7,SLC22 A12,AKR1B15,SCUBE1, S1PR2,COMP,ADAMTS 16,CIDEA,BHLHA15,IG F2BP1,CCL24,EDN2,AC HE,SFN,SLC6A2,PLXN A4,TREM2,LMOD2,SC D,GCK,EIF2S3B,PDX1,

						LIME1,PLEKHN1,RTN4 R,BBC3,GJD3,FOXP3,S EZ6,SLC51B,DCSTAMP ,CYP7A1,H4C5,SPTA1, CMA1,SLC22A2,H4C8, KCNH3,SCIN,EPHB2,L PL,RTEL1,LRFN4,ANG PTL8,CNTN2,HCN2,HS PA8,MB,RAB3B,GPLD1 ,KCNJ11,TMEM102,IL4I 1,HRH2,SLC1A7,DAGL A,MUC6,PFKL,EYA2,G LIS2,TNFSF13,UGT1A1, ZBED6,UGT1A9,SORC S2,IL2RA,LSS,POLD1,K CNJ5,GTF2I,GDF2,NAL CN,ARHGEF18,MAPK8 IP2,CDKN1A,ITGB3,AT P13A2,P2RY2,ABCA2,I NAVA,SLC29A4,TRPV6 ,GAS6,RHEX,PIEZO1,S YT7,AGRN,FDXR,DAB 2IP,PDGFA,LRRC24,CD C42EP1,EXO1,CORO1B ,WNK2,ACE2,OXT,MC HR1,KCNAB2,NLRP6,S PP1,KCNE1,ZFPM1,AN XA6,S1PR4,C1QTNF12, E2F1,ITGA7,CLDN3
GO:0048468	BP	cell developme nt	0.175272 677	0.756285 78	63	NTN3,S1PR2,COMP,BH LHA15,C1QL1,IGF2BP1 ,COL11A1,ROS1,ACHE, SFN,TNNT3,PLXNA4,F ASN,STMN2,TREM2,C ABYR,TCAP,ACTA1,L MOD2,ANKRD1,RTN4 R,HECW1,FOXP3,SEZ6, HES2,LAMC3,TBX20,S PTA1,TYMS,BMP10,TP GS1,RASAL1,EPHB2,R AB25,RIMBP3,NPM2,A NGPTL8,CNTN2,EFNA 2,LAMB3,ST14,BICDL1

						,MAPK8IP2,CDKN1A,ITGB3,ABCA2,MAP1S,LAMA3,RHEX,AGRN,FAT1,DAB2IP,SPINT1,SPP1,KRT8,ZFPM1,TFCP2L1,ANXA6,LAMB2,E2F1,TUBB2B,LAMA5,CLDN3
GO:0071944	CC	cell periphery	0.000147813	3.830286713	178	NTN3,SLC22A12,SCUBE1,ULBP3,PKP3,SLC7A14,S1PR2,COMP,PCDH A12,CDH15,ADAMTS16,PLCH2,TPSG1,COL11A1,DPEP1,ALDH3A1,ROS1,FADS2,CDH16,TMEM240,ACHE,TRBV4-2,COL10A1,SLC6A2,PLXNA4,EDA2R,MUC3A,FASN,DGCR6,TREM2,RAB44,NKD2,COL19A1,TMEM150B,LIME1,PLEKHN1,RTN4R,DTNA,ADAM21,LGALS4,TIMP3,STBD1,CHI3L1,GJD3,DOCK7,PHLDA3,MMP17,SLC22A1,SLC51B,DCSTAMP,TRAV9-2,LAMC3,SPTA1,CMA1,TRAV8-3,SLC22A2,TRBV7-9,GALR3,RASAL1,PITPNM1,APC2,KCNH3,PCDHGB2,SCIN,PCDHGA4,EPHB2,SLC5A10,SLC26A1,LPL,MRAP,LRFN4,RAB25,SLC2A14,TMPRSS9,CNTN2,EVC,EFNA2,HCN2,VTGN1,HSPA8,RAB3B,ADAMTSL2,GPLD1,CDH24,MFAP5,ACKR1,KCNJ11,TMEM102,IL4I1,EVPLL,HRH2,SLC1A7,DAGLA,SUSD2,SUSD3,PCDHAC2,LA

MB3,LYPD1,AJM1,MU
C6,RRAD,PCDHGB4,U
GT1A1,SORCS2,PCDH
GC3,IL2RA,LYPD2,AN
XA13,SERPINA12,KCN
J5,MICAL3,EPPK1,NAL
CN,HMCN2,ST14,ARH
GEF18,MRGPRF,ENTP
D8,OLFM2,DISP2,ITGB
3,P2RY2,ABCA2,SLC29
A4,MFAP3,TRPV6,ADA
MTSL5,PCDHGB7,LAM
A3,RHEX,PIEZO1,SYT7
,AGRN,FAT1,GPBAR1,
DAB2IP,B3GNT3,LRRC
24,CDC42EP1,EXO1,BC
AR1,CORO1B,SPINT1,L
RRC55,C1ORF116,TRE
H,WNK2,ACE2,CFB,CO
L7A1,LIPH,INHBE,MC
HR1,KCNAB2,NLRP6,T
ECTB,SLC6A19,FCAM
R,ANGPTL7,KRT8,KCN
E1,FNDC5,HLA-
G,TRAF7,ANXA6,S1PR
4,ABCB8,MMP9,C4A,L
AMB2,SLC22A18,TME
M63A,TMC4,LAMA5,IT
GA7,CLDN3,TNFRSF12
A

GO:0016020	CC	membrane	0.027489 157	1.560838 574	238	EEF1A2,CYP51A1,SLC2 2A12,SCUBE1,ULBP3,P KP3,SLC7A14,S1PR2,P CDHA12,CDH15,PLCH2 ,TPSG1,GALNT4,CPT1 B,RAB43,DPEP1,LDLR AD1,ALDH3A1,ROS1,F ADS2,CWH43,CDH16,T MEM240,TMEM151A,A CHE,TRBV4- 2,SLC6A2,PLXNA4,ED A2R,MUC3A,FASN,ST MN2,TREM2,PHLDA2,S
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CD,RAB44,NKD2,TME
M150B,UGT1A6,STRIT
1,LIME1,HHATL,PLEK
HN1,RTN4R,DTNA,BB
C3,ADAM21,LGALS4,T
MEM52B,STBD1,PDZK
1IP1,NAT8L,MAMDC4,
GJD3,DOK7,PHLDA3,M
MP17,SV2B,PTCHD4,S
EZ6,SLC51B,DCSTAMP
,NOMO2,MTFP1,TRAV

9-

2,LAMC3,CYP7A1,H4C
5,SPTA1,TYMS,TRAV8-
3,SLC22A2,TRBV7-
9,GALR3,CMTM1,NOM
O3,RASAL1,SYNGR4,F
ADS1,H4C8,PITPNM1,A
PC2,KCNH3,PCDHGB2,
SCIN,PCDHGA4,EPHB2
,SLC5A10,SLC26A1,LP
L,LOXL4,IGSF1,MRAP,
LRFN4,RAB25,SLC2A1
4,TMPRSS9,CNTN2,EV
C,ACAD11,EFNA2,HCN
2,VTCN1,BRICD5,HSP
A8,RAB3B,GPLD1,CDH
24,ACKR1,KCNJ11,TM
EM102,IL4I1,EVPLL,HR
H2,SLC1A7,SLC49A3,D
AGLA,TMEM125,SUSD
2,AP1M2,B3GNT8,SUS
D3,PCDHAC2,LYPD1,A
JM1,MUC6,RRAD,PFKL
,TNFSF13,PCDHGB4,T
MEM121,UGT1A1,UGT
1A9,SORCS2,PCDHGC3
,IL2RA,LYPD2,ANXA1
3,LSS,POLD1,SERPINA
12,KCNJ5,GTF2I,RHBD
D3,MICAL3,EPPK1,GL
TPD2,KLHDC7A,NALC
N,HMCN2,ST14,ARHG
EF18,MRGPRF,FDPS,F

						<p>UT7,ENTPD8,OLFM2,F AM151A,DISP2,ITGB3, ATP13A2,P2RY2,ABCA 2,SLC29A4,MFAP3,TRP V6,PAQR4,NYNRIN,PC DHGB7,LAMA3,RHEX, PIEZO1,SYT7,KIF4A,A GRN,INTS1,FAT1,FDX R,CLCN7,GPBAR1,DAB 2IP,PDGFA,B3GNT3,T MEM104,LRRC24,CDC 42EP1,BEGAIN,EXO1,B CAR1,WDR24,CORO1B ,SPINT1,LRRC55,C1OR F116,IGSF3,TREH,WNK 2,ACE2,ENTPD7,CFB,C OL7A1,UGT1A4,LIPH,S T6GALNAC1,AP5B1,M CHR1,KCNAB2,NLRP6, TECTB,SLC6A19,FCA MR,EVI5L,KRT8,KCNE 1,FNDCC5,HLA- G,PCNX3,TFCP2L1,TR AF7,ANXA6,DERL3,S1 PR4,ABCB8,C4A,SLC22 A18,MKI67,CCDC134,M ED16,MCM5,TMEM63A ,TMC4,EXTL3,GOLGA6 B,ITGA7,CLDN3,FMO1, SPHK2,TNFRSF12A</p>
GO:0005509	MF	calcium ion binding	0.001499 623	2.824017 866	35	<p>MYL1,CALML3,SCUBE 1,COMP,PCDHA12,CD H15,PLCH2,TNNC2,CD H16,CABYR,RAB44,NK D2,TUBB4A,MYL7,SPT A1,PITPNM1,PCDHGB2 ,SCIN,PCDHGA4,LPL,S PATA21,VWCE,CDH24, PCDHAC2,PCDHGB4,P CDHGC3,ANXA13,HM CN2,PCDHGB7,GAS6,S YT7,AGRN,FAT1,RASE F,ANXA6</p>

GO:0005198	MF	structural molecule activity	0.049695 351	1.303684 236	29	MYL1,MYBPC1,COMP, COL11A1,COL10A1,KRT23,MUC3A,TCAP,ACTA1,COL19A1,TUBB4A, CHI3L1,LAMC3,SPTA1, MFAP5,EVPLL,LAMB3, MUC6,EPPK1,HMCN2, MAPK8IP2,LAMA3,AGRN,COL7A1,TECTB,LAMB2,TUBB2B,LAMA5, CLDN3
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Table 3 The enriched pathway terms of the up and down regulated differentially expressed genes

Pathway ID	Pathway Name	Adjusted p value	Negative log10 of adjusted p value	Gene Count	Gene
Up regulated genes					
REAC:R-HSA-449147	Signaling by Interleukins	5.19612E-05	4.28432078	24	FOS,IL6,CEBPD,SOCS2,IRS2,CXCL2,PTGS2,SOCS3,MMP1,IL1RL1,CCL2,OSM,PELI2,GATA3,IL10,JUN,JUNB,CCL3L1,FOXO1,S100B,CCL3,FGF2,SOCS1,MAP3K8
REAC:R-HSA-162582	Signal Transduction	0.000351497	3.45407887	72	FOSB,FOS,AREG,IL6,RGS1,EGR1,RGS7,NR4A1,DUSP1,DLK1,TUBA3E,IRS2,CXCL2,EGR3,TUBA3D,GABRG3,RGS2,FOSL1,SOCS3,CXCR4,SDR9C7,THBS1,TUBB8,EGR2,CXCL3,RHOB,DISP2,FST,PCK1,CHRM3,PTGER3,ARC,IL1RL1,

					HBEGF,CCL4L2,CCL2, H4C11,AVPR1A,CALC R,PKD4,INHBB,EPO,G ATA3,JUN,ESR2,TAS2R 14,VIP,CHRD1,GRM1, JUNB,CCL3L1,JUND,F OXO1,S100B,DKK1,HT R4,FGF7,ID2,RGS16,SO X17,GAS1,PRKG2,CCL 3,FGF2,TRPC6,FZD7,SO CS1,GNG11,GPR183,LP AR6,F2RL3,ST3GAL6
REAC:R-HSA- 500792	GPCR ligand binding	0.009405 239	2.026630 152	19	CXCL2,CXCR4,CXCL3, CHRM3,PTGER3,CCL2, AVPR1A,CALCR,TAS2 R14,VIP,GRM1,CCL3L1 ,HTR4,CCL3,FZD7,GNG 11,GPR183,LPAR6,F2R L3
REAC:R-HSA- 9006934	Signaling by Receptor Tyrosine Kinases	0.015959 834	1.796971 627	19	FOSB,FOS,AREG,EGR1 ,IRS2,EGR3,GABRG3,F OSL1,THBS1,EGR2,AR C,HBEGF,JUNB,JUND, S100B,FGF7,ID2,FGF2,S OCS1
REAC:R-HSA- 416476	G alpha (q) signalling events	0.024781 954	1.605864 462	11	RGS1,RGS2,CHRM3,HB EGF,AVPR1A,GRM1,R GS16,TRPC6,GNG11,LP AR6,F2RL3
REAC:R-HSA- 112315	Transmission across Chemical Synapses	0.033876 307	1.470103 934	12	TUBA3E,TUBA3D,GAB RG3,TUBB8,CACNA1A, GRIK1,PPFIA2,GRIK2,S LC6A4,SLC38A2,GRIP1 ,GNG11
Down regulated genes					
REAC:R-HSA- 1474244	Extracellular matrix organization	4.76433E -05	4.321998 012	24	SCUBE1,COMP,ADAM TS16,COL11A1,COL10 A1,COL19A1,MMP17,L AMC3,CMA1,BMP10,L OXL4,MFAP5,LAMB3,I

					TGB3,MFAP3,LAMA3, AGRN,PDGFA,COL7A1 ,SPP1,MMP9,LAMB2,L AMA5,ITGA7
REAC:R-HSA-211859	Biological oxidations	0.149345 464	0.825807 963	12	CYP51A1,DPEP1,ALDH 3A1,UGT1A6,CYP7A1,S LC26A1,UGT1A1,UGT1 A9,FDXR,OPLAH,UGT1 A4,FMO1
REAC:R-HSA-5173105	O-linked glycosylation	0.289440 419	0.538440 822	7	ADAMTS16,GALNT4,M UC3A,ADAMTSL2,B3G NT8,MUC6,B3GNT3
REAC:R-HSA-397014	Muscle contraction	0.295106 887	0.530020 655	10	MYL1,MYBPC1,TNNC2 ,TNNT3,TCAP,ACTA1, MYL7,KCNJ11,KCNE1, ANXA6
REAC:R-HSA-556833	Metabolism of lipids	0.299103 351	0.524178 721	26	CYP51A1,AKR1B15,CI DEC,CIDEA,CPT1B,DP EP1,FADS2,ACHE,FAS N,SCD,ANKRD1,MVD, CYP7A1,FADS1,PITPN M1,ACAD11,ACBD7,U GT1A9,LSS,FDPS,ME1, FDXR,LIPH,MED16,SP HK2,MID1IP1

Table 4 Topology table for up and down regulated genes.

Regulation	Node	Degree	Betweenness	Stress	Closeness
Up	ESR2	252	0.153302	16307122	0.327825
Up	JUN	218	0.122226	20151740	0.318931
Up	PTN	83	0.04122	6599240	0.261213
Up	PTGER3	61	0.04852	9842220	0.243274
Up	CEBPB	54	0.013264	2179706	0.289255
Up	FOXO1	46	0.015398	1958960	0.286178
Up	ERBB4	42	0.021503	4864528	0.266298

Up	NR4A1	40	0.013258	2508616	0.271305
Up	FOXC1	40	0.014365	2960242	0.256879
Up	SOCS3	39	0.015854	1846382	0.268846
Up	TSPAN5	39	0.021529	3536542	0.179423
Up	ATF3	38	0.008644	888320	0.274996
Up	DLK1	38	0.024667	2025172	0.198226
Up	RASSF10	38	0.017409	2496598	0.256983
Up	SOCS1	37	0.011257	1943118	0.266745
Up	TFAP2A	37	0.01778	1917734	0.284638
Up	ID2	35	0.014538	1684376	0.259632
Up	GRM1	33	0.008081	1405306	0.252868
Up	JUNB	33	0.003916	464160	0.27105
Up	JUND	32	0.003605	581468	0.278421
Up	GRIP1	32	0.027221	4286096	0.255638
Up	GADD45G	31	0.018252	1295156	0.289018
Up	IRS2	31	0.011813	1244018	0.280018
Up	NR0B2	30	0.011956	1085608	0.273244
Up	THBS1	30	0.020429	1220078	0.234295
Up	EGR1	29	0.008524	1240050	0.268142
Up	RGS2	29	0.013439	613038	0.268846
Up	MZT1	28	0.01342	1489952	0.234054
Up	GPR183	28	0.011006	4785362	0.187047
Up	MAFF	27	0.0076	914614	0.244436
Up	PCBP2	26	0.007207	976748	0.251885
Up	LPAR6	26	0.013687	1227722	0.21789
Up	FGF2	25	0.018904	2947892	0.245305

Up	CACNA1A	24	0.014346	1032998	0.245419
Up	CA8	23	0.011729	1626402	0.212977
Up	CXCR4	23	0.011272	1056072	0.2569
Up	S100B	22	0.00813	1264412	0.248279
Up	GATA3	22	0.005995	1401804	0.251685
Up	TUBB8	22	0.010257	1276630	0.244926
Up	FOSL1	19	0.004451	290374	0.270819
Up	ZFP36	19	0.005886	855226	0.252586
Up	MAP3K8	18	0.002239	664468	0.252687
Up	CEBPD	18	0.003277	452042	0.256009
Up	BASP1	18	0.004385	972442	0.25077
Up	PTGS2	17	0.00354	684102	0.250098
Up	CTLA4	16	0.004535	561138	0.232408
Up	EEF1E1	16	0.006062	993528	0.230033
Up	PPFIA2	15	0.004649	430712	0.240218
Up	HSPE1	14	0.005538	963234	0.251486
Up	KLF4	14	0.002381	401354	0.249803
Up	PRDM1	14	0.004147	663736	0.233674
Up	PTPRR	13	0.002529	397948	0.230167
Up	SOCS2	12	2.25E-04	29864	0.225731
Up	FAM107A	12	0.004314	391420	0.23653
Up	DUSP1	11	8.29E-04	200904	0.236671
Up	IL1RAP	11	0.005075	490034	0.226294
Up	CCL2	11	0.004963	301058	0.179221
Up	GRIK2	10	0.002374	159532	0.213235
Up	PHLDA1	10	0.002297	380826	0.244135

Up	ETFRF1	10	0.004407	230860	0.208651
Up	CPA4	10	0.005088	610960	0.203854
Up	FMC1	10	0.003795	509566	0.219229
Up	TNFSF11	9	0.006207	499546	0.228066
Up	GADD45B	9	0.001894	221200	0.226326
Up	PTX3	9	0.003429	288438	0.200316
Up	PLP1	9	0.002263	205084	0.214083
Up	ZFAND5	9	0.00214	106574	0.270013
Up	NR4A2	9	0.00141	126664	0.222549
Up	NOTCH2NLA	9	0.002972	234194	0.220463
Up	CRP	8	0.002804	195986	0.192761
Up	OSM	8	0.003812	215368	0.210981
Up	NPHP3	8	0.003428	308932	0.202993
Up	C9orf72	8	0.004954	494952	0.210004
Up	NRXN1	8	0.004407	299852	0.204906
Up	ASB3	8	0.001938	714486	0.184868
Up	MAK	8	0.001972	159538	0.226601
Up	RHOB	8	0.003182	393652	0.197094
Up	TUBA3E	8	0.003786	289220	0.20426
Up	SLC38A2	8	0.002598	229690	0.192015
Up	FST	7	0.003149	1000482	0.16387
Up	HPRT1	7	0.002519	265684	0.190757
Up	PLA2G2A	7	0.001582	115638	0.227657
Up	FZD7	7	0.001934	696944	0.182393
Up	CCN2	7	0.008071	354698	0.266723
Up	SLC19A2	7	0.003778	297990	0.165545

Up	SYT6	7	0.002519	132836	0.208679
Up	FOS	6	0.001001	233150	0.246889
Up	BTG1	6	0.001312	158508	0.220019
Up	RGS7	6	0.001373	68622	0.193655
Up	MMP1	6	0.002086	85636	0.162162
Up	ADAMTS1	6	0.002369	102166	0.18102
Up	CTCFL	6	0.001763	246802	0.228066
Up	PELI2	5	6.63E-04	105816	0.222643
Up	KLF6	5	6.77E-04	75600	0.236073
Up	EYA4	5	7.59E-04	91984	0.197794
Up	KIR3DL2	5	1	6	1
Up	PFKFB3	5	3.28E-05	6506	0.215391
Up	PNRC1	5	0.00139	114074	0.222036
Up	RBMS1	5	0.001488	192558	0.183883
Up	SIK1	5	0.00146	115492	0.232988
Up	HTR4	5	5.45E-05	12090	0.216095
Up	EGR2	5	6.76E-04	100080	0.220401
Up	FAM9B	5	1	20	1
Up	ZNRF2	4	7.56E-04	76784	0.23151
Up	SGK3	4	0.001265	170160	0.224899
Up	IGFBP1	4	0.00189	182178	0.15723
Up	IMPA1	4	6.30E-04	43712	0.20232
Up	SYBU	4	3.36E-04	36546	0.209022
Up	CHRM3	4	6.68E-04	81146	0.215508
Up	GULP1	4	3.48E-04	43006	0.22665
Up	ADAMTS4	4	0.001457	106596	0.193195

Up	DUSP2	3	5.91E-06	2284	0.216389
Up	TNR	3	6.61E-04	34996	0.19117
Up	RETREG1	3	9.48E-04	107682	0.176079
Up	FOSB	2	0	0	0.242753
Up	NACA2	2	6.30E-04	71244	0.19482
Up	PCK1	2	1.12E-04	24282	0.233795
Up	TCP10L	1	0	0	1
Up	MSTN	1	0	0	0.213838
Up	CALCR	1	0	0	0.189833
Up	GRIK1	1	0	0	0.203605
Up	ELMOD1	1	0	0	0.217412
Up	DNAJC12	1	0	0	0.175398
Up	SOWAHA	1	0	0	0.19951
Up	CCN1	1	0	0	0.199209
Up	PCDHB10	1	0	0	0.21973
Down	IKBKG	297	0.219998	28468976	0.339538
Down	HSPA8	249	0.216486	22912020	0.352393
Down	SFN	139	0.096144	11786478	0.307827
Down	CDKN1A	89	0.044712	9732644	0.290314
Down	E2F1	79	0.027908	5678252	0.277108
Down	ZWINT	68	0.034002	4334154	0.248746
Down	ACTA1	65	0.031398	5160900	0.270358
Down	FOXP3	63	0.026408	4439834	0.261644
Down	BCAR1	53	0.026528	2498042	0.283595
Down	MCM5	49	0.015828	3100420	0.270151
Down	CDT1	49	0.0142	2142496	0.27268

Down	ATP13A2	48	0.040851	1858586	0.281583
Down	GLIS2	43	0.012738	2971676	0.267803
Down	GTF2I	40	0.013965	3548098	0.267352
Down	FASN	40	0.013278	1923754	0.294052
Down	TUBB2B	39	0.014139	3409940	0.261536
Down	EEF1A2	35	0.011846	1154354	0.283722
Down	MED16	35	0.010267	546374	0.274829
Down	KRT8	35	0.022582	2216918	0.295889
Down	ITGB3	32	0.017613	1787526	0.25309
Down	MKI67	32	0.012591	2306860	0.26999
Down	IGF2BP1	32	0.011046	1817704	0.264964
Down	CALML3	30	0.016001	3689680	0.234624
Down	EIF3C	29	0.013833	1898480	0.255309
Down	MAPK8IP2	28	0.014621	2092782	0.252888
Down	PPP6R1	28	0.014191	2543882	0.236742
Down	PFKL	26	0.011293	2060970	0.262422
Down	POLD1	25	0.01216	1380436	0.254103
Down	WDR62	25	0.009598	1556774	0.257776
Down	BEGAIN	25	0.008918	621044	0.231358
Down	EXO1	24	0.009378	611262	0.26679
Down	PKP3	24	0.013902	706668	0.277788
Down	CORO1B	23	0.008296	1392340	0.240911
Down	MYH7	23	0.010919	466678	0.228214
Down	PPP1R3C	22	0.009067	1597620	0.236231
Down	MAP1S	22	0.012693	971324	0.247177
Down	PHLDA3	22	0.008565	1300372	0.238826

Down	EPHB2	21	0.007088	1027538	0.246658
Down	CNTN2	21	0.008116	442262	0.277885
Down	EPPK1	21	0.006527	714440	0.285972
Down	LAMB3	21	0.011464	1023764	0.243929
Down	LIPH	21	0.010728	701480	0.212692
Down	SPTA1	20	0.006833	602872	0.253717
Down	DTNA	18	0.011282	1247794	0.206439
Down	FBXW5	18	0.005902	970060	0.233657
Down	WDR24	18	0.007909	812806	0.222925
Down	KCNAB2	18	0.006806	539108	0.227821
Down	INTS1	18	0.011943	1432184	0.240473
Down	TRAF7	17	0.006461	891258	0.235268
Down	CDC45	17	0.005438	340314	0.255083
Down	AP1M2	16	0.009031	859896	0.213953
Down	MMP9	16	0.010164	605996	0.202217
Down	SPP1	16	0.007637	828418	0.229087
Down	RTEL1	16	0.008419	692556	0.241976
Down	APC2	15	0.003969	540810	0.238342
Down	TBL3	15	0.005688	802840	0.241939
Down	TUT1	15	0.005993	741238	0.224676
Down	ACAD11	15	0.007604	390702	0.21475
Down	PDF	15	0.005927	815818	0.211967
Down	STBD1	14	0.008739	588312	0.219411
Down	MFAP3	14	0.008403	592372	0.208063
Down	CLCN7	14	0.00565	345496	0.206506
Down	ITGA7	13	0.004528	295182	0.203305

Down	EYA2	12	0.005337	373532	0.226294
Down	TCAP	12	0.005861	210724	0.271979
Down	LAMA5	12	0.004464	378806	0.203788
Down	TIMP3	12	0.005346	371996	0.169851
Down	KIF4A	11	0.004493	663298	0.235007
Down	FAT1	11	0.004601	383862	0.219821
Down	RAB3B	10	0.005664	629802	0.166921
Down	DAB2IP	10	0.001509	308434	0.247196
Down	CKM	10	0.003777	334172	0.239873
Down	MICAL3	10	0.001711	278900	0.225747
Down	MIB2	10	0.002635	175896	0.23745
Down	SERPINA12	10	0.003286	1359806	0.162038
Down	FBXL18	10	0.002126	410424	0.215728
Down	RAVER1	9	0.002356	184440	0.232255
Down	LPL	9	0.002077	256246	0.201844
Down	C19orf25	9	0.005017	454386	0.212322
Down	CDCA2	9	0.002925	429662	0.232937
Down	RAB25	9	0.003803	599076	0.208569
Down	GAS6	8	0.004121	284918	0.204339
Down	TMEM52B	8	0.00642	1133566	0.226536
Down	FDPS	7	0.001512	77870	0.268983
Down	STMN2	7	0.00198	112084	0.21843
Down	LRFN4	7	7.76E-04	119920	0.2404
Down	MEOX1	7	0.003778	227130	0.152699
Down	TRIM56	7	0.00154	235690	0.240546
Down	CDC42EP1	7	0.00145	147522	0.240382

Down	ANXA6	6	8.32E-04	55866	0.210477
Down	FDXR	6	0.00196	213120	0.185019
Down	C4A	6	0.003488	217398	0.188659
Down	LAMA3	6	0.002394	218314	0.225346
Down	KRT7	6	0.001611	172556	0.239493
Down	MVD	6	0.002525	163688	0.227445
Down	MYBPC1	5	0.001022	80464	0.199799
Down	INAVA	5	0.001535	221534	0.195974
Down	LAMB2	5	0.001901	130904	0.193643
Down	TYMS	4	6.30E-04	48926	0.213594
Down	SLC22A18	4	0.001272	66132	0.188749
Down	CYP51A1	4	0.00189	204342	0.14622
Down	DPEP1	3	0	0	1
Down	ABCB8	3	0.00126	110762	0.178958
Down	TPGS1	3	0.00126	231982	0.176275
Down	TMEM63A	3	6.52E-04	38766	0.160157
Down	OLFM2	3	1	6	1
Down	EXTL3	3	1	6	1
Down	DUSP8	2	1.55E-06	342	0.219169
Down	COL7A1	2	2.58E-04	22290	0.200038
Down	BHLHA15	2	1.00E-07	2	0.170948
Down	TUBB4A	2	2.31E-04	62654	0.256443
Down	ME1	2	3.08E-05	8426	0.195829
Down	PCDHGC3	2	6.30E-04	51874	0.15275
Down	SCD	2	6.30E-04	30588	0.206816
Down	SMCR8	1	0	0	0.173566

Down	MXD4	1	0	0	1
Down	UNC119B	1	0	0	0.168749
Down	ACKR1	1	0	0	0.15199
Down	INHBE	1	0	0	0.140804
Down	SCIN	1	0	0	0.212834
Down	DUS3L	1	0	0	0.194772
Down	LIME1	1	0	0	0.19047
Down	NAT8L	1	0	0	0.152135
Down	SUSD3	1	0	0	0.190049
Down	CCDC117	1	0	0	0.260591
Down	PIEZO1	1	0	0	0.152135
Down	CIDEA	1	0	0	0.139449
Down	EVI5L	1	0	0	0.195684
Down	FAM111B	1	0	0	0.21973
Down	ABCA2	1	0	0	0.196108
Down	AGRN	1	0	0	0.197069
Down	PDX1	1	0	0	0.215698
Down	PARP10	1	0	0	0.253494
Down	VWCE	1	0	0	1

Table 5 miRNA - target gene and TF - target gene interaction

Regulation	Target Genes	Degree	MicroRNA	Regulation	Target Genes	Degree	TF
Up	JUN	118	hsa-mir-199a-5p	Up	JUN	61	GATA2
Up	FOXO1	63	hsa-mir-33a-3p	Up	SOCS3	56	RUNX1

Up	FOXC1	62	hsa-mir-561-3p	Up	TFAP2A	55	SUZ12
Up	SOCS3	48	hsa-mir-22-5p	Up	ATF3	48	NUCKS1
Up	CEBPB	47	hsa-mir-3613-3p	Up	CEBPB	46	FOXP2
Up	TFAP2A	46	hsa-mir-1306-3p	Up	FOXO1	43	PAX3
Up	NR4A1	40	hsa-mir-125a-5p	Up	SOCS1	39	STAT5A
Up	SOCS1	26	hsa-mir-21-3p	Up	FOXC1	37	SALL4
Up	ATF3	26	hsa-mir-147a	Up	NR4A1	36	MYC
Up	TSPAN5	24	hsa-mir-181a-5p	Up	PTGER3	33	TFCP2L1
Up	ERBB4	21	hsa-mir-433-3p	Up	TSPAN5	30	ASH2L
Up	PTN	12	hsa-mir-376a-5p	Up	ERBB4	29	MEF2A
Up	DLK1	5	hsa-mir-15a-5p	Up	ESR2	28	RCOR1
Up	ESR2	1	hsa-mir-335-5p	Up	DLK1	28	LMO2
Up	PTGER3	1	hsa-mir-148a-3p	Up	PTN	27	MYCN
Down	CDKN1A	187	hsa-mir-30b-3p	Down	CDKN1A	57	TP53
Down	HSPA8	116	hsa-mir-338-5p	Down	HSPA8	39	KLF4
Down	FASN	116	hsa-mir-103a-3p	Down	FASN	39	EGR1

Down	E2F1	74	hsa-mir-150-5p	Down	ZWINT	37	AHR
Down	CDT1	45	hsa-mir-202-3p	Down	BCAR1	37	TRIM28
Down	MCM5	41	hsa-mir-145-5p	Down	E2F1	36	MITF
Down	GTF2I	33	hsa-mir-124-3p	Down	CDT1	34	SIN3B
Down	ZWINT	28	hsa-mir-126-3p	Down	TUBB2B	34	SMAD3
Down	TUBB2B	24	hsa-mir-101-3p	Down	GTF2I	33	AR
Down	BCAR1	21	hsa-mir-1296-5p	Down	ATP13A2	28	TCF7
Down	GLIS2	20	hsa-mir-31-3p	Down	MCM5	27	KLF1
Down	SFN	19	hsa-mir-200c-3p	Down	SFN	21	REST
Down	ATP13A2	13	hsa-mir-4523	Down	GLIS2	19	SOX2
Down	ACTA1	7	hsa-mir-27a-5p	Down	ACTA1	13	SRY
Down	FOXP3	1	hsa-mir-372-3p	Down	FOXP3	10	CCND1

Figures

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

Fig. 4. Modules of isolated form PPI of DEGs. (A) The most significant module was obtained from PPI network with 95 nodes and 103 edges for up regulated genes (B) The most significant module was obtained from PPI network with 79 nodes and 131 edges for down regulated genes. Up regulated genes are marked in green; down regulated genes are marked in red

Fig. 5. Target gene - miRNA regulatory network between target genes. The yellow color diamond nodes represent the key miRNAs; up regulated genes are marked in green color; down regulated genes are marked in red color.

Fig. 6. Target gene - TF regulatory network between target genes. The blue color triangle nodes represent the key TFs; up regulated genes are marked in green color; down regulated genes are marked in red color.

Fig. 7. ROC curve analyses of hub genes. A) ESR2 B) JUN C) PTN D) PTGER3 E) CEBPB F) IKBKG G) SFN I) CDKN1A J) E2F1