Identification of differentially expressed genes and signaling pathways in gestational diabetes mellitus by integrated bioinformatics analysis

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Abstract

Gestational diabetes mellitus (GDM) is a metabolic disorder during pregnancy. Numerous biomarkers have been identified that are linked with the occurrence and development of GDM. The aim of this investigation was to identify differentially expressed genes (DEGs) in GDM using a bioinformatics approach to elucidate their molecular pathogenesis. GDM associated expression profiling by high throughput sequencing dataset (GSE154377) was obtained from Gene Expression Omnibus (GEO) database including 28 normal pregnancy samples and 33 GDM samples. DEGs were identified using DESeq2. The gene ontology (GO) and REACTOME pathway enrichments of DEGs were performed by g:Profiler. Protein-protein interaction (PPI) networks were assembled with Cytoscape software and separated into modules using the PEWCC1 algorithm. MiRNA-hub gene regulatory network and TF-hub gene regulatory network were performed with the miRNet database and NetworkAnalyst database. Receiver Operating Characteristic (ROC) analyses was conducted to validate the hub genes. A total of 953 DEGs were identified, of which 478 DEGs were up regulated and 475 DEGs were down regulated. Furthermore, GO and REACTOME pathway enrichment analysis demonstrated that these DEGs were mainly enriched in multicellular organismal process, cell activation, formation of the cornified envelope and hemostasis. TRIM54, ELAVL2, PTN, KIT, BMPR1B, APP, SRC, ITGA4, RPA1 and ACTB were identified as key genes in the PPI network, miRNA-hub gene regulatory network and TF-hub gene regulatory network. TRIM54, ELAVL2, PTN, KIT, BMPR1B, APP, SRC, ITGA4, RPA1 and ACTB in GDM were validated using ROC analysis. This investigation provides further insights into the molecular pathogenesis of GDM, which might facilitate the diagnosis and treatment of GDM.

Keywords: gestational diabetes mellitus; hub gene; gene expression omnibus; bioinformatics; protein-protein interaction network

Introduction

Gestational diabetes mellitus (GDM) has emerged as most common medical complications of pregnancy, but current treatments are still suboptimal [1]. The number of cases GDM is rising worldwide and it has become a key health concern [2]. There are several important risk factors for GDM, such as advanced maternal age [3], family history of diabetes [4], obesity [5], cigarette smoking [6], genetics factors [7], hypertension and type 2 diabetes [8], and cardiovascular diseases [9]. However, GDM is a complex disorder and its biology remains poorly understood. Therefore, mining key biomarkers linked with GDM occurrence and advancement is essential for GDM early diagnosis, prognosis and treatment.

The GDM is an extremely complicated pathophysiological process and controlled by various genes and signaling pathways. Genes such as PVT1 [10], IL-6, IL-10, and TNF- α [11], CAPN10 [12], ADCYAP1 [13] and ABHD5 [14] are associated with GDM. Signaling pathways such as PI3K/AKT signaling pathway [15], AMPK signaling pathway [16], vitamin D signaling pathways [17], TLR4/NF-kappaB Signaling Pathway [18] and AGEs-RAGE signaling pathway [19] are linked with GDM. Recently, next-generation sequencing (NGS) technology is extensively applied in clinical investigation, with the marked gain relying on its capacity to together determine the expression data of massive genes at a time [20]. The public database Gene Expression Omnibus (GEO) (<http://www.ncbi.nlm.nih.gov/geo/>) [21] are powerful tools used to screen the differentially expressed genes (DEGs) generated from NGS data corresponding to the progression of GDM [22]. Therefore, there are still many related genes to be identified, which will help us better understand the molecular pathogenesis of GDM and facilitate the discovery of new diagnostic biomarkers or therapeutic target.

In the current investigation, we tested integrated bioinformatics analysis for the identification of DEGs as potential biomarkers of GDM based on the expression profiling by high throughput sequencing from the GEO database. These analysis might provide possible perspectives for the progression and development of GDM as well as identification potential candidate genes for GDM diagnose or treatment.

Materials and methods

Data resources

The NGS data used in this investigation were acquired from GEO database, which is a public repository containing the expression profiling by high throughput sequencing data submitted by research institutions around the world. We chose the expression profiling by high throughput sequencing data GSE154377 [23] from the GEO database. The NGS data of GSE154377 was consisted with 28 normal pregnancy samples and 33 GDM samples based on the platform of GPL20301 Illumina HiSeq 4000 (Homo sapiens).

Identification of DEGs

DESeq2 [24] packages of R Bioconductor (<http://www.bioconductor.org/>) was applied to significance analysis of DEGs between normal pregnancy samples and GDM samples. The log-fold change (FC) in expression and adjusted P-values (adj. P) were resolved. The criterion of statistical significance was adj. P value <0.05, $|\text{Log}_2(\text{FC})| > 1.73$ for up regulated genes and $|\text{Log}_2(\text{FC})| > -0.69$ for down regulated genes. A heatmap of the DEGs was produced using gplots in R software. All significant DEGs were shown in a volcano plot generated using ggplot2 in R software.

Gene Ontology (GO) and REACTOME pathway enrichment analysis of DEGs

Gene Ontology (GO) (<http://www.geneontology.org>) [25] is a suitable technique to classify gene expression and its properties, including biological process (BP), cellular component (CC) and molecular function (MF), which provide extensive functional annotation tools for researchers to integrate key genes with a specific function. REACTOME (<https://reactome.org/>) [26] is an online pathway database that collects information on genomic, biochemical, and enzymatic pathways. The DEGs were mapped to the REACTOME pathway database and the significantly related pathways were screened. We could use g:Profiler (<http://biit.cs.ut.ee/gprofiler/>) [27] is an online functional annotation tool to visualize the DEGs enrichment of BP, MF, CC and pathways ($P \leq 0.05$).

Construction of the PPI network and module analysis

IID interactome (Integrated Interactions Database) (<http://iid.ophid.utoronto.ca/>) [28] was used to construct PPI network. The identified DEGs were input into IID interactome to unravel a potential PPI network. Afterwards, a PPI network was constructed and visualized by Cytoscape software (version 3.8.2, <http://www.cytoscape.org/>) [29]. Subsequently, the topological properties including node degree [30], betweenness centrality [31], stress centrality [32] and closeness centrality [33] of the DEGs in the PPI network were calculated by Network Analyzer plug-in of Cytoscape to further analyze the candidate hub genes from the PPI network. The PEWCC1 plug-in [34] was used to search sub-networks of the PPI network and the default parameters (Degree cutoff ≥ 10 , node score cutoff ≥ 0.4 , K-core ≥ 4 , and max depth=100.) were set in the functional interface of Cytoscape software.

MiRNA-hub gene regulatory network construction

The miRNA-hub gene interactions were predicted with miRNet database (<https://www.mirnet.ca/>) [35], which involves 14 predicted algorithms (TarBase, miRTarBase, miRecords, miRanda (S mansoni only), miR2Disease, HMDD, PhenomiR, SM2miR, PharmacomiR, EpimiR, starBase, TransmiR, ADmiRE, and TAM 2.0). The Cytoscape 3.8.2 software [29] was used to visualize the regulatory network.

TF-hub gene regulatory network construction

The TF-hub gene interactions were predicted with NetworkAnalyst database (<https://www.networkanalyst.ca/>) [36], which involves 1 predicted algorithm (ChEA). The Cytoscape 3.8.2 software [29] was used to visualize the regulatory network.

Receiver operating characteristic curve (ROC) analysis

pROC package in R statistical software [37] was used to operate ROC curve analysis and to resolve the specificity, sensitivity, positive and negative predictive values for all the feasible thresholds of the ROC curve. The value of the hub genes were predicted based on the ROC curve analysis.

Results

Identification of DEGs

DEGs were identified by DESeq2 in the R package. In total, 953 DEGs (478 up and 475 down regulated genes) were selected based on the criteria of adj. P value <0.05 , $|\text{Log}_2(\text{FC})| > 1.73$ for up regulated genes and $|\text{Log}_2(\text{FC})| > -0.69$ for down regulated genes. Heatmap of DEGs is presented in Fig. 1, and volcano plot is presented in Fig. 2. The up and down regulated DEGs is listed in Table 1.

Gene Ontology (GO) and REACTOME pathway enrichment analysis of DEGs

All 953 DEGs were analyzed by g:Profiler software and the results of GO enrichment analysis indicated that 1) for BP, up regulated genes were particularly enriched in multicellular organismal process and developmental process, and down regulated genes in cell activation and immune system process; 2) for CC, up regulated genes were enriched in cell periphery and intrinsic component of membrane, and down regulated genes in endomembrane system and cytoplasm; 3) for GO MF, up regulated genes were significantly enriched in the transporter activity and channel activity, and down regulated genes in enzyme binding and protein binding (Table 2). REACTOME pathway enrichment analysis results were shown in Table 3 which demonstrated that up regulated genes were particularly enriched in formation of the cornified envelope and cell-cell junction organization, while down regulated genes were particularly enriched in hemostasis and neutrophil degranulation ($P < 0.05$).

Construction of the PPI network and module analysis

The PPI network of DEGs was constructed with 8472 nodes and 20624 edges (Fig.3). The node degree, betweenness centrality, stress centrality and closeness centrality methods were performed to calculate the top hub genes and are listed in Table 4. The results revealed 5 up and 5 down regulated genes identified as hub genes, including TRIM54, ELAVL2, PTN, KIT, BMPR1B, APP, SRC, ITGA4, RPA1 and ACTB. PEWCC1 was used to identify the significant modules in the PPI network and the two significant modules were selected. Module 1 consisted of 95 nodes and 103 edges (Fig.4A) and module 2 consisted of 79 nodes and 131 edges (Fig.4B). Following GO and pathway enrichment analysis, the module 1 was revealed to be associated with multicellular organismal process, developmental

process and intrinsic component of membrane, and module 2 was revealed to be associated with hemostasis, immune system, enzyme binding, cytokine signaling in immune system and protein binding.

MiRNA-hub gene regulatory network construction

To investigate interaction correlations between the hub genes and miRNAs, a miRNA-hub gene interaction network was constructed, which has 2598 nodes (hub genes:307; miRNAs: 2291) and 17035 edges. Results from the current investigation demonstrated that one target gene might be regulated by several miRNAs (Fig. 5) and are listed in Table 5. Up regulated hub genes including, ERFFI1 targeted by 70 miRNAs (ex; hsa-mir-198); CCNE1 targeted by 50 miRNAs (ex; hsa-mir-181b-5p); ELAVL2 targeted by 43 miRNAs (ex; hsa-mir-766-3p); ANTXR1 targeted by 36 miRNAs (ex; hsa-mir-624-5p); ZBTB8A targeted by 34 miRNAs (ex; hsa-mir-10b-5p). Similarly, down regulated hub genes including, SRRM2 targeted by 250 miRNAs (ex; hsa-mir-582-5p); CDKN1A targeted by 187 miRNAs (ex; hsa-mir-657); MYH9 targeted by 126 miRNAs (ex; hsa-mir-1231); APP targeted by 125 miRNAs (ex; hsa-mir-509-3-5p); ACTB targeted by 122 miRNAs (ex; hsa-mir-192-3p).

TF-hub gene regulatory network construction

To investigate interaction correlations between the hub genes and TFs, a TF-hub gene interaction network was constructed, which has 503 nodes (hub genes:309; miRNAs: 194) and 7686 edges. Results from the current investigation demonstrated that one target gene might be regulated by several TFs, (Fig. 6) and are listed in Table 5. Up regulated hub genes including, ERFFI1 targeted by 43 TFs (ex; CREM); ELAVL2 targeted by 41 TFs (ex; BMI1); KIT targeted by 34 TFs (ex; DMRT1); ZBTB8A targeted by 29 TFs (ex; GATA4); PPARGC1A targeted by 27 TFs (ex; FOXA2). Similarly, down regulated hub genes including, SMAD3 targeted by 58 TFs (ex; EP300); CDKN1A targeted by 57 TFs (ex; STAT3); ACTB targeted by 56 TFs (ex; HOXC9); PKM targeted by 55 TFs (ex; FOXP1); MYH9 targeted by 53 TFs (ex; ATF3).

Receiver operating characteristic curve (ROC) analysis

Based on the data of GSE154377, the patients were divided into the normal pregnancy group and GDM group. The ROC curves were analyzed by pROC package in R statistical software to evaluate the diagnostic accuracy of hub genes for GDM. As shown in Fig. 7, TRIM54, ELAVL2, PTN, KIT, BMPR1B, APP, SRC, ITGA4, RPA1 and ACTB achieved an AUC value of >0.90, demonstrating that these genes have high sensitivity and specificity for GDM diagnosis. Therefore, the ten hub genes identified, TRIM54, ELAVL2, PTN, KIT, BMPR1B, APP, SRC, ITGA4, RPA1 and ACTB might be considered as new biomarkers for GDM and require further investigation to validate these preliminary findings.

Discussion

A number of pre-clinical and clinical investigations have been conducted to reveal the underlying mechanisms of GDM in the past decades; however, the incidence of GDM remains high. This is primarily due to the majority of the investigation focusing genetic risk factor [38]. In the current investigation, expression profiling by high throughput sequencing dataset was analyzed and 953 DEGs (478 up and 475 down regulated genes) were identified. Existing evidences have reported that HNF4G [39], SLC15A1 [40], CXCL5 [41] and MALAT1 [42] promotes obesity, but these genes might be novel target for GDM. NPHP3-AS1 [43], LTA (lymphotoxin alpha) [44], CXCL5 [45] and MALAT1 [46] are found to be expressed in cardiovascular diseases, but these genes might be novel targets for GDM. A recent study demonstrated that XIST (X inactive specific transcript) [47] and MALAT1 [48] serves a crucial role in GDM progression. LTA (lymphotoxin alpha) [49], CXCL5 [50] and MALAT1 [51] are associated with prognosis of diabetes mellitus, but these genes might be novel targets for GDM. LTA (lymphotoxin alpha) [52], CXCL5 [53], MALAT1 [54] and TMEM70 [55] have been demonstrated to function in hypertension, but these genes might be novel targets for GDM. CXCL5 has been shown to be activated abortion [56].

GO and REACTOME pathway enrichment analyses were used to investigate the interactions of DEGs. Pathways include hemostasis [57], neutrophil degranulation [58], immune system [59] and cytokine signaling in immune system [60] are responsible for progression of GDM. LGR5 [61], GREM1 [62], GLRA3 [63], NEUROD4 [64], CYP2J2 [65], KCNH6 [66], LBP (lipopolysaccharide binding protein) [67], CXCL14 [68], RGN (regucalcin) [69], NPY2R [70],

SERPINB13 [71], WNT5A [72], EDA (ectodysplasin A) [73], HSD11B2 [74], ACVR1C [75], NEUROD1 [76], SLIT2 [77], PPARGC1A [78], IGF1 [79], OSR1 [80], CYP46A1 [81], TLR3 [82], BMP7 [83], SELP (selectin P) [84], HLA-A [85], NOTCH2 [86], LRP1 [87], CLU (clusterin) [88], FCN1 [89], CDKN1A [90], **SMAD3** [91], HLA-E [92], PTPRC (protein tyrosine phosphatase receptor type C) [93], MYH9 [94], JAK3 [95], IL6R [96], TIMP1 [97], DOCK8 [98], TNFRSF1B [99], ITGAL (integrin subunit alpha L) [100], CD47 [101], RARA (retinoic acid receptor alpha) [102], DGKD (diacylglycerol kinase delta) [103], PLEK (pleckstrin) [104], PREX1 [105], BSCL2 [106], PANX1 [107], IRF7 [108], NOTCH1 [109], STIM1 [110], TRIM13 [111], LRBA (LPS responsive beige-like anchor protein) [112], CXCR4 [113], MDM4 [114], MYO9B [115] and PDE5A [116] were revealed to be expressed in diabetes mellitus, but these genes might be novel targets for GDM. SIX1 [117], GREM1 [118], GHRHR (growth hormone releasing hormone receptor) [119], GPR37L1 [120], CYP2J2 [121], AQP4 [122], ROS1 [123], LBP (lipopolysaccharide binding protein) [124], SGCD (sarcoglycan delta) [125], CXCL14 [126], RGN (regucalcin) [127], F9 [128], KCND2 [129], AZGP1 [130], HAS2 [131], CNTN4 [132], WNT5A [133], PTHLH [134], FAP (fibroblast activation protein alpha) [135], THSD7A [136], SHROOM3 [137], ETV1 [138], CYP24A1 [139], SLIT2 [140], GJC1 [141], PPARGC1A [142], TRPM3 [143], **IGF1** [144], TRPV6 [145], TLR3 [146], BMP7 [147], DSG2 [148], POSTN (periostin) [149], ENOX1 [150], KCNA7 [151], ITGB3 [152], THBS1 [153], TRPC6 [154], SELP (selectin P) [155], VCL (vinculin) [156], P2RY1 [157], NOTCH2 [158], F2RL3 [159], PSAP (prosaposin) [160], LRP1 [161], CLU (clusterin) [162], FCN1 [163], CDKN1A [164], SMAD3 [165], CAPN1 [166], BAK1 [167], FERMT3 [168], HLA-E [169], ADA2 [170], PTPRC (protein tyrosine phosphatase receptor type C) [171], PEAR1 [172], TGFB1 [173], JAK3 [174], ALOX12 [175], ITGB2 [176], SELPLG (selectin P ligand) [177], TNFSF4 [178], BCL11B [179], IL17RA [180], CST3 [181], BCL3 [182], TNFRSF1B [183], SERPINA1 [184], CD47 [185], CD74 [186], STXBP2 [187], LEF1 [188], F13A1 [189], BSCL2 [190], VCAN (versican) [191], SUN2 [192], PPM1L [193], IRF7 [194], NOTCH1 [195], EHD3 [196], PCSK6 [197], STIM1 [198], CXCR4 [199], ATP2A2 [200], CALM3 [201], CSF1R [202], CLPP (caseinolytic mitochondrial matrix peptidase proteolytic subunit) [203], PIK3IP1 [204], CDK9 [205], USP22 [206], MDM4 [207], TUBB1 [208], PDE5A [209] and GNB5 [210] plays important roles in cardiovascular diseases progression, but these genes might

be novel targets for GDM. Polonikov et al [211], Chida et al [212], Yamada et al [213], Zhang et al [214], Kawarazaki et al [215], Ueda et al [216], Bao et al [217], Leng et al [218], **Taghvaei et al [219]**, Norling et al [220], Brown et al [221], Singh et al [222], Liu et al [223], Nie et al [224], Liu et al [225], Sharma et al [226], Liu et al [227], Jain et al [228], Novoyatleva et al [229], Yu et al [230], Sahoo et al [231], Gamboa et al [232], Zeng et al [233], Zabini et al [234], Olivi et al [235], Liu et al [236], Nabrdalik et al [237], Katayose et al [238], Topchieva et al [239], Onal et al [240], Speirs et al [241], Novelli et al [242], Le Hiress et al [243], Chang et al [244], Deng et al [245], Wang et al [246], Dhande et al [247], Yu et al [248] and Li et al [249] showed that CYP2J2, BMPR1B, ROS1, SCN7A, WNT5A, HSD11B2, CYP24A1, WNK3, **PPARGC1A**, IGF1, OSR1, TLR3, BMP7, POSTN (periostin), ITGB3, THBS1, FLNA (filamin A), TRPC6, SELP (selectin P), VCL (vinculin), NOTCH2, F2RL3, LRP1, CLU (clusterin), SMAD3, PEAR1, MYH9, TGFB1, PDGFA (platelet derived growth factor subunit A), IL6R, TIMP1, TNFRSF1B, CD47, CD74, VCAN (versican), IRF7, NOTCH1, STIM1, CXCR4 and PDE5A expression can be associated with hypertension progression, but these genes might be novel targets for GDM. ROS1 [250], WNT2 [251], PHLDA2 [252], WNT5A [253], HSD11B2 [254], CLDN1 [255], CYP24A1 [256], HRG (histidine rich glycoprotein) [257], TLR3 [258], THBS1 [259], TRPC6 [260], SELP (selectin P) [261], CLU (clusterin) [262], CDKN1A [263], ITGB1 [264], HLA-E [265], IL6R [266], TIMP1 [267], SERPINA1 [268], CD74 [269], PANX1 [270], STIM1 [271] and CXCR4 [272] were revealed to be correlated with disease outcome in patients with preeclampsia. Previously reported studies have shown that the expression of LBP (lipopolysaccharide binding protein) [273], MC1R [274], CXCL14 [275], RGN (regucalcin) [276], NPY2R [277], MFAP5 [278], WNT5A [279], EDA (ectodysplasin A) [280], THSD7A [281], NEUROD1 [282], SLIT2 [283], **PPARGC1A** [219], **IGF1** [144], OSR1 [284], TLR3 [285], BMP7 [286], POSTN (periostin) [287], LRP1B [288], THBS1 [289], NOTCH2 [290], LRP1 [291], CLU (clusterin) [292], **SMAD3** [91], TGFB1 [293], APP (amyloid beta precursor protein) [294], ITGB2 [295], IL6R [296], TIMP1 [297], CD47 [298], CD74 [299], RARA (retinoic acid receptor alpha) [300], DOCK2 [301], F13A1 [302], IRF7 [303], STIM1 [304], CXCR4 [305], MGLL (monoglyceride lipase) [306], M6PR [307], USP22 [308] and CASP2 [309] were mainly involved in progression of obesity, but these genes might be novel targets for GDM. Recent studies have shown that GLP1R [310], NEUROD1 [311], PPARGC1A [312],

IGF1 [313], LRP1B [314], NOTCH2 [315], BAK1 [316], TLR2 [317], IL6R [318], TIMP1 [319], PIK3CD [320], PRKCA (protein kinase C alpha) [321], CXCR4 [322], RAB8A [323] and M6PR [324] are associated with GDM. Abnormal expression PDE5A was linked with abortion [325].

Hub genes in the PPI network and modules are linked to the progression of GDM. TRIM54, ELAVL2, PTN (pleiotrophin), KIT (KIT proto-oncogene, receptor tyrosine kinase), SRC (SRC proto-oncogene, non-receptor tyrosine kinase), ITGA4, RPA1, ACTB (actin beta) and IGSF1 were might be the novel biomarkers for GDM.

At the same time, hub genes, miRNAs and TFs implicated with GDM, all of which were located in the core nodes in MiRNA-hub gene regulatory network and TF-hub gene regulatory network, meaning that these hub genes, miRNAs and TFs could be critical therapeutic targets to protect against GDM. hsa-mir-766-3p [326], hsa-mir-10b-5p [327], hsa-mir-657 [328], GATA4 [329], FOXA2 [330], STAT3 [331] and ATF3 [332] plays an important role in the progression of diabetes mellitus, but these miRNAs might be novel targets for GDM. hsa-mir-582-5p is closely related to obesity [333], but these miRNAs might be novel targets for GDM. Wang et al. [334] found that the altered expression of hsa-mir-657 in GDM. Improta Caria et al [335], Li et al. [336], Park et al. [337], Cheng et al. [338] and Davis, [339] demonstrated that hsa-mir-657, BMI1, GATA4, STAT3 and ATF3 played a pivotal role in the hypertension, but these miRNAs might be novel targets for GDM. Improta Caria et al [335], Patankar et al. [340], Bochkis et al. [341], Nishimura et al. [342], Su et al. [343] and Kim et al. [344] suggested that hsa-mir-657, GATA4, FOXA2, EP300, STAT3 and ATF3 could induce obesity, but these genes might be novel targets for GDM. Accumulating evidence has demonstrated that hsa-mir-657 [345], hsa-mir-1231 [346], CREM (cAMP responsive element modulator) [347], BMI1 [348], GATA4 [349], EP300 [350], STAT3 [351], FOXP1 [352] and ATF3 [353] appears to be constitutively activated in cardiovascular diseases, but these genes might be novel targets for GDM. Abnormal expression of FOXP1 was responsible for loss of pregnancy [354]. ERFFI1, CCNE1, ANTXR1, ZBTB8A, SRRM2, PKM (pyruvate kinase M1/2), hsa-mir-198, hsa-mir-181b-5p, hsa-mir-624-5p, hsa-mir-509-3-5p, hsa-mir-192-3p, DMRT1, HOXC9, were might be the novel biomarkers for GDM.

Conclusions

The findings from this bioinformatics analysis investigations identified signaling pathways and the essential hub genes that might contribute to GDM. These findings improve our understanding of the molecular pathogenesis of GDM. Our investigation has key clinical importance for the early diagnosis and treatment, as well as the prevention, of GDM and provides effective targets for the treatment of GDM. However, further validation experiments are required to confirm the function of the identified hub genes linked with GDM.

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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. [(GSE154377) <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE154377>]

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

Author Contributions

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

C. V. - Software and investigation

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Tables

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

GeneSymbol	logFC	pValue	adj.P.Val	tvalue	Up/Down	GeneName
OPN1LW	5.513445	1.08E-13	1.33E-09	7.430209	Up	opsin 1, long wave sensitive
NDP	4.18255	8.43E-05	0.006062	3.93188	Up	norrin cystine knot growth factor NDP
CXorf66	4.046972	0.000314	0.013896	3.603447	Up	chromosome X open reading frame 66
TMPRSS11B	3.991258	0.000207	0.011081	3.709816	Up	transmembrane serine protease 11B
LINC02008	3.938406	2.43E-05	0.003077	4.22139	Up	long intergenic non-protein coding RNA 2008
LINC01697	3.891591	0.000675	0.022111	3.399696	Up	long intergenic non-protein coding RNA 1697
HNF4G	3.886017	3.11E-05	0.003434	4.165549	Up	hepatocyte nuclear factor 4 gamma
HTN3	3.855467	0.000722	0.022988	3.381116	Up	histatin 3
MTND5P28	3.791132	0.000284	0.01323	3.629045	Up	MT-ND5 pseudogene 28
LINC02658	3.749396	0.000275	0.012942	3.638237	Up	long intergenic non-protein coding RNA 2658
SLC15A1	3.747731	9.18E-06	0.001667	4.43569	Up	solute carrier family 15 member 1
ADAM18	3.744252	0.000249	0.012032	3.663474	Up	ADAM metallopeptidase domain 18
LGALS17A	3.665543	0.000865	0.024898	3.331024	Up	galectin 14 pseudogene
MTND6P20	3.650359	0.000196	0.010678	3.724129	Up	MT-ND6 pseudogene 20
NPHP3-AS1	3.614647	0.000181	0.010146	3.743861	Up	NPHP3 antisense RNA 1
SERPINA10	3.598318	0.001245	0.030213	3.228435	Up	serpin family A member 10
C12orf54	3.590508	0.00037	0.015208	3.560355	Up	chromosome 12 open reading frame 54
SPATA22	3.536618	1.95E-06	0.00063	4.758353	Up	spermatogenesis associated 22
LGR5	3.535902	0.000243	0.011968	3.669005	Up	leucine rich repeat containing G protein-coupled receptor 5
RNU6-83P	3.532468	0.001496	0.03347	3.1754	Up	RNA, U6 small nuclear 83, pseudogene
OCA2	3.531677	0.000113	0.00729	3.860849	Up	OCA2 melanosomal transmembrane protein
CHEK2P2	3.523224	0.001579	0.034406	3.159792	Up	checkpoint kinase 2 pseudogene 2
PHYHIPL	3.510438	1.05E-06	0.00041	4.881476	Up	phytanoyl-CoA 2-hydroxylase interacting protein like
MTND5P17	3.509858	0.001127	0.028774	3.256804	Up	MT-ND5 pseudogene 17
MTND1P6	3.503479	0.002651	0.045307	3.005581	Up	MT-ND1 pseudogene 6
PLSCR2	3.501271	0.00175	0.036613	3.129626	Up	phospholipid scramblase 2
OR1H1P	3.500832	0.001555	0.034141	3.164149	Up	olfactory receptor family 1 subfamily H member 1 pseudogene
MIMT1	3.496863	0.001008	0.02697	3.288372	Up	MER1 repeat containing imprinted transcript 1
C3orf22	3.485741	0.000676	0.022122	3.39919	Up	chromosome 3 open reading frame 22
CDH3	3.480793	4.35E-05	0.00417	4.087837	Up	cadherin 3
LOC101927359	3.476698	0.000107	0.007035	3.874707	Up	uncharacterized LOC101927359
MTND5P23	3.472296	0.001424	0.032562	3.189774	Up	MT-ND5 pseudogene 23
LINC00906	3.468795	0.000953	0.026372	3.304029	Up	long intergenic non-protein coding RNA 906
LIPJ	3.468169	0.000369	0.015169	3.561489	Up	lipase family member J
NLRP8	3.44517	0.000862	0.02485	3.332101	Up	NLR family pyrin domain containing 8
CBX3P8	3.445133	0.000223	0.011379	3.690871	Up	chromobox 3 pseudogene 8
PAEP	3.437944	0.002141	0.0409	3.069962	Up	progesterone associated endometrial protein
RNY4P7	3.430056	0.000337	0.014383	3.585244	Up	RNY4 pseudogene 7

KCNH7-AS1	3.427803	0.001973	0.03916	3.094316	Up	KCNH7 antisense RNA 1
SIX1	3.427656	2.21E-05	0.002943	4.243042	Up	SIX homeobox 1
CUBNP3	3.421282	0.00223	0.041454	3.057715	Up	cubilin pseudogene 3
CYP27C1	3.414289	3.25E-05	0.003516	4.155216	Up	cytochrome P450 family 27 subfamily C member 1
SLC34A2	3.403709	1.04E-05	0.001765	4.407902	Up	solute carrier family 34 member 2
DSG4	3.40126	0.000746	0.023321	3.372169	Up	desmoglein 4
ASPA	3.395598	4.34E-06	0.001071	4.594369	Up	aspartoacylase
SPATA16	3.379004	0.00073	0.023055	3.378147	Up	spermatogenesis associated 16
CPN2	3.377474	0.000702	0.022707	3.388776	Up	carboxypeptidase N subunit 2
SFTA3	3.361222	0.00085	0.024662	3.336103	Up	surfactant associated 3
C8orf86	3.347714	0.000214	0.011264	3.702057	Up	chromosome 8 open reading frame 86
GREM1	3.342215	0.000634	0.02135	3.416659	Up	gremlin 1, DAN family BMP antagonist
MAGEA10	3.339161	0.000308	0.013776	3.608067	Up	MAGE family member A10
LRCOL1	3.336085	0.001761	0.036748	3.127794	Up	leucine rich colipase like 1
DDX18P2	3.334146	0.000979	0.026694	3.296526	Up	DEAD-box helicase 18 pseudogene 2
LOC100129935	3.323216	0.002591	0.044767	3.012492	Up	galectin 14 pseudogene
LRRN4CL	3.322787	0.000364	0.015029	3.565236	Up	LRRN4 C-terminal like
RAD51AP2	3.321826	0.002858	0.047155	2.982626	Up	RAD51 associated protein 2
ANKRD62	3.311208	0.000281	0.013123	3.63219	Up	ankyrin repeat domain 62
TXNDC8	3.305393	0.001998	0.039496	3.090579	Up	thioredoxin domain containing 8
KLHL31	3.298714	0.000873	0.025053	3.328638	Up	kelch like family member 31
GLRA3	3.290448	2.67E-06	0.000788	4.694779	Up	glycine receptor alpha 3
PCDHGB6	3.281157	0.000288	0.013293	3.626107	Up	protocadherin gamma subfamily B, 6
MTND5P30	3.279389	0.001001	0.026856	3.290179	Up	MT-ND5 pseudogene 30
MTCO1P22	3.276334	0.000294	0.013396	3.620554	Up	MT-CO1 pseudogene 22
NEUROD4	3.271933	0.000648	0.021519	3.410775	Up	neuronal differentiation 4
RGS5-AS1	3.271195	0.000323	0.014101	3.595763	Up	RGS5 antisense RNA 1
CRISP2	3.262188	0.000128	0.007983	3.829692	Up	cysteine rich secretory protein 2
FAM205C	3.261825	0.001293	0.030853	3.217507	Up	family with sequence similarity 205 member C
GAS1RR	3.261656	0.002178	0.041176	3.06484	Up	GAS1 adjacent regulatory RNA
PLCE1-AS2	3.257854	0.003008	0.048538	2.966893	Up	PLCE1 antisense RNA 2
CCDC160	3.25178	0.002345	0.042557	3.042632	Up	coiled-coil domain containing 160
FAM83B	3.229445	0.002217	0.041334	3.059495	Up	family with sequence similarity 83 member B
ART3	3.227592	0.002995	0.048449	2.968252	Up	ADP-ribosyltransferase 3 (inactive)
SNAP25-AS1	3.223636	0.000944	0.026225	3.306718	Up	SNAP25 antisense RNA 1
LINC02179	3.219018	0.000283	0.013182	3.630541	Up	long intergenic non-protein coding RNA 2179
FAM204CP	3.217918	0.003044	0.048837	2.963272	Up	family with sequence similarity 204 member C, pseudogene
MEI4	3.213357	0.00135	0.031558	3.205177	Up	meiotic double-stranded break formation protein 4
PCDHB7	3.206851	0.001516	0.033695	3.171611	Up	protocadherin beta 7
DMBT1L1	3.201517	0.0005	0.018378	3.480759	Up	deleted in malignant brain tumors 1 like 1 (pseudogene)
MINAR2	3.189907	0.001776	0.036962	3.125332	Up	membrane integral NOTCH2 associated receptor 2
ESRP1	3.186004	4.94E-06	0.001186	4.567488	Up	epithelial splicing regulatory protein 1
KRT85	3.18558	0.000405	0.016149	3.536738	Up	keratin 85

LINC01250	3.166207	0.001232	0.030149	3.231272	Up	long intergenic non-protein coding RNA 1250
ADAM7	3.146252	0.002852	0.047116	2.983252	Up	ADAM metallopeptidase domain 7
EPHA3	3.130622	2.55E-05	0.003077	4.210507	Up	EPH receptor A3
SLC7A9	3.127796	0.000362	0.015	3.566187	Up	solute carrier family 7 member 9
PTN	3.121738	6.88E-06	0.001442	4.497309	Up	pleiotrophin
CEACAM7	3.117185	8.15E-05	0.005999	3.940007	Up	CEA cell adhesion molecule 7
VPS33B-DT	3.11502	0.002578	0.044697	3.014001	Up	VPS33B divergent transcript
PLEKHN1	3.112252	2.20E-06	0.000683	4.733941	Up	pleckstrin homology domain containing N1
LOC112268408	3.110789	0.002661	0.045337	3.004395	Up	uncharacterized LOC112268408
CNGA1	3.108671	0.00031	0.013808	3.606984	Up	cyclic nucleotide gated channel subunit alpha 1
LOC100507144	3.104564	0.001868	0.038043	3.110403	Up	uncharacterized LOC100507144
RN7SL583P	3.091743	0.0012	0.029799	3.238954	Up	RNA, 7SL, cytoplasmic 583, pseudogene
CHRNA3	3.089636	0.002172	0.041151	3.065643	Up	cholinergic receptor nicotinic beta 3 subunit
FAM133GP	3.083474	0.000613	0.020879	3.425718	Up	family with sequence similarity 133 member A pseudogene
PWWP3B	3.082875	0.000248	0.012032	3.66385	Up	PWWP domain containing 3B
GHRHR	3.074944	0.000163	0.009601	3.770518	Up	growth hormone releasing hormone receptor
LRRC15	3.067099	0.000274	0.012942	3.638447	Up	leucine rich repeat containing 15
SHCBP1L	3.06246	0.000386	0.015653	3.549279	Up	SHC binding and spindle associated 1 like
MYH4	3.059639	0.000297	0.013428	3.618145	Up	myosin heavy chain 4
CTAGE16P	3.052947	0.001273	0.030627	3.221993	Up	CTAGE family member 16, pseudogene
LOC105369203	3.047191	4.35E-05	0.00417	4.087835	Up	uncharacterized LOC105369203
OLA1P2	3.046707	0.003035	0.048798	2.964123	Up	OLA1 pseudogene 2
LOC100129484	3.043078	0.000217	0.011328	3.698704	Up	uncharacterized LOC100129484
MTND6P12	3.042631	0.001213	0.029833	3.235749	Up	MT-ND6 pseudogene 12
CYP4Z2P	3.034917	0.001347	0.031558	3.205761	Up	cytochrome P450 family 4 subfamily Z member 2, pseudogene
MEIOC	3.030053	0.001193	0.029701	3.240469	Up	meiosis specific with coiled-coil domain
LOC100505588	3.029497	0.002764	0.046281	2.992826	Up	uncharacterized LOC100505588
MAMDC2	3.024368	0.000516	0.018631	3.472303	Up	MAM domain containing 2
ANKRD66	3.02431	0.001198	0.029776	3.23946	Up	ankyrin repeat domain 66
GPR37L1	3.023285	3.47E-05	0.003684	4.140122	Up	G protein-coupled receptor 37 like 1
CYP26A1	3.013734	0.001551	0.034101	3.164983	Up	cytochrome P450 family 26 subfamily A member 1
SCGB2B2	3.008861	8.28E-05	0.006042	3.93614	Up	secretoglobin family 2B member 2
DCAF8L1	3.008786	0.001977	0.039219	3.093623	Up	DDB1 and CUL4 associated factor 8 like 1
CYP2J2	3.00746	0.002792	0.04641	2.989729	Up	cytochrome P450 family 2 subfamily J member 2
WDR72	2.985403	9.18E-05	0.006385	3.911253	Up	WD repeat domain 72
CPEB1	2.981477	5.53E-05	0.004728	4.031834	Up	cytoplasmic polyadenylation element binding protein 1
BNC1	2.981248	0.001138	0.028918	3.253915	Up	basonuclin 1
CCDC110	2.980104	0.000199	0.010794	3.720262	Up	coiled-coil domain containing 110
GLYCAM1	2.969315	0.002187	0.041176	3.063582	Up	glycosylation dependent cell adhesion molecule 1 (pseudogene)
CCL22	2.961513	0.001749	0.036613	3.12984	Up	C-C motif chemokine ligand 22
AQP4	2.960121	4.83E-05	0.004447	4.063507	Up	aquaporin 4
FPGT-TNNI3K	2.96006	0.001576	0.034401	3.160295	Up	FPGT-TNNI3K readthrough
LOC101927884	2.947566	0.000946	0.026225	3.306124	Up	uncharacterized LOC101927884

BMPR1B	2.945795	6.42E-06	0.001381	4.511961	Up	bone morphogenetic protein receptor type 1B
SYNPR	2.938076	0.000228	0.011442	3.68553	Up	synaptoporin
IMPG1	2.936346	0.000848	0.024648	3.336789	Up	interphotoreceptor matrix proteoglycan 1
ANKRD30A	2.934217	0.000437	0.016891	3.516366	Up	ankyrin repeat domain 30A
MYH8	2.931689	0.000685	0.022264	3.395619	Up	myosin heavy chain 8
TMEM105	2.924668	7.39E-05	0.005594	3.963279	Up	TMEM105 long non-coding RNA
KRT14	2.918362	2.29E-06	0.000692	4.725558	Up	keratin 14
CLDN2	2.91664	0.001516	0.033695	3.17164	Up	claudin 2
LHFPL3-AS1	2.916058	0.000512	0.018616	3.47434	Up	LHFPL3 antisense RNA 1
SLITRK6	2.902106	0.003056	0.048926	2.96206	Up	SLIT and NTRK like family member 6
DISC1FP1	2.894594	0.000114	0.007337	3.858004	Up	DISC1 fusion partner 1
VGLL2	2.894124	0.00256	0.044663	3.016207	Up	vestigial like family member 2
RBM46	2.891768	0.001812	0.037437	3.119353	Up	RNA binding motif protein 46
MTND5P12	2.890344	8.48E-05	0.006062	3.930429	Up	MT-ND5 pseudogene 12
TCEAL6	2.889542	0.001046	0.027588	3.277866	Up	transcription elongation factor A like 6
ROS1	2.886309	0.000318	0.013947	3.600172	Up	ROS proto-oncogene 1, receptor tyrosine kinase
C10orf53	2.884227	0.000504	0.018497	3.478593	Up	chromosome 10 open reading frame 53
TECRL	2.882738	0.001604	0.034896	3.15515	Up	trans-2,3-enoyl-CoA reductase like
EYA4	2.879404	5.97E-05	0.00493	4.013875	Up	EYA transcriptional coactivator and phosphatase 4
LOC730100	2.875785	0.00114	0.028943	3.253377	Up	uncharacterized LOC730100
C16orf89	2.874808	0.002768	0.04629	2.992389	Up	chromosome 16 open reading frame 89
KCNH6	2.872739	0.001298	0.03092	3.21647	Up	potassium voltage-gated channel subfamily H member 6
SCN7A	2.867538	7.78E-05	0.005762	3.951077	Up	sodium voltage-gated channel alpha subunit 7
ISM2	2.864433	0.002963	0.048105	2.971562	Up	isthmin 2
GABRG1	2.86395	0.002861	0.047155	2.98233	Up	gamma-aminobutyric acid type A receptor subunit gamma1
SFTPC	2.863718	3.70E-05	0.00378	4.125429	Up	surfactant protein C
CRNDE	2.863195	0.000185	0.010247	3.738435	Up	colorectal neoplasia differentially expressed
LOC100129175	2.851956	0.002807	0.046533	2.988095	Up	uncharacterized LOC100129175
RIMS2	2.850549	2.85E-05	0.003258	4.185403	Up	regulating synaptic membrane exocytosis 2
CRTC1P1	2.850441	0.001454	0.033004	3.183795	Up	CRTC1 pseudogene 1
SCTR-AS1	2.846397	0.002011	0.039698	3.088583	Up	SCTR antisense RNA 1
LOC339685	2.84522	0.000513	0.018616	3.473718	Up	uncharacterized LOC339685
SCEL	2.838558	0.000784	0.023824	3.358301	Up	sciellin
TCEAL4P1	2.838441	0.000176	0.010092	3.750922	Up	transcription elongation factor A like 4 pseudogene 1
MYO3A	2.838051	3.82E-05	0.00383	4.117973	Up	myosin IIIA
ADAM30	2.831585	0.000892	0.025475	3.322576	Up	ADAM metallopeptidase domain 30
CCDC168	2.825794	0.000316	0.013923	3.602088	Up	coiled-coil domain containing 168
MTRNR2L1	2.813509	7.11E-08	7.93E-05	5.388253	Up	MT-RNR2 like 1
GPR151	2.813138	0.002917	0.047645	2.976326	Up	G protein-coupled receptor 151
NLGN4X	2.809515	2.94E-05	0.003321	4.178078	Up	neuroligin 4 X-linked
ASB5	2.80702	0.000737	0.023226	3.375553	Up	ankyrin repeat and SOCS box containing 5
LBP	2.802633	0.000806	0.024108	3.350603	Up	lipopolysaccharide binding protein
DELEC1	2.801445	0.00057	0.019974	3.445735	Up	deleted in esophageal cancer 1

DMRTA1	2.797287	0.001398	0.032282	3.195043	Up	DMRT like family A1
FAM230B	2.790151	0.000788	0.023846	3.357094	Up	family with sequence similarity 230 member B
MYF6	2.786903	0.001221	0.02999	3.233968	Up	myogenic factor 6
RBPJL	2.781603	0.00021	0.011148	3.706579	Up	recombination signal binding protein for immunoglobulin kappa J region like
RP1	2.781247	0.002073	0.040204	3.07959	Up	RP1 axonemal microtubule associated
LINC01630	2.776756	0.001854	0.037842	3.112712	Up	long intergenic non-protein coding RNA 1630
CPA4	2.775558	0.000114	0.007333	3.858755	Up	carboxypeptidase A4
TMEM139	2.76087	0.001088	0.02805	3.266713	Up	transmembrane protein 139
SLC9A2	2.752986	0.002063	0.040159	3.081041	Up	solute carrier family 9 member A2
TEKT3	2.751933	0.000292	0.013372	3.622295	Up	tektin 3
FEZF1	2.749279	0.002606	0.044931	3.010738	Up	FEZ family zinc finger 1
SGCD	2.744477	2.77E-06	0.000789	4.687422	Up	sarcoglycan delta
LOC286177	2.743338	0.003151	0.049748	2.952574	Up	uncharacterized LOC286177
ST8SIA3	2.739592	4.47E-05	0.004229	4.081858	Up	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3
SLC5A12	2.739076	0.001016	0.027068	3.286118	Up	solute carrier family 5 member 12
BRINP1	2.737461	0.000178	0.01012	3.747803	Up	BMP/retinoic acid inducible neural specific 1
VXN	2.736153	0.000515	0.018631	3.473072	Up	vexin
TMEM31	2.73473	0.002168	0.041107	3.066193	Up	transmembrane protein 31
XG	2.721822	0.002188	0.041176	3.063497	Up	Xg glycoprotein (Xg blood group)
GPR158	2.718024	0.000271	0.012846	3.641144	Up	G protein-coupled receptor 158
ELAVL2	2.710713	5.96E-05	0.00493	4.014458	Up	ELAV like RNA binding protein 2
ARSJ	2.710116	0.000442	0.017056	3.513368	Up	arylsulfatase family member J
ZNF804B	2.70973	0.000289	0.013296	3.625262	Up	zinc finger protein 804B
CFAP300	2.708049	0.001491	0.033412	3.176431	Up	cilia and flagella associated protein 300
GRHL2	2.706357	5.62E-05	0.004783	4.028283	Up	grainyhead like transcription factor 2
LOC400036	2.704866	0.003135	0.049553	2.954182	Up	DEAD-box helicase 23 pseudogene
SLC26A5	2.703945	0.002496	0.043986	3.023788	Up	solute carrier family 26 member 5
EVC	2.703266	6.49E-06	0.001384	4.509672	Up	EvC ciliary complex subunit 1
LINC00472	2.697899	0.000463	0.017514	3.501345	Up	long intergenic non-protein coding RNA 472
POU3F3	2.697838	0.000358	0.014969	3.569401	Up	POU class 3 homeobox 3
WNT2	2.6951	0.000747	0.023336	3.371581	Up	Wnt family member 2
LVRN	2.694329	0.000162	0.009595	3.771991	Up	laeverin
KIR3DL1	2.69343	0.00156	0.034148	3.163278	Up	killer cell immunoglobulin like receptor, three Ig domains and long cytoplasmic tail 1
CBLN1	2.691716	0.001876	0.038108	3.109161	Up	cerebellin 1 precursor
SLC36A3	2.691472	0.001037	0.027438	3.280157	Up	solute carrier family 36 member 3
LOC349160	2.680699	0.001812	0.037437	3.119408	Up	uncharacterized LOC349160
DECR2	2.680621	1.44E-06	0.000513	4.818799	Up	2,4-dienoyl-CoA reductase 2
SLC5A8	2.675127	0.001786	0.037143	3.123644	Up	solute carrier family 5 member 8
CLDN12	2.669284	7.39E-05	0.005594	3.963259	Up	claudin 12
STMND1	2.663163	0.000418	0.016457	3.528753	Up	stathmin domain containing 1
KCTD16	2.658392	0.000276	0.012969	3.636715	Up	potassium channel tetramerization domain containing 16
LRFN5	2.657917	0.000897	0.025499	3.321125	Up	leucine rich repeat and fibronectin type III domain containing 5

GLP1R	2.644488	0.000458	0.017448	3.504402	Up	glucagon like peptide 1 receptor
SCN11A	2.644333	0.000149	0.009026	3.792542	Up	sodium voltage-gated channel alpha subunit 11
C3orf56	2.644144	0.002196	0.041176	3.062382	Up	chromosome 3 open reading frame 56
GABRP	2.643919	0.000489	0.018121	3.486538	Up	gamma-aminobutyric acid type A receptor subunit pi
SLC16A12	2.642939	0.001471	0.033231	3.180407	Up	solute carrier family 16 member 12
AADAT	2.637926	0.000145	0.008863	3.798904	Up	aminoadipate aminotransferase
LOC101927666	2.634652	0.000814	0.024176	3.348034	Up	uncharacterized LOC101927666
RDH16	2.626915	0.002563	0.044683	3.015854	Up	retinol dehydrogenase 16
DRP2	2.621728	0.000515	0.018631	3.472582	Up	dystrophin related protein 2
PAPOLB	2.617781	0.002102	0.040484	3.075407	Up	poly(A) polymerase beta
GCM2	2.613247	0.003104	0.049344	2.95727	Up	glial cells missing transcription factor 2
MC1R	2.6116	4.51E-05	0.004256	4.079484	Up	melanocortin 1 receptor
DEPDC1-AS1	2.606883	0.00166	0.035644	3.145241	Up	DEPDC1 antisense RNA 1
SERPINA6	2.599409	0.0029	0.04749	2.978163	Up	serpin family A member 6
SLC1A1	2.59426	0.000757	0.023471	3.367951	Up	solute carrier family 1 member 1
CFAP299	2.593946	0.000632	0.021347	3.417428	Up	cilia and flagella associated protein 299
CXCL14	2.592708	0.001715	0.036256	3.135663	Up	C-X-C motif chemokine ligand 14
DSCAM-AS1	2.59025	0.00272	0.04583	2.997734	Up	DSCAM antisense RNA 1
FLG	2.589226	0.000461	0.017474	3.502371	Up	filaggrin
RGN	2.584689	0.003102	0.049344	2.957427	Up	regucalcin
RPL6P20	2.584134	0.002676	0.045415	3.002708	Up	ribosomal protein L6 pseudogene 20
LOC102724776	2.583449	0.003044	0.048837	2.963305	Up	uncharacterized LOC102724776
TRIM54	2.582009	0.001312	0.031156	3.21345	Up	tripartite motif containing 54
LOC101928228	2.579563	0.000177	0.010106	3.749409	Up	uncharacterized LOC101928228
RPL26P36	2.577256	0.001725	0.036334	3.133878	Up	ribosomal protein L26 pseudogene 36
SMC1B	2.577237	0.000326	0.014131	3.594015	Up	structural maintenance of chromosomes 1B
PPP1R14C	2.577061	0.000737	0.023226	3.375252	Up	protein phosphatase 1 regulatory inhibitor subunit 14C
SHC4	2.572754	0.001721	0.036306	3.134546	Up	SHC adaptor protein 4
CCDC178	2.568823	5.42E-05	0.004666	4.036535	Up	coiled-coil domain containing 178
MUC15	2.562581	0.000789	0.023846	3.356556	Up	mucin 15, cell surface associated
ID4	2.562465	0.001592	0.034669	3.157309	Up	inhibitor of DNA binding 4, HLH protein
NPY2R	2.553344	0.000931	0.026107	3.310675	Up	neuropeptide Y receptor Y2
HPSE2	2.550548	0.002599	0.044877	3.011531	Up	heparanase 2 (inactive)
SERPINB13	2.547395	0.001059	0.02763	3.27426	Up	serpin family B member 13
USP43	2.543343	7.56E-05	0.005671	3.957821	Up	ubiquitin specific peptidase 43
TRPM1	2.541316	0.000644	0.021466	3.41219	Up	transient receptor potential cation channel subfamily M member 1
NEUROG1	2.540745	0.000433	0.016841	3.519271	Up	neurogenin 1
F9	2.539726	0.0022	0.041176	3.061785	Up	coagulation factor IX
CREB3L3	2.534091	9.26E-05	0.006392	3.909331	Up	cAMP responsive element binding protein 3 like 3
LSP1P5	2.522544	0.001436	0.032769	3.187406	Up	LSP1 pseudogene 5
ROBO2	2.51639	1.66E-05	0.002335	4.306683	Up	roundabout guidance receptor 2
GPC6	2.515006	4.94E-05	0.004447	4.058525	Up	glypican 6
RNY3P1	2.512029	1.54E-05	0.002229	4.323431	Up	RNY3 pseudogene 1

RPP38-DT	2.503674	0.002047	0.040019	3.083326	Up	RPP38 divergent transcript
GFPT2	2.501221	0.000638	0.02144	3.414845	Up	glutamine-fructose-6-phosphate transaminase 2
WNT9A	2.500183	0.001349	0.031558	3.205328	Up	Wnt family member 9A
SSX5	2.500099	0.002573	0.044697	3.014608	Up	SSX family member 5
GREM2	2.498023	0.000434	0.016844	3.518786	Up	gremlin 2, DAN family BMP antagonist
KCND2	2.497277	0.001915	0.038394	3.103168	Up	potassium voltage-gated channel subfamily D member 2
PCSK1	2.496232	6.15E-05	0.005023	4.007076	Up	proprotein convertase subtilisin/kexin type 1
PHLDA2	2.495562	0.001617	0.035075	3.152878	Up	pleckstrin homology like domain family A member 2
DDX10P2	2.483572	0.002193	0.041176	3.062754	Up	DEAD-box helicase 10 pseudogene 2
DACH2	2.482729	0.000329	0.0142	3.59169	Up	dachshund family transcription factor 2
PLA2G2D	2.47526	0.001893	0.038276	3.106553	Up	phospholipase A2 group IID
CFAP20DC	2.470592	0.000285	0.01323	3.628628	Up	CFAP20 domain containing
MFAP5	2.469399	5.16E-05	0.004523	4.048033	Up	microfibril associated protein 5
RGPD4-AS1	2.465122	0.000244	0.011968	3.668434	Up	RGPD4 antisense RNA 1 (head to head)
GABRB1	2.462301	0.002572	0.044697	3.014703	Up	gamma-aminobutyric acid type A receptor subunit beta1
AZGP1	2.458429	0.000824	0.024177	3.344458	Up	alpha-2-glycoprotein 1, zinc-binding
SLC4A10	2.451773	2.71E-06	0.000789	4.691319	Up	solute carrier family 4 member 10
PTPN3	2.450598	8.20E-06	0.001552	4.459976	Up	protein tyrosine phosphatase non-receptor type 3
C11orf16	2.450469	0.002817	0.04667	2.986985	Up	chromosome 11 open reading frame 16
HAS2	2.440967	0.002848	0.047074	2.983733	Up	hyaluronan synthase 2
CTNNA2	2.433397	0.001317	0.031237	3.212327	Up	catenin alpha 2
IGSF3	2.427352	0.000182	0.010146	3.742314	Up	immunoglobulin superfamily member 3
FNDC7	2.42648	0.001493	0.033435	3.17597	Up	fibronectin type III domain containing 7
IGSF1	2.425892	0.000118	0.007485	3.850557	Up	immunoglobulin superfamily member 1
IGSF21	2.422478	0.000355	0.014893	3.571627	Up	immunoglobulin superfamily member 21
SLC5A4	2.418933	0.001487	0.033379	3.177249	Up	solute carrier family 5 member 4
PCDHGA9	2.418474	0.000377	0.015361	3.555989	Up	protocadherin gamma subfamily A, 9
KRT24	2.417881	0.000634	0.02135	3.416641	Up	keratin 24
ANHX	2.417712	0.002621	0.045039	3.009057	Up	anomalous homeobox
KIT	2.417683	0.000457	0.017448	3.504662	Up	KIT proto-oncogene, receptor tyrosine kinase
SNX31	2.417526	0.001533	0.03383	3.168347	Up	sorting nexin 31
SLC35F1	2.415882	0.00229	0.042181	3.049788	Up	solute carrier family 35 member F1
IHO1	2.414311	0.000753	0.023366	3.369583	Up	interactor of HORMAD1 1
ZNF750	2.414149	0.00103	0.027301	3.282261	Up	zinc finger protein 750
FAM71D	2.413063	0.002052	0.040029	3.082613	Up	family with sequence similarity 71 member D
LONRF2	2.409924	8.08E-06	0.001552	4.463113	Up	LON peptidase N-terminal domain and ring finger 2
TNFAIP8L3	2.408773	1.42E-05	0.002103	4.340094	Up	TNF alpha induced protein 8 like 3
CNTN5	2.406147	0.000611	0.020846	3.426521	Up	contactin 5
PHKA1	2.403578	5.30E-05	0.00461	4.04181	Up	phosphorylase kinase regulatory subunit alpha 1
NCCRP1	2.402669	0.002145	0.0409	3.069429	Up	NCCRP1, F-box associated domain containing
RSP01	2.398304	2.79E-05	0.003258	4.189886	Up	R-spondin 1
GRIA4	2.398157	0.000935	0.02616	3.309471	Up	glutamate ionotropic receptor AMPA type subunit 4
B3GAT1-DT	2.397891	0.001055	0.027608	3.275302	Up	B3GAT1 diverget transcript

ZMAT4	2.396372	0.00171	0.036212	3.136383	Up	zinc finger matrin-type 4
CNTN4	2.387406	0.000392	0.015831	3.545439	Up	contactin 4
PCDH11X	2.382392	0.00082	0.024176	3.345944	Up	protocadherin 11 X-linked
PLAAT5	2.370067	0.001321	0.03128	3.211471	Up	phospholipase A and acyltransferase 5
ENOX1	2.367742	0.002547	0.044513	3.017732	Up	ecto-NOX disulfide-thiol exchanger 1
LINC02345	2.367066	0.000762	0.023479	3.366221	Up	long intergenic non-protein coding RNA 2345
SLC18A1	2.365888	0.000427	0.016699	3.522972	Up	solute carrier family 18 member A1
SVOP	2.365594	0.002361	0.042658	3.040602	Up	SV2 related protein
CFAP53	2.365378	0.002807	0.046533	2.988131	Up	cilia and flagella associated protein 53
CDC20B	2.364628	0.002055	0.040046	3.082184	Up	cell division cycle 20B
OBI1-AS1	2.363385	0.000182	0.010146	3.742795	Up	OBI1 antisense RNA 1
LINC01267	2.360519	0.002313	0.042352	3.046768	Up	long intergenic non-protein coding RNA 1267
NKAPL	2.359592	0.000324	0.014101	3.595455	Up	NFKB activating protein like
WNT5A	2.358613	7.70E-05	0.005717	3.95368	Up	Wnt family member 5A
ADGRF1	2.358543	0.002252	0.041643	3.054814	Up	adhesion G protein-coupled receptor F1
EDA	2.355859	0.000403	0.016126	3.538198	Up	ectodysplasin A
GNG12-AS1	2.355706	0.002666	0.045355	3.003847	Up	GNG12, DIRAS3 and WLS antisense RNA 1
KCNA1	2.350861	0.000248	0.012032	3.664071	Up	potassium voltage-gated channel subfamily A member 1
CCDC81	2.348095	0.000479	0.017835	3.491998	Up	coiled-coil domain containing 81
VWDE	2.345836	0.00121	0.029831	3.236534	Up	von Willebrand factor D and EGF domains
TRIM71	2.344576	0.000719	0.022988	3.382419	Up	tripartite motif containing 71
COLEC12	2.344077	0.000468	0.017631	3.498331	Up	collectin subfamily member 12
RASEF	2.339961	0.000762	0.023479	3.366175	Up	RAS and EF-hand domain containing
MTND6P16	2.337388	0.002778	0.046321	2.991281	Up	MT-ND6 pseudogene 16
LOC101928850	2.337377	0.001745	0.036561	3.13054	Up	uncharacterized LOC101928850
TDRD6	2.335919	0.000981	0.026733	3.29581	Up	tudor domain containing 6
LINC01121	2.335434	0.000179	0.01012	3.747306	Up	long intergenic non-protein coding RNA 1121
SCN1A	2.332824	0.002505	0.043986	3.022779	Up	sodium voltage-gated channel alpha subunit 1
MTND2P13	2.324998	0.000311	0.013819	3.606314	Up	MT-ND2 pseudogene 13
LOC100505715	2.316277	0.001178	0.029564	3.24411	Up	uncharacterized LOC100505715
MTRNR2L2	2.313195	6.44E-05	0.005153	3.996031	Up	MT-RNR2 like 2
MROH2B	2.309703	0.002021	0.039824	3.087165	Up	maestro heat like repeat family member 2B
ATP13A5	2.30919	0.002466	0.043601	3.027536	Up	ATPase 13A5
MTCYBP35	2.309142	0.001691	0.035914	3.13982	Up	MT-CYB pseudogene 35
ITIH3	2.303498	0.000401	0.016091	3.53941	Up	inter-alpha-trypsin inhibitor heavy chain 3
TBX18	2.298837	0.001521	0.033725	3.17056	Up	T-box transcription factor 18
RGPD8	2.298546	1.34E-05	0.002019	4.353131	Up	RANBP2 like and GRIP domain containing 8
MTRNR2L8	2.291085	8.26E-05	0.006042	3.936666	Up	MT-RNR2 like 8
HSD11B2	2.288685	0.001905	0.038276	3.104702	Up	hydroxysteroid 11-beta dehydrogenase 2
LOC100128164	2.285659	0.000173	0.009978	3.754942	Up	four and a half LIM domains 1 pseudogene
VWA5B1	2.285369	0.000224	0.011379	3.690841	Up	von Willebrand factor A domain containing 5B1
FRMPD1	2.277255	0.001898	0.038276	3.105754	Up	FERM and PDZ domain containing 1
NUDT10	2.27087	0.002654	0.045307	3.005226	Up	nudix hydrolase 10

SCN2A	2.266149	0.001513	0.033695	3.172115	Up	sodium voltage-gated channel alpha subunit 2
LRP1B	2.263645	0.000622	0.021084	3.421929	Up	LDL receptor related protein 1B
TUSC8	2.26322	0.000594	0.020535	3.4344	Up	tumor suppressor candidate 8
TMC7	2.259069	0.000565	0.019862	3.447645	Up	transmembrane channel like 7
DNAH8	2.257525	2.87E-05	0.003258	4.18394	Up	dynein axonemal heavy chain 8
TACC2	2.249898	9.64E-08	9.09E-05	5.333445	Up	transforming acidic coiled-coil containing protein 2
SRRM1P1	2.240683	0.000165	0.009637	3.767174	Up	serine/arginine repetitive matrix 1 pseudogene 1
KCNK1	2.237479	0.002714	0.045771	2.998453	Up	potassium two pore domain channel subfamily K member 1
RPL31P2	2.237463	0.002088	0.040327	3.077352	Up	ribosomal protein L31 pseudogene 2
SHISAL2B	2.232438	0.000662	0.021852	3.404741	Up	shisa like 2B
ADGRV1	2.22211	0.000267	0.01268	3.645087	Up	adhesion G protein-coupled receptor V1
LMCD1-AS1	2.220982	0.002039	0.039991	3.084557	Up	LMCD1 antisense RNA 1
PTH1H	2.220149	0.002684	0.045476	3.001776	Up	parathyroid hormone like hormone
CCNA1	2.218492	0.002222	0.041364	3.058791	Up	cyclin A1
LOC101929331	2.216569	0.001331	0.031467	3.209205	Up	uncharacterized LOC101929331
FANK1	2.209783	0.001076	0.027879	3.269923	Up	fibronectin type III and ankyrin repeat domains 1
COBL	2.208342	2.38E-05	0.003075	4.22623	Up	cordon-bleu WH2 repeat protein
CA12	2.204549	0.001852	0.037842	3.113031	Up	carbonic anhydrase 12
ACVR1C	2.202767	0.000159	0.009489	3.777069	Up	activin A receptor type 1C
LIN28B	2.19221	0.002343	0.042557	3.04297	Up	lin-28 homolog B
FAP	2.190262	0.002649	0.045307	3.005779	Up	fibroblast activation protein alpha
CDH8	2.188607	0.000822	0.024176	3.345133	Up	cadherin 8
LINC02516	2.188282	0.001885	0.038231	3.107719	Up	long intergenic non-protein coding RNA 2516
HUNK	2.186613	0.001559	0.034147	3.163546	Up	hormonally up-regulated Neu-associated kinase
GDA	2.18637	0.000475	0.017713	3.494649	Up	guanine deaminase
FERMT1	2.186142	0.001741	0.036551	3.131129	Up	fermitin family member 1
PCDHAC2	2.182501	0.00315	0.049748	2.952745	Up	protocadherin alpha subfamily C, 2
DACT3	2.180069	0.000724	0.022988	3.380384	Up	dishevelled binding antagonist of beta catenin 3
THSD7A	2.174731	3.78E-05	0.003827	4.120684	Up	thrombospondin type 1 domain containing 7A
IQCH	2.17072	0.00026	0.012401	3.652197	Up	IQ motif containing H
EFCAB5	2.166213	0.000248	0.012032	3.664178	Up	EF-hand calcium binding domain 5
PEX5L	2.159847	0.001799	0.037314	3.12155	Up	peroxisomal biogenesis factor 5 like
KRT80	2.157287	0.001077	0.027891	3.269503	Up	keratin 80
DGKB	2.152441	0.002866	0.047155	2.981723	Up	diacylglycerol kinase beta
MIPOL1	2.151576	3.96E-07	0.000202	5.070865	Up	mirror-image polydactyly 1
ERVFRD-1	2.146361	0.002069	0.04018	3.080109	Up	endogenous retrovirus group FRD member 1, envelope
MROH7	2.144137	0.001891	0.038276	3.106885	Up	maestro heat like repeat family member 7
NWD1	2.138886	0.001529	0.033794	3.169182	Up	NACHT and WD repeat domain containing 1
RPL5P9	2.136476	0.001417	0.032481	3.191203	Up	ribosomal protein L5 pseudogene 9
IRX2	2.128446	0.00267	0.04539	3.003404	Up	iroquois homeobox 2
C8orf34	2.126376	0.000638	0.02144	3.414745	Up	chromosome 8 open reading frame 34
ABCA4	2.11746	0.001117	0.028579	3.259331	Up	ATP binding cassette subfamily A member 4
STRC	2.116012	0.003071	0.049015	2.960547	Up	stereocilin

PTH2R	2.115792	0.000304	0.013588	3.612101	Up	parathyroid hormone 2 receptor
NXPE1	2.113269	0.002283	0.042123	3.05065	Up	neurexophilin and PC-esterase domain family member 1
TTC6	2.111884	0.001845	0.03779	3.114092	Up	tetratricopeptide repeat domain 6
TMEM117	2.111578	0.001239	0.030205	3.229725	Up	transmembrane protein 117
HPGDS	2.109892	0.002109	0.040552	3.074442	Up	hematopoietic prostaglandin D synthase
LINC00319	2.107732	0.002376	0.042799	3.038703	Up	long intergenic non-protein coding RNA 319
POPDC2	2.105552	0.001277	0.030666	3.221072	Up	popeye domain containing 2
ADCY2	2.105369	0.002746	0.046108	2.994785	Up	adenylate cyclase 2
NEUROD1	2.103703	0.001825	0.03757	3.117299	Up	neuronal differentiation 1
DYDC2	2.103538	0.002326	0.042463	3.04516	Up	DPY30 domain containing 2
ANKS1B	2.103506	0.000361	0.015	3.566711	Up	ankyrin repeat and sterile alpha motif domain containing 1B
SPINK5	2.091698	3.77E-06	0.000972	4.623788	Up	serine peptidase inhibitor Kazal type 5
DNAH7	2.083609	0.000664	0.021877	3.404061	Up	dynein axonemal heavy chain 7
KCNIP3	2.080304	0.000407	0.016188	3.535437	Up	potassium voltage-gated channel interacting protein 3
EFHD1	2.079688	0.000366	0.015111	3.563362	Up	EF-hand domain family member D1
PTPRVP	2.07093	0.001905	0.038276	3.104597	Up	protein tyrosine phosphatase receptor type V, pseudogene
IL20RA	2.059487	0.001232	0.030149	3.231432	Up	interleukin 20 receptor subunit alpha
CLDN1	2.051894	0.00046	0.017474	3.502794	Up	claudin 1
MAL2	2.045176	0.00094	0.026167	3.307794	Up	mal, T cell differentiation protein 2
IZUMO1	2.04049	0.002425	0.043302	3.032495	Up	izumo sperm-egg fusion 1
SHROOM3	2.036624	0.000774	0.023633	3.361906	Up	shroom family member 3
KLK11	2.03325	0.001722	0.036306	3.134359	Up	kallikrein related peptidase 11
CCNE1	2.031649	8.59E-05	0.006125	3.927182	Up	cyclin E1
C5orf34	2.030955	0.001251	0.030269	3.227007	Up	chromosome 5 open reading frame 34
HAGLR	2.030678	0.000244	0.011968	3.668631	Up	HOXD antisense growth-associated long non-coding RNA
SOHLH1	2.027269	0.002949	0.048	2.973046	Up	spermatogenesis and oogenesis specific basic helix-loop-helix 1
SLC6A7	2.026896	0.002113	0.040594	3.073894	Up	solute carrier family 6 member 7
DISP3	2.017289	0.003171	0.049996	2.950641	Up	dispatched RND transporter family member 3
CCDC144A	2.017023	0.002696	0.045569	3.000434	Up	coiled-coil domain containing 144A
RNY3P15	2.012765	0.000488	0.018098	3.487286	Up	RNY3 pseudogene 15
FUT3	2.00891	0.001339	0.031528	3.20754	Up	fucosyltransferase 3 (Lewis blood group)
GABRB3	1.999488	0.00036	0.015	3.567729	Up	gamma-aminobutyric acid type A receptor subunit beta3
ANKRD45	1.998307	0.002582	0.044697	3.01351	Up	ankyrin repeat domain 45
SLC7A14	1.997464	0.00134	0.031529	3.207166	Up	solute carrier family 7 member 14
ETV1	1.994147	0.000931	0.026107	3.310687	Up	ETS variant transcription factor 1
CYP24A1	1.99389	0.001803	0.037364	3.120901	Up	cytochrome P450 family 24 subfamily A member 1
TNR	1.989575	0.000117	0.007455	3.852826	Up	tenascin R
ERRFI1	1.986467	0.000163	0.009601	3.770865	Up	ERBB receptor feedback inhibitor 1
PKHD1	1.981313	0.001264	0.030438	3.224052	Up	PKHD1 ciliary IPT domain containing fibrocystin/polyductin
RNY4P3	1.980563	0.000528	0.018925	3.466125	Up	RNY4 pseudogene 3
KRT13	1.980125	0.00216	0.041044	3.067343	Up	keratin 13
SLIT2	1.977635	0.000946	0.026225	3.306227	Up	slit guidance ligand 2
C2orf72	1.973621	0.001796	0.037284	3.122029	Up	chromosome 2 open reading frame 72

MAST1	1.967185	0.001674	0.035744	3.142734	Up	microtubule associated serine/threonine kinase 1
DTNA	1.965549	3.74E-06	0.000972	4.625455	Up	dystrobrevin alpha
MTND6P3	1.954429	0.000989	0.026772	3.293577	Up	MT-ND6 pseudogene 3
ANTXR1	1.953571	0.000557	0.019657	3.451608	Up	ANTXR cell adhesion molecule 1
ITGA8	1.943705	0.000215	0.011264	3.70068	Up	integrin subunit alpha 8
KCNA7	1.943639	0.001181	0.029566	3.243516	Up	potassium voltage-gated channel subfamily A member 7
RPL5P5	1.938703	0.001865	0.038009	3.110912	Up	ribosomal protein L5 pseudogene 5
MIR100HG	1.931116	0.000802	0.024074	3.352008	Up	mir-100-let-7a-2-mir-125b-1 cluster host gene
MTND6P7	1.926584	0.002089	0.040327	3.077268	Up	MT-ND6 pseudogene 7
GJC1	1.925965	0.002785	0.046349	2.990545	Up	gap junction protein gamma 1
WNK3	1.911953	0.000303	0.013583	3.612905	Up	WNK lysine deficient protein kinase 3
PPARGC1A	1.909247	0.001337	0.031528	3.207817	Up	PPARG coactivator 1 alpha
TRPM3	1.894528	0.001056	0.027608	3.275048	Up	transient receptor potential cation channel subfamily M member 3
PAK3	1.886078	0.000506	0.018497	3.47747	Up	p21 (RAC1) activated kinase 3
IGF1	1.885985	4.94E-05	0.004447	4.058211	Up	insulin like growth factor 1
LRRC7	1.885084	0.002344	0.042557	3.042833	Up	leucine rich repeat containing 7
UNC80	1.884923	0.000824	0.024177	3.344691	Up	unc-80 homolog, NALCN channel complex subunit
PRKN	1.883231	0.001161	0.029354	3.248193	Up	parkin RBR E3 ubiquitin protein ligase
CCDC114	1.878413	0.001388	0.032202	3.197052	Up	coiled-coil domain containing 114
POU2F3	1.867221	0.002618	0.045039	3.009403	Up	POU class 2 homeobox 3
LINC00261	1.864563	0.002192	0.041176	3.062916	Up	long intergenic non-protein coding RNA 261
SIGLEC5	1.864333	0.002118	0.0406	3.073196	Up	sialic acid binding Ig like lectin 5
OSR1	1.859268	0.00108	0.027939	3.268722	Up	odd-skipped related transcription factor 1
RNA5SP202	1.857863	2.58E-05	0.003086	4.207956	Up	RNA, 5S ribosomal pseudogene 202
ZNF599	1.852715	0.000256	0.012271	3.65655	Up	zinc finger protein 599
HRG	1.845664	0.002023	0.039829	3.086884	Up	histidine rich glycoprotein
B3GNT4	1.841526	0.002328	0.042463	3.044899	Up	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 4
CYP46A1	1.823515	0.002982	0.048357	2.969551	Up	cytochrome P450 family 46 subfamily A member 1
SH3RF2	1.819235	0.001247	0.030249	3.227811	Up	SH3 domain containing ring finger 2
TTC25	1.818112	0.001302	0.030956	3.215577	Up	tetratricopeptide repeat domain 25
CDH6	1.817889	0.002522	0.044225	3.020705	Up	cadherin 6
FHAD1	1.807752	0.001379	0.032073	3.199029	Up	forkhead associated phosphopeptide binding domain 1
FOLR2	1.806169	0.001876	0.038108	3.109204	Up	folate receptor beta
INAVA	1.80001	0.000708	0.02286	3.386569	Up	innate immunity activator
ARHGEF4	1.797538	0.001557	0.034141	3.163862	Up	Rho guanine nucleotide exchange factor 4
CSRP2	1.797297	0.00078	0.023744	3.359926	Up	cysteine and glycine rich protein 2
SETD9	1.788362	0.000831	0.024307	3.342201	Up	SET domain containing 9
TRPV6	1.786255	0.002295	0.042181	3.049106	Up	transient receptor potential cation channel subfamily V member 6
ATP1A4	1.786037	0.001294	0.030853	3.217366	Up	ATPase Na ⁺ /K ⁺ transporting subunit alpha 4
TUFT1	1.785546	0.00045	0.017213	3.508951	Up	tuftelin 1
TLR3	1.778403	0.000288	0.013293	3.625928	Up	toll like receptor 3
CIART	1.777924	0.002992	0.048449	2.96854	Up	circadian associated repressor of transcription
BNIP1	1.770915	0.001501	0.033537	3.17456	Up	BCL2 interacting protein like

ZBTB8A	1.766359	0.002771	0.046306	2.992076	Up	zinc finger and BTB domain containing 8A
ANKRD11P1	1.757155	0.00126	0.030383	3.224854	Up	ANKRD11 pseudogene 1
BMP7	1.754203	0.0025	0.043986	3.023331	Up	bone morphogenetic protein 7
GNAL	1.753	0.000812	0.024176	3.348706	Up	G protein subunit alpha L
DDX11L16	1.748222	0.000834	0.024307	3.341316	Up	DEAD/H-box helicase 11 like 16 (pseudogene)
DSG2	1.745653	0.002241	0.041536	3.056218	Up	desmoglein 2
CELF5	1.742927	0.002082	0.040319	3.078226	Up	CUGBP Elav-like family member 5
POSTN	1.741624	0.002116	0.0406	3.07341	Up	periostin
DZANK1	1.734506	0.002043	0.039991	3.083933	Up	double zinc ribbon and ankyrin repeat domains 1
STOML1	1.732747	0.001133	0.028852	3.255148	Up	stomatin like 1
CCDC150	1.731692	0.0002	0.010815	3.719213	Up	coiled-coil domain containing 150
MTND2P28	-4.90599	6.27E-18	1.54E-13	-8.62753	Down	MT-ND2 pseudogene 28
SNORD46	-4.03607	1.87E-06	0.000616	-4.76672	Down	small nucleolar RNA, C/D box 46
SCARNA21	-3.96374	1.46E-07	0.000108	-5.25768	Down	small Cajal body-specific RNA 21
MTND1P23	-3.65224	6.88E-07	0.000307	-4.96464	Down	MT-ND1 pseudogene 23
COX4I2	-3.46711	0.00184	0.03779	-3.1149	Down	cytochrome c oxidase subunit 4I2
SNORD15B	-3.36678	3.40E-12	2.40E-08	-6.96024	Down	small nucleolar RNA, C/D box 15B
SNORD67	-3.27752	8.82E-05	0.006199	-3.92082	Down	small nucleolar RNA, C/D box 67
SNORA26	-3.16261	0.000292	0.013372	-3.62225	Down	small nucleolar RNA, H/ACA box 26
SCARNA7	-3.12296	5.75E-08	7.28E-05	-5.42628	Down	small Cajal body-specific RNA 7
SCARNA6	-3.1138	3.69E-06	0.000972	-4.62793	Down	small Cajal body-specific RNA 6
SNORA49	-3.00158	1.32E-05	0.001992	-4.35741	Down	small nucleolar RNA, H/ACA box 49
SNORD89	-2.98616	3.22E-07	0.000179	-5.1101	Down	small nucleolar RNA, C/D box 89
XIST	-2.94715	2.25E-08	4.04E-05	-5.59163	Down	X inactive specific transcript
MTCO1P12	-2.91868	6.76E-10	1.84E-06	-6.17155	Down	MT-CO1 pseudogene 12
SNORA46	-2.83296	2.27E-05	0.00299	-4.23664	Down	small nucleolar RNA, H/ACA box 46
SNORD8	-2.80183	0.000218	0.011333	-3.69697	Down	small nucleolar RNA, C/D box 8
LTA	-2.74322	0.002893	0.047414	-2.97886	Down	lymphotoxin alpha
SNORA20	-2.73344	0.000125	0.007836	-3.83615	Down	small nucleolar RNA, H/ACA box 20
SNORA75	-2.70965	0.001906	0.038276	-3.10457	Down	small nucleolar RNA, H/ACA box 75
SNORD116-24	-2.70339	0.002652	0.045307	-3.00541	Down	small nucleolar RNA, C/D box 116-24
SNORD17	-2.68133	3.92E-12	2.40E-08	-6.94007	Down	small nucleolar RNA, C/D box 17
SNORA53	-2.62376	1.12E-07	9.13E-05	-5.30657	Down	small nucleolar RNA, H/ACA box 53
SNORA23	-2.55895	3.17E-07	0.000179	-5.11277	Down	small nucleolar RNA, H/ACA box 23
SNORA12	-2.34359	1.48E-06	0.000518	-4.81391	Down	small nucleolar RNA, H/ACA box 12
SNORD9	-2.31392	0.00296	0.048102	-2.97188	Down	small nucleolar RNA, C/D box 9
SCARNA10	-2.30272	1.68E-07	0.000114	-5.23166	Down	small Cajal body-specific RNA 10
SNORA73B	-2.27776	5.25E-06	0.001225	-4.55464	Down	small nucleolar RNA, H/ACA box 73B
RNU5A-1	-2.2381	2.58E-05	0.003086	-4.20766	Down	RNA, U5A small nuclear 1
LOC400541	-2.13572	0.002581	0.044697	-3.01371	Down	uncharacterized LOC400541
CCDC24	-2.06616	0.00103	0.027301	-3.28218	Down	coiled-coil domain containing 24
CXCL5	-2.00406	1.17E-06	0.000443	-4.86103	Down	C-X-C motif chemokine ligand 5
MALAT1	-1.96132	2.47E-08	4.04E-05	-5.5753	Down	metastasis associated lung adenocarcinoma transcript 1

ITGA2B	-1.95681	3.00E-07	0.000175	-5.12318	Down	integrin subunit alpha 2b
TMEM70	-1.9551	7.91E-07	0.00034	-4.93767	Down	transmembrane protein 70
TMEM150A	-1.87702	0.000292	0.013372	-3.62198	Down	transmembrane protein 150A
LGALS3BP	-1.87374	7.10E-05	0.005475	-3.97284	Down	galectin 3 binding protein
ITGB3	-1.82598	4.35E-07	0.000209	-5.05282	Down	integrin subunit beta 3
CCDC28B	-1.81435	0.001027	0.027283	-3.28297	Down	coiled-coil domain containing 28B
CNNM4	-1.8064	0.000351	0.014776	-3.57459	Down	cyclin and CBS domain divalent metal cation transport mediator 4
SPSB2	-1.80517	0.00019	0.01042	-3.73252	Down	splA/ryanodine receptor domain and SOCS box containing 2
SEC14L5	-1.77994	5.86E-05	0.004918	-4.01829	Down	SEC14 like lipid binding 5
PLXNB2	-1.76414	5.94E-08	7.28E-05	-5.42064	Down	plexin B2
MPL	-1.69211	1.12E-05	0.001787	-4.39349	Down	MPL proto-oncogene, thrombopoietin receptor
UBOX5	-1.68768	0.000939	0.026167	-3.30826	Down	U-box domain containing 5
MTCO2P12	-1.6563	2.51E-05	0.003077	-4.21361	Down	MT-CO2 pseudogene 12
EXO5	-1.63808	0.003087	0.049175	-2.95895	Down	exonuclease 5
TMEM178A	-1.6373	0.002427	0.043302	-3.03227	Down	transmembrane protein 178A
NEAT1	-1.63692	6.53E-11	3.20E-07	-6.53097	Down	nuclear paraspeckle assembly transcript 1
ITGAX	-1.63477	3.35E-10	1.17E-06	-6.28152	Down	integrin subunit alpha X
IGHD	-1.55784	1.78E-06	0.000606	-4.77683	Down	immunoglobulin heavy constant delta
F13A1	-1.55093	1.03E-05	0.001765	-4.41066	Down	coagulation factor XIII A chain
POMK	-1.54862	0.000992	0.026772	-3.29291	Down	protein O-mannose kinase
MPIG6B	-1.54393	2.05E-05	0.002771	-4.25979	Down	megakaryocyte and platelet inhibitory receptor G6b
SCARNA5	-1.53993	0.001063	0.027659	-3.27336	Down	small Cajal body-specific RNA 5
THBS1	-1.53355	2.71E-07	0.000162	-5.14246	Down	thrombospondin 1
FLNA	-1.5138	3.81E-10	1.17E-06	-6.26151	Down	filamin A
TTYH3	-1.49872	3.77E-07	0.000196	-5.08044	Down	tweety family member 3
RNU5B-1	-1.48598	0.000606	0.020737	-3.42908	Down	RNA, U5B small nuclear 1
ACAD10	-1.48224	0.000997	0.026839	-3.29128	Down	acyl-CoA dehydrogenase family member 10
TUBB1	-1.4625	1.87E-05	0.00255	-4.27993	Down	tubulin beta 1 class VI
MTATP6P1	-1.46162	0.000698	0.022616	-3.39024	Down	MT-ATP6 pseudogene 1
ATP2A3	-1.45721	1.86E-07	0.00012	-5.21255	Down	ATPase sarcoplasmic/endoplasmic reticulum Ca2+ transporting 3
BSCL2	-1.45633	0.000547	0.019444	-3.45651	Down	BSCL2 lipid droplet biogenesis associated, seipin
ARHGAP27	-1.45245	3.89E-06	0.000993	-4.61721	Down	Rho GTPase activating protein 27
TRPC6	-1.44884	0.000582	0.020311	-3.44006	Down	transient receptor potential cation channel subfamily C member 6
SELP	-1.44569	7.27E-05	0.005584	-3.96743	Down	selectin P
LMF2	-1.44542	0.001479	0.033304	-3.1787	Down	lipase maturation factor 2
ZNF865	-1.43756	2.84E-05	0.003258	-4.18559	Down	zinc finger protein 865
SCARNA1	-1.43102	0.002052	0.040029	-3.08254	Down	small Cajal body-specific RNA 1
CD79A	-1.43031	2.92E-06	0.000822	-4.67616	Down	CD79a molecule
CSF1R	-1.42263	1.30E-05	0.001977	-4.36033	Down	colony stimulating factor 1 receptor
TSPAN18	-1.42096	8.69E-08	8.60E-05	-5.3521	Down	tetraspanin 18
MEMO1	-1.41159	0.001686	0.035853	-3.14057	Down	mediator of cell motility 1
RAB27B	-1.4082	2.46E-05	0.003077	-4.21825	Down	RAB27B, member RAS oncogene family
MAP3K7CL	-1.39373	0.001733	0.036439	-3.13253	Down	MAP3K7 C-terminal like

NUP210	-1.39068	1.71E-05	0.002402	-4.29912	Down	nucleoporin 210
XKR8	-1.38657	0.001051	0.027608	-3.27656	Down	XK related 8
ZNF296	-1.3763	0.000893	0.025475	-3.32229	Down	zinc finger protein 296
HLA-A	-1.36399	4.26E-05	0.00411	-4.09299	Down	major histocompatibility complex, class I, A
VCL	-1.35636	2.75E-06	0.000789	-4.68889	Down	vinculin
PYGB	-1.35046	1.37E-07	0.000106	-5.26879	Down	glycogen phosphorylase B
ZNF185	-1.34888	7.28E-06	0.001463	-4.48526	Down	zinc finger protein 185 with LIM domain
TLN1	-1.34869	9.33E-10	2.29E-06	-6.1204	Down	taln 1
ATG16L2	-1.34232	0.000383	0.015563	-3.55153	Down	autophagy related 16 like 2
P2RY1	-1.34195	6.23E-05	0.005041	-4.00391	Down	purinergic receptor P2Y1
FCRL1	-1.33807	0.001187	0.029636	-3.24197	Down	Fc receptor like 1
VCAN	-1.33673	5.17E-06	0.001218	-4.5579	Down	versican
GP5	-1.33529	0.000375	0.015331	-3.55694	Down	glycoprotein V platelet
TREML1	-1.32677	0.000354	0.014874	-3.57241	Down	triggering receptor expressed on myeloid cells like 1
ENDOD1	-1.32673	3.35E-05	0.003601	-4.14836	Down	endonuclease domain containing 1
SF3A2	-1.32632	2.07E-05	0.002792	-4.25694	Down	splicing factor 3a subunit 2
SNHG1	-1.31645	3.57E-07	0.000191	-5.09032	Down	small nucleolar RNA host gene 1
CYBC1	-1.31003	2.16E-06	0.000683	-4.73829	Down	cytochrome b-245 chaperone 1
NOTCH2	-1.30956	6.57E-06	0.001388	-4.50727	Down	notch receptor 2
F2RL3	-1.30319	0.000544	0.019385	-3.4581	Down	F2R like thrombin or trypsin receptor 3
MLEC	-1.30219	6.56E-05	0.005188	-3.99169	Down	malectin
LIPA	-1.30205	3.04E-06	0.000836	-4.66836	Down	lipase A, lysosomal acid type
PSAP	-1.29688	3.59E-09	8.00E-06	-5.90214	Down	prosaposin
FAM185A	-1.29651	0.003014	0.048576	-2.96634	Down	family with sequence similarity 185 member A
CHST12	-1.29603	0.001818	0.037455	-3.11853	Down	carbohydrate sulfotransferase 12
ZNF142	-1.28692	0.000461	0.017474	-3.50237	Down	zinc finger protein 142
CD300E	-1.28208	4.95E-05	0.004447	-4.05786	Down	CD300e molecule
LIMS1	-1.27289	8.29E-06	0.001552	-4.45754	Down	LIM zinc finger domain containing 1
MYBBP1A	-1.2726	1.15E-05	0.001797	-4.38768	Down	MYB binding protein 1a
TLR5	-1.27091	3.23E-05	0.003516	-4.15682	Down	toll like receptor 5
ACAA1	-1.26927	5.32E-05	0.00461	-4.04102	Down	acetyl-CoA acyltransferase 1
ABCA7	-1.26175	0.000641	0.021466	-3.41379	Down	ATP binding cassette subfamily A member 7
ELAC2	-1.2384	0.000275	0.012948	-3.63763	Down	elaC ribonuclease Z 2
CAVIN2	-1.23832	0.000225	0.011379	-3.68867	Down	caveolae associated protein 2
PTPRJ	-1.23748	7.34E-07	0.000321	-4.9521	Down	protein tyrosine phosphatase receptor type J
MYCL	-1.23528	0.002527	0.044281	-3.02011	Down	MYCL proto-oncogene, bHLH transcription factor
ABCC3	-1.23485	0.000179	0.010131	-3.74645	Down	ATP binding cassette subfamily C member 3
LRP1	-1.22373	2.68E-05	0.003145	-4.19944	Down	LDL receptor related protein 1
BAX	-1.22016	3.69E-05	0.00378	-4.12579	Down	BCL2 associated X, apoptosis regulator
SUN2	-1.21453	0.001048	0.027588	-3.27739	Down	Sad1 and UNC84 domain containing 2
P2RX1	-1.21224	8.63E-05	0.006131	-3.92616	Down	purinergic receptor P2X 1
RNU4-2	-1.20679	0.000666	0.021923	-3.40305	Down	RNA, U4 small nuclear 2
DENND1C	-1.20654	2.52E-05	0.003077	-4.21316	Down	DENN domain containing 1C

PYCR2	-1.20379	2.51E-05	0.003077	-4.21399	Down	pyrroline-5-carboxylate reductase 2
SMCR8	-1.19691	7.53E-05	0.005661	-3.95896	Down	SMCR8-C9orf72 complex subunit
ENO2	-1.19673	1.87E-05	0.00255	-4.27962	Down	enolase 2
SPARC	-1.19573	0.000338	0.014421	-3.58411	Down	secreted protein acidic and cysteine rich
TMEM140	-1.19371	0.000156	0.009395	-3.78076	Down	transmembrane protein 140
CLU	-1.19052	0.000112	0.007242	-3.86311	Down	clusterin
TBXA2R	-1.18747	3.50E-05	0.003694	-4.13853	Down	thromboxane A2 receptor
LRRC25	-1.18687	0.000472	0.017694	-3.49615	Down	leucine rich repeat containing 25
CIITA	-1.18392	0.000112	0.007242	-3.86311	Down	class II major histocompatibility complex transactivator
FCN1	-1.18116	5.65E-06	0.001284	-4.5389	Down	ficolin 1
NFRKB	-1.17991	0.001479	0.033304	-3.17872	Down	nuclear factor related to kappaB binding protein
ITGB5	-1.17791	0.000832	0.024307	-3.34193	Down	integrin subunit beta 5
PRKAR2B	-1.17746	0.000123	0.007728	-3.84083	Down	protein kinase cAMP-dependent type II regulatory subunit beta
ITGA2	-1.17733	0.001413	0.032461	-3.19203	Down	integrin subunit alpha 2
PPM1L	-1.17733	0.000627	0.021185	-3.41987	Down	protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent 1L
CDKN1A	-1.17374	3.67E-05	0.00378	-4.12762	Down	cyclin dependent kinase inhibitor 1A
CCNL1	-1.17343	0.000301	0.013571	-3.61479	Down	cyclin L1
MAP4K1	-1.17148	3.68E-05	0.00378	-4.12662	Down	mitogen-activated protein kinase kinase kinase kinase 1
ADCY7	-1.16248	5.66E-05	0.004783	-4.02666	Down	adenylate cyclase 7
TKFC	-1.15685	0.002084	0.040319	-3.07803	Down	triokinase and FMN cyclase
ZC3HAV1L	-1.15209	0.002252	0.041643	-3.05477	Down	zinc finger CCCH-type containing, antiviral 1 like
MPEG1	-1.15151	1.89E-06	0.000616	-4.76529	Down	macrophage expressed 1
PANX1	-1.14895	0.001235	0.030149	-3.23074	Down	pannexin 1
NRGN	-1.14792	0.000591	0.020472	-3.43561	Down	neurogranin
RAB1B	-1.14574	3.37E-07	0.000184	-5.10152	Down	RAB1B, member RAS oncogene family
CA5BP1	-1.1382	0.001138	0.028918	-3.25407	Down	carbonic anhydrase 5B pseudogene 1
PDE5A	-1.13435	0.000138	0.00844	-3.81219	Down	phosphodiesterase 5A
CLPP	-1.12506	5.89E-05	0.004918	-4.01717	Down	caseinolytic mitochondrial matrix peptidase proteolytic subunit
NCSTN	-1.12446	4.82E-05	0.004447	-4.06399	Down	nicastatin
URB2	-1.12263	0.000647	0.021519	-3.41111	Down	URB2 ribosome biogenesis homolog
IRF7	-1.12153	0.000197	0.010736	-3.72219	Down	interferon regulatory factor 7
CHERP	-1.11812	0.000256	0.012271	-3.65642	Down	calcium homeostasis endoplasmic reticulum protein
SMAD3	-1.11811	4.97E-05	0.004447	-4.05702	Down	SMAD family member 3
CTSW	-1.11737	0.000104	0.006936	-3.88213	Down	cathepsin W
GLIPR1	-1.11571	0.00141	0.03242	-3.19266	Down	GLI pathogenesis related 1
NIBAN3	-1.11238	0.001211	0.029831	-3.23632	Down	niban apoptosis regulator 3
C2orf88	-1.10948	0.001337	0.031528	-3.20797	Down	chromosome 2 open reading frame 88
CMIP	-1.10944	9.65E-11	3.94E-07	-6.47226	Down	c-Maf inducing protein
SNHG3	-1.10866	0.001906	0.038276	-3.10448	Down	small nucleolar RNA host gene 3
LFNG	-1.10857	0.000881	0.025232	-3.32595	Down	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase
TMEM259	-1.10223	0.000105	0.006987	-3.879	Down	transmembrane protein 259
MFAP3L	-1.09951	0.000178	0.010116	-3.74857	Down	microfibril associated protein 3 like
KDM2B	-1.09588	0.000316	0.013923	-3.60202	Down	lysine demethylase 2B

CTSA	-1.08776	0.000138	0.00844	-3.81163	Down	cathepsin A
CMTM5	-1.08502	0.000602	0.020717	-3.43049	Down	CKLF like MARVEL transmembrane domain containing 5
ITGB1	-1.08493	0.000117	0.007479	-3.85139	Down	integrin subunit beta 1
TCL1A	-1.08285	0.000437	0.016891	-3.51639	Down	TCL1 family AKT coactivator A
RHBDF2	-1.0815	0.000644	0.021466	-3.41243	Down	rhomboid 5 homolog 2
MRPL28	-1.07974	0.000739	0.023226	-3.37468	Down	mitochondrial ribosomal protein L28
DENND4B	-1.07669	4.36E-06	0.001071	-4.59333	Down	DENN domain containing 4B
PIK3IP1	-1.0738	0.002438	0.04338	-3.03089	Down	phosphoinositide-3-kinase interacting protein 1
ANO6	-1.0728	0.000183	0.010146	-3.74208	Down	anoctamin 6
SIDT2	-1.0724	0.001844	0.03779	-3.11431	Down	SID1 transmembrane family member 2
VPS52	-1.07237	0.001962	0.039005	-3.09597	Down	VPS52 subunit of GARP complex
CAPN1	-1.07099	8.76E-08	8.60E-05	-5.35063	Down	calpain 1
BAK1	-1.07031	0.002622	0.045039	-3.00895	Down	BCL2 antagonist/killer 1
IGHM	-1.06891	9.10E-06	0.001665	-4.43745	Down	immunoglobulin heavy constant mu
POLR1A	-1.06714	0.0005	0.018378	-3.48087	Down	RNA polymerase I subunit A
NOTCH1	-1.06581	0.000231	0.011467	-3.68267	Down	notch receptor 1
MS4A1	-1.06515	8.76E-06	0.001615	-4.44574	Down	membrane spanning 4-domains A1
PLEC	-1.06359	7.36E-06	0.001466	-4.48313	Down	plectin
HEATR6	-1.06357	0.000833	0.024307	-3.34158	Down	HEAT repeat containing 6
SRPRA	-1.06195	3.45E-05	0.00368	-4.14139	Down	SRP receptor subunit alpha
FERMT3	-1.05969	3.37E-06	0.000907	-4.64715	Down	fermitin family member 3
TLR2	-1.05728	0.000587	0.020406	-3.43764	Down	toll like receptor 2
RNASET2	-1.05719	0.001958	0.039005	-3.09646	Down	ribonuclease T2
GSE1	-1.05705	0.000165	0.009631	-3.76795	Down	Gse1 coiled-coil protein
DNAH1	-1.05642	0.002558	0.044661	-3.01643	Down	dynein axonemal heavy chain 1
GPR183	-1.05545	0.001287	0.030786	-3.21883	Down	G protein-coupled receptor 183
TCIRG1	-1.05428	0.000767	0.023535	-3.36442	Down	T cell immune regulator 1, ATPase H ⁺ transporting V0 subunit a3
PLXDC2	-1.05364	1.13E-05	0.001796	-4.39103	Down	plexin domain containing 2
ESYT1	-1.05169	0.000207	0.011081	-3.71086	Down	extended synaptotagmin 1
LOC728975	-1.05112	0.000525	0.018855	-3.46791	Down	uncharacterized LOC728975
GIGYF1	-1.04994	9.89E-05	0.006716	-3.89329	Down	GRB10 interacting GYF protein 1
HLA-E	-1.04792	7.06E-06	0.001447	-4.49174	Down	major histocompatibility complex, class I, E
TPP1	-1.03673	7.65E-05	0.005698	-3.95523	Down	tripeptidyl peptidase 1
C1orf198	-1.03507	0.00033	0.0142	-3.59083	Down	chromosome 1 open reading frame 198
LENG8	-1.03282	0.00077	0.023545	-3.36347	Down	leukocyte receptor cluster member 8
MMD	-1.03273	0.001966	0.039069	-3.09525	Down	monocyte to macrophage differentiation associated
ARHGAP6	-1.03147	9.83E-05	0.006697	-3.89486	Down	Rho GTPase activating protein 6
INF2	-1.03092	4.89E-05	0.004447	-4.06078	Down	inverted formin 2
ADA2	-1.03056	3.22E-05	0.003516	-4.15714	Down	adenosine deaminase 2
LEPROT	-1.02826	0.000362	0.015	-3.56638	Down	leptin receptor overlapping transcript
LHFPL2	-1.02583	0.000168	0.009794	-3.76256	Down	LHFPL tetraspan subfamily member 2
RSRP1	-1.02528	0.00013	0.008082	-3.82605	Down	arginine and serine rich protein 1
PRR12	-1.02355	5.89E-05	0.004918	-4.01726	Down	proline rich 12

PTPRC	-1.02342	6.41E-06	0.001381	-4.51254	Down	protein tyrosine phosphatase receptor type C
PEAR1	-1.02315	0.000976	0.026694	-3.29731	Down	platelet endothelial aggregation receptor 1
SH3BP1	-1.02067	0.000164	0.009631	-3.76841	Down	SH3 domain binding protein 1
CBFA2T3	-1.01554	4.37E-06	0.001071	-4.59298	Down	CBFA2/RUNX1 partner transcriptional co-repressor 3
SH3BGRL2	-1.01405	0.001013	0.027022	-3.28691	Down	SH3 domain binding glutamate rich protein like 2
NBEAL2	-1.01302	1.66E-07	0.000114	-5.23428	Down	neurobeachin like 2
USP20	-1.01201	0.000312	0.013829	-3.60538	Down	ubiquitin specific peptidase 20
ACTN1	-1.01061	1.38E-07	0.000106	-5.26824	Down	actinin alpha 1
GALNT10	-1.01018	6.48E-05	0.005161	-3.99445	Down	polypeptide N-acetylgalactosaminyltransferase 10
MYH9	-1.00874	3.06E-08	4.68E-05	-5.53822	Down	myosin heavy chain 9
EML3	-1.00631	0.001341	0.031529	-3.20698	Down	EMAP like 3
CHPF2	-1.00208	0.003133	0.049553	-2.95433	Down	chondroitin polymerizing factor 2
OGT	-0.99967	6.23E-06	0.001364	-4.51837	Down	O-linked N-acetylglucosamine (GlcNAc) transferase
TGFB1	-0.99647	9.73E-06	0.001712	-4.42309	Down	transforming growth factor beta 1
SLC35E2B	-0.99475	0.002332	0.042463	-3.04436	Down	solute carrier family 35 member E2B
ITGA4	-0.99164	1.11E-05	0.001787	-4.39552	Down	integrin subunit alpha 4
SLA2	-0.99112	1.58E-05	0.002264	-4.31754	Down	Src like adaptor 2
PITPNM2	-0.99094	0.000218	0.011333	-3.69702	Down	phosphatidylinositol transfer protein membrane associated 2
DTX1	-0.99043	0.000227	0.011442	-3.68656	Down	deltex E3 ubiquitin ligase 1
CARD11	-0.98965	0.000414	0.016355	-3.53081	Down	caspase recruitment domain family member 11
MADD	-0.98635	8.67E-08	8.60E-05	-5.35256	Down	MAP kinase activating death domain
KCNA3	-0.98406	0.000815	0.024176	-3.34766	Down	potassium voltage-gated channel subfamily A member 3
MRTFA	-0.98003	7.14E-06	0.001447	-4.48947	Down	myocardin related transcription factor A
EHD3	-0.97891	1.58E-05	0.002264	-4.31736	Down	EH domain containing 3
JAK3	-0.97683	2.29E-06	0.000692	-4.72564	Down	Janus kinase 3
SMG5	-0.97651	3.42E-05	0.003666	-4.14321	Down	SMG5 nonsense mediated mRNA decay factor
BTLA	-0.97428	0.000977	0.026694	-3.29714	Down	B and T lymphocyte associated
ITM2B	-0.97395	0.000939	0.026167	-3.30808	Down	integral membrane protein 2B
SRC	-0.96844	6.51E-05	0.005166	-3.99349	Down	SRC proto-oncogene, non-receptor tyrosine kinase
DSE	-0.96802	0.001176	0.029554	-3.24454	Down	dermatan sulfate epimerase
GP9	-0.96762	0.001032	0.02733	-3.28158	Down	glycoprotein IX platelet
APP	-0.96469	0.000121	0.007643	-3.84417	Down	amyloid beta precursor protein
PCSK6	-0.96413	0.00118	0.029566	-3.24363	Down	proprotein convertase subtilisin/kexin type 6
FGD3	-0.96372	5.96E-05	0.00493	-4.01439	Down	FYVE, RhoGEF and PH domain containing 3
TMEM63A	-0.96257	0.000766	0.023535	-3.36466	Down	transmembrane protein 63A
UNC13D	-0.96254	4.23E-07	0.000207	-5.0585	Down	unc-13 homolog D
POU2F2	-0.96008	5.20E-05	0.004533	-4.04663	Down	POU class 2 homeobox 2
TGOLN2	-0.95956	1.07E-07	9.13E-05	-5.31445	Down	trans-golgi network protein 2
ALOX12	-0.95833	0.002466	0.043601	-3.02754	Down	arachidonate 12-lipoxygenase, 12S type
FHOD1	-0.95699	0.000725	0.022988	-3.38001	Down	formin homology 2 domain containing 1
TMC6	-0.95675	0.000506	0.018497	-3.47745	Down	transmembrane channel like 6
MAP1A	-0.95616	0.001254	0.030269	-3.22621	Down	microtubule associated protein 1A
STIM1	-0.956	0.000171	0.009894	-3.75824	Down	stromal interaction molecule 1

CTDSPL	-0.95589	3.63E-05	0.00378	-4.1296	Down	CTD small phosphatase like
NHSL2	-0.95568	0.000407	0.016188	-3.53524	Down	NHS like 2
FTSJ1	-0.9548	0.000213	0.011232	-3.70358	Down	FtsJ RNA 2'-O-methyltransferase 1
RAB5C	-0.95199	0.000674	0.022111	-3.40002	Down	RAB5C, member RAS oncogene family
ZYX	-0.95107	2.11E-07	0.000133	-5.18909	Down	zyxin
GUCY1B1	-0.95093	0.000202	0.010901	-3.71667	Down	guanylate cyclase 1 soluble subunit beta 1
CMTM3	-0.95034	0.001706	0.036147	-3.13716	Down	CKLF like MARVEL transmembrane domain containing 3
CNST	-0.94803	0.000133	0.008228	-3.82102	Down	consortin, connexin sorting protein
ITPR1	-0.94779	9.85E-06	0.001712	-4.42051	Down	inositol 1,4,5-trisphosphate receptor type 1
GANAB	-0.94722	2.41E-05	0.003076	-4.22326	Down	glucosidase II alpha subunit
LDLRAP1	-0.94622	7.85E-06	0.00154	-4.46915	Down	low density lipoprotein receptor adaptor protein 1
CCNL2	-0.94337	0.001671	0.035724	-3.14316	Down	cyclin L2
SCAF1	-0.94322	0.000444	0.017101	-3.51224	Down	SR-related CTD associated factor 1
RNF213	-0.94236	9.61E-07	0.000386	-4.89945	Down	ring finger protein 213
MYLK	-0.93801	0.000244	0.011968	-3.66838	Down	myosin light chain kinase
CENPT	-0.93691	0.000923	0.025996	-3.31315	Down	centromere protein T
ARL15	-0.93608	0.001004	0.02689	-3.28952	Down	ADP ribosylation factor like GTPase 15
SRSF6	-0.93462	2.87E-05	0.003258	-4.18353	Down	serine and arginine rich splicing factor 6
LILRB2	-0.93243	0.001756	0.036694	-3.12872	Down	leukocyte immunoglobulin like receptor B2
TYMP	-0.92831	0.000169	0.009825	-3.76117	Down	thymidine phosphorylase
EPM2AIP1	-0.9279	0.000549	0.019464	-3.45543	Down	EPM2A interacting protein 1
SELENON	-0.92751	0.000614	0.020887	-3.42524	Down	selenoprotein N
SNRPA	-0.92596	0.000312	0.013829	-3.60519	Down	small nuclear ribonucleoprotein polypeptide A
RUFY1	-0.92552	0.001177	0.029554	-3.2445	Down	RUN and FYVE domain containing 1
GNB5	-0.92404	0.002044	0.039991	-3.08379	Down	G protein subunit beta 5
PRUNE1	-0.92163	6.17E-05	0.005023	-4.00634	Down	prune exopolyphosphatase 1
HELZ2	-0.92021	0.001894	0.038276	-3.10633	Down	helicase with zinc finger 2
GPR137B	-0.91873	0.000789	0.023846	-3.35671	Down	G protein-coupled receptor 137B
MBD6	-0.91809	0.001696	0.035973	-3.13883	Down	methyl-CpG binding domain protein 6
MTPN	-0.91698	0.000107	0.007035	-3.87486	Down	myotrophin
PDGFA	-0.91698	0.000286	0.013232	-3.62811	Down	platelet derived growth factor subunit A
ITGB2	-0.91566	9.79E-06	0.001712	-4.42169	Down	integrin subunit beta 2
METTL26	-0.91492	0.000816	0.024176	-3.34723	Down	methyltransferase like 26
SELPLG	-0.91412	0.000977	0.026694	-3.29704	Down	selectin P ligand
ATP9A	-0.91117	0.00249	0.043911	-3.0246	Down	ATPase phospholipid transporting 9A (putative)
DAPP1	-0.90904	0.00144	0.032813	-3.18648	Down	dual adaptor of phosphotyrosine and 3-phosphoinositides 1
CORO1B	-0.90571	1.07E-05	0.001778	-4.40295	Down	coronin 1B
TRIM13	-0.90533	8.14E-06	0.001552	-4.46152	Down	tripartite motif containing 13
SIN3B	-0.90521	0.002163	0.041072	-3.06691	Down	SIN3 transcription regulator family member B
VPS37B	-0.90416	2.95E-06	0.000822	-4.67423	Down	VPS37B subunit of ESCRT-I
UPF1	-0.9016	3.35E-08	4.69E-05	-5.52211	Down	UPF1 RNA helicase and ATPase
GDI1	-0.90075	1.32E-06	0.000476	-4.83669	Down	GDP dissociation inhibitor 1
TNFSF4	-0.89928	0.002323	0.042463	-3.04544	Down	TNF superfamily member 4

PGAP6	-0.89926	0.000729	0.023053	-3.37853	Down	post-glycosylphosphatidylinositol attachment to proteins 6
DIMT1	-0.89763	8.41E-05	0.006062	-3.93238	Down	DIMT1 rRNA methyltransferase and ribosome maturation factor
RPA1	-0.89722	0.001813	0.037437	-3.11934	Down	replication protein A1
RAB37	-0.89716	0.000134	0.008296	-3.81837	Down	RAB37, member RAS oncogene family
SPN	-0.89706	0.000109	0.007142	-3.87038	Down	sialophorin
BCL11B	-0.89634	0.00012	0.007579	-3.84685	Down	BAF chromatin remodeling complex subunit BCL11B
IMPDH1	-0.89595	1.63E-05	0.00233	-4.30975	Down	inosine monophosphate dehydrogenase 1
ZBTB7B	-0.89564	1.11E-05	0.001787	-4.39371	Down	zinc finger and BTB domain containing 7B
UBA7	-0.89534	0.000336	0.014363	-3.58607	Down	ubiquitin like modifier activating enzyme 7
IL17RA	-0.89386	0.002731	0.045957	-2.99647	Down	interleukin 17 receptor A
ARHGAP45	-0.89323	1.19E-06	0.000443	-4.85691	Down	Rho GTPase activating protein 45
CBX6	-0.89155	7.04E-05	0.005444	-3.97496	Down	chromobox 6
FAM78A	-0.89123	6.04E-05	0.004955	-4.0111	Down	family with sequence similarity 78 member A
IL10RA	-0.89088	0.00059	0.020458	-3.43619	Down	interleukin 10 receptor subunit alpha
CCDC88B	-0.8901	0.000749	0.023336	-3.37094	Down	coiled-coil domain containing 88B
FGD2	-0.887	0.000318	0.013947	-3.60058	Down	FYVE, RhoGEF and PH domain containing 2
IL6R	-0.88694	0.002874	0.04719	-2.98092	Down	interleukin 6 receptor
TIMP1	-0.88474	0.002332	0.042463	-3.04433	Down	TIMP metalloproteinase inhibitor 1
CST3	-0.88244	4.94E-05	0.004447	-4.05853	Down	cystatin C
ARHGEF18	-0.88146	0.001	0.026845	-3.2906	Down	Rho/Rac guanine nucleotide exchange factor 18
SUSD3	-0.87991	0.002546	0.044513	-3.0178	Down	sushi domain containing 3
FPGT	-0.87627	0.001177	0.029554	-3.24451	Down	fucose-1-phosphate guanylyltransferase
TSPAN14	-0.87607	1.01E-06	0.000401	-4.88878	Down	tetraspanin 14
BCL3	-0.87565	0.000821	0.024176	-3.34553	Down	BCL3 transcription coactivator
CASP6	-0.87492	0.001961	0.039005	-3.0961	Down	caspase 6
TUBA4A	-0.87399	8.71E-05	0.006153	-3.92402	Down	tubulin alpha 4a
STON2	-0.87283	0.000357	0.014946	-3.57025	Down	stonin 2
GAS2L1	-0.8701	0.002448	0.043475	-3.02971	Down	growth arrest specific 2 like 1
PRAM1	-0.86941	0.000909	0.025759	-3.31732	Down	PML-RARA regulated adaptor molecule 1
DOCK8	-0.86409	3.44E-08	4.69E-05	-5.51723	Down	dedicator of cytokinesis 8
FAM117B	-0.86342	2.68E-05	0.003145	-4.19897	Down	family with sequence similarity 117 member B
GRAP2	-0.86129	0.001287	0.030786	-3.21895	Down	GRB2 related adaptor protein 2
C15orf39	-0.85788	8.10E-05	0.005983	-3.94135	Down	chromosome 15 open reading frame 39
DGKA	-0.85734	0.003058	0.048926	-2.96185	Down	diacylglycerol kinase alpha
ARHGEF1	-0.85684	4.39E-05	0.004178	-4.08616	Down	Rho guanine nucleotide exchange factor 1
RBM15	-0.85623	0.000861	0.02485	-3.33242	Down	RNA binding motif protein 15
EVL	-0.85591	2.24E-07	0.000137	-5.17847	Down	Enah/Vasp-like
ARL6IP5	-0.85568	0.000964	0.026542	-3.30096	Down	ADP ribosylation factor like GTPase 6 interacting protein 5
LRBA	-0.85445	0.000194	0.01064	-3.72615	Down	LPS responsive beige-like anchor protein
IL2RG	-0.85243	0.000449	0.017213	-3.50955	Down	interleukin 2 receptor subunit gamma
PACSIN2	-0.85239	1.42E-05	0.002103	-4.3404	Down	protein kinase C and casein kinase substrate in neurons 2
MGAT4B	-0.85231	0.000371	0.015208	-3.55994	Down	alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase B
TNFRSF1B	-0.85034	0.000653	0.021673	-3.40846	Down	TNF receptor superfamily member 1B

LIMD2	-0.84822	9.25E-06	0.001667	-4.4341	Down	LIM domain containing 2
FCMR	-0.84735	0.002891	0.047414	-2.97906	Down	Fc fragment of IgM receptor
MOB1B	-0.84594	0.001353	0.031558	-3.20455	Down	MOB kinase activator 1B
MEPCE	-0.84434	0.000598	0.020599	-3.4324	Down	methylphosphate capping enzyme
SERPINA1	-0.8439	9.42E-06	0.001685	-4.43015	Down	serpin family A member 1
PARVB	-0.84297	0.000128	0.007983	-3.83009	Down	parvin beta
CYTH4	-0.83743	0.000329	0.0142	-3.59133	Down	cytohesin 4
MINK1	-0.83717	1.35E-05	0.00202	-4.35162	Down	misshapen like kinase 1
CDK9	-0.83717	0.002799	0.046486	-2.98902	Down	cyclin dependent kinase 9
RNF166	-0.83615	7.52E-05	0.005661	-3.95934	Down	ring finger protein 166
BACH2	-0.83557	0.000479	0.017835	-3.49213	Down	BTB domain and CNC homolog 2
C16orf54	-0.83517	0.000303	0.013583	-3.61268	Down	chromosome 16 open reading frame 54
ST6GAL1	-0.83265	5.76E-06	0.001296	-4.53494	Down	ST6 beta-galactoside alpha-2,6-sialyltransferase 1
PIK3CD	-0.83256	2.41E-05	0.003076	-4.22314	Down	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit delta
CD84	-0.83207	0.000997	0.026839	-3.29142	Down	CD84 molecule
PIGS	-0.83204	0.00231	0.042348	-3.04724	Down	phosphatidylinositol glycan anchor biosynthesis class S
PAX5	-0.83198	0.002781	0.046321	-2.99094	Down	paired box 5
SLC12A6	-0.83191	0.000811	0.024176	-3.34888	Down	solute carrier family 12 member 6
TSC22D3	-0.83029	1.19E-05	0.001852	-4.37871	Down	TSC22 domain family member 3
PI4KA	-0.82863	2.97E-05	0.003326	-4.17553	Down	phosphatidylinositol 4-kinase alpha
SLC2A3	-0.82562	0.000214	0.011264	-3.70149	Down	solute carrier family 2 member 3
CDK2AP1	-0.82435	0.002237	0.041485	-3.05681	Down	cyclin dependent kinase 2 associated protein 1
RNF167	-0.82309	9.29E-05	0.006395	-3.90851	Down	ring finger protein 167
CXCR4	-0.82239	0.000939	0.026167	-3.30808	Down	C-X-C motif chemokine receptor 4
ITGAL	-0.82201	8.43E-05	0.006062	-3.9319	Down	integrin subunit alpha L
TESPA1	-0.82069	0.001242	0.030213	-3.229	Down	thymocyte expressed, positive selection associated 1
ZNF641	-0.8206	0.00135	0.031558	-3.20511	Down	zinc finger protein 641
AFF3	-0.82016	0.000985	0.026772	-3.2948	Down	AF4/FMR2 family member 3
MAP4K2	-0.82004	0.000221	0.011379	-3.69405	Down	mitogen-activated protein kinase kinase kinase kinase 2
RNPEPL1	-0.81798	3.53E-06	0.00094	-4.63733	Down	arginyl aminopeptidase like 1
TNRC18	-0.81713	0.001432	0.032712	-3.18818	Down	trinucleotide repeat containing 18
TMEM64	-0.81185	0.0011	0.028265	-3.26365	Down	transmembrane protein 64
CTTN	-0.81143	0.000508	0.018519	-3.4767	Down	cortactin
CD47	-0.81045	0.000471	0.017682	-3.49677	Down	CD47 molecule
ABI3	-0.80921	0.003	0.048449	-2.96775	Down	ABI family member 3
NUP188	-0.80778	0.0019	0.038276	-3.10549	Down	nucleoporin 188
DOK2	-0.80762	8.22E-05	0.00603	-3.93804	Down	docking protein 2
JADE2	-0.80698	9.22E-05	0.006385	-3.91037	Down	jade family PHD finger 2
APLP2	-0.80381	0.000383	0.015563	-3.55124	Down	amyloid beta precursor like protein 2
PRRC2B	-0.80096	4.09E-07	0.000205	-5.06466	Down	proline rich coiled-coil 2B
RNH1	-0.80085	0.000149	0.009015	-3.79346	Down	ribonuclease/angiogenin inhibitor 1
ITGAM	-0.79865	1.15E-05	0.001797	-4.38772	Down	integrin subunit alpha M
FBRSL1	-0.79664	0.00099	0.026772	-3.29346	Down	fibrosin like 1

DAD1	-0.7966	0.002406	0.043137	-3.03492	Down	defender against cell death 1
FTH1	-0.79596	0.002446	0.043475	-3.02996	Down	ferritin heavy chain 1
WAS	-0.79575	2.44E-05	0.003077	-4.22002	Down	WASP actin nucleation promoting factor
PKM	-0.79409	4.67E-05	0.004372	-4.07146	Down	pyruvate kinase M1/2
MICAL1	-0.79024	0.001644	0.035387	-3.14798	Down	microtubule associated monooxygenase, calponin and LIM domain containing 1
MED12	-0.78919	0.000644	0.021466	-3.41225	Down	mediator complex subunit 12
RASGRP2	-0.78853	3.55E-05	0.003732	-4.13517	Down	RAS guanyl releasing protein 2
CHST15	-0.78715	0.001528	0.033794	-3.16925	Down	carbohydrate sulfotransferase 15
ZNF407	-0.78667	0.00052	0.018756	-3.47011	Down	zinc finger protein 407
TTC7A	-0.78576	0.000256	0.012271	-3.65643	Down	tetratricopeptide repeat domain 7A
NKTR	-0.78507	0.002233	0.041471	-3.05737	Down	natural killer cell triggering receptor
RNF44	-0.78352	2.18E-06	0.000683	-4.73584	Down	ring finger protein 44
TNIK	-0.7832	4.96E-05	0.004447	-4.05744	Down	TRAF2 and NCK interacting kinase
ACTR8	-0.78285	0.001681	0.035795	-3.1415	Down	actin related protein 8
ITM2A	-0.78053	0.002761	0.046261	-2.9932	Down	integral membrane protein 2A
CD74	-0.78038	1.23E-06	0.000451	-4.85041	Down	CD74 molecule
TMEM159	-0.77781	0.002626	0.045057	-3.00842	Down	transmembrane protein 159
WDFY4	-0.77731	0.000189	0.010417	-3.73316	Down	WDFY family member 4
MINDY1	-0.77692	0.001399	0.032282	-3.19489	Down	MINDY lysine 48 deubiquitinase 1
SETD1B	-0.77688	0.001049	0.027588	-3.27716	Down	SET domain containing 1B, histone lysine methyltransferase
STRN4	-0.7768	0.00041	0.016205	-3.53368	Down	striatin 4
ARHGAP18	-0.77625	0.002128	0.040759	-3.07176	Down	Rho GTPase activating protein 18
CSF3R	-0.77608	5.45E-05	0.004668	-4.03564	Down	colony stimulating factor 3 receptor
MTHFR	-0.77535	0.002156	0.041002	-3.06789	Down	methylenetetrahydrofolate reductase
KLF2	-0.77468	1.76E-06	0.000606	-4.77956	Down	Kruppel like factor 2
MYO1G	-0.77353	0.000326	0.014131	-3.59398	Down	myosin IG
MBNL1	-0.77351	0.00024	0.01188	-3.67283	Down	muscleblind like splicing regulator 1
CHMP1A	-0.77317	0.002612	0.044998	-3.01007	Down	charged multivesicular body protein 1A
TMEM40	-0.77232	0.002399	0.043101	-3.03585	Down	transmembrane protein 40
TSC22D4	-0.77095	0.000528	0.018925	-3.46615	Down	TSC22 domain family member 4
VPS51	-0.77093	0.000908	0.025753	-3.3177	Down	VPS51 subunit of GARP complex
PRKCA	-0.77022	0.000918	0.025903	-3.31447	Down	protein kinase C alpha
FOXK1	-0.7701	6.94E-05	0.005383	-3.97838	Down	forkhead box K1
STXBP2	-0.76972	0.000203	0.010914	-3.7158	Down	syntaxin binding protein 2
MYADM	-0.76451	0.001184	0.029614	-3.24264	Down	myeloid associated differentiation marker
FBRS	-0.76411	1.24E-05	0.001918	-4.36972	Down	fibrosin
MRPL49	-0.7639	0.002087	0.040327	-3.07756	Down	mitochondrial ribosomal protein L49
VSIR	-0.76379	0.00045	0.017213	-3.50884	Down	V-set immunoregulatory receptor
RIC8A	-0.76185	0.00077	0.023545	-3.36328	Down	RIC8 guanine nucleotide exchange factor A
NCOR2	-0.75973	0.000223	0.011379	-3.6918	Down	nuclear receptor corepressor 2
RARA	-0.75606	0.000262	0.012485	-3.64997	Down	retinoic acid receptor alpha
DPYD	-0.75537	5.07E-05	0.004486	-4.05246	Down	dihydropyrimidine dehydrogenase

DMXL1	-0.75215	5.33E-06	0.001228	-4.55131	Down	Dmx like 1
PNISR	-0.75092	0.000348	0.014718	-3.57662	Down	PNN interacting serine and arginine rich protein
DGKD	-0.75064	6.00E-05	0.004932	-4.013	Down	diacylglycerol kinase delta
USP22	-0.75061	2.41E-08	4.04E-05	-5.57939	Down	ubiquitin specific peptidase 22
WDFY2	-0.74983	0.002146	0.0409	-3.06921	Down	WD repeat and FYVE domain containing 2
TBC1D10C	-0.7491	0.002373	0.042779	-3.03907	Down	TBC1 domain family member 10C
SH3BGR13	-0.7484	0.001537	0.033863	-3.16754	Down	SH3 domain binding glutamate rich protein like 3
CTDNEP1	-0.74753	0.000679	0.022149	-3.39777	Down	CTD nuclear envelope phosphatase 1
FAXDC2	-0.74702	0.000422	0.016539	-3.52616	Down	fatty acid hydroxylase domain containing 2
B4GALT1	-0.74485	0.000115	0.007342	-3.85717	Down	beta-1,4-galactosyltransferase 1
PLCB2	-0.74418	0.001646	0.035404	-3.14758	Down	phospholipase C beta 2
MIDEAS	-0.74414	3.63E-05	0.00378	-4.12956	Down	mitotic deacetylase associated SANT domain protein
AKNA	-0.74392	0.000222	0.011379	-3.693	Down	AT-hook transcription factor
CNDP2	-0.74239	0.000741	0.023226	-3.374	Down	carnosine dipeptidase 2
MDM4	-0.7411	7.01E-06	0.001447	-4.4934	Down	MDM4 regulator of p53
LGALS1	-0.73919	0.002938	0.047889	-2.97417	Down	galectin like
MAN2B1	-0.73902	0.001842	0.03779	-3.11459	Down	mannosidase alpha class 2B member 1
ATP2A2	-0.7385	0.000899	0.025541	-3.32034	Down	ATPase sarcoplasmic/endoplasmic reticulum Ca2+ transporting 2
DRAP1	-0.73622	0.002476	0.043726	-3.02631	Down	DR1 associated protein 1
MGLL	-0.73517	0.000524	0.018855	-3.46803	Down	monoglyceride lipase
CAD	-0.73466	0.003059	0.048926	-2.96174	Down	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase
CASP2	-0.73357	3.92E-05	0.003894	-4.11195	Down	caspase 2
ZMIZ1	-0.72916	1.07E-05	0.001778	-4.40181	Down	zinc finger MIZ-type containing 1
RIN3	-0.72851	4.25E-06	0.001071	-4.5987	Down	Ras and Rab interactor 3
USP39	-0.72837	0.000328	0.0142	-3.59223	Down	ubiquitin specific peptidase 39
STK10	-0.72431	2.47E-05	0.003077	-4.21788	Down	serine/threonine kinase 10
GUCY1A1	-0.724	0.003054	0.048926	-2.96223	Down	guanylate cyclase 1 soluble subunit alpha 1
YLPM1	-0.72338	0.000607	0.020764	-3.42834	Down	YLP motif containing 1
ARHGAP4	-0.72319	0.000404	0.016147	-3.53719	Down	Rho GTPase activating protein 4
LEF1	-0.72136	0.00139	0.032205	-3.19676	Down	lymphoid enhancer binding factor 1
CMTM6	-0.72086	0.002409	0.043137	-3.03453	Down	CKLF like MARVEL transmembrane domain containing 6
E2F3	-0.71983	0.001503	0.033554	-3.17415	Down	E2F transcription factor 3
WIPF1	-0.71966	5.60E-07	0.000259	-5.00459	Down	WAS/WASL interacting protein family member 1
CALM3	-0.71921	0.000348	0.014718	-3.57652	Down	calmodulin 3
RAB8A	-0.71773	0.001282	0.030728	-3.21993	Down	RAB8A, member RAS oncogene family
PLEK	-0.71655	4.74E-07	0.000224	-5.03635	Down	pleckstrin
SEPTIN9	-0.71354	3.22E-06	0.000876	-4.65642	Down	septin 9
RN7SK	-0.71244	0.002277	0.042026	-3.05157	Down	RNA component of 7SK nuclear ribonucleoprotein
IRAK3	-0.71152	7.53E-06	0.001488	-4.47822	Down	interleukin 1 receptor associated kinase 3
DOCK2	-0.70951	1.09E-05	0.001787	-4.39763	Down	dedicator of cytokinesis 2
SRRM2	-0.70753	8.83E-07	0.000367	-4.91617	Down	serine/arginine repetitive matrix 2
M6PR	-0.70709	0.00093	0.026107	-3.31085	Down	mannose-6-phosphate receptor, cation dependent

SCAF4	-0.70556	0.001328	0.031434	-3.20978	Down	SR-related CTD associated factor 4
MYO9B	-0.70522	0.000538	0.019202	-3.46104	Down	myosin IXB
DENND4C	-0.7041	6.85E-05	0.005343	-3.98142	Down	DENN domain containing 4C
KRAS	-0.70354	1.53E-05	0.002227	-4.32488	Down	KRAS proto-oncogene, GTPase
PTPN18	-0.70306	5.90E-05	0.004918	-4.01685	Down	protein tyrosine phosphatase non-receptor type 18
ATE1	-0.70243	0.00107	0.02782	-3.27142	Down	arginyltransferase 1
PREX1	-0.7024	0.000846	0.024636	-3.33725	Down	phosphatidylinositol-3,4,5-trisphosphate dependent Rac exchange factor 1
SLC44A2	-0.70141	0.001156	0.029251	-3.24948	Down	solute carrier family 44 member 2
CIC	-0.70058	0.002324	0.042463	-3.04542	Down	capicua transcriptional repressor
HDAC7	-0.6961	0.001403	0.032317	-3.19412	Down	histone deacetylase 7
PKN1	-0.6958	2.53E-05	0.003077	-4.21223	Down	protein kinase N1
SLC6A6	-0.69526	0.000535	0.019133	-3.46241	Down	solute carrier family 6 member 6
ACTB	-0.69456	0.000231	0.011467	-3.68263	Down	actin beta
WRNIP1	-0.69294	0.002658	0.045308	-3.0048	Down	WRN helicase interacting protein 1
G6PD	-0.69232	3.13E-05	0.003441	-4.16381	Down	glucose-6-phosphate dehydrogenase

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:0032501	BP	multicellular organismal process	3.03E-09	8.51786445	199	OPN1LW,NDP,HTN3,ADAM18,SERPINA10,SPATA22,LGR5,OCA2,CDH3,PAEP,SIX1,SLC34A2,DSG4,ASPA,SPATA16,GREM1,LRCOL1,TXNDC8,GLRA3,NEUROD4,MEI4,ESRP1,KRT85,EPHA3,PTN,CNGA1,CHRNA3,GHRHR,SHCBP1L,MYH4,MEIOC,GPR37L1,CYP26A1,CYP2J2,WDNR72,BNC1,AQP4,BMPRI1B,IMPG1,MYH8,KRT14,SLITRK6,VGLL2,RBM46,ROS1,EYA4,KCNH

6,SCN7A,GABRG1,SFT
PC,RIMS2,SCEL,MYO3
A,NLGN4X,LBP,DMRT
A1,MYF6,RP1,TEKT3,F
EZFI,SGCD,BRINP1,V
XN,GRHL2,SLC26A5,E
VC,POU3F3,WNT2,LVR
N,CBLN1,CLDN12,STM
ND1,LRFN5,GLP1R,SC
N11A,GABRP,SLC16A1
2,DRP2,GCM2,MC1R,S
LC1A1,CXCL14,FLG,R
GN,TRIM54,ID4,NPY2R
,SERPINB13,TRPM1,NE
UROG1,F9,ROBO2,GPC
6,WNT9A,GREM2,KCN
D2,PHLDA2,DACH2,PL
A2G2D,MFAP5,GABRB
1,AZGP1,SLC4A10,PTP
N3,HAS2,CTNNA2,IGS
F3,IGSF21,PCDHGA9,K
RT24,ANHX,KIT,IHO1,
ZNF750,CNTN5,CNTN4
,CFAP53,NKAPL,WNT5
A,ADGRF1,EDA,KCNA
1,TRIM71,TDRD6,SCN1
A,MROH2B,TBX18,HS
D11B2,SCN2A,TACC2,
KCNK1,ADGRV1,PTHL
H,CCNA1,COBL,ACVR
1C,FAP,CDH8,HUNK,G
DA,FERMT1,PCDHAC2
,DACT3,THSD7A,KRT8
0,DGKB,IRX2,ABCA4,S
TRC,PTH2R,POPDC2,A
DCY2,NEUROD1,SPIN
K5,KCNIP3,EFHD1,IL20
RA,CLDN1,MAL2,IZU
MO1,SHROOM3,SOHL
H1,DISP3,GABRB3,ETV
1,CYP24A1,TNR,ERRFI
1,PKHD1,KRT13,SLIT2,
MAST1,DTNA,ANTXR1
,ITGA8,GJC1,WNK3,PP

						ARGC1A,TRPM3,PAK3,IGF1,PRKN,OSR1,HRG,CYP46A1,TTC25,CDH6,FOLR2,INAVA,CSRP2,TRPV6,ATP1A4,TUFT1,TLR3,CIART,BMP7,GNAL,DSG2,POSTN
GO:0032502	BP	developmental process	0.000152082	3.817921215	158	NDP,HNF4G,HTN3,ADAM18,LGR5,OCA2,CDH3,PAEP,SIX1,SLC34A2,DSG4,ASPA,SPATA16,GREM1,TXNDC8,NEUROD4,MEI4,ESRP1,KRT85,EPHA3,PTN,GHRHR,SHCBP1L,MEIOC,GPOR37L1,CYP26A1,WDR72,BNC1,BMPR1B,KRT14,SLITRK6,VGLL2,RBM46,ROS1,EYA4,RIMS2,SCEL,MYO3A,NLGN4X,DMRTA1,MYF6,RP1,FEZF1,SGCD,BRINP1,VXN,GRHL2,SLC26A5,EVC,POU3F3,WNT2,CBLN1,STMND1,LRFN5,DRP2,GCM2,MC1R,SLC1A1,CXCL14,FLG,RGN,TRIM54,SHC4,ID4,NPY2R,SERPINB13,NEUROG1,ROBO2,GPC6,WNT9A,GREM2,PHLDA2,DACH2,PLA2G2D,MFAP5,GABRB1,SLC4A10,PTPN3,HAS2,CTNNA2,IGSF3,IGSF21,PCDHGA9,KRT24,ANH,KIT,IHO1,ZNF750,CNTN5,CNTN4,CFAP53,NKAPL,WNT5A,ADGRF1,EDA,KCNA1,VWDE,TRIM71,TDRD6,MROH2B,TBX18,SCN2A,TACC2,ADGRV1,PTHLH,CCNA1,COBL,AC

						VR1C,FAP,CDH8,HUN K,GDA,FERMT1,PCDH AC2,DACT3,THSD7A,K RT80,ERVFRD- 1,IRX2,STRC,POPDC2, NEUROD1,SPINK5,EFH D1,CLDN1,MAL2,SHR OOM3,SOHLH1,DISP3, GABRB3,ETV1,CYP24 A1,TNR,ERRFI1,PKHD1 ,KRT13,SLIT2,MAST1, ANTXR1,ITGA8,GJC1,P PARGC1A,PAK3,IGF1,P RKN,POU2F3,OSR1,HR G,CYP46A1,TTC25,CD H6,CSRP2,ATP1A4,TUF T1,TLR3,BMP7,DSG2,P OSTN
GO:0071944	CC	cell periphery	7.36876E -06	5.132605 428	159	OPN1LW,NDP,TMPRSS 11B,SLC15A1,LGR5,PL SCR2,CDH3,SLC34A2,D SG4,CPN2,GREM1,GLR A3,PCDHGB6,ART3,PC DHB7,ADAM7,EPHA3, SLC7A9,PTN,CEACAM 7,PLEKHN1,CNGA1,CH RNB3,GHRHR,LRR15, GPR37L1,AQP4,BMP1 B,IMPG1,KRT14,CLDN 2,SLITRK6,ROS1,KCNH 6,SCN7A,GABRG1,RIM S2,SCEL,ADAM30,GPR 151,NLGN4X,SLC9A2,S GCD,SLC5A12,VXN,XG ,GPR158,SLC26A5,EVC, WNT2,LVRN,KIR3DL1, CBLN1,SLC5A8,CLDN1 2,KCTD16,LRFN5,GLP1 R,SCN11A,GABRP,SLC 16A12,DRP2,MC1R,SLC 1A1,FLG,SHC4,MUC15, NPY2R,HPSE2,TRPM1, F9,ROBO2,GPC6,KCND

						2,MFAP5,GABRB1,AZG P1,SLC4A10,PTPN3,HA S2,CTNNA2,IGSF21,SL C5A4,PCDHGA9,KIT,T NFAIP8L3,CNTN5,PHK A1,GRIA4,CNTN4,PCD H11X,ENOX1,WNT5A, ADGRF1,EDA,KCNA1, COLEC12,SCN1A,ATP1 3A5,FRMPD1,SCN2A,L RP1B,TMC7,TACC2,KC NK1,ADGRV1,COBL,C A12,ACVR1C,FAP,CDH 8,FERMT1,PCDHAC2,T HSD7A,DGKB,ERVFRD - 1,ABCA4,PTH2R,TME M117,POPDC2,ADCY2, ANKS1B,SPINK5,KCNI P3,IL20RA,CLDN1,MA L2,IZUMO1,SHROOM3, SLC6A7,GABRB3,SLC7 A14,TNR,ERRFI1,PKHD 1,MAST1,DTNA,ANTX R1,ITGA8,KCNA7,GJC1 ,TRPM3,PAK3,IGF1,LR RC7,UNC80,POU2F3,H RG,CDH6,FOLR2,ARH GEF4,TRPV6,ATP1A4,T LR3,BMP7,GNAL,DSG2 ,POSTN,STOML1
GO:0031224	CC	intrinsic component of membrane	0.000494 326	3.305986 326	143	OPN1LW,CXORF66,TM PRSS11B,SLC15A1,AD AM18,LGR5,OCA2,PLS CR2,CDH3,SLC34A2,DS G4,LRRN4CL,GLRA3,P CDHGB6,FAM205C,AR T3,PCDHB7,MINAR2,A DAM7,EPHA3,SLC7A9, CEACAM7,CNGA1,CH RNB3,GHRHR,LRR15, GPR37L1,AQP4,BMP1 B,SYNPR,CLDN2,SLIT

RK6,ROS1,TECRL,KCN
H6,SCN7A,GABRG1,SF
TPC,ADAM30,GPR151,
NLGN4X,ASB5,TMEM1
39,SLC9A2,SGCD,ST8SI
A3,SLC5A12,TMEM31,
XG,GPR158,ARSJ,SLC2
6A5,EVC,LVRN,KIR3D
L1,SLC36A3,SLC5A8,C
LDN12,LRFN5,GLP1R,S
CN11A,GABRP,SLC16A
12,RDH16,MC1R,SLC1
A1,MUC15,NPY2R,SER
PINB13,TRPM1,CREB3
L3,ROBO2,GPC6,KCND
2,GABRB1,SLC4A10,H
AS2,IGSF3,IGSF1,IGSF2
1,SLC5A4,PCDHGA9,KI
T,SLC35F1,CNTN5,GRI
A4,CNTN4,PCDH11X,S
LC18A1,SVOP,ADGRF1
,EDA,KCNA1,COLEC12
,SCN1A,ATP13A5,HSD1
1B2,SCN2A,LRP1B,TM
C7,KCNK1,SHISAL2B,
ADGRV1,CA12,ACVR1
C,FAP,CDH8,PCDHAC2
,THSD7A,ERVFRD-
1,MROH7,ABCA4,PTH2
R,NXPE1,TMEM117,PO
PDC2,ADCY2,KCNIP3,I
L20RA,CLDN1,MAL2,I
ZUMO1,SLC6A7,DISP3,
FUT3,GABRB3,SLC7A1
4,PKHD1,ANTXR1,ITG
A8,KCNA7,GJC1,TRPM
3,UNC80,B3GNT4,CYP4
6A1,CDH6,FOLR2,TRP
V6,ATP1A4,TLR3,DSG2
,STOML1

GO:0005215	MF	transporter activity	2.49774E -06	5.602453 474	50	SLC15A1,OCA2,PLSCR 2,SLC34A2,GLRA3,SLC 7A9,CNGA1,CHRNA3,A
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						QP4,KCNH6,SCN7A,GABRG1,SLC9A2,SLC5A12,SLC26A5,SLC36A3,SLC5A8,SCN11A,GABRP,SLC16A12,SLC1A1,TRPM1,KCND2,GABRB1,AZGP1,SLC4A10,SLC5A4,SLC35F1,TNFAIP8L3,GRIA4,SLC18A1,SVOP,KCNA1,SCN1A,ATP13A5,SCN2A,TMC7,KCNK1,PEX5L,ABCA4,KCNIP3,SLC6A7,GABRB3,SLC7A14,KCNA7,GJC1,TRPM3,UNC80,TRPV6,ATP1A4
GO:0015267	MF	channel activity	2.08045E-05	4.681842376	27	GLRA3,CNGA1,CHRNB3,AQP4,KCNH6,SCN7A,GABRG1,SCN11A,GABRP,SLC1A1,TRPM1,KCND2,GABRB1,GRIA4,KCNA1,SCN1A,SCN2A,TMC7,KCNK1,PEX5L,KCNIP3,GABRB3,KCNA7,GJC1,TRPM3,UNC80,TRPV6

Down regulated genes

GO:0001775	BP	cell activation	4.37E-37	36.36000553	125	ITGA2B,ITGB3,MPL,ITGAX,MPIG6B,THBS1,FLNA,TRPC6,SELP,CD79A,HLA-A,VCL,PYGB,TLN1,P2RY1,FCRL1,GP5,TREML1,NOTCH2,F2RL3,MLEC,PSAP,ACAA1,PTPRJ,LRP1,BAX,P2RX1,CLU,FCN1,CDKN1A,NCSTN,SMAD3,GLIPR1,LFNG,CTSA,ITGB1,ANO6,CAPN1,BAK1,IGHM,MS4A1,FERMT3,TLR2,RNASET2,GPR183,TCIRG1,H
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						LA- E,ADA2,PTPRC,PEAR1, NBEAL2,MYH9,TGFB1, ITGA4,SLA2,DTX1,CA RD11,JAK3,BTLA,SRC, GP9,APP,TMEM63A,UN C13D,POU2F2,ALOX12, TMC6,RAB5C,ITPR1,LI LRB2,GPR137B,PDGFA ,ITGB2,SELPLG,TNFSF 4,RAB37,SPN,BCL11B,I MPDH1,ZBTB7B,IL17R A,ARHGAP45,CCDC88 B,IL6R,TIMP1,CST3,TS PAN14,BCL3,PRAM1,D OCK8,GRAP2,DGKA,T NFRSF1B,SERPINA1,PI K3CD,CD84,SLC2A3,IT GAL,TESPA1,CD47,ITG AM,FTH1,WAS,PKM,IT M2A,CD74,WDFY4,PR KCA,STXBP2,VSIR,RA RA,DGKD,TBC1D10C,B 4GALT1,MAN2B1,ZMI Z1,STK10,LEF1,CMTM 6,PLEK,DOCK2,PREX1, SLC44A2,PKN1,ACTB
GO:0002376	BP	immune system process	1.77E-19	18.75194 365	159	LTA,CXCL5,ITGA2B,IT GB3,MPL,TMEM178A,I TGAX,MPIG6B,THBS1, FLNA,SELP,CD79A,CS F1R,XKR8,HLA- A,VCL,PYGB,FCRL1,T REML1,CYBC1,NOTCH 2,MLEC,PSAP,CD300E, TLR5,ACAA1,PTPRJ,LR P1,BAX,P2RX1,CLU,CII TA,FCN1,ITGB5,PRKA R2B,ITGA2,CDKN1A,A DCY7,TKFC,MPEG1,N CSTN,IRF7,SMAD3,CT SW,GLIPR1,LFNG,CTS A,ITGB1,RHBDF2,ANO

6,CAPN1,BAK1,IGHM,
NOTCH1,MS4A1,TLR2,
RNASET2,GPR183,TCI
RG1,HLA-
E,ADA2,PTPRC,CBFA2
T3,NBEAL2,ACTN1,MY
H9,TGFB1,ITGA4,SLA2
,DTX1,CARD11,JAK3,B
TLA,SRC,APP,TMEM63
A,UNC13D,POU2F2,TM
C6,RAB5C,ZYX,CMTM
3,LILRB2,GPR137B,ITG
B2,SELPLG,TRIM13,TN
FSF4,RAB37,SPN,BCL1
1B,IMPDH1,ZBTB7B,IL
17RA,ARHGAP45,CCD
C88B,IL6R,CST3,TSPA
N14,BCL3,PRAM1,DOC
K8,GRAP2,RBM15,IL2R
G,TNFRSF1B,FCMR,SE
RPINA1,RNF166,BACH
2,ST6GAL1,PIK3CD,CD
84,PAX5,TSC22D3,SLC
2A3,CXCR4,ITGAL,TES
PA1,MAP4K2,TMEM64,
CD47,DOK2,ITGAM,FT
H1,WAS,PKM,RASGRP
2,TTC7A,ITM2A,CD74,
WDFY4,CSF3R,KLF2,M
YO1G,PRKCA,STXBP2,
VSIR,RARA,TBC1D10C
,FAXDC2,B4GALT1,M
AN2B1,ZMIZ1,RIN3,ST
K10,LEF1,CMTM6,WIP
F1,PLEK,IRAK3,DOCK
2,KRAS,PREX1,SLC44A
2,PKN1,ACTB,WRNIP1,
G6PD

GO:0012505	CC	endomemb rane system	3.56E-16	15.44824 976	183	ITGA2B,LGALS3BP,IT GB3,MPL,TMEM178A,I TGAX,F13A1,POMK,M PIG6B,THBS1,FLNA,AT P2A3,BSCL2,SELP,LMF
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2,CD79A,RAB27B,NUP
210,HLA-
A,VCL,PYGB,VCAN,TR
EML1,CYBC1,NOTCH2,
MLEC,PSAP,CHST12,A
CAA1,ABCA7,PTPRJ,L
RP1,BAX,SUN2,P2RX1,
SPARC,CLU,TBXA2R,F
CN1,PPM1L,PANX1,NR
GN,RAB1B,NCSTN,IRF
7,CHERP,SMAD3,CTS
W,GLIPR1,LFNG,TME
M259,CTSA,ITGB1,TCL
1A,RHBDF2,DENND4B,
ANO6,VPS52,CAPN1,B
AK1,NOTCH1,SRPRA,F
ERMT3,TLR2,RNASET
2,TCIRG1,ESYT1,HLA-
E,TPP1,MMD,ADA2,LE
PROT,LHFPL2,PTPRC,
CBFA2T3,SH3BGRL2,N
BEAL2,ACTN1,GALNT
10,MYH9,CHPF2,TGFB
1,SLC35E2B,SLA2,PITP
NM2,EHD3,JAK3,ITM2
B,SRC,DSE,APP,PCSK6,
FGD3,TMEM63A,UNC1
3D,TGOLN2,TMC6,STI
M1,RAB5C,CMTM3,CN
ST,ITPR1,GANAB,LDL
RAP1,LILRB2,EPM2AIP
1,SELENON,RUFY1,PD
GFA,ITGB2,ATP9A,TRI
M13,VPS37B,GDI1,RAB
37,IMPDH1,ARHGAP45
,CCDC88B,FGD2,TIMP1
,CST3,TSPAN14,STON2
,GRAP2,RBM15,ARL6IP
5,LRBA,IL2RG,PACSIN
2,MGAT4B,TNFRSF1B,
SERPINA1,CYTH4,MIN
K1,ST6GAL1,PIGS,SLC
2A3,RNF167,CXCR4,IT
GAL,TESPA1,MAP4K2,

						TNRC18,TMEM64,CTT N,CD47,NUP188,APLP2 ,ITGAM,DAD1,FTH1,P KM,CHST15,TNIK,ITM 2A,CD74,TMEM159,WD FY4,CHMP1A,VPS51,P RKCA,STXBP2,DGKD, WDFY2,TBC1D10C,CT DNEP1,FAXDC2,B4GA LT1,MAN2B1,ATP2A2, MGLL,RIN3,STK10,AR HGAP4,CMTM6,CALM 3,RAB8A,DOCK2,M6PR ,DENND4C,KRAS,SLC4 4A2,PKN1
GO:0005737	CC	cytoplasm	3.30E-10	9.481080 396	328	COX4I2,ITGA2B,TMEM 70,TMEM150A,LGALS3 BP,ITGB3,CCDC28B,SP SB2,MPL,EXO5,TMEM 178A,ITGAX,F13A1,PO MK,MPIG6B,THBS1,FL NA,ACAD10,TUBB1,AT P2A3,BSCL2,ARHGAP2 7,TRPC6,SELP,LMF2,C D79A,MEMO1,RAB27B, MAP3K7CL,NUP210,HL A- A,VCL,PYGB,ZNF185,T LN1,ATG16L2,P2RY1,V CAN,TREML1,ENDOD1 ,CYBC1,NOTCH2,MLE C,LIPA,PSAP,CHST12,L IMS1,MYBBP1A,ACAA 1,ABCA7,ELAC2,CAVI N2,PTPRJ,LRP1,BAX,S UN2,P2RX1,DENND1C, PYCR2,SMCR8,ENO2,S PARC,CLU,TBXA2R,LR RC25,CITTA,FCN1,ITGB 5,PRKAR2B,ITGA2,PP M1L,CDKN1A,TKFC,Z C3HAV1L,MPEG1,PAN X1,NRGN,RAB1B,PDE5

A,CLPP,NCSTN,IRF7,C
 HERP,SMAD3,CTSW,G
 LIPR1,CMIP,LFNG,TM
 EM259,MFAP3L,CTSA,I
 TGB1,TCL1A,RHBDF2,
 MRPL28,DENND4B,AN
 O6,SIDT2,VPS52,CAPN
 1,BAK1,NOTCH1,PLEC,
 SRPRA,FERMT3,TLR2,
 RNASET2,DNAH1,TCI
 RG1,ESYT1,HLA-
 E,TPP1,C1ORF198,MM
 D,ARHGAP6,INF2,ADA
 2,LEPROT,LHFPL2,PTP
 RC,SH3BP1,CBFA2T3,N
 BEAL2,USP20,ACTN1,
 GALNT10,MYH9,EML3
 ,CHPF2,OGT,TGFB1,SL
 C35E2B,SLA2,PITPNM2
 ,DTX1,CARD11,MADD,
 MRTFA,EHD3,JAK3,SM
 G5,ITM2B,SRC,DSE,AP
 P,PCSK6,FGD3,TMEM6
 3A,UNC13D,POU2F2,T
 GOLN2,ALOX12,FHOD
 1,TMC6,MAP1A,STIM1,
 FTSJ1,RAB5C,ZYX,GU
 CY1B1,CMTM3,CNST,I
 TPR1,GANAB,LDLRAP
 1,RNF213,MYLK,CENP
 T,LILRB2,TYMP,EPM2
 AIP1,SELENON,RUFY1
 ,GNB5,PRUNE1,HELZ2,
 GPR137B,MTPN,PDGF
 A,ITGB2,ATP9A,DAPP1
 ,CORO1B,TRIM13,SIN3
 B,VPS37B,UPF1,GDI1,P
 GAP6,DIMT1,RAB37,I
 MPDH1,UBA7,ARHGA
 P45,IL10RA,CCDC88B,
 FGD2,TIMP1,CST3,AR
 HGEF18,FPGT,TSPAN1
 4,BCL3,CASP6,TUBA4
 A,STON2,GAS2L1,DOC

K8,GRAP2,C15ORF39,D
GKA,ARHGEF1,EVL,A
RL6IP5,LRBA,IL2RG,P
ACSIN2,MGAT4B,TNF
RSF1B,LIMD2,MOB1B,
SERPINA1,PARVB,CYT
H4,MINK1,CDK9,RNF1
66,BACH2,ST6GAL1,PI
K3CD,PIGS,PAX5,TSC2
2D3,PI4KA,SLC2A3,CD
K2AP1,RNF167,CXCR4,
ITGAL,TESPA1,ZNF641
,AFF3,MAP4K2,TNRC1
8,TMEM64,CTTN,CD47,
ABI3,NUP188,DOK2,AP
LP2,RNH1,ITGAM,DAD
1,FTH1,WAS,PKM,MIC
AL1,RASGRP2,CHST15,
TTC7A,NKTR,TNIK,IT
M2A,CD74,TMEM159,
WDFY4,MINDY1,STRN
4,ARHGAP18,MTHFR,
MYO1G,MBNL1,CHMP
1A,VPS51,PRKCA,FOX
K1,STXBP2,MYADM,M
RPL49,RIC8A,RARA,DP
YD,DMXL1,PNISR,DG
KD,WDFY2,TBC1D10C,
SH3BGRL3,CTDNEP1,F
AXDC2,B4GALT1,PLC
B2,AKNA,CNDP2,MAN
2B1,ATP2A2,MGLL,CA
D,CASP2,ZMIZ1,RIN3,S
TK10,GUCY1A1,YLPM
1,ARHGAP4,LEF1,CMT
M6,WIPF1,CALM3,RAB
8A,PLEK,SEPTIN9,IRA
K3,DOCK2,M6PR,MYO
9B,DENND4C,KRAS,PT
PN18,ATE1,PREX1,SLC
44A2,HDAC7,PKN1,AC
TB,WRNIP1,G6PD

GO:0019899 MF enzyme 2.39E-07 6.621960 90 ITGB3,UBOX5,ITGAX,

		binding		344		FLNA,TRPC6,CSF1R,V CL,NOTCH2,MLEC,PS AP,LIMS1,CAVIN2,PTP RJ,LRP1,SMCR8,CLU,N FRKB,PRKAR2B,CDKN 1A,PANX1,CLPP,NCST N,SMAD3,ITGB1,TCL1 A,PIK3IP1,NOTCH1,TCI RG1,ARHGAP6,INF2,PT PRC,NBEAL2,PITPNM2 ,DTX1,JAK3,SMG5,SRC ,APP,FGD3,UNC13D,ST IM1,CNST,SCAF1,LILR B2,ITGB2,ATP9A,GDI1, ZBTB7B,FGD2,IL6R,TI MP1,CST3,TSPAN14,TU BA4A,PRAM1,LRBA,T NFRSF1B,MOB1B,SER PINA1,CDK9,SLC12A6, CDK2AP1,CXCR4,MAP 4K2,DOK2,WAS,MICA L1,CD74,STRN4,PRKC A,VSIR,NCOR2,RARA, DGKD,USP22,MDM4,A TP2A2,CAD,CASP2,RIN 3,LEF1,CALM3,RAB8A, PLEK,SCAF4,MYO9B,P REX1,HDAC7,PKN1,AC TB
GO:0005515	MF	protein binding	0.000108 112	3.966126 242	370	LTA,CCDC24,CXCL5,IT GA2B,TMEM70,TMEM 150A,LGALS3BP,ITGB3 ,CCDC28B,CNNM4,SPS B2,SEC14L5,PLXNB2,M PL,UBOX5,ITGAX,F13 A1,POMK,MPIG6B,THB S1,FLNA,ATP2A3,BSCL 2,ARHGAP27,TRPC6,SE LP,LMF2,CD79A,CSF1R ,MEMO1,RAB27B,MAP 3K7CL,ZNF296,HLA- A,VCL,PYGB,ZNF185,T LN1,ATG16L2,P2RY1,V

CAN,GP5,TREML1,EN
DOD1,SF3A2,CYBC1,N
OTCH2,MLEC,PSAP,FA
M185A,CD300E,LIMS1,
MYBBP1A,TLR5,ACAA
1,CAVIN2,PTPRJ,MYC
L,LRP1,BAX,SUN2,P2R
X1,DENND1C,PYCR2,S
MCR8,ENO2,SPARC,T
MEM140,CLU,TBXA2R,
LRRC25,CIITA,FCN1,N
FRKB,ITGB5,PRKAR2B
,ITGA2,CDKN1A,CCNL
1,MAP4K1,TKFC,PANX
1,NRGN,RAB1B,PDE5A
,CLPP,NCSTN,IRF7,CH
ERP,SMAD3,GLIPR1,NI
BAN3,C2ORF88,CMIP,
MFAP3L,KDM2B,CMT
M5,ITGB1,TCL1A,RHB
DF2,MRPL28,DENND4
B,PIK3IP1,ANO6,VPS52
,CAPN1,BAK1,IGHM,P
OLR1A,NOTCH1,MS4A
1,PLEC,FERMT3,TLR2,
GSE1,DNAH1,TCIRG1,
PLXDC2,ESYT1,GIGYF
1,HLA-
E,TPP1,LENG8,MMD,A
RHGAP6,INF2,ADA2,L
EPROT,LHFPL2,RSRP1,
PTPRC,PEAR1,SH3BP1,
CBFA2T3,SH3BGRL2,N
BEAL2,USP20,ACTN1,
GALNT10,MYH9,EML3
,OGT,TGFB1,ITGA4,SL
A2,PITPNM2,DTX1,CA
RD11,MADD,KCNA3,M
RTFA,EHD3,JAK3,SMG
5,BTLA,ITM2B,SRC,GP
9,APP,PCSK6,FGD3,TM
EM63A,UNC13D,POU2
F2,TGOLN2,ALOX12,F
HOD1,TMC6,MAP1A,S

TIM1,CTDSPL,NHSL2,F
 TSJ1,RAB5C,ZYX,GUC
 Y1B1,CMTM3,CNST,IT
 PR1,GANAB,LDLRAP1,
 CCNL2,SCAF1,MYLK,C
 ENPT,ARL15,SRSF6,LI
 LRB2,TYMP,EPM2AIP1
 ,SELENON,SNRPA,RUF
 Y1,GNB5,PRUNE1,HEL
 Z2,GPR137B,MBD6,MT
 PN,PDGFA,ITGB2,SELP
 LG,ATP9A,DAPP1,COR
 O1B,TRIM13,SIN3B,VP
 S37B,UPF1,GDI1,TNFS
 F4,PGAP6,RPA1,RAB37
 ,SPN,BCL11B,IMPDH1,
 ZBTB7B,UBA7,IL17RA,
 ARHGAP45,CBX6,FAM
 78A,IL10RA,CCDC88B,
 FGD2,IL6R,TIMP1,CST
 3,ARHGEF18,SUSD3,TS
 PAN14,BCL3,CASP6,TU
 BA4A,STON2,GAS2L1,
 PRAM1,DOCK8,FAM11
 7B,GRAP2,ARHGEF1,R
 BM15,EVL,ARL6IP5,LR
 BA,IL2RG,PACSIN2,M
 GAT4B,TNFRSF1B,LIM
 D2,MOB1B,MEPCE,SE
 RPINA1,PARVB,CYTH
 4,MINK1,CDK9,RNF166
 ,BACH2,C16ORF54,ST6
 GAL1,PIK3CD,CD84,PI
 GS,PAX5,SLC12A6,TSC
 22D3,PI4KA,SLC2A3,C
 DK2AP1,RNF167,CXCR
 4,ITGAL,TESPA1,MAP4
 K2,CTTN,CD47,ABI3,D
 OK2,JADE2,APLP2,PRR
 C2B,RNH1,ITGAM,FTH
 1,WAS,PKM,MICAL1,M
 ED12,CHST15,TTC7A,R
 NF44,TNIK,ACTR8,ITM
 2A,CD74,TMEM159,WD

FY4,MINDY1,SETD1B,
STRN4,ARHGAP18,CSF
3R,KLF2,MYO1G,MBN
L1,CHMP1A,TSC22D4,
VPS51,PRKCA,FOXK1,
STXBP2,MYADM,MRP
L49,VSIR,RIC8A,NCOR
2,RARA,DPYD,DMXL1,
DGKD,USP22,WDFY2,T
BC1D10C,SH3BGRL3,C
TDNEP1,FAXDC2,B4G
ALT1,PLCB2,AKNA,M
DM4,LGALSL,ATP2A2,
DRAP1,MGLL,CAD,CA
SP2,ZMIZ1,RIN3,USP39
,STK10,GUCY1A1,YLP
M1,ARHGAP4,LEF1,C
MTM6,E2F3,WIPF1,CA
LM3,RAB8A,PLEK,SEP
TIN9,IRAK3,DOCK2,SR
RM2,M6PR,SCAF4,MY
O9B,DENND4C,KRAS,P
TPN18,ATE1,PREX1,CI
C,HDAC7,PKN1,ACTB,
WRNIP1,G6PD

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-6809371	Formation of the cornified envelope	0.017403 093	1.759373 564	10	LIPJ,DSG4,KRT85,KRT14,FLG,KRT24,KRT80,S PINK5,KRT13,DSG2
REAC:R-HSA-421270	Cell-cell junction organization	0.057968 43	1.236808 462	6	CDH3,CLDN2,CLDN12, CDH8,CLDN1,CDH6

REAC:R-HSA-373080	Class B/2 (Secretin family receptors)	0.057968 43	1.236808 462	7	GHRHR,WNT2,GLP1R,WNT9A,WNT5A,PTHLH,PTH2R
REAC:R-HSA-112316	Neuronal System	0.057968 43	1.236808 462	16	GLRA3,CHRNA3,SLITRK6,KCNH6,NLGN4X,SLC1A1,KCND2,GABRB1,GRIA4,KCNA1,KCNK1,ADCY2,GABRB3,KCNA7,GJC1,GNAL
REAC:R-HSA-5576891	Cardiac conduction	0.058865 891	1.230136 275	8	SCN7A,SCN11A,KCND2,SCN1A,SCN2A,KCNK1,KCNIP3,ATP1A4
REAC:R-HSA-382551	Transport of small molecules	0.058865 891	1.230136 275	23	SLC15A1,SLC34A2,SLC7A9,AQP4,SLC9A2,SLC5A12,SLC5A8,SLC1A1,TRPM1,CREB3L3,AZGP1,SLC4A10,SLC5A4,SLC18A1,ATP13A5,ABCA4,ADCY2,SLC6A7,WNK3,TRPM3,UNC80,TRPV6,ATP1A4

Down regulated genes

REAC:R-HSA-109582	Hemostasis	9.54E-20	19.02047 251	69	ITGA2B,LGALS3BP,ITGB3,MPL,ITGAX,F13A1,MPIG6B,THBS1,FLNA,TUBB1,ATP2A3,TRPC6,SELP,RAB27B,VCL,TLN1,P2RY1,GP5,ENDO1,F2RL3,PSAP,P2RX1,SPARC,CLU,TBXA2R,PRKAR2B,ITGA2,PDE5A,CTSW,ITGB1,IGHM,FERMT3,LHFPL2,ACTN1,ITGA4,EHD3,SRC,GP9,APP,STIM1,GUCY1B1,ITPR1,GNB5,ITGB2,SELPLG,SPN,TIMP1,TUBA4A,DOCK8,DGKA,SERPINA1,CD84,ITGAL,CD47,DOK2,APLP2,ITG
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					AM,MICAL1,RASGRP2,CD74,PRKCA,STXBP2,DGKD,ATP2A2,MGLL,GUCY1A1,PLEK,DOCK2,ACTB
REAC:R-HSA-6798695	Neutrophil degranulation	6.68E-12	11.17530495	46	ITGAX,VCL,PYGB,MLEC,PSAP,ACAA1,PTPRJ,P2RX1,FCN1,NCSTN,GLIPR1,CTSA,ANO6,CAPN1,TLR2,RNASET2,TCIRG1,ADA2,PTPRC,NBEAL2,TMEM63A,UNC13D,TMC6,RAB5C,LILRB2,ITGB2,RAB37,IMPDH1,ARHGAP45,CST3,TSPAN14,TNFRSF1B,SERPINA1,SLC2A3,ITGAL,CD47,ITGAM,FTH1,PKM,TBC1D10C,B4GALT1,MAN2B1,STK10,CDMTM6,DOCK2,SLC44A2
REAC:R-HSA-168256	Immune System	1.38E-09	8.861116751	104	LTA,SPSB2,UBOX5,ITGAX,F13A1,FLNA,TUBB1,CD79A,CSF1R,NUP210,HLA-A,VCL,PYGB,TREML1,MLEC,PSAP,CD300E,TLR5,ACAA1,PTPRJ,P2RX1,CLU,CIITA,FCN1,ITGB5,CDKN1A,TKFC,PANX1,NCSTN,IRF7,SMAAD3,GLIPR1,CTSA,ITGB1,ANO6,CAPN1,IGHM,TLR2,RNASET2,TCIRG1,HLA-E,ADA2,PTPRC,NBEAL2,MYH9,ITGA4,SLA2,CARD11,JAK3,BTLA,APP,TMEM63A,UNC13D,TMC6,STIM1,RAB5C,ITPR1,RNF213,LILRB2,ITGB2,DAPPI,TNFSF4,RAB

					37,IMPDH1,UBA7,IL17 RA,ARHGAP45,IL10RA ,IL6R,TIMP1,CST3,TSP AN14,TUBA4A,GRAP2, EVL,IL2RG,TNFRSF1B, SERPINA1,PIK3CD,SLC 2A3,ITGAL,CD47,NUP1 88,ITGAM,FTH1,WAS,P KM,RASGRP2,CD74,CS F3R,STXBP2,TBC1D10 C,B4GALT1,MAN2B1, CASP2, STK10,CMTM6,WIPF1,I RAK3,DOCK2,MYO9B, PTPN18,SLC44A2,ACT B
REAC:R-HSA- 1912420	Pre-NOTCH Processing in Golgi	0.000492 38	3.307699 894	6	ATP2A3,NOTCH2,LFN G,NOTCH1,B4GALT1,A TP2A2
REAC:R-HSA- 194315	Signaling by Rho GTPases	0.011456 442	1.940950 253	26	FLNA,TUBB1,ARHGAP 27,ITGB1,ARHGAP6,M YH9,MRTFA,FGD3,MY LK,CENPT,ARHGAP45, FGD2,ARHGEF18,TUB A4A,ARHGEF1,EVL,CT TN,WAS,ARHGAP18,P RKCA,ARHGAP4,WIPF 1,MYO9B,PREX1,PKN1 ,ACTB
REAC:R-HSA- 1280215	Cytokine Signaling in Immune system	0.017394 819	1.759580 073	34	LTA,ITGAX,F13A1,FLN A,CSF1R,NUP210,HLA- A,PTPRJ,CIITA,CDKN1 A,IRF7,SMAD3,ITGB1, HLA- E,SLA2,JAK3,APP,ITGB 2,TNFSF4,UBA7,IL17R A,IL10RA,IL6R,TIMP1, GRAP2,IL2RG,TNFRSF 1B,PIK3CD,NUP188,IT GAM,CSF3R,STXBP2,I RAK3,PTPN18

Table 4 Topology table for up and down regulated genes.

Regulation	Node	Degree	Betweenness	Stress	Closeness
Up	TRIM54	133	0.012147	21844832	0.322581
Up	ELAVL2	118	0.009706	13548160	0.323122
Up	PTN	109	0.008667	10295782	0.325332
Up	KIT	105	0.005763	7684058	0.332132
Up	BMPRI1B	102	0.012139	7911102	0.352362
Up	ERRFI1	99	0.008331	11254818	0.338466
Up	CCNE1	86	0.003025	5367340	0.330825
Up	CCNA1	83	0.004101	5615582	0.34443
Up	GLP1R	78	0.010843	23727352	0.299903
Up	EDA	74	0.008686	5992546	0.315667
Up	PPARGC1A	72	0.002826	4898866	0.322485
Up	KRT13	70	0.004347	10153884	0.31577
Up	SLC15A1	64	0.00578	5083164	0.301448
Up	ANTXR1	59	0.006338	4754724	0.364739
Up	ZBTB8A	59	0.00408	8024144	0.307376
Up	KRT14	57	0.001607	3870640	0.322978
Up	NPY2R	57	0.004358	4577120	0.302607
Up	SLC18A1	56	0.005946	4356010	0.306766
Up	LRRC15	54	0.005085	12368332	0.298816
Up	PTPN3	53	0.00338	4379752	0.322377
Up	TMPRSS11B	53	0.005232	13231264	0.28515
Up	TUFT1	50	0.002391	2006556	0.308054
Up	BMP7	48	0.004125	3406724	0.310316

Up	MIPOL1	47	0.003199	7831728	0.296433
Up	DSG2	43	0.00103	1538692	0.326669
Up	MAGEA10	42	0.002659	2782598	0.311971
Up	TLR3	41	0.002523	2126014	0.311365
Up	MAST1	41	0.002679	1449942	0.345502
Up	F9	40	0.003205	3436702	0.301448
Up	DTNA	39	0.003643	2835460	0.311825
Up	DSG4	39	0.002547	6333108	0.286045
Up	LIN28B	38	0.002233	2392960	0.306429
Up	EPHA3	38	0.003012	1844952	0.317553
Up	GDA	38	0.002698	4154080	0.301995
Up	IL20RA	37	0.003001	2163774	0.306885
Up	EYA4	36	0.002123	2202158	0.300142
Up	CCL22	35	0.003053	4599286	0.300548
Up	SLC1A1	35	0.004187	3161236	0.346317
Up	PCDHAC2	35	0.004863	3849886	0.292706
Up	IGSF21	34	0.002215	2796766	0.296119
Up	SH3RF2	34	0.001943	1330190	0.342509
Up	USP43	34	0.00183	2158278	0.305694
Up	COBL	33	7.34E-04	789636	0.331775
Up	FLG	33	0.001565	2103066	0.312027
Up	SERPINB13	33	0.002022	2211972	0.303009
Up	COLEC12	32	0.002562	1515874	0.335126
Up	GFPT2	30	0.002137	2091622	0.31094
Up	SFTPC	30	0.002498	2902984	0.304276
Up	LRP1B	29	0.003228	1563906	0.344553

Up	AZGP1	29	0.001511	2326868	0.30975
Up	ETV1	28	6.64E-04	1570448	0.306701
Up	CPA4	27	0.001782	1645444	0.303476
Up	KLK11	27	0.002312	3332010	0.2924
Up	CTNNA2	27	0.001317	2711166	0.312714
Up	WNT5A	27	0.002257	1865676	0.296525
Up	KRT85	27	0.001319	2630340	0.305975
Up	FAP	27	0.001924	3392714	0.291986
Up	ROBO2	26	0.001435	2365116	0.291651
Up	KCNIP3	26	0.001472	3374664	0.28202
Up	BRINP1	25	0.0012	2988948	0.301301
Up	NCCRP1	25	8.25E-04	1228816	0.315173
Up	ART3	24	0.001611	3187858	0.283016
Up	INAVA	24	0.00154	1886482	0.291278
Up	CREB3L3	24	0.001636	2012464	0.302332
Up	SLIT2	23	0.001176	1918318	0.301259
Up	POPDC2	23	0.002173	1488558	0.271797
Up	IZUMO1	23	0.002732	4118726	0.259647
Up	MAL2	23	0.001473	2898432	0.296261
Up	RGPD8	22	0.001517	1034252	0.305586
Up	PAEP	22	0.001035	874582	0.343828
Up	ASB5	22	4.24E-04	368080	0.303583
Up	FAM83B	22	8.25E-04	1549462	0.305166
Up	SLC5A8	22	0.001364	1608962	0.276598
Up	SIX1	21	0.00131	1136652	0.295735
Up	KCND2	21	0.002331	1658754	0.303956

Up	MYH4	21	9.70E-04	980960	0.299623
Up	NEUROD1	21	0.001441	2678376	0.287985
Up	PAK3	20	6.35E-05	179392	0.297748
Up	TACC2	20	0.001037	1183890	0.309374
Up	TTC25	20	0.001315	2071982	0.276139
Up	LBP	19	0.001144	837746	0.309917
Up	HRG	19	8.05E-04	1333666	0.292607
Up	CDC20B	19	0.001052	1653682	0.279211
Up	TNR	19	0.001002	1524772	0.286092
Up	SHROOM3	18	6.22E-04	712586	0.316393
Up	PHKA1	18	8.26E-04	664362	0.301763
Up	RIMS2	18	8.17E-04	1001820	0.305575
Up	CSRP2	18	2.40E-04	457510	0.304983
Up	KRT24	18	2.78E-05	166448	0.30059
Up	LRRC7	18	6.50E-04	1043008	0.299085
Up	ITGA8	17	0.001062	974108	0.291524
Up	SIGLEC5	17	0.001041	718852	0.290351
Up	CLDN1	17	7.91E-04	1036670	0.284009
Up	IGF1	17	0.001485	2375614	0.275937
Up	MYF6	17	3.75E-04	472100	0.284503
Up	CDH8	17	7.20E-04	923698	0.293351
Up	TRIM71	17	9.54E-04	1482892	0.250325
Up	ESRP1	16	9.05E-04	638852	0.286983
Up	GPC6	16	0.001651	1480508	0.325674
Up	CPEB1	16	0.001555	915000	0.327906
Up	GRIA4	16	3.00E-04	243164	0.303519

Up	ID4	16	9.00E-04	532420	0.307977
Up	TRPV6	16	6.17E-04	609086	0.281005
Up	GJC1	16	0.001409	1565962	0.27087
Up	FERMT1	16	4.60E-04	808642	0.300267
Up	EFHD1	16	9.97E-04	2285970	0.281553
Up	ZMAT4	15	0.00194	2108242	0.331141
Up	FUT3	15	0.001643	1729770	0.26295
Up	KIR3DL1	15	6.23E-04	1269024	0.278188
Up	MC1R	15	0.001048	1221034	0.282739
Up	BNIP1	15	9.69E-04	1242002	0.277315
Up	PHYHIP1	15	4.86E-04	372398	0.288465
Up	PCDHB7	15	0.00158	1015798	0.272361
Up	IGSF1	14	7.87E-04	482056	0.268635
Up	ST8SIA3	14	8.32E-04	665984	0.291543
Up	CA12	14	6.44E-05	102792	0.268619
Up	SCEL	14	7.34E-04	388298	0.33479
Up	SLC34A2	14	0.001583	1563014	0.247542
Up	GABRB3	14	5.08E-04	274876	0.300924
Up	ANKS1B	4	4.96E-05	207240	0.331775
Up	CIART	2	5.70E-05	275826	0.319652
Up	IQCH	2	0	0	0.31964
Up	CXCL14	2	3.86E-05	97804	0.322749
Up	LONRF2	1	0	0	0.2311
Up	ITIH3	1	0	0	0.243265
Up	DACT3	1	0	0	0.240369
Up	DECR2	1	0	0	0.317752

Up	CFAP53	1	0	0	0.317752
Up	NDP	1	0	0	0.317752
Up	ANKRD45	1	0	0	0.317752
Up	CNTN4	1	0	0	0.317752
Up	GRHL2	1	0	0	0.317752
Up	STOML1	1	0	0	0.317752
Up	RBPJL	1	0	0	0.317752
Up	ERVFRD-1	1	0	0	0.317752
Up	SHC4	1	0	0	0.249331
Up	SLC9A2	1	0	0	0.28788
Up	RASEF	1	0	0	0.247252
Up	SVOP	1	0	0	0.230718
Up	SLC35F1	1	0	0	0.232315
Up	CELF5	1	0	0	0.244219
Up	ZNF599	1	0	0	0.232066
Up	C5orf34	1	0	0	0.240823
Up	ROS1	1	0	0	0.279842
Up	CRISP2	1	0	0	0.269028
Up	ASPA	1	0	0	0.239909
Up	CLDN12	1	0	0	0.246359
Up	RSPO1	1	0	0	0.256266
Up	WNK3	1	0	0	0.247598
Up	FRMPD1	1	0	0	0.260037
Up	DRP2	1	0	0	0.23771
Down	APP	2189	0.002666	3365310	0.317845
Down	SRC	504	0.400224	5.59E+08	0.465717

Down	ITGA4	496	0.008595	8040232	0.303306
Down	RPA1	493	0	0	0.2311
Down	ACTB	476	0.01213	21489770	0.335607
Down	SMAD3	398	0.010658	16678612	0.357999
Down	MYH9	364	0.006158	6598872	0.337227
Down	FLNA	353	0.007077	11964634	0.337885
Down	PKM	353	4.21E-05	68424	0.292597
Down	CDKN1A	302	0.010037	16637086	0.367027
Down	TUBA4A	281	0.004054	3547868	0.316706
Down	PRKCA	279	4.19E-05	33780	0.274616
Down	SRRM2	259	0.022533	38294108	0.381347
Down	NOTCH1	245	0.013646	27956328	0.345433
Down	VCL	233	0.005656	4112886	0.355311
Down	CDK9	211	0.031272	43724982	0.387802
Down	UPF1	199	0.048906	1.46E+08	0.371865
Down	MEPCE	186	0.005625	5736504	0.361481
Down	LGALS3BP	176	0.050731	56826626	0.397302
Down	ACTN1	172	0.005719	8627714	0.316335
Down	CAD	171	0.010289	9147932	0.323472
Down	TLN1	170	0.024835	32927066	0.377671
Down	RARA	168	0.016376	38790824	0.34524
Down	RAB5C	164	0.009051	26501322	0.32746
Down	E2F3	157	0.067172	81164158	0.404238
Down	MYBBP1A	157	0.004253	4853872	0.319216
Down	SF3A2	153	0.005345	5537860	0.321455
Down	NCSTN	148	0.013675	11620366	0.373614

Down	PLEC	148	0.007198	7735012	0.333667
Down	CLU	148	0.004284	4921862	0.315621
Down	CTTN	144	1.85E-05	34480	0.273479
Down	LRP1	143	0.035606	66738612	0.368025
Down	ITGB1	141	0.007016	11423404	0.330433
Down	OGT	139	0.017531	34670330	0.363911
Down	NCOR2	136	0.05242	67476208	0.414314
Down	TNIK	133	0.003794	7500172	0.323255
Down	CAPN1	132	0.011955	9201942	0.362783
Down	TNFRSF1B	126	0.005235	6048582	0.338347
Down	RAB8A	126	0.033442	45967308	0.398711
Down	ZYX	122	0.002615	4159134	0.316671
Down	TGFB1	121	0.030548	55611552	0.380726
Down	GANAB	121	0.004766	9084764	0.316324
Down	FTH1	112	0	0	0.240315
Down	FTSJ1	110	0.008563	21677110	0.350069
Down	WAS	105	0.006824	14951804	0.316416
Down	ATP2A2	104	0.005502	13512860	0.325454
Down	BAX	103	0.002749	7775802	0.312997
Down	SNRPA	103	0.004686	7615722	0.323146
Down	FOKK1	103	6.56E-05	124624	0.297523
Down	CBX6	102	2.60E-05	130320	0.300101
Down	HDAC7	100	7.36E-06	41282	0.289409
Down	KRAS	100	0.00505	3946654	0.314372
Down	TUBB1	99	0.010762	7334820	0.356496
Down	USP39	99	0.004163	4124064	0.333346

Down	STRN4	98	0.015639	13083920	0.371546
Down	GDI1	97	0.00808	7245854	0.355151
Down	POLR1A	95	0.004493	3158464	0.315356
Down	GIGYF1	94	0.00389	8518854	0.317868
Down	MED12	94	1.58E-05	10046	0.275586
Down	JAK3	93	0.011564	8350784	0.351704
Down	ENO2	92	0	0	0.260201
Down	RAB1B	89	0.008892	17406094	0.336899
Down	CTDSPL	86	0.005896	10405078	0.326792
Down	GRAP2	84	0.010691	20962628	0.34186
Down	TSC22D4	84	0.008449	16411146	0.350849
Down	PTPRJ	83	0.003374	6154730	0.317449
Down	CXCR4	82	0	0	0.319392
Down	MDM4	81	0	0	0.321014
Down	SRSF6	81	0.00369	2617526	0.348744
Down	IMPDH1	79	0.008468	14872056	0.324636
Down	PTPRC	78	0	0	0.245083
Down	CLPP	78	0	0	0.317752
Down	TLR2	77	4.79E-05	76992	0.322317
Down	CORO1B	77	0	0	0.317752
Down	USP22	76	0	0	0.317752
Down	SIN3B	76	0.006673	5072566	0.357084
Down	SUN2	75	0	0	0.319369
Down	PI4KA	75	5.09E-05	194840	0.320231
Down	MRPL28	75	0	0	0.317752
Down	IL17RA	75	0	0	0.317752

Down	PKN1	74	0	0	0.317752
Down	USP20	74	0.003156	4712314	0.357777
Down	CHERP	73	1.58E-04	227708	0.320717
Down	VPS52	73	5.49E-05	172518	0.322077
Down	TGOLN2	71	0	0	0.317752
Down	G6PD	70	9.99E-05	528874	0.329578
Down	POMK	69	0	0	0.317752
Down	DENND4C	69	4.16E-05	440608	0.329353
Down	PRKAR2B	69	0	0	0.317752
Down	ITGB3	66	0	0	0.317752
Down	PAX5	65	9.66E-05	409222	0.327385
Down	ITGB5	64	0	0	0.317752
Down	NOTCH2	62	0.0076	4500746	0.353023
Down	SERPINA1	61	0	0	0.317752
Down	RNF166	61	0	0	0.317752
Down	LEF1	60	0.002734	2878552	0.356893
Down	RUFY1	59	0	0	0.317752
Down	ITPR1	59	0.016504	15009770	0.367541
Down	IRF7	58	4.20E-05	254816	0.325797
Down	CDK2AP1	58	0.016675	15745286	0.373937
Down	THBS1	57	0	0	0.317752
Down	HLA-E	57	0.007079	6193594	0.359694
Down	RNH1	56	5.89E-05	307276	0.322725
Down	ELAC2	56	0.006031	7284664	0.360863
Down	PACSIN2	55	0	0	0.318476
Down	ARL6IP5	55	0	0	0.317752

Down	CCNL2	55	0	0	0.317752
Down	ATP2A3	55	0.033293	57837312	0.388567
Down	DIMT1	54	0	0	0.317752
Down	PSAP	54	0	0	0.317752
Down	CD79A	54	3.27E-04	585398	0.330711
Down	VPS51	54	0	0	0.317752
Down	CTDNEP1	53	0	0	0.321443
Down	ITGB2	53	0.002039	3160000	0.334208
Down	LIMS1	53	0.009901	17849898	0.334376
Down	CMTM5	53	0	0	0.279878
Down	GNB5	52	0.042962	1.29E+08	0.371403
Down	ESYT1	52	0.010431	19740350	0.351404
Down	EVL	52	0.002936	3873720	0.321861
Down	PYGB	50	0	0	0.243498
Down	HLA-A	7	3.15E-06	4282	0.25335
Down	CSF1R	4	0	0	0.243498
Down	MYLK	4	0.02758	53431176	0.357349
Down	MICAL1	4	0	0	0.263631
Down	ZBTB7B	3	0.011364	18936744	0.356555
Down	RIN3	3	0	0	0.28158
Down	SPARC	3	5.99E-05	100996	0.279112
Down	LFNG	3	0	0	0.25378
Down	PRAM1	3	0.007566	10658530	0.33669
Down	FERMT3	3	0.004345	6463622	0.323183
Down	APLP2	3	0.002097	5599528	0.312207
Down	ACAD10	3	5.54E-06	5790	0.281452

Down	ITGA2B	3	0.003888	5735454	0.329328
Down	VCAN	3	0.005452	8532800	0.331116
Down	LENG8	3	0.005412	6353682	0.338466
Down	EPM2AIP1	3	0.004426	3470384	0.316764
Down	MAP1A	3	0.00816	16680766	0.33231
Down	STON2	3	0.003943	9629562	0.331737
Down	ABI3	3	6.24E-05	141136	0.260663
Down	TRIM13	3	0.006012	17818956	0.328279
Down	WIPF1	3	0.006612	10493584	0.327423
Down	IL2RG	3	0	0	0.249331
Down	B4GALT1	3	0.004053	8509232	0.32549
Down	DOCK8	2	0.008903	15185354	0.333205
Down	NUP188	2	0.007135	7672290	0.329065
Down	MAP4K1	2	0.003653	4056316	0.316949
Down	PLXDC2	2	2.45E-06	6914	0.241879
Down	RASGRP2	2	0.004447	3796740	0.322389
Down	CCNL1	2	0	0	0.244253
Down	CASP6	2	3.41E-05	75570	0.268802
Down	C15orf39	2	0.008306	17301536	0.332017
Down	MBNL1	2	1.36E-05	74714	0.306896
Down	ZC3HAV1L	2	0.004666	6660660	0.327695
Down	SMG5	2	2.15E-05	101210	0.303529
Down	MRPL49	2	1.78E-05	51682	0.289293
Down	LILRB2	2	0	0	0.28788
Down	ITGAL	2	0	0	0.28788
Down	CD47	2	0	0	0.28788

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

Regulation	Target Genes	Degree	MicroRNA	Regulation	Target Genes	Degree	TF
Up	ERRFI1	70	hsa-mir-198	UP	ERRFI1	43	CREM
Up	CCNE1	50	hsa-mir-181b-5p	UP	ELAVL2	41	BMI1
Up	ELAVL2	43	hsa-mir-766-3p	UP	KIT	34	DMRT1
Up	ANTXR1	36	hsa-mir-624-5p	UP	ZBTB8A	29	GATA4
Up	ZBTB8A	34	hsa-mir-10b-5p	UP	PPARGC1A	27	FOXA2
Up	KIT	29	hsa-mir-550a-5p	UP	PTN	27	SOX2
Up	PPARGC1A	19	hsa-mir-941	UP	CCNE1	26	SIN3A
Up	CCNA1	18	hsa-mir-124-3p	UP	ANTXR1	26	SOX9
Up	PTN	12	hsa-mir-577	UP	BMPR1B	25	TCF3
Up	KRT14	11	hsa-mir-146a-5p	UP	SLC15A1	22	POU5F1
Up	BMPR1B	7	hsa-mir-200c-3p	UP	GLP1R	20	GATA1
Up	EDA	7	hsa-mir-16-5p	UP	CCNA1	14	MYC
Up	KRT13	5	hsa-mir-1343-3p	UP	KRT13	13	SOX17
Up	TRIM54	3	hsa-mir-302a-3p	UP	EDA	11	RUNX2

Up	GLP1R	1	hsa-mir-376c-3p	UP	TRIM54	7	TEAD4
Down	SRRM2	250	hsa-mir-582-5p	Down	SMAD3	58	EP300
Down	CDKN1A	187	hsa-mir-657	Down	CDKN1A	57	STAT3
Down	MYH9	126	hsa-mir-1231	Down	ACTB	56	HOXC9
Down	APP	125	hsa-mir-509-3-5p	Down	PKM	55	FOXP1
Down	ACTB	122	hsa-mir-192-3p	Down	MYH9	53	ATF3
Down	VCL	95	hsa-mir-590-5p	Down	SRC	46	TCF7
Down	FLNA	92	hsa-mir-99b-5p	Down	NOTCH1	46	RUNX1
Down	PKM	81	hsa-mir-514a-3p	Down	APP	45	TET1
Down	SMAD3	56	hsa-mir-320d	Down	VCL	45	ESRRB
Down	RPA1	41	hsa-mir-196a-3p	Down	PRKCA	43	MITF
Down	NOTCH1	35	hsa-mir-1301-3p	Down	SRRM2	37	CEBPB
Down	PRKCA	35	hsa-mir-484	Down	TUBA4A	24	SCLY
Down	SRC	27	hsa-mir-4525	Down	ITGA4	19	GATA1
Down	TUBA4A	27	hsa-mir-3619-5p	Down	FLNA	18	CUX1
Down	ITGA4	13	hsa-mir-101-3p	Down	RPA1	16	SMARCA4

Fig. 2. Volcano plot of differentially expressed genes. Genes with a significant change of more than two-fold were selected. Green dot represented up regulated significant genes and red dot represented down regulated significant genes.

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

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 blue color diamond nodes represent the key miRNAs; up regulated genes are marked in green; down regulated genes are marked in red.

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

Fig. 7. ROC curve analyses of hub genes. A) TRIM54 B) ELAVL2 C) PTN D) KIT E) BMPR1B F) APP G) SRC H) ITGA4 I) RPA1 J) ACTB