Identification and Interaction Analysis of Molecular Markers in Myocardial Infarction by Integrated Bioinformatics Analysis

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Abstract

Myocardial infarction (MI) is the leading cardiovascular diseases in worldwide, yet relatively little is known about the genes and signaling pathways involved in MI progression. The present investigation aimed to elucidate potential crucial candidate genes and pathways in MI. expression profiling by high throughput sequencing dataset (GSE132143) was downloaded from the Gene Expression Omnibus (GEO) database, which included data from 20 MI samples and 12 normal control samples. Differentially expressed genes (DEGs) were identified using t-tests in the DESeq2 R package. These DEGs were subsequently investigated by Gene Ontology (GO) and pathway enrichment analysis, a protein-protein interaction (PPI) network, modules, miRNA-hub gene regulatory network and TF-hub gene regulatory network were constructed and analyzed. Hub genes were validated by receiver operating characteristic curve (ROC) analysis. In total, 958 DEGs were identified, of which 480 were up regulated and 478 were down regulated. GO and pathway enrichment analysis results revealed that the DEGs were mainly enriched in, immune system, neuronal system, response to stimulus, and multicellular organismal process. A PPI network, modules, miRNA-hub gene regulatory network and TF-hub gene regulatory network was constructed by using Cytoscape software, and CFTR, CDK1, RPS13, RPS15A, RPS27, NOTCH1, MRPL12, NOS2, CCDC85B and ATN1 were identified as the hub genes. Our results highlight the important roles of the genes including CFTR, CDK1, RPS13, RPS15A, RPS27, NOTCH1, MRPL12, NOS2, CCDC85B and ATN1 in MI pathogenesis or therapeutic management.

Keywords: myocardial infarction; bioinformatics analysis; differentially expressed genes; expression profiling by high throughput sequencing; enrichment analysis

Introduction

Myocardial infarction (MI) is one of the most prevalent cardiovascular diseases in the world [1]. MI is broadly characterized as a sudden blockage of blood flow to heart and permanent damage to the heart muscle [2]. Myocardial infarction (MI) is a main cause of morbidity and mortality all over the world [3]. The potential highly risk factors for MI include genetic risk [4], older age [5], smoking [6], hypertension [7], diabetes mellitus [8] and obesity [9]. Although some prognostic biomarkers have been exploited, the overall survival of MI remains weak due to its difficulty in early detection [10-11]. It is therefore urgent to identify novel diagnostic and prognostic biomarkers, and therapeutic target for MI.

Molecular biology investigation have identified numerous biomarkers and signaling pathway that contribute to MI, including HMGA1 [12], STXBP2 [13], CCL19 and CCL21 [14], NLRP3 [15], CD14 [16], Nrf2 signaling pathway [17], Wnt signaling pathways [18], β 2AR, cAMP/PKA, and BDNF/TrkB signaling pathways [19], PTEN/PI3K/Akt signaling pathway [20] and TGF- β 1 signaling pathway [21]. A further study into the molecular events linked with MI is required.

One of the recent technology RNA sequencing, which allows the study of gene expression in a high throughput manner with high sensitivity, specificity and repeatability. A significant amount of data has been produced via the use of RNA sequencing and such data has been uploaded and stored in public databases. Furthermore, many bioinformatics studies on MI have been produced in recent years [22], which proved that the integrated bioinformatics techniques could help us to further investigation and better exploring the molecular mechanisms.

In this study, we identified DEGs in expression profiling by high throughput sequencing dataset GSE132143 [23] from the Gene Expression Omnibus (GEO) database (<http://www.ncbi.nlm.nih.gov/geo/>) [24]. We performed Gene Ontology (GO) and REACTOME functional and pathway enrichment analysis, and constructed and analyzed a protein–protein interaction (PPI) network, modules, miRNA-hub gene regulatory network and TF-hub gene regulatory network. Diagnostic values of hub genes were determined by receiver operating characteristic curve (ROC) analysis. Collectively, the findings of the current investigation highlighted hub genes and pathways that might contribute to the

pathology of MI. These may provide a basis for the advancement of future diagnostic and therapeutic target for MI.

Materials and Methods

Data resources

GSE132143 [23] expression profiling by high throughput sequencing dataset was downloaded from the GEO database and based on GPL18573 Illumina NextSeq 500 (Homo sapiens). The datasets contained 32 samples, including 20 MI samples and 12 normal control samples.

Identification of DEGs

DEGs between MI and normal control specimen were identified via DESeq2 package in R bioconductor [25] with $|\log FC| \geq 1.37$ for up regulated genes and $|\log FC| \leq -1.89$ for down regulated genes and adjust P value ≤ 0.05 , and Benjamini and Hochberg false discovery rate method [26]. The heatmap of DEGs in every sample of the MI and normal control group was constructed by using gplots package in R software. The volcano plot was generated by ggplot2 package in R software.

GO and REACTOME pathway enrichment analysis of DEGs

Gene ontology (GO) (<http://geneontology.org/>) [27] is a framework for the model of biology, which describes gene functions and classification includes, biological process (BP), cellular component (CC) and molecular function (MF). REACTOME pathway (<https://reactome.org/>) [28] is a collection of databases for recognition high-level gene functions and functions of the biological system. The g:Profiler (<http://biit.cs.ut.ee/gprofiler/>) [29] is an online tool that provides a comprehensive set of functional annotation tools to examine the biological content behind a number of genes. In order to analyze DEGs at the functional level, GO term enrichment analysis and REACTOME pathway enrichment analysis were conducted using g:Profiler. $P < 0.05$ was considered to indicate a statistically significant difference.

Construction of the PPI network and module analysis

Human Integrated Protein-Protein Interaction rEference (HiPPIE) interactome (<http://cbdm-01.zdv.uni-mainz.de/~mschaefer/hippie/>) [30] is an online software of interactions of genes and proteins. Cytoscape 3.8.2 (<http://www.cytoscape.org/>) [31] is an open-source tool for network visualization of genes and proteins. The hub genes were identified by using the plug-in Network Analyzer of the Cytoscape software, including node degree [32], betweenness centrality [33], stress centrality [34] and closeness centrality [35]. In order to find modules of the whole network, the PEWCC1 (<http://apps.cytoscape.org/apps/PEWCC1>) [36] plug-in of the Cytoscape software was applied.

MiRNA-hub gene regulatory network construction

To explore the interaction among the hub genes and miRNAs, we used the miRNet database (<https://www.mirnet.ca/>) [37]. Furthermore, all the known and predicted miRNA-hub gene pairs were downloaded from miRNet database and the miRNA-hub gene pairs were screened out. The miRNA-hub gene regulatory network was established via Cytoscape version 3.8.2 [31].

TF-hub gene regulatory network construction

To explore the interaction among the hub genes and TFs, we used the NetworkAnalyst database (<https://www.networkanalyst.ca/>) [38]. Furthermore, all the known and predicted TF-hub gene pairs were downloaded from NetworkAnalyst database and the TF-hub gene pairs were screened out. The TF-hub gene regulatory network was established via Cytoscape version 3.8.2 [31].

Validation of hub genes by receiver operating characteristic curve (ROC) analysis

pROC package in R statistical software [39] was used to perform ROC curve analysis and to resolve the specificity and sensitivity for all the possible thresholds of the ROC curve. The area under the curve (AUC) value of the hub genes was predicted based on the ROC curve analysis.

Results

Identification of DEGs

By using DESeq2 package to analyze the differential expression of the expression profiling by high throughput sequencing dataset, we obtained 958 DEGs composed of 480 up regulated genes and 478 down regulated genes (Table 1). All DEGs were displayed in volcano maps (Fig. 1). Heatmap analysis showed that these genes presented differential expression profiles between MI and normal control (Fig. 2).

GO and REACTOME pathway enrichment analysis of DEGs

GO analysis of genes includes BP, CC and MF. The GO enrichment analysis results showed that the up regulated genes were mainly involved in BP such as the response to stimulus and cell communication (Table 2). The down regulated genes were enriched in multicellular organismal process and anatomical structure development (Table 2). GO CC analysis indicated that the up regulated genes were mainly involved in cell periphery and membrane (Table 2). The down regulated genes were enriched in cell periphery and plasma membrane (Table 2). In addition, for the MF analysis, the up regulated genes were significantly enriched in the molecular transducer activity and transmembrane signaling receptor activity (Table 2). The down regulated genes were enriched in inorganic molecular entity transmembrane transporter activity and structural molecule activity (Table 2). REACTOME pathway enrichment analyses indicated that the up regulated genes were enriched in immune system and innate immune system (Table 3). The down regulated genes were enriched in neuronal system and extracellular matrix organization (Table 3).

Construction of the PPI network and module analysis

The PPI network of DEGs consisting of 6292 nodes and 12582 edges was constructed in the HiPPIE database. Then it was visualized through Cytoscape (Fig. 3). Based on the HiPPIE database, the DEGs with the highest PPI scores identified by the 4 centrality methods are shown in Table 4. After repeated genes removing, the hub genes were obtained using the 4 centrality methods, including CFTR, CDK1, RPS13, RPS15A, RPS27, NOTCH1, MRPL12, NOS2, CCDC85B and ATN1. A significant modules were constructed from the PPI network of the DEGs using PEWCC1, including module 1 had 59 nodes and 203 edges (Fig. 4A) and module 2 had 21 nodes and 41 edges (Fig. 4B). Enrichment analysis demonstrated that modules 1 and 2 may be associated with metabolism of amino

acids and derivatives, cellular responses to external stimuli, response to stimulus, membrane, diseases of glycosylation and multicellular organismal process.

MiRNA-hub gene regulatory network construction

2222 nodes (miRNA: 1952 and hub gene: 270) and 9722 edges were mapped in the miRNA-hub gene regulatory network (Fig. 5). Moreover, we found that TFRC was potentially targeted by 108 miRNAs (ex; hsa-mir-409-3p); TOP2A was potentially targeted by 90 miRNAs (ex; hsa-mir-320d); CDK1 was potentially targeted by 68 miRNAs (ex; hsa-mir-301a-5p); CEP55 was potentially targeted by 56 miRNAs (ex; hsa-mir-107); FKBP5 was potentially targeted by 32 miRNAs (ex; hsa-mir-205-5p); ATN1 was potentially targeted by 74 miRNAs (ex; hsa-mir-3200-3p); FSCN1 was potentially targeted by 62 miRNAs (ex; hsa-mir-29a-5p); CHERP was potentially targeted by 52 miRNAs (ex; hsa-mir-296-5p); NOTCH1 was potentially targeted by 35 miRNAs (ex; hsa-mir-139-5p); NOTCH3 was potentially targeted by 33 miRNAs (ex; hsa-mir-147a) and are shown in Table 5.

TF-hub gene regulatory network construction

356 nodes (TF: 78 and hub gene: 278) and 2152 edges were mapped in the TF-hub gene regulatory network (Fig. 6). Moreover, we found that RPS27 was potentially targeted by 18 TFs (ex; CREB1); FKBP5 was potentially targeted by 17 TFs (ex; TP63); TFRC was potentially targeted by 15 TFs (ex; FOXA1); CDK1 was potentially targeted by 14 TFs (ex; NRF1); PRDX1 was potentially targeted by 11 TFs (ex; JUND); ATN1 was potentially targeted by 19 TFs (ex; TEAD1); FSCN1 was potentially targeted by 8 TFs (ex; SREBF2); ATP6V1B1 was potentially targeted by 7 TFs (ex; GATA2); GATA1 was potentially targeted by 7 TFs (ex; E2F1); MRPL12 was potentially targeted by 7 TFs (ex; TP53) and are shown in Table 5.

Validation of hub genes by receiver operating characteristic curve (ROC) analysis

As these 10 hub genes are prominently expressed in MI, we performed a ROC curve analysis to evaluate their sensitivity and specificity for the diagnosis of MI. As shown in Fig. 7, CFTR, CDK1, RPS13, RPS15A, RPS27, NOTCH1, MRPL12, NOS2, CCDC85B and ATN1 achieved an AUC value of >0.88, demonstrating

that these hub genes have high sensitivity and specificity for MI diagnosis. The results suggested that CFTR, CDK1, RPS13, RPS15A, RPS27, NOTCH1, MRPL12, NOS2, CCDC85B and ATN1 can be used as biomarkers for the diagnosis of MI.

Discussion

Although people have continuously investigated MI, the early diagnosis and treatment of MI is still a large problem due to the lack of understanding of the molecular mechanisms that drive the occurrence and development of MI. Therefore, in-depth investigation into the factors and mechanisms of MI development are necessary for MI diagnosis and treatment. Due to well-developed RNA sequencing, it is easier to determine the general genetic modification in the progression of diseases, which can allow for the recognition of gene targets for diagnosis, therapy, and prognosis of MI.

In our investigation, a total of 958 DEGs were screened, including 480 up regulated genes and 478 down regulated genes. Lin et al [40] and Wuest et al [41] found that the role of IL1RL1 and ALOX15B in coronary artery disease. Research have shown that SERPINA3 [42], GPR78 [43] and ESM1 [44] plays a significant role in MI progression. Expression of the SCGN (secretagoin, EF-hand calcium binding protein) gene plays a role in the development of diabetes mellitus [45], but this genes might be novel target for MI.

In the present investigation, a GO and pathway enrichment analysis was conducted to further understand the regulatory roles of DEGs in MI. Immune system [46], innate immune system [47], neutrophil degranulation [48], toll-like receptor cascades [49], metabolism of amino acids and derivatives [50], neuronal system [51], extracellular matrix organization [52], degradation of the extracellular matrix [53], diseases of glycosylation [54], response to stimulus [55], cell communication [56], cell periphery [57], membrane [58], anatomical structure development [59] and plasma membrane [60] were responsible for progression of MI. PLA2G2A [61], CCL23 [62], CD53 [63], TREML4 [64], TREM2 [65], CD180 [66], HPSE (heparanase) [67], CELA2A [68], TNFRSF4 [69], AMBP (alpha-1-microglobulin/bikunin precursor) [70], SOX18 [71], PANX2 [72], RSPO2 [73], COMP (cartilage oligomeric matrix protein) [74], ASGR1 [75] and

NOXA1 [76] are involved in progression of atherosclerosis. A previous study reported that S100A9 [77], ADORA3 [78], IL1R2 [79], FPR1 [80], CCL20 [81], CD163 [82], S100A8 [83], TLR2 [84], HAS2 [85], PTX3 [86], TIMP4 [87], AREG (amphiregulin) [88], LBP (lipopolysaccharide binding protein) [89], IL18R1 [90], ALOX5AP [91], RETN (resistin) [92], F13A1 [93], FPR2 [94], SAA1 [95], FLT3 [96], AQP4 [97], FCER1G [98], CCL18 [99], HP (haptoglobin) [100], CDK1 [101], SLC7A11 [102], CFTR (CF transmembrane conductance regulator) [103], F8 [104], STC1 [44], IL18RAP [90], TIMP3 [105], PDE4D [106], CYP4A11 [107], SCN10A [108], APOB (apolipoprotein B) [109], ACE (angiotensin I converting enzyme) [110], PENK (proenkephalin) [111], HSPB6 [112], TLR9 [113], EGR1 [114], CACNG8 [115], FOXD3 [116], DBH (dopamine beta-hydroxylase) [117], FOXP3 [118], GLP1R [119], IL34 [120], CCN1 [121], ADRA2A [122], BGN (biglycan) [123], NOS2 [124], AGRN (agrin) [125], DRD1 [126], GNB3 [127], EGR2 [128], MDK (midkine) [129], NOTCH3 [130], AZIN2 [131], NOTCH1 [132], LOXL2 [133], ADAMTS14 [134] and SOD3 [135] are expressed in MI. DEFB1 [136], SLC11A1 [137], SPINK1 [138], CCR1 [139], GLUL (glutamate-ammonia ligase) [140], GPR84 [141], SIGLEC5 [142], SIGLEC7 [143], LGR5 [144], CD38 [145], GRB14 [146], PRDX1 [147], SLC19A2 [148], CADM2 [149], TRPM5 [150], COL1A1 [151], CTRB1 [152], UTS2R [153], CRTCL1 [154], MUC5B [155], TMPRSS6 [156], SLC5A2 [157] and KCNJ9 [158] expression were shown to play an important role in diabetes mellitus, but these genes might be novel target for MI. MT1A [159], LYVE1 [160], S100A12 [161], GCKR (glucokinase regulator) [162], TLR8 [163], MRC1 [164], AGTR1 [165], P2RY12 [166], MSR1 [167], NQO1 [168], FKBP5 [169], CMTM5 [170], ADH1C [171], APLNR (apelin receptor) [172], SFRP4 [173], CCL3 [174], COL1A2 [175], EGR3 [176] and IL2RB [177] expression have a role in coronary artery disease. EDN2 [178], SNX10 [179] and KCNN1 [180] were played a predominant role in progression of atrial fibrillation. EDNRB (endothelin receptor type B) [181], FGF10 [182], WNK3 [183], KNG1 [184], FCN3 [185], AQP3 [186], HPR (haptoglobin-related protein) [187], CTH (cystathionine gamma-lyase) [188], SPARCL1 [189], MAOA (monoamine oxidase A) [190], BMPRI1B (bone morphogenetic protein receptor type 1B) [191], FGF7 [192], CALCRL (calcitonin receptor like receptor) [193], MARK3 [194], ADH1B [195], AMH (anti-Mullerian hormone) [196], RET (ret proto-oncogene) [197], IGF2 [198], SLC6A9 [199], NPPA (natriuretic peptide A) [200], SCT (secretin) [201], DCX (doublecortin)

[202], ASIC1 [203], LMX1B [204], DBP (D-box binding PAR bZIP transcription factor) [205] and SLC6A9 [206] levels are correlated with disease severity in patients with hypertension. CAMP (cathelicidin antimicrobial peptide) [207], SPP1 [208], CXCL11 [209], TFRC (transferrin receptor) [210], IRAK3 [211], C3AR1 [212], GLI2 [213], THY1 [214], FOXO6 [215], RGS4 [216], WNT10B [217] and AEBP1 [218] were found to be involved in progression of obesity, but these genes might be novel target for MI. TDGF1 [219], KIF20A [220] and LTBP2 [221] were linked with progression of congenital heart defect.

A PPI network was constructed for the identified DEGs and hub genes were defined by the betweenness centrality, stress centrality and closeness centrality rank. The key modules were subsequently isolated from the PPI network. RPS13, RPS15A, RPS27, RPL26, RPS29, MRPL12, CCDC85B and ATN1 were the novel biomarkers for the progression of T2DM.

The subsequent construction of the miRNA-hub gene regulatory network and TF-hub gene regulatory network using the respective hub genes identified miRNA and TFs as potential key markers involved in MI. Chen et al [222], Li and Zhang [223], Wang et al [224], Zhao et al [225], Lin et al [226], Liao et al [227], Izadpanah et al [228], Wang et al [229] and Hakobjanyan et al [230] reported that the expression of the hsa-mir-409-3p, hsa-mir-320d, hsa-mir-107, hsa-mir-139-5p, NRF1, TEAD1, GATA2, E2F1 and TP53 are correlated with disease grades of MI. hsa-mir-301a-5p [231], hsa-mir-29a-5p [232], hsa-mir-296-5p [233], CREB1 [234] and FOXA1 [235] were linked with progression of diabetes mellitus, but these genes might be novel target for MI. hsa-mir-205-5p was involved in the progression of hypertension [236]. SREBF2 was associated with progression of coronary artery disease [237]. TOP2A, CEP55, FSCN1, CHERP, ATP6V1B1, GATA1, hsa-mir-3200-3p, hsa-mir-147a, TP63 and JUND (jun D proto-oncogene) were the novel biomarkers for the progression of MI.

In conclusion CFTR, CDK1, RPS13, RPS15A, RPS27, NOTCH1, MRPL12, NOS2, CCDC85B and ATN1 might be a critical gene for MI. In addition, immune system, neuronal system, response to stimulus, cell periphery, molecular transducer activity, multicellular organismal process and inorganic molecular entity transmembrane transporter activity play a pivotal role in the progression of MI from normal samples. Therefore, these pathways and genes can be a potential

therapeutic target for target therapy in MI. We also introduce several miRNAs and TFs that can use to target these critical genes and pathways.

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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. [(GSE132143) <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE132143>]

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)

Gene Symbol	logFC	pValue	adj.P.Val	tvalue	Regulation	Gene Name
RNY4	5.579746	5.51E-29	1.24E-25	11.17324	Up	RNA, Ro60-associated Y4
UMODL1-AS1	4.641232	0.001219	0.00548	3.234363	Up	UMODL1 antisense RNA 1
IL1RL1	4.151538	1.75E-58	3.14E-54	16.12332	Up	interleukin 1 receptor like 1
ANKRD22	4.141446	3.01E-07	5.69E-06	5.122728	Up	ankyrin repeat domain 22
RNF17	4.108169	0.000161	0.001042	3.773882	Up	ring finger protein 17
SERPINA3	3.927298	3.29E-25	4.38E-22	10.37301	Up	serpin family A member 3
ALOX15B	3.835862	1.18E-09	5.17E-08	6.083183	Up	arachidonate 15-lipoxygenase type B
RNASE2	3.752758	2.22E-18	9.86E-16	8.745419	Up	ribonuclease A family member 2
SCGN	3.723034	2.93E-13	3.81E-11	7.297616	Up	secretagogin, EF-hand calcium binding protein
CD177	3.636629	3.07E-09	1.16E-07	5.927867	Up	CD177 molecule
AOX1	3.346982	2.05E-29	5.27E-26	11.26066	Up	aldehyde oxidase 1
TUBA3C	3.255294	2.00E-24	2.32E-21	10.19912	Up	tubulin alpha 3c
RNA5SP304	3.253096	0.00245	0.009651	3.029451	Up	RNA, 5S ribosomal pseudogene 304
VSIG4	3.210108	4.37E-43	2.62E-39	13.76103	Up	V-set and immunoglobulin domain containing 4
OR4M2	3.18715	0.000186	0.001175	3.737391	Up	olfactory receptor family 4 subfamily M member 2
PLA2G2A	3.173675	1.37E-10	8.44E-09	6.419057	Up	phospholipase A2 group IIA
S100A9	3.165379	5.96E-20	3.63E-17	9.145122	Up	S100 calcium binding protein A9
CLECL1	3.110064	8.15E-06	8.95E-05	4.461245	Up	C-type lectin like 1
RNU7-154P	3.097763	2.53E-06	3.39E-05	4.705354	Up	RNA, U7 small nuclear 154 pseudogene
OR11J1P	3.076974	0.001508	0.006505	3.173052	Up	olfactory receptor family 11 subfamily J member 1 pseudogene
KRT5	3.053882	4.29E-07	7.59E-06	5.055631	Up	keratin 5
ADORA3	3.038127	1.92E-22	1.64E-19	9.745705	Up	adenosine A3 receptor
VTRNA1-3	2.994675	5.45E-05	0.000426	4.035285	Up	vault RNA 1-3
IL1R2	2.966613	1.77E-20	1.15E-17	9.275601	Up	interleukin 1 receptor type 2
SLC22A16	2.965856	9.98E-07	1.54E-05	4.892085	Up	solute carrier family 22 member 16
LCN6	2.962512	6.60E-13	7.98E-11	7.187499	Up	lipocalin 6
OR11J6P	2.921939	0.002486	0.009764	3.025091	Up	olfactory receptor family 11 subfamily J member 6 pseudogene
FPR1	2.899739	3.40E-23	3.22E-20	9.920097	Up	formyl peptide receptor 1
CCL20	2.880525	0.002778	0.010673	2.991299	Up	C-C motif chemokine ligand 20
OR11J5P	2.873974	0.006063	0.020166	2.744378	Up	olfactory receptor family 11 subfamily J member 5 pseudogene
FCGBP	2.833765	2.44E-10	1.36E-08	6.330939	Up	Fc fragment of IgG binding protein
TUBA3D	2.826436	8.97E-19	4.19E-16	8.847233	Up	tubulin alpha 3d
DEFB1	2.824242	0.006277	0.020749	2.732965	Up	defensin beta 1
MT1A	2.794836	4.32E-06	5.27E-05	4.595148	Up	metallothionein 1A
LYVE1	2.765871	2.58E-18	1.10E-15	8.728434	Up	lymphatic vessel endothelial hyaluronan receptor 1
CD163	2.752851	6.32E-23	5.68E-20	9.858199	Up	CD163 molecule
S100A8	2.74215	2.04E-13	2.74E-11	7.346254	Up	S100 calcium binding protein A8
MCEMP1	2.716497	1.26E-05	0.000128	4.367627	Up	mast cell expressed membrane protein 1

SNORA63C	2.710838	4.23E-09	1.50E-07	5.875085	Up	small nucleolar RNA, H/ACA box 63C
ADAMDEC1	2.706414	0.000105	0.000735	3.878508	Up	ADAM like decysin 1
OR52N5	2.697679	6.10E-05	0.000467	4.009009	Up	olfactory receptor family 52 subfamily N member 5
S100A12	2.691859	8.03E-07	1.29E-05	4.934546	Up	S100 calcium binding protein A12
CEP55	2.677728	2.15E-12	2.22E-10	7.024705	Up	centrosomal protein 55
TSIX	2.677281	0.001517	0.006534	3.171444	Up	TSIX transcript, XIST antisense RNA
PRR32	2.672892	0.00014	0.000932	3.807299	Up	proline rich 32
TUBAP8	2.646856	8.22E-18	3.21E-15	8.596545	Up	tubulin alpha pseudogene 8
RARRES1	2.639969	3.51E-15	7.50E-13	7.871404	Up	retinoic acid receptor responder 1
PPEF1	2.634499	4.14E-08	1.06E-06	5.48478	Up	protein phosphatase with EF-hand domain 1
TUBA3E	2.62609	1.34E-16	3.88E-14	8.270167	Up	tubulin alpha 3e
MMRN1	2.609449	4.57E-07	8.01E-06	5.043397	Up	multimerin 1
TUBAP9	2.607613	3.60E-16	9.81E-14	8.151167	Up	tubulin alpha pseudogene 9
IGLV8-61	2.601016	0.002496	0.009796	3.023796	Up	immunoglobulin lambda variable 8-61
FAM83B	2.59668	1.40E-05	0.000139	4.344196	Up	family with sequence similarity 83 member B
MTRNR2L11	2.594186	3.90E-06	4.85E-05	4.616414	Up	MT-RNR2 like 11
CHI3L2	2.586472	2.91E-08	7.87E-07	5.546483	Up	chitinase 3 like 2
TLR2	2.575405	3.82E-26	6.53E-23	10.57685	Up	toll like receptor 2
EDN2	2.563355	5.73E-06	6.68E-05	4.536064	Up	endothelin 2
DAW1	2.553361	3.73E-05	0.000315	4.123305	Up	dynein assembly factor with WD repeats 1
VN1R60P	2.54999	0.000364	0.002036	3.565248	Up	vomeroneasal 1 receptor 60 pseudogene
RNVU1-34	2.511083	0.005435	0.01846	2.78008	Up	RNA, variant U1 small nuclear 34
PTPRQ	2.479308	8.65E-07	1.37E-05	4.919996	Up	protein tyrosine phosphatase receptor type Q
RNY1	2.473187	6.23E-21	4.39E-18	9.386102	Up	RNA, Ro60-associated Y1
DMP1	2.471165	4.32E-05	0.000355	4.089639	Up	dentin matrix acidic phosphoprotein 1
NPTX2	2.470985	9.88E-15	1.93E-12	7.740761	Up	neuronal pentraxin 2
SCARNA23	2.461822	3.28E-06	4.21E-05	4.652554	Up	small Cajal body-specific RNA 23
ADH1B	2.434671	1.06E-13	1.55E-11	7.432747	Up	alcohol dehydrogenase 1B (class I), beta polypeptide
BANCR	2.426012	0.002137	0.008615	3.070478	Up	BRAF-activated non-protein coding RNA
SLC25A48	2.417088	0.001385	0.006079	3.19779	Up	solute carrier family 25 member 48
HAS2	2.41656	4.24E-12	4.08E-10	6.928801	Up	hyaluronan synthase 2
CYP4B1	2.412669	4.86E-08	1.22E-06	5.456384	Up	cytochrome P450 family 4 subfamily B member 1
PTX3	2.409897	5.51E-08	1.35E-06	5.433987	Up	pentraxin 3
TMIGD3	2.389688	9.50E-14	1.40E-11	7.447722	Up	transmembrane and immunoglobulin domain containing 3
IGLV5-45	2.388431	0.01611	0.044452	2.406423	Up	immunoglobulin lambda variable 5-45
FCGR1CP	2.386298	1.82E-08	5.25E-07	5.628699	Up	Fc fragment of IgG receptor 1c, pseudogene
CYP4Z2P	2.378179	2.24E-10	1.27E-08	6.343886	Up	cytochrome P450 family 4 subfamily Z member 2, pseudogene
TIMP4	2.371008	1.14E-21	8.91E-19	9.563326	Up	TIMP metalloproteinase inhibitor 4
CLEC4D	2.362952	6.35E-06	7.27E-05	4.514519	Up	C-type lectin domain family 4 member D
PKHD1	2.362583	0.000394	0.002175	3.544286	Up	PKHD1 ciliary IPT domain containing fibrocystin/polyductin
LCN15	2.361396	3.07E-06	3.98E-05	4.666394	Up	lipocalin 15
TBX22	2.356449	4.39E-06	5.33E-05	4.591911	Up	T-box transcription factor 22
MT1X	2.355976	7.70E-11	5.15E-09	6.506265	Up	metallothionein 1X

AREG	2.349214	7.74E-07	1.25E-05	4.941783	Up	amphiregulin
MTRNR2L1	2.315705	1.79E-05	0.00017	4.289007	Up	MT-RNR2 like 1
BMP3	2.284982	0.00529	0.018076	2.788837	Up	bone morphogenetic protein 3
FCGR1A	2.283693	1.24E-07	2.69E-06	5.286831	Up	Fc fragment of IgG receptor Ia
CYP4Z1	2.28039	2.63E-15	5.69E-13	7.907311	Up	cytochrome P450 family 4 subfamily Z member 1
SCARNA18	2.279144	4.16E-06	5.10E-05	4.603175	Up	small Cajal body-specific RNA 18
IGKV1D-8	2.277938	0.004821	0.01679	2.818735	Up	immunoglobulin kappa variable 1D-8
EDNRB	2.27515	1.09E-24	1.36E-21	10.25763	Up	endothelin receptor type B
HOPX	2.274613	5.56E-06	6.51E-05	4.542481	Up	HOP homeobox
SLC19A2	2.272137	2.31E-28	4.89E-25	11.04517	Up	solute carrier family 19 member 2
FGF10	2.268452	1.34E-05	0.000135	4.352848	Up	fibroblast growth factor 10
RNU6ATAC	2.267968	9.60E-12	8.42E-10	6.812355	Up	RNA, U6atac small nuclear (U12-dependent splicing)
SULT1B1	2.265755	1.88E-29	5.21E-26	11.26816	Up	sulfotransferase family 1B member 1
RNF175	2.241455	6.52E-13	7.97E-11	7.189055	Up	ring finger protein 175
METTL7B	2.241047	6.64E-13	8.00E-11	7.186735	Up	methyltransferase like 7B
SLC66A1L	2.238488	2.75E-08	7.53E-07	5.556597	Up	solute carrier family 66 member 1 like
RHAG	2.234748	1.76E-09	7.24E-08	6.018624	Up	Rh associated glycoprotein
BBS12	2.22376	7.34E-19	3.57E-16	8.869598	Up	Bardet-Biedl syndrome 12
NAA11	2.22176	1.49E-10	9.01E-09	6.406717	Up	N-alpha-acetyltransferase 11, NatA catalytic subunit
SIGLEC10	2.22094	1.26E-13	1.81E-11	7.41021	Up	sialic acid binding Ig like lectin 10
MUC16	2.216738	0.014897	0.041734	2.434877	Up	mucin 16, cell surface associated
PGA3	2.215169	1.41E-10	8.65E-09	6.414678	Up	pepsinogen A3
PSMC6P2	2.21118	0.00139	0.006096	3.196821	Up	proteasome 26S subunit, ATPase, 6 pseudogene 2
SYT13	2.208971	2.18E-10	1.24E-08	6.348444	Up	synaptotagmin 13
GCKR	2.208122	0.017034	0.046402	2.385967	Up	glucokinase regulator
BLM	2.202519	7.80E-15	1.58E-12	7.77072	Up	BLM RecQ like helicase
CLEC4E	2.201741	1.54E-08	4.58E-07	5.657125	Up	C-type lectin domain family 4 member E
SNORA79B	2.198363	8.76E-09	2.80E-07	5.753229	Up	small nucleolar RNA, H/ACA box 79B
CCL23	2.197519	0.005056	0.017437	2.803422	Up	C-C motif chemokine ligand 23
LILRA5	2.193247	3.83E-13	4.86E-11	7.26143	Up	leukocyte immunoglobulin like receptor A5
OR13A1	2.192713	0.005946	0.019856	2.750736	Up	olfactory receptor family 13 subfamily A member 1
OLAH	2.19267	0.000509	0.002675	3.475758	Up	oleoyl-ACP hydrolase
FAM111B	2.190301	3.70E-09	1.35E-07	5.897066	Up	family with sequence similarity 111 member B
H1-3	2.182279	2.34E-11	1.83E-09	6.682796	Up	H1.3 linker histone, cluster member
MGST1	2.180525	5.20E-12	4.89E-10	6.900083	Up	microsomal glutathione S-transferase 1
SERPINA5	2.175708	1.29E-10	8.02E-09	6.428188	Up	serpin family A member 5
PGA4	2.169584	2.23E-08	6.27E-07	5.593241	Up	pepsinogen A4
SLCO4A1	2.164331	2.12E-09	8.46E-08	5.988367	Up	solute carrier organic anion transporter family member 4A1
WNK3	2.160356	2.36E-17	8.15E-15	8.474641	Up	WNK lysine deficient protein kinase 3
RNU6-509P	2.159622	0.015302	0.042636	2.425163	Up	RNA, U6 small nuclear 509, pseudogene
CAMP	2.145519	0.001607	0.006843	3.154709	Up	cathelicidin antimicrobial peptide
KAZN-AS1	2.142912	2.21E-07	4.38E-06	5.180542	Up	KAZN antisense RNA 1
SPP1	2.13936	1.59E-11	1.30E-09	6.739139	Up	secreted phosphoprotein 1

CYP4A11	2.139264	1.81E-09	7.41E-08	6.013846	Up	cytochrome P450 family 4 subfamily A member 11
SLC11A1	2.136032	3.58E-11	2.64E-09	6.620698	Up	solute carrier family 11 member 1
LBP	2.135988	0.004083	0.014678	2.871715	Up	lipopolysaccharide binding protein
IL18R1	2.129729	4.99E-27	8.97E-24	10.76585	Up	interleukin 18 receptor 1
ALOX5AP	2.129693	2.56E-19	1.42E-16	8.986085	Up	arachidonate 5-lipoxygenase activating protein
DLGAP5	2.126079	8.58E-09	2.75E-07	5.756689	Up	DLG associated protein 5
TRPM1	2.118343	0.005435	0.018461	2.780023	Up	transient receptor potential cation channel subfamily M member 1
PGA5	2.105342	3.17E-08	8.38E-07	5.53197	Up	pepsinogen A5
MS4A4A	2.10156	5.21E-13	6.50E-11	7.219725	Up	membrane spanning 4-domains A4A
SCN10A	2.093768	1.60E-05	0.000155	4.314862	Up	sodium voltage-gated channel alpha subunit 10
RPS15AP17	2.093492	3.06E-08	8.17E-07	5.538211	Up	ribosomal protein S15a pseudogene 17
H3C7	2.092387	5.52E-09	1.88E-07	5.830827	Up	H3 clustered histone 7
SPINK1	2.092288	0.00248	0.009746	3.025777	Up	serine peptidase inhibitor Kazal type 1
RETN	2.091833	0.006533	0.021451	2.719762	Up	resistin
KNG1	2.090394	0.000456	0.002439	3.50563	Up	kininogen 1
CCR1	2.089325	1.64E-16	4.66E-14	8.246202	Up	C-C motif chemokine receptor 1
RNU5A-1	2.088339	3.86E-09	1.39E-07	5.890004	Up	RNA, U5A small nuclear 1
CSTA	2.085995	1.34E-08	4.07E-07	5.680351	Up	cystatin A
AKR1B10	2.083723	0.002081	0.008428	3.078414	Up	aldo-ketoreductase family 1 member B10
LCN10	2.082085	9.14E-05	0.000656	3.912387	Up	lipocalin 10
EEF1A1P31	2.077653	5.27E-16	1.39E-13	8.10499	Up	eukaryotic translation elongation factor 1 alpha 1 pseudogene 31
NMRAL2P	2.076921	4.54E-05	0.000368	4.078135	Up	NmrA like redox sensor 2, pseudogene
VN1R28P	2.072231	0.003277	0.012218	2.940453	Up	vomeroneural 1 receptor 28 pseudogene
IGKV2D-40	2.071097	0.016582	0.045462	2.395849	Up	immunoglobulin kappa variable 2D-40
SLA	2.070975	5.49E-16	1.43E-13	8.100123	Up	Src like adaptor
MYOT	2.064989	3.34E-09	1.24E-07	5.913712	Up	myotilin
BEND2	2.062686	8.83E-05	0.000637	3.920554	Up	BEN domain containing 2
RN7SL191P	2.061233	0.003769	0.013734	2.896892	Up	RNA, 7SL, cytoplasmic 191, pseudogene
GRM7-AS3	2.059395	0.008743	0.027172	2.621958	Up	GRM7 antisense RNA 3
RN7SKP94	2.058874	6.22E-05	0.000475	4.004117	Up	RN7SK pseudogene 94
ADH1A	2.056145	7.65E-10	3.62E-08	6.152026	Up	alcohol dehydrogenase 1A (class I), alpha polypeptide
GALNTL6	2.037105	1.22E-05	0.000124	4.374844	Up	polypeptide N-acetylgalactosaminyltransferase like 6
CYP4A22	2.032709	2.98E-10	1.61E-08	6.300046	Up	cytochrome P450 family 4 subfamily A member 22
CYP4A27P	2.02855	0.000406	0.002231	3.535845	Up	cytochrome P450 family 4 subfamily A member 27, pseudogene
TLR8	2.026412	1.80E-10	1.06E-08	6.377081	Up	toll like receptor 8
FCGR3A	2.018412	1.05E-09	4.70E-08	6.101938	Up	Fc fragment of IgG receptor IIIa
PKHD1L1	2.015925	0.000719	0.003562	3.38222	Up	PKHD1 like 1
SIGLEC12	2.011093	0.003131	0.011755	2.954528	Up	sialic acid binding Ig like lectin 12
TAS2R7	2.00703	2.95E-05	0.000259	4.177281	Up	taste 2 receptor member 7
SHISA3	1.999131	8.92E-11	5.73E-09	6.484225	Up	shisa family member 3
F13A1	1.993279	3.46E-14	5.58E-12	7.579783	Up	coagulation factor XIII A chain
RPS8P10	1.992515	9.08E-05	0.000653	3.913873	Up	ribosomal protein S8 pseudogene 10
CDH19	1.991141	6.48E-08	1.56E-06	5.40494	Up	cadherin 19

H4C13	1.989227	3.22E-06	4.15E-05	4.656473	Up	H4 clustered histone 13
FCGR1B	1.979038	3.17E-07	5.93E-06	5.113214	Up	Fc fragment of IgG receptor Ib
EPCAM	1.977482	0.003209	0.011992	2.946991	Up	epithelial cell adhesion molecule
ZDHHC20P1	1.977408	0.016427	0.045168	2.399297	Up	zinc finger DHHC-type containing 20 pseudogene 1
CR1L	1.973131	3.61E-08	9.42E-07	5.508937	Up	complement C3b/C4b receptor 1 like
CATSPERB	1.971487	1.57E-09	6.63E-08	6.036545	Up	cation channel sperm associated auxiliary subunit beta
ANAPC1P5	1.967991	1.57E-05	0.000153	4.318341	Up	ANAPC1 pseudogene 5
GLUL	1.964718	5.25E-52	6.29E-48	15.17406	Up	glutamate-ammonia ligase
BCAT1	1.96429	1.08E-17	4.04E-15	8.565251	Up	branched chain amino acid transaminase 1
NAMPTP1	1.956402	4.51E-08	1.14E-06	5.469617	Up	nicotinamidephosphoribosyltransferase pseudogene 1
CXCL11	1.956011	0.002264	0.009041	3.053218	Up	C-X-C motif chemokine ligand 11
RPL23AP57	1.954543	2.93E-06	3.83E-05	4.675892	Up	ribosomal protein L23a pseudogene 57
CLEC1B	1.954137	0.002089	0.008454	3.077239	Up	C-type lectin domain family 1 member B
SNORD89	1.952967	2.63E-11	2.02E-09	6.665678	Up	small nucleolar RNA, C/D box 89
ST6GALNAC3	1.952404	1.55E-24	1.86E-21	10.22387	Up	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 3
TIMD4	1.944744	0.002384	0.009444	3.037709	Up	T cell immunoglobulin and mucin domain containing 4
PII5	1.934166	9.42E-05	0.000672	3.904986	Up	peptidase inhibitor 15
ACTG1P12	1.927876	0.004909	0.017027	2.812926	Up	actin gamma 1 pseudogene 12
DHRS7C	1.926808	0.00016	0.001039	3.774868	Up	dehydrogenase/reductase 7C
C4orf54	1.919958	0.000731	0.003612	3.377741	Up	chromosome 4 open reading frame 54
CD53	1.91885	1.82E-14	3.27E-12	7.662853	Up	CD53 molecule
TFCP2L1	1.910287	4.98E-15	1.03E-12	7.827499	Up	transcription factor CP2 like 1
OTOGL	1.906497	1.77E-07	3.63E-06	5.221944	Up	otogelin like
MRC1	1.904979	6.16E-16	1.58E-13	8.086196	Up	mannose receptor C-type 1
CYP4A44P	1.904841	0.00441	0.015621	2.847239	Up	cytochrome P450 family 4 subfamily A member 44, pseudogene
TENT5B	1.903378	3.16E-12	3.14E-10	6.970532	Up	terminal nucleotidyltransferase 5B
SNORA54	1.898421	2.16E-09	8.61E-08	5.985073	Up	small nucleolar RNA, H/ACA box 54
TFRC	1.897404	7.58E-11	5.08E-09	6.508634	Up	transferrin receptor
NAMPT	1.897309	1.50E-09	6.34E-08	6.044689	Up	nicotinamidephosphoribosyltransferase
RPL36AP49	1.896784	0.000113	0.000778	3.861828	Up	ribosomal protein L36a pseudogene 49
CPM	1.896726	1.71E-14	3.10E-12	7.671005	Up	carboxypeptidase M
BIRC3	1.895028	3.24E-09	1.21E-07	5.918851	Up	baculoviral IAP repeat containing 3
FPR2	1.892003	9.18E-12	8.15E-10	6.818737	Up	formyl peptide receptor 2
DCXR-DT	1.891386	6.09E-05	0.000467	4.009235	Up	DCXR divergent transcript
SAA1	1.884901	0.008132	0.02567	2.646559	Up	serum amyloid A1
RNVU1-17	1.881652	0.011803	0.03465	2.517978	Up	RNA, variant U1 small nuclear 17
RRM2	1.881454	1.29E-05	0.00013	4.361373	Up	ribonucleotidoreductase regulatory subunit M2
IGHV3-75	1.875375	0.0033	0.012291	2.938352	Up	immunoglobulin heavy variable 3-75 (pseudogene)
ADH1C	1.873873	2.37E-09	9.28E-08	5.970312	Up	alcohol dehydrogenase 1C (class I), gamma polypeptide
CCL26	1.869224	0.007182	0.023197	2.68828	Up	C-C motif chemokine ligand 26
FCN3	1.867346	1.65E-07	3.42E-06	5.23522	Up	ficolin 3
SNORA24B	1.866393	0.002805	0.010762	2.988369	Up	small nucleolar RNA, H/ACA box 24B
H2BC10	1.863206	2.66E-06	3.52E-05	4.695647	Up	H2B clustered histone 10

RNU5B-1	1.862574	2.40E-08	6.69E-07	5.580627	Up	RNA, U5B small nuclear 1
NREP-AS1	1.855772	0.003909	0.014152	2.885407	Up	NREP antisense RNA 1
SLC30A10	1.852745	3.17E-09	1.19E-07	5.922534	Up	solute carrier family 30 member 10
KMO	1.846148	8.75E-08	2.02E-06	5.350894	Up	kynurenine 3-monooxygenase
AGTR1	1.842207	1.57E-08	4.65E-07	5.653996	Up	angiotensin II receptor type 1
STRIT1	1.834893	0.002172	0.008721	3.065687	Up	small transmembrane regulator of ion transport 1
LRRN3	1.832508	6.47E-10	3.15E-08	6.178558	Up	leucine rich repeat neuronal 3
GLULP4	1.827979	1.40E-19	8.12E-17	9.05222	Up	glutamate-ammonia ligase pseudogene 4
SCARNA1	1.824848	5.88E-06	6.82E-05	4.530558	Up	small Cajal body-specific RNA 1
H2BC14	1.82124	0.003105	0.011669	2.957161	Up	H2B clustered histone 14
HRAT17	1.818053	4.55E-08	1.15E-06	5.467918	Up	heart tissue-associated transcript 17
RPS17P5	1.816377	0.001238	0.005545	3.229989	Up	ribosomal protein S17 pseudogene 5
TMEM100	1.810968	8.49E-08	1.97E-06	5.356358	Up	transmembrane protein 100
CHST9	1.807261	7.42E-07	1.20E-05	4.949947	Up	carbohydrate sulfotransferase 9
C5orf64	1.804206	0.000424	0.002303	3.524769	Up	chromosome 5 putative open reading frame 64
GPR84	1.80394	0.001523	0.006551	3.170358	Up	G protein-coupled receptor 84
P2RY12	1.803474	1.78E-10	1.05E-08	6.379533	Up	purinergic receptor P2Y12
AQP3	1.80279	8.38E-17	2.50E-14	8.325739	Up	aquaporin 3 (Gill blood group)
FLT3	1.802445	1.14E-06	1.73E-05	4.864933	Up	fms related receptor tyrosine kinase 3
TUBAL3	1.800851	1.63E-06	2.35E-05	4.794022	Up	tubulin alpha like 3
RNU6-432P	1.800813	0.012579	0.036413	2.495479	Up	RNA, U6 small nuclear 432, pseudogene
ADGRF4	1.80056	0.009021	0.027887	2.611244	Up	adhesion G protein-coupled receptor F4
RPSAP72	1.794723	0.000181	0.001149	3.744428	Up	ribosomal protein SA pseudogene 72
TDRD9	1.793742	6.22E-10	3.05E-08	6.184868	Up	tudor domain containing 9
H2BC9	1.793678	1.74E-05	0.000167	4.295499	Up	H2B clustered histone 9
TFEC	1.792475	2.41E-10	1.35E-08	6.332482	Up	transcription factor EC
HPR	1.789521	1.17E-15	2.77E-13	8.007726	Up	haptoglobin-related protein
OR52N1	1.783269	7.79E-05	0.000573	3.950822	Up	olfactory receptor family 52 subfamily N member 1
SIGLEC5	1.77985	0.012403	0.036055	2.500456	Up	sialic acid binding Ig like lectin 5
HSD11B1	1.777559	2.71E-07	5.20E-06	5.14268	Up	hydroxysteroid 11-beta dehydrogenase 1
SIGLEC7	1.775476	3.41E-08	8.96E-07	5.519139	Up	sialic acid binding Ig like lectin 7
RAB39A	1.77509	2.68E-08	7.38E-07	5.560859	Up	RAB39A, member RAS oncogene family
MSR1	1.763236	7.41E-11	4.98E-09	6.512189	Up	macrophage scavenger receptor 1
TTK	1.759317	1.34E-06	1.98E-05	4.833428	Up	TTK protein kinase
SRGN	1.758712	1.49E-09	6.33E-08	6.045505	Up	serglycin
IGKV1-9	1.752989	0.008732	0.027147	2.622361	Up	immunoglobulin kappa variable 1-9
MANCR	1.749224	2.08E-06	2.87E-05	4.745385	Up	mitotically associated long non coding RNA
H2BC3	1.747613	4.57E-07	8.01E-06	5.043531	Up	H2B clustered histone 3
GPR151	1.747447	0.002455	0.009668	3.028868	Up	G protein-coupled receptor 151
EEF1AKMT4	1.745965	8.00E-11	5.27E-09	6.500552	Up	EEF1A lysine methyltransferase 4
RNU6-8	1.74219	0.000499	0.002629	3.481465	Up	RNA, U6 small nuclear 8
RNU6-7	1.739324	0.005441	0.018477	2.779719	Up	RNA, U6 small nuclear 7
GPR34	1.739002	2.53E-06	3.39E-05	4.705393	Up	G protein-coupled receptor 34

PRRG4	1.736915	1.60E-08	4.72E-07	5.650901	Up	proline rich and Gla domain 4
ZNF622P1	1.734007	1.34E-11	1.11E-09	6.764356	Up	ZNF622 pseudogene 1
SAMSN1	1.730904	1.22E-10	7.60E-09	6.437276	Up	SAM domain, SH3 domain and nuclear localization signals 1
RPL7P16	1.72837	0.004511	0.015924	2.840023	Up	ribosomal protein L7 pseudogene 16
TMPRSS12	1.727275	0.000581	0.002988	3.440491	Up	transmembrane serine protease 12
TREML4	1.727104	0.00408	0.014674	2.871883	Up	triggering receptor expressed on myeloid cells like 4
S100A3	1.72334	0.000194	0.001221	3.726257	Up	S100 calcium binding protein A3
CADM2	1.723248	2.00E-05	0.000186	4.26507	Up	cell adhesion molecule 2
SNORD96B	1.722442	0.000122	0.00083	3.842047	Up	small nucleolar RNA, C/D box 96B
SLAMF8	1.721893	1.59E-05	0.000154	4.316518	Up	SLAM family member 8
MCTP2	1.709952	2.95E-05	0.000258	4.177374	Up	multiple C2 and transmembrane domain containing 2
AQP4	1.708509	0.000906	0.004302	3.318096	Up	aquaporin 4
RPSAP47	1.706609	1.73E-10	1.02E-08	6.383673	Up	ribosomal protein SA pseudogene 47
FCER1G	1.705951	2.92E-14	4.85E-12	7.602027	Up	Fc fragment of IgE receptor Ig
SIGLEC9	1.698602	3.97E-08	1.02E-06	5.492354	Up	sialic acid binding Ig like lectin 9
HS6ST2	1.695316	1.33E-05	0.000134	4.354606	Up	heparansulfate 6-O-sulfotransferase 2
NQO1	1.694258	9.79E-10	4.45E-08	6.112814	Up	NAD(P)H quinone dehydrogenase 1
MELK	1.69103	0.000175	0.00112	3.752058	Up	maternal embryonic leucine zipper kinase
CR1	1.687769	1.07E-09	4.76E-08	6.099248	Up	complement C3b/C4b receptor 1 (Knops blood group)
LGR5	1.685453	0.006707	0.021942	2.711033	Up	leucine rich repeat containing G protein-coupled receptor 5
TREM2	1.685313	1.80E-07	3.68E-06	5.218981	Up	triggering receptor expressed on myeloid cells 2
C5orf47	1.682576	0.000533	0.00278	3.463457	Up	chromosome 5 open reading frame 47
TDGF1P3	1.682479	0.015866	0.043917	2.411988	Up	teratocarcinoma-derived growth factor 1 pseudogene 3
RPL17P5	1.675486	0.001939	0.007957	3.099414	Up	ribosomal protein L17 pseudogene 5
AASS	1.670227	1.39E-14	2.57E-12	7.696848	Up	aminoadipate-semialdehyde synthase
CCL18	1.66744	0.003106	0.01167	2.957086	Up	C-C motif chemokine ligand 18
TRHDE	1.66553	0.001624	0.006901	3.151601	Up	thyrotropin releasing hormone degrading enzyme
HP	1.66454	2.82E-16	7.79E-14	8.18082	Up	haptoglobin
MFN1P1	1.663417	0.000624	0.003179	3.420892	Up	MFN1 pseudogene 1
TAS2R8	1.663194	9.49E-05	0.000676	3.903386	Up	taste 2 receptor member 8
SNORA35B	1.662779	0.001178	0.005334	3.244172	Up	small nucleolar RNA, H/ACA box 35B
SNORA23	1.661962	1.77E-05	0.000169	4.292401	Up	small nucleolar RNA, H/ACA box 23
RNU6-1201P	1.661054	0.00885	0.027432	2.617797	Up	RNA, U6 small nuclear 1201, pseudogene
TC2N	1.658839	8.02E-08	1.87E-06	5.366685	Up	tandem C2 domains, nuclear
IRAK3	1.654092	9.42E-13	1.08E-10	7.138756	Up	interleukin 1 receptor associated kinase 3
MANEA	1.64711	1.84E-07	3.75E-06	5.214785	Up	mannosidaseendo-alpha
LY96	1.645511	1.14E-08	3.52E-07	5.709057	Up	lymphocyte antigen 96
MS4A6A	1.642181	2.23E-11	1.76E-09	6.689876	Up	membrane spanning 4-domains A6A
EEF1B2P2	1.637475	5.55E-16	1.44E-13	8.098744	Up	eukaryotic translation elongation factor 1 beta 2 pseudogene 2
OR52N3P	1.636963	0.008797	0.027323	2.619835	Up	olfactory receptor family 52 subfamily N member 3 pseudogene
CCDC68	1.635162	3.04E-08	8.14E-07	5.539097	Up	coiled-coil domain containing 68
OXGR1	1.631569	0.001906	0.007845	3.104526	Up	oxoglutarate receptor 1
SNORA14A	1.629388	5.58E-06	6.53E-05	4.541763	Up	small nucleolar RNA, H/ACA box 14A

SNORA63D	1.628392	5.51E-10	2.75E-08	6.203763	Up	small nucleolar RNA, H/ACA box 63D
BATF	1.626564	0.001109	0.005076	3.261262	Up	basic leucine zipper ATF-like transcription factor
SNORA12	1.620842	1.45E-05	0.000143	4.335552	Up	small nucleolar RNA, H/ACA box 12
CYBB	1.620824	4.99E-09	1.73E-07	5.847624	Up	cytochrome b-245 beta chain
SNORA20	1.617678	4.39E-06	5.33E-05	4.592027	Up	small nucleolar RNA, H/ACA box 20
RPL39	1.616617	2.14E-07	4.26E-06	5.186666	Up	ribosomal protein L39
ENO1-AS1	1.614146	0.012136	0.035447	2.508163	Up	ENO1 antisense RNA 1
KCNH7	1.613275	0.000284	0.001664	3.629283	Up	potassium voltage-gated channel subfamily H member 7
WDR49	1.613104	1.07E-06	1.64E-05	4.878054	Up	WD repeat domain 49
CDK1	1.607981	6.99E-07	1.14E-05	4.961638	Up	cyclin dependent kinase 1
SGPP2	1.606731	1.22E-05	0.000125	4.374084	Up	sphingosine-1-phosphate phosphatase 2
RNA5-8SN2	1.60281	0.018041	0.048624	2.364776	Up	RNA, 5.8S ribosomal N2
RNA5-8SP10	1.601955	0.01812	0.048804	2.36316	Up	RNA, 5.8S ribosomal pseudogene 10
ELL2	1.60165	8.49E-10	3.95E-08	6.135495	Up	elongation factor for RNA polymerase II 2
RNA5-8SN3	1.600955	0.018211	0.049008	2.361309	Up	RNA, 5.8S ribosomal N3
RNA5-8SN1	1.600276	0.018263	0.049117	2.360237	Up	RNA, 5.8S ribosomal N1
RPL23AP43	1.59674	4.38E-09	1.54E-07	5.869243	Up	ribosomal protein L23a pseudogene 43
RPL11P2	1.589405	0.001046	0.004841	3.277911	Up	ribosomal protein L11 pseudogene 2
RIDA	1.58823	1.72E-07	3.55E-06	5.227317	Up	reactive intermediate imine deaminase A homolog
RNU6-733P	1.585162	0.003849	0.013981	2.890312	Up	RNA, U6 small nuclear 733, pseudogene
RPL17P34	1.58308	0.000144	0.000952	3.800932	Up	ribosomal protein L17 pseudogene 34
SLC7A11	1.581975	0.001229	0.005513	3.232107	Up	solute carrier family 7 member 11
SIRPB2	1.581299	8.44E-13	9.94E-11	7.15385	Up	signal regulatory protein beta 2
DRC1	1.58022	0.01391	0.039445	2.459583	Up	dynein regulatory complex subunit 1
NDUFA4	1.577302	0.000125	0.000848	3.835636	Up	NDUFA4 mitochondrial complex associated
NECAB1	1.575598	1.27E-06	1.88E-05	4.844721	Up	N-terminal EF-hand calcium binding protein 1
TMTC1	1.572658	1.06E-30	3.47E-27	11.5186	Up	transmembrane O-mannosyltransferase targeting cadherins 1
PAFAH1B2P2	1.57226	0.001585	0.006768	3.158708	Up	PAFAH1B2 pseudogene 2
RN7SKP83	1.572085	0.007758	0.024699	2.662424	Up	RN7SK pseudogene 83
SNORD15B	1.571392	8.70E-06	9.42E-05	4.447155	Up	small nucleolar RNA, C/D box 15B
LRMDA	1.569279	1.14E-12	1.27E-10	7.112018	Up	leucine rich melanocyte differentiation associated
H2AC14	1.568373	7.29E-05	0.000542	3.96672	Up	H2A clustered histone 14
SYN2	1.568293	0.000429	0.002324	3.521584	Up	synapsin II
H3C12	1.568271	0.001592	0.006787	3.157385	Up	H3 clustered histone 12
GNMT	1.566584	1.03E-07	2.31E-06	5.321975	Up	glycine N-methyltransferase
C1orf162	1.566215	7.55E-19	3.62E-16	8.86654	Up	chromosome 1 open reading frame 162
STARD7	1.56547	5.23E-12	4.91E-10	6.899143	Up	StAR related lipid transfer domain containing 7
CTH	1.562456	1.73E-10	1.02E-08	6.383435	Up	cystathionine gamma-lyase
RPSAP53	1.561259	3.06E-10	1.66E-08	6.295672	Up	ribosomal protein SA pseudogene 53
TOP2A	1.560869	3.88E-05	0.000325	4.114363	Up	DNA topoisomerase II alpha
H3C8	1.560579	0.000125	0.000848	3.835581	Up	H3 clustered histone 8
DSPP	1.557954	0.000659	0.003323	3.406199	Up	dentin sialophosphoprotein
C1orf105	1.553019	2.24E-05	0.000205	4.239316	Up	chromosome 1 open reading frame 105

PLA1A	1.552684	1.50E-10	9.02E-09	6.40555	Up	phospholipase A1 member A
MYO16-AS1	1.550275	0.014208	0.040139	2.451962	Up	MYO16 antisense RNA 1
CARD18	1.550039	0.006733	0.021997	2.709773	Up	caspase recruitment domain family member 18
SCARNA8	1.549956	0.005527	0.018713	2.774618	Up	small Cajal body-specific RNA 8
RPSAP8	1.548701	1.84E-07	3.75E-06	5.214839	Up	ribosomal protein SA pseudogene 8
RHOU	1.547008	3.03E-16	8.31E-14	8.172136	Up	ras homolog family member U
CFTR	1.544694	1.88E-05	0.000177	4.279055	Up	CF transmembrane conductance regulator
H2BC11	1.542889	1.15E-15	2.76E-13	8.009334	Up	H2B clustered histone 11
H1-5	1.5423	7.80E-05	0.000574	3.95033	Up	H1.5 linker histone, cluster member
H4C6	1.542163	3.05E-06	3.97E-05	4.66725	Up	H4 clustered histone 6
CNTN3	1.541098	1.20E-05	0.000123	4.378264	Up	contactin 3
TAS2R9	1.538989	0.000415	0.002267	3.53023	Up	taste 2 receptor member 9
CLEC7A	1.538473	1.04E-07	2.33E-06	5.319967	Up	C-type lectin domain containing 7A
UAP1	1.537928	9.32E-14	1.38E-11	7.450184	Up	UDP-N-acetylglucosaminepyrophosphorylase 1
F8	1.536294	9.66E-10	4.40E-08	6.114986	Up	coagulation factor VIII
RPL22L1	1.536016	1.20E-15	2.81E-13	8.004165	Up	ribosomal protein L22 like 1
FKBP5	1.535956	3.39E-05	0.000291	4.145574	Up	FKBP prolylase 5
CTSC	1.53189	6.31E-10	3.09E-08	6.182497	Up	cathepsin C
CATIP	1.531775	0.003739	0.013631	2.8994	Up	ciliogenesis associated TTC17 interacting protein
MROH2B	1.529396	3.37E-06	4.30E-05	4.64712	Up	maestro heat like repeat family member 2B
AMD1	1.529031	4.53E-09	1.58E-07	5.863403	Up	adenosylmethionine decarboxylase 1
JCHAIN	1.528867	0.002329	0.009254	3.044656	Up	joining chain of multimeric IgA and IgM
RPS29	1.528524	2.36E-09	9.27E-08	5.971114	Up	ribosomal protein S29
SLC17A3	1.526651	0.000251	0.001501	3.661437	Up	solute carrier family 17 member 3
RPL34P9	1.526313	0.007877	0.025035	2.65731	Up	ribosomal protein L34 pseudogene 9
CCAT2	1.522385	0.013092	0.037581	2.48125	Up	colon cancer associated transcript 2
C3AR1	1.521761	1.27E-07	2.73E-06	5.283316	Up	complement C3a receptor 1
ATP5MD	1.521226	3.58E-05	0.000304	4.132721	Up	ATP synthase membrane subunit DAPIT
TOMM20L	1.518109	0.007005	0.022721	2.696599	Up	translocase of outer mitochondrial membrane 20 like
TDGF1	1.517903	0.009707	0.029561	2.586099	Up	teratocarcinoma-derived growth factor 1
SMIM9	1.517204	2.10E-07	4.19E-06	5.189957	Up	small integral membrane protein 9
RPS17P16	1.515806	1.10E-08	3.42E-07	5.715068	Up	ribosomal protein S17 pseudogene 16
SNORD114-1	1.51367	0.010154	0.030658	2.57053	Up	small nucleolar RNA, C/D box 114-1
SPARCL1	1.511936	1.13E-12	1.27E-10	7.11313	Up	SPARC like 1
IGHV3-48	1.509589	0.017192	0.046753	2.382576	Up	immunoglobulin heavy variable 3-48
IGSF11-AS1	1.509326	0.000633	0.003217	3.416935	Up	IGSF11 antisense RNA 1
MTHFD2	1.507945	8.50E-13	9.96E-11	7.152895	Up	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolatecyclohydrolase
RNU7-47P	1.507736	0.016611	0.045533	2.395199	Up	RNA, U7 small nuclear 47 pseudogene
MRPS36	1.500806	1.11E-07	2.46E-06	5.307513	Up	mitochondrial ribosomal protein S36
RPS15AP19	1.500194	1.44E-05	0.000142	4.337962	Up	ribosomal protein S15a pseudogene 19
ASS1P13	1.500114	0.004139	0.014847	2.867358	Up	argininosuccinatesynthetase 1 pseudogene 13
RPS15AP12	1.499685	5.04E-07	8.68E-06	5.02479	Up	ribosomal protein S15a pseudogene 12

CCN6	1.498809	5.40E-07	9.21E-06	5.01144	Up	cellular communication network factor 6
RNVU1-15	1.497703	0.00577	0.019377	2.760558	Up	RNA, variant U1 small nuclear 15
ANKRD2	1.492058	0.001325	0.005862	3.210581	Up	ankyrin repeat domain 2
CERS6-AS1	1.490253	0.00075	0.003686	3.370516	Up	CERS6 antisense RNA 1
MYO16	1.484418	2.11E-11	1.68E-09	6.698139	Up	myosin XVI
RNU5D-1	1.480081	0.000625	0.00318	3.420598	Up	RNA, U5D small nuclear 1
RNU6-883P	1.479939	0.000339	0.001924	3.583552	Up	RNA, U6 small nuclear 883, pseudogene
XK	1.476882	2.36E-09	9.28E-08	5.970688	Up	X-linked Kx blood group
CHL1	1.470314	0.000109	0.000756	3.87004	Up	cell adhesion molecule L1 like
SERPINI2	1.467813	0.000862	0.004124	3.33222	Up	serpin family I member 2
RPL10AP2	1.46755	6.84E-10	3.30E-08	6.169763	Up	ribosomal protein L10a pseudogene 2
CDCP1	1.467118	2.77E-06	3.66E-05	4.687194	Up	CUB domain containing protein 1
RPL24P7	1.46645	0.005976	0.019931	2.749073	Up	RPL24 pseudogene 7
HIGD1A	1.466146	1.66E-05	0.00016	4.306171	Up	HIG1 hypoxia inducible domain family member 1A
RPL21P134	1.464332	2.14E-06	2.95E-05	4.739288	Up	ribosomal protein L21 pseudogene 134
RPL26P36	1.461518	4.79E-05	0.000384	4.065713	Up	ribosomal protein L26 pseudogene 36
CD38	1.46149	1.53E-12	1.63E-10	7.072127	Up	CD38 molecule
RNASE6	1.460364	8.21E-08	1.91E-06	5.362446	Up	ribonuclease A family member k6
RPS6P26	1.460064	0.013738	0.039042	2.464042	Up	ribosomal protein S6 pseudogene 26
RAD9B	1.458667	2.57E-06	3.42E-05	4.702851	Up	RAD9 checkpoint clamp component B
CD180	1.457665	2.04E-07	4.08E-06	5.196045	Up	CD180 molecule
MAOA	1.455187	4.24E-11	3.02E-09	6.595554	Up	monoamine oxidase A
STC1	1.453056	4.49E-07	7.88E-06	5.047112	Up	stanniocalcin 1
RPL26	1.452966	1.55E-08	4.60E-07	5.655783	Up	ribosomal protein L26
RNU6-861P	1.45206	0.00044	0.002372	3.514638	Up	RNA, U6 small nuclear 861, pseudogene
RNU4ATAC	1.450727	1.21E-07	2.64E-06	5.291672	Up	RNA, U4atac small nuclear (U12-dependent splicing)
RPS15A	1.450304	1.54E-08	4.58E-07	5.656644	Up	ribosomal protein S15a
COX7A2	1.449687	4.24E-05	0.000349	4.093758	Up	cytochrome c oxidase subunit 7A2
COX7B	1.449099	8.98E-05	0.000647	3.916554	Up	cytochrome c oxidase subunit 7B
ASS1P3	1.44836	0.001209	0.005443	3.236753	Up	argininosuccinatesynthetase 1 pseudogene 3
BMPR1B	1.447825	0.000263	0.001561	3.649046	Up	bone morphogenetic protein receptor type 1B
SNORA74D	1.446225	2.53E-07	4.89E-06	5.155778	Up	small nucleolar RNA, H/ACA box 74D
SNORD46	1.446097	1.64E-05	0.000159	4.30866	Up	small nucleolar RNA, C/D box 46
RNU6-85P	1.445226	0.010186	0.030721	2.569448	Up	RNA, U6 small nuclear 85, pseudogene
KLHL40	1.445085	0.000238	0.001438	3.675217	Up	kelch like family member 40
PSMB3P1	1.44425	0.003972	0.01434	2.880396	Up	proteasome subunit beta 3 pseudogene 1
RNU5E-1	1.442091	6.35E-05	0.000483	3.999534	Up	RNA, U5E small nuclear 1
OSTC	1.441725	1.03E-06	1.59E-05	4.885034	Up	oligosaccharyltransferase complex non-catalytic subunit
IGHV3-53	1.440864	0.004522	0.015953	2.839243	Up	immunoglobulin heavy variable 3-53
H2AC12	1.439996	1.95E-07	3.93E-06	5.204473	Up	H2A clustered histone 12
TMEM126A	1.439784	2.71E-05	0.000241	4.196445	Up	transmembrane protein 126A
RPL21P98	1.439262	3.21E-07	5.99E-06	5.110412	Up	ribosomal protein L21 pseudogene 98
RPSAP18	1.43871	7.85E-15	1.59E-12	7.769966	Up	ribosomal protein SA pseudogene 18

SLPI	1.437392	0.001741	0.007297	3.131244	Up	secretory leukocyte peptidase inhibitor
SNX10	1.435195	1.56E-06	2.26E-05	4.803244	Up	sorting nexin 10
SERPINF2	1.434614	6.30E-05	0.000479	4.001415	Up	serpin family F member 2
APOB	1.433745	4.01E-06	4.95E-05	4.610912	Up	apolipoprotein B
PHACTR3-AS1	1.432722	0.003127	0.011742	2.954996	Up	PHACTR3 antisense RNA 1
KCNK2	1.431741	0.001982	0.008096	3.092883	Up	potassium two pore domain channel subfamily K member 2
FGF7	1.430857	3.69E-05	0.000312	4.126136	Up	fibroblast growth factor 7
RPL21P37	1.425707	7.28E-06	8.16E-05	4.485267	Up	ribosomal protein L21 pseudogene 37
RGCC	1.423871	4.13E-09	1.48E-07	5.878712	Up	regulator of cell cycle
SCGB1D2	1.423588	0.006582	0.021579	2.717307	Up	secretoglobin family 1D member 2
GRB14	1.422874	1.60E-06	2.30E-05	4.79862	Up	growth factor receptor bound protein 14
CALCRL	1.422375	0.000325	0.001859	3.594553	Up	calcitonin receptor like receptor
ZNF57	1.421947	9.28E-16	2.25E-13	8.036067	Up	zinc finger protein 57
ZWINT	1.421537	0.001447	0.006299	3.185112	Up	ZW10 interacting kinetochore protein
PRDX1	1.421094	1.48E-09	6.28E-08	6.046997	Up	peroxiredoxin 1
SPINK6	1.42106	0.000208	0.001292	3.709213	Up	serine peptidase inhibitor Kazal type 6
SDR16C5	1.420747	0.001632	0.006924	3.150211	Up	short chain dehydrogenase/reductase family 16C member 5
SAT1	1.419759	3.07E-13	3.99E-11	7.291188	Up	spermidine/spermine N1-acetyltransferase 1
CMTM5	1.416424	0.010686	0.031955	2.552795	Up	CKLF like MARVEL transmembrane domain containing 5
GPR12	1.416355	0.001055	0.004875	3.275431	Up	G protein-coupled receptor 12
ANGPTL1	1.41578	5.67E-06	6.62E-05	4.538219	Up	angiopoietin like 1
TMEM258	1.414885	1.79E-09	7.34E-08	6.015608	Up	transmembrane protein 258
OVCH1	1.41236	1.27E-07	2.73E-06	5.283233	Up	ovochymase 1
LCP1	1.411907	3.95E-09	1.42E-07	5.886312	Up	lymphocyte cytosolic protein 1
HPSE	1.411385	1.45E-09	6.21E-08	6.049631	Up	heparanase
MS4A6E	1.410285	3.05E-05	0.000266	4.17003	Up	membrane spanning 4-domains A6E
LAPTM5	1.409598	3.39E-14	5.49E-12	7.582467	Up	lysosomal protein transmembrane 5
RPS13	1.408548	2.28E-05	0.000208	4.235151	Up	ribosomal protein S13
MARK3	1.408321	1.74E-27	3.29E-24	10.86237	Up	microtubule affinity regulating kinase 3
RNU6-314P	1.408007	0.008827	0.027382	2.618689	Up	RNA, U6 small nuclear 314, pseudogene
PABPC5-AS1	1.407981	0.0026	0.010122	3.011424	Up	PABPC5 antisense RNA 1
KIF20A	1.406715	1.60E-05	0.000155	4.313939	Up	kinesin family member 20A
TMEM97	1.405702	2.93E-08	7.89E-07	5.545813	Up	transmembrane protein 97
GALNT15	1.40252	0.000217	0.001335	3.698475	Up	polypeptide N-acetylgalactosaminyltransferase 15
TNFRSF11A	1.402472	1.04E-11	8.98E-10	6.801005	Up	TNF receptor superfamily member 11a
EEF1E1	1.40119	1.37E-08	4.12E-07	5.677664	Up	eukaryotic translation elongation factor 1 epsilon 1
RPS27	1.399161	2.58E-06	3.44E-05	4.701756	Up	ribosomal protein S27
SNRPG	1.39839	1.13E-05	0.000116	4.391256	Up	small nuclear ribonucleoprotein polypeptide G
TKTL1	1.398184	1.09E-06	1.66E-05	4.874043	Up	transketolase like 1
RPL36AP46	1.396676	8.98E-08	2.05E-06	5.346292	Up	ribosomal protein L36a pseudogene 46
UGT2B4	1.396506	0.000883	0.004211	3.325499	Up	UDP glucuronosyltransferase family 2 member B4
IL18RAP	1.395923	2.98E-05	0.000261	4.175301	Up	interleukin 18 receptor accessory protein

RPS7P1	1.394955	4.19E-07	7.43E-06	5.060171	Up	ribosomal protein S7 pseudogene 1
MRPL50	1.393049	1.37E-05	0.000136	4.349111	Up	mitochondrial ribosomal protein L50
CLEC12A	1.390248	0.001819	0.007561	3.118329	Up	C-type lectin domain family 12 member A
PDE7A	1.389661	1.23E-08	3.79E-07	5.694899	Up	phosphodiesterase 7A
TIMP3	1.389553	1.80E-18	8.28E-16	8.769373	Up	TIMP metalloproteinase inhibitor 3
TMSB4XP4	1.389091	2.81E-06	3.71E-05	4.683997	Up	TMSB4X pseudogene 4
EMB	1.384816	3.95E-06	4.90E-05	4.613757	Up	embigin
AP1S2	1.381599	9.29E-05	0.000664	3.908452	Up	adaptor related protein complex 1 subunit sigma 2
PDE4D	1.381594	3.77E-09	1.37E-07	5.894038	Up	phosphodiesterase 4D
CYP4X1	1.376257	1.39E-12	1.50E-10	7.084667	Up	cytochrome P450 family 4 subfamily X member 1
C7	1.37554	6.25E-08	1.51E-06	5.411628	Up	complement C7
SHC4	1.372456	1.67E-07	3.46E-06	5.232558	Up	SHC adaptor protein 4
RNY3	1.371967	0.000713	0.003539	3.384396	Up	RNA, Ro60-associated Y3
DEPDC1B	1.371127	0.006113	0.020317	2.741635	Up	DEP domain containing 1B
GLIS1	-4.88911	8.26E-09	2.66E-07	-5.76313	Down	GLIS family zinc finger 1
TMEM130	-4.13365	1.60E-05	0.000155	-4.31446	Down	transmembrane protein 130
PRND	-4.11724	0.00016	0.001038	-3.77541	Down	prion like protein doppel
RTN4RL2	-4.02078	1.13E-07	2.49E-06	-5.30509	Down	reticulon 4 receptor like 2
CRACD	-3.86097	1.35E-09	5.85E-08	-6.06087	Down	capping protein inhibiting regulator of actin dynamics
GRIFIN	-3.84956	9.97E-07	1.54E-05	-4.89228	Down	galectin-related inter-fiber protein
GPR78	-3.68804	1.76E-05	0.000168	-4.29352	Down	G protein-coupled receptor 78
LRRC55	-3.68204	6.31E-18	2.58E-15	-8.6267	Down	leucine rich repeat containing 55
CYP2A13	-3.58005	1.82E-05	0.000172	-4.28569	Down	cytochrome P450 family 2 subfamily A member 13
ESM1	-3.56771	4.07E-08	1.04E-06	-5.48761	Down	endothelial cell specific molecule 1
CAPN6	-3.54782	8.41E-07	1.34E-05	-4.92561	Down	calpain 6
EEF1DP5	-3.50705	0.011542	0.034017	-2.52584	Down	eukaryotic translation elongation factor 1 delta pseudogene 5
ELFN2	-3.48594	1.02E-05	0.000107	-4.41371	Down	extracellular leucine rich repeat and fibronectin type III domain containing 2
AGKP1	-3.41899	1.32E-06	1.95E-05	-4.83704	Down	AGK pseudogene 1
SMIM41	-3.40035	0.003837	0.01395	-2.89127	Down	small integral membrane protein 41
ACE	-3.39135	4.80E-60	1.73E-55	-16.344	Down	angiotensin I converting enzyme
FBN3	-3.3666	4.31E-06	5.25E-05	-4.59606	Down	fibrillin 3
MTCYBP2	-3.36649	6.17E-06	7.10E-05	-4.52059	Down	MT-CYB pseudogene 2
CELA2A	-3.34078	0.000882	0.004211	-3.32556	Down	chymotrypsin like elastase 2A
ASPDH	-3.33645	7.67E-07	1.24E-05	-4.9437	Down	aspartate dehydrogenase domain containing
LY6H	-3.3042	0.002921	0.011115	-2.9759	Down	lymphocyte antigen 6 family member H
PENK	-3.29143	3.03E-09	1.15E-07	-5.92992	Down	proenkephalin
FNDC1	-3.2771	8.48E-49	7.62E-45	-14.6814	Down	fibronectin type III domain containing 1
CLEC12A-AS1	-3.27513	0.000824	0.003969	-3.34466	Down	CLEC12A antisense RNA 1
RNU6-255P	-3.25696	2.57E-06	3.42E-05	-4.70288	Down	RNA, U6 small nuclear 255, pseudogene
CCDC114	-3.23009	4.51E-05	0.000366	-4.0797	Down	coiled-coil domain containing 114
TNFRSF4	-3.2264	3.37E-12	3.35E-10	-6.96126	Down	TNF receptor superfamily member 4
TCTE1	-3.20598	0.000519	0.002715	-3.47089	Down	t-complex-associated-testis-expressed 1

FHAD1-AS1	-3.20466	5.63E-06	6.58E-05	-4.53989	Down	FHAD1 antisense RNA 1
CTRB2	-3.19766	0.000172	0.001104	-3.75629	Down	chymotrypsinogen B2
PDE6B-AS1	-3.19396	0.016971	0.046291	-2.38734	Down	PDE6B antisense RNA 1
SYT12	-3.18088	1.76E-06	2.51E-05	-4.77891	Down	synaptotagmin 12
DBH-AS1	-3.17539	8.73E-07	1.38E-05	-4.91835	Down	DBH antisense RNA 1
FATE1	-3.15854	2.19E-06	2.99E-05	-4.73544	Down	fetal and adult testis expressed 1
KNDC1	-3.1471	1.49E-05	0.000146	-4.33039	Down	kinase non-catalytic C-lobe domain containing 1
CASKP1	-3.14455	6.86E-06	7.77E-05	-4.49813	Down	calcium/calmodulin dependent serine protein kinase pseudogene 1
SLC7A4	-3.14253	6.39E-05	0.000486	-3.99774	Down	solute carrier family 7 member 4
MUC12	-3.13836	0.000144	0.000949	-3.80204	Down	mucin 12, cell surface associated
ZNF385D-AS2	-3.137	0.010737	0.032068	-2.55114	Down	ZNF385D antisense RNA 2
OMP	-3.10801	0.00307	0.011566	-2.96065	Down	olfactory marker protein
HSPB6	-3.10522	3.65E-12	3.59E-10	-6.95009	Down	heat shock protein family B (small) member 6
KDM5D	-3.09165	0.000607	0.003105	-3.42863	Down	lysine demethylase 5D
TTY14	-3.08216	0.000905	0.004299	-3.31842	Down	testis-specific transcript, Y-linked 14
SSC5D	-3.06747	1.63E-22	1.43E-19	-9.76226	Down	scavenger receptor cysteine rich family member with 5 domains
NHLRC4	-3.05493	4.01E-09	1.44E-07	-5.88376	Down	NHL repeat containing 4
AMH	-3.05356	8.17E-06	8.97E-05	-4.46078	Down	anti-Mullerian hormone
COL22A1	-3.04613	5.15E-09	1.78E-07	-5.8423	Down	collagen type XXII alpha 1 chain
PTX4	-3.04335	0.001702	0.007165	-3.1379	Down	pentraxin 4
UTY	-3.03674	0.000311	0.001788	-3.60634	Down	ubiquitously transcribed tetratricopeptide repeat containing, Y-linked
LRFN1	-3.03561	8.30E-05	0.000604	-3.93543	Down	leucine rich repeat and fibronectin type III domain containing 1
TRPM5	-3.03501	0.004501	0.015897	-2.84071	Down	transient receptor potential cation channel subfamily M member 5
APLNR	-3.0197	2.20E-29	5.28E-26	-11.2544	Down	apelin receptor
DDX3Y	-3.00674	0.000247	0.001482	-3.66542	Down	DEAD-box helicase 3 Y-linked
CHD5	-3.00243	5.69E-07	9.59E-06	-5.00144	Down	chromodomain helicase DNA binding protein 5
OFD1P7Y	-2.99908	4.35E-05	0.000357	-4.08781	Down	OFD1 pseudogene 7 Y-linked
FOSB	-2.982	1.29E-07	2.76E-06	-5.28016	Down	FosB proto-oncogene, AP-1 transcription factor subunit
UICLM	-2.97822	0.00174	0.007295	-3.13136	Down	up-regulated in colorectal cancer liver metastasis
CYSRT1	-2.97481	7.91E-06	8.74E-05	-4.46762	Down	cysteine rich tail 1
ATP1B2	-2.97341	6.57E-28	1.31E-24	-10.9511	Down	ATPase Na ⁺ /K ⁺ transporting subunit beta 2
SEZ6L2	-2.96892	3.17E-10	1.71E-08	-6.29043	Down	seizure related 6 homolog like 2
LOXHD1	-2.95005	8.51E-26	1.27E-22	-10.5014	Down	lipxygenase homology domains 1
DKKL1 CTD-	-2.94902	0.0003	0.001736	-3.61569	Down	dickkopf like acrosomal protein 1
3080P12.3	-2.93164	0.000223	0.001364	-3.69133	Down	uncharacterized LOC101928857
TLR9	-2.92385	0.001216	0.005467	-3.23521	Down	toll like receptor 9
GET4	-2.9126	4.19E-05	0.000346	-4.0969	Down	guided entry of tail-anchored proteins factor 4
BARHL1	-2.91083	0.001658	0.007018	-3.14546	Down	BarH like homeobox 1
KRTAP5-1	-2.90524	2.52E-07	4.88E-06	-5.15598	Down	keratin associated protein 5-1
CCL3L1	-2.90351	2.27E-06	3.09E-05	-4.72751	Down	C-C motif chemokine ligand 3 like 1
MUC3A	-2.90125	2.33E-17	8.13E-15	-8.47602	Down	mucin 3A, cell surface associated
RBMV2YP	-2.89787	0.001804	0.007512	-3.12081	Down	RNA binding motif protein Y-linked family 2 member Y, pseudogene

OFD1P4Y	-2.89243	0.000176	0.001122	-3.75167	Down	OFD1 pseudogene 4 Y-linked
MED14P1	-2.88792	0.000195	0.001226	-3.72506	Down	mediator complex subunit 14 pseudogene 1
ENTPD8	-2.88316	1.95E-05	0.000183	-4.27	Down	ectonucleoside triphosphate diphosphohydrolase 8
TRIL	-2.88005	1.06E-43	7.61E-40	-13.8632	Down	TLR4 interactor with leucine rich repeats
RN7SKP282	-2.87538	4.94E-05	0.000393	-4.05859	Down	RN7SK pseudogene 282
NXNL1	-2.87209	0.002172	0.008723	-3.0656	Down	nucleoredoxin like 1
RSPH6A	-2.86695	0.001099	0.005037	-3.2639	Down	radial spoke head 6 homolog A
LRRC38	-2.86614	0.000415	0.002268	-3.53009	Down	leucine rich repeat containing 38
RBMV2WP	-2.85224	0.001871	0.007734	-3.11003	Down	RNA binding motif protein Y-linked family 2 member W, pseudogene
RBMV2XP	-2.85224	0.001871	0.007734	-3.11003	Down	RNA binding motif protein Y-linked family 2 member X, pseudogene
FLYWCH1P1	-2.85167	0.012781	0.036883	-2.48983	Down	FLYWCH-type zinc finger 1 pseudogene 1
OFD1P10Y	-2.84945	0.004613	0.016205	-2.83289	Down	OFD1 pseudogene 10 Y-linked
MUC5B	-2.83758	9.25E-10	4.27E-08	-6.12188	Down	mucin 5B, oligomeric mucus/gel-forming
TTY10	-2.83734	0.005326	0.018179	-2.78665	Down	testis-specific transcript, Y-linked 10
GRID2IP	-2.81491	4.63E-07	8.08E-06	-5.04119	Down	Grid2 interacting protein
RNF208	-2.80701	1.03E-09	4.64E-08	-6.10392	Down	ring finger protein 208
SFRP4	-2.80559	9.58E-10	4.38E-08	-6.11626	Down	secreted frizzled related protein 4
ACER1	-2.80336	0.00105	0.004857	-3.27675	Down	alkaline ceramidase 1
EGR1	-2.79643	1.14E-09	5.03E-08	-6.08886	Down	early growth response 1
MAST1	-2.78643	0.000106	0.000738	-3.87721	Down	microtubule associated serine/threonine kinase 1
ESPN	-2.77946	7.62E-06	8.47E-05	-4.47559	Down	espin
CCDC63	-2.7779	1.74E-07	3.58E-06	-5.22545	Down	coiled-coil domain containing 63
ADAMTS14	-2.77508	5.98E-13	7.35E-11	-7.20105	Down	ADAM metalloproteinase with thrombospondin type 1 motif 14
PRRT1	-2.76987	3.11E-08	8.27E-07	-5.53503	Down	proline rich transmembrane protein 1
COL1A1	-2.7648	4.37E-12	4.19E-10	-6.92468	Down	collagen type I alpha 1 chain
STIM1-AS1	-2.76439	0.000124	0.000841	-3.83827	Down	STIM1 antisense RNA 1
APLP1	-2.76348	3.42E-17	1.12E-14	-8.43114	Down	amyloid beta precursor like protein 1
ARHGAP33	-2.73208	4.43E-17	1.42E-14	-8.4009	Down	Rho GTPase activating protein 33
DUOXA2	-2.72376	0.000224	0.001367	-3.69061	Down	dual oxidase maturation factor 2
ZNF839P1	-2.72326	0.001312	0.005816	-3.21335	Down	zinc finger protein 839 pseudogene 1
IGDCC3	-2.7068	3.17E-05	0.000275	-4.16094	Down	immunoglobulin superfamily DCC subclass member 3
HBA1	-2.70354	1.60E-08	4.74E-07	-5.65021	Down	hemoglobin subunit alpha 1
RTN4R	-2.70303	8.57E-12	7.72E-10	-6.82863	Down	reticulon 4 receptor
DOC2A	-2.68864	1.40E-07	2.97E-06	-5.26478	Down	double C2 domain alpha
PTPRVP	-2.68667	2.81E-05	0.000249	-4.18823	Down	protein tyrosine phosphatase receptor type V, pseudogene
TMEM121	-2.67382	1.20E-06	1.79E-05	-4.85638	Down	transmembrane protein 121
EPS8L2	-2.67091	1.78E-08	5.17E-07	-5.63197	Down	EPS8 like 2
CILP2	-2.66831	1.59E-05	0.000154	-4.31613	Down	cartilage intermediate layer protein 2
BCORP1	-2.66043	0.001467	0.006366	-3.18113	Down	BCL6 corepressor pseudogene 1
RIMBP2	-2.65867	0.001	0.004667	-3.29045	Down	RIMS binding protein 2
CA7	-2.65493	0.000783	0.00381	-3.35861	Down	carbonic anhydrase 7
FZD10-AS1	-2.65402	8.30E-06	9.09E-05	-4.45731	Down	FZD10 antisense divergent transcript
GNG8	-2.64512	0.001051	0.004859	-3.27649	Down	G protein subunit gamma 8

C10orf90	-2.63237	0.000445	0.002394	-3.51161	Down	chromosome 10 open reading frame 90
PALM3	-2.62953	0.001466	0.006363	-3.18132	Down	paralemmin 3
PPDPF	-2.62731	1.83E-10	1.07E-08	-6.37501	Down	pancreatic progenitor cell differentiation and proliferation factor
MTND6P24	-2.62664	0.01694	0.046233	-2.388	Down	MT-ND6 pseudogene 24
PRR12	-2.62536	1.14E-12	1.27E-10	-7.11302	Down	proline rich 12
ELFN1-AS1	-2.62504	0.000224	0.001368	-3.6904	Down	ELFN1 antisense RNA 1
GLI2	-2.6227	7.56E-16	1.87E-13	-8.06117	Down	GLI family zinc finger 2
OIT3	-2.61731	6.24E-05	0.000476	-4.00361	Down	oncoprotein induced transcript 3
RP1L1	-2.60824	1.80E-07	3.68E-06	-5.21903	Down	RP1 like 1
C2CD4D	-2.60552	9.06E-05	0.000651	-3.91449	Down	C2 calcium dependent domain containing 4D
SLC16A13	-2.60311	4.82E-09	1.67E-07	-5.85333	Down	solute carrier family 16 member 13
IER3-AS1	-2.59841	0.001292	0.005745	-3.21781	Down	IER3 antisense RNA 1
DUX4L26	-2.59701	0.002646	0.010262	-3.00617	Down	double homeobox 4 like 26 (pseudogene)
HMCN2	-2.59332	2.21E-13	2.94E-11	-7.33515	Down	hemicentin 2
R3HDML	-2.5901	0.011063	0.032856	-2.54069	Down	R3H domain containing like
KRTAP10-7	-2.58854	0.016217	0.044688	-2.40399	Down	keratin associated protein 10-7
ATP6V1B1	-2.57882	0.000557	0.002881	-3.45183	Down	ATPase H ⁺ transporting V1 subunit B1
NAT8L	-2.57001	3.28E-06	4.21E-05	-4.65255	Down	N-acetyltransferase 8 like
SRCIN1	-2.56661	9.07E-15	1.81E-12	-7.75162	Down	SRC kinase signaling inhibitor 1
NRGN	-2.56324	1.74E-08	5.07E-07	-5.63633	Down	neurogranin
PRKY	-2.56199	1.10E-08	3.41E-07	-5.71527	Down	protein kinase Y-linked (pseudogene)
GCSIR	-2.56155	0.000338	0.001919	-3.58443	Down	GPR55 cis regulatory suppressor of immune response RNA
TLCD3B	-2.55905	0.004609	0.016197	-2.83318	Down	TLC domain containing 3B
HBA2	-2.55637	1.02E-07	2.30E-06	-5.3224	Down	hemoglobin subunit alpha 2
THY1	-2.55521	9.72E-12	8.49E-10	-6.81066	Down	Thy-1 cell surface antigen
OFD1P8Y	-2.55452	0.004509	0.015917	-2.84018	Down	OFD1 pseudogene 8 Y-linked
RET	-2.55272	1.30E-14	2.44E-12	-7.70568	Down	ret proto-oncogene
CACNG8	-2.54658	1.41E-07	2.99E-06	-5.26385	Down	calcium voltage-gated channel auxiliary subunit gamma 8
FOXD3	-2.54645	0.000113	0.000783	-3.85981	Down	forkhead box D3
MAPK8IP1P1	-2.54579	0.014191	0.0401	-2.45239	Down	mitogen-activated protein kinase 8 interacting protein 1 pseudogene 1
STX1B	-2.54292	6.58E-13	7.98E-11	-7.18793	Down	syntaxin 1B
DBH	-2.54094	0.000237	0.001436	-3.67564	Down	dopamine beta-hydroxylase
GZMM	-2.52033	0.001709	0.007189	-3.13669	Down	granzyme M
CLDN5	-2.51806	2.10E-17	7.41E-15	-8.48797	Down	claudin 5
PPIAP39	-2.51602	0.00024	0.001448	-3.67281	Down	peptidylprolylisomerase A pseudogene 39
AMBP	-2.51577	0.000259	0.00154	-3.65339	Down	alpha-1-microglobulin/bikunin precursor
IGF2	-2.51532	1.44E-08	4.32E-07	-5.66855	Down	insulin like growth factor 2
MXRA5Y	-2.51245	1.69E-10	1.00E-08	-6.38708	Down	matrix remodeling associated 5 Y-linked (pseudogene)
FOXP3	-2.51209	5.20E-05	0.00041	-4.04637	Down	forkhead box P3
GLP1R	-2.50999	2.54E-08	7.05E-07	-5.57025	Down	glucagon like peptide 1 receptor
ZNF683	-2.50826	0.001445	0.006294	-3.1855	Down	zinc finger protein 683
SYCE1	-2.5066	0.000828	0.003987	-3.34326	Down	synaptonemal complex central element protein 1
CYP2F1	-2.50653	6.04E-06	6.97E-05	-4.52515	Down	cytochrome P450 family 2 subfamily F member 1

LKAAEAR1	-2.50603	0.009467	0.028991	-2.59473	Down	LKAAEAR motif containing 1
TCF7L1	-2.50142	3.95E-12	3.83E-10	-6.93904	Down	transcription factor 7 like 1
SLC6A1-AS1	-2.48806	1.30E-09	5.65E-08	-6.06746	Down	SLC6A1 antisense RNA 1
NTN5	-2.48779	9.33E-06	9.97E-05	-4.43218	Down	netrin 5
DPRX	-2.48757	0.001582	0.006761	-3.15923	Down	divergent-paired related homeobox
MTND5P19	-2.48481	0.017196	0.046762	-2.38248	Down	MT-ND5 pseudogene 19
GYG2P1	-2.47504	3.22E-05	0.000278	-4.15758	Down	glycogenin 2 pseudogene 1
MTND2P12	-2.47088	0.004689	0.016426	-2.82765	Down	MT-ND2 pseudogene 12
SARDH	-2.46482	2.22E-09	8.81E-08	-5.98071	Down	sarcosine dehydrogenase
LYPD1	-2.45426	0.004416	0.015637	-2.84681	Down	LY6/PLAUR domain containing 1
L1TD1	-2.45214	0.010908	0.032464	-2.54564	Down	LINE1 type transposase domain containing 1
PRRT2	-2.45178	1.54E-13	2.16E-11	-7.38349	Down	proline rich transmembrane protein 2
SLC6A9	-2.44763	4.00E-16	1.06E-13	-8.13862	Down	solute carrier family 6 member 9
RNU6-321P	-2.44484	0.001516	0.00653	-3.17168	Down	RNA, U6 small nuclear 321, pseudogene
ACHE	-2.4389	2.27E-14	4.00E-12	-7.63413	Down	acetylcholinesterase (Cartwright blood group)
PNPLA7	-2.43362	2.02E-11	1.61E-09	-6.70477	Down	patatin like phospholipase domain containing 7
C17orf50	-2.43052	0.010256	0.030877	-2.56708	Down	chromosome 17 open reading frame 50
IL34	-2.42559	3.58E-12	3.54E-10	-6.9529	Down	interleukin 34
CLIP3	-2.42499	1.84E-10	1.07E-08	-6.37395	Down	CAP-Gly domain containing linker protein 3
RNU1-31P	-2.41842	3.87E-06	4.81E-05	-4.61821	Down	RNA, U1 small nuclear 31, pseudogene
DEFB124	-2.41708	7.20E-05	0.000536	-3.96972	Down	defensin beta 124
TM7SF2	-2.41624	1.13E-37	5.82E-34	-12.8286	Down	transmembrane 7 superfamily member 2
ZSWIM9	-2.41143	1.75E-08	5.08E-07	-5.63547	Down	zinc finger SWIM-type containing 9
CTRB1	-2.41047	1.41E-05	0.00014	-4.34234	Down	chymotrypsinogen B1
PIK3R6	-2.40855	1.96E-15	4.45E-13	-7.94414	Down	phosphoinositide-3-kinase regulatory subunit 6
RNASE10	-2.40739	0.007658	0.024452	-2.66679	Down	ribonuclease A family member 10 (inactive)
NRXN2	-2.40499	2.03E-10	1.17E-08	-6.35874	Down	neurexin 2
TMPRSS6	-2.40366	0.000383	0.002127	-3.55145	Down	transmembrane serine protease 6
ZFXH2	-2.40102	5.30E-10	2.66E-08	-6.21001	Down	zinc finger homeobox 2
PODNL1	-2.39752	3.98E-07	7.12E-06	-5.06971	Down	podocan like 1
ADGRB1	-2.3927	2.63E-06	3.50E-05	-4.69758	Down	adhesion G protein-coupled receptor B1
C16orf78	-2.3906	0.000424	0.002303	-3.52469	Down	chromosome 16 open reading frame 78
MRGPRE	-2.38919	0.00096	0.004515	-3.30191	Down	MAS related GPR family member E
FIGNL2-DT	-2.38916	0.003786	0.013791	-2.8955	Down	FIGNL2 divergent transcript
SHANK1	-2.38796	4.81E-06	5.77E-05	-4.57295	Down	SH3 and multiple ankyrin repeat domains 1
GUCY1B2	-2.38687	0.000511	0.002683	-3.47483	Down	guanylatecyclase 1 soluble subunit beta 2 (pseudogene)
KCNN1	-2.38554	0.002291	0.009132	-3.04961	Down	potassium calcium-activated channel subfamily N member 1
NPPA	-2.3854	0.002748	0.010582	-2.99456	Down	natriuretic peptide A
MTCO3P22	-2.38323	0.008232	0.025929	-2.6424	Down	MT-CO3 pseudogene 22
UPK3BP1	-2.38283	7.41E-05	0.00055	-3.96272	Down	uroplakin 3B pseudogene 1
PHF21B	-2.38254	6.95E-06	7.85E-05	-4.49516	Down	PHD finger protein 21B
MLIP-IT1	-2.38121	0.003684	0.013469	-2.90399	Down	MLIP intronic transcript 1
UPK3B	-2.37776	1.96E-06	2.74E-05	-4.7574	Down	uroplakin 3B

UTS2R	-2.3705	0.002076	0.008412	-3.07916	Down	urotensin 2 receptor
PLPPR3	-2.36936	0.008809	0.027346	-2.61937	Down	phospholipid phosphatase related 3
DPYSL5	-2.36884	0.01321	0.037842	-2.47805	Down	dihydropyrimidinase like 5
C1QTNF9	-2.36667	3.11E-17	1.03E-14	-8.44223	Down	C1q and TNF related 9
MYCN	-2.36507	3.04E-08	8.14E-07	-5.53893	Down	MYCN proto-oncogene, bHLH transcription factor
IQCN	-2.36358	4.19E-14	6.64E-12	-7.55489	Down	IQ motif containing N
SYCE1L	-2.3627	0.000689	0.003442	-3.39388	Down	synaptonemal complex central element protein 1 like
FAM171A2	-2.36011	3.16E-06	4.08E-05	-4.66	Down	family with sequence similarity 171 member A2
ENTPD2	-2.35956	1.18E-09	5.17E-08	-6.08324	Down	ectonucleoside triphosphate diphosphohydrolase 2
BICDL2	-2.35952	0.004821	0.01679	-2.81877	Down	BICD family like cargo adaptor 2
LMTK3	-2.35747	9.81E-07	1.52E-05	-4.89548	Down	lemur tyrosine kinase 3
OGDHL	-2.35098	3.39E-13	4.36E-11	-7.27805	Down	oxoglutarate dehydrogenase L
OFD1P9Y	-2.35018	0.010683	0.03195	-2.55291	Down	OFD1 pseudogene 9 Y-linked
ZNF628	-2.34926	2.25E-08	6.32E-07	-5.5916	Down	zinc finger protein 628
PSD2	-2.34798	0.001056	0.004879	-3.27515	Down	pleckstrin and Sec7 domain containing 2
IL2RB	-2.34781	1.14E-09	5.05E-08	-6.08791	Down	interleukin 2 receptor subunit beta
ASGR1	-2.34753	0.004	0.014427	-2.87813	Down	asialoglycoprotein receptor 1
CCN1	-2.34567	1.08E-06	1.65E-05	-4.87672	Down	cellular communication network factor 1
KRT18P58	-2.34189	0.003655	0.013386	-2.90647	Down	keratin 18 pseudogene 58
TMEM132E	-2.34128	0.016615	0.04554	-2.39511	Down	transmembrane protein 132E
MTCO1P23	-2.33854	0.007951	0.025226	-2.65415	Down	MT-CO1 pseudogene 23
IGSF9	-2.33842	0.000443	0.002386	-3.51289	Down	immunoglobulin superfamily member 9
SLC5A2	-2.33461	1.86E-06	2.63E-05	-4.768	Down	solute carrier family 5 member 2
FRMD1	-2.33169	0.003686	0.013472	-2.90388	Down	FERM domain containing 1
TINCR	-2.33096	3.33E-05	0.000287	-4.14965	Down	TINCR ubiquitin domain containing
CROCCP4	-2.33006	0.000907	0.004304	-3.31779	Down	CROCC pseudogene 4
FIGNL2	-2.32742	2.97E-06	3.88E-05	-4.67274	Down	fidgetin like 2
CDSN	-2.32601	0.002325	0.009237	-3.04528	Down	corneodesmosin
RAB43	-2.32013	0.00016	0.00104	-3.77454	Down	RAB43, member RAS oncogene family
CACNA1G	-2.3186	1.19E-11	1.01E-09	-6.78111	Down	calcium voltage-gated channel subunit alpha1 G
SOX18	-2.31637	1.21E-06	1.82E-05	-4.85334	Down	SRY-box transcription factor 18
EFCC1	-2.31374	9.15E-12	8.14E-10	-6.81925	Down	EF-hand and coiled-coil domain containing 1
TMEM145	-2.31353	0.000263	0.00156	-3.64933	Down	transmembrane protein 145
ADRA2A	-2.31285	6.71E-09	2.22E-07	-5.79806	Down	adrenoceptor alpha 2A
P2RY8	-2.31022	7.12E-18	2.88E-15	-8.61294	Down	P2Y receptor family member 8
RPL18AP14	-2.30597	0.002898	0.011041	-2.97838	Down	ribosomal protein L18a pseudogene 14
KCNJ9	-2.30447	9.20E-05	0.000659	-3.91091	Down	potassium inwardly rectifying channel subfamily J member 9
PERCC1	-2.30111	0.00217	0.008717	-3.06597	Down	proline and glutamate rich with coiled coil 1
PANX2	-2.29938	0.004126	0.014809	-2.86836	Down	pannexin 2
ACOXL	-2.29881	0.000511	0.002681	-3.47501	Down	acyl-CoA oxidase like
MRPL12	-2.29849	5.75E-08	1.40E-06	-5.42656	Down	mitochondrial ribosomal protein L12
KCNF1	-2.2959	0.001876	0.007749	-3.10919	Down	potassium voltage-gated channel modifier subfamily F member 1
DUOX2	-2.29502	3.40E-10	1.81E-08	-6.27923	Down	dual oxidase 2

SNX19P4	-2.28619	2.92E-06	3.82E-05	-4.67642	Down	sorting nexin 19 pseudogene 4
BRSK1	-2.28322	5.23E-09	1.80E-07	-5.83973	Down	BR serine/threonine kinase 1
PSAT1P3	-2.28151	0.001777	0.007422	-3.12524	Down	phosphoserine aminotransferase 1 pseudogene 3
AQP12B	-2.28151	0.00146	0.006347	-3.18246	Down	aquaporin 12B
PDE4C	-2.27831	1.12E-06	1.69E-05	-4.86984	Down	phosphodiesterase 4C
CHERP	-2.27507	4.49E-10	2.30E-08	-6.23601	Down	calcium homeostasis endoplasmic reticulum protein
ARID5A	-2.27456	2.37E-11	1.84E-09	-6.68092	Down	AT-rich interaction domain 5A
COL20A1	-2.27281	0.007612	0.024328	-2.6688	Down	collagen type XX alpha 1 chain
FOXO6	-2.27206	9.53E-06	0.000102	-4.42747	Down	forkhead box O6
RSPO2	-2.26961	0.006776	0.022115	-2.70767	Down	R-spondin 2
MXRA5	-2.26826	1.80E-10	1.06E-08	-6.37763	Down	matrix remodeling associated 5
ETS1-AS1	-2.26747	4.32E-06	5.26E-05	-4.59557	Down	ETS1 antisense RNA 1
SEZ6L	-2.26711	1.34E-06	1.97E-05	-4.83439	Down	seizure related 6 homolog like
SLC34A3	-2.26426	8.79E-07	1.39E-05	-4.9169	Down	solute carrier family 34 member 3
ISLR2	-2.26368	7.31E-16	1.84E-13	-8.06518	Down	immunoglobulin superfamily containing leucine rich repeat 2
C1QTNF12	-2.25484	6.17E-05	0.000471	-4.0063	Down	C1q and TNF related 12
IQCA1	-2.25295	1.03E-10	6.51E-09	-6.46319	Down	IQ motif containing with AAA domain 1
TMEM59L	-2.25074	3.58E-06	4.53E-05	-4.63426	Down	transmembrane protein 59 like
LMNTD2	-2.24913	0.00123	0.005519	-3.23172	Down	lamin tail domain containing 2
SNORD37	-2.24319	0.001456	0.006328	-3.1834	Down	small nucleolar RNA, C/D box 37
B4GALNT4	-2.24123	7.74E-05	0.00057	-3.95225	Down	beta-1,4-N-acetyl-galactosaminyltransferase 4
OXER1	-2.23961	2.42E-09	9.45E-08	-5.96682	Down	oxoeicosanoid receptor 1
FBXL16	-2.23826	3.88E-07	6.97E-06	-5.07483	Down	F-box and leucine rich repeat protein 16
BGN	-2.23532	1.02E-09	4.59E-08	-6.10609	Down	biglycan
KLK10	-2.23502	0.003998	0.014424	-2.87829	Down	kallikrein related peptidase 10
NOS2	-2.23486	8.89E-08	2.04E-06	-5.34813	Down	nitric oxide synthase 2
SSPOP	-2.23408	7.10E-12	6.50E-10	-6.85557	Down	SCO-spondin, pseudogene
AGRN	-2.23361	2.43E-20	1.56E-17	-9.24168	Down	agrin
KCNC3	-2.22953	2.78E-08	7.59E-07	-5.55472	Down	potassium voltage-gated channel subfamily C member 3
RNU1-129P	-2.22634	0.013814	0.039221	-2.46205	Down	RNA, U1 small nuclear 129, pseudogene
MYO3B-AS1	-2.22206	0.006159	0.020437	-2.73918	Down	MYO3B antisense RNA 1
GP5	-2.22182	0.001462	0.006351	-3.18211	Down	glycoprotein V platelet
NXPH4	-2.22096	0.000762	0.00373	-3.36634	Down	neurexophilin 4
RN7SKP57	-2.22006	7.00E-05	0.000525	-3.97614	Down	RN7SK pseudogene 57
RHCG	-2.2183	0.013078	0.037549	-2.48164	Down	Rh family C glycoprotein
ILDR1	-2.21663	0.011963	0.035027	-2.51324	Down	immunoglobulin like domain containing receptor 1
DPPA2P1	-2.21463	0.004363	0.015485	-2.85061	Down	developmental pluripotency associated 2 pseudogene 1
ATN1	-2.21455	1.28E-09	5.56E-08	-6.0702	Down	atrophin 1
TMEM240	-2.21328	5.50E-07	9.33E-06	-5.00791	Down	transmembrane protein 240
GABRD	-2.21257	0.000126	0.00085	-3.83465	Down	gamma-aminobutyric acid type A receptor subunit delta
TMPRSS9	-2.21056	1.76E-07	3.62E-06	-5.22295	Down	transmembrane serine protease 9
ERICH4	-2.20739	1.87E-09	7.61E-08	-6.0085	Down	glutamate rich 4
DUSP8	-2.20557	1.74E-13	2.39E-11	-7.36744	Down	dual specificity phosphatase 8

SEC1P	-2.20125	4.40E-05	0.00036	-4.08523	Down	secretory blood group 1, pseudogene
LRRC36	-2.20092	0.006616	0.021682	-2.71556	Down	leucine rich repeat containing 36
LAMP5	-2.19636	0.004457	0.015761	-2.84389	Down	lysosomal associated membrane protein family member 5
FOXN4	-2.1962	0.006671	0.021835	-2.71283	Down	forkhead box N4
PCGF2	-2.19263	7.89E-09	2.55E-07	-5.77072	Down	polycomb group ring finger 2
H3-4	-2.18887	0.008728	0.027143	-2.62253	Down	H3.4 histone
PRRG3	-2.18611	5.58E-10	2.78E-08	-6.20184	Down	proline rich and Gla domain 3
DRD1	-2.18589	0.013624	0.038814	-2.46704	Down	dopamine receptor D1
MAMSTR	-2.18365	5.31E-11	3.72E-09	-6.56199	Down	MEF2 activating motif and SAP domain containing transcriptional regulator
ANKRD24	-2.18362	9.58E-07	1.49E-05	-4.90012	Down	ankyrin repeat domain 24
BEGAIN	-2.18234	3.85E-10	2.00E-08	-6.25983	Down	brain enriched guanylate kinase associated
FOXI2	-2.18159	0.002899	0.011044	-2.97824	Down	forkhead box I2
RPL23AP66	-2.18022	0.003306	0.012312	-2.93771	Down	ribosomal protein L23a pseudogene 66
COL9A1	-2.18	2.87E-09	1.09E-07	-5.9391	Down	collagen type IX alpha 1 chain
KRTAP10-11	-2.17351	0.011701	0.034405	-2.52104	Down	keratin associated protein 10-11
GRIK4	-2.16696	3.70E-05	0.000313	-4.12527	Down	glutamate ionotropic receptor kainate type subunit 4
BAALC-AS2	-2.16416	0.005768	0.019374	-2.76069	Down	BAALC antisense RNA 2
CCL3	-2.16136	0.000955	0.004498	-3.30341	Down	C-C motif chemokine ligand 3
COL11A2	-2.1607	2.66E-11	2.03E-09	-6.66427	Down	collagen type XI alpha 2 chain
RN7SL202P	-2.15989	0.005109	0.017562	-2.8001	Down	RNA, 7SL, cytoplasmic 202, pseudogene
LTBP4	-2.15753	1.25E-14	2.35E-12	-7.71093	Down	latent transforming growth factor beta binding protein 4
TRIM50	-2.1574	1.78E-06	2.53E-05	-4.77679	Down	tripartite motif containing 50
ADGRG5	-2.14625	7.15E-05	0.000533	-3.97109	Down	adhesion G protein-coupled receptor G5
SAMD11P1	-2.14455	9.60E-06	0.000102	-4.42592	Down	sterile alpha motif domain containing 11 pseudogene 1
SLC17A7	-2.13874	7.48E-10	3.56E-08	-6.1555	Down	solute carrier family 17 member 7
WHRN	-2.13771	7.30E-06	8.17E-05	-4.48489	Down	whirlin
MBD6	-2.13614	3.52E-09	1.29E-07	-5.90532	Down	methyl-CpG binding domain protein 6
ZNF414	-2.13232	2.39E-09	9.34E-08	-5.96896	Down	zinc finger protein 414
ISLR	-2.1306	2.62E-36	1.18E-32	-12.583	Down	immunoglobulin superfamily containing leucine rich repeat
KIF26B	-2.12741	7.13E-06	8.02E-05	-4.48968	Down	kinesin family member 26B
RFX1	-2.12674	3.57E-10	1.87E-08	-6.27188	Down	regulatory factor X1
SHANK2	-2.12333	1.93E-08	5.53E-07	-5.61843	Down	SH3 and multiple ankyrin repeat domains 2
TNFRSF18	-2.12084	0.01253	0.036332	-2.49686	Down	TNF receptor superfamily member 18
MRPS21P7	-2.12048	0.002107	0.008517	-3.07466	Down	mitochondrial ribosomal protein S21 pseudogene 7
RNU6-1306P	-2.12009	0.006834	0.022266	-2.70483	Down	RNA, U6 small nuclear 1306, pseudogene
MYH11	-2.11903	1.68E-09	6.98E-08	-6.02654	Down	myosin heavy chain 11
ADRA1D	-2.11595	0.000191	0.0012	-3.73117	Down	adrenoceptor alpha 1D
SCT	-2.11518	0.000784	0.00381	-3.35848	Down	secretin
ZNF469	-2.11477	1.93E-13	2.61E-11	-7.35371	Down	zinc finger protein 469
BIRC7	-2.11335	0.006668	0.021825	-2.713	Down	baculoviral IAP repeat containing 7
IQSEC3	-2.11314	1.33E-11	1.11E-09	-6.76538	Down	IQ motif and Sec7 domain ArfGEF 3
CDH23	-2.10915	9.84E-36	3.93E-32	-12.478	Down	cadherin related 23
SDSL	-2.10885	2.54E-11	1.96E-09	-6.67098	Down	serine dehydratase like

CECR3	-2.10827	0.000711	0.003532	-3.38514	Down	cat eye syndrome chromosome region, candidate 3
LTBP2	-2.10749	4.84E-08	1.21E-06	-5.45694	Down	latent transforming growth factor beta binding protein 2
KRTAP12-1	-2.10631	0.014011	0.039687	-2.45699	Down	keratin associated protein 12-1
COMP	-2.10261	0.003359	0.013189	-2.91212	Down	cartilage oligomeric matrix protein
ARHGEF16	-2.10106	2.11E-06	2.90E-05	-4.74286	Down	Rho guanine nucleotide exchange factor 16
RASA4	-2.10077	1.08E-06	1.65E-05	-4.87636	Down	RAS p21 protein activator 4
CYP2W1	-2.0992	0.000428	0.002322	-3.52188	Down	cytochrome P450 family 2 subfamily W member 1
MSI1	-2.09799	5.68E-15	1.17E-12	-7.81086	Down	musashi RNA binding protein 1
PCDHA2	-2.08955	0.002206	0.008837	-3.06107	Down	protocadherin alpha 2
KIAA1210	-2.08779	7.13E-05	0.000532	-3.97194	Down	KIAA1210
SLC26A10	-2.08301	8.04E-08	1.87E-06	-5.36616	Down	solute carrier family 26 member 10
PRXL2AP1	-2.08172	0.008009	0.025359	-2.65169	Down	peroxiredoxin like 2A pseudogene 1
DNAAF3	-2.08085	8.79E-11	5.68E-09	-6.4865	Down	dynein axonemal assembly factor 3
HR	-2.07873	2.63E-07	5.05E-06	-5.1485	Down	HR lysine demethylase and nuclear receptor corepressor
SLC9A3P3	-2.07738	0.002318	0.009212	-3.04617	Down	solute carrier family 9 member 3 pseudogene 3
IL1RAPL2	-2.07354	8.07E-05	0.00059	-3.9424	Down	interleukin 1 receptor accessory protein like 2
SP2	-2.07256	4.94E-12	4.68E-10	-6.9074	Down	Sp2 transcription factor
KHSRPP1	-2.07131	0.005217	0.017862	-2.7933	Down	KH-type splicing regulatory protein pseudogene 1
IER3	-2.07119	4.97E-06	5.93E-05	-4.56595	Down	immediate early response 3
CRISPLD1	-2.07016	2.04E-08	5.82E-07	-5.60875	Down	cysteine rich secretory protein LCCL domain containing 1
F8A2	-2.06923	1.57E-05	0.000153	-4.31845	Down	coagulation factor VIII associated 2
PBX4	-2.06696	0.007316	0.02356	-2.68212	Down	PBX homeobox 4
MTND1P6	-2.06619	0.002189	0.00878	-3.06334	Down	MT-ND1 pseudogene 6
C10orf71	-2.0658	7.44E-21	5.04E-18	-9.36737	Down	chromosome 10 open reading frame 71
PRRT1B	-2.06053	0.000135	0.000899	-3.81775	Down	proline rich transmembrane protein 1B
EHD2	-2.06051	2.21E-11	1.75E-09	-6.69146	Down	EH domain containing 2
DCX	-2.05781	0.002866	0.010945	-2.98178	Down	doublecortin
KRTAP5-AS1	-2.05712	4.73E-05	0.000381	-4.06836	Down	KRTAP5-1/KRTAP5-2 antisense RNA 1
GNB3	-2.05583	2.26E-09	8.95E-08	-5.97759	Down	G protein subunit beta 3
DOCK6	-2.05447	1.93E-13	2.61E-11	-7.35371	Down	dedicator of cytokinesis 6
SLC4A11	-2.05006	3.15E-08	8.33E-07	-5.53309	Down	solute carrier family 4 member 11
ASIC1	-2.04668	5.01E-10	2.53E-08	-6.2187	Down	acid sensing ion channel subunit 1
PTGDS	-2.04612	3.04E-11	2.30E-09	-6.64459	Down	prostaglandin D2 synthase
SOD3	-2.04605	7.56E-08	1.78E-06	-5.37723	Down	superoxide dismutase 3
SLC6A1	-2.0448	5.66E-26	9.15E-23	-10.5398	Down	solute carrier family 6 member 1
KDM6B	-2.03993	3.62E-11	2.66E-09	-6.61885	Down	lysine demethylase 6B
OPCML	-2.03832	3.96E-13	4.99E-11	-7.25701	Down	opioid binding protein/cell adhesion molecule like
RXFP4	-2.0331	8.74E-05	0.000632	-3.92304	Down	relaxin family peptide/INSL5 receptor 4
DNM1P29	-2.02973	0.009965	0.03019	-2.57705	Down	dynammin 1 pseudogene 29
ZBTB12	-2.02859	4.33E-08	1.10E-06	-5.47684	Down	zinc finger and BTB domain containing 12
EGR2	-2.02834	3.61E-06	4.56E-05	-4.63271	Down	early growth response 2
AHDC1	-2.02789	1.25E-10	7.77E-09	-6.43363	Down	AT-hook DNA binding motif containing 1
MDK	-2.0266	2.50E-10	1.39E-08	-6.32692	Down	midkine

NOXA1	-2.02565	1.08E-06	1.65E-05	-4.8768	Down	NADPH oxidase activator 1
ZMYND15	-2.0256	4.21E-06	5.15E-05	-4.60055	Down	zinc finger MYND-type containing 15
WDR62	-2.02471	1.19E-08	3.68E-07	-5.70049	Down	WD repeat domain 62
NDUFB2-AS1	-2.02398	0.002752	0.010591	-2.99418	Down	NDUFB2 antisense RNA 1
LLPH-DT	-2.0236	0.000159	0.001036	-3.77597	Down	LLPH divergent transcript
TTBK1	-2.01969	4.45E-05	0.000363	-4.08255	Down	tau tubulin kinase 1
LTBP3	-2.01804	5.27E-17	1.62E-14	-8.38053	Down	latent transforming growth factor beta binding protein 3
NOTCH3	-2.01692	3.41E-13	4.37E-11	-7.27725	Down	notch receptor 3
RGS4	-2.01611	3.42E-06	4.35E-05	-4.64411	Down	regulator of G protein signaling 4
IGFN1	-2.01476	0.003933	0.01423	-2.88349	Down	immunoglobulin like and fibronectin type III domain containing 1
CCNHP1	-2.01377	0.008975	0.027774	-2.61301	Down	cyclin H pseudogene 1
DYRK1B	-2.01145	8.49E-12	7.67E-10	-6.83001	Down	dual specificity tyrosine phosphorylation regulated kinase 1B
GIPC3	-2.01129	2.45E-14	4.23E-12	-7.62456	Down	GIPC PDZ domain containing family member 3
TTLL10	-2.00745	0.000338	0.001918	-3.58461	Down	tubulin tyrosine ligase like 10
KIAA1755	-2.00452	1.17E-14	2.23E-12	-7.71958	Down	KIAA1755
OXT	-2.00451	0.01498	0.041924	-2.43286	Down	oxytocin/neurophysin I prepropeptide
NR1D1	-2.0012	4.47E-08	1.13E-06	-5.47103	Down	nuclear receptor subfamily 1 group D member 1
LCN1P1	-2.00098	0.004434	0.015691	-2.84553	Down	lipocalin 1 pseudogene 1
AEBP1	-2.00076	4.08E-11	2.93E-09	-6.6012	Down	AE binding protein 1
DNM1P46	-1.99973	1.07E-07	2.39E-06	-5.3146	Down	dynamin 1 pseudogene 46
KANK4	-1.99864	9.41E-06	0.0001	-4.4302	Down	KN motif and ankyrin repeat domains 4
PDZD7	-1.99656	0.000164	0.001057	-3.76925	Down	PDZ domain containing 7
S1PR5	-1.98781	0.000292	0.001699	-3.62228	Down	sphingosine-1-phosphate receptor 5
UNC80	-1.9843	0.000237	0.001436	-3.67566	Down	unc-80 homolog, NALCN channel complex subunit
CALML6	-1.98229	0.006138	0.020383	-2.74034	Down	calmodulin like 6
FSCN1	-1.98091	1.61E-10	9.59E-09	-6.39435	Down	fascin actin-bundling protein 1
SLC1A7	-1.9797	9.74E-12	8.49E-10	-6.81026	Down	solute carrier family 1 member 7
SPATA32	-1.97839	0.012148	0.035471	-2.50781	Down	spermatogenesis associated 32
WNK2	-1.97507	2.93E-10	1.59E-08	-6.30238	Down	WNK lysine deficient protein kinase 2
KIR3DX1	-1.97437	0.008635	0.02693	-2.62616	Down	killer cell immunoglobulin like receptor, three Ig domains X1 (pseudogene)
ATCAY	-1.97351	1.32E-05	0.000133	-4.35701	Down	ATCAY kinesin light chain interacting caytaxin
SLC4A1	-1.97305	0.000749	0.003684	-3.37085	Down	solute carrier family 4 member 1 (Diego blood group)
PIANP	-1.97293	0.000497	0.002622	-3.48225	Down	PILR alpha associated neural protein
CPLX1	-1.9726	1.56E-07	3.28E-06	-5.24485	Down	complexin 1
CDRT15P3	-1.97253	0.001858	0.007687	-3.11209	Down	CDRT15 pseudogene 3
FOXD2-AS1	-1.97222	0.000895	0.00426	-3.32152	Down	FOXD2 adjacent opposite strand RNA 1
LRRC3	-1.97183	2.68E-09	1.03E-07	-5.95001	Down	leucine rich repeat containing 3
MN1	-1.97157	2.92E-21	2.18E-18	-9.46573	Down	MN1 proto-oncogene, transcriptional regulator
UPK2	-1.97049	0.01386	0.039335	-2.46088	Down	uroplakin 2
GAPDHP15	-1.97032	1.13E-05	0.000116	-4.39131	Down	glyceraldehyde-3-phosphate dehydrogenase pseudogene 15
LMX1B	-1.96935	7.79E-10	3.66E-08	-6.14925	Down	LIM homeobox transcription factor 1 beta
APCDD1L	-1.9693	2.02E-16	5.67E-14	-8.22085	Down	APC down-regulated 1 like
AZIN2	-1.96918	8.98E-16	2.20E-13	-8.04	Down	antizyme inhibitor 2

C16orf74	-1.96917	0.000488	0.00258	-3.48721	Down	chromosome 16 open reading frame 74
MTCO3P43	-1.969	0.001288	0.005728	-3.21874	Down	MT-CO3 pseudogene 43
P2RX2	-1.96722	0.00992	0.030076	-2.57862	Down	purinergic receptor P2X 2
TNNT3	-1.96705	4.10E-07	7.30E-06	-5.06427	Down	troponin T3, fast skeletal type
OASL	-1.96687	1.86E-09	7.57E-08	-6.00986	Down	2'-5'-oligoadenylate synthetase like
DBP	-1.96673	3.00E-08	8.05E-07	-5.54153	Down	D-box binding PAR bZIP transcription factor
SOX8	-1.96619	2.27E-06	3.08E-05	-4.72781	Down	SRX-box transcription factor 8
KIF26A	-1.96566	2.61E-15	5.69E-13	-7.9085	Down	kinesin family member 26A
CARNS1	-1.96474	8.26E-19	3.91E-16	-8.85639	Down	carosine synthase 1
CCDC85B	-1.96323	3.13E-08	8.30E-07	-5.53427	Down	coiled-coil domain containing 85B
CDHR5	-1.9623	1.03E-07	2.31E-06	-5.32162	Down	cadherin related family member 5
SAMD11	-1.96228	6.09E-08	1.48E-06	-5.41623	Down	sterile alpha motif domain containing 11
BOC	-1.96112	2.02E-12	2.11E-10	-7.03318	Down	BOC cell adhesion associated, oncogene regulated
MGAT5B	-1.95866	0.005012	0.017313	-2.80623	Down	alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase B
IPO9-AS1	-1.95826	1.33E-05	0.000133	-4.35562	Down	IPO9 antisense RNA 1
CRTC1	-1.95752	1.80E-09	7.38E-08	-6.0146	Down	CREB regulated transcription coactivator 1
PNMA3	-1.95473	3.28E-05	0.000283	-4.1531	Down	PNMA family member 3
ADGRE3	-1.95424	0.000644	0.003263	-3.41233	Down	adhesion G protein-coupled receptor E3
RPL13AP11	-1.95296	7.13E-10	3.41E-08	-6.16312	Down	ribosomal protein L13a pseudogene 11
PRRT4	-1.95181	1.90E-05	0.000178	-4.27662	Down	proline rich transmembrane protein 4
BAHCC1	-1.95038	2.18E-11	1.73E-09	-6.6933	Down	BAH domain and coiled-coil containing 1
ESPNL	-1.95024	0.012811	0.036951	-2.48897	Down	espin like
LRRC43	-1.94951	3.10E-06	4.02E-05	-4.66393	Down	leucine rich repeat containing 43
RN7SL774P	-1.94769	0.011299	0.033429	-2.53331	Down	RNA, 7SL, cytoplasmic 774, pseudogene
KLK13	-1.94498	0.016512	0.045337	-2.39739	Down	kallikrein related peptidase 13
FOXS1	-1.94449	8.04E-09	2.59E-07	-5.76757	Down	forkhead box S1
CHAD	-1.94355	1.41E-05	0.00014	-4.34263	Down	chondroadherin
RNF224	-1.94175	0.001586	0.00677	-3.15848	Down	ring finger protein 224
TMEM18-DT	-1.93908	0.014914	0.041773	-2.43446	Down	TMEM18 divergent transcript
TP63	-1.93803	6.80E-12	6.24E-10	-6.86174	Down	tumor protein p63
IGHEP2	-1.93791	3.55E-06	4.49E-05	-4.63634	Down	immunoglobulin heavy constant epsilon P2 (pseudogene)
CDH3	-1.93534	0.000213	0.001317	-3.7029	Down	cadherin 3
FBXO39	-1.9351	4.82E-05	0.000386	-4.06399	Down	F-box protein 39
EGR3	-1.93493	0.000255	0.001523	-3.65671	Down	early growth response 3
TBX21	-1.93015	0.001107	0.005069	-3.26176	Down	T-box transcription factor 21
LRCOL1	-1.92831	0.005781	0.019399	-2.75997	Down	leucine rich colipase like 1
CCDC120	-1.92827	2.62E-09	1.01E-07	-5.9536	Down	coiled-coil domain containing 120
EPPK1	-1.92743	1.46E-05	0.000144	-4.33391	Down	epiplakin 1
RHPN1	-1.92522	1.44E-06	2.10E-05	-4.81921	Down	rophilin Rho GTPase binding protein 1
ERFL	-1.92385	0.000573	0.002955	-3.44394	Down	ETS repressor factor like
SBK2	-1.92338	0.001966	0.008042	-3.09525	Down	SH3 domain binding kinase family member 2
NOTCH1	-1.92318	1.21E-09	5.30E-08	-6.07852	Down	notch receptor 1
TMEM86B	-1.92194	9.00E-05	0.000648	-3.91598	Down	transmembrane protein 86B

CACNA1S	-1.92186	0.005317	0.018156	-2.78719	Down	calcium voltage-gated channel subunit alpha1 S
LOXL2	-1.91923	5.44E-10	2.72E-08	-6.20586	Down	lysyl oxidase like 2
KLHL38	-1.91876	7.33E-11	4.94E-09	-6.51365	Down	kelch like family member 38
GATA1	-1.91777	0.008277	0.026021	-2.64056	Down	GATA binding protein 1
COL5A1	-1.91427	1.88E-13	2.56E-11	-7.3574	Down	collagen type V alpha 1 chain
CASKIN1	-1.91056	8.88E-06	9.58E-05	-4.44273	Down	CASK interacting protein 1
KCNK7	-1.91023	1.76E-07	3.62E-06	-5.223	Down	potassium two pore domain channel subfamily K member 7
OR10V3P	-1.90801	0.009463	0.028988	-2.59485	Down	olfactory receptor family 10 subfamily V member 3 pseudogene
ZFY	-1.90697	0.001128	0.005146	-3.25645	Down	zinc finger protein Y-linked
COL9A2	-1.90528	1.49E-06	2.16E-05	-4.81317	Down	collagen type IX alpha 2 chain
SPDYE7P	-1.9051	3.68E-07	6.68E-06	-5.08492	Down	speedy/RINGO cell cycle regulator family member E7, pseudogene
MTCO3P16	-1.90379	0.006171	0.02046	-2.73856	Down	MT-CO3 pseudogene 16
ADGRF1	-1.90155	0.010333	0.031067	-2.56448	Down	adhesion G protein-coupled receptor F1
CBARP	-1.90116	0.000417	0.002276	-3.52883	Down	CACN subunit beta associated regulatory protein
DLGAP4	-1.90101	9.12E-13	1.06E-10	-7.14311	Down	DLG associated protein 4
WNT10B	-1.89834	0.000179	0.001142	-3.74657	Down	Wnt family member 10B
PRKX-AS1	-1.89728	0.000186	0.001174	-3.73771	Down	PRKX antisense RNA 1
LRRC37A11P	-1.89707	7.15E-05	0.000533	-3.97133	Down	leucine rich repeat containing 37 member A11, pseudogene
MRC2	-1.89563	3.92E-13	4.97E-11	-7.25814	Down	mannose receptor C type 2
CCNP	-1.89354	0.017941	0.048399	-2.36683	Down	cyclin P
SLC25A6P4	-1.8922	0.002428	0.009588	-3.03212	Down	solute carrier family 25 member 6 pseudogene 4

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

GO ID	CATEGORY	GO Name	Adjusted p value	negative log10 of adjusted p value	Gene Count	Gene
Up regulated genes						
GO:0050896	BP	response to stimulus	4.9346E-05	4.30674763	213	IL1RL1,SERPINA3,ALOX15 B,RNASE2,CD177,VSIG4,O R4M2,PLA2G2A,S100A9,A DORA3,IL1R2,FPR1,CCL20, DEFB1,MT1A,LYVE1,CD16 3,S100A8,MCEMP1,ADAM DEC1,OR52N5,S100A12,CE P55,PPEF1,MMRN1,IGLV8- 61,FAM83B,MTRNR2L1,T LR2,EDN2,PTPRQ,NPTX2, HAS2,PTX3,TMIGD3,IGLV 5- 45,TIMP4,CLEC4D,PKHD1, MT1X,AREG,MTRNR2L1,B MP3,FCGR1A,IGKV1D- 8,EDNRB,FGF10,SULT1B1, RNF175,SIGLEC10,MUC16, SYT13,GCKR,BLM,CLEC4E ,CCL23,LILRA5,OR13A1,M GST1,SERPINA5,WNK3,CA MP,SPP1,SLC11A1,LBP,IL1 8R1,ALOX5AP,DLGAP5,TR PM1,H3C7,SPINK1,RETN,K NG1,CCR1,AKR1B10,IGKV 2D-

						40,SLA,MYOT,TLR8,FCGR3A,PKHD1L1,TAS2R7,SHISA3,F13A1,H4C13,FCGR1B,EPCAM,CR1L,CATSPERB,GLUL,CXCL11,CLEC1B,CD53,MRC1,TFRC,NAMPT,BIRC3,FPR2,SAA1,CCL26,FCN3,H2BC10,SLC30A10,KMO,AGTR1,TMEM100,GPR84,P2RY12,AQP3,FLT3,ADGRF4,TFEC,HPR,OR52N1,SIGLEC5,SIGLEC7,RAB39A,MSR1,TTK,SRGN,IGKV1-9,GPR151,GPR34,SAMSN1,TREML4,SLAMF8,MCTP2,AQP4,FCER1G,SIGLEC9,NQO1,MELK,CR1,LGR5,TREM2,CCL18,TRHDE,HP,TAS2R8,IRAK3,LY96,CCDC68,OXGR1,BATF,CYBB,RPL39,CDK1,RIDA,SLC7A11,H3C12,CTH,TOP2A,H3C8,CARD18,RHOU,CFTR,H2BC11,H4C6,TAS2R9,CLEC7A,F8,FKBP5,CTSC,MROH2B,JCHAIN,SLC17A3,C3AR1,TDGF1,SPARCL1,IGHV3-48,CCN6,ANKRD2,MYO16,CHL1,HIGD1A,CD38,RNASE6,RAD9B,CD180,MAOA,STC1,RPL26,RPS15A,BMPR1B,IGHV3-53,SLPI,SNX10,SERPINF2,APOB,KCNK2,FGF7,RGCC,GRB14,CALCRL,PRDX1,CP1,HPSE,LAPTM5,MARK3,TNFRSF11A,EEF1E1,IL18RAP,CLEC12A,PDE7A,TIMP3,EMB,PDE4D,C7,SHC4,DEPDC1B
GO:0007154	BP	cell communication	0.006449939	2.190444375	155	IL1RL1,ALOX15B,SCGN,CD177,OR4M2,PLA2G2A,S100A9,ADORA3,IL1R2,FPR1,CCL20,DEFB1,S100A8,OR52N5,S100A12,CEP55,PPEF1,FAM83B,MTRNR2L1,TLR2,EDN2,NPTX2,TMIGD3,TIMP4,CLEC4D,PKHD1,AREG,MTRNR2L1,BMP3,FCGR1A,EDNRB,FGF10,RNF175,MUC16,SYT13,BLM,CLEC4E,CCL23,LILRA5,OR13A1,WNK3,SPP1,LBP,IL18R1,DLGAP5,TRPM1,SCN10A,H3C7,SPINK1,RETN,KNK1,CCR1,IGKV2D- 40,SLA,TLR8,FCGR3A,TAS2R7,SHISA3,F13A1,FCGR1B,EPCAM,GLUL,CXCL11,CLEC1B,CD53,TFRC,NAMPT,BIRC3,FPR2,SAA1,CCL26,SLC30A10,KMO,AGTR1,TMEM100,GPR84,P2RY12,AQP3,FLT3,ADGRF4,OR52N1,RAB39A,TTK,SRGN,GPR151,GPR34,TREML4,MCTP2,FCER1G,SIGLEC9,NQO1,MELK,CR1,LGR5,TREM2,CCL18,TRHDE,TAS2R8,IRA

						K3,LY96,CCDC68,OXGR1, BATF,CYBB,CDK1,SLC7A1 1,SYN2,H3C12,CTH,H3C8,R HOU,CFTR,H2BC11,TAS2R 9,CLEC7A,CTSC,MROH2B, C3AR1,TDGF1,SPARCL1,IG HV3- 48,CCN6,MYO16,CHL1,CD 38,RAD9B,CD180,MAOA,S TC1,RPL26,BMPR1B,IGHV 3- 53,SERPINF2,APOB,KCNK2 ,FGF7,RGCC,GRB14,CALC RL,PRDX1,CMTM5,GPR12, ANGPTL1,LCP1,HPSE,LAP TM5,MARK3,TNFRSF11A,E EF1E1,IL18RAP,PDE7A,TI MP3,PDE4D,SHC4,DEPDC1 B IL1RL1,SERPINA3,ALOX15 B,CD177,OR4M2,PLA2G2A, S100A9,CLECL1,ADORA3,I L1R2,SLC22A16,FPR1,LYV E1,CD163,S100A8,MCEMP1 ,ADAMDEC1,OR52N5,S100 A12,CEP55,MMRN1,IGLV8- 61,TLR2,PTPRQ,DMP1,AD H1B,HAS2,PTX3,TMIGD3,I GLV5- 45,TIMP4,CLEC4D,PKHD1, FCGR1A,IGKV1D- 8,EDNRB,SLC19A2,FGF10, RHAG,SIGLEC10,MUC16,S YT13,CLEC4E,LILRA5,OR1 3A1,MGST1,SERPINA5,SLC O4A1,CYP4A11,SLC11A1,I L18R1,TRPM1,MS4A4A,SC N10A,KNG1,CCR1,CSTA,IG KV2D- 40,SLA,MYOT,ADH1A,TLR 8,FCGR3A,PKHD1L1,SIGLE C12,TAS2R7,F13A1,CDH19, FCGR1B,EPCAM,CATSPER B,GLUL,CLEC1B,CD53,OT OGL,MRC1,TFRC,NAMPT, CPM,FPR2,ADH1C,FCN3,S LC30A10,AGTR1,LRRN3,T MEM100,GPR84,P2RY12,A QP3,FLT3,OR52N1,SIGLEC 5,SIGLEC7,RAB39A,MSR1,I GKV1- 9,GPR151,GPR34,PRRG4,T REML4,S100A3,CADM2,AQ P4,FCER1G,SIGLEC9,MEL K,CR1,LGR5,TREM2,TRHD E,TAS2R8,IRAK3,LY96,OX GR1,CYBB,KCNH7,SLC7A1 1,SIRPB2,SYN2,DSPP,RHO U,CFTR,H2BC11,CNTN3,T AS2R9,CLEC7A,UAP1,F8,C TSC,CATIP,SLC17A3,C3AR 1,TDGF1,SMIM9,SPARCL1, IGHV3- 48,CCN6,MYO16,XK,CHL1, CDCP1,CD38,CD180,STC1, BMPR1B,IGHV3- 53,SLPI,SERPINF2,APOB,K CNK2,GRB14,CALCRL,SD R16C5,GPR12,ANGPTL1,LC P1,HPSE,LAPTM5,MARK3,
GO:0071944	CC	cell periphery	1.36E-09	8.867810114	170	

GO:0016020	CC	membrane	2.24211E-06	5.649343059	223	KIF20A,TMEM97,TNFRSF11A,IL18RAP,CLEC12A,TIMP3,EMB,AP1S2,PDE4D,C7,SHC4 IL1RL1,ALOX15B,SCGN,CD177,VSIG4,OR4M2,PLA2G2A,S100A9,CLECL1,KRT5,ADORA3,IL1R2,SLC22A16,FPR1,DEFB1,LYVE1,CD163,S100A8,MCEMP1,OR52N5,S100A12,CEP55,RARRES1,IGLV8- 61,FAM83B,TLR2,PTPRQ,ADH1B,SLC25A48,HAS2,CYP4B1,TMIGD3,IGLV5-45,CLEC4D,PKHD1,AREG,FCGR1A,CYP4Z1,IGKV1D-8,EDNRB,SLC19A2,FGF10,RNF175,RHAG,SIGLEC10,MUC16,SYT13,CLEC4E,LILRA5,OR13A1,MGST1,SERPINA5,SLCO4A1,CYP4A11,SLC11A1,LBP,IL18R1,ALOX5AP,TRPM1,MS4A4A,SCN10A,H3C7,KNG1,CCR1,CSTA,IGKV2D- 40,SLA,MYOT,ADH1A,GALNTL6,CYP4A22,TLR8,FCGR3A,PKHD1L1,SIGLEC12,TAS2R7,SHISA3,CDH19,H4C13,FCGR1B,EPCAM,CR1L,CATSPERB,GLUL,CLEC1B,ST6GALNAC3,TIMD4,DHR57C,CD53,TFCP2L1,MRC1,TFRC,NAMPT,CPM,BIRC3,FPR2,ADH1C,SLC30A10,KMO,AGTR1,STRIT1,LRRN3,TMEM100,CHST9,GPR84,P2RY12,AQP3,FLT3,ADGRF4,OR52N1,SIGLEC5,HSD11B1,SIGLEC7,RAB39A,MSR1,TTK,IGKV1- 9,GPR151,GPR34,PRRG4,TMPRSS12,TREML4,S100A3,CADM2,SLAMF8,MCTP2,AQP4,FCER1G,SIGLEC9,HS6ST2,MELK,CR1,LGR5,TREM2,TRHDE,TAS2R8,IRAK3,MANEA,LY96,MS4A6A,OXGR1,CYBB,KCNH7,CDK1,SPPP2,SLC7A11,SIRPB2,NDUFA4,TMTC1,SYN2,H3C12,C1ORF162,STARD7,H3C8,PLA1A,RHOU,CFTR,H2BC11,H4C6,CNTN3,TAS2R9,CLEC7A,UAP1,F8,FKBP5,CTSC,CATIP,RPS29,SLC17A3,C3AR1,ATP5MD,TOMM20L,TDGF1,SMIM9,IGHV3- 48,MRPS36,MYO16,XK,CHL1,CDCP1,HIGD1A,CD38,CD180,MAOA,STC1,RPL26,RPS15A,COX7A2,COX7B,BMPR1B,OSTC,IGHV3- 53,TMEM126A,SNX10,APOB,KCNK2,GRB14,CALCRL,SDR16C5,CMTM5,GPR12,TMEM258,LCP1,HPSE,MS4A6E,LAPTM5,RPS13,MARK3,KIF20A,TMEM97,GALNT1

GO:0060089	MF	molecular transducer activity	0.000421239	3.375471183	51	5,TNFRSF11A,EEF1E1,UGT2B4,IL18RAP,MRPL50,CLEC12A,EMB,AP1S2,PDE4D,CYP4X1,C7,SHC4,IL1RL1,OR4M2,ADORA3,IL1R2,FPR1,LYVE1,OR52N5,TLR2,TMIGD3,PKHD1,FCGR1A,EDNRB,CLEC4E,OR13A1,IL18R1,CCR1,MYOT,TLR8,FCGR3A,PKHD1L1,TAS2R7,FCGR1B,CLEC1B,MRC1,FPR2,AGTR1,GPR84,P2RY12,FLT3,ADGRF4,OR52N1,SIGLEC7,GPR151,GPR34,TREML4,SLAMF8,FCER1G,CR1,LGR5,TREM2,TAS2R8,LY96,OXGR1,TAS2R9,CLEC7A,C3AR1,BMPR1B,CALCRL,GPR12,TNFRSF11A,IL18RAP
GO:0004888	MF	transmembrane signaling receptor activity	0.001403098	2.852912115	43	IL1RL1,OR4M2,ADORA3,IL1R2,FPR1,LYVE1,OR52N5,TLR2,TMIGD3,FCGR1A,EDNRB,OR13A1,IL18R1,CCR1,MYOT,TLR8,FCGR3A,TAS2R7,FCGR1B,CLEC1B,MRC1,FPR2,AGTR1,GPR84,P2RY12,FLT3,ADGRF4,OR52N1,GPR151,GPR34,FCER1G,CR1,LGR5,TREM2,TAS2R8,OXGR1,TAS2R9,C3AR1,BMPR1B,CALCRL,GPR12,TNFRSF11A,IL18RAP
Down regulated genes						
GO:0032501	BP	multicellular organismal process	0.002147964	2.667973087	186	GLIS1,RTN4RL2,CRACD,ESM1,ACE,CELA2A,LY6H,PENK,TNFRSF4,CTRB2,KND C1,OMP,HSPB6,SSC5D,AMH,COL22A1,LRFN1,TRPM5,APLNR,DDX3Y,CHD5,FOSB,ATP1B2,SEZ6L2,LOXHD1,DKKL1,TLR9,BARHL1,KRTAP5-1,TRIL,NXNL1,RSPH6A,SFRP4,ACER1,EGR1,MAST1,ESPN,CCDC63,COL1A1,APLP1,ARHGAP33,IGDCC3,RTN4R,DOC2A,EPSS8L2,GNG8,PPDPF,GLI2,RP1L1,KRTAP10-7,ATP6V1B1,SRIN1,NRG N,THY1,RET,CACNG8,FOX D3,STX1B,DBH,CLDN5,AMBP,IGF2,FOXP3,GLP1R,ZNF683,NTN5,PRRT2,SLC6A9,ACHE,IL34,DEFB124,CTRB1,PIK3R6,NRXN2,ZFHX2,ADGRB1,SHANK1,NPPA,UTS2R,DPYSL5,ENTPD2,ZNF628,CCN1,TMEM132E,IGSF9,CDSN,CACNA1G,SOX18,ADRA2A,PERCC1,PANX2,DUOX2,BSK1,CHERP,FOXO6,RSPO2,ISLR2,BGN,NOS2,AGRN,GP5,ATN1,GABRD,FOXN4,PCGF2,DRD1,BEGAIN,COL9A1,KRTAP10-11,CCL3,COL11A2,LTBP4,SLC17A7,WHRN,KIF26B,SHANK2,TNFRSF18,MYH11,A

						DRA1D,SCT,BIRC7,CDH23, KRTAP12- 1,COMP,MSI1,PCDHA2,IL1 RAPL2,SP2,PBX4,EHD2,DC X,GNB3,DOCK6,ASIC1,SL C6A1,KDM6B,OPCML,EGR 2,MDK,ZMYND15,WDR62, TTBK1,LTBP3,NOTCH3,RG S4,IGFN1,DYRK1B,OXT,N R1D1,PDZD7,S1PR5,SPATA 32,ATCAY,SLC4A1,MN1,U PK2,LMX1B,AZIN2,P2RX2, TNNT3,DBP,SOX8,KIF26A, BOC,CRTC1,ESPNL,KLK13 ,FOXSI,CHAD,TP63,CDH3, EGR3,TBX21,LRCOL1,CCD C120,EPPK1,NOTCH1,CAC NA1S,LOXL2,GATA1,COL5 A1,COL9A2,ADGRF1,DLG AP4,WNT10B,MRC2
GO:0048856	BP	anatomical structure development	0.005847965	2.232995209	148	RTN4RL2,ESM1,ACE,FBN3 ,CELA2A,LY6H,PENK,KND C1,OMP,HSPB6,SSC5D,AM H,COL22A1,LRFN1,APLNR ,CHD5,ATP1B2,SEZ6L2,DK KL1,TLR9,BARHL1,KRTAP 5- 1,RSPH6A,SFRP4,ACER1,E GR1,MAST1,CCDC63,COL1 A1,APLP1,ARHGAP33,RTN 4R,DOC2A,GNG8,PPDPF,G LI2,RP1L1,KRTAP10- 7,ATP6V1B1,SRCIN1,NRG N,THY1,RET,FOXD3,STX1 B,CLDN5,IGF2,FOXP3,ZNF 683,NTN5,ACHE,IL34,PIK3 R6,NRXN2,ZFHX2,ADGRB 1,SHANK1,NPPA,DPYSL5, CCN1,TMEM132E,IGSF9,C DSN,SOX18,PERCC1,DUO X2,BRSK1,CHERP,FOXO6, RSPO2,ISLR2,BGN,AGRN, RHCG,ATN1,FOXN4,PCGF 2,DRD1,MAMSTR,FOXI2,C OL9A1,KRTAP10- 11,CCL3,COL11A2,LTBP4,S LC17A7,WHRN,KIF26B,SH ANK2,TNFRSF18,MYH11,S CT,BIRC7,CDH23,KRTAP12 - 1,COMP,MSI1,PCDHA2,IL1 RAPL2,IER3,CRISPLD1,PB X4,EHD2,DCX,KDM6B,OP CML,EGR2,MDK,ZMYND1 5,WDR62,TTBK1,LTBP3,N OTCH3,RGS4,IGFN1,DYRK 1B,OXT,NR1D1,PDZD7,S1P R5,ATCAY,SLC4A1,MN1,U PK2,LMX1B,P2RX2,TNNT3 ,DBP,SOX8,KIF26A,BOC,C RTC1,KLK13,FOXSI,CHAD ,TP63,CDH3,EGR3,TBX21,C CDC120,EPPK1,NOTCH1,L OXL2,GATA1,COL5A1,CO L9A2,ADGRF1,WNT10B TMEM130,PRND,RTN4RL2, GPR78,LRRC55,ACE,FBN3, LY6H,PENK,TNFRSF4,SYT 12,SLC7A4,MUC12,SSC5D, COL22A1,LRFN1,TRPM5,A
GO:0071944	CC	cell periphery	9.01283E-06	5.045138949	161	

						PLNR,ATP1B2,SEZ6L2,TLR9,MUC3A,ENTPD8,TRIL,LRRC38,MUC5B,GRID2IP,MAST1,ADAMTS14,COL1A1,APLP1,ARHGAP33,DUOXA2,IGDCC3,RTN4R,EPSS8L2,RIMBP2,GNNG8,C10ORF90,PALM3,SLC16A13,HMCN2,ATP6V1B1,NRGN,THY1,RET,CACNG8,STX1B,CLDN5,AMBP,GLP1R,SYCE1,NTN5,LYPD1,PRRT2,SLC6A9,ACHE,CLIP3,TM7SF2,PIK3R6,NRXN2,TMPRSS6,PODNL1,ADGRB1,MRGPRE,SHANK1,KCNN1,NPPA,UPK3B,UTS2R,PLPPR3,ENTPD2,PSD2,IL2RB,ASGR1,CCN1,IGSF9,SLC5A2,FRMD1,CACNA1G,ADRA2A,P2RY8,KCNJ9,PANX2,KCNF1,DUOX2,COL20A1,MXRA5,SLC34A3,ISLR2,OXER1,BGN,NOS2,AGRN,KCNC3,GP5,RHCG,ILDR1,TMEM240,GABRD,TMPRSS9,LAMP5,DRD1,COL9A1,GRIK4,COL11A2,LTBP4,ADGRG5,SLC17A7,WHRN,SHANK2,TNFRSF18,ADRA1D,CDH23,LTBP2,COMP,RAA4,CYP2W1,PCDHA2,IL1RAPL2,EHD2,GNB3,SLC4A11,ASIC1,SOD3,SLC6A1,OPCML,RXFP4,MDK,NOXA1,LTBP3,NOTCH3,RGS4,AEBP1,PDZD7,S1PR5,UNC80,FSCN1,SLC1A7,WNK2,SLC4A1,PIANP,UPK2,APCDD1L,P2RX2,CDHR5,BOC,CRTC1,ADGRE3,CHAD,CDH3,EPPK1,NOTCH1,CACNA1S,LOXL2,COL5A1,KCNK7,COL9A2,ADGRF1,CBARP,DLGAP4
GO:0005886	CC	plasma membrane	0.005336788	2.272720017	136	TMEM130,PRND,RTN4RL2,GPR78,LRRRC55,ACE,LY6H,PENK,TNFRSF4,SYT12,SLC7A4,MUC12,LRFN1,TRPM5,APLNR,ATP1B2,SEZ6L2,TLR9,MUC3A,ENTPD8,LRRC38,MUC5B,GRID2IP,MAST1,APLP1,ARHGAP33,DUOXA2,IGDCC3,RTN4R,EPSS8L2,RIMBP2,GNNG8,C10ORF90,PALM3,SLC16A13,HMCN2,ATP6V1B1,NRGN,THY1,RET,CACNG8,STX1B,CLDN5,AMBP,GLP1R,SYCE1,LYPD1,PRRT2,SLC6A9,ACHE,CLIP3,TM7SF2,PIK3R6,NRXN2,TMPRSS6,ADGRB1,MRGPRE,SHANK1,KCNN1,UPK3B,UTS2R,PLPPR3,ENTPD2,PSD2,IL2RB,ASGR1,IGSF9,SLC5A2,FRMD1,CACNA1G,ADRA2A,P2RY8,KCNJ9,PANX2,KCNF1,DUOX2,SLC34A3,ISLR2,OXER1,BGN,NOS2,AGRN,KCNC3,GP5,RHCG,ILDR1,TMEM240,

GO:0015318	MF	inorganic molecular entity transmembrane transporter activity	0.058426335	1.233391358	29	GABRD,TMPRSS9,LAMP5, DRD1,GRIK4,ADGRG5,SLC 17A7,WHRN,SHANK2,TNF RSF18,ADRA1D,CDH23,RA SA4,CYP2W1,PCDHA2,IL1 RAPL2,EHD2,GNB3,SLC4A 11,ASIC1,SLC6A1,OPCML, RXFP4,NOXA1,NOTCH3,R GS4,PDZD7,S1PR5,UNC80, FSCN1,SLC1A7,WNK2,SLC 4A1,PIANP,UPK2,APCDD1 L,P2RX2,CDHR5,BOC,CRT C1,ADGRE3,CDH3,EPPK1, NOTCH1,CACNA1S,KCNK 7,ADGRF1,CBARP,DLGAP4 LRRC55,SLC7A4,TRPM5,A TP1B2,LRRC38,SLC16A13, ATP6V1B1,CACNG8,SLC6 A9,KCNN1,SLC5A2,CACN A1G,KCNJ9,KCNF1,SLC34 A3,KCNC3,RHCG,GABRD, GRIK4,SLC17A7,SLC4A11, ASIC1,SLC6A1,UNC80,SLC 1A7,SLC4A1,P2RX2,CACN A1S,KCNK7
GO:0005198	MF	structural molecule activity	0.094978184	1.02237614	24	FBN3,HSPB6,COL22A1,MU C3A,COL1A1,OIT3,HMCN2 ,CLDN5,CCN1,PANX2,MRP L12,MXRA5,BGN,AGRN,C OL9A1,COL11A2,LTBP4,M YH11,LTBP2,COMP,AEBP1 ,EPPK1,COL5A1,COL9A2

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-168256	Immune System	1.83563E-05	4.736214648	81	IL1RL1,SERPINA3,RNASE2,CD177,T UBA3C,PLA2G2A,S100A9,IL1R2,FP R1,CCL20,TUBA3D,DEFB1,S100A8, MCEMP1,S100A12,TUBA3E,TLR2,P TX3,CLEC4D,AREG,FCGR1A,FGF10 ,SIGLEC10,MUC16,CLEC4E,LILRA5, MGST1,CAMP,SLC11A1,LBP,IL18R1 ,RETN,CCR1,IGKV2D- 40,TLR8,FCGR3A,SIGLEC12,F13A1, FCGR1B,CD53,MRC1,BIRC3,FPR2,S AA1,FCN3,GPR84,FLT3,TUBAL3,SI GLEC5,SIGLEC7,TREML4,FCER1G, SIGLEC9,CR1,TREM2,HP,IRAK3,LY 96,BATF,CYBB,RHOU,CLEC7A,CTS C,C3AR1,IGHV3- 48,RNASE6,CD180,MAOA,IGHV3- 53,SLPI,APOB,FGF7,LCPI,HPSE,MA RK3,KIF20A,TNFRSF11A,IL18RAP,C LEC12A,APIS2,C7
REAC:R-HSA-168249	Innate Immune System	1.83563E-05	4.736214648	51	SERPINA3,RNASE2,CD177,PLA2G2 A,S100A9,FPR1,DEFB1,S100A8,MCE MP1,S100A12,TLR2,PTX3,CLEC4D,F CGR1A,MUC16,CLEC4E,MGST1,CA MP,SLC11A1,LBP,RETN,IGKV2D- 40,TLR8,FCGR3A,CD53,BIRC3,FPR2 ,SAA1,FCN3,GPR84,SIGLEC5,FCER1 G,SIGLEC9,CR1,TREM2,HP,IRAK3,L Y96,CYBB,CLEC7A,CTSC,C3AR1,IG HV3-48,RNASE6,CD180,IGHV3-

REAC:R-HSA-6798695	Neutrophil degranulation	9.54101E-05	4.020405579	29	53,SLPI,APOB,HPSE,CLEC12A,C7SERPINA3,RNASE2,CD177,S100A9,FR1,S100A8,MCEMP1,S100A12,TLR2,PTX3,CLEC4D,MGST1,CAMP,SLC11A1,RETN,CD53,FPR2,GPR84,SIGLEC5,FCER1G,SIGLEC9,CR1,HP,CYBB,CTSC,C3AR1,SLPI,HPSE,CLEC12A
REAC:R-HSA-168898	Toll-like Receptor Cascades	0.012127308	1.916235606	12	S100A9,S100A8,S100A12,TLR2,LBP,TLR8,BIRC3,SAA1,IRAK3,LY96,CD180,APOB
REAC:R-HSA-71291	Metabolism of amino acids and derivatives	0.024436592	1.611959361	18	GLUL,BCAT1,KMO,NQO1,AASS,RP L39,RIDA,GNMT,CTH,RPL22L1,AMD1,RPS29,RPL26,RPS15A,SAT1,RPS13,EEF1E1,RPS27
REAC:R-HSA-8953897	Cellular responses to external stimuli	0.024436592	1.611959361	24	TUBA3C,TUBA3D,MT1A,TUBA3E,MT1X,H1-3,H2BC14,TUBAL3,H2BC9,H2BC3,CYBB,RPL39,H2AC14,H2BC11,H1-5,RPL22L1,FKBP5,RPS29,HIGD1A,RPL26,RPS15A,PRDX1,RPS13,RPS27
Down regulated genes					
REAC:R-HSA-112316	Neuronal System	0.000114227	3.942232869	24	SYT12,LRFN1,GNNG8,NRNG,CACNG8,ACHE,NRXN2,SHANK1,KCNN1,KCNJ9,PANX2,KCNF1,KCNC3,BEGAIN,GRIK4,SLC17A7,SHANK2,IL1RAPL2,GNB3,SLC6A1,SLC1A7,CPLX1,KCNK7,DLGAP4
REAC:R-HSA-1474244	Extracellular matrix organization	0.000114227	3.942232869	20	CAPN6,FBN3,CTRB2,COL22A1,ADAMTS14,COL1A1,CTRB1,TMPRSS6,COL20A1,BGN,AGRN,COL9A1,COL1A2,LTBP4,LTBP2,COMP,LTBP3,LOXL2,COL5A1,COL9A2
REAC:R-HSA-6794362	Protein-protein interactions at synapses	0.012465304	1.904297133	8	SYT12,LRFN1,NRXN2,SHANK1,BEGAIN,SHANK2,IL1RAPL2,DLGAP4
REAC:R-HSA-1474228	Degradation of the extracellular matrix	0.015320837	1.814717503	10	CAPN6,FBN3,CTRB2,COL1A1,CTRB1,TMPRSS6,COL9A1,COL11A2,COL5A1,COL9A2
REAC:R-HSA-500792	GPCR ligand binding	0.030591053	1.514405578	19	PENK,APLN,CCCL3L1,GNNG8,GLP1R,UTS2R,PLPPR3,ADRA2A,OXER1,DRD1,CCL3,ADRA1D,SCT,GNB3,RXFP4,OXT,S1PR5,ADGRE3,WNT10B
REAC:R-HSA-3781865	Diseases of glycosylation	0.093732211	1.028111137	8	MUC12,MUC3A,MUC5B,ADAMTS14,BGN,AGRN,NOTCH3,NOTCH1

Table 4 Topology table for up and down regulated genes.

Regulation	Node	Degree	Betweenness	Stress	Closeness
Up	CFTR	800	0.250818	2.82E+08	0.382037
Up	CDK1	289	0.059973	1.09E+08	0.333174
Up	RPS13	255	0.037331	50801568	0.35159
Up	RPS15A	233	0.031358	47775876	0.332312
Up	RPS27	213	0.025226	52139390	0.332277
Up	PRDX1	201	0.034128	55983910	0.348223
Up	NDUFA4	190	0.041688	59296328	0.316656
Up	FKBP5	157	0.031733	44198116	0.315591
Up	RPL26	156	0.014756	28200346	0.320904
Up	RHOU	133	0.032899	14114804	0.299016
Up	TOP2A	132	0.022582	21447746	0.337518
Up	TFRC	127	0.026876	31508150	0.324479
Up	S100A9	124	0.023694	18575534	0.334877
Up	CEP55	123	0.022005	29250578	0.306355
Up	SNRPG	121	0.022174	58988410	0.287667
Up	MRPL50	117	0.017338	16197166	0.294992
Up	RPS29	111	0.007838	10474252	0.313312
Up	BLM	108	0.021289	16918168	0.325049

Up	AGTR1	100	0.022019	17157708	0.305566
Up	ZWINT	99	0.018375	20533060	0.291506
Up	SPP1	99	0.018586	9330572	0.314503
Up	C3AR1	94	0.016166	25287748	0.264361
Up	TTK	91	0.017179	19765014	0.304974
Up	BIRC3	90	0.014977	24960018	0.299957
Up	KRT5	90	0.008929	25389258	0.305804
Up	S100A8	88	0.012007	12637402	0.333298
Up	SAT1	82	0.014165	15900742	0.297742
Up	APOB	78	0.01467	14861278	0.302962
Up	MARK3	76	0.010936	15499698	0.29433
Up	FPR2	74	0.011396	18351388	0.256034
Up	BMPRI1B	71	0.013222	16342524	0.29051
Up	EEF1E1	67	0.006446	9571868	0.295922
Up	VSIG4	64	0.011875	13237432	0.278326
Up	MELK	63	0.009324	6151010	0.281124
Up	P2RY12	63	0.008425	7797394	0.272302
Up	PDE4D	54	0.007393	10017988	0.303913
Up	CMTM5	54	0.011555	15349250	0.261776
Up	CTH	54	0.011322	13403074	0.277137
Up	KNG1	53	0.008809	6029112	0.28506
Up	GLUL	51	0.007775	12036292	0.288989
Up	HP	51	0.005073	7718948	0.292292
Up	RRM2	50	0.006974	4018526	0.318226
Up	TLR2	50	0.009032	7171472	0.28207
Up	PPEF1	49	0.002383	6116412	0.275197
Up	ATP5MD	49	0.005997	5678794	0.29341
Up	NAMPT	48	0.005236	8796778	0.285864
Up	CSTA	47	0.0056	3242708	0.312876
Up	CCR1	46	0.008862	10277030	0.260572
Up	TDGF1	45	0.006828	11958282	0.265074
Up	RPL39	43	0.003737	9890538	0.279749
Up	KIF20A	42	0.0056	10002414	0.277112
Up	IL1R2	42	0.007887	2661112	0.297096
Up	SERPINA3	42	0.007121	5931062	0.279762
Up	DEPDC1B	42	0.003267	3787682	0.261395
Up	KLHL40	42	0.006323	6412684	0.260551
Up	SERPINA5	41	0.005996	5510082	0.271082
Up	API52	39	0.006525	11289512	0.276333
Up	BCAT1	38	0.007672	4563422	0.267509
Up	FLT3	37	0.004	5164642	0.274106
Up	PLA2G2A	35	0.004359	5431086	0.276091
Up	NQO1	34	0.002866	9438888	0.275329
Up	COX7A2	34	0.003955	2248426	0.279252
Up	MTHFD2	34	0.004247	7481058	0.27486
Up	TUBA3E	34	0.003142	6571258	0.277846
Up	HIGD1A	33	0.003446	5562624	0.282146
Up	AMD1	32	0.008064	2564908	0.281351
Up	EDNRB	31	0.004132	10397624	0.254141
Up	STARD7	31	0.004386	8133746	0.262958
Up	TIMP3	30	0.005329	5535204	0.271761
Up	SLC19A2	30	0.007143	2466610	0.27182
Up	SLC22A16	30	0.003748	5590640	0.231168
Up	BATF	29	0.005488	8241746	0.246551
Up	LAPTM5	29	0.002531	5891300	0.255805
Up	LCP1	29	0.003421	10760010	0.256367
Up	DLGAP5	28	0.003726	3577874	0.310085
Up	RIDA	28	0.003761	2634098	0.263586
Up	F8	27	0.003666	5060182	0.265499
Up	FCGR1A	27	0.003253	3749296	0.248646
Up	CLEC12A	27	0.004847	4563254	0.248371
Up	TUBAL3	27	0.001767	5494636	0.269076
Up	TMEM126A	27	0.004645	1707450	0.287773
Up	ELL2	26	0.003436	3333898	0.250877
Up	CDH19	26	0.004185	1563734	0.272008
Up	UAP1	25	0.002146	2800316	0.274177
Up	IRAK3	25	0.002929	4503640	0.259916
Up	CTSC	25	0.002683	4792556	0.257143
Up	MANEA	25	0.004902	1598406	0.248244
Up	CLEC7A	25	0.005317	2453022	0.27107

Up	GRB14	24	0.003207	4733128	0.272137
Up	GNMT	24	0.001794	2840784	0.262881
Up	FAM83B	24	0.002446	4019758	0.270802
Up	RPL22L1	24	0.004024	2944142	0.283123
Up	JCHAIN	24	0.004353	4653652	0.252134
Up	SIGLEC5	24	0.003229	1035168	0.250897
Up	SLA	23	0.002594	3046528	0.271714
Up	CPM	23	0.002164	3067630	0.259937
Up	SCGN	22	0.003827	7053140	0.244529
Up	SERPINF2	21	0.001762	2060048	0.253639
Up	RAB39A	21	0.002987	3242160	0.275848
Up	FCGR3A	20	0.003232	3079286	0.261689
Up	TNFRSF11A	19	0.001994	2676430	0.259798
Up	PTX3	19	0.004185	3863002	0.223943
Up	SRGN	19	0.001867	1548928	0.257754
Up	LBP	19	0.001897	2861646	0.255503
Up	SYN2	19	0.001206	3610072	0.24756
Up	MMRN1	19	0.001393	927204	0.252144
Up	OSTC	19	0.002529	2572846	0.272574
Up	TMEM258	19	0.002276	3475832	0.257691
Up	F13A1	18	0.001232	1483048	0.25413
Up	HSD11B1	18	0.003099	2861348	0.256347
Up	S100A3	17	0.00276	4485872	0.243989
Up	MYOT	17	0.001723	1802236	0.260411
Up	BBS12	17	0.00243	8403578	0.23358
Up	TRHDE	17	0.00403	3288960	0.265847
Up	TMPRSS12	17	0.002815	3369698	0.239721
Up	CDCP1	16	0.003614	2357734	0.278387
Up	SLPI	15	9.63E-04	976730	0.259733
Up	AKR1B10	15	0.001132	493918	0.266952
Up	MGST1	14	9.56E-04	1544300	0.273665
Up	CCDC68	14	0.001456	2365346	0.237504
Up	SIGLEC9	2	8.70E-06	23072	0.225419
Up	ADH1B	2	4.07E-05	37458	0.22735
Up	TLR8	2	0	0	0.213827
Up	CAMP	2	7.42E-05	96406	0.218962
Up	CCL23	1	0	0	0.206716
Up	RGCC	1	0	0	0.249921
Up	CD38	1	0	0	0.207418
Up	EPCAM	1	0	0	0.276442
Up	LY96	1	0	0	0.220019
Up	HS6ST2	1	0	0	0.216991
Up	SHC4	1	0	0	0.219581
Up	ALOX15B	1	0	0	0.214096
Up	FCN3	1	0	0	0.182974
Up	MTRNR2L1	1	0	0	0.258294
Up	IL1RL1	1	0	0	0.213269
Up	FGF7	1	0	0	0.229943
Up	CNTN3	1	0	0	0.228714
Up	CCL26	1	0	0	0.206716
Up	CD163	1	0	0	0.226189
Up	SLC30A10	1	0	0	0.244996
Up	FCER1G	1	0	0	0.207418
Up	RHAG	1	0	0	0.208291
Down	NOTCH1	250	0.055026	75882802	0.332417
Down	MRPL12	195	0.037118	50798784	0.313578
Down	NOS2	158	0.017276	30450186	0.318499
Down	CCDC85B	151	0.033004	20747204	0.302234
Down	ATN1	114	0.02349	18276352	0.303108
Down	GLP1R	109	0.025463	18684482	0.290591
Down	APLN	103	0.021689	18858734	0.291736
Down	ATP6V1B1	99	0.022959	9935628	0.299714
Down	LRFN1	93	0.015879	12549670	0.28071
Down	GATA1	89	0.015617	23510800	0.300372
Down	FSCN1	88	0.013048	8110734	0.32723
Down	CHERP	84	0.011161	20724310	0.296983
Down	EPPK1	84	0.012839	12039586	0.333016
Down	FOXP3	83	0.011715	20499710	0.28292
Down	NOTCH3	80	0.015072	8290510	0.312643
Down	ADGRG5	80	0.015847	20888478	0.264461

Down	TCTE1	80	0.015977	7802718	0.285838
Down	FOXSI	79	0.012498	20736510	0.282526
Down	DKKL1	78	0.016678	18615684	0.276503
Down	COL1A1	76	0.013725	12697230	0.29859
Down	MYH11	73	0.009346	5311188	0.31947
Down	DYRK1B	71	0.011062	18710680	0.285747
Down	GET4	68	0.010111	18051758	0.298392
Down	CCDC120	68	0.017344	9691046	0.297898
Down	RET	67	0.010929	10583060	0.304811
Down	PCGF2	64	0.010749	21781650	0.281439
Down	APLP1	61	0.014188	6846322	0.296521
Down	MDK	59	0.009935	11348532	0.286815
Down	WDR62	58	0.008676	12733168	0.289908
Down	ISLR	58	0.010523	20009526	0.260238
Down	IQCNI	57	0.010111	16769670	0.269053
Down	FATE1	57	0.011652	14232246	0.251328
Down	FOXI2	53	0.007592	8828670	0.261211
Down	DCX	48	0.009089	5176554	0.304163
Down	EGR1	47	0.006697	16123798	0.27545
Down	MAST1	47	0.007072	12364366	0.29121
Down	MYCN	46	0.0041	6582592	0.280085
Down	NPPA	46	0.009645	4323078	0.272408
Down	FRMD1	45	0.009925	7849260	0.246165
Down	COL5A1	40	0.005986	5359170	0.28479
Down	DUSP8	40	0.005631	2465084	0.282869
Down	RHPN1	40	0.006169	4790624	0.257553
Down	SFRP4	40	0.005898	8543724	0.267816
Down	CPLX1	39	0.007959	3871650	0.275028
Down	ZNF414	39	0.006946	10943040	0.246175
Down	RFX1	38	0.007136	2569940	0.29763
Down	LOXL2	38	0.005758	9246234	0.275077
Down	SLC4A1	37	0.005974	7496290	0.263079
Down	SYCE1	37	0.005509	11144044	0.255753
Down	DDX3Y	37	0.002711	5323020	0.281363
Down	SHANK2	36	0.005424	4374242	0.3001
Down	LTBP4	36	0.005445	2434208	0.266839
Down	BIRC7	35	0.003199	5467760	0.251148
Down	GNB3	35	0.00595	9751722	0.264328
Down	BEGAIN	33	0.003947	3860650	0.270814
Down	TLR9	33	0.004504	7136794	0.260045
Down	DLGAP4	33	0.00457	5414044	0.281388
Down	SHANK1	32	0.003386	4979252	0.259476
Down	STX1B	32	0.004463	9748988	0.239712
Down	THY1	32	0.003414	4184066	0.262049
Down	KLHL38	32	0.004726	5878076	0.26425
Down	IL2RB	31	0.004268	8195548	0.269745
Down	EHD2	30	0.003516	11343860	0.241776
Down	P2RY8	29	0.003672	4881448	0.246967
Down	DPYSL5	28	0.003752	5602212	0.264183
Down	MRC2	28	0.00602	3155886	0.285009
Down	ADGRB1	27	0.003534	4457434	0.253628
Down	CHD5	27	0.002936	5717864	0.271035
Down	P2RX2	26	0.004522	6083842	0.242437
Down	PTGDS	25	0.003159	4128644	0.268204
Down	IGF2	24	0.002926	3579840	0.254367
Down	AHDC1	24	0.002394	2714014	0.284854
Down	FAM171A2	24	0.003962	4336600	0.250468
Down	MGAT5B	23	0.003457	1490980	0.239338
Down	KIF26B	23	0.003064	1399770	0.286384
Down	DOCK6	23	0.00371	4300742	0.254511
Down	ASGR1	23	0.003218	3830722	0.282424
Down	FOXDI	23	0.00188	986110	0.270464
Down	BGN	22	0.004658	1408836	0.280173
Down	CDSN	22	0.002468	1014552	0.281514
Down	AGRN	22	0.003369	1782196	0.290981
Down	ARID5A	22	0.002375	2661748	0.264206
Down	LITDI	22	0.003525	5054094	0.240491
Down	LMX1B	21	0.002896	2846334	0.268789
Down	EGR2	21	0.002473	1703458	0.254934
Down	GLI2	20	0.002149	2685102	0.281477

Down	ADRA2A	20	0.001974	3308074	0.251751
Down	ARHGEF16	20	0.00193	4148570	0.270872
Down	WNK2	20	0.001619	3205596	0.269745
Down	ADRA1D	19	0.001854	3465836	0.250139
Down	GABRD	19	0.002153	2302972	0.235169
Down	CAPN6	19	0.002692	4506702	0.244093
Down	LYPD1	19	0.002765	4063698	0.241118
Down	SOX8	19	0.003288	2741798	0.250787
Down	IER3	18	0.004052	2238378	0.283851
Down	NOXA1	18	0.002917	2744574	0.267611
Down	EPS8L2	18	0.001633	1924974	0.278289
Down	KDM6B	18	0.002083	2000150	0.252823
Down	AMBP	17	8.61E-04	1420600	0.275873
Down	BOC	17	0.002632	3509404	0.255742
Down	KLK10	17	0.001916	2746686	0.246484
Down	BAHCC1	16	0.002208	3217268	0.259081
Down	WHRN	16	0.002154	2204088	0.243168
Down	MUC5B	16	0.003777	2428884	0.25688
Down	OPCML	16	0.001443	1865180	0.251409
Down	SYT12	16	0.002859	4959848	0.230735
Down	RGS4	15	0.002083	3512584	0.257101
Down	NR1D1	15	0.002637	2458946	0.259177
Down	HR	15	0.001354	2193650	0.262738
Down	ACHE	15	0.002614	1339788	0.27682
Down	CDH3	15	0.001266	415460	0.294178
Down	SRCIN1	15	0.001085	1237478	0.267919
Down	TRIM50	15	0.001172	1853618	0.236255
Down	C1QTNF9	15	0.001478	1276520	0.225274
Down	LTBP3	15	0.001739	1944214	0.243837
Down	FBN3	15	0.001381	2246422	0.25167
Down	CCL3	14	0.001829	714350	0.242465
Down	DRD1	14	0.002047	3743596	0.239639
Down	CCN1	14	0.001042	583294	0.268605
Down	TNNT3	14	0.00141	1015768	0.216983
Down	KRTAP10-7	3	1.01E-04	108030	0.237012
Down	TP63	2	1.10E-05	54194	0.241859
Down	CTRB1	2	1.23E-05	15314	0.225881
Down	KLK13	2	1.23E-05	15314	0.225881
Down	GNG8	1	0	0	0.209073
Down	DOC2A	1	0	0	0.196489
Down	DBP	1	0	0	0.197793
Down	NRGN	1	0	0	0.225169
Down	ATCAY	1	0	0	0.200856
Down	PLPPR3	1	0	0	0.209156
Down	C10orf71	1	0	0	0.22225
Down	SEZ6L2	1	0	0	0.229055
Down	TMPPRS6	1	0	0	0.229943
Down	NXPH4	1	0	0	0.230195
Down	PRRT2	1	0	0	0.211122
Down	RXFP4	1	0	0	0.221834
Down	ATP1B2	1	0	0	0.242952

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

Regulation	Target Genes	Degree	MicroRNA	Regulation	Target Genes	Degree	TF
Up	TFRC	108	hsa-mir-409-3p	Up	RPS27	18	CREB1
Up	TOP2A	90	hsa-mir-320d	Up	FKBP5	17	TP63
Up	CDK1	68	hsa-mir-301a-5p	Up	TFRC	15	FOXA1
Up	CEP55	56	hsa-mir-107	Up	CDK1	14	NRF1
Up	FKBP5	32	hsa-mir-205-5p	Up	PRDX1	11	JUND
Up	PRDX1	31	hsa-mir-18a-3p	Up	CFTR	10	RUNX2
Up	NDUFA4	28	hsa-mir-185-5p	Up	RHOU	10	SOX17
Up	RPS15A	25	hsa-mir-571	Up	RPS13	10	FOXF2
Up	RHOU	24	hsa-mir-340-5p	Up	RPS15A	9	FOXC1
Up	RPL26	17	hsa-mir-200a-5p	Up	TOP2A	8	SRF
Up	CFTR	12	hsa-mir-4452	Up	CEP55	7	NFIC
Up	RPS27	11	hsa-mir-103a-3p	Up	RPL26	7	ZNF354C

Up	RPS13	7	hsa-mir-126-3p	Up	SNRPG	5	ELK4
Up	S100A9	7	hsa-mir-1343-3p	Up	NDUFA4	3	RELA
Up	SNRPG	6	hsa-mir-155-5p	Up	S100A9	2	USF2
Down	ATN1	74	hsa-mir-3200-3p	Down	ATN1	19	TEAD1
Down	FSCN1	62	hsa-mir-29a-5p	Down	FSCN1	8	SREBF2
Down	CHERP	52	hsa-mir-296-5p	Down	ATP6V1B1	7	GATA2
Down	NOTCH1	35	hsa-mir-139-5p	Down	GATA1	7	E2F1
Down	NOTCH3	33	hsa-mir-147a	Down	MRPL12	7	TP53
Down	EPPK1	16	hsa-mir-148b-3p	Down	CHERP	7	PPARG
Down	APLNR	13	hsa-mir-373-3p	Down	GLP1R	6	ARID3A
Down	CCDC85B	11	hsa-mir-603	Down	FOXP3	6	STAT3
Down	MRPL12	9	hsa-mir-128-3p	Down	NOTCH3	6	KLF5
Down	LRFN1	6	hsa-mir-145-5p	Down	EPPK1	5	E2F6
Down	NOS2	5	hsa-mir-497-5p	Down	APLNR	4	PRDM1
Down	GATA1	4	hsa-mir-4454	Down	NOS2	4	IRF2
Down	ATP6V1B1	2	hsa-mir-1229-3p	Down	NOTCH1	3	GATA3
Down	GLP1R	1	hsa-mir-376c-3p	Down	LRFN1	3	YY1
Down	TCTE1	1	hsa-mir-7-5p	Down	CCDC85B	3	TFAP2A

Figures

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

Fig. 4. Modules of isolated form PPI of DEGs. (A) The most significant module was obtained from PPI network with 59 nodes and 203 edges for up regulated genes (B) The most significant module was obtained from PPI network with 21 nodes and 41 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 gray 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) CFTR B) CDK1 C) RPS13 D) RPS15A E) RPS27 F) NOTCH1 G) MRPL12 H) NOS2 I) CCDC85B J) ATN1