Identification of Key Pathways and Genes in Dementia via Integrated Bioinformatics Analysis

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Abstract

To provide a better understanding of dementia at the molecular level, this study aimed to identify the genes and key pathways associated with dementia by using integrated bioinformatics analysis. Based on the expression profiling by high throughput sequencing dataset GSE153960 derived from the Gene Expression Omnibus (GEO), the differentially expressed genes (DEGs) between patients with dementia and healthy controls were identified. With DEGs, we performed a series of functional enrichment analyses. Then, a protein–protein interaction (PPI) network, modules, miRNA-hub gene regulatory network and TF-hub gene regulatory network was constructed, analyzed and visualized, with which the hub genes miRNAs and TFs nodes were screened out. Finally, validation of hub genes was performed by using receiver operating characteristic curve (ROC) analysis. A total of 948 DEGs were screened out, among which 475 genes were up regulated; while 473 were down regulated. Functional enrichment analyses indicated that DEGs were mainly involved in defense response, ion transport, neutrophil degranulation and neuronal system. The hub genes (CDK1, TOP2A, MAD2L1, RSL24D1, CDKN1A, NOTCH3, MYB, PWP2, WNT7B and HSPA12B) were identified from PPI network, modules, miRNA-hub gene regulatory network and TF-hub gene regulatory network. We identified a series of key genes along with the pathways that were most closely related with dementia initiation and progression. Our results provide a more detailed molecular mechanism for the advancement of dementia, shedding light on the potential biomarkers and therapeutic targets.

Keywords: dementia; expression profiling by high throughput sequencing; bioinformatics; differentially expressed gene; protein-protein interaction network

Introduction

Dementia is a neuropsychiatric syndrome characterized by losses of cognitive and emotional abilities [Cantone et al. 2014]. Dementia patients show varying levels of behavior disturbance includes agitation, aggression, and rejection of care [Marx et al. 2019]. The numbers of cases of dementia are increasing globally and it has become an essential mental health concern. According to a survey, the prevalence of dementia is expected to reaching 110 million in 2050 [Lyketsos, 2020]. The prevalence of dementia fast elevates from about 2-3% among those aged 70–75 years to 20–25% among those aged 85 years or more [Aarsland, 2020]. Alzheimer's disease is the neurodegenerative origin of dementia [Chancellor et al. 2014]. Many investigations suggest that modifications in multiple genes and signaling pathways are associated in controlling the advancement of dementia. However, an inadequacy of investigation on the precise molecular mechanisms of dementia advancement limits the treatment efficacy of the disease at present. Therefore, understanding the molecular mechanisms of dementia occurrence and progression is of utmost essential for diagnosis, prognosis and targeted therapy in the future.

In recent decades, more and more researchers have devoted themselves to exploring the molecular mechanisms by which signaling pathways regulates the progression of dementia. Signaling pathways includes TGF-β signaling pathway [Kandasamy et al. 2020], TLR4/MyD88/NF-κB signaling pathway [Wang et al. 2020], Akt/mTOR signaling pathway [Xu et al. 2019], SIRT1/PGC-1α signaling pathway [Yao et al. 2019] and VEGF–VEGFR2 signaling pathway [Wang et al. 2014] are involved in the initiation and progression of dementia. Further, a series of genes such as UBQLN2 [Deng et al. 2011], PRKAR1B [Cohn-Hokke et al. 2014], apolipoprotein E (APOE) [Regland et al. 1999], TREM2 [Guerreiro et al. 2013] and PON1 [Alam et al. 2014], have been predicted as target genes for diagnosing and treatment of dementia. However, the interactions between genes, signal pathway, miRNAs and transcription factors (TFs) warrant further comprehensive analysis.

RNA sequencing has increasingly become a promising tool in studying neuropsychiatric disorders [Hardwick et al. 2019]. These genomic data offer possibilities for identifying certain disease-related genes. Recently, many

investigations have been performed according to expression profiling by high throughput sequencing data profiles to elucidate the pathogenesis of dementia [Rajkumar et al. 2020].

In the current study, we downloaded expression profiling by high throughput sequencing dataset, GSE153960 [Prudencio et al. 2020], from the NCBI Gene Expression Omnibus database (NCBI GEO) (http://www.ncbi.nlm.nih.gov/geo/) [Clough and Barrett, 2016]), including gene expression data from 263 patients with dementia and 277 healthy controls. We identified differentially expressed genes (DEGs) using the limma R bioconductor package with standard data processing. To further understand the function of genes, Gene Ontology (GO) enrichment analysis, REACTOME pathway enrichment analysis, protein-protein interaction (PPI) network construction and analysis, module analysis, miRNA-hub regulatory gene network construction and analysis and TF-hub regulatory gene network construction and analysis were performed in sequence. Finally, selected hub genes were verified by receiver operating characteristic curve (ROC) analysis. We anticipated that these investigations will implement further insight of dementia pathogenesis and development at the molecular level.

Material and Methods

RNA sequencing data

The expression profiling by high throughput sequencing dataset (GEO access number: GSE153960, contributed by Prudencio et al. [2020], were downloaded from the NCBI GEO, which was currently the largest fully public gene expression resource. There were a total of 540 samples in this analysis, including 263 patients with dementia and 277 healthy controls.

Identification of DEGs

The DEGs were identified by using limma package in R between patients with dementia and healthy controls [Ritchie et al. 2015], with the criteria of |log fold change (FC)| > 0.6 for up regulated genes, |log fold change (FC)| < -0.7 for down regulated genes and p-value < 0.05 followed by multiple-testing correction using the Benjamini-Hochberg procedure to obtain the adjusted p-value [Hardcastle, 2016].

GO and REACTOME pathway enrichment analysis

ToppGene (ToppFun) (https://toppgene.cchmc.org/enrichment.jsp) [Chen et al 2009] is a tool which provides a comprehensive set of functional annotation tools for researchers to investigate the biological meaning of genes. Identified DEGs were investigated further using ToppGene, Gene Ontology (GO) (http://geneontology.org/) [Thomas, 2017] and REACTOME (https://reactome.org/) [Fabregat et al. 2018] pathway enrichment analyses. $P<0.05$ and gene counts of >5 were considered to indicate a statistically significant difference in the functional enrichment analysis.

PPI network construction and module analysis

Identified DEGs were mapped into the online Search Tool for the Retrieval of Interacting Genes (STRING) database [Szklarczyk et al. 2011] to evaluate the interactive relationships among the DEGs. Interactions with a combined score >0.4 were defined as statistically significant. Cytoscape software (version 3.8.2) (www.cytoscape.org) [Shannon et al. 2003] was used to visualize the integrated regulatory networks. According to the node degree [Przulj et al 2004], betweenness centrality [Nguyen et al 2011], stress centrality [Shi and Zhang, 2011] and closeness centrality [Fadhal et al 2014] in the Cytoscape plugin Network Analyzer, the top five ranked genes were defined as hub genes. . The Cytoscape plugin PEWCC1 (http://apps.cytoscape.org/apps/PEWCC1) [Zaki et al 2013] was used to further detect deeper connected regions within the PPI network.

MiRNA-hub gene regulatory network construction

MiRNA-hub gene regulatory was constructed employing the hub genes. MiRNA targets were extracted from miRNet database (https://www.mirnet.ca/) [Fan and Xia, 2018]. The regulatory interactions between miRNA and hub genes were obtained. The miRNA-target regulatory networks were visualized by Cytoscape.

TF-hub gene regulatory network construction

TF-hub gene regulatory was constructed employing the hub genes. TF targets were extracted from NetworkAnalyst database (https://www.networkanalyst.ca/) [Zhou

et al 2019. The regulatory interactions between TF and hub genes were obtained. The TF-target regulatory networks were visualized by Cytoscape.

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

The multivariate modeling with selected hub genes were used to identify biomarkers with high sensitivity and specificity for dementia diagnosis. Used one data as training set and other as validation set iteratively. The receiver operator characteristic curves were plotted and area under curve (AUC) was determined independently to check the conduct of each model using the R packages "pROC" [Robin et al 2011]. An AUC > 0.9 marked that the model had a positive fitting effect.

Results

Identification of DEGs

There were 263 patients with dementia and 277 healthy controls in our present study. Via Limma in R bioconductor package, we identified 948 DEGs from GSE153960. Among them, 475 genes were up regulated; while 473 were down regulated (Table 1). A heatmap of the up regulated and down regulated genes, was produced using the gplots package and R software. A volcano plot of all of the DEGs was generated using ggplot2 package and R software. The heatmap and volcano plot are shown in Fig. 1 and and Fig. 2, respectively.

GO and REACTOME pathway enrichment analysis

GO and REACTOME enrichment analysis for DEGs was performed using the ToppGene. We uploaded all DEGs to identify the GO categories and REACTOME pathways of the DEGs. The enriched GO terms were classified into biological process (BP), cellular component (CC) and molecular function (MF). GO analysis results showed that for BP, up regulated genes were significantly enriched in defense response and cell activation (Table 2). Down regulated genes were significantly enriched in BP, including ion transport and trans-synaptic signaling (Table 2). Up regulated genes were significantly enriched in CC, including whole membrane and intrinsic component of plasma membrane (Table 2). Down regulated genes were significantly enriched in CC, including integral component

of plasma membrane and neuron projection (Table 2). GO MF showed that the up regulated genes were significantly enriched in molecular transducer activity and signaling receptor binding (Table 2). Down regulated genes were significantly enriched in MF, including transporter activity and transmembrane signaling receptor activity (Table 2). Moreover, REACTOME pathways were over represented in the up regulated genes, including neutrophil degranulation and innate immune system, while the down regulated genes were significantly enriched in REACTOME pathways, including neuronal system and NCAM signaling for neurite out-growth (Table 3).

PPI network construction and module analysis

By using the STRING database, the PPI network of DEGs was established and consisted of 3837 nodes and 7530 edges (Fig .3). The PPI network was observed by Cytoscape, and the cut-off criterion of hub gene selection with high node degree, betweenness centrality, stress centrality and closeness centrality. A top 10 genes were selected for key biomarker identification (Table 4). They consisted of 5 up regulated genes (CDK1, TOP2A, MAD2L1, RSL24D1 and CDKN1A) and 5 down regulated genes (NOTCH3, MYB, PWP2, WNT7B and HSPA12B). The 2 most significant modules were extracted from the PPI network by PEWCC1, which included a module 1 consisted of 9 nodes and 17 edges (Fig.4A), which are mainly associated with molecular transducer activity and innate immune system and module 2 consisted of 8 nodes and 15 edges (Fig.4B), which are mainly associated with GPCR ligand binding, neuronal system, trans-synaptic signaling and integral component of plasma membrane.

MiRNA-hub gene regulatory network construction

The miRNA-hub gene regulatory network was shown in Fig. 5, consisting of 2303 nodes and 9686 interactions. The nodes with high topological score can be regarded as key network nodes. The results, output by the powerful visualization system, indicated that 444 miRNAs (ex; hsa-mir-1248) might target CDKN1A, 127 miRNAs (ex; hsa-mir-6887-3p) might target TGFBR1, 113 miRNAs (ex; hsa-mir-101-5p) might target EIF4A2, 109 miRNAs (ex; hsa-mir-488-5p) might target CDK1, 107 miRNAs (ex; hsa-mir-548l) might target HSPA13, 88 miRNAs (ex; hsa-mir-6886-5p) might target WNT7B, 56 miRNAs (ex; hsa-mir-107) might

target CHTF18, 47 miRNAs (ex; hsa-mir-150-3p) might target MYB, 43 miRNAs (ex; hsa-mir-195-5p) might target NR4A1 and 41 miRNAs (ex; hsa-mir-206) might target NOTCH3 and are listed in Table 5.

TF-hub gene regulatory network construction

The TF-hub gene regulatory network was shown in Fig. 6, consisting of 577 nodes and 5405 interactions. The nodes with high topological score can be regarded as key network nodes. The results, output by the powerful visualization system, indicated that 105 TFs (ex; MLLT1) might target CDKN1A, 63 TFs (ex; STAT1) might target EIF4A2, 37 TFs (ex; TBP) might target U2AF1, 33 TFs (ex; ELF1) might target SFN, 24 TFs (ex; HMBOX1) might target BTK, 71 TFs (ex; BCL11B) might target KIFC2, 61 TFs (ex; TEAD3) might target CALML6, 49 TFs (ex; KAT2A) might target NR4A1, 44 TFs (ex; SP3) might target MYB and 32 TFs (ex; FOSL2) might target ADCY4 and are listed in Table 5.

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

ROC curve analysis using “pROC” packages was performed to calculate the capacity of 5 up regulated and 5 down genes to distinguish patients with dementia from healthy controls. CDK1, TOP2A, MAD2L1, RSL24D1, CDKN1A, NOTCH3, MYB, PWP2, WNT7B and HSPA12B all exhibited excellent diagnostic efficiency (AUC > 0.9) (Fig. 7).

Discussion

As dementia is the most frequent neurodegenerative disorder worldwide, it is important to understand the molecular mechanism of dementia, which might provide a novel field in diagnosis and therapy of dementia. In this investigation, we got a total of 948 DEGs including 475 up regulated and 473 down regulated genes. Sanfilippo et al [2020], Kamboh et al [2006], Hartlage-Rübsamen et al [2015], Pey et al [2014], Yu et al [2015] and Wang et al [2016] found that CHI3L2, SERPINA3, CCL2, CD163, HLA-DRB5 and GSTM1 are expressed in Alzheimer's disease patients. BCL2A1 is implicated in the growth of amyotrophic lateral sclerosis [Iaccarino et al. 2011], but this gene might be associated with progression

of dementia. HES5 [Kondo et al. 2019] and CYP2D6 [Chamnanphon et al. 2020] are detected in brain cells and is highly correlated with dementia.

The DEGs obtained were remarkably enriched in GO terms and pathway under defense response, whole membrane, molecular transducer activity, neutrophil degranulation, ion transport, integral component of plasma membrane, transporter activity and neuronal system. Defense response [Licastro and Chiappelli, 2003], cell activation [Schubert and Rudolphi, 1998], whole membrane [Paonessa et al. 2019], intrinsic component of plasma membrane [Verdier et al. 2004], neutrophil degranulation [Licastro et al. 1994], innate immune system [van der Willik et al. 2019], hemostasis [Loures et al. 2019], ion transport [Benos et al. 1994], neuron projection [Bondareff et al. 1982], transporter activity [Jellinger et al. 2020], neuronal system [Seeley, 2008] and axon guidance [Zhou et al. 2012] were responsible for progression of dementia. HGF (hepatocyte growth factor) [Sharma, 2010], HLA-DRB1 [Lu et al. 2017], CHI3L1 [Lananna et al. 2020], S100A8 [Lodeiro et al. 2017], S100A9 [Wang et al. 2018], S100A12 [Shepherd et al. 2006], FCGR2B [Costa et al. 2020], HP (haptoglobin) [Song et al. 2015], AIF1 [Sanfilippo et al 2020], CCR1 [Halks-Miller et al. 2003], ALOX5AP [Manev and Manev, 2006], FPR2 [Iribarren et al. 2005], CR1 [Mahmoudi et al. 2018], CFI (complement factor I) [Lashkari et al. 2018], AQP4 [Zeppenfeld et al. 2017], SLC11A1 [Jamieson et al. 2005], CTSS (cathepsin S) [Lemere et al. 1995], CXCR2 [Ryu et al. 2015], IL10 [Babić Leko et al. 2020], IL18 [Scarabino et al. 2020], CYP19A1 [Song et al. 2019], BTK (Bruton tyrosine kinase) [Keaney et al. 2019], C7 [Zhang et al. 2019], PLA2G7 [Koshy et al. 2010], SOCS3 [Cao et al. 2018], OLR1 [Wang et al. 2018], LIPA (lipase A, lysosomal acid type) [von Trotha et al. 2006], CD86 [Busse et al. 2015], TLR5 [Herrera-Rivero et al. 2019], CD44 [Pinner et al. 2017], CD68 [Matsumura et al. 2015], CD74 [Kiyota et al. 2015], LTF (lactotransferrin) [Wang et al. 2010], LYZ (lysozyme) [Sandin et al. 2016], S100A10 [King et al. 2020], AQP1 [Nikpour et al. 2020], GPR84 [Audoy-Rémus et al. 2015], HPSE (heparanase) [García et al. 2017], NGFR (nerve growth factor receptor) [Cheng et al. 2012], RHOQ (ras homolog family member Q) [Tian et al. 2021], EGF (epidermal growth factor) [Birecree et al. 1988], CDK1 [Hilgeroth et al. 2014], PKD1 [Chen et al. 2020], HTR6 [Kan et al. 2004], GRIN1 [Wang et al. 2021], AGRN (agrin) [Rauch et al. 2011] and GP6 [Laske et al. 2008] have been shown as a promising biomarkers in Alzheimer's disease. Field et al

[2010], Lincoln et al [2009], Ziliotto et al [2018], El Sharkawi et al [2019], Cossins et al [1997], Mirowska-Guzel et al [2011], Asouri et al [2020], Cardamone et al [2018], Begovich et al [2005], Bennetts et al [1999], Iparraguirre et al [2017] and Oldoni et al [2020] reported that HLA-DPB1, HLA-DQA1, CCL18, CCL20, MMP7, IL1A, IL2RA, CYBB (cytochrome b-245 beta chain), PTPN22, HLA-DMB, ANXA2 and CHIT1expression were associated with progression of multiple sclerosis, but these genes might be liable for advancement of dementia. Chang et al [2015], Jamshidi et al [2014], Campolo et al [2020], Bottero et al [2018], Gao et al [2019], Haga et al [2020], Klaver et al [2018], Greenbaum et al [2013] and Aguirre et al [2020] reported that expression of HLA-DQB1, HLA-DRA, TLR7, TLR8, PTPRC (protein tyrosine phosphatase receptor type C), OSMR (oncostatin M receptor), FABP5, LAMP2, CHRNA5 and IL13RA1 could be an index for Parkinson's disease progression, but these genes might be responsible for progression of dementia. Shmuel-Galia et al. [2017], Paloneva et al. [2000], Abu-Rumeileh et al. [2020], Wojta et al. [2020], Ries et al. [2016], Bernstein et al. [2020], Qian and Ke [2020], Kitic et al. [2014], Gorevic et al. [1985], Bonham et al. [2018], Shi et al. [2017], Maddison and Giorgini [2015], Wang et al. [2017], Pase et al. [2020], Daniele et al. [2015], Hayward and Lee [2014], Wang et al. [2020], Kim et al. [2006], Götz et al. [1998], Budge et al. [2018], Loeffler et al. [1996], Cacciagli et al. [2014], Stoffel et al. [2018], Koper et al. [2018], Philippe et al. [2015], Cursano et al. [2020], Butler et al. [2019], Cho et al. [2021] and Casiglia et al. [2013] presented that expression of TLR6, TYROBP (transmembrane immune signaling adaptor TYROBP), SERPINA1, CCR5, ANXA1, SLC7A2, HAMP (hepcidin antimicrobial peptide), TSLP (thymic stromal lymphopoietin), B2M, CXCR4, C3, KYNU (kynureninase), CASP1, CD14, TLR1, TLR2, TREM2, HCK (HCK proto-oncogene, Src family tyrosine kinase), MAOB (monoamine oxidase B), GPNMB (glycoprotein nmb), CP (ceruloplasmin), AP1S2, SMPD3, CXCL11, SHANK3, CRHR1, DRD4, NOTCH3 and GNB3 were associated with progression of dementia. Yamamoto et al. [2017], Wang et al. [2017], Stringer et al. [2020] and Brenner et al. [2019] demonstrated that that the expression of SPP1, C5AR1, CACNA1H and CACNA1A are associated with the prognosis of amyotrophic lateral sclerosis, but these genes might be associated with advancement of dementia. TGFBR1 [Zheng et al. 2021], SCN4A [Bergareche et al. 2015], KCNT1 [McTague et al. 2018], SLC13A5 [Matricardi et al. 2020]

and CACNA1B [Gorman et al. 2019] were reported to be associated with progression of epilepsy, but these genes might be involved in dementia.

A PPI network and modules were constructed with DEGs, which revealed that the top hub genes with highest node degree, betweenness centrality, stress centrality and closeness centrality.TOP2A, MAD2L1, RSL24D1, CDKN1A, PWP2, WNT7B, HSPA12B, CCNG1, GADD45A, SFN (stratifin), CEP55, PTTG1, GRM2, SHANK1 and GRM4 were might be the novel biomarkers for dementia progression.

A miRNA-hub gene regulatory network and TF-hub gene regulatory network with the hub genes were constructed, and identified as the key genes, miRNAs and TFs in dementia. Hsa-mir-1248 [Hewel et al. 2019], hsa-mir-195-5p [Takousis et al. 2019] and SP3 [Boutillier et al. 2007] might play important role in Alzheimer's disease, but these genes might be linked with progression of dementia. hsa-mir-101-5p has been reported in multiple sclerosis [Chen et al. 2017], but this gene might be liable for progression of dementia. Reports indicate that hsa-mir-206 [Grasso et al. 2019], hsa-mir-107 [Nelson et al. 2018], STAT1 [Ebner et al. 2011], TBP (TATA-binding protein) [Bruni et al. 2004] and KAT2A [Nematollahi et al. 2016] were found in dementia. BCL11B has been shown to be activated in amyotrophic lateral sclerosis [Lennon et al. 2016], but this gene might be liable for advancement of dementia. Fan et al. [2020] and Rouillard et al. [2018] found that FOSL2 and NR4A1 might be involved in the development of Parkinson's disease, but these genes might be linked with dementia progression. Hsa-mir-6887-3p, hsa-mir-488-5p, hsa-mir-548l, hsa-mir-6886-5p, hsa-mir-150-3p, MLLT1, ELF1, HMBOX1, TEAD3, EIF4A2, HSPA13, KIFC2, U2AF1, CALML6 and ADCY4 were might be the novel biomarkers for dementia progression.

` In conclusion, we used a series of bioinformatics analysis methods to identify the key genes and pathways associated in dementia initiation and progression from expression profiling by high throughput sequencing data containing patients with dementia and healthy controls. Our results provide a more detailed molecular mechanism for the advancement of dementia, shedding light on the potential biomarkers and therapeutic targets. However, the interacting

molecular mechanism and function of genes need to be confirmed in more experiments.

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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. [(GSE153960) (https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE153960)]

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

Gene Symbol	logFC	pValue	adj.P.Val	t value	Regulation	Gene Name
CHI3L2	2.057359	2.79E-12	6.02E-11	7.151524	Up	chitinase 3 like 2
SERPINA3	2.038899	3.91E-16	1.84E-14	8.400369	Up	serpin family A member 3
TGFB2-OT1	1.878194	2.81E-12	6.06E-11	7.150304	Up	TGFB2 overlapping transcript 1
SLAMF8	1.765528	1.28E-15	5.40E-14	8.241442	Up	SLAM family member 8
CCL2	1.69641	1.30E-15	5.48E-14	8.239506	Up	C-C motif chemokine ligand 2
CD163	1.640185	1.72E-14	5.78E-13	7.886108	Up	CD163 molecule
HLA-DRB5	1.630125	2.08E-10	3.23E-09	6.478609	Up	major histocompatibility complex, class II, DR beta 5
SERPINA5	1.555842	7.09E-14	2.08E-12	7.687277	Up	serpin family A member 5
CLEC5A	1.488497	3.38E-14	1.06E-12	7.791951	Up	C-type lectin domain containing 5A
BCL2A1	1.470264	1.24E-15	5.24E-14	8.245968	Up	BCL2 related protein A1
CD44	1.469417	2.84E-13	7.36E-12	7.488226	Up	CD44 molecule (Indian blood group)

CSTA	1.441465	5.53E-14	1.66E-12	7.722364	Up	cystatin A
MSR1	1.423322	1.74E-16	8.87E-15	8.506955	Up	macrophage scavenger receptor 1
CHIT1	1.4064	3.55E-11	6.29E-10	6.760897	Up	chitinase 1
LYZ	1.382117	1.16E-12	2.68E-11	7.282726	Up	lysozyme
LTF	1.356901	9.01E-09	1.07E-07	5.839709	Up	lactotransferrin
GPNMB	1.32367	2.84E-14	9.13E-13	7.816226	Up	glycoprotein nmb
FCER1G	1.321987	4.93E-14	1.50E-12	7.738815	Up	Fc fragment of IgE receptor Ig
MS4A4A	1.312422	1.00E-12	2.35E-11	7.303744	Up	membrane spanning 4-domains A4A
GTF2A1L	1.266975	5.61E-08	5.93E-07	5.507857	Up	general transcription factor IIA subunit 1 like
FPR1	1.265243	9.02E-13	2.13E-11	7.319483	Up	formyl peptide receptor 1
TLR8	1.241432	1.05E-13	2.95E-12	7.631986	Up	toll like receptor 8
SFN	1.239731	2.10E-11	3.87E-10	6.842905	Up	stratifin
HLA-DQB1	1.235479	5.65E-08	5.97E-07	5.506588	Up	major histocompatibility complex, class II, DQ beta 1
SIGLEC7	1.232269	2.55E-10	3.89E-09	6.445376	Up	sialic acid binding Ig like lectin 7
CHI3L1	1.229335	6.31E-12	1.28E-10	7.028033	Up	chitinase 3 like 1
MS4A6A	1.2269	1.63E-11	3.07E-10	6.882057	Up	membrane spanning 4-domains A6A
RNASE2	1.224535	4.48E-12	9.31E-11	7.079931	Up	ribonuclease A family member 2
ANKRD22	1.216325	2.45E-11	4.46E-10	6.818685	Up	ankyrin repeat domain 22
SERPINA1	1.208572	2.58E-12	5.61E-11	7.163088	Up	serpin family A member 1
LY96	1.207197	1.92E-18	1.52E-16	9.08535	Up	lymphocyte antigen 96
LINC00836	1.179389	1.27E-13	3.51E-12	7.604751	Up	long intergenic non-protein coding RNA 836
VSIG4	1.165762	1.63E-12	3.67E-11	7.231586	Up	V-set and immunoglobulin domain containing 4
FCGR1A	1.164483	1.84E-14	6.13E-13	7.877198	Up	Fc fragment of IgG receptor Ia
CHRNA1	1.16074	1.51E-11	2.86E-10	6.894459	Up	cholinergic receptor nicotinic alpha 1 subunit
AQP9	1.154651	2.62E-13	6.83E-12	7.50024	Up	aquaporin 9
STEAP4	1.152085	2.98E-11	5.33E-10	6.788316	Up	STEAP4 metalloreductase
ALOX5AP	1.142816	5.72E-13	1.39E-11	7.386272	Up	arachidonate 5-lipoxygenase activating protein
SPP1	1.131466	1.28E-10	2.07E-09	6.557289	Up	secreted phosphoprotein 1
GPR65	1.120357	1.96E-11	3.63E-10	6.853876	Up	G protein-coupled receptor 65
HLA-DRA	1.112508	1.01E-09	1.39E-08	6.217718	Up	major histocompatibility complex, class II, DR alpha
APOC1	1.104864	3.41E-09	4.37E-08	6.00952	Up	apolipoprotein C1
FPR3	1.104439	3.67E-07	3.35E-06	5.149041	Up	formyl peptide receptor 3
S100A9	1.089191	2.12E-09	2.81E-08	6.091321	Up	S100 calcium binding protein A9
C1QB	1.08872	7.04E-11	1.19E-09	6.652589	Up	complement C1q B chain
TLR2	1.081519	2.31E-13	6.08E-12	7.517967	Up	toll like receptor 2
TLR7	1.080775	1.06E-11	2.07E-10	6.948588	Up	toll like receptor 7
GPR183	1.078688	1.34E-06	1.12E-05	4.888719	Up	G protein-coupled receptor 183
HLA-DQA1	1.077488	1.39E-06	1.16E-05	4.881405	Up	major histocompatibility complex, class II, DQ alpha 1
HAMP	1.071171	2.31E-07	2.19E-06	5.239194	Up	hepcidin antimicrobial peptide
RNASE6	1.068114	3.20E-10	4.81E-09	6.408293	Up	ribonuclease A family member k6
LY86	1.064046	1.13E-10	1.85E-09	6.576719	Up	lymphocyte antigen 86
S100A8	1.058157	1.10E-08	1.30E-07	5.803995	Up	S100 calcium binding protein A8

TFEC	1.053666	1.34E-14	4.63E-13	7.920784	Up	transcription factor EC
RGS18	1.050344	6.11E-14	1.82E-12	7.708371	Up	regulator of G protein signaling 18
CCL18	1.050186	8.25E-13	1.96E-11	7.332675	Up	C-C motif chemokine ligand 18
FCGR2A	1.043765	5.53E-10	8.02E-09	6.317674	Up	Fc fragment of IgG receptor IIa
S100A3	1.043369	1.60E-11	3.02E-10	6.884937	Up	S100 calcium binding protein A3
CP	1.03399	6.67E-09	8.14E-08	5.892754	Up	ceruloplasmin
C21orf62	1.030994	1.15E-10	1.87E-09	6.574224	Up	chromosome 21 open reading frame 62
PLA2G7	1.027658	1.13E-19	1.27E-17	9.436097	Up	phospholipase A2 group VII
SBSPON	1.02672	0.00152	0.006496	3.187114	Up	somatomedin B and thrombospondin type 1 domain containing
CD48	1.02127	3.37E-07	3.10E-06	5.165565	Up	CD48 molecule
TKTL1	1.021124	3.62E-11	6.41E-10	6.757762	Up	transketolase like 1
APLNR	1.016089	7.42E-07	6.47E-06	5.008861	Up	apelin receptor
LILRA6	1.011874	7.71E-08	7.94E-07	5.448677	Up	leukocyte immunoglobulin like receptor A6
FCGR2B	1.009126	7.16E-06	5.31E-05	4.533068	Up	Fc fragment of IgG receptor IIb
AQP1	1.008517	6.32E-07	5.57E-06	5.041082	Up	aquaporin 1 (Colton blood group)
SCIN	1.006935	5.21E-09	6.48E-08	5.936032	Up	scinderin
SAMSN1	0.996386	1.37E-12	3.13E-11	7.257384	Up	SAM domain, SH3 domain and nuclear localization signals 1
CCR1	0.996208	4.08E-11	7.15E-10	6.739136	Up	C-C motif chemokine receptor 1
FAM177B	0.992272	5.75E-12	1.18E-10	7.04203	Up	family with sequence similarity 177 member B
SIGLEC5	0.992048	4.65E-07	4.19E-06	5.101997	Up	sialic acid binding Ig like lectin 5
ALOX15B	0.987902	1.26E-06	1.06E-05	4.901651	Up	arachidonate 15-lipoxygenase type B
CPVL	0.987098	6.96E-12	1.41E-10	7.013151	Up	carboxypeptidasevitellogenic like
OLR1	0.983844	4.07E-10	6.02E-09	6.368579	Up	oxidized low density lipoprotein receptor 1
FCGR3A	0.983734	4.87E-10	7.13E-09	6.338807	Up	Fc fragment of IgG receptor IIIa
CERNA2	0.982782	5.47E-06	4.15E-05	4.591509	Up	competing endogenous lncRNA 2 for microRNA let-7b
CD86	0.98011	1.76E-09	2.35E-08	6.123467	Up	CD86 molecule
HGF	0.977524	1.45E-18	1.18E-16	9.120757	Up	hepatocyte growth factor
LILRB3	0.977073	3.89E-07	3.54E-06	5.137344	Up	leukocyte immunoglobulin like receptor B3
C3AR1	0.972002	9.23E-10	1.29E-08	6.232352	Up	complement C3a receptor 1
SLC7A2	0.971717	1.61E-21	2.97E-19	9.944688	Up	solute carrier family 7 member 2
STON1-GTF2A1L	0.971196	0.000164	0.000931	3.795821	Up	STON1-GTF2A1L readthrough
IFI30	0.967681	2.82E-08	3.10E-07	5.634976	Up	IFI30 lysosomalthiolreductase
C1QC	0.9671	2.88E-09	3.73E-08	6.03902	Up	complement C1q C chain
DNASE2B	0.966574	3.89E-10	5.77E-09	6.375855	Up	deoxyribonuclease 2 beta
CTSS	0.966034	1.29E-11	2.49E-10	6.918323	Up	cathepsin S
CBSL	0.96267	1.39E-05	9.80E-05	4.385126	Up	cystathionine beta-synthase like
LOC100507144	0.959419	2.15E-07	2.05E-06	5.253117	Up	uncharacterized LOC100507144
GPR34	0.958125	1.61E-10	2.55E-09	6.520263	Up	G protein-coupled receptor 34
CYBB	0.957002	1.27E-11	2.45E-10	6.920909	Up	cytochrome b-245 beta chain
SIGLEC9	0.949729	2.61E-10	3.98E-09	6.441431	Up	sialic acid binding Ig like lectin 9
HP	0.948902	0.000502	0.002533	3.500997	Up	haptoglobin
IL10	0.94532	7.73E-09	9.32E-08	5.866749	Up	interleukin 10

MTHFD2	0.94409	6.43E-16	2.89E-14	8.334153	Up	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolatecyclohydrolase
CD68	0.942514	1.68E-08	1.91E-07	5.728791	Up	CD68 molecule
LAPTM5	0.94173	1.57E-10	2.50E-09	6.524427	Up	lysosomal protein transmembrane 5
AIF1	0.941266	2.49E-09	3.27E-08	6.063584	Up	allograft inflammatory factor 1
CYP19A1	0.941219	2.13E-08	2.39E-07	5.686026	Up	cytochrome P450 family 19 subfamily A member 1
RAB38	0.940889	1.46E-12	3.31E-11	7.248276	Up	RAB38, member RAS oncogene family
PPBP	0.940793	2.04E-10	3.18E-09	6.481415	Up	pro-platelet basic protein
RBM46	0.940787	3.20E-10	4.81E-09	6.408229	Up	RNA binding motif protein 46
EMP1	0.940147	1.57E-11	2.97E-10	6.887908	Up	epithelial membrane protein 1
MS4A7	0.938493	2.38E-09	3.12E-08	6.071934	Up	membrane spanning 4-domains A7
HSPE1-MOB4	0.930941	5.47E-08	5.78E-07	5.512852	Up	HSPE1-MOB4 readthrough
LOC100652840	0.923419	1.85E-06	1.51E-05	4.821826	Up	M-phase phosphoprotein 10 (U3 small nucleolarribonucleoprotein) pseudogene
RGS1	0.922476	0.000254	0.001384	3.682457	Up	regulator of G protein signaling 1
GRHL3	0.920707	7.24E-05	0.000444	3.998995	Up	grainyhead like transcription factor 3
CD180	0.917819	2.76E-09	3.59E-08	6.046369	Up	CD180 molecule
HLA-DRB1	0.915605	6.47E-08	6.76E-07	5.481385	Up	major histocompatibility complex, class II, DR beta 1
CR1	0.910799	2.87E-09	3.72E-08	6.039603	Up	complement C3b/C4b receptor 1 (Knops blood group)
FCGR1CP	0.909095	1.96E-08	2.21E-07	5.700684	Up	Fc fragment of IgG receptor Ic, pseudogene
CTSC	0.909067	3.26E-15	1.27E-13	8.115044	Up	cathepsin C
RASSF9	0.907988	1.15E-05	8.22E-05	4.428346	Up	Ras association domain family member 9
VAMP8	0.905566	9.41E-11	1.55E-09	6.606283	Up	vesicle associated membrane protein 8
S100A4	0.903653	7.98E-07	6.92E-06	4.99414	Up	S100 calcium binding protein A4
FBP1	0.902752	1.52E-09	2.06E-08	6.148177	Up	fructose-bisphosphatase 1
EVI2B	0.902533	4.81E-11	8.35E-10	6.713043	Up	ecotropic viral integration site 2B
CYTL1	0.899964	2.42E-09	3.18E-08	6.068837	Up	cytokine like 1
ABCF2-H2BE1	0.899866	9.84E-05	0.000587	3.923777	Up	ABCF2-H2BE1 readthrough
TNFSF8	0.899179	1.38E-08	1.60E-07	5.763207	Up	TNF superfamily member 8
DNAJC5B	0.897858	1.31E-09	1.79E-08	6.172859	Up	DnaJ heat shock protein family (Hsp40) member C5 beta
ANXA1	0.893996	1.75E-09	2.34E-08	6.124366	Up	annexin A1
CDH19	0.891343	2.38E-11	4.33E-10	6.823641	Up	cadherin 19
C1QA	0.887832	5.93E-08	6.24E-07	5.497535	Up	complement C1q A chain
HLA-DPA1	0.886134	1.70E-08	1.94E-07	5.72588	Up	major histocompatibility complex, class II, DP alpha 1
TYROBP	0.884289	5.55E-08	5.87E-07	5.509994	Up	transmembrane immune signaling adaptor TYROBP
AQP4	0.882274	5.56E-18	3.90E-16	8.951309	Up	aquaporin 4
CCR5	0.882119	1.05E-07	1.05E-06	5.391037	Up	C-C motif chemokine receptor 5
IL1RL1	0.875124	9.94E-05	0.000593	3.921199	Up	interleukin 1 receptor like 1
C5AR1	0.874734	1.57E-06	1.30E-05	4.85551	Up	complement C5a receptor 1
ADORA3	0.874266	6.46E-08	6.75E-07	5.481661	Up	adenosine A3 receptor
SLC7A7	0.873098	1.11E-08	1.31E-07	5.802082	Up	solute carrier family 7 member 7
HOXB7	0.871808	0.008329	0.014367	2.648139	Up	homeobox B7
NCF2	0.871484	2.27E-09	2.99E-08	6.079789	Up	neutrophil cytosolic factor 2

BATF	0.870381	3.01E-08	3.30E-07	5.622858	Up	basic leucine zipper ATF-like transcription factor
CD84	0.870231	3.72E-09	4.73E-08	5.994757	Up	CD84 molecule
LILRA2	0.869718	1.85E-08	2.10E-07	5.710657	Up	leukocyte immunoglobulin like receptor A2
PIRT	0.869486	4.28E-07	3.87E-06	5.11865	Up	phosphoinositide interacting regulator of transient receptor potential channels
HOXC10	0.867748	0.017979	0.028182	2.37326	Up	homeobox C10
PLBD1	0.865486	3.17E-09	4.08E-08	6.02223	Up	phospholipase B domain containing 1
CDCP1	0.86446	2.79E-09	3.63E-08	6.044299	Up	CUB domain containing protein 1
TIFA	0.860908	3.27E-18	2.43E-16	9.018477	Up	TRAF interacting protein with forkhead associated domain
VNN1	0.860144	1.58E-07	1.54E-06	5.312265	Up	vanin 1
ADGRE1	0.859199	8.33E-06	6.11E-05	4.499734	Up	adhesion G protein-coupled receptor E1
C7	0.858473	3.68E-06	2.87E-05	4.676734	Up	complement C7
MFAP5	0.85696	8.10E-07	7.02E-06	4.991104	Up	microfibril associated protein 5
TMIGD3	0.854966	4.11E-13	1.03E-11	7.434675	Up	transmembrane and immunoglobulin domain containing 3
CKS2	0.848641	3.76E-17	2.17E-15	8.707011	Up	CDC28 protein kinase regulatory subunit 2
IGSF6	0.848304	4.83E-08	5.15E-07	5.535855	Up	immunoglobulin superfamily member 6
SLCO4A1-AS1	0.845877	1.86E-09	2.48E-08	6.114054	Up	SLCO4A1 antisense RNA 1
S100A10	0.845646	6.54E-07	5.75E-06	5.03404	Up	S100 calcium binding protein A10
CRISPLD1	0.844854	4.52E-11	7.87E-10	6.722963	Up	cysteine rich secretory protein LCCL domain containing 1
S100A11	0.842516	2.74E-09	3.57E-08	6.047184	Up	S100 calcium binding protein A11
EMP3	0.83991	1.82E-13	4.91E-12	7.552285	Up	epithelial membrane protein 3
PTPRC	0.839547	1.83E-09	2.44E-08	6.116726	Up	protein tyrosine phosphatase receptor type C
HPGDS	0.838218	1.24E-08	1.45E-07	5.783191	Up	hematopoietic prostaglandin D synthase
FCGR1B	0.833855	1.86E-08	2.11E-07	5.709789	Up	Fc fragment of IgG receptor Ib
VNN2	0.832403	2.04E-09	2.71E-08	6.09819	Up	vanin 2
ANGPT1	0.831093	5.87E-14	1.75E-12	7.71414	Up	angiopoietin 1
IL18	0.829948	7.13E-08	7.40E-07	5.463156	Up	interleukin 18
DAPP1	0.827495	7.80E-10	1.10E-08	6.260522	Up	dual adaptor of phosphotyrosine and 3-phosphoinositides 1
TREM2	0.823445	9.55E-07	8.19E-06	4.957627	Up	triggering receptor expressed on myeloid cells 2
ZNF844	0.823036	1.85E-05	0.000127	4.320431	Up	zinc finger protein 844
CD300LF	0.822888	7.30E-06	5.41E-05	4.52874	Up	CD300 molecule like family member f
SUCNR1	0.814503	1.29E-09	1.75E-08	6.17632	Up	succinate receptor 1
MAOB	0.814462	2.97E-15	1.17E-13	8.127937	Up	monoamine oxidase B
BIRC7	0.813827	0.000169	0.000959	3.787595	Up	baculoviral IAP repeat containing 7
SLA	0.81323	5.13E-11	8.86E-10	6.70282	Up	Src like adaptor
PIK3AP1	0.812233	9.81E-10	1.36E-08	6.222066	Up	phosphoinositide-3-kinase adaptor protein 1
CXCR4	0.810069	2.71E-05	0.00018	4.232932	Up	C-X-C motif chemokine receptor 4
C6	0.809027	4.27E-08	4.59E-07	5.558494	Up	complement C6
LPCAT2	0.807716	2.05E-09	2.72E-08	6.096986	Up	lysophosphatidylcholineacyltransferase 2
DENND2D	0.807287	3.42E-10	5.13E-09	6.397034	Up	DENN domain containing 2D
CD14	0.806094	1.86E-08	2.10E-07	5.710533	Up	CD14 molecule
U2AF1	0.805142	5.48E-06	4.15E-05	4.591357	Up	U2 small nuclear RNA auxiliary factor 1
LINC02432	0.802437	5.88E-06	4.43E-05	4.576006	Up	long intergenic non-protein coding RNA 2432

SULT1C2	0.80003	0.000182	0.001026	3.768326	Up	sulfotransferase family 1C member 2
PDE4DIPP4	0.798781	1.13E-09	1.56E-08	6.197576	Up	PDE4DIP pseudogene 4
TASL	0.798212	7.75E-09	9.35E-08	5.86626	Up	TLR adaptor interacting with endolysosomal SLC15A4
LCP1	0.796904	2.98E-09	3.86E-08	6.032723	Up	lymphocyte cytosolic protein 1
TLR1	0.796299	1.69E-13	4.58E-12	7.562946	Up	toll like receptor 1
FPR2	0.79466	3.31E-07	3.04E-06	5.169451	Up	formyl peptide receptor 2
TNFRSF11B	0.791292	1.35E-11	2.59E-10	6.91146	Up	TNF receptor superfamily member 11b
SCIMP	0.791147	5.77E-07	5.12E-06	5.059302	Up	SLP adaptor and CSK interacting membrane protein
PLCXD3	0.789862	1.03E-12	2.42E-11	7.299224	Up	phosphatidylinositol specific phospholipase C X domain containing 3
BTK	0.788863	1.32E-08	1.53E-07	5.772267	Up	Bruton tyrosine kinase
APOC2	0.788213	3.62E-08	3.93E-07	5.588757	Up	apolipoprotein C2
SOD2	0.786522	3.39E-20	4.33E-18	9.581734	Up	superoxide dismutase 2
S100A12	0.785313	6.02E-06	4.52E-05	4.570839	Up	S100 calcium binding protein A12
ANXA2	0.783926	1.55E-06	1.28E-05	4.858524	Up	annexin A2
TSPAN8	0.782721	0.000715	0.003456	3.403093	Up	tetraspanin 8
SIGLEC8	0.781343	3.09E-06	2.44E-05	4.714362	Up	sialic acid binding Ig like lectin 8
CD53	0.781082	9.91E-10	1.37E-08	6.220442	Up	CD53 molecule
CYP4F3	0.781057	5.40E-07	4.81E-06	5.072302	Up	cytochrome P450 family 4 subfamily F member 3
SIGLEC14	0.779606	2.41E-05	0.000162	4.259698	Up	sialic acid binding Ig like lectin 14
RPE65	0.778812	3.98E-06	3.08E-05	4.66027	Up	retinoid isomerohydrolase RPE65
CLUL1	0.777708	4.91E-09	6.13E-08	5.946338	Up	clusterin like 1
AKR1C2	0.777382	6.07E-17	3.36E-15	8.644739	Up	aldo-ketoreductase family 1 member C2
SLC1A5	0.776022	1.56E-06	1.29E-05	4.857198	Up	solute carrier family 1 member 5
ACP5	0.775673	0.000178	0.001006	3.773868	Up	acid phosphatase 5, tartrate resistant
MT1A	0.775575	4.33E-08	4.65E-07	5.555896	Up	metallothionein 1A
HLA-DOA	0.77534	3.91E-07	3.56E-06	5.136579	Up	major histocompatibility complex, class II, DO alpha
LOC101927692	0.77494	4.74E-09	5.93E-08	5.952377	Up	uncharacterized LOC101927692
IL1A	0.774625	1.10E-07	1.10E-06	5.381503	Up	interleukin 1 alpha
SLC11A1	0.773866	1.21E-05	8.62E-05	4.416711	Up	solute carrier family 11 member 1
L3MBTL4-AS1	0.773816	1.09E-08	1.28E-07	5.806059	Up	L3MBTL4 antisense RNA 1
TSLP	0.773307	3.30E-09	4.24E-08	6.015314	Up	thymic stromal lymphopoietin
GAPT	0.773177	1.16E-05	8.31E-05	4.425598	Up	GRB2 binding adaptor protein, transmembrane
MAPK8IP1P1	0.771269	0.000152	0.00087	3.814896	Up	mitogen-activated protein kinase 8 interacting protein 1 pseudogene 1
IL13RA1	0.770923	8.73E-13	2.06E-11	7.324207	Up	interleukin 13 receptor subunit alpha 1
PELATON	0.767207	1.06E-05	7.62E-05	4.446643	Up	plaque enriched lncRNA in atherosclerotic and inflammatory bowel macrophage regulation
CLIC4	0.765249	2.66E-16	1.30E-14	8.451315	Up	chloride intracellular channel 4
TNFAIP6	0.764725	1.00E-10	1.65E-09	6.596071	Up	TNF alpha induced protein 6
ADAMDEC1	0.764208	3.71E-11	6.56E-10	6.753837	Up	ADAM like decysin 1
SLC26A7	0.762628	1.38E-08	1.60E-07	5.76427	Up	solute carrier family 26 member 7
KLHL6	0.762526	4.19E-06	3.23E-05	4.649216	Up	kelch like family member 6
HTRA4	0.760809	3.85E-07	3.51E-06	5.139228	Up	HtrA serine peptidase 4

FKBP5	0.759661	1.66E-13	4.49E-12	7.566028	Up	FKBP prolylisomerase 5
SEMA3D	0.756906	2.72E-11	4.91E-10	6.802759	Up	semaphorin 3D
MACC1	0.755131	3.89E-09	4.93E-08	5.986834	Up	MET transcriptional regulator MACC1
SOHLH2	0.754278	6.13E-09	7.53E-08	5.90761	Up	spermatogenesis and oogenesis specific basic helix-loop-helix 2
LUM	0.751977	2.41E-06	1.94E-05	4.766256	Up	lumican
TNFSF15	0.751817	9.99E-08	1.01E-06	5.399805	Up	TNF superfamily member 15
RAB42	0.751817	0.000177	0.000999	3.776164	Up	RAB42, member RAS oncogene family
GNG12	0.750793	3.97E-16	1.86E-14	8.398262	Up	G protein subunit gamma 12
TLR5	0.749183	2.56E-09	3.35E-08	6.059096	Up	toll like receptor 5
MPZL2	0.748658	3.79E-07	3.46E-06	5.142559	Up	myelin protein zero like 2
TNFRSF12A	0.748404	2.41E-08	2.69E-07	5.663342	Up	TNF receptor superfamily member 12A
FYB1	0.746504	5.84E-08	6.15E-07	5.50042	Up	FYN binding protein 1
DYNLT3	0.74604	2.21E-15	8.83E-14	8.1682	Up	dynein light chain Tctex-type 3
TNFSF13B	0.746014	3.57E-16	1.70E-14	8.412387	Up	TNF superfamily member 13b
TNC	0.745929	0.000578	0.002869	3.462085	Up	tenascin C
DSC2	0.74533	1.06E-13	2.99E-12	7.629708	Up	desmocollin 2
PMP2	0.743433	2.23E-12	4.90E-11	7.184859	Up	peripheral myelin protein 2
GADD45A	0.741681	1.14E-10	1.86E-09	6.575403	Up	growth arrest and DNA damage inducible alpha
FGF7	0.740888	2.50E-05	0.000168	4.251707	Up	fibroblast growth factor 7
RBM47	0.740154	1.30E-07	1.28E-06	5.350277	Up	RNA binding motif protein 47
GLIPR1	0.739826	1.41E-12	3.21E-11	7.253018	Up	GLI pathogenesis related 1
SOCS3	0.738603	3.49E-05	0.000228	4.173625	Up	suppressor of cytokine signaling 3
FABP5	0.737251	9.42E-14	2.69E-12	7.646867	Up	fatty acid binding protein 5
BIRC3	0.73425	1.48E-11	2.82E-10	6.897061	Up	baculoviral IAP repeat containing 3
C2orf88	0.733842	3.28E-12	6.99E-11	7.127156	Up	chromosome 2 open reading frame 88
TMEM156	0.733753	1.59E-07	1.55E-06	5.310986	Up	transmembrane protein 156
TGFBR1	0.732499	4.69E-16	2.16E-14	8.376044	Up	transforming growth factor beta receptor 1
CFI	0.73184	1.80E-06	1.48E-05	4.82727	Up	complement factor I
CEP55	0.729637	6.56E-07	5.77E-06	5.033574	Up	centrosomal protein 55
OGFRL1	0.72949	5.90E-24	2.52E-21	10.59128	Up	opioid growth factor receptor like 1
CD74	0.729434	4.94E-06	3.78E-05	4.613534	Up	CD74 molecule
RNASE4	0.728752	1.42E-07	1.39E-06	5.332811	Up	ribonuclease A family member 4
RPL17-C18orf32	0.728448	1.25E-11	2.42E-10	6.922754	Up	RPL17-C18orf32 readthrough
GBP3	0.727564	4.72E-08	5.04E-07	5.539876	Up	guanylate binding protein 3
SCN7A	0.726621	1.38E-05	9.74E-05	4.386694	Up	sodium voltage-gated channel alpha subunit 7
CLEC7A	0.726407	4.22E-06	3.25E-05	4.647727	Up	C-type lectin domain containing 7A
PTP4A1	0.721979	2.44E-11	4.44E-10	6.819539	Up	protein tyrosine phosphatase 4A1
OGN	0.72023	0.000361	0.001894	3.589814	Up	osteoglycin
RPL10AP6	0.719557	2.03E-11	3.74E-10	6.848474	Up	ribosomal protein L10a pseudogene 6
TNNI2	0.719215	2.51E-08	2.79E-07	5.655866	Up	troponin I2, fast skeletal type
C3	0.719155	8.50E-07	7.34E-06	4.981383	Up	complement C3
RSL24D1	0.716258	1.83E-20	2.49E-18	9.65607	Up	ribosomal L24 domain containing 1

SOAT1	0.715834	7.46E-26	6.56E-23	11.07783	Up	sterol O-acyltransferase 1
IP6K3	0.714366	3.79E-06	2.94E-05	4.670814	Up	inositol hexakisphosphate kinase 3
OSGIN2	0.714042	3.81E-20	4.82E-18	9.567569	Up	oxidative stress induced growth inhibitor family member 2
GPC3	0.711972	3.32E-05	0.000217	4.185512	Up	glypican 3
SNX20	0.711041	2.98E-06	2.36E-05	4.72209	Up	sorting nexin 20
RPL22L1	0.708553	4.62E-21	7.43E-19	9.820164	Up	ribosomal protein L22 like 1
LILRA4	0.708051	0.000165	0.000939	3.793592	Up	leukocyte immunoglobulin like receptor A4
LINC01480	0.707921	2.01E-06	1.64E-05	4.804035	Up	long intergenic non-protein coding RNA 1480
MCUB	0.706698	2.08E-06	1.68E-05	4.797731	Up	mitochondrial calcium uniporter dominant negative subunit beta
TNFAIP8L2	0.706508	7.03E-07	6.16E-06	5.019733	Up	TNF alpha induced protein 8 like 2
RGS2	0.706372	3.95E-14	1.22E-12	7.770069	Up	regulator of G protein signaling 2
SPOCD1	0.706007	1.61E-05	0.000112	4.351817	Up	SPOC domain containing 1
MYOT	0.704081	4.97E-15	1.86E-13	8.057626	Up	myotilin
CALHM6	0.703805	2.50E-07	2.35E-06	5.223858	Up	calcium homeostasis modulator family member 6
HCLS1	0.703663	3.86E-07	3.51E-06	5.139166	Up	hematopoietic cell-specific Lyn substrate 1
HLA-DQB2	0.70354	5.43E-06	4.12E-05	4.593181	Up	major histocompatibility complex, class II, DQ beta 2
PDPN	0.703107	4.04E-10	5.97E-09	6.369842	Up	podoplanin
LAIR1	0.702962	1.34E-06	1.12E-05	4.88787	Up	leukocyte associated immunoglobulin like receptor 1
F5	0.702026	2.44E-05	0.000164	4.256887	Up	coagulation factor V
CASP1	0.701118	9.35E-09	1.11E-07	5.833144	Up	caspase 1
FAS	0.699359	1.54E-13	4.20E-12	7.57654	Up	Fas cell surface death receptor
EIF3E	0.698268	4.74E-24	2.15E-21	10.61601	Up	eukaryotic translation initiation factor 3 subunit E
DRAM2	0.697889	3.07E-22	7.18E-20	10.13871	Up	DNA damage regulated autophagy modulator 2
CCL20	0.697396	7.28E-06	5.40E-05	4.529326	Up	C-C motif chemokine ligand 20
HAVCR2	0.69604	3.19E-09	4.10E-08	6.021211	Up	hepatitis A virus cellular receptor 2
TDRD15	0.694375	8.39E-06	6.15E-05	4.498162	Up	tudor domain containing 15
HLA-DPB1	0.694356	2.49E-07	2.34E-06	5.22477	Up	major histocompatibility complex, class II, DP beta 1
ANO6	0.694177	5.11E-16	2.33E-14	8.364735	Up	anoctamin 6
ITGB2	0.693752	2.30E-06	1.85E-05	4.776761	Up	integrin subunit beta 2
NFIL3	0.69305	9.32E-20	1.06E-17	9.459077	Up	nuclear factor, interleukin 3 regulated
LINC01857	0.692969	1.10E-15	4.69E-14	8.262181	Up	long intergenic non-protein coding RNA 1857
RPL21P93	0.692317	6.38E-10	9.14E-09	6.294156	Up	ribosomal protein L21 pseudogene 93
PRSS21	0.691534	9.59E-12	1.89E-10	6.963982	Up	serine protease 21
TGFBI	0.691242	8.73E-05	0.000526	3.953162	Up	transforming growth factor beta induced
CXCL5	0.690648	1.08E-13	3.04E-12	7.627144	Up	C-X-C motif chemokine ligand 5
KIF20A	0.6893	1.10E-06	9.34E-06	4.929108	Up	kinesin family member 20A
F13A1	0.687571	4.67E-06	3.58E-05	4.625904	Up	coagulation factor XIII A chain
NAMPTP1	0.685683	1.09E-08	1.28E-07	5.805907	Up	nicotinamidephosphoribosyltransferasepseudogene 1
ITGBL1	0.68549	0.000178	0.001005	3.774328	Up	integrin subunit beta like 1
ASAH1	0.684798	1.95E-16	9.80E-15	8.492171	Up	N-acylsphingosineamidohydrolase 1
HSD17B13	0.684405	4.67E-10	6.84E-09	6.345978	Up	hydroxysteroid 17-beta dehydrogenase 13

RPS3AP26	0.68297	7.25E-19	6.50E-17	9.206817	Up	RPS3A pseudogene 26
CD302	0.68218	3.50E-18	2.57E-16	9.009879	Up	CD302 molecule
IFITM2	0.682134	8.13E-08	8.35E-07	5.438534	Up	interferon induced transmembrane protein 2
P2RY8	0.680253	0.000111	0.000654	3.894217	Up	P2Y receptor family member 8
PLXDC2	0.680157	1.33E-16	6.92E-15	8.542901	Up	plexin domain containing 2
HPSE	0.679944	7.38E-10	1.05E-08	6.269734	Up	heparanase
IMPA1	0.679819	7.94E-21	1.19E-18	9.755822	Up	inositol monophosphatase 1
S100A6	0.678303	3.29E-10	4.94E-09	6.403471	Up	S100 calcium binding protein A6
PCED1B-AS1	0.677754	1.52E-06	1.26E-05	4.86185	Up	PCED1B antisense RNA 1
NAMPT	0.677579	6.68E-13	1.61E-11	7.36369	Up	nicotinamidephosphoribosyltransferase
KDELR3	0.677349	7.45E-11	1.25E-09	6.643676	Up	KDEL endoplasmic reticulum protein retention receptor 3
RRM2B	0.677203	1.11E-24	6.23E-22	10.77936	Up	ribonucleotidereductase regulatory TP53 inducible subunit M2B
APOL4	0.676576	2.74E-05	0.000182	4.229994	Up	apolipoprotein L4
AP1S2	0.675672	1.24E-21	2.40E-19	9.975234	Up	adaptor related protein complex 1 subunit sigma 2
ARL11	0.675622	1.16E-06	9.80E-06	4.918177	Up	ADP ribosylation factor like GTPase 11
SLC5A3	0.674719	1.96E-15	7.93E-14	8.184306	Up	solute carrier family 5 member 3
SDCBP	0.67386	2.39E-28	5.88E-25	11.69781	Up	syndecan binding protein
RNASE3	0.672162	2.69E-06	2.15E-05	4.74313	Up	ribonuclease A family member 3
CYTIP	0.672027	1.43E-05	0.000101	4.379151	Up	cytohesin 1 interacting protein
GBP1	0.671552	1.36E-07	1.34E-06	5.341343	Up	guanylate binding protein 1
C4A	0.671401	3.12E-05	0.000205	4.199743	Up	complement C4A (Rodgers blood group)
DNAJB9	0.671252	1.41E-20	1.99E-18	9.687327	Up	DnaJ heat shock protein family (Hsp40) member B9
PTPN22	0.669852	8.68E-11	1.45E-09	6.619336	Up	protein tyrosine phosphatase non-receptor type 22
SNX10	0.669114	1.42E-08	1.64E-07	5.758602	Up	sorting nexin 10
GPR82	0.668616	0.000102	0.00061	3.913648	Up	G protein-coupled receptor 82
ARHGDIB	0.668484	5.82E-08	6.14E-07	5.501025	Up	Rho GDP dissociation inhibitor beta
IQGAP2	0.667682	1.80E-05	0.000124	4.327129	Up	IQ motif containing GTPase activating protein 2
LINC02099	0.667142	8.38E-09	1.01E-07	5.852433	Up	long intergenic non-protein coding RNA 2099
H3C11	0.666538	8.53E-05	0.000515	3.959045	Up	H3 clustered histone 11
TRPC5OS	0.666451	2.60E-09	3.40E-08	6.05651	Up	TRPC5 opposite strand
ITGAD	0.66396	1.32E-06	1.10E-05	4.892151	Up	integrin subunit alpha D
IL2RA	0.663727	2.10E-05	0.000143	4.291302	Up	interleukin 2 receptor subunit alpha
UGCG	0.663322	1.41E-21	2.68E-19	9.960276	Up	UDP-glucose ceramideglucosyltransferase
ARHGAP15	0.661609	3.17E-06	2.50E-05	4.708696	Up	Rho GTPase activating protein 15
GBP2	0.661374	1.12E-05	8.02E-05	4.434216	Up	guanylate binding protein 2
FGL2	0.66067	1.08E-06	9.16E-06	4.933424	Up	fibrinogen like 2
LANCL3	0.659974	2.38E-13	6.23E-12	7.514039	Up	LanC like 3
BMP5	0.65879	0.000484	0.002454	3.51085	Up	bone morphogenetic protein 5
MYOM3	0.657109	0.000105	0.000623	3.90797	Up	myomesin 3
FGF2	0.656508	2.06E-19	2.17E-17	9.362348	Up	fibroblast growth factor 2
OTOS	0.655804	5.12E-08	5.44E-07	5.525103	Up	otospiralin
LOC112267968	0.655499	2.16E-05	0.000146	4.285717	Up	uncharacterized LOC112267968

PTGS1	0.655473	3.51E-08	3.82E-07	5.594383	Up	prostaglandin-endoperoxide synthase 1
GLRX	0.655085	6.67E-15	2.44E-13	8.017403	Up	glutaredoxin
HLA-DMB	0.654745	5.21E-05	0.000328	4.078641	Up	major histocompatibility complex, class II, DM beta
PPDPFL	0.654375	0.000336	0.001779	3.608644	Up	pancreatic progenitor cell differentiation and proliferation factor like
RGS10	0.654236	1.14E-06	9.66E-06	4.921538	Up	regulator of G protein signaling 10
LYVE1	0.654141	1.13E-06	9.61E-06	4.922778	Up	lymphatic vessel endothelial hyaluronan receptor 1
EVI2A	0.654081	2.35E-07	2.22E-06	5.235996	Up	ecotropic viral integration site 2A
CLIC1	0.653922	3.18E-07	2.94E-06	5.177255	Up	chloride intracellular channel 1
MGST1	0.653865	1.07E-13	3.01E-12	7.628516	Up	microsomal glutathione S-transferase 1
PTTG1	0.653622	2.14E-12	4.72E-11	7.191313	Up	PTTG1 regulator of sister chromatid separation, securin
NPC2	0.651945	3.81E-08	4.12E-07	5.579595	Up	NPC intracellular cholesterol transporter 2
FAM111B	0.651861	5.43E-06	4.12E-05	4.59309	Up	family with sequence similarity 111 member B
PLP2	0.65135	1.79E-08	2.03E-07	5.717262	Up	proteolipid protein 2
SRGN	0.650762	5.38E-07	4.79E-06	5.073126	Up	serglycin
B3GNT5	0.650265	1.84E-08	2.09E-07	5.712045	Up	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5
OR52N4	0.649014	9.87E-08	9.95E-07	5.402142	Up	olfactory receptor family 52 subfamily N member 4
CNN3	0.648544	1.47E-16	7.59E-15	8.529229	Up	calponin 3
CAPG	0.648338	5.61E-07	4.99E-06	5.064671	Up	capping actin protein, gelsolin like
TOP2A	0.647312	0.000433	0.002224	3.540845	Up	DNA topoisomerase II alpha
CASP5	0.646834	1.41E-06	1.18E-05	4.877666	Up	caspase 5
HCK	0.64668	1.06E-06	9.00E-06	4.937207	Up	HCK proto-oncogene, Src family tyrosine kinase
NABP1	0.64614	1.83E-12	4.09E-11	7.214147	Up	nucleic acid binding protein 1
CDK1	0.645707	3.63E-10	5.41E-09	6.387396	Up	cyclin dependent kinase 1
FCAR	0.645516	7.18E-05	0.000441	4.000968	Up	Fc fragment of IgA receptor
MAD2L1	0.64527	5.64E-11	9.68E-10	6.687897	Up	mitotic arrest deficient 2 like 1
FRRS1	0.644905	3.01E-06	2.38E-05	4.719727	Up	ferric chelate reductase 1
DCSTAMP	0.644445	1.96E-05	0.000134	4.307495	Up	dendrocyte expressed seven transmembrane protein
ITIH2	0.644007	0.000289	0.001554	3.648295	Up	inter-alpha-trypsin inhibitor heavy chain 2
LAMP2	0.642807	2.33E-15	9.30E-14	8.160902	Up	lysosomal associated membrane protein 2
SHISAL2A	0.642787	1.34E-06	1.12E-05	4.888926	Up	shisa like 2A
GGH	0.641518	9.54E-11	1.57E-09	6.604182	Up	gamma-glutamyl hydrolase
C1orf87	0.641452	0.00172	0.00717	3.150454	Up	chromosome 1 open reading frame 87
ATP5MD	0.641311	1.86E-16	9.39E-15	8.498499	Up	ATP synthase membrane subunit DAPIT
CD37	0.641269	4.19E-05	0.00027	4.130284	Up	CD37 molecule
GPR84	0.641013	1.90E-05	0.00013	4.314663	Up	G protein-coupled receptor 84
TMED5	0.639791	9.74E-25	5.74E-22	10.79355	Up	transmembrane p24 trafficking protein 5
OSMR	0.639714	4.18E-09	5.27E-08	5.974391	Up	oncostatin M receptor
LSP1	0.639534	0.000121	0.000707	3.872795	Up	lymphocyte specific protein 1
PPP1CB	0.638757	1.29E-25	1.05E-22	11.01803	Up	protein phosphatase 1 catalytic subunit beta
KLHL31	0.638635	2.86E-11	5.15E-10	6.79461	Up	kelch like family member 31
ACP3	0.638576	1.08E-05	7.74E-05	4.442802	Up	acid phosphatase 3

RPL17P6	0.638112	2.34E-13	6.15E-12	7.516222	Up	ribosomal protein L17 pseudogene 6
LINC01235	0.637611	1.11E-05	7.97E-05	4.435706	Up	long intergenic non-protein coding RNA 1235
LINC00706	0.636903	6.05E-06	4.54E-05	4.569928	Up	long intergenic non-protein coding RNA 706
CALCRL	0.636527	8.39E-12	1.67E-10	6.98457	Up	calcitonin receptor like receptor
PROS1	0.635805	5.49E-13	1.34E-11	7.392495	Up	protein S
CPB1	0.635424	4.92E-06	3.76E-05	4.614464	Up	carboxypeptidase B1
CPM	0.63489	1.97E-08	2.23E-07	5.699344	Up	carboxypeptidase M
CRYZ	0.634403	1.21E-17	7.93E-16	8.852151	Up	crystallin zeta
LINC01088	0.633962	0.001404	0.006084	3.210413	Up	long intergenic non-protein coding RNA 1088
HLA-DMA	0.633684	8.52E-06	6.24E-05	4.494691	Up	major histocompatibility complex, class II, DM alpha
SLC38A2	0.633105	6.34E-22	1.34E-19	10.05418	Up	solute carrier family 38 member 2
MAFB	0.632674	6.50E-08	6.79E-07	5.480475	Up	MAF bZIP transcription factor B
ST8SIA4	0.631922	8.88E-12	1.76E-10	6.975844	Up	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4
KYNU	0.631679	2.40E-06	1.93E-05	4.767749	Up	kynureninase
GPX8	0.631669	0.000653	0.003195	3.428411	Up	glutathione peroxidase 8 (putative)
HSP90AB3P	0.631287	3.31E-10	4.97E-09	6.402365	Up	heat shock protein 90 alpha family class B member 3, pseudogene
RPL9P8	0.63121	3.00E-18	2.26E-16	9.029189	Up	ribosomal protein L9 pseudogene 8
HOXC4	0.630924	0.020286	0.03139	2.327857	Up	homeobox C4
STK26	0.630871	9.30E-11	1.54E-09	6.608246	Up	serine/threonine kinase 26
KCNJ5	0.62918	0.000155	0.000887	3.809615	Up	potassium inwardly rectifying channel subfamily J member 5
CCNG1	0.628797	9.79E-21	1.43E-18	9.730849	Up	cyclin G1
CHST9	0.628613	1.33E-11	2.56E-10	6.913261	Up	carbohydrate sulfotransferase 9
ACTR6	0.628277	7.03E-17	3.85E-15	8.625642	Up	actin related protein 6
PLA2G2A	0.628137	0.000204	0.001136	3.739718	Up	phospholipase A2 group IIA
CDKN1A	0.628123	9.40E-06	6.83E-05	4.473055	Up	cyclin dependent kinase inhibitor 1A
MMP7	0.627991	4.53E-12	9.41E-11	7.078182	Up	matrix metallopeptidase 7
TNFAIP8L3	0.627413	1.25E-07	1.24E-06	5.357138	Up	TNF alpha induced protein 8 like 3
PRRG4	0.627395	1.54E-05	0.000108	4.362139	Up	proline rich and Gla domain 4
C1orf162	0.627391	3.83E-11	6.74E-10	6.748859	Up	chromosome 1 open reading frame 162
PI15	0.626881	4.58E-07	4.12E-06	5.105029	Up	peptidase inhibitor 15
PLEK	0.626315	2.36E-07	2.23E-06	5.234888	Up	pleckstrin
LIPA	0.626069	2.91E-10	4.42E-09	6.423432	Up	lipase A, lysosomal acid type
MSLN	0.625256	5.54E-06	4.20E-05	4.588951	Up	mesothelin
OSTC	0.624321	3.37E-21	5.62E-19	9.857736	Up	oligosaccharyltransferase complex non-catalytic subunit
LOC101929331	0.623577	4.18E-05	0.000269	4.13111	Up	uncharacterized LOC101929331
ANGPTL5	0.623074	2.10E-07	2.00E-06	5.257635	Up	angiopoietin like 5
HILPDA	0.622023	3.45E-06	2.70E-05	4.690707	Up	hypoxia inducible lipid droplet associated
NGFR	0.621832	0.000225	0.001238	3.714674	Up	nerve growth factor receptor
HSPA13	0.620823	4.64E-17	2.63E-15	8.679517	Up	heat shock protein family A (Hsp70) member 13
CRTAM	0.619031	0.021452	0.033014	2.306618	Up	cytotoxic and regulatory T cell molecule
CRNDE	0.618001	0.008103	0.014051	2.657562	Up	colorectal neoplasia differentially expressed
CYP1B1	0.617941	2.80E-07	2.61E-06	5.201918	Up	cytochrome P450 family 1 subfamily B member 1

FKBP7	0.617471	2.66E-13	6.93E-12	7.497871	Up	FKBP prolylisomerase 7
PHEX	0.616303	1.26E-06	1.06E-05	4.901164	Up	phosphate regulating endopeptidase homolog X-linked
SERPINB1	0.616188	5.21E-14	1.57E-12	7.731029	Up	serpin family B member 1
PIFO	0.616067	2.12E-07	2.02E-06	5.255631	Up	primary cilia formation
HOTAIRM1	0.61595	0.030508	0.045354	2.169107	Up	HOXA transcript antisense RNA, myeloid-specific 1
RHOQ	0.615385	5.98E-24	2.53E-21	10.58983	Up	ras homolog family member Q
ZBTB33	0.615321	2.10E-19	2.19E-17	9.360019	Up	zinc finger and BTB domain containing 33
PKIB	0.614222	0.00067	0.003265	3.421458	Up	cAMP-dependent protein kinase inhibitor beta
ERBIN	0.613961	9.03E-17	4.87E-15	8.593079	Up	erbb2 interacting protein
ACSL1	0.613725	5.73E-11	9.82E-10	6.685362	Up	acyl-CoA synthetase long chain family member 1
AP1AR	0.613691	1.95E-19	2.07E-17	9.368638	Up	adaptor related protein complex 1 associated regulatory protein
SLC2A5	0.61365	5.31E-07	4.73E-06	5.075908	Up	solute carrier family 2 member 5
PLS1	0.61321	4.15E-11	7.26E-10	6.73648	Up	plastin 1
RP2	0.612878	2.28E-14	7.44E-13	7.84724	Up	RP2 activator of ARL3 GTPase
LRRC25	0.612536	2.53E-05	0.000169	4.248743	Up	leucine rich repeat containing 25
TSPAN19	0.612035	1.62E-08	1.85E-07	5.734813	Up	tetraspanin 19
ARL6IP5	0.611773	3.42E-19	3.35E-17	9.299882	Up	ADP ribosylation factor like GTPase 6 interacting protein 5
GK	0.610892	5.55E-19	5.09E-17	9.239925	Up	glycerol kinase
TC2N	0.609079	9.38E-06	6.82E-05	4.473351	Up	tandem C2 domains, nuclear
CHRNA5	0.608913	7.18E-10	1.02E-08	6.274253	Up	cholinergic receptor nicotinic alpha 5 subunit
HACD4	0.608889	3.45E-11	6.12E-10	6.765607	Up	3-hydroxyacyl-CoA dehydratase 4
F3	0.608579	1.46E-07	1.43E-06	5.32765	Up	coagulation factor III, tissue factor
PWAR5	0.608483	0.013871	0.02241	2.468597	Up	PraderWilli/Angelman region RNA 5
GMFG	0.608119	4.32E-08	4.64E-07	5.556571	Up	glia maturation factor gamma
RAB20	0.607149	5.73E-06	4.33E-05	4.581468	Up	RAB20, member RAS oncogene family
RPL39	0.607035	3.46E-16	1.65E-14	8.416601	Up	ribosomal protein L39
EGF	0.60673	2.42E-06	1.94E-05	4.765532	Up	epidermal growth factor
EIF4A2	0.606084	1.04E-12	2.43E-11	7.29836	Up	eukaryotic translation initiation factor 4A2
B2M	0.605881	2.74E-10	4.16E-09	6.433531	Up	beta-2-microglobulin
C4B	0.605268	0.000214	0.001184	3.727623	Up	complement C4B (Chido blood group)
STEAP1	0.605216	1.40E-09	1.90E-08	6.162592	Up	STEAP family member 1
SPTSSA	0.605	1.91E-20	2.60E-18	9.65056	Up	serine palmitoyltransferase small subunit A
BTG3	0.6047	5.08E-11	8.78E-10	6.704286	Up	BTG anti-proliferation factor 3
KITLG	0.604562	7.70E-10	1.09E-08	6.262582	Up	KIT ligand
GAS2L3	0.604212	1.47E-05	0.000103	4.372412	Up	growth arrest specific 2 like 3
H3C8	0.604196	0.000146	0.00084	3.824599	Up	H3 clustered histone 8
TLR6	0.60399	1.56E-09	2.11E-08	6.143677	Up	toll like receptor 6
MILR1	0.603478	3.92E-05	0.000253	4.14644	Up	mast cell immunoglobulin like receptor 1
SCEL	0.603285	3.93E-07	3.58E-06	5.135176	Up	sciellin
TLR10	0.602596	7.23E-07	6.32E-06	5.013936	Up	toll like receptor 10
ARG1	0.602336	7.67E-07	6.68E-06	5.001952	Up	arginase 1
LINC01736	0.602061	3.60E-05	0.000234	4.166301	Up	long intergenic non-protein coding RNA 1736

HEXB	0.601841	5.54E-27	8.63E-24	11.36119	Up	hexosaminidase subunit beta
CXCR2	0.6014	5.74E-06	4.34E-05	4.581092	Up	C-X-C motif chemokine receptor 2
AK6	0.601364	1.57E-21	2.92E-19	9.947764	Up	adenylate kinase 6
MSX2	0.600845	0.000641	0.003145	3.433425	Up	mshhomeobox 2
GEM	0.600484	2.95E-08	3.24E-07	5.62657	Up	GTP binding protein overexpressed in skeletal muscle
FAM81B	0.600007	0.001385	0.006024	3.214341	Up	family with sequence similarity 81 member B
GSTM1	-2.45254	4.93E-10	7.20E-09	-6.33701	Down	glutathione S-transferase mu 1
NPIPA8	-1.52079	4.32E-07	3.91E-06	-5.11668	Down	nuclear pore complex interacting protein family member A8
CFAP157	-1.46652	1.16E-09	1.59E-08	-6.19412	Down	cilia and flagella associated protein 157
MAPK15	-1.46357	3.15E-12	6.74E-11	-7.13331	Down	mitogen-activated protein kinase 15
MTND1P23	-1.42041	1.40E-10	2.25E-09	-6.54208	Down	MT-ND1 pseudogene 23
HES5	-1.37979	1.00E-15	4.33E-14	-8.27437	Down	hes family bHLH transcription factor 5
LOC102723360	-1.33333	4.54E-08	4.86E-07	-5.54726	Down	uncharacterized LOC102723360
PKD1P5	-1.32389	1.11E-19	1.26E-17	-9.43744	Down	polycystin 1, transient receptor potential channel interacting pseudogene 5
CYP2D6	-1.32229	5.64E-26	5.54E-23	-11.1085	Down	cytochrome P450 family 2 subfamily D member 6
PTGDR2	-1.27048	4.46E-26	4.61E-23	-11.1343	Down	prostaglandin D2 receptor 2
MEG9	-1.23691	4.32E-16	2.01E-14	-8.38711	Down	maternally expressed 9
FGF17	-1.23456	2.38E-13	6.23E-12	-7.51396	Down	fibroblast growth factor 17
F8A3	-1.22799	7.00E-13	1.68E-11	-7.35683	Down	coagulation factor VIII associated 3
LMNTD2-AS1	-1.22267	7.98E-13	1.90E-11	-7.33741	Down	LMNTD2 antisense RNA 1
VWA5B2	-1.20371	2.27E-16	1.12E-14	-8.47211	Down	von Willebrand factor A domain containing 5B2
SLC4A1	-1.19544	5.04E-14	1.53E-12	-7.73555	Down	solute carrier family 4 member 1 (Diego blood group)
ADAMTS7P1	-1.18883	7.13E-15	2.60E-13	-8.00805	Down	ADAMTS7 pseudogene 1
IQCN	-1.16821	1.07E-24	6.14E-22	-10.7826	Down	IQ motif containing N
UPK3BL2	-1.15263	1.45E-20	2.04E-18	-9.68406	Down	uroplakin 3B like 2
PCDHA14	-1.14332	3.50E-10	5.23E-09	-6.39348	Down	protocadherin alpha 14 pseudogene
CALML6	-1.13696	1.12E-18	9.49E-17	-9.1532	Down	calmodulin like 6
SLC26A10	-1.13487	1.19E-15	5.06E-14	-8.25109	Down	solute carrier family 26 member 10
DNAH3	-1.1219	2.46E-07	2.31E-06	-5.2274	Down	dynein axonemal heavy chain 3
SLC13A5	-1.12028	1.23E-15	5.18E-14	-8.24758	Down	solute carrier family 13 member 5
KCNT1	-1.11423	3.28E-08	3.58E-07	-5.60719	Down	potassium sodium-activated channel subfamily T member 1
HGFAC	-1.11168	6.09E-16	2.75E-14	-8.34128	Down	HGF activator
LINC02688	-1.09814	1.29E-12	2.97E-11	-7.26637	Down	long intergenic non-protein coding RNA 2688
LOC339059	-1.09622	2.85E-13	7.39E-12	-7.48756	Down	uncharacterized LOC339059
FAM153B	-1.09555	9.86E-08	9.94E-07	-5.40231	Down	family with sequence similarity 153 member B
LOC729652	-1.08557	7.11E-20	8.42E-18	-9.49195	Down	uncharacterized LOC729652
ALAS2	-1.08473	3.56E-09	4.54E-08	-6.00233	Down	5'-aminolevulinate synthase 2
AMIGO3	-1.08275	1.25E-07	1.24E-06	-5.35801	Down	adhesion molecule with Ig like domain 3
PDE4C	-1.08147	5.04E-08	5.36E-07	-5.52802	Down	phosphodiesterase 4C
CCDC78	-1.08104	1.01E-24	5.81E-22	-10.79	Down	coiled-coil domain containing 78
GOLGA8O	-1.0764	5.18E-08	5.50E-07	-5.52274	Down	golgin A8 family member O
IQSEC3P3	-1.07638	4.75E-09	5.94E-08	-5.95204	Down	IQ motif and Sec7 domain 3 pseudogene 3

PKD1P4	-1.06548	2.11E-28	5.40E-25	-11.7114	Down	polycystin 1, transient receptor potential channel interacting pseudogene 4
IL21R-AS1	-1.05286	2.72E-16	1.33E-14	-8.44828	Down	IL21R antisense RNA 1
TRIM17	-1.04487	1.71E-11	3.21E-10	-6.87457	Down	tripartite motif containing 17
SOGA3	-1.04078	1.25E-22	3.44E-20	-10.2427	Down	SOGA family member 3
NUTM2E	-1.03011	4.41E-09	5.54E-08	-5.96503	Down	NUT family member 2E
EME2	-1.02724	4.43E-28	1.00E-24	-11.6323	Down	essential meiotic structure-specific endonuclease subunit 2
LOC100130587	-1.02601	9.25E-17	4.98E-15	-8.58998	Down	uncharacterized LOC100130587
TNFRSF25	-1.02586	2.04E-10	3.17E-09	-6.48166	Down	TNF receptor superfamily member 25
LOC400553	-1.02452	3.19E-10	4.80E-09	-6.40883	Down	uncharacterized LOC400553
CSPG4P13	-1.02337	1.13E-13	3.18E-12	-7.62034	Down	chondroitin sulfate proteoglycan 4 pseudogene 13
HERC2P5	-1.02272	1.04E-13	2.93E-12	-7.6333	Down	hect domain and RLD 2 pseudogene 5
ANKRD20A11P	-1.01891	9.28E-11	1.54E-09	-6.60852	Down	ankyrin repeat domain 20 family member A11, pseudogene
FTCD	-1.01531	1.59E-11	3.00E-10	-6.8861	Down	formimidoyltransferasecyclodeaminase
C13orf46	-1.01283	3.38E-24	1.63E-21	-10.6541	Down	chromosome 13 open reading frame 46
ANKRD19P	-1.01102	8.92E-09	1.07E-07	-5.84148	Down	ankyrin repeat domain 19, pseudogene
CACNA1H	-1.01041	4.00E-15	1.53E-13	-8.08728	Down	calcium voltage-gated channel subunit alpha1 H
KRT18P15	-1.00072	6.59E-17	3.62E-15	-8.63418	Down	keratin 18 pseudogene 15
RGS11	-0.99855	1.93E-32	2.91E-28	-12.6764	Down	regulator of G protein signaling 11
STX16-NPEPL1	-0.99691	3.36E-19	3.31E-17	-9.30209	Down	STX16-NPEPL1 readthrough (NMD candidate)
PKD1P2	-0.99211	7.14E-06	5.30E-05	-4.53368	Down	polycystin 1, transient receptor potential channel interacting pseudogene 2
GNB3	-0.9921	2.01E-13	5.34E-12	-7.5384	Down	G protein subunit beta 3
FAM66E	-0.99043	3.13E-14	9.98E-13	-7.80249	Down	family with sequence similarity 66 member E
IGFN1	-0.9863	2.39E-10	3.68E-09	-6.45553	Down	immunoglobulin like and fibronectin type III domain containing 1
WDR97	-0.98542	2.68E-19	2.72E-17	-9.32969	Down	WD repeat domain 97
KCNK4-TEX40	-0.98169	1.49E-07	1.45E-06	-5.32396	Down	KCNK4-TEX40 readthrough
OXCT2P1	-0.97824	1.45E-17	9.23E-16	-8.82936	Down	3-oxoacid CoA-transferase 2 pseudogene 1
DNAH2	-0.97652	4.57E-17	2.59E-15	-8.68153	Down	dynein axonemal heavy chain 2
EGR4	-0.97636	4.35E-05	0.000278	-4.12181	Down	early growth response 4
PRR22	-0.97524	1.37E-25	1.09E-22	-11.0112	Down	proline rich 22
MUSTN1	-0.97441	1.78E-12	3.99E-11	-7.21826	Down	musculoskeletal, embryonic nuclear protein 1
LOC728138	-0.96938	1.72E-11	3.23E-10	-6.87366	Down	KIAA2013 pseudogene
SOHLH1	-0.96598	1.96E-05	0.000134	-4.30731	Down	spermatogenesis and oogenesis specific basic helix-loop-helix 1
CCDC154	-0.96493	4.17E-18	3.04E-16	-8.98766	Down	coiled-coil domain containing 154
RTEL1-TNFRSF6B	-0.96471	6.45E-23	1.94E-20	-10.3189	Down	RTEL1-TNFRSF6B readthrough (NMD candidate)
DEFA1	-0.96346	1.56E-07	1.52E-06	-5.31533	Down	defensin alpha 1
PLA2G4B	-0.96033	2.06E-22	5.10E-20	-10.1849	Down	phospholipase A2 group IVB
GRAPL	-0.95833	6.42E-10	9.20E-09	-6.29304	Down	GRB2 related adaptor protein like
WBP11P1	-0.95681	3.86E-09	4.90E-08	-5.98806	Down	WBP11 pseudogene 1
TUB-AS1	-0.95318	6.20E-15	2.29E-13	-8.0273	Down	TUB antisense RNA 1
LAT	-0.95179	2.53E-25	1.84E-22	-10.9433	Down	linker for activation of T cells
SRRM3	-0.94996	2.41E-08	2.69E-07	-5.66324	Down	serine/arginine repetitive matrix 3

POTEI	-0.94916	7.12E-06	5.29E-05	-4.53424	Down	POTE ankyrin domain family member I
KRT8P15	-0.94464	7.47E-19	6.64E-17	-9.20309	Down	keratin 8 pseudogene 15
DUX4L27	-0.94225	7.23E-11	1.22E-09	-6.64836	Down	double homeobox 4 like 27 (pseudogene)
POLR2J2	-0.94105	8.56E-25	5.26E-22	-10.8079	Down	RNA polymerase II subunit J2
MIRLET7BHG	-0.94065	5.58E-24	2.40E-21	-10.5976	Down	MIRLET7B host gene
CFAP74	-0.93965	6.00E-15	2.22E-13	-8.03193	Down	cilia and flagella associated protein 74
CFAP99	-0.93745	1.01E-18	8.68E-17	-9.16607	Down	cilia and flagella associated protein 99
TMEM249	-0.93661	6.02E-10	8.68E-09	-6.30379	Down	transmembrane protein 249
CCER2	-0.93548	2.82E-23	9.46E-21	-10.4135	Down	coiled-coil glutamate rich protein 2
ZFR2	-0.9347	2.90E-14	9.30E-13	-7.81327	Down	zinc finger RNA binding protein 2
SLC7A10	-0.93113	8.22E-13	1.95E-11	-7.33321	Down	solute carrier family 7 member 10
PLEKHG5	-0.93104	8.43E-10	1.19E-08	-6.24748	Down	pleckstrin homology and RhoGEF domain containing G5
MIR124-1HG	-0.93091	9.08E-06	6.62E-05	-4.48056	Down	MIR124-1 host gene
TBC1D29P	-0.93087	3.98E-19	3.81E-17	-9.28107	Down	TBC1 domain family member 29, pseudogene
FER1L5	-0.93004	2.85E-16	1.38E-14	-8.44202	Down	fer-1 like family member 5
SMARCE1P5	-0.92523	1.20E-16	6.34E-15	-8.55613	Down	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1 pseudogene 5
PKD1P3	-0.92515	6.37E-24	2.64E-21	-10.5826	Down	polycystin 1, transient receptor potential channel interacting pseudogene 3
SEPT5-GP1BB	-0.92436	2.51E-12	5.46E-11	-7.16743	Down	SEPT5-GP1BB readthrough
RNY1	-0.92326	1.14E-07	1.14E-06	-5.37403	Down	RNA, Ro60-associated Y1
PDE6B-AS1	-0.92095	7.39E-16	3.27E-14	-8.31553	Down	PDE6B antisense RNA 1
LOC101929538	-0.91899	2.82E-14	9.07E-13	-7.81724	Down	uncharacterized LOC101929538
CYP2D7	-0.91876	9.01E-24	3.64E-21	-10.5434	Down	cytochrome P450 family 2 subfamily D member 7 (gene/pseudogene)
GAS2L1P2	-0.91866	1.13E-15	4.82E-14	-8.25832	Down	growth arrest specific 2 like 1 pseudogene 2
CA1	-0.91853	1.34E-08	1.56E-07	-5.76878	Down	carbonic anhydrase 1
KCNH3	-0.91791	5.01E-05	0.000317	-4.08786	Down	potassium voltage-gated channel subfamily H member 3
TBC1D3C	-0.91693	0.000285	0.001532	-3.65245	Down	TBC1 domain family member 3C
GLYCTK	-0.91655	2.46E-29	7.81E-26	-11.938	Down	glycerate kinase
AZU1	-0.91523	1.98E-10	3.09E-09	-6.48668	Down	azurocidin 1
GPR199P	-0.91402	7.14E-08	7.40E-07	-5.46299	Down	G protein-coupled receptor 199, pseudogene
DNASE1L2	-0.91285	4.22E-20	5.23E-18	-9.55519	Down	deoxyribonuclease 1 like 2
GLULP2	-0.91101	2.06E-10	3.20E-09	-6.47991	Down	glutamate-ammonia ligase pseudogene 2
CSPG4P10	-0.90988	3.01E-21	5.13E-19	-9.87098	Down	chondroitin sulfate proteoglycan 4 pseudogene 10
SHANK1	-0.90961	1.94E-08	2.19E-07	-5.7029	Down	SH3 and multiple ankyrin repeat domains 1
KIAA2012	-0.90914	1.28E-10	2.08E-09	-6.55659	Down	KIAA2012
CFAP46	-0.9082	2.17E-14	7.13E-13	-7.85365	Down	cilia and flagella associated protein 46
CCDC188	-0.90774	4.53E-13	1.13E-11	-7.42054	Down	coiled-coil domain containing 188
LINC01310	-0.90376	1.33E-12	3.04E-11	-7.2624	Down	long intergenic non-protein coding RNA 1310
OR7E157P	-0.90282	5.71E-09	7.05E-08	-5.92007	Down	olfactory receptor family 7 subfamily E member 157 pseudogene
ADAM33	-0.90072	1.03E-14	3.64E-13	-7.95765	Down	ADAM metallopeptidase domain 33
ABO	-0.8972	9.30E-19	8.07E-17	-9.17587	Down	ABO, alpha 1-3-N-acetylgalactosaminyltransferase and alpha 1-3-galactosyltransferase
LOC105379252	-0.89676	1.70E-11	3.20E-10	-6.87535	Down	family with sequence similarity 95 member B1-

						like
RNF207	-0.8955	9.78E-22	1.96E-19	-10.0034	Down	ring finger protein 207
MEG3	-0.8926	6.83E-09	8.31E-08	-5.88863	Down	maternally expressed 3
RIPOR3	-0.89182	1.21E-11	2.35E-10	-6.92794	Down	RIPOR family member 3
ACAP3	-0.89141	1.19E-27	2.42E-24	-11.5264	Down	ArfGAP with coiled-coil, ankyrin repeat and PH domains 3
ADGRB1	-0.88744	1.19E-15	5.05E-14	-8.25141	Down	adhesion G protein-coupled receptor B1
WNT7B	-0.88409	5.94E-16	2.68E-14	-8.34467	Down	Wnt family member 7B
CELF3	-0.88404	2.26E-06	1.83E-05	-4.77979	Down	CUGBP Elav-like family member 3
ZDHHC11B	-0.88401	5.56E-19	5.10E-17	-9.23967	Down	zinc finger DHHC-type containing 11B
LINC02395	-0.88356	2.00E-10	3.12E-09	-6.48494	Down	long intergenic non-protein coding RNA 2395
CHD5	-0.88057	2.69E-05	0.000179	-4.2343	Down	chromodomain helicase DNA binding protein 5
SEMA3G	-0.87927	5.09E-12	1.05E-10	-7.06057	Down	semaphorin 3G
USHBP1	-0.87867	3.39E-12	7.20E-11	-7.12227	Down	USH1 protein network component harmonin binding protein 1
OBSCN-AS1	-0.87867	3.32E-09	4.26E-08	-6.0141	Down	OBSCN antisense RNA 1
ACTG1P12	-0.87815	1.04E-07	1.04E-06	-5.39292	Down	actin gamma 1 pseudogene 12
VWA5B1	-0.87567	2.28E-06	1.84E-05	-4.7781	Down	von Willebrand factor A domain containing 5B1
POTEF	-0.87507	2.93E-06	2.33E-05	-4.72509	Down	POTE ankyrin domain family member F
NPIPA5	-0.87201	1.25E-08	1.46E-07	-5.78132	Down	nuclear pore complex interacting protein family member A5
SPTBN5	-0.87078	4.96E-13	1.22E-11	-7.40717	Down	spectrin beta, non-erythrocytic 5
DLGAP3	-0.87022	4.56E-06	3.50E-05	-4.63107	Down	DLG associated protein 3
MMP23B	-0.86972	7.01E-18	4.86E-16	-8.92199	Down	matrix metallopeptidase 23B
STH	-0.86661	4.65E-15	1.74E-13	-8.06675	Down	saitohin
LINC01238	-0.86416	2.41E-21	4.19E-19	-9.89753	Down	long intergenic non-protein coding RNA 1238
SCRT1	-0.86136	3.64E-06	2.84E-05	-4.67915	Down	scratch family transcriptional repressor 1
CNKSR1	-0.86127	2.52E-29	7.81E-26	-11.9357	Down	connector enhancer of kinase suppressor of Ras 1
FAM163B	-0.86088	4.64E-05	0.000296	-4.10629	Down	family with sequence similarity 163 member B
KIF26A	-0.85947	5.61E-15	2.08E-13	-8.04113	Down	kinesin family member 26A
CCM2L	-0.85907	2.51E-19	2.57E-17	-9.33772	Down	CCM2 like scaffold protein
FOXL2NB	-0.85879	2.82E-12	6.09E-11	-7.14964	Down	FOXL2 neighbor
KCNQ2	-0.858	7.06E-07	6.18E-06	-5.01881	Down	potassium voltage-gated channel subfamily Q member 2
LCNL1	-0.85733	2.67E-17	1.59E-15	-8.7509	Down	lipocalin like 1
JMJD7-PLA2G4B	-0.85512	2.13E-19	2.22E-17	-9.35813	Down	JMJD7-PLA2G4B readthrough
CFAP73	-0.85415	2.59E-05	0.000173	-4.24314	Down	cilia and flagella associated protein 73
SHANK3	-0.85278	4.63E-13	1.15E-11	-7.41732	Down	SH3 and multiple ankyrin repeat domains 3
HTR6	-0.85055	0.000263	0.001428	-3.67318	Down	5-hydroxytryptamine receptor 6
EZHIP	-0.85003	1.02E-19	1.16E-17	-9.44777	Down	EZH inhibitory protein
CES4A	-0.84926	4.27E-22	9.45E-20	-10.1004	Down	carboxylesterase 4A
NR4A1	-0.84783	2.08E-11	3.83E-10	-6.84432	Down	nuclear receptor subfamily 4 group A member 1
HMCN2	-0.84654	1.26E-11	2.43E-10	-6.92247	Down	hemicentin 2
MST1R	-0.84634	5.47E-16	2.49E-14	-8.35573	Down	macrophage stimulating 1 receptor
PLCH2	-0.84549	3.05E-23	1.01E-20	-10.4046	Down	phospholipase C eta 2
DNAAF1	-0.84541	8.46E-09	1.01E-07	-5.85085	Down	dynein axonemal assembly factor 1

NTSR1	-0.84447	4.35E-06	3.35E-05	-4.64132	Down	neurotensin receptor 1
MAMDC4	-0.84364	2.05E-15	8.23E-14	-8.17847	Down	MAM domain containing 4
ERC2-IT1	-0.84352	2.84E-09	3.68E-08	-6.04156	Down	ERC2 intronic transcript 1
CCDC57	-0.84333	2.11E-22	5.18E-20	-10.1821	Down	coiled-coil domain containing 57
SMCR5	-0.84317	4.42E-19	4.17E-17	-9.26814	Down	Smith-Magenis syndrome chromosome region, candidate 5
TTC6	-0.8418	6.11E-06	4.58E-05	-4.56761	Down	tetratricopeptide repeat domain 6
CA4	-0.84138	9.21E-06	6.71E-05	-4.47743	Down	carbonic anhydrase 4
SSPOP	-0.84112	3.71E-19	3.58E-17	-9.28966	Down	SCO-spondin, pseudogene
LOC317727	-0.84103	6.53E-07	5.74E-06	-5.03441	Down	ataxin 2 like pseudogene
ADAMTSL4-AS1	-0.84032	5.50E-20	6.69E-18	-9.52306	Down	ADAMTSL4 antisense RNA 1
TGM1	-0.83882	4.02E-15	1.53E-13	-8.08672	Down	transglutaminase 1
PWP2	-0.83862	7.42E-05	0.000454	-3.99305	Down	PWP2 small subunit processome component
VPS9D1-AS1	-0.83841	1.23E-10	2.00E-09	-6.56293	Down	VPS9D1 antisense RNA 1
ATP2C2-AS1	-0.83741	1.49E-20	2.09E-18	-9.68063	Down	ATP2C2 antisense RNA 1
LCN15	-0.83729	5.15E-07	4.60E-06	-5.08169	Down	lipocalin 15
LINC02418	-0.83693	8.11E-12	1.62E-10	-6.98963	Down	long intergenic non-protein coding RNA 2418
ADGRA2	-0.83653	1.20E-20	1.71E-18	-9.70643	Down	adhesion G protein-coupled receptor A2
GPS2P2	-0.83561	7.28E-07	6.36E-06	-5.0125	Down	G protein pathway suppressor 2 pseudogene 2
CCDC33	-0.83478	3.47E-05	0.000227	-4.17509	Down	coiled-coil domain containing 33
KNCN	-0.83418	2.00E-07	1.91E-06	-5.26727	Down	kinocilin
MYO15B	-0.83326	3.53E-14	1.11E-12	-7.78561	Down	myosin XVB
C9orf139	-0.83257	3.97E-13	1.00E-11	-7.43983	Down	chromosome 9 putative open reading frame 139
BICDL1	-0.83222	2.19E-12	4.82E-11	-7.18771	Down	BICD family like cargo adaptor 1
LOC101929269	-0.83164	4.41E-10	6.48E-09	-6.35535	Down	uncharacterized LOC101929269
LENG8	-0.83136	1.57E-26	2.01E-23	-11.2482	Down	leukocyte receptor cluster member 8
CEL	-0.83116	5.56E-14	1.67E-12	-7.72172	Down	carboxyl ester lipase
ADGRD2	-0.82978	0.000135	0.000784	-3.84402	Down	adhesion G protein-coupled receptor D2
GRIN1	-0.82685	3.67E-05	0.000238	-4.16185	Down	glutamate ionotropic receptor NMDA type subunit 1
LRRC56	-0.82666	2.37E-21	4.17E-19	-9.89938	Down	leucine rich repeat containing 56
TBX2	-0.82553	2.43E-11	4.42E-10	-6.82032	Down	T-box transcription factor 2
SCNN1D	-0.82527	2.14E-29	7.79E-26	-11.9528	Down	sodium channel epithelial 1 subunit delta
PDIA2	-0.824	1.61E-14	5.42E-13	-7.89585	Down	protein disulfideisomerase family A member 2
CFAP100	-0.82349	4.10E-06	3.17E-05	-4.65397	Down	cilia and flagella associated protein 100
NOTCH3	-0.82342	1.19E-12	2.76E-11	-7.27805	Down	notch receptor 3
VWA7	-0.82313	8.11E-10	1.14E-08	-6.25408	Down	von Willebrand factor A domain containing 7
ALS2CL	-0.82246	1.21E-16	6.37E-15	-8.55528	Down	ALS2 C-terminal like
RPL13AP11	-0.82229	1.93E-17	1.19E-15	-8.79297	Down	ribosomal protein L13a pseudogene 11
POLR2J3	-0.82063	1.93E-29	7.79E-26	-11.9638	Down	RNA polymerase II subunit J3
PZP	-0.82026	4.03E-07	3.66E-06	-5.13038	Down	PZP alpha-2-macroglobulin like
RPL19P9	-0.82019	1.03E-07	1.04E-06	-5.39372	Down	ribosomal protein L19 pseudogene 9
CCDC183-AS1	-0.81814	8.24E-23	2.42E-20	-10.2908	Down	CCDC183 antisense RNA 1
C2CD4C	-0.81813	3.19E-09	4.10E-08	-6.02151	Down	C2 calcium dependent domain containing 4C

KIF12	-0.81798	2.34E-06	1.89E-05	-4.77232	Down	kinesin family member 12
KRTAP5-8	-0.81777	2.05E-13	5.43E-12	-7.53566	Down	keratin associated protein 5-8
IDUA	-0.8171	1.03E-22	2.93E-20	-10.2648	Down	alpha-L-iduronidase
UPK3B	-0.81553	1.90E-12	4.21E-11	-7.20932	Down	uroplakin 3B
RUFY4	-0.81481	6.35E-11	1.08E-09	-6.66907	Down	RUN and FYVE domain containing 4
IQANK1	-0.81292	5.40E-13	1.32E-11	-7.3948	Down	IQ motif and ankyrin repeat containing 1
SCN4A	-0.81274	3.18E-10	4.79E-09	-6.40913	Down	sodium voltage-gated channel alpha subunit 4
DNAH1	-0.81258	1.83E-28	4.89E-25	-11.7266	Down	dynein axonemal heavy chain 1
PKD1	-0.81209	3.12E-17	1.83E-15	-8.73093	Down	polycystin 1, transient receptor potential channel interacting
LIME1	-0.81193	9.62E-25	5.74E-22	-10.7949	Down	Lck interacting transmembrane adaptor 1
CROCC	-0.81127	2.15E-26	2.53E-23	-11.214	Down	ciliary rootlet coiled-coil, rootletin
SDR42E2	-0.81096	4.87E-11	8.44E-10	-6.71116	Down	short chain dehydrogenase/reductase family 42E, member 2
AGAP1-IT1	-0.81004	4.56E-19	4.29E-17	-9.26436	Down	AGAP1 intronic transcript 1
STPG3-AS1	-0.80861	2.17E-13	5.73E-12	-7.5275	Down	STPG3 antisense RNA 1
CCT7P1	-0.80659	1.88E-16	9.46E-15	-8.49729	Down	chaperonin containing TCP1 subunit 7 pseudogene 1
AGAP12P	-0.80579	1.74E-12	3.90E-11	-7.22196	Down	ArfGAP with GTPase domain, ankyrin repeat and PH domain 12, pseudogene
MYLK2	-0.80561	2.28E-10	3.51E-09	-6.46365	Down	myosin light chain kinase 2
PRR29	-0.80537	1.05E-07	1.05E-06	-5.39075	Down	proline rich 29
C20orf203	-0.80474	1.41E-14	4.84E-13	-7.91353	Down	chromosome 20 open reading frame 203
KRT18P5	-0.80468	2.30E-18	1.78E-16	-9.06241	Down	keratin 18 pseudogene 5
AMN	-0.8042	2.32E-13	6.09E-12	-7.51778	Down	amnion associated transmembrane protein
KCNH4	-0.8034	0.000204	0.001137	-3.73941	Down	potassium voltage-gated channel subfamily H member 4
CORO6	-0.80264	2.06E-11	3.80E-10	-6.84595	Down	coronin 6
ATP10A	-0.80227	2.03E-13	5.39E-12	-7.5368	Down	ATPase phospholipid transporting 10A (putative)
ZNF541	-0.80135	1.55E-14	5.25E-13	-7.90104	Down	zinc finger protein 541
TBC1D26	-0.80079	6.47E-11	1.10E-09	-6.6662	Down	TBC1 domain family member 26
GOLGA6L3	-0.80077	6.82E-08	7.09E-07	-5.47167	Down	golgin A6 family like 3
NPIPB3	-0.80061	2.58E-24	1.31E-21	-10.6843	Down	nuclear pore complex interacting protein family member B3
MUC20	-0.80048	1.46E-18	1.19E-16	-9.1199	Down	mucin 20, cell surface associated
LDLRAD2	-0.80034	5.97E-08	6.27E-07	-5.49648	Down	low density lipoprotein receptor class A domain containing 2
PDCL3P6	-0.80004	8.78E-11	1.46E-09	-6.61751	Down	PDCL3 pseudogene 6
LOC285097	-0.7997	1.90E-17	1.18E-15	-8.79448	Down	uncharacterized FLJ38379
DBH-AS1	-0.79942	8.03E-28	1.69E-24	-11.5688	Down	DBH antisense RNA 1
PROM2	-0.79843	7.40E-26	6.56E-23	-11.0788	Down	prominin 2
LOC105374338	-0.79827	1.33E-07	1.31E-06	-5.3457	Down	uncharacterized LOC105374338
HRC	-0.7979	2.79E-12	6.02E-11	-7.15162	Down	histidine rich calcium binding protein
BRICD5	-0.79719	6.77E-19	6.11E-17	-9.2154	Down	BRICHOS domain containing 5
LOC101928682	-0.79682	7.99E-10	1.13E-08	-6.25651	Down	uncharacterized LOC101928682
ZMIZ1-AS1	-0.79597	4.04E-20	5.04E-18	-9.56048	Down	ZMIZ1 antisense RNA 1
LRRC10B	-0.79541	1.11E-05	7.94E-05	-4.43685	Down	leucine rich repeat containing 10B
PKD1P6	-0.7939	1.68E-20	2.32E-18	-9.66625	Down	polycystin 1, transient receptor potential channel interacting pseudogene 6

AGAP2	-0.79316	2.68E-05	0.000178	-4.23556	Down	ArfGAP with GTPase domain, ankyrin repeat and PH domain 2
C6orf141	-0.7923	7.32E-07	6.39E-06	-5.01159	Down	chromosome 6 open reading frame 141
C19orf71	-0.79217	2.92E-08	3.21E-07	-5.62832	Down	chromosome 19 open reading frame 71
RPS3AP31	-0.79194	1.87E-06	1.53E-05	-4.81973	Down	RPS3A pseudogene 31
C20orf204	-0.79013	3.33E-12	7.08E-11	-7.12499	Down	chromosome 20 open reading frame 204
MGAT5B	-0.78989	2.30E-05	0.000156	-4.27084	Down	alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase B
LOC107984399	-0.78898	7.61E-11	1.28E-09	-6.6402	Down	uncharacterized LOC107984399
PCK1	-0.7888	1.07E-06	9.09E-06	-4.93491	Down	phosphoenolpyruvatecarboxykinase 1
FER1L4	-0.78731	3.33E-18	2.46E-16	-9.01618	Down	fer-1 like family member 4 (pseudogene)
FBN3	-0.78683	1.17E-11	2.26E-10	-6.93393	Down	fibrillin 3
LINC01237	-0.78635	2.68E-16	1.31E-14	-8.45006	Down	long intergenic non-protein coding RNA 1237
CRIP3	-0.78618	1.32E-16	6.88E-15	-8.54379	Down	cysteine rich protein 3
CHTF18	-0.78599	2.98E-21	5.10E-19	-9.87207	Down	chromosome transmission fidelity factor 18
B3GAT1-DT	-0.78523	8.56E-13	2.03E-11	-7.32722	Down	B3GAT1 diverget transcript
TDRD10	-0.78474	9.89E-13	2.32E-11	-7.30586	Down	tudor domain containing 10
LINC01347	-0.78457	6.35E-24	2.64E-21	-10.5831	Down	long intergenic non-protein coding RNA 1347
ADCY4	-0.7841	3.80E-11	6.69E-10	-6.75042	Down	adenylatecyclase 4
CCDC183	-0.78322	1.05E-13	2.96E-12	-7.63174	Down	coiled-coil domain containing 183
SLC22A13	-0.78279	4.26E-09	5.36E-08	-5.97104	Down	solute carrier family 22 member 13
NPAS4	-0.78256	8.32E-05	0.000503	-3.96505	Down	neuronal PAS domain protein 4
MMD2	-0.78246	5.68E-20	6.86E-18	-9.51924	Down	monocyte to macrophage differentiation associated 2
JAG2	-0.78179	5.45E-19	5.01E-17	-9.24215	Down	jagged canonical Notch ligand 2
PILRB	-0.78144	7.95E-22	1.63E-19	-10.0277	Down	paired immunoglobin like type 2 receptor beta
SMPD3	-0.78002	2.90E-08	3.19E-07	-5.62956	Down	sphingomyelinphosphodiesterase 3
BEGAIN	-0.78	2.86E-11	5.14E-10	-6.79472	Down	brain enriched guanylate kinase associated
CLEC18A	-0.77999	1.26E-14	4.36E-13	-7.92984	Down	C-type lectin domain family 18 member A
HSPA12B	-0.77906	1.08E-11	2.11E-10	-6.94543	Down	heat shock protein family A (Hsp70) member 12B
ST6GALNAC1	-0.77898	2.44E-12	5.32E-11	-7.17154	Down	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 1
ATXN7L2	-0.77895	5.47E-22	1.18E-19	-10.0714	Down	ataxin 7 like 2
CYP4F29P	-0.77857	1.17E-07	1.16E-06	-5.37052	Down	cytochrome P450 family 4 subfamily F member 29, pseudogene
MYB	-0.77766	1.01E-08	1.20E-07	-5.81886	Down	MYB proto-oncogene, transcription factor
MTND2P28	-0.77728	0.000105	0.000623	-3.90765	Down	MT-ND2 pseudogene 28
HBD	-0.7771	1.33E-09	1.81E-08	-6.171	Down	hemoglobin subunit delta
CACNA1B	-0.77612	2.07E-12	4.58E-11	-7.19618	Down	calcium voltage-gated channel subunit alpha1 B
CLEC18C	-0.77554	4.47E-08	4.79E-07	-5.55013	Down	C-type lectin domain family 18 member C
COL7A1	-0.77519	1.70E-15	6.99E-14	-8.20326	Down	collagen type VII alpha 1 chain
RNF213-AS1	-0.775	7.97E-19	7.03E-17	-9.19505	Down	RNF213 antisense RNA 1
RHOT1P1	-0.77369	4.50E-09	5.64E-08	-5.96177	Down	ras homolog family member T1 pseudogene 1
AP1G2	-0.77343	1.41E-15	5.88E-14	-8.22857	Down	adaptor related protein complex 1 subunit gamma 2
NUTM2D	-0.77325	3.69E-16	1.75E-14	-8.40797	Down	NUT family member 2D
CCDC116	-0.77301	2.67E-14	8.62E-13	-7.82497	Down	coiled-coil domain containing 116
CELF5	-0.77288	1.80E-05	0.000124	-4.32633	Down	CUGBP Elav-like family member 5

LINC00304	-0.77287	3.82E-06	2.96E-05	-4.66889	Down	long intergenic non-protein coding RNA 304
PRSS30P	-0.77249	2.02E-11	3.74E-10	-6.84879	Down	serine protease 30, pseudogene
REM1	-0.77141	1.43E-07	1.39E-06	-5.33225	Down	RRAD and GEM like GTPase 1
ARHGAP33	-0.7712	8.17E-32	6.88E-28	-12.5295	Down	Rho GTPase activating protein 33
LOC101929719	-0.77097	3.21E-07	2.96E-06	-5.17538	Down	uncharacterized LOC101929719
ADAMTS13	-0.77089	7.09E-32	6.88E-28	-12.544	Down	ADAM metallopeptidase with thrombospondin type 1 motif 13
NPIPB11	-0.77087	2.09E-20	2.79E-18	-9.64024	Down	nuclear pore complex interacting protein family member B11
ZGLP1	-0.77068	5.33E-16	2.43E-14	-8.35919	Down	zinc finger GATA like protein 1
CEROX1	-0.77015	5.91E-13	1.43E-11	-7.38147	Down	cytoplasmic endogenous regulator of oxidative phosphorylation 1
GALNT9	-0.76926	4.69E-05	0.000299	-4.10351	Down	polypeptide N-acetylgalactosaminyltransferase 9
TTC34	-0.76905	1.33E-26	1.79E-23	-11.2659	Down	tetratricopeptide repeat domain 34
GRM2	-0.76873	0.00012	0.000702	-3.87483	Down	glutamate metabotropic receptor 2
GP1BB	-0.76773	1.71E-09	2.29E-08	-6.12811	Down	glycoprotein Ib platelet subunit beta
IQSEC3	-0.76721	9.62E-07	8.24E-06	-4.95622	Down	IQ motif and Sec7 domain ArfGEF 3
FAM71F2	-0.76642	2.23E-27	4.24E-24	-11.4593	Down	family with sequence similarity 71 member F2
NPIPA1	-0.76601	6.31E-21	9.79E-19	-9.78318	Down	nuclear pore complex interacting protein family member A1
CYP21A1P	-0.76576	3.42E-08	3.72E-07	-5.59952	Down	cytochrome P450 family 21 subfamily A member 1, pseudogene
CROCCP1	-0.7645	6.96E-10	9.90E-09	-6.27964	Down	CROCC pseudogene 1
MAST1	-0.76362	2.80E-08	3.09E-07	-5.63575	Down	microtubule associated serine/threonine kinase 1
HBA1	-0.76305	4.38E-07	3.95E-06	-5.11411	Down	hemoglobin subunit alpha 1
FBXW4P1	-0.7623	4.61E-21	7.43E-19	-9.82047	Down	F-box and WD repeat domain containing 4 pseudogene 1
PRSS53	-0.76208	6.33E-20	7.56E-18	-9.50615	Down	serine protease 53
CLDN9	-0.76191	3.60E-11	6.37E-10	-6.75878	Down	claudin 9
MTUS2	-0.76132	2.62E-06	2.10E-05	-4.74865	Down	microtubule associated scaffold protein 2
LOC107987373	-0.76084	0.00369	0.00736	-2.91621	Down	39S ribosomal protein L23, mitochondrial
LOC100653233	-0.76026	3.34E-06	2.62E-05	-4.69775	Down	uncharacterized LOC100653233
MARCHF4	-0.75915	8.57E-06	6.27E-05	-4.49332	Down	membrane associated ring-CH-type finger 4
ITIH4	-0.75829	6.88E-19	6.21E-17	-9.21326	Down	inter-alpha-trypsin inhibitor heavy chain 4
LOC100506551	-0.75774	2.98E-06	2.36E-05	-4.72164	Down	uncharacterized LOC100506551
COL5A3	-0.75752	3.56E-14	1.11E-12	-7.78466	Down	collagen type V alpha 3 chain
CROCC2	-0.75534	0.000171	0.000967	-3.78535	Down	ciliary rootlet coiled-coil, rootletin family member 2
STRC	-0.7553	1.54E-09	2.08E-08	-6.14633	Down	stereocilin
BTNL9	-0.75505	5.26E-12	1.08E-10	-7.05554	Down	butyrophilin like 9
MTCO1P12	-0.75469	1.51E-11	2.87E-10	-6.89373	Down	MT-CO1 pseudogene 12
SPRN	-0.75393	6.37E-06	4.77E-05	-4.55848	Down	shadow of prion protein
ARL5C	-0.75323	7.85E-07	6.82E-06	-4.9973	Down	ADP ribosylation factor like GTPase 5C
ADAMTS7P4	-0.75293	3.63E-10	5.42E-09	-6.38714	Down	ADAMTS7 pseudogene 4
EPHA10	-0.75268	5.97E-08	6.27E-07	-5.49638	Down	EPH receptor A10
CACNA1A	-0.75262	1.21E-07	1.21E-06	-5.36287	Down	calcium voltage-gated channel subunit alpha1 A
FLT4	-0.75253	7.81E-11	1.31E-09	-6.63605	Down	fms related receptor tyrosine kinase 4
FOXD4L3	-0.75219	2.25E-05	0.000152	-4.27579	Down	forkhead box D4 like 3

LINC01164	-0.75205	0.000766	0.003662	-3.38414	Down	long intergenic non-protein coding RNA 1164
CYP2D8P	-0.75204	1.16E-10	1.88E-09	-6.57336	Down	ccytochrome P450 family 2 subfamily D member 8, pseudogene
ABCC8	-0.75184	2.88E-14	9.24E-13	-7.81435	Down	ATP binding cassette subfamily C member 8
KRT18P4	-0.75151	9.97E-16	4.30E-14	-8.27543	Down	keratin 18 pseudogene 4
ARHGAP19-SLIT1	-0.75107	8.83E-08	8.99E-07	-5.42306	Down	ARHGAP19-SLIT1 readthrough (NMD candidate)
TSPOAP1	-0.75033	3.18E-12	6.79E-11	-7.13193	Down	TSPO associated protein 1
LOC101929457	-0.74988	5.08E-14	1.54E-12	-7.73455	Down	uncharacterized LOC101929457
GGT3P	-0.74932	6.01E-08	6.30E-07	-5.49527	Down	gamma-glutamyltransferase 3 pseudogene
KRT8P31	-0.74923	4.31E-10	6.35E-09	-6.35903	Down	keratin 8 pseudogene 31
ZNF469	-0.74918	6.21E-14	1.85E-12	-7.70612	Down	zinc finger protein 469
TBC1D3D	-0.74858	0.000882	0.004135	-3.34429	Down	TBC1 domain family member 3D
DRD4	-0.74729	1.05E-11	2.06E-10	-6.94999	Down	dopamine receptor D4
PTPRVP	-0.74719	7.21E-07	6.30E-06	-5.01457	Down	protein tyrosine phosphatase receptor type V, pseudogene
KRT18P6	-0.74656	3.16E-06	2.50E-05	-4.70907	Down	keratin 18 pseudogene 6
KRTAP5-7	-0.74655	1.41E-11	2.70E-10	-6.90435	Down	keratin associated protein 5-7
RPL19P6	-0.7452	6.58E-15	2.41E-13	-8.01915	Down	ribosomal protein L19 pseudogene 6
CDK5R2	-0.74471	5.92E-05	0.000369	-4.04796	Down	cyclin dependent kinase 5 regulatory subunit 2
EFCAB12	-0.7447	1.02E-11	2.01E-10	-6.95398	Down	EF-hand calcium binding domain 12
CACNA1I	-0.74469	6.89E-06	5.13E-05	-4.54136	Down	calcium voltage-gated channel subunit alpha1 I
LOC284395	-0.74401	1.46E-08	1.68E-07	-5.75392	Down	uncharacterized LOC284395
ASIC3	-0.74387	5.80E-20	6.99E-18	-9.51665	Down	acid sensing ion channel subunit 3
LY6G5B	-0.74312	5.58E-18	3.91E-16	-8.95092	Down	lymphocyte antigen 6 family member G5B
FAM71F1	-0.74272	1.41E-11	2.69E-10	-6.90507	Down	family with sequence similarity 71 member F1
NEURL1	-0.74258	1.54E-05	0.000108	-4.36219	Down	neuralized E3 ubiquitin protein ligase 1
SLFN12L	-0.74087	2.47E-07	2.32E-06	-5.22645	Down	schlafen family member 12 like
TIE1	-0.73955	1.36E-11	2.61E-10	-6.91003	Down	tyrosine kinase with immunoglobulin like and EGF like domains 1
FENDRR	-0.73929	4.78E-11	8.30E-10	-6.71413	Down	FOXF1 adjacent non-coding developmental regulatory RNA
CPSF1P1	-0.73845	5.16E-05	0.000326	-4.08096	Down	CPSF1 pseudogene 1
PRICKLE4	-0.73776	1.63E-08	1.86E-07	-5.73389	Down	prickle planar cell polarity protein 4
LINC02280	-0.73745	5.34E-08	5.66E-07	-5.517	Down	long intergenic non-protein coding RNA 2280
ALX4	-0.73713	3.61E-06	2.82E-05	-4.68091	Down	ALX homeobox 4
CUX2	-0.73645	0.001265	0.005592	-3.24082	Down	cut like homeobox 2
CPNE7	-0.73625	0.001072	0.004877	-3.28871	Down	copine 7
CLDN34	-0.73611	9.62E-08	9.73E-07	-5.40693	Down	claudin 34
FOXL1	-0.736	2.07E-07	1.97E-06	-5.26076	Down	forkhead box L1
GRM4	-0.73551	0.00124	0.005507	-3.24658	Down	glutamate metabotropic receptor 4
INHA	-0.7351	4.67E-12	9.66E-11	-7.07386	Down	inhibin subunit alpha
CABLES1	-0.73507	2.93E-11	5.26E-10	-6.79092	Down	Cdk5 and Abl enzyme substrate 1
ITGA2B	-0.73471	1.06E-17	7.03E-16	-8.86994	Down	integrin subunit alpha 2b
LOC440300	-0.73411	1.79E-17	1.12E-15	-8.80273	Down	chondroitin sulfate proteoglycan 4 pseudogene
NPAP1	-0.73393	1.70E-07	1.64E-06	-5.29862	Down	nuclear pore associated protein 1
RTEL1	-0.73376	5.45E-24	2.36E-21	-10.6002	Down	regulator of telomere elongation helicase 1

DNAJC5G	-0.73323	0.00131	0.005753	-3.23066	Down	DnaJ heat shock protein family (Hsp40) member C5 gamma
LGALS4	-0.73305	4.41E-12	9.17E-11	-7.08248	Down	galectin 4
SLC8A2	-0.7316	0.000107	0.000633	-3.90353	Down	solute carrier family 8 member A2
BAIAP2L2	-0.73072	1.24E-12	2.85E-11	-7.27259	Down	BAR/IMD domain containing adaptor protein 2 like 2
XKR7	-0.73062	0.000619	0.00305	-3.44311	Down	XK related 7
ZFHX2	-0.72976	4.11E-25	2.69E-22	-10.8895	Down	zinc finger homeobox 2
POLR3DP1	-0.72907	1.34E-17	8.65E-16	-8.839	Down	RNA polymerase III subunit D pseudogene 1
TTC16	-0.72843	3.37E-12	7.17E-11	-7.12305	Down	tetratricopeptide repeat domain 16
MIAT	-0.72803	2.91E-05	0.000192	-4.2166	Down	myocardial infarction associated transcript
CCDC114	-0.72784	1.16E-07	1.16E-06	-5.37144	Down	coiled-coil domain containing 114
SH3D21	-0.72773	3.85E-17	2.22E-15	-8.70365	Down	SH3 domain containing 21
LOC101927551	-0.72768	3.47E-15	1.34E-13	-8.10659	Down	uncharacterized LOC101927551
SLC1A7	-0.72713	0.000167	0.000949	-3.79071	Down	solute carrier family 1 member 7
CFAP65	-0.72685	2.51E-07	2.36E-06	-5.22336	Down	cilia and flagella associated protein 65
CARMIL3	-0.72673	1.62E-16	8.30E-15	-8.51693	Down	capping protein regulator and myosin 1 linker 3
OBSCN	-0.72653	3.42E-10	5.12E-09	-6.39721	Down	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
CRLF1	-0.72635	1.31E-05	9.30E-05	-4.39811	Down	cytokine receptor like factor 1
MTATP6P1	-0.72634	2.01E-10	3.14E-09	-6.48366	Down	MT-ATP6 pseudogene 1
CNGB1	-0.72632	0.001275	0.00563	-3.23841	Down	cyclic nucleotide gated channel subunit beta 1
RPL5P14	-0.72619	1.30E-08	1.51E-07	-5.77493	Down	ribosomal protein L5 pseudogene 14
VWA3A	-0.72567	8.95E-08	9.11E-07	-5.4206	Down	von Willebrand factor A domain containing 3A
SBSN	-0.72556	4.99E-09	6.22E-08	-5.94342	Down	suprabasin
SLC7A5P1	-0.72546	1.56E-12	3.52E-11	-7.2385	Down	solute carrier family 7 member 5 pseudogene 1
GP6	-0.72508	6.70E-09	8.17E-08	-5.89211	Down	glycoprotein VI platelet
GLB1L3	-0.72497	5.13E-05	0.000324	-4.08221	Down	galactosidase beta 1 like 3
PLPPR3	-0.72494	0.000927	0.004315	-3.33007	Down	phospholipid phosphatase related 3
CATSPERG	-0.72453	1.45E-17	9.21E-16	-8.82974	Down	cation channel sperm associated auxiliary subunit gamma
FBXL16	-0.72405	2.24E-05	0.000152	-4.27706	Down	F-box and leucine rich repeat protein 16
COX4I2	-0.7233	9.98E-09	1.18E-07	-5.82152	Down	cytochrome c oxidase subunit 4I2
CYSLTR2	-0.72304	1.39E-18	1.14E-16	-9.12596	Down	cysteinyl leukotriene receptor 2
FOXL2	-0.72245	1.41E-09	1.91E-08	-6.16137	Down	forkhead box L2
PRB2	-0.7219	0.001387	0.006031	-3.21391	Down	proline rich protein BstNI subfamily 2
B4GALNT3	-0.72073	2.48E-07	2.33E-06	-5.2254	Down	beta-1,4-N-acetyl-galactosaminyltransferase 3
SULT1A2	-0.72051	8.94E-11	1.48E-09	-6.61463	Down	sulfotransferase family 1A member 2
COL11A2	-0.72035	1.26E-21	2.41E-19	-9.97416	Down	collagen type XI alpha 2 chain
KIFC2	-0.71935	5.44E-09	6.74E-08	-5.92849	Down	kinesin family member C2
RSPH6A	-0.71913	2.30E-10	3.54E-09	-6.46219	Down	radial spoke head 6 homolog A
COL9A1	-0.71871	1.30E-17	8.38E-16	-8.84378	Down	collagen type IX alpha 1 chain
RRP7BP	-0.71869	4.12E-27	6.93E-24	-11.3932	Down	ribosomal RNA processing 7 homolog B, pseudogene
CATIP	-0.71851	3.03E-10	4.58E-09	-6.4168	Down	ciliogenesis associated TTC17 interacting protein
ZBTB44-DT	-0.71839	9.23E-14	2.63E-12	-7.64983	Down	ZBTB44 divergent transcript
KCNK4	-0.71836	0.00012	0.000702	-3.87478	Down	potassium two pore domain channel subfamily K

						member 4
TPT1P5	-0.71834	2.54E-09	3.33E-08	-6.06021	Down	tumor protein, translationally-controlled 1 pseudogene 5
C1orf159	-0.7181	3.26E-26	3.49E-23	-11.1687	Down	chromosome 1 open reading frame 159
AJM1	-0.718	5.15E-14	1.55E-12	-7.73262	Down	apical junction component 1 homolog
RPL18AP10	-0.71697	4.04E-07	3.67E-06	-5.13011	Down	ribosomal protein L18a pseudogene 10
OTOG	-0.71691	2.31E-08	2.59E-07	-5.67059	Down	otogelin
RHBDF1P1	-0.71671	2.89E-09	3.74E-08	-6.03834	Down	RHBDF1 pseudogene 1
LAMA5	-0.7155	1.28E-13	3.54E-12	-7.60356	Down	laminin subunit alpha 5
ACTG1P14	-0.71537	9.75E-16	4.22E-14	-8.27833	Down	actin gamma 1 pseudogene 14
SNAI3-AS1	-0.71519	3.39E-15	1.31E-13	-8.10983	Down	SNAI3 antisense RNA 1
ND1	-0.71413	2.89E-22	6.79E-20	-10.1456	Down	NADH dehydrogenase subunit 1
GOLGA8B	-0.71376	2.88E-15	1.13E-13	-8.13228	Down	golgin A8 family member B
LOC100419506	-0.71366	3.81E-11	6.71E-10	-6.74985	Down	ribosomal protein L4 pseudogene
LRRC74B	-0.71321	6.54E-06	4.89E-05	-4.55261	Down	leucine rich repeat containing 74B
TRIM54	-0.71305	0.003458	0.007311	-2.93674	Down	tripartite motif containing 54
C4orf50	-0.71292	5.79E-05	0.000361	-4.0534	Down	chromosome 4 open reading frame 50
CBFA2T3	-0.71288	8.81E-09	1.05E-07	-5.84362	Down	CBFA2/RUNX1 partner transcriptional co-repressor 3
LRRC29	-0.71286	4.83E-24	2.17E-21	-10.614	Down	leucine rich repeat containing 29
HIC2	-0.71268	3.98E-23	1.28E-20	-10.3742	Down	HIC ZBTB transcriptional repressor 2
GRIP2	-0.71218	7.43E-10	1.05E-08	-6.26861	Down	glutamate receptor interacting protein 2
JCADP1	-0.71215	2.02E-10	3.14E-09	-6.48351	Down	JCAD pseudogene 1
CASKIN1	-0.71214	4.30E-12	8.96E-11	-7.08619	Down	CASK interacting protein 1
EXD3	-0.71107	3.99E-23	1.28E-20	-10.3741	Down	exonuclease 3'-5' domain containing 3
RBFOX3	-0.71024	0.002766	0.007311	-3.00641	Down	RNA binding fox-1 homolog 3
RHOXF1-AS1	-0.71022	7.53E-05	0.00046	-3.98937	Down	RHOXF1 antisense RNA 1
CXCL11	-0.71005	4.02E-05	0.000259	-4.14014	Down	C-X-C motif chemokine ligand 11
BSN	-0.70977	1.78E-05	0.000123	-4.32888	Down	bassoon presynaptic cytomatrix protein
POTEE	-0.70936	0.000626	0.003078	-3.44024	Down	POTE ankyrin domain family member E
B3GNT4	-0.7089	5.36E-05	0.000337	-4.07179	Down	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 4
RPL23AP74	-0.70858	4.92E-11	8.52E-10	-6.70951	Down	ribosomal protein L23a pseudogene 74
MST1L	-0.70836	1.14E-12	2.65E-11	-7.28463	Down	macrophage stimulating 1 like
PRR36	-0.70836	1.28E-06	1.07E-05	-4.89815	Down	proline rich 36
TMEM271	-0.7082	1.33E-06	1.11E-05	-4.8903	Down	transmembrane protein 271
PNPLA7	-0.70794	5.71E-18	3.98E-16	-8.94794	Down	patatin like phospholipase domain containing 7
SPPL2B	-0.70779	1.07E-25	9.03E-23	-11.0379	Down	signal peptide peptidase like 2B
INS-IGF2	-0.70717	5.48E-05	0.000344	-4.06625	Down	INS-IGF2 readthrough
CBARP	-0.70672	9.84E-15	3.50E-13	-7.96374	Down	CACN subunit beta associated regulatory protein
BCL6B	-0.70668	6.55E-10	9.37E-09	-6.28971	Down	BCL6B transcription repressor
LOC400622	-0.70665	0.000104	0.00062	-3.90922	Down	uncharacterized LOC400622
GPR20	-0.70645	1.12E-07	1.12E-06	-5.37752	Down	G protein-coupled receptor 20
UBAP1L	-0.70613	1.65E-22	4.31E-20	-10.2106	Down	ubiquitin associated protein 1 like
LOC100128882	-0.70612	3.06E-09	3.95E-08	-6.02869	Down	uncharacterized LOC100128882

SLC25A6P4	-0.70543	6.29E-10	9.04E-09	-6.29633	Down	solute carrier family 25 member 6 pseudogene 4
CFP	-0.70486	1.18E-12	2.74E-11	-7.27949	Down	complement factor properdin
GOLGA6B	-0.70485	4.92E-07	4.41E-06	-5.09112	Down	golgin A6 family member B
DTX2P1-UPK3BP1-PMS2P11	-0.70447	7.50E-34	4.42E-29	-13.0044	Down	DTX2P1-UPK3BP1-PMS2P11 readthrough, transcribed pseudogene
AGER	-0.70359	1.01E-14	3.58E-13	-7.96031	Down	advanced glycosylation end-product specific receptor
LCN12	-0.70356	7.83E-10	1.11E-08	-6.25989	Down	lipocalin 12
CEP170B	-0.70347	1.05E-11	2.06E-10	-6.95016	Down	centrosomal protein 170B
COL16A1	-0.70346	3.29E-13	8.40E-12	-7.46701	Down	collagen type XVI alpha 1 chain
CRHR1	-0.70325	1.94E-05	0.000133	-4.31043	Down	corticotropin releasing hormone receptor 1
ATP8	-0.70298	1.86E-12	4.15E-11	-7.21177	Down	ATP synthase F0 subunit 8
AGRN	-0.7029	2.66E-12	5.78E-11	-7.15836	Down	agrin
MEIS3	-0.70269	5.92E-05	0.000369	-4.04789	Down	Meishomeobox 3
SLC38A5	-0.70246	4.10E-10	6.06E-09	-6.36726	Down	solute carrier family 38 member 5
CICP27	-0.70225	4.30E-06	3.32E-05	-4.64334	Down	capicua transcriptional repressor pseudogene 27
INE1	-0.70217	2.96E-21	5.08E-19	-9.87292	Down	inactivation escape 1
P2RX5-TAX1BP3	-0.7016	4.70E-07	4.22E-06	-5.10019	Down	P2RX5-TAX1BP3 readthrough (NMD candidate)
SLC25A2	-0.70111	1.99E-08	2.24E-07	-5.69794	Down	solute carrier family 25 member 2
SEPTIN12	-0.70105	3.33E-07	3.07E-06	-5.16781	Down	septin 12
DLL4	-0.70091	1.01E-13	2.87E-12	-7.63666	Down	delta like canonical Notch ligand 4
IGSF9B	-0.70084	1.23E-11	2.38E-10	-6.9255	Down	immunoglobulin superfamily member 9B
CELSR3	-0.70066	3.16E-09	4.07E-08	-6.02285	Down	cadherin EGF LAG seven-pass G-type receptor 3
CRHR2	-0.70051	0.000765	0.003658	-3.3845	Down	corticotropin releasing hormone receptor 2
CHST5	-0.70022	7.08E-17	3.87E-15	-8.62483	Down	carbohydrate sulfotransferase 5

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

GO ID	CATEGORY	GO Name	P Value	FDR B&H	FDR B&Y	Bonferroni	Gene Count	Gene
Up regulated genes								
GO:0006952	BP	defense response	1.73E-47	3.32E-44	3.07E-43	9.96E-44	146	PIK3AP1,HGF,SERPINA3,RPL39,HLA-DPA1,HLA-DPB1,HLA-DQA1,HLA-DQB1,HLA-DQB2,CLEC5A,HLA-DRA,HLA-DRB1,CTSC,ACP5,HLA-DRB5,VSIG4,TMIGD3,CLEC7A,TLR7,LY96,CHI3L1,TLR6,F3,TLR8,CD163,S100A8,S100A9,TYROBP,S100A12,ADORA3,SERPINA1,FCER1G,FCGR1A,FCGR1B,FCGR2B,HP,IFI

								30,AIF1,PLA2G2A,CCL2,CCR1,CCR5,CCL18,CCL20,MMP7,CXCL5,LY86,ALOX5AP,CD300LF,BATF,ANXA1,FPR1,FPR2,FPR3,BIRC3,IFITM2,SUCNR1,RAB20,PPBP,CR1,CFI,AQP4,ARG1,SLC7A2,SLC11A1,TIFA,HAMP,IL1A,VAMP8,IL2RA,TSLP,CTSS,CXCR2,CYBB,SLAMF8,IL10,IL18,SPP1,CYP19A1,B2M,GBP1,GBP2,GBP3,PTPN22,NCF2,ITGB2,ERBIN,PTGS1,FGL2,CD84,PTPRC,VNN1,CXCR4,BTK,C1QA,C1QB,C1QC,C3,C3AR1,C4A,C4B,C5AR1,C6,C7,KYNU,PLA2G7,TNFAIP8L2,LILRB3,LILRA2,CAPG,SOCS3,CASP1,SIGLEC14,OLR1,TLR10,HAVCR2,RNASE2,LIPA,RNASE3,RNASE6,NAMPT,CD14,ANO6,CD86,TNFSF8,CD37,TLR1,TLR2,TLR5,CRTAM,CD44,TREM2,CD48,CD68,SERPINB1,CD74,LSP1,IL1RL1,LTF,TNFAIP6,CALCRL,OSMR,CD180,LYZ,HCK,LILRA4
GO:0001775	BP	cell activation	8.60E-46	1.24E-42	1.14E-41	4.95E-42	132	CDKN1A,HEXB,SERPINA3,HLA-DMA,HLA-DMB,HLA-DOA,HLA-DPA1,HLA-DPB1,HLA-DQA1,CLEC5A,CTSC,ACP3,VSIG4,CLEC7A,TLR7,CHI3L1,DNAJB9,TLR6,CHIT1,TLR8,FABP5,S100A8,S100A9,TYROBP,S100A11,S100A12,SERPINA1,FCAR,FCER1G,MGST1,FCGR2A,FCGR2B,FCGR3A,HP,CLIC1,AIF1,CCL2,GPNMB,CCL20,PLEK,SDCBP,CD300LF,BATF,ANXA1,ANXA2,FPR1,FPR2,GMFG,NPC2,SUCNR1,PPBP,CR1,FAS,MILR1,SLC2A5,ARG1,PDPN,SLC7A2,SLC11A1,ASAH1,TNFSF13B,HAMP,VAMP8,FYB1,IL2RA,TSLP,CTSS,CXCR2,CYBB,SLAMF8,IL10,IL18,IQGAP2,SIGLEC9,B2M,GAPT,GPR84,SIGLEC5,PTPN22,SAMSN1,DCSTAMP,ITGAD,HPSE,ITGB2,FGL2,CD84,GGH,PTPRC,VNN1,CXCR4,BTK,C1QA,C3,C3AR1,MAFB,C5AR1,GLIPR1,TNFAIP8L2,LILRB3,LILRA2,LAIR1,SIGLEC14,LAMP2,GPR183,LCP1,OLR1,HAVCR2,TGFBR1,RNASE2,RNASE3,NAMPT,CD14,ANO6,CD86,TNFSF8,CD37,TLR1,TLR2,CRTAM,CD

								44,TREM2,CD48,CD53,CD68,SERPINB1,CD74,IL1RL1,LTF,TNFAIP6,MPZL2,CD180,LYZ
GO:0098805	CC	whole membrane	2.28E-19	1.81E-17	1.25E-16	1.27E-16	98	MAOB,HLA-DMA,HLA-DMB,HLA-DOA,HLA-DPA1,HLA-DPB1,HLA-DQA1,HLA-DQB1,HLA-DQB2,CLEC5A,HLA-DRA,HLA-DRB1,HLA-DRB5,ACP3,TLR7,LY96,TLR6,TLR8,CD163,FABP5,RAB38,ACSL1,TYROBP,S100A10,FCAR,FCER1G,FCGR1A,MGST1,FCGR1B,FCGR2A,SNX10,GPNMB,SDCBP,STEAP1,ANGPT1,ANXA1,ANXA2,FPR1,FPR2,BIRC3,CP,DRAM2,RAB20,CR1,FAS,AQP1,AQP4,SLC2A5,ARG1,MSR1,PDPN,SLC11A1,SLC26A7,VAMP8,CXCR2,CYBB,IQGAP2,SIGLEC9,SNX20,B2M,GPR84,SIGLEC5,BCL2A1,DCSTAMP,HPSE,ITGB2,LAPTM5,GK,PTPRC,VNN1,BTK,NGFR,AP1S2,C3AR1,C5AR1,GLIPR1,KDELR3,LILRB3,LAIR1,SIGLEC14,STEAP4,LAMP2,OLR1,TGFBR1,RHOQ,EGF,CD14,ANO6,TLR1,TLR2,CD44,CD48,CD53,CD68,CD74,RASSF9,HCK,SERPINA5
GO:0031226	CC	intrinsic component of plasma membrane	2.09E-16	9.63E-15	6.64E-14	1.16E-13	93	IGSF6,HLA-DPA1,HLA-DQA1,CLEC5A,HLA-DRA,TSPAN19,TMIGD3,EVI2B,LY96,TLR6,F3,CHRNA1,CHRNA5,CD163,PHEX,SLC38A2,TYROBP,ADORA3,ITGBL1,FCAR,FCER1G,FCGR2B,APLNR,SCN7A,CCR1,CCR5,GPNMB,SDCBP,STEAP1,GPR65,CP,CR1,AQP1,AQP4,AQP9,SLC1A5,MILR1,SLC2A5,SLC5A3,MSR1,PDPN,SLC7A2,SIGLEC7,SLC11A1,SLC26A7,IL2RA,CXCR2,CYBB,IL13RA1,SIGLEC9,GPR84,NCF2,ITGAD,ITGB2,LAPTM5,CD84,LYVE1,PTPRC,GPC3,KCNJ5,NGFR,C3AR1,C5AR1,C6,C7,TNFSF15,LILRB3,LILRA2,GPR34,P2RY8,CALHM6,GPR183,SLC7A7,OLR1,TLR10,TGFBR1,SEMA3D,CD14,TNFSF8,CD37,TLR1,TLR2,CRTAM,TSPAN8,CD44,TREM2,CD48,CD53,CD74,CALCRL,OSMR,ADGRE1,LILRA4
GO:0060089	MF	molecular transducer activity	1.74E-10	1.74E-07	1.30E-06	1.74E-07	83	CDKN1A,IGSF6,HLA-DOA,HLA-DPA1,HLA-DQA1,HLA-DQB1,HLA-DQB2,HLA-

								DRA,CLEC7A,EVI2A,TLR7,LY96,TLR6,F3,CHRNA1,TLR8,CHRNA5,ADORA3,CKS2,FCER1G,FCGR1A,FCGR1B,FCGR2B,FCGR3A,APLNR,CCL2,CCR1,CCR5,MYOT,GPR65,FPR1,FPR2,FPR3,SUCNR1,CR1,FAS,SLC1A5,SIGLEC7,PKIB,IL2RA,CXCR2,SLAMF8,IL10,IL13RA1,SIGLEC8,GPR82,GPR84,ITGB2,GADD45A,LYVE1,PTPRC,CXCR4,NGFR,C3AR1,C5AR1,SFN,OGFRL1,LILRB3,LILRA2,GPR34,P2RY8,GPR183,TNFRSF11B,TLR10,CCNG1,TGFBR1,EGF,CD14,CD86,TLR1,TLR2,TLR5,OR52N4,CD44,TREM2,CD48,CD74,IL1RL1,CDK1,CALCRL,OSMR,ADGRE1,LILRA4
GO:0005102	MF	signaling receptor binding	6.87E-09	1.72E-06	1.29E-05	6.87E-06	78	PIK3AP1,HGF,HLA-DOA,HLA-DPA1,HLA-DQA1,HLA-DQB1,HLA-DQB2,HLA-DRA,CLEC7A,CYTL1,LY96,TLR6,S100A4,S100A8,S100A9,TYROBP,S100A12,ITGBL1,KITLG,FCGR1A,FGF2,CCL2,FGF7,GPNMB,CCL18,CCL20,HILPDA,CXCL5,SDCBP,MACC1,ANGPT1,CD300LF,ANXA1,ANXA2,FPR1,FPR2,GMFG,PPBP,AQP1,PDPN,ASAH1,TNFSF13B,HAMP,IL1A,FYB1,TSLP,IL10,IL18,SPP1,B2M,ITGB2,ERBIN,BMP5,PTPRC,NGFR,C3,OSGIN2,TNFSF15,LAMP2,LCP1,OGN,TNFRSF11B,TGFBI,TGFBR1,SEMA3D,NAMPT,EGF,CD86,TNFSF8,TLR1,TLR2,TLR5,CRTAM,TSPAN8,CD44,CD74,HCK,LILRA4
Down regulated genes								
GO:0006811	BP	ion transport	1.96E-05	7.06E-03	6.25E-02	7.64E-02	54	TSPOAP1,CBARP,ASIC3,SLC22A13,AGER,SCN4A,PKD1,SCNN1D,HRC,SMPD3,CXCL11,CNGB1,KCNT1,REM1,HTR6,SHANK3,SLC1A7,CRHR1,CRHR2,SLC4A1,SLC8A2,MAPK15,PLCH2,SLC13A5,RNF207,SLC26A10,MYB,LCN12,SLC38A5,KCNK4,LIME1,XKR7,ABCC8,KCNQ2,CACNA1I,CACNA1H,COX4I2,CA1,CA4,SHANK1,CACNA1A,CACNA1B,DRD4,NTSR1,GRIN1,GRM2,ATP10A,KCNH4,KCNH3,SLC25A2,HBA1,SLC7A5P1,AGRN,SLC7A10
GO:0099537	BP	trans-synaptic	2.87E-05	7.06E-03	6.25E-02	1.12E-01	31	CEL,TSPOAP1,PLEKHG5,AGER,SCN4A,BEGAIN,

		signaling						HTR6,SHANK3,CRHR1,CRHR2,MYLK2,SLC8A2,IGSF9B,NPAS4,ADGRB1,KCNQ2,CACNA1I,CACNA1H,BSN,SHANK1,CACNA1A,CACNA1B,CUX2,DRD4,NTSR1,GRIN1,GRM2,GRM4,NEURL1,GRIP2,AGRN
GO:0005887	CC	integral component of plasma membrane	2.66E-06	4.12E-04	2.77E-03	1.24E-03	52	GP6,CEL,PLPPR3,ASIC3,DLGAP3,PROM2,SLC22A13,AGER,SCN4A,PKD1,ADCY4,FLT4,HTR6,PILRB,DLL4,SHANK3,SLC1A7,CRHR1,CRHR2,SLC4A1,MST1R,SLC8A2,LAT,SLC26A10,TNFRSF25,ADGRB1,SLC38A5,SEMA3G,ITGA2B,KCNK4,JAG2,ABCC8,KCNQ2,CACNA1H,NOTCH3,GP1BB,SHANK1,CACNA1A,CYSLTR2,DRD4,GPR20,NTSR1,GRIN1,GRM2,GRM4,KCNH4,KCNH3,TIE1,ADGRD2,SLC7A10,PTGDR2,EPHA10
GO:0043005	CC	neuron projection	8.88E-04	1.53E-02	1.03E-01	4.12E-01	42	TSPOAP1,CBARP,SPTBN5,DLGAP3,AGER,SCN4A,CNGB1,ACAP3,BEGAIN,ADCY4,HTR6,SHANK3,CRHR1,CRHR2,MYLK2,SLC8A2,KNCN,MAST1,IGSF9B,INHA,ADGRB1,RGS11,KCNQ2,CACNA1H,STRC,BSN,GNB3,CDK5R2,SHANK1,CACNA1A,CACNA1B,DRD4,NTSR1,GRIN1,GRM2,GRM4,NEURL1,GRIP2,AGRN,SLC7A10,EPHA10,ARHGAP33
GO:0005215	MF	transporter activity	2.11E-04	7.75E-03	5.56E-02	1.55E-01	43	TSPOAP1,CBARP,ASIC3,SLC22A13,AGER,SCN4A,PKD1,SCNN1D,HRC,CNGB1,KCNT1,REM1,SHANK3,SLC1A7,CRHR1,SLC4A1,SLC8A2,SLC13A5,RNF207,SLC26A10,CPNE7,SLC38A5,KCNK4,XKR7,ABCC8,KCNQ2,CACNA1I,CACNA1H,COX4I2,SHANK1,CACNA1A,CACNA1B,DRD4,NTSR1,GRIN1,GRM2,KCNH4,KCNH3,SLC25A2,HBA1,SLC7A5P1,AGRN,SLC7A10
GO:0004888	MF	transmembranesignaling receptor activity	6.73E-02	3.57E-01	1.00E+00	1.00E+00	30	GP6,CRLF1,AGER,PKD1,FLT4,HTR6,ADGRA2,SHANK3,CRHR1,CRHR2,MST1R,TNFRSF25,ADGRB1,ABCC8,GP1BB,SHANK1,CYSLTR2,DRD4,GPR20,NTSR1,GRIN1,GRM2,GRM4,CELSR3,TIE1,NEURL1,ADGRD2,AGRN,PTGDR2,EPHA10

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

Pathway ID	Pathway Name	P-value	FDR B&H	FDR B&Y	Bonferroni	Gene Count	Gene
1457780	Neutrophil degranulation	8.98E-29	7.23E-26	5.26E-25	7.23E-26	67	HEXB,SERPINA3,CLEC5A,CTSC,ACP3,CHI3L1,CHIT1,FABP5,S100A8,S100A9,TYROBP,S100A11,S100A12,SERPINA1,FCAR,FCER1G,MGST1,FCGR2A,HP,SDCBP,ANXA2,FPR1,FPR2,GMFG,NPC2,PPBP,CR1,SLC2A5,ARG1,SLC11A1,ASAH1,VAMP8,CTSS,CXCR2,CYBB,IQGAP2,SIGLEC9,B2M,GPR84,SIGLEC5,HPSE,ITGB2,FGL2,GGH,PTPRC,VNN1,C3,C3AR1,C5AR1,GLIPR1,LILRB3,LAIR1,SIGLEC14,LAMP2,OLR1,RNASE2,RNASE3,CD14,ANO6,TLR2,CD44,CD53,CD68,SERPINB1,LTF,TNFAIP6,LYZ
1269203	Innate Immune System	4.32E-26	1.74E-23	1.27E-22	3.48E-23	106	CDKN1A,HEXB,PIK3AP1,HGF,SERPINA3,CLEC5A,CTSC,ACP3,CLEC7A,TLR7,LY96,CHI3L1,TLR6,CHIT1,TLR8,FABP5,S100A8,S100A9,TYROBP,S100A11,S100A12,SERPINA1,FCAR,KITLG,FCER1G,FCGR1A,MGST1,FCGR2A,FCGR3A,HP,FGF2,PLA2G2A,FGF7,LY86,SDCBP,ANGPT1,ANXA2,FPR1,FPR2,GMFG,BIRC3,NPC2,PPBP,CR1,CFI,SLC2A5,ARG1,SLC11A1,ASAH1,VAMP8,IL2RA,CTSS,PROS1,CXCR2,CYBB,IQGAP2,SIGLEC9,B2M,GPR84,SIGLEC5,NCF2,HPSE,ITGB2,FGL2,GGH,PTPRC,VNN1,BTK,C1QA,C1QB,C1QC,C3,C3AR1,C4A,C4B,C5AR1,C6,C7,GLIPR1,LILRB3,LAIR1,CASP1,SIGLEC14,LAMP2,OLR1,TLR10,RNASE2,RNASE3,RNASE6,EGF,CD14,ANO6,CD86,TLR1,TLR2,TLR5,CD44,TREM2,CD53,CD68,SERPINB1,LTF,TNFAIP6,CD180,LYZ,HCK
1269201	Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell	4.99E-09	3.66E-07	2.66E-06	4.02E-06	19	TYROBP,FCGR1A,FCGR2B,FCGR3A,CD300LF,LILRA6,SIGLEC7,SIGLEC9,SIGLEC8,B2M,SIGLEC5,ITGB2,C3,LILRB3,LILRA2,LAIR1,CRTAM,TREM2,LILRA4
1269576	G alpha (i) signalling events	3.24E-06	1.25E-04	9.05E-04	2.61E-03	21	ADORA3,APLNR,CCR1,CCR5,CCL20,CXCL5,ANXA1,FPR1,FPR2,FPR3,SUCNR1,PPBP,CXCR2,GNG12,CXCR4,C3,C3AR1,C5AR1,RGS1,RGS10,RGS18

1269318	Signaling by Interleukins	1.35E-04	4.18E-03	3.04E-02	1.09E-01	30	CDKN1A,HGF,F13A1,KITLG,H3C11,H3C8,FGF2,CCL2,FGF7,CCR1,CCR5,CCL20,ANGPT1,BATF,ANXA1,FPR1,IL1A,IL2RA,IL10,IL13RA1,IL18,ITGB2,SOCS3,CASP1,HAVCR2,EGF,CD86,IL1RL1,OSMR,HCK
1269340	Hemostasis	2.78E-03	5.10E-02	3.71E-01	1.00E+00	30	HGF,SERPINA3,F3,F5,F13A1,S100A10,SERPINA1,FCER1G,H3C11,H3C8,PLEK,ANGPT1,ANXA2,PPBP,PDPN,SRGN,IL2RA,PROS1,ITGB2,CD84,GNG12,LAMP2,SLC7A7,OLR1,KIF20A,EGF,CD44,CD48,CD74,SERPINA5
1269544	GPCR ligand binding	6.98E-03	1.00E-01	7.29E-01	1.00E+00	22	ADORA3,APLNR,CCR1,CCR5,CCL20,CXCL5,GPR65,ANXA1,FPR1,FPR2,FPR3,SUCNR1,PPBP,CXCR2,GNG12,CXCR4,C3,C3AR1,C5AR1,GPR183,CALCRL,ADGRE1
Down regulated genes							
1268763	Neuronal System	1.07E-05	2.80E-03	1.91E-02	5.59E-03	17	TSPOAP1,DLGAP3,BEGAIN,ADCY4,SHANK3,SLC1A7,KCNK4,ABCC8,KCNQ2,GNB3,SHANK1,CACNA1A,CACNA1B,GRIN1,KCNH4,KCNH3,GRIP2
1270312	NCAM signaling for neurite out-growth	6.61E-03	1.51E-01	1.00E+00	1.00E+00	10	CNKSR1,SPTBN5,COL9A1,LAT,ITGA2B,FGF17,CACNA1I,CACNA1H,GRIN1,AGRN
1270303	Axon guidance	1.27E-02	1.81E-01	1.00E+00	1.00E+00	15	CNKSR1,SPTBN5,SCN4A,AGAP2,COL9A1,SHANK3,LAT,ITGA2B,FGF17,KCNQ2,CACNA1I,CACNA1H,GRIN1,AGRN,EPHA10
1269544	GPCR ligand binding	1.32E-02	1.82E-01	1.00E+00	1.00E+00	13	PLPPR3,CXCL11,HTR6,WNT7B,CRHR1,CRHR2,GNB3,CYSLTR2,DRD4,NTSR1,GRM2,GRM4,PTGDR2
1269903	Transmembrane transport of small molecules	1.05E-01	4.96E-01	1.00E+00	1.00E+00	14	ASIC3,SCNN1D,ADCY4,SLC1A7,SLC4A1,SLC8A2,SLC13A5,LCN12,SLC38A5,LCN15,ABCC8,GNB3,ATP10A,SLC7A10
1269340	Hemostasis	1.25E-01	4.96E-01	1.00E+00	1.00E+00	13	GP6,SLC8A2,LAT,MYB,KIF26A,KIF12,ITGA2B,ITIH4,CABLES1,GNB3,GP1BB,KIFC2,SLC7A10

Table 4 Topology table for up and down regulated genes

Category	Node	Degree	Betweenness	Stress	Closeness
Up	CDK1	402	0.197084	47028580	0.367116
Up	TOP2A	191	0.081627	13073002	0.341251
Up	MAD2L1	146	0.040284	8144352	0.324233
Up	RSL24D1	133	0.034596	8777264	0.30143

Up	CDKN1A	122	0.030348	6995294	0.331404
Up	RHOQ	111	0.052089	7439940	0.320307
Up	HCK	111	0.035255	11066684	0.322733
Up	BTK	90	0.02356	5280320	0.301359
Up	TGFBR1	89	0.036693	10570252	0.318499
Up	SFN	88	0.030706	5847364	0.333362
Up	EIF4A2	86	0.02546	4672448	0.306096
Up	RPL39	85	0.014424	6331184	0.300297
Up	BIRC3	82	0.02467	6593536	0.30953
Up	U2AF1	80	0.03024	6114556	0.299524
Up	HSPA13	79	0.023849	4111210	0.312225
Up	RPL22L1	78	0.011772	4945670	0.300133
Up	SOCS3	67	0.018611	4368764	0.312709
Up	PPP1CB	61	0.024464	3908348	0.30841
Up	CCNG1	61	0.00591	1238240	0.315876
Up	ITGB2	58	0.028427	5334096	0.316946
Up	CASP1	58	0.018625	2471864	0.308981
Up	CD44	56	0.025232	4779164	0.315098
Up	VAMP8	54	0.02368	2898878	0.297872
Up	IQGAP2	54	0.007736	2790576	0.313552
Up	FAS	54	0.014105	5340678	0.283707
Up	EIF3E	51	0.015213	3479548	0.297457
Up	LCP1	51	0.009397	1985584	0.313347
Up	NGFR	47	0.016065	3746024	0.308459
Up	TLR2	46	0.012377	2255708	0.298824
Up	PLS1	46	0.007749	1638298	0.310834
Up	STK26	44	0.017254	2794926	0.299664
Up	CXCR4	44	0.017176	4261588	0.314607
Up	TNNI2	42	0.00668	8295678	0.245961
Up	CKS2	40	0.004636	968814	0.317892
Up	FGF2	39	0.01534	1981338	0.289378
Up	CCR5	37	0.008114	1662686	0.277388
Up	ANXA2	37	0.014813	3649912	0.313963
Up	SOD2	36	0.01232	2200890	0.297526
Up	S100A9	36	0.008539	1250402	0.271902
Up	GPC3	34	0.004643	1075058	0.239167
Up	BATF	33	0.00659	1842444	0.271191
Up	HOXB7	32	0.005224	2604922	0.247644
Up	ARHGAP15	32	0.006037	1575176	0.265688
Up	GADD45A	32	0.007594	1064172	0.31996
Up	LAMP2	32	0.007823	3053920	0.254799
Up	ACTR6	31	0.010083	2336460	0.236878
Up	DNAJB9	31	0.002157	834952	0.264315

Up	ANXA1	30	0.00939	2103520	0.301549
Up	DNAJC5B	30	0.001424	1100202	0.266278
Up	PTPN22	30	0.003095	1739114	0.273025
Up	ERBIN	30	0.012972	2825982	0.312887
Up	C3	29	0.011276	3367732	0.238335
Up	S100A4	29	0.006124	1593532	0.303601
Up	DYNLT3	29	0.004175	1869030	0.22383
Up	BMP5	28	0.005191	833118	0.253134
Up	GEM	27	0.003998	3127856	0.244674
Up	S100A10	27	0.010457	853366	0.299758
Up	SDCBP	26	0.007881	1442622	0.298081
Up	SERPINA1	26	0.011803	1824802	0.301004
Up	ARHGDIB	25	0.00217	1032648	0.304275
Up	GLRX	23	0.006494	1256738	0.295623
Up	B2M	23	0.009862	1122844	0.292869
Up	OGN	22	0.003355	1546298	0.256554
Up	HCLS1	22	0.004584	751498	0.2831
Up	KIF20A	22	0.002995	1053136	0.316946
Up	BIRC7	21	0.002067	803284	0.295213
Up	RRM2B	21	0.004262	946508	0.293901
Up	HGF	20	0.006487	729002	0.264479
Up	RGS2	20	0.003947	2415788	0.251971
Up	MMP7	20	0.00531	450650	0.261611
Up	BCL2A1	20	0.004104	382146	0.268816
Up	MSX2	20	0.003782	1705198	0.231098
Up	CXCR2	20	0.005673	1759130	0.230723
Up	PTTG1	20	0.003325	436594	0.313552
Up	CEP55	20	0.005756	585852	0.31559
Up	ACSL1	19	0.008972	975302	0.291512
Up	LUM	19	0.001751	1357886	0.250245
Up	TLR7	19	0.002068	466520	0.26195
Up	CCR1	18	0.002536	1830672	0.225753
Up	TLR1	18	1.00E-03	270250	0.25409
Up	S100A6	18	0.005993	566808	0.300274
Up	ANGPT1	18	0.001995	247354	0.260297
Up	NAMPT	17	0.006404	866924	0.292757
Up	TYROBP	16	0.006739	3350394	0.21767
Up	SERPINA5	16	0.005047	1140526	0.204445
Up	SOAT1	16	0.007372	834918	0.293183
Up	C1QA	16	0.003569	907138	0.244051
Up	SPP1	16	0.003897	481758	0.273668
Up	EGF	15	0.003463	1877948	0.246736
Up	NCF2	15	0.003176	846020	0.252984

Up	GPX8	15	0.003073	745356	0.29249
Up	CCL2	14	0.002658	610374	0.238379
Up	CPVL	14	0.004372	636758	0.294624
Up	RAB20	14	0.006334	466976	0.201863
Up	KYNU	14	0.004584	733080	0.292534
Up	HP	14	0.005264	634858	0.244051
Up	MTHFD2	14	0.006469	723768	0.291556
Up	FCGR2A	13	0.002775	672196	0.305195
Up	FCGR2B	13	0.002454	818192	0.253118
Up	RASSF9	13	0.003768	327690	0.246181
Up	CD74	12	0.00413	277206	0.30281
Up	CSTA	12	0.00461	539282	0.291489
Up	CP	12	0.0037	233612	0.236849
Up	MSLN	12	0.004721	1874812	0.200764
Up	LTF	11	0.006533	917294	0.301099
Up	C6	11	0.002184	776286	0.231461
Up	ARL11	11	0.003483	486670	0.292869
Up	TMED5	11	0.003557	612564	0.29672
Up	LYZ	10	0.002369	389198	0.296079
Up	ARL6IP5	10	0.004541	404738	0.297249
Up	FGF7	10	0.001158	492864	0.211408
Up	HOXC4	10	0.001703	539558	0.220917
Up	HOXC10	10	0.001805	548562	0.216662
Up	FCGR3A	10	0.001167	993240	0.224814
Up	RGS1	10	1.49E-04	62882	0.218265
Up	S100A11	9	0.001746	228728	0.296354
Up	DSC2	9	0.002704	467128	0.222106
Up	PIK3AP1	9	0.001407	319970	0.250147
Up	RGS18	9	1.22E-04	135174	0.215457
Up	RGS10	9	0.002616	1549108	0.303649
Up	S100A8	3	6.23E-05	17078	0.23881
Up	FCGR1A	3	8.90E-05	110248	0.245034
Up	CD14	3	1.41E-04	20250	0.249886
Up	TLR10	2	0	0	0.230418
Up	CR1	2	7.30E-05	24248	0.202417
Up	CNN3	2	1.30E-07	104	0.238721
Up	TLR6	2	0	0	0.238929
Up	SLC11A1	1	0	0	0.191503
Up	TLR8	1	0	0	0.231587
Up	CXCL5	1	0	0	0.187479
Up	PPBP	1	0	0	0.187479
Up	SIGLEC7	1	0	0	0.238231
Up	FCER1G	1	0	0	0.183558

Up	C1QB	1	0	0	0.196185
Up	C1QC	1	0	0	0.196185
Up	S100A12	1	0	0	0.197508
Up	TNFSF15	1	0	0	0.191647
Up	LY86	1	0	0	0.207587
Up	ACP5	1	0	0	0.214878
Up	SRGN	1	0	0	0.239615
Up	IL1A	1	0	0	0.236062
Up	IL18	1	0	0	0.236062
Up	LY96	1	0	0	0.230086
Up	NFIL3	1	0	0	0.213348
Up	C3AR1	1	0	0	0.192474
Up	CLEC7A	1	0	0	0.230086
Up	FPR1	1	0	0	0.231698
Up	HTRA4	1	0	0	0.236382
Up	VNN2	1	0	0	0.240683
Up	AP1S2	1	0	0	0.228075
Up	CPM	1	0	0	0.197916
Up	HLA-DQA1	1	0	0	0.232443
Up	KCNJ5	1	0	0	0.187736
Up	CD163	1	0	0	0.196185
Up	SIGLEC14	1	0	0	0.178768
Up	ANKRD22	1	0	0	0.218029
Up	TREM2	1	0	0	0.178768
Up	VSIG4	1	0	0	0.192474
Up	HLA-DMA	1	0	0	0.232443
Up	AIF1	1	0	0	0.238602
Up	ITGBL1	1	0	0	0.212615
Up	PLP2	1	0	0	0.184184
Up	CYBB	1	0	0	0.201916
Up	ITGAD	1	0	0	0.240683
Up	CFI	1	0	0	0.192474
Up	HLA-DRA	1	0	0	0.232443
Up	HLA-DQB1	1	0	0	0.232443
Up	SLA	1	0	0	0.23226
Up	HLA-DPB1	1	0	0	0.232443
Up	IL10	1	0	0	0.230086
Up	DAPP1	1	0	0	0.231587
Up	CLEC5A	1	0	0	0.178768
Down	NOTCH3	164	0.091402	23838154	0.331777
Down	MYB	114	0.041442	7392588	0.330405
Down	PWP2	85	0.032395	5057778	0.296812
Down	WNT7B	76	0.019782	2626426	0.277709

Down	HSPA12B	73	0.006667	2161072	0.27609
Down	NR4A1	72	0.025505	4889526	0.31345
Down	FLT4	66	0.020378	5735870	0.321085
Down	MAPK15	64	0.021292	3346718	0.301643
Down	GRIN1	64	0.023937	4117674	0.295965
Down	KIFC2	63	0.016898	4559514	0.286568
Down	CALML6	59	0.009409	2030892	0.270981
Down	OBSCN	54	0.008442	8694380	0.248188
Down	CORO6	51	0.005529	1012934	0.270961
Down	PDIA2	45	0.012294	5298738	0.267821
Down	CHTF18	43	0.008614	1782478	0.30522
Down	ADCY4	41	0.011029	6899344	0.256743
Down	GNB3	40	0.010425	6470774	0.261736
Down	LAT	39	0.009974	2962082	0.3025
Down	DNAH1	38	0.002688	5473740	0.231489
Down	DNAH3	35	0.002569	5296504	0.231447
Down	DNAH2	35	0.002776	5189040	0.232584
Down	KCNH3	34	0.007586	1205362	0.212568
Down	CHD5	34	0.009884	1545622	0.296537
Down	KCNH4	34	0.007586	1205362	0.212568
Down	PNPLA7	34	0.008145	3168532	0.244191
Down	AP1G2	33	0.014151	1680394	0.295441
Down	POLR2J3	33	0.015995	1968346	0.294127
Down	PDE4C	31	0.005427	2684966	0.25
Down	TIE1	30	0.003319	1939470	0.246545
Down	REM1	29	0.004314	1853664	0.270179
Down	ITGA2B	29	0.008146	945330	0.270008
Down	EPHA10	29	0.00243	2289996	0.235742
Down	GP1BB	29	0.003547	2615204	0.260403
Down	GRAPL	29	0.005118	2545348	0.25409
Down	SHANK1	28	0.009431	998326	0.259119
Down	PKD1	26	0.00671	1877922	0.302071
Down	MST1R	26	0.005428	1662648	0.310658
Down	DNAJC5G	25	4.01E-04	267002	0.263425
Down	CACNA1A	23	0.008785	1982682	0.30143
Down	CNKSR1	23	0.006291	3201818	0.241927
Down	PLEKHG5	23	0.00133	464342	0.26406
Down	CACNA1B	23	0.010784	1739420	0.301786
Down	ATXN7L2	22	0.009932	1793842	0.20617
Down	MYLK2	20	0.00364	1889536	0.254174
Down	ADGRA2	20	0.002251	1605348	0.251162
Down	JAG2	19	0.003135	341490	0.270789
Down	FOXL2	19	0.004964	2129576	0.251277

Down	CBFA2T3	18	0.005802	2970336	0.235496
Down	DRD4	17	0.005015	2287930	0.231112
Down	ADGRB1	17	0.007025	1023980	0.296125
Down	SLC4A1	16	0.005579	1584818	0.249528
Down	CDK5R2	16	0.001136	151486	0.279531
Down	RGS11	16	0.002225	1716534	0.214974
Down	KIF26A	16	0.002655	1291994	0.248462
Down	LRRC10B	16	5.10E-04	746332	0.248945
Down	ZNF469	16	0.005113	850154	0.221172
Down	MEIS3	16	0.003919	544578	0.252784
Down	AGRN	15	0.003672	694362	0.296262
Down	LAMA5	14	0.004736	1018384	0.211641
Down	RTEL1	14	0.005158	701906	0.292267
Down	KCNQ2	14	0.012494	2580574	0.244565
Down	ABCC8	14	0.003882	1444224	0.250653
Down	TBX2	13	0.002103	795172	0.237582
Down	HBA1	13	0.00606	870296	0.232217
Down	TTC16	13	0.002938	2785128	0.239825
Down	ASIC3	12	0.003761	656668	0.241805
Down	CACNA1H	12	0.002209	244700	0.238587
Down	COL7A1	12	0.003033	1172566	0.20475
Down	GRM2	12	0.002335	349216	0.236805
Down	TTC6	12	0.002417	2559988	0.239795
Down	USHBP1	10	0.002714	449390	0.221363
Down	CABLES1	10	5.91E-04	469160	0.246039
Down	BCL6B	10	0.003553	579104	0.292892
Down	NTSR1	10	0.002558	556770	0.216381
Down	CCDC33	10	0.005748	1111714	0.203404
Down	CELSR3	9	2.04E-04	146192	0.201672
Down	DLL4	9	5.96E-04	69464	0.263281
Down	DLGAP3	9	5.84E-04	140240	0.230987
Down	TNFRSF25	9	0.001238	364564	0.237068
Down	AGAP2	9	0.001386	378968	0.226273
Down	AGER	8	0.001241	255066	0.246103
Down	GRM4	8	4.80E-04	146670	0.242233
Down	SCNN1D	8	0.001816	281882	0.291025
Down	CACNA1I	8	0.001429	289364	0.235742
Down	PLA2G4B	7	0.001088	429840	0.241958
Down	TBC1D26	7	0.003666	372828	0.215494
Down	TRIM17	6	8.96E-04	142824	0.292936
Down	PZP	6	7.80E-04	420298	0.199979
Down	TRIM54	6	0.001716	358752	0.219979
Down	PRICKLE4	6	4.54E-04	135962	0.225475

Down	HBD	6	0.0021	332484	0.188557
Down	HGFAC	6	0.001463	255144	0.219125
Down	SLC8A2	5	4.48E-05	11786	0.231517
Down	SPTBN5	5	5.71E-04	188288	0.207744
Down	FOXD4L3	5	0.001565	1879774	0.173066
Down	ARL5C	5	4.48E-05	10724	0.201746
Down	CRHR1	5	0.002615	1085972	0.202813
Down	COL5A3	4	5.51E-04	233718	0.207295
Down	LIME1	4	2.25E-05	12626	0.240215
Down	GSTM1	4	0.001073	135528	0.291578
Down	TSPOAP1	4	6.75E-04	133888	0.215264
Down	HTR6	4	2.33E-04	111870	0.235511
Down	CRHR2	4	5.22E-04	358806	0.144352
Down	BSN	4	0.001564	139830	0.188344
Down	CLDN9	4	5.31E-04	151246	0.20146
Down	SCN4A	4	2.58E-04	89070	0.21238
Down	EGR4	4	0.001564	182706	0.207363
Down	SEMA3G	3	6.53E-04	157670	0.203491
Down	CUX2	3	1.12E-04	22356	0.23996
Down	CCDC114	3	0.001043	2377910	0.15888
Down	NPAS4	3	0.001043	201686	0.144651
Down	CFP	3	2.55E-04	58480	0.227656
Down	FOXL1	3	6.86E-06	714	0.203642
Down	BEGAIN	3	0.001043	140566	0.217448
Down	COL11A2	3	5.22E-04	200148	0.20335
Down	HES5	3	2.07E-05	8016	0.224446
Down	CA4	3	0.001043	360206	0.19975
Down	CEL	1	0	0	0.231433

Table 5 miRNA - hub gene and TF – hub gene interaction

Regulation	Hub Genes	Degree	MicroRNA	Regulation	Hub Genes	Degree	TF
Up	CDKN1A	444	hsa-mir-1248	Up	CDKN1A	105	MLLT1
Up	TGFBR1	127	hsa-mir-6887-3p	Up	EIF4A2	63	STAT1
Up	EIF4A2	113	hsa-mir-101-5p	Up	U2AF1	37	TBP
Up	CDK1	109	hsa-mir-488-5p	Up	SFN	33	ELF1
Up	HSPA13	107	hsa-mir-548l	Up	BTK	24	HMBOX1
Up	TOP2A	104	hsa-mir-421	Up	RPL22L1	19	CREB1
Up	SFN	91	hsa-mir-6756-5p	Up	CDK1	18	GLI4
Up	BIRC3	83	hsa-mir-222-3p	Up	RHOQ	18	ZBTB11
Up	MAD2L1	57	hsa-mir-1297	Up	HSPA13	15	ATF2
Up	RSL24D1	46	hsa-mir-3679-3p	Up	MAD2L1	15	RFXANK
Up	RHOQ	38	hsa-mir-7158-5p	Up	TGFBR1	12	FOXM1
Up	U2AF1	33	hsa-mir-183-5p	Up	RSL24D1	10	MXD3
Up	RPL39	13	hsa-mir-30c-5p	Up	RPL39	8	GTF2E2
Up	BTK	13	hsa-mir-4269	Up	BIRC3	7	STAT3
Up	HCK	3	hsa-mir-146a-5p	Up	HCK	6	EBF1

Down	WNT7B	88	hsa-mir-6886-5p	Down	KIFC2	71	BCL11B
Down	CHTF18	56	hsa-mir-107	Down	CALML6	61	TEAD3
Down	MYB	47	hsa-mir-150-3p	Down	NR4A1	49	KAT2A
Down	NR4A1	43	hsa-mir-195-5p	Down	MYB	44	SP3
Down	NOTCH3	41	hsa-mir-206	Down	ADCY4	32	FOSL2
Down	KIFC2	35	hsa-mir-374a-5p	Down	CHTF18	27	HMGN3
Down	HSPA12B	20	hsa-mir-6719-3p	Down	GRIN1	18	SREBF2
Down	OBSCN	19	hsa-mir-140-3p	Down	WNT7B	17	RARA
Down	PWP2	18	hsa-mir-19b-3p	Down	PWP2	16	ZFP2
Down	FLT4	12	hsa-mir-296-5p	Down	MAPK15	7	EGR1
Down	CALML6	6	hsa-mir-30a-5p	Down	PDIA2	7	HIC1
Down	CORO6	5	hsa-mir-556-5p	Down	NOTCH3	6	PKNOX1
Down	GRIN1	5	hsa-mir-3677-5p	Down	OBSCN	5	SETDB1
Down	ADCY4	3	hsa-mir-1290	Down	FLT4	3	KLF8
Down	PDIA2	2	hsa-mir-155-5p	Down	HSPA12B	3	THRB

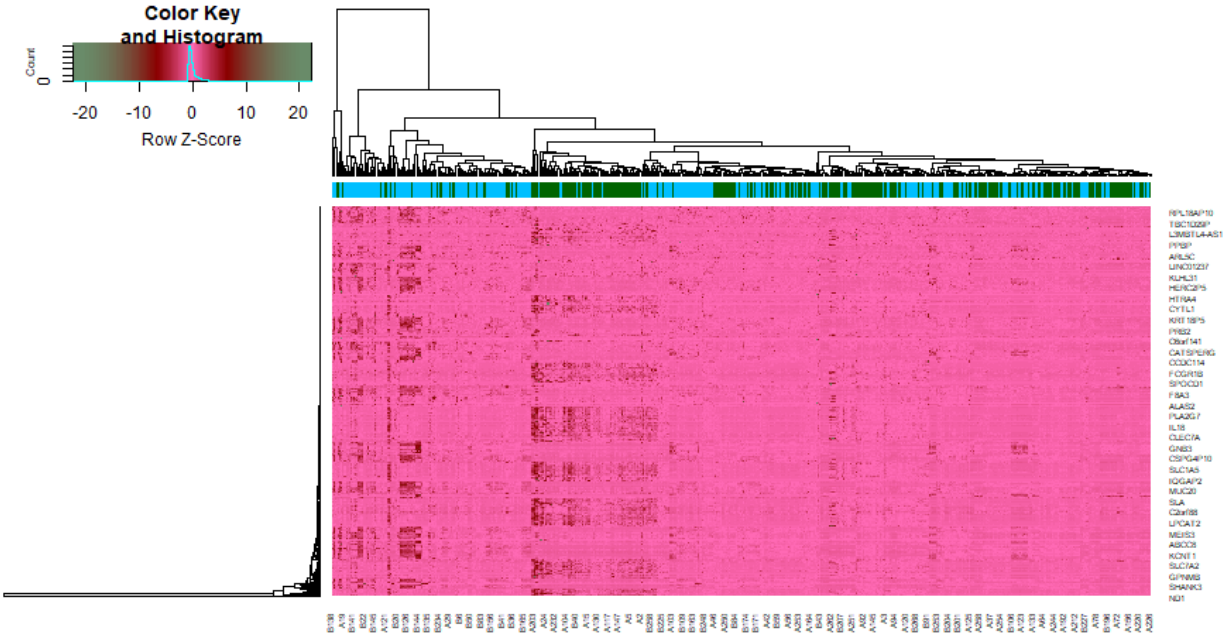

Fig. 1. Heat map of differentially expressed genes. Legend on the top left indicate log fold change of genes. (A1 – A277= healthy controls; B1 – B263 = patients with dementia)

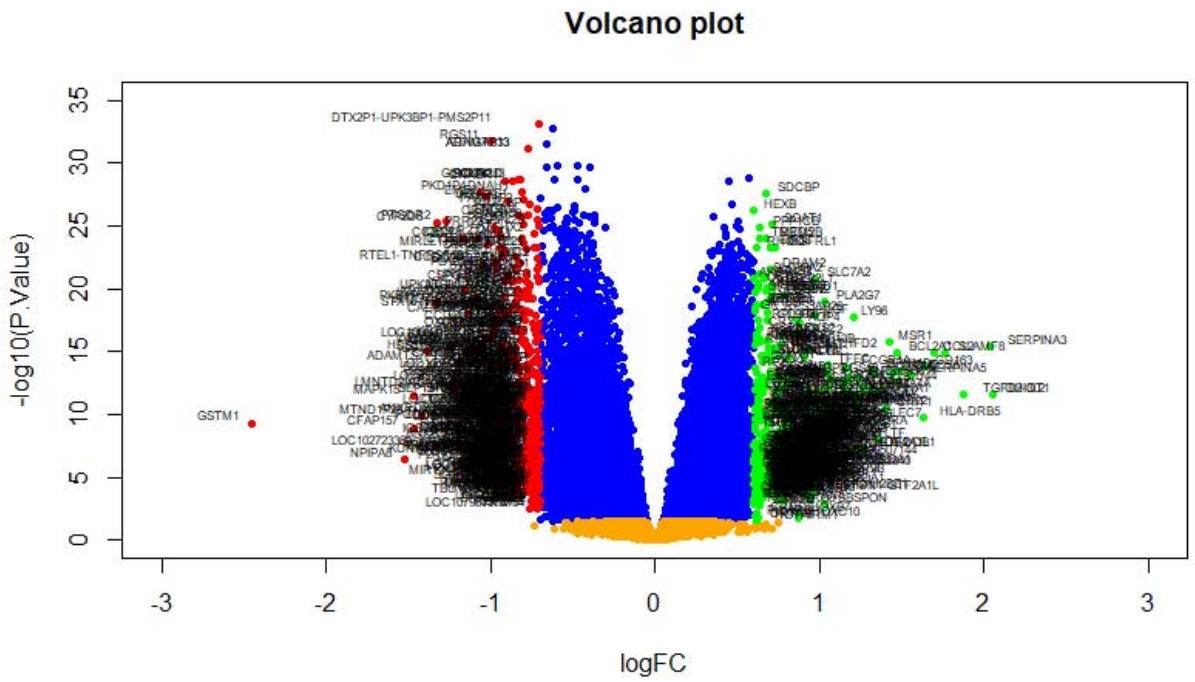

Fig. 2. Volcano plot of differentially expressed genes. Genes with a significant change of more than two-fold were selected. Green dot represented up regulated significant genes and red dot represented down regulated significant genes.

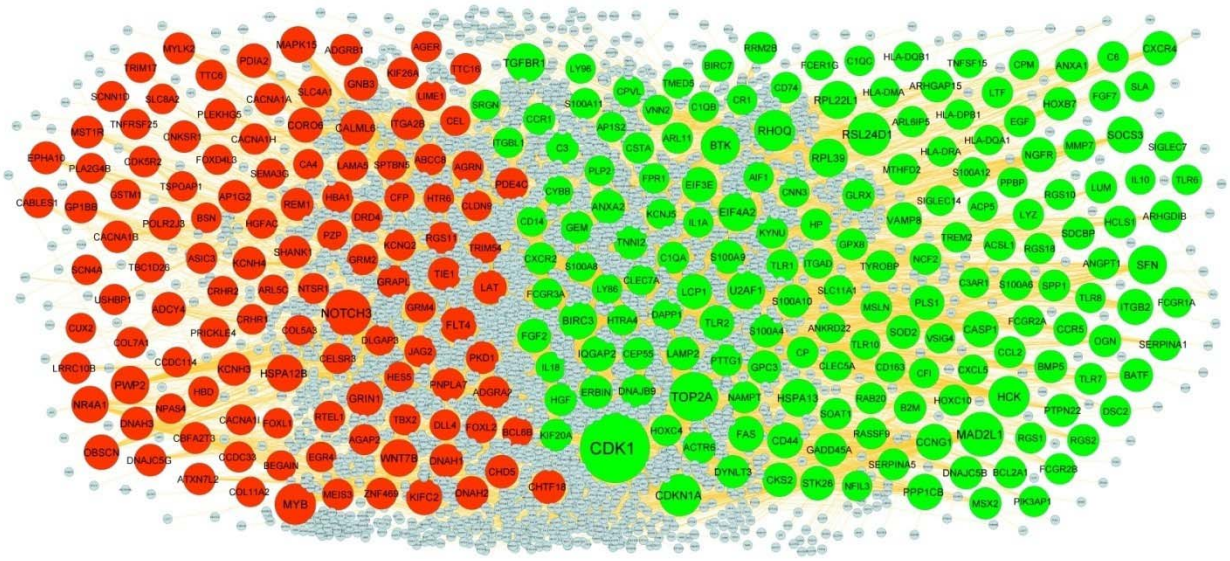

Fig. 3. PPI network of DEGs. The PPI network of DEGs was constructed using Cytoscap. Up regulated genes are marked in green; down regulated genes are marked in red

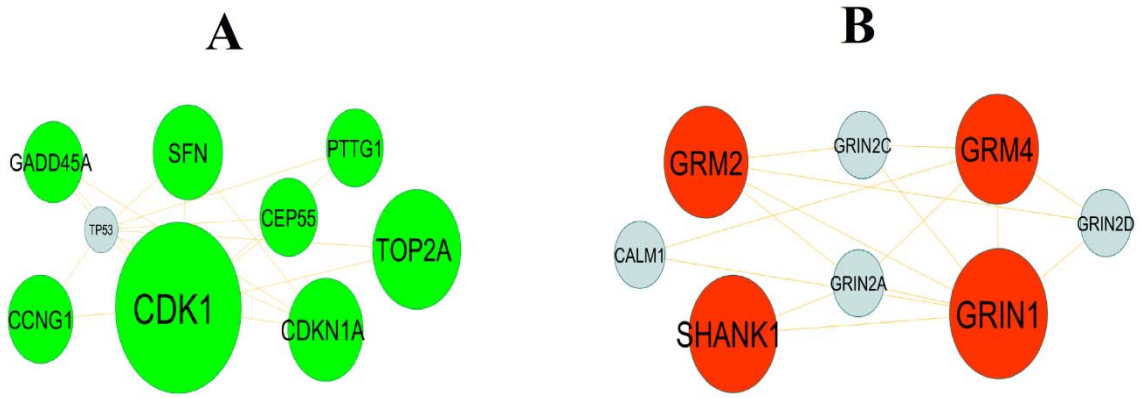

Fig. 4. Modules of isolated form PPI of DEGs. (A) The most significant module was obtained from PPI network with 9 nodes and 17 edges for up regulated genes (B) The most significant module was obtained from PPI network with 8 nodes and 15 edges for down regulated genes. Up regulated genes are marked in green; down regulated genes are marked in red.

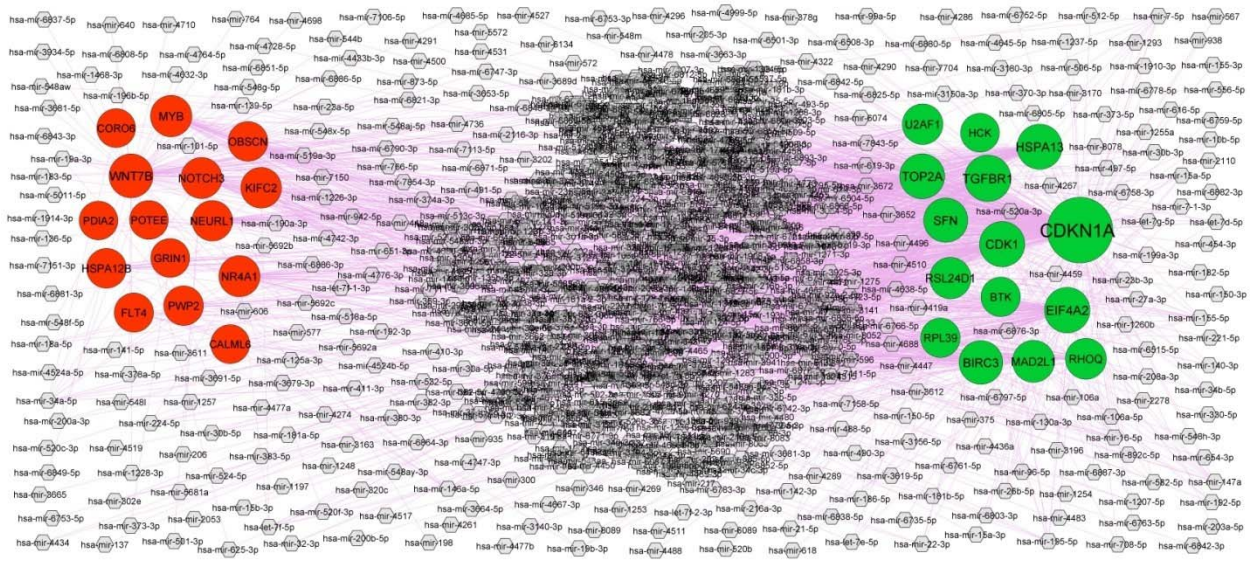

Fig. 5. MiRNA - hub gene regulatory network. The purple color diamond nodes represent the key miRNAs; up regulated genes are marked in green; down regulated genes are marked in red.

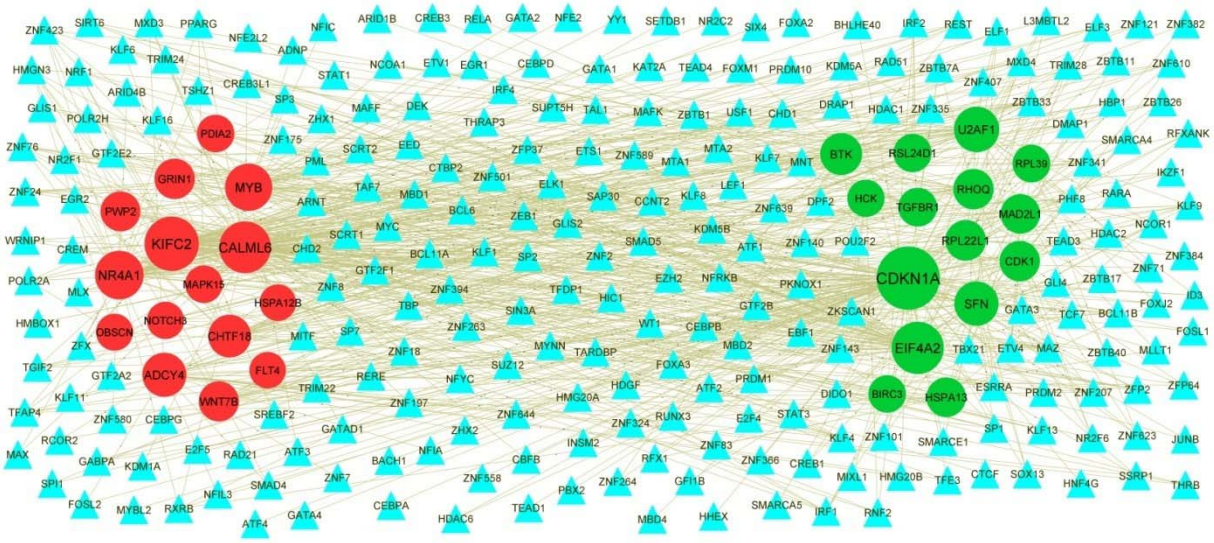

Fig. 6. TF - hub gene regulatory network. The blue color triangle nodes represent the key TFs; up regulated genes are marked in green; down regulated genes are marked in red.

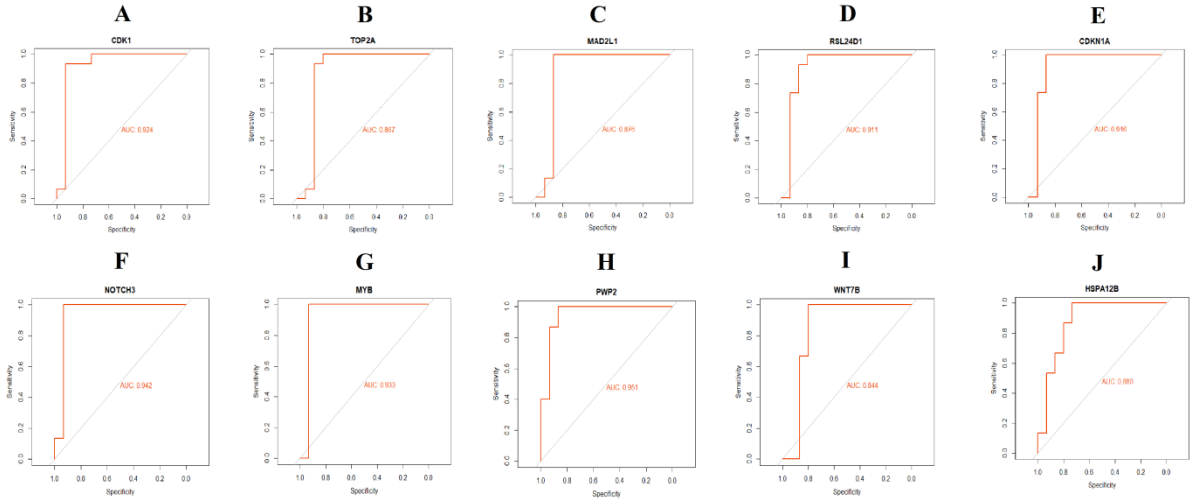

Fig. 7 ROC curve validated the sensitivity, specificity of hub genes as a predictive biomarker for dementia prognosis. A) CDK1 B) TOP2A C) MAD2L1 D) RSL24D1 E) CDKN1A F) NOTCH3 G) MYB H) PWP2 I) WNT7B J) HSPA12B