Analysis of key genes and pathways associated with the pathogenesis of Type 2 diabetes mellitus

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Abstract

Type 2 diabetes mellitus (T2DM) is the most common endocrine disorder which poses a serious threat to human health. This investigation aimed to screen the candidate genes differentially expressed in T2DM by bioinformatics analysis. The expression profiling by high throughput sequencing of GSE81608 dataset was retrieved from the gene expression omnibus (GEO) database and analyzed to identify the differentially expressed genes (DEGs) between T2DM and normal controls. Then, Gene Ontology (GO) and pathway enrichment analysis, protein-protein interaction (PPI) network, modules, miRNA-hub gene regulatory network construction and TF-hub gene regulatory network construction, and topological analysis were performed. Receiver operating characteristic curve (ROC) analysis was also performed to verify the diagnostics value and expression of identified hub genes. A total of 927 DEGs (461 were up regulated and 466 down regulated genes) were identified in T2DM. GO and REACTOME results showed that DEGs mainly enriched in protein metabolic process, establishment of localization, metabolism of proteins and metabolism. The top centrality hub genes APP, MYH9, TCTN2, USP7, SYNPO, GRB2, HSP90AB1, UBC, HSPA5 and SQSTM1 were screened out as the critical genes among the DEGs from the PPI network, modules, miRNA-hub gene regulatory network construction and TF-hub gene regulatory network. ROC analysis provide diagnostics value of hub genes. This study identified key genes, signal pathways and therapeutic agents, which might help us, improve our understanding of the mechanisms of HGPS and identify some new therapeutic agents for T2DM.

Keywords: bioinformatics analysis; differentially expressed genes; hub genes; Type 2 diabetes mellitus; protein-protein interaction network

Introduction

Type 2 diabetes mellitus (T2DM) is a complex metabolic disorder and is characterized primarily by a decrease in insulin secretion, typically accompanied by insulin resistance [1]. Globally, it is predicted that 25 million adults (20–79 years) have diabetes, projected to reach 629 million by 2045 and is the ninth leading cause of death [2-3]. T2DM is mainly associated with macrovascular complications include stroke, coronary artery disease and peripheral arterial disease, and microvascular include diabetic retinopathy, diabetic nephropathy, and diabetic neuropathy, and non-vascular diabetes complications include nonalcoholic fatty liver disease, psychiatric disease, obesity, cancer, cognitive impairment, infections and disability [4]. There are several important risk factors for T2DM, such as age, sex, family history of diabetes, hypertension, obesity, abdominal obesity, stress in the workplace or home, a sedentary lifestyle, smoking, insufficient fruit and vegetable consumption, physical activity, genetic and environmental [5]. Our understanding of the occurrence and development mechanism of T2DM has been greatly improved; however, the cause and potential molecular mechanism of T2DM are still unclear [6]. Therefore, it is necessary to identify key genes and pathways for understanding the molecular mechanism and discovering potential biomarkers for T2DM.

In recent decades, more and more researchers have devoted themselves to exploring the potential mechanisms for progression of T2DM. For instance, it has been demonstrated that the HHEX, CDKN2A/B, and IGF2BP2 [7], CDKAL1 and HHEX/IDE [8], ADIPOQ, PPAR- γ , and RXR- α [9], ABCC8 and KCNJ11 [10], TCF7L2, SLC30A8, PCSK1 and PCSK2 [11], PI3K/AKT-and AMPK signaling pathway [12], mTOR signaling pathway [13], insulin signaling pathway [14], AGE/RAGE/JNK, STAT3/SCOS3 and RAS signaling pathway [15] and ERK signaling pathway [16] were involved in progression of T2DM. Therefore, it is of great practical significance to explore the genes and signaling pathways of T2DM on islet cells.

RNA sequencing technology can rapidly detect gene expression on a global basis and are particularly useful in screening for differentially expressed genes (DEGs) in diseases [17]. RNA sequencing which allow the investigation of gene expression in a high throughput manner with high sensitivity, specificity and

repeatability. Significant amounts of data have been produced via the use of RNA sequencing and the majority of such data has been uploaded and stored in public databases. Previous investigations concerning T2DM gene expression profiling have identified hundreds of DEGs [18]. However, the comparative analysis of DEGs across a range of independent investigation might yield only a relatively limited amount of useful data with regard to T2DM advancement. The disadvantages of these single investigations might be overcome by bioinformatics analysis, as this approach would make it possible to analyze the signaling pathways and interaction networks linked with the identified DEGs. This knowledge might help in elucidating the molecular mechanisms underlying T2DM.

In the present investigation, expression profiling by high throughput sequencing dataset was downloaded from the Gene Expression Omnibus (GEO) (GEO, <http://www.ncbi.nlm.nih.gov/geo/>) [19]: GSE81608 [20]. DEGs were identified in T2DM. Additionally, gene ontology (GO), REACTOME pathway enrichment analysis was performed and protein-protein interaction (PPI) networks, modules, miRNA-hub gene regulatory network construction and TF-hub gene regulatory network were constructed to identify the hub genes, miRNA and TFs in T2DM. Finally, hub genes were validated by receiver operating characteristic curve (ROC). Collectively, the findings of the present investigation highlighted crucial genes and signaling pathways that might contribute to the pathology of T2DM. These may provide a basis for the advancement of future diagnostic, prognostic and therapeutic tools for T2DM.

Materials and Methods

Data resources

Expression profiling by high throughput sequencing dataset GSE81608 [20] was downloaded from the GEO database. The data was produced using a GPL16791 Illumina HiSeq 2500 (Homo sapiens). The GSE81608 dataset contained data from 1600 samples, including 949 T2DM, and 651 healthy control samples.

Identification of DEGs

Limma package in R software [21] is a tool to identify DEGs by comparing samples from GEO series. Limma package in R software was used to search for in

messenger RNAs (mRNAs; DEGs) that were differentially expressed between T2DM and healthy control samples. The cutoff criteria were an adjusted p-value of <0.05 , whereas the logFC value were > 0.181 for up regulated genes and < -0.27 for down regulated genes. DEG of this dataset was visualized with volcano map and hierarchical clustering heat map. The volcano plot was drawn using ggplot2 package in R software. Hierarchical clustering heat maps of DEG expression (up regulated genes and down regulated genes) were visualized with gplots package in R software.

GO and REACTOME pathway enrichment analysis of DEGs

GO enrichment analysis (<http://geneontology.org/>) [22] implement the annotation of biological processes (BP), cellular components (CC) and molecular functions (MF) of DEGs. REACTOME (<https://reactome.org/>) [23] is a database that stores large amounts of data on genomics, biological pathways, signaling pathways, diseases, drugs, and chemicals. The present investigation used Database for g:Profiler (<http://biit.cs.ut.ee/gprofiler/>) [24] to perform GO and REACTOME pathway enrichment analysis. $P<0.05$ was considered to indicate a statistically significant difference.

Construction of the PPI network and module analysis

The IID interactome database (<http://iid.ophid.utoronto.ca/>) may be searched for associations between known and predicted proteins, and is commonly used to predict PPI information in molecular biology [25]. Cytoscape 3.8.2 (<http://www.cytoscape.org/>) [26] was used to visualize the results from the PPI network. In this investigation, node degree [27], betweenness centrality [28], stress centrality [29] and closeness centrality [30], which constitutes a fundamental parameter in network theory, was adopted to evaluate the nodes in a network. The node degree betweenness centrality, stress centrality and closeness centrality methods were calculated using Cytoscape plugin Network Analyzer. Module analysis on the PPI network results was performed using the PEWCC1 (<http://apps.cytoscape.org/apps/PEWCC1>) [31] clustering algorithm that comes with Cytoscape. Module analysis might be used to find out more connected gene groups. In addition, the module analysis were further analyzed for GO and pathway enrichment analysis.

MiRNA-hub gene regulatory network construction

Prediction of miRNA-hub genes was performed by miRNet database (<https://www.mirnet.ca/>) [32]. According to the regulatory interaction, miRNA-hub gene regulatory network was constructed based on miRNet by Cytoscape 3.8.2 software [26].

TF-hub gene regulatory network construction

Prediction of TF-hub genes was performed by NetworkAnalyst database (<https://www.networkanalyst.ca/>) [33]. According to the regulatory interaction, TF-hub gene regulatory network was constructed based on NetworkAnalyst by Cytoscape 3.8.2 software [26].

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

ROC curve analysis was performed to evaluate the sensitivity and specificity of the hub genes for T2DM diagnosis using the R package “pROC” [34]. An area under the curve (AUC) value was determined and used to label the ROC effect.

Results

Identification of DEGs

A total of 927 genes were identified to be differentially expressed between T2DM and normal control samples with the threshold of adjusted p-value of <0.05 , and logFC value were > 0.181 for up regulated genes and < -0.27 for down regulated genes. Among these DEGs, 461 were up regulated and 466 down regulated genes in T2DM compared with normal control samples and are listed in Table 1. A heat map (Fig. 1) and a volcano plot (Fig. 2) for the identified DEGs was generated.

GO and REACTOME pathway enrichment analysis of DEGs

To identify the pathways which had the most significant involvement with the genes identified, up regulated and down regulated genes were submitted into g:Profiler for GO and REACTOME pathway enrichment analysis and are listed in Table 2 and Table 3. GO enrichment analysis revealed that in BP terms, the up regulated genes were mainly enriched in protein metabolic process and positive

regulation of biological process. Down regulated genes were mainly enriched in establishment of localization and cellular metabolic process. In CC terms, up regulated genes were mainly enriched in intracellular anatomical structure and endomembrane system, whereas down regulated genes were mainly enriched in cytoplasm and intracellular anatomical structure. In MF terms, up regulated genes were mainly enriched in heterocyclic compound binding and protein binding, whereas down regulated genes were mainly enriched in catalytic activity and protein binding. REACTOME pathway enrichment analysis demonstrated that up regulated genes were significantly enriched in metabolism of proteins and NR1H3 & NR1H2 regulate gene expression linked to cholesterol transport and efflux. Down regulated genes were significantly enriched in the metabolism and the citric acid (TCA) cycle and respiratory electron transport.

Construction of the PPI network and module analysis

Following the analysis based on the PPI networks, 4424 nodes and 8670 edges were identified in Cytoscape (Fig. 3). The genes with higher scores were the hub genes, as the genes of higher node degree, betweenness centrality, stress centrality and closeness centrality might be linked with T2DM. The top hub genes were APP, MYH9, TCTN2, USP7, SYNPO, GRB2, HSP90AB1, UBC, HSPA5 and SQSTM1, and are listed in Table 4. A total of two modules were selected through PEWCC1 analysis, and module 1 had nodes 98 and edges 117 (Fig. 4A) and module 2 had nodes 81 and edges 248 (Fig. 4B). Enrichment analysis demonstrated that modules 1 and 2 might be linked with RNA polymerase II transcription, intracellular anatomical structure, metabolism of proteins, protein metabolic process, positive regulation of biological process, metabolism, immune system, establishment of localization, cytoplasm, neutrophil degranulation, cellular metabolic process, intracellular anatomical structure and protein binding.

MiRNA-hub gene regulatory network construction

The hub genes of the DEGs in T2DM were performed by online databases miRNet. Based on the miRNAs, a miRNA -hub gene regulatory network was constructed with 2630 nodes (miRNA: 2345 and hub gene: 285) and 20765 interaction pairs (Fig. 5). PRKDC was the gene targets of 163 miRNAs (ex; hsa-mir-142-5p), MYH9 was the gene targets of 126 miRNAs (ex; hsa-mir-181b-3p) ,

APP was the gene targets of 125 miRNAs (ex; hsa-mir-216b-5p), ILF3 was the gene targets of 107 miRNAs (ex; hsa-mir-3157-3p), SKIL was the gene targets 91 of miRNAs (ex; hsa-mir-1294), HSPA8 was the gene targets of 116 of miRNAs (ex; hsa-mir-3661), HSP90AB1 was the gene targets of 103 of miRNAs (ex; hsa-mir-200a-3p), SQSTM1 was the gene targets of 94 of miRNAs (ex; hsa-mir-520d-5p), HSPA5 was the gene targets of 88 of miRNAs (ex; hsa-mir-573) and GRB2 was the gene targets of 65 of miRNAs (ex; hsa-mir-1291), and are listed in Table 5.

TF-hub gene regulatory network construction

The hub genes of the DEGs in T2DM were performed by online databases NetworkAnalyst. Based on the TFs, a TF -hub gene regulatory network was constructed with 477 nodes (TF: 192 and hub gene: 285) and 8507 interaction pairs (Fig. 6). BCL6 was the gene targets of 60 TFs (ex; NOTCH1), MYH9 was the gene targets of 53 TFs (ex; PPARD), NCOR2 was the gene targets of 50 TFs (ex; HIF1A), APP was the gene targets of 45 TFs (ex; SMARCA4), NDRG1 was the gene targets of 44 TFs (ex; SUZ12), UBC was the gene targets of 64 TFs (ex; TAF7L), HSP90AB1 was the gene targets of 49 TFs (ex; RUNX2), TUBA1C was the gene targets of 47 TFs (ex; MITF), HSPA5 was the gene targets of 44 TFs (ex; YAP1) and HSPA8 was the gene targets of 39 TFs (ex; E2F1), and are listed in Table 5.

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

Validated by ROC curves, we found that 10 hub genes had high sensitivity and specificity, including APP (AUC = 0.853), MYH9 (AUC = 0.852), TCTN2 (AUC = 0.881), USP7 (AUC = 0.862), SYNPO (AUC = 0.893), GRB2 (AUC = 0.850), HSP90AB1 (AUC = 0.870), UBC (AUC = 0.865), HSPA5 (AUC = 0.902) and SQSTM1 (AUC = 0.875) (Fig. 7). The hub genes might be biomarkers of T2DM and have positive implications for early medical intervention of the disease.

Discussion

Although there are various investigations on T2DM have been conducted, the mortality of T2DM is still high. This might be due to the lack of valid biomarkers for detection of early stage T2DM and of valid treatment for T2DM. Therefore, molecular mechanisms of T2DM are necessary for scientists to find the treat and diagnosis method of T2DM. Because of the fast advancement of RNA sequencing technology, it is more convenient to find out the genetic modification of development of diseases. RNA sequencing facilitates us to examine the gene, the genetic modification in T2DM, which had been proved to be a better approach to find novel biomarkers in other metabolic diseases.

In the present investigation, we observed whether there were more beneficial genes which could be better biomarkers for the diagnosis, prognosis and therapeutic for T2DM. In order to find out the significant gene of T2DM, we analyzed the T2DM expression profiling by high throughput sequencing of GSE81608 in limma, where a total number of 927 DEGs were obtained between T2DM and normal control, comprising was 461 up regulated and 466 down regulated genes. CTBP1 [35] and TRNC [36] are involved in the pathogenesis of T2DM. Previous studies have demonstrated that SST (somatostatin) serve an essential role in obesity [37], but this gene might be novel target for T2DM.

Then, databases including GO and REACTOME were selected to do gene enrichment analysis. Metabolism of proteins [38], metabolism [39], the citric acid (TCA) cycle and respiratory electron transport [40], gluconeogenesis [41], immune system [42], heterocyclic compound binding [43], protein binding [44], establishment of localization [45], cellular metabolic process [46], cytoplasm [47] and catalytic activity [48] were the GO terms and signaling pathways responsible for the advancement of T2DM. A previous study showed that IGFBP2 [49], APOH (apolipoprotein H) [50], ANXA2 [51], BAX (BCL2 associated X, apoptosis regulator) [52], PCSK1N [53], PDK4 [54], CPE (carboxypeptidase E) [55], OCLN (occludin) [56], CD44 [57], NDN (necdin, MAGE family member) [58], MLXIPL (MLX interacting protein like) [59], CD36 [60], SREBF1 [61], NR4A1 [62], PCSK2 [63], CHGB (chromogranin B) [64], PDK3 [65], PDCD4 [66], EIF5A [67], NRP1 [68], ABCA1 [69], DNMT1 [70], MYH9 [71], HMGB1 [72], B4GALT5 [73], B2M [74], MAP3K12 [75], KSR2 [76], NPY (neuropeptide Y) [77], CHGA (chromogranin A) [78], CD47 [79], DLK1 [80], PDK4 [81], CPE (carboxypeptidase E) [82], OCLN (occludin) [83], CXXC4 [84], PEMT

(phosphatidylethanolamine N-methyltransferase) [85], FADS2 [86], RREB1 [87], HNRNPAB (heterogeneous nuclear ribonucleoprotein A/B) [88], CPT1A [89], ALDH1B1 [90], ESRRA (estrogen related receptor alpha) [91], NISCH (nischarin) [92], SSTR3 [93], ND1 [94], NCOR2 [95], RBP4 [96], GSTP1 [97], CYB5A [98], G6PC2 [99], DNAJC15 [100], TMED6 [101], PSMD6 [102], CLU (clusterin) [103], TTR (transthyretin) [104], TXN (thioredoxin) [105], LAMTOR1 [106], GLUL (glutamate-ammonia ligase) [107], NEU1 [108], HSPA8 [109], AP3S2 [110], COX4I1 [111], MT2A [112], MTCH2 [113], ESD (esterase D) [114], UBE2L6 [115], SCD (stearoyl-CoA desaturase) [116], MGST3 [117], NQO1 [118], NSMCE2 [119] and PRSS1 [120] played an important role in T2DM. Quintela et al [121], Yuan et al [122], Cacace et al [123], Hao et al [124], Beckelman et al [125], Liu et al [126], Sekiguchi et al [127], Castillon et al [128], O'Donnell-Luria et al [129], Coupland et al [130], Koufaris et al [131], Qvist et al [132], Richter et al [133], Torres et al [134], Jeong et al [135], Bermejo-Bescós et al [136], Ramon-Duaso et al [137], Guilarte, [138], Mukaetova-Ladinska et al [139], Fazeli et al [140], Butler et al [141], Nackenoff et al [142], Konyukh et al [143], Hu et al [144], Kaur et al [145], Nakamura et al [146], Liu et al [147], Obara et al [148], Herrmann et al [149], Ozgen et al [150], Masciullo et al [151], Perrone et al [152], Su et al [153], Zhao et al [154], Iqbal et al [155], Gal et al [156], Wang et al [157], Stefanović et al [158], Zahola et al [159], Bik-Multanowski et al [160], Mata et al [161], Li et al [162], Payton et al [163] and Chai et al [164] indicated that UBA6, TIA1, DPP6, USP7, EEF2, ITM2B, DPH1, PAK3, KMT2E, MAPT (microtubule associated protein tau), HCFC1, BRD1, TAOK2, PHF1, STMN2, APP (amyloid beta precursor protein), MBNL2, APLP1, MAP2, SRRM2, CST3, SRRM2, CST3, PLD3, SEZ6L2, DOC2A, PI4KA, GNAO1, TRA2A, MIDN (midnolin), HOOK3, MCPH1, SACS (sacsin molecular chaperone), TUBA4A, ASAH1, ATP6V1B2, SVBP (small vasohibin binding protein), AIFM1, UBC (ubiquitin C), IFI30, SCGN (secretagoin, EF-hand calcium binding protein), MTRNR2L12, GBA (glucosylceramidase beta), TXN2, NQO2 and PPIL1 were involved in the development and progression of cognitive impairment, but these genes might be novel target for T2DM. RPS3A [165], PGAM5 [166], RPL7 [167], TLK1 [168], DDR1 [169], ILF3 [170], TNRC6A [171], GGCX (gamma-glutamyl carboxylase) [172], S100A6 [173], LSAMP (limbic system associated membrane protein) [174], KCNA5 [175], LUC7L3 [176], ATAD3C [177], SRSF3 [178], MCU (mitochondrial calcium uniporter) [179], ATP2A2 [180], GAA (glucosidase

alpha, acid) [181], MAGI1 [182], WIPF2 [183], VAMP8 [184], UCHL1 [185], CLIC1 [186], PSMB5 [187], GRB2 [188], ZMPSTE24 [189], COX6B1 [190], SQSTM1 [191], COTL1 [192], CD63 [193], NDUFB7 [194], BEX1 [195] and MTRNR2L8 [196] plays a major role in mediating cardiovascular diseases progression, but these genes might be novel target for T2DM. HLA-A [197], VEGFA (vascular endothelial growth factor A) [198], RPS26 [199], BMP6 [200], HLA-B [201], IER3IP1 [202], MT1E [203], ACADM (acyl-CoA dehydrogenase medium chain) [204] and GAPDH (glyceraldehyde-3-phosphate dehydrogenase) [205] are associated with progression of type 1 diabetes mellitus, but these genes might be novel target for T2DM. PEMT (phosphatidylethanolamine N-methyltransferase) [206], INSM1 [207], BCL6 [208], RUNX1T1 [209], PGRMC2 [210], ARID1B [211], CITED2 [212], KLF13 [213], PPT1 [214], ARRDC3 [215], HSPA5 [216], MDH2 [217] and COA3 [218] have been previously reported to be a key biomarkers for the early detection of obesity, but these genes might be novel target for T2DM. A previous study demonstrated that IGFBP5 [219], PRDX6 [220], PKM (pyruvate kinase M1/2) [221], PRDX1 [222] and USP22 [223] were more highly expressed in diabetic nephropathy, but these genes might be novel target for T2DM. Durgin et al [224], Zhang et al [225], Hamada et al [226], Gong et al [227], Li et al [228], Lin et al [229] and Schweigert et al [230] suggested that CYB5R3, CACNA1A, GLCCI1, CAP1, HSP90AB1, BLVRA (biliverdin reductase A) and CRIP1 were involved in the progression of hypertension, but these genes might be novel target for T2DM.

By PPI network and module analysis, we identified the hub genes that might affect the origin or advancement of T2DM. TCTN2, SYNPO (synaptopodin), PSMD12, PSMC4, TUBA1C, PSMC5, PSMD7 and RAD23A were novel biomarkers for the progression of T2DM.

In addition, miRNA-hub gene regulatory network construction and TF-hub gene regulatory network were constructed. In addition, miRNA-mRNA networks were constructed. The roles of hub genes, miRNA and TF in the pathogenesis of T2DM are discussed. Hsa-mir-142-5p [231], hsa-mir-1291 [232], NOTCH1 [233], PPARG (peroxisome proliferator-activated receptor delta) [234], HIF1A [235], RUNX2 [236] and E2F1 [237] levels are correlated with disease severity in patients with T2DM. Previous studies have demonstrated that hsa-mir-216b-5p [238] and hsa-mir-200a-3p [239] appears to be expressed in type 1 diabetes, but

these genes might be novel target for T2DM. Hsa-mir-1294 [240], SUZ12 [241] and YAP1 [242] were responsible for progression of cognitive impairment, but these genes might be novel target for T2DM. Hsa-mir-573 [243] and SMARCA4 [244] were linked with progression of hypertension, but these genes might be novel target for T2DM. PRKDC (protein kinase, DNA-activated, catalytic subunit), SKIL (SKI like proto-oncogene), NDRG1, hsa-mir-181b-3p, hsa-mir-3157-3p, hsa-mir-3661, hsa-mir-520d-5p, TAF7L and MITF (Microphthalmia-associated transcription factor) were novel biomarkers for the progression of T2DM.

In conclusion, the present study identified ten hub genes (APP, MYH9, TCTN2, USP7, SYNPO, GRB2, HSP90AB1, UBC, HSPA5 and SQSTM1) with crucial role in progression of T2DM; our results suggested these genes could add a new dimension to our understanding of the T2DM and might be served as potential biomarkers that will be assisting endocrinologist in developing novel therapeutic strategies for T2DM patients. However, there are some limitations in this study. Further larger clinical sample size and in-depth clinical experiment are needed to clarify the clear mechanism and warrant the prognostic value of these DEGs in T2DM.

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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. [(GSE81608) (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE81608>)]

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

Author Contributions

V. A - Methodology and validation

V. R - Formal analysis and validation

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

C. V - Software and investigation

S. K - Supervision and resources

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Tables

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

Gene Symbol	logFC	p Value	adj.P.Vale	t value	Regulations	Gene Name
CTBP1	1.474016	2.19E-79	4.17E-75	19.96953	Up	C-terminal binding protein 1
RPS14P1	1.285412	1.46E-44	6.94E-41	14.448	Up	ribosomal protein S14 pseudogene 1
RPL21P80	1.153779	3.86E-41	1.34E-37	13.82375	Up	ribosomal protein L21 pseudogene 80
PCMTD1	1.135899	7.29E-22	4.87E-19	9.751538	Up	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1
GAS2	1.122312	3.55E-14	9.86E-12	7.646372	Up	growth arrest specific 2
RPL21P11	1.084727	3.88E-31	6.42E-28	11.85596	Up	ribosomal protein L21 pseudogene 11
RPL21P16	1.055074	1.76E-27	1.92E-24	11.0667	Up	ribosomal protein L21 pseudogene 16
CPNE8	1.026604	1.52E-10	2.59E-08	6.446126	Up	copine 8
RPL9P8	0.98054	1.87E-41	7.11E-38	13.88221	Up	ribosomal protein L9 pseudogene 8
RPL21P2	0.977007	8.67E-34	1.94E-30	12.4018	Up	ribosomal protein L21 pseudogene 2
NPY	0.951123	1.58E-08	1.78E-06	5.682019	Up	neuropeptide Y
IGFBP2	0.941036	1.07E-20	6.91E-18	9.458884	Up	insulin like growth factor binding protein 2
TWSG1	0.910784	3.95E-15	1.22E-12	7.934279	Up	twisted gastrulation BMP signaling modulator 1
VGF	0.899294	8.54E-17	3.26E-14	8.415794	Up	VGF nerve growth factor inducible
APOH	0.886565	1.86E-08	2.06E-06	5.653523	Up	apolipoprotein H
BCYRN1P1	0.883965	4.56E-10	6.98E-08	6.272524	Up	brain cytoplasmic RNA 1, pseudogene 1
MZT2B	0.870462	5.83E-40	1.71E-36	13.60369	Up	mitotic spindle organizing protein 2B
RPL21	0.854196	8.11E-19	4.06E-16	8.969797	Up	ribosomal protein L21
NME7	0.844284	1.69E-10	2.83E-08	6.42956	Up	NME/NM23 family member 7
MZT2A	0.835727	2.34E-25	2.34E-22	10.58601	Up	mitotic spindle organizing protein 2A
SGSM2	0.830962	3.17E-30	4.65E-27	11.66308	Up	small G protein signaling modulator 2
RIN2	0.823708	3.95E-14	1.09E-11	7.631854	Up	Ras and Rabinteractor 2
SH3GL1	0.788298	6.78E-20	3.80E-17	9.25305	Up	SH3 domain containing GRB2 like 1, endophilin A2
RPL17	0.77636	2.17E-18	1.02E-15	8.855363	Up	ribosomal protein L17
RPL9P7	0.766544	1.52E-16	5.62E-14	8.345122	Up	ribosomal protein L9 pseudogene 7
RPL21P97	0.765139	5.01E-19	2.58E-16	9.025258	Up	ribosomal protein L21 pseudogene 97
CHGA	0.762231	2.12E-14	6.22E-12	7.714878	Up	chromogranin A
BCYRN1	0.747901	1.15E-07	1.10E-05	5.326007	Up	brain cytoplasmic RNA 1
TRNP	0.747857	2.10E-15	6.97E-13	8.015113	Up	tRNA
RPL21P53	0.747113	1.45E-20	9.06E-18	9.42516	Up	ribosomal protein L21 pseudogene 53
RPL21P134	0.74419	4.00E-28	4.48E-25	11.20893	Up	ribosomal protein L21 pseudogene 134
PHF1	0.742234	5.65E-16	2.01E-13	8.181586	Up	PHD finger protein 1
SRGAP2C	0.735167	5.38E-10	8.13E-08	6.246219	Up	SLIT-ROBO Rho GTPase activating protein 2C
HMG2P41	0.732565	8.72E-14	2.22E-11	7.525521	Up	high mobility group nucleosomal binding domain 2 pseudogene 4
ALYREF	0.709141	4.79E-18	2.17E-15	8.762089	Up	Aly/REF export factor
RPL21P75	0.703422	3.35E-17	1.33E-14	8.529557	Up	ribosomal protein L21 pseudogene 75

RUNX1T1	0.701702	3.36E-10	5.23E-08	6.320955	Up	RUNX1 partner transcriptional co-repressor 1
ANXA2	0.695469	2.91E-05	0.001438	4.192432	Up	annexin A2
THAP5	0.695018	1.24E-06	9.30E-05	4.868105	Up	THAP domain containing 5
COX7A1	0.692838	9.60E-06	0.000549	4.440384	Up	cytochrome c oxidase subunit 7A1
SEZ6L	0.68747	3.48E-09	4.52E-07	5.940588	Up	seizure related 6 homolog like
STMN2	0.680995	2.95E-06	0.000202	4.691299	Up	stathmin 2
RPL21P51	0.673726	3.94E-20	2.34E-17	9.314022	Up	ribosomal protein L21 pseudogene 51
XIST	0.672006	5.67E-12	1.16E-09	6.940221	Up	X inactive specific transcript
CD47	0.660398	1.69E-07	1.55E-05	5.254217	Up	CD47 molecule
BAX	0.6396	1.42E-18	6.91E-16	8.905118	Up	BCL2 associated X, apoptosis regulator
SELENOM	0.627347	1.61E-05	0.000854	4.326094	Up	selenoprotein M
RPL21P93	0.624329	6.69E-14	1.75E-11	7.561349	Up	ribosomal protein L21 pseudogene 93
RPL21P119	0.613383	5.52E-14	1.46E-11	7.587191	Up	ribosomal protein L21 pseudogene 119
DLK1	0.608249	0.000151	0.005723	3.798086	Up	delta like non-canonical Notch ligand 1
UBA6	0.601934	6.42E-06	0.000393	4.527061	Up	ubiquitin like modifier activating enzyme 6
RPL21P28	0.598296	2.87E-17	1.18E-14	8.548338	Up	ribosomal protein L21 pseudogene 28
PCSK1N	0.598244	4.94E-13	1.15E-10	7.287506	Up	proprotein convertase subtilisin/kexin type 1 inhibitor
ND3	0.595436	7.10E-23	5.52E-20	9.99929	Up	NADH dehydrogenase subunit 3
ZC3HAV1	0.595393	5.77E-07	4.60E-05	5.019251	Up	zinc finger CCCH-type containing, antiviral 1
ZNF83	0.584609	8.99E-07	6.89E-05	4.931948	Up	zinc finger protein 83
ZNF516	0.583289	1.43E-09	1.96E-07	6.08809	Up	zinc finger protein 516
TMEM209	0.582278	8.67E-05	0.003636	3.935269	Up	transmembrane protein 209
S100A6	0.581788	0.000265	0.009023	3.655227	Up	S100 calcium binding protein A6
RNU4ATAC	0.580741	8.08E-08	8.11E-06	5.390325	Up	RNA, U4atac small nuclear (U12-dependent splicing)
FXVD5	0.575523	0.001701	0.039275	3.143327	Up	FXVD domain containing ion transport regulator 5
NSUN6	0.572444	1.42E-08	1.63E-06	5.701046	Up	NOP2/Sun RNA methyltransferase 6
RPL21P98	0.569015	4.41E-13	1.04E-10	7.30324	Up	ribosomal protein L21 pseudogene 98
PDK4	0.562534	0.001442	0.034584	3.191688	Up	pyruvate dehydrogenase kinase 4
CPE	0.557447	3.78E-24	3.27E-21	10.30388	Up	carboxypeptidase E
RNU4-2	0.556358	9.63E-14	2.41E-11	7.512117	Up	RNA, U4 small nuclear 2
OCLN	0.555643	9.70E-06	0.000554	4.438028	Up	occludin
TIAL1	0.55498	2.51E-05	0.001264	4.226285	Up	TIA1 cytotoxic granule associated RNA binding protein like 1
CDCP1	0.554294	4.36E-05	0.00203	4.098948	Up	CUB domain containing protein 1
PGRMC2	0.554056	5.82E-07	4.63E-05	5.017602	Up	progesterone receptor membrane component 2
NPIPA1	0.552615	3.29E-07	2.80E-05	5.127837	Up	nuclear pore complex interacting protein family member A1
SKIL	0.552182	7.40E-05	0.00318	3.973284	Up	SKI like proto-oncogene
TLE5	0.551705	2.25E-09	3.00E-07	6.013492	Up	TLE family member 5, transcriptional modulator
RPS3A	0.551302	1.11E-15	3.76E-13	8.096998	Up	ribosomal protein S3A
RNA5-8SP6	0.534271	5.15E-07	4.17E-05	5.041352	Up	RNA, 5.8S ribosomal pseudogene 6
LMO1	0.524608	5.79E-05	0.002576	4.032072	Up	LIM domain only 1
RPS2	0.515349	1.26E-07	1.19E-05	5.309164	Up	ribosomal protein S2
H3P6	0.513379	1.25E-08	1.47E-06	5.722103	Up	H3 histone pseudogene 6
HLA-A	0.508443	2.45E-07	2.15E-05	5.184145	Up	major histocompatibility complex, class I, A

CXXC4	0.505817	9.30E-05	0.003864	3.918104	Up	CXXC finger protein 4
SNORD10	0.505339	5.94E-07	4.72E-05	5.013344	Up	small nucleolar RNA, C/D box 10
PGAM5	0.504362	4.35E-07	3.56E-05	5.074121	Up	PGAM family member 5, mitochondrial serine/threonine protein phosphatase
PPP1R14C	0.500165	0.000709	0.019885	3.392755	Up	protein phosphatase 1 regulatory inhibitor subunit 14C
RPL21P18	0.495652	2.80E-10	4.44E-08	6.349961	Up	ribosomal protein L21 pseudogene 18
NPDC1	0.495075	9.32E-08	9.16E-06	5.364161	Up	neural proliferation, differentiation and control 1
VEGFA	0.491315	7.62E-07	5.93E-05	4.964671	Up	vascular endothelial growth factor A
MIER1	0.488953	4.92E-05	0.002243	4.070427	Up	MIER1 transcriptional regulator
RPS26P47	0.487273	1.70E-11	3.25E-09	6.779146	Up	ribosomal protein S26 pseudogene 47
SNORD116-2	0.484757	8.62E-06	0.000501	4.463641	Up	small nucleolar RNA, C/D box 116-2
NME3	0.48391	6.02E-05	0.002665	4.022619	Up	NME/NM23 nucleoside diphosphate kinase 3
MTND5P11	0.482773	2.26E-24	2.00E-21	10.35647	Up	MT-ND5 pseudogene 11
SCARNA22	0.482326	0.000864	0.023379	3.337726	Up	small Cajal body-specific RNA 22
PEMT	0.481371	0.00068	0.019231	3.404002	Up	phosphatidylethanolamine N-methyltransferase
MAN1A1	0.479744	0.000123	0.004864	3.850151	Up	mannosidase alpha class 1A member 1
GARS1-DT	0.47794	4.35E-09	5.52E-07	5.903104	Up	GARS1 divergent transcript
RPS26P3	0.474877	3.32E-10	5.18E-08	6.323257	Up	ribosomal protein S26 pseudogene 3
OVCA2	0.47414	3.81E-06	0.000252	4.637818	Up	OVCA2 serine hydrolase domain containing
PARM1	0.472187	9.63E-09	1.16E-06	5.767609	Up	prostate androgen-regulated mucin-like protein 1
CD44	0.469788	0.000703	0.019755	3.395174	Up	CD44 molecule (Indian blood group)
ANKRD36	0.464217	2.99E-07	2.57E-05	5.145782	Up	ankyrin repeat domain 36
SLC22A17	0.461136	4.23E-05	0.001984	4.105784	Up	solute carrier family 22 member 17
NDN	0.458218	3.26E-05	0.001578	4.166065	Up	necdin, MAGE family member
LSAMP	0.457372	2.82E-07	2.45E-05	5.157171	Up	limbic system associated membrane protein
DCUN1D4	0.455019	0.001436	0.034501	3.192821	Up	defective in cullin neddylation 1 domain containing 4
NDRG1	0.452572	5.27E-07	4.25E-05	5.036817	Up	N-myc downstream regulated 1
SNHG8	0.452034	9.92E-05	0.004093	3.902492	Up	small nucleolar RNA host gene 8
IGFBP5	0.450197	3.63E-05	0.001741	4.141593	Up	insulin like growth factor binding protein 5
RHOB	0.449872	0.000149	0.005669	3.801427	Up	ras homolog family member B
RPL7	0.448946	3.87E-08	4.08E-06	5.523736	Up	ribosomal protein L7
RPL21P46	0.447428	6.35E-12	1.29E-09	6.92375	Up	ribosomal protein L21 pseudogene 46
MLXIPL	0.447422	4.32E-05	0.002016	4.10085	Up	MLX interacting protein like
JUNB	0.447023	3.15E-05	0.001532	4.174113	Up	JunB proto-oncogene, AP-1 transcription factor subunit
RPL3P4	0.444286	4.12E-07	3.39E-05	5.084716	Up	ribosomal protein L3 pseudogene 4
KCNA5	0.436338	4.38E-06	0.000285	4.608406	Up	potassium voltage-gated channel subfamily A member 5
POLR2J2	0.434874	1.06E-08	1.27E-06	5.751497	Up	RNA polymerase II subunit J2
EPB41L4A-AS1	0.433771	1.46E-07	1.36E-05	5.280562	Up	EPB41L4A antisense RNA 1
APP	0.433287	4.07E-06	0.000267	4.623855	Up	amyloid beta precursor protein
TIA1	0.432879	8.46E-05	0.003563	3.940994	Up	TIA1 cytotoxic granule associated RNA binding protein
RANBP3	0.431976	7.23E-10	1.06E-07	6.198819	Up	RAN binding protein 3
RAD52	0.431833	0.00028	0.009456	3.641218	Up	RAD52 homolog, DNA repair protein
ARGLU1	0.430628	0.000144	0.005523	3.809728	Up	arginine and glutamate rich 1

CD36	0.430483	3.83E-06	0.000253	4.636707	Up	CD36 molecule
RPL36A	0.430377	4.90E-12	1.01E-09	6.961335	Up	ribosomal protein L36a
NENF	0.430075	0.000643	0.018345	3.41961	Up	neudesinneurotrophic factor
RN7SL2	0.428215	0.000305	0.010146	3.618998	Up	RNA component of signal recognition particle 7SL2
TMEM45B	0.427303	0.001038	0.026836	3.285967	Up	transmembrane protein 45B
RPL36AP7	0.426888	7.84E-07	6.07E-05	4.958916	Up	ribosomal protein L36a pseudogene 7
MBNL2	0.424434	0.000125	0.004939	3.844825	Up	muscleblind like splicing regulator 2
FADS2	0.423554	8.50E-11	1.52E-08	6.535472	Up	fatty acid desaturase 2
WSB1	0.423551	5.24E-06	0.000332	4.570366	Up	WD repeat and SOCS box containing 1
SREBF1	0.422354	1.74E-08	1.94E-06	5.665195	Up	sterol regulatory element binding transcription factor 1
TMEM167A	0.420194	0.001254	0.031082	3.231981	Up	transmembrane protein 167A
GUSBP14	0.419306	7.34E-14	1.90E-11	7.548793	Up	GUSB pseudogene 14
DDX17	0.417942	2.18E-06	0.000157	4.753325	Up	DEAD-box helicase 17
NR4A1	0.416967	0.000462	0.014185	3.509099	Up	nuclear receptor subfamily 4 group A member 1
APLP1	0.415548	0.000105	0.004287	3.888001	Up	amyloid beta precursor like protein 1
RPS26P25	0.414785	5.10E-07	4.15E-05	5.043363	Up	ribosomal protein S26 pseudogene 25
CDH10	0.414033	0.000164	0.00608	3.777994	Up	cadherin 10
MAP2	0.413883	0.000176	0.006476	3.759522	Up	microtubule associated protein 2
TLK1	0.413402	0.00069	0.019448	3.400106	Up	tousled like kinase 1
UBBP4	0.412618	6.00E-18	2.69E-15	8.735616	Up	ubiquitin B pseudogene 4
TMCO3	0.411759	0.00034	0.011068	3.59058	Up	transmembrane and coiled-coil domains 3
ATP1B1	0.40652	0.000182	0.006608	3.752135	Up	ATPase Na ⁺ /K ⁺ transporting subunit beta 1
GSTT1	0.40489	0.000285	0.009604	3.636266	Up	glutathione S-transferase theta 1
PCSK2	0.404255	0.000619	0.017842	3.429901	Up	proproteinconvertasesubtilisin/kexin type 2
INSM1	0.403589	2.84E-05	0.001415	4.197687	Up	INSM transcriptional repressor 1
INO80E	0.402009	2.23E-10	3.69E-08	6.386086	Up	INO80 complex subunit E
PLOD2	0.401754	0.001336	0.032613	3.213913	Up	procollagen-lysine,2-oxoglutarate 5-dioxygenase 2
RPS10	0.40171	1.79E-06	0.00013	4.79359	Up	ribosomal protein S10
ANKRD36C	0.401548	4.32E-05	0.002016	4.100913	Up	ankyrin repeat domain 36C
JPX	0.401337	5.37E-13	1.25E-10	7.275861	Up	JPX transcript, XIST activator
RPL21P29	0.400799	2.70E-13	6.62E-11	7.371107	Up	ribosomal protein L21 pseudogene 29
HLA-B	0.398782	0.000933	0.024837	3.3162	Up	major histocompatibility complex, class I, B
EIF1AX	0.394846	0.000537	0.01591	3.46839	Up	eukaryotic translation initiation factor 1A X-linked
DDX18	0.394434	0.000101	0.004141	3.898292	Up	DEAD-box helicase 18
ARID1B	0.392437	1.59E-05	0.000845	4.329018	Up	AT-rich interaction domain 1B
SUMF2	0.391423	6.39E-05	0.002799	4.00852	Up	sulfatase modifying factor 2
SPINT2	0.387605	0.000226	0.00793	3.696872	Up	serine peptidase inhibitor, Kunitz type 2
STXBP5	0.386323	0.000215	0.007595	3.70958	Up	syntaxin binding protein 5
GPBP1L1	0.386026	0.000349	0.011266	3.583826	Up	GC-rich promoter binding protein 1 like 1
SRRM2	0.385583	5.71E-08	5.84E-06	5.453704	Up	serine/arginine repetitive matrix 2
UBXN6	0.384223	5.16E-06	0.000327	4.573893	Up	UBX domain protein 6
CST3	0.383961	2.80E-05	0.001398	4.201105	Up	cystatin C
TMEM123	0.383093	0.001642	0.038299	3.153773	Up	transmembrane protein 123

MPP6	0.382761	0.001424	0.03427	3.195322	Up	membrane palmitoylated protein 6
PRSS3	0.379637	0.000691	0.019453	3.399823	Up	serine protease 3
RAB8A	0.377471	0.000729	0.020275	3.384963	Up	RAB8A, member RAS oncogene family
PTPN18	0.377271	8.90E-05	0.003723	3.928734	Up	protein tyrosine phosphatase non-receptor type 18
NUDT4B	0.375718	5.71E-06	0.000354	4.55239	Up	nudix hydrolase 4B
HMGN2P6	0.37317	8.08E-08	8.11E-06	5.390423	Up	high mobility group nucleosomal binding domain 2 pseudogene 6
DYNC2I1	0.372574	1.15E-05	0.000636	4.401462	Up	dynein 2 intermediate chain 1
RNU2-2P	0.372044	5.33E-06	0.000335	4.566756	Up	RNA, U2 small nuclear 2, pseudogene
SNORA11D	0.372008	0.002239	0.048286	3.061447	Up	small nucleolar RNA, H/ACA box 11D
EMC10	0.370313	0.000334	0.010933	3.594916	Up	ER membrane protein complex subunit 10
DPP6	0.369036	0.001339	0.032654	3.213189	Up	dipeptidyl peptidase like 6
POLR2J3	0.368783	1.74E-05	0.000914	4.308638	Up	RNA polymerase II subunit J3
C1orf122	0.36843	0.001619	0.03793	3.157877	Up	chromosome 1 open reading frame 122
DNASE2	0.367364	0.000262	0.008942	3.658467	Up	deoxyribonuclease 2, lysosomal
CHGB	0.366149	1.96E-05	0.001013	4.282365	Up	chromogranin B
PDK3	0.365998	0.000157	0.005885	3.788188	Up	pyruvate dehydrogenase kinase 3
RPL36AP37	0.365114	0.000477	0.014563	3.50032	Up	ribosomal protein L36a pseudogene 37
PLD3	0.364676	0.00112	0.028428	3.264421	Up	phospholipase D family member 3
FCGRT	0.364573	0.000501	0.015112	3.487583	Up	Fc fragment of IgG receptor and transporter
RN7SL1	0.364473	0.002242	0.048311	3.06109	Up	RNA component of signal recognition particle 7SL1
ALCAM	0.364461	0.000492	0.014903	3.492185	Up	activated leukocyte cell adhesion molecule
RPS27	0.363101	2.19E-08	2.42E-06	5.624481	Up	ribosomal protein S27
ATP8A1	0.362212	1.82E-05	0.00095	4.299122	Up	ATPase phospholipid transporting 8A1
TLE3	0.36187	0.000131	0.005115	3.833117	Up	TLE family member 3, transcriptional corepressor
ZFX	0.361143	0.001731	0.039825	3.138164	Up	zinc finger protein X-linked
CYB5R3	0.358593	0.000382	0.012124	3.559641	Up	cytochrome b5 reductase 3
RAB3GAP2	0.357043	0.001077	0.027473	3.275673	Up	RAB3 GTPase activating non-catalytic protein subunit 2
RPL15P18	0.356774	4.87E-09	6.10E-07	5.88413	Up	ribosomal protein L15 pseudogene 18
MTCO1P2	0.3567	0.000532	0.015826	3.471082	Up	MT-CO1 pseudogene 2
RNR2	0.355028	5.25E-22	3.64E-19	9.786714	Up	1-rRNA
FTX	0.354506	2.50E-10	4.07E-08	6.367953	Up	FTX transcript, XIST regulator
RPL21P19	0.354214	5.65E-06	0.000351	4.554314	Up	ribosomal protein L21 pseudogene 19
NUDT4	0.354085	0.001505	0.0359	3.179238	Up	nudix hydrolase 4
RPL21P128	0.353736	2.31E-15	7.59E-13	8.003071	Up	ribosomal protein L21 pseudogene 128
ATP13A3	0.351606	0.001301	0.031996	3.221481	Up	ATPase 13A3
USP7	0.351254	0.001361	0.033113	3.20841	Up	ubiquitin specific peptidase 7
MEX3D	0.350471	6.96E-05	0.003017	3.988077	Up	mex-3 RNA binding family member D
ADGRG1	0.349339	0.000379	0.012048	3.561978	Up	adhesion G protein-coupled receptor G1
SUN1	0.349329	0.001559	0.03682	3.168932	Up	Sad1 and UNC84 domain containing 1
ITGAV	0.345799	0.00154	0.036541	3.172425	Up	integrin subunit alpha V
LUC7L3	0.344626	0.000902	0.024159	3.32575	Up	LUC7 like 3 pre-mRNA splicing factor
RGPD5	0.344154	7.31E-05	0.003145	3.976202	Up	RANBP2 like and GRIP domain containing 5
RPL21P105	0.3437	1.34E-12	2.94E-10	7.147677	Up	ribosomal protein L21 pseudogene 105

SEZ6L2	0.343462	8.70E-05	0.003644	3.934455	Up	seizure related 6 homolog like 2
CDK10	0.342461	0.000541	0.015984	3.466496	Up	cyclin dependent kinase 10
RPL21P7	0.340677	8.78E-13	1.99E-10	7.20703	Up	ribosomal protein L21 pseudogene 7
ELF2	0.340647	0.000111	0.004458	3.875783	Up	E74 like ETS transcription factor 2
ARL4C	0.339133	6.31E-05	0.002772	4.011638	Up	ADP ribosylation factor like GTPase 4C
MXRA7P1	0.338508	6.96E-06	0.000419	4.509836	Up	MXRA7 pseudogene 1
CCDC186	0.338292	0.000749	0.020697	3.377648	Up	coiled-coil domain containing 186
ATAD3C	0.338127	7.90E-06	0.000464	4.482682	Up	ATPase family AAA domain containing 3C
RPL9P25	0.337992	5.00E-06	0.000319	4.580412	Up	ribosomal protein L9 pseudogene 25
ELL2P1	0.337472	2.16E-18	1.02E-15	8.855545	Up	elongation factor for RNA polymerase II 2 pseudogene 1
FAM102A	0.334028	0.000615	0.017752	3.431681	Up	family with sequence similarity 102 member A
H3-3A	0.332578	0.000165	0.0061	3.776846	Up	H3.3 histone A
RPL39	0.332129	5.54E-05	0.002478	4.042426	Up	ribosomal protein L39
EEF2	0.331883	5.13E-07	4.16E-05	5.042172	Up	eukaryotic translation elongation factor 2
RPS26P15	0.331872	1.27E-07	1.20E-05	5.306605	Up	ribosomal protein S26 pseudogene 15
SAMD12	0.33076	0.000197	0.007041	3.731463	Up	sterile alpha motif domain containing 12
UPK3BL1	0.328408	0.00018	0.006558	3.754786	Up	uropod protein 3B like 1
PAFAH1B1	0.328304	0.002178	0.047368	3.069839	Up	platelet activating factor acetylhydrolase 1b regulatory subunit 1
MCTS1	0.325819	0.000449	0.013864	3.516522	Up	MCTS1 re-initiation and release factor
FGF7P3	0.325584	2.35E-16	8.61E-14	8.291084	Up	fibroblast growth factor 7 pseudogene 3
TNRC6B	0.324738	4.14E-06	0.000271	4.620155	Up	trinucleotide repeat containing adaptor 6B
RREB1	0.324583	2.67E-05	0.00134	4.211896	Up	ras responsive element binding protein 1
ITM2B	0.324018	6.54E-06	0.000398	4.523094	Up	integral membrane protein 2B
SRSF3	0.323004	0.002185	0.047468	3.06878	Up	serine and arginine rich splicing factor 3
HSPA1B	0.322825	0.000243	0.00841	3.678086	Up	heat shock protein family A (Hsp70) member 1B
PDCD4	0.321215	0.000458	0.014094	3.511258	Up	programmed cell death 4
FAM229B	0.32053	0.001985	0.044394	3.097653	Up	family with sequence similarity 229 member B
EIF5A	0.320022	5.27E-05	0.002374	4.054465	Up	eukaryotic translation initiation factor 5A
KRT10	0.319788	0.000664	0.018862	3.410766	Up	keratin 10
UNC80	0.3189	0.000572	0.016763	3.45169	Up	unc-80 homolog, NALCN channel complex subunit
DPH1	0.317036	0.00015	0.005669	3.800712	Up	diphthamide biosynthesis 1
NRP1	0.316879	0.001596	0.037518	3.161974	Up	neuropilin 1
DDR1	0.315885	0.002139	0.046761	3.075171	Up	discoidin domain receptor tyrosine kinase 1
PAK3	0.315642	0.001233	0.03073	3.23684	Up	p21 (RAC1) activated kinase 3
HNRNPAB	0.31556	0.000624	0.01796	3.42761	Up	heterogeneous nuclear ribonucleoprotein A/B
RPS26P8	0.314553	7.05E-05	0.003047	3.985203	Up	ribosomal protein S26 pseudogene 8
EGFEM1P	0.314407	4.78E-09	6.01E-07	5.887039	Up	EGF like and EMI domain containing 1, pseudogene
OTUD4	0.314026	0.00016	0.005946	3.784815	Up	OTU deubiquitinase 4
LSR	0.313715	1.02E-05	0.000576	4.427448	Up	lipolysis stimulated lipoprotein receptor
SNORD3B-2	0.313053	1.77E-06	0.000129	4.796	Up	small nucleolar RNA, C/D box 3B-2
FOSB	0.311504	9.77E-05	0.00405	3.906109	Up	FosB proto-oncogene, AP-1 transcription factor subunit
CPT1A	0.31039	0.000325	0.010699	3.60217	Up	carnitinepalmitoyltransferase 1A
ILF3	0.309346	0.000348	0.011264	3.584385	Up	interleukin enhancer binding factor 3

DOC2A	0.308827	3.24E-11	6.05E-09	6.68232	Up	double C2 domain alpha
RPL41P6	0.308188	2.90E-05	0.001436	4.193403	Up	ribosomal protein L41 pseudogene 6
TRNQ	0.306615	0.000182	0.006628	3.751111	Up	tRNA
FAR2P2	0.306113	0.000181	0.006584	3.753265	Up	fatty acyl-CoA reductase 2 pseudogene 2
A1BG	0.304071	0.000207	0.007341	3.718944	Up	alpha-1-B glycoprotein
KMT2E	0.300576	0.002329	0.0497	3.049652	Up	lysine methyltransferase 2E (inactive)
ALDH1B1	0.3004	0.001207	0.030202	3.243133	Up	aldehyde dehydrogenase 1 family member B1
ZNF189	0.300182	0.001066	0.027328	3.278513	Up	zinc finger protein 189
PDCD2	0.299528	0.000573	0.016784	3.451149	Up	programmed cell death 2
BMS1P20	0.299317	4.94E-05	0.002249	4.069544	Up	BMS1 pseudogene 20
ITSN2	0.298834	0.000337	0.011014	3.59254	Up	intersectin 2
PRXL2C	0.298104	0.000509	0.015279	3.483341	Up	peroxiredoxin like 2C
CLSTN1	0.296198	0.000795	0.021853	3.360949	Up	calsynenin 1
ESRRA	0.295162	1.10E-05	0.000614	4.410375	Up	estrogen related receptor alpha
ABCA1	0.293634	0.000881	0.023681	3.332327	Up	ATP binding cassette subfamily A member 1
PI4KA	0.293606	0.000441	0.01367	3.521384	Up	phosphatidylinositol 4-kinase alpha
PNISR	0.29356	0.000949	0.025072	3.311392	Up	PNN interacting serine and arginine rich protein
VWA1	0.293559	1.21E-05	0.000663	4.390089	Up	von Willebrand factor A domain containing 1
SLF2	0.293105	0.001924	0.043325	3.106845	Up	SMC5-SMC6 complex localization factor 2
RPS26	0.291732	0.001731	0.039825	3.138254	Up	ribosomal protein S26
GNAO1	0.291484	9.75E-05	0.004047	3.906537	Up	G protein subunit alpha o1
FRG1BP	0.29043	1.62E-06	0.000118	4.814235	Up	FSHD region gene 1 family member B, pseudogene
NISCH	0.290075	0.001675	0.038816	3.147863	Up	nischarin
RPL9P28	0.289842	5.89E-06	0.000364	4.545444	Up	ribosomal protein L9 pseudogene 28
DNMT1	0.28893	0.001047	0.026989	3.283586	Up	DNA methyltransferase 1
MCU	0.286565	3.79E-05	0.001812	4.131711	Up	mitochondrial calcium uniporter
USP27X	0.286159	6.61E-05	0.00288	4.000619	Up	ubiquitin specific peptidase 27 X-linked
HMGN1P38	0.283893	4.04E-05	0.001914	4.116729	Up	high mobility group nucleosome binding domain 1 pseudogene 3
CSKMT	0.282948	6.71E-10	9.95E-08	6.210615	Up	citrate synthase lysine methyltransferase
TOP1	0.282915	0.001545	0.036592	3.171551	Up	DNA topoisomerase I
HMGN2P1	0.282831	7.51E-08	7.59E-06	5.403866	Up	high mobility group nucleosomal binding domain 2 pseudogene 1
ITGB1P1	0.282659	3.68E-05	0.001762	4.138566	Up	integrin subunit beta 1 pseudogene 1
MYH9	0.282628	0.000727	0.020233	3.385935	Up	myosin heavy chain 9
SYNPO	0.282591	0.000189	0.006834	3.742144	Up	synaptopodin
ATP2A2	0.281957	0.000268	0.009104	3.652678	Up	ATPase sarcoplasmic/endoplasmic reticulum Ca2+ transporting 2
GAA	0.281659	0.000639	0.018255	3.421382	Up	glucosidase alpha, acid
RPL41P3	0.27995	8.82E-05	0.003691	3.931082	Up	ribosomal protein L41 pseudogene 3
TRA2A	0.277281	0.001453	0.034801	3.189385	Up	transformer 2 alpha homolog
LENG8	0.276588	2.02E-07	1.81E-05	5.220641	Up	leukocyte receptor cluster member 8
RPL41P5	0.275765	6.84E-05	0.002971	3.992301	Up	ribosomal protein L41 pseudogene 5
SFTPA1	0.275626	8.75E-06	0.000507	4.460364	Up	surfactant protein A1
PIKFYVE	0.274637	0.000963	0.025335	3.307282	Up	phosphoinositide kinase, FYVE-type zinc finger containing
CCDC18-	0.274441	0.000116	0.004629	3.864689	Up	CCDC18 antisense RNA 1

AS1							
PDXDC2P-NPIP14P	0.273908	7.52E-10	1.10E-07	6.192371	Up		nuclear pore complex-interacting protein
RPS25P2	0.270903	0.000144	0.005501	3.811211	Up		ribosomal protein S25 pseudogene 2
MAFG	0.270117	8.41E-05	0.00355	3.942689	Up		MAF bZIP transcription factor G
U2AF2	0.269571	4.77E-06	0.000306	4.590367	Up		U2 small nuclear RNA auxiliary factor 2
SLC35E2B	0.269373	0.001396	0.033793	3.201047	Up		solute carrier family 35 member E2B
LPCAT4	0.269036	0.001553	0.036725	3.169974	Up		lysophosphatidylcholineacyltransferase 4
ST14	0.268932	0.000611	0.017676	3.4335	Up		ST14 transmembrane serine protease matriptase
MIDN	0.268354	0.001768	0.040546	3.131976	Up		midnolin
HOOK3	0.267489	0.000813	0.022273	3.3547	Up		hook microtubule tethering protein 3
SLMO2-ATP5E	0.266988	0.000287	0.009625	3.635033	Up		SLMO2-ATP5E readthrough
HNRNPH1	0.266848	4.70E-05	0.002155	4.081502	Up		heterogeneous nuclear ribonucleoprotein H1
NBPF12	0.266768	0.000161	0.006013	3.781738	Up		NBPF member 12
CHCHD2P2	0.266572	0.000125	0.004922	3.845946	Up		coiled-coil-helix-coiled-coil-helix domain containing 2 pseudogene
TNRC6A	0.265649	0.001947	0.043688	3.103305	Up		trinucleotide repeat containing adaptor 6A
TCTN2	0.26518	0.001087	0.027652	3.273064	Up		tectonic family member 2
SSTR3	0.265012	0.000713	0.019968	3.391203	Up		somatostatin receptor 3
ZSWIM1	0.263879	0.000741	0.02051	3.380431	Up		zinc finger SWIM-type containing 1
FRG1JP	0.263268	2.50E-06	0.000176	4.725601	Up		FSHD region gene 1 family member J, pseudogene
WDR17	0.261331	4.58E-05	0.002116	4.087257	Up		WD repeat domain 17
LENG9	0.260459	3.41E-07	2.88E-05	5.120644	Up		leukocyte receptor cluster member 9
NPIPA5	0.259831	0.002296	0.049117	3.053895	Up		nuclear pore complex interacting protein family member A5
NUTM2B-AS1	0.258578	2.15E-08	2.39E-06	5.627528	Up		NUTM2B antisense RNA 1
FBXO44	0.25832	0.000637	0.018215	3.422177	Up		F-box protein 44
SIPA1L3	0.257457	0.000149	0.005669	3.80121	Up		signal induced proliferation associated 1 like 3
HMGB1	0.256879	0.000324	0.010682	3.602821	Up		high mobility group box 1
SRSF9P1	0.2564	0.000826	0.022518	3.350402	Up		serine and arginine rich splicing factor 9 pseudogene 1
ZXDC	0.256259	0.001081	0.027566	3.274523	Up		ZXD family zinc finger C
MAN2B2	0.255435	0.001141	0.028914	3.259015	Up		mannosidase alpha class 2B member 2
PPP1R37	0.255146	5.04E-08	5.24E-06	5.476299	Up		protein phosphatase 1 regulatory subunit 37
BCL2L2-PABPN1	0.254617	0.001768	0.040546	3.131995	Up		BCL2L2-PABPN1 readthrough
TSIX	0.254558	2.66E-06	0.000185	4.71253	Up		TSIX transcript, XIST antisense RNA
MAPT	0.254238	6.82E-05	0.002968	3.992839	Up		microtubule associated protein tau
ZCCHC3	0.254221	0.002036	0.045181	3.089951	Up		zinc finger CCHC-type containing 3
GANAB	0.25409	0.002052	0.045422	3.087678	Up		glucosidase II alpha subunit
RPL41	0.254	0.000141	0.005454	3.815092	Up		ribosomal protein L41
PABPN1	0.253521	0.000414	0.012957	3.538721	Up		poly(A) binding protein nuclear 1
NAA40	0.252484	0.001374	0.033347	3.205632	Up		N-alpha-acetyltransferase 40, NatD catalytic subunit
B4GALT5	0.25192	0.000256	0.00877	3.66459	Up		beta-1,4-galactosyltransferase 5
FGF7P8	0.251644	1.99E-07	1.80E-05	5.223331	Up		fibroblast growth factor 7 pseudogene 8
CELF3	0.250908	1.31E-06	9.78E-05	4.857361	Up		CUGBP Elav-like family member 3
PRKDC	0.250799	0.002059	0.045525	3.086656	Up		protein kinase, DNA-activated, catalytic subunit

HIVEP1	0.250042	0.000272	0.009236	3.64849	Up	HIVEP zinc finger 1
RGPD8	0.24914	0.001907	0.043055	3.109584	Up	RANBP2 like and GRIP domain containing 8
KIAA0895L	0.248637	0.000488	0.014793	3.494615	Up	KIAA0895 like
HSPA8P8	0.24862	1.86E-06	0.000135	4.785835	Up	heat shock protein family A (Hsp70) member 8 pseudogene 8
NOL3	0.24829	0.000537	0.01591	3.468422	Up	nucleolar protein 3
UBN2	0.248245	0.000515	0.015407	3.480027	Up	ubnuclein 2
SNORD3B-1	0.248082	0.000381	0.012093	3.560775	Up	small nucleolar RNA, C/D box 3B-1
SNRNP70	0.247862	0.000273	0.009258	3.647639	Up	small nuclear ribonucleoprotein U1 subunit 70
TMEM159	0.247826	0.001581	0.037269	3.164836	Up	transmembrane protein 159
RBM33	0.247317	0.00054	0.015947	3.467331	Up	RNA binding motif protein 33
MAGI1	0.247238	0.000332	0.010852	3.597094	Up	membrane associated guanylate kinase, WW and PDZ domain containing 1
NBPF14	0.247211	0.001434	0.034455	3.19339	Up	NBPF member 14
DLEU2	0.246246	8.88E-07	6.82E-05	4.93426	Up	deleted in lymphocytic leukemia 2
FURIN	0.244745	0.000255	0.00875	3.665756	Up	furin, paired basic amino acid cleaving enzyme
WIPF2	0.244272	0.001598	0.037518	3.161708	Up	WAS/WASL interacting protein family member 2
CEBPZOS	0.243736	8.63E-05	0.003624	3.936351	Up	CEBPZ opposite strand
UMAD1	0.243619	7.15E-09	8.79E-07	5.818704	Up	UBAP1-MVB12-associated (UMA) domain containing 1
SNORD3A	0.242038	0.001401	0.033856	3.20012	Up	small nucleolar RNA, C/D box 3A
RPL41P1	0.241074	0.000709	0.019887	3.392522	Up	ribosomal protein L41 pseudogene 1
HNRNPL	0.238866	0.002335	0.049809	3.048821	Up	heterogeneous nuclear ribonucleoprotein L
RCN1P2	0.238833	2.78E-08	3.03E-06	5.582827	Up	reticulocalbin 1 pseudogene 2
MCPH1	0.23857	0.001404	0.03387	3.199463	Up	microcephalin 1
HCFC1	0.23638	0.000831	0.022605	3.348725	Up	host cell factor C1
SNORA81	0.236326	0.001667	0.038738	3.149203	Up	small nucleolar RNA, H/ACA box 81
GTF2IRD2B	0.236128	0.000882	0.023688	3.331873	Up	GTF2I repeat domain containing 2B
CACNA1A	0.236076	0.000237	0.008278	3.684442	Up	calcium voltage-gated channel subunit alpha1 A
RPL17P43	0.235907	0.001354	0.032994	3.210008	Up	ribosomal protein L17 pseudogene 43
SYT7	0.235793	0.001196	0.030041	3.245613	Up	synaptotagmin 7
RNU4-1	0.235414	1.45E-07	1.35E-05	5.282363	Up	RNA, U4 small nuclear 1
GGCX	0.235237	0.00057	0.016729	3.452462	Up	gamma-glutamyl carboxylase
SLC35E2A	0.235195	4.42E-06	0.000287	4.606706	Up	solute carrier family 35 member E2A
RPL28	0.235141	0.001052	0.027103	3.282203	Up	ribosomal protein L28
TFAP4	0.233953	4.92E-07	4.01E-05	5.050106	Up	transcription factor AP-4
RGL2	0.233729	0.000372	0.011906	3.566824	Up	ral guanine nucleotide dissociation stimulator like 2
RPS10P28	0.233253	5.25E-05	0.002371	4.05504	Up	ribosomal protein S10 pseudogene 28
HIF1A-AS2	0.232811	0.002133	0.046648	3.076073	Up	HIF1A antisense RNA 2
SDK1	0.232184	7.32E-06	0.000438	4.498972	Up	sidekick cell adhesion molecule 1
SACS	0.231787	1.24E-05	0.000676	4.384897	Up	sacin molecular chaperone
ANKRD18A	0.231539	0.000601	0.017471	3.438099	Up	ankyrin repeat domain 18A
CITED2	0.230839	0.000156	0.005865	3.790214	Up	Cbp/p300 interacting transactivator with Glu/Asp rich carboxy-terminal domain 2
NFASC	0.230788	0.001249	0.031048	3.233128	Up	neurofascin
PTMAP2	0.229398	6.89E-05	0.002988	3.990659	Up	prothymosin alpha pseudogene 2

B2M	0.229397	0.00011	0.004435	3.877282	Up	beta-2-microglobulin
MLLT10P1	0.227392	0.000157	0.005881	3.789055	Up	MLLT10 pseudogene 1
SON	0.226282	0.00067	0.019007	3.408244	Up	SON DNA and RNA binding protein
GRAMD4	0.225983	1.02E-05	0.000579	4.426313	Up	GRAM domain containing 4
RPL7P26	0.225397	0.001237	0.0308	3.235995	Up	ribosomal protein L7 pseudogene 26
NAIPP4	0.225183	1.25E-05	0.00068	4.383041	Up	NAIP pseudogene 4
HMG2P2	0.224878	4.52E-05	0.002097	4.090238	Up	high mobility group nucleosomal binding domain 2 pseudogene 2
SLC18A2	0.224659	0.000375	0.011987	3.564422	Up	solute carrier family 18 member A2
RMST	0.222931	7.01E-05	0.003035	3.986416	Up	rhabdomyosarcoma 2 associated transcript
RGL3	0.222739	0.002037	0.045181	3.089792	Up	ral guanine nucleotide dissociation stimulator like 3
GLCCI1	0.222701	0.001726	0.039764	3.138972	Up	glucocorticoid induced 1
BRD1	0.222046	0.000113	0.004558	3.869823	Up	bromodomain containing 1
TRMT9B	0.221844	0.000241	0.008364	3.680367	Up	tRNA methyltransferase 9B (putative)
TMUB1	0.221765	1.99E-10	3.32E-08	6.403974	Up	transmembrane and ubiquitin like domain containing 1
CAPN12	0.221658	6.64E-06	0.000403	4.520024	Up	calpain 12
PRH1-PRR4	0.220566	1.06E-06	8.03E-05	4.898714	Up	PRH1-PRR4 readthrough
SEC22B3P	0.22003	0.000741	0.02051	3.3805	Up	SEC22 homolog B3, pseudogene
CSNK1G2	0.219891	1.66E-05	0.000873	4.320137	Up	casein kinase 1 gamma 2
TOP1P1	0.219441	8.76E-08	8.69E-06	5.375711	Up	DNA topoisomerase I pseudogene 1
FAR2P3	0.219075	0.000193	0.006941	3.736292	Up	fatty acyl-CoA reductase 2 pseudogene 3
SNORD81	0.217346	4.69E-07	3.84E-05	5.059332	Up	small nucleolar RNA, C/D box 81
SSBP4	0.215959	0.000126	0.004952	3.843425	Up	single stranded DNA binding protein 4
RNF152	0.21572	0.001042	0.026883	3.284896	Up	ring finger protein 152
MAP3K12	0.21505	0.000145	0.005541	3.808387	Up	mitogen-activated protein kinase kinasekinase 12
SNORD3C	0.214839	0.001336	0.032613	3.21374	Up	small nucleolar RNA, C/D box 3C
DEC2R2	0.214699	0.000783	0.021558	3.365327	Up	2,4-dienoyl-CoA reductase 2
PLXNB2	0.213714	0.000995	0.025904	3.298104	Up	plexin B2
MALAT1	0.213406	0.000199	0.007096	3.729056	Up	metastasis associated lung adenocarcinoma transcript 1
GUSBP1	0.213084	0.000158	0.005904	3.787054	Up	GUSB pseudogene 1
SKP1P1	0.211385	0.002069	0.045704	3.085136	Up	S-phase kinase associated protein 1 pseudogene 1
SLC6A17	0.211288	0.00018	0.006557	3.755057	Up	solute carrier family 6 member 17
NBPF20	0.211211	5.11E-06	0.000325	4.575956	Up	NBPF member 20
MPRIP	0.210727	0.000137	0.005318	3.82214	Up	myosin phosphatase Rho interacting protein
GUSBP15	0.208689	4.07E-06	0.000267	4.623875	Up	GUSB pseudogene 15
FAM3C2P	0.208395	0.000153	0.005784	3.794913	Up	FAM3C pseudogene
BCL6	0.208367	0.000947	0.02506	3.312116	Up	BCL6 transcription repressor
PCDHB@	0.208149	5.35E-08	5.55E-06	5.465433	Up	protocadherin beta cluster
RAI1	0.208006	2.11E-05	0.00108	4.265645	Up	retinoic acid induced 1
SSR4	0.207945	1.34E-05	0.000725	4.36696	Up	signal sequence receptor subunit 4
RPL17P27	0.20794	1.52E-05	0.000812	4.339099	Up	ribosomal protein L17 pseudogene 27
AHDC1	0.207521	4.72E-05	0.002166	4.08009	Up	AT-hook DNA binding motif containing 1
TAOK2	0.207402	8.16E-09	9.90E-07	5.796083	Up	TAO kinase 2
SEMA6A	0.207007	0.000529	0.015773	3.472621	Up	semaphorin 6A

BMP6	0.204439	0.000316	0.010464	3.6098	Up	bone morphogenetic protein 6
UBE2Q2P2	0.204437	1.27E-08	1.48E-06	5.72047	Up	ubiquitin conjugating enzyme E2 Q2 pseudogene 2
NUTM2A-AS1	0.204424	0.000229	0.008024	3.693144	Up	NUTM2A antisense RNA 1
ECHDC3	0.203215	0.000484	0.014716	3.496864	Up	enoyl-CoA hydratase domain containing 3
AQP4-AS1	0.202953	1.16E-09	1.62E-07	6.122413	Up	AQP4 antisense RNA 1
RPS15AP19	0.202443	0.001846	0.041914	3.11914	Up	ribosomal protein S15a pseudogene 19
PRR34-AS1	0.200773	0.000176	0.006476	3.7594	Up	PRR34 antisense RNA 1
RPS10P5	0.200553	2.91E-05	0.001438	4.19248	Up	ribosomal protein S10 pseudogene 5
RGPD6	0.199989	0.001197	0.030046	3.245374	Up	RANBP2 like and GRIP domain containing 6
SHISAL1	0.197634	0.00028	0.009449	3.64166	Up	shisa like 1
IGL	0.197544	4.03E-13	9.66E-11	7.315782	Up	immunoglobulin lambda locus
KLF13	0.196919	0.000107	0.004348	3.882936	Up	Kruppel like factor 13
BMS1P2	0.195776	1.10E-05	0.000614	4.410205	Up	BMS1 pseudogene 2
TMEM132B	0.194815	0.00167	0.038738	3.148813	Up	transmembrane protein 132B
RPPH1	0.194633	0.002317	0.049512	3.051134	Up	ribonuclease P RNA component H1
NPIP11	0.193989	0.000254	0.00875	3.666089	Up	nuclear pore complex interacting protein family member B11
APOL4	0.193418	7.23E-07	5.68E-05	4.97506	Up	apolipoprotein L4
GUSBP2	0.19337	3.43E-07	2.89E-05	5.119674	Up	GUSB pseudogene 2
ZNF783	0.19295	0.000805	0.022098	3.357453	Up	zinc finger family member 783
ND1	0.192877	1.05E-05	0.000591	4.420561	Up	NADH dehydrogenase subunit 1
LERFS	0.192725	1.71E-05	0.000896	4.313417	Up	lncRNA negative regulator of fibroblast-like synovocyte migration SYNCRIP interacting
RPL21P1	0.190925	2.01E-07	1.81E-05	5.221398	Up	ribosomal protein L21 pseudogene 1
EP300-AS1	0.190833	0.002201	0.047756	3.066616	Up	EP300 antisense RNA 1
FGF7P6	0.190229	8.41E-08	8.39E-06	5.383119	Up	fibroblast growth factor 7 pseudogene 6
RPL23A	0.189109	0.000144	0.005504	3.810805	Up	ribosomal protein L23a
RPS2P46	0.188953	0.000725	0.020213	3.386403	Up	ribosomal protein S2 pseudogene 46
TMEM79	0.188926	2.42E-05	0.001231	4.234237	Up	transmembrane protein 79
RGPD4	0.188137	0.000627	0.017999	3.426676	Up	RANBP2 like and GRIP domain containing 4
MZF1	0.188005	0.000636	0.018215	3.422572	Up	myeloid zinc finger 1
NAIPP2	0.187962	4.05E-05	0.001918	4.115953	Up	NAIP pseudogene 2
DPH6-DT	0.187939	5.50E-08	5.68E-06	5.460291	Up	DPH6 divergent transcript
STXBP5-AS1	0.187044	7.73E-09	9.41E-07	5.805367	Up	STXBP5 antisense RNA 1
KSR2	0.186677	0.000251	0.008648	3.669911	Up	kinase suppressor of ras 2
HMG1P36	0.186039	0.000422	0.013151	3.533456	Up	high mobility group nucleosome binding domain 1 pseudogene 36
ZZEF1	0.185636	0.000801	0.022003	3.358852	Up	zinc finger ZZ-type and EF-hand domain containing 1
CRYZL2P	0.185381	0.000481	0.014646	3.498588	Up	crystallin zeta like 2, pseudogene
RNA18SP2	0.184869	0.001151	0.029127	3.256539	Up	RNA, 18S ribosomal pseudogene 2
INTS6L	0.18451	0.00123	0.030695	3.237545	Up	integrator complex subunit 6 like
NCOR2	0.18356	0.001336	0.032613	3.213779	Up	nuclear receptor corepressor 2
PDCD6IPP2	0.183477	4.65E-06	0.0003	4.595975	Up	PDCD6IP pseudogene 2
TENM3	0.183004	0.001545	0.036592	3.171473	Up	teneurintransmembrane protein 3
SUZ12P1	0.182867	0.000172	0.00634	3.765502	Up	SUZ12 pseudogene 1

TRNC	-1.77362	2.96E-28	3.42E-25	-11.2376	Down	tRNA
MTND4P24	-1.63404	2.54E-40	8.06E-37	-13.6713	Down	MT-ND4 pseudogene 24
RPS4Y1	-1.52484	3.15E-17	1.27E-14	-8.53724	Down	ribosomal protein S4 Y-linked 1
RPL7P47	-1.39853	3.96E-46	2.51E-42	-14.7268	Down	ribosomal protein L7 pseudogene 47
SST	-1.34161	2.00E-12	4.36E-10	-7.09024	Down	somatostatin
MICOS10P3	-1.21011	3.05E-45	1.66E-41	-14.5694	Down	MICOS10 pseudogene 3
PTBP2	-1.15934	2.89E-15	9.25E-13	-7.97449	Down	polypyrimidine tract binding protein 2
FXVD2	-1.14088	2.40E-10	3.93E-08	-6.37418	Down	FXVD domain containing ion transport regulator 2
RPL36AP21	-1.06563	1.39E-37	3.79E-34	-13.1509	Down	ribosomal protein L36a pseudogene 21
RPS27AP16	-1.04028	3.49E-34	8.31E-31	-12.4815	Down	RPS27A pseudogene 16
EEF1A1P9	-1.02205	1.57E-41	6.65E-38	-13.896	Down	eukaryotic translation elongation factor 1 alpha 1 pseudogene 9
FXVD6-FXVD2	-0.98977	7.09E-20	3.90E-17	-9.24787	Down	FXVD6-FXVD2 readthrough
TRNS1	-0.98749	7.65E-23	5.83E-20	-9.99138	Down	tRNA
FTL	-0.97976	1.26E-48	9.61E-45	-15.1633	Down	ferritin light chain
TRNT	-0.97078	3.84E-11	7.09E-09	-6.65679	Down	tRNA
SAR1A	-0.95721	7.68E-14	1.98E-11	-7.54275	Down	secretion associated Ras related GTPase 1A
MTND1P23	-0.95118	3.03E-16	1.09E-13	-8.25971	Down	MT-ND1 pseudogene 23
RPL10P8	-0.89287	1.50E-31	2.85E-28	-11.9424	Down	ribosomal protein L10 pseudogene 8
RPL10P15	-0.88648	2.06E-31	3.57E-28	-11.9134	Down	ribosomal protein L10 pseudogene 15
TUBA4A	-0.87452	6.14E-10	9.14E-08	-6.22497	Down	tubulin alpha 4a
RPS3AP47	-0.85603	4.27E-29	5.61E-26	-11.4208	Down	RPS3A pseudogene 47
MT2A	-0.854	3.62E-06	0.000242	-4.64829	Down	metallothionein 2A
IFI30	-0.853	4.26E-07	3.50E-05	-5.07814	Down	IFI30 lysosomal thioredoxin reductase
CNOT6L	-0.84121	8.91E-14	2.25E-11	-7.5226	Down	CCR4-NOT transcription complex subunit 6 like
RBP4	-0.83075	2.80E-06	0.000193	-4.70201	Down	retinol binding protein 4
PSPHP1	-0.81912	1.37E-36	3.48E-33	-12.9582	Down	phosphoserine phosphatase pseudogene 1
RPL36AP50	-0.80991	2.82E-29	3.98E-26	-11.4599	Down	ribosomal protein L36a pseudogene 50
IAPP	-0.80147	0.001218	0.030454	-3.24037	Down	islet amyloid polypeptide
TRNM	-0.79749	1.58E-10	2.69E-08	-6.43952	Down	tRNA
GPX2	-0.7926	5.62E-09	7.00E-07	-5.85966	Down	glutathione peroxidase 2
GSTP1	-0.77863	2.04E-07	1.82E-05	-5.21866	Down	glutathione S-transferase pi 1
HSPE1P4	-0.77559	2.02E-17	8.47E-15	-8.59047	Down	heat shock protein family E (Hsp10) member 1 pseudogene 4
RPL7P23	-0.77025	4.92E-22	3.47E-19	-9.7938	Down	ribosomal protein L7 pseudogene 23
FTLP2	-0.76845	1.04E-32	2.08E-29	-12.1821	Down	ferritin light chain pseudogene 2
RPS10P11	-0.76409	7.76E-25	7.39E-22	-10.4653	Down	ribosomal protein S10 pseudogene 11
RPL10P16	-0.75141	6.66E-23	5.29E-20	-10.006	Down	ribosomal protein L10 pseudogene 16
RPL7P15	-0.74852	9.29E-25	8.64E-22	-10.4469	Down	ribosomal protein L7 pseudogene 15
IFI27L2	-0.73744	5.50E-07	4.41E-05	-5.02851	Down	interferon alpha inducible protein 27 like 2
MTCH2	-0.73219	1.95E-07	1.77E-05	-5.22718	Down	mitochondrial carrier 2
VAMP8	-0.72844	5.75E-06	0.000356	-4.55081	Down	vesicle associated membrane protein 8
SAT1	-0.72797	4.97E-05	0.002261	-4.06799	Down	spermidine/spermine N1-acetyltransferase 1
HEPACAM2	-0.72721	5.28E-06	0.000333	-4.56887	Down	HEPACAM family member 2

RPL23AP18	-0.72679	2.55E-28	3.03E-25	-11.2519	Down	ribosomal protein L23a pseudogene 18
FTLP3	-0.72647	5.14E-24	4.35E-21	-10.2724	Down	ferritin light chain pseudogene 3
PSMB7	-0.72557	6.67E-06	0.000403	-4.51911	Down	proteasome 20S subunit beta 7
CYB5A	-0.71038	5.49E-06	0.000343	-4.56075	Down	cytochrome b5 type A
RPS3AP5	-0.70819	1.67E-24	1.52E-21	-10.3872	Down	RPS3A pseudogene 5
TRNR	-0.70395	2.11E-11	4.02E-09	-6.7464	Down	tRNA
TRNN	-0.69791	9.90E-10	1.41E-07	-6.14787	Down	tRNA
UQCC2	-0.6969	1.74E-08	1.94E-06	-5.66516	Down	ubiquinol-cytochrome c reductase complex assembly factor 2
ETFB	-0.68813	2.38E-07	2.10E-05	-5.18969	Down	electron transfer flavoprotein subunit beta
RPL7P9	-0.67807	7.17E-20	3.90E-17	-9.24666	Down	ribosomal protein L7 pseudogene 9
SCGN	-0.67616	8.32E-12	1.62E-09	-6.88425	Down	secretagogin, EF-hand calcium binding protein
USP22	-0.67594	9.10E-08	8.98E-06	-5.3686	Down	ubiquitin specific peptidase 22
RPL18AP6	-0.673	7.00E-19	3.56E-16	-8.98679	Down	ribosomal protein L18a pseudogene 6
RPS3AP6	-0.6723	4.56E-26	4.83E-23	-10.7487	Down	RPS3A pseudogene 6
RPL7P48	-0.66897	1.60E-31	2.90E-28	-11.9365	Down	ribosomal protein L7 pseudogene 48
DDIT3	-0.66778	0.000116	0.004629	-3.86483	Down	DNA damage inducible transcript 3
TMEM251	-0.66466	2.36E-06	0.000168	-4.73668	Down	transmembrane protein 251
PIIB	-0.66306	7.39E-09	9.05E-07	-5.81316	Down	peptidylprolyl isomerase B
RTF2	-0.66116	8.35E-06	0.000487	-4.4707	Down	replication termination factor 2
RPS28	-0.66076	7.58E-09	9.26E-07	-5.80867	Down	ribosomal protein S28
RPS15P4	-0.65935	1.09E-17	4.71E-15	-8.66474	Down	ribosomal protein S15 pseudogene 4
CAMK2D	-0.6557	9.94E-07	7.54E-05	-4.91195	Down	calcium/calmodulin dependent protein kinase II delta
G6PC2	-0.65506	0.00039	0.012347	-3.55439	Down	glucose-6-phosphatase catalytic subunit 2
MTND2P28	-0.65118	3.00E-29	4.08E-26	-11.4541	Down	MT-ND2 pseudogene 28
RPL31P4	-0.64938	1.01E-18	5.02E-16	-8.94381	Down	ribosomal protein L31 pseudogene 4
RPL7P1	-0.6445	1.09E-20	6.91E-18	-9.45702	Down	ribosomal protein L7 pseudogene 1
MTRNR2L12	-0.64341	1.39E-15	4.66E-13	-8.06759	Down	MT-RNR2 like 12
DDX3Y	-0.64255	2.87E-08	3.11E-06	-5.57705	Down	DEAD-box helicase 3 Y-linked
HSPE1P2	-0.63929	3.16E-17	1.27E-14	-8.53666	Down	heat shock protein family E (Hsp10) member 1 pseudogene 2
DRG1	-0.63917	1.78E-05	0.000934	-4.30352	Down	developmentally regulated GTP binding protein 1
BCAP31	-0.63727	1.64E-06	0.00012	-4.81112	Down	B cell receptor associated protein 31
ASAH1	-0.63454	5.46E-07	4.39E-05	-5.02989	Down	N-acylsphingosineamidohydrolase 1
RPL15P22	-0.63241	5.45E-22	3.71E-19	-9.78276	Down	ribosomal protein L15 pseudogene 22
RPL9	-0.6246	7.19E-11	1.30E-08	-6.56128	Down	ribosomal protein L9
ATP6V1B2	-0.6243	3.01E-05	0.001473	-4.18461	Down	ATPase H ⁺ transporting V1 subunit B2
DNAJC15	-0.62222	1.82E-07	1.67E-05	-5.24021	Down	DnaJ heat shock protein family (Hsp40) member C15
VPS25	-0.62201	0.000145	0.005536	-3.80889	Down	vacuolar protein sorting 25 homolog
EIF1AY	-0.61644	9.39E-06	0.000539	-4.44517	Down	eukaryotic translation initiation factor 1A Y-linked
MTCO2P2	-0.61625	2.69E-10	4.29E-08	-6.3561	Down	MT-CO2 pseudogene 2
ATP5PB	-0.61548	1.03E-05	0.00058	-4.42551	Down	ATP synthase peripheral stalk-membrane subunit b
CDC42BPA	-0.61283	1.36E-07	1.28E-05	-5.29439	Down	CDC42 binding protein kinase alpha
RPS28P5	-0.61031	6.23E-18	2.76E-15	-8.73101	Down	ribosomal protein S28 pseudogene 5
PSMC4	-0.60897	6.83E-06	0.000413	-4.51375	Down	proteasome 26S subunit, ATPase 4

TMED6	-0.60771	9.42E-06	0.000541	-4.44438	Down	transmembrane p24 trafficking protein 6
ATP6V1D	-0.6077	1.27E-05	0.000688	-4.37972	Down	ATPase H ⁺ transporting V1 subunit D
CSNK2B	-0.5997	4.56E-05	0.00211	-4.08843	Down	casein kinase 2 beta
ATP5MGP3	-0.59951	4.20E-31	6.66E-28	-11.8487	Down	ATP synthase membrane subunit g pseudogene 3
RPL7P6	-0.59715	2.27E-14	6.61E-12	-7.70542	Down	ribosomal protein L7 pseudogene 6
RPL10P4	-0.59686	4.53E-23	3.67E-20	-10.0465	Down	ribosomal protein L10 pseudogene 4
UCHL1	-0.59269	0.000312	0.010351	-3.61311	Down	ubiquitin C-terminal hydrolase L1
RPS3AP20	-0.59121	3.37E-15	1.06E-12	-7.95458	Down	RPS3A pseudogene 20
PSMC5	-0.58847	8.30E-05	0.003511	-3.94587	Down	proteasome 26S subunit, ATPase 5
SLC25A5	-0.5873	1.15E-05	0.000636	-4.40117	Down	solute carrier family 25 member 5
EEF1A1P22	-0.58354	1.63E-30	2.48E-27	-11.7245	Down	eukaryotic translation elongation factor 1 alpha 1 pseudogene 22
RPL36AP28	-0.583	1.63E-20	9.99E-18	-9.4125	Down	ribosomal protein L36a pseudogene 28
MTND4P12	-0.58279	1.19E-07	1.13E-05	-5.31953	Down	MT-ND4 pseudogene 12
TRNA	-0.58124	5.61E-06	0.000349	-4.55591	Down	tRNA
ATXN7L3B	-0.58007	1.14E-05	0.000635	-4.40204	Down	ataxin 7 like 3B
RPS3AP26	-0.57945	6.02E-20	3.47E-17	-9.26636	Down	RPS3A pseudogene 26
RPS3AP25	-0.57923	3.64E-17	1.43E-14	-8.51968	Down	RPS3A pseudogene 25
NDUFA9	-0.57851	0.000257	0.008787	-3.66369	Down	NADH:ubiquinoneoxidoreductase subunit A9
PPT1	-0.57828	5.19E-05	0.00235	-4.05774	Down	palmitoyl-protein thioesterase 1
RPL39P12	-0.57444	6.47E-20	3.68E-17	-9.25824	Down	ribosomal protein L39 pseudogene 12
PIR	-0.57417	2.96E-08	3.19E-06	-5.57147	Down	pirin
SMIM24	-0.57307	0.001082	0.027582	-3.27417	Down	small integral membrane protein 24
MLLT11	-0.57118	0.000157	0.005885	-3.78811	Down	MLLT11 transcription factor 7 cofactor
SARS1	-0.57061	1.97E-05	0.001015	-4.28162	Down	seryl-tRNA synthetase 1
RPS3AP43	-0.56793	1.94E-28	2.38E-25	-11.2779	Down	RPS3A pseudogene 43
CYCSP3	-0.56658	5.64E-20	3.31E-17	-9.27361	Down	CYCS pseudogene 3
H3C9P	-0.56451	3.49E-14	9.78E-12	-7.64852	Down	H3 clustered histone 9, pseudogene
TMEM106C	-0.56259	0.000319	0.010533	-3.60736	Down	transmembrane protein 106C
SSR2	-0.55671	0.000192	0.006896	-3.73845	Down	signal sequence receptor subunit 2
ARRDC3	-0.55364	0.00106	0.02724	-3.2801	Down	arrestin domain containing 3
TSPYL5	-0.55266	1.21E-05	0.000665	-4.38914	Down	TSPY like 5
PCP4	-0.55085	0.002036	0.045181	-3.09	Down	Purkinje cell protein 4
RPS3AP49	-0.55006	2.35E-15	7.66E-13	-8.00083	Down	RPS3A pseudogene 49
RPS15P2	-0.549	1.65E-18	7.94E-16	-8.88751	Down	ribosomal protein S15 pseudogene 2
TRNI	-0.54667	8.09E-07	6.24E-05	-4.95275	Down	tRNA
ARL6IP1	-0.54562	3.77E-06	0.00025	-4.64007	Down	ADP ribosylation factor like GTPase 6 interacting protein 1
TOX4	-0.54494	2.01E-05	0.001033	-4.27692	Down	TOX high mobility group box family member 4
TSPAN7	-0.54452	0.000324	0.010678	-3.60314	Down	tetraspanin 7
PSMD7	-0.54222	0.000107	0.004344	-3.88352	Down	proteasome 26S subunit, non-ATPase 7
RPL7P32	-0.54052	8.14E-11	1.47E-08	-6.5422	Down	ribosomal protein L7 pseudogene 32
TIMM17A	-0.54025	0.000255	0.008766	-3.665	Down	translocase of inner mitochondrial membrane 17A
BLVRB	-0.54014	0.000126	0.004954	-3.84307	Down	biliverdin reductase B
ATP5F1C	-0.53933	3.79E-05	0.001813	-4.13132	Down	ATP synthase F1 subunit gamma

RPS3AP21	-0.53899	8.90E-16	3.06E-13	-8.12441	Down	RPS3A pseudogene 21
SH3BGRL3	-0.53822	0.00021	0.007439	-3.7151	Down	SH3 domain binding glutamate rich protein like 3
PRPS2	-0.53753	1.61E-05	0.000854	-4.32634	Down	phosphoribosyl pyrophosphate synthetase 2
MRPL54	-0.53538	7.10E-05	0.003065	-3.98335	Down	mitochondrial ribosomal protein L54
RPS27P17	-0.53464	5.03E-10	7.64E-08	-6.25691	Down	ribosomal protein S27 pseudogene 17
NDUFA12	-0.53433	0.000142	0.005463	-3.81407	Down	NADH:ubiquinoneoxidoreductase subunit A12
ATP6V1E1	-0.53365	4.65E-05	0.002136	-4.08386	Down	ATPase H ⁺ transporting V1 subunit E1
GRAMD2B	-0.53356	6.07E-06	0.000373	-4.53906	Down	GRAM domain containing 2B
EEF1A1P12	-0.53355	1.28E-16	4.78E-14	-8.36634	Down	eukaryotic translation elongation factor 1 alpha 1 pseudogene 12
RAB21	-0.53177	0.000551	0.016223	-3.46142	Down	RAB21, member RAS oncogene family
PRDX1	-0.53131	0.000179	0.006553	-3.7557	Down	peroxiredoxin 1
CTSA	-0.53115	0.000232	0.008132	-3.68947	Down	cathepsin A
NIT2	-0.5293	0.000342	0.011123	-3.58859	Down	nitrilase family member 2
BUD23	-0.52874	0.000609	0.017618	-3.4346	Down	BUD23 rRNAmethyltransferase and ribosome maturation factor
ATP5MC1	-0.52481	0.000345	0.011201	-3.58632	Down	ATP synthase membrane subunit c locus 1
LCLAT1	-0.5244	0.000507	0.015249	-3.48434	Down	lysocardiolipinacyltransferase 1
UBE2L5	-0.52356	7.34E-25	7.17E-22	-10.4708	Down	ubiquitin conjugating enzyme E2 L5
MPC1	-0.52344	0.00043	0.013381	-3.52817	Down	mitochondrial pyruvate carrier 1
PSMD6	-0.52003	0.000256	0.00877	-3.66442	Down	proteasome 26S subunit, non-ATPase 6
CLIC1	-0.51993	0.000285	0.009599	-3.63672	Down	chloride intracellular channel 1
THYN1	-0.51925	0.000518	0.015496	-3.47825	Down	thymocyte nuclear protein 1
GBA	-0.5191	5.82E-05	0.002587	-4.03081	Down	glucosylceramidase beta
ENO1	-0.51877	5.03E-05	0.002282	-4.06521	Down	enolase 1
ESD	-0.51809	0.000908	0.024302	-3.3237	Down	esterase D
REEP5	-0.51715	5.99E-05	0.002652	-4.02406	Down	receptor accessory protein 5
FDPS	-0.517	0.001077	0.027473	-3.27569	Down	farnesyl diphosphate synthase
IDH1	-0.51672	0.000105	0.004267	-3.88938	Down	isocitrate dehydrogenase (NADP(+)) 1
HOPX	-0.51644	0.000233	0.008144	-3.68887	Down	HOP homeobox
PSMB5	-0.51427	1.91E-05	0.000988	-4.28861	Down	proteasome 20S subunit beta 5
RPS24P8	-0.514	4.58E-14	1.23E-11	-7.61222	Down	ribosomal protein S24 pseudogene 8
MRPS35	-0.51317	0.000385	0.012208	-3.55761	Down	mitochondrial ribosomal protein S35
XRCC6	-0.51246	0.000184	0.006687	-3.74862	Down	X-ray repair cross complementing 6
PSMB3	-0.51184	0.000277	0.009386	-3.64385	Down	proteasome 20S subunit beta 3
PRDX6	-0.50942	0.000566	0.016615	-3.45453	Down	peroxiredoxin 6
ZNF165	-0.50861	7.86E-05	0.00335	-3.95886	Down	zinc finger protein 165
NDUFV3	-0.50647	9.19E-06	0.00053	-4.44984	Down	NADH:ubiquinoneoxidoreductase subunit V3
CLU	-0.50421	6.46E-06	0.000395	-4.5257	Down	clusterin
RPL36API3	-0.50417	1.36E-08	1.57E-06	-5.70845	Down	ribosomal protein L36a pseudogene 13
CDV3	-0.50276	0.000495	0.014945	-3.49079	Down	CDV3 homolog
GLMP	-0.50089	9.28E-06	0.000534	-4.44771	Down	glycosylated lysosomal membrane protein
PLEKHB2	-0.49916	0.000221	0.007817	-3.70172	Down	pleckstrin homology domain containing B2
MDH2	-0.4975	0.000106	0.004325	-3.88529	Down	malate dehydrogenase 2
EIF3K	-0.49682	0.000537	0.015906	-3.46886	Down	eukaryotic translation initiation factor 3 subunit K

TTR	-0.49514	0.000355	0.011452	-3.57891	Down	transthyretin
SDR39U1	-0.4931	0.000303	0.010084	-3.62108	Down	short chain dehydrogenase/reductase family 39U member 1
PTGR2	-0.49288	4.28E-05	0.001999	-4.10344	Down	prostaglandin reductase 2
NME2P1	-0.49286	2.14E-11	4.05E-09	-6.74477	Down	NME2 pseudogene 1
GNPDA1	-0.49283	0.00027	0.009154	-3.65102	Down	glucosamine-6-phosphate deaminase 1
GHITM	-0.49196	0.000345	0.011198	-3.58661	Down	growth hormone inducible transmembrane protein
HPF1	-0.48964	8.15E-05	0.003454	-3.95012	Down	histone PARylation factor 1
GRB2	-0.48936	0.000667	0.018939	-3.40943	Down	growth factor receptor bound protein 2
RPL10P9	-0.48309	4.59E-14	1.23E-11	-7.61179	Down	ribosomal protein L10 pseudogene 9
EEF1A1P16	-0.47667	2.13E-20	1.29E-17	-9.38232	Down	eukaryotic translation elongation factor 1 alpha 1 pseudogene 16
MT1E	-0.47613	0.001443	0.034584	-3.19157	Down	metallothionein 1E
RAB3B	-0.47506	1.69E-08	1.91E-06	-5.66984	Down	RAB3B, member RAS oncogene family
RPS27AP5	-0.47453	6.60E-12	1.32E-09	-6.91798	Down	ribosomal protein S27a pseudogene 5
RPL7P44	-0.47441	1.63E-19	8.49E-17	-9.15395	Down	ribosomal protein L7 pseudogene 44
MDH1	-0.47432	7.70E-05	0.0033	-3.9638	Down	malate dehydrogenase 1
RPL34P18	-0.47406	8.45E-10	1.22E-07	-6.17359	Down	ribosomal protein L34 pseudogene 18
ATP5PO	-0.4708	0.000403	0.012677	-3.54563	Down	ATP synthase peripheral stalk subunit OSCP
POLR3K	-0.47059	0.000999	0.025998	-3.29689	Down	RNA polymerase III subunit K
UBE2L6	-0.47009	0.00024	0.008347	-3.68111	Down	ubiquitin conjugating enzyme E2 L6
CYSTM1	-0.46993	7.92E-06	0.000464	-4.48191	Down	cysteine rich transmembrane module containing 1
C11orf54	-0.46706	4.56E-05	0.002111	-4.08812	Down	chromosome 11 open reading frame 54
TRAPPC2L	-0.46693	0.000315	0.01046	-3.61013	Down	trafficking protein particle complex 2 like
PSMA4	-0.46531	0.00229	0.049022	-3.05465	Down	proteasome 20S subunit alpha 4
SCD	-0.46504	5.38E-06	0.000337	-4.56473	Down	stearoyl-CoA desaturase
KLHL41	-0.46491	0.000341	0.011089	-3.58963	Down	kelch like family member 41
REG1A	-0.46408	0.000123	0.004868	-3.84948	Down	regenerating family member 1 alpha
COX6CP1	-0.46393	1.80E-14	5.44E-12	-7.73651	Down	cytochrome c oxidase subunit 6C pseudogene 1
RPL27AP6	-0.4626	8.86E-13	2.00E-10	-7.20572	Down	ribosomal protein L27a pseudogene 6
PIGP	-0.46187	0.001669	0.038738	-3.14901	Down	phosphatidylinositol glycan anchor biosynthesis class P
SUCLG1	-0.46129	0.002025	0.045059	-3.09164	Down	succinate-CoA ligase GDP/ADP-forming subunit alpha
NAPA	-0.46093	0.000225	0.007921	-3.69787	Down	NSF attachment protein alpha
RPL31P17	-0.46077	7.57E-17	2.94E-14	-8.43059	Down	ribosomal protein L31 pseudogene 17
VAT1	-0.45987	0.000289	0.009676	-3.63335	Down	vesicle amine transport 1
TXN2	-0.45817	0.001775	0.040657	-3.13085	Down	thioredoxin 2
HSPE1P3	-0.45727	5.89E-08	6.02E-06	-5.44795	Down	heat shock protein family E (Hsp10) member 1 pseudogene 3
GAPDHP65	-0.4563	2.40E-23	1.99E-20	-10.1128	Down	glyceraldehyde 3 phosphate dehydrogenase pseudogene 65
NTPCR	-0.45604	0.001094	0.027791	-3.27126	Down	nucleoside-triphosphatase, cancer-related
UBE2B	-0.45399	0.000398	0.012573	-3.54868	Down	ubiquitin conjugating enzyme E2 B
PRXL2A	-0.45369	0.000318	0.010512	-3.60839	Down	peroxiredoxin like 2A
CUTA	-0.45315	7.51E-06	0.000446	-4.49344	Down	cutA divalent cation tolerance homolog
HMGB1P37	-0.45312	7.75E-16	2.71E-13	-8.14189	Down	high mobility group box 1 pseudogene 37
RPS28P9	-0.45125	5.57E-11	1.03E-08	-6.60005	Down	ribosomal protein S28 pseudogene 9
GTF2A2	-0.45055	0.001522	0.036218	-3.17589	Down	general transcription factor IIA subunit 2

TUBAP2	-0.44961	3.55E-11	6.59E-09	-6.66865	Down	tubulin alpha pseudogene 2
DAP	-0.44955	0.000957	0.025228	-3.30906	Down	death associated protein
ACADM	-0.44797	0.000544	0.016041	-3.46532	Down	acyl-CoA dehydrogenase medium chain
CAP1	-0.44673	0.000409	0.012847	-3.54164	Down	cyclase associated actin cytoskeleton regulatory protein 1
TXN	-0.44586	2.22E-06	0.000159	-4.7498	Down	thioredoxin
RPS7P10	-0.44374	1.44E-12	3.15E-10	-7.13738	Down	ribosomal protein S7 pseudogene 10
SNRPGP2	-0.44352	3.36E-14	9.47E-12	-7.65374	Down	small nuclear ribonucleoprotein polypeptide G pseudogene 2
ERICH5	-0.44351	3.42E-05	0.001648	-4.15554	Down	glutamate rich 5
BLVRA	-0.44243	0.001061	0.02724	-3.27981	Down	biliverdinreductase A
TMEM68	-0.44224	5.75E-05	0.00256	-4.03387	Down	transmembrane protein 68
PSMB2	-0.43901	5.92E-05	0.002626	-4.02675	Down	proteasome 20S subunit beta 2
SCAMP3	-0.43891	0.001131	0.028674	-3.26177	Down	secretory carrier membrane protein 3
EEF1A1P13	-0.43853	4.07E-13	9.68E-11	-7.31458	Down	eukaryotic translation elongation factor 1 alpha 1 pseudogene 13
COA3	-0.43703	0.000143	0.005485	-3.81233	Down	cytochrome c oxidase assembly factor 3
DYNLRB1	-0.43637	1.69E-05	0.000887	-4.31608	Down	dynein light chain roadblock-type 1
UQCRH	-0.43618	0.002156	0.047054	-3.0729	Down	ubiquinol-cytochrome c reductase hinge protein
SUMO2P6	-0.43513	3.86E-15	1.21E-12	-7.93714	Down	SUMO2 pseudogene 6
MGST3	-0.43337	0.00065	0.018518	-3.41644	Down	microsomal glutathione S-transferase 3
MRPS15	-0.43316	0.001656	0.038561	-3.15123	Down	mitochondrial ribosomal protein S15
LAMTOR1	-0.43303	0.002161	0.047092	-3.07219	Down	late endosomal/lysosomal adaptor, MAPK and MTOR activator 1
GLUL	-0.43294	7.24E-05	0.003116	-3.97875	Down	glutamate-ammonia ligase
PCMTD2	-0.43114	0.001587	0.037393	-3.16369	Down	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2
UBE2V1P2	-0.43098	2.04E-07	1.82E-05	-5.21844	Down	UBE2V1 pseudogene 2
RPL23AP12	-0.43088	9.29E-20	4.92E-17	-9.21739	Down	ribosomal protein L23a pseudogene 12
NEU1	-0.43082	0.00205	0.045422	-3.08791	Down	neuraminidase 1
ALG3	-0.43078	4.08E-05	0.001927	-4.11456	Down	ALG3 alpha-1,3- mannosyltransferase
ORC3	-0.4304	0.001385	0.033567	-3.20336	Down	origin recognition complex subunit 3
GTF2B	-0.42837	0.001243	0.030925	-3.23465	Down	general transcription factor IIB
RPS27AP11	-0.428	5.01E-12	1.03E-09	-6.95828	Down	RPS27A pseudogene 11
EXOSC1	-0.42776	0.000601	0.017471	-3.43796	Down	exosome component 1
RPL6P19	-0.42775	4.72E-12	9.79E-10	-6.96692	Down	ribosomal protein L6 pseudogene 19
FARSA	-0.42724	0.000306	0.010171	-3.61814	Down	phenylalanyl-tRNA synthetase subunit alpha
FKBP1C	-0.42718	4.00E-08	4.21E-06	-5.51775	Down	FKBP prolyl isomerase 1C
SNORD58B	-0.42684	4.16E-09	5.30E-07	-5.91065	Down	small nucleolar RNA, C/D box 58B
SVBP	-0.42653	4.18E-05	0.001968	-4.10879	Down	small vasohibin binding protein
NR0B2	-0.42613	0.000402	0.012666	-3.54647	Down	nuclear receptor subfamily 0 group B member 2
PTGFRN	-0.4258	9.95E-06	0.000565	-4.43256	Down	prostaglandin F2 receptor inhibitor
ZMPSTE24	-0.42548	0.001254	0.031082	-3.23213	Down	zinc metalloproteinase STE24
GAPDH	-0.42428	1.25E-10	2.17E-08	-6.47557	Down	glyceraldehyde-3-phosphate dehydrogenase
IER3IP1	-0.42412	0.001989	0.044432	-3.09705	Down	immediate early response 3 interacting protein 1
CAPZB	-0.42407	0.000602	0.017478	-3.43761	Down	capping actin protein of muscle Z-line subunit beta
LBHD1	-0.42384	0.000961	0.025307	-3.30779	Down	LBH domain containing 1

FTH1	-0.42333	5.29E-06	0.000333	-4.56862	Down	ferritin heavy chain 1
DNAJA1	-0.42299	0.000443	0.0137	-3.52057	Down	DnaJ heat shock protein family (Hsp40) member A1
RPL15P14	-0.42247	1.50E-17	6.36E-15	-8.62629	Down	ribosomal protein L15 pseudogene 14
PPIL1	-0.42158	2.54E-05	0.001278	-4.22338	Down	peptidylprolylisomerase like 1
EEF1A1P8	-0.42156	2.72E-16	9.85E-14	-8.27318	Down	eukaryotic translation elongation factor 1 alpha 1 pseudogene 8
PSMD12	-0.42077	0.00198	0.044344	-3.09834	Down	proteasome 26S subunit, non-ATPase 12
TRNE	-0.41945	1.63E-05	0.000863	-4.32342	Down	tRNA
COX6B1	-0.41892	8.34E-05	0.003528	-3.94445	Down	cytochrome c oxidase subunit 6B1
RPL7P2	-0.41268	9.98E-12	1.92E-09	-6.85757	Down	ribosomal protein L7 pseudogene 2
NDUFB7	-0.41261	0.002	0.044641	-3.0953	Down	NADH:ubiquinoneoxidoreductase subunit B7
IBTK	-0.41138	0.000948	0.02507	-3.31181	Down	inhibitor of Bruton tyrosine kinase
SQSTM1	-0.41137	0.000705	0.019811	-3.39419	Down	sequestosome 1
EEF1A1P35	-0.4109	2.36E-17	9.77E-15	-8.57206	Down	eukaryotic translation elongation factor 1 alpha 1 pseudogene 35
TRNK	-0.41012	0.001834	0.041719	-3.12105	Down	tRNA
ARG2	-0.40998	0.002075	0.045802	-3.08432	Down	arginase 2
FKBP2	-0.40995	6.17E-05	0.002718	-4.0171	Down	FKBP prolylisomerase 2
RNR1	-0.40959	1.18E-15	3.98E-13	-8.08859	Down	s-rRNA
SUMO2P17	-0.40806	1.06E-09	1.51E-07	-6.13613	Down	SUMO2 pseudogene 17
MORF4L2	-0.40779	0.00078	0.021497	-3.36633	Down	mortality factor 4 like 2
DHDDS	-0.4037	0.000531	0.015816	-3.47167	Down	dehydrodolichyldiphosphate synthase subunit
ARCN1	-0.40218	0.001721	0.039674	-3.13981	Down	archain 1
RPS3AP36	-0.40086	8.34E-20	4.47E-17	-9.22964	Down	RPS3A pseudogene 36
RNF6	-0.40049	0.001054	0.027143	-3.28159	Down	ring finger protein 6
SMIM4	-0.39841	0.001368	0.033242	-3.20703	Down	small integral membrane protein 4
ATP5F1B	-0.39835	0.000648	0.018456	-3.41756	Down	ATP synthase F1 subunit beta
GABARAP	-0.39762	9.75E-11	1.73E-08	-6.5144	Down	GABA type A receptor-associated protein
HSPA5	-0.39609	0.001652	0.038497	-3.1519	Down	heat shock protein family A (Hsp70) member 5
RAD23A	-0.3953	0.000502	0.015142	-3.48683	Down	RAD23 homolog A, nucleotide excision repair protein
RPS28P4	-0.39301	1.57E-08	1.78E-06	-5.68274	Down	ribosomal protein S28 pseudogene 4
CYCSP24	-0.39294	2.10E-14	6.22E-12	-7.71604	Down	CYCS pseudogene 24
COTL1	-0.39288	0.001598	0.037518	-3.16162	Down	coactosin like F-actin binding protein 1
RPS3AP44	-0.39056	3.54E-18	1.62E-15	-8.79783	Down	RPS3A pseudogene 44
MPP1	-0.38941	0.000175	0.006423	-3.76195	Down	membrane palmitoylated protein 1
NSMCE2	-0.38873	0.000263	0.00896	-3.65726	Down	NSE2 (MMS21) homolog, SMC5-SMC6 complex SUMO ligase
HMG2P21	-0.38828	2.65E-12	5.65E-10	-7.04986	Down	high mobility group nucleosomal binding domain 2 pseudogene 2
MTRNR2L1	-0.38658	3.61E-08	3.86E-06	-5.53609	Down	MT-RNR2 like 1
PEF1	-0.3863	0.00226	0.04858	-3.05874	Down	penta-EF-hand domain containing 1
RPL10P6	-0.38617	2.63E-09	3.50E-07	-5.98699	Down	ribosomal protein L10 pseudogene 6
RPS3AP7	-0.38579	2.94E-12	6.18E-10	-7.03537	Down	RPS3A pseudogene 7
ATP5MFP2	-0.3854	2.47E-22	1.77E-19	-9.86745	Down	ATP synthase membrane subunit f pseudogene 2
MBIP	-0.38484	0.000522	0.015597	-3.47608	Down	MAP3K12 binding inhibitory protein 1
TATDN3	-0.38481	0.001356	0.033022	-3.20958	Down	TatDDNase domain containing 3
RPS10P17	-0.38179	3.26E-08	3.50E-06	-5.55428	Down	ribosomal protein S10 pseudogene 17

H2BC12	-0.38158	0.001832	0.041697	-3.12139	Down	H2B clustered histone 12
PRDX5	-0.38143	2.95E-05	0.001453	-4.18914	Down	peroxiredoxin 5
CRYBB2	-0.38121	3.92E-10	6.02E-08	-6.29669	Down	crystallin beta B2
SUMO2P20	-0.37938	2.28E-12	4.93E-10	-7.07181	Down	SUMO2 pseudogene 20
ZNF410	-0.37837	0.001685	0.038977	-3.14611	Down	zinc finger protein 410
TUBG1	-0.37749	0.001403	0.03387	-3.19961	Down	tubulin gamma 1
SPCS2	-0.37723	0.001021	0.026486	-3.29066	Down	signal peptidase complex subunit 2
GALT	-0.37694	0.000139	0.005365	-3.81949	Down	galactose-1-phosphate uridylyltransferase
BEX1	-0.37536	2.09E-05	0.001072	-4.26798	Down	brain expressed X-linked 1
RPL7P13	-0.37485	2.38E-14	6.88E-12	-7.6992	Down	ribosomal protein L7 pseudogene 13
NDUFB8	-0.37453	7.21E-05	0.003108	-3.97958	Down	NADH:ubiquinone oxidoreductase subunit B8
ZBTB8OSP2	-0.37078	1.04E-20	6.86E-18	-9.46148	Down	zinc finger and BTB domain containing 8 opposite strand pseudogene 2
NSFL1C	-0.36983	0.000263	0.008949	-3.65781	Down	NSFL1 cofactor
TMEM183A	-0.36855	0.000507	0.015249	-3.48407	Down	transmembrane protein 183A
RPS17P2	-0.36789	7.51E-12	1.47E-09	-6.89927	Down	ribosomal protein S17 pseudogene 2
ARMC2-AS1	-0.36688	2.05E-25	2.11E-22	-10.5991	Down	ARMC2 antisense RNA 1
MTFR1L	-0.36657	0.002218	0.048012	-3.06432	Down	mitochondrial fission regulator 1 like
HSPA8	-0.36575	0.000238	0.00831	-3.68273	Down	heat shock protein family A (Hsp70) member 8
RPS20P10	-0.36572	8.82E-12	1.71E-09	-6.87571	Down	ribosomal protein S20 pseudogene 10
POLE3	-0.36557	0.000625	0.01796	-3.42748	Down	DNA polymerase epsilon 3, accessory subunit
RPL17P5	-0.36539	3.65E-13	8.79E-11	-7.3297	Down	ribosomal protein L17 pseudogene 5
EEF1A1P19	-0.36469	7.00E-11	1.28E-08	-6.56529	Down	eukaryotic translation elongation factor 1 alpha 1 pseudogene 19
RPS27P7	-0.36457	7.24E-12	1.43E-09	-6.9046	Down	ribosomal protein S27 pseudogene 7
H2AC19	-0.3645	0.00211	0.046377	-3.07937	Down	H2A clustered histone 19
TRNH	-0.36284	0.000466	0.014263	-3.50677	Down	tRNA
RAB3GAP1	-0.36283	0.002006	0.044687	-3.09447	Down	RAB3 GTPase activating protein catalytic subunit 1
COA8	-0.36228	0.001138	0.028843	-3.2599	Down	cytochrome c oxidase assembly factor 8
COX14	-0.36213	0.000464	0.014207	-3.50826	Down	cytochrome c oxidase assembly factor COX14
EIF5A2	-0.36181	0.000165	0.0061	-3.77667	Down	eukaryotic translation initiation factor 5A2
UBBP1	-0.36172	1.62E-09	2.22E-07	-6.06724	Down	ubiquitin B pseudogene 1
ATP5MGP4	-0.36115	3.10E-15	9.83E-13	-7.96558	Down	ATP synthase membrane subunit g pseudogene 4
RPL31P2	-0.36003	5.84E-09	7.25E-07	-5.8532	Down	ribosomal protein L31 pseudogene 2
RPS10P22	-0.35964	1.78E-13	4.44E-11	-7.42812	Down	ribosomal protein S10 pseudogene 22
MT1G	-0.35661	0.000918	0.024508	-3.32074	Down	metallothionein 1G
AIFM1	-0.35618	0.00019	0.006856	-3.74038	Down	apoptosis inducing factor mitochondria associated 1
RPS7P11	-0.35591	1.62E-09	2.22E-07	-6.06714	Down	ribosomal protein S7 pseudogene 11
PPP1R1A	-0.35494	0.001664	0.038735	-3.14973	Down	protein phosphatase 1 regulatory inhibitor subunit 1A
TXNP5	-0.35432	1.01E-07	9.84E-06	-5.34995	Down	thioredoxin pseudogene 5
GCNT3	-0.35175	6.22E-05	0.002739	-4.01505	Down	glucosaminyl (N-acetyl) transferase 3, mucin type
PRSS1	-0.35162	3.71E-06	0.000247	-4.64323	Down	serine protease 1
TCEAL4	-0.35157	0.001368	0.033242	-3.20692	Down	transcription elongation factor A like 4
PSMF1	-0.35154	0.00208	0.045864	-3.08357	Down	proteasome inhibitor subunit 1

TRNY	-0.35146	0.001577	0.037208	-3.1655	Down	tRNA
RPL15P7	-0.35122	1.27E-09	1.76E-07	-6.10754	Down	ribosomal protein L15 pseudogene 7
HMGN2P19	-0.35078	2.31E-10	3.81E-08	-6.38038	Down	high mobility group nucleosomal binding domain 2 pseudogene 1
CCDC28B	-0.35008	0.002068	0.045694	-3.08537	Down	coiled-coil domain containing 28B
RPL35P1	-0.34973	2.03E-09	2.75E-07	-6.02984	Down	ribosomal protein L35 pseudogene 1
CYCSP39	-0.34969	2.71E-13	6.62E-11	-7.37069	Down	CYCS pseudogene 39
EEF1A1P24	-0.34899	8.34E-17	3.21E-14	-8.41882	Down	eukaryotic translation elongation factor 1 alpha 1 pseudogene 24
USP9Y	-0.34852	1.12E-05	0.000626	-4.40562	Down	ubiquitin specific peptidase 9 Y-linked
PKM	-0.34839	0.000103	0.004198	-3.89425	Down	pyruvate kinase M1/2
RPL7P50	-0.34813	7.93E-18	3.47E-15	-8.70243	Down	ribosomal protein L7 pseudogene 50
RPL28P3	-0.34505	3.60E-09	4.67E-07	-5.93477	Down	ribosomal protein L28 pseudogene 3
SUMO2P3	-0.34474	7.00E-13	1.60E-10	-7.23884	Down	SUMO2 pseudogene 3
SCNM1	-0.34436	0.000813	0.022273	-3.35464	Down	sodium channel modifier 1
CDC23	-0.3433	0.000971	0.025489	-3.30499	Down	cell division cycle 23
CANX	-0.34183	0.000446	0.013793	-3.51834	Down	calnexin
SPINK4	-0.34142	0.001734	0.039855	-3.13776	Down	serine peptidase inhibitor Kazal type 4
SLC25A6P2	-0.33937	1.36E-17	5.83E-15	-8.63792	Down	solute carrier family 25 member 6 pseudogene 2
NDUFA4P1	-0.33899	7.21E-12	1.43E-09	-6.90516	Down	NDUFA4 pseudogene 1
UBE2L4	-0.33748	8.82E-10	1.26E-07	-6.16659	Down	ubiquitin conjugating enzyme E2 L4 (pseudogene)
RPLP0P9	-0.33611	4.30E-06	0.00028	-4.61241	Down	ribosomal protein lateral stalk subunit P0 pseudogene
NQO1	-0.33534	7.91E-06	0.000464	-4.4824	Down	NAD(P)H quinone dehydrogenase 1
CTNNAL1	-0.33523	0.000131	0.005101	-3.83429	Down	catenin alpha like 1
ETV6	-0.3352	0.001945	0.043673	-3.10358	Down	ETS variant transcription factor 6
MRPS11	-0.33369	0.000982	0.02572	-3.30166	Down	mitochondrial ribosomal protein S11
GPI	-0.33349	0.0018	0.041159	-3.12665	Down	glucose-6-phosphate isomerase
RPL7P19	-0.33116	7.34E-06	0.000438	-4.4985	Down	ribosomal protein L7 pseudogene 19
HMGB1P1	-0.33092	3.24E-06	0.00022	-4.67136	Down	high mobility group box 1 pseudogene 1
TRUB1	-0.32869	0.000764	0.021089	-3.37204	Down	TruBpseudouridine synthase family member 1
RPL39P27	-0.32699	3.42E-10	5.29E-08	-6.31839	Down	ribosomal protein L39 pseudogene 27
HMGN2P18	-0.32623	1.69E-14	5.15E-12	-7.74457	Down	high mobility group nucleosomal binding domain 2 pseudogene 1
CRIP1	-0.32531	0.000709	0.019885	-3.39276	Down	cysteine rich protein 1
RPL37AP1	-0.32523	4.73E-12	9.79E-10	-6.96667	Down	ribosomal protein L37a pseudogene 1
UFD1	-0.3246	0.000986	0.025803	-3.30056	Down	ubiquitin recognition factor in ER associated degradation 1
PXK	-0.32391	0.001856	0.042076	-3.11764	Down	PX domain containing serine/threonine kinase like
ZNF326	-0.3234	0.00083	0.022591	-3.3491	Down	zinc finger protein 326
RPL39P32	-0.32252	7.80E-07	6.05E-05	-4.96006	Down	ribosomal protein L39 pseudogene 32
SNRPEP4	-0.32224	4.61E-05	0.002121	-4.08577	Down	SNRPE pseudogene 4
RPL17P36	-0.32176	3.69E-06	0.000246	-4.64418	Down	ribosomal protein L17 pseudogene 36
RPL41P4	-0.32162	1.22E-08	1.44E-06	-5.7269	Down	ribosomal protein L41 pseudogene 4
TUBA1C	-0.32135	0.002099	0.046178	-3.08083	Down	tubulin alpha 1c
MTRNR2L8	-0.32104	6.50E-06	0.000396	-4.52457	Down	MT-RNR2 like 8
RPL24P4	-0.32073	2.88E-07	2.49E-05	-5.15335	Down	RPL24 pseudogene 4
RPL26P30	-0.32051	5.20E-07	4.21E-05	-5.03928	Down	ribosomal protein L26 pseudogene 30

RPL3P2	-0.31988	1.16E-07	1.11E-05	-5.32402	Down	ribosomal protein L3 pseudogene 2
RPL39P10	-0.3196	1.28E-10	2.20E-08	-6.47269	Down	ribosomal protein L39 pseudogene 10
SNRPCP12	-0.31936	5.69E-13	1.31E-10	-7.26794	Down	small nuclear ribonucleoprotein polypeptide C pseudogene 12
NANS	-0.31548	0.000943	0.02503	-3.31304	Down	N-acetylneuraminase
HSP90AB2P	-0.31496	3.92E-10	6.02E-08	-6.29687	Down	heat shock protein 90 alpha family class B member 2, pseudogene
EDARADD	-0.31464	0.000948	0.025071	-3.3116	Down	EDAR associated death domain
RPL7P58	-0.3131	2.60E-12	5.56E-10	-7.05287	Down	ribosomal protein L7 pseudogene 58
HSP90AB1	-0.31307	2.92E-10	4.60E-08	-6.34311	Down	heat shock protein 90 alpha family class B member 1
SPCS2P4	-0.313	5.03E-05	0.002282	-4.06541	Down	signal peptidase complex subunit 2 pseudogene 4
TMED4	-0.31249	2.88E-05	0.001427	-4.19515	Down	transmembrane p24 trafficking protein 4
FTLP17	-0.31234	8.11E-23	6.06E-20	-9.98527	Down	ferritin light chain pseudogene 17
RPL34P27	-0.3123	1.24E-10	2.16E-08	-6.47702	Down	ribosomal protein L34 pseudogene 27
TTY15	-0.31214	4.89E-08	5.11E-06	-5.48176	Down	testis-specific transcript, Y-linked 15
PTMAP8	-0.31168	4.58E-13	1.08E-10	-7.29792	Down	prothymosin alpha pseudogene 8
RPL23AP69	-0.30985	5.07E-14	1.35E-11	-7.5985	Down	ribosomal protein L23a pseudogene 69
PDZD8	-0.30983	0.001014	0.026326	-3.29256	Down	PDZ domain containing 8
COX8A	-0.3096	0.001805	0.041222	-3.12584	Down	cytochrome c oxidase subunit 8A
RPL23AP3	-0.3084	1.30E-12	2.88E-10	-7.15139	Down	ribosomal protein L23a pseudogene 3
FABP5P11	-0.30689	4.21E-05	0.001976	-4.10706	Down	fatty acid binding protein 5 pseudogene 11
CHCHD6	-0.30681	0.001447	0.034671	-3.19066	Down	coiled-coil-helix-coiled-coil-helix domain containing 6
AP3S2	-0.30669	0.000326	0.010727	-3.60127	Down	adaptor related protein complex 3 subunit sigma 2
RPL39P38	-0.3065	2.30E-06	0.000165	-4.74208	Down	ribosomal protein L39 pseudogene 38
TIMM8BP2	-0.30482	1.68E-10	2.83E-08	-6.42989	Down	translocase of inner mitochondrial membrane 8B pseudogene 2
XPOT	-0.30481	0.001507	0.035927	-3.17875	Down	exportin for tRNA
AK2P2	-0.30475	6.39E-12	1.29E-09	-6.92279	Down	adenylate kinase 2 pseudogene 2
MOB4P2	-0.30419	1.40E-06	0.000104	-4.84332	Down	MOB4 pseudogene 2
RPL23AP75	-0.304	7.48E-16	2.64E-13	-8.14633	Down	ribosomal protein L23a pseudogene 75
MTCO2P22	-0.30294	5.44E-09	6.80E-07	-5.86517	Down	MT-CO2 pseudogene 22
RPL7P12	-0.30227	2.08E-14	6.22E-12	-7.71734	Down	ribosomal protein L7 pseudogene 12
RPS27AP1	-0.30196	8.70E-14	2.22E-11	-7.52589	Down	RPS27A pseudogene 1
WDR89	-0.30152	0.000169	0.006225	-3.77081	Down	WD repeat domain 89
TPI1P1	-0.30011	5.51E-05	0.002473	-4.04371	Down	triosephosphateisomerase 1 pseudogene 1
RPL6P3	-0.29989	3.36E-13	8.17E-11	-7.34082	Down	ribosomal protein L6 pseudogene 3
CACYBPP2	-0.29981	6.49E-06	0.000396	-4.52498	Down	calcyclin binding protein pseudogene 2
RPS20P6	-0.29975	1.82E-13	4.50E-11	-7.4255	Down	ribosomal protein S20 pseudogene 6
PARN	-0.29953	0.001076	0.027473	-3.27587	Down	poly(A)-specific ribonuclease
PLA1A	-0.29843	0.00176	0.040439	-3.13327	Down	phospholipase A1 member A
WDR73	-0.29808	0.001639	0.038254	-3.1543	Down	WD repeat domain 73
FTH1P23	-0.29682	3.74E-07	3.12E-05	-5.10325	Down	ferritin heavy chain 1 pseudogene 23
RPL5P5	-0.29556	6.48E-14	1.70E-11	-7.56553	Down	ribosomal protein L5 pseudogene 5
COX4I1	-0.29554	6.69E-05	0.002912	-3.99764	Down	cytochrome c oxidase subunit 4I1
ALDOA	-0.29552	0.000994	0.0259	-3.29834	Down	aldolase, fructose-bisphosphate A
RPL17P18	-0.29521	0.000358	0.011537	-3.57676	Down	ribosomal protein L17 pseudogene 18

TMEM45A	-0.29497	0.000507	0.015249	-3.48414	Down	transmembrane protein 45A
LDLRAP1	-0.294	0.001288	0.031773	-3.22433	Down	low density lipoprotein receptor adaptor protein 1
AK2P1	-0.29357	8.72E-06	0.000507	-4.46113	Down	adenylate kinase 2 pseudogene 1
RPL17P8	-0.29299	2.71E-12	5.73E-10	-7.04707	Down	ribosomal protein L17 pseudogene 8
MTRNR2L10	-0.29272	1.23E-10	2.15E-08	-6.47884	Down	MT-RNR2 like 10
RPL22P2	-0.2924	1.26E-05	0.000687	-4.38018	Down	ribosomal protein L22 pseudogene 2
EIF4EP5	-0.2918	3.73E-09	4.82E-07	-5.92869	Down	eukaryotic translation initiation factor 4E pseudogene 5
RPL36AP45	-0.2914	2.35E-06	0.000168	-4.73774	Down	ribosomal protein L36a pseudogene 45
ATP5MDP1	-0.29073	8.75E-06	0.000507	-4.46052	Down	ATP synthase membrane subunit DAPIT pseudogene 1
RPL39P19	-0.28815	4.20E-07	3.45E-05	-5.08096	Down	ribosomal protein L39 pseudogene 19
RPL26P6	-0.28765	0.001911	0.043097	-3.10897	Down	ribosomal protein L26 pseudogene 6
TPI1	-0.28628	0.002268	0.048726	-3.05766	Down	triosephosphateisomerase 1
EEF1A1P5	-0.28553	1.19E-07	1.13E-05	-5.31926	Down	eukaryotic translation elongation factor 1 alpha 1 pseudogene 5
PRORP	-0.28521	0.000364	0.011686	-3.57248	Down	protein only RNase P catalytic subunit
SNRPGP10	-0.2849	2.43E-07	2.14E-05	-5.18542	Down	small nuclear ribonucleoprotein polypeptide G pseudogene 10
EEF1B2P6	-0.2846	1.33E-05	0.00072	-4.36856	Down	eukaryotic translation elongation factor 1 beta 2 pseudogene 6
NQO2	-0.28447	0.001315	0.032295	-3.21842	Down	N-ribosyldihydronicotinamide:quinonereductase 2
RPL23AP65	-0.28402	2.51E-05	0.001264	-4.22608	Down	ribosomal protein L23a pseudogene 65
RPL7P11	-0.28298	4.22E-14	1.15E-11	-7.62331	Down	ribosomal protein L7 pseudogene 11
CD63	-0.28254	5.62E-07	4.48E-05	-5.02445	Down	CD63 molecule
RPS15AP12	-0.2825	1.17E-08	1.38E-06	-5.73422	Down	ribosomal protein S15a pseudogene 12
RPL14	-0.28079	5.42E-05	0.002436	-4.04785	Down	ribosomal protein L14
RPL7P24	-0.28048	8.77E-16	3.04E-13	-8.12636	Down	ribosomal protein L7 pseudogene 24
RPS29P5	-0.27846	4.73E-08	4.96E-06	-5.48777	Down	ribosomal protein S29 pseudogene 5
RPL36AP16	-0.27753	3.16E-09	4.12E-07	-5.95679	Down	ribosomal protein L36a pseudogene 16
UBC	-0.27639	0.000466	0.014256	-3.50712	Down	ubiquitin C
RPSAP54	-0.27631	9.80E-07	7.47E-05	-4.91478	Down	ribosomal protein SA pseudogene 54
ATP5MC2	-0.27566	0.000302	0.010072	-3.62161	Down	ATP synthase membrane subunit c locus 2
UQCRHL	-0.27518	1.61E-07	1.49E-05	-5.2628	Down	ubiquinol-cytochrome c reductase hinge protein like
CORO1C	-0.27502	0.001554	0.036725	-3.16987	Down	coronin 1C
RPL15P20	-0.27449	1.36E-09	1.88E-07	-6.09611	Down	ribosomal protein L15 pseudogene 20
DNAJC19P9	-0.274	0.000114	0.00458	-3.8681	Down	DnaJ heat shock protein family (Hsp40) member C19 pseudogene
HIGD1AP14	-0.27375	6.93E-10	1.02E-07	-6.20549	Down	HIG1 hypoxia inducible domain family member 1A pseudogene 1
FABP5P8	-0.27319	4.75E-09	5.99E-07	-5.88828	Down	fatty acid binding protein 5 pseudogene 8
HMBS	-0.27266	0.000468	0.014321	-3.50546	Down	hydroxymethylbilane synthase
RPSAP17	-0.27253	1.27E-08	1.49E-06	-5.71973	Down	ribosomal protein SA pseudogene 17
PPP2CBP1	-0.27127	1.19E-12	2.65E-10	-7.16403	Down	protein phosphatase 2 catalytic subunit beta pseudogene 1
RPL24P8	-0.27089	1.51E-08	1.72E-06	-5.68998	Down	RPL24 pseudogene 8
ETV5	-0.27005	0.001333	0.032586	-3.21453	Down	ETS variant transcription factor 5

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

GO ID	CATEGORY	GO Name	Adjusted p value	negative log10 of adjusted p value	Gene Count	Gene
Up regulated genes						
GO:0019538	BP	protein metabolic process	0.023917063	1.621292161	123	CTBP1,PCMTD1,IGFBP2,TW SG1,VGF,APOH,RPL21,RPL1 7,PHF1,ANXA2,BAX,UBA6,P CSK1N,ZC3HAV1,PKK4,CPE ,OCLN,RPS3A,RPS2,HLA- A,PGAM5,PPP1R14C,VEGFA ,MIER1,PEMT,MAN1A1,CD4 4,NDN,DCUN1D4,IGFBP5,RP L7,MLXIPL,APP,TIA1,CD36, RPL36A,WSB1,SREBF1,NR4 A1,TLK1,PCSK2,INSM1,INO 80E,PLOD2,RPS10,EIF1AX,S UMF2,SPINT2,UBXN6,CST3, PRSS3,RAB8A,PTPN18,DPP6 ,CHGB,PKK3,RPS27,RAB3G AP2,USP7,MEX3D,ITGAV,C DK10,RPL39,EEF2,MCTS1,T NRC6B,ITM2B,PDCC4,EIF5 A,KRT10,DPH1,NRP1,DDR1, PAK3,OTUD4,ILF3,KMT2E,P DCD2,ABCA1,VWA1,RPS26, DNMT1,USP27X,CSKMT,TO P1,MYH9,SFTPA1,PIKFYVE, U2AF2,ST14,TNRC6A,FBXO 44,HMGB1,PPP1R37,MAPT, GANAB,RPL41,NAA40,B4G ALT5,PRKDC,NOL3,SNRNP7 0,FURIN,HNRNP,HCFC1,G GCX,RPL28,TFAP4,B2M,GR AMD4,BRD1,TMUB1,CAPN1 2,CSNK1G2,RNF152,MAP3K 12,PLXNB2,BCL6,TAOK2,B MP6,APOL4,RPL23A,KSR2
GO:0048518	BP	positive regulation of biological process	0.103228346	0.986201031	131	CTBP1,NPY,IGFBP2,TW SG1, APOH,RIN2,SH3GL1,CHGA, PHF1,SRGAP2C,ANXA2,ST MN2,CD47,BAX,ZC3HAV1,Z NF516,S100A6,OCLN,TIAL1, SKIL,TLE5,LMO1,RPS2,HLA - A,VEGFA,MIER1,PEMT,PAR M1,CD44,NDN,DCUN1D4,IG FBP5,RHOB,MLXIPL,JUNB, KCNA5,APP,TIA1,CD36,NEN F,SREBF1,DDX17,NR4A1,M AP2,ATP1B1,INSM1,HLA- B,ARID1B,STXBP5,GPBP1L1 ,CST3,EMC10,ATP8A1,RAB3 GAP2,USP7,MEX3D,ADGRG 1,ITGAV,CDK10,ELF2,EEF2, PAFAH1B1,MCTS1,TNRC6B, RREB1,PDCC4,EIF5A,KRT10 ,NRP1,DDR1,PAK3,HNRNPA B,OTUD4,FOSB,CPT1A,ILF3, KMT2E,PDCC2,ITSN2,PRXL 2C,CLSTN1,ESRRA,ABCA1, SLF2,DNMT1,MCU,USP27X, MYH9,SYNPO,ATP2A2,TRA 2A,SFTPA1,MAFG,U2AF2,T NRC6A,HMGB1,ZXDC,MAP

GO:0005622	CC	intracellular anatomical structure	4.57833E-06	5.339293274	267	<p>T,ZCCHC3,B4GALT5,CELF3,PRKDC,HIVEP1,SNRNP70,MAGI1,FURIN,WIPF2,HCFC1,SYT7,TFAP4,RGL2,CITED2,B2M,GRAMD4,BRD1,CSNK1G2,SSBP4,RNF152,MAP3K12,PLXNB2,BCL6,TAOK2,SEMA6A,BMP6,ECHDC3,KLF13,TMEM79,MZF1,KSR2,NCOR2,TENM3</p> <p>CTBP1,PCMTD1,GAS2,NPY,I GFBP2,VGF,APOH,MZT2B,RPL21,NME7,MZT2A,SGSM2,RIN2,SH3GL1,RPL17,CHGA,PHF1,SRGAP2C,ALYREF,RUNX1T1,ANXA2,THAP5,COX7A1,SEZ6L,STMN2,CD47,BAX,SELENOM,DLK1,UBA6,PCSK1N,ND3,ZC3HAV1,ZNF83,ZNF516,S100A6,NSUN6,PDK4,CPE,OCN,TIAL1,PGRMC2,NPIPA1,SKIL,TLE5,RPS3A,LMO1,RPS2,HLA-A,CXXC4,PGAM5,PPP1R14C,VEGFA,MIER1,NME3,PEN1,MAN1A1,OVCA2,PARM1,CD44,SLC22A17,NDN,LSAMP,DCUN1D4,NDRG1,IGFBP5,RHOB,RPL7,MLXIP1,JUNB,KCNA5,POLR2J2,APP,TIA1,RANBP3,RAD52,ARGLU1,CD36,RPL36A,NENF,MBNL2,FADS2,WSB1,SREBF1,TMEM167A,DDX17,NR4A1,APLP1,MAP2,TLK1,PCSK2,INSM1,INO80E,PLOD2,RPS10,HLA-B,E1F1AX,DDX18,ARID1B,SUMF2,SPINT2,STXBP5,GPBP1L1,SRRM2,UBXN6,CST3,TMEM123,PRSS3,RAB8A,PTPN18,NUDT4B,DYNC2I1,EMC10,DNAH2,CHGB,PKD3,PLD3,FCGRT,RPS27,ATP8A1,TLE3,ZFX,CYB5R3,RAB3GAP2,NUDT4,USP7,MEX3D,SUN1,ITGAV,LUC7L3,SEZ6L2,CDK10,ELF2,ARL4C,CCDC186,ATAD3C,RPL39,EEF2,PAFAH1B1,MCTSI,TNRC6B,REB1,ITM2B,SRSF3,PDCC4,EIF5A,KRT10,DPH1,NRP1,PAK3,HNRNPAB,OTUD4,FOSB,CPT1A,ILF3,DOC2A,A1BG,KMT2E,ALDH1B1,ZNF189,PDCC2,ITSN2,CLSTN1,ESRRA,ABCA1,PI4KA,PNISR,VWA1,SLF2,RPS26,GNAO1,NISCH,DNMT1,MCU,USP27X,CSKMT,TOPI,MYH9,SYNPO,ATP2A2,GAA,TRA2A,LENG8,SFTPA1,PIKFYVE,MAFG,U2AF2,SLC35E2B,LPCAT4,MIDN,HOOK3,HNRNP1,NBPF12,TNRC6A,TCTN2,SSTR3,ZSWIM1,NPIPA5,FBXO44,SIPA1L3,HMGB1,ZXDC,MAN2B2,BCL2L2-PABPN1,MAPT,ZCCHC3,GANAB,RPL41,PABPN1,NAA40,B4GALT5,CELF3,PRKDC,HI</p>
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						VEP1,NOL3,UBN2,SNRNP70, TMEM159,MAGI1,FURIN,WI PF2,CEBPZOS,HNRNP1,MC PH1,HCFC1,CACNA1A,SYT7 ,GGCX,RPL28,TFAP4,SACS, CITED2,NFASC,B2M,SON,G RAMD4,SLC18A2,GLCCI1,B RD1,TRMT9B,TMUB1,CAPN 12,CSNK1G2,SSBP4,RNF152, MAP3K12,DECR2,SLC6A17, NBP420,MPIRIP,BCL6,SSR4, TAOK2,BMP6,ECHDC3,KLF 13,NPIP11,APOL4,ZNF783, ND1,RPL23A,TMEM79,RGP D4,MZF1,KSR2,INTS6L,NCO R2
GO:0012505	CC	endomembrane system	0.029110496	1.535950391	101	NPY,VGF,APOH,RPL21,SH3 GL1,CHGA,ANXA2,SEZ6L,S TMN2,CD47,BAX,SELENOM ,PCSK1N,S100A6,CPE,PGRM C2,NPIPA1,SKIL,RPS3A,HL A- A,VEGFA,PEMT,MAN1A1,P ARM1,CD44,NDRG1,IGFBP5 ,RHOB,KCNA5,APP,RANBP3 ,CD36,RPL36A,NENF,FADS2 ,SREBF1,TMEM167A,NR4A1 ,PCSK2,PLOD2,HLA- B,SUMF2,STXBP5,UBXN6,C ST3,PRSS3,RAB8A,EMC10,C HGB,PLD3,FCGRT,ATP8A1, CYB5R3,RAB3GAP2,SUN1,I TGAV,SEZ6L2,CCDC186,EE F2,PAFAH1B1,ITM2B,EIF5A, NRP1,PAK3,DOC2A,A1BG,I TSN2,CLSTN1,ABCA1,VWA 1,RPS26,NISCH,SYNPO,ATP 2A2,GAA,SFTPA1,PIKFYVE, SLC35E2B,LPCAT4,HOO3, TNRC6A,SIPA1L3,HMGB1,G ANAB,RPL41,B4GALT5,NOL 3,TMEM159,FURIN,SYT7,G GCX,NFASC,B2M,GRAMD4, SLC18A2,TMUB1,SLC6A17, BCL6,SSR4,TMEM79,RGPD4 CTBP1,RPL21,NME7,RPL17, PHF1,ALYREF,RUNX1T1,A NXA2,THAP5,UBA6,ZC3HA V1,ZNF83,ZNF516,NSUN6,P DK4,TIAL1,PGRMC2,SKIL,R PS3A,RPS2,HLA- A,CXXC4,MIER1,NME3,ND N,RHOB,RPL7,MLXIPL,JUN B,POLR2J2,APP,TIA1,RAD52 ,RPL36A,MBNL2,SREBF1,D DX17,NR4A1,TLK1,INSM1,R PS10,EIF1AX,DDX18,ARID1 B,GPBP1L1,SRRM2,RAB8A, NUDT4B,DNASE2,PKD3,RPS 27,ATP8A1,ZFX,CYB5R3,NU DT4,ATP13A3,MEX3D,LUC7 L3,CDK10,ELF2,ARL4C,ATA D3C,RPL39,EEF2,MCTS1,TN RC6B,RREB1,ITM2B,SRSF3, PDCD4,EIF5A,DDR1,PAK3,H NRNPAB,OTUD4,FOSB,ILF3 ,ALDH1B1,ZNF189,PDCD2,E SRRA,ABCA1,PI4KA,PNISR, RPS26,GNAO1,DNMT1,TOPI ,MYH9,ATP2A2,TRA2A,PIK
GO:1901363	MF	heterocyclic compound binding	0.050253518	1.298833533	129	

GO:0005515	MF	protein binding	0.543492863	0.264806155	251	<p>FYVE,MAFG,U2AF2,HNRNP H1,TNRC6A,HMGB1,ZXDC, BCL2L2- PABPN1,MAPT,ZCCHC3,GA NAB,RPL41,PABPN1,CELF3, PRKDC,HIVEP1,NOL3,SNRN P70,RBM33,MAGI1,HNRNP ,HCF1,RPL28,TFAP4,SON,T RMT9B,CSNK1G2,SSBP4,M AP3K12,BCL6,AHDC1,TAOK 2,KLF13,ZNF783,RPL23A,M ZF1,KSR2,NCOR2 CTBP1,PCMTD1,GAS2,CPNE 8,NPY,IGFBP2,TWSG1,VGF, APOH,MZT2B,RPL21,NME7, MZT2A,SH3GL1,RPL17,PHF 1,SRGAP2C,RUNX1T1,ANX A2,THAP5,COX7A1,SEZ6L,S TMN2,CD47,BAX,SELENOM ,DLK1,UBA6,PCSK1N,ND3,Z C3HAV1,ZNF83,ZNF516,S10 0A6,FXD5,PDK4,CPE,OCL N,TIAL1,CDCP1,PGRMC2,S KIL,TLE5,RPS3A,LMO1,RPS 2,HLA- A,PGAM5,NPDC1,VEGFA,M IER1,NME3,PEMT,PARM1,C D44,ANKRD36,SLC22A17,N DN,LSAMP,DCUN1D4,NDR G1,IGFBP5,RHOB,RPL7,ML XIPL,JUNB,KCNA5,POLR2J2 ,APP,TIA1,RANBP3,RAD52, ARGLU1,CD36,RPL36A,NEN F,TMEM45B,MBNL2,FADS2, WSB1,SREBF1,TMEM167A, DDX17,NR4A1,APLP1,CDH1 0,MAP2,TLK1,ATP1B1,PCSK 2,INSM1,INO80E,RPS10,AN KRD36C,HLA- B,E1F1AX,DDX18,ARID1B,S UMF2,STXBP5,GPBP1L1,SR RM2,UBXN6,CST3,TMEM12 3,MPP6,PRSS3,RAB8A,PTPN 18,DYNC2I1,CHGB,PDK3,PL D3,FCGR2,ALCAM,RPS27,A TP8A1,TLE3,CYB5R3,RAB3 GAP2,NUDT4,USP7,ADGRG 1,SUN1,ITGAV,LUC7L3,CD K10,ELF2,ARL4C,FAM102A, EEF2,SAMD12,PAFAH1B1,M CTS1,TNRC6B,ITM2B,SRSF3 ,PDCD4,FAM229B,E1F5A,KR T10,DPH1,NRP1,DDR1,PAK3 ,HNRNPAB,OTUD4,FOSB,CP T1A,ILF3,DOC2A,KMT2E,PD CD2,ITSN2,CLSTN1,ESRRA, ABCA1,PI4KA,VWA1,SLF2, RPS26,GNAO1,NISCH,DNM T1,MCU,CSKMT,TOPI,MYH 9,SYNPO,ATP2A2,TRA2A,L ENG8,SFTPA1,PIKFYVE,MA FG,U2AF2,ST14,MIDN,HOO K3,HNRNP1,TNRC6A,SST R3,WDR17,FBXO44,SIPA1L3 ,HMGB1,ZXDC,MAN2B2,PP PIR37,BCL2L2- PABPN1,MAPT,ZCCHC3,GA NAB,RPL41,PABPN1,NAA40 ,PRKDC,HIVEP1,KIAA0895L ,NOL3,SNRN70,TMEM159,</p>
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						MAGI1,FURIN,WIPF2,UMAD1,HNRNPL,MCPH1,HCFC1,CACNA1A,SYT7,RPL28,TFA P4,RGL2,SDK1,SACS,ANKRD18A,CITED2,NFASC,B2M,SON,GRAMD4,SLC18A2,RGL3,BRD1,TMUB1,CSNK1G2,SBP4,RNF152,MAP3K12,DECR2,PLXNB2,SLC6A17,MPRIIP,BCL6,AHDC1,TAOK2,SEMA6A,BMP6,SHISAL1,KLF13,APOL4,ZNF783,ND1,RPL23A,TMEM79,RGPD4,MZF1,KS R2,NCOR2,TENM3
Down regulated genes						
GO:0051234	BP	establishment of localization	0.000213201	3.671209808	116	RPS4Y1,FXVD2,FXVD6-FXVD2,FTL,SAR1A,TUBA4A,RBP4,GSTP1,VAMP8,PSMB7,CYB5A,UQCC2,RPS28,CAMK2D,G6PC2,BCAP31,ASAH1,RPL9,ATP6V1B2,DNAJC15,VPS25,ATP5PB,PSMC4,TMED6,ATP6V1D,UCHL1,PSMC5,SLC25A5,NDUFA9,PPT1,SSR2,ARRDC3,ARL6IP1,PSMD7,TIMM17A,ATP5F1C,ATP6V1E1,RAB21,CTSA,NIT2,ATP5MC1,MPC1,PSMD6,CLIC1,REEP5,IDH1,PSMB5,XRC6,PSMB3,PRDX6,CLU,TTR,GRB2,RAB3B,ATP5PO,CYSTM1,TRAPPC2L,PSMA4,NAPAA,VAT1,UBE2B,CAP1,TXN,P SMB2,SCAMP3,DYNLRB1,LAMTOR1,GLUL,NEU1,SVBP,NR0B2,ZMPSTE24,IER3IP1,CAPZB,FTH1,DNAJA1,PSMD12,COX6B1,IBTK,SQSTM1,ARCN1,ATP5F1B,GABARAP,HSPA5,COTL1,PEF1,SPCS2,NSFL1C,HSPA8,RAB3GAP1,COA8,EIF5A2,AIFM1,GCNT3,PSMF1,PKM,CDC23,CANX,GPI,UFD1,PXK,TUBA1C,HP90AB1,TMED4,PDZD8,COX8A,AP3S2,XPOT,COX4I1,ALDOA,LDLRAP1,CD63,RPL14,UBC,ATP5MC2,CORO1C
GO:0044237	BP	cellular metabolic process	0.000561829	3.250396124	192	RPS4Y1,PTBP2,CNOT6L,RBP4,IAPP,GPX2,GSTP1,VAMP8,SAT1,PSMB7,CYB5A,UQC2,ETFB,USP22,PPIB,RTF2,RPS28,CAMK2D,G6PC2,BCAP31,ASAH1,RPL9,ATP6V1B2,DNAJC15,VPS25,EIF1AY,ATP5PB,CDC42BPA,PSMC4,ATP6V1D,UCHL1,PSMC5,NDUFA9,PPT1,PIR,MLLT11,SARS1,ARRDC3,TSPYL5,ARL6IP1,TOX4,PSMD7,TIMM17A,BLVRB,ATP5F1C,SH3BGRL3,PRPS2,MRPL54,NDUFA12,ATP6V1E1,PRDX1,CTSA,NIT2,BUD23,ATP5MC1,LCLAT1,UBE2L5,MPC1,PSMD6,GBA,E NO1,ESD,FDPS,IDH1,HOPX,PSMB5,MRPS35,XRCC6,PSMB3,PRDX6,ZNF165,NDUFV3,CLU,GLMP,MDH2,EIF3K,TTTR,PTGR2,GNPDA1,GHITM,H

GO:0005737	CC	cytoplasm	1.84E-12	11.73552798	221	<p>PF1,GRB2,RAB3B,RPS27AP5,MDH1,ATP5PO,POLR3K,UBE2L6,PSMA4,SCD,KLHL41,PIGP,SUCLG1,TXN2,UBE2B,GTF2A2,DAP,ACADM,TXN,BLVRA,PSMB2,COA3,UQCRH,MGST3,MRPS15,LAMTOR1,GLUL,PCMTD2,NEU1,ALG3,ORC3,GTF2B,EXOSC1,FARSA,FKBP1C,SVBP,NR0B2,ZMPSTE24,GAPDH,LBHD1,DNAJA1,PPIL1,PSMD12,COX6B1,NDUFB7,IBTK,SQSTM1,ARG2,MORF4L2,DHDDS,RNF6,ATP5F1B,GABARAP,HSPA5,RAD23A,MPP1,NSMCE2,PEF1,MBIP,TATDN3,H2BC12,PRDX5,ZNF410,SPCS2,GALT,BEX1,NSFL1C,MTFR1L,HSPA8,POLE3,H2AC19,RAB3GAP1,COA8,EIF5A2,AIFM1,PPP1R1A,GCNT3,PRSS1,TCF12,EAL4,PSMF1,USP9Y,PKM,SCNM1,CDC23,SPINK4,NQO1,ETV6,MRPS11,GPI,TRUB1,UFD1,PXK,ZNF326,NANS,HSP90AB1,COX8A,PARN,PLA1A,COX4I1,ALDOA,LDLRAP1,TP11,PRORP,NQO2,CD63,RPL14,UBC,ATP5MC2,UQCRHL,CORO1C,HMB5,ETV5RPS4Y1,FTL,SAR1A,TUBA4A,MT2A,IFI30,CNOT6L,RBP4,GPX2,GSTP1,IFI27L2,MTC,H2,VAMP8,SAT1,HEPACAM2,PSMB7,CYB5A,UQCC2,ETFB,SCGN,PPIB,RPS28,CAMK2D,G6PC2,MTRNR2L12,DDX3Y,BCAP31,ASAH1,RPL9,ATP6V1B2,DNAJC15,VPS25,ATP5PB,CDC42BPA,PSMC4,TMED6,ATP6V1D,UCHL1,PSMC5,SLC25A5,ATXN7L3B,NDUFA9,PPT1,PIR,MLLT11,SARS1,TMEM106C,SSR2,ARRDC3,PCP4,ARL6IP1,PSMD7,TIMM17A,BLVRB,ATP5F1C,SH3BGL3,PRPS2,MRPL54,NDUFA12,ATP6V1E1,GRAMD2B,RAB21,PRDX1,CTSA,NIT2,BUD23,ATP5MC1,LCLAT1,MP1,PSMD6,CLIC1,GBA,ENO1,ESD,REEP5,FDPS,IDH1,HOPX,PSMB5,MRPS35,XRCC6,PSMB3,PRDX6,NDUFV3,CLU,CDV3,GLMP,PLEKHB2,MDH2,EIF3K,TTR,PTGR2,GNPDA1,GHITM,GRB2,MT1E,RAB3B,RPS27AP5,MDH1,ATP5PO,POLR3K,UBE2L6,CYSTM1,TRAPPC2L,PSMA4,SCD,KLHL41,REG1A,PIGP,SUCLG1,NAPA,VAT1,TXN2,UBE2B,PRXL2A,ACADM,CAP1,TXN,BLVRA,PSMB2,SCAMP3,COA3,DYNLRB1,UQCRH,MGST3,MRPS15,LAMTOR1,GLUL,PCMTD2,NEU1,ALG3,EXOSC1,FARSA,FKBP1C,SVBP,NR0B2,PTGFRN,ZMPSTE2</p>
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						4,GAPDH,IER3IP1,CAPZB,FTH1,DNAJA1,PSMD12,COX6B1,NDUFB7,IBTK,SQSTM1,ARG2,DHDDS,ARCN1,RNF6,ATP5F1B,GABARAP,HSPA5,RAD23A,COTL1,MPP1,MTRNR2L1,PEF1,MBIP,H2BC12,PRDX5,TUBG1,SPCS2,GALT,BEX1,NSFL1C,MTFR1L,HSPA8,RAB3GAP1,COA8,COX14,EIF5A2,MT1G,AIFM1,PPP1R1A,GCNT3,PSMF1,CCDC28B,USP9Y,PKM,CDC23,CANX,NQO1,CTNNA1,ETV6,MRPS11,GPI,TRUB1,CRIP1,UFD1,PXK,TUBA1C,MTRNR2L8,NANS,EDARADD,HSP90AB1,TMED4,PDZD8,COX8A,CHCHD6,AP3S2,XPOT,PARN,PLA1A,WDR73,COX4I1,ALDOA,LDLRAP1,MTRNR2L10,TPST1,PRORP,NQO2,CD63,RPL14,UBC,ATP5MC2,UQCRLH,CORO1C,HMBB
GO:0005622	CC	intracellular anatomical structure	5.44E-11	10.26453138	247	RPS4Y1,PTBP2,FTL,SAR1A,TUBA4A,MT2A,IFI30,CNOT6L,RBP4,GPX2,GSTP1,IFI27L2,MTCH2,VAMP8,SAT1,HEPACAM2,PSMB7,CYB5A,UQCRC2,ETFB,SCGN,USP22,PPIB,RTF2,RPS28,CAMK2D,G6PC2,MTRNR2L12,DDX3Y,BCAP31,ASAH1,RPL9,ATP6V1B2,DNAJC15,VPS25,ATP5PB,CDC42BPA,PSMC4,TMED6,ATP6V1D,UCHL1,PSMC5,SLC25A5,ATXN7L3B,NDUFA9,PTP1,PIR,MLLT11,SARS1,TMEM106C,SSR2,ARRDC3,TSPYL5,PCP4,ARL6IP1,TOX4,PSMD7,TIMM17A,BLVRB,ATP5F1C,SH3BGRL3,PRPS2,MRPL54,NDUFA12,ATP6V1E1,GRAMD2B,RAB21,PRDX1,CTSA,NIT2,BUD23,ATP5MC1,CLAT1,UBE2L5,MPC1,PSMD6,CLIC1,THYN1,GBA,ENO1,ESD,REEP5,FDPS,IDH1,HOPX,PSMB5,MRPS35,XRCC6,PSMB3,PRDX6,ZNF165,NDUV3,CLU,CDV3,GLMP,PLEKHB2,MDH2,EIF3K,TTR,SDR39U1,PTGR2,GNPDA1,GHITM,HPF1,GRB2,MT1E,RAB3B,PS27AP5,MDH1,ATP5PO,POLR3K,UBE2L6,CYSTM1,C11ORF54,TRAPPC2L,PSMA4,SCD,KLHL41,REG1A,PIGP,SUCLG1,NAPA,VAT1,TXN2,UBE2B,PRXL2A,GTF2A2,ACADM,CAP1,TXN,BLVRA,PSMB2,SCAMP3,COA3,DYNLRB1,UQCRLH,MGST3,MRPS15,LAMTOR1,GLUL,PCMTD2,NEU1,ALG3,ORC3,GTF2B,EXOSC1,FARSA,FKBP1C,SVBP,NR0B2,PTGFRN,ZMPSTE24,GAPDH,IER3IP1,CAPZB,LBHD1,FTH1,DNAJA1,PPIL1,PSMD12,COX6B1,NDUFB7,IBT

GO:0003824	MF	catalytic activity	6.46E-08	7.189593031	130	<p>K,SQSTM1,ARG2,MORF4L2,DHDDS,ARCN1,RNF6,ATP5F1B,GABARAP,HSPA5,RAD23A,COTL1,MPP1,NSMCE2,MTRNR2L1,PEF1,MBIP,TATDN3,H2BC12,PRDX5,ZNF410,TUBG1,SPCS2,GALT,BEX1,NSFL1C,MTRF1L,HSPA8,POLE3,H2AC19,RAB3GAP1,COA8,COX14,EIF5A2,MT1G,AIFM1,PPP1R1A,GCNT3,TCEAL4,PSMF1,CCDC28B,USP9Y,PKM,SCNM1,CDC23,CANX,NQO1,CTNNAL1,ETV6,MRPS11,GPI,TRUB1,CRIP1,UFD1,PXK,ZNF326,TUBA1C,MTRNR2L8,NANS,EDARADD,HSAP90AB1,TMED4,PDZD8,COX8A,CHCHD6,AP3S2,XPOT,PARN,PLA1A,WDR73,COX4I1,ALDOA,LDLRAP1,MTRNR2L10,TPI1,PRORP,NQO2,CD63,RPL14,UBC,ATP5MC2,UQCRHL,CORO1C,HMBS,ETV5SAR1A,TUBA4A,IFI30,CNOT6L,GPX2,GSTP1,SAT1,PSMB7,CYB5A,ETFB,USP22,PPIB,CAMK2D,G6PC2,DDX3Y,ASAH1,ATP6V1B2,ATP5PB,CD42BPA,PSMC4,UCHL1,PSMC5,NDUFA9,PPT1,PIR,SARS1,PSMD7,BLVRB,ATP5F1C,S3H3BGR13,PRPS2,NDUFA12,ATP6V1E1,RAB21,PRDX1,CSTA,NIT2,BUD23,ATP5MC1,LCLAT1,UBE2L5,PSMD6,GBA,ENO1,ESD,FDPS,IDH1,PSMB5,XRCC6,PSMB3,PRDX6,NDUFV3,MDH2,SDR39U1,PTGR2,GNPDA1,RAB3B,MDH1,ATP5PO,POLR3K,UBE2L6,C11ORF54,PSMA4,SCD,PIGP,SUCLG1,VAT1,TXN2,NTPC,R,UBE2B,ACADM,TXN,BLVRA,TMEM68,PSMB2,DYNLRB1,UQCRH,MGST3,GLUL,PMTD2,NEU1,ALG3,GTF2B,FARSA,FKBP1C,ZMPSTE24,GAPDH,FTH1,PPIL1,COX6B1,NDUFB7,SQSTM1,ARG2,DHDDS,RNF6,ATP5F1B,HSPA5,MPP1,NSMCE2,TATDN3,PRDX5,TUBG1,SPCS2,GALT,HSPA8,POLE3,AIFM1,GCNT3,PRSS1,USP9Y,PKM,CDC23,NQO1,GPI,TRUB1,UFD1,PXK,TUBA1C,NANS,COX8A,PARN,PLA1A,COX4I1,ALDOA,TPI1,PRORP,NQO2,ATP5MC2,UQCRHL,HMBS</p>
						<p>RPS4Y1,SST,PTBP2,FXDY2,FTL,SAR1A,TUBA4A,MT2A,IFI30,CNOT6L,RBP4,IAPP,GSTP1,MTCH2,VAMP8,SAT1,HEPACAM2,PSMB7,CYB5A,UQCC2,ETFB,SCGN,USP22,PPIB,RTF2,RPS28,CAMK2D,MTRNR2L12,BCAP31,ASAH1,RPL9,ATP6V1B2,DNAJC15,VPS25,EIF1AY,ATP5PB,CDC4</p>
GO:0005515	MF	protein binding	0.001861874	2.730049815	231	<p>RPS4Y1,SST,PTBP2,FXDY2,FTL,SAR1A,TUBA4A,MT2A,IFI30,CNOT6L,RBP4,IAPP,GSTP1,MTCH2,VAMP8,SAT1,HEPACAM2,PSMB7,CYB5A,UQCC2,ETFB,SCGN,USP22,PPIB,RTF2,RPS28,CAMK2D,MTRNR2L12,BCAP31,ASAH1,RPL9,ATP6V1B2,DNAJC15,VPS25,EIF1AY,ATP5PB,CDC4</p>

2BPA,PSMC4,ATP6V1D,UCH
L1,PSMC5,SLC25A5,ATXN7
L3B,NDUFA9,PPT1,PIR,MLL
T11,SARS1,TMEM106C,SSR2
,ARRDC3,TSPYL5,PCP4,ARL
6IP1,TOX4,TSPAN7,PSMD7,
BLVRB,ATP5F1C,SH3BGRL
3,PRPS2,MRPL54,NDUFA12,
ATP6V1E1,GRAMD2B,RAB2
1,PRDX1,BUD23,ATP5MC1,
LCLAT1,UBE2L5,MPC1,PSM
D6,CLIC1,GBA,ENO1,ESD,R
EEP5,FDPS,IDH1,HOPX,PSM
B5,XRCC6,PSMB3,PRDX6,Z
NF165,NDUFV3,CLU,PLEKH
B2,MDH2,EIF3K,TTR,PTGR2
,GNPDA1,GHITM,HPF1,GRB
2,MT1E,RAB3B,RPS27AP5,M
DH1,ATP5PO,POLR3K,UBE2
L6,CYSTM1,C11ORF54,TRA
PPC2L,PSMA4,SCD,KLHL41,
REG1A,PIGP,NAPA,VAT1,T
XN2,UBE2B,CUTA,GTF2A2,
DAP,ACADM,CAP1,TXN,ER
ICH5,BLVRA,PSMB2,SCAM
P3,COA3,DYNLRB1,UQCRH,
MGST3,LAMTOR1,GLUL,PC
MTD2,NEU1,ALG3,ORC3,GT
F2B,EXOSC1,FARSA,SVBP,
NR0B2,PTGFRN,ZMPSTE24,
GAPDH,IER3IP1,CAPZB,LB
HD1,FTH1,DNAJA1,PPIL1,PS
MD12,NDUFB7,IBTK,SQST
M1,ARG2,MORF4L2,DHDDS
,ARCN1,RNF6,ATP5F1B,GA
BARAP,HSPA5,RAD23A,CO
TL1,MPP1,NSMCE2,MTRNR
2L1,PEF1,MBIP,H2BC12,PRD
X5,CRYBB2,ZNF410,TUBG1,
GALT,BEX1,NSFL1C,TMEM
183A,MTFR1L,HSPA8,POLE
3,H2AC19,RAB3GAP1,COX1
4,EIF5A2,MT1G,AIFM1,PPP1
R1A,TCEAL4,PSMF1,CCDC2
8B,USP9Y,PKM,SCNM1,CDC
23,CANX,SPINK4,NQO1,CT
NNAL1,ETV6,MRPS11,GPI,U
FD1,PXK,ZNF326,TUBA1C,
MTRNR2L8,EDARADD,HSP
90AB1,PDZD8,COX8A,CHC
HD6,XPOT,WDR89,PARN,W
DR73,COX4H1,ALDOA,TME
M45A,LDLRAP1,MTRNR2L1
0,TPI1,PRORP,NQO2,CD63,R
PL14,UBC,ATP5MC2,CORO1
C,HMBS,ETV5

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

Pathway ID	Pathway Name	Adjusted p value	Negative log10 of adjusted p value	Gene Count	Gene
Up regulated genes					
REAC:R-HSA-392499	Metabolism of proteins	0.013327181	1.875261715	55	CTBP1,IGFBP2,VGF,RPL21,RPL17,UBA6,CPE,RPS3A,RPS2,HLA-A,MAN1A1,LSAMP,DCUN1D4,IGFBP5,RPL7,APP,RAD52,RPL36A,WSB1,DX17,PCSK2,INO80E,RPS10,EIF1AX,SUMF2,CST3,RAB8A,CHGB,RPS27,USP7,RPL39,EEF2,ITM2B,EIF5A,DPH1,VWA1,RPS26,GNAO1,DNMT1,TPST1,SFTPA1,FBXO44,GANAB,RPL41,B4GALT5,PRKDC,FURIN,HCFC1,GGCX,RPL28,B2M,RNF152,SSR4,RPL23A,NCOR2
REAC:R-HSA-9029569	NR1H3 & NR1H2 regulate gene expression linked to cholesterol transport and efflux	0.125045697	0.902931247	5	ARL4C,TNRC6B,ABCA1,TNRC6A,NCOR2
REAC:R-HSA-422475	Axon guidance	0.132834136	0.876690304	21	RPL21,RPL17,RPS3A,RPS2,RHOB,RPL7,RPL36A,RPS10,ALCAM,RPS27,ITGAV,RPL39,NRP1,PAK3,RPS26,MYH9,RPL41,RPL28,NFASC,SEMA6A,RPL23A
REAC:R-HSA-73857	RNA Polymerase II Transcription	1	0	25	NPY,BAX,OCLN,SKIL,LMO1,VEGFA,NDRG1,JUNB,SREBF1,NR4A1,ARID1B,USP7,ELF2,TNRC6B,SRSF3,KMT2E,ZNF189,ESRRA,U2AF2,TNRC6A,PABPN1,CITED2,BRD1,BCL6,NCOR2
REAC:R-HSA-1852241	Organelle biogenesis and maintenance	1	0	7	RAB8A,DYNLC2II,PAFAH1B1,ESRRA,TCTN2,SSTR3,HCFC1
REAC:R-HSA-6798695	Neutrophil degranulation	1	0	16	ANXA2,CD47,CD44,CD36,HLA-B,CST3,PRSS3,ATP8A1,CYB5R3,ITGAV,EEF2,A1BG,GAA,HMGB1,NFASC,B2M
Down regulated genes					
REAC:R-HSA-1430728	Metabolism	2.56E-11	10.59159661	77	RPS4Y1,RBP4,GPX2,GSTP1,SAT1,PSMB7,CYB5A,ETFB,RPS28,G6PC2,ASAHI,RPL9,ATP5PB,PSMC4,PSMC5,NDUFA9,PPT1,SARS1,PSMD7,BLVRB,ATP5F1C,PRPS2,NDUFA12,CTSA,ATP5MC1,LCLAT1,MPC1,PSMD6,GBA,ENO1,ESD,FDPS,IDH1,PSMB5,PSMB3,NDUFV3,MDH2,TTR,PTGR2,GNPDA1,MDH1,ATP5PO,PSMA4,SCD,SUCLG1,TXN2,ACADM,TXN,BLVRA,PSMB2,UQCRH,MGST3,GLUL,NEU1,GAPDH,PSMD12,

					COX6B1,NDUFB7,ARG2,ATP5F1B,GALT,COX14,PRSS1,PSMF1,NQO1,GPI,HSP90AB1,COX8A,PLA1A,COX4I1,ALDOA,TPI1,NQO2,RPL14,UBC,ATP5MC2,HMBS
REAC:R-HSA-1428517	The citric acid (TCA) cycle and respiratory electron transport	2.21E-08	7.655421329	19	ETFB,ATP5PB,NDUFA9,ATP5F1C,NDUFA12,ATP5MC1,MPC1,NDUFV3,MDH2,ATP5PO,SUCLG1,UQCRH,COX6B1,NDUFB7,ATP5F1B,COX14,COX8A,COX4I1,ATP5MC2
REAC:R-HSA-6798695	Neutrophil degranulation	1.20688E-06	5.918337455	28	FTL,GSTP1,VAMP8,PSMB7,ASAHI,ATP6V1D,PSMD7,CTSA,NIT2,PSMD6,IDH1,XRCC6,PRDX6,TTOR,CYSTMI,VAT1,CAP1,LAMTOR1,NEU1,FTH1,PSMD12,COTL1,HSPA8,PKM,GPI,HSP90AB1,ALDOA,CD63
REAC:R-HSA-70263	Gluconeogenesis	1.32437E-05	4.877991388	8	G6PC2,ENO1,MDH2,MDH1,GAPDH,GPI,ALDOA,TPI1
REAC:R-HSA-392499	Metabolism of proteins	0.00012311	3.909706731	60	RPS4Y1,TUBA4A,IAPP,PSMB7,ETFB,USP22,RPS28,RPL9,PSMC4,UCHL1,PSMC5,SARS1,SSR2,PSMD7,MRPL54,RAB21,CTSA,PSMD6,GBA,PSMB5,MRPS35,PSMB3,EIF3K,TTOR,RAB3B,UBE2L6,TRAPPC2L,PSMA4,KLHL41,PIGP,NAPA,UBE2B,TXN,PSMB2,MRPS15,NEU1,ALG3,EXOSC1,FARSA,CAPZB,PSMD12,DHDDS,ARCNI1,HSPA5,RAD23A,NSMCE2,H2BC12,SPCS2,HSPA8,EIF5A2,GCNT3,PSMF1,CANX,MRPS11,UFD1,TUBA1C,NANS,PARN,RPL14,UBC
REAC:R-HSA-168256	Immune System	0.008098179	2.091612637	58	FTL,TUBA4A,MT2A,IFI30,GSTP1,VAMP8,PSMB7,CAMK2D,BCAP31,ASAHI,ATP6V1B2,PSMC4,ATP6V1D,PSMC5,PSMD7,ATP6V1E1,CTSA,NIT2,PSMD6,IDH1,PSMB5,XRCC6,PSMB3,PRDX6,CLU,TTR,GRB2,POLR3K,UBE2L6,CYSTMI,PSMA4,KLHL41,VAT1,UBE2B,CAP1,TTN,PSMB2,LAMTOR1,NEU1,CAPZB,FTH1,PSMD12,SQSTM1,RNF6,HSPA5,COTL1,HSPA8,PSMF1,PKM,CDC23,CANX,GPI,TUBA1C,EDARADD,HSP90AB1,ALDOA,CD63,UBC

Table 4 Topology table for up and down regulated genes.

Regulation	Node	Degree	Betweenness	Stress	Closeness
Up	APP	674	0.277552	48171576	0.396397
Up	MYH9	231	0.067132	12987566	0.351087
Up	TCTN2	203	0.074204	9822804	0.31559
Up	USP7	156	0.048917	10011292	0.341756
Up	SYNPO	148	0.019807	5325396	0.315343
Up	BCL6	99	0.03129	4924434	0.316788
Up	PRKDC	97	0.02396	5704444	0.339213
Up	U2AF2	77	0.016653	3792650	0.316448
Up	SKIL	72	0.021529	2766174	0.31763
Up	CTBP1	72	0.018919	3933722	0.30334
Up	TOP1	66	0.012706	3485932	0.318522
Up	NDRG1	65	0.014232	2582316	0.327508
Up	NCOR2	62	0.014748	2563224	0.327727
Up	ILF3	62	0.010796	3729048	0.325197
Up	MAPT	59	0.011654	2038018	0.335304
Up	SNRNP70	56	0.013306	2811964	0.337737
Up	NME7	54	0.009971	2818468	0.302345
Up	HCFC1	54	0.011189	4114590	0.285724
Up	SRRM2	53	0.008517	2842260	0.304719
Up	DDX17	48	0.010257	2309956	0.34835
Up	RUNX1T1	45	0.007377	1300474	0.298327
Up	TNRC6B	44	0.005765	1772074	0.294513
Up	RPS3A	43	0.008663	1580346	0.314044
Up	BAX	43	0.010013	1360956	0.305287
Up	ANXA2	42	0.006725	1415220	0.32746
Up	RAB8A	38	0.009675	2880488	0.28541
Up	ALYREF	37	0.006723	3260410	0.299114
Up	OTUD4	36	0.009901	1095992	0.306175
Up	TNRC6A	36	0.006285	1066772	0.298629
Up	LMO1	36	0.007004	1983992	0.281738
Up	NR4A1	35	0.007386	1366096	0.293516
Up	DNMT1	35	0.007153	1311716	0.318247
Up	JUNB	34	0.007201	2171380	0.289501
Up	HNRNPH1	34	0.004039	1126254	0.310822
Up	HNRNPL	33	0.002406	639204	0.306684
Up	EEF2	32	0.00508	1312314	0.31811
Up	RPS2	32	0.005007	944774	0.30743
Up	PGAM5	32	0.004601	1343578	0.295695
Up	CD44	31	0.005854	812632	0.311523
Up	B2M	31	0.005781	1559068	0.265885
Up	RAD52	30	0.004293	852988	0.296289
Up	ATP2A2	30	0.007054	1516120	0.312823
Up	SREBF1	30	0.007025	2186330	0.278526
Up	PAFAH1B1	29	0.005215	2372866	0.276438
Up	NDN	29	0.007043	1329464	0.296547
Up	SRSF3	28	0.003437	1013722	0.303174
Up	APLP1	27	0.006221	892288	0.276818
Up	GANAB	27	0.004094	990330	0.298347
Up	RPL7	26	0.003381	933236	0.310757
Up	MPRIIP	26	0.001472	342632	0.295873
Up	INO80E	25	0.005901	1721260	0.272453
Up	CACNA1A	24	0.010596	1171628	0.281863
Up	CHGB	24	0.006952	765394	0.299337
Up	RPL28	24	0.002372	585818	0.299074
Up	ITSN2	24	0.003281	939596	0.286093
Up	RPS10	23	0.004922	897446	0.326132
Up	RPL23A	23	0.003289	505840	0.311962
Up	PHF1	22	0.003983	1034682	0.277426
Up	HNRNPAB	22	0.001844	495324	0.3108
Up	SH3GL1	22	0.003033	986094	0.270008
Up	HMGB1	21	0.002117	776702	0.290681
Up	PKD3	19	0.002946	742934	0.275937
Up	ARID1B	19	0.004	716712	0.264217
Up	ABCA1	18	0.003966	549762	0.275216
Up	ESRRA	18	0.002502	368532	0.276023
Up	TRA2A	18	0.001473	605004	0.285005

Up	MAGI1	18	0.00426	637328	0.277722
Up	VEGFA	17	0.004134	836256	0.248525
Up	ZC3HAV1	17	0.001292	489318	0.274227
Up	HIVEP1	16	0.001767	378796	0.2718
Up	SIPA1L3	16	0.001056	218866	0.285465
Up	MPP6	16	0.002628	324224	0.275972
Up	RPL17	16	0.001736	515376	0.297165
Up	SSR4	16	0.001986	441016	0.283617
Up	RPS27	15	0.002603	522416	0.297905
Up	SON	15	4.63E-04	263370	0.282512
Up	PDCD4	15	0.001508	323916	0.276732
Up	TMEM79	15	0.004325	604778	0.229337
Up	MAFG	14	0.002447	382134	0.252123
Up	SGSM2	14	0.002229	327358	0.278544
Up	NOL3	14	6.71E-04	214960	0.264091
Up	S100A6	14	9.74E-04	248722	0.280861
Up	MZT2A	14	2.68E-04	75218	0.276801
Up	RPL21	14	0.001091	579282	0.289843
Up	MCPH1	14	8.71E-04	244188	0.255857
Up	LUC7L3	13	0.001174	368838	0.272386
Up	DDX18	13	0.001648	394268	0.31722
Up	TLE3	13	0.002428	330598	0.309193
Up	EIF5A	13	0.002018	470016	0.279742
Up	LENG8	13	0.001599	412736	0.24473
Up	OCN	12	0.001253	314884	0.263462
Up	PABPN1	12	0.001338	370074	0.285705
Up	BRD1	11	0.001735	432360	0.250156
Up	KRT10	11	5.29E-04	212650	0.28389
Up	RPS26	11	6.46E-04	207408	0.291102
Up	TMEM209	11	0.002671	362732	0.281917
Up	TLK1	11	0.001007	270716	0.252627
Up	NPDC1	11	7.46E-04	230746	0.250595
Up	ST14	11	0.001157	228876	0.261871
Up	UBA6	10	0.00209	401360	0.269055
Up	MAP3K12	10	0.00226	336206	0.272201
Up	MAP2	10	0.001373	254464	0.319327
Up	ITGAV	10	0.00199	532090	0.270371
Up	CPE	10	0.001881	615956	0.227778
Up	TFAP4	10	7.77E-04	213056	0.26184
Up	MIER1	10	0.0015	272476	0.264123
Up	CPT1A	9	5.45E-04	93620	0.276438
Up	RGL2	9	6.06E-04	170470	0.251865
Up	CYB5R3	9	9.29E-04	184034	0.256748
Up	DDR1	9	0.001327	189372	0.266558
Up	ATP1B1	9	0.001955	400240	0.267073
Up	NME3	9	0.001643	194338	0.301808
Up	MZT2B	9	1.10E-04	28768	0.258413
Up	ALDH1B1	9	9.67E-04	319144	0.277583
Up	PI4KA	9	7.40E-04	268444	0.277879
Up	CSNK1G2	9	0.001421	396030	0.252931
Up	CITED2	9	0.002327	530770	0.263431
Up	RANBP3	9	0.001499	304686	0.236853
Up	NRP1	8	8.45E-04	148358	0.258398
Up	PGRMC2	8	4.66E-04	87082	0.262275
Up	HLA-B	5	0	0	0.210049
Up	HLA-A	4	7.39E-05	16916	0.249408
Up	EIF1AX	1	0	0	0.28389
Up	ARL4C	1	0	0	0.28389
Up	RPL41	1	0	0	0.28389
Up	UBXN6	1	0	0	0.28389
Up	CDK10	1	0	0	0.267235
Up	DPH1	1	0	0	0.266639
Up	AHDC1	1	0	0	0.259871
Up	SEZ6L2	1	0	0	0.191166
Up	PDCD2	1	0	0	0.222239
Up	PTPN18	1	0	0	0.285576
Up	NISCH	1	0	0	0.285576
Up	RBM33	1	0	0	0.285576
Up	WIPF2	1	0	0	0.285576
Up	MCU	1	0	0	0.225479

Up	ZZEF1	1	0	0	0.241075
Up	FCGRT	1	0	0	0.210049
Up	EMC10	1	0	0	0.239898
Up	PLD3	1	0	0	0.239898
Up	FADS2	1	0	0	0.239898
Up	FAM102A	1	0	0	0.212614
Up	SEMA6A	1	0	0	0.222463
Up	ZFX	1	0	0	0.232008
Up	USP27X	1	0	0	0.21869
Down	GRB2	431	0.172947	23419584	0.399693
Down	HSP90AB1	225	0.07414	15655320	0.364663
Down	UBC	224	0.075316	15138294	0.356148
Down	HSPA5	144	0.05737	10318564	0.363554
Down	SQSTM1	123	0.036494	6909982	0.339317
Down	XRCC6	121	0.034438	8751842	0.335228
Down	HSPA8	120	0.03154	6567910	0.365537
Down	TUBA1C	91	0.023847	3670590	0.328896
Down	TUBG1	81	0.017666	3231832	0.324267
Down	PSMC5	80	0.015146	3450624	0.332456
Down	CSNK2B	77	0.019998	5358078	0.32002
Down	CDC23	75	0.021091	6346650	0.302076
Down	SAT1	69	0.01963	4672960	0.296746
Down	GAPDH	63	0.012495	2722934	0.342046
Down	GABARAP	62	0.01438	2298584	0.299175
Down	RAD23A	56	0.009202	1854168	0.312778
Down	PKM	51	0.009281	2445062	0.320972
Down	DNAJA1	51	0.008274	2322170	0.320763
Down	PSMB3	50	0.005865	1322226	0.308051
Down	EXOSC1	50	0.01119	2195338	0.294709
Down	DDIT3	48	0.01172	2529152	0.297345
Down	NDUFA9	47	0.013121	3147348	0.291102
Down	CANX	46	0.01141	2049224	0.314089
Down	IBTK	45	0.008641	1736696	0.290891
Down	SCNM1	45	0.006692	2252600	0.281594
Down	PSMC4	42	0.003699	829472	0.31331
Down	NDUFA12	42	0.004926	813880	0.250837
Down	MBIP	42	0.01045	2311340	0.274601
Down	PSMD7	41	0.002834	722504	0.302179
Down	USP22	41	0.011629	3407576	0.279884
Down	PSMD6	40	0.001629	559916	0.281863
Down	CLU	40	0.00841	1216580	0.309431
Down	AIFM1	39	0.005419	1729814	0.299966
Down	MORF4L2	39	0.011082	2538970	0.275662
Down	PRDX1	38	0.005407	1341464	0.312403
Down	ARL6IP1	37	0.012555	1641598	0.244635
Down	CAPZB	36	0.004358	1050292	0.311742
Down	PSMD12	34	0.001447	422448	0.305161
Down	PSMB7	34	0.001154	364868	0.289577
Down	BCAP31	34	0.013785	1768344	0.327824
Down	PSMB5	34	0.003403	666674	0.313199
Down	NR0B2	34	0.005798	1517314	0.302138
Down	TUBA4A	33	0.005178	1530624	0.307217
Down	RNF6	33	0.003643	1333208	0.262166
Down	MPP1	32	0.007264	815422	0.302924
Down	CAMK2D	32	0.008412	1997208	0.289805
Down	PSMF1	32	0.006012	1557236	0.280594
Down	ALDOA	31	0.004458	960392	0.311391
Down	PSMA4	30	0.002283	522348	0.297505
Down	PSMB2	30	0.003431	769210	0.296309
Down	UCHL1	28	0.00501	791348	0.328067
Down	TXN2	28	0.00596	1364924	0.272084
Down	ORC3	28	0.005692	1623144	0.284273
Down	CLIC1	27	0.004327	824568	0.304447
Down	UBE2L6	27	0.006391	1958890	0.274499
Down	GBA	26	0.004796	875116	0.282061
Down	ENO1	26	0.00367	1143078	0.306876
Down	RPL14	26	0.004161	1610674	0.298569
Down	FTH1	24	0.004084	777832	0.276783
Down	TXN	24	0.003003	482510	0.302717
Down	GSTP1	24	0.004232	1080546	0.295201

Down	REEP5	24	0.005234	1041918	0.267817
Down	TOX4	23	0.005025	1370332	0.276058
Down	TTR	23	0.003317	617718	0.272823
Down	CORO1C	23	0.001258	341072	0.296269
Down	GTF2B	22	0.004837	1919700	0.246228
Down	PPIB	21	0.002633	702460	0.286557
Down	UFD1	20	0.00202	299278	0.298952
Down	GLUL	20	0.003636	572524	0.266767
Down	SCAMP3	19	0.002153	497590	0.274738
Down	FTL	19	0.004867	440140	0.298006
Down	SLC25A5	19	0.001986	352068	0.310844
Down	UBE2B	19	0.002118	572844	0.260713
Down	ZNF326	19	0.002394	916478	0.295359
Down	LAMTOR1	19	0.004398	814628	0.252454
Down	ZNF410	18	0.004751	566192	0.302386
Down	PRDX6	18	0.002313	594114	0.280327
Down	DRG1	18	0.002816	810156	0.295122
Down	ATP6V1B2	18	0.002914	816976	0.270388
Down	ZNF165	18	0.003519	739876	0.262493
Down	NDUFV3	18	0.001755	335550	0.259292
Down	EIF3K	18	0.004959	1105612	0.27343
Down	NSFL1C	17	0.003491	339954	0.287189
Down	ARCN1	17	0.002733	778374	0.290204
Down	TPI1	17	0.001365	553820	0.293848
Down	ARRDC3	17	0.001321	468292	0.265518
Down	NDUFB8	16	0.001576	271076	0.25175
Down	PRDX5	15	0.00314	356484	0.304824
Down	RPS28	15	0.00171	509708	0.276317
Down	TCEAL4	15	0.002744	249400	0.281451
Down	VAMP8	15	0.003131	687744	0.270437
Down	TRAPPC2L	14	0.004206	559988	0.293516
Down	CNOT6L	14	0.002421	339456	0.257721
Down	ATP6V1D	14	0.002838	320770	0.28589
Down	DYNLRB1	14	0.001865	358956	0.26184
Down	EDARADD	13	0.001601	322314	0.258051
Down	PEF1	13	0.001577	414800	0.268957
Down	FARSA	13	0.001697	508804	0.2652
Down	POLE3	12	0.004074	517276	0.286019
Down	COX4I1	12	0.002449	321508	0.261561
Down	ETV5	12	0.003438	1053244	0.236334
Down	NAPA	12	0.002141	556788	0.283217
Down	VPS25	12	0.002068	519502	0.245014
Down	BEX1	12	0.001246	267736	0.267979
Down	XPOT	11	0.001347	381778	0.281774
Down	MT2A	11	0.001882	359724	0.241562
Down	NDUFB7	11	0.001	155788	0.238231
Down	MRPS35	11	0.00194	415706	0.264107
Down	MRPS15	11	0.001587	179036	0.276058
Down	PLEKHB2	11	0.001437	374900	0.236057
Down	NSMCE2	11	0.001999	798156	0.237464
Down	CTNNA1	11	0.001959	302074	0.253119
Down	PPIL1	11	0.001172	393624	0.278019
Down	PRPS2	10	0.001596	384080	0.259383
Down	COX6B1	10	5.69E-04	148866	0.236765
Down	ETV6	10	0.002363	207722	0.296408
Down	CAP1	10	5.76E-04	164992	0.273972
Down	SPCS2	10	0.001427	294448	0.282801
Down	GRAMD2B	10	0.002536	387376	0.231425
Down	CDC42BPA	10	0.001848	460620	0.252858
Down	ATP6V1E1	2	1.68E-05	7358	0.256421
Down	MPC1	1	0	0	0.230293
Down	TRUB1	1	0	0	0.28389
Down	NANS	1	0	0	0.267235
Down	MDH1	1	0	0	0.267235
Down	GHITM	1	0	0	0.266639
Down	COA3	1	0	0	0.207341
Down	NEU1	1	0	0	0.224518
Down	UQCC2	1	0	0	0.285576
Down	RBP4	1	0	0	0.214355
Down	CUTA	1	0	0	0.226925

Down	GPX2	1	0	0	0.228591
Down	PXK	1	0	0	0.230257
Down	TSPYL5	1	0	0	0.254722
Down	ALG3	1	0	0	0.239898
Down	ZMPSTE24	1	0	0	0.239898
Down	SCD	1	0	0	0.239898
Down	UQCRH	1	0	0	0.200544
Down	EIF5A2	1	0	0	0.232008
Down	ATXN7L3B	1	0	0	0.21869

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

Regulation	Target Genes	Degree	MicroRNA	Regulation	Target Genes	Degree	TF
Up	PRKDC	163	hsa-mir-142-5p	Up	BCL6	60	NOTCH1
Up	MYH9	126	hsa-mir-181b-3p	Up	MYH9	53	PPARD
Up	APP	125	hsa-mir-216b-5p	Up	NCOR2	50	HIF1A
Up	ILF3	107	hsa-mir-3157-3p	Up	APP	45	SMARCA4
Up	SKIL	91	hsa-mir-1294	Up	NDRG1	44	SUZ12
Up	NCOR2	81	hsa-mir-4708-3p	Up	TOP1	41	CREM
Up	U2AF2	65	hsa-mir-196a-5p	Up	ILF3	41	DACH1
Up	NDRG1	60	hsa-mir-374a-5p	Up	MAPT	38	YAP1
Up	TOP1	45	hsa-mir-424-5p	Up	SKIL	37	GATA2
Up	CTBP1	45	hsa-mir-944	Up	PRKDC	36	NUCKS1
Up	BCL6	35	hsa-mir-4701-3p	Up	CTBP1	35	ELF1
Up	USP7	34	hsa-mir-93-5p	Up	U2AF2	34	KDM6A
Up	MAPT	23	hsa-mir-2278	Up	SYNPO	28	SMAD4
Up	SYNPO	15	hsa-mir-138-5p	Up	USP7	27	NANOG
Up	TCTN2	9	hsa-mir-34a-5p	Up	TCTN2	10	SRF
Down	HSPA8	116	hsa-mir-3661	Down	UBC	64	TAF7L
Down	HSP90AB1	103	hsa-mir-200a-3p	Down	HSP90AB1	49	RUNX2
Down	SQSTM1	94	hsa-mir-520d-5p	Down	TUBA1C	47	MITF
Down	HSPA5	88	hsa-mir-573	Down	HSPA5	44	YAP1
Down	GRB2	65	hsa-mir-1291	Down	HSPA8	39	E2F1
Down	SAT1	56	hsa-mir-301b-3p	Down	GAPDH	38	SOX11
Down	UBC	55	hsa-mir-9-5p	Down	GABARAP	38	HOXB4
Down	GAPDH	54	hsa-mir-5690	Down	GRB2	37	TFAP2A
Down	TUBA1C	53	hsa-mir-603	Down	CSNK2B	35	THAP11
Down	CDC23	51	hsa-mir-376a-5p	Down	PSMC5	33	STAT4
Down	TUBG1	32	hsa-mir-182-5p	Down	SQSTM1	30	EP300
Down	XRCC6	31	hsa-mir-618	Down	CDC23	27	TEAD4
Down	GABARAP	26	hsa-mir-34b-3p	Down	SAT1	25	SALL4
Down	PSMC5	10	hsa-mir-452-5p	Down	XRCC6	23	YY1
Down	CSNK2B	9	hsa-mir-149-3p	Down	TUBG1	22	SOX2

Figures

Volcano plot

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 98 nodes and 117 edges for up regulated genes (B) The most significant module was obtained from PPI network with 81 nodes and 248 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 chocolate 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 T2DM. A) APP B) MYH9 C) TCTN2 D) USP7 E) SYNPO F) GRB2 G) HSP90AB1 H) UBC I) HSPA5 J) SQSTM1