Identification of biomarkers, pathways and potential therapeutic targets for heart failure using bioinformatics analysis

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Abstract

Heart failure (HF) is a complex cardiovascular diseases associated with high mortality. To discover key molecular changes in HF, we analyzed next-generation sequencing (NGS) data of HF. In this investigation, differentially expressed genes (DEGs) were analyzed using limma in R package from GSE161472 of the Gene Expression Omnibus (GEO). Then, gene enrichment analysis, protein-protein interaction (PPI) network, miRNA-hub gene regulatory network and TF-hub gene regulatory network construction, and topological analysis were performed on the DEGs by the Gene Ontology (GO), REACTOME pathway, STRING, HiPPIE, miRNet, NetworkAnalyst and Cytoscape. Finally, we performed receiver operating characteristic curve (ROC) analysis of hub genes. A total of 930 DEGs (9464 up regulated genes and 466 down regulated genes) were identified in HF. GO and REACTOME pathway enrichment results showed that DEGs mainly enriched in localization, small molecule metabolic process, SARS-CoV infections and the citric acid (TCA) cycle and respiratory electron transport. Subsequently, the PPI network, miRNA-hub gene regulatory network and TF-hub gene regulatory network were constructed, and 10 hub genes in these network were focused on by centrality analysis and module analysis. Furthermore, data showed that HSP90AA1, ARRB2, MYH9, HSP90AB1, FLNA, EGFR, PIK3R1, CUL4A, YEATS4 and KAT2B were good diagnostic values. In summary, this study suggests that HSP90AA1, ARRB2, MYH9, HSP90AB1, FLNA, EGFR, PIK3R1, CUL4A, YEATS4 and KAT2B may act as the key genes in HF.

Keywords: Heart Failure; Bioinformatics Analysis; Next Generation Sequencing; Differentially Expressed Gene; Hub Gene

Introduction

Heart failure (HF) is one of the chronic cardiovascular diseases, affecting 1% to 2% of the adult population worldwide [1]. HF is said to be inefficiency of the heart to supply the peripheral tissues with the appropriate amount of blood and oxygen to meet their metabolic requirement and is linked with a high risk for subsequent mortality and morbidity [2]. Multiple risk factors might cause HF, including diabetics [3], hypertension [4], obesity [5], genetics [6], environmental triggers [7], and immunity, inflammation, and oxidative stress [8]. Although there are extensive investigation available regarding the etiologies and mechanisms underlying HF, the precise molecular mechanisms remain unclear [9-10]. Therefore, essential molecular markers of HF that are identifiable with more powerful technologies are urgently required.

Understanding the status of various genes and signaling pathway in early diagnosis of HF could improve the effect of initial treatment. COL1A1 [11], CXCL14 [12], MECP2 [13], RBM20 [14], PGC-1 [15], Wnt signaling pathway [16], TGF β 1/Smad3 signaling pathway [17], AT1-CARP signaling pathway [18], Akt signaling pathway [19] and neuregulin-1/ErbB signaling [20] were responsible for progression of HF. Therefore, we aimed to further explore the molecular pathogenesis of HF and identify specific molecular targets. However, these data still demand further clinical interpretation.

Next-generation sequencing (NGS) technology plays a crucial role in the analysis of gene expression, which served as important tools in cardiovascular research with great clinical application [21]. Recently, a large number of gene expression profiling studies have been reported with the use of NGS technology. The integrated bioinformatics analysis will be more positive and provide valuable novel molecular targets to foster the advancement of specific diagnosis and new therapeutic strategies.

In this investigation, NGS dataset (GSE161472) was downloaded from the GEO database (<http://www.ncbi.nlm.nih.gov/geo/>) [22], and crucial genes identified by combining bioinformatics analyses in HF. Gene ontology (GO) terms and REACTOME pathways associated with HF were investigated, and the hub genes associated with HF were identified by protein–protein interaction (PPI)

network, modules, miRNA-hub gene regulatory network and TF-hub gene regulatory network construction and analysis. Subsequently, we validated the hub genes by receiver operating characteristic curve (ROC) analysis. Furthermore, we investigated the potential candidate molecular markers for their utility in diagnosis, prognosis, and drug targeting in HF.

Material and methods

Data resources

This study investigated DEGs in HF versus normal samples by analyzing GSE161472 GEO expression profiling by high throughput sequencing data downloaded from the GEO database. GEO serves as a public repository for experimental high-throughput raw NGS data. Expression profiling by high throughput sequencing profile was generated with the GPL11154 Illumina HiSeq 2000 (Homo sapiens). The GSE161472 dataset included 84 samples, containing 47 HF and 37 normal control samples.

Identification of DEGs

The analysis of screening DEGs between HF and normal control samples was analyzed by limma in R package [23]. Moreover, the threshold for the DEGs was set as $P\text{-value} \leq 0.05$, and $|\log_2\text{foldchange (FC)}| > 0.22$ for up regulated genes and $|\log_2\text{foldchange (FC)}| < -0.18$ for down regulated genes. The heat map and volcano plot of the DEGs were plotted using gplots and ggplot2, respectively.

GO and REACTOME pathway enrichment analysis of DEGs

The GO terms (<http://www.geneontology.org>) database primarily adds three categories: biological process (BP), cellular component (CC), and molecular function (MF) [24]. The REACTOME pathway (<https://reactome.org/>) [25] database compiles genomic, chemical, and systematic functional information. The g:Profiler (<http://biit.cs.ut.ee/gprofiler/>) [26] online tool implements methods to analyze and anticipate functional profiles of gene and gene clusters. In this investigation, GO terms and REACTOME pathways were analyzed using the g:Profiler with the enrichment threshold of $P < 0.05$.

Construction of the PPI network and module analysis

The Human Integrated Protein-Protein Interaction rEference (HiPPIE) interactome (<http://cbdm-01.zdv.uni-mainz.de/~mschaefer/hippie/>) [27] database provides a significant association of protein-protein interaction (PPI). Cytoscape 3.8.2 (<http://www.cytoscape.org/>) [28] is used for the visual exploration of interaction networks. In this investigation, DEGs PPI networks were analyzed by the HiPPIE database and subsequently visualized by using Cytoscape. In addition, the node degree [29], betweenness centrality [30], stress centrality [31] and closeness centrality [32] of each protein node in the PPI network was calculated using plug-in Network Analyzer of the Cytoscape software. PEWCC1 (<http://apps.cytoscape.org/apps/PEWCC1>) [33] plug-in of the Cytoscape software was then used to screen out modules of PPI networks, and the degree cutoff = 2, node score cutoff = 0.2, k-core = 2, and max depth = 100.

MiRNA-hub gene regulatory network construction

The miRNet database (<https://www.mirnet.ca/>) [34], a web biological database for prediction of known and unknown miRNA and hub genes relationships, was used to construct the miRNA-hub gene regulatory network, which was visualized in Cytoscape 3.8.2 [28].

TF-hub gene regulatory network construction

TF-hub gene regulatory network analysis is useful to analyze the interactions between hub genes and TF which might provide insights into the mechanisms of generation or development of diseases. NetworkAnalyst database (<https://www.networkanalyst.ca/>) [35] and Cytoscape 3.8.2 [28] software were used to build the TF-hub gene regulatory network.

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

Then ROC curve analysis was implemented to calculate the sensitivity (true positive rate) and specificity (true negative rate) of the hub genes for HF diagnosis and we investigated how large the area under the curve (AUC) was by using pROC package in R statistical software [36]. The diagnostic values of the hub genes were predicted based on the ROC curve analysis.

Results

Identification of DEGs

Dataset GSE161472 was downloaded from the GEO database and analyzed using R packages (limma). Volcano plot was constructed to visualize fold changes of the DEGs (Fig. 1). A total of 930 DEGs were identified in GSE161472, among which a total of 464 were up regulated genes and 466 were down regulated genes and are listed in Table 1. The DEGs in the NSG data are shown as volcano plots in Fig. 1. The 464 up regulated genes and 466 down regulated genes are shown in heatmap and were shown in Fig. 2.

GO and REACTOME pathway enrichment analysis of DEGs

The top 930 DEGs were chosen to perform GO term and REACTOME pathway analyses. We detected enrichment in several BP GO terms such as localization, organic substance transport, small molecule metabolic process and cellular metabolic process and are listed in Table 2. In terms of CC, cytoplasm, membrane, intracellular anatomical structure and organelle lumen and are listed in Table 2. What's more, some MF GO terms, such as protein binding, enzyme binding, catalytic activity and nucleoside phosphate binding, and are listed in Table 2. As to REACTOME pathway enrichment analysis, SARS-CoV infections, asparagine N-linked glycosylation, the citric acid (TCA) cycle and respiratory electron transport, and respiratory electron transport were mostly associated with these genes and are listed in Table 3.

Construction of the PPI network and module analysis

Using Cytoscape, a HIPPIE interactome database was used to establish a PPI network of these DEGs, with 4194 nodes and 8352 edges (Fig. 3). Based on the HIPPIE database, the DEGs with the highest PPI scores identified by the 4 centrality methods are shown in Table 4. The hub genes were obtained using the 4 centrality methods, including HSP90AA1, ARRB2, MYH9, HSP90AB1, FLNA, EGFR, PIK3R1, CUL4A, YEATS4 and KAT2B. A significant module was constructed from the PPI network of the DEGs using PEWCC1, including module 1 had 35 nodes and 124 edges (Fig. 4A) and module 2 had 14 nodes and 34 edges (Fig. 4B). GO and REACTOME pathway enrichment analysis showed that genes in these modules were markedly enriched in disease, immune system, cytoplasm, neutrophil degranulation, protein binding, infectious disease, SARS-CoV

infections, localization, organic substance transport, the citric acid (TCA) cycle and respiratory electron transport, respiratory electron transport and metabolism.

MiRNA-hub gene regulatory network construction

According to the information in miRNet database and Cytoscape databases, the miRNA-hub gene regulatory network relationships of miRNA and hub genes were obtained (Fig. 5). After comparing the targets with hub genes, we found that MYH9 was the potential target of 226 miRNAs (ex; hsa-mir-520e); TUBB was the potential target of 202 miRNAs (ex; hsa-mir-8084); XPO1 was the potential target of 198 miRNAs (ex; hsa-mir-125a-5p); HSP90AA1 was the potential target of 188 miRNAs (ex; hsa-mir-133a-3p); HSP90AB1 was the potential target of 162 miRNAs (ex; hsa-mir-4801); PIK3R1 was the potential target of 131 miRNAs (ex; hsa-mir-138-5p); NCOA2 was the potential target of 114 miRNAs (ex; hsa-mir-539-5p); EGFR was the potential target of 83 miRNAs (ex; hsa-mir-132-3p); IFIT3 was the potential target of 78 miRNAs (ex; hsa-mir-449a); PSMB9 was the potential target of 68 miRNAs (ex; hsa-mir-200c-5p).

TF-hub gene regulatory network construction

According to the information in NetworkAnalyst database and Cytoscape databases, the TF-hub gene regulatory network relationships of TF and hub genes were obtained (Fig. 6). After comparing the targets with hub genes, we found that HSP90AA1 was the potential target of 35 TFs (ex; RUNX1T1); XPO1 was the potential target of 33 TFs (ex; STAT1); SMARCA4 was the potential target of 33 TFs (ex; EGR1); HSPA5 was the potential target of 22 TFs (ex; FOSB); ARRB2 was the potential target of 20 TFs (ex; ARNT); KAT2B was the potential target of 47 TFs (ex; TWIST1); ZBTB16 was the potential target of 47 TFs (ex; GATA2); ZBTB16 was the potential target of 39 TFs (ex; GATA2); NCOA2 was the potential target of 34 TFs (ex; AHR); PIK3R1 was the potential target of 34 TFs (ex; GTF2H1); EGFR was the potential target of 27 TFs (ex; STAT5B).

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

A ROC curve was plotted to evaluate the diagnostic value of HSP90AA1, ARRB2, MYH9, HSP90AB1, FLNA, EGFR, PIK3R1, CUL4A, YEATS4 and

KAT2B (Fig. 7). The AUCs for the 10 hub genes were 0.953, 0.941, 0.976, 0.948, 0.931, 0.969, 0.958, 0.906, 0.912 and 0.950, respectively. These hub genes show good diagnostics values.

Discussion

Although many relevant investigation of HF have been operated, early diagnoses, adequacy of treatment and prognosis for HF remain poorly concluded. For diagnosis and treatment, it is vital to more interpret the molecular mechanisms resulting in occurrence and advancement. Bioinformatics analysis is progressively adopted to screen out biomarkers have a guiding role in the diagnosis and treatment of HF [37].

In this investigation, we performed a series of bioinformatics analysis to screen key genes and pathways. The expression profiling by high throughput sequencing data found that 464 up regulated genes and 466 down regulated genes were identified in HF samples compared to normal control samples. ZFP57 [38] and ANK1 [39] contributes to the progression of diabetics, but these genes might be novel target for HF. TNC (tenascin C) has been shown to be activated in cardiac hypertrophy [40]. CCL2 is mainly involved in the progression of myocardial infarction [41]. SPP1[42] and IGSF1 [43] plays an important role in obesity, but these genes might be novel target for HF. Kiczak et al [44] found that TIMP1 was highly expressed in the HF.

GO and REACTOME pathway enrichment analyses were used to investigate the interactions of these DEGs. SARS-CoV infections [45], asparagine N-linked glycosylation [46], neutrophil degranulation [47], immune system [48], respiratory electron transport [49], metabolism [50], complex I biogenesis [51], neddylation [52], localization [53], membrane [54], protein binding [55], small molecule metabolic process [56] and were responsible for progression of HF. Han et al [57], Yamada et al [58], Wang et al [59], García-Manzanares et al [60], Raitoharju et al [61], King et al [62], Hirokawa et al [63], Kahali et al [64], Sun et al [65] and Kuhn et al [66] found expression of DHCR24, STXBP2, CLEC5A, XPO1, ADAM8, IRF3, DOT1L, PPP1R3B, IFIT3 and PCSK6 in myocardial infarction and indicated it as a potential gene markers. Expression of CYP1B1 [67], SLC7A1 [68], MYH9 [69], LAT2 [70], FXYS5 [71], CAMK1 [72],

TGFBR1 [73], HSP90AB1 [74], PLEKHA7 [75], AGTRAP (angiotensin II receptor associated protein) [76], SLC16A9 [77], ACADSB (acyl-CoA dehydrogenase short/branched chain) [78], IMPA1 [79], CD300LG [80], CIRBP (cold inducible RNA binding protein) [81], PIK3R1 [82], YEATS4 [83], USP2 [84], NEDD9 [85], CHCHD5 [86] and ERAP1 [87] promotes hypertension. HSPB1 [88], CRYAB (crystallin alpha B) [89], ANXA5 [90], CCR2 [91], RGS4 [92], TNFRSF1A [93], XBP1 [94], NKX2-5 [95], NEU1 [96], GSTP1 [97], COMT (catechol-O-methyltransferase) [98], LIMK1 [99], CAMKK1 [100], CD276 [101], SMARCA4 [102], ADORA2B [103], ACOT1 [104], RGN (regucalcin) [105], PPA2 [106], KAT2B [107], PDK1 [108], CS (citrate synthase) [109], FGF12 [110], AQP4 [111], LMOD2 [112], SELENBP1 [113], MB (myoglobin) [114], S100A1 [115], RYR2 [116], GPC5 [117], JARID2 [118], EGFR (epidermal growth factor receptor) [119], FUNDC1 [120], S1PR1 [121], EPAS1 [122] and OSBPL11 [123] genes are a potential biomarkers for the detection and prognosis of HF at an early age. A previous study reported that CALR (calreticulin) [124], BSCL2 [125], PKD1 [126], TMEM16 [127], CHST15 [128], NAA10 [129], TCF3 [130], CNN1 [131], TAF1A [132], ACAD9 [133], KLHL24 [134], MYOM2 [135], TRIM63 [136], CTNNA3 [137], NLRC5 [138], KLF9 [139], MYLK3 [140], RBM20 [141], GSTK1 [142], UQCRC1 [143], NDUFS2 [144] and COX6B1 [145] are expressed in cardiomyopathy. Other research have revealed that RTN4 [146], NCF2 [147], ARHGAP9 [148], LIPG (lipase G, endothelial type) [149], BCL3 [150], HSPG2 [151], APOBR (apolipoprotein B receptor) [152], ITGA2 [153], PPIA (peptidylprolylisomerase A) [154], IRAK1 [155], VKORC1 [156], RNLS (renalase, FAD dependent amine oxidase) [157], HLA-F [158], FBXL17 [159], COL11A2 [160] and NDUFC2 [161] are expressed in coronary heart disease, suggesting that it might also function in coronary heart disease transformation and development. CCR1 [162], MANF (mesencephalic astrocyte derived neurotrophic factor) [163], HSP90AA1 [164], ARRB2 [165], SLC39A13 [166], P4HA2 [167], HECTD3 [168], CNPY2 [169], ECHDC2 [170], NDUFS4 [171] and IMMT (inner membrane mitochondrial protein) [172] are a key initiators of ischemic cardiac diseases. Mounting evidence indicates that expression of PEA3 [173], CD48 [174], EDEM2 [175], CD55 [176], NCOR2 [177], EXT2 [178], SPRED1 [179], PDIA6 [180], CD300E [181], TCF19 [182], ABHD15 [183], OXSM (3-oxoacyl-ACP synthase, mitochondrial) [184], MGST3 [185], COQ7 [186], ACSL5 [187], ANK1 [188], PYGM (glycogen

phosphorylase, muscle associated) [189], FBXO40 [190], SLC2A4 [191], HLA-DOA [192], TAP2 [193], HLA-DPA1 [194], NSMCE2 [195], NDUFA4 [196], HMG20A [197], AMY2B [198] and ACYP2 [199] might be involved in the pathogenesis of diabetics, but these genes might be novel target for HF. Recent evidence indicates that the SIRPA (signal regulatory protein alpha) [200], PFN1 [201], EIF6 [202], AHR (aryl hydrocarbon receptor) [203], RUNX1 [204], IDO1 [205], PDHB (pyruvate dehydrogenase E1 subunit beta) [206], NDUFS1 [207], MTUS1 [208], ZNF418 [209] and MTMR14 [210] are the key biomarkers in cardiac hypertrophy. Previous studies had shown that the expression of CLIC1 [211], ARPC1B [212], FLNA (filamin A) [213], HILPDA (hypoxia inducible lipid droplet associated) [214], RTN3 [215], G0S2 [216], CALU (calumenin) [217], MYDGF (myeloid derived growth factor) [218], LTBR (lymphotoxin beta receptor) [219], GGCX (gamma-glutamyl carboxylase) [220], SAMD1 [221], ACAT1 [222], NNT (nicotinamide nucleotide transhydrogenase) [223] and ATG14 [224] were closely related to the occurrence of atherosclerosis. HSPA5 [225], NMB (neuromedin B) [226], ELP5 [227], NLGN2 [228], RAB23 [229], MBOAT7 [230], CEP19 [231], PFKP (phosphofructokinase, platelet) [232], TKT (transketolase) [233], P4HB [234], CRYM (crystallin mu) [235], AMT (aminomethyltransferase) [236], MACROD2 [237], NUDT3 [238], DLD (dihydrolipoamide dehydrogenase) [239], NCOA2 [240], ZBTB16 [241], TFAM (transcription factor A, mitochondrial) [242], RASAL2 [243], NDUFB6 [244], HELZ2 [245] and CIITA (class II major histocompatibility complex transactivator) [246] were reported to be expressed in obesity, but these genes might be novel target for HF. TGFB1 [247], CD63 [248], DACT1 [249] and PSMB10 [250] have been reported to be crucial for the progression of atrial fibrillation. FAM20C [251] and CD74 [252] are important in the development of cardiac arrhythmia.

To explore the pathogenesis of HF, we constructed PPI network and isolated modules from PPI network for systematic analysis. The genes in the PPI network and modules with higher score were the hub genes that affected the progression of disease. CLTA (clathrin light chain A), RAI14, MPRIP (myosin phosphatase Rho interacting protein), AP2A1, CUL4A and NDUFA13 were the novel biomarkers for the progression of HF.

We further constructed a miRNA-hub gene regulatory network and TF-hub gene regulatory network for better understanding of the interaction between

miRNA and hub genes, and TF and hub genes. Hsa-mir-125a-5p [253], hsa-mir-539-5p [254] and RUNX1T1 [255] were linked with progression of obesity, but these genes might be novel target for HF. Hsa-mir-138-5p [256] and STAT1 [257] were involved in the progression of HF. Hsa-mir-200c-5p [258] and STAT5B [259] were associated with development of diabetics, but these genes might be novel target for HF. EGR1 [260] and GATA2 [261] were liable for advancement of coronary heart disease. FOSB [262] and AHR [263] were associated with development of ischemic cardiac diseases. TWIST1 was responsible for progression of atherosclerosis [264]. TUBB (tubulin beta class I), hsa-mir-520e, hsa-mir-8084, hsa-mir-133a-3p, hsa-mir-4801, hsa-mir-132-3p, hsa-mir-449a, ARNT, and GTF2H1 were the novel biomarkers for the progression of HF.

In summary, the present data provide a comprehensive bioinformatics analysis of DEGs that might be related to the progression of HF. We have identified 930 candidate DEGs with NGS data and integrated bioinformatics analyses. A variety of novel genes and signaling pathways might be associated in the pathogenesis of HF. We also conclude that HSP90AA1, ARRB2, MYH9, HSP90AB1, FLNA, EGFR, PIK3R1, CUL4A, YEATS4 and KAT2B might be associated with progression of HF. These findings could lead to an increase in our understanding of the etiology and underlying molecular events of HF.

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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. [(GSE161472) <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE161472>)]

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

Author Contributions

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

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References

1. Tanai E, Frantz S. Pathophysiology of Heart Failure. Compr Physiol. 2015;6(1):187-214. doi:[10.1002/cphy.c140055](https://doi.org/10.1002/cphy.c140055)
2. Yap J. Risk stratification in heart failure: Existing challenges and potential promise. Int J Cardiol. 2020;313:97-98. doi:[10.1016/j.ijcard.2020.04.042](https://doi.org/10.1016/j.ijcard.2020.04.042)
3. Ohkuma T, Komorita Y, Peters SAE, Woodward M. Diabetes as a risk factor for heart failure in women and men: a systematic review and meta-analysis of 47 cohorts including 12 million individuals. Diabetologia. 2019;62(9):1550-1560. doi:[10.1007/s00125-019-4926-x](https://doi.org/10.1007/s00125-019-4926-x)

4. Messerli FH, Rimoldi SF, Bangalore S. The Transition From Hypertension to Heart Failure: Contemporary Update. *JACC Heart Fail.* 2017;5(8):543-551. doi:[10.1016/j.jchf.2017.04.012](https://doi.org/10.1016/j.jchf.2017.04.012)
5. Ayinapudi K, Samson R, Le Jemtel TH, Marrouche NF, Oparil S. Weight Reduction for Obesity-Induced Heart Failure with Preserved Ejection Fraction. *Curr Hypertens Rep.* 2020;22(8):47. doi:[10.1007/s11906-020-01074-w](https://doi.org/10.1007/s11906-020-01074-w)
6. Skrzynia C, Berg JS, Willis MS, Jensen BC. Genetics and heart failure: a concise guide for the clinician. *Curr Cardiol Rev.* 2015;11(1):10-17. doi:[10.2174/1573403x09666131117170446](https://doi.org/10.2174/1573403x09666131117170446)
7. Escolar V, Lozano A, Larburu N, Kerexeta J, Álvarez R, Juez B, Echebarria A, Azcona A, Artola G. Impact of environmental factors on heart failure decompensations. *ESC Heart Fail.* 2019;6(6):1226-1232. doi:[10.1002/ehf2.12506](https://doi.org/10.1002/ehf2.12506)
8. Ayoub KF, Pothineni NVK, Rutland J, Ding Z, Mehta JL. Immunity, Inflammation, and Oxidative Stress in Heart Failure: Emerging Molecular Targets. *Cardiovasc Drugs Ther.* 2017;31(5-6):593-608. doi:[10.1007/s10557-017-6752-z](https://doi.org/10.1007/s10557-017-6752-z)
9. Ziaeian B, Fonarow GC. Epidemiology and aetiology of heart failure. *Nat Rev Cardiol.* 2016;13(6):368-378. doi:[10.1038/nrcardio.2016.25](https://doi.org/10.1038/nrcardio.2016.25)
10. Latronico MV, Elia L, Condorelli G, Catalucci D. Heart failure: targeting transcriptional and post-transcriptional control mechanisms of hypertrophy for treatment. *Int J Biochem Cell Biol.* 2008;40(9):1643-1648. doi:[10.1016/j.biocel.2008.03.002](https://doi.org/10.1016/j.biocel.2008.03.002)
11. Hua X, Wang YY, Jia P, Xiong Q, Hu Y, Chang Y, Lai S, Xu Y, Zhao Z, Song J. Multi-level transcriptome sequencing identifies COL1A1 as a candidate marker in human heart failure progression. *BMC Med.* 2020;18(1):2. doi:[10.1186/s12916-019-1469-4](https://doi.org/10.1186/s12916-019-1469-4)
12. Zeng L, Gu N, Chen J, Jin G, Zheng Y. IRX1 hypermethylation promotes heart failure by inhibiting CXCL14 expression. *Cell Cycle.* 2019;18(23):3251-3262. doi:[10.1080/15384101.2019.1673099](https://doi.org/10.1080/15384101.2019.1673099)
13. Wang C, Wang F, Cao Q, Li Z, Huang L, Chen S. The Effect of Mecp2 on Heart Failure. *Cell Physiol Biochem.* 2018;47(6):2380-2387. doi:[10.1159/000491610](https://doi.org/10.1159/000491610)

14. Ma J, Lu L, Guo W, Ren J, Yang J. Emerging Role for RBM20 and its Splicing Substrates in Cardiac Function and Heart Failure. *Curr Pharm Des.* 2016;22(31):4744-4751. doi:[10.2174/1381612822666160701145322](https://doi.org/10.2174/1381612822666160701145322)
15. Schilling J, Kelly DP. The PGC-1 cascade as a therapeutic target for heart failure. *J Mol Cell Cardiol.* 2011;51(4):578-583. doi:[10.1016/j.yjmcc.2010.09.021](https://doi.org/10.1016/j.yjmcc.2010.09.021)
16. Stylianidis V, Hermans KCM, Blankesteijn WM. Wnt Signaling in Cardiac Remodeling and Heart Failure. *Handb Exp Pharmacol.* 2017;243:371-393. doi:[10.1007/164_2016_56](https://doi.org/10.1007/164_2016_56)
17. Chen K, Chen W, Liu SL, Wu TS, Yu KF, Qi J, Wang Y, Yao H, Huang XY, Han Y, et al. Epigallocatechingallate attenuates myocardial injury in a mouse model of heart failure through TGF β 1/Smad3 signaling pathway. *Mol Med Rep.* 2018;17(6):7652-7660. doi:[10.3892/mmr.2018.8825](https://doi.org/10.3892/mmr.2018.8825)
18. Wang X, Meng H, Wang Q, Shao M, Lu W, Chen X, Jiang Y, Li C, Wang Y, Tu P. et al. Baoyuan decoction ameliorates apoptosis via AT1-CARP signaling pathway in H9C2 cells and heart failure post-acute myocardial infarction rats. *J Ethnopharmacol.* 2020;252:112536. doi:[10.1016/j.jep.2019.112536](https://doi.org/10.1016/j.jep.2019.112536)
19. Ananthakrishnan R, Moe GW, Goldenthal MJ, Marín-García J. Akt signaling pathway in pacing-induced heart failure. *Mol Cell Biochem.* 2005;268(1-2):103-110. doi:[10.1007/s11010-005-3699-3](https://doi.org/10.1007/s11010-005-3699-3)
20. Xu Y, Li X, Liu X, Zhou M. Neuregulin-1/ErbB signaling and chronic heart failure. *Adv Pharmacol.* 2010;59:31-51. doi:[10.1016/S1054-3589\(10\)59002-1](https://doi.org/10.1016/S1054-3589(10)59002-1)
21. Abplanalp WT, John D, Cremer S, Assmus B, Dorsheimer L, Hoffmann J, Becker-Pergola G, Rieger MA, Zeiher AM, Vasa-Nicotera M, et al. Single-cell RNA-sequencing reveals profound changes in circulating immune cells in patients with heart failure. *Cardiovasc Res.* 2021;117(2):484-494. doi:[10.1093/cvr/cvaa101](https://doi.org/10.1093/cvr/cvaa101)
22. Clough E, Barrett T. The Gene Expression Omnibus Database. *Methods Mol Biol.* 2016;1418:93-110. doi:[10.1007/978-1-4939-3578-9_5](https://doi.org/10.1007/978-1-4939-3578-9_5)
23. Ritchie ME, Phipson B, Wu D, Hu Y, Law CW, Shi W, Smyth GK. limma powers differential expression analyses for RNA-sequencing and microarray studies. *Nucleic Acids Res.* 2015;43(7):e47. doi:[10.1093/nar/gkv007](https://doi.org/10.1093/nar/gkv007)

24. Thomas PD. The Gene Ontology and the Meaning of Biological Function. *Methods Mol Biol.* 2017;1446:15–24. doi:[10.1007/978-1-4939-3743-1_2](https://doi.org/10.1007/978-1-4939-3743-1_2)
25. Fabregat A, Jupe S, Matthews L, Sidiropoulos K, Gillespie M, Garapati P, Haw R, Jassal B, Korninger F, May B et al The Reactome Pathway Knowledgebase. *Nucleic Acids Res.* 2018;46(D1):D649–D655. doi:[10.1093/nar/gkx1132](https://doi.org/10.1093/nar/gkx1132)
26. Reimand J, Kull M, Peterson H, Hansen J, Vilo J. g:Profiler--a web-based toolset for functional profiling of gene lists from large-scale experiments. *Nucleic Acids Res.* 2007;35(Web Server issue):W193–W200. doi:[10.1093/nar/gkm226](https://doi.org/10.1093/nar/gkm226)
27. Alanis-Lobato G, Andrade-Navarro MA, Schaefer MH. HIPPIE v2.0: enhancing meaningfulness and reliability of protein-protein interaction networks. *Nucleic Acids Res.* 2017;45(D1):D408–D414. doi:[10.1093/nar/gkw985](https://doi.org/10.1093/nar/gkw985)
28. Shannon P, Markiel A, Ozier O, Baliga NS, Wang JT, Ramage D, Amin N, Schwikowski B, Ideker T Cytoscape: a software environment for integrated models of biomolecular interaction networks. *Genome Res* 2003;13(11):2498–2504. doi:[10.1101/gr.1239303](https://doi.org/10.1101/gr.1239303)
29. Przulj N, Wigle DA, Jurisica I. Functional topology in a network of protein interactions. *Bioinformatics.* 2004;20(3):340–348. doi:[10.1093/bioinformatics/btg415](https://doi.org/10.1093/bioinformatics/btg415)
30. Nguyen TP, Liu WC, Jordán F. Inferring pleiotropy by network analysis: linked diseases in the human PPI network. *BMC Syst Biol.* 2011;5:179. doi:[10.1186/1752-0509-5-179](https://doi.org/10.1186/1752-0509-5-179)
31. Shi Z, Zhang B. Fast network centrality analysis using GPUs. *BMC Bioinformatics.* 2011;12:149. doi:[10.1186/1471-2105-12-149](https://doi.org/10.1186/1471-2105-12-149)
32. Fadhal E, Gamielien J, Mwambene EC. Protein interaction networks as metric spaces: a novel perspective on distribution of hubs. *BMC Syst Biol.* 2014;8:6. doi:[10.1186/1752-0509-8-6](https://doi.org/10.1186/1752-0509-8-6)
33. Zaki N, Efimov D, Berenguères J. Protein complex detection using interaction reliability assessment and weighted clustering coefficient. *BMC Bioinformatics.* 2013;14:163. doi:[10.1186/1471-2105-14](https://doi.org/10.1186/1471-2105-14)
34. Fan Y, Xia J (2018) miRNet-Functional Analysis and Visual Exploration of miRNA-Target Interactions in a Network Context. *Methods Mol Biol* 1819:215–233. doi:[10.1007/978-1-4939-8618-7_10](https://doi.org/10.1007/978-1-4939-8618-7_10)

35. Zhou G, Soufan O, Ewald J, Hancock REW, Basu N, Xia J (2019) NetworkAnalyst 3.0: a visual analytics platform for comprehensive gene expression profiling and meta-analysis. *Nucleic Acids Res* 47:W234-W241. doi:[10.1093/nar/gkz240](https://doi.org/10.1093/nar/gkz240)
36. Robin X, Turck N, Hainard A, Tiberti N, Lisacek F, Sanchez JC, Müller M. pROC: an open-source package for R and S+ to analyze and compare ROC curves. *BMC Bioinformatics* 2011;12:77. doi:[10.1186/1471-2105-12-77](https://doi.org/10.1186/1471-2105-12-77)
37. Li X, Li B, Jiang H. Identification of time-series differentially expressed genes and pathways associated with heart failure post-myocardial infarction using integrated bioinformatics analysis. *Mol Med Rep.* 2019;19(6):5281-5290. doi:[10.3892/mmr.2019.10190](https://doi.org/10.3892/mmr.2019.10190)
38. Touati A, Errea-Dorronsoro J, Nouri S, Halleb Y, Pereda A, Mahdhaoui N, Ghith A, Saad A, Perez de Nanclares G, H'mida Ben Brahim D. Transient neonatal diabetes mellitus and hypomethylation at additional imprinted loci: novel ZFP57 mutation and review on the literature. *Acta Diabetol.* 2019;56(3):301-307. doi:[10.1007/s00592-018-1239-3](https://doi.org/10.1007/s00592-018-1239-3)
39. Sun L, Zhang X, Wang T, Chen M, Qiao H. Association of ANK1 variants with new-onset type 2 diabetes in a Han Chinese population from northeast China. *Exp Ther Med.* 2017;14(4):3184-3190. doi:[10.3892/etm.2017.4866](https://doi.org/10.3892/etm.2017.4866)
40. Song L, Wang L, Li F, Yukht A, Qin M, Ruther H, Yang M, Chaux A, Shah PK, Sharifi BG. Bone Marrow-Derived Tenascin-C Attenuates Cardiac Hypertrophy by Controlling Inflammation. *J Am Coll Cardiol.* 2017;70(13):1601-1615. doi:[10.1016/j.jacc.2017.07.789](https://doi.org/10.1016/j.jacc.2017.07.789)
41. Dewald O, Zymek P, Winkelmann K, Koerting A, Ren G, Abou-Khamis T, Michael LH, Rollins BJ, Entman ML, Frangogiannis NG. CCL2/Monocyte Chemoattractant Protein-1 regulates inflammatory responses critical to healing myocardial infarcts. *Circ Res.* 2005;96(8):881-889. doi:[10.1161/01.RES.0000163017.13772.3a](https://doi.org/10.1161/01.RES.0000163017.13772.3a)
42. Yang H, Graham LC, Reagan AM, Grabowska WA, Schott WH, Howell GR. Transcriptome profiling of brain myeloid cells revealed activation of Itgal, Trem1, and Spp1 in western diet-induced obesity. *J Neuroinflammation.* 2019;16(1):169. doi:[10.1186/s12974-019-1527-z](https://doi.org/10.1186/s12974-019-1527-z)
43. Ghanny S, Zidell A, Pedro H, Joustra SD, Losekoot M, Wit JM, Aisenberg J. The IGSF1 Deficiency Syndrome May Present with Normal Free T4 Levels, Severe Obesity, or Premature Testicular Growth. *J Clin Res Pediatr*

- Endocrinol. 2020;10.4274/jcrpe.galenos.2020.2020.0125.
doi:[10.4274/jcrpe.galenos.2020.2020.0125](https://doi.org/10.4274/jcrpe.galenos.2020.2020.0125)
- 44.Kiczak L, Tomaszek A, Bania J, Paslawska U, Zacharski M, Noszczyk-Nowak A, Janiszewski A, Skrzypczak P, Ardehali H, Jankowska EA, et al. Expression and complex formation of MMP9, MMP2, NGAL, and TIMP1 in porcine myocardium but not in skeletal muscles in male pigs with tachycardia-induced systolic heart failure. *Biomed Res Int.* 2013;2013:283856. doi:[10.1155/2013/283856](https://doi.org/10.1155/2013/283856)
 - 45.Belhadjer Z, Méot M, Bajolle F, Khraiche D, Legendre A, Abakka S, Auriau J, Grimaud M, Oualha M, Beghetti M, et al. Acute Heart Failure in Multisystem Inflammatory Syndrome in Children in the Context of Global SARS-CoV-2 Pandemic. *Circulation.* 2020;142(5):429-436. doi:[10.1161/CIRCULATIONAHA.120.048360](https://doi.org/10.1161/CIRCULATIONAHA.120.048360)
 - 46.Yang S, Chatterjee S, Cipollo J. The Glycoproteomics-MS for Studying Glycosylation in Cardiac Hypertrophy and Heart Failure. *Proteomics Clin Appl.* 2018;12(5):e1700075. doi:[10.1002/prca.201700075](https://doi.org/10.1002/prca.201700075)
 - 47.Bai B, Cheng M, Jiang L, Xu J, Chen H, Xu Y. High Neutrophil to Lymphocyte Ratio and Its Gene Signatures Correlate With Diastolic Dysfunction in Heart Failure With Preserved Ejection Fraction. *Front Cardiovasc Med.* 2021;8:614757. doi:[10.3389/fcvm.2021.614757](https://doi.org/10.3389/fcvm.2021.614757)
 - 48.De Angelis E, Pecoraro M, Rusciano MR, Ciccarelli M, Popolo A. Cross-Talk between Neurohormonal Pathways and the Immune System in Heart Failure: A Review of the Literature. *Int J Mol Sci.* 2019;20(7):1698. doi:[10.3390/ijms20071698](https://doi.org/10.3390/ijms20071698)
 - 49.Casademont J, Miró O. Electron transport chain defects in heart failure. *Heart Fail Rev.* 2002;7(2):131-139. doi:[10.1023/a:1015372407647](https://doi.org/10.1023/a:1015372407647)
 - 50.Fukushima A, Milner K, Gupta A, Lopaschuk GD. Myocardial Energy Substrate Metabolism in Heart Failure : from Pathways to Therapeutic Targets. *Curr Pharm Des.* 2015;21(25):3654-3664. doi:[10.2174/1381612821666150710150445](https://doi.org/10.2174/1381612821666150710150445)
 - 51.Pisano A, Cerbelli B, Perli E, Pelullo M, Bargelli V, Preziuso C, Mancini M, He L, Bates MG, Lucena JR, et al. Impaired mitochondrial biogenesis is a common feature to myocardial hypertrophy and end-stage ischemic heart failure. *Cardiovasc Pathol.* 2016;25(2):103-112. doi:[10.1016/j.carpath.2015.09.009](https://doi.org/10.1016/j.carpath.2015.09.009)

52. Zou J, Ma W, Littlejohn R, Li J, Stansfield BK, Kim IM, Liu J, Zhou J, Weintraub NL, Su H. Transient inhibition of neddylation at neonatal stage evokes reversible cardiomyopathy and predisposes the heart to isoproterenol-induced heart failure. *Am J Physiol Heart Circ Physiol*. 2019;316(6):H1406-H1416. doi:[10.1152/ajpheart.00806.2018](https://doi.org/10.1152/ajpheart.00806.2018)
53. Treskatsch S, Feldheiser A, Shaqura M, Dehe L, Habazettl H, Röpke TK, Shakibaei M, Schäfer M, Spies CD, Mousa SA. Cellular localization and adaptive changes of the cardiac delta opioid receptor system in an experimental model of heart failure in rats. *Heart Vessels*. 2016;31(2):241-250. doi:[10.1007/s00380-014-0620-6](https://doi.org/10.1007/s00380-014-0620-6)
54. Dangers L, Bréchet N, Schmidt M, Lebreton G, Hékimian G, Nieszkowska A, Besset S, Trouillet JL, Chastre J, Leprince P, et al. Extracorporeal Membrane Oxygenation for Acute Decompensated Heart Failure. *Crit Care Med*. 2017;45(8):1359-1366. doi:[10.1097/CCM.0000000000002485](https://doi.org/10.1097/CCM.0000000000002485)
55. Rodríguez-Calvo R, Girona J, Alegret JM, Bosquet A, Ibarretxe D, Masana L. Role of the fatty acid-binding protein 4 in heart failure and cardiovascular disease. *J Endocrinol*. 2017;233(3):R173-R184. doi:[10.1530/JOE-17-0031](https://doi.org/10.1530/JOE-17-0031)
56. Chen L, Song J, Hu S. Metabolic remodeling of substrate utilization during heart failure progression. *Heart Fail Rev*. 2019;24(1):143-154. doi:[10.1007/s10741-018-9713-0](https://doi.org/10.1007/s10741-018-9713-0)
57. Han F, Chen Q, Su J, Zheng A, Chen K, Sun S, Wu H, Jiang L, Xu X, Yang M, et al. MicroRNA-124 regulates cardiomyocyte apoptosis and myocardial infarction through targeting Dhcr24. *J Mol Cell Cardiol*. 2019;132:178-188. doi:[10.1016/j.yjmcc.2019.05.007](https://doi.org/10.1016/j.yjmcc.2019.05.007)
58. Yamada Y, Sakuma J, Takeuchi I, Yasukochi Y, Kato K, Oguri M, Fujimaki T, Horibe H, Muramatsu M, Sawabe M, et al. Identification of STXBP2 as a novel susceptibility locus for myocardial infarction in Japanese individuals by an exome-wide association study. *Oncotarget*. 2017;8(20):33527-33535. doi:[10.18632/oncotarget.16536](https://doi.org/10.18632/oncotarget.16536)
59. Wang X, Hu Y, Wang Y, Shen D, Tao G. CLEC5A knockdown protects against the cardiac dysfunction after Myocardial infarction by suppressing macrophage polarization, NLRP3 inflammasome activation and pyroptosis. *Biochem Cell Biol*. 2021;10.1139/bcb-2020-0672. doi:[10.1139/bcb-2020-0672](https://doi.org/10.1139/bcb-2020-0672)

60. García-Manzanares M, Tarazón E, Ortega A, Gil-Cayuela C, Martínez-Dolz L, González-Juanatey JR, Lago F, Portolés M, Roselló-Lletí E, Rivera M. XPO1 Gene Therapy Attenuates Cardiac Dysfunction in Rats with Chronic Induced Myocardial Infarction. *J Cardiovasc Transl Res.* 2020;13(4):593-600. doi:[10.1007/s12265-019-09932-y](https://doi.org/10.1007/s12265-019-09932-y)
61. Raitoharju E, Seppälä I, Levula M, Kuukasjärvi P, Laurikka J, Nikus K, Huovila AP, Oksala N, Klopp N, Illig T, et al. Common variation in the ADAM8 gene affects serum sADAM8 concentrations and the risk of myocardial infarction in two independent cohorts. *Atherosclerosis.* 2011;218(1):127-133. doi:[10.1016/j.atherosclerosis.2011.05.005](https://doi.org/10.1016/j.atherosclerosis.2011.05.005)
62. King KR, Aguirre AD, Ye YX, Sun Y, Roh JD, Ng RP Jr, Kohler RH, Arlauckas SP, Iwamoto Y, Savol A, et al. IRF3 and type I interferons fuel a fatal response to myocardial infarction. *Nat Med.* 2017;23(12):1481-1487. doi:[10.1038/nm.4428](https://doi.org/10.1038/nm.4428)
63. Hirokawa M, Morita H, Tajima T, Takahashi A, Ashikawa K, Miya F, Shigemizu D, Ozaki K, Sakata Y, Nakatani D, et al. A genome-wide association study identifies PLCL2 and AP3D1-DOT1L-SF3A2 as new susceptibility loci for myocardial infarction in Japanese. *Eur J Hum Genet.* 2015;23(3):374-380. doi:[10.1038/ejhg.2014.110](https://doi.org/10.1038/ejhg.2014.110)
64. Kahali B, Chen Y, Feitosa MF, Bielak LF, O'Connell JR, Musani SK, Hegde Y, Chen Y, Stetson LC, Guo X, et al. A Noncoding Variant Near PPP1R3B Promotes Liver Glycogen Storage and MetS, but Protects Against Myocardial Infarction. *J Clin Endocrinol Metab.* 2021;106(2):372-387. doi:[10.1210/clinem/dgaa855](https://doi.org/10.1210/clinem/dgaa855)
65. Kuhn TC, Knobel J, Burkert-Rettenmaier S, Li X, Meyer IS, Jungmann A, Sicklinger F, Backs J, Lasitschka F, Müller OJ, et al. Secretome Analysis of Cardiomyocytes Identifies PCSK6 (Proprotein Convertase Subtilisin/Kexin Type 6) as a Novel Player in Cardiac Remodeling After Myocardial Infarction. *Circulation.* 2020;141(20):1628-1644. doi:[10.1161/CIRCULATIONAHA.119.044914](https://doi.org/10.1161/CIRCULATIONAHA.119.044914)
66. Sun J, Zhang Q, Liu X, Shang X. Downregulation of IFIT3 relieves the inflammatory response and myocardial fibrosis of mice with myocardial infarction and improves their cardiac function. *Exp Anim.* 2021;10.1538/expanim.21-0060. doi:[10.1538/expanim.21-0060](https://doi.org/10.1538/expanim.21-0060)

67. Pingili AK, Jennings BL, Mukherjee K, Akroush W, Gonzalez FJ, Malik KU. 6 β -Hydroxytestosterone, a metabolite of testosterone generated by CYP1B1, contributes to vascular changes in angiotensin II-induced hypertension in male mice. *Biol Sex Differ.* 2020;11(1):4. doi:[10.1186/s13293-019-0280-4](https://doi.org/10.1186/s13293-019-0280-4)
68. Wang Y, Jin L. miRNA-145 is associated with spontaneous hypertension by targeting SLC7A1. *Exp Ther Med.* 2018;15(1):548-552. doi:[10.3892/etm.2017.5371](https://doi.org/10.3892/etm.2017.5371)
69. Liu L, Wang C, Mi Y, Liu D, Li L, Fan J, Nan L, Jia N, Du Y. Association of MYH9 Polymorphisms with Hypertension in Patients with Chronic Kidney Disease in China. *Kidney Blood Press Res.* 2016;41(6):956-965. doi:[10.1159/000452597](https://doi.org/10.1159/000452597)
70. Pinho MJ, Gomes P, Serrão MP, Bonifácio MJ, Soares-da-Silva P. Organ-specific overexpression of renal LAT2 and enhanced tubular L-DOPA uptake precede the onset of hypertension. *Hypertension.* 2003;42(4):613-618. doi:[10.1161/01.HYP.0000091822.00166.B1](https://doi.org/10.1161/01.HYP.0000091822.00166.B1)
71. Huang X, Wang B, Yang D, Shi X, Hong J, Wang S, Dai X, Zhou X, Geng YJ. Reduced expression of FXRD domain containing ion transport regulator 5 in association with hypertension. *Int J Mol Med.* 2012;29(2):231-238. doi:[10.3892/ijmm.2011.837](https://doi.org/10.3892/ijmm.2011.837)
72. Zhang S, Liu J, Zheng K, Chen L, Sun Y, Yao Z, Sun Y, Lin Y, Lin K, Yuan L. Exosomal miR-211 contributes to pulmonary hypertension via attenuating CaMK1/PPAR- γ axis. *Vascul Pharmacol.* 2021;136:106820. doi:[10.1016/j.vph.2020.106820](https://doi.org/10.1016/j.vph.2020.106820)
73. Zhao H, Wang Y, Zhang X, Guo Y, Wang X. miR-181b-5p inhibits endothelial-mesenchymal transition in monocrotaline-induced pulmonary arterial hypertension by targeting endocan and TGFBR1. *Toxicol Appl Pharmacol.* 2020;386:114827. doi:[10.1016/j.taap.2019.114827](https://doi.org/10.1016/j.taap.2019.114827)
74. Li M, Mulkey F, Jiang C, O'Neil BH, Schneider BP, Shen F, Friedman PN, Momozawa Y, Kubo M, Niedzwiecki D, et al. Identification of a Genomic Region between SLC29A1 and HSP90AB1 Associated with Risk of Bevacizumab-Induced Hypertension: CALGB 80405 (Alliance). *Clin Cancer Res.* 2018;24(19):4734-4744. doi:[10.1158/1078-0432.CCR-17-1523](https://doi.org/10.1158/1078-0432.CCR-17-1523)
75. Endres BT, Priestley JR, Palygin O, Flister MJ, Hoffman MJ, Weinberg BD, Grzybowski M, Lombard JH, Staruschenko A, Moreno C, et al. Mutation of

- Plekha7 attenuates salt-sensitive hypertension in the rat. *Proc Natl Acad Sci U S A*. 2014;111(35):12817-12822. doi:[10.1073/pnas.1410745111](https://doi.org/10.1073/pnas.1410745111)
76. Wakui H, Uneda K, Tamura K, Ohsawa M, Azushima K, Kobayashi R, Ohki K, Dejima T, Kanaoka T, Tsurumi-Ikeya Y, et al. Renal tubule angiotensin II type 1 receptor-associated protein promotes natriuresis and inhibits salt-sensitive blood pressure elevation. *J Am Heart Assoc*. 2015;4(3):e001594. doi:[10.1161/JAHA.114.001594](https://doi.org/10.1161/JAHA.114.001594)
77. Simino J, Sung YJ, Kume R, Schwander K, Rao DC. Gene-alcohol interactions identify several novel blood pressure loci including a promising locus near SLC16A9. *Front Genet*. 2013;4:277. doi:[10.3389/fgene.2013.00277](https://doi.org/10.3389/fgene.2013.00277)
78. Kamide K, Kokubo Y, Yang J, Matayoshi T, Inamoto N, Takiuchi S, Horio T, Miwa Y, Yoshii M, Tomoike H, et al. Association of genetic polymorphisms of ACADSB and COMT with human hypertension. *J Hypertens*. 2007;25(1):103-110. doi:[10.1097/HJH.0b013e3280103a40](https://doi.org/10.1097/HJH.0b013e3280103a40)
79. Rafikov R, McBride ML, Zemskova M, Kurdyukov S, McClain N, Niihori M, Langlais PR, Rafikova O. Inositol monophosphatase 1 as a novel interacting partner of RAGE in pulmonary hypertension. *Am J Physiol Lung Cell Mol Physiol*. 2019;316(3):L428-L444. doi:[10.1152/ajplung.00393.2018](https://doi.org/10.1152/ajplung.00393.2018)
80. Støy J, Grarup N, Hørlyck A, Ibsen L, Rungby J, Poulsen PL, Brandslund I, Christensen C, Hansen T, Pedersen O, et al. Blood pressure levels in male carriers of Arg82Cys in CD300LG. *PLoS One*. 2014;9(10):e109646. doi:[10.1371/journal.pone.0109646](https://doi.org/10.1371/journal.pone.0109646)
81. Liu J, Ke X, Wang L, Zhang Y, Yang J. Deficiency of cold-inducible RNA-binding protein exacerbated monocrotaline-induced pulmonary artery hypertension through Caveolin1 and CAVIN1. *J Cell Mol Med*. 2021;25(10):4732-4743. doi:[10.1111/jcmm.16437](https://doi.org/10.1111/jcmm.16437)
82. Zhang W, Zhang S, Li ZF, Huang C, Ren S, Zhou R, Jiang A, Yang AN. Knockdown of PIK3R1 by shRNA inhibits the activity of the splenic macrophages associated with hypersplenism due to portal hypertension. *Pathol Res Pract*. 2010;206(11):760-767. doi:[10.1016/j.prp.2010.07.009](https://doi.org/10.1016/j.prp.2010.07.009)
83. Schneider TM, Eadon MT, Cooper-DeHoff RM, Cavanaugh KL, Nguyen KA, Arwood MJ, Tillman EM, Pratt VM, Dexter PR, McCoy AB, et al. Multi-Institutional Implementation of Clinical Decision Support for APOL1,

- NAT2, and YEATS4 Genotyping in Antihypertensive Management. *J Pers Med*. 2021;11(6):480. doi:[10.3390/jpm11060480](https://doi.org/10.3390/jpm11060480)
84. Pouly D, Debonneville A, Ruffieux-Daidié D, Maillard M, Abriel H, Loffing J, Staub O. Mice carrying ubiquitin-specific protease 2 (Usp2) gene inactivation maintain normal sodium balance and blood pressure. *Am J Physiol Renal Physiol*. 2013;305(1):F21-F30. doi:[10.1152/ajprenal.00012.2013](https://doi.org/10.1152/ajprenal.00012.2013)
85. Wang J, Yang K, Yuan JX. NEDD9, a Hypoxia-upregulated Mediator for Pathogenic Platelet-Endothelial Cell Interaction in Pulmonary Hypertension. *Am J Respir Crit Care Med*. 2021;203(12):1455-1458. doi:[10.1164/rccm.202101-0007ED](https://doi.org/10.1164/rccm.202101-0007ED)
86. Wu L, Gao L, Zhao X, Zhang M, Wu J, Mi J. A new risk locus in CHCHD5 for hypertension and obesity in a Chinese child population: a cohort study. *BMJ Open*. 2017;7(9):e016241. doi:[10.1136/bmjopen-2017-016241](https://doi.org/10.1136/bmjopen-2017-016241)
87. Zee RYL, Rivera A, Inostroza Y, Ridker PM, Chasman DI, Romero JR. Gene Variation of Endoplasmic Reticulum Aminopeptidases 1 and 2, and Risk of Blood Pressure Progression and Incident Hypertension among 17,255 Initially Healthy Women. *Int J Genomics*. 2018;2018:2308585. doi:[10.1155/2018/2308585](https://doi.org/10.1155/2018/2308585)
88. Marunouchi T, Inomata S, Sanbe A, Takagi N, Tanonaka K. Protective effect of geranylgeranylacetone via enhanced induction of HSPB1 and HSPB8 in mitochondria of the failing heart following myocardial infarction in rats. *Eur J Pharmacol*. 2014;730:140-147. doi:[10.1016/j.ejphar.2014.02.037](https://doi.org/10.1016/j.ejphar.2014.02.037)
89. Zhang Y, Li C, Meng H, Guo D, Zhang Q, Lu W, Wang Q, Wang Y, Tu P. BYD Ameliorates Oxidative Stress-Induced Myocardial Apoptosis in Heart Failure Post-Acute Myocardial Infarction via the P38 MAPK-CRYAB Signaling Pathway. *Front Physiol*. 2018;9:505. doi:[10.3389/fphys.2018.00505](https://doi.org/10.3389/fphys.2018.00505)
90. Schurgers LJ, Burgmaier M, Ueland T, Schutters K, Aakhus S, Hofstra L, Gullestad L, Aukrust P, Hellmich M, Narula J, et al. Circulating annexin A5 predicts mortality in patients with heart failure. *J Intern Med*. 2016;279(1):89-97. doi:[10.1111/joim.12396](https://doi.org/10.1111/joim.12396)
91. Orllepp JR, Vesper K, Mevissen V, Schmitz F, Janssens U, Franke A, Hanrath P, Weber C, Zerres K, Hoffmann R. Chemokine receptor (CCR2)

- genotype is associated with myocardial infarction and heart failure in patients under 65 years of age. *J Mol Med (Berl)*. 2003;81(6):363-367. doi:[10.1007/s00109-003-0435-x](https://doi.org/10.1007/s00109-003-0435-x)
- 92.Mittmann C, Chung CH, Höppner G, Michalek C, Nose M, Schüler C, Schuh A, Eschenhagen T, Weil J, Pieske B, et al. Expression of ten RGS proteins in human myocardium: functional characterization of an upregulation of RGS4 in heart failure. *Cardiovasc Res*. 2002;55(4):778-786. doi:[10.1016/s0008-6363\(02\)00459-5](https://doi.org/10.1016/s0008-6363(02)00459-5)
 - 93.Stojanov S, DeJaco C, Lohse P, Huss K, Duftner C, Belohradsky BH, Herold M, Schirmer M. Clinical and functional characterisation of a novel TNFRSF1A c.605T>A/V173D cleavage site mutation associated with tumour necrosis factor receptor-associated periodic fever syndrome (TRAPS), cardiovascular complications and excellent response to etanercept treatment. *Ann Rheum Dis*. 2008;67(9):1292-1298. doi:[10.1136/ard.2007.079376](https://doi.org/10.1136/ard.2007.079376)
 - 94.Duan Q, Chen C, Yang L, Li N, Gong W, Li S, Wang DW. MicroRNA regulation of unfolded protein response transcription factor XBP1 in the progression of cardiac hypertrophy and heart failure in vivo. *J Transl Med*. 2015;13:363. doi:[10.1186/s12967-015-0725-4](https://doi.org/10.1186/s12967-015-0725-4)
 - 95.Deng B, Wang JX, Hu XX, Duan P, Wang L, Li Y, Zhu QL. Nkx2.5 enhances the efficacy of mesenchymal stem cells transplantation in treatment heart failure in rats. *Life Sci*. 2017;182:65-72. doi:[10.1016/j.lfs.2017.06.014](https://doi.org/10.1016/j.lfs.2017.06.014)
 - 96.Heimerl M, Sieve I, Ricke-Hoch M, Erschow S, Battmer K, Scherr M, Hilfiker-Kleiner D. Neuraminidase-1 promotes heart failure after ischemia/reperfusion injury by affecting cardiomyocytes and invading monocytes/macrophages. *Basic Res Cardiol*. 2020;115(6):62. doi:[10.1007/s00395-020-00821-z](https://doi.org/10.1007/s00395-020-00821-z)
 - 97.Simeunovic D, Odanovic N, Pljesa-Ercegovac M, Radic T, Radovanovic S, Coric V, Milinkovic I, Matic M, Djukic T, Ristic A, et al. Glutathione Transferase P1 Polymorphism Might Be a Risk Determinant in Heart Failure. *Dis Markers*. 2019;2019:6984845. doi:[10.1155/2019/6984845](https://doi.org/10.1155/2019/6984845)
 - 98.Krakoff LR, Buccino RA, Spann JF Jr, De Champlain J. Cardiac catechol O-methyltransferase and monoamine oxidase activity in congestive heart

- failure. Am J Physiol. 1968;215(3):549-552. doi:[10.1152/ajplegacy.1968.215.3.549](https://doi.org/10.1152/ajplegacy.1968.215.3.549)
99. Su Q, Zhang P, Yu D, Wu Z, Li D, Shen F, Liao P, Yin G. Upregulation of miR-93 and inhibition of LIMK1 improve ventricular remodeling and alleviate cardiac dysfunction in rats with chronic heart failure by inhibiting RhoA/ROCK signaling pathway activation. Aging (Albany NY). 2019;11(18):7570-7586. doi:[10.18632/aging.102272](https://doi.org/10.18632/aging.102272)
100. Beghi S, Cavaliere F, Manfredini M, Ferrarese S, Corazzari C, Beghi C, Buschini A. Polymorphism rs7214723 in CAMKK1: a new genetic variant associated with cardiovascular diseases. Biosci Rep. 2021;41(7):BSR20210326. doi:[10.1042/BSR20210326](https://doi.org/10.1042/BSR20210326)
101. Anzalone R, Corrao S, Lo Iacono M, Loria T, Corsello T, Cappello F, Di Stefano A, Giannuzzi P, Zummo G, Farina F, et al. Isolation and characterization of CD276+/HLA-E+ human subendocardial mesenchymal stem cells from chronic heart failure patients: analysis of differentiative potential and immunomodulatory markers expression. Stem Cells Dev. 2013;22(1):1-17. doi:[10.1089/scd.2012.0402](https://doi.org/10.1089/scd.2012.0402)
102. Ito S, Asahina H, Yamaguchi N, Tomaru U, Hasegawa T, Hatanaka Y, Hatanaka KC, Taguchi H, Harada T, Ohira H, et al. A case of radio-insensitive SMARCA4-deficient thoracic undifferentiated carcinoma with severe right heart failure. Respir Med Case Rep. 2021;32:101364. doi:[10.1016/j.rmcr.2021.101364](https://doi.org/10.1016/j.rmcr.2021.101364)
103. Zhai YJ, Liu P, He HR, Zheng XW, Wang Y, Yang QT, Dong YL, Lu J. The association of ADORA2A and ADORA2B polymorphisms with the risk and severity of chronic heart failure: a case-control study of a northern Chinese population. Int J Mol Sci. 2015;16(2):2732-2746. doi:[10.3390/ijms16022732](https://doi.org/10.3390/ijms16022732)
104. Xia C, Dong R, Chen C, Wang H, Wang DW. Cardiomyocyte specific expression of Acyl-coA thioesterase 1 attenuates sepsis induced cardiac dysfunction and mortality. Biochem Biophys Res Commun. 2015;468(4):533-540. doi:[10.1016/j.bbrc.2015.10.078](https://doi.org/10.1016/j.bbrc.2015.10.078)
105. Yamaguchi M. Regulatory role of regucalcin in heart calcium signaling: Insight into cardiac failure (Review). Biomed Rep. 2014;2(3):303-308. doi:[10.3892/br.2014.245](https://doi.org/10.3892/br.2014.245)

106. Zhao A, Shen J, Ding Y, Sheng M, Zuo M, Lv H, Wang J, Shen Y, Wang H, Sun L. Long-read sequencing identified a novel nonsense and a de novo missense of PPA2 in trans in a Chinese patient with autosomal recessive infantile sudden cardiac failure. *Clin Chim Acta*. 2021;519:163-171. doi:[10.1016/j.cca.2021.03.029](https://doi.org/10.1016/j.cca.2021.03.029)
107. Hou YS, Wang JZ, Shi S, Han Y, Zhang Y, Zhi JX, Xu C, Li FF, Wang GY, Liu SL. Identification of epigenetic factor KAT2B gene variants for possible roles in congenital heart diseases. *Biosci Rep*. 2020;40(4):BSR20191779. doi:[10.1042/BSR20191779](https://doi.org/10.1042/BSR20191779)
108. Mora A, Davies AM, Bertrand L, Sharif I, Budas GR, Jovanović S, Mouton V, Kahn CR, Lucocq JM, Gray GA, et al. Deficiency of PDK1 in cardiac muscle results in heart failure and increased sensitivity to hypoxia. *EMBO J*. 2003;22(18):4666-4676. doi:[10.1093/emboj/cdg469](https://doi.org/10.1093/emboj/cdg469)
109. Jaenisch RB, Bertagnolli M, Borghi-Silva A, Arena R, Lago PD. Respiratory Muscle Training Improves Diaphragm Citrate Synthase Activity and Hemodynamic Function in Rats with Heart Failure. *Braz J Cardiovasc Surg*. 2017;32(2):104-110. doi:[10.21470/1678-9741-2017-0002](https://doi.org/10.21470/1678-9741-2017-0002)
110. Li Q, Zhao Y, Wu G, Chen S, Zhou Y, Li S, Zhou M, Fan Q, Pu J, Hong K, et al. De Novo FGF12 (Fibroblast Growth Factor 12) Functional Variation Is Potentially Associated With Idiopathic Ventricular Tachycardia. *J Am Heart Assoc*. 2017;6(8):e006130. doi:[10.1161/JAHA.117.006130](https://doi.org/10.1161/JAHA.117.006130)
111. Cheng Y, Chao J, Dai D, Dai Y, Zhu D, Liu B. AQP4-knockout aggravation of isoprenaline-induced myocardial injury is mediated by p66Shc and endoplasmic reticulum stress. *Clin Exp Pharmacol Physiol*. 2017;44(11):1106-1115. doi:[10.1111/1440-1681.12812](https://doi.org/10.1111/1440-1681.12812)
112. Pappas CT, Farman GP, Mayfield RM, Konhilas JP, Gregorio CC. Cardiac-specific knockout of Lmod2 results in a severe reduction in myofilament force production and rapid cardiac failure. *J Mol Cell Cardiol*. 2018;122:88-97. doi:[10.1016/j.yjmcc.2018.08.009](https://doi.org/10.1016/j.yjmcc.2018.08.009)
113. Kühn EC, Slagman A, Kühn-Heid ECD, Seelig J, Schwiebert C, Minich WB, Stoppe C, Möckel M, Schomburg L. Circulating levels of selenium-binding protein 1 (SELENBP1) are associated with risk for major adverse cardiac events and death. *J Trace Elem Med Biol*. 2019;52:247-253. doi:[10.1016/j.jtemb.2019.01.005](https://doi.org/10.1016/j.jtemb.2019.01.005)

114. O'Brien PJ, O'Grady M, McCutcheon LJ, Shen H, Nowack L, Horne RD, Mirsalimi SM, Julian RJ, Grima EA, Moe GW, et al. Myocardial myoglobin deficiency in various animal models of congestive heart failure. *J Mol Cell Cardiol.* 1992;24(7):721-730. doi:[10.1016/0022-2828\(92\)93386-x](https://doi.org/10.1016/0022-2828(92)93386-x)
115. Weber C, Neacsu I, Krautz B, Schlegel P, Sauer S, Raake P, Ritterhoff J, Jungmann A, Remppis AB, Stangassinger M, et al. Therapeutic safety of high myocardial expression levels of the molecular inotrope S100A1 in a preclinical heart failure model. *Gene Ther.* 2014;21(2):131-138. doi:[10.1038/gt.2013.63](https://doi.org/10.1038/gt.2013.63)
116. Dobrev D, Wehrens XH. Role of RyR2 phosphorylation in heart failure and arrhythmias: Controversies around ryanodine receptor phosphorylation in cardiac disease. *Circ Res.* 2014;114(8):1311-1319. doi:[10.1161/CIRCRESAHA.114.300568](https://doi.org/10.1161/CIRCRESAHA.114.300568)
117. Arking DE, Reinier K, Post W, Jui J, Hilton G, O'Connor A, Prineas RJ, Boerwinkle E, Psaty BM, Tomaselli GF, et al. Genome-wide association study identifies GPC5 as a novel genetic locus protective against sudden cardiac arrest. *PLoS One.* 2010;5(3):e9879. doi:[10.1371/journal.pone.0009879](https://doi.org/10.1371/journal.pone.0009879)
118. Bovill E, Westaby S, Reji S, Sayeed R, Crisp A, Shaw T. Induction by left ventricular overload and left ventricular failure of the human Jumonji gene (JARID2) encoding a protein that regulates transcription and reexpression of a protective fetal program. *J Thorac Cardiovasc Surg.* 2008;136(3):709-716. doi:[10.1016/j.jtcvs.2008.02.020](https://doi.org/10.1016/j.jtcvs.2008.02.020)
119. Watanabe H, Ichihara E, Kano H, Ninomiya K, Tanimoto M, Kiura K. Congestive Heart Failure During Osimertinib Treatment for Epidermal Growth Factor Receptor (EGFR)-mutant Non-small Cell Lung Cancer (NSCLC). *Intern Med.* 2017;56(16):2195-2197. doi:[10.2169/internalmedicine.8344-16](https://doi.org/10.2169/internalmedicine.8344-16)
120. Li W, Yin L, Sun X, Wu J, Dong Z, Hu K, Sun A, Ge J. Alpha-lipoic acid protects against pressure overload-induced heart failure via ALDH2-dependent Nrf1-FUNDC1 signaling. *Cell Death Dis.* 2020;11(7):599. doi:[10.1038/s41419-020-02805-2](https://doi.org/10.1038/s41419-020-02805-2)
121. Cannavo A, Rengo G, Liccardo D, Pagano G, Zincarelli C, De Angelis MC, Puglia R, Di Pietro E, Rabinowitz JE, Barone MV, et al. β 1-adrenergic receptor and sphingosine-1-phosphate receptor 1 (S1PR1)

reciprocal downregulation influences cardiac hypertrophic response and progression to heart failure: protective role of S1PR1 cardiac gene therapy. *Circulation*. 2013;128(15):1612-1622.

doi:[10.1161/CIRCULATIONAHA.113.002659](https://doi.org/10.1161/CIRCULATIONAHA.113.002659)

122. Heaton MP, Bassett AS, Whitman KJ, Krafur GM, Lee SI, Carlson JM, Clark HJ, Smith HR, Pelster MC, Basnayake V, et al. Evaluation of EPAS1 variants for association with bovine congestive heart failure. *F1000Res*. 2019;8:1189. doi:[10.12688/f1000research.19951.1](https://doi.org/10.12688/f1000research.19951.1)
123. Bouchard L, Faucher G, Tchernof A, Deshaies Y, Marceau S, Lescelleur O, Biron S, Bouchard C, Pérusse L, Vohl MC. Association of OSBPL11 gene polymorphisms with cardiovascular disease risk factors in obesity. *Obesity (Silver Spring)*. 2009;17(7):1466-1472. doi:[10.1038/oby.2009.71](https://doi.org/10.1038/oby.2009.71)
124. Frustaci A, De Luca A, Galea N, Verardo R, Guida V, Carrozzo R, Chimenti C, Frustaci E, Sansone L, Russo MA. Novel dilated cardiomyopathy associated to Calreticulin and Myo7A gene mutation in Usher syndrome. *ESC Heart Fail*. 2021;8(3):2310-2315. doi:[10.1002/ehf2.13260](https://doi.org/10.1002/ehf2.13260)
125. Zhou H, Lei X, Yan Y, Lydic T, Li J, Weintraub NL, Su H, Chen W. Targeting ATGL to rescue BSCL2 lipodystrophy and its associated cardiomyopathy. *JCI Insight*. 2019;5(14):e129781. doi:[10.1172/jci.insight.129781](https://doi.org/10.1172/jci.insight.129781)
126. Miura A, Kondo H, Yamamoto T, Okumura Y, Nishio H. Sudden Unexpected Death of Infantile Dilated Cardiomyopathy with JPH2 and PKD1 Gene Variants. *Int Heart J*. 2020;61(5):1079-1083. doi:[10.1536/ihj.20-155](https://doi.org/10.1536/ihj.20-155)
127. Gong F, Gu J, Wang H. Up regulated Tmbim1 activation promotes high fat diet (HFD)-induced cardiomyopathy by enhancement of inflammation and oxidative stress. *Biochem Biophys Res Commun*. 2018;504(4):797-804. doi:[10.1016/j.bbrc.2018.08.059](https://doi.org/10.1016/j.bbrc.2018.08.059)
128. Watanabe K, Arumugam S, Sreedhar R, Thandavarayan RA, Nakamura T, Nakamura M, Harima M, Yoneyama H, Suzuki K. Small interfering RNA therapy against carbohydrate sulfotransferase 15 inhibits cardiac remodeling in rats with dilated cardiomyopathy. *Cell Signal*. 2015;27(7):1517-1524. doi:[10.1016/j.cellsig.2015.03.004](https://doi.org/10.1016/j.cellsig.2015.03.004)

129. Shishido A, Morisada N, Tominaga K, Uemura H, Haruna A, Hanafusa H, Nozu K, Iijima K. Japanese boy with NAA10-related syndrome and hypertrophic cardiomyopathy. *Hum Genome Var.* 2020;7:23. doi:[10.1038/s41439-020-00110-0](https://doi.org/10.1038/s41439-020-00110-0)
130. Su D, Ju Y, Han W, Yang Y, Wang F, Wang T, Tang J. Tcf3-activated lncRNA Gas5 regulates newborn mouse cardiomyocyte apoptosis in diabetic cardiomyopathy. *J Cell Biochem.* 2020;121(11):4337-4346. doi:[10.1002/jcb.29630](https://doi.org/10.1002/jcb.29630)
131. Lu D, Zhang L, Bao D, Lu Y, Zhang X, Liu N, Ge W, Gao X, Li H, Zhang L. Calponin1 inhibits dilated cardiomyopathy development in mice through the ϵ PKC pathway. *Int J Cardiol.* 2014;173(2):146-153. doi:[10.1016/j.ijcard.2014.02.032](https://doi.org/10.1016/j.ijcard.2014.02.032)
132. Long PA, Theis JL, Shih YH, Maleszewski JJ, Abell Aleff PC, Evans JM, Xu X, Olson TM. Recessive TAF1A mutations reveal ribosomopathy in siblings with end-stage pediatric dilated cardiomyopathy. *Hum Mol Genet.* 2017;26(15):2874-2881. doi:[10.1093/hmg/ddx169](https://doi.org/10.1093/hmg/ddx169)
133. Jacobi-Polishook T, Yosha-Orpaz N, Sagi Y, Lev D, Lerman-Sagie T. Successful pregnancy in a patient with mitochondrial cardiomyopathy due to ACAD9 deficiency. *JIMD Rep.* 2020;56(1):9-13. doi:[10.1002/jmd2.12157](https://doi.org/10.1002/jmd2.12157)
134. Hedberg-Oldfors C, Abramsson A, Osborn DPS, Danielsson O, Fazlinezhad A, Nilipour Y, Hübbert L, Nennesmo I, Visuttijai K, Bharj J, et al. Cardiomyopathy with lethal arrhythmias associated with inactivation of KLHL24. *Hum Mol Genet.* 2019;28(11):1919-1929. doi:[10.1093/hmg/ddz032](https://doi.org/10.1093/hmg/ddz032)
135. Auxerre-Plantié E, Nielsen T, Grunert M, Olejniczak O, Perrot A, Özcelik C, Harries D, Matinmehr F, Dos Remedios C, Mühlfeld C, Kraft T, et al. Identification of MYOM2 as a candidate gene in hypertrophic cardiomyopathy and Tetralogy of Fallot, and its functional evaluation in the *Drosophila* heart. *Dis Model Mech.* 2020;13(12):dmm045377. doi:[10.1242/dmm.045377](https://doi.org/10.1242/dmm.045377)
136. Salazar-Mendiguchía J, Ochoa JP, Palomino-Doza J, Domínguez F, Díez-López C, Akhtar M, Ramiro-León S, Clemente MM, Pérez-Cejas A, Robledo M, et al. Mutations in TRIM63 cause an autosomal-recessive form of hypertrophic cardiomyopathy. *Heart.* 2020;106(17):1342-1348. doi:[10.1136/heartjnl-2020-316913](https://doi.org/10.1136/heartjnl-2020-316913)

137. Janssens B, Mohapatra B, Vatta M, Goossens S, Vanpoucke G, Kools P, Montoye T, van Hengel J, Bowles NE, van Roy F, et al. Assessment of the CTNNA3 gene encoding human alpha T-catenin regarding its involvement in dilated cardiomyopathy. *Hum Genet.* 2003;112(3):227-236. doi:[10.1007/s00439-002-0857-5](https://doi.org/10.1007/s00439-002-0857-5)
138. Wang B, Wu Y, Ge Z, Zhang X, Yan Y, Xie Y. NLRC5 deficiency ameliorates cardiac fibrosis in diabetic cardiomyopathy by regulating EndMT through Smad2/3 signaling pathway. *Biochem Biophys Res Commun.* 2020;528(3):545-553. doi:[10.1016/j.bbrc.2020.05.151](https://doi.org/10.1016/j.bbrc.2020.05.151)
139. Zhang WY, Wang J, Li AZ. A study of the effects of SGLT-2 inhibitors on diabetic cardiomyopathy through miR-30d/KLF9/VEGFA pathway. *Eur Rev Med Pharmacol Sci.* 2020;24(11):6346-6359. doi:[10.26355/eurev_202006_21533](https://doi.org/10.26355/eurev_202006_21533)
140. Williams JL, Paudyal A, Awad S, Nicholson J, Grzesik D, Botta J, Meimaridou E, Maharaj AV, Stewart M, Tinker A, et al. Mylk3 null C57BL/6N mice develop cardiomyopathy, whereas Nnt null C57BL/6J mice do not. *Life Sci Alliance.* 2020;3(4):e201900593. doi:[10.26508/lsa.201900593](https://doi.org/10.26508/lsa.201900593)
141. Lennermann D, Backs J, van den Hoogenhof MMG. New Insights in RBM20 Cardiomyopathy. *Curr Heart Fail Rep.* 2020;17(5):234-246. doi:[10.1007/s11897-020-00475-x](https://doi.org/10.1007/s11897-020-00475-x)
142. Sasagawa S, Nishimura Y, Okabe S, Murakami S, Ashikawa Y, Yuge M, Kawaguchi K, Kawase R, Okamoto R, Ito M, et al. Downregulation of GSTK1 Is a Common Mechanism Underlying Hypertrophic Cardiomyopathy. *Front Pharmacol.* 2016;7:162. doi:[10.3389/fphar.2016.00162](https://doi.org/10.3389/fphar.2016.00162)
143. Gusic M, Schottmann G, Feichtinger RG, Du C, Scholz C, Wagner M, Mayr JA, Lee CY, Yépez VA, Lorenz N, et al. Bi-Allelic UQCRFS1 Variants Are Associated with Mitochondrial Complex III Deficiency, Cardiomyopathy, and Alopecia Totalis. *Am J Hum Genet.* 2020;106(1):102-111. doi:[10.1016/j.ajhg.2019.12.005](https://doi.org/10.1016/j.ajhg.2019.12.005)
144. Loeffen J, Elpeleg O, Smeitink J, Smeets R, Stöckler-Ipsiroglu S, Mandel H, Sengers R, Trijbels F, van den Heuvel L. Mutations in the complex I NDUFS2 gene of patients with cardiomyopathy and

- encephalomyopathy. *Ann Neurol.* 2001;49(2):195-201. doi:[10.1002/1531-8249\(20010201\)49:2<195::aid-ana39>3.0.co;2-m](https://doi.org/10.1002/1531-8249(20010201)49:2<195::aid-ana39>3.0.co;2-m)
145. Abdulhag UN, Soiferman D, Schueler-Furman O, Miller C, Shaag A, Elpeleg O, Edvardson S, Saada A. Mitochondrial complex IV deficiency, caused by mutated COX6B1, is associated with encephalomyopathy, hydrocephalus and cardiomyopathy. *Eur J Hum Genet.* 2015;23(2):159-164. doi:[10.1038/ejhg.2014.85](https://doi.org/10.1038/ejhg.2014.85)
146. Domarkienė I, Pranculis A, Germanas S, Jakaitienė A, Vitkus D, Dženkevičiūtė V, Kučinskienė Z, Kučinskas V. RTN4 and FBXL17 Genes are Associated with Coronary Heart Disease in Genome-Wide Association Analysis of Lithuanian Families. *Balkan J Med Genet.* 2013;16(2):17-22. doi:[10.2478/bjmg-2013-0026](https://doi.org/10.2478/bjmg-2013-0026)
147. Mo XG, Liu W, Yang Y, Imani S, Lu S, Dan G, Nie X, Yan J, Zhan R, Li X, et al. NCF2, MYO1F, S1PR4, and FCN1 as potential noninvasive diagnostic biomarkers in patients with obstructive coronary artery: A weighted gene co-expression network analysis. *J Cell Biochem.* 2019;120(10):18219-18235. doi:[10.1002/jcb.29128](https://doi.org/10.1002/jcb.29128)
148. Takefuji M, Asano H, Mori K, Amano M, Kato K, Watanabe T, Morita Y, Katsumi A, Itoh T, Takenawa T, et al. Mutation of ARHGAP9 in patients with coronary spastic angina. *J Hum Genet.* 2010;55(1):42-49. doi:[10.1038/jhg.2009.120](https://doi.org/10.1038/jhg.2009.120)
149. Vergeer M, Cohn DM, Boekholdt SM, Sandhu MS, Prins HM, Ricketts SL, Wareham NJ, Kastelein JJ, Khaw KT, Kamphuisen PW, et al. Lack of association between common genetic variation in endothelial lipase (LIPG) and the risk for CAD and DVT. *Atherosclerosis.* 2010;211(2):558-564. doi:[10.1016/j.atherosclerosis.2010.04.004](https://doi.org/10.1016/j.atherosclerosis.2010.04.004)
150. Prasongsukarn K, Dechkhajorn W, Benjathummarak S, Maneerat Y. TRPM2, PDLIM5, BCL3, CD14, GBA Genes as Feasible Markers for Premature Coronary Heart Disease Risk. *Front Genet.* 2021;12:598296. doi:[10.3389/fgene.2021.598296](https://doi.org/10.3389/fgene.2021.598296)
151. Cai H, Wang XL, Wilcken DE. Genetic polymorphism of heparan sulfate proteoglycan (perlecan, HSPG2), lipid profiles and coronary artery disease in the Australian population. *Atherosclerosis.* 2000;148(1):125-129. doi:[10.1016/s0021-9150\(99\)00213-0](https://doi.org/10.1016/s0021-9150(99)00213-0)

152. Castrechini S, Rivasi AP. Apolipoprotein B, apolipoprotein E, and angiotensin-converting enzyme polymorphisms in 2 Italian populations at different risk for coronary artery disease and comparison of allele frequencies among European populations. *Hum Biol.* 1999;71(6):933-945
153. Grinshtein YI, Kosinova AA, Grinshtein IY, Subbotina TN, Savchenko AA. The Prognostic Value of Combinations of Genetic Polymorphisms in the ITGB3, ITGA2, and CYP2C19*2 Genes in Predicting Cardiovascular Outcomes After Coronary Bypass Grafting. *Genet Test Mol Biomarkers.* 2018;22(4):259-265. doi:[10.1089/gtmb.2017.0177](https://doi.org/10.1089/gtmb.2017.0177)
154. Vinitha A, Kutty VR, Vivekanand A, Reshmi G, Divya G, Sumi S, Santosh KR, Pratapachandran NS, Ajit MS, Kartha CC, et al. PPIA rs6850: A > G single-nucleotide polymorphism is associated with raised plasma cyclophilin A levels in patients with coronary artery disease. *Mol Cell Biochem.* 2016;412(1-2):259-268. doi:[10.1007/s11010-015-2632-7](https://doi.org/10.1007/s11010-015-2632-7)
155. Ramkaran P, Khan S, Phulukdaree A, Moodley D, Chuturgoon AA. miR-146a polymorphism influences levels of miR-146a, IRAK-1, and TRAF-6 in young patients with coronary artery disease. *Cell Biochem Biophys.* 2014;68(2):259-266. doi:[10.1007/s12013-013-9704-7](https://doi.org/10.1007/s12013-013-9704-7)
156. Watzka M, Nebel A, El Mokhtari NE, Ivandic B, Müller J, Schreiber S, Oldenburg J. Functional promoter polymorphism in the VKORC1 gene is no major genetic determinant for coronary heart disease in Northern Germans. *Thromb Haemost.* 2007;97(6):998-1002.
157. Stec A, Ksiazek A, Buraczynska M. Rs10887800 renalase gene polymorphism is associated with an increased risk of coronary artery disease in hemodialyzed patients. *Int Urol Nephrol.* 2016;48(6):871-876. doi:[10.1007/s11255-016-1270-7](https://doi.org/10.1007/s11255-016-1270-7)
158. Zidi I, Kharrat N, Abdelhedi R, Hassine AB, Laaribi AB, Yahia HB, Abdelmoula NB, Abid L, Rebai A, Rizzo R. Nonclassical human leukocyte antigen (HLA-G, HLA-E, and HLA-F) in coronary artery disease. *Hum Immunol.* 2016;77(4):325-329. doi:[10.1016/j.humimm.2016.01.008](https://doi.org/10.1016/j.humimm.2016.01.008)
159. Domarkienė I, Pranculis A, Germanas S, Jakaitienė A, Vitkus D, Dženkevičiūtė V, Kučinskienė Z, Kučinskas V. RTN4 and FBXL17 Genes are Associated with Coronary Heart Disease in Genome-Wide Association Analysis of Lithuanian Families. *Balkan J Med Genet.* 2013;16(2):17-22. doi:[10.2478/bjmg-2013-0026](https://doi.org/10.2478/bjmg-2013-0026)

160. Sheu JJ, Lin YJ, Chang JS, Wan L, Chen SY, Huang YC, Chan C, Chiu IW, Tsai FJ. Association of COL11A2 polymorphism with susceptibility to Kawasaki disease and development of coronary artery lesions. *Int J Immunogenet.* 2010;37(6):487-492. doi:[10.1111/j.1744-313X.2010.00952.x](https://doi.org/10.1111/j.1744-313X.2010.00952.x)
161. Raffa S, Chin XLD, Stanzione R, Forte M, Bianchi F, Cotugno M, Marchitti S, Micaloni A, Gallo G, Schirone L, et al. The reduction of NDUFC2 expression is associated with mitochondrial impairment in circulating mononuclear cells of patients with acute coronary syndrome. *Int J Cardiol.* 2019;286:127-133. doi:[10.1016/j.ijcard.2019.02.027](https://doi.org/10.1016/j.ijcard.2019.02.027)
162. Chen C, Peng H, Zeng Y, Dong G. CD14, CD163, and CCR1 are involved in heart and blood communication in ischemic cardiac diseases. *J Int Med Res.* 2020;48(9):300060520951649. doi:[10.1177/0300060520951649](https://doi.org/10.1177/0300060520951649)
163. Tadimalla A, Belmont PJ, Thuerauf DJ, Glassy MS, Martindale JJ, Gude N, Sussman MA, Glembotski CC. Mesencephalic astrocyte-derived neurotrophic factor is an ischemia-inducible secreted endoplasmic reticulum stress response protein in the heart. *Circ Res.* 2008;103(11):1249-1258. doi:[10.1161/CIRCRESAHA.108.180679](https://doi.org/10.1161/CIRCRESAHA.108.180679)
164. Zhu WS, Guo W, Zhu JN, Tang CM, Fu YH, Lin QX, Tan N, Shan ZX. Hsp90aa1: a novel target gene of miR-1 in cardiac ischemia/reperfusion injury. *Sci Rep.* 2016;6:24498. doi:[10.1038/srep24498](https://doi.org/10.1038/srep24498)
165. Wang Y, Jin L, Song Y, Zhang M, Shan D, Liu Y, Fang M, Lv F, Xiao RP, Zhang Y. β -arrestin 2 mediates cardiac ischemia-reperfusion injury via inhibiting GPCR-independent cell survival signalling. *Cardiovasc Res.* 2017;113(13):1615-1626. doi:[10.1093/cvr/cvx147](https://doi.org/10.1093/cvr/cvx147)
166. Wang J, Cheng X, Zhao H, Yang Q, Xu Z. Downregulation of the zinc transporter SLC39A13 (ZIP13) is responsible for the activation of CaMKII at reperfusion and leads to myocardial ischemia/reperfusion injury in mouse hearts. *J Mol Cell Cardiol.* 2021;152:69-79. doi:[10.1016/j.yjmcc.2020.12.002](https://doi.org/10.1016/j.yjmcc.2020.12.002)
167. Natarajan R, Salloum FN, Fisher BJ, Ownby ED, Kukreja RC, Fowler AA. Activation of hypoxia-inducible factor-1 via prolyl-4 hydroxylase-2 gene silencing attenuates acute inflammatory responses in postischemic

- myocardium. *Am J Physiol Heart Circ Physiol*. 2007;293(3):H1571-H1580. doi:[10.1152/ajpheart.00291.2007](https://doi.org/10.1152/ajpheart.00291.2007)
168. Zhou W, Zhong Z, Lin D, Liu Z, Zhang Q, Xia H, Peng S, Liu A, Lu Z, Wang Y, Ye S, et al. Hypothermic oxygenated perfusion inhibits HECTD3-mediated TRAF3 polyubiquitination to alleviate DCD liver ischemia-reperfusion injury. *Cell Death Dis*. 2021;12(2):211. doi:[10.1038/s41419-021-03493-2](https://doi.org/10.1038/s41419-021-03493-2)
169. Cui Y, Wang Y, Liu G. Protective effect of Barbaloin in a rat model of myocardial ischemia reperfusion injury through the regulation of the CNPY2- $\square$ PERK pathway. *Int J Mol Med*. 2019;43(5):2015-2023. doi:[10.3892/ijmm.2019.4123](https://doi.org/10.3892/ijmm.2019.4123)
170. Du J, Li Z, Li QZ, Guan T, Yang Q, Xu H, Pritchard KA, Camara AK, Shi Y. Enoyl coenzyme a hydratase domain-containing 2, a potential novel regulator of myocardial ischemia injury. *J Am Heart Assoc*. 2013;2(5):e000233. doi:[10.1161/JAHA.113.000233](https://doi.org/10.1161/JAHA.113.000233)
171. Zhang H, Gong G, Wang P, Zhang Z, Kolwicz SC, Rabinovitch PS, Tian R, Wang W. Heart specific knockout of Ndufs4 ameliorates ischemia reperfusion injury. *J Mol Cell Cardiol*. 2018;123:38-45. doi:[10.1016/j.yjmcc.2018.08.022](https://doi.org/10.1016/j.yjmcc.2018.08.022)
172. Tombo N, Imam Aliagan AD, Feng Y, Singh H, Bopassa JC. Cardiac ischemia/reperfusion stress reduces inner mitochondrial membrane protein (mitofilin) levels during early reperfusion. *Free Radic Biol Med*. 2020;158:181-194. doi:[10.1016/j.freeradbiomed.2020.06.039](https://doi.org/10.1016/j.freeradbiomed.2020.06.039)
173. Savastano S, Valentino R, Di Somma C, Orio F, Pivonello C, Passaretti F, Brancato V, Formisano P, Colao A, Beguinot F, et al. Serum 25-Hydroxyvitamin D Levels, phosphoprotein enriched in diabetes gene product (PED/PEA-15) and leptin-to-adiponectin ratio in women with PCOS. *Nutr Metab (Lond)*. 2011;8:84. doi:[10.1186/1743-7075-8-84](https://doi.org/10.1186/1743-7075-8-84)
174. Ramos-Lopez E, Ghebru S, Van Autreve J, Aminkeng F, Herwig J, Seifried E, Seidl C, Van der Auwera B, Badenhop K. Neither an intronic CA repeat within the CD48 gene nor the HERV-K18 polymorphisms are associated with type 1 diabetes. *Tissue Antigens*. 2006;68(2):147-152. doi:[10.1111/j.1399-0039.2006.00637.x](https://doi.org/10.1111/j.1399-0039.2006.00637.x)
175. Alhaidan Y, Christesen HT, Højlund K, Al Balwi MA, Brusgaard K. A novel gene in early childhood diabetes: EDEM2 silencing decreases

- SLC2A2 and PXD1 expression, leading to impaired insulin secretion. *Mol Genet Genomics*. 2020;295(5):1253-1262. doi:[10.1007/s00438-020-01695-5](https://doi.org/10.1007/s00438-020-01695-5)
176. Ma XW, Chang ZW, Qin MZ, Sun Y, Huang HL, He Y. Decreased expression of complement regulatory proteins, CD55 and CD59, on peripheral blood leucocytes in patients with type 2 diabetes and macrovascular diseases. *Chin Med J (Engl)*. 2009;122(18):2123-2128.
177. Cividini F, Scott BT, Suarez J, Casteel DE, Heinz S, Dai A, Diemer T, Suarez JA, Benner CW, Ghassemian M, Dillmann WH. Ncor2/PPAR α -Dependent Upregulation of MCUb in the Type 2 Diabetic Heart Impacts Cardiac Metabolic Flexibility and Function. *Diabetes*. 2021;70(3):665-679. doi:[10.2337/db20-0779](https://doi.org/10.2337/db20-0779)
178. Ren Q, Xiao J, Han X, Yang W, Ji L. Impact of variants of the EXT2 gene on Type 2 diabetes and its related traits in the Chinese han population. *Endocr Res*. 2015;40(2):79-82. doi:[10.3109/07435800.2014.952015](https://doi.org/10.3109/07435800.2014.952015)
179. Meng S, Cao JT, Zhang B, Zhou Q, Shen CX, Wang CQ. Downregulation of microRNA-126 in endothelial progenitor cells from diabetes patients, impairs their functional properties, via target gene Spred-1. *J Mol Cell Cardiol*. 2012;53(1):64-72. doi:[10.1016/j.yjmcc.2012.04.003](https://doi.org/10.1016/j.yjmcc.2012.04.003)
180. Al-Fadhli FM, Afqi M, Sairafi MH, Almuntashri M, Alharby E, Alharbi G, Abdud Samad F, Hashmi JA, Zaytuni D, Bahashwan AA, et al. Biallelic loss of function variant in the unfolded protein response gene PDIA6 is associated with asphyxiating thoracic dystrophy and neonatal-onset diabetes. *Clin Genet*. 2021;99(5):694-703. doi:[10.1111/cge.13930](https://doi.org/10.1111/cge.13930)
181. Haseda F, Imagawa A, Nishikawa H, Mitsui S, Tsutsumi C, Fujisawa R, Sano H, Murase-Mishiba Y, Terasaki J, Sakaguchi S, et al. Antibody to CMRF35-Like Molecule 2, CD300e A Novel Biomarker Detected in Patients with Fulminant Type 1 Diabetes. *PLoS One*. 2016;11(8):e0160576. doi:[10.1371/journal.pone.0160576](https://doi.org/10.1371/journal.pone.0160576)
182. Cheung YH, Watkinson J, Anastassiou D. Conditional meta-analysis stratifying on detailed HLA genotypes identifies a novel type 1 diabetes locus around TCF19 in the MHC. *Hum Genet*. 2011;129(2):161-176. doi:[10.1007/s00439-010-0908-2](https://doi.org/10.1007/s00439-010-0908-2)
183. Xia W, Pessentheiner AR, Hofer DC, Amor M, Schreiber R, Schoiswohl G, Eichmann TO, Walenta E, Itariu B, Prager G, et al. Loss of ABHD15 Impairs the Anti-lipolytic Action of Insulin by Altering PDE3B

- Stability and Contributes to Insulin Resistance. *Cell Rep.* 2018;23(7):1948-1961. doi:[10.1016/j.celrep.2018.04.055](https://doi.org/10.1016/j.celrep.2018.04.055)
184. Gao T, Qian S, Shen S, Zhang X, Liu J, Jia W, Chen Z, Ye J. Reduction of mitochondrial 3-oxoacyl-ACP synthase (OXSM) by hyperglycemia is associated with deficiency of α -lipoic acid synthetic pathway in kidney of diabetic mice. *Biochem Biophys Res Commun.* 2019;512(1):106-111. doi:[10.1016/j.bbrc.2019.02.155](https://doi.org/10.1016/j.bbrc.2019.02.155)
185. Thameem F, Yang X, Permana PA, Wolford JK, Bogardus C, Prochazka M. Evaluation of the microsomal glutathione S-transferase 3 (MGST3) locus on 1q23 as a Type 2 diabetes susceptibility gene in Pima Indians. *Hum Genet.* 2003;113(4):353-358. doi:[10.1007/s00439-003-0980-y](https://doi.org/10.1007/s00439-003-0980-y)
186. Shigeta Y, Izumi K, Shichiri M. Influence of the administration of coenzyme Q7 on abnormality of vibratory perception in diabetics. *J Vitaminol (Kyoto).* 1965;11(3):199-203. doi:[10.5925/jnsv1954.11.199](https://doi.org/10.5925/jnsv1954.11.199)
187. Xia Q, Chesi A, Manduchi E, Johnston BT, Lu S, Leonard ME, Parlin UW, Rappaport EF, Huang P, Wells AD, et al. The type 2 diabetes presumed causal variant within TCF7L2 resides in an element that controls the expression of ACSL5. *Diabetologia.* 2016;59(11):2360-2368. doi:[10.1007/s00125-016-4077-2](https://doi.org/10.1007/s00125-016-4077-2)
188. Sun L, Zhang X, Wang T, Chen M, Qiao H. Association of ANK1 variants with new-onset type 2 diabetes in a Han Chinese population from northeast China. *Exp Ther Med.* 2017;14(4):3184-3190. doi:[10.3892/etm.2017.4866](https://doi.org/10.3892/etm.2017.4866)
189. Baker DJ, Timmons JA, Greenhaff PL. Glycogen phosphorylase inhibition in type 2 diabetes therapy: a systematic evaluation of metabolic and functional effects in rat skeletal muscle. *Diabetes.* 2005;54(8):2453-2459. doi:[10.2337/diabetes.54.8.2453](https://doi.org/10.2337/diabetes.54.8.2453)
190. Zhang L, Chen Z, Wang Y, Tweardy DJ, Mitch WE. Stat3 activation induces insulin resistance via a muscle-specific E3 ubiquitin ligase Fbxo40. *Am J Physiol Endocrinol Metab.* 2020;318(5):E625-E635. doi:[10.1152/ajpendo.00480.2019](https://doi.org/10.1152/ajpendo.00480.2019)
191. Esteves JV, Yonamine CY, Machado UF. SLC2A4 expression and its epigenetic regulation as biomarkers for insulin resistance treatment in diabetes mellitus. *Biomark Med.* 2020;14(6):413-416. doi:[10.2217/bmm-2019-0481](https://doi.org/10.2217/bmm-2019-0481)

192. Santin I, Castellanos-Rubio A, Aransay AM, Gutierrez G, Gaztambide S, Rica I, Vicario JL, Noble JA, Castaño L, Bilbao JR. Exploring the diabetogenicity of the HLA-B18-DR3 CEH: independent association with T1D genetic risk close to HLA-DOA. *Genes Immun.* 2009;10(6):596-600. doi:[10.1038/gene.2009.41](https://doi.org/10.1038/gene.2009.41)
193. Penfornis A, Tuomilehto-Wolf E, Faustman DL, Hitman GA; DiMe (Childhood Diabetes in Finland) Study Group. Analysis of TAP2 polymorphisms in Finnish individuals with type I diabetes. *Hum Immunol.* 2002;63(1):61-70. doi:[10.1016/s0198-8859\(01\)00365-2](https://doi.org/10.1016/s0198-8859(01)00365-2)
194. Varney MD, Valdes AM, Carlson JA, Noble JA, Tait BD, Bonella P, Lavant E, Fear AL, Louey A, Moonsamy P, et al. HLA DPA1, DPB1 alleles and haplotypes contribute to the risk associated with type 1 diabetes: analysis of the type 1 diabetes genetics consortium families. *Diabetes.* 2010;59(8):2055-2062. doi:[10.2337/db09-0680](https://doi.org/10.2337/db09-0680)
195. Payne F, Colnaghi R, Rocha N, Seth A, Harris J, Carpenter G, Bottomley WE, Wheeler E, Wong S, Saudek V, et al. Hypomorphism in human NSMCE2 linked to primordial dwarfism and insulin resistance. *J Clin Invest.* 2014;124(9):4028-4038. doi:[10.1172/JCI73264](https://doi.org/10.1172/JCI73264)
196. Yagil C, Varadi-Levi R, Yagil Y. A novel mutation in the NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 4 (Ndufa4) gene links mitochondrial dysfunction to the development of diabetes in a rodent model. *Dis Model Mech.* 2018;11(11):dmm036699. doi:[10.1242/dmm.036699](https://doi.org/10.1242/dmm.036699)
197. Huang T, Wang L, Bai M, Zheng J, Yuan D, He Y, Wang Y, Jin T, Cui W. Influence of IGF2BP2, HMG20A, and HNF1B genetic polymorphisms on the susceptibility to Type 2 diabetes mellitus in Chinese Han population. *Biosci Rep.* 2020;40(5):BSR20193955. doi:[10.1042/BSR20193955](https://doi.org/10.1042/BSR20193955)
198. Arendt M, Fall T, Lindblad-Toh K, Axelsson E. Amylase activity is associated with AMY2B copy numbers in dog: implications for dog domestication, diet and diabetes. *Anim Genet.* 2014;45(5):716-722. doi:[10.1111/age.12179](https://doi.org/10.1111/age.12179)
199. AlDehaini DMB, Al-Bustan SA, Malalla ZHA, Ali ME, Sater M, Giha HA. The influence of TERC, TERT and ACYP2 genes polymorphisms on plasma telomerase concentration, telomeres length and T2DM. *Gene.* 2021;766:145127. doi:[10.1016/j.gene.2020.145127](https://doi.org/10.1016/j.gene.2020.145127)

200. Jiang DS, Zhang XF, Gao L, Zong J, Zhou H, Liu Y, Zhang Y, Bian ZY, Zhu LH, Fan GC, et al. Signal regulatory protein- α protects against cardiac hypertrophy via the disruption of toll-like receptor 4 signaling. *Hypertension*. 2014;63(1):96-104. doi:[10.1161/HYPERTENSIONAHA.113.01506](https://doi.org/10.1161/HYPERTENSIONAHA.113.01506)
201. Yang D, Wang Y, Jiang M, Deng X, Pei Z, Li F, Xia K, Zhu L, Yang T, Chen M. Downregulation of Profilin-1 Expression Attenuates Cardiomyocytes Hypertrophy and Apoptosis Induced by Advanced Glycation End Products in H9c2 Cells. *Biomed Res Int*. 2017;2017:9716087. doi:[10.1155/2017/9716087](https://doi.org/10.1155/2017/9716087)
202. Romano N, Ricciardi S, Gallo P, Ceci M. Upregulation of eIF6 inhibits cardiac hypertrophy induced by phenylephrine. *Biochem Biophys Res Commun*. 2018;495(1):601-606. doi:[10.1016/j.bbrc.2017.11.046](https://doi.org/10.1016/j.bbrc.2017.11.046)
203. Lund AK, Goens MB, Nuñez BA, Walker MK. Characterizing the role of endothelin-1 in the progression of cardiac hypertrophy in aryl hydrocarbon receptor (AhR) null mice. *Toxicol Appl Pharmacol*. 2006;212(2):127-135. doi:[10.1016/j.taap.2005.07.005](https://doi.org/10.1016/j.taap.2005.07.005)
204. Zhang D, Liang C, Li P, Yang L, Hao Z, Kong L, Tian X, Guo C, Dong J, Zhang Y, et al. Runt-related transcription factor 1 (Runx1) aggravates pathological cardiac hypertrophy by promoting p53 expression. *J Cell Mol Med*. 2021;10.1111/jcmm.16704. doi:[10.1111/jcmm.16704](https://doi.org/10.1111/jcmm.16704)
205. Liu Y, Li S, Gao Z, Li S, Tan Q, Li Y, Wang D, Wang Q. Indoleamine 2,3-Dioxygenase 1 (IDO1) Promotes Cardiac Hypertrophy via a PI3K-AKT-mTOR-Dependent Mechanism. *Cardiovasc Toxicol*. 2021;21(8):655-668. doi:[10.1007/s12012-021-09657-y](https://doi.org/10.1007/s12012-021-09657-y)
206. Mitra A, Basak T, Ahmad S, Datta K, Datta R, Sengupta S, Sarkar S. Comparative Proteome Profiling during Cardiac Hypertrophy and Myocardial Infarction Reveals Altered Glucose Oxidation by Differential Activation of Pyruvate Dehydrogenase E1 Component Subunit β . *J Mol Biol*. 2015;427(11):2104-2120. doi:[10.1016/j.jmb.2014.10.026](https://doi.org/10.1016/j.jmb.2014.10.026)
207. Zou R, Tao J, Qiu J, Shi W, Zou M, Chen W, Li W, Zhou N, Wang S, Ma L, et al. Ndufs1 Deficiency Aggravates the Mitochondrial Membrane Potential Dysfunction in Pressure Overload-Induced Myocardial Hypertrophy. *Oxid Med Cell Longev*. 2021;2021:5545261. doi:[10.1155/2021/5545261](https://doi.org/10.1155/2021/5545261)

208. Ito S, Asakura M, Liao Y, Min KD, Takahashi A, Shindo K, Yamazaki S, Tsukamoto O, Asanuma H, Mogi M, et al. Identification of the Mtus1 Splice Variant as a Novel Inhibitory Factor Against Cardiac Hypertrophy. *J Am Heart Assoc.* 2016;5(7):e003521. doi:[10.1161/JAHA.116.003521](https://doi.org/10.1161/JAHA.116.003521)
209. Pan L, Sheng M, Huang Z, Zhu Z, Xu C, Teng L, He L, Gu C, Yi C, Li J. Zinc-finger protein 418 overexpression protects against cardiac hypertrophy and fibrosis. *PLoS One.* 2017;12(10):e0186635. doi:[10.1371/journal.pone.0186635](https://doi.org/10.1371/journal.pone.0186635)
210. Zhang JL, Zhang DH, Li YP, Wu LM, Liang C, Yao R, Wang Z, Feng SD, Wang ZM, Zhang YZ. Myotubularin-related protein 14 suppresses cardiac hypertrophy by inhibiting Akt. *Cell Death Dis.* 2020;11(2):140. doi:[10.1038/s41419-020-2330-6](https://doi.org/10.1038/s41419-020-2330-6)
211. Zhu J, Xu Y, Ren G, Hu X, Wang C, Yang Z, Li Z, Mao W, Lu D. Tanshinone IIA Sodium sulfonate regulates antioxidant system, inflammation, and endothelial dysfunction in atherosclerosis by downregulation of CLIC1. *Eur J Pharmacol.* 2017;815:427-436. doi:[10.1016/j.ejphar.2017.09.047](https://doi.org/10.1016/j.ejphar.2017.09.047)
212. Li J, Chen Y, Gao J, Chen Y, Zhou C, Lin X, Liu C, Zhao M, Xu Y, Ji L, et al. Evala ameliorates atherosclerosis by promoting re-endothelialization of injured arteries via Rac1/Cdc42/Arpc1b. *Cardiovasc Res.* 2021;117(2):450-461. doi:[10.1093/cvr/cvaa011](https://doi.org/10.1093/cvr/cvaa011)
213. Bandaru S, Ala C, Salimi R, Akula MK, Ekstrand M, Devarakonda S, Karlsson J, Van den Eynden J, Bergström G, Larsson E, et al. Targeting Filamin A Reduces Macrophage Activity and Atherosclerosis. *Circulation.* 2019;140(1):67-79. doi:[10.1161/CIRCULATIONAHA.119.039697](https://doi.org/10.1161/CIRCULATIONAHA.119.039697)
214. Maier A, Wu H, Cordasic N, Oefner P, Dietel B, Thiele C, Weidemann A, Eckardt KU, Warnecke C. Hypoxia-inducible protein 2 Hig2/Hilpda mediates neutral lipid accumulation in macrophages and contributes to atherosclerosis in apolipoprotein E-deficient mice. *FASEB J.* 2017;31(11):4971-4984. doi:[10.1096/fj.201700235R](https://doi.org/10.1096/fj.201700235R)
215. Chen Y, Xiang R, Zhao S. The potential role of RTN3 in monocyte recruitment and atherosclerosis. *Mol Cell Biochem.* 2012;361(1-2):67-70. doi:[10.1007/s11010-011-1089-6](https://doi.org/10.1007/s11010-011-1089-6)

216. Wang X, Meng H, Ruan J, Chen W, Meng F. Low G0S2 gene expression levels in peripheral blood may be a genetic marker of acute myocardial infarction in patients with stable coronary atherosclerotic disease: A retrospective clinical study. *Medicine (Baltimore)*. 2021;100(3):e23468. doi:[10.1097/MD.00000000000023468](https://doi.org/10.1097/MD.00000000000023468)
217. Hernández-Romero D, Ruiz-Nodar JM, Marín F, Tello-Montoliu A, Roldán V, Mainar L, Pérez-Andreu V, Antón AI, Bonaque JC, Valdés M, et al. CALU A29809G polymorphism in coronary atherothrombosis: Implications for coronary calcification and prognosis. *Ann Med*. 2010;42(6):439-446. doi:[10.3109/07853890.2010.499131](https://doi.org/10.3109/07853890.2010.499131)
218. Meng B, Li Y, Ding Y, Xu X, Wang L, Guo B, Zhu B, Zhang J, Xiang L, Dong J, et al. Myeloid-derived growth factor inhibits inflammation and alleviates endothelial injury and atherosclerosis in mice. *Sci Adv*. 2021;7(21):eabe6903. doi:[10.1126/sciadv.abe6903](https://doi.org/10.1126/sciadv.abe6903)
219. Grandoch M, Feldmann K, Göthert JR, Dick LS, Homann S, Klatt C, Bayer JK, Waldheim JN, Rabausch B, Nagy N, et al. Deficiency in lymphotoxin β receptor protects from atherosclerosis in apoE-deficient mice. *Circ Res*. 2015;116(8):e57-e68. doi:[10.1161/CIRCRESAHA.116.305723](https://doi.org/10.1161/CIRCRESAHA.116.305723)
220. Shyu HY, Fong CS, Fu YP, Shieh JC, Yin JH, Chang CY, Wang HW, Cheng CW. Genotype polymorphisms of GGCX, NQO1, and VKORC1 genes associated with risk susceptibility in patients with large-artery atherosclerotic stroke. *Clin Chim Acta*. 2010;411(11-12):840-845. doi:[10.1016/j.cca.2010.02.071](https://doi.org/10.1016/j.cca.2010.02.071)
221. Tian S, Cao Y, Wang J, Bi Y, Zhong J, Meng X, Sun W, Yang R, Gan L, Wang X, et al. The miR-378c-Samd1 circuit promotes phenotypic modulation of vascular smooth muscle cells and foam cells formation in atherosclerosis lesions. *Sci Rep*. 2021;11(1):10548. doi:[10.1038/s41598-021-89981-z](https://doi.org/10.1038/s41598-021-89981-z)
222. Su YR, Dove DE, Major AS, Hasty AH, Boone B, Linton MF, Fazio S. Reduced ABCA1-mediated cholesterol efflux and accelerated atherosclerosis in apolipoprotein E-deficient mice lacking macrophage-derived ACAT1. *Circulation*. 2005;111(18):2373-2381. doi:[10.1161/01.CIR.0000164236.19860.13](https://doi.org/10.1161/01.CIR.0000164236.19860.13)
223. Vozenilek AE, Vetkoetter M, Green JM, Shen X, Traylor JG, Klein RL, Orr AW, Woolard MD, Krzywanski DM. Absence of Nicotinamide

- Nucleotide Transhydrogenase in C57BL/6J Mice Exacerbates Experimental Atherosclerosis. *J Vasc Res.* 2018;55(2):98-110. doi:[10.1159/000486337](https://doi.org/10.1159/000486337)
224. Zhang H, Ge S, Ni B, He K, Zhu P, Wu X, Shao Y. Augmenting ATG14 alleviates atherosclerosis and inhibits inflammation via promotion of autophagosome-lysosome fusion in macrophages. *Autophagy.* 2021;1-13. doi:[10.1080/15548627.2021.1909833](https://doi.org/10.1080/15548627.2021.1909833)
 225. Xiang R, Fan LL, Huang H, Chen YQ, He W, Guo S, Li JJ, Jin JY, Du R, Yan R, et al. Increased Reticulon 3 (RTN3) Leads to Obesity and Hypertriglyceridemia by Interacting With Heat Shock Protein Family A (Hsp70) Member 5 (HSPA5). *Circulation.* 2018;138(17):1828-1838. doi:[10.1161/CIRCULATIONAHA.117.030718](https://doi.org/10.1161/CIRCULATIONAHA.117.030718)
 226. Pigeyre M, Bokor S, Romon M, Gottrand F, Gilbert CC, Valtueña J, Gómez-Martínez S, Moreno LA, Amouyel P, Dallongeville J, et al. Influence of maternal educational level on the association between the rs3809508 neuromedin B gene polymorphism and the risk of obesity in the HELENA study. *Int J Obes (Lond).* 2010;34(3):478-486. doi:[10.1038/ijo.2009.260](https://doi.org/10.1038/ijo.2009.260)
 227. Belalcazar LM, Papandonatos GD, McCaffery JM, Peter I, Pajewski NM, Erar B, Allred ND, Balasubramanyam A, Bowden DW, Brautbar A, et al. A common variant in the CLDN7/ELP5 locus predicts adiponectin change with lifestyle intervention and improved fitness in obese individuals with diabetes. *Physiol Genomics.* 2015;47(6):215-224. doi:[10.1152/physiolgenomics.00109.2014](https://doi.org/10.1152/physiolgenomics.00109.2014)
 228. Parente DJ, Garriga C, Baskin B, Douglas G, Cho MT, Araujo GC, Shinawi M. Neuroligin 2 nonsense variant associated with anxiety, autism, intellectual disability, hyperphagia, and obesity. *Am J Med Genet A.* 2017;173(1):213-216. doi:[10.1002/ajmg.a.37977](https://doi.org/10.1002/ajmg.a.37977)
 229. Jenkins D, Seelow D, Jehue FS, Perlyn CA, Alonso LG, Bueno DF, Donnai D, Josifova D, Mathijssen IM, Morton JE, et al. RAB23 mutations in Carpenter syndrome imply an unexpected role for hedgehog signaling in cranial-suture development and obesity. *Am J Hum Genet.* 2007;80(6):1162-1170. doi:[10.1086/518047](https://doi.org/10.1086/518047)
 230. Zusi C, Morandi A, Maguolo A, Corradi M, Costantini S, Mosca A, Crudele A, Mantovani A, Alisi A, Miraglia Del Giudice E, et al. Association between MBOAT7 rs641738 polymorphism and non-alcoholic

- fatty liver in overweight or obese children. *Nutr Metab Cardiovasc Dis.* 2021;31(5):1548-1555. doi:[10.1016/j.numecd.2021.01.020](https://doi.org/10.1016/j.numecd.2021.01.020)
231. Yıldız Bölükbaşı E, Mumtaz S, Afzal M, Woehlbier U, Malik S, Tolun A. Homozygous mutation in CEP19, a gene mutated in morbid obesity, in Bardet-Biedl syndrome with predominant postaxial polydactyly. *J Med Genet.* 2018;55(3):189-197. doi:[10.1136/jmedgenet-2017-104758](https://doi.org/10.1136/jmedgenet-2017-104758)
 232. Andreasen CH, Mogensen MS, Borch-Johnsen K, Sandbaek A, Lauritzen T, Sørensen TI, Hansen L, Almind K, Jørgensen T, Pedersen O, et al. Non-replication of genome-wide based associations between common variants in INSIG2 and PFKP and obesity in studies of 18,014 Danes. *PLoS One.* 2008;3(8):e2872. doi:[10.1371/journal.pone.0002872](https://doi.org/10.1371/journal.pone.0002872)
 233. Tian N, Liu Q, Li Y, Tong L, Lu Y, Zhu Y, Zhang P, Chen H, Hu L, Meng J, et al. Transketolase Deficiency in Adipose Tissues Protects Mice From Diet-Induced Obesity by Promoting Lipolysis. *Diabetes.* 2020;69(7):1355-1367. doi:[10.2337/db19-1087](https://doi.org/10.2337/db19-1087)
 234. Jang I, Pottekat A, Poothong J, Yong J, Lagunas-Acosta J, Charbono A, Chen Z, Scheuner DL, Liu M, Itkin-Ansari P, et al. PDIA1/P4HB is required for efficient proinsulin maturation and β cell health in response to diet induced obesity. *Elife.* 2019;8:e44528. doi:[10.7554/eLife.44528](https://doi.org/10.7554/eLife.44528)
 235. Ohkubo Y, Sekido T, Nishio SI, Sekido K, Kitahara J, Suzuki S, Komatsu M. Loss of μ -crystallin causes PPAR γ activation and obesity in high-fat diet-fed mice. *Biochem Biophys Res Commun.* 2019;508(3):914-920. doi:[10.1016/j.bbrc.2018.12.038](https://doi.org/10.1016/j.bbrc.2018.12.038)
 236. Simmons RM, McKnight SM, Edwards AK, Wu G, Satterfield MC. Obesity increases hepatic glycine dehydrogenase and aminomethyltransferase expression while dietary glycine supplementation reduces white adipose tissue in Zucker diabetic fatty rats. *Amino Acids.* 2020;52(10):1413-1423. doi:[10.1007/s00726-020-02901-9](https://doi.org/10.1007/s00726-020-02901-9)
 237. Kim HR, Jin HS, Eom YB. Association of MACROD2 gene variants with obesity and physical activity in a Korean population. *Mol Genet Genomic Med.* 2021;9(4):e1635. doi:[10.1002/mgg3.1635](https://doi.org/10.1002/mgg3.1635)
 238. Williams MJ, Eriksson A, Shaik M, Voisin S, Yamskova O, Paulsson J, Thombare K, Fredriksson R, Schiöth HB. The Obesity-Linked Gene Nudt3 Drosophila Homolog Aps Is Associated With Insulin Signaling. *Mol Endocrinol.* 2015;29(9):1303-1319. doi:[10.1210/ME.2015-1077](https://doi.org/10.1210/ME.2015-1077)

239. Arrabal S, Lucena MA, Canduela MJ, Ramos-Uriarte A, Rivera P, Serrano A, Pavón FJ, Decara J, Vargas A, Baixeras E, et al. Pharmacological Blockade of Cannabinoid CB1 Receptors in Diet-Induced Obesity Regulates Mitochondrial Dihydrolipoamide Dehydrogenase in Muscle. *PLoS One*. 2015;10(12):e0145244. doi:[10.1371/journal.pone.0145244](https://doi.org/10.1371/journal.pone.0145244)
240. Lu Y, Habtetsion TG, Li Y, Zhang H, Qiao Y, Yu M, Tang Y, Zhen Q, Cheng Y, Liu Y. Association of NCOA2 gene polymorphisms with obesity and dyslipidemia in the Chinese Han population. *Int J Clin Exp Pathol*. 2015;8(6):7341-7349.
241. Bendlová B, Vaňková M, Hill M, Vacínová G, Lukášová P, Vejražková D, Šedová L, Šeda O, Včelák J. ZBTB16 gene variability influences obesity-related parameters and serum lipid levels in Czech adults. *Physiol Res*. 2017;66(Suppl 3):S425-S431. doi:[10.33549/physiolres.933731](https://doi.org/10.33549/physiolres.933731)
242. Vernochet C, Mourier A, Bezy O, Macotela Y, Boucher J, Rardin MJ, An D, Lee KY, Ilkayeva OR, Zingaretti CM, et al. Adipose-specific deletion of TFAM increases mitochondrial oxidation and protects mice against obesity and insulin resistance. *Cell Metab*. 2012;16(6):765-776. doi:[10.1016/j.cmet.2012.10.016](https://doi.org/10.1016/j.cmet.2012.10.016)
243. Zhu X, Xie S, Xu T, Wu X, Han M. Rasal2 deficiency reduces adipogenesis and occurrence of obesity-related disorders. *Mol Metab*. 2017;6(6):494-502. doi:[10.1016/j.molmet.2017.03.003](https://doi.org/10.1016/j.molmet.2017.03.003)
244. Lomba A, Milagro FI, García-Díaz DF, Campión J, Marzo F, Martínez JA. A high-sucrose isocaloric pair-fed model induces obesity and impairs NDUFB6 gene function in rat adipose tissue. *J Nutrigenet Nutrigenomics*. 2009;2(6):267-272. doi:[10.1159/000308465](https://doi.org/10.1159/000308465)
245. Yoshino S, Satoh T, Yamada M, Hashimoto K, Tomaru T, Katano-Toki A, Kakizaki S, Okada S, Shimizu H, Ozawa A, et al. Protection against high-fat diet-induced obesity in Helz2-deficient male mice due to enhanced expression of hepatic leptin receptor. *Endocrinology*. 2014;155(9):3459-3472. doi:[10.1210/en.2013-2160](https://doi.org/10.1210/en.2013-2160)
246. Deng T, Lyon CJ, Minze LJ, Lin J, Zou J, Liu JZ, Ren Y, Yin Z, Hamilton DJ, Reardon PR, et al. Class II major histocompatibility complex plays an essential role in obesity-induced adipose inflammation. *Cell Metab*. 2013;17(3):411-422. doi:[10.1016/j.cmet.2013.02.009](https://doi.org/10.1016/j.cmet.2013.02.009)

247. Zheng W, Yan C, Wang X, Luo Z, Chen F, Yang Y, Liu D, Gai X, Hou J, Huang M. TheTGFB1 functional polymorphism rs1800469 and susceptibility to atrial fibrillation in two Chinese Han populations. *PLoS One*. 2013;8(12):e83033. doi:[10.1371/journal.pone.0083033](https://doi.org/10.1371/journal.pone.0083033)
248. Choudhury A, Chung I, Blann AD, Lip GY. Platelet surface CD62P and CD63, mean platelet volume, and soluble/platelet P-selectin as indexes of platelet function in atrial fibrillation: a comparison of "healthy control subjects" and "disease control subjects" in sinus rhythm. *J Am Coll Cardiol*. 2007;49(19):1957-1964. doi:[10.1016/j.jacc.2007.02.038](https://doi.org/10.1016/j.jacc.2007.02.038)
249. Hou J, Yue Y, Hu B, Xu G, Su R, Lv L, Huang J, Yao J, Guan Y, Wang K, et al. DACT1 Involvement in the Cytoskeletal Arrangement of Cardiomyocytes in Atrial Fibrillation by Regulating Cx43. *Braz J Cardiovasc Surg*. 2019;34(6):711-722. doi:[10.21470/1678-9741-2019-0033](https://doi.org/10.21470/1678-9741-2019-0033)
250. Li J, Wang S, Bai J, Yang XL, Zhang YL, Che YL, Li HH, Yang YZ. Novel Role for the Immunoproteasome Subunit PSMB10 in Angiotensin II-Induced Atrial Fibrillation in Mice. *Hypertension*. 2018;71(5):866-876. doi:[10.1161/HYPERTENSIONAHA.117.10390](https://doi.org/10.1161/HYPERTENSIONAHA.117.10390)
251. Pollak AJ, Haghighi K, Kunduri S, Arvanitis DA, Bidwell PA, Liu GS, Singh VP, Gonzalez DJ, Sanoudou D, Wiley SE, et al. Phosphorylation of serine96 of histidine-rich calcium-binding protein by the Fam20C kinase functions to prevent cardiac arrhythmia. *Proc Natl Acad Sci U S A*. 2017;114(34):9098-9103. doi:[10.1073/pnas.1706441114](https://doi.org/10.1073/pnas.1706441114)
252. Cheng WL, Kao YH, Chen YC, Lin YK, Chen SA, Chen YJ. Macrophage migration inhibitory factor increases atrial arrhythmogenesis through CD74 signaling. *Transl Res*. 2020;216:43-56. doi:[10.1016/j.trsl.2019.10.002](https://doi.org/10.1016/j.trsl.2019.10.002)
253. Khalyfa A, Kheirandish-Gozal L, Bhattacharjee R, Khalyfa AA, Gozal D. Circulating microRNAs as Potential Biomarkers of Endothelial Dysfunction in Obese Children. *Chest*. 2016;149(3):786-800. doi:[10.1378/chest.15-0799](https://doi.org/10.1378/chest.15-0799)
254. Zamanillo R, Sánchez J, Serra F, Palou A. Breast Milk Supply of MicroRNA Associated with Leptin and Adiponectin Is Affected by Maternal Overweight/Obesity and Influences Infancy BMI. *Nutrients*. 2019;11(11):2589. doi:[10.3390/nu11112589](https://doi.org/10.3390/nu11112589)

255. Zhou Y, Hambly BD, Simmons D, McLachlan CS. RUNX1T1 rs34269950 is associated with obesity and metabolic syndrome. QJM. 2020;hcaa208. doi:[10.1093/qjmed/hcaa208](https://doi.org/10.1093/qjmed/hcaa208)
256. Zhuo XZ, Bai K, Wang Y, Liu P, Xi W, She J, Liu J. Long-chain non-coding RNA-GAS5 / hsa-miR-138-5p attenuates high glucose-induced cardiomyocyte damage by targeting CYP11B2. Biosci Rep. 2021;BSR20202232. doi:[10.1042/BSR20202232](https://doi.org/10.1042/BSR20202232)
257. Wu L, Archacki SR, Zhang T, Wang QK. Induction of high STAT1 expression in transgenic mice with LQTS and heart failure. Biochem Biophys Res Commun. 2007;358(2):449-454. doi:[10.1016/j.bbrc.2007.04.119](https://doi.org/10.1016/j.bbrc.2007.04.119)
258. Mirza AH, Kaur S, Nielsen LB, Størting J, Yarani R, Roursgaard M, Mathiesen ER, Damm P, Svare J, Mortensen HB, et al. Breast Milk-Derived Extracellular Vesicles Enriched in Exosomes From Mothers With Type 1 Diabetes Contain Aberrant Levels of microRNAs. Front Immunol. 2019;10:2543. doi:[10.3389/fimmu.2019.02543](https://doi.org/10.3389/fimmu.2019.02543)
259. Brizzi MF, Dentelli P, Pavan M, Rosso A, Gambino R, Grazia De Cesaris M, Garbarino G, Camussi G, Pagano G, Pegoraro L. Diabetic LDL inhibits cell-cycle progression via STAT5B and p21(waf). J Clin Invest. 2002;109(1):111-119. doi:[10.1172/JCI13617](https://doi.org/10.1172/JCI13617)
260. Peng J, Xiang Y. Value analysis of CD69 combined with EGR1 in the diagnosis of coronary heart disease. Exp Ther Med. 2019;17(3):2047-2052. doi:[10.3892/etm.2019.7175](https://doi.org/10.3892/etm.2019.7175)
261. Muiya NP, Wakil S, Al-Najai M, Tahir AI, Baz B, Andres E, Al-Boudari O, Al-Tassan N, Al-Shahid M, Meyer BF, et al. A study of the role of GATA2 gene polymorphism in coronary artery disease risk traits. Gene. 2014;544(2):152-158. doi:[10.1016/j.gene.2014.04.064](https://doi.org/10.1016/j.gene.2014.04.064)
262. Alfonso-Jaume MA, Bergman MR, Mahimkar R, Cheng S, Jin ZQ, Karliner JS, Lovett DH. Cardiac ischemia-reperfusion injury induces matrix metalloproteinase-2 expression through the AP-1 components FosB and JunB. Am J Physiol Heart Circ Physiol. 2006;291(4):H1838-H1846. doi:[10.1152/ajpheart.00026.2006](https://doi.org/10.1152/ajpheart.00026.2006)
263. Wang B, Xu A. Aryl hydrocarbon receptor pathway participates in myocardial ischemia reperfusion injury by regulating mitochondrial apoptosis. Med Hypotheses. 2019;123:2-5. doi:[10.1016/j.mehy.2018.12.004](https://doi.org/10.1016/j.mehy.2018.12.004)

264. Mahmoud MM, Kim HR, Xing R, Hsiao S, Mammoto A, Chen J, Serbanovic-Canic J, Feng S, Bowden NP, Maguire R, et al. TWIST1 Integrates Endothelial Responses to Flow in Vascular Dysfunction and Atherosclerosis. *Circ Res.* 2016;119(3):450-462. doi:[10.1161/CIRCRESAHA.116.308870](https://doi.org/10.1161/CIRCRESAHA.116.308870)

Figures

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

Fig. 2. Heat map of differentially expressed genes. Legend on the top left indicate log fold change of genes. (A1 – A37 = normal control samples; B1 – B47 = HF samples)

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

Fig. 4. Modules of isolated form PPI of DEGs. (A) The most significant module was obtained from PPI network with 35 nodes and 124 edges for up regulated genes (B) The most significant module was obtained from PPI network with 14 nodes and 34 edges for down regulated genes. Up regulated genes are marked in green; down regulated genes are marked in red

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

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

Fig. 7. ROC curve analyses of hub genes. A) HSP90AA1 B) ARRB2 C) MYH9 D) HSP90AB1 E) FLNA F) EGFR G) PIK3R1 H) CUL4A I) YEATS4 J) KAT2B

Tables

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

Gene Symbol	logFC	pValue	adj.P.Val	t value	Regulation	Gene Name
ZFP57	1.224999	2.14E-05	0.003206	4.509255	Up	ZFP57 zinc finger protein
TNC	1.122396	0.000645	0.027465	3.547613	Up	tenascin C
RNASE2	1.027472	1.78E-06	0.000833	5.144701	Up	ribonuclease A family member 2
CCL2	0.99544	0.0012	0.040517	3.35554	Up	C-C motif chemokine ligand 2
SPP1	0.873203	0.000506	0.023804	3.620881	Up	secreted phosphoprotein 1

KRT18	0.86356	0.000739	0.029864	3.505992	Up	keratin 18
TIMP1	0.846651	0.000294	0.016519	3.781328	Up	TIMP metalloproteinase inhibitor 1
CNN1	0.80833	0.00089	0.033515	3.448633	Up	calponin 1
TBC1D3L	0.795101	0.000564	0.025323	3.588131	Up	TBC1 domain family member 3L
DDX11	0.783764	4.41E-10	7.70E-06	7.079934	Up	DEAD/H-box helicase 11
CRLF1	0.743021	0.000265	0.015442	3.811524	Up	cytokine receptor like factor 1
ITGA3	0.741614	7.66E-08	0.000185	5.903327	Up	integrin subunit alpha 3
SDF2L1	0.692187	4.11E-07	0.000356	5.503602	Up	stromal cell derived factor 2 like 1
DHCR24	0.66763	0.000524	0.02437	3.610307	Up	24-dehydrocholesterol reductase
CYP1B1	0.667586	0.001627	0.049168	3.258738	Up	cytochrome P450 family 1 subfamily B member 1
HSPB1	0.663728	0.00064	0.027341	3.549831	Up	heat shock protein family B (small) member 1
CALR	0.648199	4.45E-09	3.41E-05	6.559875	Up	calreticulin
PLP2	0.632977	5.55E-07	0.000442	5.43104	Up	proteolipid protein 2
CD300E	0.632444	0.001185	0.040123	3.359543	Up	CD300e molecule
SERPINH1	0.624614	9.89E-06	0.002207	4.710643	Up	serpin family H member 1
S100A11	0.616077	2.05E-05	0.003152	4.51963	Up	S100 calcium binding protein A11
CAPG	0.605376	0.000115	0.009153	4.050937	Up	capping actin protein, gelsolin like
G0S2	0.586767	0.001044	0.037112	3.399133	Up	G0/G1 switch 2
FSCN1	0.579453	2.65E-06	0.000981	5.046164	Up	fascin actin-bundling protein 1
SH3BGRL3	0.577715	9.13E-05	0.007905	4.115034	Up	SH3 domain binding glutamate rich protein like 3
STXBP2	0.577692	1.62E-06	0.000802	5.168126	Up	syntaxin binding protein 2
PDIA4	0.577622	1.31E-06	0.000718	5.221421	Up	protein disulfideisomerase family A member 4
PYCR1	0.57611	0.000142	0.010507	3.990254	Up	pyrroline-5-carboxylate reductase 1
CSTA	0.572099	0.000533	0.02454	3.604988	Up	cystatin A
MNDA	0.570341	0.000388	0.02001	3.700429	Up	myeloid cell nuclear differentiation antigen
CDK2AP2	0.563929	8.15E-05	0.007313	4.146639	Up	cyclin dependent kinase 2 associated protein 2
CLCF1	0.559634	0.000617	0.026855	3.561185	Up	cardiotrophin like cytokine factor 1
PFKP	0.548707	0.001031	0.036851	3.402981	Up	phosphofructokinase, platelet
SLC7A1	0.542981	0.000677	0.028265	3.532721	Up	solute carrier family 7 member 1
RTN4	0.540935	0.001448	0.045624	3.296161	Up	reticulon 4
RUNX1	0.536499	0.000116	0.009153	4.048996	Up	RUNX family transcription factor 1
MFSD2A	0.528795	0.00019	0.012619	3.908525	Up	major facilitator superfamily domain containing 2A
CRYAB	0.521683	0.000753	0.030242	3.500341	Up	crystallin alpha B
MTFP1	0.513792	0.000403	0.020443	3.688557	Up	mitochondrial fission process 1
CLEC10A	0.513156	3.04E-05	0.003934	4.415474	Up	C-type lectin domain containing 10A
LRRC59	0.512434	1.67E-05	0.002908	4.574069	Up	leucine rich repeat containing 59
LILRA6	0.511502	1.95E-06	0.000853	5.122379	Up	leukocyte immunoglobulin like receptor A6
NCF2	0.510261	8.16E-05	0.007313	4.146238	Up	neutrophil cytosolic factor 2
HYOU1	0.508652	1.13E-07	0.000208	5.811898	Up	hypoxia up-regulated 1
PI4KAP1	0.508565	0.001035	0.036888	3.401747	Up	phosphatidylinositol 4-kinase alpha pseudogene 1
CCR1	0.508242	0.000547	0.025004	3.597535	Up	C-C motif chemokine receptor 1
TUBB6	0.508065	0.000617	0.026855	3.560899	Up	tubulin beta 6 class V

MYH9	0.506252	0.001081	0.037791	3.388193	Up	myosin heavy chain 9
BSCL2	0.502388	0.000129	0.009821	4.017479	Up	BSCL2 lipid droplet biogenesis associated, seipin
CALU	0.501481	0.000357	0.018991	3.72491	Up	calumenin
HSP90B1	0.493927	6.27E-06	0.001664	4.828226	Up	heat shock protein 90 beta family member 1 mesencephalic astrocyte derived neurotrophic factor
MANF	0.49332	4.97E-05	0.005423	4.282646	Up	tubulin beta 3 class III
TUBB3	0.48338	0.001467	0.045982	3.291846	Up	transketolase
TKT	0.472263	3.19E-06	0.00112	4.999166	Up	proliferation and apoptosis adaptor protein 15
PEA15	0.471374	0.000235	0.014244	3.847352	Up	F-box protein 27
FBXO27	0.470041	2.02E-06	0.000853	5.113807	Up	PVR cell adhesion molecule leukocyte associated immunoglobulin like receptor 1
PVR	0.461959	0.000354	0.018981	3.726891	Up	ankyrin repeat domain 13A
LAIR1	0.461304	0.000648	0.027539	3.545943	Up	arrestin domain containing 4
ANKRD13A	0.458515	0.001301	0.042645	3.330124	Up	myeloid derived growth factor
ARRDC4	0.455249	8.08E-05	0.007292	4.149203	Up	signal regulatory protein alpha
MYDGF	0.442572	1.93E-05	0.003097	4.536344	Up	prolyl 3-hydroxylase family member 4 (inactive)
SIRPA	0.437948	6.88E-05	0.006627	4.19355	Up	chloride intracellular channel 1
P3H4	0.437004	7.30E-05	0.00693	4.177202	Up	heat shock protein family A (Hsp70) member 5 heat shock protein 90 alpha family class A member 1
CLIC1	0.436357	3.21E-05	0.004108	4.400731	Up	annexin A5
HSPA5	0.435138	0.000162	0.011415	3.953189	Up	pleckstrin homology domain containing A7
HSP90AA1	0.432769	0.000121	0.009345	4.037281	Up	prolyl 4-hydroxylase subunit alpha 2
ANXA5	0.430833	9.73E-05	0.008246	4.097546	Up	sphingomyelin synthase 2
PLEKHA7	0.430517	0.000179	0.01219	3.925565	Up	centromere protein U
P4HA2	0.429533	0.000125	0.009618	4.026796	Up	neuromedin B
SGMS2	0.426985	0.000616	0.026855	3.561532	Up	collagen type V alpha 1 chain
CENPU	0.425563	5.81E-06	0.001608	4.847661	Up	ATP binding cassette subfamily C member 3
NMB	0.425512	0.000663	0.02786	3.539067	Up	procollagen-lysine,2-oxoglutarate 5-dioxygenase 2
COL5A1	0.424422	0.00107	0.03763	3.391434	Up	SAC3 domain containing 1
ABCC3	0.424346	0.000185	0.012432	3.915687	Up	dishevelled binding antagonist of beta catenin 1
PLOD2	0.421726	0.000163	0.011424	3.952237	Up	interferon induced transmembrane protein 2
SAC3D1	0.417839	1.31E-05	0.002577	4.637246	Up	tumor protein p53 inducible protein 13
DACT1	0.417316	0.000804	0.031533	3.480344	Up	C-C motif chemokine receptor 2
IFITM2	0.415944	0.000776	0.030782	3.491181	Up	CD48 molecule
TP53I13	0.415031	1.66E-06	0.000802	5.162827	Up	ORMDL sphingolipid biosynthesis regulator 2
CCR2	0.414803	0.001295	0.042642	3.331416	Up	protein disulfideisomerase family A member 6
CD48	0.414536	0.000319	0.01756	3.75811	Up	retinoic acid induced 14
ORMDL2	0.41319	9.60E-05	0.008171	4.101119	Up	PRELI domain containing 1 calcium voltage-gated channel auxiliary subunit beta 1
PDIA6	0.412615	3.14E-06	0.001118	5.003514	Up	tubulin beta class I
RAI14	0.412392	0.001384	0.044303	3.310538	Up	mitogen-activated protein kinase kinase 1
PRELID1	0.411245	0.000154	0.011059	3.967643	Up	ST3 beta-galactoside alpha-2,3-sialyltransferase 4
CACNB1	0.410792	4.74E-06	0.001369	4.899449	Up	
TUBB	0.410417	0.001615	0.048901	3.261217	Up	
MAP2K1	0.41029	0.000485	0.02321	3.633446	Up	
ST3GAL4	0.410126	6.38E-05	0.006374	4.214234	Up	

MMD	0.405867	2.20E-05	0.003227	4.500787	Up	monocyte to macrophage differentiation associated
RGS4	0.403324	0.000542	0.02485	3.600297	Up	regulator of G protein signaling 4
ZYX	0.401683	4.63E-05	0.00524	4.301846	Up	zyxin
MRGPRF	0.398775	0.000896	0.033648	3.446871	Up	MAS related GPR family member F
IMPDH1	0.395853	0.000558	0.025268	3.591368	Up	inosine monophosphate dehydrogenase 1
SEC24D	0.395438	0.001056	0.037362	3.395761	Up	SEC24 homolog D, COPII coat complex component
LAT2	0.395431	3.05E-05	0.003934	4.414543	Up	linker for activation of T cells family member 2
PGM3	0.39518	1.89E-05	0.003097	4.541889	Up	phosphoglucomutase 3
ITGA7	0.394428	7.58E-05	0.007073	4.166611	Up	integrin subunit alpha 7
PHLDA2	0.39404	0.000738	0.029857	3.506467	Up	pleckstrin homology like domain family A member 2
TRIM47	0.393406	0.000119	0.009306	4.040356	Up	tripartite motif containing 47
DCLK1	0.39321	0.000513	0.024097	3.616547	Up	doublecortin like kinase 1
FARP1	0.393034	0.001425	0.045111	3.301071	Up	FERM, ARH/RhoGEF and pleckstrin domain protein 1
DOK2	0.392357	0.000275	0.01572	3.801569	Up	docking protein 2
FXVD5	0.39205	0.000197	0.012834	3.897324	Up	FXVD domain containing ion transport regulator 5
ELP5	0.391828	0.000609	0.026706	3.564968	Up	elongatoracetyltransferase complex subunit 5
CLEC5A	0.391684	4.13E-06	0.0013	4.934192	Up	C-type lectin domain containing 5A
NANS	0.39166	1.79E-05	0.002972	4.556291	Up	N-acetylneuraminate synthase
FAM78B	0.391579	0.00042	0.020902	3.676838	Up	family with sequence similarity 78 member B
SHKBP1	0.390441	3.71E-06	0.001212	4.961044	Up	SH3KBP1 binding protein 1
SLC52A2	0.390128	0.000103	0.008553	4.081469	Up	solute carrier family 52 member 2
RPS2	0.389446	5.81E-06	0.001608	4.847544	Up	ribosomal protein S2
REEP3	0.389438	7.58E-08	0.000185	5.905589	Up	receptor accessory protein 3
TGFB1	0.388921	0.000252	0.014924	3.826628	Up	transforming growth factor beta 1
MPRIP	0.386935	0.001186	0.040151	3.359094	Up	myosin phosphatase Rho interacting protein
VASN	0.386371	0.000646	0.027477	3.547192	Up	vasorin
ARPC1B	0.384751	0.000266	0.015447	3.810509	Up	actin related protein 2/3 complex subunit 1B
SLC20A1	0.384426	0.00073	0.029689	3.509768	Up	solute carrier family 20 member 1
FZD8	0.383954	3.25E-05	0.004128	4.3972	Up	frizzled class receptor 8
AGTRAP	0.383635	1.92E-05	0.003097	4.536867	Up	angiotensin II receptor associated protein
PLOD3	0.382457	2.75E-07	0.000288	5.599965	Up	procollagen-lysine,2-oxoglutarate 5-dioxygenase 3
SLC44A3	0.382075	3.77E-06	0.001219	4.957496	Up	solute carrier family 44 member 3
CENPV	0.378846	2.28E-05	0.0033	4.491424	Up	centromere protein V
CLEC11A	0.378487	0.001022	0.036636	3.405753	Up	C-type lectin domain containing 11A
MYO1G	0.376607	4.96E-05	0.005423	4.283068	Up	myosin IG
NKX3-1	0.37512	0.000799	0.031418	3.481964	Up	NK3 homeobox 1
CCT2	0.375116	0.000323	0.01771	3.754203	Up	chaperonin containing TCP1 subunit 2
FLNA	0.373909	0.000123	0.0095	4.031236	Up	filamin A
IER5L	0.372959	1.32E-05	0.002577	4.635088	Up	immediate early response 5 like
KLHL25	0.372406	1.08E-05	0.002339	4.686763	Up	kelch like family member 25
ARHGAP9	0.371625	0.000605	0.026614	3.566828	Up	Rho GTPase activating protein 9
POLD2	0.369517	1.64E-05	0.002902	4.578557	Up	DNA polymerase delta 2, accessory subunit

SIRPB2	0.367136	0.00019	0.012625	3.90756	Up	signal regulatory protein beta 2
AHNAK2	0.366866	0.000384	0.019906	3.702966	Up	AHNAK nucleoprotein 2
ALG3	0.366274	3.66E-06	0.001211	4.964495	Up	ALG3 alpha-1,3- mannosyltransferase
BVES-AS1	0.365988	1.08E-05	0.002339	4.687811	Up	BVES antisense RNA 1
LIPG	0.364925	0.000877	0.033236	3.453507	Up	lipase G, endothelial type
L3HYPDH	0.363919	0.000784	0.031004	3.487922	Up	trans-L-3-hydroxyproline dehydratase
MICALL2	0.363576	2.84E-05	0.003765	4.433161	Up	MICAL like 2
COX6A1	0.362848	5.91E-05	0.006076	4.235216	Up	cytochrome c oxidase subunit 6A1
RPN2	0.362819	1.31E-05	0.002577	4.637612	Up	ribophorin II
HILPDA	0.362026	0.000392	0.02017	3.697404	Up	hypoxia inducible lipid droplet associated
TNFAIP8L2	0.360924	0.000554	0.02516	3.593563	Up	TNF alpha induced protein 8 like 2
CD320	0.360226	4.06E-06	0.001298	4.938562	Up	CD320 molecule
SIGLEC9	0.359194	0.001543	0.047802	3.275869	Up	sialic acid binding Ig like lectin 9
TNFRSF1A	0.357954	5.38E-05	0.005754	4.260707	Up	TNF receptor superfamily member 1A
LINC00622	0.357673	8.77E-05	0.007724	4.126217	Up	long intergenic non-protein coding RNA 622
GTSF1	0.355681	0.001579	0.04833	3.26837	Up	gametocyte specific factor 1
PRAF2	0.355212	0.000254	0.014995	3.824501	Up	PRA1 domain family member 2
BCL3	0.354363	0.001613	0.048901	3.261653	Up	BCL3 transcription coactivator
SCRIB	0.354292	4.03E-05	0.004814	4.339214	Up	scribble planar cell polarity protein
RPLP0	0.353489	8.26E-05	0.007387	4.142891	Up	ribosomal protein lateral stalk subunit P0
LHFPL2	0.352538	0.001574	0.04833	3.269431	Up	LHFPL tetraspan subfamily member 2
OSTC	0.351111	0.000415	0.020744	3.680094	Up	oligosaccharyltransferase complex non-catalytic subunit
GALE	0.350814	0.000245	0.014702	3.835172	Up	UDP-galactose-4-epimerase
PPIB	0.348003	0.001157	0.039445	3.36699	Up	peptidylprolyl isomerase B
ATP13A2	0.348001	6.59E-06	0.001712	4.815096	Up	ATPase cation transporting 13A2
YBX3	0.346688	0.001113	0.038469	3.37907	Up	Y-box binding protein 3
DDX39A	0.346486	6.66E-05	0.00651	4.202522	Up	DEXD-box helicase 39A
CHST15	0.346107	0.001467	0.045982	3.291979	Up	carbohydrate sulfotransferase 15
HOMER3	0.345717	0.001062	0.037482	3.393865	Up	homer scaffold protein 3
POLR3D	0.345507	0.000127	0.009736	4.021909	Up	RNA polymerase III subunit D
TMED9	0.345393	0.000222	0.013746	3.863031	Up	transmembrane p24 trafficking protein 9
GNG12	0.344962	0.001398	0.044529	3.307175	Up	G protein subunit gamma 12
GTF2H4	0.343634	1.66E-06	0.000802	5.163143	Up	general transcription factor IIH subunit 4
NXPH3	0.343391	0.000102	0.00851	4.085522	Up	neurexophilin 3
CXCL6	0.34288	7.37E-05	0.006962	4.174671	Up	C-X-C motif chemokine ligand 6
LILRB3	0.342718	0.000763	0.030481	3.496327	Up	leukocyte immunoglobulin like receptor B3
FIBCD1	0.341485	0.001428	0.045172	3.300421	Up	fibrinogen C domain containing 1
CBR1	0.341407	4.72E-05	0.005274	4.296574	Up	carbonyl reductase 1
DPAGT1	0.340778	5.99E-08	0.000182	5.960904	Up	dolichyl-phosphate N-acetylglucosaminylphosphotransferase 1
HIC1	0.33953	0.000262	0.015259	3.815358	Up	HIC ZBTB transcriptional repressor 1
ST6GALNAC4	0.339157	0.000178	0.012145	3.927471	Up	ST6 N-acetylglactosaminide alpha-2,6-sialyltransferase 4
CD63	0.338271	5.35E-05	0.005735	4.262255	Up	CD63 molecule

EHD2	0.337585	0.000171	0.011733	3.939022	Up	EH domain containing 2
TMED5	0.337169	0.000156	0.011139	3.96471	Up	transmembrane p24 trafficking protein 5
CD276	0.336462	0.000922	0.034267	3.437975	Up	CD276 molecule
FKBP2	0.33637	4.85E-05	0.005367	4.289363	Up	FKBP prolyl isomerase 2
LMAN2L	0.335963	4.21E-05	0.004952	4.327348	Up	lectin, mannose binding 2 like
CNPY3	0.335429	1.54E-06	0.000785	5.181345	Up	canopy FGF signaling regulator 3
ZNF467	0.335383	0.000237	0.014374	3.843941	Up	zinc finger protein 467
LMNB2	0.335076	0.000226	0.013883	3.857843	Up	lamin B2
PDIA3	0.334513	3.93E-05	0.004746	4.345855	Up	protein disulfide isomerase family A member 3
ZDHHC12	0.331578	0.000752	0.030227	3.500768	Up	zinc finger DHHC-type palmitoyltransferase 12
DBNL	0.331109	4.62E-06	0.001347	4.90593	Up	drebrin like
ACAP3	0.329606	2.54E-05	0.003492	4.462688	Up	ArfGAP with coiled-coil, ankyrin repeat and PH domains 3
CRELD2	0.329221	0.000369	0.019414	3.714737	Up	cysteine rich with EGF like domains 2
BCL9L	0.328792	0.000882	0.033328	3.451631	Up	BCL9 like
CCZ1B	0.327871	0.001452	0.04568	3.29516	Up	CCZ1 homolog B, vacuolar protein trafficking and biogenesis associated
ASCC2	0.327273	4.91E-05	0.005397	4.285839	Up	activating signal cointegrator 1 complex subunit 2
P4HB	0.326734	3.53E-05	0.004346	4.374806	Up	prolyl 4-hydroxylase subunit beta
TMEM198	0.326491	3.47E-05	0.004291	4.379913	Up	transmembrane protein 198
PFN1	0.326301	0.000195	0.012757	3.900469	Up	profilin 1
EBNA1BP2	0.324439	0.00086	0.032806	3.459269	Up	EBNA1 binding protein 2
SLC25A39	0.324417	2.97E-07	0.00029	5.581642	Up	solute carrier family 25 member 39
ZDHHC16	0.322971	7.36E-06	0.001827	4.787103	Up	zinc finger DHHC-type palmitoyltransferase 16
B3GAT3	0.322572	1.94E-07	0.00026	5.683079	Up	beta-1,3-glucuronyltransferase 3
TLCD1	0.321918	5.62E-05	0.005926	4.248836	Up	TLC domain containing 1
HSPG2	0.321897	0.00017	0.011692	3.940468	Up	heparansulfate proteoglycan 2
AGPAT1	0.321136	9.90E-08	0.000198	5.842963	Up	1-acylglycerol-3-phosphate O-acyltransferase 1
YIF1A	0.320271	0.000271	0.015611	3.805417	Up	Yip1 interacting factor homolog A, membrane trafficking protein
YJEFN3	0.320051	0.001533	0.047627	3.277899	Up	YjeF N-terminal domain containing 3
XPO1	0.318841	7.57E-05	0.007073	4.166981	Up	exportin 1
SEC23B	0.318583	0.000137	0.01022	4.001735	Up	SEC23 homolog B, COPII coat complex component
XBP1	0.317966	6.09E-06	0.001657	4.83538	Up	X-box binding protein 1
MCEMP1	0.317081	0.00108	0.037772	3.388589	Up	mast cell expressed membrane protein 1
FAM114A1	0.316352	0.001217	0.040827	3.351117	Up	family with sequence similarity 114 member A1
FAM222B	0.315258	0.000253	0.014937	3.825999	Up	family with sequence similarity 222 member B
FAM27C	0.31426	3.04E-05	0.003934	4.415335	Up	family with sequence similarity 27 member C
SEC11C	0.31363	0.001276	0.042274	3.336188	Up	SEC11 homolog C, signal peptidase complex subunit
LRFN3	0.313012	3.39E-06	0.001155	4.983987	Up	leucine rich repeat and fibronectin type III domain containing 3
KLC2	0.312745	0.001645	0.049537	3.255287	Up	kinesin light chain 2
APOBR	0.31271	0.000195	0.012757	3.900526	Up	apolipoprotein B receptor
MIIP	0.312588	0.000336	0.018331	3.742673	Up	migration and invasion inhibitory protein
NKX2-5	0.310849	0.000266	0.015447	3.811048	Up	NK2 homeobox 5

TMUB1	0.309133	3.15E-05	0.004044	4.405656	Up	transmembrane and ubiquitin like domain containing 1
PKNOX2	0.307335	0.000436	0.021436	3.665316	Up	PBX/knotted 1 homeobox 2
ALG8	0.307029	1.92E-05	0.003097	4.537639	Up	ALG8 alpha-1,3-glucosyltransferase
STIP1	0.306752	2.10E-06	0.000861	5.104216	Up	stress induced phosphoprotein 1
LTBR	0.306372	7.46E-05	0.007008	4.170993	Up	lymphotoxin beta receptor
ZNF692	0.305857	7.65E-05	0.007088	4.16419	Up	zinc finger protein 692
ATG101	0.30536	7.15E-06	0.001796	4.794275	Up	autophagy related 101
CBX6	0.305044	9.87E-08	0.000198	5.843654	Up	chromobox 6
GALNT7	0.304277	0.000262	0.015259	3.815487	Up	polypeptide N-acetylgalactosaminyltransferase 7
ARHGDI	0.302976	0.000102	0.00851	4.08528	Up	Rho GDP dissociation inhibitor alpha
SEPSECS-AS1	0.302961	1.02E-05	0.002257	4.702384	Up	SEPSECS antisense RNA 1 (head to head)
NXT1	0.302811	0.00075	0.030192	3.501392	Up	nuclear transport factor 2 like export factor 1
CALML4	0.302558	0.001204	0.040612	3.354572	Up	calmodulin like 4
PLXNA4	0.302118	5.81E-05	0.006036	4.240098	Up	plexin A4
ZNF668	0.300703	0.00015	0.010921	3.974769	Up	zinc finger protein 668
TNFSF8	0.300573	5.85E-05	0.006037	4.238231	Up	TNF superfamily member 8
ARRB2	0.300061	0.000295	0.016559	3.780258	Up	arrestin beta 2
RGS19	0.299956	0.000356	0.018991	3.725841	Up	regulator of G protein signaling 19
JTB	0.299631	4.01E-07	0.000356	5.509437	Up	jumping translocation breakpoint
NEU1	0.298949	7.40E-06	0.001829	4.785528	Up	neuraminidase 1
RTN3	0.298709	0.000102	0.00851	4.085138	Up	reticulon 3
SLC25A5	0.29869	9.84E-05	0.008296	4.094319	Up	solute carrier family 25 member 5
NLGN2	0.298311	4.92E-06	0.001415	4.889602	Up	neuroligin 2
POLR2J4	0.298103	6.58E-05	0.006477	4.205659	Up	RNA polymerase II subunit J4, pseudogene
AUP1	0.297831	7.21E-07	0.000518	5.367279	Up	AUP1 lipid droplet regulating VLDL assembly factor
SLC38A10	0.297822	1.44E-07	0.000228	5.754254	Up	solute carrier family 38 member 10
LGI2	0.297612	0.000361	0.019094	3.721683	Up	leucine rich repeat LGI family member 2
DOHH	0.297485	0.000689	0.028604	3.527432	Up	deoxyhypusine hydroxylase
ST14	0.29666	0.000443	0.021697	3.660922	Up	ST14 transmembrane serine protease matriptase
TESK1	0.296587	0.00014	0.010383	3.995431	Up	testis associated actin remodelling kinase 1
TBC1D2	0.296468	3.20E-07	0.0003	5.563722	Up	TBC1 domain family member 2
ITGA2	0.29522	0.001255	0.041826	3.341375	Up	integrin subunit alpha 2
HSPBP1	0.295083	0.000169	0.011651	3.941877	Up	HSPA (Hsp70) binding protein 1
OPN3	0.294553	0.000488	0.023275	3.631897	Up	opsin 3
RPL4P5	0.293787	1.03E-05	0.00227	4.699585	Up	ribosomal protein L4 pseudogene 5
DPEP2	0.293585	0.000103	0.008553	4.080461	Up	dipeptidase 2
SCAMP2	0.293062	9.31E-05	0.008027	4.109691	Up	secretory carrier membrane protein 2
KCTD21	0.292847	4.07E-06	0.001298	4.938084	Up	potassium channel tetramerization domain containing 21
ADAM8	0.292593	0.000118	0.00927	4.043615	Up	ADAM metallopeptidase domain 8
PNPLA6	0.291501	4.32E-07	0.000361	5.491725	Up	patatin like phospholipase domain containing 6
ANKRD13B	0.29141	2.78E-05	0.003698	4.439465	Up	ankyrin repeat domain 13B
NCLN	0.290701	0.000185	0.012417	3.916473	Up	nicalin

DHX34	0.29064	1.14E-05	0.002422	4.67336	Up	DExH-box helicase 34
EIF6	0.289426	0.000206	0.013198	3.885433	Up	eukaryotic translation initiation factor 6
FZD2	0.288318	8.84E-05	0.007765	4.124207	Up	frizzled class receptor 2
CSE1L	0.287822	3.34E-06	0.00115	4.988	Up	chromosome segregation 1 like
IRAK1	0.286433	0.001296	0.042642	3.33116	Up	interleukin 1 receptor associated kinase 1
SLC30A1	0.286242	0.000961	0.035144	3.424906	Up	solute carrier family 30 member 1
FURIN	0.285797	0.000543	0.02488	3.599634	Up	furin, paired basic amino acid cleaving enzyme
SHTN1	0.285099	0.001542	0.047802	3.275904	Up	shootin 1
ANO10	0.284169	0.000277	0.015838	3.799016	Up	anoctamin 10
FJX1	0.283925	0.001274	0.042273	3.336652	Up	four-jointed box kinase 1
GAL3ST4	0.283398	1.61E-05	0.002863	4.583164	Up	galactose-3-O-sulfotransferase 4
SGMS1	0.282987	5.57E-06	0.001562	4.858071	Up	sphingomyelin synthase 1
ALDH16A1	0.281646	0.000137	0.01022	4.001741	Up	aldehyde dehydrogenase 16 family member A1 ER degradation enhancing alpha-mannosidase like
EDEM2	0.281611	0.001354	0.043818	3.317382	Up	protein 2
PLXNA3	0.281561	0.001462	0.045966	3.292913	Up	plexin A3
SLC5A3	0.281452	9.72E-08	0.000198	5.847257	Up	solute carrier family 5 member 3
SCAMP4	0.28067	9.51E-07	0.00058	5.299736	Up	secretory carrier membrane protein 4
KLHL17	0.280454	1.60E-05	0.002847	4.585648	Up	kelch like family member 17
FUT11	0.279844	7.99E-05	0.007271	4.152159	Up	fucosyltransferase 11
LACC1	0.279461	0.000638	0.027336	3.551021	Up	laccase domain containing 1
GNB1L	0.279328	0.000427	0.021166	3.671657	Up	G protein subunit beta 1 like
COLGALT1	0.278177	0.001437	0.045408	3.298544	Up	collagen beta(1-O)galactosyltransferase 1
SFXN3	0.277442	0.001661	0.04987	3.252085	Up	sideroflexin 3
PGLS	0.276369	2.15E-05	0.003206	4.507013	Up	6-phosphogluconolactonase
RBM47	0.275698	0.000639	0.027336	3.550574	Up	RNA binding motif protein 47
TM9SF1	0.275656	9.08E-05	0.007875	4.116612	Up	transmembrane 9 superfamily member 1
SPATA2L	0.274571	0.00076	0.030386	3.497547	Up	spermatogenesis associated 2 like FAM20C golgi associated secretory pathway
FAM20C	0.274567	0.00069	0.028619	3.527002	Up	kinase
LPCAT1	0.274544	2.21E-06	0.000881	5.091798	Up	lysophosphatidylcholineacyltransferase 1
RUSC1	0.273906	8.44E-06	0.002029	4.751702	Up	RUN and SH3 domain containing 1
PPIA	0.273888	0.000614	0.026855	3.562374	Up	peptidylprolylisomerase A
TMEM214	0.273688	0.000148	0.010798	3.980041	Up	transmembrane protein 214
RAB23	0.273579	0.001298	0.042643	3.330713	Up	RAB23, member RAS oncogene family
TBC1D8B	0.273572	0.000277	0.015841	3.798597	Up	TBC1 domain family member 8B
SAMD1	0.272723	0.001284	0.042382	3.334275	Up	sterile alpha motif domain containing 1
RAB11FIP5	0.272394	0.00066	0.027817	3.54057	Up	RAB11 family interacting protein 5
PAK1IP1	0.271911	5.31E-05	0.005713	4.26457	Up	PAK1 interacting protein 1
PUSL1	0.271653	0.00013	0.009866	4.015416	Up	pseudouridine synthase like 1
PACS1	0.271392	0.000766	0.030545	3.49515	Up	phosphofurin acidic cluster sorting protein 1
ELOVL1	0.271274	0.000394	0.020219	3.695362	Up	ELOVL fatty acid elongase 1
EIF3I	0.270884	0.000158	0.01124	3.960043	Up	eukaryotic translation initiation factor 3 subunit I
RPUSD1	0.270125	0.001099	0.038176	3.383176	Up	RNA pseudouridine synthase domain containing 1

PARD6A	0.269973	0.001504	0.046936	3.283862	Up	par-6 family cell polarity regulator alpha
NME2	0.269842	0.001358	0.043855	3.316452	Up	NME/NM23 nucleoside diphosphate kinase 2
DHRS13	0.269704	0.000152	0.011003	3.971121	Up	dehydrogenase/reductase 13
SUPT3H	0.269519	1.74E-05	0.002942	4.564059	Up	SPT3 homolog, SAGA and STAGA complex component
NRROS	0.269456	0.000527	0.024377	3.608801	Up	negative regulator of reactive oxygen species
HHLA3	0.26928	0.000664	0.027869	3.53869	Up	HERV-H LTR-associating 3
BMS1P2	0.268734	0.00025	0.014831	3.829107	Up	BMS1 pseudogene 2
TBCK	0.268465	0.000539	0.024766	3.601924	Up	TBC1 domain containing kinase
TRAF7	0.268331	6.20E-07	0.000467	5.404138	Up	TNF receptor associated factor 7
C19orf38	0.267804	0.000886	0.033444	3.450049	Up	chromosome 19 open reading frame 38
NAGA	0.267516	0.000119	0.009306	4.04098	Up	alpha-N-acetylgalactosaminidase
P2RX4	0.267022	0.000272	0.015626	3.804775	Up	purinergic receptor P2X 4
STRBP	0.266715	0.000226	0.013883	3.857878	Up	spermatid perinuclear RNA binding protein
CLTA	0.26664	1.04E-05	0.00227	4.698255	Up	clathrin light chain A
GORAB	0.266273	0.000655	0.02771	3.542939	Up	golgin, RAB6 interacting
CNPY4	0.265996	0.000633	0.02725	3.553117	Up	canopy FGF signaling regulator 4
SLC5A6	0.265925	0.000109	0.008869	4.066027	Up	solute carrier family 5 member 6
AHR	0.265629	2.00E-05	0.003152	4.526266	Up	aryl hydrocarbon receptor
HGS	0.265499	1.98E-05	0.003146	4.529721	Up	hepatocyte growth factor-regulated tyrosine kinase substrate
CLIP2	0.264802	1.26E-05	0.00253	4.648875	Up	CAP-Gly domain containing linker protein 2
PAOX	0.263484	0.000245	0.014702	3.835136	Up	polyamine oxidase
TAF1A	0.263003	9.73E-06	0.002207	4.714942	Up	TATA-box binding protein associated factor, RNA polymerase I subunit A
NAA10	0.262709	6.23E-05	0.006274	4.220682	Up	N-alpha-acetyltransferase 10, NatA catalytic subunit
DPY19L1	0.262459	4.21E-05	0.004952	4.327758	Up	dpy-19 like C-mannosyltransferase 1
POLD1	0.262369	0.000227	0.013884	3.857433	Up	DNA polymerase delta 1, catalytic subunit
SLC39A13	0.262152	0.00024	0.014483	3.841368	Up	solute carrier family 39 member 13
SRM	0.26212	0.000897	0.033648	3.446399	Up	spermidine synthase
IMPDH2	0.262005	0.000194	0.012744	3.902678	Up	inosine monophosphate dehydrogenase 2
GABPB1-AS1	0.261903	6.43E-05	0.006413	4.211889	Up	GABPB1 antisense RNA 1
APBA3	0.261056	0.000662	0.027833	3.539639	Up	amyloid beta precursor protein binding family A member 3
CAMK1	0.260942	1.97E-05	0.003146	4.530152	Up	calcium/calmodulin dependent protein kinase I
C20orf96	0.260728	3.04E-05	0.003934	4.415582	Up	chromosome 20 open reading frame 96
ARHGAP33	0.26061	6.17E-06	0.001657	4.832341	Up	Rho GTPase activating protein 33
EFNA5	0.260324	0.000951	0.034899	3.428312	Up	ephrin A5
GLIS2	0.259939	0.001382	0.044303	3.310978	Up	GLIS family zinc finger 2
USB1	0.259863	0.000348	0.018763	3.732333	Up	U6 snRNA biogenesis phosphodiesterase 1
HNRNPH3	0.259528	0.000697	0.028675	3.523932	Up	heterogeneous nuclear ribonucleoprotein H3
AP2A1	0.259307	1.43E-05	0.002626	4.614494	Up	adaptor related protein complex 2 subunit alpha 1
UFSP1	0.259287	5.27E-05	0.005689	4.266378	Up	UFM1 specific peptidase 1 (inactive)
GDPD5	0.258978	0.000167	0.011526	3.945826	Up	glycerophosphodiesterphosphodiesterase domain containing 5
WDR27	0.258903	3.36E-09	3.08E-05	6.623787	Up	WD repeat domain 27

HSPA13	0.258302	0.001262	0.042006	3.339566	Up	heat shock protein family A (Hsp70) member 13
VAT1	0.258103	1.17E-05	0.002439	4.666332	Up	vesicle amine transport 1
CBX1	0.258057	1.34E-06	0.000718	5.215879	Up	chromobox 1
LRP10	0.257516	0.000219	0.013608	3.867894	Up	LDL receptor related protein 10
TCF3	0.256674	0.000553	0.02516	3.594358	Up	transcription factor 3
AP2S1	0.256657	0.000626	0.027019	3.556833	Up	adaptor related protein complex 2 subunit sigma 1
IRF3	0.256171	2.35E-07	0.000276	5.637827	Up	interferon regulatory factor 3
CCT3	0.255919	9.13E-06	0.002097	4.731565	Up	chaperonin containing TCP1 subunit 3 calcium/calmodulin dependent protein kinase kinase 1
CAMKK1	0.25571	0.000396	0.020284	3.69388	Up	
C8orf49	0.254247	0.000694	0.028628	3.525257	Up	chromosome 8 putative open reading frame 49
ATN1	0.253874	4.13E-06	0.0013	4.93419	Up	atrophin 1
FICD	0.252546	3.97E-05	0.004774	4.343558	Up	FIC domain protein adenyllyltransferase
TYRO3	0.251636	0.001606	0.048766	3.263059	Up	TYRO3 protein tyrosine kinase
ZSWIM7	0.251602	0.000577	0.025689	3.581373	Up	zinc finger SWIM-type containing 7
PCYOX1L	0.250554	0.000362	0.019116	3.720676	Up	prenylcysteine oxidase 1 like
FAM136A	0.250554	1.78E-06	0.000833	5.145354	Up	family with sequence similarity 136 member A
NLE1	0.250199	2.53E-05	0.003492	4.464083	Up	notchless homolog 1
SLC35C1	0.25016	0.001579	0.04833	3.268338	Up	solute carrier family 35 member C1
INTS8	0.249958	2.93E-05	0.003836	4.425106	Up	integrator complex subunit 8 nuclear pore complex interacting protein pseudogene 1
NPIPP1	0.249823	0.001468	0.045982	3.291712	Up	
NUDT5	0.249601	0.001302	0.042645	3.329829	Up	nudix hydrolase 5
OLAH	0.249177	0.000103	0.008553	4.082454	Up	oleoyl-ACP hydrolase
BAG2	0.248614	2.19E-05	0.003215	4.50257	Up	BAG cochaperone 2
PPARD	0.248222	3.72E-06	0.001212	4.960809	Up	peroxisome proliferator activated receptor delta
VKORC1	0.247541	0.000447	0.021843	3.657796	Up	vitamin K epoxide reductase complex subunit 1
NCAPH2	0.247486	8.82E-06	0.002046	4.74044	Up	non-SMC condensin II complex subunit H2
MAP1S	0.247006	6.74E-05	0.006563	4.199117	Up	microtubule associated protein 1S
CYSLTR1	0.246828	9.56E-05	0.008148	4.102434	Up	cysteinyl leukotriene receptor 1
CANX	0.246537	6.49E-05	0.00644	4.209622	Up	calnexin
GAPT	0.246468	0.000116	0.009153	4.047889	Up	GRB2 binding adaptor protein, transmembrane
PAPOLA	0.246046	0.000216	0.013542	3.870959	Up	poly(A) polymerase alpha
HM13	0.245973	0.001386	0.044303	3.309949	Up	histocompatibility minor 13
DCAF13	0.245824	0.001619	0.048974	3.260427	Up	DDB1 and CUL4 associated factor 13
FANCE	0.245809	0.000106	0.008701	4.0729	Up	FA complementation group E
NR2C2AP	0.245472	0.000406	0.020473	3.686796	Up	nuclear receptor 2C2 associated protein
MAPK13	0.245299	0.00042	0.020902	3.676667	Up	mitogen-activated protein kinase 13 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4
SMARCA4	0.245265	0.000221	0.013678	3.864851	Up	
SSR2	0.243149	0.000131	0.009879	4.014327	Up	signal sequence receptor subunit 2
MFS12	0.242194	0.000946	0.03478	3.429774	Up	major facilitator superfamily domain containing 12
ANKRD52	0.241882	4.50E-05	0.005142	4.309649	Up	ankyrin repeat domain 52
PKD1	0.241699	0.000408	0.020523	3.685348	Up	polycystin 1, transient receptor potential channel interacting

RALY	0.240652	8.92E-05	0.007801	4.121486	Up	RALY heterogeneous nuclear ribonucleoprotein
BBS7	0.240501	0.000206	0.013201	3.884951	Up	Bardet-Biedl syndrome 7
DAD1	0.240178	0.000186	0.01245	3.91446	Up	defender against cell death 1
CD55	0.239229	0.000559	0.025268	3.591082	Up	CD55 molecule (Cromer blood group)
NOP2	0.239005	0.000231	0.014092	3.852372	Up	NOP2 nucleolar protein
ESYT1	0.238678	2.08E-06	0.00086	5.106718	Up	extended synaptotagmin 1
NCOR2	0.238175	2.16E-05	0.003206	4.506773	Up	nuclear receptor corepressor 2
SH3GL1	0.23784	0.000394	0.020219	3.695395	Up	SH3 domain containing GRB2 like 1, endophilin A2
SPCS3	0.237435	0.000528	0.024398	3.608092	Up	signal peptidase complex subunit 3
SNAPC2	0.237313	0.000392	0.020186	3.696831	Up	small nuclear RNA activating complex polypeptide 2
PAK4	0.237197	6.27E-06	0.001664	4.828091	Up	p21 (RAC1) activated kinase 4
RASGRP4	0.236994	0.000397	0.020284	3.693079	Up	RAS guanyl releasing protein 4
NAB2	0.236918	0.000225	0.013869	3.859293	Up	NGFI-A binding protein 2
CYTH2	0.236404	2.28E-05	0.0033	4.492015	Up	cytohesin 2
PLCB3	0.235545	0.000249	0.014822	3.83012	Up	phospholipase C beta 3
ANKRD50	0.235412	0.000243	0.014647	3.837052	Up	ankyrin repeat domain 50
RNF167	0.235395	4.25E-05	0.004975	4.325171	Up	ring finger protein 167
APOBEC3B	0.235106	0.001065	0.037482	3.393007	Up	apolipoprotein B mRNA editing enzyme catalytic subunit 3B
TMEM241	0.235063	0.000234	0.014219	3.848619	Up	transmembrane protein 241
RAVER1	0.234903	2.84E-05	0.003765	4.433203	Up	ribonucleoprotein, PTB binding 1
HECTD3	0.234538	4.39E-05	0.005081	4.316262	Up	HECT domain E3 ubiquitin protein ligase 3
MBOAT7	0.234387	0.0003	0.016708	3.775873	Up	membrane bound O-acyltransferase domain containing 7
APIB1	0.234294	5.22E-05	0.005649	4.26893	Up	adaptor related protein complex 1 subunit beta 1
PAPSS1	0.234287	0.000459	0.022292	3.650149	Up	3'-phosphoadenosine 5'-phosphosulfate synthase 1
CD300LF	0.234256	1.90E-05	0.003097	4.540054	Up	CD300 molecule like family member f
ARHGEF40	0.23423	0.001391	0.044395	3.308795	Up	Rho guanine nucleotide exchange factor 40
NRAS	0.234066	0.001001	0.036118	3.412218	Up	NRAS proto-oncogene, GTPase
TMED2	0.233863	0.000857	0.032719	3.460579	Up	transmembrane p24 trafficking protein 2
GMNN	0.233749	0.000881	0.03331	3.452058	Up	geminin DNA replication inhibitor
NAGK	0.233287	0.000188	0.012521	3.911577	Up	N-acetylglucosamine kinase
GGCX	0.232875	5.42E-05	0.005776	4.259026	Up	gamma-glutamyl carboxylase
RHOJ	0.23277	0.000772	0.030683	3.492706	Up	ras homolog family member J
RFC4	0.23276	0.000248	0.014794	3.831434	Up	replication factor C subunit 4
PORCN	0.23263	0.001031	0.036851	3.403182	Up	porcupine O-acyltransferase
SLC24A3	0.232269	7.93E-05	0.007258	4.154329	Up	solute carrier family 24 member 3
GDAP2	0.232256	0.000123	0.0095	4.030748	Up	ganglioside induced differentiation associated protein 2
ERGIC1	0.232147	4.36E-06	0.001341	4.920292	Up	endoplasmic reticulum-golgi intermediate compartment 1
BRMS1	0.231781	0.001343	0.043559	3.319937	Up	BRMS1 transcriptional repressor and anoikis regulator
RPN1	0.23169	0.000495	0.023504	3.62737	Up	ribophorin I
SLC38A6	0.231439	0.001343	0.043559	3.32002	Up	solute carrier family 38 member 6
GCNT1	0.231228	0.001271	0.042229	3.337433	Up	glucosaminyl (N-acetyl) transferase 1

TCF19	0.231095	0.000455	0.02215	3.652361	Up	transcription factor 19
MFS10	0.230972	0.001272	0.042244	3.337092	Up	major facilitator superfamily domain containing 10
RPS19	0.23037	0.000481	0.023097	3.635762	Up	ribosomal protein S19
SURF4	0.230259	0.000551	0.025154	3.595175	Up	surfeit 4
YIPF2	0.22946	0.00054	0.024769	3.601588	Up	Yip1 domain family member 2
ABHD15	0.228602	0.000148	0.010798	3.979789	Up	abhydrolase domain containing 15
GSTP1	0.228242	4.26E-06	0.001321	4.926665	Up	glutathione S-transferase pi 1
DOT1L	0.228078	0.001601	0.04872	3.264	Up	DOT1 like histone lysine methyltransferase
TMEM150B	0.227801	4.70E-05	0.005274	4.297561	Up	transmembrane protein 150B
GPAA1	0.227515	3.56E-05	0.004358	4.373153	Up	glycosylphosphatidylinositol anchor attachment 1
ATXN2L	0.227344	1.86E-08	0.000107	6.232361	Up	ataxin 2 like
SF3B4	0.227333	3.84E-05	0.004639	4.35272	Up	splicing factor 3b subunit 4
TGFBR1	0.227257	0.0002	0.012926	3.893432	Up	transforming growth factor beta receptor 1
SPATA33	0.227209	3.24E-05	0.004128	4.397736	Up	spermatogenesis associated 33
COMT	0.227093	0.001333	0.043368	3.322299	Up	catechol-O-methyltransferase
RPSAP26	0.226712	0.001551	0.04793	3.274142	Up	ribosomal protein SA pseudogene 26
SCAMP3	0.226637	0.000116	0.009153	4.049314	Up	secretory carrier membrane protein 3
CLPTM1L	0.226627	0.001275	0.042274	3.336341	Up	CLPTM1 like
PPP1R11	0.226343	5.73E-08	0.000182	5.97138	Up	protein phosphatase 1 regulatory inhibitor subunit 11
LIMK1	0.225911	0.000564	0.025323	3.588066	Up	LIM domain kinase 1
EXT2	0.225802	1.46E-05	0.002654	4.610171	Up	exostosinglycosyltransferase 2
RHOG	0.225679	0.001584	0.048419	3.267469	Up	ras homolog family member G
C2CD2L	0.22564	2.60E-05	0.003545	4.457044	Up	C2CD2 like
MROH1	0.224693	6.69E-05	0.006523	4.201382	Up	maestro heat like repeat family member 1
TMBIM1	0.224538	4.49E-05	0.005142	4.310313	Up	transmembrane BAX inhibitor motif containing 1
CNPY2	0.224296	0.000406	0.020473	3.686725	Up	canopy FGF signaling regulator 2
IFT46	0.223876	0.000609	0.026706	3.565	Up	intraflagellar transport 46
BICD2	0.223796	3.49E-06	0.001164	4.976486	Up	BICD cargo adaptor 2
CEP19	0.223793	0.000104	0.008553	4.080088	Up	centrosomal protein 19
ERGIC2	0.223641	8.71E-05	0.007696	4.128369	Up	ERGIC and golgi 2
ADORA2B	0.223586	0.001525	0.047456	3.279479	Up	adenosine A2b receptor
LILRA1	0.22355	0.001206	0.040621	3.353952	Up	leukocyte immunoglobulin like receptor A1
HSP90AB1	0.223453	2.36E-05	0.003377	4.48311	Up	heat shock protein 90 alpha family class B member 1
HMG20B	0.223194	0.001208	0.040633	3.353453	Up	high mobility group 20B
SPRED1	0.222241	3.17E-06	0.00112	5.000871	Up	sprouty related EVH1 domain containing 1
CCNYL1	0.22216	0.000685	0.028517	3.529004	Up	cyclin Y like 1
MED8	0.221953	7.72E-05	0.007135	4.161812	Up	mediator complex subunit 8
GPR137	0.221901	0.000672	0.028122	3.535101	Up	G protein-coupled receptor 137
LINC00899	0.221878	0.00036	0.019094	3.721952	Up	long intergenic non-protein coding RNA 899
EPHB3	0.221237	1.40E-05	0.002601	4.619664	Up	EPH receptor B3
LRRC3	0.221106	0.001176	0.039875	3.361959	Up	leucine rich repeat containing 3
FAM219A	0.220892	4.60E-05	0.005232	4.303595	Up	family with sequence similarity 219 member A

POMT2	0.220238	2.65E-05	0.003574	4.452384	Up	protein O-mannosyltransferase 2
MTCO2P12	-1.41863	6.98E-05	0.006678	-4.1897	Down	MT-CO2 pseudogene 12
FAM81B	-1.24747	5.57E-07	0.000442	-5.42996	Down	family with sequence similarity 81 member B
MTCO3P12	-1.04149	2.73E-06	0.001005	-5.03812	Down	MT-CO3 pseudogene 12
C14orf180	-0.91724	8.06E-07	0.000553	-5.34034	Down	chromosome 14 open reading frame 180
ASB15	-0.91673	1.04E-06	0.000611	-5.27859	Down	ankyrin repeat and SOCS box containing 15
PHKG1	-0.88703	2.92E-05	0.003835	-4.42593	Down	phosphorylase kinase catalytic subunit gamma 1
SSTR5-AS1	-0.88544	0.001209	0.040633	-3.35326	Down	SSTR5 antisense RNA 1
ANK1	-0.84299	0.000462	0.022404	-3.64802	Down	ankyrin 1
IGSF1	-0.82587	8.71E-05	0.007696	-4.1283	Down	immunoglobulin superfamily member 1
MT1X	-0.80319	0.000382	0.019839	-3.70463	Down	metallothionein 1X
SMCO1	-0.80049	0.000959	0.035099	-3.42555	Down	single-pass membrane protein with coiled-coil domains 1
FGF12	-0.76661	1.27E-05	0.002539	-4.64584	Down	fibroblast growth factor 12
IDO1	-0.73682	8.12E-05	0.007304	-4.14763	Down	indoleamine 2,3-dioxygenase 1
F2RL3	-0.73297	1.69E-05	0.002916	-4.5703	Down	F2R like thrombin or trypsin receptor 3
RASD1	-0.72309	0.001207	0.040621	-3.35381	Down	ras related dexamethasone induced 1
AQP4	-0.72286	0.000818	0.031843	-3.47497	Down	aquaporin 4
GBP4	-0.71494	2.94E-07	0.00029	-5.58436	Down	guanylate binding protein 4
PYGM	-0.71265	0.000946	0.03478	-3.4298	Down	glycogen phosphorylase, muscle associated
FLJ42969	-0.70984	0.000621	0.026888	-3.55917	Down	uncharacterized LOC441374
FBXO40	-0.68051	0.000198	0.012834	-3.89672	Down	F-box protein 40
EIF4EBP3	-0.67331	6.90E-06	0.001756	-4.80368	Down	eukaryotic translation initiation factor 4E binding protein 3
CRYM	-0.65044	0.000487	0.023262	-3.63238	Down	crystallin mu
APOLD1	-0.64319	0.000432	0.021337	-3.66797	Down	apolipoprotein L domain containing 1
COQ10A	-0.63692	6.32E-05	0.006327	-4.21687	Down	coenzyme Q10A
SLC5A1	-0.63603	0.00064	0.027341	-3.54994	Down	solute carrier family 5 member 1
LCNL1	-0.63498	0.000226	0.013883	-3.85841	Down	lipocalin like 1
ACOT1	-0.62868	1.27E-07	0.000217	-5.78494	Down	acyl-CoA thioesterase 1
TMEM182	-0.62698	6.85E-05	0.006613	-4.19468	Down	transmembrane protein 182
SLC2A4	-0.62515	6.76E-05	0.006565	-4.19845	Down	solute carrier family 2 member 4
CXCL9	-0.61794	6.57E-05	0.006477	-4.20626	Down	C-X-C motif chemokine ligand 9
CARNS1	-0.61735	7.28E-05	0.00693	-4.17773	Down	carnosine synthase 1
MIR1-1HG	-0.60997	4.20E-05	0.004952	-4.32844	Down	MIR1-1 host gene
RGCC	-0.60981	1.40E-05	0.002601	-4.62027	Down	regulator of cell cycle
SHISA3	-0.59027	0.001317	0.042978	-3.32621	Down	shisa family member 3
LMOD2	-0.58597	3.37E-05	0.004226	-4.38794	Down	leiomodin 2
KLHL24	-0.58365	2.23E-06	0.000881	-5.08898	Down	kelch like family member 24
TSC22D3	-0.57675	5.50E-05	0.005821	-4.25504	Down	TSC22 domain family member 3
MYBPC1	-0.56836	0.001548	0.047912	-3.27469	Down	myosin binding protein C1
NUDT8	-0.5655	1.41E-05	0.002605	-4.61816	Down	nudix hydrolase 8
NEK10	-0.56374	5.09E-07	0.000417	-5.45216	Down	NIMA related kinase 10
MYOM2	-0.55345	0.000954	0.034958	-3.42733	Down	myomesin 2

PLA1A	-0.54813	0.000106	0.008701	-4.07306	Down	phospholipase A1 member A
EFHC2	-0.54373	9.37E-05	0.008047	-4.10798	Down	EF-hand domain containing 2
ZNF189	-0.54089	1.58E-06	0.000799	-5.17452	Down	zinc finger protein 189
CLGN	-0.53439	0.000105	0.008627	-4.07629	Down	calmegin
CD300LG	-0.53313	0.001551	0.04793	-3.27415	Down	CD300 molecule like family member g
C1orf53	-0.53126	3.92E-08	0.000164	-6.05989	Down	chromosome 1 open reading frame 53
HPCAL4	-0.52773	0.000567	0.025398	-3.58649	Down	hippocalcin like 4
LINC00881	-0.52203	0.001051	0.037234	-3.39714	Down	long intergenic non-protein coding RNA 881
SNHG17	-0.51907	2.41E-05	0.003415	-4.47746	Down	small nucleolar RNA host gene 17
TMEM143	-0.51534	0.000273	0.015667	-3.80328	Down	transmembrane protein 143
SELENBP1	-0.51243	0.00142	0.045026	-3.30233	Down	selenium binding protein 1
CD74	-0.51208	2.46E-05	0.003452	-4.47213	Down	CD74 molecule
GBP1	-0.50313	9.36E-05	0.008047	-4.10814	Down	guanylate binding protein 1
PPP1R12B	-0.50215	0.000233	0.014214	-3.84909	Down	protein phosphatase 1 regulatory subunit 12B
TRIM22	-0.50163	0.000179	0.01219	-3.92595	Down	tripartite motif containing 22
EFCAB2	-0.49591	0.000115	0.009153	-4.05118	Down	EF-hand calcium binding domain 2
MB	-0.49328	0.000345	0.018662	-3.73462	Down	myoglobin
IFIT3	-0.48935	2.01E-05	0.003152	-4.52512	Down	interferon induced protein with tetratricopeptide repeats 3
PHYH	-0.48125	2.06E-05	0.003152	-4.51826	Down	phytanoyl-CoA 2-hydroxylase
RD3L	-0.48085	0.000294	0.016519	-3.78152	Down	retinal degeneration 3 like
IRF6	-0.47961	0.001368	0.044032	-3.31406	Down	interferon regulatory factor 6
ACAT1	-0.47573	0.000498	0.02359	-3.62539	Down	acetyl-CoA acetyltransferase 1
TRIM63	-0.47558	1.69E-05	0.002916	-4.57043	Down	tripartite motif containing 63
COX7A1	-0.47508	1.67E-05	0.002908	-4.57443	Down	cytochrome c oxidase subunit 7A1
MTATP6P1	-0.47393	2.46E-05	0.003453	-4.47126	Down	MT-ATP6 pseudogene 1
TMEM178B	-0.47239	0.000522	0.024319	-3.61135	Down	transmembrane protein 178B
S100A1	-0.47177	0.001567	0.048208	-3.27079	Down	S100 calcium binding protein A1
ATP6V0E2	-0.47055	0.001442	0.045509	-3.2974	Down	ATPase H ⁺ transporting V0 subunit e2
CCT6B	-0.46771	1.35E-05	0.002587	-4.62918	Down	chaperonin containing TCP1 subunit 6B
HLA-DOA	-0.46145	3.48E-06	0.001164	-4.97773	Down	major histocompatibility complex, class II, DO alpha
HLA-DRA	-0.46046	0.001543	0.047802	-3.27586	Down	major histocompatibility complex, class II, DR alpha
ZBTB16	-0.45952	0.000183	0.012319	-3.91958	Down	zinc finger and BTB domain containing 16
PPP1R3B	-0.45433	0.000119	0.009306	-4.04084	Down	protein phosphatase 1 regulatory subunit 3B
HLA-F	-0.45308	2.03E-06	0.000853	-5.11208	Down	major histocompatibility complex, class I, F
P2RX6	-0.45013	0.000715	0.029171	-3.51609	Down	purinergic receptor P2X 6
TXLNB	-0.4497	0.000409	0.020558	-3.68419	Down	taxilin beta
NEAT1	-0.44877	0.000594	0.026258	-3.5727	Down	nuclear paraspeckle assembly transcript 1
ADPRHL1	-0.44742	1.34E-05	0.002587	-4.63194	Down	ADP-ribosylhydrolase like 1
LINC00863	-0.4438	1.68E-12	7.70E-08	-8.30655	Down	long intergenic non-protein coding RNA 863
LYRM9	-0.44164	0.00029	0.016341	-3.78619	Down	LYR motif containing 9
CTNNA3	-0.43916	0.000324	0.017773	-3.75281	Down	catenin alpha 3
TAP2	-0.43792	1.98E-06	0.000853	-5.11841	Down	transporter 2, ATP binding cassette subfamily B member

ARRDC2	-0.4375	2.09E-07	0.000267	-5.66554	Down	arrestin domain containing 2
SLC16A9	-0.4357	5.48E-05	0.005819	-4.25574	Down	solute carrier family 16 member 9
OSBP2	-0.43483	8.09E-05	0.007293	-4.14862	Down	oxysterol binding protein 2
MYZAP	-0.43444	0.000131	0.009879	-4.01411	Down	myocardial zonulaadherens protein
AMT	-0.43398	0.001005	0.036171	-3.4112	Down	aminomethyltransferase
NLRC5	-0.4317	6.41E-06	0.001683	-4.82243	Down	NLR family CARD domain containing 5
SCN7A	-0.43066	2.41E-05	0.003415	-4.47762	Down	sodium voltage-gated channel alpha subunit 7
GLIDR	-0.43015	9.68E-08	0.000198	-5.84827	Down	glioblastoma down-regulated RNA
KLF9	-0.42921	5.70E-07	0.000444	-5.42439	Down	Kruppel like factor 9
AMY2B	-0.42885	0.000152	0.011003	-3.97149	Down	amylase alpha 2B
CFAP58	-0.42686	1.83E-07	0.00026	-5.69731	Down	cilia and flagella associated protein 58
PIFO	-0.42626	0.000625	0.027019	-3.5571	Down	primary cilia formation
MYLK3	-0.42548	0.000504	0.023791	-3.62192	Down	myosin light chain kinase 3
PCSK6	-0.42542	0.00029	0.016341	-3.78593	Down	proproteinconvertasesubtilisin/kexin type 6 major histocompatibility complex, class II, DP alpha 1
HLA-DPA1	-0.42433	0.001234	0.041318	-3.34683	Down	
DECR1	-0.4214	0.000141	0.010416	-3.99408	Down	2,4-dienoyl-CoA reductase 1
PGPEP1L	-0.42136	0.000187	0.012512	-3.91221	Down	pyroglutamyl-peptidase I like
WVOX	-0.42017	8.26E-07	0.000553	-5.33431	Down	WW domain containing oxidoreductase
DOCK9	-0.41981	4.10E-07	0.000356	-5.50416	Down	dedicator of cytokinesis 9
ASB4	-0.41715	0.001402	0.044633	-3.30622	Down	ankyrin repeat and SOCS box containing 4 phenazine biosynthesis like protein domain containing
PBLD	-0.41181	2.05E-05	0.003152	-4.52068	Down	
CIRBP	-0.41176	2.55E-05	0.003492	-4.46262	Down	cold inducible RNA binding protein
PLEKHB1	-0.40976	0.000897	0.033648	-3.44648	Down	pleckstrin homology domain containing B1
ZNF883	-0.40957	0.000551	0.025154	-3.59513	Down	zinc finger protein 883
ACADSB	-0.40801	4.22E-06	0.00132	-4.92857	Down	acyl-CoA dehydrogenase short/branched chain
HSPB3	-0.40711	8.73E-06	0.002046	-4.74312	Down	heat shock protein family B (small) member 3
TCP11L2	-0.40505	0.001664	0.049882	-3.25165	Down	t-complex 11 like 2
RYR2	-0.40486	0.00035	0.018838	-3.73081	Down	ryanodine receptor 2
PARP14	-0.40325	1.17E-05	0.002437	-4.66791	Down	poly(ADP-ribose) polymerase family member 14
NDUFA1	-0.40048	1.52E-05	0.002736	-4.59812	Down	NADH:ubiquinoneoxidoreductase subunit A1
MX1	-0.39971	5.64E-05	0.005926	-4.24823	Down	MX dynamin like GTPase 1
ZBED5-AS1	-0.39898	0.000213	0.013493	-3.87491	Down	ZBED5 antisense RNA 1
ACADM	-0.3976	3.05E-06	0.001102	-5.01106	Down	acyl-CoA dehydrogenase medium chain defective in cullin neddylation 1 domain containing 2
DCUN1D2	-0.39529	2.10E-05	0.003176	-4.51355	Down	
C10orf71-AS1	-0.39208	0.001639	0.049452	-3.25647	Down	C10orf71 antisense RNA 1
CDS2	-0.39064	8.81E-09	5.78E-05	-6.40413	Down	CDP-diacylglycerol synthase 2
HEG1	-0.38998	0.00043	0.021293	-3.66923	Down	heart development protein with EGF like domains 1
RGN	-0.38951	0.000691	0.028627	-3.52636	Down	regucalcin
ZNF682	-0.38867	0.001578	0.04833	-3.26851	Down	zinc finger protein 682
CEBPB-AS1	-0.38724	6.09E-07	0.000466	-5.40862	Down	CEBPB antisense RNA 1
NNT	-0.38528	8.61E-06	0.00204	-4.74655	Down	nicotinamide nucleotide transhydrogenase
SUGCT	-0.3847	0.000128	0.009736	-4.02101	Down	succinyl-CoA:glutarate-CoAtransferase

NUDT6	-0.38168	0.00089	0.033515	-3.44863	Down	nudix hydrolase 6
PTPRB	-0.38138	0.000114	0.009153	-4.05223	Down	protein tyrosine phosphatase receptor type B
LIFR	-0.37953	6.30E-06	0.001664	-4.8268	Down	LIF receptor subunit alpha
MTMR14	-0.37937	8.51E-06	0.002029	-4.74968	Down	myotubularin related protein 14
CEP85	-0.37825	0.000977	0.035493	-3.41986	Down	centrosomal protein 85
ATAD2	-0.37766	0.000895	0.033645	-3.44718	Down	ATPase family AAA domain containing 2 potassium voltage-gated channel subfamily D member 3
KCND3	-0.37747	4.91E-05	0.005397	-4.28564	Down	guanine deaminase adipogenesis associated Mth938 domain containing
GDA	-0.37657	0.000284	0.016028	-3.79229	Down	interferon stimulated exonuclease gene 20
AAMDC	-0.37476	1.36E-05	0.002587	-4.62852	Down	synuclein gamma potassium voltage-gated channel subfamily A member 7
ISG20	-0.37364	9.40E-05	0.008062	-4.10694	Down	long intergenic non-protein coding RNA 1460
SNCG	-0.37343	0.000616	0.026855	-3.56168	Down	kinesin family member 22
KCNA7	-0.36943	0.000284	0.016028	-3.79235	Down	3-hydroxybutyrate dehydrogenase 2
LINC01460	-0.36934	2.05E-05	0.003152	-4.52061	Down	myosin light chain kinase family member 4
KIF22	-0.36929	1.98E-06	0.000853	-5.1183	Down	lactate dehydrogenase C
BDH2	-0.36908	0.00074	0.029864	-3.50566	Down	von Willebrand factor C domain containing 2
MYLK4	-0.36892	0.001127	0.038746	-3.37518	Down	apolipoprotein L3
LDHC	-0.36871	0.000699	0.028687	-3.52292	Down	long intergenic non-protein coding RNA 1003
VWC2	-0.36812	0.000355	0.018991	-3.726	Down	spermatogenesis associated 24
APOL3	-0.36775	6.61E-05	0.006483	-4.20465	Down	proteasome 20S subunit beta 9
LINC01003	-0.36571	5.03E-05	0.00548	-4.27914	Down	ornithine decarboxylase antizyme 2 HECT and RLD domain containing E3 ubiquitin protein ligase family member 6
SPATA24	-0.36556	0.000148	0.010798	-3.98025	Down	coiled-coil domain containing 68
PSMB9	-0.36262	0.000848	0.032542	-3.46392	Down	cytochrome b5 domain containing 2
OAZ2	-0.36181	2.35E-06	0.000906	-5.07557	Down	kizunacentrosomal protein
HERC6	-0.36101	0.000139	0.010341	-3.99704	Down	chromosome 15 open reading frame 40
CCDC68	-0.35907	0.000532	0.024527	-3.60575	Down	ankyrin repeat family A member 2
CYB5D2	-0.35868	2.23E-05	0.00326	-4.49723	Down	sulfotransferase family 1C member 2 radical S-adenosyl methionine domain containing 2
KIZ	-0.35735	4.03E-05	0.004814	-4.3396	Down	succinate dehydrogenase complex subunit C
C15orf40	-0.35598	8.41E-05	0.00746	-4.13803	Down	NADH:ubiquinone oxidoreductase subunit S4 AU RNA binding methylglutaconyl-CoA hydratase
ANKRA2	-0.35459	1.36E-06	0.000718	-5.212	Down	KIAA1217
SULT1C2	-0.35379	0.00066	0.027817	-3.54037	Down	chromosome 4 open reading frame 36
RSAD2	-0.35236	0.001388	0.044312	-3.30961	Down	ubiquinol-cytochrome c reductase binding protein
SDHC	-0.35068	1.88E-07	0.00026	-5.69062	Down	modulator of apoptosis 1
NDUFS4	-0.34874	8.53E-07	0.000553	-5.32652	Down	long intergenic non-protein coding RNA 888
AUH	-0.34801	0.000149	0.010824	-3.97819	Down	rhophilin associated tail protein 1B
KIAA1217	-0.34606	7.61E-05	0.007078	-4.16553	Down	3-hydroxy-3-methylglutaryl-CoA lyase
C4orf36	-0.34358	8.28E-06	0.002024	-4.7567	Down	
UQCRB	-0.34329	0.000267	0.015447	-3.80996	Down	
MOAP1	-0.33984	1.09E-05	0.002339	-4.68452	Down	
LINC00888	-0.33758	5.46E-06	0.00154	-4.86317	Down	
ROPN1B	-0.33728	0.000619	0.026874	-3.5599	Down	
HMGCL	-0.33721	1.39E-05	0.002601	-4.62306	Down	

ZNF33B	-0.33705	0.000211	0.013411	-3.87801	Down	zinc finger protein 33B
BATF2	-0.33646	0.000604	0.026587	-3.56747	Down	basic leucine zipper ATF-like transcription factor 2
VN1R28P	-0.33333	0.000415	0.020744	-3.68016	Down	vomeronal 1 receptor 28 pseudogene
RCSD1	-0.33328	1.79E-06	0.000833	-5.14328	Down	RCSD domain containing 1
CLK1	-0.33245	4.44E-05	0.005109	-4.31344	Down	CDC like kinase 1
FLJ37453	-0.33219	9.12E-07	0.000574	-5.31008	Down	uncharacterized LOC729614
FBXO4	-0.33219	0.000108	0.008833	-4.06768	Down	F-box protein 4
TYW1B	-0.33173	0.000545	0.024944	-3.59856	Down	tRNA-yW synthesizing protein 1 homolog B
OXSM	-0.33163	2.58E-07	0.000277	-5.61571	Down	3-oxoacyl-ACP synthase, mitochondrial
FAM219B	-0.3315	5.35E-06	0.001517	-4.86862	Down	family with sequence similarity 219 member B
TAPBPL	-0.33114	0.000237	0.014356	-3.8447	Down	TAP binding protein like
PIK3R1	-0.33091	0.000133	0.009995	-4.01036	Down	phosphoinositide-3-kinase regulatory subunit 1
MGST3	-0.3309	0.00012	0.009308	-4.03951	Down	microsomal glutathione S-transferase 3
PCBD2	-0.32933	8.99E-05	0.007841	-4.1194	Down	pterin-4 alpha-carbinolaminatedehydratase 2
C4orf3	-0.32838	7.25E-06	0.001811	-4.79072	Down	chromosome 4 open reading frame 3
BBS2	-0.32824	0.00012	0.009308	-4.03935	Down	Bardet-Biedl syndrome 2
CIITA	-0.32634	0.00047	0.022673	-3.64319	Down	class II major histocompatibility complex transactivator
RBM20	-0.32592	0.000406	0.020473	-3.68691	Down	RNA binding motif protein 20
YEATS4	-0.32537	2.60E-06	0.000971	-5.05078	Down	YEATS domain containing 4
COQ6	-0.32345	3.13E-05	0.004024	-4.40774	Down	coenzyme Q6, monooxygenase
DCAF6	-0.3213	1.87E-06	0.000849	-5.13354	Down	DDB1 and CUL4 associated factor 6
GPC5	-0.32116	0.000223	0.013762	-3.8623	Down	glypican 5
SLC2A11	-0.32114	0.000243	0.014647	-3.83697	Down	solute carrier family 2 member 11
USP2	-0.32065	0.000934	0.034489	-3.43397	Down	ubiquitin specific peptidase 2
SLCO5A1	-0.32054	0.001601	0.04872	-3.264	Down	solute carrier organic anion transporter family member 5A1
DTWD2	-0.31941	3.77E-05	0.00459	-4.35772	Down	DTW domain containing 2
PDE7A	-0.31813	7.08E-05	0.006766	-4.1855	Down	phosphodiesterase 7A
IFIT2	-0.31803	0.000281	0.015958	-3.79464	Down	interferon induced protein with tetratricopeptide repeats 2
MRPS21	-0.31718	3.45E-06	0.001164	-4.97994	Down	mitochondrial ribosomal protein S21
SCAPER	-0.317	0.000113	0.009143	-4.05551	Down	S-phase cyclin A associated protein in the ER
DCAF8	-0.3152	1.64E-07	0.000243	-5.72395	Down	DDB1 and CUL4 associated factor 8
PEX7	-0.31503	0.000506	0.023804	-3.62093	Down	peroxisomal biogenesis factor 7
RWDD2B	-0.31417	2.44E-07	0.000276	-5.6286	Down	RWD domain containing 2B
SPRYD4	-0.31186	9.95E-07	0.000594	-5.28867	Down	SPRY domain containing 4
C16orf86	-0.31134	2.16E-05	0.003208	-4.50575	Down	chromosome 16 open reading frame 86
C1orf54	-0.31079	0.001297	0.042642	-3.33107	Down	chromosome 1 open reading frame 54
SAMD9L	-0.30936	0.000685	0.028517	-3.52933	Down	sterile alpha motif domain containing 9 like
KLHDC2	-0.30927	5.93E-05	0.006078	-4.2345	Down	kelch domain containing 2
TBC1D7	-0.30782	0.000641	0.027347	-3.54949	Down	TBC1 domain family member 7
GLRX5	-0.30521	4.51E-06	0.001344	-4.91195	Down	glutaredoxin 5
GBP1P1	-0.30435	0.000648	0.027533	-3.54629	Down	guanylate binding protein 1 pseudogene 1
ATPAF1	-0.30267	1.19E-05	0.002458	-4.66215	Down	ATP synthase mitochondrial F1 complex assembly factor 1

C11orf1	-0.30257	0.000571	0.025504	-3.58445	Down	chromosome 11 open reading frame 1
UQCRC2	-0.30252	2.17E-05	0.003209	-4.50483	Down	ubiquinol-cytochrome c reductase core protein 2
NRSN2-AS1	-0.30187	0.000336	0.018336	-3.74224	Down	NRSN2 antisense RNA 1
PNPLA4	-0.30182	1.35E-05	0.002587	-4.62902	Down	patatin like phospholipase domain containing 4
ADCYAP1R1	-0.30146	0.000812	0.031688	-3.477	Down	ADCYAP receptor type 1
MGME1	-0.30137	2.77E-08	0.000141	-6.14056	Down	mitochondrial genome maintenance exonuclease 1
DYRK3	-0.30099	6.62E-05	0.006483	-4.20423	Down	dual specificity tyrosine phosphorylation regulated kinase 3
JARID2	-0.30073	4.53E-06	0.001344	-4.91056	Down	jumonji and AT-rich interaction domain containing 2
MACROD2	-0.30047	5.03E-10	7.70E-06	-7.05053	Down	mono-ADP ribosylhydrolase 2
ZC3H6	-0.30027	1.64E-06	0.000802	-5.16623	Down	zinc finger CCCH-type containing 6
PRX	-0.29908	0.000135	0.01016	-4.0044	Down	periaxin
C22orf46	-0.29908	1.18E-05	0.002439	-4.66533	Down	CTA-216E10.6
FPGS	-0.29763	1.50E-06	0.000772	-5.18827	Down	folylpolyglutamate synthase
ZNF226	-0.29688	8.75E-07	0.000558	-5.32026	Down	zinc finger protein 226
COX14	-0.29668	7.96E-05	0.007269	-4.15336	Down	cytochrome c oxidase assembly factor COX14
NDUFB3	-0.2961	1.79E-05	0.002972	-4.55564	Down	NADH:ubiquinoneoxidoreductase subunit B3
LIFR-AS1	-0.29604	0.000466	0.022546	-3.6458	Down	LIFR antisense RNA 1
TFAM	-0.2952	6.99E-07	0.00051	-5.37493	Down	transcription factor A, mitochondrial
PDHB	-0.29514	2.00E-06	0.000853	-5.11645	Down	pyruvate dehydrogenase E1 subunit beta
AIFM1	-0.29499	0.000104	0.008553	-4.08012	Down	apoptosis inducing factor mitochondria associated 1
DPH6	-0.29357	5.86E-05	0.006037	-4.23758	Down	diphthamine biosynthesis 6
PTRHD1	-0.29326	2.03E-06	0.000853	-5.11223	Down	peptidyl-tRNA hydrolase domain containing 1
GSTK1	-0.29269	4.34E-05	0.005035	-4.31944	Down	glutathione S-transferase kappa 1
ST7-AS1	-0.29249	0.001528	0.0475	-3.27897	Down	ST7 antisense RNA 1
SUSD5	-0.29166	0.000142	0.010456	-3.9921	Down	sushi domain containing 5
ZNF629	-0.29101	4.52E-06	0.001344	-4.91136	Down	zinc finger protein 629
PCCB	-0.29049	5.12E-05	0.005563	-4.2744	Down	propionyl-CoA carboxylase subunit beta
PSMB10	-0.29048	1.38E-05	0.002601	-4.62449	Down	proteasome 20S subunit beta 10
NMNAT1	-0.29008	1.09E-05	0.002339	-4.68526	Down	nicotinamide nucleotide adenyllyltransferase 1
TRAPPC6A	-0.28972	0.000157	0.011189	-3.96211	Down	trafficking protein particle complex 6A
COQ7 CTC-	-0.28943	3.31E-06	0.00115	-4.99018	Down	coenzyme Q7, hydroxylase
338M12.4	-0.2893	0.000715	0.029171	-3.51604	Down	uncharacterized LOC101928649
NDUFA13	-0.28928	0.000793	0.031217	-3.48449	Down	NADH:ubiquinoneoxidoreductase subunit A13
LINGO4	-0.2892	4.53E-06	0.001344	-4.91105	Down	leucine rich repeat and Ig domain containing 4
ZNF554	-0.28875	6.14E-06	0.001657	-4.83347	Down	zinc finger protein 554
FAM229B	-0.28859	0.000925	0.034353	-3.43695	Down	family with sequence similarity 229 member B
DNASE1L1	-0.28732	9.53E-05	0.008144	-4.10306	Down	deoxyribonuclease 1 like 1
ASB5	-0.28706	0.001305	0.042672	-3.32915	Down	ankyrin repeat and SOCS box containing 5
NSMCE2	-0.28504	1.32E-05	0.002577	-4.63597	Down	NSE2 (MMS21) homolog, SMC5-SMC6 complex SUMO ligase
ME3	-0.28447	0.000398	0.020301	-3.6925	Down	malic enzyme 3
NDUFS1	-0.28381	0.000341	0.018567	-3.73785	Down	NADH:ubiquinoneoxidoreductase core subunit S1
SEC14L1	-0.28362	1.89E-05	0.003097	-4.54163	Down	SEC14 like lipid binding 1

UPF3AP2	-0.2823	0.000256	0.015035	-3.82187	Down	UPF3A pseudogene 2
NEDD9	-0.28211	0.001038	0.036914	-3.40105	Down	neural precursor cell expressed, developmentally down-regulated 9
NDUFA10	-0.28124	0.001169	0.039751	-3.36363	Down	NADH:ubiquinoneoxidoreductase subunit A10
AGTPBP1	-0.28087	0.00025	0.014831	-3.82912	Down	ATP/GTP binding protein 1
TADA2B	-0.27985	2.59E-07	0.000277	-5.61419	Down	transcriptional adaptor 2B
C11orf54	-0.27935	0.000496	0.023504	-3.62711	Down	chromosome 11 open reading frame 54
MYL6B	-0.27878	2.24E-06	0.000881	-5.08755	Down	myosin light chain 6B
TOLLIP-AS1	-0.27839	0.000446	0.021801	-3.6587	Down	TOLLIP antisense RNA 1 (head to head)
MDH2	-0.27805	0.000114	0.009153	-4.05241	Down	malate dehydrogenase 2
NUDT3	-0.2774	4.69E-05	0.005274	-4.29836	Down	nudix hydrolase 3
ECHDC2	-0.2772	0.001571	0.048296	-3.26999	Down	enoyl-CoA hydratase domain containing 2 coiled-coil-helix-coiled-coil-helix domain containing 5
CHCHD5	-0.27694	3.47E-05	0.004291	-4.37973	Down	carbonyl reductase 4
UQCRCF1	-0.27567	8.92E-06	0.002059	-4.73758	Down	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1
DNAJC30	-0.27509	4.59E-06	0.001347	-4.90763	Down	DnaJ heat shock protein family (Hsp40) member C30
BTN3A3	-0.27501	0.000298	0.01662	-3.77811	Down	butyrophilin subfamily 3 member A3
CCDC28A	-0.27499	0.000721	0.029331	-3.51376	Down	coiled-coil domain containing 28A
DHRS12	-0.27378	0.001139	0.03902	-3.37186	Down	dehydrogenase/reductase 12
EGFR	-0.27307	0.000351	0.018907	-3.7294	Down	epidermal growth factor receptor
AKAP7	-0.27306	0.000425	0.021109	-3.67278	Down	A-kinase anchoring protein 7
PHF7	-0.27213	0.001493	0.046656	-3.2862	Down	PHD finger protein 7
NDUFS2	-0.27187	0.000389	0.020041	-3.69963	Down	NADH:ubiquinoneoxidoreductase core subunit S2
HIBADH	-0.27067	0.000401	0.020372	-3.69049	Down	3-hydroxyisobutyrate dehydrogenase
PPA2	-0.2703	0.00028	0.015924	-3.796	Down	inorganic pyrophosphatase 2
RAVER2	-0.26991	0.000616	0.026855	-3.56174	Down	ribonucleoprotein, PTB binding 2
FRMPD1	-0.26927	0.000261	0.015246	-3.81633	Down	FERM and PDZ domain containing 1
RASAL2	-0.26858	0.000573	0.025565	-3.58342	Down	RAS protein activator like 2
ZNF483	-0.26847	0.000114	0.009153	-4.05391	Down	zinc finger protein 483
HCP5	-0.26842	0.000821	0.031902	-3.47362	Down	HLA complex P5
NDUFA2	-0.26792	0.000283	0.016026	-3.79305	Down	NADH:ubiquinoneoxidoreductase subunit A2
ZNF160	-0.26636	0.000526	0.024377	-3.60931	Down	zinc finger protein 160
FBXL17	-0.26592	5.86E-05	0.006037	-4.23765	Down	F-box and leucine rich repeat protein 17
BORCS7	-0.26516	2.62E-05	0.003558	-4.45447	Down	BLOC-1 related complex subunit 7
COX7B	-0.26388	2.03E-05	0.003152	-4.52286	Down	cytochrome c oxidase subunit 7B succinate dehydrogenase complex iron sulfur subunit B
SDHB	-0.2632	6.81E-05	0.006587	-4.19634	Down	
PARL	-0.26309	1.11E-07	0.000208	-5.81494	Down	presenilin associated rhomboid like
AFG3L2	-0.26293	0.001386	0.044303	-3.31005	Down	AFG3 like matrix AAA peptidase subunit 2
ZNF25	-0.26245	2.24E-05	0.003263	-4.49617	Down	zinc finger protein 25
NDUFA4	-0.26226	0.000474	0.022813	-3.6405	Down	NDUFA4 mitochondrial complex associated
FUNDC1	-0.26211	3.33E-05	0.0042	-4.39106	Down	FUN14 domain containing 1
TRAK1	-0.26161	5.71E-05	0.005976	-4.24469	Down	trafficking kinesin protein 1
IFI35	-0.26133	0.000561	0.025304	-3.58976	Down	interferon induced protein 35

TMEM204	-0.26113	0.001103	0.038279	-3.38204	Down	transmembrane protein 204
GTF2IRD2B	-0.26107	0.00137	0.044057	-3.31363	Down	GTF2I repeat domain containing 2B
S1PR1	-0.26104	0.000485	0.02321	-3.63336	Down	sphingosine-1-phosphate receptor 1
ACYP2	-0.26069	0.000301	0.016729	-3.77514	Down	acylphosphatase 2
SLC31A2	-0.26024	0.000577	0.025689	-3.58155	Down	solute carrier family 31 member 2
MTUS1	-0.2602	4.32E-05	0.005024	-4.32067	Down	microtubule associated scaffold protein 1
TAL1	-0.26018	3.23E-05	0.004127	-4.39875	Down	TAL bHLH transcription factor 1, erythroid differentiation factor
HLTF	-0.25995	0.000273	0.015667	-3.80353	Down	helicase like transcription factor
DLD	-0.25959	0.000639	0.027336	-3.55045	Down	dihydrolipoamide dehydrogenase
ICA1L	-0.25902	0.000976	0.035476	-3.42026	Down	islet cell autoantigen 1 like
ZNF234	-0.25877	0.000102	0.008513	-4.08455	Down	zinc finger protein 234
CXCL11	-0.25859	2.04E-06	0.000853	-5.111	Down	C-X-C motif chemokine ligand 11
GMPR2	-0.25813	1.98E-07	0.00026	-5.67856	Down	guanosine monophosphate reductase 2
ACAD9	-0.25613	1.63E-07	0.000243	-5.72454	Down	acyl-CoA dehydrogenase family member 9
IPP	-0.25601	0.000126	0.009649	-4.02543	Down	intracisternal A particle-promoted polypeptide
NIT2	-0.25546	8.87E-05	0.007777	-4.12325	Down	nitrilase family member 2
ATP8A1	-0.25541	0.001659	0.049816	-3.25264	Down	ATPase phospholipid transporting 8A1
DDI2	-0.25515	7.10E-06	0.001792	-4.79629	Down	DNA damage inducible 1 homolog 2
BBS12	-0.25373	0.000147	0.010755	-3.98226	Down	Bardet-Biedl syndrome 12
RNLS	-0.25349	0.000876	0.033236	-3.45368	Down	renalase, FAD dependent amine oxidase
LNX1	-0.25258	5.59E-05	0.005909	-4.25027	Down	ligand of numb-protein X 1
CHCHD7	-0.25246	7.98E-05	0.007271	-4.1525	Down	coiled-coil-helix-coiled-coil-helix domain containing 7
MRPL45	-0.25223	2.34E-06	0.000906	-5.0775	Down	mitochondrial ribosomal protein L45
ATAD1	-0.25218	0.000202	0.013015	-3.88985	Down	ATPase family AAA domain containing 1
TRMT11	-0.25183	0.000148	0.010806	-3.97912	Down	tRNA methyltransferase 11 homolog
HMG20A	-0.2515	8.75E-06	0.002046	-4.74231	Down	high mobility group 20A
FAM214A	-0.25113	0.001593	0.048584	-3.26548	Down	family with sequence similarity 214 member A
KAT2B	-0.25078	0.000937	0.034519	-3.43271	Down	lysine acetyltransferase 2B
ARL15	-0.25036	0.000215	0.013509	-3.87234	Down	ADP ribosylation factor like GTPase 15
MCEE	-0.25012	0.001355	0.043818	-3.31716	Down	methylmalonyl-CoA epimerase
CEP192	-0.2493	0.000235	0.014244	-3.84734	Down	centrosomal protein 192
CIR1	-0.2492	1.76E-05	0.002972	-4.55998	Down	corepressor interacting with RBPJ, CIR1
SLC30A9	-0.24913	4.92E-08	0.000174	-6.00709	Down	solute carrier family 30 member 9
TMCC1	-0.2489	1.27E-05	0.002539	-4.6448	Down	transmembrane and coiled-coil domain family 1 calcineurin like phosphoesterase domain containing 1
CPPED1	-0.24784	0.00106	0.037459	-3.39454	Down	
MKRN2	-0.24677	1.29E-07	0.000217	-5.78048	Down	makorin ring finger protein 2
SUCLG2	-0.24674	6.57E-05	0.006477	-4.20618	Down	succinate-CoA ligase GDP-forming subunit beta
RASGRP3	-0.24661	0.00028	0.015924	-3.79617	Down	RAS guanyl releasing protein 3
ZNF418	-0.2458	0.000182	0.012315	-3.9207	Down	zinc finger protein 418
GPANK1	-0.24567	2.36E-05	0.003377	-4.48286	Down	G-patch domain and ankyrin repeats 1
IP6K2	-0.24547	0.000552	0.025154	-3.59484	Down	inositol hexakisphosphate kinase 2
EXOSC7	-0.24523	0.000146	0.010746	-3.98295	Down	exosome component 7

MAST4	-0.245	0.000686	0.028517	-3.52872	Down	microtubule associated serine/threonine kinase family member 4
FZD4	-0.24494	1.52E-05	0.002736	-4.59901	Down	frizzled class receptor 4
ATE1	-0.24398	0.000306	0.01692	-3.7704	Down	arginyltransferase 1
SNAPC5	-0.24333	8.93E-05	0.007801	-4.12133	Down	small nuclear RNA activating complex polypeptide 5
PDK1	-0.24315	0.000531	0.024516	-3.60618	Down	pyruvate dehydrogenase kinase 1
FLJ38576	-0.24289	0.001359	0.04387	-3.31612	Down	uncharacterized LOC651430
EIF4EBP2	-0.24252	0.001023	0.036636	-3.40558	Down	eukaryotic translation initiation factor 4E binding protein 2
HCG18	-0.2422	0.000693	0.028628	-3.52585	Down	HLA complex group 18
ABCA11P	-0.24069	0.000568	0.025398	-3.58628	Down	ATP binding cassette subfamily A member 11, pseudogene
SMIM20	-0.23997	0.000732	0.029715	-3.50896	Down	small integral membrane protein 20
ZNF32	-0.23992	0.000211	0.013411	-3.87762	Down	zinc finger protein 32
RAB12	-0.23978	0.000935	0.034492	-3.43356	Down	RAB12, member RAS oncogene family
LANCL2	-0.23831	6.90E-05	0.006634	-4.19268	Down	LanC like 2
UQCRCQ	-0.23789	0.001563	0.048144	-3.27165	Down	ubiquinol-cytochrome c reductase complex III subunit VII
TANC1	-0.23699	0.00122	0.040906	-3.35023	Down	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1
NDUFB6	-0.2364	0.000214	0.013493	-3.8733	Down	NADH:ubiquinone oxidoreductase subunit B6
FDX1	-0.23549	0.000357	0.018991	-3.72465	Down	ferredoxin 1
TMEM198B	-0.23389	0.000668	0.027985	-3.53686	Down	transmembrane protein 198B (pseudogene)
SEC31B	-0.23382	0.001133	0.038901	-3.37346	Down	SEC31 homolog B, COPII coat complex component
KIAA0232	-0.23377	4.01E-05	0.004811	-4.34077	Down	KIAA0232
SARS2	-0.23376	0.001251	0.041719	-3.34241	Down	seryl-tRNA synthetase 2, mitochondrial
ASH1L-AS1	-0.23328	0.001035	0.036888	-3.40186	Down	ASH1L antisense RNA 1
ZNF383	-0.23266	1.47E-05	0.002674	-4.60716	Down	zinc finger protein 383
THAP4	-0.23226	0.00066	0.027817	-3.54053	Down	THAP domain containing 4
TMEM44-AS1	-0.23208	0.001285	0.042382	-3.33402	Down	TMEM44 antisense RNA 1
NAA38	-0.23206	4.16E-05	0.004924	-4.331	Down	N-alpha-acetyltransferase 38, NatC auxiliary subunit
TRAM2-AS1	-0.23157	0.000765	0.030543	-3.49543	Down	TRAM2 antisense RNA 1 (head to head)
MRPL16	-0.23147	0.000434	0.021371	-3.66687	Down	mitochondrial ribosomal protein L16
MRPS28	-0.2312	1.22E-06	0.000695	-5.23763	Down	mitochondrial ribosomal protein S28
ABCB7	-0.23103	0.000115	0.009153	-4.05176	Down	ATP binding cassette subfamily B member 7
MRPS33	-0.23065	0.000352	0.018917	-3.72889	Down	mitochondrial ribosomal protein S33
NDUFB2	-0.23009	2.61E-05	0.003549	-4.4559	Down	NADH:ubiquinone oxidoreductase subunit B2
OXA1L	-0.22969	0.000254	0.015006	-3.82379	Down	OXA1L mitochondrial inner membrane protein
ZNF721	-0.22935	1.33E-06	0.000718	-5.21785	Down	zinc finger protein 721
TACC1	-0.22935	0.000533	0.02454	-3.60524	Down	transforming acidic coiled-coil containing protein 1
IMPA1	-0.22911	3.82E-05	0.004634	-4.35371	Down	inositol monophosphatase 1
LRIF1	-0.22902	0.000181	0.012294	-3.92185	Down	ligand dependent nuclear receptor interacting factor 1
TFDP2	-0.22826	0.001104	0.038299	-3.38164	Down	transcription factor Dp-2
CCNB1IP1	-0.22772	0.000554	0.02516	-3.59364	Down	cyclin B1 interacting protein 1
PSMB8	-0.22471	0.001614	0.048901	-3.26137	Down	proteasome 20S subunit beta 8

PCYT1A	-0.22311	5.94E-06	0.001624	-4.84204	Down	phosphate cytidyltransferase 1, choline, alpha
CCDC25	-0.22224	0.000933	0.034489	-3.43405	Down	coiled-coil domain containing 25
LINC00909	-0.22221	0.00013	0.009821	-4.01718	Down	long intergenic non-protein coding RNA 909
TYW1	-0.22017	1.33E-06	0.000718	-5.2164	Down	tRNA-yW synthesizing protein 1 homolog
RFX5	-0.21984	0.000218	0.013604	-3.86871	Down	regulatory factor X5
WASF4P	-0.2196	0.001363	0.043913	-3.31536	Down	WASP family member 4, pseudogene
MIR762HG	-0.21927	0.000988	0.035749	-3.41639	Down	MIR762 host gene
ERCC5	-0.21895	1.23E-05	0.002513	-4.6551	Down	ERCC excision repair 5, endonuclease
AP5S1	-0.21894	5.44E-05	0.005788	-4.25785	Down	adaptor related protein complex 5 subunit sigma 1
INO80C	-0.21818	6.96E-05	0.006673	-4.19047	Down	INO80 complex subunit C
NT5C3A	-0.21788	1.91E-05	0.003097	-4.53813	Down	5'-nucleotidase, cytosolic IIIA
COX7C	-0.21764	9.91E-05	0.008338	-4.09238	Down	cytochrome c oxidase subunit 7C
ACSL5	-0.21703	0.000158	0.01124	-3.95993	Down	acyl-CoA synthetase long chain family member 5
RARB	-0.21673	0.000616	0.026855	-3.56165	Down	retinoic acid receptor beta
CECR2	-0.21605	0.000333	0.018175	-3.74554	Down	CECR2 histone acetyl-lysine reader
GP6	-0.21523	0.001302	0.042645	-3.32988	Down	glycoprotein VI platelet
TIMM23B	-0.21522	9.64E-06	0.002203	-4.71752	Down	translocase of inner mitochondrial membrane 23 homolog B
CHRA1	-0.21496	0.00049	0.02337	-3.63037	Down	chromatin accessibility complex subunit 1
ZNF287	-0.21433	0.000271	0.015608	-3.80583	Down	zinc finger protein 287
RMDN1	-0.21392	0.000783	0.030993	-3.48829	Down	regulator of microtubule dynamics 1
KBTBD4	-0.21199	2.73E-05	0.003668	-4.44399	Down	kelch repeat and BTB domain containing 4
COPZ2	-0.21192	0.000707	0.028926	-3.51964	Down	COPI coat complex subunit zeta 2
RGMB	-0.21107	3.45E-05	0.004291	-4.38126	Down	repulsive guidance molecule BMP co-receptor b
HELZ2	-0.21102	0.00089	0.033515	-3.44864	Down	helicase with zinc finger 2
NBPF3	-0.21072	0.000563	0.025315	-3.58875	Down	NBPF member 3
PRKAG1	-0.21054	6.45E-05	0.006413	-4.21135	Down	protein kinase AMP-activated non-catalytic subunit gamma 1
ERAP1	-0.20996	0.000813	0.031706	-3.47656	Down	endoplasmic reticulum aminopeptidase 1
CNBP	-0.20952	0.000256	0.015035	-3.82151	Down	CCHC-type zinc finger nucleic acid binding protein
MZF1-AS1	-0.2089	0.00052	0.024271	-3.61284	Down	MZF1 antisense RNA 1
TMEM14B	-0.20889	2.05E-05	0.003152	-4.51974	Down	transmembrane protein 14B
ZMYM2	-0.20682	5.97E-05	0.006096	-4.23247	Down	zinc finger MYM-type containing 2
ORC2	-0.2066	3.87E-07	0.000356	-5.5181	Down	origin recognition complex subunit 2
COL11A2	-0.20656	0.001242	0.041492	-3.34459	Down	collagen type XI alpha 2 chain
COX11	-0.20638	1.94E-06	0.000853	-5.12414	Down	cytochrome c oxidase copper chaperone COX11
ANAPC15	-0.20615	0.000281	0.015941	-3.79533	Down	anaphase promoting complex subunit 15
COX6B1	-0.2056	0.000699	0.028687	-3.52294	Down	cytochrome c oxidase subunit 6B1
CLNS1A	-0.20515	1.16E-06	0.000667	-5.25082	Down	chloride nucleotide-sensitive channel 1A
EPAS1	-0.20487	0.000194	0.012744	-3.90226	Down	endothelial PAS domain protein 1
LAP3	-0.20467	0.000715	0.029171	-3.51597	Down	leucineaminopeptidase 3
OXCT1-AS1	-0.20422	0.000202	0.012997	-3.89094	Down	OXCT1 antisense RNA 1
OSBPL11	-0.20325	0.000655	0.027712	-3.54264	Down	oxysterol binding protein like 11
POLR2L	-0.20266	0.001323	0.043124	-3.32469	Down	RNA polymerase II, I and III subunit L

CS	-0.2022	0.001155	0.039403	-3.36756	Down	citrate synthase
AFF1	-0.20165	0.000269	0.015546	-3.80773	Down	AF4/FMR2 family member 1
FBXO21	-0.20142	0.000853	0.032626	-3.46205	Down	F-box protein 21
RNMT	-0.20118	0.000194	0.012744	-3.90276	Down	RNA guanine-7 methyltransferase
METTL25	-0.20098	0.000563	0.025315	-3.58882	Down	methyltransferase like 25
WDR37	-0.20088	5.83E-05	0.006037	-4.2388	Down	WD repeat domain 37
TUBGCP5	-0.20068	0.000986	0.035729	-3.41706	Down	tubulin gamma complex associated protein 5
TRAPPC13	-0.20033	0.000579	0.025749	-3.58038	Down	trafficking protein particle complex 13
GHITM	-0.19956	1.66E-05	0.002908	-4.57625	Down	growth hormone inducible transmembrane protein
ATG14	-0.19835	0.001523	0.047439	-3.28002	Down	autophagy related 14
PIK3C2B	-0.19725	0.000918	0.034198	-3.43911	Down	phosphatidylinositol-4-phosphate 3-kinase catalytic subunit type 2 beta
GTF2IRD2P1	-0.1971	0.000842	0.032406	-3.46578	Down	GTF2I repeat domain containing 2 pseudogene 1
ATCAY	-0.19636	0.000202	0.012997	-3.89063	Down	ATCAY kinesin light chain interacting caytaxin
TMEM242	-0.19577	0.000354	0.018981	-3.72687	Down	transmembrane protein 242
SPAG7	-0.1952	0.000321	0.017615	-3.75614	Down	sperm associated antigen 7
HCG4B	-0.19503	0.00083	0.032108	-3.47031	Down	HLA complex group 4B
SYF2	-0.19409	0.001139	0.03902	-3.37179	Down	SYF2 pre-mRNA splicing factor
OSBPL1A	-0.19382	0.000165	0.011497	-3.94914	Down	oxysterol binding protein like 1A
ZNF304	-0.19377	7.46E-05	0.007008	-4.1713	Down	zinc finger protein 304
N4BP2L2	-0.19368	0.000819	0.03188	-3.47436	Down	NEDD4 binding protein 2 like 2
RBMS2	-0.19329	1.50E-05	0.002708	-4.60282	Down	RNA binding motif single stranded interacting protein 2
ZNF766	-0.19224	1.78E-05	0.002972	-4.55706	Down	zinc finger protein 766
TXNRD3	-0.19149	0.001333	0.043368	-3.32223	Down	thioredoxinreductase 3
STK16	-0.19146	1.39E-05	0.002601	-4.62165	Down	serine/threonine kinase 16
LINC00235	-0.19116	0.001133	0.038901	-3.37348	Down	long intergenic non-protein coding RNA 235
ACAD8	-0.18976	0.001575	0.04833	-3.2693	Down	acyl-CoA dehydrogenase family member 8
FKBP3	-0.18963	0.000856	0.032719	-3.46077	Down	FKBP prolylisomerase 3
MED6	-0.18929	1.91E-05	0.003097	-4.5391	Down	mediator complex subunit 6
LARP4	-0.18913	0.000294	0.016519	-3.78142	Down	La ribonucleoprotein 4
NCOA4	-0.18857	7.78E-05	0.007165	-4.15954	Down	nuclear receptor coactivator 4
ENY2	-0.18757	0.001386	0.044303	-3.3099	Down	ENY2 transcription and export complex 2 subunit
CMTR1	-0.1875	0.000186	0.012453	-3.91398	Down	cap methyltransferase 1
SLU7	-0.18719	0.000602	0.026543	-3.56827	Down	SLU7 homolog, splicing factor
HDDC2	-0.18682	0.000519	0.024249	-3.61343	Down	HD domain containing 2
TATDN2P3	-0.18634	0.000219	0.01362	-3.86724	Down	TatDDNase domain containing 2 pseudogene 3
YTHDC2	-0.18442	8.38E-05	0.007449	-4.13895	Down	YTH domain containing 2
IMMT	-0.1841	0.000246	0.014738	-3.83366	Down	inner membrane mitochondrial protein
GEN1	-0.18385	0.000926	0.034389	-3.43638	Down	GEN1 Holliday junction 5' flap endonuclease
SERPINB6	-0.18358	0.000622	0.026911	-3.55862	Down	serpin family B member 6
RSRC2	-0.18335	6.12E-05	0.006222	-4.22566	Down	arginine and serine rich coiled-coil 2
XRN1	-0.18325	9.77E-06	0.002207	-4.71386	Down	5'-3' exoribonuclease 1
LMBR1L	-0.18204	0.000208	0.013268	-3.88229	Down	limb development membrane protein 1 like

NCOA2	-0.18173	0.000635	0.027298	-3.5523	Down	nuclear receptor coactivator 2
C6orf89	-0.18159	7.38E-05	0.006962	-4.17423	Down	chromosome 6 open reading frame 89
NDUFB8	-0.18156	0.000116	0.009153	-4.04896	Down	NADH:ubiquinoneoxidoreductase subunit B8
NSUN4	-0.18155	4.73E-05	0.005274	-4.29596	Down	NOP2/Sun RNA methyltransferase 4
NDUFC2	-0.18131	0.001361	0.043877	-3.31584	Down	NADH:ubiquinoneoxidoreductase subunit C2
ZNHIT3	-0.18057	0.00078	0.030921	-3.48927	Down	zinc finger HIT-type containing 3
KLHL5	-0.18055	0.000654	0.027681	-3.54355	Down	kelch like family member 5
CUL4A	-0.18016	0.000515	0.02411	-3.61546	Down	cullin 4A

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:0051179	BP	localization	1.49135E-05	4.8264212	220	RNASE2,CCL2,SPP1,KRT18,TIMP1,TBC1D3L,ITGA3,DHCR24,CYP1B1,HSPB1,CALR,PLP2,S100A11,FSCN1,STXBP2,PDIA4,MNDA,SLC7A1,RTN4,MFSD2A,CRYAB,CLEC10A,NCF2,HYOU1,CCR1,MYH9,BCL2,HSP90B1,MANF,PEA15,LAIR1,ANKRD13A,ARRDC4,SIRPA,CLIC1,HSPA5,HP90AA1,ANXA5,NMB,CO15A1,ABCC3,CCR2,CD48,PRELID1,CACNB1,TUBB,MAP2K1,ST3GAL4,MMD,RGS4,IMPDH1,SEC24D,LAT2,PHLDA2,DCLK1,DOCK2,FXRD5,ELP5,CLEC5A,SLC52A2,RPS2,TGFB1,ARPC1B,SLC20A1,PLOD3,SLC44A3,CENPV,MYO1G,NKX3-1,CCT2,FLNA,ARHGAP9,LIPG,MICAL2,COX6A1,HILPDA,CD320,SIGLEC9,TNFRSF1A,PRAF2,BCL3,SCRIB,RPLP0,LHFPL2,PIIB,ATP13A2,DDX39A,HOMER3,TMED9,CXCL6,LILRB3,CD63,EHD2,TMED5,LMAN2L,ZDHHC12,DBNL,ACAP3,PFN1,SLC25A39,B3GAT3,HSPG2,YIF1A,YJFN3,XPO1,SEC23B,XBP1,MCEMP1,KLC2,APOBR,MIIIP,NKX2-5,ARHGDI,NXT1,PLXNA4,ARRB2,NEU1,RTN3,SLC25A5,NLGN2,AUP1,SLC38A10,TESK1,TBC1D2,ITGA2,SCAMP2,ADAM8,ANKRD13B,EIF6,CSE1L,SLC30A1,FURIN,SHTN1,ANO10,EDEM2,PLXNA3,SLC5A3,SCAMP4,SFXN3,TM9SF1,LPCAT1,PPIA,RAB23,T

						BC1D8B,RAB11FIP5,PAC S1,PARD6A,NME2,NRRO S,TBCK,P2RX4,CLTA,CN PY4,SLC5A6,HGS,SLC39A 13,IMPDH2,APBA3,CAMK 1,ARHGAP33,EFNA5,GLIS 2,AP2A1,VAT1,LRP10,AP2 S1,CCT3,TYRO3,PCYOX1 L,SLC35C1,PPARD,MAP1 S,CYSLTR1,CANX,HM13, SSR2,MFSD12,PKD1,BBS7 ,CD55,ESYT1,NCOR2,SH3 GL1,SPCS3,PAK4,CYTH2, ANKRD50,TMEM241,MB OAT7,AP1B1,CD300LF,NR AS,TMED2,RHOJ,PORCN, SLC24A3,ERGIC1,SLC38A 6,GCNT1,MFSD10,RPS19, SURF4,YIPF2,GSTP1,GPA A1,TGFBR1,COMT,SCAM P3,LIMK1,EXT2,RHOG,C2 CD2L,TMBIM1,IFT46,BIC D2,CEP19,ERGIC2,HSP90 AB1,SPRED1,EPHB3 SPPI1,KRT18,TBC1D3L,HS PB1,CALR,STXBP2,PDIA4 ,SLC7A1,MFSD2A,MYH9, HSP90B1,PEA15,ARRDC4, HSPA5,HSP90AA1,NMB,A BCC3,PRELID1,RGS4,SEC 24D,SLC52A2,RPS2,TGFB 1,NKX3- 1,FLNA,LIPG,MICALL2,C D320,PRAF2,SCRIB,RPLP 0,ATP13A2,DDX39A,HOM ER3,TMED9,CD63,TMED5 ,LMAN2L,ZDHHC12,B3G AT3,YIF1A,YJEFN3,XPO1, SEC23B,XBP1,APOBR,NX T1,ARRB2,SLC25A5,NLG N2,AUP1,SLC38A10,TBC1 D2,SCAMP2,ADAM8,CSE 1L,FURIN,EDEM2,SLC5A 3,SCAMP4,SFXN3,PPIA,R AB23,TBC1D8B,RAB11FI P5,PARD6A,TBCK,P2RX4, CLTA,SLC5A6,HGS,APBA 3,CAMK1,ARHGAP33,EF NA5,AP2A1,LRP10,AP2S1, SLC35C1,PPARD,CANX,H M13,SSR2,MFSD12,PKD1, BBS7,ESYT1,SPCS3,ANK RD50,TMEM241,AP1B1,T MED2,PORCN,SLC38A6, MFSD10,RPS19,SCAMP3, C2CD2L,BICD2,HSP90AB 1
GO:0071702	BP	organic substance transport	0.000182418	3.738933041	100	SPPI1,KRT18,TBC1D3L,HS PB1,CALR,STXBP2,PDIA4 ,SLC7A1,MFSD2A,MYH9, HSP90B1,PEA15,ARRDC4, HSPA5,HSP90AA1,NMB,A BCC3,PRELID1,RGS4,SEC 24D,SLC52A2,RPS2,TGFB 1,NKX3- 1,FLNA,LIPG,MICALL2,C D320,PRAF2,SCRIB,RPLP 0,ATP13A2,DDX39A,HOM ER3,TMED9,CD63,TMED5 ,LMAN2L,ZDHHC12,B3G AT3,YIF1A,YJEFN3,XPO1, SEC23B,XBP1,APOBR,NX T1,ARRB2,SLC25A5,NLG N2,AUP1,SLC38A10,TBC1 D2,SCAMP2,ADAM8,CSE 1L,FURIN,EDEM2,SLC5A 3,SCAMP4,SFXN3,PPIA,R AB23,TBC1D8B,RAB11FI P5,PARD6A,TBCK,P2RX4, CLTA,SLC5A6,HGS,APBA 3,CAMK1,ARHGAP33,EF NA5,AP2A1,LRP10,AP2S1, SLC35C1,PPARD,CANX,H M13,SSR2,MFSD12,PKD1, BBS7,ESYT1,SPCS3,ANK RD50,TMEM241,AP1B1,T MED2,PORCN,SLC38A6, MFSD10,RPS19,SCAMP3, C2CD2L,BICD2,HSP90AB 1
GO:0005737	CC	cytoplasm	2.92E-09	8.534597387	336	TNC,RNASE2,SPP1,KRT18 ,TIMP1,DDX11,CRLF1,IT GA3,SDF2L1,DHCR24,CY P1B1,HSPB1,CALR,PLP2,S ERPINH1,S100A11,CAPG, G0S2,FSCN1,SH3BGRL3,S TXBP2,PDIA4,PYCR1,CST A,MNDA,CDK2AP2,PFKP, RTN4,MFSD2A,CRYAB,M TFP1,LRRC59,NCF2,HYO U1,CCR1,TUBB6,MYH9,B SCL2,CALU,HSP90B1,MA NF,TUBB3,TKT,PEA15,FB

XO27,PVR,LAIR1,ANKRD13A,ARRDC4,MYDGF,SIRPA,P3H4,CLIC1,HSPA5,HP90AA1,ANXA5,PLEKHA7,P4HA2,SGMS2,CENPU,COL5A1,PLOD2,DACT1,IFTM2,TP53I13,CCR2,ORMDL2,PDIA6,RAI14,PRELID1,TUBB,MAP2K1,ST3GAL4,MMD,RGS4,ZYX,IMPDH1,SEC24D,PGM3,PHLDA2,TRIM47,FARP1,DOK2,ELP5,CLEC5A,NANS,SHKBP1,RPS2,REEP3,TGFB1,MPRIP,VASN,ARPC1B,FZD8,AGTRAP,PLOD3,CENPV,CLEC11A,MYO1G,NKX3-1,CCT2,FLNA,KLHL25,ARHGAP9,AHNAK2,ALG3,LIPG,MICALL2,COX6A1,RPN2,HILPDA,TNFAIP8L2,CD320,SIGLEC9,TNFRSF1A,GTSEF1,PRAF2,BCL3,SCRIB,RPLP0,LHFPL2,OSTC,GALE,PPIB,ATP13A2,YBX3,DDX39A,CHST15,HOMER3,POLR3D,TMED9,GNG12,LILRB3,CBR1,DPAGT1,ST6GALNAC4,CD63,EHD2,TMED5,FKBP2,LMAN2L,CNPY3,PDIA3,ZDHHC12,DBNL,CRELD2,P4HB,TMEM198,PFN1,SLC25A39,ZDHHC16,B3GAT3,HSPG2,AGPAT1,YIF1A,YJEFN3,XPO1,SEC23B,XBP1,MCEMP1,FAM114A1,SEC11C,KLC2,TMUB1,PKNOX2,ALG8,STIP1,LTBR,ATG101,GALNT7,ARHGDI1A,NXT1,ARRB2,RGS19,ITB,NEU1,RTN3,SLC25A5,AUP1,SLC38A10,DOHH,TESK1,TBC1D2,ITGA2,HSPBP1,SCAMP2,ADAM8,PNPLA6,ANKRD13B,NCLN,EIF6,FZD2,CSE1L,IRAK1,SLC30A1,FURIN,SHTN1,GAL3ST4,SGMS1,EDEM2,SLC5A3,SCAMP4,KLHL17,FUT11,LACC1,COLGALT1,SFXN3,PGLS,TM9SF1,SPATA2L,FAM20C,LPCAT1,RUSC1,PIA,TMEM214,RAB23,TBC1D8B,RAB11FIP5,PUSL1,PACS1,ELOVL1,EIF3I,PARD6A,NME2,DHRS13,NRROS,TBCK,TRAF7,NAGA,P2RX4,STRBP,CLTA,GORAB,AHR,HGS,CLIP2,NAA10,POLD1,SLC39A13,SRM,IMPDH2,APBA3,CAMK1,ARHGAP33,GLIS2,AP2A1,GDPD5,HSPA13,VAT1,TCF3,AP2S1,IRF3,CCT3,CAMKK1,ATN1,FICD,TYRO3,PCYOX1L,FAM136A,SLC35C1,NUDT5,OLAH,BAG2,VKORC1,MAP1S,CANX,GAPT,PAPOLA,HM13,DCAF1

GO:0016020 CC membrane 1.92278E-06 5.716070067 279

3,MAPK13,SSR2,MFSD12,PKD1,BBS7,DAD1,CD55,ESYT1,SH3GL1,SPCS3,SNAPC2,PAK4,RASGRP4,CYTH2,PLCB3,ANKRD50,RNF167,APOBEC3B,TMEM241,RAVER1,HECTD3,MBOAT7,AP1B1,PAPSS1,ARHGEF40,NRAS,TMED2,GMNN,NAGK,GGCX,RHOJ,PORCN,GDAP2,ERGIC1,BRMS1,RPN1,GCNT1,MFSD10,RPS19,SURF4,YIPF2,GSTP1,TMEM150B,GPA1,ATXN2L,TGFBR1,SPATA33,COMT,SCAMP3,PPP1R11,LI-MK1,EXT2,RHOG,C2CD2L,TMBIM1,CNPY2,IFT46,BICD2,CEP19,ERGIC2,HS-P90AB1,SPRED1,CCNYL1,GPR137,EPHB3,POMT2,TNC,KRT18,TBC1D3L,CR-LF1,ITGA3,SDF2L1,DHCR24,CYP1B1,HSPB1,CALR,PLP2,CD300E,SERPINH1,F-SCN1,STXBP2,CSTA,PFK-P,SLC7A1,RTN4,MFSD2A,CRYAB,MTFP1,CLEC10A,LRRCS9,LILRA6,NCF2,HY-OU1,CCR1,MYH9,BSCL2,CALU,HSP90B1,TKT,PVR,LAIR1,ANKRD13A,ARRD-C4,SIRPA,CLIC1,HSPA5,H-SP90AA1,ANXA5,PLEKH-A7,SGMS2,ABCC3,PLOD2,IFITM2,TP53I13,CCR2,CD48,ORMDL2,PDIA6,CACN-B1,TUBB,MAP2K1,ST3GA-L4,MMD,RGS4,ZYX,MRG-PRF,SEC24D,LAT2,ITGA7,PHLDA2,DCLK1,FARP1,F-XYD5,CLEC5A,SLC52A2,RPS2,REEP3,VASN,SLC20-A1,FZD8,AGTRAP,PLOD3,SLC44A3,CENPV,MYO1G,FLNA,SIRPB2,AHNAK2,ALG3,MICAL2,COX6A1,RPN2,HILPDA,CD320,SIG-LEC9,TNFRSF1A,PRAF2,B-CL3,SCRIB,RPLP0,LHFPL2,OSTC,PPIB,ATP13A2,D-DX39A,CHST15,HOMER3,TMED9,GNG12,LILRB3,FI-BCD1,DPAGT1,ST6GALN-AC4,CD63,EHD2,TMED5,CD276,FKBP2,LMAN2L,L-MNB2,PDIA3,ZDHHC12,D-BNL,P4HB,TMEM198,PFN1,SLC25A39,ZDHHC16,B3-GAT3,TLCD1,HSPG2,AGP-AT1,YIF1A,XPO1,SEC23B,XBP1,MCEMP1,SEC11C,L-RFN3,KLC2,APOBR,TMU-B1,ALG8,LTBR,ATG101,G-ALNT7,ARHGDIA,PLXNA4,TNFSF8,ARRB2,RGS19,J-TB,NEU1,RTN3,SLC25A5,NLGN2,AUP1,SLC38A10,S-T14,TBC1D2,ITGA2,DPEP2,SCAMP2,ADAM8,PNPL

						<p>A6,ANKRD13B,NCLN,DH X34,FZD2,CSE1L,IRAK1,S LC30A1,FURIN,ANO10,G AL3ST4,SGMS1,ALDH16 A1,EDEM2,PLXNA3,SLC5 A3,SCAMP4,FUT11,GNB1 L,COLGALT1,SFXN3,TM9 SF1,LPCAT1,PPIA,TMEM2 14,RAB23,RAB11FIP5,EL OVL1,PARD6A,NME2,DH RS13,NRROS,TRAF7,C19 ORF38,P2RX4,CLTA,SLC5 A6,HGS,NAA10,DPY19L1, POLD1,SLC39A13,IMPDH 2,APBA3,ARHGAP33,EFN A5,AP2A1,GDPD5,VAT1,L RP10,AP2S1,FICD,TYRO3, PCYOX1L,SLC35C1,VKO RC1,NCAPH2,CYSLTR1,C ANX,GAPT,HM13,SMARC A4,SSR2,MFSD12,PKD1,B BS7,DAD1,CD55,ESYT1,N COR2,SH3GL1,SPCS3,RAS GRP4,CYTH2,PLCB3,RNF 167,TMEM241,MBOAT7,A P1B1,CD300LF,ARHGEF4 0,NRAS,TMED2,GGCX,R HOJ,PORCN,SLC24A3,GD AP2,ERGIC1,RPN1,SLC38 A6,GCNT1,MFSD10,RPS19 ,SURF4,YIPF2,ABHD15,G STP1,TMEM150B,GPAA1, ATXN2L,TGFBR1,COMT, SCAMP3,CLPTM1L,LIMK 1,EXT2,RHOG,C2CD2L,T MBIM1,BICD2,ERGIC2,A DORA2B,LILRA1,HSP90A B1,SPRED1,CCNYL1,GPR 137,EPHB3,LRRC3,POMT2 ZFP57,TNC,RNASE2,CCL2 ,SPP1,KRT18,TIMP1,CNN1 ,DDX11,CRLF1,ITGA3,SD F2L1,DHCR24,HSPB1,CAL R,PLP2,CD300E,SERPINH 1,S100A11,CAPG,G0S2,FS CN1,SH3BGR13,STXBP2, PDIA4,PYCR1,CSTA,MND A,CDK2AP2,CLCF1,PFKP, SLC7A1,RTN4,RUNX1,MF SD2A,CRYAB,MTFP1,CLE C10A,LRRC59,NCF2,HYO U1,CCR1,TUBB6,MYH9,B SCL2,CALU,HSP90B1,MA NF,TUBB3,TKT,PEA15,FB XO27,PVR,LAIR1,ANKRD 13A,ARRDC4,MYDGF,SIR PA,CLIC1,HSPA5,HSP90A A1,ANXA5,PLEKHA7,P4H A2,SGMS2,CENPU,NMB,C OL5A1,DACT1,TP53I13,C CR2,CD48,ORMDL2,PDIA 6,RAI14,PRELID1,CACNB 1,TUBB,MAP2K1,MMD,R GS4,ZYX,IMPDH1,SEC24 D,LAT2,ITGA7,PHLDA2,D CLK1,FARP1,DOK2,FXFD 5,ELP5,SHKBP1,SLC52A2, RPS2,REEP3,TGFB1,MPRI P,VASN,ARPC1B,FZD8,A GTRAP,PLOD3,SLC44A3,</p>
GO:0005515	MF	protein binding	1.46774E-05	4.833349985	383	

CENPV,CLEC11A,MYO1G
 ,NKX3-
 1,CCT2,FLNA,KLHL25,AR
 HGAP9,POLD2,AHNAK2,
 ALG3,LIPG,MICALL2,CO
 X6A1,RPN2,HILPDA,TNF
 AIP8L2,CD320,SIGLEC9,T
 NFRSF1A,PRAF2,BCL3,SC
 RIB,RPLP0,LHFPL2,OSTC,
 GALE,PPIB,ATP13A2,YB
 X3,DDX39A,CHST15,HO
 MER3,TMED9,GNG12,GT
 F2H4,NXPH3,CXCL6,LILR
 B3,FIBCD1,DPAGT1,HIC1,
 CD63,EHD2,TMED5,CD27
 6,FKBP2,LMAN2L,CNPY3
 ,ZNF467,LMNB2,PDIA3,D
 BNL,ACAP3,CRELD2,BCL
 9L,ASCC2,P4HB,PFN1,EB
 NA1BP2,ZDHHC16,B3GA
 T3,TLCD1,HSPG2,AGPAT
 1,YIF1A,YJEFN3,XPO1,SE
 C23B,XBP1,MCEMP1,FA
 M114A1,FAM222B,SEC11
 C,LRFN3,KLC2,MIIP,NKX
 2-
 5,TMUB1,PKNOX2,ALG8,
 STIP1,LTBR,ZNF692,ATG
 101,CBX6,ARHGDIA,NXT
 1,PLXNA4,TNFSF8,ARRB
 2,RGS19,JTB,NEU1,RTN3,
 SLC25A5,NLGN2,AUP1,L
 GI2,DOHH,ST14,TESK1,T
 BC1D2,ITGA2,HSPBP1,SC
 AMP2,KCTD21,ADAM8,A
 NKRD13B,NCLN,EIF6,FZ
 D2,CSE1L,IRAK1,SLC30A
 1,FURIN,SHTN1,SGMS1,A
 LDH16A1,PLXNA3,SLC5A
 3,SCAMP4,KLHL17,FUT11
 ,LACC1,GNB1L,SFXN3,P
 GLS,RBM47,SPATA2L,FA
 M20C,RUSC1,PPIA,RAB23
 ,TBC1D8B,SAMD1,RAB11
 FIP5,PAK1IP1,PACS1,ELO
 VL1,EIF3I,RPUSD1,PARD
 6A,NME2,SUPT3H,NRROS
 ,TRAF7,C19ORF38,NAGA,
 P2RX4,STRBP,CLTA,GOR
 AB,CNPY4,SLC5A6,AHR,
 HGS,CLIP2,TAF1A,NAA10
 ,POLD1,SLC39A13,SRM,I
 MPDH2,APBA3,CAMK1,A
 RHGAP33,EFNA5,GLIS2,H
 NRNP3,AP2A1,UFSPI,G
 DPD5,WDR27,HSPA13,VA
 T1,CBX1,LRP10,TCF3,AP2
 S1,IRF3,CCT3,CAMKK1,A
 TN1,FICD,TYRO3,ZSWIM
 7,FAM136A,NLE1,INTS8,
 NUDT5,BAG2,PPARD,VK
 ORC1,NCAPH2,MAP1S,C
 ANX,PAPOLA,HM13,DCA
 F13,NR2C2AP,MAPK13,S
 MARCA4,SSR2,MFSD12,A
 NKRD52,PKD1,RALY,BBS
 7,CD55,NOP2,ESYT1,NCO
 R2,SH3GL1,SPCS3,PAK4,
 RASGRP4,NAB2,CYTH2,P
 LCB3,ANKRD50,RNF167,

						<p>APOBEC3B,TMEM241,RA VER1,HECTD3,MBOAT7, AP1B1,PAPSS1,CD300LF, NRAS,TMED2,GMNN,NA GK,RHOJ,RFC4,PORCN,G DAP2,ERGIC1,BRMS1,RP N1,SLC38A6,GCNT1,TCF1 9,MFSD10,RPS19,SURF4, YIPF2,ABHD15,GSTP1,DO T1L,GPAA1,ATXN2L,SF3 B4,TGFBR1,SPATA33,CO MT,SCAMP3,CLPTM1L,PP P1R11,LIMK1,EXT2,RHO G,C2CD2L,MROH1,TMBI M1,CNPY2,IFT46,BICD2,C EP19,ERGIC2,ADORA2B, HSP90AB1,HMG20B,SPRE D1,CCNYL1,MED8,EPHB3 ,LRR3</p>
GO:0019899	MF	enzyme binding	0.014919002	1.826260217	72	<p>TIMP1,ITGA3,SDF2L1,DH CR24,HSPB1,CALR,CSTA, RTN4,NCF2,HSP90B1,SIR PA,HSPA5,HSP90AA1,DA CT1,TUBB,FARP1,DOK2, RPS2,FZD8,NKX3- 1,CCT2,FLNA,MICALL2,P PIB,YBX3,HIC1,P4HB,PFN 1,XPO1,XBP1,LTBR,ARH GDIA,NXT1,ARRB2,ITB,S LC25A5,AUP1,TESK1,HSP BP1,KCTD21,CSE1L,FURI N,RAB11FIP5,PARD6A,N ME2,CLTA,HGS,POLD1,A PBA3,ARHGAP33,AP2A1, CBX1,TCF3,BAG2,HM13,S MARCA4,PKD1,NCOR2,S H3GL1,AP1B1,GMNN,BR MS1,RPS19,YIPF2,GSTP1, SCAMP3,PPP1R11,RHOG, BICD2,HSP90AB1,SPRED 1,CCNYL1</p>
Down regulated genes						
GO:0044281	BP	small molecule metabolic process	0.00019486	3.710276942	71	<p>IDO1,CRYM,COQ10A,AC OT1,CARNS1,CD74,PHYH ,ACAT1,PPP1R3B,SLC16A 9,AMT,DECR1,ACADSB,A CADM,RGN,GDA,BDH2,L DHC,PSMB9,OAZ2,SULT1 C2,AUH,HMGCL,OXSM, MGST3,PCBD2,COQ6,PDE 7A,PEX7,PNPLA4,ADCYA P1R1,MACROD2,FPGS,PD HB,PCCB,PSMB10,NMNA T1,COQ7,ME3,MDH2,NU DT3,ECHDC2,CBR4,DNAJ C30,HIBADH,PPA2,SDHB, DLD,GMPR2,ACAD9,NIT2 ,RNLS,KAT2B,MCEE,SUC LG2,IP6K2,PDK1,FDX1,S ARS2,THAP4,IMPA1,PSM B8,NT5C3A,ACSL5,PRKA G1,COX11,CS,ATCAY,OS BPL1A,ACAD8,NCOA2 ASB15,PHKG1,IGSF1,IDO 1,RASD1,PYGM,FBXO40, EIF4EBP3,CRYM,COQ10A ,ACOT1,CARNS1,RGCC,K LHL24,TSC22D3,NEK10,P LA1A,ZNF189,CD74,TRIM 22,PHYH,IRF6,ACAT1,TRI</p>
GO:0044237	BP	cellular metabolic process	0.016078482	1.793754943	261	

M63,COX7A1,S100A1,ATP
6V0E2,ZBTB16,PPP1R3B,
ADPRHL1,SLC16A9,AMT,
NLR5,KLF9,P1FO,MYLK
3,PCSK6,DECR1,WWOX,
ASB4,PBLD,CIRBP,ACAD
SB,PARP14,NDUFA1,MX1
,ACADM,DCUN1D2,CDS2
,HEG1,RGN,ZNF682,NNT,
PTPRB,MTMR14,CEP85,A
TAD2,GDA,ISG20,KIF22,B
DH2,MYLK4,LDHC,PSMB
9,OAZ2,HERC6,SULT1C2,
SDHC,NDUFS4,AUH,UQC
RB,ROPN1B,HMGCL,ZNF
33B,BATF2,CLK1,FBXO4,
TYW1B,OXSM,PIK3R1,M
GST3,PCBD2,CHTA,RBM2
0,YEATS4,COQ6,DCAF6,
GPC5,USP2,DTWD2,PDE7
A,MRPS21,DCAF8,PEX7,T
BC1D7,GLRX5,UQCRC2,P
NPLA4,ADCYAP1R1,MG
ME1,DYRK3,JARID2,MAC
ROD2,PRX,FPGS,ZNF226,
NDUFB3,TFAM,PDHB,AIF
M1,DPH6,GSTK1,ZNF629,
PCCB,PSMB10,NMNAT1,
COQ7,NDUFA13,ZNF554,
DNASE1L1,ASB5,NSMCE
2,ME3,NDUFS1,NEDD9,N
DUFA10,AGTPBP1,TADA
2B,MDH2,NUDT3,ECHDC
2,CBR4,UQCRFS1,DNAJC
30,EGFR,AKAP7,NDUFS2,
HIBADH,PPA2,RAVER2,Z
NF483,NDUFA2,ZNF160,F
BXL17,COX7B,SDHB,AFG
3L2,ZNF25,NDUFA4,FUN
DC1,TRAK1,S1PR1,ACYP
2,TAL1,HLTF,DLN,ZNF23
4,GMPR2,ACAD9,NIT2,D
DI2,RNLS,LNX1,ATAD1,T
RMT11,HMG20A,KAT2B,
MCEE,CEP192,CIR1,SLC3
0A9,CPPED1,MKRN2,SUC
LG2,ZNF418,IP6K2,EXOS
C7,MAST4,FZD4,ATE1,SN
APC5,PDK1,E1F4EBP2,ZN
F32,LANCL2,UQCRQ,ND
UFB6,FDX1,SARS2,ZNF38
3,THAP4,MRPL16,MRPS2
8,MRPS33,NDUFB2,OXA1
L,ZNF721,TACC1,IMPA1,
LRIF1,TFDP2,CCNB1IP1,P
SMB8,PCYT1A,TYW1,RF
X5,ERCC5,AP5S1,INO80C,
NT5C3A,COX7C,ACSL5,R
ARB,CECR2,CHRA1,ZN
F287,RGMB,HELZ2,PRKA
G1,ERAP1,CNBP,ORC2,C
OX11,ANAPC15,COX6B1,
CLNS1A,EPAS1,POLR2L,
CS,FBXO21,RNMT,GHIT
M,ATG14,PIK3C2B,ATCA
Y,SYF2,OSBPL1A,ZNF304
,N4BP2L2,RBMS2,ZNF766
,STK16,ACAD8,FKBP3,M
ED6,LARP4,NCOA4,ENY2
,CMTR1,SLU7,HDDC2,GE

GO:0005622	CC	intracellular anatomical structure	5.04E-10	9.297214292	357	<p>N1,SERPINB6,XRN1,NCOA2,C6ORF89,NSUN4,NDUFC2,ZNHIT3,KLHL5,CUL4A</p> <p>FAM81B,ASB15,PHKG1,ANK1,MT1X,FGF12,IDO1,ASD1,AQP4,GBP4,PYGM,FBXO40,EIF4EBP3,CRYM,COQ10A,SLC5A1,ACOT1,SLC2A4,CARNS1,RGCC,SISA3,LMOD2,KLHL24,TSC22D3,MYBPC1,MYOM2,PLA1A,EFHC2,ZNF189,C LGN,CD300LG,TMEM143,SELENBP1,CD74,GBP1,PP1R12B,TRIM22,EFCAB2,MB,IFIT3,PHYH,IRF6,ACAT1,TRIM63,COX7A1,S100A1,ATP6V0E2,CCT6B,HLA-DOA,HLA-DRA,ZBTB16,PPP1R3B,HLA-LA-F,P2RX6,TXLNB,CTNNA3,TAP2,ARRDC2,OSBP2,MYZAP,AMT,NLR5,KLF9,CFAP58,PIFO,MYLK3,PCSK6,HLA-DPA1,DEC1,PGPEP1L,WWOX,DOCK9,ASB4,PBLD,CIRBP,PLEKHB1,ACADSB,HSPB3,RYR2,PARP14,NDUFA1,MX1,ACADM,DCUN1D2,CDS2,RGN,ZNF682,NNT,SUGCT,NUDT6,PTPRB,MTMR14,CEP85,ATAD2,GDA,AAMDC,ISG20,SNCG,KIF22,BDH2,LDHC,APOL3,SPATA24,PSMB9,OAZ2,HERC6,CCDC68,KIZ,C15ORF40,ANKRA2,SULT1C2,RSAD2,SDHC,NDUFS4,AUH,KIAA1217,UQCRB,MOAP1,ROPN1B,HMGCL,ZNF33B,BATF2,RCSD1,CLK1,FBXO4,OXSM,TAPBPL,PIK3R1,MGST3,PCBD2,C4ORF3,BBS2,CIITA,RBM20,YEATS4,COQ6,DCAF6,GPC5,SLC2A11,USP2,SLCO5A1,DTWD2,PDE7A,IFIT2,MRPS21,SCAPER,DCAF8,PEX7,SPRYD4,SAMD9L,KLHDC2,TBC1D7,GLRX5,ATPAF1,C11ORF1,UQCRC2,PNPLA4,ADCYAP1R1,MGME1,DYRK3,JARID2,MACROD2,ZC3H6,PRX,FPGS,ZNF226,COX14,NDUFB3,TFAM,PDHB,AIFM1,DPH6,GSTK1,ZNF629,PCCB,PSMB10,NMNAT1,TRAPPC6A,COQ7,NDUFA13,ZNF554,DNAH1L1,ASB5,NSMCE2,ME3,NDUFS1,SEC14L1,NEDD9,NDUFA10,AGTPBP1,TADA2B,C11ORF54,MYL6B,MDH2,NUDT3,ECHDC2,CHCHD5,CBR4,UQCRFS1,DNAJC30,EGFR,AKAP7,PHF7,NDUF</p>
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GO:0043233	CC	organelle lumen	0.008137513	2.089508331	146	<p>S2,HIBADH,PPA2,RAVER2,FRMPD1,RASAL2,ZNF483,NDUFA2,ZNF160,FBXL17,BORCS7,COX7B,SDHB,AFG3L2,ZNF25,NDUFA4,FUNDC1,TRAK1,IFI35,S1P R1,SLC31A2,MTUS1,TAL1,HLTF,DLD,ICA1L,ZNF234,GMPR2,ACAD9,IPP,NIT2,ATP8A1,DDI2,LNX1,CHCHD7,MRPL45,ATAD1,TRMT11,HMG20A,KAT2B,MCEE,CEP192,CIR1,SLC30A9,TMCC1,CPPED1,SUCLG2,RASGRP3,ZNF418,IP6K2,EXOSC7,MAST4,FZD4,ATE1,SNAPC5,PKD1,EIF4EBP2,SMIM20,ZNF32,LANCL2,UQCRQ,NDUFB6,FDX1,SEC31B,SARS2,ZNF383,NAA38,MRPL16,MRPS28,ABCB7,MRPS33,NDUFB2,OXA1L,ZNF721,TACC1,IMPA1,LRIF1,TFDP2,CCNB1IP1,PSMB8,PCYT1A,RFX5,ERCC5,AP5S1,INO80C,NT5C3A,COX7C,ACSL5,RARB,CECR2,CHRA1,ZNF287,RMDN1,COPZ2,RGMB,HELZ2,NBPF3,PRKAG1,ERAP1,CNBP,TMEM14B,ZMYM2,ORC2,COL11A2,COX11,ANAPC15,COX6B1,CLNS1A,EPAS1,LAP3,OSBPL11,POLR2L,CS,AFF1,FBXO21,RNMT,WDR37,TUBGCP5,TRAPPC13,GHITM,ATG14,PIK3C2B,ATCAY,SPAG7,SYF2,OSBPL1A,ZNF304,N4BP2L2,RBMS2,ZNF766,TXNRD3,STK16,ACAD8,FKBP3,MED6,LARP4,NCOA4,ENY2,CMTR1,SLU7,HDDC2,YTHDC2,IMMT,GEN1,SERPINB6,XRN1,LMBR1L,NCOA2,C6ORF89,NSUN4,NDUFC2,ZNHT3,KLHL5,CUL4A</p> <p>CRYM,RGCC,SELENBP1,CD74,PPP1R12B,TRIM22,PHYH,IRF6,ACAT1,S100A1,ZBTB16,TAP2,AMT,KLF9,PCSK6,DECR1,WWOX,CIRBP,ACADSB,HSPB3,ACADM,CEP85,ATAD2,ISG20,KIF22,SPATA24,PSMB9,HERC6,RSAD2,AUH,HMGCL,CITTA,YEATS4,DCAF6,GPC5,SLC2A11,USP2,MRPS21,SCAPER,DCAF8,PEX7,KLHDC2,GLRX5,C11ORF1,UQCRC2,DYRK3,JARID2,MACROD2,FPGS,TFAM,PDHB,AIFM1,DPH6,GSTK1,PCCB,PSMB10,NMNAT1,NDUFA13,ZNF554,DNASE1L1,NSMCE2,ME3,NDUFS1,SEC14L1,NEDD9,NDUFA10,AGTPBP1,TADA2B,C11ORF54,MDH2,CH</p>
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						CHD5,CBR4,EGFR,PHF7,NDUFS2,HIBADH,PPA2,FBXL17,SDHB,S1PR1,MTUS1,TAL1,HLTF,DLD,NIT2,DDI2,CHCHD7,KAT2B,MCEE,CIR1,CPPED1,SUCLG2,IP6K2,EXOSC7,SNAPC5,PDK1,LANCL2,NDUFB6,FDX1,SARS2,ZNF383,NAA38,MRPL16,MRPS28,MRPS33,OXA1L,LRIF1,TFDP2,CCNB1IP1,PSMB8,ERCC5,AP5S1,INO80C,ACSL5,RARB,CHRA1,HELZ2,PRKAG1,ERAP1,ZMYM2,ORC2,COL11A2,ANAPC15,CLNS1A,EPAS1,LAP3,OSBPL11,POLR2L,CS,AFF1,RNMT,PIK3C2B,SYF2,TXNRD3,STK16,ACAD8,MED6,ENY2,CMTR1,SLU7,IMMT,GEN1,NCOA2,C6ORF89,NSUN4,CUL4A
GO:0003824	MF	catalytic activity	1.72558E-06	5.76306544	175	PHKG1,IDO1,RASD1,GBP4,PYGM,FBXO40,CRYM,ACOT1,CARNS1,NUDT8,NEK10,PLA1A,SELENBP1,GBP1,TRIM22,PHYH,ACAT1,TRIM63,COX7A1,ATP6V0E2,PPP1R3B,ADPRHL1,AMT,AMY2B,MYLK3,PCSK6,DECR1,PGPEP1L,WWOX,ASB4,PBLD,ACADSB,PARP14,NDUFA1,MX1,ACADM,CDS2,RGN,NT,SUGCT,NUDT6,PTPRB,MTMR14,ATAD2,GDA,ISG20,KIF22,BDH2,MYLK4,LDHC,PSMB9,HERC6,SULT1C2,RSAD2,SDHC,NDUFS4,AUH,HMGCL,CLK1,FBXO4,TYW1B,OXSM,MGST3,PCBD2,CIITA,COQ6,USP2,DTWD2,PDE7A,GLRX5,PNPLA4,MGME1,DYRK3,JARID2,MACROD2,FPGS,NDUFB3,PDHB,AIFM1,DPH6,PTRHD1,GSTK1,PCCB,PSMB10,NMNAT1,COQ7,NDUFA13,DNAH1L1,NSMCE2,ME3,NDUFS1,NDUFA10,AGTPBP1,C11ORF54,MYL6B,MDH2,NUDT3,ECHDC2,CBR4,UQCRRF1,DHRS12,EGFR,AKAP7,NDUFS2,HIBADH,PPA2,NDUFA2,COX7B,SDHB,AFG3L2,NDUFA4,ACYP2,HLTF,DLD,GMPR2,ACAD9,NIT2,DDI2,RNLS,LNX1,TRMT11,KAT2B,MCEE,CPPED1,MKRN2,SUCLG2,IP6K2,EXOSC7,MAST4,ATE1,PDK1,RAB12,UQCRRQ,NDUFB6,FDX1,SARS2,THAP4,NDUFB2,IMPA1,CCNB1IP1,PSMB8,PCYT1A,TYW1,ERCC5,NT5C3A,COX7C,ACSL5,CHRA1,HELZ2,PRKAG1,ERAP1,COX11,COX6B

GO:1901265	MF	nucleoside phosphate binding	0.01702265	1.768972841	70	1,LAP3,POLR2L,CS,FBXO 21,RNMT,METTL25,PIK3 C2B,ATCAY,TXNRD3,ST K16,ACAD8,FKBP3,MED6 ,CMTR1,SLU7,HDDC2,YT HDC2,GEN1,XRN1,NSUN 4,NDUFC2,CUL4A PHKG1,RASD1,GBP4,PYG M,CRYM,CARNS1,NEK10 ,GBP1,ACAT1,CCT6B,P2R X6,TAP2,NLRC5,MYLK3, DECR1,ACADSB,MX1,AC ADM,NNT,NUDT6,ATAD2 ,KIF22,BDH2,MYLK4,HM GCL,CLK1,TYW1B,CITTA, COQ6,DYRK3,FPGS,AIFM 1,DPH6,PCCB,NMNAT1,N DUFA13,ME3,CBR4,EGFR ,AKAP7,NDUFS2,HIBADH ,AFG3L2,HLTF,DLD,ACA D9,ATP8A1,BBS12,RNLS, ATAD1,ARL15,SUCLG2,IP 6K2,MAST4,PDK1,RAB12, LANCL2,KIAA0232,SARS 2,ABCB7,TYW1,NT5C3A, ACSL5,HELZ2,PRKAG1,PI K3C2B,TXNRD3,STK16,A CAD8,YTHDC2
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Table 3 The enriched pathway terms of the up and down regulated differentially expressed genes

Pathway ID	Pathway Name	Adjusted p value	Negative log10 of adjusted p value	Gene Count	Gene
Up regulated genes					
REAC:R-HSA-9679506	SARS-CoV Infections	1.79986E-05	4.744760661	19	HSP90AA1,TUBB,ST3GAL 4,IMPDH1,RPN2,ST6GAL NAC4,FURIN,EDEM2,IMP DH2,AP2A1,AP2S1,CYSLT R1,CANX,DAD1,BRMS1,R PN1,COMT,HSP90AB1,H MG20B
REAC:R-HSA-446203	Asparagine N-linked glycosylation	0.001564455	2.805637058	24	CALR,TUBB6,TUBB3,ST3 GAL4,SEC24D,PGM3,NAN S,ALG3,RPN2,TMED9,DP AGT1,ST6GALNAC4,LMA N2L,PDIA3,ALG8,NEU1,E DEM2,SLC35C1,CANX,D AD1,CD55,TMED2,NAGK, RPN1
REAC:R-HSA-6798695	Neutrophil degranulation	0.005152656	2.287968817	30	RNASE2,S100A11,MNDA, LAIR1,SIRPA,HSP90AA1, TUBB,IMPDH1,CLEC5A,C CT2,ARHGAP9,SIGLEC9, LILRB3,CD63,DBNL,MCE MP1,NEU1,ADAM8,LPCA T1,PPIA,NME2,IMPDH2,V AT1,CD55,NRAS,SURF4,G STP1,RHOG,TMBIM1,HSP 90AB1
REAC:R-HSA-168256	Immune System	0.030763983	1.511957444	81	RNASE2,CCL2,TIMP1,CR LF1,CALR,CD300E,S100A 11,FSCN1,STXBP2,MNDA, CLCF1,CLEC10A,LILRA6, NCF2,CCR1,TUBB6,MYH9 ,HSP90B1,TUBB3,FBXO27 ,PVR,LAIR1,SIRPA,HSPA5 ,HSP90AA1,IFITM2,CCR2, TUBB,MAP2K1,IMPDH1,S

					EC24D,LAT2,CLEC5A,ARPC1B,CCT2,FLNA,KLHL25,ARHGAP9,SIGLEC9,TNFRSF1A,RPLP0,POLR3D,ILRB3,CD63,CNPY3,PDIA3,DBNL,P4HB,MCEMP1,KLC2,LTBR,TNFSF8,NEU1,ADAM8,IRAK1,LPCAT1,PIA,NME2,TRAF7,CLTA,IMPDH2,AP2A1,VAT1,AP2S1,IRF3,CANX,MAPK13,SMARCA4,CD55,RASGRP4,HECTD3,AP1B1,CD300LF,NRAS,SURF4,GSTP1,LIMK1,RHOG,TMBIM1,LILRA1,HSP90AB1
REAC:R-HSA-5663205	Infectious disease	0.030763983	1.511957444	43	CALR,TUBB6,MYH9,TUBB3,HSP90AA1,TUBB,MAP2K1,ST3GAL4,IMPDH1,RPS2,ARPC1B,RPN2,RPLP0,GNG12,GTF2H4,ST6GALNAC4,XPO1,SLC25A5,DPEP2,FURIN,EDEM2,PPIA,PACS1,P2RX4,CLTA,HGS,IMPDH2,AP2A1,CBX1,AP2S1,CYSLTR1,CANX,DAD1,NCOR2,SH3GL1,AP1B1,BRMS1,RPN1,RPS19,COMT,ADORA2B,HSP90AB1,HMG20B
REAC:R-HSA-1643685	Disease	0.037823878	1.422233951	66	CYP1B1,CALR,TUBB6,MYH9,TUBB3,HSP90AA1,TUBB,MAP2K1,ST3GAL4,IMPDH1,RPS2,MPRIIP,ARPC1B,FZD8,AGTRAP,ALG3,RPN2,CD320,RPLP0,GAL E,GNG12,GTF2H4,DPAGT1,ST6GALNAC4,B3GAT3,HSPG2,XPO1,ALG8,ARRB2,NEU1,SLC25A5,DPEP2,FURIN,EDEM2,PPIA,PACS1,P2RX4,CLTA,HGS,IMPDH2,AP2A1,CBX1,AP2S1,SLC35C1,CYSLTR1,CANX,DAD1,NCOR2,SH3GL1,AP1B1,PAPSS1,NRAS,GGCX,PORCN,BRMS1,RPN1,RPS19,TGFBF1,COMT,EXT2,RHOG,ADORA2B,HSP90AB1,HMG20B,SPRED1,POMT2
					Down regulated genes
REAC:R-HSA-1428517	The citric acid (TCA) cycle and respiratory electron transport	1.59E-19	18.7992737	34	COQ10A,NDUFA1,NNT,L DHC,SDHC,NDUFS4,UQCRB,UQCRC2,COX14,NDUFB3,PDHB,NDUFA13,ME3,NDUFS1,NDUFA10,MDH2,UQCRFS1,NDUFS2,NDUFA2,COX7B,SDHB,NDUFA4,DLD,ACAD9,SUCLG2,PDK1,UQCRQ,NDUFB6,NDUFB2,COX7C,COX11,COX6B1,CS,NDUFC2
REAC:R-HSA-611105	Respiratory electron transport	7.73E-17	16.11175861	25	COQ10A,NDUFA1,SDHC,NDUFS4,UQCRB,UQCRC2,COX14,NDUFB3,NDUFA13,NDUFS1,NDUFA10,UQCRFS1,NDUFS2,NDUFA2,COX7B,SDHB,NDUFA4,ACAD9,UQCRQ,NDUFB6,ND

REAC:R-HSA-1430728	Metabolism	1.28E-07	6.891525601	88	UFB2,COX7C,COX11,COX6B1,NDUFC2,PHKG1,IDO1,PYGM,CRYM,COQ10A,ACOT1,CARN S1,PLA1A,PHYH,ACAT1,AMT,DECR1,ACADSB,PARP14,NDUFA1,ACADM,CD S2,NNT,MTMR14,GDA,BDH2,LDHC,PSMB9,OAZ2,SULT1C2,SDHC,NDUFS4,AUH,UQCRB,HMGCL,PIK3R1,MGST3,COQ6,GPC5,GLRX5,UQCRC2,PNPLA4,COX14,NDUFB3,PDHB,GSTK1,PCCB,PSMB10,NMNAT1,COQ7,NDUFA13,ME3,NDUFS1,NDUFA10,MDH2,NUDT3,CBR4,UQCRFS1,NDUFS2,HIBADH,PPA2,NDUFA2,COX7B,SDHB,NDUFA4,DLD,GMPT2,ACAD9,RNLS,MCEE,SUCLG2,IP6K2,PKD1,UQCRQ,NDUFB6,FDX1,ABC7,NDUFB2,IMPA1,PSMB8,PCYT1A,COX7C,ACSL5,HELZ2,COX11,COX6B1,CS,PIK3C2B,OSBPL1A,ACAD8,MED6,NCOA2,NDUFC2
REAC:R-HSA-6799198	Complex I biogenesis	4.57E-07	6.340126791	12	NDUFA1,NDUFS4,NDUFB3,NDUFA13,NDUFS1,NDUFA10,NDUFS2,NDUFA2,ACAD9,NDUFB6,NDUFB2,NDUFC2
REAC:R-HSA-913531	Interferon Signaling	0.000694263	3.158475852	16	GBP4,GBP1,TRIM22,IFI35,IRF6,HLA-DRA,HLA-F,HLA-DPA1,MX1,ISG20,RSAD2,CIITA,IFIT2,IFI35,IP6K2,PSMB8
REAC:R-HSA-8951664	Neddylation	0.00637316	2.195645204	16	ASB15,FBXO40,ZBTB16,ASB4,DCUN1D2,PSMB9,FBXO4,DCAF6,DCAF8,PSMB10,ASB5,PSMB8,EPAS1,FBXO21,KLHL5,CUL4A

Table 5 Topology table for up and down regulated genes.

Regulation	Node	Degree	Betweenness	Stress	Closeness
Up	HSP90AA1	310	0.105186	29473478	0.36184
Up	ARRB2	299	0.124612	20082640	0.373275
Up	MYH9	228	0.070579	13829408	0.350409
Up	HSP90AB1	209	0.053187	14659960	0.364926
Up	FLNA	190	0.044393	10880514	0.339624
Up	HSPA5	188	0.065912	17060132	0.357216
Up	TNFRSF1A	124	0.03477	6034056	0.341033
Up	CCT3	109	0.030755	10034828	0.325417
Up	HGS	108	0.0419	4478216	0.338828
Up	CCT2	105	0.025763	9543988	0.326278
Up	RPS2	98	0.026105	9920886	0.300444
Up	TUBB	98	0.018976	5951558	0.346959
Up	SMARCA4	97	0.026302	7085132	0.315429
Up	XPO1	95	0.027487	6316348	0.32321
Up	HSPB1	82	0.024042	5627972	0.328348
Up	CBX1	77	0.023271	2963688	0.295012
Up	IRAK1	70	0.013772	2975710	0.310754
Up	CANX	69	0.031114	4061074	0.317555
Up	NCOR2	63	0.01861	4457204	0.30931

Up	LTBR	62	0.022577	4090604	0.289372
Up	BAG2	60	0.007715	1816876	0.322911
Up	TCF3	53	0.012495	1863634	0.290354
Up	AP2A1	53	0.008801	1319284	0.323085
Up	RUNX1	50	0.011362	2037902	0.2995
Up	ATP13A2	48	0.017498	2377446	0.286094
Up	CRYAB	46	0.01341	1926656	0.28586
Up	HSP90B1	46	0.009218	1902636	0.326456
Up	CLTA	45	0.005735	1109224	0.325064
Up	PARD6A	44	0.012789	2482316	0.281221
Up	SCRIB	44	0.011391	1698702	0.303533
Up	CBX6	44	0.010962	2091228	0.279217
Up	IRF3	43	0.011483	1268188	0.291931
Up	MAP2K1	42	0.008477	3474166	0.288357
Up	TGFBR1	42	0.012857	1622142	0.307382
Up	RPS19	42	0.006526	1230086	0.300768
Up	TGFB1	41	0.011855	1307696	0.271111
Up	PPIA	41	0.011088	1183456	0.315358
Up	RPLP0	41	0.00609	1193560	0.316143
Up	PDIA3	41	0.010754	2026544	0.28588
Up	P4HB	40	0.009139	1460992	0.306058
Up	DDX39A	40	0.009277	3461020	0.281145
Up	EIF3I	39	0.011686	2461912	0.288913
Up	SLC25A5	39	0.004345	1770966	0.302176
Up	STIP1	38	0.00649	1203034	0.328116
Up	CALR	38	0.007663	1234138	0.294597
Up	KLC2	37	0.009778	3937578	0.259484
Up	KRT18	36	0.006854	1519388	0.314837
Up	NOP2	36	0.005849	1965080	0.288436
Up	TUBB3	35	0.007708	1258792	0.309812
Up	RTN4	35	0.01073	2762978	0.262868
Up	MPRIP	34	0.004201	989642	0.295282
Up	LIMK1	32	0.006918	2144466	0.268335
Up	EBNA1BP2	32	0.005269	1377772	0.28379
Up	SF3B4	31	0.003896	1956276	0.274106
Up	EIF6	31	0.008563	2417368	0.274519
Up	SAMD1	31	0.009166	1376104	0.258588
Up	RFC4	30	0.006575	2168370	0.284657
Up	ATG101	30	0.007382	1799294	0.257034
Up	CENPU	30	0.011364	2467378	0.262292
Up	RAI14	29	0.002282	626954	0.294556
Up	RALY	29	0.00385	1632114	0.283311
Up	AHR	28	0.005258	929864	0.307563
Up	YBX3	28	0.005719	845400	0.297186
Up	RPN1	27	0.005333	1003358	0.3108
Up	MED8	27	0.004526	1083086	0.267598
Up	IMPDH2	27	0.004069	1758294	0.275041
Up	ARHGDIA	26	0.003333	1061284	0.277535
Up	BCL3	26	0.004098	2433738	0.261801
Up	AP1B1	26	0.004584	646688	0.307856
Up	CSE1L	26	0.004087	983540	0.319394
Up	CLEC11A	26	0.007713	989062	0.244177
Up	LACC1	26	0.008891	984630	0.22798
Up	ARPC1B	25	0.002145	341520	0.289332
Up	DBNL	25	0.004635	1916854	0.253798
Up	CALU	25	0.003243	596042	0.301221
Up	PFKP	24	0.003824	640598	0.301265
Up	DOK2	24	0.005036	520896	0.28733
Up	HSPG2	24	0.007308	2105818	0.258875
Up	PPARD	24	0.003881	645368	0.295782
Up	SUPT3H	23	0.002695	460336	0.268541
Up	PAK4	23	0.004208	1419282	0.274429
Up	CBR1	23	0.006943	699274	0.302002
Up	USB1	23	0.007624	2548172	0.255064
Up	POLD1	22	0.005181	1242286	0.275855
Up	HOMER3	22	0.005901	1424406	0.26673
Up	ZYX	22	0.004633	1394100	0.27931
Up	ATN1	22	0.003907	840334	0.260225
Up	AUP1	22	0.005522	1774450	0.264626
Up	TUBB6	22	0.002315	591814	0.31184

Up	PLXNA3	22	0.004444	727980	0.261735
Up	GMNN	21	0.003885	1174334	0.25811
Up	DOT1L	21	0.004261	572126	0.272662
Up	BRMS1	21	0.002845	890982	0.264676
Up	CSTA	20	0.005657	457012	0.291992
Up	MAP1S	20	0.004369	910238	0.263644
Up	HNRNP3	20	0.002747	490102	0.294949
Up	IFT46	20	0.007227	935380	0.219966
Up	PDIA6	20	0.005345	560676	0.289892
Up	POLR3D	19	0.005844	1305130	0.270656
Up	BBS7	19	0.004865	957796	0.257634
Up	AGTRAP	19	0.006353	793272	0.222547
Up	CHST15	19	0.006162	780822	0.24939
Up	PFN1	18	0.003623	1201860	0.275946
Up	GSTP1	18	0.002817	478532	0.304923
Up	HMG20B	18	0.003377	843174	0.271076
Up	AP2S1	17	0.001625	204508	0.296262
Up	FSCN1	17	0.00176	409310	0.294597
Up	RPN2	17	0.003654	460022	0.303489
Up	SCAMP3	17	0.00318	339394	0.296808
Up	FAM219A	17	0.005901	920154	0.212573
Up	BSCL2	17	0.006041	755562	0.245076
Up	TAF1A	16	0.003506	949442	0.252453
Up	SH3GL1	16	0.00252	724566	0.241032
Up	RAB11FIP5	16	0.002924	347802	0.294494
Up	CYTH2	16	0.004501	445180	0.299757
Up	LRRC59	16	0.00254	543436	0.288001
Up	GTF2H4	15	0.002776	569404	0.246039
Up	ITGA2	15	0.003974	487382	0.260661
Up	EXT2	15	0.002771	291208	0.236305
Up	ATXN2L	15	0.00164	534306	0.280299
Up	NAGK	2	7.97E-05	17502	0.214081
Up	HYOU1	2	6.81E-04	85588	0.264143
Up	ITGA3	2	0	0	0.231032
Up	PPIB	2	9.40E-06	3604	0.253002
Up	REEP3	2	3.44E-04	30714	0.230537
Up	STXBP2	2	1.94E-04	35736	0.24843
Up	GNG12	2	0	0	0.26386
Up	POLD2	1	0	0	0.216223
Up	P4HA2	1	0	0	0.234351
Up	RGS4	1	0	0	0.280206
Up	RTN3	1	0	0	0.208162
Up	PKD1	1	0	0	0.239463
Up	IMPDH1	1	0	0	0.215723
Up	EHD2	1	0	0	0.226343
Up	SHTN1	1	0	0	0.212315
Up	NKX2-5	1	0	0	0.204228
Up	YIF1A	1	0	0	0.222464
Up	TNC	1	0	0	0.280206
Up	TYRO3	1	0	0	0.244818
Up	SH3BGR13	1	0	0	0.280206
Up	NXT1	1	0	0	0.244276
Up	VASN	1	0	0	0.213297
Up	ANXA5	1	0	0	0.222334
Up	ANKRD13A	1	0	0	0.280206
Up	NAB2	1	0	0	0.210693
Up	ASCC2	1	0	0	0.236225
Up	PRELID1	1	0	0	0.222322
Up	PLOD3	1	0	0	0.189292
Up	PUSL1	1	0	0	0.215723
Up	CNPY3	1	0	0	0.232867
Up	PLCB3	1	0	0	0.219506
Up	PLP2	1	0	0	0.185662
Up	PACS1	1	0	0	0.214772
Up	TRAF7	1	0	0	0.196265
Up	PDIA4	1	0	0	0.222334
Up	NAA10	1	0	0	0.271831
Up	VKORC1	1	0	0	0.207935
Up	SERPINH1	1	0	0	0.226343
Up	OSTC	1	0	0	0.222464

Up	APBA3	1	0	0	0.231965
Up	NANS	1	0	0	0.267377
Up	COMT	1	0	0	0.186588
Up	ZNF668	1	0	0	0.213504
Up	COX6A1	1	0	0	0.210693
Up	MIIP	1	0	0	0.211575
Up	TRIM47	1	0	0	0.207935
Up	DACT1	1	0	0	0.218283
Up	TIMP1	1	0	0	0.231517
Up	CLIC1	1	0	0	0.271831
Up	PAPOLA	1	0	0	0.202336
Up	P3H4	1	0	0	0.226343
Down	EGFR	457	0.205087	31778098	0.38925
Down	PIK3R1	129	0.029988	6125958	0.324159
Down	CUL4A	86	0.029651	3569628	0.307472
Down	YEATS4	78	0.026514	4703300	0.288397
Down	KAT2B	78	0.020104	5566144	0.303907
Down	IMMT	66	0.021652	2718504	0.309264
Down	LNK1	61	0.020473	5411208	0.269525
Down	PSMB9	54	0.015817	2213722	0.27022
Down	ZBTB16	54	0.012719	3403640	0.301243
Down	AIFM1	51	0.011528	2517548	0.30468
Down	IFIT3	44	0.005977	2200814	0.271585
Down	NCOA2	43	0.00903	2936252	0.283445
Down	ORC2	42	0.00981	2693738	0.281334
Down	KIF22	40	0.011169	1798164	0.271444
Down	DLD	39	0.011045	1859202	0.28676
Down	HMG20A	39	0.011156	1841296	0.274699
Down	TAL1	38	0.006576	1348134	0.283752
Down	PDK1	38	0.009524	1204636	0.262505
Down	NDUFA13	38	0.007856	1020548	0.271726
Down	WWOX	38	0.009767	2640520	0.28015
Down	MED6	35	0.007727	2053870	0.271567
Down	CNBP	34	0.004331	1017186	0.279925
Down	IFIT2	33	0.001855	811294	0.264126
Down	NEDD9	31	0.003258	1626964	0.266917
Down	ZMYM2	31	0.006147	1681486	0.289632
Down	NDUFS1	31	0.007983	1660148	0.294287
Down	GSTK1	30	0.003699	600696	0.274825
Down	SLC2A4	28	0.00827	863248	0.292542
Down	POLR2L	27	0.005489	1205152	0.25792
Down	NDUFS4	27	0.004631	531618	0.254075
Down	EXOSC7	26	0.00872	3029252	0.233802
Down	TRIM63	25	0.007324	1205550	0.272645
Down	CLNS1A	25	0.005597	685370	0.29244
Down	ACAD9	25	0.004525	585172	0.24672
Down	PRKAG1	24	0.005618	1741160	0.257856
Down	EPAS1	24	0.003693	1197012	0.283886
Down	HLTF	24	0.005	1387306	0.280995
Down	NDUFS2	24	0.002997	648248	0.271392
Down	NDUFA10	24	0.006564	1037876	0.268129
Down	PDHB	23	0.00466	708824	0.272255
Down	LRIF1	23	0.00614	754416	0.256421
Down	TACC1	22	0.005807	845206	0.268696
Down	CCT6B	22	0.002537	398772	0.265783
Down	COX6B1	21	0.005409	660090	0.266917
Down	PEX7	20	0.003911	698310	0.265783
Down	AFF1	20	0.003658	666254	0.257508
Down	TADA2B	20	0.001756	416586	0.252408
Down	JARID2	19	0.004313	1176778	0.256625
Down	MRPL45	19	0.00259	830040	0.234024
Down	AFG3L2	19	0.003668	569724	0.283464
Down	TUBGCP5	18	0.005516	1403916	0.241504
Down	USP2	18	0.00299	1093242	0.273677
Down	STK16	18	0.003886	762212	0.229176
Down	NDUFB8	18	0.00125	338722	0.242314
Down	KLHDC2	18	0.003505	738710	0.257729
Down	PSMB8	17	2.11E-04	40700	0.2252
Down	CEP192	17	0.003195	413690	0.256547
Down	NDUFA2	17	0.001519	415996	0.260225

Down	DECR1	17	0.004216	618826	0.285122
Down	S100A1	16	0.003936	883538	0.250388
Down	CLK1	16	0.002694	581140	0.246241
Down	ERCC5	15	0.002811	739870	0.252621
Down	BBS2	15	0.001912	344104	0.242482
Down	UQCRFS1	15	0.001609	410728	0.249583
Down	TFDP2	14	0.003063	561542	0.239122
Down	RYSR2	14	0.002974	1029164	0.258652
Down	TSC22D3	14	0.001711	590994	0.267769
Down	SNCG	14	0.002632	641292	0.259372
Down	XRN1	14	0.00346	725826	0.263313
Down	NSUN4	14	0.001857	406812	0.24223
Down	UQCRB	14	0.00271	354782	0.240991
Down	MRPL16	14	0.003276	798096	0.25746
Down	UQCRC2	13	0.001984	323946	0.260856
Down	INO80C	13	0.003952	1337910	0.228726
Down	NDUFA4	13	0.001854	576890	0.259083
Down	SELENBP1	13	0.006052	590728	0.256924
Down	UQCRQ	13	0.001044	173988	0.262719
Down	COQ7	13	0.003186	432406	0.236039
Down	NCOA4	12	0.001289	285214	0.274951
Down	PPP1R12B	12	0.001031	147258	0.276055
Down	CIITA	12	0.002312	345020	0.274951
Down	DCAF6	12	0.003437	450830	0.257113
Down	NSMCE2	12	0.003586	614470	0.265044
Down	TRAPPC13	12	0.003395	951662	0.232132
Down	PPA2	12	0.003142	406886	0.229376
Down	SLU7	11	0.00155	340894	0.244818
Down	MYL6B	11	5.60E-04	77222	0.275964
Down	ATE1	11	0.005206	873822	0.23708
Down	ANAPC15	11	0.0043	1490158	0.202894
Down	RWDD2B	11	0.002933	816092	0.224621
Down	WDR37	11	0.002434	257170	0.273498
Down	MDH2	10	0.001131	379138	0.27015
Down	RARB	10	0.001572	202540	0.250943
Down	TAP2	10	0.001655	494660	0.220487
Down	DCAF8	10	0.001607	156804	0.274573
Down	CIRBP	10	0.001095	236180	0.253645
Down	GHITM	10	0.003112	518496	0.267616
Down	CEP85	10	0.003491	482348	0.242076
Down	EFHC2	10	0.003356	386606	0.233476
Down	LIFR	9	0.001828	331854	0.24469
Down	ANK1	9	0.003345	407186	0.196513
Down	PSMB10	9	0.002359	251676	0.266662
Down	MOAP1	9	0.001976	558852	0.220603
Down	COQ6	9	0.002198	500396	0.239778
Down	PTPRB	9	0.001789	201664	0.287074
Down	CD74	9	0.002426	444702	0.231914
Down	SUCLG2	9	0.002002	374116	0.229314
Down	NMNAT1	9	0.001016	209774	0.246401
Down	OSBPL1A	9	0.001842	370658	0.244947
Down	MRPS21	9	0.002572	472608	0.225782
Down	SEC31B	9	1.32E-04	56026	0.277995
Down	SYF2	9	0.001532	379850	0.258381
Down	MKRN2	9	0.001743	256576	0.227398
Down	SDHB	8	0.001664	366050	0.240963
Down	FBXO4	8	1.91E-04	42572	0.247491
Down	ENY2	8	1.95E-04	44450	0.23297
Down	S1PR1	8	0.00192	388468	0.232621
Down	N4BP2L2	8	0.001974	629170	0.223329
Down	FBXL17	8	0.001302	356674	0.223639
Down	PARL	8	0.001604	163762	0.224501
Down	HLA-DPA1	3	5.67E-04	41006	0.232583
Down	MYLK4	2	0	0	0.277572
Down	PIK3C2B	1	0	0	0.280206
Down	RFX5	1	0	0	0.215667
Down	CS	1	0	0	0.222322
Down	DCUN1D2	1	0	0	0.235179
Down	BBS12	1	0	0	0.204866
Down	NDUFC2	1	0	0	0.213678

Down	PYGM	1	0	0	0.200258
Down	IP6K2	1	0	0	0.265716
Down	KLHL24	1	0	0	0.224753
Down	MCEE	1	0	0	0.182043
Down	PCYT1A	1	0	0	0.197699
Down	PHYH	1	0	0	0.209986
Down	SLC5A1	1	0	0	0.280206
Down	NDUFB3	1	0	0	0.213678

Table 6 miRNA - target gene and TF - target gene interaction

Regulation	Target Genes	Degree	MicroRNA	Regulation	Target Genes	Degree	TF
Up	MYH9	226	hsa-mir-520e	UP	HSP90AA1	35	RUNX1T1
Up	TUBB	202	hsa-mir-8084	UP	XPO1	33	STAT1
Up	XPO1	198	hsa-mir-125a-5p	UP	SMARCA4	33	EGR1
Up	HSP90AA1	188	hsa-mir-133a-3p	UP	HSPA5	22	FOSB
Up	HSP90AB1	162	hsa-mir-4801	UP	ARRB2	20	ARNT
Up	HSPA5	123	hsa-mir-320d	UP	HSP90AB1	20	JUNB
Up	FLNA	106	hsa-mir-212-3p	UP	HGS	18	TSG101
Up	CCT3	54	hsa-mir-342-3p	UP	TUBB	16	STAT3
Up	ARRB2	54	hsa-mir-3127-3p	UP	MYH9	16	MAX
Up	CCT2	48	hsa-mir-16-1-3p	UP	CCT3	15	XRCC6
Up	HGS	47	hsa-mir-4739	UP	HSPB1	15	FOS
Up	SMARCA4	44	hsa-mir-1296-5p	UP	RPS2	13	CREB1
Up	RPS2	40	hsa-mir-3943	UP	FLNA	9	VHL
Up	TNFRSF1A	22	hsa-mir-29a-3p	UP	TNFRSF1A	6	DAXX
Up	HSPB1	22	hsa-mir-148a-3p	UP	CCT2	3	YY1
Down	PIK3R1	131	hsa-mir-138-5p	Down	KAT2B	47	TWIST1
Down	NCOA2	114	hsa-mir-539-5p	Down	ZBTB16	39	GATA2
Down	EGFR	83	hsa-mir-132-3p	Down	NCOA2	34	AHR
Down	IFIT3	78	hsa-mir-449a	Down	PIK3R1	34	GTF2H1
Down	PSMB9	68	hsa-mir-200c-5p	Down	EGFR	27	STAT5B
Down	KAT2B	62	hsa-mir-320c	Down	ORC2	22	CDC5L
Down	ZBTB16	53	hsa-mir-3908	Down	LNK1	21	FOXO1
Down	CUL4A	53	hsa-mir-16-5p	Down	IMMT	13	POU3F2
Down	DLD	41	hsa-mir-30d-5p	Down	PSMB9	10	TOPORS
Down	ORC2	40	hsa-mir-7-5p	Down	CUL4A	10	USF1
Down	YEATS4	35	hsa-mir-376a-5p	Down	AIFM1	8	MYC
Down	IMMT	33	hsa-mir-182-5p	Down	YEATS4	6	MLLT10
Down	KIF22	33	hsa-mir-146a	Down	IFIT3	5	STAT2
Down	AIFM1	13	hsa-mir-484	Down	KIF22	4	ELK1
Down	LNK1	5	hsa-let-7b-5p	Down	DLD	3	NFYA