Supplemental Material
Material and Methods

In vivo studies

Dose exploration study Mice were individually housed with carousel feeders and maintained on standard rodent diet (Lab Diet 5001, meal) and tap water *ad libitum*. They were then given chow containing halofuginone at 0.8, 2.5, 8 and 25 PPM to reach a targeted dose of 0.1, 0.3, 1 and 3 mg/kg, respectively. Four days later, mice were euthanized. Blood samples were collected for pharmacokinetics (PK, drug concentration) analysis. Liver and left ventricles were flash frozen in liquid nitrogen for gene expression analysis.

PK analysis (halofuginone in blood) was performed using liquid chromatography/tandem mass spectrometric (LC/MS/MS) detection. Briefly, blood samples were mixed with acetonitrile and then centrifuged. Ten µl of supernatant was injected into the LC/MS/MS system. The mobile phase consisted of a gradient that transitioned linearly from 90% aqueous 0.1% formic acid and 10% acetonitrile to 100% acetonitrile in 1.5 minutes (850 µL/min flow rate). A 2x20mm, 2.5µ, Xbridge C18 analytical column was used. The eluent flowed into an API 5000-1 mass spectrometer (AB Sciex, Framingham, MA) using positive ESI multiple-reaction monitoring. Halofuginone was characterized by the transition of the m/z 416.1 parent mass (M+H)+ precursor ion to its m/z 100.1 product ion, generated at optimized collision energy.

AngII/PE Mice were individually housed with carousel feeders and maintained on standard rodent diet (Lab Diet 5001, meal) and tap water *ad libitum*. On day 0, under Isoflurane (2-2.5%) anesthesia, an osmotic pump containing halofuginone (Alzet model 1004, Durect Corporation, Cupertino, CA) was implanted subcutaneously in the mice. These pumps deliver halofuginone at a rate of 0.046 mg/kg/day (low dose group) or 0.138 mg/kg/day (high
Two control groups and vehicle groups also received osmotic pumps which delivered saline on day 0. The high control AngII/PE group were pair fed to match the food consumption of the mice in halofuginone 0.138mg/kg/day. All other groups were fed *ad libitum*. On day 10, both halofuginone treated groups and control groups received a second osmotic pump (Alzet model 1002) which delivered angiotensin-II (Cat#A9525, Sigma-Aldrich, St. Louis, MO) at 0.432 mg/kg/day and phenylephrine HCL (Cat#P6126, Sigma-Aldrich) at 100mg/kg/day. On day 24, mice were euthanized. Organ weights were recorded. Left ventricles were pulverized under liquid nitrogen and used for hydroxyproline analysis and gene expression analysis.

**Hydroxyproline LC-MS/MS Method** Weighed tissue samples were hydrolyzed in 6N HCl at 110°C for 16 hours. Sample preparation consisted of a 10-fold dilution of hydrolysate with water followed by the addition of acetonitrile containing DL-Proline as an internal standard. Analytical standards were prepared by diluting a stock of hydroxyproline with the DL-Proline solution. LC-MS/MS analysis was performed using positive mode ESI and a HILIC gradient on a silica LC column. Quantitation was performed using Analyst mass spectrometry software and collagen concentrations calculated using Microsoft Excel.

**TAC** Transverse aortic constriction (TAC) was performed as previously reported (1). Briefly, mice were anesthetized with Nembutal (60 mg/kg, ip), and ventilated with a rodent ventilator (Harvard Apparatus, Holliston, MA). Body temperature was maintained by a heated surgical pad. The chest was opened through a midline sternotomy using aseptic technique. Transverse aorta was exposed with a small rodent retractor. A 7-0 suture was placed around the aorta between the innominate and left carotid arteries; a 27-G needle was placed alongside the transverse aorta. Then, the suture was tied snugly around the needle. Aortic constriction was generated by sliding out the needle. Sham operation underwent a similar surgical procedure without constricting the aorta. The incision was closed by layers using 5–0 suture. The endotracheal tube was removed after spontaneous breathing was regained. Animals were treated with halofuginone (0.3 mg/kg/day in chow) right after the TAC surgery.
until the end of the study. LV hemodynamics were evaluated at the end of study. Briefly, mice were anesthetized with 2% isoflurane in oxygen and a 1 F Millar Mikro-tip catheter transducer was inserted into the left ventricle through the right carotid artery to measure left ventricular pressure and both systolic and diastolic left ventricular function (dP/dtmax and dP/dtmin, respectively). After baseline hemodynamic measurement, mice were administered dobutamine at a dose of 1 μg/μl/g/min by intravenous infusion through the right jugular vein for 3 min to determine the cardiac contractile reserve in response to the dobutamine challenge; the difference in maximal change in dP/dtmax between dobutamine challenge and baseline (ΔdP/dtmax) was calculated. Plasma was collected at the end of the study and proANP levels were measured using an ELISA (Cat#04-BI-20892, Alpco, Boston, MA). Echocardiographic examination was performed to evaluate cardiac structure and function in accordance with the American Society of Echocardiography (ASE) guidelines. Anesthesia was induced by placing mice in a chamber using 100% oxygen at 3% isoflurane and maintained at 1.5% isoflurane via nose cone. Scans were performed using VEVO 2100 ultrasound system (VisualSonics, Inc. Toronto, ON, Canada). Short axis images of the left ventricle at the papillary level and parasternal LV long axis images were obtained and stored as digital video loops. Static images and 2D digital loops were stored and analyzed offline on VEVO 2100 workstation (ver. 1.6.0).

I/R 14-week old C57BL/6 mice were injected intraperitoneally with or without halofuginone (6 μg/mice/day, roughly 2 mg/kg/day for 30 g mouse), three days before the ischemic surgery. Ischemia was induced by ligation of the left anterior descending coronary artery for 30 min and reperfusion for 24 hr. The heart was harvested after injection of 2% Evans blue dye with LAD occluded. Then, the heart was sliced into five pieces and stained by 1% triphenyl tetrazolium chloride (TTC). Infarct area, area at risk and LV area were quantified to evaluate the extent of I/R injury.

Fibroblast experiments
Human cardiac fibroblasts (normal human cardiac fibroblast-ventricle, Cat#CC2904, Lonza, Walkersville, MD) were passaged in FGM-3 media (Cat#CC4526, Lonza) until passage 6 or 7. They were then seeded in EMEM media and then treated with EMEM containing ficoll for 24-48hr to stimulate collagen deposition \(^{(2)}\). At the same time of ficoll treatment, compounds such as halofuginone, borrelidin (Cat# B3061-1MG, Sigma-Aldrich), L-proline (Cat#P5607, Sigma-Aldrich), L-threonine (Cat# T8441, Sigma-Aldrich) were added to the media to test their effects. In addition to compound treatment, these cells were also transfected with BacMam virus that carries constitutively active GCN2 (S808G and F855L mutations) with increasing multiplicity of transfection (virus to cell ratio). These cells were then stimulated with ficoll to induce collagen deposition. For collagen deposition analysis, at the end of the treatment, cells were fixed with methanol and immunostained with mouse anti-mature type I collagen antibody (Cat#C2456-.5ML, Sigma-Aldrich), secondary antibody (Cat#A21236, Life Technologies, Grand Island, NY) and Hoechst (Cat#H3569, Life Technologies). Fluorescent images were obtained using Operetta High Content Imaging System (Perkin Elmer, Waltham, MA). Collagen intensities and nuclei numbers were calculated by Harmony software (Perkin Elmer). For Western blots, cells were lysed with RIPA buffer with protease and phosphatase inhibitor cocktails (Cat# 89901, #78429 and #78426, Thermo Fisher, Rockford, IL) and total cellular protein were harvested by centrifugation removal of cell debris. Cell media were also stored for Western Blot analysis. For Western, about 10 μg of total protein or 15ul of cell media were separated on 4-12% SDS-PAGE gel and then transferred to nitrocellulose membrane. The membranes were blotted with pGCN2 antibody (phospho-T899, Cat# ab75836, Abcam, Cambridge, MA), total GCN2 antibody (Cat#3302S, Cell Signaling Technology, Boston, MA), α-tubulin antibody (Cat#SC-8035, Santa Cruz Biotechnology, Santa Cruz, CA), donkey-anti-rabbit IRDye 680 secondary antibody (Cat# 926-68023, Li-Cor, Lincoln, NE), anti-procollagen I antibody (Cat#SC-8782, Santa Cruz Biotechnology, Santa Cruz, CA), and donkey-anti-goat IRDye 680 secondary antibody (Cat#926-68024, Li-Cor). The images were scanned using Odyssey Imager (Li-Cor) and quantification was done using the Odyssey software.
Real Time RT-PCR and transcriptomics analysis

In cellular experiments, total cellular RNA was isolated using the RNeasy mini kit (Cat#74106, Qiagen, Valencia, CA). In animal experiments, frozen tissues were pulverized under liquid nitrogen and then total RNA were isolated using TRizol reagent (Cat#10296028, Life Technologies) and the RNeasy mini kit. Real-time RT-PCR analysis was carried out using QuantiTect RT-PCR (Cat#204445, Qiagen). Primer and probe sets used in cellular studies were Hs00984230_m1 (B2M), Hs01090850_m1 (CHOP), Hs00383231_m1 (NPPA) and Hs00164004_m1 (COL1A1). Primer and probe sets used in animal studies were Mm00492097_m1 (CHOP), Mm00437762_m1 (B2M), Mm00801666_g1 (COL1A1), Mm00803785_m1 (ASNS), Mm00440359_m1 (MYH6) and Mm00782868_sH (LC3B).

For transcriptomics analysis, RNA was isolated as described above. Poly-A mRNA enrichment was carried out using TruSeq™ RNA sample prep v2 kit (Illumina Inc. San Diego, USA) according to manufacturer's instructions. Then cDNA libraries were prepared and sequenced on Illumina’s HiSeq1000 by using Illumina’s Paired End 2x50bp SBS sequencing kits v5 (Illumina) for whole-transcriptome sequencing. Quality assessment of the reads was performed using ArrayStudio. An average of 60 million reads was generated for each sample. The reads were mapped to the Human Reference at an average of 95%. Read mapping and expression estimation was analyzed using methodology as described before (3). The number of reads for each transcript from each samples was converted to fragments per kilo base per million (FPKM). General linear regression or ANOVA test was used to identify significant differences between tested conditions. FDR (false discovery rate) was used to determine the significance threshold. An FDR < 0.1 along with fold change greater than 2 was considered to indicate significant expression abundance. Pathway enrichment analysis was conducted using Ingenuity Pathway Analysis. The analysis was conducted on the differentially expressed genes from comparing halofuginone treated vs. control samples. The significantly enriched pathways were selected by using p-value of 0.01.
**Cardiomyocyte experiment**

Human iPSC-derived cardiomyocytes were purchased from Cellular Dynamics International (CDI, Madison, WI). Upon defrosting, cells were allowed to mature in maintenance media (CDI) for 10-14 days. Cells were placed in serum-free media for 24 hrs before treatment. These cells were then transfected with BacMam virus that carries constitutively active GCN2 (S808G and F855L mutations) with increasing multiplicity of transfection (virus to cell ratio). Western blot was used to determine total and p-GCN2, total and p-Elf2α, tubulin and LC3B (Cell Signaling, cat#12741) levels as described above.

**Proteomic analysis**

**Cell treatment for expression proteomics experiment**

NHCF-V cells were treated with 100 nM halofuginone, 300 nM halofuginone, 300 nM halofuginone and 4 mM L-proline, or DMSO for 24 hours. The experiment was done in two biological replicates.

**Sample preparation for MS**

Cells were lysed in 2 % SDS for 3 min at 95 °C in a thermomixer (Thermo Fisher Scientific), followed by digestion of DNA with Benzonase at 37 °C for 1.5 h. Lysates were cleared by centrifugation and protein concentrations in the supernatants were determined by the BCA assay. Proteins were reduced by DTT and alkylated with iodacetamide and separated on 4–12% NuPAGE (Invitrogen), and stained with colloidal Coomassie. Gel lanes were cut into three slices covering the entire separation range (~2 cm) and subjected to in-gel digestion. Peptide samples were labelled with 10-plex TMT (TMT10, Thermo Fisher Scientific, Waltham, MA) reagents, enabling relative quantification of a broad range of 10 conditions in a single experiment. The labeling reaction was performed in 40 mM triethylammoniumbicarbonate, pH 8.53 at 22 °C and quenched with glycine. Labeled peptide
extracts were combined to a single sample per experiment, and subjected to additional fractionation on an Ultimate3000 (Dionex, Sunnyvale, CA) by using reversed-phase chromatography at pH 12 [1 mm Xbridge column (Waters, Milford, MA)], as previously described (6).

**LC-MS/MS analysis**

Samples were dried in vacuum and resuspended in 0.05 % trifluoroacetic acid (TFA) in water. Of the sample, 50% was injected into an Ultimate3000 nanoRLSC HPLC (Dionex, Sunnyvale, CA) coupled to a Q-Exactive Mass Spectrometer (Thermo Fisher Scientific). Peptides were trapped on a 5 mm x 300 μm C18 column (Pepmap100, 5 μm, 300 Å, Thermo Fisher Scientific) in water with 0.05 % TFA at 60 °C. Separation was performed on custom 50 cm x 100 μm (ID) reversed-phase columns (Reprosil) at 55°C. Gradient elution was performed from 2% acetonitrile to 40% acetonitrile in 0.1% formic acid and 3.5 % DMSO over 2 hours. Samples were online-injected into Q-Exactive plus mass spectrometers operating with a data-dependent top 10 method. MS spectra were acquired by using 70,000 resolution and an ion target of 3x10⁵. Higher energy collisional dissociation (HCD) scans were performed with 35% NCE at 35,000 resolution (at m/z 200), and the ion target settings was set to 2x10⁵ so as to avoid coalescence (7).

**Protein identification and quantification**

Mascot 2.4 (Matrix Science, Boston, MA) was used for protein identification by using a 10 parts per million mass tolerance for peptide precursors and 20 mD (HCD) mass tolerance for fragment ions. Carbamidomethylation of cysteine residues and TMT modification of lysine residues were set as fixed modifications and methionine oxidation, and N-terminal acetylation of proteins and TMT modification of peptide N-termini were set as variable modifications. The search database consisted of a customized version of the International Protein Index protein sequence database combined with a decoy version of this database was created by using a script supplied by Matrix Science. Unless stated otherwise, we accepted protein identifications as described (8).
Reporter ion intensities were read from raw data and multiplied with ion accumulation times (the unit is milliseconds) so as to yield a measure proportional to the number of ions; this measure is referred to as ion area \(^9\). Spectra matching to peptides were filtered according to the following criteria: mascot ion score >15, signal-to-background of the precursor ion >4, and signal-to-interference >0.5 \(^{10}\). Fold-changes were corrected for isotope purity as described and adjusted for interference caused by co-eluting nearly isobaric peaks as estimated by the signal-to-interference measure \(^{11}\). Protein quantification was derived from individual spectra matching to distinct peptides by using a sum-based bootstrap algorithm; 95% confidence intervals were calculated for all protein fold-changes that were quantified with more than three spectra \(^9\). Protein fold changes were only reported for proteins with at least 2 quantified unique peptide matches. Protein FDR for quantified proteins was < 0.01.

**Statistical analysis**

Quantified proteins were divided into bins according to the number of quantified spectrum sequence matches. Each bin consists of at least 300 proteins. This data quality–dependent binning strategy is analogous to the procedure described previously \(^{12}\). For each protein fold change (FC) a p-value is calculated using a Z-test with a robust estimation of the standard deviation (using the 15.87, 50, and 84.13 percentiles). The standard deviation is calculated, per bin, from a distribution of proteins log \(_2\) transformed fold change differences from the two biological replicates divided by the square root of two:

\[
\frac{\log_2(FC_{\text{rep1}}) - \log_2(FC_{\text{rep2}})}{\sqrt{2}}
\]

Subsequently, an adjustment for multiple hypothesis testing was performed on the full data set by using Benjamini-Hochberg (BH) correction \(^{13}\). Proteins were counted as regulated when having a p-value of \(\leq 0.05\) and changed in their expression in both replicates by 30 % in the same direction.
Clustering of proteins significantly regulated after either 100nM or 300nM Halofuginone was done in Tibco Spotfire 6.0.2 using Euclidian distance and complete linkage. GO-term enrichment analysis for the main cluster of regulated proteins was done using the webtool Gorilla (14). The enrichment analysis was done for each cluster using all identified proteins as background.
| Accession No. | Gene Name | Fold Change (log2) | FDR |
|--------------|-----------|--------------------|-----|
| IPI00021033  | COL3A1    | -2.59              | 1.9E-41 |
| IPI00297646  | COL1A1    | -2.29              | 3.45E-36 |
| IPI00873137  | COL1A2    | -2.22              | 5.51E-34 |
| IPI00028714  | MGP       | -2.56              | 6.33E-29 |
| IPI0171160   | LRRC17    | -2.48              | 4.73E-22 |
| IPI0020986   | LUM       | -2.15              | 3.3E-19  |
| IPI00329573  | COL12A1   | -1.63              | 2.72E-18 |
| IPI00012119  | DCN       | -1.96              | 9.95E-18 |
| IPI00299738  | PCOLCE    | -2.11              | 4.91E-17 |
| IPI00902794  | MAGED4    | -2.40              | 1.3E-16  |
| IPI00398845  | MAGED1    | -2.07              | 1.46E-16 |
| IPI00879004  | TOP2A     | 2.03               | 7.76E-16 |
| IPI00216088  | CRABP2    | -2.03              | 1.85E-15 |
| IPI00011735  | IFRD1     | 1.88               | 5.93E-15 |
| IPI00168691  | SHCBP1    | 2.21               | 2.22E-14 |
| IPI00290110  | PDCD4     | -1.60              | 4.76E-14 |
| IPI00220488  | FOXS1     | -2.18              | 6.25E-13 |
| IPI0014572   | SPARC     | -1.71              | 1.05E-12 |
| IPI00045512  | HMCN1     | -1.35              | 1.16E-12 |
| IPI00477611  | COL5A1    | -1.90              | 1.41E-12 |
| IPI00017557  | SFRP4     | -1.67              | 3.5E-12  |
| IPI00645849  | ECM1      | -1.72              | 4.71E-12 |
| IPI00739099  | COL5A2    | -1.80              | 1.35E-11 |
| IPI00291136  | COL6A1    | -1.22              | 1.95E-11 |
| IPI00304840  | COL6A2    | -1.25              | 2.07E-11 |
| IPI00296165  | C1R       | -1.57              | 4.83E-11 |
| IPI00180266  | WWTR1     | -1.61              | 5.3E-11  |
| IPI00552815  | COL5A1    | -1.80              | 8.5E-11  |
| IPI00001872  | PCDHGA12  | -1.93              | 1.36E-10 |
| IPI00396383  | VWA1      | -1.50              | 1.38E-10 |
| IPI00307829  | CGNL1     | -1.61              | 2.49E-10 |
| IPI00007960  | POSTN     | -1.28              | 5.32E-10 |
| IPI00013880  | SEMA5A    | -1.60              | 1.07E-09 |
| IPI00030431  | ANTXR1    | -1.22              | 1.13E-09 |
| IPI00008894  | CPA4      | -1.49              | 1.23E-09 |
| IPI00304227  | CDH11     | -1.60              | 1.44E-09 |
| IPI0007256   | ZHX2      | -1.28              | 2.79E-09 |
| IPI0027721   | PDGFRA    | -1.54              | 4.84E-09 |
| IPI00852735  | FAT4      | -1.43              | 5.33E-09 |
| IPI00023648  | ISLR      | -1.53              | 5.79E-09 |
| IPI00877788  | MEIS1     | -1.71              | 6.42E-09 |
| IPI00060423  | CTHRC1    | -1.60              | 9.47E-09 |
| IPI00793751  | MFAP4     | -1.40              | 1E-08   |
| IPI00871279  | SLC38A1   | 1.49               | 1.09E-08 |
| IPI00008822  | PRRX1     | -1.47              | 1.31E-08 |
| IPI00719836  | CXCL12    | -1.84              | 1.34E-08 |
| IPI00020977  | CTGF      | -1.48              | 1.75E-08 |
| IPI00165931  | PLXNA4    | -1.44              | 1.89E-08 |
| IPI0022200   | COL6A3    | -1.02              | 2.34E-08 |
| IPI00153049  | MXRA8     | -1.39              | 2.49E-08 |
| IPI00007874  | SOX17     | -1.60              | 2.75E-08 |
| IPI00783931  | COL18A1   | -1.33              | 3.03E-08 |
| IPI00305289  | KIF11     | 1.44               | 5.14E-08 |
| Gene Symbol | Gene Name | Fold Change | p Value |
|-------------|-----------|-------------|---------|
| IPI00024621 | OLFML3   | -1.46       | 5.99E-08|
| IPI00012792 | CDH5     | -1.50       | 7.02E-08|
| IPI00105407 | AKR1B10  | -1.36       | 7.51E-08|
| IPI00409626 | PCDH9    | -1.41       | 7.55E-08|
| IPI00550368 | TENC1    | -1.36       | 1.21E-07|
| IPI00152835 | BMPER    | -1.46       | 1.45E-07|
| IPI00888378 | GATSL2   | -1.72       | 2.11E-07|
| IPI00916930 | STK17B   | -1.32       | 2.5E-07 |
| IPI00293203 | SULF1    | -1.36       | 3.6E-07 |
| IPI00001597 | LOXL1    | -1.02       | 4.51E-07|
| IPI00006114 | SERPINF1 | -1.28       | 5.73E-07|
| IPI00383814 | TMEM132A | -1.25       | 6.28E-07|
| IPI00165044 | C4ORF18  | -1.21       | 7.05E-07|
| IPI0017640  | SLIT3    | -1.25       | 8.38E-07|
| IPI00151360 | GTPBP2   | 1.41        | 8.93E-07|
| IPI00856078 | LDB1     | -1.36       | 1.02E-06|
| IPI00028908 | NID2     | -1.24       | 1.13E-06|
| IPI00221375 | NRG1     | -1.34       | 1.53E-06|
| IPI00783565 | SL6A6    | -1.44       | 1.53E-06|
| IPI00415037 | ADAM12   | -1.24       | 1.88E-06|
| IPI00176193 | COL14A1  | -1.26       | 2.8E-06 |
| IPI00022300 | METTL7A  | -1.18       | 3.05E-06|
| IPI00296147 | TMEM119  | -1.38       | 3.13E-06|
| IPI00009205 | TCF25    | -1.07       | 3.19E-06|
| IPI00337314 | STON1    | -1.17       | 6.21E-06|
| IPI00847609 | SVEP1    | -1.08       | 6.97E-06|
| IPI00069711 | CD248    | -1.13       | 8.39E-06|
| IPI00430439 | VGLL4    | -1.24       | 9.65E-06|
| IPI00015902 | PDGFRB   | -1.30       | 1.08E-05|
| IPI00079935 | HIC1     | -1.45       | 1.14E-05|
| IPI00038139 | VWA5B2   | -1.43       | 1.17E-05|
| IPI00414128 | APCDD1L  | -1.16       | 1.31E-05|
| IPI00298388 | PIK3IP1  | -1.40       | 1.44E-05|
| IPI00064429 | DKK2P586H2123 | -1.09       | 1.46E-05|
| IPI00028415 | PBX1     | -1.10       | 2.07E-05|
| IPI00024242 | EBF3     | -1.20       | 2.24E-05|
| IPI00063787 | CCDC72   | -1.38       | 2.35E-05|
| IPI00651738 | ADI1     | -1.08       | 2.38E-05|
| IPI00297235 | CCPG1    | 1.35        | 2.49E-05|
| IPI00029449 | VANGL2   | -1.07       | 2.71E-05|
| IPI00024089 | ABCG1    | 1.31        | 2.97E-05|
| IPI00329482 | LAMA4    | -1.07       | 3.09E-05|
| IPI00743696 | COL4A1   | -1.11       | 3.42E-05|
| IPI00376689 | KIAA1199 | -0.88       | 3.86E-05|
| IPI00030757 | ADAMTS2  | -1.14       | 4.11E-05|
| IPI00003128 | P4HA2    | -0.91       | 6.38E-05|
| IPI00215611 | CRIP1    | -1.17       | 8.13E-05|
| IPI00298281 | LAMC1    | -0.87       | 8.14E-05|
| IPI00328113 | FBN1     | -0.87       | 8.42E-05|
| IPI00004307 | LAMP3    | 1.28        | 8.43E-05|
| IPI00297333 | AKR1C1   | -1.08       | 9.04E-05|
| IPI00893234 | OBSL1    | -1.07       | 9.36E-05|
| IPI00028565 | GBP2     | -1.07       | 9.57E-05|
| IPI0018769  | THBS2    | -0.87       | 9.62E-05|
| IPI0032055  | CA5B     | -1.26       | 9.66E-05|
| Gene ID         | Gene Symbol | Log Ratio | P Value     |
|----------------|-------------|-----------|-------------|
| IPI00026941    | PRSS23      | -0.96     | 9.69E-05    |
| IPI00059135    | PPP1R14A    | -1.06     | 9.87E-05    |
| IPI0027780     | MMP2        | -0.89     | 0.0001      |
| IPI00152540    | CD109       | -1.12     | 0.000103    |
| IPI00218487    | GJA1        | -1.10     | 0.000113    |
| IPI00853454    | LAMB1       | -0.79     | 0.000122    |
| IPI00297124    | IL6ST       | -0.79     | 0.000128    |
| IPI00005110    | TBX3        | -1.22     | 0.000128    |
| IPI00022621    | MFAP2       | -0.96     | 0.000141    |
| IPI00018606    | CGCLCA-T    | -0.85     | 0.000143    |
| IPI00433279    | SLFN5       | 1.18      | 0.00015     |
| IPI00024284    | HSPG2       | -0.81     | 0.000152    |
| IPI00025817    | CCND3       | -1.37     | 0.000158    |
| IPI00164831    | STARD5      | -0.99     | 0.000164    |
| IPI00059169    | CCDC102A    | -1.15     | 0.000168    |
| IPI00399164    | ARID5B      | -0.95     | 0.000198    |
| IPI00154603    | FGF2        | 1.19      | 0.000199    |
| IPI00024887    | BMP6        | -1.04     | 0.000203    |
| IPI00298057    | PPL         | -1.08     | 0.000204    |
| IPI00016915    | IGFBP7      | -1.22     | 0.000227    |
| IPI00165249    | PFTK1       | -1.16     | 0.000237    |
| IPI00013257    | SSBP4       | -1.12     | 0.000253    |
| IPI00329563    | UBE2L6      | -1.27     | 0.000279    |
| IPI00479997    | STMN1       | -0.94     | 0.00029     |
| IPI00007811    | CDK4        | -1.04     | 0.000305    |
| IPI00290526    | CCDC8       | -1.01     | 0.000342    |
| IPI00435947    | WIPF2       | -1.01     | 0.000349    |
| IPI00018387    | FURIN       | -1.06     | 0.000409    |
| IPI00010474    | SLC7A11     | 1.11      | 0.000424    |
| IPI00017696    | C1S         | -0.99     | 0.000423    |
| IPI00020164    | PTP4A1      | 1.25      | 0.000446    |
| IPI00374285    | FLJ41603    | -0.87     | 0.000452    |
| IPI00783987    | C3          | -0.92     | 0.000458    |
| IPI00289258    | MYO10       | -1.28     | 0.000475    |
| IPI00745313    | AEBP1       | -0.92     | 0.00048     |
| IPI00328243    | PLD3        | -0.88     | 0.000485    |
| IPI00872222    | C10ORF54    | -1.07     | 0.000499    |
| IPI00030618    | PCDH18      | -0.96     | 0.00051     |
| IPI00307591    | ZNF609      | -0.88     | 0.000546    |
| IPI00549569    | ISYNA1      | -1.00     | 0.000553    |
| IPI00872929    | APOBEC3C    | -0.71     | 0.000594    |
| IPI00012575    | PIR         | -0.92     | 0.000601    |
| IPI00080170    | TSPAN9      | -0.98     | 0.000601    |
| IPI00328431    | UNC5B       | 0.99      | 0.000606    |
| IPI00024105    | C1QTNF5     | -1.06     | 0.00062     |
| IPI00872194    | COLEC12     | -1.18     | 0.000654    |
| IPI00290560    | DEPC6       | -0.96     | 0.000682    |
| IPI00026944    | NID1        | -0.88     | 0.000682    |
| IPI00871728    | FAM115A     | -1.25     | 0.00076     |
| IPI00215977    | IGF2        | -1.08     | 0.000862    |
| IPI00514311    | CTNBP2NL    | -0.79     | 0.000864    |
| IPI00017567    | ENG         | -0.93     | 0.000865    |
| IPI00885020    | SH3D19      | -0.80     | 0.000866    |
| IPI00025418    | COL7A1      | -0.90     | 0.000903    |
| IPI00009802    | VCAN        | -0.93     | 0.000913    |
| Gene Symbol | Description | Log2 Fold | P-Value |
|-------------|-------------|-----------|---------|
| PHF21A | -0.89 | 0.000919 |
| LAMA2 | -0.82 | 0.000973 |
| BMPR2 | -0.91 | 0.000998 |
| C11orf67 | -0.93 | 0.001057 |
| P4HA3 | -0.89 | 0.001057 |
| TPST1 | -0.89 | 0.001057 |
| TGFBI | -0.86 | 0.001084 |
| BACH1 | -0.94 | 0.001135 |
| PIN4 | -0.97 | 0.001187 |
| TRAFD1 | -0.95 | 0.001187 |
| CDKN2C | -0.93 | 0.001244 |
| ERN1 | 1.21 | 0.001251 |
| HYPK | -0.92 | 0.001267 |
| LMO4 | -1.27 | 0.001409 |
| FAT1 | -0.95 | 0.001409 |
| MAP1LC3B2 | 1.10 | 0.001469 |
| CERCAM | -0.98 | 0.001763 |
| GDF15 | 1.29 | 0.001834 |
| INHBA | -0.82 | 0.001847 |
| NCAM2 | -0.79 | 0.001872 |
| PALMD | -0.94 | 0.001958 |
| PDE5A | -1.06 | 0.001991 |
| NUAK1 | -0.97 | 0.002029 |
| Q15156_HUMAN | -1.09 | 0.002144 |
| IL17RD | -1.14 | 0.002179 |
| AKR1C3 | -1.00 | 0.00218 |
| TFP12 | -1.14 | 0.002193 |
| ITM2B | -0.85 | 0.002257 |
| C1qtnf1 | -1.41 | 0.002315 |
| ZYG11BL | -0.96 | 0.002317 |
| EFEMP2 | -0.77 | 0.002519 |
| RUNX2 | -0.77 | 0.002544 |
| CCDC80 | -0.90 | 0.002727 |
| KIF26B | -0.96 | 0.002732 |
| F2R | -0.96 | 0.002817 |
| S100A4 | -0.96 | 0.002835 |
| FOXC2 | -0.89 | 0.002839 |
| CRIP | -0.91 | 0.002926 |
| GPR124 | -0.87 | 0.002926 |
| NPR2 | -0.97 | 0.003217 |
| MAP1A | -0.58 | 0.003262 |
| RBP1 | -0.95 | 0.003532 |
| SDF4 | -1.02 | 0.003553 |
| C6orf115 | -0.89 | 0.003585 |
| WBP2 | -0.77 | 0.0038 |
| IRF2BP2 | -0.79 | 0.00406 |
| SPC25 | -0.81 | 0.004231 |
| UBL5 | -0.77 | 0.004239 |
| MAGED2 | -0.85 | 0.004268 |
| EMILIN1 | -0.92 | 0.004474 |
| APLP2 | -0.60 | 0.004691 |
| FBLN2 | -0.73 | 0.004713 |
| SH3BGRL | -0.95 | 0.004905 |
| SRPX | -0.89 | 0.004947 |
| Protein ID       | Symbol | Expression Value | FDR   |
|-----------------|--------|------------------|-------|
| IPI00009793     | C1RL   | -0.99            | 0.00519 |
| IPI00473118     | MATN2  | -0.86            | 0.005228 |
| IPI00296099     | THBS1  | -0.56            | 0.005422 |
| IPI00069232     | GPRASP2| -0.90            | 0.005793 |
| IPI00030781     | STAT1  | -0.75            | 0.005841 |
| IPI00855785     | FN1    | -0.62            | 0.005841 |
| IPI00012303     | SELENBP1| -0.79          | 0.006263 |
| IPI00099179     | SUFU   | -0.86            | 0.006415 |
| IPI00303280     | LRRC32 | -0.80            | 0.006531 |
| IPI00445977     | LHFPL2 | -0.76            | 0.006587 |
| IPI00266899     | CDC2   | -0.78            | 0.006638 |
| IPI00218260     | NFIX   | -0.79            | 0.006681 |
| IPI00000695     | GNA14  | -0.71            | 0.007023 |
| IPI00386516     | KIAA0174| -0.67           | 0.00723 |
| IPI00442121     | ALAD   | -0.71            | 0.00766 |
| IPI00760962     | KANK2  | -0.90            | 0.007979 |
| IPI00465099     | BNC2   | -0.80            | 0.007999 |
| IPI00848032     | TBC1D9 | -0.83            | 0.008103 |
| IPI00044369     | PLXDC2 | -0.80            | 0.008182 |
| IPI00025478     | IRF9   | -0.77            | 0.008314 |
| IPI00005401     | GALNT5 | -0.84            | 0.008593 |
| IPI00029568     | PTX3   | 1.09             | 0.008656 |
| IPI0002732      | EXT1L2 | -0.79            | 0.009022 |
| IPI00059930     | NACC2  | -0.87            | 0.009057 |
| IPI00029260     | CD14   | -0.76            | 0.009177 |
| IPI00010948     | TRIM26 | -0.75            | 0.009263 |
| IPI0006377      | POMP   | -0.70            | 0.009278 |
| IPI0054042      | GTF2I  | -0.85            | 0.009348 |
| IPI0004409      | DDR2   | 0.85             | 0.009371 |
| IPI00291579     | KIF23  | 0.84             | 0.00981 |
| IPI00153060     | ANGPTL4| 1.18             | 0.009913 |
| IPI00290435     | KIF2C  | 1.09             | 0.00997 |
| IPI00412829     | TEK    | -0.81            | 0.010161 |
| IPI00294839     | ENTPD4 | -0.76            | 0.010276 |
| IPI00604494     | CCDC92 | -0.82            | 0.010413 |
| IPI00513732     | TLE4   | -1.18            | 0.010567 |
| IPI00299758     | CHST12 | -0.70            | 0.010721 |
| IPI00743698     | PTPRA  | -0.88            | 0.010746 |
| IPI00032292     | TIMP1  | -0.91            | 0.010839 |
| IPI00100980     | EHD2   | -0.75            | 0.012155 |
| IPI00003420     | MAPRE2 | -0.87            | 0.012382 |
| IPI00748895     | ANK1   | -0.81            | 0.012509 |
| IPI00455408     | GLTPD1 | -0.82            | 0.01273 |
| IPI00218803     | FBLN1  | -0.67            | 0.013732 |
| IPI00292150     | LTBP2  | -0.86            | 0.014594 |
| IPI00045106     | HHIP   | -0.69            | 0.014726 |
| IPI00031681     | CDK2   | -0.74            | 0.014926 |
| IPI00029819     | NOTCH3 | -0.64            | 0.0152 |
| IPI00739386     | PRAGMIN| -0.82            | 0.015573 |
| IPI00893155     | GPC1   | -0.77            | 0.015578 |
| IPI00410259     | PHILDB2| 0.88             | 0.015645 |
| IPI00013159     | ETV6   | -0.89            | 0.015657 |
| IPI00179438     | DAB2   | -0.67            | 0.015661 |
| IPI00019209     | SEMA3C | -0.72            | 0.015983 |
| IPI00170548     | ATAD2  | 1.10             | 0.015992 |
| Gene ID       | Gene Symbol | log2 Fold Change | p-value |
|--------------|-------------|------------------|---------|
| IPI00010445  | GLT8D2      | -0.71            | 0.016018|
| IPI00383108  | APBB1       | -1.00            | 0.016027|
| IPI00550644  | TTC38       | -0.67            | 0.016855|
| IPI00386562  | FBLIM1      | -0.57            | 0.016992|
| IPI00166657  | FBXW8       | -0.71            | 0.017379|
| IPI00329760  | OS9         | -0.70            | 0.017402|
| IPI00007132  | RHOBTB3     | -0.75            | 0.017428|
| IPI00410351  | NCOR1       | -0.65            | 0.017985|
| IPI00029723  | FSTL1       | -1.01            | 0.018592|
| IPI00005733  | TGFBR1      | 0.80             | 0.018763|
| IPI00304895  | MOCOS       | 1.10             | 0.01897 |
| IPI00397015  | AHDC1       | -0.62            | 0.019076|
| IPI00023532  | LOC26010    | -0.62            | 0.01941 |
| IPI00059764  | ZNF428      | -0.74            | 0.01975 |
| IPI00871938  | PTGFRN      | -0.66            | 0.020564|
| IPI00014174  | MORF4L2     | -0.71            | 0.02105 |
| IPI00032936  | ERF         | -0.67            | 0.021323|
| IPI00296353  | ARHGAP18    | -0.72            | 0.021323|
| IPI00784258  | LTB1P1      | -0.78            | 0.022073|
| IPI00479296  | ABCA8       | -0.75            | 0.022169|
| IPI00005751  | ATF6        | 0.98             | 0.022706|
| IPI00329753  | FAM164A     | -0.74            | 0.023095|
| IPI00002816  | CTSF        | -0.72            | 0.023251|
| IPI00019448  | TSGA14      | -0.64            | 0.024085|
| IPI00298409  | PDCL        | -0.72            | 0.024451|
| IPI00290071  | WDR42A      | -0.59            | 0.024979|
| IPI0021389   | CCS         | -0.60            | 0.025359|
| IPI00395488  | VASN        | -0.54            | 0.025643|
| IPI00872795  | PPAP2A      | -0.66            | 0.025829|
| IPI00020470  | GLT8D1      | -0.70            | 0.025882|
| IPI00441959  | NIN         | -0.80            | 0.025912|
| IPI00006142  | ARMCX2      | -0.70            | 0.025912|
| IPI00151036  | RNF13       | -0.73            | 0.026486|
| IPI00004312  | STAT2       | -0.85            | 0.026725|
| IPI00022498  | MT2A        | -0.69            | 0.026842|
| IPI0001735   | NCOB2       | -0.72            | 0.02768 |
| IPI00290462  | CBR3        | -0.69            | 0.027917|
| IPI00289342  | EPHB4       | -0.70            | 0.029661|
| IPI00006608  | APP         | -0.64            | 0.030421|
| IPI00023673  | LGALS3BP    | -0.60            | 0.030488|
| IPI0011564   | SDC4        | -0.70            | 0.031128|
| IPI00013925  | GALT        | -0.58            | 0.031468|
| IPI00444572  | SIPA1L2     | -0.82            | 0.031697|
| IPI00872398  | TNPO3       | -0.69            | 0.032035|
| IPI00807364  | FNBP1L      | -0.67            | 0.032161|
| IPI00020228  | FZD6        | -0.77            | 0.033086|
| IPI00604444  | PLAU        | 1.00             | 0.033319|
| IPI00328798  | BCL9L       | -0.58            | 0.033883|
| IPI00031789  | IL1RAP      | 0.80             | 0.034161|
| IPI00006288  | SLIT2       | -0.74            | 0.034178|
| IPI00001690  | CUL7        | -0.85            | 0.034879|
| IPI0031018   | MAFK        | 0.73             | 0.036848|
| IPI0028082   | RECK        | -0.56            | 0.037492|
| IPI00291901  | IRF3        | -0.56            | 0.03777 |
| Gene ID     | Gene Symbol | Ratio  | p-value |
|------------|-------------|--------|---------|
| IPI00028516| KIAA0513    | -0.81  | 0.038046|
| IPI0015808 | GNL2        | 0.66   | 0.038847|
| IPI0011689 | EEF2K       | -0.72  | 0.038973|
| IPI00030023| HNMT        | -0.67  | 0.039413|
| IPI0023098 | FOXP1       | -0.59  | 0.040448|
| IPI0005609 | VWA5A       | -0.96  | 0.041404|
| IPI00444945| BAX         | -0.56  | 0.041404|
| IPI00647915| TAGLN2      | -0.45  | 0.0417  |
| IPI0011901 | ADAM19      | -0.78  | 0.042204|
| IPI00470422| ANKMY2      | -0.77  | 0.04271 |
| IPI0000760 | DDAH2       | -0.62  | 0.04271 |
| IPI00024307| EFNB1       | -0.78  | 0.043376|
| IPI00217469| HIST1H1A    | 0.66   | 0.043402|
| IPI0180240 | TMSL3       | -0.76  | 0.04417 |
| IPI0023529 | CDK6        | -0.66  | 0.044447|
| IPI0029817 | NEU1        | -0.59  | 0.045283|
| IPI0176903 | PTRF        | -0.41  | 0.045283|
| IPI00022431| AHSAG       | -0.63  | 0.04617 |
| IPI00515115| ABLIM1      | -0.58  | 0.046785|
| IPI0008157 | KIAA1211    | -0.72  | 0.047257|
| IPI00296461| SMPD1       | -0.65  | 0.047504|
| IPI0182728 | VPS4B       | -0.47  | 0.047533|
| IPI0021250 | DAPK1       | -0.71  | 0.047628|
| IPI00607575| RXRB        | -0.55  | 0.047703|
| IPI0030026 | SULT1A1     | -0.59  | 0.048529|
| IPI00003369| LIMD1       | -0.58  | 0.048997|
| IPI00031679| C3ORF26     | 0.65   | 0.049734|
| Input IDs | Gene Name                                      | Fold Change | FDR   |
|----------|-----------------------------------------------|-------------|-------|
| TRIB3    | tribbles pseudokinase 3                       | 77.3699     | 0.001 |
| IGFBP1   | insulin-like growth factor binding protein 1  | 59.1483     | 0.0037|
| DDT3     | DNA-damage-inducible transcript 3            | 42.6177     | 0.0096|
| CHAC1    | ChaC, cation transport regulator homolog 1 (E. coli) | 28.9237     | 0.0006|
| IL1A     | interleukin 1, alpha                          | 21.9582     | 0.0276|
| ADM2     | adrenomedullin 2                              | 20.9329     | 0.0011|
| SH3BGR   | SH3 domain binding glutamate-rich protein     | 18.8094     | 0.0078|
| GDF15    | growth differentiation factor 15              | 16.0542     | 0.0134|
| PSAT1    | phosphoserine aminotransferase 1              | 15.309      | 0.0072|
| MTHFD2   | methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase | 15.2944     | 0.0072|
| SLC7A1   | solute carrier family 7 (cationic amino acid transporter, y+ system), member 1 | 13.9985     | 0.0033|
| PMAIP1   | phorbol-12-myristate-13-acetate-induced protein 1 | 13.6756     | 0.0162|
| FGF2     | fibroblast growth factor 2 (basic)            | 11.6312     | 0.0222|
| PTX3     | pentraxin 3, long                             | 11.0769     | 0.0071|
| TNFSF4   | tumor necrosis factor (ligand) superfamily, member 4 | 10.3411     | 0.0067|
| CD274    | CD274 molecule                                | 9.3607      | 0.0289|
| FAM129A  | family with sequence similarity 129, member A | 9.0446      | 0.0019|
| LAMP3    | lysosomal-associated membrane protein 3       | 8.9245      | 0.0011|
| SLC1A5   | solute carrier family 1 (neutral amino acid transporter), member 5 | 8.9045      | 0.001 |
| CEGBP    | CCAAT/enhancer binding protein (C/EBP), gamma | 8.8581      | 0.0072|
| SLC6A9   | solute carrier family 6 (neurotransmitter transporter, glycine), member 9 | 8.8506      | 0.0007|
| RCAN1    | regulator of calcineurin 1                    | 8.6199      | 0.0075|
| HSPA5    | heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa) | 8.3931      | 0.0125|
| KCNG1    | potassium voltage-gated channel, subfamily G, member 1 | 8.2696      | 0.0019|
| MXD1     | MAX dimerization protein 1                    | 8.2591      | 0.0174|
| ULBP1    | UL16 binding protein 1                        | 8.1037      | 0.0108|
| SLCN5    | schlafen family member 5                     | 7.9528      | 0.011 |
| IL6      | interleukin 6                                 | 7.8984      | 0.0132|
| MOCOS    | molybdenum cofactor sulfatase                | 7.7674      | 0.0048|
| SESN2    | sestrin 2                                     | 7.6075      | 0.0041|
| CSTA     | cystatin A (stefin A)                         | 7.5472      | 0.0012|
| WARS     | tryptophanyl-tRNA synthetase                  | 7.5415      | 0.0042|
| SLC38A1  | solute carrier family 38, member 1            | 7.4784      | 0.0072|
| TCEA1    | transcription elongation factor A (SII), 1    | 7.1435      | 0.0088|
| HBEGF    | heparin-binding EGF-like growth factor        | 7.1356      | 0.0329|
| ATF5     | activating transcription factor 5             | 7.0858      | 0.0013|
| DDT4     | DNA-damage-inducible transcript 4            | 6.9259      | 0.0019|
| GOT1     | glutamic-oxaloacetic transaminase 1, soluble  | 6.7169      | 0.0096|
| SLC7A5   | solute carrier family 7 (amino acid transporter light chain, L system), member 5 | 6.6366      | 0.0006|
| SLC1A4   | solute carrier family 1 (glutamate/neural amino acid transporter), member 4 | 6.6105      | 0.0052|
| PDCD1LG2 | programmed cell death 1 ligand 2             | 6.1914      | 0.0158|
| OLAH     | oleoyl-ACP hydrolase                         | 6.1863      | 0.0124|
| TM6SF1   | transmembrane 6 superfamily member 1         | 6.1043      | 0.0062|
| IL20RB   | interleukin 20 receptor beta                 | 6.068       | 0.003 |
| ASB1     | ankyrin repeat and SOCS box containing 1     | 6.054       | 0.0098|
| ERN1     | endoplasmic reticulum to nucleus signaling 1 | 5.9348      | 0.0232|
| TFGB2    | transforming growth factor, beta 2           | 5.9312      | 0.0216|
| SLC7A11  | solute carrier family 7 (anionogenic amino acid transporter light chain, xC-system), member 11 | 5.872       | 0.0074|
| NUDT2    | nudix (nucleoside diphosphate linked moiety X)-type motif 2 | 5.7771      | 0.0081|
| BNC1     | basoirucin 1                                 | 5.7208      | 0.0276|
| E2F7     | E2F transcription factor 7                   | 5.63        | 0.011 |
| C6orf48  | chromosome 6 open reading frame 48           | 5.5415      | 0.0089|
| SLC3A2   | solute carrier family 3 (amino acid transporter heavy chain), member 2 | 5.5085      | 0.0312|
| KRT34    | keratin 34                                   | 5.48        | 0.0298|
| SGTB     | small glutamine-rich tetra/tricopeptide repeat (TPR)-containing, beta | 5.4322      | 0.0172|
| Gene   | Description                                                                 | Log2FoldChange | p-value |
|--------|------------------------------------------------------------------------------|---------------|---------|
| PDE1C  | phosphodiesterase 1C, calmodulin-dependent 70kDa                            | 5.4311        | 0.0351  |
| SNHG12 | small nucleolar RNA host gene 12 (non-protein coding)                       | 5.3914        | 0.0312  |
| SLC22A15| solute carrier family 22, member 15                                         | 5.3707        | 0.0069  |
| UAP1   | UDP-N-acetylglucosamine pyrophosphorylase 1                                 | 5.3111        | 0.0245  |
| GTPBP2 | GTP binding protein 2                                                        | 5.2464        | 0.0062  |
| GDNF   | glial cell derived neurotrophic factor                                      | 5.2364        | 0.0743  |
| ARHGEF2| Rho/Rac guanine nucleotide exchange factor (GEF) 2                         | 5.1597        | 0.0137  |
| FAM167A| family with sequence similarity 167, member A                              | 5.0891        | 0.0115  |
| PPP1R15A| protein phosphatase 1, regulatory subunit 15A                             | 5.058         | 0.0334  |
| CPEB4  | cytoplasmic polyadenylation element binding protein 4                       | 5.0001        | 0.0461  |
| GARS   | UDP-N-acetylglucosamine pyrophosphorylase 1                                 | 4.9869        | 0.0111  |
| TUBE1  | tubulin, epsilon 1                                                          | 4.9337        | 0.0159  |
| IARS   | isoleucyl-IRNA synthetase                                                   | 4.9244        | 0.0003  |
| SNACP1 | small nuclear RNA activating complex, polypeptide 1, 43kDa                  | 4.9145        | 0.0279  |
| SCN9A  | sodium channel, voltage-gated, type IX, alpha subunit                      | 4.9126        | 0.0041  |
| SAT1   | spermide/spermine N1-acetyltransferase 1                                   | 4.8622        | 0.0351  |
| TSLP   | thymic stromal lymphopoietin                                                | 4.8375        | 0.0262  |
| ETV5   | ets variant 5                                                               | 4.7634        | 0.0066  |
| RPLP0P2| ribosomal protein, large, P0 pseudogene 2                                  | 4.7731        | 0.0091  |
| RH1    | ribonuclease/angiogenin inhibitor 1                                         | 4.7653        | 0.0036  |
| AKNA   | AT-hook transcription factor                                                | 4.7611        | 0.0074  |
| RGBM   | repulsive guidance molecule family member b                                | 4.6311        | 0.0257  |
| LRRN4CL| LRRN4 C-terminal like                                                       | 4.6138        | 0.0012  |
| RND3   | Rho family GTPase 3                                                         | 4.6025        | 0.0399  |
| MYC    | v-my avian myelocytomatosis viral oncogene homolog                          | 4.5655        | 0.0182  |
| FIBIN  | fin bud initiation factor homolog (zebrafish)                               | 4.5399        | 0.0053  |
| ALDH1L2| aldehyde dehydrogenase 1 family, member L2                                 | 4.505         | 0.0036  |
| MYEF2  | myelin expression factor 2                                                  | 4.4932        | 0.0293  |
| XPOT   | exportin, tRNA                                                              | 4.4591        | 0.0007  |
| DDR2   | discoidin domain receptor tyrosine kinase 2                                | 4.4544        | 0.011   |
| GPR1   | G protein-coupled receptor 1                                                | 4.4461        | 0.0078  |
| PHGDH  | phosphoglycerate dehydrogenase                                              | 4.3318        | 0.019   |
| RAB39B | RAB39B, member RAS oncogene family                                          | 4.3211        | 0.0272  |
| TNC    | tenascin C                                                                  | 4.3052        | 0.006   |
| GPT2   | glutamic pyruvate transaminase (alanine aminotransferase) 2                 | 4.2223        | 0.0042  |
| SNHG5  | small nucleolar RNA host gene 5 (non-protein coding)                        | 4.2218        | 0.0172  |
| FRMPD4 | FERM and PDZ domain containing 4                                            | 4.217         | 0.021   |
| GRPEL2 | GrpE-like 2, mitochondrial (E. coli)                                        | 4.2162        | 0.0182  |
| MARCH4 | membrane-associated ring finger (C3HC4) 4, E3 ubiquitin protein ligase      | 4.2092        | 0.0159  |
| CXCL3  | chemokine (C-X-C motif) ligand 3                                            | 4.1775        | 0.0705  |
| IL1B   | interleukin 1, beta                                                         | 4.1288        | 0.0293  |
| MAP1LC3B| microtubule-associated protein 1 light chain 3 beta                        | 4.1226        | 0.0128  |
| NFIL3  | nuclear factor, interleukin 3 regulated                                     | 4.0894        | 0.0242  |
| SNHG1  | small nucleolar RNA host gene 1 (non-protein coding)                        | 4.0614        | 0.0113  |
| NUPR1  | nuclear protein, transcriptional regulator, 1                              | 4.0379        | 0.0296  |
| MAP1LC3B2| microtubule-associated protein 1 light chain 3 beta 2                       | 4.0258        | 0.0289  |
| BEX4   | brain expressed, X-linked 4                                                 | 3.9957        | 0.0223  |
| PTPRH  | protein tyrosine phosphatase, receptor type, H                             | 3.9776        | 0.0002  |
| ODC1   | ornithine decarboxylase 1                                                   | 3.9672        | 0.0255  |
| MICALCL| MICAL C-terminal like                                                       | 3.9637        | 0.0333  |
| PVR    | poliovirus receptor                                                         | 3.9208        | 0.0299  |
| FOSL1  | FOS-like antigen 1                                                          | 3.8538        | 0.0181  |
| CBS    | cystathionine-beta-synthase                                                 | 3.8521        | 0.0172  |
| NGF    | nerve growth factor (beta polypeptide)                                     | 3.8339        | 0.0304  |
| SCRG1  | stimulator of chondrogenesis 1                                              | 3.8315        | 0.0105  |
| ARF1   | ADP-ribosylation factor 1                                                   | 3.8218        | 0.044   |
| H1F0   | H1 histone family, member 0                                                 | 3.7992        | 0.0536  |
| COL15A1| collagen, type XV, alpha 1                                                  | 3.788         | 0.0132  |
| MAMDC2 | MAM domain containing 2                                                     | 3.7422        | 0.0334  |
| HSPA13 | heat shock protein 70kDa family, member 13                                  | 3.6922        | 0.0111  |
| HSPA9  | heat shock 70kDa protein 9 (mortalin)                                       | 3.6672        | 0.0053  |
| Gene Name | Description                                                                 | Log2 Fold Change | P Value   |
|-----------|------------------------------------------------------------------------------|------------------|-----------|
| PRKCE     | protein kinase C, epsilon                                                     | 3.6667           | 0.0184    |
| RAPH1     | Ras association (RafGDS/AF-6) and pleckstrin homology domains 1              | 3.6642           | 0.0121    |
| SFTA1P    | surfactant associated 1, pseudogene                                         | 3.6615           | 0.0324    |
| NBR2      | neighbor of BRCA1 gene 2 (non-protein coding)                               | 3.6572           | 0.0118    |
| SLMO2     | slowmo homolog 2 (Drosophila)                                                | 3.619            | 0.0266    |
| ANXA1     | annexin A1                                                                  | 3.6067           | 0.0255    |
| EIF2S2    | eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa           | 3.5807           | 0.012     |
| SRXN1     | suffredoxin 1                                                               | 3.5714           | 0.0048    |
| ADAMTS5   | ADAM metalloproteinase with thrombospondin type 1 motif, 5                  | 3.5598           | 0.0101    |
| GFTP1     | glutamine--fructose-6-phosphate transaminase 1                              | 3.5425           | 0.013     |
| CSNK2A1   | casein kinase 2, alpha 1 polypeptide                                         | 3.5303           | 0.0229    |
| KLC2      | kinesin light chain 2                                                        | 3.4925           | 0.0757    |
| GK        | glycerol kinase                                                             | 3.4554           | 0.0183    |
| SKA1      | spindle and kinetochore associated complex subunit 1                         | 3.4499           | 0.0432    |
| MT1H      | metallothionein 1H                                                          | 3.4471           | 0.0348    |
| IQGAP3    | IQ motif containing GTPase activating protein 3                              | 3.446            | 0.0108    |
| SLC31A1   | solute carrier family 31 (copper transporter), member 1                     | 3.434            | 0.0128    |
| SLC43A3   | solute carrier family 43, member 3                                           | 3.4283           | 0.0576    |
| DUSP5     | dual specificity phosphatase 5                                               | 3.3861           | 0.0315    |
| UNC5B     | unc-5 homolog B (C. elegans)                                                 | 3.3715           | 0.0006    |
| FOXD1     | forkhead box D1                                                             | 3.34             | 0.0293    |
| EXOSC6    | exosome component 6                                                          | 3.3318           | 0.0164    |
| DUSP1     | dual specificity phosphatase 1                                               | 3.2622           | 0.0239    |
| PLIN2     | perilipin 2                                                                  | 3.2456           | 0.0004    |
| TRIM25    | tripartite motif containing 25                                               | 3.2442           | 0.0079    |
| ANGPTL4   | angiopeptin-like 4                                                           | 3.2037           | 0.0111    |
| RNF187    | ring finger protein 187                                                       | 3.2856           | 0.0007    |
| DUSP1     | dual specificity phosphatase 1                                               | 3.2622           | 0.0239    |
| PLIN2     | perilipin 2                                                                  | 3.2456           | 0.0004    |
| TRIM25    | tripartite motif containing 25                                               | 3.2442           | 0.0079    |
| ANGPTL1   | angiopeptin-like 1                                                           | 3.2265           | 0.0079    |
| SYT1      | synaptotagmin I                                                              | 3.224            | 0.024     |
| NRB2F     | nuclear receptor binding factor 2                                            | 3.201            | 0.0236    |
| STC2      | stanniocalcin 2                                                              | 3.1865           | 0.0282    |
| NPC1      | Niemann-Pick disease, type C1                                                | 3.1845           | 0.0323    |
| GCLM      | glutamate-cysteine ligase, modifier subunit                                  | 3.1744           | 0.0191    |
| XBP1      | X-box binding protein 1                                                      | 3.1712           | 0.0066    |
| RNF41     | ring finger protein 41, E3 ubiquitin protein ligase                          | 3.1567           | 0.0255    |
| ELOVL6    | ELOVL fatty acid elongase 6                                                  | 3.1567           | 0.0255    |
| Dyrk3     | dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3             | 3.1449           | 0.0593    |
| ARHGAP9   | Rho GTPase activating protein 9                                               | 3.1398           | 0.019     |
| EIF4EBP1  | eukaryotic translation initiation factor 4E binding protein 1                | 3.1376           | 0.0088    |
| ADRB2     | adrenocceptor beta 2, surface                                                | 3.1356           | 0.0267    |
| MT1F      | metallothionein 1F                                                           | 3.1322           | 0.0182    |
| KCTD15    | potassium channel tetramerization domain containing 15                       | 3.1286           | 0.0052    |
| TNFRSF10B | tumor necrosis factor receptor superfamily, member 10b                       | 3.1218           | 0.0276    |
| SEPHS2    | selenophosphate synthetase 2                                                 | 3.0473           | 0.0215    |
| SLC44A2   | solute carrier family 44 (choline transporter), member 2                    | 3.0473           | 0.0727    |
| SHMT2     | serine hydroxymethyltransferase 2 (mitochondrial)                           | 3.0461           | 0.0431    |
| CSAGALNACT2| chondroitin sulfate N-acetylgalactosamine transferase 2                      | 3.0324           | 0.0364    |
| ARHGAP24  | Rho GTPase activating protein 24                                             | 3.0286           | 0.008     |
| APOLD1    | apolipoprotein L domain containing 1                                         | 3.023            | 0.0546    |
| FYN       | FYN proto-oncogene, Src family tyrosine kinase                              | 3.0206           | 0.0562    |
| SLTM      | SAFB-like, transcription modulator                                          | 3.0202           | 0.0203    |
| UGGG      | UDP-glucose ceramide glucosyltransferase                                     | 3.0079           | 0.0297    |
| SLC35F2   | solute carrier family 35, member F2                                          | 3.0024           | 0.0218    |
| CD55      | CD55 molecule, decay accelerating factor for complement (Cromer blood group)| 2.999            | 0.0229    |
| DKK1      | dickkopf WNT signaling pathway inhibitor 1                                   | 2.9937           | 0.0308    |
| OCLN      | occludin                                                                     | 2.9831           | 0.0343    |
| PPP1R15B  | protein phosphatase 1, regulatory subunit 15B                                | 2.9725           | 0.0251    |
| PNMA2     | paraneoplastic Ma antigen 2                                                  | 2.972            | 0.001     |
| Gene Symbol | Description | Log2FC | P-Value |
|-------------|-------------|--------|---------|
| LRRC8D | leucine rich repeat containing 8 family, member D | 2.9699 | 0.0425 |
| UHRF1BP1 | UHRF1 binding protein 1 | 2.9572 | 0.0101 |
| UPP1 | uridine phosphorylase 1 | 2.9549 | 0.0328 |
| PYROXD1 | pyridine nucleotide-disulphide oxidoreductase domain 1 | 2.9535 | 0.0291 |
| LIF | leukemia inhibitory factor | 2.9522 | 0.0242 |
| KIAA0754 | KIAA0754 | 2.945 | 0.0103 |
| SLC35B3 | solute carrier family 35 (adenosine 3'-phospho 5'-phosphosulfate transporter), member B3 | 2.9396 | 0.0682 |
| RAP1GDS1 | RAP1, GTP-GDP dissociation stimulator 1 | 2.9345 | 0.0536 |
| KCTD16 | potassium channel tetramerization domain containing 16 | 2.9178 | 0.028 |
| SLC25A33 | solute carrier family 25 (pyrimidine nucleotide carrier), member 33 | 2.9084 | 0.0355 |
| PYROXD1 | pyridine nucleotide-disulphide oxidoreductase domain 1 | 2.9072 | 0.0466 |
| C5orf28 | chromosome 5 open reading frame 28 | 2.9007 | 0.0101 |
| EXOSC8 | exosome component 8 | 2.8995 | 0.0127 |
| GLRB | glycine receptor, beta | 2.8965 | 0.034 |
| ATP8B1 | ATPase, aminophospholipid transporter, class I, type 8B, member 1 | 2.8767 | 0.0452 |
| TMEM170A | transmembrane protein 170A | 2.8766 | 0.0308 |
| C5orf28 | chromosome 5 open reading frame 28 | 2.8707 | 0.0392 |
| ADAMTS1 | ADAM metallopeptidase with thrombospondin type 1 motif, 1 | 2.8574 | 0.0324 |
| PDF | peptide deformylase (mitochondrial) | 2.8447 | 0.0116 |
| EIF4EBP3 | eukaryotic translation initiation factor 4E binding protein 3 | 2.8378 | 0.0228 |
| HOXB2 | homeobox B2 | 2.8245 | 0.0463 |
| PPP3CB | protein phosphatase 3, catalytic subunit, beta isoform | 2.8233 | 0.0257 |
| IRF1 | interferon regulatory factor 1 | 2.8172 | 0.0091 |
| EIF1B | eukaryotic translation initiation factor 1B | 2.8147 | 0.0297 |
| C12orf65 | chromosome 12 open reading frame 65 | 2.8113 | 0.095 |
| DDX21 | DEAD (Asp-Glu-Ala-Asp) box helicase 21 | 2.8024 | 0.0171 |
| MED30 | mediator complex subunit 30 | 2.797 | 0.0404 |
| FAM13B | family with sequence similarity 13, member B | 2.7827 | 0.0312 |
| IFI16 | interferon, gamma-inducible protein 16 | 2.7752 | 0.0239 |
| RTG1 | B-cell translocation gene 1, anti-proliferative | 2.7682 | 0.0297 |
| TNFRSF11B | tumor necrosis factor receptor superfamily, member 11b | 2.7585 | 0.0686 |
| TSC22D1 | TSC22 domain family, member 1 | 2.7584 | 0.0385 |
| CDC42EP3 | CDC42 effector protein (Rho GTPase binding) 3 | 2.7572 | 0.0129 |
| C4orf32 | chromosome 4 open reading frame 32 | 2.7538 | 0.0238 |
| KITLG | KIT ligand | 2.7518 | 0.0036 |
| MYCT1 | myc target 1 | 2.7471 | 0.0306 |
| TTC39B | tetratricopeptide repeat domain 39B | 2.7455 | 0.0709 |
| SYT7 | synaptotagmin VII | 2.7427 | 0.0076 |
| CEBPB | CCAAT/enhancer binding protein (C/EBP), beta | 2.7415 | 0.0145 |
| KCTD13 | potassium channel tetramerization domain containing 13 | 2.7412 | 0.018 |
| ZNF655 | zinc finger protein 655 | 2.7376 | 0.0389 |
| ERRF1 | ERBB receptor feedback inhibitor 1 | 2.7337 | 0.0018 |
| MID1IP1 | MID1 interacting protein 1 | 2.7287 | 0.0443 |
| MT1E | metallothionein 1E | 2.7262 | 0.0242 |
| LOC100507217 | uncharacterized LOC100507217 | 2.721 | 0.0521 |
| GADD45A | growth arrest and DNA-damage-inducible, alpha | 2.7158 | 0.0752 |
| FAM86DP | family with sequence similarity 86, member D, pseudogene | 2.7149 | 0.0063 |
| TIFA | TRAF-interacting protein with forkhead-associated domain | 2.7133 | 0.0579 |
| PHLD1A | pleckstrin homology-like domain, family A, member 1 | 2.7129 | 0.0187 |
| EPAS1 | endothelial PAS domain protein 1 | 2.7128 | 0.0007 |
| SFXN4 | sideroflexin 4 | 2.7087 | 0.0071 |
| RASSF8 | Ras association (RalGDS/AF-6) domain family (N-terminal) member 8 | 2.6903 | 0.0103 |
| DDX10 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 | 2.6792 | 0.0333 |
| THAP10 | THAP domain containing 10 | 2.6775 | 0.0108 |
| GAS5 | growth arrest-specific 5 (non-protein coding) | 2.6765 | 0.0113 |
| SARS | serine-IRNA synthetase | 2.6744 | 0.0007 |
| RAB32 | RAB32, member RAS oncogene family | 2.6708 | 0.0258 |
| PVT1 | PVT1 oncogene (non-protein coding) | 2.6654 | 0.0318 |
| ST7L | suppression of tumorigenicity 7 like | 2.6634 | 0.029 |
| WNT3 | wingless-type MMTV integration site family, member 3 | 2.6627 | 0.0226 |
| Gene        | Description                                                                 | Log2 Fold Change | p-value  |
|-------------|------------------------------------------------------------------------------|------------------|----------|
| SUGT1P1     | SUGT1 pseudogene 1                                                           | 2.662            | 0.0305   |
| EIF1        | eukaryotic translation initiation factor 1                                   | 2.6588           | 0.0163   |
| TSEN15      | TSEN15 tRNA splicing endonuclease subunit                                    | 2.6358           | 0.0161   |
| KLF11       | Kruppel-like factor 1                                                        | 2.634            | 0.0223   |
| SCN8A       | sodium channel, voltage gated, type VIII, alpha subunit                     | 2.6313           | 0.0367   |
| SPRY2       | sprouty homolog 2 (Drosophila)                                               | 2.6296           | 0.0299   |
| PRKAG1      | protein kinase, AMP-activated, gamma 1 non-catalytic subunit                 | 2.6286           | 0.0621   |
| NSMAF       | neutral sphingomyelinase (N-SMase) activation associated factor              | 2.6245           | 0.0329   |
| FAM110B     | family with sequence similarity 110, member B                               | 2.6226           | 0.0383   |
| C22orf23    | chromosome 22 open reading frame 23                                         | 2.6205           | 0.0292   |
| TARS        | threonyl-tRNA synthetase                                                     | 2.6147           | 0.0048   |
| ZNF770      | zinc finger protein 770                                                      | 2.6142           | 0.0268   |
| IDH1        | isocitrate dehydrogenase 1 (NADP+), soluble                                 | 2.6128           | 0.0045   |
| RRP15       | ribosomal RNA processing 15 homolog (S. cerevisiae)                         | 2.61              | 0.0203   |
| DLEU1       | deleted in lymphocytic leukemia 1 (non-protein coding)                      | 2.6099           | 0.0084   |
| EBF2        | early B-cell factor 2                                                        | 2.6084           | 0.014    |
| SEH1L       | SEH1-like (S. cerevisiae)                                                    | 2.6063           | 0.0159   |
| LONP1       | ion peptidase 1, mitochondrial                                              | 2.5978           | 0.0058   |
| ATF6        | activating transcription factor 6                                            | 2.5865           | 0.0177   |
| CD97        | CD97 molecule                                                                | 2.5852           | 0.0431   |
| ARHGAP26    | Rho GTase activating protein 26                                              | 2.5823           | 0.0012   |
| FGF16       | fibroblast growth factor 12                                                  | 2.5721           | 0.0592   |
| ZNF121      | zinc finger protein 121                                                      | 2.572            | 0.0647   |
| CASP3       | caspase 3, apoptosis-related cysteine peptidase                             | 2.5687           | 0.0652   |
| SH3RF1      | SH3 domain containing ring finger 1                                          | 2.5653           | 0.0159   |
| SYT13       | synaptolagmin-like 3                                                        | 2.5622           | 0.0104   |
| KCTD5       | potassium channel tetramerization domain containing 9                       | 2.5591           | 0.0474   |
| SGGAP1      | SLIT-ROBO Rho GTase activating protein 1                                     | 2.5533           | 0.0155   |
| CEP120      | centrosomal protein 120KDa                                                   | 2.5507           | 0.0463   |
| C9orf72     | chromosome 9 open reading frame 72                                           | 2.5474           | 0.0162   |
| PCF11       | PCF11 cleavage and polyadenylation factor subunit                           | 2.5438           | 0.0429   |
| HIST1H2BN   | histone cluster 1, H2bn                                                      | 2.5396           | 0.0419   |
| SERPINE1    | serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1 | 2.5377           | 0.0095   |
| FAM24B      | family with sequence similarity 24, member B                                | 2.5371           | 0.0038   |
| NPS2        | neuronal PAS domain protein 2                                                | 2.5343           | 0.0015   |
| SGCG        | sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein)               | 2.5329           | 0.0318   |
| ABCA3       | ATP-binding cassette, sub-family A (ABC1), member 3                          | 2.5304           | 0.0236   |
| ZCCHC2      | zinc finger, CCHC domain containing 2                                        | 2.5272           | 0.0427   |
| NAA38       | N(alpha)-acetyltransferase 38, NatC auxiliary subunit                        | 2.5216           | 0.0209   |
| AFAP1L1     | actin filament associated protein 1-like 1                                  | 2.5197           | 0.0127   |
| KIAA1524    | KIAA1524                                                                     | 2.5173           | 0.0537   |
| C9orf64     | chromosome 9 open reading frame 64                                           | 2.5165           | 0.0301   |
| GPCPD1      | glycophosphocholine phosphodiesterase GDE1 homolog (S. cerevisiae)          | 2.5155           | 0.0196   |
| WDFY2       | WD repeat and FYVE domain containing 2                                       | 2.515            | 0.0303   |
| H1FX        | H1 histone family, member X                                                  | 2.5103           | 0.0402   |
| YIPF4       | Yip1 domain family, member 4                                                 | 2.5069           | 0.0351   |
| SPAG1       | sperm associated antigen 1                                                   | 2.5043           | 0.0337   |
| ZC3H12C     | zinc finger CCCH-type containing 12C                                         | 2.4986           | 0.0314   |
| MAPK6       | mitogen-activated protein kinase 6                                           | 2.4973           | 0.0246   |
| TMEM116     | transmembrane protein 116                                                   | 2.4911           | 0.0302   |
| NAV3        | neuron navigator 3                                                           | 2.4878           | 0.0193   |
| AP4E1       | adaptor-related protein complex 4, epsilon 1 subunit                        | 2.484            | 0.0256   |
| ZDBF2       | zinc finger, DBF-type containing 2                                           | 2.4838           | 0.0625   |
| CDC42SE2    | CDC42 small effector 2                                                       | 2.4807           | 0.0358   |
| DYNLL2      | dynein, light chain, LC8-type 2                                              | 2.4791           | 0.0216   |
| CNNM4       | cyclin M4                                                                    | 2.4765           | 0.0049   |
| PPP1R10     | protein phosphatase 1, regulatory subunit 10                                 | 2.4773           | 0.0451   |
| MARS        | methionyl-tRNA synthetase                                                   | 2.4709           | 0.0029   |
| AIM2P2      | aminoacyl tRNA synthetase complex-interacting multifunctional protein 2      | 2.4702           | 0.0072   |
| ZXDC        | ZXD family zinc finger C                                                     | 2.4608           | 0.0236   |
| Gene | Description | Log2FoldChange | P.Value |
|------|-------------|----------------|---------|
| ZNF800 | zinc finger protein 800 | 2.4583 | 0.0291 |
| NKAPL | NFKB activating protein-like | 2.4565 | 0.0396 |
| EZH2 | enhancer of zeste 2 polycomb repressive complex 2 subunit | 2.4542 | 0.0325 |
| PSPH | phosphoserine phosphatase | 2.4529 | 0.0101 |
| RHBD1 | rhomboid domain containing 1 | 2.4527 | 0.0072 |
| CHIC2 | cysteine-rich hydrophobic domain 2 | 2.4516 | 0.0713 |
| CRNDE | colorectal neoplasia differentially expressed (non-protein coding) | 2.4497 | 0.0699 |
| JAK2 | Janus kinase 2 | 2.4488 | 0.025 |
| FIP1L1 | factor interacting with PAPOLA and CPSF1 | 2.4447 | 0.0414 |
| STK40 | serine/threonine kinase 40 | 2.4444 | 0.0172 |
| CH25H | cholesteryl 25-hydroxylase | 2.4422 | 0.0506 |
| RNF6 | ring finger protein (C3H2C3 type) 6 | 2.4401 | 0.0771 |
| C17orf51 | chromosome 17 open reading frame 51 | 2.4391 | 0.0095 |
| ANKRD27 | ankyrin repeat domain 27 (VPS9 domain) | 2.4361 | 0.0052 |
| ZNF594 | zinc finger protein 594 | 2.4335 | 0.0224 |
| BAG2 | BCL2-associated athanogene 2 | 2.4319 | 0.0183 |
| TUFT1 | tuftelin 1 | 2.4312 | 0.0431 |
| TMEM209 | transmembrane protein 209 | 2.4293 | 0.0057 |
| PDCD10 | programmed cell death 10 | 2.4285 | 0.0239 |
| FAM83G | family with sequence similarity 83, member G | 2.4263 | 0.0243 |
| PFDN2 | prefoldin subunit 2 | 2.4241 | 0.021 |
| PTP4A2 | protein tyrosine phosphatase type IVA, member 2 | 2.4222 | 0.0084 |
| ETS2 | v-ets avian erythroblastosis virus E26 oncogene homolog 2 | 2.4157 | 0.0183 |
| EIF3J | eukaryotic translation initiation factor 3, subunit J | 2.4128 | 0.0259 |
| CDK17 | cyclin-dependent kinase 17 | 2.4118 | 0.0342 |
| ALOX5AP | arachidonate 5-lipoxygenase-activating protein | 2.4099 | 0.0122 |
| C1GALT1 | core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase | 2.4087 | 0.0299 |
| DUS4L | dihydrouridine synthase 4-like (S. cerevisiae) | 2.4083 | 0.0527 |
| SLC2A3 | solute carrier family 2 (facilitated glucose transporter), member 3 | 2.4064 | 0.0398 |
| DNAJB6 | DnaJ (Hsp40) homolog, subfamily B, member 6 | 2.3992 | 0.0359 |
| C6orf211 | chromosome 6 open reading frame 211 | 2.3949 | 0.0299 |
| PPTC7 | PTC7 protein phosphatase homolog (S. cerevisiae) | 2.3944 | 0.0252 |
| HES1 | hes family bHLH transcription factor 1 | 2.3942 | 0.0414 |
| ZNF670 | zinc finger protein 670 | 2.3915 | 0.092 |
| C11orf70 | chromosome 11 open reading frame 70 | 2.3869 | 0.0444 |
| C5orf34 | chromosome 5 open reading frame 34 | 2.3798 | 0.0347 |
| CDC42BPA | CDC42 binding protein kinase alpha (DMPK-like) | 2.3784 | 0.024 |
| DNAJ3 | DnaJ (Hsp40) homolog, subfamily A, member 3 | 2.3782 | 0.0215 |
| SPRY4 | sprouty homolog 4 (Drosophila) | 2.3776 | 0.041 |
| HSPBAP1 | HSPB (heat shock 27kDa) associated protein | 2.3772 | 0.0413 |
| NTF3 | neurotrophin 3 | 2.3736 | 0.0194 |
| PRMT3 | protein arginine methyltransferase 3 | 2.3683 | 0.0229 |
| PFN2 | prefoldin subunit 6 | 2.3667 | 0.0328 |
| TRIM11 | tripartite motif containing 11 | 2.3648 | 0.0393 |
| CDYL | chromodomain protein, Y-like | 2.3622 | 0.0219 |
| AFA1P1 | actin filament associated protein 1 | 2.3611 | 0.0185 |
| RMND5A | required for meiotic nuclear division 5 homolog A (S. cerevisiae) | 2.3591 | 0.0299 |
| HCG18 | HLA complex group 18 (non-protein coding) | 2.3587 | 0.0203 |
| EPRS | glutamyl-prolyl-tRNA synthetase | 2.3585 | 0.0019 |
| HSD17B10 | hydroxysteroid (17-beta) dehydrogenase 10 | 2.3581 | 0.0118 |
| EPHA2 | EPH receptor A2 | 2.3562 | 0.0193 |
| LOC90246 | uncharacterized LOC90246 | 2.3533 | 0.0079 |
| CRIM1 | cysteine rich transmembrane BMP regulator 1 (chordin-like) | 2.3508 | 0.0184 |
| UBE2S | ubiquitin-conjugating enzyme E2S | 2.3472 | 0.0245 |
| AGPAT9 | 1-acylglycerol-3-phosphate O-acyltransferase 9 | 2.3466 | 0.0664 |
| ULBP2 | UL16 binding protein 2 | 2.345 | 0.0297 |
| STAC | SH3 and cysteine rich domain | 2.3445 | 0.0271 |
| SKIL | SKI-like proto-oncogene | 2.3421 | 0.0329 |
| CCR10 | chemokine (C-C motif) receptor 10 | 2.3405 | 0.0267 |
| PPIL4 | peptidylprolyl isomerase (cyclophilin)-like 4 | 2.3327 | 0.0538 |
| Gene | Description | Log2 Fold Change | p-value |
|------|-------------|-----------------|---------|
| MT1X | metallothionein 1X | 2.3295 | 0.045 |
| PIGA | phosphatidylinositol glycan anchor biosynthesis, class A | 2.3276 | 0.0403 |
| ADAMTS6 | ADAM metallopeptidase with thrombospondin type 1 motif, 6 | 2.3251 | 0.0161 |
| LONRF1 | origin recognition complex, subunit 6 | 2.3211 | 0.0586 |
| BCDIN3D | BCDIN3 domain containing kinase 2 | 2.3167 | 0.0227 |
| ADCK2 | adenine-rich, angiogenic inducer, 61 | 2.3139 | 0.0508 |
| CYR61 | zinc finger protein 507 | 2.311 | 0.0339 |
| PTPDC1 | protein tyrosine phosphatase domain containing 1 | 2.3085 | 0.0017 |
| SMEK2 | CEP homolog 2, suppressor of mek1 (Dictyostelium) | 2.3046 | 0.0201 |
| BIR2 | baculoviral IAP repeat containing 2 | 2.3032 | 0.0397 |
| PROSC | proline synthetase co-transcribed homolog (bacterial) | 2.2988 | 0.0263 |
| ZNF699 | BCDIN3 domain containing 2 | 2.2987 | 0.0605 |
| WD40R3 | WD repeat domain 43 | 2.2977 | 0.0189 |
| LOC344887 | LON peptidase N-terminal domain and ring finger 1 | 2.2963 | 0.0291 |
| SMEK2 | SMEK homolog 2, suppressor of mek1 (Dictyostelium) | 2.2963 | 0.0291 |
| NEK7 | NIMA-related kinase 7 | 2.2946 | 0.0278 |
| LPXN | leupaxin | 2.2911 | 0.0183 |
| MKNK2 | MAP kinase interacting serine/threonine kinase 2 | 2.2874 | 0.0504 |
| KDM6B | lysine (K)-specific demethylase 6B | 2.2874 | 0.0257 |
| SMURF2 | SMAD specific E3 ubiquitin protein ligase 2 | 2.2776 | 0.0277 |
| KDM6B | lysine (K)-specific demethylase 6B | 2.2752 | 0.0402 |
| TPBI | topoisomerase (DNA) I | 2.2748 | 0.0141 |
| SMP6 | transmembrane protein 129, E3 ubiquitin protein ligase | 2.2741 | 0.0377 |
| SETD8 | SET domain containing (lysine methyltransferase) 8 | 2.2736 | 0.0326 |
| SMARCA2 | human T-cell leukemia virus type 1 integration site 1A | 2.2719 | 0.0125 |
| XYN | xyloltransferase I | 2.2705 | 0.0125 |
| CRLF3 | cytokine receptor-like factor 3 | 2.2685 | 0.0268 |
| BMP2 | bone morphogenetic protein 2 | 2.2679 | 0.0406 |
| ZNF25 | zinc finger protein 25 | 2.2679 | 0.023 |
| SETD8 | SET domain containing (lysine methyltransferase) 8 | 2.2664 | 0.0158 |
| SLC30A1 | solute carrier family 30 (zinc transporter), member 1 | 2.2647 | 0.0236 |
| ENTP6D | echinocysteine thiolate phosphatase diphosphatohydrolase 6 (putative) | 2.2616 | 0.0111 |
| CDK13 | cyclin-dependent kinase 13 | 2.2578 | 0.0564 |
| TRIM58 | tripartite motif containing 58 | 2.2578 | 0.0536 |
| APOL6 | apolipoprotein L, 6 | 2.2567 | 0.0195 |
| MSC | musculin | 2.2554 | 0.0257 |
| IFIT2 | interferon-induced protein with tetratricopeptide repeats 2 | 2.2538 | 0.0345 |
| HMOX1 | heme oxygenase (decycling) 1 | 2.253 | 0.0301 |
| FHL2 | four and a half LIM domains 2 | 2.2529 | 0.013 |
| LOC642361 | uncharacterized LOC642361 | 2.2494 | 0.0257 |
| SRPSF3 | serine/arginine-rich splicing factor 3 | 2.2444 | 0.0529 |
| SPG2 | spastic paraplegia 20 (Troyer syndrome) | 2.2416 | 0.0496 |
| CLIP1 | CAP-GLY domain containing linker protein 1 | 2.2397 | 0.0101 |
| EFHD2 | EEF-hand domain family, member D2 | 2.239 | 0.0093 |
| TNFRSF10D | prevalent necrosis factor receptor superfamily, member 10d, decay with truncated death domain | 2.2371 | 0.0124 |
| TLK2 | toucule-like kinase 2 | 2.2357 | 0.0978 |
| LOC645166 | lymphocyte-specific protein 1 pseudogene | 2.2336 | 0.0294 |
| UBIAD1 | UbA prenyltransferase domain containing 1 | 2.2282 | 0.0093 |
| PKD1P1 | polyohytic kidney disease 1 (autosomal dominant) pseudogene 1 | 2.2276 | 0.0068 |
| SNX24 | sorting nexin 24 | 2.2261 | 0.0128 |
| Gene  | Description                                                                 | Log2 Fold Change | p-Value  |
|-------|-----------------------------------------------------------------------------|------------------|----------|
| NAMPT | nicotinamide phosphoribosyltransferase                                      | 2.2238           | 0.036    |
| SNTB1 | syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1) | 2.2155           | 0.003    |
| RBBP6 | retinoblastoma binding protein 6                                            | 2.2151           | 0.0357   |
| DTD1  | D-tyrosyl-tRNA deacylase 1                                                 | 2.215            | 0.0048   |
| NANOS1 | nanos homolog 1 (Drosophila)                                               | 2.2145           | 0.0183   |
| RRM2B | ribonucleotide reductase M2 B (TP53 inducible)                              | 2.2129           | 0.0521   |
| SLC9A1 | solute carrier family 9, subfamily A (NHE1, cation proton antiporter 1), member 1 | 2.2112           | 0.0137   |
| YARS  | tyrosyl-tRNA synthetase                                                     | 2.2093           | 0.0042   |
| USP25 | ubiquitin specific peptidase 25                                            | 2.2083           | 0.0218   |
| RAP1B | RAP1B, member of RAS oncogene family                                        | 2.2075           | 0.0242   |
| MT2A  | metallothionein 2A                                                         | 2.2055           | 0.006    |
| SLC22A4 | solute carrier family 22 (organic cation/zwitterion transporter), member 4 | 2.2049           | 0.0283   |
| FNBP4 | formin binding protein 4                                                    | 2.2047           | 0.0524   |
| PLD6  | phospholipase D family, member 6                                            | 2.2044           | 0.0714   |
| PXK   | PX domain containing serine/threonine kinase                               | 2.1989           | 0.004    |
| CBX4  | chromobox homolog 4                                                        | 2.1964           | 0.0297   |
| ARHGAP39 | Rho GTPase activating protein 39                                           | 2.196            | 0.0183   |
| TMEM47 | transmembrane protein 47                                                   | 2.1954           | 0.0247   |
| SLC4A7 | solute carrier family 4, sodium bicarbonate cotransporter, member 7       | 2.1948           | 0.0303   |
| RELB  | v-rel avian reticuloendotheliosis viral oncogene homolog B                  | 2.1943           | 0.0853   |
| GRK6  | G protein-coupled receptor kinase 6                                        | 2.1941           | 0.0579   |
| TBPX15 | T-box 15                                                                   | 2.1935           | 0.0072   |
| NARS  | asparaginyl-tRNA synthetase                                                 | 2.1895           | 0.0062   |
| FLJ46906 | uncharacterized LOC441172                                              | 2.1892           | 0.0072   |
| LOC100132891 | uncharacterized LOC100132891                                | 2.1873           | 0.0127   |
| SAE1  | SUMO1 activating enzyme subunit 1                                          | 2.1848           | 0.0181   |
| CRY1  | cryptochrome circadian clock 1                                              | 2.181            | 0.0916   |
| ERP29 | endoplasmic reticulum protein 29                                            | 2.1792           | 0.0199   |
| ARPC5L | actin related protein 2/3 complex, subunit 5-like                         | 2.1773           | 0.0292   |
| CKS1B | CDC28 protein kinase regulatory subunit 1B                                 | 2.1764           | 0.0207   |
| SLC25A25 | solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25 | 2.1745           | 0.074    |
| RMI1  | RecQ mediated genome instability 1                                         | 2.1724           | 0.0176   |
| NDC80 | NDC80 kinetochore complex component                                        | 2.1722           | 0.08     |
| TMEM128 | transmembrane protein 128                                                  | 2.1722           | 0.0297   |
| SART3 | squamous cell carcinoma antigen recognized by T cells 3                   | 2.1713           | 0.0121   |
| EIF1AX | eukaryotic translation initiation factor 1A, X-linked                      | 2.1712           | 0.0212   |
| SPC25 | SPC25, NDC80 kinetochore complex component                                  | 2.1703           | 0.066    |
| RASSF9 | Ras association (Rat1GDS/AF-6) domain family (N-terminal) member 9        | 2.1689           | 0.0175   |
| DIRC2 | disrupted in renal carcinoma 2                                             | 2.1688           | 0.0409   |
| RHEB  | Ras homolog enriched in brain                                              | 2.1668           | 0.0202   |
| FADS3 | fatty acid desaturase 3                                                   | 2.1654           | 0.0136   |
| RMND1 | required for meiotic nuclear division 1 homolog (S. cerevisiae)             | 2.1617           | 0.0177   |
| NEK10 | NIMA-related kinase 10                                                      | 2.1607           | 0.0174   |
| SPTLC1 | serine palmitoyltransferase, long chain base subunit 1                    | 2.1596           | 0.0738   |
| FBXL14 | F-box and leucine-rich repeat protein 14                                   | 2.1587           | 0.0103   |
| MAN2A1 | mannosidase, alpha, class 2A, member 1                                     | 2.1584           | 0.0431   |
| YWHAE | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon | 2.1572           | 0.0454   |
| MTRR  | 5-methyltetrahydrofolate-homocysteine methyltransferase reductase         | 2.1567           | 0.065    |
| C15orf61 | chromosome 15 open reading frame 61                                       | 2.156            | 0.0343   |
| CCDC113 | coiled-coil domain containing 113                                        | 2.1498           | 0.0148   |
| CLIP4 | CAP-GLY domain containing linker protein family, member 4                 | 2.1454           | 0.0284   |
| FST   | follistatin                                                                | 2.1426           | 0.0128   |
| SLC4A5 | solute carrier family 4 (sodium bicarbonate cotransporter), member 5      | 2.1403           | 0.0017   |
| TET3  | tet methylcytosine dioxygenase 3                                          | 2.1364           | 0.0208   |
| EEF1E1 | eukaryotic translation elongation factor 1 epsilon 1                       | 2.1361           | 0.0233   |
| HAGH  | hydroxyacylglutathione hydrolase                                           | 2.136            | 0.0159   |
| GLRX  | glutaredoxin (thioltransferase)                                            | 2.1315           | 0.0056   |
| HINT3 | histidine triad nucleotide binding protein 3                               | 2.1305           | 0.0182   |
| Gene Symbol | Description | Z score | Benjamini-corrected p value |
|-------------|-------------|---------|---------------------------|
| AARS        | alanyl-tRNA synthetase | 2.1298  | 0.0242                    |
| BRSK1       | BR serine/threonine kinase 1 | 2.1275  | 0.0475                    |
| ORM1        | ORMDL sphingolipid biosynthesis regulator 1 | 2.1261  | 0.0394                    |
| MAFK        | v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog K | 2.1259  | 0.037                     |
| KIF18A      | kinesin family member 18A | 2.1235  | 0.0394                    |
| DCLRE1A     | DNA cross-link repair 1A | 2.1207  | 0.0219                    |
| CNBP        | CCHC-type zinc finger, nucleic acid binding protein | 2.1184  | 0.0403                    |
| IL11        | interleukin 11 | 2.1174  | 0.0371                    |
| USP36       | ubiquitin specific peptidase 36 | 2.117  | 0.0149                    |
| VT11A       | vesicle transport through interaction with t-SNAREs 1A | 2.1152  | 0.0177                    |
| GLRX2       | glutaredoxin 2 | 2.1136  | 0.0357                    |
| RAD54B      | RAD54 homolog B (S. cerevisiae) | 2.1118  | 0.0833                    |
| SEC63       | SEC63 homolog (S. cerevisiae) | 2.1102  | 0.0162                    |
| CHAC2       | ChaC. cation transport regulator homolog 2 (E. coli) | 2.1101  | 0.0303                    |
| YRDC        | yrdC N(6)-threonylcarbamoyltransferase domain containing | 2.1089  | 0.0161                    |
| PNO1        | partner of NOB1 homolog (S. cerevisiae) | 2.1084  | 0.0405                    |
| NDJAF2      | NADH dehydrogenase (ubiquinone) complex I, assembly factor | 2.1046  | 0.0292                    |
| CECR2       | cat eye syndrome chromosome region, candidate 2 | 2.1045  | 0.0292                    |
| UBR4        | ubiquitin protein ligase E3 component n-recognition 4 | 2.0997  | 0.0612                    |
| ZDHHC21     | zinc finger, DHHC-type containing 21 | 2.0978  | 0.0426                    |
| TBRG1       | transforming growth factor beta regulator 1 | 2.0972  | 0.0044                    |
| MAP1B       | microtubule-associated protein 1B | 2.0967  | 0.0131                    |
| TTC17       | tetra-tricopeptide repeat domain 17 | 2.0941  | 0.0075                    |
| TXNIP       | thioredoxin interacting protein | 2.0935  | 0.0888                    |
| RPSAP52     | ribosomal protein SA pseudogene 52 | 2.0923  | 0.0755                    |
| ZNF319      | zinc finger protein 319 | 2.0914  | 0.0335                    |
| RRS1        | RRS1 ribosome biogenesis regulator homolog (S. cerevisiae) | 2.091  | 0.0049                    |
| GORAB       | golgin, RAB6-interacting | 2.0902  | 0.0349                    |
| SRGBP2      | SLIT-ROBO Rho GTPase activating protein 2 | 2.0891  | 0.0177                    |
| ZNF518B     | zinc finger protein 518B | 2.0886  | 0.0281                    |
| ESAM        | endothelial cell adhesion molecule | 2.087  | 0.0643                    |
| WBP4        | WW domain binding protein 4 | 2.087  | 0.0461                    |
| SDSL        | serine dehydratase-like | 2.0868  | 0.0384                    |
| TRIM35      | tripartite motif containing 35 | 2.0845  | 0.0027                    |
| XIAP        | X-linked inhibitor of apoptosis | 2.0811  | 0.0359                    |
| ZC3H6       | zinc finger CCCH-type containing 6 | 2.0811  | 0.0314                    |
| BBS10       | Bardet-Biedl syndrome 10 | 2.0792  | 0.0314                    |
| FKB4P4      | FK506 binding protein 4, 59kDa | 2.0775  | 0.0299                    |
| NLRP1       | NLR family, pyrin domain containing 1 | 2.0766  | 0.05                    |
| GABPB2      | GA binding protein transcription factor, beta subunit 2 | 2.0698  | 0.028                     |
| XRC2        | X-ray repair complementing defective repair in Chinese hamster cells 2 | 2.0659  | 0.0593                    |
| OTUD6B      | OTU domain containing 6B | 2.0653  | 0.0052                    |
| TPPO1       | transportin 1 | 2.063  | 0.024                     |
| PPARD       | peroxisome proliferator-activated receptor delta | 2.0617  | 0.0109                    |
| RPL39L      | ribosomal protein L39-like | 2.0612  | 0.0315                    |
| RASSF1      | Ras association (RatGDS/AF-6) domain family member 1 | 2.0605  | 0.0566                    |
| CCD82       | coiled-coil domain containing 82 | 2.0597  | 0.0254                    |
| RAB21       | RAB21, member RAS oncogene family | 2.0568  | 0.0699                    |
| TWIST2      | twist family bHLH transcription factor 2 | 2.0568  | 0.0186                    |
| GNAI1       | guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1 | 2.0561  | 0.0498                    |
| GCC1        | GRIP and coiled-coil domain containing 1 | 2.0536  | 0.0052                    |
| HAUS6       | HAUS augmin-like complex, subunit 6 | 2.0518  | 0.0081                    |
| PAWR        | PRK, apoptosis, WT1, regulator | 2.0506  | 0.0795                    |
| CHD1        | chromodomain helicase DNA binding protein 1 | 2.0505  | 0.0484                    |
| RSL24D1     | ribosomal L24 domain containing 1 | 2.0465  | 0.0112                    |
| RNFL68      | ring finger protein 16B, E3 ubiquitin protein ligase | 2.0432  | 0.0251                    |
| SOCS6       | suppressor of cytokine signaling 6 | 2.0424  | 0.0275                    |
| ZSWIM6      | zinc finger, SWIM-type containing 6 | 2.0422  | 0.0433                    |
| XPO6        | exportin 6 | 2.0418  | 0.0177                    |
| CCPG1       | cell cycle progression 1 | 2.0409  | 0.0159                    |
| COTL1       | coactosin-like F-actin binding protein 1 | 2.0399  | 0.0283                    |
| Gene Symbol | Description | Log2FoldChange | FDR |
|-------------|-------------|----------------|------|
| DKC1 | dyskeratosis congenita 1, dyskerin | 2.0391 | 0.0037 |
| CENPV | centromere protein V | 2.0348 | 0.0169 |
| DNAJB9 | DnaJ (Hsp40) homolog, subfamily B, member 9 | 2.0348 | 0.0431 |
| C10orf25 | chromosome 10 open reading frame 25 | 2.0347 | 0.0656 |
| MIF4GD | MIF4G domain containing | 2.0342 | 0.0159 |
| IER2 | immediate early response 2 | 2.0333 | 0.0224 |
| TGS1 | trimethylguanosine synthase 1 | 2.0333 | 0.0415 |
| ZNF22 | zinc finger protein 22 | 2.0307 | 0.0833 |
| SLC19A2 | solute carrier family 19 (thiamine transporter), member 2 | 2.028 | 0.0386 |
| ADNP | activity-dependent neuroprotector | 2.0348 | 0.0159 |
| DCUN1D2 | DCN1, defective in cullin neddylation 1, domain containing 2 | 2.0348 | 0.0224 |
| USP12 | ubiquitin specific peptidase 12 | 2.0265 | 0.035 |
| NOM1 | nucleolar protein with MIF4G domain 1 | 2.0218 | 0.0532 |
| DLG3 | discs, large homolog 3 (Drosophila) | 2.0213 | 0.0052 |
| FAM89A | family with sequence similarity 89, member A | 2.0181 | 0.0931 |
| SLC12A6 | solute carrier family 12 (potassium/chloride transporter), member 6 | 2.0181 | 0.0433 |
| MOAP1 | modulator of apoptosis 1 | 2.0151 | 0.0378 |
| NXX3-1 | NK3 homeobox 1 | 2.0132 | 0.0304 |
| NRI1D2 | nuclear receptor subfamily 1, group D, member 2 | 2.0128 | 0.0529 |
| HMBX1 | homeobox containing 1 | 2.0111 | 0.0242 |
| GNA13 | guanine nucleotide binding protein (G protein), alpha 13 | 2.0106 | 0.0281 |
| NOP58 | NOP58 ribonucleoprotein | 2.0099 | 0.0366 |
| SRSF10 | serine/arginine-rich splicing factor 10 | 2.0089 | 0.0821 |
| HK2 | hexokinase 2 | 2.0082 | 0.0177 |
| FLJ10038 | uncharacterized protein FLJ10038 | 2.0074 | 0.0191 |
| LOC285074 | anaphase promoting complex subunit 1 pseudogene | 2.0069 | 0.0204 |
| IGF2BP2 | insulin-like growth factor 2 mRNA binding protein 2 | 2.0059 | 0.0552 |
| SUPV3L1 | suppressor of var1, 3-like 1 (S. cerevisiae) | 2.0036 | 0.0111 |
| LRRFIP1 | leucine rich repeat (in FLII) interacting protein 1 | 2.0024 | 0.0132 |
| BTBD3 | BTB (POZ) domain containing 3 | 2.0017 | 0.022 |
| TEMEM38A | transmembrane protein 38A | -2.0001 | 0.0522 |
| FADS2 | fatty acid desaturase 2 | -2.0003 | 0.0048 |
| NDRG3 | NDRG family member 3 | -2.0007 | 0.0296 |
| KLHDC2 | kelch domain containing 2 | -2.0069 | 0.0127 |
| SCR2 | secernin 2 | -2.0087 | 0.0862 |
| TMC2 | transmembrane and tetricopeptide repeat containing 2 | -2.0095 | 0.0205 |
| NXN | nucleoredoxin | -2.0105 | 0.0103 |
| TSPAN13 | tetraspanin 13 | -2.0121 | 0.0662 |
| NFIX | nuclear factor I/X (CCAA'T'-binding transcription factor) | -2.0135 | 0.0462 |
| CNN1 | calponin 1, basic, smooth muscle | -2.0138 | 0.0062 |
| ABHD14A | abhydrolase domain containing 14A | -2.0144 | 0.0297 |
| CARD16 | caspase recruitment domain family, member 16 | -2.015 | 0.0827 |
| JPH2 | junctophilin 2 | -2.0155 | 0.0007 |
| BTD | biotinidase | -2.0156 | 0.0645 |
| ABCB7 | ATP-binding cassette, sub-family B (MDR/TAP), member 7 | -2.017 | 0.0111 |
| SPATA13 | spermatogenesis associated 13 | -2.019 | 0.0247 |
| CHAF1B | chromatin assembly factor 1, subunit B (p60) | -2.0198 | 0.0112 |
| GDF11 | growth differentiation factor 11 | -2.0207 | 0.0096 |
| KIAA0895L | KIAA0895-like | -2.0209 | 0.0209 |
| GMIP | GEM interacting protein | -2.0225 | 0.0074 |
| MMRN2 | multimerin 2 | -2.0225 | 0.003 |
| FN1 | fibronectin 1 | -2.0239 | 0.0372 |
| GCHHR | GTP cyclohydrolase I feedback regulator | -2.025 | 0.0336 |
| ADD1 | adducin 1 (alpha) | -2.0261 | 0.0312 |
| ANK3 | ankyrin 3, node of Ranvier (ankyrin G) | -2.0268 | 0.0367 |
| ACAD10 | acyl-CoA dehydrogenase family, member 10 | -2.0278 | 0.0535 |
| GAB1 | GRB2-associated binding protein 1 | -2.0285 | 0.0662 |
| TRIM3 | tripartite motif containing 3 | -2.0287 | 0.0441 |
| GLIS2 | GLIS family zinc finger 2 | -2.0305 | 0.0505 |
| SH3BP5 | SH3-domain binding protein 5 (BTK-associated) | -2.0317 | 0.0292 |
| NRM | nurin (nuclear envelope membrane protein) | -2.0318 | 0.0653 |
| C2orf27A | chromosome 2 open reading frame 27A | -2.0331 | 0.0356 |
| Gene          | Description                                                      | Log2 Ratio | p-value |
|--------------|------------------------------------------------------------------|------------|---------|
| FAM127A      | family with sequence similarity 127, member A                    | -2.0387    | 0.0658  |
| AKR1A1       | aldo-keto reductase family 1, member A1 (aldehyde reductase)     | -2.0394    | 0.0467  |
| DNAJC22      | DnaJ (Hsp40) homolog, subfamily C, member 22                     | -2.0406    | 0.0111  |
| CHKB         | choline kinase beta                                              | -2.0446    | 0.0054  |
| FBXO3        | F-box protein 3                                                  | -2.0505    | 0.0654  |
| BDH2         | 3-hydroxybutyrate dehydrogenase, type 2                          | -2.0564    | 0.0244  |
| SELO         | selenoprotein O                                                  | -2.058     | 0.0319  |
| ARHGAP31     | Rho GTPase activating protein 31                                 | -2.0593    | 0.0643  |
| GALNT11      | polypeptide N-acetylgalactosaminyltransferase 11                 | -2.0612    | 0.0206  |
| AP4M1        | adaptor-related protein complex 4, mu 1 subunit                  | -2.0613    | 0.083   |
| DALRD3       | DALR anticodon binding domain containing 3                       | -2.0617    | 0.0321  |
| MMP24        | matrix metallopeptidase 24 (membrane-inserted)                   | -2.0617    | 0.0189  |
| BEX1         | brain expressed, X-linked 1                                      | -2.0637    | 0.0132  |
| FAM171B      | family with sequence similarity 171, member B                    | -2.0641    | 0.0257  |
| SGSM2        | small G protein signaling modulator 2                            | -2.0648    | 0.0445  |
| ZNF423       | zinc finger protein 42                                            | -2.0665    | 0.0405  |
| HSPB2        | heat shock 27kDa protein 2                                        | -2.0684    | 0.0639  |
| ZNF821       | zinc finger protein 82                                            | -2.0724    | 0.0562  |
| CLN5         | ceroid-lipofuscinosis, neuronal 5                                | -2.0741    | 0.0223  |
| FLT3LG       | fms-related tyrosine kinase 3 ligand                             | -2.08      | 0.066   |
| MEX3A        | mex-3 RNA binding family member A                                | -2.0814    | 0.0032  |
| PPAP2B       | phosphatidic acid phosphatase type 2B                            | -2.085     | 0.0789  |
| ENC1         | ectodermal-neural cortex 1 (with BTB domain)                     | -2.0852    | 0.0551  |
| SAMM50       | SAMM50 sorting and assembly machinery component                  | -2.0862    | 0.0285  |
| PLXDC2       | plexin domain containing 2                                       | -2.0865    | 0.0268  |
| FAM167B      | family with sequence similarity 167, member B                    | -2.0877    | 0.0053  |
| ZNF226       | zinc finger protein 22                                            | -2.0892    | 0.0122  |
| PPAPDC1B     | phosphatidic acid phosphatase type 2 domain containing 1B         | -2.0896    | 0.0118  |
| ATG4A        | autophagy related 4A, cysteine peptidase                         | -2.0905    | 0.029   |
| CARD6        | caspase recruitment domain family, member 6                      | -2.0911    | 0.0072  |
| FAM109B      | family with sequence similarity 109, member B                    | -2.0917    | 0.0291  |
| NAP1L3       | nucleosome assembly protein 1-like 3                             | -2.0924    | 0.0484  |
| CDKNA2A      | cyclin-dependent kinase inhibitor 2A                             | -2.0932    | 0.023   |
| RNF122       | ring finger protein 12                                            | -2.0943    | 0.0183  |
| ITGA8        | integrin, alpha 8                                                | -2.0946    | 0.0025  |
| PRUNE2       | prune homolog 2 (Drosophila)                                     | -2.0956    | 0.0247  |
| ADAM19       | ADAM metalloproteinase domain 19                                 | -2.0985    | 0.0307  |
| CD9          | CD9 molecule                                                     | -2.099     | 0.0477  |
| PAICS        | phosphoribosylaminomimidazole carboxylase,                      | -2.0999    | 0.0263  |
|             | phosphoribosylaminomimidazole succinocarboxamide synthetase      |            |         |
| KIAA1377     | KIAA1377                                                         | -2.1013    | 0.0276  |
| SYNC         | syncoilin, intermediate filament protein                          | -2.1034    | 0.024   |
| LOXL1        | lysyl oxidase-like 1                                             | -2.1038    | 0.0689  |
| C17orf62     | chromosome 17 open reading frame 62                              | -2.1051    | 0.0414  |
| PTGER2       | prostaglandin E receptor 2 (subtype EP2), 53kDa                  | -2.1097    | 0.0006  |
| PTOV1        | prostate tumor overexpressed 1                                  | -2.1103    | 0.0328  |
| ADAM12       | ADAM metalloproteinase domain 12                                 | -2.1109    | 0.0114  |
| RXFP1        | relaxin/insulin-like family peptide receptor 1                   | -2.113     | 0.0079  |
| LPPR2        | lipid phosphate phosphatase-related protein type 2               | -2.1153    | 0.0458  |
| KCN4         | potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4 | -2.1163 | 0.0074 |
| AGT          | angiotensinogen (serpin peptidase inhibitor, clade A, member 8) | -2.1168 | 0.0137 |
| BAMB1        | BMP and activin membrane-bound inhibitor                        | -2.1191    | 0.0172  |
| CYB561D2     | cytochrome b561 family, member D2                                | -2.1208    | 0.028   |
| SERPINH1     | serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1) | -2.1216 | 0.0623 |
| STAT6        | signal transducer and activator of transcription 6, interleukin-4 induced | -2.1227 | 0.0174 |
| BNC2         | basonuclin 2                                                     | -2.1261    | 0.0496  |
| NPR3         | natriuretic peptide receptor 3                                  | -2.1289    | 0.0955  |
| SIDT2        | SID1 transmembrane family, member 2                              | -2.1302    | 0.0291  |
| PDLIM1       | PDZ and LIM domain 1                                             | -2.1308    | 0.057   |
| GLT8D2       | glycosyltransferase 8 domain containing 2                        | -2.1338    | 0.0321  |
| Gene Symbol | Description                                                                 | Fold Change | p-Value  |
|-------------|-----------------------------------------------------------------------------|-------------|----------|
| PLEKHG2     | pleckstrin homology domain containing, family G (with RhoGef domain) member 2 | -2.1345     | 0.0218   |
| C1orf132    | chromosome 14 open reading frame 132                                        | -2.1384     | 0.0496   |
| BTG2        | BTG family, member 2                                                         | -2.1385     | 0.0075   |
| VANGL2      | VANGL planar cell polarity protein 2                                         | -2.1394     | 0.0289   |
| TMEM173     | transmembrane protein 173                                                   | -2.1401     | 0.0398   |
| NIPAL1      | NIPA-like domain containing 1                                                | -2.1419     | 0.013    |
| FAM20C      | family with sequence similarity 20, member C                                 | -2.142      | 0.0961   |
| IGF2        | insulin-like growth factor 2 (somatomedin A)                                | -2.1441     | 0.0569   |
| TKT         | transketolase                                                               | -2.1453     | 0.029    |
| SNTA1       | syntrophin, alpha 1                                                          | -2.149      | 0.0074   |
| FRMD3       | FERM domain containing 3                                                    | -2.1504     | 0.0032   |
| GSDMD       | gasdermin D                                                                 | -2.1533     | 0.0372   |
| ADAMTS12    | ADAM metalloepidase with thrombospondin type 1 motif, 12                     | -2.1536     | 0.0367   |
| NXPH3       | neurexophilin 3                                                             | -2.1536     | 0.0007   |
| SH3D19      | SH3 domain containing 1                                                      | -2.1555     | 0.0072   |
| SHROOM3     | shroom family member 3                                                       | -2.1589     | 0.0638   |
| ANTXR1      | anthrax toxin receptor 1                                                     | -2.161      | 0.0419   |
| SGSH        | N-sulfogalactosamine sulfohydrolase                                         | -2.1611     | 0.0391   |
| UAP1L1      | UDP-N-acetylgalactosamine pyrophosphorylase 1 like 1                         | -2.1636     | 0.0079   |
| TNR5F21     | tumor necrosis factor receptor superfamily, member 21                        | -2.1648     | 0.0327   |
| TM4SF1      | transmembrane 4 L six family member 1                                        | -2.1666     | 0.0125   |
| MGAT4B      | mannosyl (alpha-1,3,4)-glucosamine beta-1,N-acetylgalactosaminyltransferase, isozyme B | -2.1667 | 0.0459 |
| KDELR3      | KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3    | -2.1669     | 0.0146   |
| IFI35       | interferon-induced protein 3                                                 | -2.1708     | 0.0902   |
| REEP2       | receptor accessory protein 2                                                 | -2.1722     | 0.0111   |
| HIC1        | hypermethylated in cancer 1                                                  | -2.1748     | 0.0943   |
| ITPKB       | inositol-trisphosphate 3-kinase B                                           | -2.1783     | 0.0007   |
| ZNF154      | zinc finger protein 154                                                      | -2.1804     | 0.0433   |
| EHMT2       | euchromatic histone-lysine N-methyltransferase 2                            | -2.1817     | 0.0437   |
| MR1         | major histocompatibility complex, class I-related                           | -2.1834     | 0.0084   |
| KAZALD1     | Kazal-type serine peptidase inhibitor domain 1                              | -2.1836     | 0.0248   |
| KCTD8       | potassium channel tetramerization domain containing 8                       | -2.1857     | 0.0221   |
| EVL         | Enah/Vasp-like                                                              | -2.1867     | 0.0242   |
| SCAND1      | SCAN domain containing 1                                                     | -2.187      | 0.018    |
| GSN         | gelsolin                                                                   | -2.1922     | 0.0048   |
| ABHD5       | abhydrolase domain containing 5                                              | -2.1936     | 0.0382   |
| LR3P3       | low density lipoprotein receptor-related protein 3                           | -2.1945     | 0.0371   |
| PARP4       | poly (ADP-ribose) polymerase family, member 4                               | -2.1952     | 0.0613   |
| GALT        | galactose-1-phosphate uridylyltransferase                                   | -2.1973     | 0.035    |
| C1QTNF1     | C1q and tumor necrosis factor related protein 1                             | -2.1981     | 0.0773   |
| MAST4       | microtubule associated serine/threonine kinase family member 4              | -2.2003     | 0.0224   |
| GPRC5C      | G protein-coupled receptor, class C, group 5, member C                       | -2.2008     | 0.0223   |
| SLIT3       | slit homolog 3 (Drosophila)                                                  | -2.2021     | 0.0379   |
| CTSK        | cathepsin K                                                                 | -2.2028     | 0.0025   |
| LR4P4       | low density lipoprotein receptor-related protein 4                           | -2.2036     | 0.0004   |
| VW5A5       | von Willebrand factor A domain containing 5A                                | -2.2055     | 0.0382   |
| BST2        | bone marrow stromal cell antigen 2                                           | -2.2064     | 0.0506   |
| SNRP4       | small nuclear ribonucleoprotein polyprotein A                               | -2.2108     | 0.0215   |
| HYAL2       | hyaluronoglucosaminidase 2                                                   | -2.2136     | 0.017    |
| SPR         | sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase)            | -2.2182     | 0.0413   |
| WDR18       | WD repeat domain 18                                                          | -2.2199     | 0.0729   |
| FZD1        | frizzled class receptor 1                                                    | -2.2214     | 0.0125   |
| PBXIP1      | pre-B-cell leukemia homeobox interacting protein 1                           | -2.2229     | 0.0294   |
| AHNAK2      | AHNAK nucleoprotein 2                                                        | -2.2248     | 0.0795   |
| BPHL        | biphenyl hydrolase-like (serine hydrolase)                                  | -2.2249     | 0.0807   |
| TPST1       | tyrosylprotein sulfotransferase 1                                            | -2.2272     | 0.0186   |
| PBX1        | pre-B-cell leukemia homeobox 1                                               | -2.2274     | 0.0489   |
| LLGL1       | lethal giant larvae homolog 1 (Drosophila)                                   | -2.2283     | 0.045    |
| TRAK1       | trafficking protein, kinesin binding 1                                       | -2.2312     | 0.0277   |
| MDGA1       | MAM domain containing glycosylophosphatidylinositol anchor 1                | -2.2325     | 0.0221   |
| Gene     | Description                                      | Log2 Fold Change | p-value   |
|----------|--------------------------------------------------|------------------|-----------|
| GALK1    | galactokinase 1                                 | -2.235           | 0.0281    |
| RTLE1    | regulator of telomere elongation helicase 1     | -2.2415          | 0.0172    |
| ARHGEF40 | Rho guanine nucleotide exchange factor (GEF) 40  | -2.2464          | 0.0452    |
| PLXND1   | plexin D1                                       | -2.2497          | 0.0498    |
| KIAA1462 | KIAA1462                                        | -2.2518          | 0.0234    |
| SNED1    | sushi, nidogen and EGF-like domains 1            | -2.2529          | 0.0667    |
| APOL1    | apolipoprotein L, 1                             | -2.2531          | 0.0692    |
| CLSTN3   | calystenin 3                                    | -2.255            | 0.0065    |
| TUBG2    | tubulin, gamma 2                                | -2.2555          | 0.0252    |
| GYG2     | glycogenin 2                                    | -2.256           | 0.0141    |
| TMEM119  | transmembrane protein 119                       | -2.2562          | 0.0072    |
| SCFD2    | sec1 family domain containing 2                 | -2.2607          | 0.0555    |
| HMCN1    | hemicentin 1                                    | -2.2612          | 0.0108    |
| STK38L   | serine/threonine kinase 38 like                 | -2.2629          | 0.0142    |
| PCYOX1   | prenylcysteine oxidase 1                        | -2.2637          | 0.0318    |
| MFSD3    | major facilitator superfamily domain containing 3| -2.2685          | 0.0134    |
| POSTN    | peristin, osteoblast specific factor             | -2.2686          | 0.0038    |
| NACAD    | NAC alpha domain containing                     | -2.2707          | 0.0116    |
| GALNT1   | polypeptide N-acetylgalactosaminyltransferase 1  | -2.2719          | 0.009     |
| PLCD3    | phospholipase C, delta 3                        | -2.2729          | 0.0732    |
| GSTA4    | glutathione S-transferase alpha 4               | -2.2734          | 0.0247    |
| KCNK15   | potassium channel, subfamily K, member 15       | -2.2747          | 0.0085    |
| QARS     | glutamyl-ribosome synthetase                    | -2.2748          | 0.0533    |
| ENDOD1   | endonuclease domain containing 1                | -2.2781          | 0.0341    |
| SH3BP1   | SH3-domain binding protein 1                    | -2.2789          | 0.0413    |
| HTR2B    | 5-hydroxytryptamine (serotonin) receptor 2B, G protein-coupled | -2.2843 | 0.0075    |
| CAPN5    | calpain 5                                       | -2.2874          | 0.0655    |
| PTG1     | pituitary tumor-transforming 1                  | -2.2885          | 0.0132    |
| FAM127C  | family with sequence similarity 127, member C   | -2.2896          | 0.0443    |
| USP35    | ubiquitin specific peptidase 35                 | -2.2899          | 0.061     |
| B3GALT4  | UDP-Gal:betaGlcNAc beta 1.3-galactosyltransferase, polypeptide 4 | -2.2901 | 0.0053    |
| SH3PXD2A | SH3 and PX domains 2A                           | -2.2911          | 0.0563    |
| ADA      | adenosine deaminase                             | -2.2943          | 0.033     |
| GALM     | galactose mutarotase (aldose 1-epimerase)       | -2.2946          | 0.0429    |
| PCSK7    | proprotein convertase subtilisin/kexin type 7   | -2.295           | 0.0183    |
| ACSF2    | acyl-CoA synthetase family member 2             | -2.2965          | 0.0235    |
| C19orf10 | chromosome 19 open reading frame 10            | -2.2975          | 0.0318    |
| MYL6     | myosin, light chain 6, alkali, smooth muscle and non-muscle | -2.2981 | 0.0256    |
| TANC1    | tetrapeptide repeat, ankyrin repeat and coiled-coil containing 1 | -2.2991 | 0.0374    |
| TEMOBB   | transmembrane protein 8B                        | -2.3028          | 0.0524    |
| ZC3H12A  | zinc finger CCCH-type containing 12A            | -2.3073          | 0.034     |
| LGR4     | leucine-rich repeat containing G protein-coupled receptor 4 | -2.3078 | 0.0519    |
| EFN3B    | ephrin-B3                                       | -2.3125          | 0.0018    |
| LYPD1    | LY6/PLAUR domain containing 1                   | -2.3144          | 0.0159    |
| RARB     | retinoic acid receptor, beta                    | -2.3148          | 0.0851    |
| FMO4     | flavin containing monoxygenase 4                | -2.3156          | 0.0013    |
| ST6GAL1  | ST6 beta-galactosamine alpha-2,6-sialyltransferase 1 | -2.3206 | 0.0294    |
| CARHSP1  | calcium regulated heat stable protein 1, 24kDa  | -2.3241          | 0.0724    |
| SLC17A5  | solute carrier family 17 (acidic sugar transporter), member 5 | -2.3313 | 0.0223    |
| CCDC102B | coiled-coil domain containing 102B              | -2.3333          | 0.0097    |
| ZNF414   | zinc finger protein 414                         | -2.3342          | 0.054     |
| MAP3K8   | mitogen-activated protein kinase kinase kinase 8| -2.3349          | 0.0055    |
| AKR1C3   | aldo-keto reductase family 1, member C          | -2.339           | 0.0454    |
| PAPSS1   | 3'-phosphoadenosine 5'-phosphosulfate synthase 1| -2.3411          | 0.0172    |
| PCDH10   | protocadherin 10                               | -2.3418          | 0.0125    |
| LIPH     | lipase, member H                                | -2.3452          | 0.0597    |
| DDAH2    | dimethylarginine dimethylaminohydrolase 2       | -2.3503          | 0.0196    |
| COMTD1   | catechol-O-methyltransferase domain containing 1| -2.3506          | 0.0456    |
| KPTN     | kaptin (actin binding protein)                  | -2.3512          | 0.0292    |
| ADAMTS2  | ADAM metallopeptidase with thrombospondin type 1 motif, 2 | -2.3537 | 0.0318    |
| TARBP2   | TAR (HIV-1) RNA binding protein 2               | -2.3565          | 0.0278    |
| P4HA3    | prolyl 4-hydroxylase, alpha polypeptide III     | -2.3575          | 0.0312    |
| Gene Name  | Description                                      | Log2 Fold Change | p-value  |
|-----------|--------------------------------------------------|-----------------|----------|
| ST3GAL4   | ST3 beta-galactoside alpha-2,3-sialyltransferase 4 | -2.3578         | 0.0483   |
| PCDHB14   | protocadherin beta 14                            | -2.3586         | 0.0041   |
| DEPTOR    | DEP domain containing MTOR-interacting protein   | -2.3588         | 0.0086   |
| GPR158    | G protein-coupled receptor 158                   | -2.3626         | 0.0105   |
| MCEE      | methylmalonyl CoA epimerase                      | -2.3652         | 0.0297   |
| FANCL     | Fanconi anemia, complementation group L          | -2.3724         | 0.0829   |
| MTMR11    | myotubularin related protein 11                  | -2.3798         | 0.0664   |
| SUSD5     | sushi domain containing 5                        | -2.381          | 0.0116   |
| CCL26     | chemokine (C-C motif) ligand 26                  | -2.3816         | 0.0492   |
| UNC5C     | unc-5 homolog C (C. elegans)                    | -2.3864         | 0.0047   |
| MYH10     | myosin, heavy chain 10, non-muscle               | -2.3886         | 0.0245   |
| SLC16A12  | solute carrier family 16, member 12              | -2.3891         | 0.0229   |
| LRRC16A   | leucine rich repeat containing 16A               | -2.39           | 0.0694   |
| SYNM      | synemin, intermediate filament protein            | -2.3902         | 0.0502   |
| NTHL1     | nth endonuclease III-like 1 (E. coli)            | -2.3909         | 0.0845   |
| ABCA6     | ATP-binding cassette, sub-family A (ABC1), member 6 | -2.393         | 0.0279   |
| SAMD14    | sterile alpha motif domain containing 14         | -2.3933         | 0.0356   |
| TUBA4A    | tubulin, alpha 4a                                | -2.4049         | 0.0551   |
| SCD5      | stearoyl-CoA desaturase 5                        | -2.407          | 0.0224   |
| C1R       | complement component 1, r subcomponent           | -2.4078         | 0.0153   |
| B3GNT9    | UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9 | -2.4088     | 0.0189   |
| TBC1D16   | TBC1 domain family, member 16                    | -2.4116         | 0.0401   |
| AXIN2     | axin 2                                           | -2.4137         | 0.0268   |
| VAMP1     | vesicle-associated membrane protein 1 (synaptobrevin 1) | -2.4184     | 0.0106   |
| CXCL6     | chemokine (C-X-C motif) ligand 6                 | -2.4211         | 0.037    |
| ZNF503    | zinc finger protein 503                          | -2.4216         | 0.0073   |
| B9D1      | B9 protein domain 1                              | -2.4233         | 0.0442   |
| KIAA1161  | KIAA1161                                         | -2.4244         | 0.0006   |
| ACE2      | angiotensin I converting enzyme 2                | -2.4246         | 0.0052   |
| MYO1E     | myosin I E                                      | -2.4283         | 0.0353   |
| ARHGAP18  | Rho GTPase activating protein 18                 | -2.431          | 0.006    |
| RILP      | Rab interacting lysosomal protein                | -2.4386         | 0.0106   |
| ACTB      | actin, beta                                      | -2.4405         | 0.0291   |
| FAM168A   | family with sequence similarity 168, member A    | -2.4416         | 0.0349   |
| OCEL1     | occludin/ELL domain containing 1                 | -2.4421         | 0.0161   |
| PTGES     | prostaglandin E synthase                         | -2.4435         | 0.0792   |
| HRNRPA1P10| heterogeneous nuclear ribonucleoprotein A1 pseudogene 10 | -2.446       | 0.0393   |
| BBS9      | Bardet-Biedl syndrome 9                          | -2.4485         | 0.0051   |
| UBA1      | ubiquitin-like modifier activating enzyme 1      | -2.4512         | 0.0845   |
| CCDC69    | coiled-coil domain containing 69                 | -2.4522         | 0.0098   |
| CKB       | creatine kinase, brain                           | -2.4523         | 0.0084   |
| PIAS2     | protein inhibitor of activated STAT, 2           | -2.4587         | 0.0918   |
| POLR2A    | polymerase (RNA) II (DNA directed) polypeptide A, 220kDa | -2.4622     | 0.0128   |
| ARAP1     | ArtGAP with RhoGAP domain, ankyrin repeat and PH domain 1 | -2.4631   | 0.0824   |
| SARDH     | sarcosine dehydrogenase                          | -2.4634         | 0.0487   |
| LIG1      | ligase I, DNA, ATP-dependent                     | -2.4638         | 0.0284   |
| EPS8L2    | EPS8-like 2                                      | -2.4645         | 0.0521   |
| PDLIM7    | PDZ and LIM domain 7 (enigma)                    | -2.4646         | 0.0413   |
| DSEL      | dermatan sulfate epimerase-like                  | -2.466          | 0.0048   |
| PRKAR1A   | protein kinase, cAMP-dependent, regulatory, type I, alpha | -2.4668  | 0.0213   |
| KCNK6     | potassium channel, subfamily K, member 6         | -2.4693         | 0.0712   |
| NAT6      | N-acetyltransferase 6 (GCN5-related)             | -2.4731         | 0.0199   |
| RECK      | reversion-inducing-cysteine-rich protein with kazal motifs | -2.4775    | 0.0183   |
| ACOX2     | acyl-CoA oxidase 2, branched chain               | -2.4821         | 0.0528   |
| PLD2      | phospholipase D2                                 | -2.4855         | 0.0423   |
| TMEM37    | transmembrane protein 37                         | -2.4858         | 0.0041   |
| SUPT5H    | suppressor of Ty 5 homolog (S. cerevisiae)       | -2.4869         | 0.0387   |
| HSPB1     | heat shock 27kDa protein 1                       | -2.4887         | 0.0324   |
| F10       | coagulation factor X                             | -2.4905         | 0.0137   |
| NDUFB9    | NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa | -2.4911    | 0.0511   |
| POLD1     | polymerase (DNA directed), delta 1, catalytic subunit | -2.5061   | 0.0461   |
| DAAM2     | dishevelled associated activator of morphogenesis 2 | -2.5071    | 0.0164   |
| Gene | Description | Log2 Fold Change | p-value |
|------|-------------|-----------------|---------|
| LEPR2 | leprecan-like 2 | -2.5113 | 0.034 |
| OSBPL7 | oxysterol binding protein-like 7 | -2.512 | 0.0084 |
| OBSL1 | obscurin-like 1 | -2.5134 | 0.0321 |
| SECTM1 | secreted and transmembrane 1 | -2.5165 | 0.0627 |
| KCNJ8 | potassium inwardly-rectifying channel, subfamily J, member 8 | -2.517 | 0.0343 |
| FAM180A | family with sequence similarity 180, member A | -2.5235 | 0.055 |
| MXR5 | matrix-remodelling associated 5 | -2.5247 | 0.0094 |
| RAC3 | ras-related C3 botulinum toxin substrate 3 (rho family, small GTP binding protein Rac3) | -2.5247 | 0.0355 |
| VASH1 | vasoedin 1 | -2.5253 | 0.0956 |
| KIF20A | kinesin family member 20A | -2.5266 | 0.0277 |
| PGBD3 | piggyBac transposable element derived 3 | -2.5312 | 0.0697 |
| MXD4 | MAX dimerization protein 4 | -2.5335 | 0.0254 |
| HIBCH | 3-hydroxyisobutyryl-CoA hydrolase | -2.536 | 0.023 |
| CASB | carbonic anhydrase VB, mitochondrial | -2.5366 | 0.0036 |
| ABCA7 | ATP-binding cassette, sub-family A (ABC1), member 7 | -2.5375 | 0.02 |
| PHTF1 | putative homeodomain transcription factor 1 | -2.5508 | 0.0453 |
| PKIG | protein kinase (cAMP-dependent, catalytic) inhibitor gamma | -2.5532 | 0.0474 |
| NICAL2 | NICAL-like 2 | -2.5541 | 0.0719 |
| EEF2K | eukaryotic elongation factor-2 kinase | -2.5589 | 0.0624 |
| OSR1 | odd-skipped related transcription factor 1 | -2.5619 | 0.0406 |
| IL11RA | interleukin 11 receptor, alpha | -2.564 | 0.0496 |
| PRRT3 | proline-rich transmembrane protein 3 | -2.568 | 0.036 |
| ZBTB4 | zinc finger and BTB domain containing 4 | -2.583 | 0.0297 |
| C1orf54 | chromosome 1 open reading frame 54 | -2.587 | 0.0019 |
| TYMS | thymidylate synthetase | -2.5898 | 0.0076 |
| STAT4 | signal transducer and activator of transcription 4 | -2.5926 | 0.0114 |
| CCDC8 | coiled-coil domain containing 8 | -2.5929 | 0.0249 |
| SUOX | sulfite oxidase | -2.6005 | 0.0548 |
| TEAD2 | TEA domain family member 2 | -2.6019 | 0.0107 |
| SLC2A13 | solute carrier family 2 (facilitated glucose transporter), member 13 | -2.6058 | 0.0078 |
| TRAF5 | TNF receptor-associated factor 5 | -2.6068 | 0.0707 |
| STAT1 | signal transducer and activator of transcription 1, 91kDa | -2.6109 | 0.003 |
| ARHGGEF37 | Rho guanine nucleotide exchange factor (GEF) 37 | -2.6119 | 0.0068 |
| CLEC3B | C-type lectin domain family 3, member B | -2.6128 | 0.003 |
| STON1 | stonin 1 | -2.6163 | 0.0204 |
| SLC7A8 | solute carrier family 7 (amino acid transporter light chain, L system), member 8 | -2.6171 | 0.0021 |
| TUBA1A | tubulin, alpha 1a | -2.6185 | 0.0203 |
| MPZL1 | myelin protein zero-like 1 | -2.6235 | 0.0432 |
| TSPAN9 | tetratraspanin 9 | -2.6265 | 0.0085 |
| FNIP2 | folliculin interacting protein 2 | -2.6325 | 0.0622 |
| BAII | brain-specific angiogenesis inhibitor 2 | -2.6341 | 0.0345 |
| ARM9 | armadillo repeat containing 9 | -2.6348 | 0.0291 |
| MAN1C1 | mannosidase, alpha, class 1C, member 1 | -2.6353 | 0.0036 |
| HSPB7 | heat shock 27kDa protein family, member 7 (cardiovascular) | -2.6361 | 0.0131 |
| GDF5 | growth differentiation factor 5 | -2.6365 | 0.0739 |
| COL27A1 | collagen, type XXVII, alpha 1 | -2.6372 | 0.0091 |
| RCAN2 | regulator of calcineurin 2 | -2.639 | 0.0057 |
| NEM2 | naked cuticle homolog 2 (Drosophila) | -2.6477 | 0.0296 |
| ANX3 | annexin A6 | -2.6515 | 0.0297 |
| NT5DC1 | 5'-nucleotidase domain containing 1 | -2.6535 | 0.0242 |
| MAP4K3 | mitogen-activated protein kinase kinase kinase 3 | -2.6535 | 0.0423 |
| ST3GA6 | ST3 beta-galactosidase alpha-2,3-sialyltransferase 6 | -2.669 | 0.0197 |
| SF3A2 | splicing factor 3a, subunit 2, 66kDa | -2.6754 | 0.0265 |
| SETMAR | SET domain and mariner transposase fusion gene | -2.6801 | 0.0324 |
| B4GALT4 | beta-1,4-N-acetylgalactosaminyl transferase 4 | -2.6848 | 0.0276 |
| ACAP3 | ArfGAP with coiled-coil, ankyrin repeat and PH domains 3 | -2.6928 | 0.0169 |
| CDK2N2 | cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4) | -2.694 | 0.0104 |
| NEAT1 | nuclear paraspeckle assembly transcript 1 (non-protein coding) | -2.7007 | 0.01 |
| CDH6 | cadherin 6, type 2, K-cadherin (fetal kidney) | -2.7013 | 0.0075 |
| CNP14 | canopy FGF signaling regulator 4 | -2.7031 | 0.0172 |
| MAP3K6 | mitogen-activated protein kinase kinase kinase 6 | -2.7066 | 0.0414 |
| Gene Symbol | Description | Log2 Fold Change | P-value |
|-------------|-------------|-----------------|---------|
| SMO         | smoothened, frizzled class receptor | -2.7194 | 0.0219 |
| ARHGEF1     | Rho guanine nucleotide exchange factor (GEF) 1 | -2.7217 | 0.0593 |
| FZD2        | frizzled class receptor 2 | -2.7279 | 0.0344 |
| ZCCHC24     | zinc finger, CCHC domain containing 24 | -2.7279 | 0.0562 |
| CTHRC1      | collagen triple helix repeat containing 1 | -2.7281 | 0.0407 |
| GNG2        | guanine nucleotide binding protein (G protein), gamma 2 | -2.7302 | 0.0395 |
| ASH2L       | ash2 (absent, small, or homeotic)-like (Drosophila) | -2.731 | 0.0333 |
| FAM114A1    | family with sequence similarity 114, member A1 | -2.7349 | 0.0312 |
| TRO         | trophin | -2.742 | 0.0311 |
| SMARC3      | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3 | -2.7439 | 0.0482 |
| KCTD12      | potassium channel tetramerization domain containing 12 | -2.7451 | 0.0107 |
| MARCKS1L    | MARCKS-like 1 | -2.7456 | 0.0326 |
| FURIN       | furin (paired basic amino acid cleaving enzyme) | -2.7495 | 0.0052 |
| ARHGAP28    | Rho GTPase activating protein 28 | -2.7525 | 0.009 |
| C1orf85     | chromosome 1 open reading frame 85 | -2.7556 | 0.0277 |
| IGFBP5      | insulin-like growth factor binding protein 5 | -2.7562 | 0.0127 |
| HEY2        | hes-related family bHLH transcription factor with YRPW motif 2 | -2.7615 | 0.0083 |
| CLN3        | ceroid-lipofuscinosis, neuronal 3 | -2.7629 | 0.0468 |
| SLC9A9      | solute carrier family 9, subfamily A (NHE9, cation proton antiporter 9), member 9 | -2.764 | 0.0006 |
| PCDH18      | protocadherin 18 | -2.7657 | 0.0647 |
| PTPLAD2     | protein tyrosine phosphatase-like A domain containing 2 | -2.7717 | 0.0113 |
| FBLN1       | fibulin 1 | -2.7735 | 0.02 |
| ACAT2       | acetyl-CoA acetyltransferase 2 | -2.7753 | 0.0084 |
| ALDH1A3     | aldehyde dehydrogenase 1 family, member A3 | -2.778 | 0.0159 |
| F11R        | F11 receptor | -2.7806 | 0.0033 |
| ANO1        | anoctamin 1, calcium activated chloride channel | -2.793 | 0.0405 |
| MTUS1       | microtubule associated tumor suppressor 1 | -2.7939 | 0.0032 |
| PNMAL1      | paraneoplastic Ma antigen family-like 1 | -2.7939 | 0.0052 |
| CHPF2       | chondroitin polymerizing factor 2 | -2.7955 | 0.0425 |
| TOMM40L     | translocase of outer mitochondrial membrane 40 homolog (yeast)-like | -2.8071 | 0.0215 |
| SLC12A2     | solute carrier family 12 (sodium/potassium/chloride transporter), member 2 | -2.8109 | 0.0011 |
| ATP1B1      | ATPase, Na+/K+ transporting, beta 1 polypeptide | -2.8118 | 0.0152 |
| S1PR3       | sphingosine-1-phosphate receptor 3 | -2.8182 | 0.0952 |
| PTN         | pleiotrophin | -2.822 | 0.0012 |
| ACTG1       | actin, gamma 1 | -2.823 | 0.0341 |
| SFRP4       | secreted frizzled-related protein 4 | -2.8254 | 0.0439 |
| MAP4K2      | mitogen-activated protein kinase kinase kinase kinase 2 | -2.829 | 0.0349 |
| USP21       | ubiquitin specific peptidase 21 | -2.8303 | 0.0184 |
| CSR2P2      | cysteine and glycine-rich protein 2 | -2.8338 | 0.0024 |
| LOC100134868| uncharacterized LOC100134868 | -2.8361 | 0.0079 |
| GDPD5       | glycerophosphodiester phosphodiesterase domain containing 5 | -2.8365 | 0.0422 |
| SALL2       | spalt-like transcription factor 2 | -2.8406 | 0.0177 |
| DPYSL3      | dihydropyrimidinase-like 3 | -2.8413 | 0.0194 |
| OLFML2B     | olfactomedin-like 2B | -2.8466 | 0.0105 |
| HLA-DMA     | major histocompatibility complex, class II, DM alpha | -2.8509 | 0.0264 |
| RG57B       | regulator of G-protein signaling 7 binding protein | -2.8522 | 0.0071 |
| STMN3       | stathmin-like 3 | -2.8585 | 0.0397 |
| CDH11       | cadherin 11, type 2, OB-cadherin (osteoblast) | -2.8804 | 0.0763 |
| JUP         | junction plakoglobin | -2.8903 | 0.0432 |
| ENG         | endoglin | -2.8945 | 0.0598 |
| EMLIN1      | elastin microfibril interacter 1 | -2.8971 | 0.0266 |
| AKAP13      | A kinase (PRKA) anchor protein 13 | -2.8992 | 0.0389 |
| FZD4        | frizzled class receptor 4 | -2.904 | 0.0365 |
| MC1R        | melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor) | -2.9066 | 0.0131 |
| ABCG2       | ATP-binding cassette, sub-family G (WHITE), member 2 | -2.9085 | 0.0000118 |
| SPEG        | SPEG complex locus | -2.9091 | 0.0562 |
| TCN2        | transcobalamin II | -2.9102 | 0.0263 |
| ELN         | elastin | -2.917 | 0.0207 |
| PRRX1       | paired related homeobox 1 | -2.9172 | 0.0784 |
| Gene    | Description                                                                 | Log2 Fold Change | P-value |
|---------|------------------------------------------------------------------------------|------------------|---------|
| FSCN1   | fascin actin-bundling protein 1                                                | -2.9212          | 0.065   |
| PTGS1   | prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase) | -2.9227          | 0.0035  |
| MIR614  | microRNA 614                                                                  | -2.9263          | 0.0313  |
| TREX1   | three prime repair exonuclease 1                                              | -2.9271          | 0.0506  |
| ACVR1L  | activin A receptor type II-like 1                                             | -2.9273          | 0.0312  |
| FILIP1L | filamin A interacting protein 1-like                                          | -2.9477          | 0.0104  |
| FAM117A | family with sequence similarity 117, member A                                | -2.9501          | 0.0195  |
| SEMA3F  | sema domain, immunoglobulin domain (lg), short basic domain, secreted, (semaphorin) 3F | -2.9567          | 0.0538  |
| ARSI    | arylsulfatase family, member I                                                | -2.9754          | 0.0018  |
| MUSTN1  | musculoskeletal, embryonic nuclear protein 1                                  | -2.9806          | 0.0162  |
| FAM69B  | family with sequence similarity 69, member B                                  | -2.9822          | 0.0295  |
| ROGD1   | rogdi homolog (Drosophila)                                                    | -2.9827          | 0.0197  |
| LRRC45  | leucine rich repeat containing 45                                             | -2.9903          | 0.0557  |
| GEN1    | gluthione peroxidase 3 (plasma)                                               | -2.9959          | 0.0101  |
| RAB11FIP1| RAB11 family interacting protein 1 (class I)                                  | -3.0273          | 0.015   |
| A2M     | alpha-2-macroglobulin                                                         | -3.0301          | 0.0108  |
| SIPA1   | signal-induced proliferation-associated 1                                    | -3.0618          | 0.0207  |
| KRT19   | keratin 19                                                                    | -3.0648          | 0.0065  |
| PROCR   | protein C receptor, endothelial                                              | -3.0778          | 0.0172  |
| ESCR    | endothelial cell surface expressed chemotaxis and apoptosis regulator         | -3.0946          | 0.0103  |
| KANK2   | KN motif and ankyrin repeat domains 2                                         | -3.116           | 0.0489  |
| IFI44   | interferon-induced protein 44                                                 | -3.1222          | 0.0016  |
| FAM26E  | family with sequence similarity 26, member E                                  | -3.1225          | 0.0234  |
| HGD     | homogentisate 1,2-dioxxygenase                                                | -3.1285          | 0.0007  |
| GAMT    | guanidinoacetate N-methyltransferase                                          | -3.1288          | 0.0244  |
| ADOR2A  | adenosine A2a receptor                                                        | -3.1311          | 0.0019  |
| CBR3    | carbonyl reductase 3                                                          | -3.1415          | 0.0574  |
| SEMA5A  | sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A | -3.1466          | 0.0163  |
| GSTM2   | glutathione S-transferase mu 2 (muscle)                                       | -3.1474          | 0.0367  |
| SH3RF2  | SH3 domain containing ring finger 2                                           | -3.1522          | 0.0294  |
| IFI44   | interferon-induced protein 44                                                 | -3.1587          | 0.0085  |
| MAGED1  | melanoma antigen family D. 1                                                 | -3.1667          | 0.0539  |
| FAM46B  | family with sequence similarity 46, member B                                  | -3.172           | 0.001   |
| COL3A1  | collagen, type III, alpha 1                                                   | -3.1798          | 0.0117  |
| PSD3    | pleckstrin and Sec7 domain containing 3                                       | -3.1808          | 0.0043  |
| SH3PX2B | SH3 and PX domains 2B                                                         | -3.1947          | 0.0503  |
| HNRNPA1 | heterogeneous nuclear ribonucleoprotein A1                                   | -3.197           | 0.0382  |
| IFNAR2  | interferon (alpha, beta and omega) receptor 2                                | -3.2012          | 0.0159  |
| PLC1    | phospholipase C-1, type 1                                                    | -3.2114          | 0.01    |
| TNS3    | tensin 3                                                                      | -3.2226          | 0.0413  |
| MEOX2   | mesenchyme homeobox 2                                                         | -3.2261          | 0.0137  |
| FES     | FES proto-oncogene, tyrosine kinase                                           | -3.2312          | 0.0149  |
| CACNB3  | calcium channel, voltage-dependent, beta 3 subunit                           | -3.241           | 0.0159  |
| CA12    | carbonic anhydrase XII                                                        | -3.2507          | 0.0154  |
| COL14A1 | collagen, type XIV, alpha 1                                                   | -3.2761          | 0.0177  |
| ADAMTS10| ADAM metallopeptidase with thrombospondin type 1 motif, 10                    | -3.277           | 0.0431  |
| FRRS1   | ferric-chelate reductase 1                                                    | -3.2772          | 0.0093  |
| AQP3    | aquaporin 3 (Gill blood group)                                                | -3.2888          | 0.0066  |
| OSR2    | odd-skipped related transcription factor 2                                   | -3.2929          | 0.0087  |
| SAR32   | seryl-tRNA synthetase 2, mitochondrial                                        | -3.3056          | 0.081   |
| HTRA3   | HtrA serine peptidase 3                                                       | -3.3112          | 0.0309  |
| MXRA8   | matrix-remodelling associated 8                                              | -3.3151          | 0.0277  |
| AKR1C2  | aldo-keto reductase family 1, member C2                                       | -3.3237          | 0.0483  |
| BFSF1   | beaded filament structural protein 1, filensin                              | -3.3264          | 0.0326  |
| HCF1CR1 | host cell factor C1 regulator 1 (XPO1 dependent)                              | -3.3415          | 0.0196  |
| SLC27A3 | solute carrier family 27 (fatty acid transporter), member 3                  | -3.3541          | 0.0125  |
| PLEKHA4 | pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 4 | -3.3739          | 0.0318  |
| Gene symbol | Gene name | Description | Log2 fold change | P-value |
|-------------|-----------|-------------|-----------------|---------|
| SSH3        | slingshot protein phosphatase 3 | -3.3867 | 0.0326 |
| SERTAD4     | SERTA domain containing 4 | -3.4171 | 0.0091 |
| ECM2        | extracellular matrix protein 2, female organ and adipocyte specific | -3.4236 | 0.0258 |
| CRIP1       | cysteine-rich protein 1 (intestinal) | -3.4291 | 0.0032 |
| PDGFRB      | platelet-derived growth factor receptor, beta polypeptide | -3.4378 | 0.0613 |
| GREM2       | gremlin 2, DAN family BMP antagonist | -3.4421 | 0.0012 |
| TCF4        | transcription factor 4 | -3.4613 | 0.0161 |
| SCUBE3      | signal peptide, CUB domain, EGF-like 3 | -3.4651 | 0.0125 |
| ROR2        | receptor tyrosine kinase-like orphan receptor 2 | -3.4722 | 0.0141 |
| ADAMTS14    | ADAM metalloproteinase with thrombospondin type 1 motif, 14 | -3.4726 | 0.0294 |
| ABCA8       | ATP-binding cassette, sub-family A (ABC1), member 8 | -3.4897 | 0.0122 |
| PDGFRB      | platelet-derived growth factor receptor, alpha polypeptide | -3.5024 | 0.0551 |
| IFITM1      | interferon induced transmembrane protein 1 | -3.5079 | 0.0227 |
| SFRP1       | secreted frizzled-related protein 1 | -3.514 | 0.0199 |
| SCUBE3      | signal peptide, CUB domain, EGF-like 3 | -3.515 | 0.0534 |
| ML1C        | megalencephalic leukoencephalopathy with subcortical cysts 1 | -3.5345 | 0.0159 |
| ABLIM1      | actin binding LIM protein 1 | -3.5402 | 0.0057 |
| EHOD3       | EH-domain containing 3 | -3.5426 | 0.0373 |
| KCNMB4      | potassium large conductance calcium-activated channel, subfamily M, beta member 4 | -3.5684 | 0.0211 |
| PRSS23      | protease, serine, 23 | -3.5731 | 0.0381 |
| SOX4        | SRY (sex determining region Y)-box 4 | -3.5813 | 0.0202 |
| C14orf37    | chromosome 14 open reading frame 37 | -3.5833 | 0.035 |
| RNASE4      | ribonuclease, RNase A family, 4 | -3.6062 | 0.0269 |
| GBP1        | guanylate binding protein 1, interferon-inducible | -3.6514 | 0.0263 |
| GJA1        | gap junction protein, alpha 1, 43kDa | -3.6585 | 0.0242 |
| PDE3A       | phosphodiesterase 3A, cGMP-inhibited | -3.6604 | 0.0199 |
| ALDOC       | aldolase C, fructose-bisphosphate | -3.6652 | 0.0552 |
| RG53        | regulator of G-protein signaling 3 | -3.6707 | 0.0391 |
| PDE1A       | phosphodiesterase 1A, calmodulin-dependent | -3.6831 | 0.051 |
| ARHGEF3     | Rho guanine nucleotide exchange factor (GEF) 3 | -3.7081 | 0.0319 |
| DB2B        | LIM domain binding 2 | -3.709 | 0.0326 |
| GNPTAB      | N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits | -3.7141 | 0.0442 |
| DCDLD1      | discoidin, CUB and LCLL domain containing 1 | -3.7205 | 0.0325 |
| MCC         | mutated in colorectal cancers | -3.7496 | 0.0318 |
| NOTCH3      | notch 3 | -3.785 | 0.0693 |
| RGS2        | regulator of G-protein signaling 2 | -3.7931 | 0.0162 |
| WNT2B       | wingless-type MMTV integration site family, member 2B | -3.8013 | 0.0004 |
| RASSF2      | Ras association (RalGDS/AF-6) domain family member 2 | -3.8087 | 0.0012 |
| APOA1       | apolipoprotein A-I | -3.8354 | 0.0064 |
| CST4        | cystatin S | -3.8541 | 0.0122 |
| TSPAN8      | tetraspanin 8 | -3.8706 | 0.0163 |
| TRIM34      | tripartite motif containing 34 | -3.9039 | 0.0154 |
| SULF1       | sulfatase 1 | -3.9172 | 0.0343 |
| PPAP2A      | phosphatidylinositol-4-phosphate phosphatase type 2A | -3.9685 | 0.0163 |
| QPRT        | quinolinate phosphoribosyltransferase | -4.0154 | 0.0018 |
| NYNRIN      | NYN domain and retroviral integrase containing | -4.0195 | 0.0082 |
| FAM65C      | family with sequence similarity 65, member C | -4.0279 | 0.0223 |
| HMGS1       | 3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble) | -4.0574 | 0.0252 |
| IDH2        | isocitrate dehydrogenase 2 (NADP+), mitochondrial | -4.0661 | 0.0319 |
| BTN3A3      | butyrophilin, subfamily 3, member A3 | -4.0726 | 0.0581 |
| DENND2A     | DENNI/MADD domain containing 2A | -4.0814 | 0.0044 |
| EPB46       | EPH receptor B6 | -4.1029 | 0.0384 |
| ISYNA1      | inositol-3-phosphate synthase 1 | -4.1083 | 0.0428 |
| CD248       | CD248 molecule, endosialin | -4.1086 | 0.0872 |
| B4GALNT1    | beta-1,4-N-acetyl-galactosaminyl transferase 1 | -4.111 | 0.0468 |
| WNT17A      | wingless-type MMTV integration site family, member 7A | -4.1202 | 0.0016 |
| IL17RD      | interleukin 17 receptor D | -4.1311 | 0.0114 |
| MGP         | matrix Gla protein | -4.1312 | 0.0297 |
| S100A3      | S100 calcium binding protein A3 | -4.1655 | 0.0457 |
| ARHGEF25    | Rho guanine nucleotide exchange factor (GEF) 25 | -4.1695 | 0.036 |
| LOC728392   | uncharacterized LOC728392 | -4.2029 | 0.0354 |
| Gene Symbol    | Description                                           | Log2 Fold Change | p-value |
|---------------|-------------------------------------------------------|-----------------|---------|
| GBP2          | guanylate binding protein 2, interferon-inducible     | -4.208          | 0.013   |
| EMCN          | endomucin                                             | -4.2581         | 0.0018  |
| FOXS1         | forkhead box S1                                       | -4.2596         | 0.0878  |
| GNA14         | guanine nucleotide binding protein (G protein), alpha 14 | -4.2768         | 0.000642|
| GALNT5        | polypeptide N-acetylgalactosaminyltransferase 5       | -4.2813         | 0.0287  |
| ARRB1         | arrestin, beta 1                                      | -4.2979         | 0.0238  |
| SOX17         | SRY (sex determining region Y)-box 17                | -4.3142         | 0.0081  |
| AKR1B10       | aldo-keto reductase family 1, member B10 (aldoase reductase) | -4.3256         | 0.0872  |
| DNAJB5        | DnaJ (Hsp40) homolog, subfamily B, member 5           | -4.326          | 0.0227  |
| GPRC5B        | G protein-coupled receptor, class C, group 5, member B | -4.3846         | 0.0087  |
| PCOLCE        | procollagen C-endopeptidase enhancer                 | -4.4012         | 0.0102  |
| HSD3B7        | hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7 | -4.4154         | 0.021   |
| PRSS35        | protease, serine, 35                                  | -4.4453         | 0.0003  |
| MMP11         | matrix metalloproteinase 11 (stromelysin 3)           | -4.4458         | 0.064   |
| SHC3          | SHC (Src homology 2 domain containing) transforming protein 3 | -4.466          | 0.0658  |
| GATS          | GATS, stromal antigen 3 opposite strand               | -4.4748         | 0.0132  |
| ART4          | ADP-ribosyltransferase 4 (Dombrock blood group)      | -4.478          | 0.0178  |
| GXYLT2        | glucoside xylosyltransferase 2                        | -4.4979         | 0.027   |
| ALAD          | aminolevulinate dehydratase                           | -4.5101         | 0.0207  |
| CCDC74A       | coiled-coil domain containing 74A                     | -4.5721         | 0.0315  |
| CCL11         | chemokine (C-C motif) ligand 11                       | -4.5793         | 0.0159  |
| RUSC1         | RUN and SH3 domain containing 1                       | -4.6584         | 0.0098  |
| FAM171A2      | family with sequence similarity 171, member A2        | -4.7237         | 0.0113  |
| SULT1B1       | sulfotransferase family, cytosolic, 1B, member 1      | -4.729          | 0.0497  |
| TENC1         | tensin like C1 domain containing phosphatase (tensi 2) | -4.7615         | 0.0324  |
| IL1R1         | interleukin 1 receptor, type I                       | -4.7739         | 0.0308  |
| TGFB3         | transforming growth factor, beta 3                    | -4.8069         | 0.0005  |
| RASL11A       | RAS-like, family 11, member A                         | -4.811          | 0.0064  |
| GBP4          | guanylate binding protein 4                           | -4.8186         | 0.0042  |
| OLFML1        | olinkomedin-like 1                                    | -4.8305         | 0.001   |
| SLC6A6        | solute carrier family 6 (neurotransmitter transporter), member 6 | -4.8789         | 0.012   |
| DACT2         | dishevelled-binding antagonist of beta-catenin 2      | -4.8816         | 0.0475  |
| ARHGDI       | Rho GDP dissociation inhibitor (GDI) beta             | -4.8946         | 0.0195  |
| MGAT3         | mannosyl (beta,1,4-)glycoprotein beta,1,4-N-acetylglucosaminyltransferase | -4.9033         | 0.0271  |
| PLA2G4A       | phospholipase A2, group IVA (cytosolic, calcium-dependent) | -4.9246         | 0.024   |
| C1orf110      | chromosome 1 open reading frame 110                   | -5.0708         | 0.0063  |
| SYNO         | synaptotodin                                           | -5.133          | 0.0439  |
| SCARA3        | scavenger receptor class A, member 3                  | -5.1614         | 0.0183  |
| MALL          | malt, T-cell differentiation protein-like             | -5.1856         | 0.0139  |
| PRR5L         | proline rich 5 like                                   | -5.2195         | 0.0167  |
| HRCT1         | histidine rich carboxyl terminus 1                    | -5.2433         | 0.0461  |
| SLC2A12       | solute carrier family 2 (facilitated glucose transporter), member 12 | -5.2596         | 0.0199  |
| STAR5D        | SIAR-related lipid transfer (START) domain containing 5 | -5.3069         | 0.0626  |
| PPP1R14A      | protein phosphatase 1, regulatory (inhibitor) subunit 14A | -5.3592         | 0.0364  |
| SNCG          | synuclein, gamma (breast cancer-specific protein 1)   | -5.4075         | 0.0291  |
| DACT3         | dishevelled-binding antagonist of beta-catenin 3      | -5.4645         | 0.0449  |
| FABP4         | fatty acid binding protein 4, adipocyte              | -5.5551         | 0.0137  |
| RARRES3       | retinoic acid receptor responder (tazarotene induced) 3 | -5.6063         | 0.0411  |
| IQCA1         | IQ motif containing with AAA domain 1                | -5.6458         | 0.0297  |
| ZNF438        | zinc finger protein 436                               | -5.6578         | 0.009   |
| CCDC28B       | coiled-coil domain containing 28B                    | -5.7695         | 0.0008  |
| LMC1D1        | LIM and cysteine-rich domains 1                       | -5.8182         | 0.022   |
| CSTF3         | cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa | -5.8307         | 0.0111  |
| CGNL1         | cingulin-like 1                                       | -5.9086         | 0.0207  |
| COLE12        | collectin sub-family member 12                       | -5.9256         | 0.0092  |
| PPL           | periplakin                                            | -5.9588         | 0.0398  |
| CST1          | cystatin SN                                          | -5.9746         | 0.0158  |
| SOST          | sclerostin                                            | -6.04           | 0.002   |
| NDRG4         | NDRG family member 4                                 | -6.0832         | 0.0039  |
| PIK3IP1       | phosphoinositide-3-kinase interacting protein 1       | -6.1187         | 0.0291  |
| UBA7          | ubiquitin-like modifier activating enzyme 7           | -6.1223         | 0.0505  |
| Gene Symbol | Protein Name | Score | P-Value |
|-------------|-------------|-------|---------|
| S100A4      | S100 calcium binding protein A4 | -6.1297 | 0.026 |
| GATA5       | GATA binding protein 5 | -6.4107 | 0.0122 |
| METTL7A     | methyltransferase like 7A | -6.496 | 0.0007 |
| ISLR        | immunoglobulin superfamily containing leucine-rich repeat | -6.5361 | 0.0513 |
| PYCARD      | PYD and CARD domain containing | -6.6336 | 0.0291 |
| CALCRL      | calcitonin receptor-like | -6.6968 | 0.0182 |
| CLIC3       | chloride intracellular channel 3 | -6.7191 | 0.0335 |
| PDZRN3      | PDZ domain containing ring finger 3 | -6.8007 | 0.0213 |
| CSDC2       | cold shock domain containing C2, RNA binding | -6.9821 | 0.0152 |
| ST3GAL5     | ST3 beta-galactoside alpha-2,3-sialyltransferase 5 | -7.062 | 0.0662 |
| TMEM35      | transmembrane protein 35 | -7.1062 | 0.0011 |
| C7          | complement component 7 | -7.1894 | 0.0069 |
| OLFML3      | olfactomedin-like 3 | -7.2129 | 0.0259 |
| SULT1E1     | sulfotransferase family 1E, estrogen-preferring, member 1 | -7.231 | 0.0693 |
| CD24        | CD24 molecule | -7.352 | 0.0101 |
| GJA4        | gap junction protein, alpha 4, 37kDa | -7.6894 | 0.0007 |
| LUM         | lumican | -7.8005 | 0.013 |
| UACA        | uveal autoantigen with coiled-coil domains and ankyrin repeats | -7.8359 | 0.0066 |
| CDH5        | cadherin 5, type 2 (vascular endothelium) | -7.9762 | 0.0137 |
| LRRC17      | leucine rich repeat containing 17 | -8.5469 | 0.045 |
| MRV1        | murine retrovirus integration site 1 homolog | -9.1291 | 0.0323 |
| CD14        | CD14 molecule | -9.2644 | 0.0083 |
| FAM198B     | family with sequence similarity 198, member B | -9.3918 | 0.0212 |
| LOC730101   | uncharacterized LOC730101 | -9.4264 | 0.0068 |
| CXCL12      | chemokine (C-X-C motif) ligand 12 | -9.5053 | 0.0436 |
| ADH1B       | alcohol dehydrogenase 1B (class I), beta polypeptide | -10.0297 | 0.0079 |
| SLC40A1     | solute carrier family 40 (iron-regulated transporter), member 1 | -11.179 | 0.0198 |
| PALMD       | pemphigus vulgaris-like | -12.3135 | 0.0207 |
| LGR5        | leucine-rich repeat containing G protein-coupled receptor 5 | -13.4966 | 0.0007 |
| LMOD1       | leiomodin 1 (smooth muscle) | -13.6545 | 0.0242 |
| FMO2        | flavin containing monoxygenase 2 (non-functional) | -15.1042 | 0.0124 |
| SELENBP1    | selenium binding protein 1 | -15.8376 | 0.0068 |
| PMCH        | pro-melanin-concentrating hormone | -19.1428 | 0.0007 |
Table S3. See attached Excel file.

Table S4

| Ingenuity Canonical Pathways                                      | -log(p-value) |
|------------------------------------------------------------------|---------------|
| Axonal Guidance Signaling                                        | 7.39          |
| RhoA Signaling                                                   | 5.89          |
| tRNA Charging                                                    | 5.73          |
| Hepatic Fibrosis / Hepatic Stellate Cell Activation              | 5.15          |
| Germ Cell-Sertoli Cell Junction Signaling                       | 4.54          |
| Human Embryonic Stem Cell Pluripotency                          | 4.26          |
| Tight Junction Signaling                                         | 4.26          |
| Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid  | 4.18          |
| Arthritis                                                       |
| Sertoli Cell-Sertoli Cell Junction Signaling                     | 3.77          |
| Actin Cytoskeleton Signaling                                     | 3.71          |
| p38 MAPK Signaling                                               | 3.61          |
| Aryl Hydrocarbon Receptor Signaling                              | 3.52          |
| Role of Macrophages, Fibroblasts and Endothelial Cells           | 3.49          |
| Epithelial Adherens Junction Signaling                           | 3.21          |
| Glucocorticoid Receptor Signaling                                | 3.01          |
| NRF2-mediated Oxidative Stress Response                          | 2.93          |

Ingenuity pathway analysis based on the transcriptomic data from 200nM halofuginone treatment.

Table S2, S3 and S4. Halofuginone mediated transcriptomic changes in cardiac fibroblast. Normal human cardiac fibroblasts were incubated with 200 nM halofuginone for 24hrs (n=3). Expression of mRNA levels was profiled using RNAseq. Using Fold change >2 and false discovery rate (FDR) <0.1, there were 569 upregulated mRNAs and 608 downregulated mRNAs following halofuginone treatment. These differentially regulated mRNAs were listed in supplementary table 2. Raw Fragments Per Kilobase of transcript per Million mapped reads (FPKM) values were listed in supplementary table 3. The 16 most enriched pathways identified, using Ingenuity pathway analysis, are listed in table 4.
**Table S5**

| Ingenuity Canonical Pathways                                      | -log(p-value) |
|---------------------------------------------------------------|---------------|
| Hepatic Fibrosis / Hepatic Stellate Cell Activation            | 5.56          |
| Inhibition of Matrix Metalloproteases                          | 5.32          |
| Axonal Guidance Signaling                                      | 5.20          |
| GADD45 Signaling                                               | 4.00          |
| Intrinsic Prothrombin Activation Pathway                       | 3.16          |
| LXR/RXR Activation                                             | 2.92          |
| Oncostatin M Signaling                                         | 2.76          |
| Methylglyoxal Degradation III                                  | 2.74          |
| Regulation of Cellular Mechanics by Calpain Protease           | 2.53          |
| Acute Phase Response Signaling                                 | 2.35          |
| Cell Cycle Control of Chromosomal Replication                  | 2.31          |
| Pyridoxal 5'-phosphate Salvage Pathway                         | 2.24          |
| Cell Cycle: G1/S Checkpoint Regulation                         | 2.24          |
| Human Embryonic Stem Cell Pluripotency                        | 2.12          |
| Agrin Interactions at Neuromuscular Junction                    | 2.11          |
| Aryl Hydrocarbon Receptor Signaling                             | 2.10          |
| PPAR Signaling                                                 | 2.05          |
| Inhibition of Angiogenesis by TSP1                             | 2.04          |
| Complement System                                              | 2.04          |

Ingenuity pathway analysis based on the proteomic data from 300nM halofuginone treatment.

**Table S1 and S5.** Halofuginone mediated proteomic changes in cardiac fibroblast.

Normal human cardiac fibroblasts were incubated with 100 and 300 nM halofuginone for 24 hrs (n=2). Expression of protein levels was profiled. Differentially regulated protein were listed in supplementary table 1. Ingenuity pathway analysis was conducted on the differentially regulated proteome by 300 nM and listed in supplementary table 5.
Figure S1

A

|        | 250kd | 150kd | pGCN2 | Total GCN2 | β-actin |
|--------|-------|-------|-------|------------|--------|
| Borrelidin | -     | +     | +     | +          |        |
| L-Proline  | -     | -     | -     | +          |        |
| L-Threonine | -     | -     | +     | -          |        |

B

|        | 250kd | 150kd | pGCN2 | Total GCN2 | β-actin |
|--------|-------|-------|-------|------------|--------|
| Borrelidin | -     | +     | +     | +          |        |
| L-Proline  | -     | -     | -     | +          |        |
| L-Threonine | -     | -     | +     | -          |        |
Figure S1. Borrelidin induced AAR (amino acid response) in fibroblast. Human cardiac fibroblast were treated with Borrelidin (100 nM), L-proline (2 mM) and L-threonine (2 mM) for 24 hrs. Protein levels of pGCN2 (phosphorylated general control nonderepressible 2), total GCN2, β-actin were examined by Western Blot (A) and mRNA level of CHOP (C/EBP homologous protein) was examined by RT-PCR (Reverse transcription polymerase chain reaction B, n=4). One way ANOVA (analysis of variance) was used for statistically analysis of log transformed data. ***p<0.001, ****p<0.0001. Wild type (WT) or GCN2 knockout (GCN2KO) mouse embryonic fibroblasts (MEF) were treated with increasing concentrations of Halofuginone for 24hrs. CHOP mRNA was examined by RT-PCR. Unpaired t-test was used for statistically analysis of log transformed data, **** p<0.0001 (C, n=4).
Figure S2. Halofuginone improves fractional area change (FAC) in TAC (transverse aortic constriction) mouse model. C57Bl/6J mice were subjected to TAC to induced heart failure and treated with halofuginone as described in figure 6. Fractional area change (FAC) was measured by echocardiography. There were 6, 9 and 7 mice in the sham, TAC and TAC + halofuginone groups Unpaired t-test. *** p< 0.001.
Figure S3. Halofuginone reduces infarct size in cardiac ischemic reperfusion (I/R) injury. C57BL/6 mice (11 mice in each group) were treated with 6 μg of halofuginone daily (~2 mg/kg) for 3 days. I/R injury was then induced by ligation of coronary artery for 30 min and reperfusion for 24 hrs. The heart was harvested with staining with Evans blue and TTC (triphenyl tetrazolium chloride) dye. Representative heart images from control (A) and halofuginone (B) treated animals were shown. Infarct size (as percentage of area at risk) and area at risk (as percentage of LV (left ventricle)) were plotted in C. Unpaired t-test, **p<0.01.
Figure S4

A

B

| Borrelidin | L-Proline | L-Threonine |
|------------|-----------|-------------|
| -          | +         | +           |

| Borrelidin | L-Proline | L-Threonine |
|------------|-----------|-------------|
| -          | +         | +           |
**Figure S4. Borrelidin inhibits collagen deposition in cardiac fibroblast.** Normal human cardiac fibroblasts were incubated with media containing ficoll to stimulate collagen deposition. Borrelidin was added at the time of ficoll treatment. The deposition of mature collagen by fibroblasts was examined by immunohistochemistry (A, n=5). Fibroblasts were treated with 10 nM borrelidin, 2 mM L-proline and 2 mM L-threonine for 24hr. At the end of the treatment, collagen deposition and COL1A1 mRNA (Type I collagen 1α1 messenger ribonucleic acid, B, n=4) were measured by immunohistochemistry and RT-PCR, respectively. One way ANOVA (analysis of variance) comparisons were used to analyze raw collagen deposition data and log transformed gene expression data, *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001.

**Figure S5**

**Figure S5. Amino acid starvation inhibits collagen deposition.** WI38 fibroblast cells were stimulated with either complete DMEM (Dulbecco's Modified Eagle Medium) media with ficoll...
or DMEM media deficient in L-Lysine, L-Leucine, L-Arginine and L-gulatmine with ficoll (A, n=5). 24 hours later, cells were fixed with methanol and immunostained with anti-mature type I collagen antibody. Normal human cardiac fibroblasts were stimulated with ficoll media and treated with L-Leucinol, a L-Leucine analog\(^{(15,16)}\) and inhibitor of Leucyl-tRNA (leucyl-transfer ribonucleic acid) synthetase (B, n=5). 24 hours later, cells were fixed with methanol and immunostained with anti-mature type I collagen antibody. Unpaired t-test *** p< 0.001.
**Figure S6**

### A

| Description                                      | Heart function/link to heart failure                                                                 |
|--------------------------------------------------|-------------------------------------------------------------------------------------------------------|
| matrix Gla protein                               | marker for HF                                                                                       |
| taurin transporter                               | taurine deficiency promotes cardiac alterations                                                    |
| collagen triple helix repeat protein             | linked to left-sided congenital heart disease                                                      |
| stromal cell-derived factor 1                    | GWAS: myocardial infarction, coronary arterial disease                                              |
| PDGF receptor                                    | heart remodeling, fibrosis                                                                           |
| collectin                                        | induced after ischemia/reperfusion                                                                   |
| carbonyl reductase                               | linked to congestive HF                                                                              |
| homeobox factor                                  | GWAS: heart PR interval                                                                             |
| osteonectin                                      | cardiac remodeling                                                                                  |
| paired homeobox factor                           | GWAS: link to atrial fibrillation                                                                   |
| microfibril-associated glycoprotein 4            | linked to left-sided congenital heart disease                                                       |
| ligand of Robo receptor                          | involved in heart development                                                                      |
| osteoblast factor pentoside                      | overexpressed in HCM                                                                               |
| bmp-binding endothelial regulator                | cardio protective anti-atherosclerotic                                                               |
| programmed cell death protein 4                  | cardiac valvulogenesis                                                                              |
| neuropilin 1                                     | induces CTGF promotes cardiac repair                                                                 |
| t-box transcription factor                        | reprogrammes mature cardiac myocytes                                                                 |
| medG DNA methyltransferase                       | linked to congenital heart defect                                                                    |

### B

**Figure S6:** Two key differentially regulated pathways. The top 100 down-regulated proteins (from proteomic study) in cardiac fibroblasts were grouped according to their
functions or properties based on Ingenuity description and the published literature. Differentially expressed heart failure related proteins were shown in panel A. Differentially expressed TGFβ (Transforming growth factor β) and Wnt-related proteins were shown in panel B.

Figure S7

Figure S7. Overexpression of GCN2 (general control nonderepressible 2) activates AAR (amino acid response) and reduces collagen deposition. Normal human cardiac fibroblasts were transfected with BacMam virus encoding a constitutively active form of GCN2 or treated with halofuginone in the presence of ficoll media. The expression of total GCN2, p-GCN2 (phosphorylated GCN2), total eIF2α (eukaryotic translation initiation factor 2α), p-eIF2α (phosphorylated eIF2α) and tubulin were detected by Western Blot (A). Deposition of collagen was determined by immunohistochemistry (B) and quantitated by image analysis (C, n=3). A BacMam virus that does not carry any protein was used as negative control and
had no effect on AAR activation or collagen deposition at similar MOT (multiplicity of transfection, data not shown).

**Figure S8**

![Western Blot Images](image)

**Figure S8.** Over expression of GCN2 (general control nonderepressible 2) activates AAR (amino acid response) and enhance autophagy in cardiomyocytes. Human iPSC (induced pluripotent stem cells) derived cardiomyocytes were transfected with a BacMam virus encoding a constitutively active form of GCN2. The expression of total GCN2, p-GCN2 (phosphorylated GCN2), total eIF2α (eukaryotic translation initiation factor 2α), p-eIF2α (phosphorylated-eIF2α), LC3BI (microtubule-associated proteins 1A/1B light chain 3B-I), LC3BII and tubulin were detected by Western Blot (A). Band intensity values normalized by the housekeeper Tubulin were used to compare relative expression levels. LC3B ratio is shown as the normalized value of LC3BII over LC3BI. (B)
Supplemental References

1. Richards DA, Bao W, Rambo MV, Burgert M, Jucker BM, Lenhard SC. Examining the relationship between exercise tolerance and isoproterenol-based cardiac reserve in murine models of heart failure. J Appl Physiol. 2013; 114:1202-1210.

2. Chen CZ, Peng YX, Wang ZB, Fish PV, Kaar JL, Koepsel RR, Russell AJ, Lareu R R, Raghunath M. The Scar-in-a-Jar: studying potential antifibrotic compounds from the epigenetic to extracellular level in a single well. Br J Pharmacol. 2009; 158:1196-1209.

3. Li B, Ruotti V, Stewart RM, Thomson JA, Dewey CN. RNA-Seq gene expression estimation with read mapping uncertainty. Bioinformatics. 2010; 26:493-500.

4. Becher I, Dittmann A, Savitski MM, Hopf C, Drewes G, Bantscheff M. Chemoproteomics reveals time-dependent binding of histone deacetylase inhibitors to endogenous repressor complexes. ACS Chem Biol. 2014; 9:1736-1746.

5. Bantscheff M, Eberhard D, Abraham Y, Bastuck S, Boesche M, Hobson S, Mathieson T, Perrin J, Raida M, Rau C, Reader V, Sweetman G, Bauer A, Bouwmeester T, Hopf C, Kruse U, Neubauer G, Ramsden N, Rick J, Kuster B, Drewes G. Quantitative chemical proteomics reveals mechanisms of action of clinical ABL kinase inhibitors. Nat Biotechnol. 2007; 25:1035-1044.

6. Kruse U, Pallasch CP, Bantscheff M, Eberhard D, Frenzel L, Ghidelli S, Maier SK, Werner T, Wendtner CM, Drewes G. Chemoproteomics-based kinase profiling and target deconvolution of clinical multi-kinase inhibitors in primary chronic lymphocytic leukemia cells. Leukemia. 2011; 25:89-100.

7. Werner T, Sweetman G, Savitski MF, Mathieson T, Bantscheff M, Savitski MM. Ion coalescence of neutron encoded TMT 10-plex reporter ions. Anal Chem. 2014; 86:3594-3601.

8. Bantscheff M, Hopf C, Savitski MM, Dittmann A, Grandi P, Michon AM, Schlegl J, Abraham Y, Becher I, Bergamini G, Boesche M, Delling M, Dumptfeld B, Eberhard D, Huthmacher C, Mathieson T, Poelckel D, Reader V, Strunk K, Sweetman G, Kruse U, Neubauer G, Ramsden NG, Drewes G. Chemoproteomics profiling of HDAC inhibitors reveals selective targeting of HDAC complexes. Nat Biotechnol. 2011; 29:255-265.

9. Savitski MM, Sweetman G, Askenazi M, Marto JA, Lang M, Zinn N, Bantscheff M. Delayed fragmentation and optimized isolation width settings for improvement of protein identification and accuracy of isobaric mass tag quantification on Orbitrap-type mass spectrometers. Anal Chem. 2011; 83:8959-8967.

10. Savitski MM, Fischer F, Mathieson T, Sweetman G, Lang M, Bantscheff M. Targeted data acquisition for improved reproducibility and robustness of proteomic mass spectrometry assays. J Am Soc Mass Spectrom. 2010; 21:1668-1679.
11. Savitski MM, Mathieson T, Zinn N, Sweetman G, Doce C, Becher I, Pachl F, Kuster B, Bantscheff M. Measuring and managing ratio compression for accurate iTRAQ/TMT quantification. *J Proteome Res.* 2013; 12:3586-3598.

12. Cox J, Mann M. MaxQuant enables high peptide identification rates, individualized p.p.b.-range mass accuracies and proteome-wide protein quantification. *Nat Biotechnol.* 2008; 26:1367-1372.

13. Benjamini Y, Drai D, Elmer G, Kafkafi N, Golani I. Controlling the false discovery rate in behavior genetics research. *Behav Brain Res.* 2001; 125:279-284.

14. Eden E, Navon R, Steinfeld I, Lipson D, Yakhini Z. GOrilla: a tool for discovery and visualization of enriched GO terms in ranked gene lists. *BMC Bioinformatics.* 2009; 10:48.

15. Rouget P, Chapeville F. Reactions sequence of leucine activation catalysed by leucyl-RNA synthetase. 1. Kinetic studies. *Eur J Biochem.* 1968; 4:305-309.

16. Vaughan MH, Hansen BS. Control of initiation of protein synthesis in human cells. Evidence for a role of uncharged transfer ribonucleic acid. *J Biol Chem.* 1973; 248:7087-7096.