Supplemental Material

Data S1

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 dose group). 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 removel 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^{TM} 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-eIF2α, 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 (4). Gel lanes were cut into three slices covering the entire separation range (~2 cm) and subjected to in-gel digestion (5). 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 × 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 $3x10^6$. 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 $2x10^5$ 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:

$$\frac{(\log_2(\mathrm{FC}_{\mathrm{rep1}}) - \log_2(\mathrm{FC}_{\mathrm{rep2}}))}{\sqrt{2}}$$

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 ≤ 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.

Table S1: Differentially Regulated Protein by 300nM Halofuginone

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
IPI00171160	LRRC17	-2.48	4.73E-22
IPI00020986	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
IPI00014572	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
IPI00007256	ZHX2	-1.28	2.79E-09
IPI00027721	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
IPI00022200	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

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
IPI00017640	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	SLC6A6	-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
IPI00023205	TCF25	-1.07	3.19E-06
IPI00337314	STON1	-1.17	6.21E-06
IPI00847609	SVEP1	-1.08	6.97E-06
IPI00006971	CD248	-1.13	8.39E-06
IPI00430439	VGLL4	-1.24	9.65E-06
IPI00015902	PDGFRB	-1.30	1.08E-05
IPI00007993	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	DKFZP586H2123	-1.09	1.46E-05
IPI00028415	PBX1	-1.10	2.07E-05
IPI00024242	EBF3	-1.20	2.24E-05
IPI00006378	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
IPI00029733	AKR1C1	-1.08	9.04E-05
IPI00893234	OBSL1	-1.07	9.36E-05
IPI00028565	GBP2	-1.07	9.57E-05
IPI00018769	THBS2	-0.87	9.62E-05
IPI00032055	CA5B	-1.26	9.66E-05

IPI00026941	PRSS23		-0.96	9.69E-05
IPI00059135	PPP1R14A		-1.06	9.87E-05
IPI00027780	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	CSGLCA-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	0.00042
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
IPI00880170	TSPAN9		-0.98	0.000601
IPI00328431	UNC5B		0.99	0.000606
IPI00024105	C1QTNF5		-1.06	0.00062
IPI00872194	COLEC12		-1.18	0.000654
IPI00290560	DEPDC6		-0.96	0.000682
IPI00026944	NID1		-0.88	0.000682
IPI00871728	FAM115A		-1.25	0.00076
IPI00215977	IGF2		-1.08	0.000862
IPI00514311	CTTNBP2NL		-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

IPI00737174	PHF21A	-0.89	0.000919
IPI00873889	LAMA2	-0.82	0.000973
IPI00783156	BMPR2	-0.91	0.000998
IPI00100775	C11ORF67	-0.93	0.001057
IPI00908609	P4HA3	-0.89	0.001057
IPI00030106	TPST1	-0.89	0.001057
IPI00018219	TGFBI	-0.86	0.001084
IPI00024235	BACH1	-0.94	0.001135
IPI00006658	PIN4	-0.97	0.001187
IPI00009146	TRAFD1	-0.95	0.001187
IPI00744724	PID1	-0.93	0.001193
IPI00001564	CDKN2C	-0.93	0.001244
IPI00015974	ERN1	1.21	0.001251
IPI00024781	HYPK	-0.92	0.001267
IPI00873001	LMO4	-1.27	0.001409
IPI00031411	FAT1	-0.95	0.001409
IPI00151462	MAP1LC3B2	1.10	0.001469
IPI00295595	CERCAM	-0.98	0.001763
IPI00306543	GDF15	1.29	0.001834
IPI00028670	INHBA	-0.82	0.001847
IPI00376427	NCAM2	-0.79	0.001872
IPI00015578	PALMD	-0.94	0.001958
IPI00294595	PDE5A	-1.06	0.001991
IPI00028566	NUAK1	-0.97	0.002029
IPI00876842	Q15156_HUMAN	-1.09	0.002144
IPI00641705	IL17RD	-1.14	0.002179
IPI00291483	AKR1C3	-1.00	0.00218
IPI00009198	TFPI2	-1.14	0.002193
IPI00031821	ITM2B	-0.85	0.002257
IPI00745915	C1QTNF1	-1.41	0.002315
IPI00376483	ZYG11BL	-0.96	0.002317
IPI00556657	EFEMP2	-0.77	0.002519
IPI00640084	RUNX2	-0.77	0.002544
IPI00844310	CCDC80	-0.90	0.002727
IPI00868928	KIF26B	-0.96	0.002732
IPI00296869	F2R	-0.96	0.002817
IPI00032313	S100A4	-0.96	0.002835
IPI00019155	FOXC2	-0.89	0.002839
IPI00023080	CRIPT	-0.91	0.002926
IPI00743456	GPR124	-0.87	0.002926
IPI00024685	NPR2	-0.97	0.003217
IPI00020356	MAP1A	-0.58	0.003262
IPI00219718	RBP1	-0.95	0.003532
IPI00106646	SDF4	-1.02	0.003553
IPI00855846	C6ORF115	-0.89	0.003585
IPI00032050	WBP2	-0.77	0.0038
IPI00376199	IRF2BP2	-0.79	0.00406
IPI00010219	SPC25	-0.81	0.004231
IPI00013241	UBL5	-0.77	0.004239
IPI00009542	MAGED2	-0.85	0.004268
IPI00013079	EMILIN1	-0.92	0.004474
IPI00031030	APLP2	-0.60	0.004691
IPI00465038	FBLN2	-0.73	0.004713
IPI00025318	SH3BGRL	-0.95	0.004905
IPI00289795	SRPX	-0.89	0.004947

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
IPI00030280	LRRC32	-0.80	0.006531
IPI00445977	LHFPL2	-0.76	0.006587
IPI00026689	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
IPI00002732	EXTL2	-0.79	0.009022
IPI00059930	NACC2	-0.87	0.009057
IPI00029260	CD14	-0.76	0.009177
IPI00010948	TRIM26	-0.75	0.009263
IPI00006377	POMP	-0.70	0.009278
IPI00054042	GTF2I	-0.85	0.009348
IPI00004409	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	PHLDB2	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

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	LTBP1	-0.78	0.022073
IPI00479296	ABCA8	-0.75	0.022169
IPI00002511	ATF6	0.98	0.022706
IPI00329753	FAM164A	-0.74	0.023095
IPI00002816	CTSF	-0.72	0.023251
IPI00883790	SEC14L1	-0.74	0.02351
IPI00019448	TSGA14	-0.64	0.024085
IPI00298409	PDCL	-0.72	0.024451
IPI00290071	WDR42A	-0.59	0.024979
IPI00021389	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
IPI00001735	NCOR2	-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
IPI00011564	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
IPI00604414	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
IPI00031018	MAFK	0.73	0.036848
IPI00028082	RECK	-0.56	0.037492
IPI00291901	IRF3	-0.56	0.03777

IPI00028516	KIAA0513	-0.81	0.038046
IPI00015808	GNL2	0.66	0.038847
IPI00011689	EEF2K	-0.72	0.038973
IPI00030023	HNMT	-0.67	0.039413
IPI00023098	FOXP1	-0.59	0.040448
IPI00005609	VWA5A	-0.96	0.041404
IPI00444945	BAX	-0.56	0.041404
IPI00647915	TAGLN2	-0.45	0.0417
IPI00011901	ADAM19	-0.78	0.042204
IPI00470422	ANKMY2	-0.77	0.04271
IPI00000760	DDAH2	-0.62	0.04271
IPI00024307	EFNB1	-0.78	0.043376
IPI00217469	HIST1H1A	0.66	0.043402
IPI00180240	TMSL3	-0.76	0.04417
IPI00023529	CDK6	-0.66	0.044447
IPI00029817	NEU1	-0.59	0.045283
IPI00176903	PTRF	-0.41	0.045283
IPI00022431	AHSG	-0.63	0.04617
IPI00515115	ABLIM1	-0.58	0.046785
IPI00008157	KIAA1211	-0.72	0.047257
IPI00296461	SMPD1	-0.65	0.047504
IPI00182728	VPS4B	-0.47	0.047533
IPI00021250	DAPK1	-0.71	0.047628
IPI00607575	RXRB	-0.55	0.047703
IPI00300026	SULT1A1	-0.59	0.048529
IPI00003369	LIMD1	-0.58	0.048997
IPI00031679	C3ORF26	0.65	0.049734

Table S2: Differentially Regulated mRNA by 200 nM Halofuginone

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
DDIT3	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	0.0007
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	0.0068
CD274	CD274 molecule	9.3607	0.0289
FAM129A	family with sequence similarity 129, member A	9.0446	0.0018
LAMP3	lysosomal-associated membrane protein 3	8.9245	0.0019
SLC1A5	solute carrier family 1 (neutral amino acid transporter), member 5	8.9045	0.001
CEBPG	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
SLFN5	schlafen family member 5	7.9528	0.011
IL6	interleukin 6	7.8984	0.0132
MOCOS	molybdenum cofactor sulfurase	7.7853	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
DDIT4	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/neutral 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
TGFB2	transforming growth factor, beta 2	5.9312	0.0216
SLC7A11	solute carrier family 7 (anionic 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	basonuclin 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 tetratricopeptide repeat (TPR)-containing, beta	5.4322	0.0172

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	5.2362	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	glycyl-tRNA synthetase	4.9869	0.0011
TUBE1	tubulin, epsilon 1	4.9337	0.0159
IARS	isoleucyl-tRNA synthetase	4.9244	0.0003
SNAPC1	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	spermidine/spermine N1-acetyltransferase 1	4.8622	0.0351
TSLP	thymic stromal lymphopoietin	4.8375	0.0262
ETV5	ets variant 5	4.7834	0.0066
RPLP0P2	ribosomal protein, large, P0 pseudogene 2	4.7731	0.0091
RNH1	ribonuclease/angiogenin inhibitor 1	4.7653	0.0036
AKNA	AT-hook transcription factor	4.7611	0.0074
RGMB	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-myc 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

PRKCE	protein kinase C, epsilon	3.6667	0.0184
RAPH1	Ras association (RalGDS/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	sulfiredoxin 1	3.5714	0.0048
ADAMTS5	ADAM metallopeptidase with thrombospondin type 1 motif, 5	3.5598	0.0101
GFPT1	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
SMYD3	SET and MYND domain containing 3	3.4361	0.0141
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
DLC1	DLC1 Rho GTPase activating protein	3.3238	0.0354
HYOU1	hypoxia up-regulated 1	3.3143	0.0776
ANGPTL4	angiopoietin-like 4	3.3037	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	angiopoietin-like 1	3.2265	0.0079
SYT1	synaptotagmin I	3.224	0.024
NRBF2	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	3.16	0.0691
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	adrenoceptor 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
CSGALNACT2	chondroitin sulfate N-acetylgalactosaminyltransferase 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
UGCG	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

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
TMEM71	transmembrane protein 71	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
CARS	cysteinyl-tRNA synthetase	2.8707	0.0392
ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	2.8574	0.0324
PDF	peptide deformylase (mitochondrial)	2.8483	0.0533
EIF4EBP3	eukaryotic translation initiation factor 4E binding protein 3	2.8447	0.0116
ESYT1	extended synaptotagmin-like protein 1	2.8378	0.0228
HOXB2	homeobox B2	2.8245	0.0436
PPP3CB	protein phosphatase 3, catalytic subunit, beta isozyme	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
BTG1	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
ERRFI1	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
PHLDA1	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	seryl-tRNA 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

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 11	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	lon 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 GTPase activating protein 26	2.5823	0.0012
FGF16	fibroblast growth factor 16	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	2.5682	0.0159
SYTL3	synaptotagmin-like 3	2.5622	0.0104
KCTD9	potassium channel tetramerization domain containing 9	2.5591	0.0474
SRGAP1	SLIT-ROBO Rho GTPase activating protein 1	2.5533	0.0155
CEP120	centrosomal protein 120kDa	2.5507	0.0463
C9orf72	chromosome 9 open reading frame 72	2.5474	0.0182
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	0.0938
NPAS2	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	glycerophosphocholine 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	2.4785	0.0049
PPP1R10	protein phosphatase 1, regulatory subunit 10	2.4773	0.0451
MARS	methionyl-tRNA synthetase	2.4709	0.0029
AIMP2	aminoacyl tRNA synthetase complex-interacting multifunctional protein 2	2.4702	0.0072
ZXDC	ZXD family zinc finger C	2.4608	0.0236

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
RHBDD1	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	cholesterol 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)	2.437	0.0193
ANKRD11	ankyrin repeat domain 11	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 1	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
DNAJA3	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 1	2.3772	0.0413
NTF3	neurotrophin 3	2.3736	0.0194
PRMT3	protein arginine methyltransferase 3	2.3683	0.0229
PFDN6	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
AFAP1	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	0.0064
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

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	LON peptidase N-terminal domain and ring finger 1	2.3238	0.0278
ORC6	origin recognition complex, subunit 6	2.3211	0.0586
BCDIN3D	BCDIN3 domain containing	2.3186	0.0237
ADCK2	aarF domain containing kinase 2	2.3167	0.0227
ISCU	iron-sulfur cluster assembly enzyme	2.316	0.0215
PTPDC1	protein tyrosine phosphatase domain containing 1	2.314	0.096
CYR61	cysteine-rich, angiogenic inducer, 61	2.3139	0.0508
ZNF507	zinc finger protein 507	2.312	0.024
LOC100288842	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5 pseudogene	2.311	0.0339
ADORA2B	adenosine A2b receptor	2.3085	0.0017
SMEK2	SMEK homolog 2, suppressor of mek1 (Dictyostelium)	2.307	0.045
ZNF773	zinc finger protein 773	2.3046	0.0201
BIRC2	baculoviral IAP repeat containing 2	2.3032	0.0397
PROSC	proline synthetase co-transcribed homolog (bacterial)	2.2988	0.0263
ZNF699	zinc finger protein 699	2.2987	0.0605
WDR43	WD repeat domain 43	2.2977	0.0189
LOC344887	NmrA-like family domain containing 1 pseudogene	2.2963	0.0291
PTPN14	protein tyrosine phosphatase, non-receptor type 14	2.2953	0.0185
NEK7	NIMA-related kinase 7	2.2946	0.0278
LPXN	leupaxin	2.292	0.0489
MKNK2	MAP kinase interacting serine/threonine kinase 2	2.2911	0.0183
DLG1	discs, large homolog 1 (Drosophila)	2.29	0.0701
COX19	cytochrome c oxidase assembly homolog 19 (S. cerevisiae)	2.2881	0.0248
TOP1	topoisomerase (DNA) I	2.2874	0.0504
TPBG	trophoblast glycoprotein	2.2874	0.0257
SMURF2	SMAD specific E3 ubiquitin protein ligase 2	2.28	0.0101
PCNXL2	pecanex-like 2 (Drosophila)	2.2787	0.0077
TMEM129	transmembrane protein 129, E3 ubiquitin protein ligase	2.2776	0.04
KDM6B	lysine (K)-specific demethylase 6B	2.2752	0.0402
MICALL1	MICAL-like 1	2.2748	0.0141
MEX3C	mex-3 RNA binding family member C	2.2741	0.0377
CDKN2D	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	2.2736	0.0326
XYLT1	xylosyltransferase I	2.2719	0.0125
FOXC1	forkhead box C1	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
ENTPD6	ectonucleoside triphosphate diphosphohydrolase 6 (putative)	2.2616	0.0111
CDK13	cyclin-dependent kinase 13	2.2578	0.0646
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
SRSF3	serine/arginine-rich splicing factor 3	2.2444	0.0529
SPG20	spastic paraplegia 20 (Troyer syndrome)	2.2416	0.0496
CLIP1	CAP-GLY domain containing linker protein 1	2.2397	0.0101
EFHD2	EF-hand domain family, member D2	2.239	0.0093
TNFRSF10D	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain	2.2371	0.0124
TLK2	tousled-like kinase 2	2.2357	0.0978
LOC645166	lymphocyte-specific protein 1 pseudogene	2.2336	0.0294
UBIAD1	UbiA prenyltransferase domain containing 1	2.2282	0.0093
PKD1P1	polycystic kidney disease 1 (autosomal dominant) pseudogene 1	2.2276	0.0068
SNX24	sorting nexin 24	2.2261	0.0128

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	0.0653
GRK6	G protein-coupled receptor kinase 6	2.1941	0.0579
TBX15	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 (RalGDS/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

AARS	alanyl-tRNA synthetase	2.1298	0.0242
BRSK1	BR serine/threonine kinase 1	2.1275	0.0475
ORMDL1	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
VTI1A	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
NDUFAF2	NADH dehydrogenase (ubiquinone) complex I, assembly factor 2	2.1046	0.0292
CECR2	cat eye syndrome chromosome region, candidate 2	2.1045	0.0292
UBR4	ubiquitin protein ligase E3 component n-recognin 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	tetratricopeptide 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
SRGAP2	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
FKBP4	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
XRCC2	X-ray repair complementing defective repair in Chinese hamster cells 2	2.0659	0.0593
OTUD6B	OTU domain containing 6B	2.0653	0.0052
TNPO1	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 (RalGDS/AF-6) domain family member 1	2.0605	0.0566
CCDC82	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	PRKC, 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	0.012
RNF168	ring finger protein 168, 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

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	0.0683
SLC19A2	solute carrier family 19 (thiamine transporter), member 2	2.028	0.0386
ADNP	activity-dependent neuroprotector homeobox	2.0269	0.0329
DCUN1D2	DCN1, defective in cullin neddylation 1, domain containing 2	2.0269	0.0249
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
NKX3-1	NK3 homeobox 1	2.0132	0.0304
NR1D2	nuclear receptor subfamily 1, group D, member 2	2.0128	0.0529
HMBOX1	homeobox containing 1	2.011	0.0242
GNA13	guanine nucleotide binding protein (G protein), alpha 13	2.0106	0.0261
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	0.052
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
TMEM38A	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
SCRN2	secernin 2	-2.0087	0.0862
TMTC2	transmembrane and tetratricopeptide repeat containing 2	-2.0095	0.0205
NXN	nucleoredoxin	-2.0105	0.0103
TSPAN13	tetraspanin 13	-2.0121	0.0062
NFIX	nuclear factor I/X (CCAAT-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
GCHFR	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	nurim (nuclear envelope membrane protein)	-2.0318	0.0653
C2orf27A	chromosome 2 open reading frame 27A	-2.0331	0.0356

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 423	-2.0665	0.0405
HSPB2	heat shock 27kDa protein 2	-2.0684	0.0638
ZNF821	zinc finger protein 821	-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 226	-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
CDKN2A	cyclin-dependent kinase inhibitor 2A	-2.0932	0.023
RNF122	ring finger protein 122	-2.0943	0.0183
ITGA8	integrin, alpha 8	-2.0946	0.0025
PRUNE2	prune homolog 2 (Drosophila)	-2.0956	0.0247
ADAM19	ADAM metallopeptidase domain 19	-2.0985	0.0307
CD9	CD9 molecule	-2.099	0.0477
PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	-2.0999	0.0263
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 metallopeptidase 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
KCNN4	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
BAMBI	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

PLEKHG2	pleckstrin homology domain containing, family G (with RhoGef domain) member 2	-2.1345	0.0218
C14orf132	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 metallopeptidase with thrombospondin type 1 motif, 12	-2.1536	0.0367
NXPH3	neurexophilin 3	-2.1536	0.0007
SH3D19	SH3 domain containing 19	-2.1555	0.0072
SHROOM3	shroom family member 3	-2.1589	0.0638
ANTXR1	anthrax toxin receptor 1	-2.161	0.0419
SGSH	N-sulfoglucosamine sulfohydrolase	-2.1611	0.0391
UAP1L1	UDP-N-acetylglucosamine pyrophosphorylase 1 like 1	-2.1636	0.0079
TNFRSF21	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-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, 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 35	-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
LRP3	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
LRP4	low density lipoprotein receptor-related protein 4	-2.2036	0.0004
VWA5A	von Willebrand factor A domain containing 5A	-2.2055	0.0382
BST2	bone marrow stromal cell antigen 2	-2.2064	0.0506
SNRPA	small nuclear ribonucleoprotein polypeptide 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 glycosylphosphatidylinositol anchor 1	-2.2325	0.0221

GALK1	galactokinase 1	-2.235	0.0281
RTEL1	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	calsyntenin 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	periostin, 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	glutaminyl-tRNA 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
PTTG1	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	-2.2955	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	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1	-2.2991	0.0374
TMEM8B	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
EFNB3	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 monooxygenase 4	-2.3156	0.0013
ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltranferase 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 C3	-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

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	0.0686
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	0.0064
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 IE	-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
HNRNPA1P10	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	ArfGAP 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

LEPREL2	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	0.0055
MXRA5	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	vasohibin 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
CA5B	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
MICALL2	MICAL-like 2	-2.5541	0.0719
EEF2K	eukaryotic elongation factor-2 kinase	-2.5589	0.0624
OSR1	odd-skipped related transciption 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	-2.5887	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
ARHGEF37	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	tetraspanin 9	-2.6265	0.0085
FNIP2	folliculin interacting protein 2	-2.6325	0.0622
BAI2	brain-specific angiogenesis inhibitor 2	-2.6341	0.0345
ARMC9	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
NKD2	naked cuticle homolog 2 (Drosophila)	-2.6477	0.0296
ANXA6	annexin A6	-2.6515	0.0297
NT5DC1	5'-nucleotidase domain containing 1	-2.6535	0.0242
FIBCD1	fibrinogen C domain containing 1	-2.6654	0.0423
ST3GAL6	ST3 beta-galactoside 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
B4GALNT4	beta-1,4-N-acetyl-galactosaminyl transferase 4	-2.6848	0.0276
ACAP3	ArfGAP with coiled-coil, ankyrin repeat and PH domains 3	-2.6928	0.0169
CDKN2C	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
CNPY4	canopy FGF signaling regulator 4	-2.7031	0.0172
MAP3K6	mitogen-activated protein kinase kinase kinase 6	-2.7066	0.0414

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	trophinin	-2.742	0.0311
SMARCD3	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
MARCKSL1	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
CSRP2	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
RGS7BP	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
EMILIN1	elastin microfibril interfacer 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

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
ACVRL1	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 (Ig), 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	0.0182
FAM69B	family with sequence similarity 69, member B	-2.9822	0.0295
ROGDI	rogdi homolog (Drosophila)	-2.9827	0.0197
LRRC45	leucine rich repeat containing 45	-2.9903	0.0557
TMEM25	transmembrane protein 25	-2.9959	0.0101
GPX3	glutathione peroxidase 3 (plasma)	-3.0008	0.0074
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
ECSCR	endothelial cell surface expressed chemotaxis and apoptosis regulator	-3.0946	0.0103
KANK2	KN motif and ankyrin repeat domains 2	-3.116	0.0489
CFI	complement factor I	-3.1222	0.0016
FAM26E	family with sequence similarity 26, member E	-3.1225	0.0234
HGD	homogentisate 1,2-dioxygenase	-3.1265	0.0007
GAMT	guanidinoacetate N-methyltransferase	-3.1268	0.0244
ADORA2A	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
SH3PXD2B	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
PLCL1	phospholipase C-like 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 transciption factor 2	-3.2929	0.0087
SARS2	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
BFSP1	beaded filament structural protein 1, filensin	-3.3264	0.0326
HCFC1R1	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

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 metallopeptidase with thrombospondin type 1 motif, 14	-3.4726	0.0294
ABCA8	ATP-binding cassette, sub-family A (ABC1), member 8	-3.4897	0.0122
PDGFRA	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
GSTM4	glutathione S-transferase mu 4	-3.515	0.0534
MLC1	megalencephalic leukoencephalopathy with subcortical cysts 1	-3.5345	0.0159
ABLIM1	actin binding LIM protein 1	-3.5402	0.0057
EHD3	EH-domain containing 3	-3.5426	0.0373
KCNMB4	potassium large conductance calcium-activated channel, subfamily M, beta member 4	-3.5684	0.021
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
RGS3	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
LDB2	LIM domain binding 2	-3.709	0.0326
GNPTAB	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits	-3.7141	0.0442
DCBLD1	discoidin, CUB and LCCL 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	phosphatidic acid 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
HMGCS1	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	DENN/MADD domain containing 2A	-4.0814	0.0044
EPHB6	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
WNT7A	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	-4.1855	0.0457
ARHGEF25	Rho guanine nucleotide exchange factor (GEF) 25	-4.1895	0.036
LOC728392	uncharacterized LOC728392	-4.2029	0.0354

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	0.0000642
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 (aldose 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 metallopeptidase 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 (tensin 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	olfactomedin-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
ARHGDIB	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
SYNPO	synaptopodin	-5.133	0.0439
SCARA3	scavenger receptor class A, member 3	-5.1614	0.0183
MALL	mal, 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
STARD5	StAR-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
ZNF436	zinc finger protein 436	-5.6578	0.009
CCDC28B	coiled-coil domain containing 28B	-5.7698	0.0098
LMCD1	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	-5.9066	0.0207
COLEC12	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

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	-6.9987	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
MRVI1	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	palmdelphin	-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 monooxygenase 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 Arthritis	4.18
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 differentiatially 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.

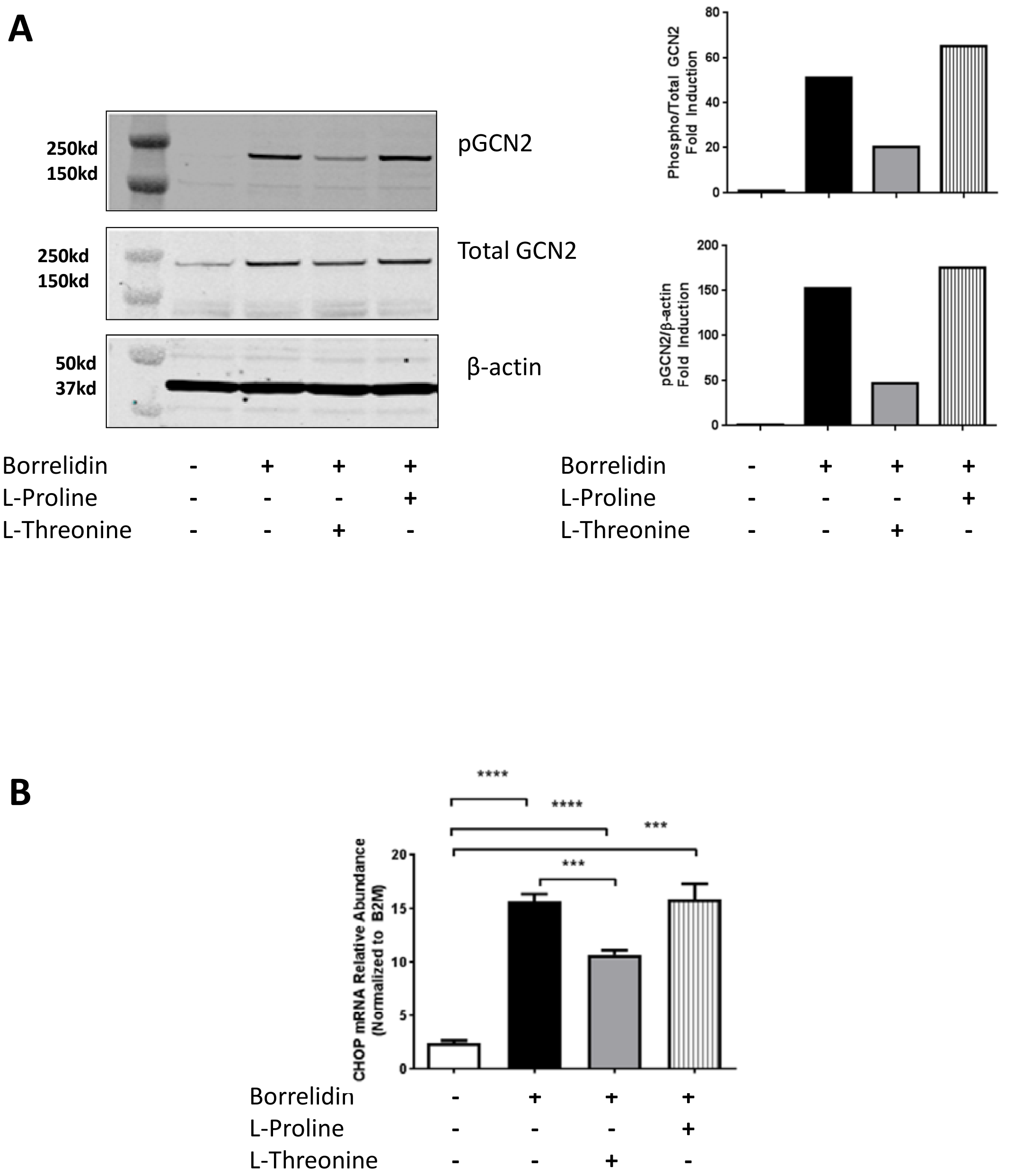
Table S5

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. Differentiatially 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
250kd
150kd
Total GCN2
50kd
37kd
β-actin
Borrelidin - + + +
L-Proline - - - +
L-Threonine - - + -
Phospho/Total GCN2 Fold Induction
0
20
40
60
80
pGCN2/β-actin Fold Induction
0
50
100
150
200
Borrelidin - + + +
L-Proline - - - +
L-Threonine - - + -
B
****
****
***
***
CHOP mRNA Relative Abundance (Normalized to B2M)
0
5
10
15
20
Borrelidin - + + +
L-Proline - - - +
L-Threonine - - + -

C

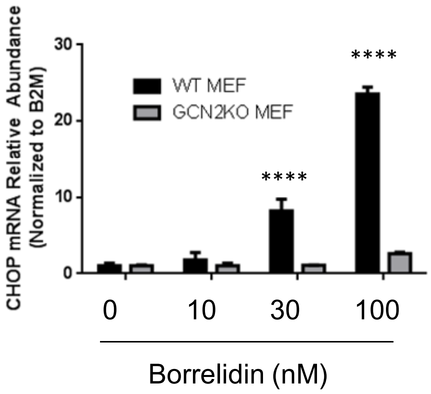


Figure S1. Borrelidin induced AAR (amino acid response) in fibroblast. Human cardiac fibroblast were treated with Borrelidin (100 nM), L-proline (2 mM) and L-threonine (2 mM) for 24 hrs. Protein levels of pGCN2 (phosphorylated general control nonderepressible 2), total GCN2, β-actin were examined by 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

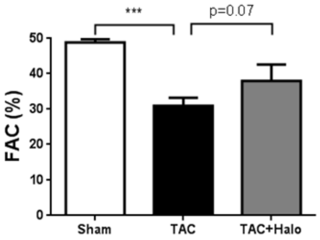


Figure S2. Halofuginone improves fractional area change (FAC) in TAC (transverse aortic constriction) mouse model. C57Bl/6J mice were subjected to TAC to induced heart failure and treated with halofuginone as described in figure 6. Fractional area change (FAC) was measured by echocardiography. There were 6, 9 and 7 mice in the sham, TAC and TAC + halofuginone groups Unpaired t-test. ***, $p< 0.001$.

Figure S3

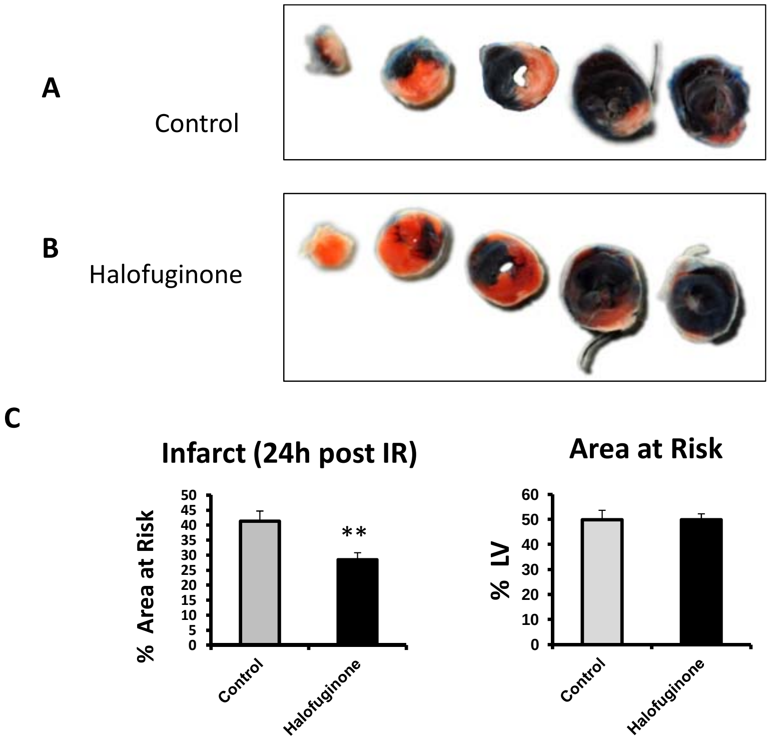


Figure S3. Halofuginone reduces infarct size in cardiac ischemic reperfusion (I/R) injury. C57BL/6 mice (11 mice in each group) were treated with 6 µg of halofuginone daily (~2 mg/kg) for 3 days. I/R injury was then induced by ligation of coronary artery for 30 min and reperfusion for 24 hrs. The heart 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 percetage 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

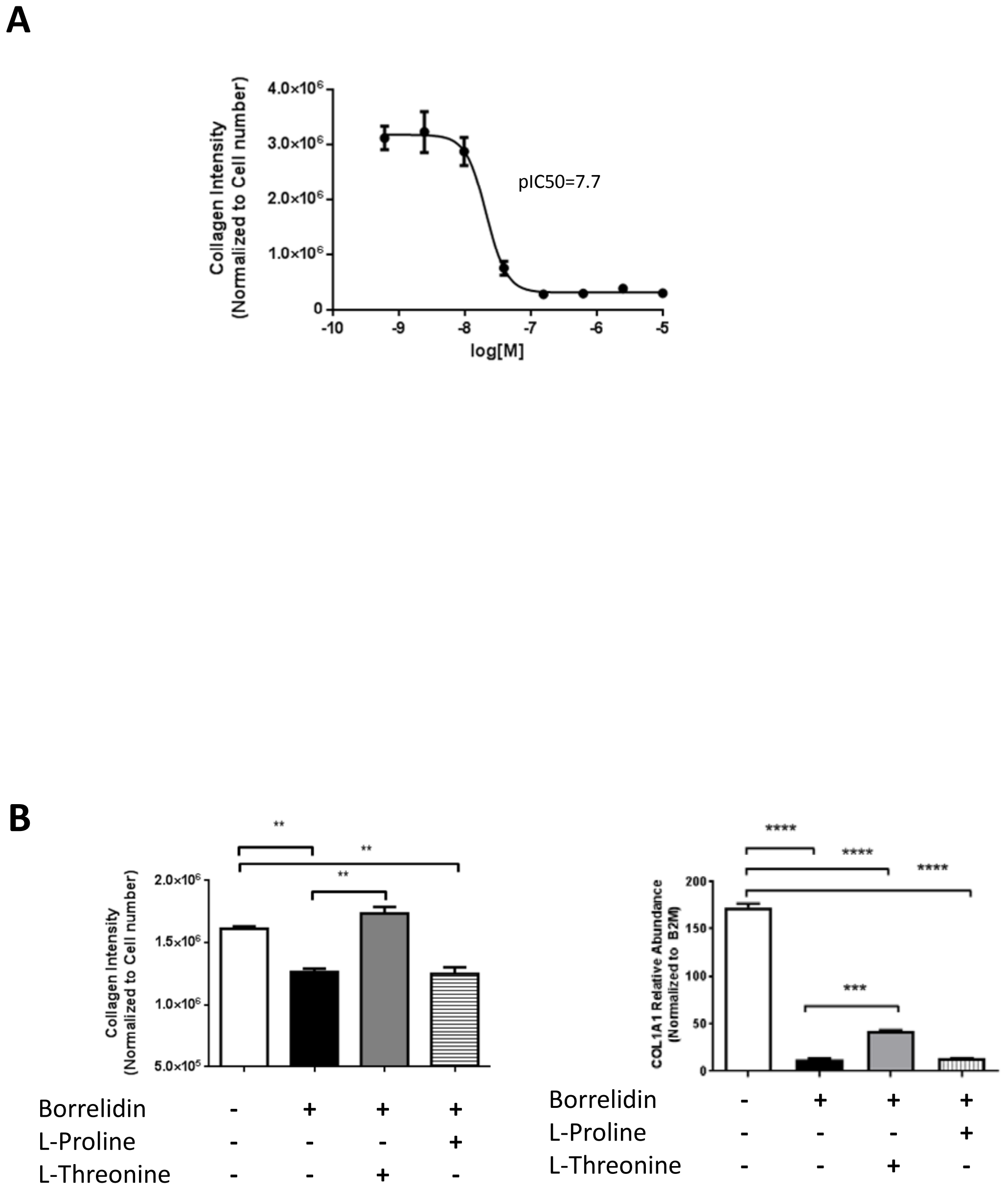

A
Collagen Intensity (Normalized to Cell number)
4.0×10^6
3.0×10^6
2.0×10^6
1.0×10^6
0
-10
-9
-8
-7
-6
-5
log[M]
pIC50=7.7
B
Collagen Intensity (Normalized to Cell number)
2.0×10^6
1.5×10^6
1.0×10^6
5.0×10^5
**
**
**
COL1A1 Relative Abundance (Normalized to B2M)
200
150
100
50
0
****
****
****
***
Borrelidin - + + +
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

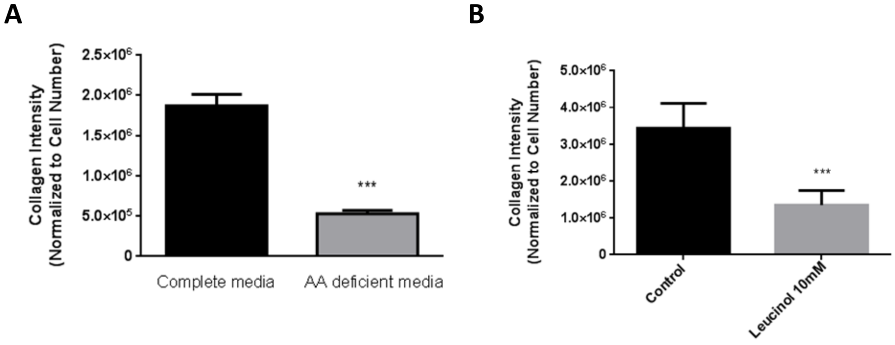
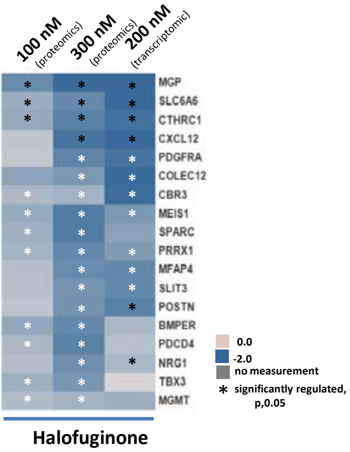


Figure S5. Amino acid starvation inhibits collagen deposition. WI38 fibroblast cells were stimulated with either complete DMEM (Dulbecco's Modified Eagle Medium) media with ficoll or DMEM media deficient in L-Lysine, L-Leucine, L-Arginine and L-gulatmine with ficoll (A, n=5). 24 hours later, cells were 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 mesoderm homeobox	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 periostin	overexpressed in HCM
bmp-binding endothelial regulator	cardio protective anti-arteriosclerotic
programmed cell death protein 4	cardiac valvulogenesis
neuregulin 1	induces CTGF promotes cardiac repair
t-box transcription factor	reprogrammes mature cardiac myocytes
meG DNA methyltransferase	linked to congenital heart defect



B

description
transcription factor
collagen triple helix repeat protein
Frizzle-like
edit heparan sulfate
Cys-rich
osteonectin
transcription regulator TAZ
insulin-like growth factor-binding protein 7
connective tissue growth factor
CDK14
activates TGFBb

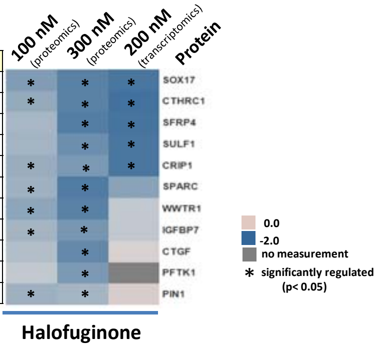


Figure S6: Two key differentially regulated pathways. The top 100 down-regulated proteins (from proteomic study) in cardiac fibroblasts were grouped according to their functions or properties based on Ingenuity description and the published literature. Differentially expressed heart failure related proteins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

Figure S7

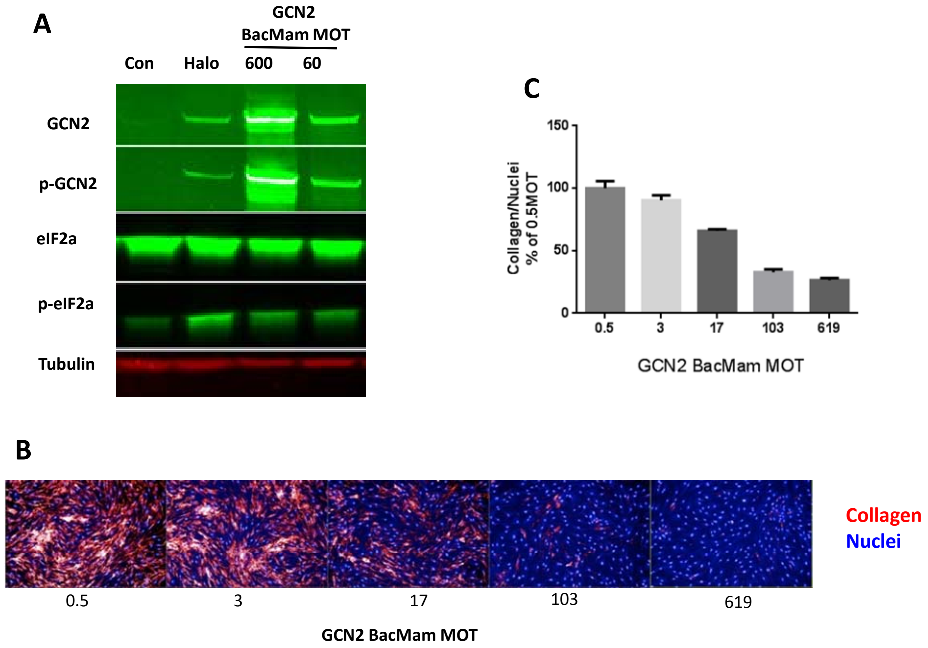


Figure S7. Overexpression of GCN2 (general control nonderepressible 2) activates AAR (amino acid response) and reduces collagen deposition. Normal human cardiac fibroblasts were transfected with BacMam virus encoding a constitively active form of GCN2 or treated with halofuginone in the presence of ficoll 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

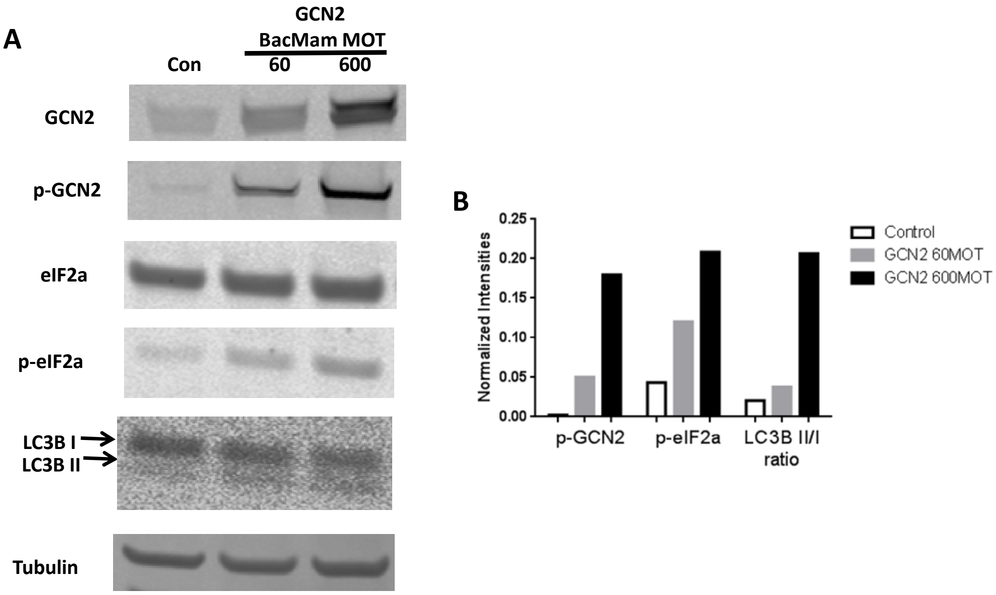


Figure S8. Over expression of GCN2 (general control nonderepressible 2) activates AAR (amino acid response) and enhance autophagy in cardiomyocytes. Human iPSC (induced pluripotent stem cells) derived cardiomyocytes were transfected with a BacMam virus encoding a constitutively active form of GCN2. The 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)

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