Extracellular vesicle-derived miR-144 as a novel mechanism for chronic intermittent hypoxia-induced endothelial dysfunction

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Supplementary Materials and Methods

Mice
All animal experiments were approved by Capital Medical University Animal Experimentation Ethics Committee, and in compliance with the National Institutes of Health Guidelines on the Use of Laboratory Animals. C57BL/6 mice were purchased from Beijing Vital River Laboratory Animal Technology Co. Twelve-week-old male mice were used. Unrestrained, freely moving mice were individually housed in chambers and received CIH treatment with fractional oxygen concentration cycled between 5% and 21% every 3 min, 8-10 h during the daytime for 15 or 30 days using a BioSpherix OxyCycler A84 system (BioSpherix, Redfield, NY, USA). Control mice were maintained in normoxic conditions for the same duration. Re-Nor post-CIH-treated mice were kept under normoxic conditions for 15 days after 30-day CIH treatment. For euthanasia, C57BL/6 mice were anesthetized with 5% isoflurane followed by terminal cardiac bleed before EV isolation, artery dissection and biochemical parameter measurement. Diastolic (DBP) and systolic (SBP) blood pressures were measured by tail-cuff plethysmography (BP-2000; Visitech Systems, Apex, North Carolina, USA).

Clinical Samples
The study design was approved by the Medical Ethics Committee of Beijing Anzhen Hospital (2017005) and conformed to the principles outlined in the Declaration of Helsinki. The research protocols were performed in accordance with the Board of Ethics at Beijing Anzhen Hospital. Written informed consent was obtained from all participants. All the subjects enrolled in this study were attending the department of Otolaryngology-Head and Neck Surgery, Beijing Anzhen Hospital, Capital Medical University. All clinical samples and clinical information were collected at Beijing Anzhen Hospital. All patients (aged 42–67 years) were male and underwent baseline anthropometric and blood pressure assessments, as well as overnight polysomnography detection, which was interpreted using standard approaches. All fasting blood samples for erythrocyte-derived EV (E-EV) purification were collected with standard EDTA anticoagulation. RNA integrity was assessed using a Bioanalyzer 2100 (Agilent Technologies, Chandler, Arizona, USA). Probes possessing “P” flags in all conditions were selected according to the quantile algorithm. Probes possessing “P” flags in all conditions were selected according to the quantile algorithm. The exclusion criteria for the non-OSA group were: subjects with hyperglycemia, cancer and infection, chronic obstructive pulmonary disease, chronic bronchitis, restrictive lung diseases, respiratory failure, aortic coarctation, Cushing syndrome, pheochromocytoma, primary aldosteronism, renal parenchymal disease, renovascular hypertension, thyroid disorders, stroke, coronary heart disease, and those who could not provide a complete medical history. The inclusion criteria for the non-OSA group was: AHI < 5/h (n=6), All participants were male. The exclusion criteria for the non-OSA group were: subjects with hyperglycemia, cancer and infection, chronic obstructive pulmonary disease, chronic bronchitis, restrictive lung diseases, respiratory failure, aortic coarctation, Cushing syndrome, pheochromocytoma, primary aldosteronism, renal parenchymal disease, renovascular hypertension, thyroid disorders, stroke, coronary heart disease, and those who could not provide a complete medical history. Detailed patient characteristics are presented in Table S5.

Cells and Tissues
Cell culture was carried out as previously described[1]. H5V endothelial cells (a kind gift from Prof. Yu Huang, Chinese University of Hong Kong, China), 293A cells, and murine erythroblastemia (MEL) cells were cultured in DMEM supplemented with 10% EV-free FBS (Exo-FBS™ EVs-depleted FBS, System Biosciences, USA), 100 IU/mL penicillin, and 100 μg/mL streptomycin. HUVECs were cultured in Endothelial Cell Medium (ScienCell Research Labs, USA) and 10% EV-free FBS. Mouse aortic rings (2 mm in length) were dissected in sterile PBS and incubated in DMEM (Gibco, USA) with or without EVs, Tempol (100 μM, Sigma, USA), Tiron (1 mM, Sigma, USA), DETCA (0.1 mM, Sigma, USA), or Oltipraz (100 μM, Sigma, USA). For intermittent hypoxia treatment, H5V cells, MEL cells, and aortic rings were exposed to an intermittent hypoxia generating system (OxyCycler model C42; Biospherix, Redfield, NY, USA) with the fractional ambient oxygen concentration cycling between 5%–21% per hour for the indicated time. For continuous hypoxia treatment, MEL cells were under the treatment of constant 5% oxygen concentration for the indicated time (OxyCycler model C42; Biospherix, Redfield, NY, USA). Prolyl hydroxylases (PHD) inhibitor dimethylxallylglycine (DMOG, MCE, China) was used as HIF-1α stabilizer to mimic the hypoxia status. The transcriptional inhibitor actinomycin D (MCE, China) was used to inhibit the expression of endogenous miRNA in recipient endothelial cells.

Microarray Analysis
RNA from aortas or from HUVECs was isolated using Trizol (Thermo Fisher Scientific, USA). Total RNA was quantified using a NanoDrop ND-2000 (Thermo Scientifics, USA). RNA integrity was assessed using a Bioanalyzer 2100 (Agilent Technologies, Chandler, Arizona, USA). Sample labeling, microarray hybridization, and washing were performed according to the manufacturer’s standard protocols. Genespring (version 13.1, Agilent Technologies, USA) was used to complete a basic analysis of the raw data. Raw data were normalized by the quantile algorithm. Probes possessing “P” flags in all conditions were selected for further analysis. Differentially expressed genes were then identified according to
fold change and P values calculated by the t-test. The threshold for up- and down-regulated genes was a fold change equal to or exceeding two, and a P value ≤ 0.05. Afterwards, GO analysis and KEGG analysis were applied to determine the roles of differentially expressed mRNAs. Hierarchical Clustering displayed distinguishable gene expression patterns among samples. Genes with overlapping differential expression under various conditions were identified using Venn diagrams.

**EV Isolation from Serum and Red Blood Cells**

S-EV isolation was carried out as previously described [1]. Blood from mice was clotted for 1 h at room temperature without anticoagulation, and centrifuged at 1,200×g for 10 min to obtain serum. Thereafter, the serum was centrifuged at 3,000×g for 10 min at 4°C. The supernatant was diluted in sterile PBS in a 1:1 ratio and centrifuged again at 14,000×g for 30 min followed by 2-h ultracentrifugation at 110,000×g (Beckman Coulter, Optima MAX-XP, USA) at 4°C. The EV pellet was washed in PBS, resuspended and passed through a 0.2-μm filter, and centrifuged at 110,000×g for 1 h at 4°C. The pellet fraction was then collected and resuspended in PBS or culture medium and used for subsequent functional wire myography studies (Danish Myo Technology 6200, Aarhus, Denmark) or purity evaluation by transmission electron microscopy using a NanoSight NS300 (Malvern Instruments, UK) or Western blotting.

E-EV isolation was carried out as previously described [2]. Red blood cells from normoxia- or CIH-treated mice were separated from EDTA-anticoagulated plasma by centrifugation at 3,000 rpm for 10 min. The upper plasma and leukocyte layer were removed by carefully pipetting and the fraction of red blood cells was then passed through a WBC Syringe Filter (Acrodisc PSF WBC Syringe Filter with Leukos, Pall, USA) to remove residual white blood cells. Approximately 350 μL of red blood cells were collected from the bottom of the microfuge tube. After washing in PBS, ~1×10^10 red blood cells from CIH-treated mice were resuspended in EV-free 1640 culture medium and lightly shaken under normoxia or intermittent hypoxia conditions for 20 min. The collected RBC-derived conditioned media were centrifuged progressively at 300×g for 10 min, 2,000×g for 10 min, 12,000×g for 45 min to remove RBCs, dead cells and cell debris. The supernatant was then passed through a 0.2μm microporous membrane filter (Millipore, MA, USA) and ultracentrifuged at 110,000×g for 70 min (Beckman Coulter, CA, USA). The EV pellets were washed with PBS to exclude contaminating proteins followed by a second ultracentrifugation at 110,000×g for 70 min. All the centrifugation steps were performed at 4°C. The EV pellet fraction was collected for qPCR, or resuspended in PBS or culture medium for subsequent cell culture and in vivo mouse treatments.

**Transmission Electron Microscopy**

Electron microscopy analysis of whole-mounted EVs was performed as previously described [1]. Briefly, S-EV pellets were fixed with 2% PFA and mounted onto grids. The grids were further fixed with 1% glutaraldehyde for 10 min and then negatively stained with methyl cellulose-UA for 10 min. After air drying, the grids were viewed using an FEI Tecnai electron microscope (FEI Tecnai, USA).

**Western Blotting and Silver Staining**

Protein samples prepared from C57BL/6 mouse aortas under the different conditions or H5V cells treated with agonimRs (Ribobio, Guangzhou, China) or S-EVs were electrophoresed through 10% SDS-poly-acrylamide gels, and transferred onto Immobilon-P polyvinylidene difluoride membranes (Millipore Corp., Bedford, MA, USA). Blots were incubated with antibodies and signals were detected using the ECL system (Pierce ECL Western Blotting Substrate, Thermo Fisher, Pittsburgh, USA). The primary antibodies used included anti-NRF2 (1:1000, Cell Signaling Technology, USA), anti-CAT (1:1000, Abcam), anti-β-ACTIN (1:5000, Abcam), anti-HIF-1α (1:1000, Abcam), and anti-GATA1 (1:1000, Abcam), anti-TSG101 (1:1000, System Bioscience), anti-C9 (1:1000, System Bioscience), anti-CD9 (1:1000, System Bioscience), anti-CD81 (1:1000, System Bioscience), anti-CD63 (1:1000, System Bioscience), anti-HBA1 (1:1000, ABclonal), anti-Calnexin (1:1000, Cell Signaling Technology), anti-Alix (1:1000, System Bioscience). Silver stain was used as a loading control. Briefly, gels were fixed in 50% methanol plus 50% acetic acid for 20 min followed by sensitizing in 0.02% sodium thiosulfate for 20 min. Thereafter, gels were immersed in silver reaction buffer (0.1% silver nitrate in 0.08% formalin) for 20 min and developed with 2% sodium carbonate in 0.04% formalin.

**Fluorescent Labeling of S-EVs and Confocal Microscopy**

S-EVs were labeled with the fluorescent dye, PKH67 (Sigma, USA) as previously described [1]. The PKH67-labeled S-EV pellet was re-suspended in serum free-culture medium and incubated with mouse aortas. After incubation, aortas were cut open, washed, fixed, and visualized under confocal microscopy. Endothelial cell nuclei were stained blue with DAPI (excitation wavelength: 405 nm). EVs were stained green with PKH67 (excitation wavelength: 488 nm). Confocal microscopy images were captured with a Fluoview 1000 (FV1000, Olympus, Tokyo, Japan) and analyzed with Fluoview Version 1.5 (FV3000, Olympus).
Measurement of Superoxide Anion Production
Fluorimetric measurements were performed using the Fluoview FV3000 laser scanning confocal system (Olympus, Tokyo, Japan). H5V cells or aortas were incubated with DHE (5 μM in PBS containing CaCl₂, MgCl₂ and glucose) at 37°C for 10 min in the dark. After incubation, cells or tissues were washed three times in PBS. Images were taken of DHE fluorescence with an excitation wavelength of 510 nm and an emission wavelength of 590 nm. Auto-fluorescence of elastin was observed at an excitation wavelength of 488 nm and an emission wavelength of 520 nm.

Organ Culture of Aortic Rings with S-EVs or E-EVs
Mouse aortic rings (2 mm in length) were dissected in sterile PBS and incubated in DMEM (Gibco, USA) with or without S-EVs or E-EVs. The medium was prepared with S-EVs (from 1 mL mouse blood, ~100 μg) or with E-EVs (from 1×10⁶ red blood cells, ~50 μg) suspended in 1 mL DMEM supplemented with 10% EV-free FBS (Exo-FBS™ EVs-depleted FBS, System Biosciences), 100 IU/mL penicillin, and 100 μg/mL streptomycin. EV-free serum was used as a negative control for all experiments. After the incubation period, aortic rings were treated with DHE staining for superoxidative anion measurement or mounted for wire myography to measure isometric forces.

Vascular functional study
Vascular relaxation including endothelium-dependent relaxation, flow-mediated dilatation and endothelial-independent relaxation was performed as a previous report[1]. After mice were euthanized, thoracic aortae were removed and placed in oxygenated ice-cold PSS solution containing 130 mM NaCl, 4.7 mM KCl, 1.6 mM CaCl₂, 1.17 mM MgSO₄·H₂O, 14.9 mM NaHCO₃, 1.2 mM KH₂PO₄, 5.5 mM D-glucose, and 0.026 mM EDTA. Changes in the isometric tone of the aortic rings were recorded by wire myography (Danish Myo Technology 6200, Aarhus, Denmark). The rings were adjusted to an optimal baseline tension of 3 mN and allowed to equilibrate for one hour. Rings were rinsed in PSS solution before contraction with 60 mM KCl. EDR was measured in phenylephrine (3 μM) precontracted rings by recording concentration responses to cumulative addition of acetylcholine. One group of rings was incubated with ROS scavengers, Tiron (1 mM) and DETCA (0.1 mM) for 30 min before the assay. Endothelium-independent relaxation to sodium nitroprusside was performed in aortic rings denuded of endothelium using fine forceps. Acetylcholine, phenylephrine, and sodium nitroprusside were purchased from Sigma-Aldrich (Sigma Aldrich, USA).

For flow-mediated dilatation (FMD) assay, segments of second-order resistance mesenteric arteries were dissected in sterilized PBS and cultured in DMEM for 48 h. Thereafter, each vessel was cannulated between two glass cannulas onto pressure myograph. The vessel diameter was recorded using Zeiss Axiovert 40 microscope (model 110P) aided with video camera (Danish Myo Technology, Aarhus, Denmark). Phe (10 μM) was used to produce steady constriction in the artery stabilized at 80 mmHg intraluminal pressure; and FMD was triggered by pressure change that equals ~15 dynes/cm² shear stress. By the end of each experiment, perfusion solution was switched to a Ca²⁺-free, EGTA (2 mM)-containing Krebs solution to induce maximum passive dilatation. FMD was presented as % of diameter changes: (flow-mediated dilatation- Phe tone)/(passive dilatation - Phe tone).

Electroporation of EVs
Electroporation of EVs was performed using a Gene Pulser Xcell electroporator (BioRad, USA). S-EVs or E-EVs were diluted in OptiMEM (Thermo Fisher Scientific) to a total volume of 100 μL and were electroporated with 400 pM scrambled negative control (NC) or indicated anti-miRs (Ribobio, Guangzhou, China) at 250 V. Aggregates of EVs formed during electroporation were dissociated by vigorous pipetting and immediately used to treat H5V cells or injected into mice via the tail vein.

RNA Extraction
RNA for pri-miRNA or mRNA detection from mouse aortas, mouse aortic endothelial cells, red blood cells, or H5V cells was isolated using Trizol (Thermo Fisher Scientific, USA). For isolation of microRNA from aortic endothelial cells, C57BL/6 mouse aortas were cleared of adventitial adipose tissue. The lumen was quickly flushed with 150 μL cell or tissue lysis buffer (mirVana miRNA Isolation Kit, Thermo Fisher Scientific, USA) three times using a 23 g syringe connected to a microfuge tube. The intimal miRNA was isolated from the eluate using an mirVana miRNA Isolation Kit (Thermo Fisher Scientific, USA) according to the manufacturer’s protocol. The same kit was used to extract miRNA from mouse red blood cells. For isolation of miRNAs from EVs, 5 pg of the synthetic Caenohabditis elegans miRNA, cel-miR-39, was added to each sample as a spike-in control for purification efficiency.

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miRNA and pri-miRNA Analysis
Isolated total RNAs were reverse-transcribed into complementary DNA by the M-MLV RT system (Thermo Fisher Scientific, USA). Real-time PCR for miRNAs was performed using Taqman Fast Universal PCR Master Mix (Applied Biosystems, USA). Reactions were carried out in Applied Biosystems 7900 instrument (Applied Biosystems, USA). Primer catalog numbers were: mmu482914 for mmu-miR-1a-3p; mmu480907 for mmu-miR-125b-5p; mmu478412 for mmu-miR-106b-5p; mmu482681 for mmu-miR-126a-3p; mmu481324 for mmu-miR-142a-5p; mmu483162 for mmu-let-7a-1-3p; mmu480919 for mmu-miR-132-3p mmu480947 for mmu-miR-150-5p; mmu478494 for mmu-miR-10b-5p; mmu480953 for mmu-miR-155-5p; mmu478384 for mmu-miR-27a-3p; and mmu482959 for mmu-miR-144-3p (TheromFisher, USA). Quantification of mRNAs and pri-miRNAs was performed using SYBR Green Supermix (Bio-Rad, USA). The primers used to amplify pri-miRNAs and mRNAs are shown in Table S6. Expression levels of mRNAs, pri-miRNAs, were normalized to control β-actin. Spike-in (cel-miR-39, miRNeasy Serum/Plasma Spike-In Control kit, QIAGEN, USA) as well as U6 was utilized as the reference to evaluate the levels of EV miRNAs. In EV-treated endothelial cells, U6 was used as the internal control for miR-144 expression. Real-time PCR was performed using an Applied Biosystems 7900 instrument (Applied Biosystems, USA).

Plasmid Construction and Luciferase Reporter Gene Assays
The 3’-UTR of mouse Nrf2 fragments was cloned into pMir luciferase reporter vector (Promega) at the XhoI and NotI sites. A 2,000-bp mouse miR-144 promoter fragment was cloned into MluI/XhoI sites of the reporter vector, pGL3-basic (miR-144-Luc), as wild type plasmid. For the mutant plasmid, GATA1 binding site GAAGATAAACA was mutated to TTCTATTTGT. After confirmation by DNA sequencing, the purified plasmid was transiently transfected into 293A cells using Lipofectamine 2000 reagent at a ratio of 1 μL Lipofectamine 2000/1 μg of DNA according to the manufacturer’s protocol (Thermo Fisher Scientific). The indicated reporter constructs (0.2 μg) were co-transfected with the indicated expression vectors and the internal control pRL-TK reporter (30 ng, Promega, USA). Luciferase activity was assessed using the Dual-Luciferase Reporter Assay System (Promega).

Lentiviral Treatment
C57BL/6 mouse aortas was transfected with lentiviruses (titer 10⁹/mL) overexpressing Nrf2 (from Vigene Biosciences, China) 293A cells or MEL cells were transfected with lentiviruses (titer 10⁹/mL) overexpressing Hif-1α (Hif-1α OE) (a kind gift from Prof. Rui Chen, Capital Medical University, China) or Gata1 (from Vigene Biosciences, China), or Hif-1α shRNA or Gata1 shRNA to silence Hif-1α and Gata1, respectively (Santa Crus, USA).

Statistical Analysis
Statistical analysis is summarized in the figure legends. In most cases, the results represent the mean ± standard error of the mean (SEM) of n separate experiments. Concentration-response curves were compared by two-way analysis of variance (two-way ANOVA) followed by Bonferroni post-hoc test. Two-tailed Student’s t-test was used when two groups were compared. One-way analysis of variance (ANOVA) was performed to determine whether there was a significant difference between more than two datasets, followed by Bonferroni’s post hoc test. P < 0.05 indicates statistical difference between groups.
Supplementary Figures

Figure S1. Endothelial function and physiological indices of C57BL/6 mice under normoxia and chronic intermittent hypoxia (CIH) conditions.

A, CIH treatment impaired endothelium-dependent relaxation in carotid arteries in a time-dependent manner. B, Levels of blood pressure in mice exposed to normoxia, CIH-15d and CIH-30d conditions. C, Levels of systolic blood pressure in mice exposed to normoxia, CIH-30d and CIH-30d plus 15-day normal oxygen conditions. D-F, Levels of blood glucose (D), blood triglyceride (E) and blood cholesterol (F) in mice exposed to normoxia and CIH-30d conditions. TG, triglyceride; CHO, cholesterol. Results are the mean ± SEM (n = 4-12). *P < 0.05 vs. Nor. #P < 0.05 vs. CIH. One-way ANOVA (B, C), two-way ANOVA (A) and two-tailed t test (E).
Figure S2. Endothelial function, endothelial superoxide anion production and profiles of differentially expressed genes in aortas from mice exposed to normoxia or chronic intermittent hypoxia (CIH) conditions.

A-B, Transcriptome microarray assays identified differentially expressed genes in aortas from mice treated with normoxia (N), CIH (C) or Re-Nor post-CIH (R). Kyoto Encyclopedia of Genes and Genomes (KEGG) and Gene ontology (GO) analysis predicted the functions of some of these genes to be associated with angiogenesis (A) or inflammation (B).

C, mRNA expression of NOX subunits, Nox2 and p47phox, in mouse aortas was promoted by CIH treatment for 30 days.

D-E, Thirty-minute pretreatment with ROS scavengers, Tempol (100 μM), or Tiron (1 mM) and DETCA (0.1 mM), or NRF2 agonist, Oltipraz (0.5 g/kg in saline, gavage once per day for 4 days before functional evaluation), blocked increased superoxide anion production in aortic endothelial cells (D) and reversed CIH-induced endothelial dysfunction in carotid aortas after CIH incubation for 30 days (E). Results are the mean ± SEM (n = 4). *P < 0.05 vs. Nor. #P < 0.05 vs. CIH. One-way ANOVA (D), two-way ANOVA (E) and two-tailed t test (C).
Figure S3. CIH S-EVs impair endothelial function, augment superoxide anion radical generation and decrease NRF2 expression in endothelial cells.

A, sodium nitroprusside-induced endothelium-independent relaxation of mouse aortas following serum extracellular vesicle (S-EV) treatment. B, Forty-eight-h treatment with CIH S-EVs impaired acetylcholine-induced endothelium-dependent relaxation (EDR) in mouse aortas in a dose-dependent manner. 1:n dilution means S-EVs from 1 mL blood were suspended in n mL S-EV-free medium. C, 30-day CIH S-EV treatment had a more severe adverse effect on endothelial function compared with 15-day CIH S-EV treatment. D, CIH S-EV treatment reduced the protein level of the antioxidant transcription factor, NRF2, and its downstream target, CAT, in H5V cells. The lower panels show the relative levels of NRF2 and CAT.

E-F, CIH S-EV-incubation increased superoxide anion production in H5V cells, which was blocked by 30 min-pretreatment with ROS scavengers, Tempol (100 μM), or Tiron (1 mM) and DETCA (0.1 mM) (E). Summary of the dihydroethidium (DHE) fluorescence intensity (F). G, CIH S-EV did not change the mRNA levels of NOX subunits or Xdh in H5V cells. H, Lentivirus-mediated overexpression of Nrf2 in mouse aortas after 48-h infection. Results are the mean ± SEM (n = 4). *P < 0.05 vs. Nor S-EV. **P < 0.05 vs. CIH S-EV. One-way ANOVA (D, F, G) and two-way ANOVA (B, C).
**Figure S4. Blood pressure influenced by E-EVs and anti-miR-144-loaded CIH E-EVs.**

A-B, qPCR determined the expression levels of miR-144 in E-EVs from OSA patients (A), CIH-exposed mice (B), and their control groups (U6 as the reference). C-E, The influence of Nor E-EVs, CIH E-EVs and anti-miR-144-loaded CIH S-EVs on systolic blood pressure (A), mean blood pressure (B) and diastolic blood pressure (C) under normoxia or chronic intermittent hypoxia. Results are the mean ± SEM (n = 4-13). *P < 0.05 vs. OSA E-EV (A), or Nor E-EV (B), or Nor E-EV anti-Scr (C-E). ²P < 0.05 vs. CIH E-EV anti-Scr. Two-tailed t test (A, B); One-way ANOVA (C-E).
Table S1. Differentially expressed proteins in aortas from CIH-treated mice.

| No. | Target ID | Gene ID | Gene Symbol | Fold (IH vs.N) | Reg. (IH vs.N) | p Value (IH vs.N) | Fold (RNpIH vs.IH) | Reg. (RNpIH vs.IH) | p Value (RNpIH vs.IH) |
|-----|-----------|---------|-------------|----------------|---------------|------------------|------------------|---------------|----------------------|
| 1   | AK084136  | 319388  | Irx3os      | -5.45          | down          | 0.00             | 1.95             | up             | 0.05                 |
| 2   | NM_010480 | 15519   | Hsp90aa1    | -4.23          | down          | 0.00             | 1.85             | up             | 0.04                 |
| 3   | NM_009786 | 12301   | Cacybp      | -4.16          | down          | 0.01             | 1.94             | up             | 0.04                 |
| 4   | NM_172391 | 268390  | Ahsa2       | -4.06          | down          | 0.01             | 1.79             | up             | 0.04                 |
| 5   | AK039015  |         |             | -3.87          | down          | 0.00             | 1.80             | up             | 0.02                 |
| 6   | NM_013863 | 29810   | Bag3        | -3.62          | down          | 0.00             | 1.83             | up             | 0.02                 |
| 7   | AK018597  | 26359   | Anxa10      | -3.21          | down          | 0.01             | 1.89             | up             | 0.00                 |
| 8   | ENSMUST00000135943 | 66234 | Msmo1       | -3.18          | down          | 0.00             | 1.55             | up             | 0.03                 |
| 9   | NM_175692 | 319317  | Snhgl1      | -3.17          | down          | 0.01             | 1.93             | up             | 0.05                 |
| 10  | NM_025819 | 66875   | Swt1        | -3.16          | down          | 0.00             | 1.59             | up             | 0.04                 |
| 11  | AK199574  | 70788   | Klhl30      | -3.13          | down          | 0.00             | 1.28             | up             | 0.02                 |
| 12  | BG080251  | 97177   | Gm12670     | -3.11          | down          | 0.00             | 1.49             | up             | 0.02                 |
| 13  | AK171865  | 105203  | Fam208b     | -3.06          | down          | 0.00             | 1.77             | up             | 0.03                 |
| 14  | AK087131  |         |             | -3.04          | down          | 0.00             | 1.89             | up             | 0.02                 |
| 15  | NM_025844 | 66917   | Chordc1     | -3.01          | down          | 0.01             | 1.72             | up             | 0.05                 |
| 16  | NM_010177 | 14103   | Fasl        | -3.01          | down          | 0.00             | 1.97             | up             | 0.02                 |
| 17  | NM_028094 | 72094   | Ugt2a3      | -2.98          | down          | 0.00             | 1.90             | up             | 0.00                 |
| 18  | ENSMUST00000192142 | 108664 | Atp6v1h     | -2.93          | down          | 0.00             | 1.85             | up             | 0.02                 |
| 19  | ENSMUST00000172726 |         |             | -2.90          | down          | 0.00             | 1.78             | up             | 0.04                 |
| 20  | AK039495  | 30056   | Timm9       | -2.89          | down          | 0.00             | 1.85             | up             | 0.00                 |
| 21  | NM_177225 | 320679  | Samd12      | -2.86          | down          | 0.00             | 1.99             | up             | 0.03                 |
| 22  | NM_177583 | 208117  | Aph1b       | -2.85          | down          | 0.00             | 1.92             | up             | 0.01                 |
| 23  | ENSMUST00000132911 | 269536 | Tex10       | -2.83          | down          | 0.00             | 1.92             | up             | 0.04                 |
| 24  | NM_009471 | 22247   | Umps        | -2.83          | down          | 0.01             | 1.95             | up             | 0.03                 |
| 25  | NM_001039710 | 67876  | Coq10b      | -2.82          | down          | 0.00             | 1.82             | up             | 0.04                 |
|   | GeneID       | Description   | Fold Change | Regulation | p-value |
|---|-------------|---------------|-------------|------------|---------|
| 26| ENSMUST00000051437 | -2.81 | down | 0.02 | 1.97 up | 0.03 |
| 27| NM_001122954  | 18784 Pla2g5 | -2.77 | down | 0.01 | 1.93 up | 0.04 |
| 28| XM_006527126  | 271564 Vps13a | -2.76 | down | 0.00 | 1.98 up | 0.01 |
| 29| AV310571     | -2.75 | down | 0.01 | 1.69 up | 0.02 |
| 30| NM_001162486  | 408191 Gm5415 | -2.75 | down | 0.00 | 1.56 up | 0.00 |
| 31| ENSMUST00000067978 | 224224 Impg2 | -2.73 | down | 0.00 | 1.75 up | 0.00 |
| 32| XM_006535986  | 18764 LOC100862442 | -2.72 | down | 0.00 | 1.67 up | 0.03 |
| 33| NM_145521     | 227721 Ppapdc3 | -2.70 | down | 0.01 | 1.90 up | 0.00 |
| 34| NM_009551     | 22682 Zfand5 | -2.69 | down | 0.00 | 1.74 up | 0.01 |
| 35| NM_001256112  | 76824 Mtfr1l | -2.67 | down | 0.00 | 1.39 up | 0.01 |
| 36| ENSMUST00000190232 | -2.66 | down | 0.01 | 1.66 up | 0.00 |
| 37| AK080258      | -2.65 | down | 0.00 | 1.54 up | 0.00 |
| 38| NM_009837     | 12464 Cct4 | -2.64 | down | 0.00 | 1.74 up | 0.01 |
| 39| NM_026674     | 68318 Aph1c | -2.63 | down | 0.00 | 1.75 up | 0.02 |
| 40| XM_006534815  | 18764 Pkd2 | -2.63 | down | 0.00 | 1.91 up | 0.01 |
| 41| NM_177788     | 277978 Exoc3l | -2.59 | down | 0.00 | 1.35 up | 0.01 |
| 42| NM_153786     | 215031 Vgll2 | -2.58 | down | 0.02 | 1.80 up | 0.02 |
| 43| ENSMUST00000145024 | 16847 Lepr | -2.57 | down | 0.00 | 1.87 up | 0.04 |
| 44| NM_146118     | 227731 Slc25a25 | -2.56 | down | 0.00 | 1.88 up | 0.01 |
| 45| NM_027805     | 71474 Ppp6r2 | -2.56 | down | 0.01 | 1.50 up | 0.05 |
| 46| NM_181040     | 230649 Atpaf1 | -2.56 | down | 0.00 | 1.78 up | 0.00 |
| 47| ENSMUST00000099029 | -2.56 | down | 0.00 | 1.65 up | 0.00 |
| 48| ENSMUST00000152019 | -2.54 | down | 0.00 | 1.78 up | 0.01 |
| 49| AK171523      | 407830 BC010981 | -2.54 | down | 0.00 | 1.54 up | 0.02 |
| 50| NAP111319-1   | -2.54 | down | 0.00 | 1.52 up | 0.01 |
| 51| AK047768      | 11472 Actn2 | -2.52 | down | 0.01 | 1.70 up | 0.00 |
| 52| NM_029295     | 75458 Cklf | -2.52 | down | 0.00 | 1.42 up | 0.02 |
| 53| ENSMUST00000178218 | 216877 Dhx33 | -2.52 | down | 0.00 | 1.71 up | 0.02 |
| 54| NAP061415-1   | -2.51 | down | 0.00 | 1.47 up | 0.03 |
| 55| TC1636899     | -2.51 | down | 0.00 | 1.84 up | 0.03 |
| 56| NM_008351     | 16159 Il12a | -2.51 | down | 0.00 | 1.99 up | 0.02 |
|   | Gene Reference | Gene Name | Fold Change | Direction | Expression | Fold Change | Direction |
|---|----------------|-----------|-------------|-----------|------------|-------------|-----------|
| 57 | NM_001082485   | Zfp266    | -2.50       | down      | 0.00       | 1.97        | up        | 0.02 |
| 58 | NM_199062      | Zfp781    | -2.50       | down      | 0.00       | 1.80        | up        | 0.00 |
| 59 | ENSMUST0000160058 |         | -2.50       | down      | 0.01       | 1.63        | up        | 0.03 |
| 60 | ENSMUST0000162574 |         | -2.49       | down      | 0.00       | 1.54        | up        | 0.02 |
| 61 | NM_010477      | Hspd1     | -2.48       | down      | 0.01       | 1.67        | up        | 0.03 |
| 62 | NAP099731-001  |          | -2.48       | down      | 0.00       | 1.96        | up        | 0.00 |
| 63 | AK157456       | Gm830     | -2.48       | down      | 0.02       | 1.82        | up        | 0.04 |
| 64 | AK134128       | Gspt1     | -2.48       | down      | 0.00       | 1.54        | up        | 0.02 |
| 65 | NM_009543      | Rnf103    | -2.47       | down      | 0.00       | 1.59        | up        | 0.03 |
| 66 | AK172643       | Tmed5     | -2.47       | down      | 0.01       | 1.89        | up        | 0.01 |
| 67 | AI606402       | 4930415C11Rik | -2.47 | down      | 0.00       | 1.90        | up        | 0.01 |
| 68 | ENSMUST0000121742 |       | -2.47       | down      | 0.00       | 1.91        | up        | 0.00 |
| 69 | NM_001081152   | Npat      | -2.46       | down      | 0.01       | 1.92        | up        | 0.03 |
| 70 | ENSMUST0000030015 |       | -2.46       | down      | 0.00       | 1.55        | up        | 0.01 |
| 71 | NM_175250      | Sult2a8   | -2.46       | down      | 0.00       | 2.00        | up        | 0.01 |
| 72 | NM_177431      | Adams20   | -2.45       | down      | 0.00       | 1.99        | up        | 0.00 |
| 73 | ENSMUST0000185704 |       | -2.45       | down      | 0.00       | 1.96        | up        | 0.00 |
| 74 | AK016918       | Nbas      | -2.44       | down      | 0.02       | 1.62        | up        | 0.00 |
| 75 | ENSMUST0000117199 |       | -2.44       | down      | 0.00       | 1.87        | up        | 0.01 |
| 76 | NM_025676      | Mcm8      | -2.44       | down      | 0.00       | 1.92        | up        | 0.01 |
| 77 | NM_010902      | Nfe2l2    | -2.44       | down      | 0.00       | 1.86        | up        | 0.04 |
| 78 | NM_009908      | Cmas      | -2.44       | down      | 0.00       | 1.46        | up        | 0.01 |
| 79 | NM_025875      | Rhm8a     | -2.43       | down      | 0.00       | 1.74        | up        | 0.02 |
| 80 | NM_145953      | Cth       | -2.43       | down      | 0.04       | 1.95        | up        | 0.02 |
| 81 | AK137479       | Vps37a    | -2.43       | down      | 0.00       | 1.46        | up        | 0.04 |
| 82 | NM_009549      | Zfp185    | -2.42       | down      | 0.01       | 1.51        | up        | 0.01 |
| 83 | NM_146189      | Mybpc2    | -2.42       | down      | 0.05       | 1.56        | up        | 0.03 |
| 84 | NM_133940      | Fbx114    | -2.41       | down      | 0.00       | 1.77        | up        | 0.01 |
| 85 | NM_023773      | Mphosph8  | -2.41       | down      | 0.00       | 1.75        | up        | 0.02 |
| 86 | NM_001029977   | Gm4788    | -2.41       | down      | 0.00       | 1.90        | up        | 0.00 |
| 87 | NM_177356      | Lamp3     | -2.40       | down      | 0.00       | 1.68        | up        | 0.01 |
|   | Gene Name   | Accession | Log2 Fold Change | Direction | FDR   | p Value |
|---|-------------|-----------|-----------------|-----------|-------|---------|
| 88| ENSMUST00000119147 | -2.40 | down | 0.00 | 1.66 | up | 0.00 |
| 89| NM_201369 | 381695 | N4bp2l2 | -2.40 | down | 0.00 | 1.64 | up | 0.00 |
| 90| NAP069232-1 | -2.39 | down | 0.00 | 1.66 | up | 0.01 |
| 91| NM_008650 | 17850 | Mut | -2.39 | down | 0.00 | 1.56 | up | 0.01 |
| 92| AK162903 | 72465 | Zfp131 | -2.39 | down | 0.00 | 1.61 | up | 0.04 |
| 93| NM_030072 | 665270 | Plb1 | -2.39 | down | 0.00 | 1.40 | up | 0.01 |
| 94| NM_028059 | 72020 | Zfp654 | -2.39 | down | 0.01 | 1.98 | up | 0.05 |
| 95| BC019993 | 21340 | Taf1b | -2.38 | down | 0.00 | 1.33 | up | 0.01 |
| 96| NM_177304 | 320981 | Enpp6 | -2.38 | down | 0.00 | 1.92 | up | 0.04 |
| 97| NM_029851 | 110350 | Dynceh1 | -2.38 | down | 0.00 | 1.77 | up | 0.02 |
| 98| NM_009398 | 21930 | Tnfaip6 | -2.38 | down | 0.01 | 1.65 | up | 0.01 |
| 99| NM_007729 | 12814 | Col11a1 | -2.38 | down | 0.00 | 1.54 | up | 0.03 |
| 100| AK178446 | 1E+08 | Gm14410 | -2.38 | down | 0.00 | 1.85 | up | 0.01 |
| 101| NM_175308 | 100465 | Mob3c | -2.38 | down | 0.00 | 1.59 | up | 0.04 |
| 102| NAP111303-1 | -2.37 | down | 0.00 | 1.88 | up | 0.00 |
| 103| NM_178722 | 240186 | Zfp438 | -2.37 | down | 0.00 | 1.83 | up | 0.02 |
| 104| NM_010330 | 13723 | Emb | -2.35 | down | 0.00 | 1.72 | up | 0.01 |
| 105| NM_029790 | 76894 | Mettl15 | -2.35 | down | 0.00 | 1.48 | up | 0.05 |
| 106| NM_029555 | 76263 | Gstk1 | -2.35 | down | 0.00 | 1.47 | up | 0.03 |
| 107| NM_001144855 | 68507 | Ppfa4 | -2.35 | down | 0.00 | 1.57 | up | 0.00 |
| 108| NM_011082 | 18703 | Pigr | -2.35 | down | 0.01 | 1.57 | up | 0.02 |
| 109| NM_145368 | 209186 | Acnat2 | -2.35 | down | 0.00 | 1.66 | up | 0.02 |
| 110| NM_026578 | 68147 | Gar1 | -2.35 | down | 0.00 | 1.82 | up | 0.01 |
| 111| ENSMUST00000066241 | -2.34 | down | 0.00 | 1.47 | up | 0.04 |
| 112| NAP005004-001 | -2.33 | down | 0.00 | 1.81 | up | 0.01 |
| 113| NM_001287388 | 21349 | Tal1 | -2.33 | down | 0.00 | 1.88 | up | 0.00 |
| 114| NM_026637 | 110175 | Ggct | -2.33 | down | 0.00 | 1.99 | up | 0.05 |
| 115| NM_028787 | 74150 | Scl35f5 | -2.33 | down | 0.01 | 1.99 | up | 0.01 |
| 116| NM_025421 | 66204 | Acyp1 | -2.33 | down | 0.00 | 1.80 | up | 0.01 |
| 117| ENSMUST00000188463 | 103268 | Cep571l | -2.33 | down | 0.01 | 1.94 | up | 0.01 |
| 118| NM_009826 | 12421 | Rbicc1 | -2.33 | down | 0.00 | 1.62 | up | 0.02 |
|   | Ensembl gene ID | Entrez gene ID | Gene Symbol | Fold Change | Expression Direction | Log2 Fold Change | p-value |
|---|----------------|----------------|-------------|-------------|----------------------|-----------------|---------|
| 119 | AF425084 | 97848 | Serpinb6c | -2.32 | down | 0.01 | 1.76 | up | 0.04 |
| 120 | XM_006497255 | 329324 | Syt14 | -2.32 | down | 0.00 | 1.69 | up | 0.01 |
| 121 | NM_053090 | 84652 | Fam126a | -2.31 | down | 0.01 | 1.66 | up | 0.04 |
| 122 | NM_178610 | 52705 | Krr1 | -2.31 | down | 0.00 | 1.56 | up | 0.01 |
| 123 | NM_001081254 | 545136 | Fam186b | -2.31 | down | 0.00 | 1.51 | up | 0.03 |
| 124 | NM_021421 | 52477 | Angel2 | -2.31 | down | 0.00 | 1.65 | up | 0.03 |
| 125 | NM_001114332 | 72472 | Slc16a10 | -2.31 | down | 0.00 | 1.96 | up | 0.01 |
| 126 | ENSMUST00000142299 | - | - | -2.31 | down | 0.01 | 1.69 | up | 0.01 |
| 127 | NM_009017 | 19369 | Raet1b | -2.31 | down | 0.00 | 1.70 | up | 0.03 |
| 128 | NM_134072 | 105387 | Akr1c14 | -2.31 | down | 0.00 | 1.72 | up | 0.02 |
| 129 | NM_001164493 | 208439 | Klhl29 | -2.31 | down | 0.01 | 1.81 | up | 0.02 |
| 130 | ENSMUST00000122407 | - | - | -2.30 | down | 0.00 | 1.83 | up | 0.00 |
| 131 | DW711327 | - | - | -2.30 | down | 0.00 | 1.38 | up | 0.01 |
| 132 | AK016293 | 114670 | 4930573O21Rik | -2.30 | down | 0.01 | 1.64 | up | 0.01 |
| 133 | NM_025513 | 66362 | Exosc3 | -2.29 | down | 0.00 | 1.85 | up | 0.00 |
| 134 | XM_006514760 | 544763 | Hbq1b | -2.29 | down | 0.00 | 1.79 | up | 0.00 |
| 135 | NM_013642 | 19252 | Dusp1 | -2.29 | down | 0.01 | 1.57 | up | 0.03 |
| 136 | NM_011721 | 22427 | Wrn | -2.29 | down | 0.00 | 1.72 | up | 0.00 |
| 137 | NM_025903 | 15983 | Ifrd2 | -2.29 | down | 0.00 | 1.74 | up | 0.01 |
| 138 | NM_197943 | 97761 | Sgsm2 | -2.29 | down | 0.00 | 1.71 | up | 0.01 |
| 139 | NM_025483 | 66315 | Senp7 | -2.29 | down | 0.03 | 1.77 | up | 0.04 |
| 140 | NM_001281851 | 330409 | Cecr2 | -2.28 | down | 0.00 | 1.64 | up | 0.00 |
| 141 | NM_009152 | 20346 | Sema3a | -2.28 | down | 0.01 | 1.78 | up | 0.00 |
| 142 | NM_146532 | 258525 | Olfr1170 | -2.28 | down | 0.00 | 1.45 | up | 0.03 |
| 143 | NM_053137 | 93883 | Pcdhb12 | -2.27 | down | 0.00 | 1.69 | up | 0.00 |
| 144 | ENSMUST00000139879 | 22608 | Ybx1 | -2.27 | down | 0.00 | 1.99 | up | 0.00 |
| 145 | NM_001013833 | 19091 | Prkg1 | -2.27 | down | 0.00 | 1.80 | up | 0.01 |
| 146 | NM_0288817 | 74205 | Acs13 | -2.26 | down | 0.00 | 1.91 | up | 0.01 |
| 147 | NM_008892 | 18968 | Pola1 | -2.26 | down | 0.00 | 1.85 | up | 0.01 |
| 148 | NAP094867-001 | - | - | -2.26 | down | 0.00 | 1.66 | up | 0.02 |
| 149 | ENSMUST00000199146 | - | - | -2.26 | down | 0.00 | 1.66 | up | 0.00 |
| Gene ID   | Description  | Fold Change | Regulation | Log2 Fold | Regulation |
|-----------|--------------|-------------|------------|-----------|------------|
| NM_028011 | Tom1l1       | -2.26       | down       | 0.00      | 1.99       | up         | 0.00       |
| NM_026904 | Anapc10      | -2.25       | down       | 0.00      | 1.65       | up         | 0.02       |
| BC027541  |             | -2.25       | down       | 0.00      | 1.69       | up         | 0.01       |
| NM_001161765 | Fmo5    | -2.25       | down       | 0.01      | 1.64       | up         | 0.03       |
| NM_138672 | Stab1        | -2.25       | down       | 0.00      | 1.61       | up         | 0.04       |
| NM_146009 | Cep290       | -2.25       | down       | 0.02      | 1.61       | up         | 0.02       |
| NM_009838 |             | -2.25       | down       | 0.00      | 1.63       | up         | 0.01       |
| NM_133702 | Nol11        | -2.24       | down       | 0.01      | 1.57       | up         | 0.00       |
| NM_001290350 | Zfp37   | -2.24       | down       | 0.00      | 1.55       | up         | 0.04       |
| NM_028108 | Naa50        | -2.24       | down       | 0.00      | 1.58       | up         | 0.02       |
| NM_001102458 | Azin1   | -2.24       | down       | 0.01      | 1.54       | up         | 0.03       |
| NM_009846 |             | -2.24       | down       | 0.00      | 1.38       | up         | 0.04       |
| NM_025722 | 4921524J17Rik | -2.24   | down       | 0.00      | 1.84       | up         | 0.03       |
| NM_001081021 | Zfp780b  | -2.24       | down       | 0.00      | 1.74       | up         | 0.04       |
| ENSMUST00000125228 | Zfp60 | -2.24       | down       | 0.01      | 1.43       | up         | 0.03       |
| NM_008467 | Kpna4        | -2.23       | down       | 0.00      | 1.92       | up         | 0.01       |
| NM_173734 | Tmem87a      | -2.23       | down       | 0.01      | 1.83       | up         | 0.00       |
| ENSMUST00000151080 | Pgr   | -2.23       | down       | 0.02      | 1.96       | up         | 0.04       |
| NM_008690 | Nfkbie       | -2.23       | down       | 0.00      | 1.81       | up         | 0.01       |
| NM_175357 | Crbn         | -2.23       | down       | 0.00      | 1.79       | up         | 0.02       |
| NM_029068 | Snx16        | -2.23       | down       | 0.00      | 1.38       | up         | 0.03       |
| NM_201529 | Lmo7         | -2.23       | down       | 0.00      | 1.45       | up         | 0.04       |
| ENSMUST00000151163 | Lin7c | -2.23       | down       | 0.00      | 1.54       | up         | 0.02       |
| XM_006530046 | Gmi14409 | -2.23       | down       | 0.00      | 1.58       | up         | 0.01       |
| NM_016746 | Ccnc         | -2.22       | down       | 0.00      | 1.65       | up         | 0.00       |
| NM_008379 | Kpnbl        | -2.22       | down       | 0.00      | 1.86       | up         | 0.01       |
| NM_001033851 | Cpn8    | -2.22       | down       | 0.00      | 1.58       | up         | 0.00       |
| CO430613  |             | -2.22       | down       | 0.00      | 1.99       | up         | 0.01       |
| NM_053075 | Rheb         | -2.22       | down       | 0.00      | 1.96       | up         | 0.00       |
| NM_028116 | Pygo1        | -2.22       | down       | 0.01      | 1.90       | up         | 0.03       |
| NM_028924 | Tc2n         | -2.22       | down       | 0.00      | 1.84       | up         | 0.01       |
| ID     | NM/Accession | Symbol | log2FC | Direction | Fold Change | p-value |
|--------|--------------|--------|--------|-----------|-------------|---------|
| 181    | NM_029564    | Tax1bp3| -2.22  | down      | 1.60        | 0.01    |
| 182    | NM_001301859 | Uba3   | -2.22  | down      | 1.77        | 0.00    |
| 183    | ENSMUST0000041638 | Gtf3c3 | -2.22  | down      | 1.89        | 0.00    |
| 184    | NM_025820    | Crnk1l | -2.22  | down      | 1.87        | 0.02    |
| 185    | NM_029749    | Usp42  | -2.21  | down      | 1.70        | 0.02    |
| 186    | NM_001205101 | Gm13212| -2.21  | down      | 1.89        | 0.01    |
| 187    | NM_026554    | Ncbp2  | -2.21  | down      | 1.81        | 0.03    |
| 188    | NM_001005358 | Zfp960 | -2.21  | down      | 1.87        | 0.01    |
| 189    | NM_011919    | ing1   | -2.21  | down      | 1.80        | 0.01    |
| 190    | NM_176987    | simc1  | -2.21  | down      | 1.67        | 0.02    |
| 191    | NM_001190356 | Gm4832 | -2.21  | down      | 1.40        | 0.02    |
| 192    | NM_00142952  | Fam46c | -2.21  | down      | 1.62        | 0.02    |
| 193    | NM_181517    | Ipo7   | -2.21  | down      | 1.93        | 0.01    |
| 194    | NM_001033156 | Fbxo33 | -2.21  | down      | 1.82        | 0.02    |
| 195    | XM_006543774 | Gm6570 | -2.21  | down      | 1.52        | 0.03    |
| 196    | XM_006531843 | 1700055N04Rik | -2.20  | down      | 1.97        | 0.00    |
| 197    | NM_139232    | Fgd4   | -2.20  | down      | 1.85        | 0.01    |
| 198    | NM_026396    | Brix1  | -2.20  | down      | 1.87        | 0.04    |
| 199    | NM_177588    | Thns1l | -2.20  | down      | 1.74        | 0.01    |
| 200    | NM_173446    | Fam155a| -2.20  | down      | 1.88        | 0.00    |
| 201    | NM_026850    | Pdc13  | -2.19  | down      | 1.75        | 0.01    |
| 202    | NM_175394    | Wtap   | -2.19  | down      | 1.70        | 0.01    |
| 203    | NM_001014397 | Gm13154| -2.19  | down      | 1.80        | 0.03    |
| 204    | NM_145492    | Zfp521 | -2.19  | down      | 1.75        | 0.02    |
| 205    | NM_146016    | Em16   | -2.19  | down      | 1.58        | 0.01    |
| 206    | NM_145943    | Sde2   | -2.19  | down      | 1.83        | 0.02    |
| 207    | NM_144811    | Cbx7   | -2.18  | down      | 1.89        | 0.05    |
| 208    | NM_011496    | AurbkB | -2.18  | down      | 1.89        | 0.01    |
| 209    | XM_011244594 | 1E+08  | Gm3325 | -2.18  | 1.60        | 0.01    |
| 210    | NM_011693    | Vcam1  | -2.18  | down      | 1.54        | 0.01    |
| 211    | NM_009770    | Btg3   | -2.17  | down      | 1.79        | 0.01    |
| Gene ID          | Gene Symbol | Log2 Fold Change | Direction | Expression | Log2 Fold Change | Direction |
|-----------------|-------------|-----------------|-----------|------------|-----------------|-----------|
| NM_001012638    | Acd         | -2.17           | down      | 0.00       | 1.96            | up        |
| NM_0026348      | Itgb3bp     | -2.17           | down      | 0.00       | 1.99            | up        |
| NM_001039184    | Cep350      | -2.17           | down      | 0.00       | 1.69            | up        |
| NM_021273       | Ckb         | -2.17           | down      | 0.00       | 1.40            | up        |
| NM_001142963    | Gm10778     | -2.17           | down      | 0.00       | 1.75            | up        |
| ENSMUST00000119319 |           | -2.17           | down      | 0.00       | 1.88            | up        |
| FJ422280        |             | -2.17           | down      | 0.01       | 1.91            | up        |
| NM_010016       | Cd55        | -2.17           | down      | 0.00       | 1.57            | up        |
| NM_019727       | Snx1        | -2.17           | down      | 0.00       | 1.74            | up        |
| NM_001256055    | Eif3j2      | -2.17           | down      | 0.01       | 1.63            | up        |
| NM_007874       | Reep5       | -2.17           | down      | 0.00       | 1.41            | up        |
| NM_025992       | Herc6       | -2.16           | down      | 0.00       | 1.57            | up        |
| NM_007597       | Canx        | -2.16           | down      | 0.00       | 1.44            | up        |
| XM_006503340    | Caap1       | -2.16           | down      | 0.01       | 1.51            | up        |
| ENSMUST0000120745 |          | -2.16           | down      | 0.00       | 1.59            | up        |
| NM_019570       | Rev1        | -2.16           | down      | 0.00       | 1.94            | up        |
| NM_011129       |             | -2.16           | down      | 0.00       | 1.39            | up        |
| NM_025825       | Appbp2      | -2.16           | down      | 0.00       | 1.58            | up        |
| NM_023233       | Trim13      | -2.16           | down      | 0.00       | 1.69            | up        |
| NM_026654       | Toe1        | -2.16           | down      | 0.00       | 1.93            | up        |
| NM_008303       | Hspe1       | -2.16           | down      | 0.02       | 1.69            | up        |
| NM_020283       | B3galt1     | -2.16           | down      | 0.00       | 1.65            | up        |
| ENSMUST0000120890 |          | -2.15           | down      | 0.00       | 1.88            | up        |
| ENSMUST00000182000 |      | -2.15           | down      | 0.00       | 1.69            | up        |
| ENSMUST00000120408 |      | -2.15           | down      | 0.00       | 1.81            | up        |
| XM_011251171    | GtpU21140Imeg| -2.15           | down      | 0.00       | 1.79            | up        |
| NM_031165       | Hspa8       | -2.15           | down      | 0.01       | 1.75            | up        |
| NM_001015099    | G2e3        | -2.15           | down      | 0.01       | 1.56            | up        |
| NM_011976       | Sema4g      | -2.14           | down      | 0.01       | 1.86            | up        |
| NM_175226       | Rnf139      | -2.14           | down      | 0.00       | 1.94            | up        |
| ENSMUST0000117894 |          | -2.14           | down      | 0.00       | 1.85            | up        |
| Gene          | Accession | Log2 Fold Change | Direction | Log2 Value | p Value |
|--------------|-----------|-----------------|-----------|------------|---------|
| Strbp        | NM_009261 | -2.14           | down      | 0.00       | 1.75    | up 0.00 |
| Tmprss9      | NM_001081688 | -2.14           | down      | 0.00       | 1.63    | up 0.00 |
| AK214641     | AK214641   | -2.14           | down      | 0.04       | 1.99    | up 0.03 |
| Nfyb         | NM_010914  | -2.14           | down      | 0.00       | 1.23    | up 0.04 |
| ENSMUST0000119165 | -2.14    | down           | 0.00      | 1.80       | up 0.01 |
| NAP095021-001 | -2.14     | down           | 0.00      | 1.71       | up 0.02 |
| 2610044O15Rik8 | NM_153780 | -2.14           | down      | 0.01       | 1.87    | up 0.02 |
| Triqk        | NM_173746  | -2.14           | down      | 0.00       | 1.83    | up 0.03 |
| Rfxap        | NM_133231  | -2.14           | down      | 0.00       | 1.66    | up 0.01 |
| Atp11c       | NM_001001798 | -2.13          | down      | 0.01       | 1.88    | up 0.02 |
| Lmo2         | NM_008505  | -2.13           | down      | 0.01       | 1.82    | up 0.04 |
| Dusp19       | NM_024438  | -2.13           | down      | 0.00       | 1.85    | up 0.02 |
| Esco1        | NM_001081222 | -2.13          | down      | 0.00       | 1.70    | up 0.01 |
| Stap2        | NM_145934  | -2.13           | down      | 0.01       | 1.65    | up 0.01 |
| Milt3        | NM_027326  | -2.13           | down      | 0.00       | 1.78    | up 0.00 |
| Tspan13      | NM_025359  | -2.13           | down      | 0.00       | 1.59    | up 0.01 |
| Trip13       | NM_027182  | -2.13           | down      | 0.00       | 1.75    | up 0.01 |
| Copg1        | NM_201244  | -2.13           | down      | 0.02       | 1.84    | up 0.03 |
| Olfr560      | NM_147113  | -2.12           | down      | 0.00       | 1.65    | up 0.02 |
| Atp11c       | NM_028932  | -2.12           | down      | 0.00       | 1.78    | up 0.01 |
| Mrps6        | NM_080456  | -2.12           | down      | 0.00       | 1.94    | up 0.02 |
| Apcdd1       | AK172004   | -2.12           | down      | 0.00       | 1.52    | up 0.03 |
| Phf3         | ENSMUST0000188847 | -2.12     | down      | 0.00       | 1.65    | up 0.02 |
| Olfr560      | NM_147113  | -2.12           | down      | 0.00       | 1.65    | up 0.02 |
| Rbsn         | NM_030081  | -2.12           | down      | 0.00       | 1.59    | up 0.03 |
| Mrps6        | NM_080456  | -2.12           | down      | 0.00       | 1.40    | up 0.01 |
| Apcdd1       | AK172004   | -2.12           | down      | 0.00       | 1.36    | up 0.04 |
| Phf3         | ENSMUST0000188847 | -2.12     | down      | 0.00       | 1.34    | up 0.01 |
| Dhh          | NM_007857  | -2.12           | down      | 0.00       | 1.34    | up 0.01 |
|    | Gene Symbol   | Description | Log2FoldChange | Direction | P_Value | q_Value |
|----|---------------|-------------|----------------|-----------|---------|---------|
| 274| NM_011277     | Rnf2        | -2.12          | down      | 0.01    | 1.68    | up      | 0.04    |
| 275| NM_001025373  | Zfp943      | -2.12          | down      | 0.00    | 1.83    | up      | 0.00    |
| 276| ENSMUST00000153501 |          | -2.12          | down      | 0.01    | 1.93    | up      | 0.01    |
| 277| NM_001039521  | Rrn3        | -2.12          | down      | 0.00    | 1.70    | up      | 0.00    |
| 278| NM_133167     | Parvb       | -2.11          | down      | 0.04    | 1.78    | up      | 0.03    |
| 279| NM_019865     | Rpl36a      | -2.11          | down      | 0.00    | 1.46    | up      | 0.02    |
| 280| AK155848      | 2610209C05Rik | -2.11        | down      | 0.00    | 1.48    | up      | 0.01    |
| 281| ENSMUST0000087143 |        | -2.11          | down      | 0.00    | 1.70    | up      | 0.03    |
| 282| NM_026054     | Zfp943      | -2.11          | down      | 0.00    | 1.78    | up      | 0.01    |
| 283| ENSMUST0000118547 |      | -2.11          | down      | 0.00    | 1.61    | up      | 0.02    |
| 284| NM_028110     | Dennd2d     | -2.11          | down      | 0.01    | 1.73    | up      | 0.03    |
| 285| NAP115053-1   |            | -2.11          | down      | 0.00    | 1.48    | up      | 0.03    |
| 286| NM_007604     | Capza2      | -2.11          | down      | 0.00    | 1.68    | up      | 0.00    |
| 287| NM_013834     | Sfrp1       | -2.11          | down      | 0.00    | 1.44    | up      | 0.03    |
| 288| NM_173181     | Zc2hc1a     | -2.11          | down      | 0.00    | 1.95    | up      | 0.02    |
| 289| NAP059691-1   |            | -2.11          | down      | 0.00    | 1.70    | up      | 0.01    |
| 290| AF369981      | Ppm1a       | -2.11          | down      | 0.00    | 1.64    | up      | 0.03    |
| 291| AK162394      | Tbxas1      | -2.10          | down      | 0.04    | 1.46    | up      | 0.03    |
| 292| NM_001199956  | Gm9839      | -2.10          | down      | 0.00    | 1.40    | up      | 0.02    |
| 293| XM_006540799  | Ube3a       | -2.10          | down      | 0.00    | 1.71    | up      | 0.02    |
| 294| NM_001024846  | Zfp62       | -2.10          | down      | 0.00    | 1.51    | up      | 0.00    |
| 295| NM_010849     | Myc         | -2.10          | down      | 0.01    | 1.79    | up      | 0.00    |
| 296| XM_006543383  | Gm5093      | -2.10          | down      | 0.00    | 1.67    | up      | 0.01    |
| 297| NM_001271016  | Ube2w       | -2.10          | down      | 0.00    | 1.60    | up      | 0.01    |
| 298| NM_145969     | Dennd6a     | -2.10          | down      | 0.00    | 1.44    | up      | 0.04    |
| 299| NM_146249     | Zfp119b     | -2.10          | down      | 0.00    | 1.52    | up      | 0.01    |
| 300| NM_026479     | Zcchc10     | -2.10          | down      | 0.00    | 1.65    | up      | 0.02    |
| 301| NM_029271     | Mrpl32      | -2.10          | down      | 0.00    | 1.87    | up      | 0.03    |
| 302| NM_025901     | Polr3k      | -2.10          | down      | 0.00    | 1.85    | up      | 0.00    |
| 303| NM_176962     | Zfp944      | -2.10          | down      | 0.00    | 1.74    | up      | 0.01    |
| Rank | ENSMUST00000134741 | 224902 | Safb2 | -2.09 | down | 0.00 | 1.65 | up | 0.01 |
|------|-------------------|--------|-------|--------|------|------|------|---|------|
| 306  | NM_023210         | 66471  | Anp32e | -2.09 | down | 0.00 | 1.98 | up | 0.00 |
| 307  | NM_029434         | 75782  | Lca5  | -2.09 | down | 0.00 | 2.00 | up | 0.01 |
| 308  | NM_001164593      | 239618 | Pdzn4 | -2.09 | down | 0.03 | 1.75 | up | 0.03 |
| 309  | ENSMUST00000080175| -2.09 | down | 0.00 | 1.79 | up | 0.02 |
| 310  | NM_021326         | 57782  | Rbak  | -2.09 | down | 0.00 | 1.82 | up | 0.04 |
| 311  | NM_001081420      | 230234 | Fam206a | -2.09 | down | 0.00 | 1.82 | up | 0.00 |
| 312  | NM_001290548      | 320267 | Fubp3 | -2.09 | down | 0.00 | 1.82 | up | 0.00 |
| 313  | NM_016957         | 15331  | Hmgn2 | -2.09 | down | 0.01 | 1.87 | up | 0.02 |
| 314  | NM_009716         | 11911  | Atf4  | -2.09 | down | 0.00 | 1.30 | up | 0.01 |
| 315  | NM_028487         | 73274  | Gpbp1 | -2.09 | down | 0.00 | 1.68 | up | 0.00 |
| 316  | NM_178379         | 70383  | Cox10 | -2.09 | down | 0.00 | 1.76 | up | 0.01 |
| 317  | AK201505          | 104175 | Sbk1  | -2.09 | down | 0.00 | 1.82 | up | 0.01 |
| 318  | AK132208          | 20042  | Rps12 | -2.09 | down | 0.00 | 1.55 | up | 0.02 |
| 319  | XM_006529444      | 226442 | Zfp281 | -2.09 | down | 0.01 | 1.30 | up | 0.00 |
| 320  | NM_00177525       | 1E+08  | EU599041 | -2.09 | down | 0.01 | 1.96 | up | 0.01 |
| 321  | NM_001001932      | 216238 | Eea1  | -2.08 | down | 0.00 | 1.75 | up | 0.01 |
| 322  | NM_009087         | 20018  | Polr1d | -2.08 | down | 0.00 | 1.68 | up | 0.00 |
| 323  | XM_006515438      | 11855  | Arhgap5 | -2.08 | down | 0.00 | 1.43 | up | 0.01 |
| 324  | ENSMUST00000093546| -2.08 | down | 0.00 | 1.46 | up | 0.02 |
| 325  | NM_178069         | 224092 | Lsg1  | -2.08 | down | 0.01 | 1.84 | up | 0.01 |
| 326  | NM_172586         | 218100 | Zfp322a | -2.08 | down | 0.00 | 1.49 | up | 0.03 |
| 327  | NM_001164676      | 381067 | Zfp229 | -2.08 | down | 0.01 | 1.70 | up | 0.01 |
| 328  | NM_010288         | 14609  | Gja1  | -2.08 | down | 0.02 | 1.55 | up | 0.01 |
| 329  | NM_177715         | 239217 | Kctd12 | -2.08 | down | 0.01 | 1.85 | up | 0.05 |
| 330  | NM_029570         | 76295  | Atp11b | -2.08 | down | 0.00 | 1.39 | up | 0.02 |
| 331  | NM_009946         | 12890  | Cplx2 | -2.08 | down | 0.01 | 1.80 | up | 0.01 |
| 332  | ENSMUST00000119605| -2.08 | down | 0.00 | 1.83 | up | 0.00 |
| 333  | AK034948          | 67712  | Slc25a37 | -2.08 | down | 0.02 | 1.84 | up | 0.04 |
| 334  | XM_006522805      | 433003 | Gm5481 | -2.08 | down | 0.00 | 1.34 | up | 0.03 |
| 335  | NM_133774         | 170459 | Stard4 | -2.08 | down | 0.01 | 1.65 | up | 0.04 |
| S.No. | Gene Symbol | Description | Log2 Fold Change | Direction | P-Value |
|-------|-------------|-------------|------------------|-----------|---------|
| 336   | ENSMUST00000118023 | -2.07 | down | 0.01 | 1.75 | up | 0.00 |
| 337   | NM_172833    | 240354 Malt1 | -2.07 | down | 0.00 | 1.81 | up | 0.02 |
| 338   | NM_009881    | 12593 Cdy1 | -2.07 | down | 0.01 | 1.76 | up | 0.02 |
| 339   | NM_001033348 | 241694 Ralgapa2 | -2.07 | down | 0.00 | 1.42 | up | 0.00 |
| 340   | NM_001079830 | 94093 Trim33 | -2.07 | down | 0.00 | 1.53 | up | 0.01 |
| 341   | AK040904     | 1E+08 Gm26510 | -2.07 | down | 0.00 | 1.37 | up | 0.04 |
| 342   | NM_025970    | 67106 Zbtb8os | -2.07 | down | 0.00 | 1.73 | up | 0.01 |
| 343   | AK040596     | -2.07 | down | 0.00 | 1.28 | up | 0.04 |
| 344   | ENSMUST00000178086 | -2.07 | down | 0.00 | 1.69 | up | 0.01 |
| 345   | NM_025885    | 381379 Med19 | -2.07 | down | 0.00 | 1.85 | up | 0.01 |
| 346   | NM_080558    | 70599 Ssfa2 | -2.07 | down | 0.00 | 1.81 | up | 0.02 |
| 347   | NM_011643    | 22063 Trpc1 | -2.07 | down | 0.01 | 1.56 | up | 0.02 |
| 348   | XM_006495473 | 19888 Rp1 | -2.07 | down | 0.03 | 1.65 | up | 0.05 |
| 349   | AK048998     | 382421 Gm5176 | -2.07 | down | 0.00 | 1.38 | up | 0.05 |
| 350   | NM_028334    | 69736 Nup37 | -2.07 | down | 0.00 | 1.84 | up | 0.01 |
| 351   | NM_024242    | 71340 Riok1 | -2.06 | down | 0.00 | 1.70 | up | 0.01 |
| 352   | NM_001111320 | 15926 Idh1 | -2.06 | down | 0.00 | 1.98 | up | 0.00 |
| 353   | NM_001025572 | 106585 Ankrd12 | -2.06 | down | 0.00 | 1.70 | up | 0.05 |
| 354   | NM_144787    | 76804 Kdm4c | -2.06 | down | 0.00 | 1.64 | up | 0.01 |
| 355   | NM_001289781 | 78697 Pus7 | -2.06 | down | 0.04 | 1.51 | up | 0.04 |
| 356   | NM_007638    | 12468 Cct7 | -2.06 | down | 0.00 | 1.43 | up | 0.02 |
| 357   | NM_194269    | 378462 Morn2 | -2.06 | down | 0.01 | 1.91 | up | 0.00 |
| 358   | NM_212457    | 406217 Bex4 | -2.06 | down | 0.00 | 1.75 | up | 0.03 |
| 359   | NM_133818    | 98404 Ai597479 | -2.06 | down | 0.00 | 1.88 | up | 0.01 |
| 360   | NM_009831    | 12450 Ccng1 | -2.06 | down | 0.00 | 1.69 | up | 0.02 |
| 361   | NM_145455    | 218490 Btf3 | -2.06 | down | 0.00 | 1.68 | up | 0.01 |
| 362   | NM_153319    | 27494 Amot | -2.06 | down | 0.01 | 1.80 | up | 0.03 |
| 363   | NM_001199350 | 619547 Rpl34-ps1 | -2.06 | down | 0.00 | 1.56 | up | 0.03 |
| 364   | NM_026536    | 68055 Atp5s | -2.05 | down | 0.00 | 1.80 | up | 0.00 |
| 365   | NAP113774-1  | -2.05 | down | 0.00 | 1.71 | up | 0.01 |
| 366   | NM_177712    | 238692 Zfp874a | -2.05 | down | 0.01 | 1.73 | up | 0.02 |
|   |   |   |   |   |   |   |   |   |   |   |   |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 367 | NM_172865 | 242362 | Manea | -2.05 | down | 0.00 | 1.82 | up | 0.00 |
| 368 | NM_001170454 | 231151 | Tada2b | -2.05 | down | 0.00 | 1.70 | up | 0.01 |
| 369 | ENSMUST000000121467 |   |   | -2.05 | down | 0.00 | 1.82 | up | 0.00 |
| 370 | NM_001170849 | 212624 | Luc7l2 | -2.05 | down | 0.00 | 1.54 | up | 0.02 |
| 371 | NM_027617 | 70951 | Spata1 | -2.05 | down | 0.00 | 1.78 | up | 0.00 |
| 372 | NM_178766 | 319653 | Slc25a40 | -2.05 | down | 0.00 | 1.67 | up | 0.01 |
| 373 | NM_001024910 |   |   | -2.05 | down | 0.00 | 1.70 | up | 0.00 |
| 374 | ENSMUST00000141874 | 20402 | Zfp106 | -2.05 | down | 0.01 | 1.84 | up | 0.03 |
| 375 | NM_029610 | 73919 | Lyrm1 | -2.05 | down | 0.00 | 1.79 | up | 0.00 |
| 376 | NM_177039 | 319942 | A530016L24Rik | -2.05 | down | 0.00 | 1.23 | up | 0.01 |
| 377 | NAP111293-1 |   |   | -2.05 | down | 0.00 | 1.89 | up | 0.00 |
| 378 | NM_028677 | 66101 | Ppih | -2.05 | down | 0.01 | 1.85 | up | 0.04 |
| 379 | NM_001289658 | 76223 | Agbl3 | -2.05 | down | 0.00 | 1.93 | up | 0.02 |
| 380 | NM_028990 | 101118 | Tmem168 | -2.05 | down | 0.00 | 1.75 | up | 0.01 |
| 381 | NM_031391 | 83602 | Gtf2a1 | -2.05 | down | 0.00 | 1.57 | up | 0.02 |
| 382 | NM_001081090 | 66580 | Esf1 | -2.05 | down | 0.00 | 1.61 | up | 0.00 |
| 383 | NM_133740 | 71974 | Prmt3 | -2.05 | down | 0.00 | 1.91 | up | 0.03 |
| 384 | NM_007552 | 12151 | Bmi1 | -2.04 | down | 0.00 | 1.80 | up | 0.02 |
| 385 | NM_001170454 | 231151 | Tada2b | -2.05 | down | 0.00 | 1.70 | up | 0.01 |
| 386 | NM_027203 | 69757 | Leng1 | -2.04 | down | 0.00 | 1.79 | up | 0.01 |
| 387 | NM_133895 | 100561 | Slc15a4 | -2.04 | down | 0.00 | 1.30 | up | 0.03 |
| 388 | NM_028319 | 72672 | Zfp518a | -2.04 | down | 0.00 | 1.37 | up | 0.05 |
| 389 | XM_006527909 | 19108 | Prkx | -2.04 | down | 0.01 | 1.98 | up | 0.00 |
| 390 | XM_006540002 | 26436 | Psg16 | -2.04 | down | 0.00 | 1.82 | up | 0.03 |
| 391 | NM_001001176 | 407786 | Taf9b | -2.04 | down | 0.00 | 1.78 | up | 0.03 |
| 392 | NM_013843 | 24132 | Zfp53 | -2.04 | down | 0.00 | 1.93 | up | 0.00 |
| 393 | TC1602431 |   |   | -2.04 | down | 0.00 | 1.42 | up | 0.01 |
| 394 | NM_020595 | 57329 | Otor | -2.04 | down | 0.00 | 1.42 | up | 0.02 |
| 395 | XM_006505459 | 12444 | Ccnd2 | -2.04 | down | 0.00 | 1.69 | up | 0.02 |
| 396 | NM_007890 | 13548 | Dyrk1a | -2.04 | down | 0.00 | 1.59 | up | 0.01 |
| 397 | NM_008186 | 14884 | Gtf2h1 | -2.04 | down | 0.01 | 1.97 | up | 0.02 |
|   |   |   |   |
|---|---|---|---|
| 398| NM_152234 | 56085 | Ubqln1 | -2.04 | down | 0.00 | 1.34 | up | 0.01 |
| 399| XM_006515301 | 1E+08 | Gm29738 | -2.03 | down | 0.01 | 1.56 | up | 0.02 |
| 400| NM_027807 | 75717 | Cul5 | -2.03 | down | 0.00 | 1.64 | up | 0.01 |
| 401| NM_026046 | 67230 | Zfp329 | -2.03 | down | 0.00 | 1.19 | up | 0.03 |
| 402| NM_001080706 | 107182 | Btaf1 | -2.03 | down | 0.01 | 1.59 | up | 0.04 |
| 403| NM_173761 | 228994 | Ythdf1 | -2.03 | down | 0.00 | 1.54 | up | 0.01 |
| 404| ENSMUST00000147830 | 17763 | Mtcp1 | -2.03 | down | 0.02 | 1.42 | up | 0.02 |
| 405| NM_079835 | 547431 | Btnl2 | -2.03 | down | 0.01 | 1.97 | up | 0.01 |
| 406| NM_025776 | 66810 | Rbm22 | -2.03 | down | 0.00 | 1.90 | up | 0.03 |
| 407| NM_053155 | 94040 | Clmn | -2.03 | down | 0.04 | 1.75 | up | 0.00 |
| 408| NM_001122675 | 227449 | Zcchc2 | -2.03 | down | 0.00 | 1.59 | up | 0.05 |
| 409| NM_013778 | 27384 | Akr1c13 | -2.03 | down | 0.02 | 1.86 | up | 0.01 |
| 410| NM_001162921 | 244871 | Zc3h12c | -2.03 | down | 0.00 | 1.99 | up | 0.00 |
| 411| NM_172645 | 226551 | Suco | -2.03 | down | 0.00 | 1.88 | up | 0.01 |
| 412| NM_011794 | 23827 | Bpnt1 | -2.03 | down | 0.00 | 1.61 | up | 0.03 |
| 413| NM_028626 | 73724 | Mcee | -2.03 | down | 0.01 | 1.88 | up | 0.02 |
| 414| ENSMUST00000119137 | - | - | - | - | - | - | - | - |
| 415| NM_029330 | 75540 | Fpgt | -2.03 | down | 0.00 | 1.70 | up | 0.03 |
| 416| NM_054087 | 116914 | Slc19a2 | -2.03 | down | 0.00 | 1.54 | up | 0.03 |
| 417| NM_029505 | 64933 | Ap3m2 | -2.02 | down | 0.01 | 1.83 | up | 0.01 |
| 418| NM_025564 | 66441 | Magohb | -2.02 | down | 0.00 | 1.89 | up | 0.02 |
| 419| XM_006523251 | 68842 | Tulp4 | -2.02 | down | 0.00 | 1.64 | up | 0.00 |
| 420| NM_001177750 | 1E+08 | Gm10767 | -2.02 | down | 0.00 | 1.58 | up | 0.02 |
| 421| NM_001290196 | 76803 | 2410141K09Rik | -2.02 | down | 0.00 | 1.46 | up | 0.03 |
| 422| NM_001081193 | 380664 | Lemd3 | -2.02 | down | 0.00 | 1.73 | up | 0.01 |
| 423| NM_001127189 | 1E+08 | Gm13157 | -2.02 | down | 0.00 | 1.58 | up | 0.01 |
| 424| NM_001008421 | 217431 | Nol10 | -2.02 | down | 0.00 | 1.75 | up | 0.04 |
| 425| NM_009466 | 22235 | Ugdh | -2.02 | down | 0.00 | 1.56 | up | 0.02 |
| 426| NM_181322 | 13018 | Cctf | -2.02 | down | 0.00 | 1.76 | up | 0.01 |
| 427| ENSMUST00000181799 | - | - | - | - | - | - | - | - |
| 428| AK042006 | 77766 | Elp4 | -2.02 | down | 0.01 | 1.43 | up | 0.01 |
| ID         | GenBank | Symbol | Log2 Ratio | Direction | Fold Change | P-value |
|------------|---------|--------|------------|-----------|-------------|---------|
| NM_175028  | 240442  | Adnp2  | -2.02      | down      | 1.33        | up 0.04 |
| NM_029606  | 76380   | Cep112 | -2.02      | down      | 1.77        | up 0.01 |
| NM_020588  | 57439   | Tmem183a | -2.02     | down      | 1.99        | up 0.01 |
| NM_030261  | 75747   | Sesn3  | -2.02      | down      | 1.99        | up 0.00 |
| NM_026246  | 18120   | Mrpl49 | -2.01      | down      | 1.88        | up 0.01 |
| NM_025800  | 66849   | Ppp1r2 | -2.01      | down      | 1.77        | up 0.02 |
| ENSMUST0000091097 | -2.01 | down | 1.36 | up 0.02 |
| NM_172854  | 241327  | Olfml2a | -2.01     | down      | 1.72        | up 0.04 |
| NM_013703  | 22359   | Vldlr  | -2.01      | down      | 1.56        | up 0.04 |
| ENSMUST0000029106 | 72147 | down | 1.51 | up 0.03 |
| ENSMUST0000119351 | -2.01 | down | 1.38 | up 0.02 |
| NM_001038015 | 67980 | down | 1.74 | up 0.01 |
| ENSMUST00000121873 | -2.01 | down | 1.62 | up 0.00 |
| NM_025682  | 66645   | Pspc1  | -2.01      | down      | 1.28        | up 0.02 |
| ENSMUST0000071770 | -2.01 | down | 1.58 | up 0.03 |
| NM_078477  | 118445  | Klf16  | -2.01      | down      | 1.63        | up 0.01 |
| NM_013673  | 20684   | Sp100  | -2.01      | down      | 1.54        | up 0.04 |
| NM_001167885 | 225888 | down | 1.52 | up 0.03 |
| NM_033564  | 93734   | Mpv17l | -2.01      | down      | 1.82        | up 0.01 |
| NM_001001185 | 408058 | down | 1.71 | up 0.03 |
| NAP095730-001 | -2.01 | down | 1.69 | up 0.01 |
| NM_009879  | 12589   | Ifit81 | -2.01      | down      | 1.65        | up 0.00 |
| NM_011134  | 18979   | Pon1   | -2.01      | down      | 2.00        | up 0.04 |
| NM_175515  | 380614  | Intu   | -2.01      | down      | 1.63        | up 0.02 |
| NM_029512  | 76080   | Ttipal | -2.01      | down      | 1.62        | up 0.01 |
| NM_001160399 | 240261 | down | 1.73 | up 0.03 |
| ENSMUST0000012147 | -2.01 | down | 1.81 | up 0.01 |
| NM_133832  | 98711   | Rdh10  | -2.00      | down      | 1.66        | up 0.01 |
| NM_026055  | 67248   | Rpl39  | -2.00      | down      | 1.45        | up 0.03 |
| NM_172054  | 98258   | Tndc9  | -2.00      | down      | 1.47        | up 0.00 |
| NM_001044386 | 22764 | down | 1.50 | up 0.02 |
|    |     |     |     |     |     |     |     |
|----|-----|-----|-----|-----|-----|-----|-----|
| 460 | NM_026503 | 68002 | Sdhaf4 | -2.00 | down | 0.00 | 1.66 | up | 0.03 |
| 461 | NM_001081680 | 238722 | Zfp72 | -2.00 | down | 0.00 | 1.71 | up | 0.02 |
| 462 | ENSMUST0000016337 | -2.00 | down | 0.00 | 1.41 | up | 0.02 |
| 463 | NM_011508 | 20918 | Eif1 | -2.00 | down | 0.00 | 1.65 | up | 0.01 |
| 464 | AK139740 | -2.00 | down | 0.00 | 1.61 | up | 0.00 |
| 465 | NM_001033422 | 331401 | Thoc2 | -2.00 | down | 0.00 | 1.31 | up | 0.02 |
| 466 | NM_175025 | 235574 | Atp2c1 | -2.00 | down | 0.00 | 1.63 | up | 0.00 |
| 467 | NM_001083927 | 21887 | Tle3 | -2.00 | down | 0.02 | 1.65 | up | 0.02 |
| 468 | NM_010085 | 13525 | Adam26a | 2.00 | up | 0.00 | -1.40 | down | 0.01 |
| 469 | NM_001080934 | 217316 | Scl16a5 | 2.00 | up | 0.00 | -1.56 | down | 0.02 |
| 470 | ENSMUST00000127159 | 78656 | Brd8 | 2.00 | up | 0.00 | -1.96 | down | 0.00 |
| 471 | NM_147003 | 259005 | Olfr139 | 2.00 | up | 0.00 | -1.48 | down | 0.03 |
| 472 | NM_146453 | 258445 | Olfr693 | 2.01 | up | 0.05 | -1.89 | down | 0.00 |
| 473 | NM_001002896 | 107993 | Bfsp2 | 2.01 | up | 0.00 | -1.56 | down | 0.00 |
| 474 | NM_001159775 | 258236 | Olfr391-ps | 2.02 | up | 0.00 | -1.86 | down | 0.00 |
| 475 | NM_007439 | 11682 | Alk | 2.02 | up | 0.00 | -1.46 | down | 0.02 |
| 476 | NM_001113187 | 98582 | Khdc1b | 2.02 | up | 0.00 | -1.45 | down | 0.01 |
| 477 | NM_010929 | 18132 | Notch4 | 2.02 | up | 0.00 | -1.81 | down | 0.01 |
| 478 | NM_027442 | 70503 | Ddo | 2.02 | up | 0.00 | -1.65 | down | 0.00 |
| 479 | AK047978 | 414118 | Zmiz1os1 | 2.02 | up | 0.00 | -1.55 | down | 0.00 |
| 480 | NM_029689 | 76651 | 1700122O11Rik | 2.02 | up | 0.00 | -1.63 | down | 0.01 |
| 481 | AK089900 | 78610 | Uvrag | 2.02 | up | 0.00 | -1.71 | down | 0.01 |
| 482 | AK087460 | 2.02 | up | 0.00 | -1.80 | down | 0.00 |
| 483 | ENSMUST0000029440 | 99543 | Olfml3 | 2.02 | up | 0.00 | -1.55 | down | 0.01 |
| 484 | NM_008435 | 16538 | Kcns1 | 2.03 | up | 0.00 | -1.76 | down | 0.00 |
| 485 | AK031474 | 382062 | AB124611 | 2.03 | up | 0.00 | -1.50 | down | 0.00 |
| 486 | AK007903 | 69818 | 1810059C17Rik | 2.03 | up | 0.00 | -1.89 | down | 0.00 |
| 487 | NM_017461 | 54204 | 43709 | 2.03 | up | 0.00 | -1.52 | down | 0.01 |
| 488 | NM_026685 | 68344 | Tmem174 | 2.03 | up | 0.00 | -1.76 | down | 0.01 |
| 489 | ENSMUST00000130479 | 319845 | Bbs9 | 2.03 | up | 0.00 | -1.39 | down | 0.02 |
| 490 | AK029733 | 666539 | Gm8154 | 2.04 | up | 0.00 | -1.55 | down | 0.01 |
|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| 491 | NM_173070 | 229562 | Sprr4 | 2.04 | up | 0.01 | -1.73 | down | 0.00 |
| 492 | ENSMUST00000145908 | 330222 | Sdk1 | 2.04 | up | 0.00 | -1.93 | down | 0.00 |
| 493 | AK034480 | 2.04 | up | 0.02 | -1.79 | down | 0.01 |
| 494 | NM_009987 | 13051 | Cx3cr1 | 2.04 | up | 0.00 | -1.73 | down | 0.02 |
| 495 | NM_013887 | 30044 | Opn4 | 2.04 | up | 0.00 | -1.69 | down | 0.00 |
| 496 | NM_026338 | 67722 | Acl11 | 2.04 | up | 0.01 | -1.70 | down | 0.00 |
| 497 | AK182364 | 11821 | Aprt | 2.05 | up | 0.00 | -1.54 | down | 0.00 |
| 498 | NM_133204 | 170734 | Zscan5b | 2.05 | up | 0.00 | -1.82 | down | 0.00 |
| 499 | NM_001101463 | 231885 | Gm4871 | 2.05 | up | 0.00 | -1.56 | down | 0.00 |
| 500 | NM_183224 | 329731 | Fam19a3 | 2.05 | up | 0.00 | -1.65 | down | 0.01 |
| 501 | NM_175280 | 78774 | Cfap61 | 2.05 | up | 0.00 | -1.78 | down | 0.01 |
| 502 | NM_026785 | 68612 | Ube2c | 2.05 | up | 0.00 | -1.32 | down | 0.04 |
| 503 | AK082467 | 110333 | Rmst | 2.05 | up | 0.00 | -1.72 | down | 0.01 |
| 504 | XM_006506255 | 320127 | Dgki | 2.06 | up | 0.02 | -1.83 | down | 0.00 |
| 505 | NM_001289756 | 11814 | Apoc3 | 2.06 | up | 0.02 | -1.97 | down | 0.00 |
| 506 | NM_146833 | 258830 | Olfr103 | 2.06 | up | 0.00 | -1.44 | down | 0.00 |
| 507 | NM_021291 | 30962 | Slc7a9 | 2.07 | up | 0.00 | -1.86 | down | 0.00 |
| 508 | NM_009470 | 22242 | Umod | 2.07 | up | 0.00 | -1.77 | down | 0.02 |
| 509 | NM_010057 | 13396 | Dlx6 | 2.07 | up | 0.01 | -1.45 | down | 0.02 |
| 510 | AA822459 | 2.07 | up | 0.00 | -1.61 | down | 0.01 |
| 511 | NM_032610 | 80297 | Sptbn4 | 2.07 | up | 0.00 | -1.78 | down | 0.01 |
| 512 | NM_144835 | 217995 | Heatr1 | 2.08 | up | 0.00 | -1.91 | down | 0.00 |
| 513 | BI661026 | 2.08 | up | 0.00 | -1.80 | down | 0.01 |
| 514 | NM_146600 | 258593 | Olfr700 | 2.08 | up | 0.00 | -1.59 | down | 0.04 |
| 515 | NM_011771 | 22780 | Ikzf3 | 2.08 | up | 0.01 | -1.94 | down | 0.00 |
| 516 | NM_009036 | 19668 | Rbpjl | 2.08 | up | 0.02 | -1.50 | down | 0.00 |
| 517 | NM_133894 | 100559 | Ugt2b38 | 2.09 | up | 0.03 | -1.70 | down | 0.01 |
| 518 | NM_001293795 | 107770 | Tm6sf2 | 2.09 | up | 0.00 | -1.40 | down | 0.00 |
| 519 | AK131776 | 1E+08 | Gm40421 | 2.09 | up | 0.00 | -1.81 | down | 0.02 |
| 520 | NM_001145537 | 668433 | 4930544D05Rik | 2.09 | up | 0.00 | -1.53 | down | 0.00 |
| 521 | XM_006511606 | 1E+08 | Gm10634 | 2.09 | up | 0.00 | -1.48 | down | 0.01 |
| Gene Id     | Start Coordinates | Gene Name | Value | P-value | Log2Ratio | Down-Regulated | Down-Regulated P-value |
|-------------|--------------------|-----------|-------|---------|------------|----------------|-----------------------|
| NM_133254   | 246787             | Slc5a2    | 2.09  | up      | 0.00       | -1.43          | down                  |
| NM_172550   | 216119             | Ybey      | 2.09  | up      | 0.03       | -1.89          | down                  |
| NM_023670   | 140488             | Igf2bp3   | 2.09  | up      | 0.05       | -1.59          | down                  |
| ENSMUST0000019243 |              |           | 2.09  | up      | 0.02       | -1.73          | down                  |
| NM_025520   | 66373              | Lsm5      | 2.09  | up      | 0.00       | -1.94          | down                  |
| BC107389    | 382913             | Neil2     | 2.10  | up      | 0.00       | -1.33          | down                  |
| NM_010235   | 14283              | Fosl1     | 2.10  | up      | 0.00       | -1.81          | down                  |
| ENSMUST00000105802 |           |           | 2.11  | up      | 0.02       | -1.62          | down                  |
| ENSMUST00000103672 |          |           | 2.11  | up      | 0.01       | -1.57          | down                  |
| NM_027024   | 69294              | Cst13     | 2.11  | up      | 0.00       | -1.94          | down                  |
| NM_194268   | 225631             | Onecut2   | 2.11  | up      | 0.02       | -1.51          | down                  |
| ENSMUST00000151328 |        |           | 2.12  | up      | 0.00       | -1.63          | down                  |
| ENSMUST00000186455 |        |           | 2.12  | up      | 0.00       | -1.97          | down                  |
| NM_001029935 | 214158             | Trim38    | 2.12  | up      | 0.00       | -1.53          | down                  |
| NM_010235   | 14608              | Gpr83     | 2.12  | up      | 0.00       | -1.73          | down                  |
| ENSMUST00000120250 |         |           | 2.12  | up      | 0.02       | -1.91          | down                  |
| NM_134193   | 171227             | Vmn1r232  | 2.12  | up      | 0.03       | -1.80          | down                  |
| AK051890    | 791272             | Gm10091   | 2.13  | up      | 0.00       | -1.66          | down                  |
| NM_007401   | 11499              | Adam5     | 2.13  | up      | 0.00       | -1.57          | down                  |
| NM_025487   | 66322              | 1700011A15Rik | 2.13 | up   | 0.00       | -1.48          | down                  |
| BF319608    |                   |           | 2.13  | up      | 0.00       | -1.81          | down                  |
| NM_027402   | 384061             | Fndc5     | 2.13  | up      | 0.00       | -1.91          | down                  |
| XM_006497797 | 19730              | Ralgds    | 2.14  | up      | 0.00       | -1.99          | down                  |
| AK040132    |                   |           | 2.14  | up      | 0.01       | -1.84          | down                  |
| ENSMUST00000127388 |        |           | 2.14  | up      | 0.00       | -1.95          | down                  |
| NM_008665   | 17932              | Myt1      | 2.14  | up      | 0.03       | -1.72          | down                  |
| ENSMUST00000107564 |        |           | 2.14  | up      | 0.00       | -1.48          | down                  |
| AK007031    | 73588              | St8sia3os | 2.14  | up      | 0.00       | -1.58          | down                  |
| NM_146904   | 57251              | Olfr870   | 2.15  | up      | 0.00       | -1.64          | down                  |
| NM_001123367 | 1E+08              | Gm3448    | 2.15  | up      | 0.00       | -1.85          | down                  |
| AK053272    | 1E+08              | Gm9963    | 2.15  | up      | 0.00       | -1.76          | down                  |
|   | Ensembl ID   | RefSeq ID       | Symbol   | Fold Change | Change Type | Log2 Fold Change | p-Value |
|---|--------------|-----------------|----------|-------------|--------------|-----------------|---------|
| 553 | AK171018     | 69305           | Dcups   | 2.16        | up           | 0.00            | -1.86   |
| 554 | AK133420     | 12983           | Csf2rb  | 2.16        | up           | 0.00            | -1.24   |
| 555 | NM_177354    | 238328          | Vash1   | 2.16        | up           | 0.00            | -1.66   |
| 556 | NM_153519    | 213272          | Txndc2  | 2.16        | up           | 0.00            | -1.80   |
| 557 | DV059070     | 109215          | Lncbate1| 2.16        | up           | 0.00            | -1.78   |
| 558 | NM_053118    | 93746           | Gprc5d  | 2.16        | up           | 0.00            | -1.90   |
| 559 | NM_010824    | 17523           | Mpo     | 2.16        | up           | 0.01            | -1.47   |
| 560 | NM_001081397 | 244281          | Myo16   | 2.16        | up           | 0.00            | -1.41   |
| 561 | AK042193     | 320763          | A430034D21Rik | 2.16     | up           | 0.00            | -1.75   |
| 562 | XM_006535747 | 50791           | Magi2   | 2.16        | up           | 0.00            | -1.38   |
| 563 | NM_013631    | 18770           | Pklr    | 2.17        | up           | 0.00            | -1.37   |
| 564 | BC114968     | 59005           | Trappc2l| 2.17        | up           | 0.01            | -1.58   |
| 565 | AK154713     | 381680          | Nxpe5   | 2.17        | up           | 0.01            | -1.78   |
| 566 | NM_009659    | 11686           | Alox12b | 2.17        | up           | 0.00            | -1.97   |
| 567 | NM_009602    | 11444           | Chrb2   | 2.17        | up           | 0.01            | -2.00   |
| 568 | NM_199257    | 234129          | Tpte    | 2.17        | up           | 0.00            | -1.53   |
| 569 | NM_028852    | 74281           | Spatc1  | 2.17        | up           | 0.02            | -1.43   |
| 570 | AK217931     | 80987           | Nckipsd | 2.17        | up           | 0.00            | -1.85   |
| 571 | NM_001011814 | 258055          | Olf524  | 2.17        | up           | 0.00            | -1.84   |
| 572 | NM_008657    | 17878           | Myf6    | 2.17        | up           | 0.04            | -1.33   |
| 573 | ENSMUST0000053635 |       |         | 2.18        | up           | 0.00            | -1.51   |
| 574 | NM_008375    | 16204           | Fabp6   | 2.19        | up           | 0.00            | -1.57   |
| 575 | NM_001114679 | 667214          | 99301111J21Rik | 2.19     | up           | 0.00            | -1.95   |
| 576 | AK084558     |                |         | 2.19        | up           | 0.00            | -1.85   |
| 577 | NM_007919    | 13706           | Cela2a  | 2.19        | up           | 0.00            | -1.61   |
| 578 | NM_019474    | 29846           | Olf156  | 2.19        | up           | 0.01            | -1.97   |
| 579 | BC048482     | 27281           | Hrasls  | 2.19        | up           | 0.00            | -1.93   |
| 580 | NM_008729    | 18163           | Ctmd2   | 2.19        | up           | 0.00            | -1.80   |
| 581 | BC042796     | 1E+08           | Gm32478 | 2.20        | up           | 0.00            | -1.84   |
| 582 | NM_010299    | 14667           | Gm2a    | 2.20        | up           | 0.03            | -1.91   |
| 583 | BC103784     | 633640          | Gm7120  | 2.20        | up           | 0.00            | -1.64   |

28
|   |   |   |   |   |   |
|---|---|---|---|---|---|
| 584 | NM_207235 | 227789 | Olfr358 | 2.21 | up | 0.00 | -1.92 | down | 0.00 |
| 585 | NM_008936 | 19127 | Prop1 | 2.21 | up | 0.00 | -1.88 | down | 0.00 |
| 586 | NM_207230 | 216783 | Olfr320 | 2.21 | up | 0.00 | -1.52 | down | 0.01 |
| 587 | NM_001013411 | 432450 | Nkain2 | 2.21 | up | 0.00 | -1.63 | down | 0.00 |
| 588 | ENSMUST00000143224 | 546134 | Gramd2 | 2.21 | up | 0.00 | -1.60 | down | 0.02 |
| 589 | ENSMUST0000088673 | 2.21 | up | 0.00 | -1.94 | down | 0.00 |
| 590 | NM_0083535 | 16161 | Il12rb1 | 2.22 | up | 0.00 | -1.43 | down | 0.01 |
| 591 | NM_001029933 | 232966 | Zfp114 | 2.22 | up | 0.01 | -1.47 | down | 0.01 |
| 592 | NM_198106 | 208169 | Slc9c1 | 2.23 | up | 0.01 | -1.87 | down | 0.01 |
| 593 | ENSMUST00000100417 | 14055 | Ezh1 | 2.23 | up | 0.01 | -1.83 | down | 0.00 |
| 594 | NM_027908 | 71761 | Amdhd1 | 2.23 | up | 0.00 | -1.83 | down | 0.00 |
| 595 | NM_001085528 | 435791 | Gm13271 | 2.23 | up | 0.00 | -1.72 | down | 0.00 |
| 596 | AA267875 | 2.23 | up | 0.00 | -1.69 | down | 0.00 |
| 597 | AK019365 | 68191 | Tacolos | 2.24 | up | 0.00 | -1.82 | down | 0.00 |
| 598 | NM_144810 | 213417 | Klhdc8a | 2.24 | up | 0.02 | -1.58 | down | 0.00 |
| 599 | ENSMUST00000150402 | 15247 | Hiat1 | 2.25 | up | 0.00 | -1.88 | down | 0.00 |
| 600 | ENSMUST00000176687 | 2.25 | up | 0.02 | -1.29 | down | 0.02 |
| 601 | AK020279 | 77123 | 9130214F15Rik | 2.25 | up | 0.01 | -1.79 | down | 0.00 |
| 602 | BC058197 | 76051 |赣c | 2.25 | up | 0.01 | -1.56 | down | 0.00 |
| 603 | NM_001167746 | 69926 | Dnah17 | 2.25 | up | 0.00 | -1.87 | down | 0.00 |
| 604 | NM_008205 | 14997 | H2-M9 | 2.26 | up | 0.01 | -1.72 | down | 0.00 |
| 605 | NM_146666 | 258660 | Olfr736 | 2.26 | up | 0.00 | -1.49 | down | 0.05 |
| 606 | CD548909 | 2.26 | up | 0.00 | -1.81 | down | 0.00 |
| 607 | BX519376 | 98401 | AI594674 | 2.26 | up | 0.01 | -1.59 | down | 0.02 |
| 608 | NM_007550 | 12144 | Blm | 2.26 | up | 0.00 | -1.84 | down | 0.00 |
| 609 | AK042948 | 1E+08 | LOC101056015 | 2.27 | up | 0.00 | -1.85 | down | 0.00 |
| 610 | AK028492 | 2.27 | up | 0.00 | -1.47 | down | 0.01 |
| 611 | AK015936 | 75231 | 4930529I22Rik | 2.27 | up | 0.00 | -1.65 | down | 0.00 |
| 612 | XM_006515852 | 238331 | Zdhcp22 | 2.27 | up | 0.00 | -1.75 | down | 0.00 |
| 613 | NM_022886 | 64929 | Scl | 2.27 | up | 0.00 | -1.79 | down | 0.00 |
| 614 | NM_026421 | 67870 | Enoph1 | 2.28 | up | 0.00 | -1.73 | down | 0.01 |
| Gene ID       | NM/Genbank Accession | Gene Symbol | Log2 Fold Change | p-value | q-value |
|--------------|----------------------|-------------|------------------|---------|---------|
| AK040329     | 84544                | Cd96        | 2.28             | 0.00    | -1.88   |
| NM_029064    | 74711                | Ttd9        | 2.29             | 0.00    | -1.97   |
| NM_028749    | 74091                | Npl         | 2.29             | 0.01    | -1.70   |
| NM_153106    | 242726               | Padi6       | 2.29             | 0.01    | -1.60   |
| ENSMUST00000173109 | 53357            | Pla2g6      | 2.30             | 0.00    | -1.28   |
| NM_023370    | 22295                | Cdh23       | 2.31             | 0.00    | -1.88   |
| NM_146739    | 258734               | Olfr502     | 2.32             | 0.00    | -1.49   |
| NM_029310    | 75497                | Fabp12      | 2.32             | 0.00    | -1.90   |
| NM_146967    | 258969               | Olfr1226    | 2.33             | 0.00    | -1.59   |
| AK164443     | 21975                | Top3a       | 2.33             | 0.00    | -1.80   |
| BC022662     | 2.33                 |             |                  | 0.02    |         |
| NM_009491    | 22307                | Vmn2r10     | 2.33             | 0.00    | -1.87   |
| AK080358     | 668311               | Gm9099      | 2.34             | 0.00    | -1.73   |
| XM_011246586 | 68327                | Tsr3        | 2.34             | 0.00    | -1.98   |
| NM_001011518 | 258219               | Olfr94      | 2.34             | 0.00    | -1.83   |
| NM_138673    | 192188               | Stab2       | 2.34             | 0.00    | -1.38   |
| XM_006531872 | 225852               | Gm550       | 2.34             | 0.00    | -1.54   |
| NM_177791    | 279499               | Kctd19      | 2.35             | 0.01    | -1.62   |
| DV065341     | 72767                | 2810427A07Rik | 2.35       | 0.00    | -1.69   |
| NM_178412    | 229688               | Chil6       | 2.35             | 0.02    | -1.67   |
| ENSMUST00000195258 | 19206          | Ptc1        | 2.36             | 0.00    | -1.70   |
| AK090034     | 1E+08                | Gm3161      | 2.36             | 0.00    | -1.85   |
| AK136711     | 244757               | Gli126      | 2.36             | 0.00    | -1.56   |
| NM_030100    | 78428                | Wibg        | 2.37             | 0.00    | -1.95   |
| NM_007709    | 12705                | Cited1      | 2.37             | 0.00    | -1.73   |
| NM_134220    | 171254               | Vmn1r198    | 2.38             | 0.00    | -1.73   |
| NM_133720    | 70086                | Cysltr2     | 2.38             | 0.00    | -1.97   |
| XM_006504899 | 1E+08                | Gm15411     | 2.39             | 0.00    | -1.76   |
| NM_027790    | 71412                | Dhrs2       | 2.39             | 0.00    | -1.85   |
| NM_134212    | 171246               | Vmn1r200    | 2.39             | 0.01    | -1.60   |
| ENSMUST00000130873 | 12111            | Bgn         | 2.40             | 0.04    | -1.83   |
| Gene ID       | Accession     | Symbol  | log2 Fold Change | log2 Fold Change | P-value |
|--------------|---------------|---------|------------------|------------------|---------|
| NM_172900    | 243958        | Siglecg | 2.40             | 0.02             | 1.61    |
| XM_006520654 | 20273         | Scn8a   | 2.40             | 0.00             | 1.99    |
| NM_146353    | 258350        | Olfr706 | 2.40             | 0.00             | 1.56    |
| ENSMUST00000140066 | 54139 | Irf6    | 2.40             | 0.00             | 2.00    |
| ENSMUST00000110031 | 11992 | Auh    | 2.41             | 0.00             | 1.92    |
| ENSMUST00000146477 | 99237 | Tm9sf4 | 2.42             | 0.00             | 1.91    |
| CK334688     | 105271        | AU017674| 2.43             | 0.00             | 1.55    |
| ENSMUST00000190711 | 14859 | Gsta3  | 2.43             | 0.01             | 1.63    |
| XM_011242052 | 24099         | Tnfsf13b| 2.44             | 0.00             | 1.50    |
| AK031735     | 2.44          | Rgr     | 2.44             | 0.03             | 1.68    |
| ENSMUST00000146433 | 2.44 |        | 2.44             | 0.01             | 1.56    |
| XM_006516464 | 116852        | Akr1c20 | 2.44             | 0.02             | 1.53    |
| NM_011741    | 22635         | Zan     | 2.45             | 0.00             | 1.84    |
| NM_198628    | 279029        | Stkld1  | 2.45             | 0.01             | 1.54    |
| NM_001301682 | 330470        | Bsph1   | 2.46             | 0.00             | 1.88    |
| AK046275     | 75868         | 4930588A03Rik | 2.47       | 0.00             | 1.51    |
| NM_029440    | 381693        | Wdr95   | 2.48             | 0.00             | 1.79    |
| ENSMUST00000119421 | 2.48 |        | 2.48             | 0.00             | 1.87    |
| ENSMUST0000017983 | 2.49 |        | 2.49             | 0.00             | 1.82    |
| ENSMUST00000120183 | 2.49 |        | 2.49             | 0.03             | 1.98    |
| NM_027104    | 71886         | 2310002L09Rik | 2.49       | 0.00             | 1.33    |
| ENSMUST00000121277 | 2.50 |        | 2.50             | 0.00             | 1.82    |
| AK135767     | 629734        | Gm6999  | 2.50             | 0.00             | 1.56    |
| NM_016718    | 29862         | Ninj2   | 2.51             | 0.00             | 1.80    |
| NM_007720    | 12776         | Ccr8    | 2.51             | 0.00             | 1.73    |
| NM_029031    | 74637         | Shpk    | 2.52             | 0.00             | 1.90    |
| NM_009362    | 21784         | Tff1    | 2.52             | 0.00             | 1.77    |
| NM_007860    | 13370         | Dio1    | 2.53             | 0.00             | 1.65    |
| AK160242     | 665225        | Gm7544  | 2.54             | 0.00             | 1.77    |
| NM_001291001 | 70426         | Tekt5   | 2.55             | 0.00             | 1.96    |
| Gene ID      | Gene Symbol | Log2 Fold Change | Gene ID      | Gene Symbol | Log2 Fold Change |
|-------------|-------------|------------------|-------------|-------------|------------------|
| AK037200    | Gm26795     | 2.56 up          | NM_153598   | Ugt2b34     | 2.56 up          |
| AK033044    | Raxos1      | 2.57 up          | NM_183288   | Arhgap27    | 2.58 up          |
| NM_011978   | Slc27a2     | 2.58 up          | AK082204    |             | 2.58 up          |
| NM_007407   | Adcyap1r1   | 2.58 up          | NM_001164682| Mpp4        | 2.59 up          |
| AK033044    |             |                  |             |             |                  |
| NM_025621   | 4921504E06Rik | 2.60 up       | NM_027600   | 4921504E06Rik | 2.60 up       |
| NM_025621   | 2310050C09Rik | 2.61 up       | NM_025621   | 2310050C09Rik | 2.61 up       |
| AK155734    | AK155734    | 2.64 up          | ENSMUST00000121186 | 2.65 up |
| NM_001127686| Hbb-bh2     | 2.60 up          | X-m_006524267 | S6gal2     | 2.60 up          |
| ENSMUST00000124702 | 2.67 up |                  | ENSMUST00000124944 | 2.69 up |
| NM_027105   | Krtap26-1   | 2.71 up          | NM_001080809 | Cps1       | 2.72 up          |
| NM_026516   | Tmem178     | 2.72 up          | NM_029464   | Tex26       | 2.73 up          |
| NM_027105   | Krtap26-1   | 2.71 up          | NM_026516   | Tmem178     | 2.72 up          |
| NM_029464   | Tex26       | 2.73 up          | TC1666663   |             | 2.73 up          |
| NM_019471   | Mmp10       | 2.75 up          | ENSMUST0000043170 | 2.76 up |
| ENSMUST00000142944 | 2.76 up |                  | NM_019471   | Mmp10       | 2.75 up          |
| NM_011978   | Slc27a2     | 2.58 up          | AK141100    | Cit         | 2.76 up          |
| AK141100    | 9630028H03Rik | 2.77 up       | NM_0177591  | Igsf1       | 2.78 up          |
| ENSMUST00000143959 | 2.78 up |                  | 705         | Pex1        | 2.78 up          |
| ENSMUST00000155469 | 13839 |                  | 706         | Epha5       | 2.81 up          |
| XM_006544087 | LOC102641508 | 2.81 up       | 707         | LOC102641508 | 2.81 up       |

**Note:** All values are normalized to the control group. The table shows genes with a significant change in expression compared to the control. The Log2 Fold Change values indicate the magnitude of change, with 'up' indicating an increase and 'down' indicating a decrease. The p-values for each change are not shown here.
| Gene ID | Accession | Gene ID | Accession | Fold Change | Status | p-Value | Fold Change | Status |
|--------|-----------|--------|-----------|-------------|--------|---------|-------------|--------|
| NM_010127 | 19009 | Pou6f1 | 2.82 | up | 0.01 | -1.79 | down | 0.01 |
| NM_177900 | 330790 | Hapln4 | 2.87 | up | 0.00 | -1.33 | down | 0.04 |
| AK218396 | 2.87 | up | 0.00 | -1.93 | down | 0.00 |
| NM_178673 | 213262 | Fstl5 | 2.90 | up | 0.00 | -1.48 | down | 0.01 |
| NM_182957 | 66773 | Gm17019 | 2.92 | up | 0.00 | -1.76 | down | 0.00 |
| ENSMUST00000069035 | 2.95 | up | 0.00 | -1.72 | down | 0.01 |
| XM_006524202 | 225049 | Ttc7 | 2.97 | up | 0.00 | -1.75 | down | 0.00 |
| NM_146951 | 258953 | Olfr340 | 2.98 | up | 0.01 | -1.44 | down | 0.01 |
| NM_001033238 | 208650 | Cblb | 2.99 | up | 0.00 | -1.85 | down | 0.00 |
| NM_001013753 | 219228 | Olfr1306 | 3.00 | up | 0.00 | -1.72 | down | 0.00 |
| ENSMUST00000107861 | 258023 | Olfr1306 | 3.01 | up | 0.00 | -1.71 | down | 0.00 |
| NM_178247 | 347708 | Dppa1 | 3.03 | up | 0.01 | -1.59 | down | 0.00 |
| AK029692 | 74923 | 4930471D02Rik | 3.05 | up | 0.00 | -1.68 | down | 0.01 |
| NM_023816 | 76389 | Ankrd36 | 3.08 | up | 0.00 | -1.85 | down | 0.00 |
| XM_006528656 | 3.12 | LOC101055948 | up | 0.00 | -1.46 | down | 0.01 |
| XM_006517153 | 18548 | Pcsk1 | 3.14 | up | 0.00 | -1.94 | down | 0.00 |
| NM_008811 | 18598 | Pdha2 | 3.15 | up | 0.00 | -1.70 | down | 0.00 |
| AK020961 | 77981 | B230110C06Rik | 3.18 | up | 0.00 | -1.99 | down | 0.05 |
| NM_010420 | 15209 | Hesx1 | 3.24 | up | 0.00 | -1.99 | down | 0.01 |
| NM_183031 | 321019 | Gpr183 | 3.25 | up | 0.00 | -1.75 | down | 0.00 |
| NM_009903 | 12740 | Cldn4 | 3.26 | up | 0.01 | -1.93 | down | 0.01 |
| AK086943 | 629554 | Gm6980 | 3.28 | up | 0.00 | -1.62 | down | 0.00 |
| NM_011440 | 20669 | Sox14 | 3.28 | up | 0.00 | -1.81 | down | 0.00 |
| ENSMUST00000107861 | 72605 | Car10 | 3.35 | up | 0.00 | -1.82 | down | 0.00 |
| AK088235 | 70966 | 4931415C17Rik | 3.35 | up | 0.00 | -1.95 | down | 0.01 |
| NM_178245 | 244813 | Bsx | 3.39 | up | 0.00 | -1.86 | down | 0.01 |
| BI499719 | 3.45 | up | 0.00 | -1.64 | down | 0.01 |
| NM_001159389 | 320995 | Rfx6 | 3.55 | up | 0.00 | -1.75 | down | 0.00 |
| ENSMUST00000154712 | 75062 | Sf3a3 | 3.55 | up | 0.00 | -1.80 | down | 0.00 |
| NM_023894 | 104384 | Rhox9 | 3.69 | up | 0.00 | -1.97 | down | 0.00 |
Table S2. KEGG pathway analysis of the differentially expressed proteins in aortas from CIH-treated mice.

| Term_ID     | Term_description                                      | Gene | Bg | Ratio | P  | FDR | Fold | GeneSymbols                                                                 |
|-------------|-------------------------------------------------------|------|----|-------|----|-----|------|----------------------------------------------------------------------------|
| path:mmu03013 | RNA transport                                         | 0.058| 0.021| 0.001| 0.133| 2.815| Eif1;Gm5415;Gm9839;Ncbp2;Nup37;Thoc2;Rbm8a;Nup153;Eif1ax;Eif3j2;Pym1;Magohb;Kpnbl |
| path:mmu03040 | Splicesome                                             | 0.049| 0.016| 0.001| 0.133| 2.991| Ncbp2;Sf5a3;Thoc2;Ppih;Magohb;Rbm22;Hspa8;Sf3b6;Crnk11;Rbm8a;Lsm5         |
| path:mmu00053 | Ascorbate and aldurate metabolism                      | 0.018| 0.003| 0.006| 0.369| 5.357| Ugdh;Ugt2b34;Ugt2a3;Ugt2b38                                               |
| path:mmu04146 | Peroxisome                                             | 0.031| 0.010| 0.008| 0.369| 3.013| Ddo;Slc27a2;Idh1;Gstkl;Mpv17l;Pex1;Acs13                                   |
| path:mmu00980 | Metabolism of xenobiotics by cytochrome P450           | 0.027| 0.008| 0.009| 0.369| 3.338| Gsta3;Ugt2b34;Gstkl;Ugt2b38;Ugt2a3;Cyp2f2                                  |
| path:mmu00982 | Drug metabolism                                        | 0.027| 0.008| 0.010| 0.369| 3.238| Gsta3;Ugt2b34;Gstkl;Ugt2b38;Ugt2a3;Fmo5                                   |
| path:mmu00520 | Amino sugar and nucleotide sugar metabolism             | 0.022| 0.006| 0.011| 0.369| 3.690| Gnpda2;Npl;Ugdh;Fpgt;Cmas                                                   |
| path:mmu04612 | Antigen processing and presentation                    | 0.031| 0.011| 0.013| 0.369| 2.782| Creb1;Nflyb;H2-M9;Hsp90aa1;Rfxap;Hspa8;Canx                               |
| path:mmu00040 | Pentose and glucuronate interconversions               | 0.018| 0.004| 0.014| 0.369| 4.254| Ugdh;Ugt2b34;Ugt2a3;Ugt2b38                                               |
| path:mmu00860 | Porphyrin and chlorophyllII metabolism                 | 0.018| 0.005| 0.026| 0.625| 3.528| Cox10;Ugt2b34;Ugt2a3;Ugt2b38                                               |
| path:mmu00592 | alpha-Linolenic acid metabolism                         | 0.013| 0.003| 0.031| 0.672| 4.339| Pla2g5;Pla2g6;Pib1                                                          |
| path:mmu00565 | Ether lipid metabolism                                 | 0.018| 0.006| 0.035| 0.704| 3.214| Pla2g5;Enpp6;Pla2g6;Pib1                                                   |
| path:mmu04211 | Longevity regulating pathway                           | 0.027| 0.011| 0.038| 0.706| 2.411| Creb1;Atf4;Rheb;Rb1cc1;Creb5;Sesn3                                         |
| path:mmu04330 | Notch signaling pathway                                | 0.018| 0.006| 0.046| 0.786| 2.952| Aphi1b;Aphi1c;Rbpi1;Notch4                                                  |
| path:mmu04310 | Wnt signaling pathway                                  | 0.036| 0.018| 0.049| 0.786| 1.981| Gm5415;Gm9839;Fosl1;Cacybp;Ccnd2;Dkk4;Sfrp1;Myc                           |
| path:mmu00983 | Drug metabolism                                        | 0.018| 0.006| 0.055| 0.786| 2.782| Umps;Ugt2b34;Ugt2a3;Ugt2b38                                               |
| Pathway                                      | Log2 Fold Change | p-Value | q-Value | Expression Score | Genes                                                                 |
|----------------------------------------------|------------------|---------|---------|------------------|----------------------------------------------------------------------|
| path:mmu05203  Viral carcinogenesis          | 0.49             | 0.028   | 0.055   | 0.786            | Creb1;Gtf2a1;H2-M9;Rbpjl;Ube3a;Atf4;Creb5;Ccnd2;Gtf2h1;Sp100;Ccr8    |
| path:mmu05143  African trypanosomiasis       | 0.013            | 0.004   | 0.076   | 0.925            | Il12a;Fasl;Vcam1                                                      |
| path:mmu03018  RNA degradation               | 0.022            | 0.010   | 0.079   | 2.178            | Btg3;Exosc3;Dcps;Lsm5;Hspd1                                           |
| path:mmu00620  Pyruvate metabolism           | 0.013            | 0.005   | 0.087   | 2.855            | Acyp1;Pklr;Pdha2                                                      |
| path:mmu00480  Glutathione metabolism        | 0.018            | 0.007   | 0.088   | 2.371            | Ggtc;Gsta3;Idh1;Gstk1                                                |
| path:mmu04120  Ubiquitin mediated proteolysis| 0.031            | 0.017   | 0.093   | 1.808            | Anapc10;Ube3a;Ube2c;Cblb;Uba3;Cul5                                    |
| path:mmu04919  Thyroid hormone signaling path| 0.027            | 0.014   | 0.099   | 1.887            | Thra;Rheb;Slc16a10;Dio1;Notch4;Myc                                        |
| path:mmu00590  Arachidonic acid metabolism   | 0.022            | 0.011   | 0.100   | 2.031            | Pla2g6;Alox12b;Pla2g5;Tbxas1;Pib1                                      |
| path:mmu05204  Chemical carcinogenesis       | 0.022            | 0.011   | 0.115   | 1.944            | Gsta3;Ugt2b34;Gstk1;Ugt2b38;Ugt2a3                                     |
| path:mmu01200  Carbon metabolism             | 0.027            | 0.015   | 0.115   | 1.808            | Pklr;Idh1;Mcee;Cps1;Mut;Pdha2                                          |
| path:mmu04962  Vasopressin-regulated water reabsorption | 0.013 | 0.005 | 0.115 | 2.523 | Creb1;Dyn2h1;Creb5 |
| path:mmu05152  Tuberculosis                  | 0.036            | 0.022   | 0.120   | 1.625            | Creb1;Nfyb;Atp6v1h;Malt1;Rfxap;Hspd1;Il12a;Eea1                        |
| path:mmu04340  Hedgehog signaling pathway    | 0.013            | 0.005   | 0.121   | 2.465            | Ptc1h1;Dhh;Cnd2                                                       |
| path:mmu03022  Basal transcription factors   | 0.013            | 0.005   | 0.121   | 2.465            | Gtf2a1;Gtf2h1;Taf9b                                                 |
| path:mmu03015  mRNA surveillance pathway     | 0.022            | 0.012   | 0.126   | 1.883            | Ncbp2;Gspt1;Magohb;Pym1;Rbm8a                                         |
| path:mmu04915  Estrogen signaling pathway    | 0.022            | 0.012   | 0.126   | 1.883            | Creb1;Hsp90aa1;Atf4;Creb5;Hspa8                                       |
| path:mmu04940  Type I diabetes mellitus      | 0.018            | 0.009   | 0.128   | 2.066            | Il12a;H2-M9;Fasl;Hspd1                                               |
| path:mmu05215  Prostate cancer               | 0.022            | 0.012   | 0.131   | 1.864            | Creb1;Hsp90aa1;Atf4;Creb5;Braf                                         |
| path:mmu04977  Vitamin digestion and absorption | 0.009           | 0.003   | 0.141   | 3.013            | Slc19a2;Pib1                                                       |
| path:mmu04918  Thyroid hormone synthesis     | 0.018            | 0.009   | 0.143   | 1.981            | Creb1;Creb5;Atf4;Canx                                               |
| path:mmu05030  Cocaine addiction             | 0.013            | 0.006   | 0.147   | 2.260            | Creb1;Creb5;Atf4                                                      |
| path:mmu00591  Linoleic acid metabolism       | 0.013            | 0.006   | 0.160   | 2.170            | Pla2g5;Pla2g6;Pib1                                                  |
| path:mmu01230  Biosynthesis of amino acids    | 0.018            | 0.009   | 0.164   | 1.878            | Cth;Cps1;Pklr;Idh1                                                 |
| path:mmu03460  Fanconi anemia pathway         | 0.013            | 0.006   | 0.167   | 2.127            | Rev1;Top3a;B1m                                                       |
| path:mmu04950  Maturity onset diabetes of the young | 0.009           | 0.003   | 0.171   | 2.679            | Rfx6;Pklr                                                          |
| path:mmu00630  Glyoxylate and dicarboxylate metabolism | 0.009 | 0.004 | 0.191 | 2.494 | Mcee;Mut |
| path:mmu05418  Fluid shear stress and atherosclerosis | 0.027 | 0.017 | 0.200 | 1.528 | Hsp90aa1;Gsta3;Klf2;Dusp1;Vcam1;Nfe212 |
| path:mmu03020  RNA polymerase                 | 0.009            | 0.004   | 0.201   | 2.411            | Polr3k;Polr1d                                                      |
| path:mmu00280  Valine, leucine and isoleucine degradation | 0.013 | 0.007 | 0.201 | 1.937 | Mcee;Auh;Mut |
| path:mmu03320  PPAR signaling pathway        | 0.018            | 0.010   | 0.208   | 1.702            | Apoc3;S1c27a2;Acs13;Fabp6                                              |
| Pathway                                  | q-value | p-value  | Fold Change | Genes                                                                 |
|------------------------------------------|---------|----------|-------------|----------------------------------------------------------------------|
| Insulin secretion                        | 0.018   | 0.010    | 2.08        | 1.702 Creb1;Creb5;Atf4;Adcyap1r1                                       |
| Propanoate metabolism                    | 0.009   | 0.004    | 2.11        | 2.333 Mcee;Mut                                                        |
| Legionellosis                            | 0.013   | 0.007    | 0.216       | 1.870 Il12a;Hspd1;Hspa8                                              |
| Th1 and Th2 cell differentiation          | 0.018   | 0.011    | 0.220       | 1.663 Il12a;Rbpj1;Nfkbi;Il12rb1                                      |
| Citrate cycle (TCA cycle)                | 0.009   | 0.004    | 0.221       | 2.260 Idh1;Pdha2                                                     |
| Lysine degradation                       | 0.013   | 0.007    | 0.223       | 1.839 Ezh1;Nsd1;Kmt5b                                               |
| Protein digestion and absorption         | 0.018   | 0.011    | 0.238       | 2.333 Mcee;Mut                                                      |
| Progesterone-mediated oocyte maturation  | 0.018   | 0.011    | 0.238       | 1.663 Il12a;Rbpj1;Nfkbi;Il12rb1                                      |
| Retinol metabolism                       | 0.018   | 0.011    | 0.244       | 1.870 Il12a;Hspd1;Hspa8                                              |
| HTLV-I infection                         | 0.044   | 0.035    | 0.254       | 1.282 Creb1;Anapc10;H2-M9;Fosl1;Nfyb;Atf4;Ccam1;Myc;Canx             |
| Allograft rejection                      | 0.013   | 0.008    | 0.260       | 1.695 Il12a;H2-M9;Fasl                                              |
| Sulfur metabolism                        | 0.004   | 0.001    | 0.266       | 3.287 Bpnt1                                                          |
| Alanine, aspartate and glutamate         | 0.009   | 0.005    | 0.273       | 1.955 Ddo;Cps1                                                      |
| Thyroid cancer                           | 0.009   | 0.005    | 0.273       | 1.955 Braf;Myc                                                       |
| Glycerophospholipid metabolism           | 0.018   | 0.012    | 0.281       | 1.491 Dgki;Pla2g5;Pla2g6;Pbl1                                        |
| p53 signaling pathway                    | 0.013   | 0.008    | 0.283       | 1.619 Ccn1;Sesn3;Ccn2                                               |
| Amphetamine addiction                    | 0.013   | 0.008    | 0.290       | 1.595 Creb1;Creb5;Atf4                                               |
| Acute myeloid leukemia                    | 0.013   | 0.008    | 0.298       | 1.572 Braf;Myc;Mpo                                                   |
| Serotonicynic synapsee                   | 0.022   | 0.016    | 0.302       | 1.370 Htr6;Alox12b;Dusp1;Trpc1;Braf                                  |
| Pyrimidine metabolism                    | 0.018   | 0.012    | 0.306       | 1.432 Umps;Pola1;Polr3k;Polr1d                                       |
| Jak-STAT signaling pathway               | 0.027   | 0.020    | 0.306       | 1.315 Lepr;Ccn2;Csf2rb;Il12a;Myc;Il12rb1                             |
| Protein processing in endoplasmic         | 0.027   | 0.020    | 0.311       | 1.307 Hsp90aa1;Atf4;Ubqln1;Hspa8;Nfe212;Canx                       |
| Glucagon signaling pathway               | 0.018   | 0.013    | 0.312       | 1.418 Creb1;Creb5;Atf4;Pdha2                                        |
| Adipocytokine signaling pathway          | 0.013   | 0.009    | 0.313       | 1.528 Acs13;Lepr;Nfkbi                                               |
| Bladder cancer                           | 0.009   | 0.005    | 0.314       | 1.764 Braf;Myc                                                       |
| Homologous recombination                 | 0.009   | 0.005    | 0.314       | 1.764 Top3a;Blm                                                     |
| Measles                                  | 0.022   | 0.017    | 0.323       | 1.329 Ccn2;Cblb;Hspa8;Il12a;Fasl                                     |
| Fatty acid biosynthesis                   | 0.004   | 0.002    | 0.325       | 2.583 Acs13                                                          |
| Pathway | Description                                      | p-value | q-value | FDR | z-value | Genes                                                                 |
|---------|--------------------------------------------------|---------|---------|-----|---------|-----------------------------------------------------------------------|
| mmu04672 | Intestinal immune network for IgA production     | 0.009   | 0.005   | 0.335 | 0.980   | Pigr;Tnfsl3b                                                           |
| mmu05210 | Colorectal cancer                                | 0.013   | 0.009   | 0.336 | 0.980   | Braf;Ralgs;Myc                                                          |
| mmu04668 | TNF signaling pathway                            | 0.018   | 0.013   | 0.350 | 0.980   | Creb1;Creb5;Atf4;Vcam1                                                |
| mmu05161 | Hepatitis B                                      | 0.022   | 0.018   | 0.362 | 0.980   | Creb1;Atf4;Creb5;Fasl;Myc                                              |
| mmu03010 | Ribosome                                         | 0.027   | 0.022   | 0.365 | 0.980   | Rpl39;Mrpl32;Rpl34-ps1;Rps12;Mrps6;Rpl36a                              |
| mmu05220 | Chronic myeloid leukemia                         | 0.013   | 0.010   | 0.367 | 0.980   | Braf;Cblb;Myc                                                          |
| mmu00450 | Selenocompound metabolism                        | 0.004   | 0.002   | 0.380 | 0.980   | 2.127 Cth                                                             |
| mmu00910 | Nitrogen metabolism                              | 0.004   | 0.002   | 0.380 | 0.980   | 2.127 Cpsl                                                            |
| mmu04725 | Cholinergic synapse                               | 0.018   | 0.014   | 0.381 | 0.980   | 1.280 Creb1;Chrmh2;Creb5;Atf4                                          |
| mmu05144 | Malaria                                          | 0.009   | 0.006   | 0.395 | 0.980   | 1.476 Il12a;Vcam1                                                      |
| mmu00270 | Cysteine and methionine metabolism               | 0.009   | 0.006   | 0.395 | 0.980   | 1.476 Cth;Enoph1                                                       |
| mmu04725 | Cholinergic synapse                               | 0.018   | 0.014   | 0.400 | 0.980   | 1.247 Lsg1;Heatr1;Gar1;Rikol                                               |
| mmu05169 | Epstein-Barr virus infection                     | 0.031   | 0.027   | 0.407 | 0.980   | 1.151 H2-M9;Rbpj1;Polar3k;Nfbkbi;Polar1d;Hspa8;Myc                      |
| mmu00220 | Arginine biosynthesis                            | 0.004   | 0.002   | 0.413 | 0.980   | 1.903 Cpsl                                                            |
| mmu01210 | 2-Oxocarboxylic acid metabolism                  | 0.004   | 0.002   | 0.413 | 0.980   | 1.903 Idh1                                                            |
| mmu00100 | Steroid biosynthesis                             | 0.004   | 0.002   | 0.413 | 0.980   | 1.903 Msmo1                                                           |
| mmu04012 | ErbB signaling pathway                           | 0.013   | 0.010   | 0.419 | 0.980   | 1.276 Braf;Cblb;Myc                                                      |
| mmu04145 | Phagosome                                        | 0.027   | 0.022   | 0.395 | 0.980   | 1.186 Myc;Ccnd2;Lmo2;Mpo;Mllt3;Bmi1                                    |
| mmu03008 | Ribosome biogenesis in eukaryotes                | 0.018   | 0.014   | 0.400 | 0.980   | 1.247 Lsg1;Heatr1;Gar1;Rikol                                            |
| mmu05169 | Epstein-Barr virus infection                     | 0.031   | 0.027   | 0.407 | 0.980   | 1.151 H2-M9;Rbpj1;Polar3k;Nfbkbi;Polar1d;Hspa8;Myc                      |
| mmu00220 | Arginine biosynthesis                            | 0.004   | 0.002   | 0.413 | 0.980   | 1.903 Cpsl                                                            |
| mmu01210 | 2-Oxocarboxylic acid metabolism                  | 0.004   | 0.002   | 0.413 | 0.980   | 1.903 Idh1                                                            |
| mmu00100 | Steroid biosynthesis                             | 0.004   | 0.002   | 0.413 | 0.980   | 1.903 Msmo1                                                           |
| mmu04012 | ErbB signaling pathway                           | 0.013   | 0.010   | 0.419 | 0.980   | 1.276 Braf;Cblb;Myc                                                      |
| mmu00140 | Steroid hormone biosynthesis                     | 0.013   | 0.011   | 0.434 | 0.980   | 1.247 Ugt2b34;Ugt2a3;Ugt2b38                                           |
| mmu04142 | Lysosome                                         | 0.018   | 0.015   | 0.450 | 0.980   | 1.166 Lamp3;Gm2a;Ap3m2;Atp6v1h                                           |
| mmu00514 | Other types of O-glycan biosynthesis             | 0.004   | 0.003   | 0.461 | 0.980   | 1.644 St6gal2                                                          |
| mmu04152 | AMPK signaling pathway                           | 0.018   | 0.015   | 0.462 | 0.980   | 1.148 Creb1;Lepr;Creb5;Rheb                                              |
| mmu04024 | cAMP signaling pathway                           | 0.027   | 0.024   | 0.464 | 0.980   | 1.101 Creb1;Htr6;Ptc1;Creb5;Braf;Adcyap1r1                               |
| Path | Description | Score | q-value | p-value | Genes |
|------|-------------|-------|---------|---------|-------|
| path:mmu04144 | Endocytosis | 0.036 | 0.033 | 0.473 | 0.980 | 1.071 |
| path:mmu00360 | Phenylalanine metabolism | 0.004 | 0.003 | 0.476 | 0.980 | 1.572 |
| path:mmu04060 | Cytokine-cytokine receptor interaction | 0.036 | 0.033 | 0.477 | 0.980 | 1.067 |
| path:mmu05213 | Endometrial cancer | 0.009 | 0.007 | 0.480 | 0.980 | 1.247 |
| path:mmu04270 | Vascular smooth muscle contraction | 0.018 | 0.016 | 0.480 | 0.980 | 1.121 |
| path:mmu05321 | Inflammatory bowel disease (IBD) | 0.009 | 0.007 | 0.489 | 0.980 | 1.226 |
| path:mmu05340 | Histidine metabolism | 0.004 | 0.003 | 0.490 | 0.980 | 1.507 |
| path:mmu04068 | FoxO signaling pathway | 0.018 | 0.016 | 0.498 | 0.980 | 1.186 |
| path:mmu04730 | Long-term depression | 0.009 | 0.007 | 0.506 | 0.980 | 1.166 |
| path:mmu04713 | Circadian entrainment | 0.013 | 0.012 | 0.512 | 0.980 | 1.116 |
| path:mmu04721 | Cholinergic neurotransmission | 0.009 | 0.008 | 0.515 | 0.980 | 1.096 |
| path:mmu05200 | Pathways in cancer | 0.067 | 0.066 | 0.520 | 0.980 | 1.012 |
| path:mmu04210 | Apoptosis | 0.018 | 0.017 | 0.522 | 0.980 | 1.064 |
| path:mmu04925 | Aldosterone synthesis and secretion | 0.013 | 0.012 | 0.526 | 0.980 | 1.085 |
| path:mmu00601 | Glycosphingolipid biosynthesis | 0.004 | 0.003 | 0.532 | 0.980 | 1.339 |
| path:mmu05230 | Central carbon metabolism in cancer | 0.009 | 0.008 | 0.532 | 0.980 | 1.130 |
| path:mmu04623 | Cytosolic DNA-sensing pathway | 0.009 | 0.008 | 0.532 | 0.980 | 1.130 |
| path:mmu04360 | Axon guidance | 0.022 | 0.022 | 0.535 | 0.980 | 1.033 |
| path:mmu04659 | Th17 cell differentiation | 0.013 | 0.013 | 0.539 | 0.980 | 1.064 |
| path:mmu05332 | Graft-versus-host disease | 0.009 | 0.008 | 0.541 | 0.980 | 1.113 |
| path:mmu04660 | T cell receptor signaling pathway | 0.013 | 0.013 | 0.546 | 0.980 | 1.053 |
| path:mmu04972 | Pancreatic secretion | 0.013 | 0.013 | 0.546 | 0.980 | 1.053 |
| path:mmu05223 | Non-small cell lung cancer | 0.009 | 0.008 | 0.549 | 0.980 | 1.096 |
| path:mmu00230 | Purine metabolism | 0.022 | 0.022 | 0.550 | 0.980 | 1.016 |
| path:mmu04910 | Insulin signaling pathway | 0.018 | 0.017 | 0.551 | 0.980 | 1.026 |
| path:mmu04064 | NF-kappa B signaling pathway | 0.013 | 0.013 | 0.553 | 0.980 | 1.043 |
| path:mmu00010 | Glycolysis / Gluconeogenesis | 0.009 | 0.008 | 0.557 | 0.980 | 1.079 |
| path:mmu04720 | Long-term potentiation | 0.009 | 0.008 | 0.557 | 0.980 | 1.079 |
| path:mmu05146 | Amoebiasis | 0.013 | 0.013 | 0.566 | 0.980 | 1.023 |
**MAPK signaling pathway**

Pathway: mmu04010

0.036 0.036 0.566 0.980 0.987

Genes: Atf4; Dusp5; Dusp1; Hspa8; Braf; Ppm1a; Fasl; Myc

**Circadian rhythm**

Pathway: mmu04710

0.004 0.004 0.581 0.980 1.166

Genes: Cebp

**Insulin resistance**

Pathway: mmu04931

0.013 0.013 0.585 0.980 0.995

Genes: Ceb1; Cldn1; Cldn5; Cldn9; Crea; Pkm2; Pklr;

**Apoptosis**

Pathway: mmu04751

0.004 0.004 0.593 0.980 1.130

Genes: Atf4; Fas; Bak1; Casp8; Casp3; Fasl; Myc

**Galactose metabolism**

Pathway: mmu00052

0.004 0.004 0.593 0.980 1.130

Genes: Ganc

**Arrhythmogenic right ventricular cardiomyopathy (ARVC)**

Pathway: mmu05412

0.009 0.009 0.597 0.980 1.004

Genes: Actn2; Gja1

**B cell receptor signaling pathway**

Pathway: mmu04662

0.009 0.009 0.597 0.980 1.004

Genes: Malt1; Nfkbie

**Circadian rhythm**

Pathway: mmu04710

0.004 0.004 0.581 0.980 1.166

Genes: Cebp

**Insulin resistance**

Pathway: mmu04931

0.013 0.013 0.585 0.980 0.995

Genes: Ceb1; Scl27a2; Ceb5

**Apoptosis**

Pathway: mmu04751

0.004 0.004 0.593 0.980 1.130

Genes: Atf4; Fas; Bak1; Casp8; Casp3; Fasl; Myc

**Galactose metabolism**

Pathway: mmu00052

0.004 0.004 0.593 0.980 1.130

Genes: Ganc

**Arrhythmogenic right ventricular cardiomyopathy (ARVC)**

Pathway: mmu05412

0.009 0.009 0.597 0.980 1.004

Genes: Actn2; Gja1

**B cell receptor signaling pathway**

Pathway: mmu04662

0.009 0.009 0.597 0.980 1.004

Genes: Malt1; Nfkbie

**Circadian rhythm**

Pathway: mmu04710

0.004 0.004 0.581 0.980 1.166

Genes: Cebp

**Insulin resistance**

Pathway: mmu04931

0.013 0.013 0.585 0.980 0.995

Genes: Ceb1; Scl27a2; Ceb5

**Apoptosis**

Pathway: mmu04751

0.004 0.004 0.593 0.980 1.130

Genes: Atf4; Fas; Bak1; Casp8; Casp3; Fasl; Myc

**Galactose metabolism**

Pathway: mmu00052

0.004 0.004 0.593 0.980 1.130

Genes: Ganc

**Arrhythmogenic right ventricular cardiomyopathy (ARVC)**

Pathway: mmu05412

0.009 0.009 0.597 0.980 1.004

Genes: Actn2; Gja1

**B cell receptor signaling pathway**

Pathway: mmu04662

0.009 0.009 0.597 0.980 1.004

Genes: Malt1; Nfkbie

**Circadian rhythm**

Pathway: mmu04710

0.004 0.004 0.581 0.980 1.166

Genes: Cebp

**Insulin resistance**

Pathway: mmu04931

0.013 0.013 0.585 0.980 0.995

Genes: Ceb1; Scl27a2; Ceb5

**Apoptosis**

Pathway: mmu04751

0.004 0.004 0.593 0.980 1.130

Genes: Atf4; Fas; Bak1; Casp8; Casp3; Fasl; Myc

**Galactose metabolism**

Pathway: mmu00052

0.004 0.004 0.593 0.980 1.130

Genes: Ganc

**Arrhythmogenic right ventricular cardiomyopathy (ARVC)**

Pathway: mmu05412

0.009 0.009 0.597 0.980 1.004

Genes: Actn2; Gja1
Proteoglycans in cancer

Neuroactive ligand-receptor interaction

Ferroptosis
cGMP-PKG signaling pathway
Gap junction
Hepatocellular carcinoma
Autophagy
Viral myocarditis
Relaxin signaling pathway
Nucleotide excision repair
Hepatitis B
Type II diabetes mellitus
Endocrine resistance
Chagas disease (American trypanosomiasis)
Phospholipase D signaling pathway
Adrenergic signaling in cardiomyocytes
Regulation of lipolysis in adipocytes
Huntington's disease
mTOR signaling pathway
Hippo signaling pathway

Pathway: Pathway Name
path:mmu05205 Proteoglycans in cancer
path:mmu04080 Neuroactive ligand-receptor interaction
path:mmu04216 Ferroptosis
cGMP-PKG signaling pathway
path:mmu05225 Gap junction
Hepatocellular carcinoma
Autophagy
Viral myocarditis
Relaxin signaling pathway
Nucleotide excision repair
Hepatitis B
Type II diabetes mellitus
Endocrine resistance
Chagas disease (American trypanosomiasis)
Phospholipase D signaling pathway
Adrenergic signaling in cardiomyocytes
Regulation of lipolysis in adipocytes
Huntington's disease
mTOR signaling pathway
Hippo signaling pathway

Signaling pathways regulating pluripotency of stem cells
Type II diabetes mellitus
Hematopoietic cell lineage
N-Glycan biosynthesis
Cholesterol metabolism
Fatty acid degradation
Cellular senescence
Arginine and proline metabolism
Fatty acid metabolism
Chagas disease (American trypanosomiasis)
Phospholipase D signaling pathway
Adrenergic signaling in cardiomyocytes
Regulation of lipolysis in adipocytes
Huntington's disease
mTOR signaling pathway
Hippo signaling pathway

0.022  0.025  0.679  0.980  0.878  Ptch1;Cblb;Braf;Fasl;Myc
0.031  0.035  0.679  0.980  0.888  Htr6;Thr6;Lepr;Cysltr2;Gpr83;Chrb2;Adcyap1r1
0.004  0.005  0.684  0.980  0.882  Acs13
0.018  0.021  0.688  0.980  0.861  Creb1;Creb5;Prkg1;Atf4
0.009  0.011  0.693  0.980  0.841  Prkg1;Gja1
0.018  0.021  0.697  0.980  0.851  Braf;Nfe2l2;Gsta3;Myc
0.013  0.016  0.703  0.980  0.834  Rb1cc1;Uvrag;Rheb
0.009  0.011  0.705  0.980  0.822  H2-M9;Cd55
0.013  0.016  0.708  0.980  0.828  Creb1;Creb5;Atf4
0.004  0.005  0.710  0.980  0.822  Gtf2h1
0.022  0.026  0.715  0.980  0.841  H2-M9;Il12a;Fasl;Sp100;Taf9b
0.013  0.016  0.722  0.980  0.810  Creb1;Creb5;Atf4
0.009  0.011  0.722  0.980  0.795  Fosl1;Hsp90aa1
0.009  0.011  0.733  0.980  0.778  Braf;Notch4
0.013  0.017  0.736  0.980  0.792  Hesx1;Myc;Bmi1
0.004  0.006  0.741  0.980  0.753  Pklr
0.009  0.012  0.744  0.980  0.761  Cd55;Cd24a
0.004  0.006  0.748  0.980  0.738  St6gal2
0.004  0.006  0.748  0.980  0.738  Apoc3
0.004  0.006  0.755  0.980  0.723  Acs13
0.018  0.023  0.762  0.980  0.778  H2-M9;Myc;Ccnd2;Rheb
0.004  0.006  0.762  0.980  0.709  Ckb
0.004  0.006  0.768  0.980  0.695  Acs13
0.009  0.012  0.774  0.980  0.716  Il12a;Fasl
0.013  0.018  0.778  0.980  0.738  Dgki;Ralgsd;Rheb
0.013  0.018  0.778  0.980  0.738  Creb1;Creb5;Atf4
0.004  0.007  0.787  0.980  0.657  Prkg1
0.018  0.024  0.790  0.980  0.746  Creb1;Dnah17;Creb5;Dnah2
0.013  0.019  0.801  0.980  0.709  Braf;Atp6v1h;Rheb
0.013  0.019  0.804  0.980  0.704  Amot;Myc;Ccnd2
| Path              | Category                  | p-value 1 | p-value 2 | p-value 3 | p-value 4 | p-value 5 | Genes                                    |
|-------------------|---------------------------|-----------|-----------|-----------|-----------|-----------|------------------------------------------|
| mmu05145          | Toxoplasmosis             | 0.009     | 0.013     | 0.805     | 0.980     | 0.670     | Il12a;Hspa8                              |
| mmu05034          | Alcoholism                | 0.018     | 0.024     | 0.806     | 0.980     | 0.727     | Braf;Creb1;Creb5;Atf4                    |
| mmu04510          | Focal adhesion            | 0.018     | 0.024     | 0.806     | 0.980     | 0.727     | Braf;Arhgap5;Parvb;Ccnd2                 |
| mmu00561          | Glycerolipid metabolism   | 0.004     | 0.007     | 0.820     | 0.980     | 0.593     | Dgki                                     |
| mmu04213          | Longevity regulating pathway | 0.004  | 0.008     | 0.825     | 0.980     | 0.583     | Hspa8                                    |
| mmu04137          | Mitophagy                 | 0.004     | 0.008     | 0.830     | 0.980     | 0.574     | Atf4                                     |
| mmu05217          | Basal cell carcinoma      | 0.004     | 0.008     | 0.830     | 0.980     | 0.574     | Ptc1                                     |
| mmu04114          | Oocyte meiosis            | 0.009     | 0.014     | 0.836     | 0.980     | 0.623     | Anapc10;Pgr                              |
| mmu04530          | Tight junction            | 0.013     | 0.021     | 0.846     | 0.980     | 0.650     | Amot;Mpp4;Clnd4                          |
| mmu05140          | Leishmaniasis             | 0.004     | 0.008     | 0.848     | 0.980     | 0.540     | Il12a                                    |
| mmu05164          | Influenza A               | 0.013     | 0.021     | 0.849     | 0.980     | 0.646     | Il12a;Fasl;Hspa8                         |
| mmu05167          | Kaposi's sarcoma-associated herpesvirus infection | 0.018 | 0.027     | 0.856     | 0.980     | 0.667     | Creb1;H2-M9;Myc;Ccr8                    |
| mmu05211          | Renal cell carcinoma      | 0.004     | 0.008     | 0.857     | 0.980     | 0.524     | Braf                                     |
| mmu04611          | Platelet activation       | 0.009     | 0.015     | 0.862     | 0.980     | 0.583     | Prkg1;Tbxas1                             |
| mmu05214          | Glioma                    | 0.004     | 0.009     | 0.865     | 0.980     | 0.509     | Braf                                     |
| mmu04520          | Adherens junction         | 0.004     | 0.009     | 0.868     | 0.980     | 0.502     | Lmo7                                     |
| mmu04917          | Prolactin signaling pathway | 0.004   | 0.009     | 0.868     | 0.980     | 0.502     | Ccnd2                                    |
| mmu04380          | Osteoclast differentiation | 0.009     | 0.016     | 0.874     | 0.980     | 0.565     | Creb1;Fosl1                              |
| mmu05133          | Pertussis                 | 0.004     | 0.009     | 0.883     | 0.980     | 0.476     | Il12a                                    |
| mmu05218          | Melanoma                  | 0.004     | 0.009     | 0.883     | 0.980     | 0.476     | Braf                                     |
| mmu04970          | Salivary secretion        | 0.004     | 0.010     | 0.889     | 0.980     | 0.464     | Prkg1                                    |
| mmu05132          | Salmonella infection      | 0.004     | 0.010     | 0.889     | 0.980     | 0.464     | Dync2h1                                  |
| mmu00190          | Oxidative phosphorylation | 0.009     | 0.016     | 0.890     | 0.980     | 0.540     | Cox10;Atp6v1h                            |
| mmu05160          | Hepatitis C               | 0.009     | 0.016     | 0.890     | 0.980     | 0.540     | Braf;Clnd4                               |
| mmu05206          | MicroRNAs in cancer       | 0.022     | 0.035     | 0.894     | 0.980     | 0.643     | Ccng1;Ccnd2;Notch4;Myc;Bmi1              |
| mmu01521          | EGFR tyrosine kinase inhibitor resistance | 0.004   | 0.010     | 0.895     | 0.980     | 0.452     | Braf                                     |
| mmu04014          | Ras signaling pathway     | 0.018     | 0.029     | 0.899     | 0.980     | 0.610     | Ralgds;Fasl;Pla2g5;Pla2g6                |
| mmu04350          | TGF-beta signaling pathway | 0.004   | 0.010     | 0.909     | 0.980     | 0.425     | Myc                                     |
| Pathway                                  | Significance | Proteins                                      |
|------------------------------------------|--------------|----------------------------------------------|
| Chemokine signaling pathway              | 0.013        | 0.024                                        |
| FC gamma R-mediated phagocytosis         | 0.004        | 0.011                                        |
| Complement and coagulation cascades      | 0.004        | 0.011                                        |
| GnRH signaling pathway                   | 0.004        | 0.011                                        |
| Small cell lung cancer                   | 0.004        | 0.011                                        |
| Gastric cancer                           | 0.009        | 0.019                                        |
| Phosphatidylinositol signaling system    | 0.004        | 0.012                                        |
| Rap1 signaling pathway                   | 0.013        | 0.026                                        |
| Toll-like receptor signaling pathway     | 0.004        | 0.012                                        |
| AGE-RAGE signaling pathway in diabetic   | 0.004        | 0.012                                        |
| NOD-like receptor signaling pathway      | 0.009        | 0.021                                        |
| HIF-1 signaling pathway                  | 0.004        | 0.013                                        |
| Alzheimer's disease                      | 0.009        | 0.022                                        |
| Necroptosis                              | 0.009        | 0.022                                        |
| Glutamatergic synapse                    | 0.004        | 0.014                                        |
| Calcium signaling pathway                | 0.009        | 0.022                                        |
| Inflammatory mediator regulation of TRP  | 0.004        | 0.015                                        |
| Apelin signaling pathway                 | 0.004        | 0.017                                        |
| Olfactory transduction                   | 0.084        | 0.138                                        |
| Regulation of actin cytoskeleton         | 0.004        | 0.026                                        |

**Table S3.** Go enrichment of the differentially expressed proteins in aortas from CIH-treated mice.
| Term_ID   | Term description       | Bg Ratio | P_value   | Category | Fold     | GeneSymbols                                                                                                                                 |
|-----------|------------------------|----------|-----------|----------|----------|--------------------------------------------------------------------------------------------------------------------------------------------|
| GO:0006355| regulation of          | 8.81E-02 | 1.06E-07  | Process  | 1.72E+00 | Gtf2a1;Rbpjl;Dlx6;Rbak;Zfx;Rnf2;Klf16;Npat;Zbtb46;Mllt3;Rrn3;Trim33;Rfx6;Thra;Pou6f1;Rb1cc1;Myf6;Ctnnd2;Zfp37;Nfyb;Nsd1;Tal1;Creb5;Klf2;EU599041;Kdm4c;Adnp2;Myc;Ccnc;Zfp329;Ctf9;Onecut2;Ctcf;Gm14409;Zfp229;Cep290;Zfp72;Zfp131;Med19;Sa fb2;Ikzf5;Zfp62;Irfl6;Esf1;Zfp874a;Zfp521;Gtf2h1;Zfp119b;Sox14;Zfp518a;Ybx1;Churc1;Fasl;Kmt5b;Creb1;Pgr;Taf1b;Zfp53;Mphosph8;Bsx;Nfe2l2;Elp4;Vgll2;Pspc1;Hspa8;Hesx1;Notch4;Eaf1;Prop1;Atf4;Gpbp1;Zfp60;Itgb3bp;Khdrbs2;Ezh1;Zfp654;Btf3;Mty1;Taf9b;Tle3;Fosl1;Cited1;Zfp281;2610044O15Rik8;Brd8;Bmi1;Igsl1;Nol11;Psr1t3;Cdyl;Cbx7;241014K09Rik;Ikzf3;Zfp780b;Zfp322a;Sp100 |
| GO:0006351| transcription, DNA-    | 7.89E-02 | 3.35E-06  | Process  | 1.66E+00 | Gtf2a1;Rbpjl;Ccnc;Polr3k;Btf3;Sox14;Zfp518a;Ybx1;Churc1;Rbak;Myt1;Zfp329;Zfx;Rnf2;Ctf9;Fasl;Klf16;Onecut2;Kmt5b;Taf9b;Creb1;Tle3;Sp100;Pgr;Ctcf;Adnp2;Cited1;Zfp281;Npat;Swt1;Taf1b;Mphosph8;Brd8;Zbtb46;Bsx;Cep290;Zfp131;Nfe2l2;Med19;Mllt3;Rrn3;Trim33;Bmi1;Rfx6;Thra;Ikzf5;Safb2;Nol11;Zfp62;Pou6f1;Rb1cc1;Elp4;Vgll2;Fubp3;Irfl6;Esf1;Pspc1;Ctnnd2;Hesx1;Cdyl;Hspa8;Zfp37;Eaf1;Notch4;Cbx7;Nfyb;Nsd1;Tal1;Atf4;Ikzf3;Creb5;Gpbp1;Klf2;Kdm4c;Itgb3bp;Zfp521;Gtf2h1;Khdrbs2;Zfp322a;Ezh1;Zfp654;Polr1d;Myc |
| GO:0005634  nucleus     | 2.48E-01  | 7.35E-06  | Component | 1.30E+00 | Grf2a1;Rbpjl;Dlx6;Lamp3;Fam206a;RbKB;Azin1;Zfx;Rnf2;Rbm22;Cknk11;Ppm1a;Klf16;Tax1bp3;Ube2w2;Zscan5b;Tek5;Npat;Rfxap;Top3a;Zbtb46;Mllt3;Rrn3;Bex4;Trim33;Rfx6;Thra;Ube3a;Lac7l2;Pouf61;Sf3a3;Sesn3;Rblcc1;Dhx33;Myf6;Lmo2;Ctnnd2;Ugdh;Dcps;Zfp37;Pygo1;Nflyb;Nsd1;Tar1;Ncbp2;Creb5;Exoc3;Klf2;Herc6;Kdm4c;Nckipso;4933402N03Rik;Bag3;BIm;Fubp3;Vps37a;Cul5;Mye;Ppwd1;Lsm5;Adnp2;CcnC;Acd;Zfp329;Txdn9;Ralga2a;Ctn9;Onee2t2;Crbn;Pdc13;Ctcf;Dyrk1a;N4bp212;Ube2c;St1p1;Pllp7;Cep290;Zfp72;Zfp131;Med19;TeX10;Senp7;Saib2;Ikgx5;Polal;Zfp62;Ralgs;Cblb;Cps1;Irf6;Esf1;Padi6;Ingl1;Igf2bp3;Lemd3;Ublq1n1;Dusp1;Amp32e;Zfp521;Gtf2h1;Miat;Braf;Ybey;Mettl3;Sbrbp;Polr3k;Zfp119b;Toel;Ptc1;Sox14;Zfp518a;Ybx1;Churc1;Zfp438;Fasl;Kmt5b;Creb1;Pgr;Rev1;Hmgn2;Taf1b;Mphosph8;Bsx;Sf3b6;Nfe212;Kpb1b;Mif;Cacybp;Malt1;Thoc2;Elp4;Vgl12;Brix1;Pym1;Mpo;Pspcl1;Hspa8;Ipo7;C2n2;Ckb;Hex1;Eaf1;Notch4;Prop1;Zfp106;Wtap;Neil2;Afr4;Gpbb1;G2e3;Ccn1;Umps;Zfp60;Esco1;Dgki;Igb3b;Magohb;Khdrbs2;Ezh1;Zfp654;Ssa2;Naa50;Btf3;Vldlr;Nkbi;Mcm8;Gtf3c3;Pus7;Gnpda2;Cep350;Magi2;Cnd2;My1;Nol10;Mom2;Uba3;Taf9b;Sde2;Tle3;Fos1;Cited1;Lsg1;Zfp281;Swt1;Brd8;Bmi1;Appbp2;Gm5415;Enoph1;Ifrd2;Nol11;Arhgap27;Krr1;Gar1;Cdy1;Cmas;Cbx7;Hsp90a1;Aurbkb;Ikzf3;Nup37;Serpinb9;Prrkx;Zfp322a;Cecr2;Polr1d;Wrm;Sp100;Rbm8a;Kpna4 |
| GO:0001782  negative regulation of cell division | 2.97E-04  | 1.69E-05  | Process   | 2.13E+01  | Ptc1;Intu;Myc;BIm |
| GO:0003676  nucleic acid binding | 3.64E-02  | 8.26E-05  | Function  | 1.85E+00  | Polr3k;Toel;Zfp518a;Ybx1;Rbkb;Zfp329;Zfx;Rbm22;Klf16;Eaa1;Cccf;Zfp281;Top3a;Zbtb46;Sf3b6;Zfp131;Saib2;Ikgx5;Polal;Zfp62;Sf3a3;Zcchc2;Dhx33;Zcchc10;Krr1;Rbsn;Pspcl1;Zfp37;Igf2bp3;Lemd3;Zfp106;Neil2;Ncbp2;Ikzf3;Zfp60;Klf2;Zfp521;Zfp322a;Khdrbs2;BIm;Wrm;Zfp654;Adnp2 |
| GO:00061077  chaperone-mediated protein folding | 1.86E-03  | 1.58E-04  | Process   | 5.92E+00  | Cct6a;Cct7;Cct4;Hspa1;Hspa8;Chordc1;Canx |
GO:0005515  protein binding  2.09E-01  2.06E-04  Function  1.28E+00  Gtf2a1;Cct7;Tff1;Rnf2;Sfrp1;Tax1bp3;Lin7c;Ube2w;Pkd2;Epha5;Zbtb46;Mllt3;Trim33;Rfx6;Sema3a;Thra;Ube3a;Rb1cc1;Sesn3;Tada2b;Lmo2;Capza2;Sptbn4;Pogo1;Ccr8;Anapc10;Nsd1;Slc7a9;Tal1;Btg3;Klf2;Bag3;Stap2;Blm;Prkg1;Slc5a2;Cul5;Myc;Lsm5;Chrhb2;Htr6;Alk;Acd;Cct4;Ctr9;Ctcf;Dyrk1a;N4bp2l2;Hpca;Stip1;Nup153;Cep290;Bbs9;Med19;Snp7;Kctd12;Pola1;Gstl1;Ralgds;Cblb;Cps1;Padi6;Ccm2;Igf2bp3;Tspan13;Cd96;Raet1b;Miat;Braf;Khdc1b;Cct6a;Mettl3;Ptc1;Sema4g;Ybx1;Ppfa4;Reep5;Il12a;Canx;Creb1;Rpl39;Pgr;Rev1;Taf1b;Zfp53;Ift81;Csf2rb;Bsx;Nfe2l2;Exoc3l;Kpnbl;Parvb;Gja1;Cacybp;Malt1;Thoc2;Vgl2;Usp33;Stoml3;Pspc1;Hspa8;Ipo7;Hexx1;Ckb;Myo16;Notch4;Prop1;Il12rb1;Wtap;Dhh;Cd24a;Atf4;Scn8a;Gpbp1;Tmem178;Trpc1;Khdrbs2;Cit;Ezh1;Cldn4;Cdhl2;Naa50;Lepr;Nkbie;Sgldg;Vldlr;Cep350;Mag2;Ccn2;Myt1;Dnah17;Uba5;Adam5;Ee1;Tle3;Cep55;Tom111;Cited1;Zfp281;Tmem108;Actn2;Trip13;Adcyap1r1;Amot;Appbp2;Bmi1;Trim38;Uvrq;Spac1;Map2;Prmt3;Snnx1;Gar1;Dusp19;Fndc5;Sle9c1;Chx7;B6sp2;Hsp90aa1;Aurkb;Ikzf3;Cth;Mpv17l;Pldcd1;Serpinb9;Wnm;Polr1d;Kpna4;Sp100;Chordc1;Stab1;Impg2;Tnfaip6;HaplN4;Stab2

GO:0005540  hyaluronic acid binding  1.00E-03  3.59E-04  Function  7.84E+00  Stab1;Impg2;Tnfaip6;HaplN4;Stab2

GO:0006458  'de novo' protein folding  5.93E-04  4.17E-04  Process  1.06E+01  Cct6a;Hspd1;Cct4;Cct7

GO:0060509  Type I pneumocyte differentiation  2.97E-04  6.23E-04  Process  1.60E+01  Creb1;Thra;Klf2

GO:0044183  protein binding involved in protein folding  1.13E-03  6.54E-04  Function  6.94E+00  Cct6a;Pdcl3;Cct7;Cct4;Hspd1

GO:0072341  modified amino acid binding  3.05E-04  6.83E-04  Function  1.55E+00  Cps1;Mut;Prmt3

GO:0045893  positive regulation of transcription, DNA-templated  2.53E-02  8.21E-04  Process  1.87E+00  Rbpj1;Ptc1;Churc1;Sfrp1;Ppm1a;Creb1;Pgr;Ctcf;Cited1;Zfp281;Npat;Rfxap;Cep290;Nfe2l2;Mllt3;Rrn3;Rfx6;Myf6;Irf6;Ing1;Nfyb;Nsd1;Tal1;Atf4;Creb5;Gpbp1;Klf2;Blm;Fubp3;Myc

GO:1904871  positive regulation of protein localization to Cajal body  3.39E-04  9.77E-04  Process  1.40E+01  Cct6a;Cct4;Cct7
GO:0005929 cillum 1.13E-02 1.26E-03 Component 2.31E+00 Htr6;Ptdch1;Pkd2;Lca5;Till9;Dynce2h1;StomI3;Dnah17;Tulp4;Dnah2;Cep290;Cct4;Bbs9;Slc9c1;Rpl1;lf81;Umod

GO:0050667 homocysteine metabolic process 3.81E-04 1.44E-03 Process 1.24E+01 Cth;Cps1;Mut

GO:1904851 positive regulation of establishment of protein localization to telomere 3.81E-04 1.44E-03 Process 1.24E+01 Cct6a;Cct4;Cct7

GO:0045292 mRNA cis splicing, via spliceosome 3.81E-04 1.44E-03 Process 1.24E+01 Dcps;Rbm22;Ncbp2

GO:0042026 protein refolding 3.81E-04 1.44E-03 Process 1.24E+01 Hsp90aa1;Hspd1;Hspa8

GO:0046850 regulation of bone remodeling 3.81E-04 1.44E-03 Process 1.24E+01 Lepr;Suco;Gja1

GO:0030644 cellular chloride ion homeostasis 3.81E-04 1.44E-03 Process 1.24E+01 Ckb;Fasl;Tbxas1

GO:0032212 positive regulation of telomere maintenance via telomerase 1.36E-03 1.52E-03 Process 5.82E+00 Cct6a;Aurkb;Cct7;Acd;Cct4

GO:0000184 nuclear-transcribed mRNA catabolic process, nonsense-mediated decay 1.36E-03 1.52E-03 Process 5.82E+00 Ncbp2;Gspt1;Magohb;Pym1;Rbm8a

GO:0051082 unfolded protein binding 3.49E-03 1.68E-03 Function 3.61E+00 Cct6a;Hsp90aa1;Cct7;Hspe1;Cct4;Hspa8;Hspd1;Canx

GO:0044297 cell body 4.22E-03 1.69E-03 Component 3.29E+00 Cct6a;Cct7;Cacybp;Map2;Alk;Usp33;Cct4;Rdh10;Braf

GO:0051973 positive regulation of telomerase activity 1.40E-03 1.75E-03 Process 5.64E+00 Hsp90aa1;Aurkb;Acd;Cct4;Myc
GO:0005737  cytoplasm  2.67E-01  2.11E-03  Component  1.19E+00
Gtf2a1; Cct7; Tll19; Dennd6a; Azin1; Tff1; Rbm22; Ppm1a; Tax1bp3; Stab1; Lin7c; Serpinb6c; In
tu; Pkd2; Slc23a3; Ube2w; Npat; Tnfsf13b; Bex4; Thra; Vash1; Ube3a; Rb1cc1; Dhz33; Sesan3; S
nix16; Sbk1; Spbn8; Dcep; Dyn2c1h; Fbx114; Dennd2d; Anapc10; Ncbf2; Btg3; Exosc3; Here6; N
yx; Bag3; Stapp2; Blm; Cilmn; Prkg1; Fuhrp3; Cul5; Myc; Lsm5; Fabp6; Amh1d1; Arhgap5; Idh1; H
spe1; Alox12b; Tnnd9c; Ralgap2a; Cct4; Ppp6r2; Rpl1; Crbn; Cep112; Tc7; Pdic13; Aprt; Hpauc;
Ube2c; Cfpaf61; Stip1; Cep5711; Rdh10; Cep290; Bbs9; Tex10; Cst13; Eml6; Safs2; Pola1; Pla2g6;
Ralgds; Cblb; Cps1; Irf6; Padi6; Stab2; Ccm2; Igef2bp3; Cdf96; Ubqln1; Dusp1; Anp32e; Braf; Txn
dc2; Khdc1b; Cct6a; Mett13; Srbp; Pdlim2; Plkr; Toe1; Ppih1; Ybx1; Riolk1; Scel; H112a; Arhgef16;
Canx; Mpp4; Pgr; 23110050c09Rik; Mphosph8; Bsx; Ythdf1; Nfe2l2; Mif; Parvb; Gja1; Canx;
Ccnd2; Pex1; Dnah2; Ssfa2; Naa50; Btfl3; Nkbi; Gnapda2; Cep350; Mag12; Ccnd2; Pex1; Dnah17;
Uba3; Fgpt; Eea1; Agbl3; Cep55; Tom111; Cited1; Lsg1; Npl; Atp1; Sept1; Hspd1; Adcyap1r1; Amot;
Appb2; Sept4; Bm11; Gsta3; Enol1; Trim13; Spact1; Zhce2c; Map2; Prmt3; Chif6; Arhgap27; Snx1;
Krn1; Sgsm2; Dusp19; Bgn; Bfsp2; Sept10; Hsp90aa1; Akurbk; Lca5; Hrals; Rbhb; E NF3; Pbx1c1;
Mpv171; Serpin9b; Ppplr2; Cplx2; Prkx; Zfpl322a; Wrm; Kpna4; Sp100; Zfand5; Trapp2c;
Flg; Aliob12c; Cltn4; Cela2a

GO:0061436  establishment of skin barrier  8.90E-04  2.15E-03  Process  7.09E+00
Flg; Aliob12c; Cltn4; Cela2a

GO:0064136  metal ion binding  9.80E-04  2.15E-03  Function  7.09E+00

GO:0046792  nuclear periphery  8.95E-04  2.38E-03  Component  6.89E+00
Nup153; Kpnb1; Map2; Atf4

GO:0045333  cellular respiration  9.32E-04  2.57E-03  Process  6.77E+00
Cqco10b; Slc25a25; Cox10; Sdhaf1
GO:0007601 visual perception 5.51E-03 2.72E-03 Process 2.86E+00 Bfsp2;Impg2;Rgr;Sox14;Opn4;Nyx;Col11a1;Rdh10;Rp1;Chrb2

GO:0005832 chaperonin-containing T-complex 4.69E-04 2.94E-03 Component 9.86E+00 Cct6a;Cct4;Cct7

GO:0030879 mammary gland development 1.61E-03 3.32E-03 Process 4.90E+00 Creb1;Arhgap5;Pch1;Pgr;Notch4

GO:0071498 cellular response to fluid shear stress metabolic process 5.08E-04 3.54E-03 Process 9.31E+00 Nfe2l2;Klf2;Pkd2

GO:0008152 mammary gland development 1.61E-03 3.32E-03 Process 4.90E+00 Creb1;Arhgap5;Pch1;Pgr;Notch4

GO:0006457 metabolic process 1.84E-02 3.56E-03 Process 9.31E+00 Nfe2l2;Klf2;Pkd2

GO:0006457 protein folding 4.03E-03 4.07E-03 Process 3.13E+00 Cct6a;Hsp90aal1;Cct7;Hspe1;Cct4;Hspa8;Hspd1;Canx

GO:0016485 gestation with mouth forming second 1.14E-03 5.54E-03 Process 5.51E+00 Amot;Ugdh;Nsd1;Rnf2

GO:0001702 protein folding 4.03E-03 4.07E-03 Process 3.13E+00 Cct6a;Hsp90aal1;Cct7;Hspe1;Cct4;Hspa8;Hspd1;Canx
GO:0000974  Prp19 complex  5.96E-04  6.10E-03  Component  7.75E+00  Crnk1l1;Rbm22;Hspa8
GO:0030133  transport vesicle  1.83E-03  6.43E-03  Component  4.21E+00  Aph1b;Pigr;Atp2c1;Tmem168;Bgn
GO:0007028  cytoplasm organization  2.12E-04  6.83E-03  Process  1.49E+01  Padi6;Rrn3
GO:0036003  positive regulation of transcription from RNA polymerase II promoter in response to stress  2.12E-04  6.83E-03  Process  1.49E+01  Nfe2l2;Klf2
GO:0002904  positive regulation of B cell apoptotic process  2.12E-04  6.83E-03  Process  1.49E+01  Cd24a;Myc
GO:0090238  positive regulation of arachidonic acid secretion  2.12E-04  6.83E-03  Process  1.49E+01  Mif;Pla2g6
GO:0008616  queuosine biosynthetic process  2.12E-04  6.83E-03  Process  1.49E+01  Txndc9;Pdcl3
GO:0006360  transcription from RNA polymerase I promoter  2.12E-04  6.83E-03  Process  1.49E+01  Taf1b;Gtf2h1
GO:1904874  positive regulation of telomerase RNA localization to Cajal body  6.36E-04  6.90E-03  Process  7.44E+00  Cct6a;Cct4;Cct7
GO:0030890  positive regulation of B cell proliferation  1.91E-03  6.93E-03  Process  4.14E+00  Mif;Gpr183;Tnfsf13b;Chrnb2;Bmi1
GO:0042113  B cell activation  1.23E-03  7.19E-03  Process  5.13E+00  Malt1;Hspd1;Chrnb2;Ikzf3
GO:0009378  four-way junction helicase activity  2.18E-04  7.26E-03  Function  1.44E+01  Wrm;Blm
| GO:0000405 | bubble DNA binding | 2.18E-04 | 7.26E-03 | Function | 1.44E+01 | Wrn;Blm |
| GO:0034185 | apolipoprotein binding | 6.54E-04 | 7.53E-03 | Function | 7.21E+00 | Vldlr;Hspd1;Canx |
| GO:0003700 | DNA binding transcription factor activity | 3.71E-02 | 8.29E-03 | Function | 1.53E+00 | Rbpj;Myt1;Zfp438;Klf16;Onecut2;Creb1;Fosl1;Prgr;Ctcf;Cited1;Zfp281;2610044O15Rik;Gm14409;Zfp229;Zfp53;Bsx;Zfp72;Nfe2l2;Rfx6;Thra;Pou6f1;Tada2b;Irf6;Nfyb;Zfp874a;2410141K09Rik;Tal1;Atf4;Creb5;Gpbp1;Zfp60;Klf2;EU599041;Zfp780b;Zfp322a;Myc |
| GO:0017124 | SH3 domain binding | 5.49E-03 | 8.55E-03 | Function | 2.58E+00 | Zfp106;Uvrag;Tom111;Gja1;Nckipsd;Cblb;Arhgap27;Khdrbs2;Cit |
| GO:0051371 | muscle alpha-actinin binding | 6.98E-04 | 9.08E-03 | Function | 6.76E+00 | Mybpc2;Pdlim2;Pkd2 |
| GO:0006606 | protein import into nucleus | 2.88E-03 | 9.83E-03 | Process | 3.28E+00 | Nup153;Hspa8;Ipo7;Kpnb1;Kpna4;Ing1 |
| GO:0030490 | maturation of SSU-rRNA | 7.20E-04 | 9.91E-03 | Process | 6.57E+00 | Tsr3;Nol11;Riok1 |
| GO:0031396 | regulation of protein ubiquitination | 7.20E-04 | 9.91E-03 | Process | 6.57E+00 | Ubqln1;Hsp90aa1;Rnf139 |
| GO:0006352 | DNA-templated transcription, initiation | 7.20E-04 | 9.91E-03 | Process | 6.57E+00 | Myc;Rrn3;Taf9b |
| GO:0071499 | cellular response to laminar fluid shear stress | 2.54E-04 | 1.01E-02 | Process | 1.24E+01 | Nfe2l2;Klf2 |
| GO:0051168 | nuclear export | 2.54E-04 | 1.01E-02 | Process | 1.24E+01 | Malt1;Lsg1 |
| GO:0044539 | long-chain fatty acid import | 2.54E-04 | 1.01E-02 | Process | 1.24E+01 | Slec27a2;Acsl3 |
| GO:0044806 | G-quadruplex DNA unwinding | 2.54E-04 | 1.01E-02 | Process | 1.24E+01 | Wrn;Blm |
| GO:0006207 | 'de novo' pyrimidine nucleobase biosynthetic process | 2.54E-04 | 1.01E-02 | Process | 1.24E+01 | Cps1;Umps |
| GO:0033135 | regulation of peptidyl-serine phosphorylation | 2.54E-04 | 1.01E-02 | Process | 1.24E+01 | Nsd1;Sptbn4 |
| GO:0031514 | motile cilium | 3.71E-03 | 1.04E-02 | Component | 2.91E+00 | Sept4;Intu;Pkd2;Dnah17;Dnah2;Slc9c1;Dyn2h1 |
| GO:0000403 | Y-form DNA binding | 2.62E-04 | 1.07E-02 | Function | 1.20E+01 | Wrn;Blm |
| GO:0017171 | serine hydrolase activity | 2.62E-04 | 1.07E-02 | Function | 1.20E+01 | Pla2g6;Cela2a |
| GO:0045505 | dynein intermediate chain binding | 1.40E-03 | 1.14E-02 | Function | 4.51E+00 | Dnah17;BC048507;Dyn2h1;Dnah2 |
| GO:0003682 | chromatin binding | 2.04E-02 | 1.21E-02 | Function | 1.69E+00 | Rbpj1;Sox14;Ybx1;Rnf2;Ctcf;Cited1;Nup153;Mllt3;Bmi1;Pola1;Tada2b;Lmo2;Hexx1;Cdyl;Prop1;Cbx7;Nsd1;Tal1;Kdm4c;Gtf2h1;Wrn;Ezh1 |
| GO:0008270 | zinc ion binding | 2.91E-02 | 1.21E-02 | Function | 1.57E+00 | Polr3k;Mmp10;Ptc1;Myt1;Churc1;Rnf2;Agl3;Pgr;Rnf139;Nup153;Top3a;Trim33;Thra;Izfit5;Trim13;Sf3a3;Zcchc2;Usp33;Zcchc10;Zfp37;Nsd1;Adamts20;Dhh;Neil2;Esco1;Kdm4c;Bmi1;Zfad5;Chordc1 |
| GO:0035690 | cellular response to drug | 2.20E-03 | 1.27E-02 | Process | 3.58E+00 | Rbm22;Bmi1;Braf;Nfe2l2;Myc |
| GO:0051959 | dynein light intermediate chain binding | 1.44E-03 | 1.27E-02 | Function | 4.37E+00 | Dnah17;BC048507;Dyn2h1;Dnah2 |
| GO:0001502 | cartilage condensation | 8.05E-04 | 1.36E-02 | Process | 5.88E+00 | Otor;Thra;Col11a1 |
| GO:0004842 | ubiquitin-protein transferase activity | 1.47E-02 | 1.38E-02 | Function | 1.81E+00 | Khdc8a;Rnf139;Ube3a;Ube2w;Malt1;G2e3;Herc6;Trim13;Khld29;Lmo7;Rnf103;Ube2c;Cblb;Khld30;Mphosph8;Rnf2;Fbx114 |
| GO:0043584 | nose development | 2.97E-04 | 1.38E-02 | Process | 1.06E+01 | Hes1;Rdh10 |
| GO:0045656 | negative regulation of monocyte differentiation | 2.97E-04 | 1.38E-02 | Process | 1.06E+01 | Zbtb46;Myc |
| GO:0009313 | oligosaccharide catabolic process | 2.97E-04 | 1.38E-02 | Process | 1.06E+01 | Gm2a;Ctbs |
| GO:ID          | Term                                | P-value | E-value | Type     | FDR     | Genes                                                                 |
|---------------|-------------------------------------|---------|---------|----------|---------|-----------------------------------------------------------------------|
| GO:0051480    | regulation of cytosolic calcium ion concentration | 1.48E-03 | 1.40E-02 | Process  | 4.25E+00 | Trpc1;Tmem178;Cul5;Cdhl23                                             |
| GO:0034366    | spherical high-density lipoprotein particle | 2.98E-04 | 1.46E-02 | Component | 1.03E+01 | Apoc3;Pon1                                                             |
| GO:0070765    | gamma-secretase complex              | 2.98E-04 | 1.46E-02 | Component | 1.03E+01 | Aph1b;Aph1c                                                            |
| GO:0000151    | ubiquitin ligase complex             | 3.96E-03 | 1.46E-02 | Component | 2.72E+00 | Ccnc;Ube2c;4933402N03Rik;Mphosph8;Rnf2;Hspa8;Bmi1                    |
| GO:0051880    | G-quadruplex DNA binding             | 3.05E-04 | 1.47E-02 | Function  | 1.03E+01 | Wrn;Blm                                                                |
| GO:0008479    | queuine tRNA-ribosyltransferase activity binding | 3.05E-04 | 1.47E-02 | Function  | 1.03E+01 | Txndc9;Pdcl3                                                           |
| GO:0005113    | patched binding                      | 3.05E-04 | 1.47E-02 | Function  | 1.03E+01 | Dhh;Pch1                                                               |
| GO:0015030    | Cajal body                           | 1.49E-03 | 1.54E-02 | Component | 4.13E+00 | Lsg1;Angel2;Toe1;Npat                                                  |
| GO:0060997    | dendritic spine morphogenesis        | 8.47E-04 | 1.56E-02 | Process   | 5.58E+00 | Ctnnd2;Epha5;Prmt3                                                    |
| GO:0071013    | catalytic step 2 spliceosome         | 4.13E-03 | 1.81E-02 | Component | 2.61E+00 | Sf3a3;Magohb;Rbm22;Sf3b6;Crnkl1;Rbm8a;Ppwd1                          |
| GO:0061820    | telomeric D-loop disassembly         | 3.39E-04 | 1.81E-02 | Process   | 9.31E+00 | Wrn;Blm                                                                |
| GO:0002070    | epithelial cell maturation           | 3.39E-04 | 1.81E-02 | Process   | 9.31E+00 | Pgr;Gja1                                                               |
| GO:0034379    | very-low-density lipoprotein particle assembly | 3.39E-04 | 1.81E-02 | Process   | 9.31E+00 | Apoc3;Acs13                                                            |
| GO:0010518    | positive regulation of phospholipase activity | 3.39E-04 | 1.81E-02 | Process   | 9.31E+00 | Hpcal;Pla2g5                                                          |
| GO ID          | Description                              | p-value | FDR   | Type     | Genes                                      |
|---------------|------------------------------------------|---------|-------|----------|--------------------------------------------|
| GO:0050847    | progesterone receptor signaling pathway   | 3.39E-04 | 1.81E-02 | Process  | Ube3a;Pgr                                 |
| GO:0048680    | positive regulation of axon regeneration | 3.39E-04 | 1.81E-02 | Process  | Braf;Mif                                  |
| GO:0034498    | early endosome to Golgi transport         | 3.39E-04 | 1.81E-02 | Process  | Snx1;Rbsn                                 |
| GO:0071481    | cellular response to X-ray               | 3.39E-04 | 1.81E-02 | Process  | Ccnd2;Sfrp1                               |
| GO:0048845    | venous blood vessel morphogenesis        | 3.39E-04 | 1.81E-02 | Process  | Notch4;Ccm2                               |
| GO:0030496    | midbody                                  | 5.11E-03 | 1.84E-02 | Component | Uvrag;Cep55;Ptch1;Aurkb;Lyrm1;Txndc9;Cit;Sept1 |
| GO:0073339    | binding of sperm to zona pellucida       | 1.61E-03 | 1.85E-02 | Process  | Cct6a;Zan;Cct4;Cct7                        |
| GO:0008380    | RNA splicing                             | 1.06E-02 | 1.87E-02 | Process  | Dcps;Wtap;Ncbp2;Sf3a3;Thoc2;Ybx1;Magohb;Rbm22;Hspa8;Sf3b6;Crnkl1;Lsm5;Ppwd1 |
| GO:0072669    | tRNA-splicing ligase complex             | 3.41E-04 | 1.91E-02 | Component | Zbtb8os;AI597479                          |
| GO:0061164    | RNA polymerase I CORE element sequence-  | 3.49E-04 | 1.92E-02 | Function | Taf1b;Rm3                                 |
|               | specific DNA binding                     |         |       |          |                                            |
| GO:0043140    | ATP-dependent 3’→5’ DNA helicase activity | 3.49E-04 | 1.92E-02 | Function | Wrn;Blm                                   |
| GO:0102391    | decanoate-CoA ligase activity            | 3.49E-04 | 1.92E-02 | Function | Slc27a2;Acsd3                             |
| GO:0004033    | aldo-keto reductase (NADP) activity      | 3.49E-04 | 1.92E-02 | Function | Akr1c20;Akr1c13                           |
| GO          | Term                                                                 | FDR     | p-value   | Process/Function | Genes Associated |
|-------------|----------------------------------------------------------------------|---------|-----------|------------------|------------------|
| GO:0008035  | high-density lipoprotein particle binding                           | 3.49E-04 | 1.92E-02  | Function         | Pon1;Hspd1       |
| GO:0008020  | G-protein coupled photoreceptor activity                            | 3.49E-04 | 1.92E-02  | Function         | Rgr;Opn4         |
| GO:0035145  | exon-exon junction complex                                           | 8.95E-04 | 1.93E-02  | Component        | Pym1;Rbm8a;Magohb|
| GO:0008569  | ATP-dependent microtubule motor activity, minus-end-directed         | 9.16E-04 | 1.95E-02  | Function         | Dnah17;Dyn2h1;Dnah2|
| GO:0043085  | positive regulation of catalytic activity                           | 1.65E-03 | 2.02E-02  | Process          | Aph1b;Aph1c;Myc;Hspa8|
| GO:0061512  | protein localization to cilium                                      | 9.32E-04 | 2.03E-02  | Process          | Bbs9;Dyn2h1;Tulp4|
| GO:0050821  | protein stabilization                                               | 6.44E-03 | 2.19E-02  | Process          | Creb1;Cct6a;Hsp90aa1;Cct7;Usp33;Cct4;Bag3;Hspd1;Taf9b|
| GO:0003824  | catalytic activity                                                  | 2.04E-02 | 2.22E-02  | Function         | St6gal2;Pklr;Enpp6;Azin1;Ppm1a;Ganc;Npl;Cps1;Ugdh;Cdy1;Ckb;Mut;Sle27a2;Neil2;Cth ;Umps;Acs13;Auh;Wrn;B1m;Prkg1|
| GO:0009048  | dosage compensation by inactivation of X chromosome                 | 3.81E-04 | 2.29E-02  | Process          | Eif1;Ctf1       |
| GO:0014050  | negative regulation of glutamate secretion                         | 3.81E-04 | 2.29E-02  | Process          | Prkg1;Htr6      |
| GO:0034374  | low-density lipoprotein particle remodeling                        | 3.81E-04 | 2.29E-02  | Process          | Pla2g5;Mpo     |
| GO:0080009  | mRNA methylation                                                    | 3.81E-04 | 2.29E-02  | Process          | Mettl3;Wtap |
| GO ID          | GO Term                                      | p-value | q-value | FDR   | Count | Genes          |
|---------------|----------------------------------------------|---------|---------|-------|-------|----------------|
| GO:0042994    | cytoplasmic sequestering of transcription factor | 3.81E-04 | 2.29E-02 | Process | 8.27E+00 | Thra;Pkd2      |
| GO:0043030    | regulation of macrophage activation          | 3.81E-04 | 2.29E-02 | Process | 8.27E+00 | Shpk;Pla2g5    |
| GO:0030814    | regulation of cAMP metabolic process         | 3.81E-04 | 2.29E-02 | Process | 8.27E+00 | Cep290;Pkd2    |
| GO:0006032    | chitin catabolic process                     | 3.81E-04 | 2.29E-02 | Process | 8.27E+00 | Chil6;Ctbs     |
| GO:0032926    | negative regulation of activin receptor signaling pathway | 3.81E-04 | 2.29E-02 | Process | 8.27E+00 | Lemd3;Magi2    |
| GO:2000234    | positive regulation of rRNA processing       | 3.81E-04 | 2.29E-02 | Process | 8.27E+00 | Heatr1;Riok1   |
| GO:0002329    | pre-B cell differentiation                   | 3.81E-04 | 2.29E-02 | Process | 8.27E+00 | Cd24a;Atp11c   |
| GO:0045494    | photoreceptor cell maintenance               | 1.74E-03 | 2.38E-02 | Process | 3.63E+00 | Cep290;Rp1;Lca5;Cdh23 |
| GO:0004568    | chitinase activity                           | 3.92E-04 | 2.43E-02 | Function | 8.01E+00 | Chil6;Ctbs    |
| GO:0042623    | ATPase activity, coupled RNA activity        | 3.92E-04 | 2.43E-02 | Function | 8.01E+00 | Pex1;Hspa8    |
| GO:0000340    | RNA 7-methylguanosine cap binding            | 3.92E-04 | 2.43E-02 | Function | 8.01E+00 | Dcps;Ncbp2    |
| GO:0000398    | mRNA splicing, via spliceosome               | 4.49E-03 | 2.43E-02 | Process | 2.46E+00 | Mettl3;Ncbp2;Sf3a3;Pspc1;Sf3b6;CrnkI1;Lsm5 |
| GO:0004402    | histone acetyltransferase activity           | 1.74E-03 | 2.43E-02 | Function | 3.61E+00 | Cdyl;Elp4;Tada2b;Taf9b |
| GO:0005509 | calcium ion binding | 2.57E-02 | 2.45E-02 | Function | 1.53E+00 | Vldlr;Canx;Stab1;Pon1;Pkd2;Hpca;Actn2;Fstl5;Slc25a25;Umod;Rptn;Pla2g5;Cblb;Cps1;Padi6;Stab2;Notch4;Myl1;Anxa10;Dhh;Atp2c1;Syt14;Braf;Chordc1;Cdhd23 |
| GO:0008023 | transcription elongation factor complex | 9.80E-04 | 2.47E-02 | Component | 4.72E+00 | Mllt3;Elp4;Eaf1 |
| GO:0008139 | nuclear localization sequence binding | 1.00E-03 | 2.49E-02 | Function | 4.70E+00 | Nup153;Kpnb1;Kpna4 |
| GO:0007159 | leukocyte cell-cell adhesion | 1.02E-03 | 2.57E-02 | Process | 4.65E+00 | Cd24a;Umod;Vcam1 |
| GO:0008023 | regulation of T cell receptor signaling pathway | 4.24E-04 | 2.81E-02 | Process | 7.44E+00 | Malt1;Cblb |
| GO:0061337 | cardiac conduction | 4.24E-04 | 2.81E-02 | Process | 7.44E+00 | Sptbn4;Gja1 |
| GO:0046632 | alpha-beta T cell differentiation | 4.24E-04 | 2.81E-02 | Process | 7.44E+00 | Braf;Bim |
| GO:0007220 | Notch receptor processing | 4.24E-04 | 2.81E-02 | Process | 7.44E+00 | Aph1b;Aph1c |
| GO:0031145 | anaphase-promoting complex-dependent catabolic process response to cAMP | 4.24E-04 | 2.81E-02 | Process | 7.44E+00 | Anapc10;Ube2c |
| GO:0051591 | endocrine pancreas development | 1.06E-03 | 2.86E-02 | Process | 4.47E+00 | Braf;Pkrl;Cited1 |
| GO:0031018 | carbohydrate metabolic process | 1.06E-03 | 2.86E-02 | Process | 4.47E+00 | Rfx6;Onecut2;Myt1 |
| GO:0005975 | low-density lipoprotein receptor activity | 7.88E-03 | 2.92E-02 | Process | 2.00E+00 | St6gal2;Ganc;Pkrl;Ctbs;Gnpda2;Ppp1r2;Npl;Shpk;Glb112;Pdha2 |
| GO:0005041 | photoreceptor activity | 4.36E-04 | 2.98E-02 | Function | 7.21E+00 | Stab1;Stab2 |
| GO:0009881 | photoreceptor activity | 4.36E-04 | 2.98E-02 | Function | 7.21E+00 | Rgr;Opn4 |
GO:0031519 PcG protein complex 1.07E-03 3.08E-02 Component 4.34E+00 Bmi1;Rnf2;Cbx7

GO:0015031 protein transport 2.51E-02 3.09E-02 Process 1.51E+00 Btf3;Pex1;Tmed5;Lin7c;Tom111;Lsg1;Vps13a;Cep290;Bbs9;Kpnb1;Slc15a4;Appbp2;Snx 24;Ap3m2;Snx16;Snx1;Rbsn;Ipo7;Timm9;Lca5;Copg1;Nup37;Vps37a;Kpna4

GO:0004623 phospholipase A2 activity 1.09E-03 3.10E-02 Function 4.33E+00 Pla2g5;Pla2g6;Plb1

GO:0007286 spermatid development 3.73E-03 3.12E-02 Process 2.54E+00 Sept4;Strbp;Dhh;Trip13;Cdy1;Pygo1

GO:0003723 RNA binding 6.28E-02 3.14E-02 Function 1.30E+00 Cct6a;Mettl3;Strbp;Btf3;Pus7;Hspe1;Gspt1;Ybx1;Nol10;Cct4;Rbm22;Crmk11;Canx;Gm50 93;Rpl39;Lsm5;Stip1;Ythdf1;Sf3b6;Heatr1;Kpnb1;Hspd1;Safb2;Kctd12;Nol11;Luc712;Sf 3a3;Trmo;Thoc2;Dhx33;Brix1;Mrpl32;Eif1ax;Esf1;Krr1;Rps12;Gar1;Pym1;Pspc1;Hspa8; Cbx7;Igf2bp3;Zfp106;Hsp90aa1;Ncbp2;Exosc3;Auh;Magohb;Khdrbs2;Fup3;Rbm8a;Khd dc1b

GO:0043231 intracellular membrane-bounded organelle 3.35E-02 3.15E-02 Component 1.42E+00 Pch1;Lamp3;Dennd6a;Ybx1;Ugt2b38;Fmo5;Ppp6r2;Tax1bp3;Fosl1;Pon1;Rdh10;Hspd1; Safb2;Btaf1;Snx16;Snx1;Rbsn;Ugt2a3;Mpo;Eaf1;Sle27a2;Ugt2b34;Gpb1;Mpv171;Acs13; Atp2c1;Braf;Vps37a;Cyp2f2;Trappc2;Pdha2

GO:0051087 chaperone binding 3.75E-02 3.23E-02 Function 2.52E+00 Hspe1;Stip1;Ahsa2;Bag3;Hspd1;Timm9

GO:0006397 mRNA processing 1.39E-02 3.34E-02 Process 1.70E+00 Dcps;Mettl3;Wtap;Ncbp2;Sf3a3;Thoc2;Ybx1;Magohb;Rbm22;Khdrbs2;Hspa8;Sf3b6;Crm k11;Lsm5;Ppwd1

GO:0001763 morphogenesis of a branching structure 4.66E-04 3.38E-02 Process 6.77E+00 Ctnnd2;Notch4

GO:0046641 positive regulation of alpha-beta T cell proliferation 4.66E-04 3.38E-02 Process 6.77E+00 Cd24a;Blm

GO:0033603 positive regulation of dopamine secretion 4.66E-04 3.38E-02 Process 6.77E+00 Htr6;Chrnbb2

GO:0032816 positive regulation of natural killer cell activation 4.66E-04 3.38E-02 Process 6.77E+00 Il12a;Raet1b
GO:2000009 negative regulation of protein localization to cell surface 4.66E-04 3.38E-02 Process 6.77E+00 Actn2;Tax1bp3

GO:0070613 regulation of protein processing 4.66E-04 3.38E-02 Process 6.77E+00 Notch4;Rnf139

GO:0018298 protein-chromophore linkage 4.66E-04 3.38E-02 Process 6.77E+00 Rgr;Opn4

GO:0004553 hydrolase activity, hydrolyzing O-glycosyl compounds 1.13E-03 3.44E-02 Function 4.16E+00 Ganc;Glb1l2;Ctbs

GO:0070979 protein K11-linked ubiquitination 1.14E-03 3.50E-02 Process 4.14E+00 Anapc10;Ube2w;Ube2c

GO:0035102 PRC1 complex 4.69E-04 3.56E-02 Component 6.58E+00 Rnf2;Cbx7

GO:0017069 snRNA binding 4.80E-04 3.58E-02 Function 6.56E+00 Toe1;Ncbp2

GO:0016772 transferase activity, transferring phosphorus-containing groups 4.80E-04 3.58E-02 Function 6.56E+00 Ckb;Fpgt

GO:0008026 ATP-dependent helicase activity 4.80E-04 3.58E-02 Function 6.56E+00 Wrn;Blm

GO:0008061 chitin binding 4.80E-04 3.58E-02 Function 6.56E+00 Chil6;Ctbs

GO:0070410 co-SMAD binding 4.80E-04 3.58E-02 Function 6.56E+00 Cited1;Trim33

GO:0001228 transcriptional activator activity, RNA polymerase II transcription regulatory region 5.93E-03 3.60E-02 Function 2.12E+00 Rfx6;Rbpjl;Ctcf;Ikzf3;Myt1;Myf6;Lmo2;Zfp131
sequence-specific DNA binding

| GO:0030154 | cell differentiation | 3.61E-02 | 3.69E-02 | Process | 1.40E+00 | Mettl3;Strbp;Sema4g;Myt1;Morn2;Tff1;Sfrp1;Creb1;Tle3;Cited1;Adam26a;Zfp281;Ifi81;Trip13;Adcyap1r1;Rfx6;Sema3a;Sept4;Usp42;Myf6;Irf6;Notch4;Cdy1;Sle9c1;Zfp37;Tal1;Cplx2;Prkx;Zfp521;Cit;Braf;Txdnc2 |
| GO:0045429 | positive regulation of nitric oxide biosynthetic process | 1.99E-03 | 3.71E-02 | Process | 3.17E+00 | Raet1b;Klf2;Hsp90aa1;Pkd2 |
| GO:0036126 | sperm flagellum | 1.96E-03 | 3.78E-02 | Component | 3.15E+00 | Sept4;Tekt5;Hsp90aa1;Txdnc2 |
| GO:0050840 | extracellular matrix binding | 1.18E-03 | 3.79E-02 | Function | 4.01E+00 | Olfml2a;Bgn;Zan |
| GO:0007283 | spermatogenesis | 1.67E-02 | 3.86E-02 | Process | 1.61E+00 | Mif;Tle3;Mettl3;Strbp;Sept4;Adam26a;Usp42;Morn2;Zfx;Ift81;Sle9c1;Cit;Trip13;Cdy1;Txdnc2;Zfp37;Adcyap1r1 |
| GO:0000978 | RNA polymerase II proximal promoter sequence-specific DNA binding | 1.92E-02 | 3.90E-02 | Function | 1.56E+00 | Creb1;Rfx6;Nsd1;Fosl1;Rbpjl;Pgr;Tal1;Atf4;Ctfc;Zfp281;Fubp3;Ybx1;Myf6;Bsx;Hesx1;Klf16;Onecut2;Myc;Bmi1 |
| GO:0002237 | response to molecule of bacterial origin | 5.08E-04 | 3.98E-02 | Process | 6.20E+00 | Malt1;Cd24a |
| GO:0045577 | regulation of B cell differentiation | 5.08E-04 | 3.98E-02 | Process | 6.20E+00 | Cd24a;Ikzf3 |
| GO:0046548 | retinal rod cell development | 5.08E-04 | 3.98E-02 | Process | 6.20E+00 | Rp1;Miat |
| GO:0060644 | mammary gland epithelial cell differentiation | 5.08E-04 | 3.98E-02 | Process | 6.20E+00 | Irf6;Ptc1 |
| GO:0035970  | peptidyl-threonine dephosphorylation | 5.08E-04 | 3.98E-02 | Process | 6.20E+00 | Dusp5;Ppm1a |
|-------------|--------------------------------------|----------|----------|---------|----------|-------------|
| GO:004237   | cellular metabolic process central nervous system projection neuron axonogenesis | 5.08E-04 | 3.98E-02 | Process | 6.20E+00 | Wrn;Blm |
| GO:0021952  | GO:0021952  | 5.08E-04 | 3.98E-02 | Process | 6.20E+00 | Sptbn4;Chrb2 |
| GO:0043235  | receptor complex | 5.96E-03 | 4.10E-02 | Component | 2.07E+00 | Pigr;Lepr;Kctd12;Vldlr;Impg2;Plxdc1;Trpc1;Adcyap1r1 |
| GO:0005719  | nuclear euchromatin development | 1.19E-03 | 4.13E-02 | Component | 3.88E+00 | Creb1;Myc;Cecr2 |
| GO:0001824  | blastocyst development | 1.23E-03 | 4.20E-02 | Process | 3.85E+00 | N4bp2l2;Thoc2;G2e3 |
| GO:0017017  | MAP kinase tyrosine/threonine phosphatase activity | 5.23E-04 | 4.21E-02 | Function | 6.01E+00 | Dusp5;Dusp1 |
| GO:0042752  | regulation of circadian rhythm | 2.08E-03 | 4.22E-02 | Process | 3.04E+00 | Creb1;Ube3a;Opn4;Pspc1 |
| GO:0005681  | spliceosomal complex | 6.05E-03 | 4.39E-02 | Component | 2.04E+00 | Rheb;Sf3a3;Rbm22;Hspa8;Sf3b6;Crnk11;Lsm5;Ppwd1 |
| GO:0046982  | protein heterodimerization activity | 2.47E-02 | 4.48E-02 | Function | 1.47E+00 | Mettl3;Gtf2a1;Myc;Sox14;Ralgapa2;Uba3;Il12a;Taf9b;Nfe2l2;Hspd1;Thra;Pola1;Snx1;Nfyb;Tal1;Atf4;Ikzf3;Syt14;Khdrbs2;Braf;Cul5;Lsm5;Chrb2 |
| GO:0003677  | DNA binding | 7.56E-02 | 4.49E-02 | Function | 1.25E+00 | Gtf2a1;Strrbp;Rbpbj;Dlx6;Mcm8;Sox14;Zfp518a;Ybx1;Chrc1;Myt1;Acd;Zfp329;Zfx;Klf16;Onecut2;Sp100;Creb1;Fosl1;Pgr;Ctcf;Adnp2;Rev1;Zfp281;Taf1b;Rfxap;Top3a;Bsx;Zfp131;Nfe2l2;Trim33;Rfx6;Thra;Ikzf5;Safb2;Pola1;Pou6f1;Myf6;Lmo2;Irf6;Hexx1;Zfp37;Prop1;Lemd3;Nfyb;Neil2;Tal1;Atf4;Ikzf3;Creb5;Zfp60;Klf2;Gpbp1;Zfp521;Zfp322a;Polarid1;Bln;Wrn;Zfp654;Zfand5;Myc |
| GO:0016604  | nuclear body | 1.18E-02 | 4.53E-02 | Component | 1.70E+00 | Safb2;Toe1;Pou6f1;Lsg1;Eaf1;Acd;Rnf2;Miat;Cdyl;Med19;Myc;Ppwd1;Bmi1 |
| GO:0045503 | dynein light chain binding | 1.26E-03 | 4.55E-02 | Function | 3.73E+00 | Dnah17;Dync2h1;Dnah2 |
| GO:0015020 | glucuronosyltransferase activity | 1.26E-03 | 4.55E-02 | Function | 3.73E+00 | Ugt2b34;Ugt2a3;Ugt2b38 |
| GO:0006828 | manganese ion transport | 5.51E-04 | 4.62E-02 | Process | 5.73E+00 | Atp2c1;Trpc1 |
| GO:0043268 | positive regulation of potassium ion transport | 5.51E-04 | 4.62E-02 | Process | 5.73E+00 | Mif;Actn2 |
| GO:0043616 | keratinocyte proliferation | 5.51E-04 | 4.62E-02 | Process | 5.73E+00 | Irf6;Ptch1 |
| GO:0042438 | melanin biosynthetic process | 5.51E-04 | 4.62E-02 | Process | 5.73E+00 | Cited1;Trpc1 |
| GO:0016574 | histone ubiquitination | 5.51E-04 | 4.62E-02 | Process | 5.73E+00 | Rnf2;Bmi1 |
| GO:0021795 | cerebral cortex cell migration | 5.51E-04 | 4.62E-02 | Process | 5.73E+00 | Htr6;Cx3cr1 |
| GO:0043508 | negative regulation of JUN kinase activity | 5.51E-04 | 4.62E-02 | Process | 5.73E+00 | Dusp19;Sfrp1 |
| GO:0045580 | regulation of T cell differentiation | 5.51E-04 | 4.62E-02 | Process | 5.73E+00 | Braf;Mettl3 |
| GO:0030514 | negative regulation of BMP signaling pathway | 2.16E-03 | 4.78E-02 | Process | 2.92E+00 | Lemd3;Ppm1a;Sfrp1;Trim33 |
| GO:0007155 | cell adhesion | 2.23E-02 | 4.82E-02 | Process | 1.48E+00 | Siglecg;Tm9sf4;Tnfaip6;Pcdh17;Vcam1;Ninj2;Emb;Stab1;Sdk1;Cx3cr1;Pcdhb12;Parvb;Mybpc2;Hapl4;Stab2;Ctnnd2;Zan;Cd24a;Cd96;Prkx;Cdhh3 |
| GO:1990124 | messenger ribonucleoprotein complex | 5.54E-04 | 4.87E-02 | Component | 5.56E+00 | Ybx1;Hspa8 |
Table S4. Differentially expressed protein in S-EV-treated HUVECs.

| GeneSymbol | GeneName | Description | RefSeq Accession | EnsemblID | Fold (IH SEV vs.N SEV) | Regulation p value | IH SEV1 | IH SEV2 | IH SEV3 | Nor SEV1 | Nor SEV2 | Nor SEV3 |
|------------|----------|-------------|------------------|-----------|------------------------|------------------|---------|---------|---------|----------|----------|----------|
|            |          | heterogeneous nuclear ribonucleoprotein A3 pseudogene 12 | ENST00000437410 | -2.078 | down | 0.006 | 6.935 | 7.045 | 6.979 | 8.286 | 7.649 | 8.190 |
| Gene Name      | Description                                                                 | Species                  | Transcript ID    | Expression Value | Fold Change | Gene ID  | Standard Deviation |
|---------------|-----------------------------------------------------------------------------|--------------------------|------------------|------------------|-------------|----------|-------------------|
| TMEM33        | transmembrane protein 33                                                   | Homo sapiens transmembrane protein 33 | NM_018126        | -2.040           | down        | 0.046    | 5.624            |
|               | Rho guanine nucleotide exchange factor (GEF) 35                             | Homo sapiens Rho guanine nucleotide exchange factor | NM_001003702     | -2.087           | down        | 0.030    | 7.238            |
| ARHGEF35      | UBX domain protein 8                                                        | Homo sapiens UBX domain protein 8 | NM_001282199     | 2.216            | up          | 0.000    | 8.555            |
| UBXN8         | TAO kinase 2                                                                | Homo sapiens TAO kinase 2 | NM_004783        | 2.037            | up          | 0.001    | 6.516            |
| TAOK2         | RAB13, member RAS oncogene family                                           | Homo sapiens RAB13, member RAS oncogene family | NM_002870        | -2.082           | down        | 0.002    | 9.962            |
| RAB13         | heterogeneous nuclear ribonucleoprotein A1 pseudogene 36                    | Homo sapiens DDB1 and CUL4 associated factor 8 | NM_015726        | -2.232           | down        | 0.000    | 6.682            |
| Inc-ZNF91-2   | Inc-ZNF91-2:1                                                               | Homo sapiens DDB1 and CUL4 associated factor 8 | NM_015726        | -2.232           | down        | 0.000    | 6.682            |
| DCAF8         | coiled-coil domain containing 71                                            | Homo sapiens coiled-coil domain containing 71 | NM_022903        | 2.161            | up          | 0.001    | 8.941            |
| Lnc-ZNF91-2   | LNCipedia lincRNA                                                           | Homo sapiens coiled-coil domain containing 71 | NM_022903        | 2.161            | up          | 0.001    | 8.941            |
| Gene          | Description                                                                 | Accession       | Log2 Fold Change | P value | Non-OSA (n=6) | OSA (n=6) | P value |
|--------------|------------------------------------------------------------------------------|-----------------|-----------------|---------|---------------|-----------|---------|
| AKAP12       | A kinase (PRKA) anchor protein 12                                             | ENST00000490177 | -2.277          | 0.000   | 12.374        | 12.448    | 12.517  | 13.742 | 13.460 | 13.698 |
| lnc-NKD2-3   | lnc-NKD2-3:7 cyclin-dependent kinase 11A                                      | ENST00000401096 | -3.736          | 0.003   | 3.599         | 4.249     | 4.027   | 6.007  | 5.594  | 6.158  |
| CDK11A       | Homo sapiens cyclin-dependent kinase 11A                                      | NM_033529       | -2.027          | 0.001   | 9.155         | 9.337     | 9.341   | 10.422 | 10.076 | 10.392 |
| ND6          | NADH dehydrogenase, subunit 6 (complex I)                                    | ENST00000361681 | -3.965          | 0.015   | 5.667         | 5.351     | 5.382   | 7.635  | 6.555  | 8.172  |
| PEG10        | paternally expressed 10                                                       | NM_001040152    | -3.521          | 0.000   | 8.683         | 8.889     | 8.619   | 10.691 | 10.234 | 10.714 |
| DNAJC7       | DnaJ (Hsp40) homolog, subfamily C, member 7                                   | ENST00000316603 | 2.197           | 0.001   | 11.865        | 11.534    | 11.739  | 10.505 | 10.711 | 10.515 |
| HIST1H2BE    | histone cluster 1, H2be nuclear factor, erythroid 2-like 2                   | NM_003523       | -2.443          | 0.005   | 6.026         | 6.544     | 6.457   | 7.607  | 7.362  | 7.924  |
| NFE2L2       | Homo sapiens nuclear factor, erythroid 2-like 2                              | NM_006164       | -2.373          | 0.004   | 2.788         | 2.966     | 2.630   | 3.373  | 3.305  | 4.304  |

Table S5. Blood metabolic indexes of participants with or without OSA.
Table S6. mRNA and pri-mRNA primer sequence.

| Gene   | Forward Primer          | Reverse Primer          |
|--------|-------------------------|-------------------------|
| Nox2   | ACCACCCTCTATGACTGGAAATG | TTGGATACCTTGGGCACTT     |
| p47phox| TGGTGGGTGGTCAGGAAAGG   | AGGAATCGGACGCTGTTGC     |
| Nox4   | GTGTCTGCATGGTGTTGATT   | CAGCCAGGAGGGTGAGTGTC    |
| Xdh    | CACAGAACACCATGAAAACCCA | GAAGCCCACCTTTGTATTTAGCC |
| β-actin| GCATTGTTACCACTGGGACG   | CAGAGGCATACAGGGACAGCA   |
| Pri-miR-144 | GACCCCTAGCAATCCCC      | CGGTTCCTCCAGCCATTCC     |
| Pri-miR-27a | TAGGCAGGGCAAGCAAGAAT   | AGCAGGGTCAGTTGAAGAT     |

Reference

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2. Peng L, Li Y, Li X, Du Y, Li L, Hu C et al. Extracellular vesicles derived from intermittent hypoxia-treated red blood cells impair endothelial function through regulating enos phosphorylation and et-1 expression. Cardiovasc Drugs Ther. 2020.