SUPPLEMENTAL MATERIAL

EXTENDED METHODS

Human Valve Tissue

A whole genome expression microarray analysis was carried out on a random sample of 11 myxomatous and 11 non-myxomatous human mitral valves obtained during surgeries performed at Mayo Clinic in Rochester, MN. All studied valves were from patients older than 18 years of age at the time of surgery, and that had consented for the use of tissue for biomedical research purposes. Study protocol for tissue acquisition required the tissue to be processed immediately upon resection (i.e., within 5 minutes). Myxomatous mitral valve tissue was from patients with mitral regurgitation that underwent valve repair. A diagnosis of MMVD was made by the surgeon's visual assessment during cardiopulmonary bypass, and confirmed by a staff cardiovascular pathologist on the basis of macroscopic and microscopic (i.e., by Verhoeff-van Gieson [VVG]) staining. The portion of the mitral valve evaluated by the pathologist was dependent upon whether the patient had anterior, posterior or bileaflet mitral valve prolapse. Those with mitral stenosis, rheumatic heart disease, active endocarditis or mitral valve disease of known genetic origin (i.e. Marfan's syndrome, Loey's-Dietz) were not eligible for inclusion in the current study. In contrast, non-myxomatous mitral valves were obtained from explanted hearts in patients undergoing cardiac transplant operations. Explanted hearts were free of mitral valve disease, which was confirmed by the surgeon's evaluation of gross morphology. In spite of their non-diseased macroscopic appearance, mitral valves from transplant hearts were likely exposed to undue stress and thus are not truly "normal". The valves were, however, non-myxomatous and have historically been deemed as the best available controls for such exploratory and descriptive studies. In the interest of brevity and clarity, in manuscript figures, we refer to control, non-myxomatous valves as "normal" valves. Patient-specific data including demographics, surgical indication and baseline medications were abstracted from medical records (Tables S3-S5). Approximately two-thirds (7/11) of patients with myxomatous mitral valves were male versus 82% (9/11) of those with non-myxomatous valves (p=0.18). Patients with myxomatous valves had a mean (SD) age of 67 (10) years as compared to 49 (15) years in the non-myxomatous group ($p<0.05$). All study protocols were approved by the Mayo Clinic Institutional Review Board.

Animal Model

Protocols pertaining to all animal studies were approved by the Mayo Clinic Institutional Animal Care and Use Committee (IACUC) and conformed to guidelines set forth by the National Institutes of Health and the Guide for the Care and Use of Laboratory Animals. C57BL/6 mice were aged to 3 months and maintained on standard mouse chow (Picolab5053; LabDiet) and housed in a pathogen-free facility. Mitral valves (both anterior and posterior leaflets) from 16 mice were employed for cell culture experiments (see Cell Culture below), whereas 46 mice were used for minipump experiments (see Angiotensin II minipumps below). Animals were euthanized using intraperitoneal injection of pentobarbital sodium (0.5 mL).

Angiotensin II Minipumps

Young C57BL/6 mice were randomized to receive 14 days of 1) pressor doses of AngII (1000 ng/kg/min) for 2 weeks (n=21), or 2) normal saline (n=23), via osmotic minipumps (Alzet ®). Using standard techniques, intra-peritoneal ketamine/xylazine injection at the minimum weight-adjusted dose was used as anesthesia. Under sterile conditions, one-centimeter transverse incisions were made in the upper back, and a cavity dissected for subcutaneous minipump implantation. Vicryl 6-0 sutures (Ethicon Inc) were used for incision closure. Daily non-invasive blood pressure measurements were carried out using tail-cuff methods, and mice were euthanized on day 15 post-minipump implantation. Mitral valves from 28 mice (AngII n=13, saline n=15) were harvested for quantitative real-time PCR (qRT-PCR), and valves from 16 mice (AngII n=8, saline n=8) were used for immunohistochemical analysis. All mice implanted with minipumps thrived normally. During the series of experiments, 1 mouse (AngII) was excluded because the minipump became dislodged prior to completion of the 14-days, and another mouse (AngII) was excluded due to premature death at day 10 post-implantation. The latter mouse died due to aortic aneurysm rupture.

Echocardiography

On day 14 after minipump implantation, C57BL/6 mice receiving infusions of AngII or saline underwent echocardiographic evaluation using standard methods described elsewhere [1–4]. Apical 4-chamber, parasternal long-axis and modified 2-chamber views of the mitral valve were obtained. Specifically, the mitral valve was assessed for evidence of mitral regurgitation by measuring transvalvular blood velocity through the mitral valve orifice during diastole. Short- and long-axis views of the left ventricle were obtained to evaluate ventricular function, dimension and mass[5].

Cell Culture

Mitral valves interstitial cells from 4 non-myxomatous human mitral valves (separate from valves used for the microarray) and 16 C57BL/6 mice (pooled in groups of four) were harvested. Both anterior and posterior murine mitral valve leaflets were used. Mitral valves were pooled in keeping with standard culture techniques to ensure the growth of a large and sufficient number of cells for quantitative assays. Valvular cells were grown in complete media using standard outgrowth techniques (40% Dulbecco's modified Eagles medium, 40% Ham's F-10, 20% fetal bovine serum, 100U/mL penicillin and 100 ug/mL streptomycin) between passages 2 and 8, and harvested at 90–100% confluence. Isolated cells stained positive for vimentin and negative for CD68 and CD31, consistent with cells of fibroblast origin (i.e., MVICs). Cells were treated separately for 20 minutes and 24 hours with human recombinant transforming growth factor-β2 (TGF-β2) (R&D Systems; 10 ng/mL), human recombinant bone morphogenetic protein 4 (BMP4) (Gibco ®, Life Technologies;100 ng/mL) or normal saline as control. Twenty-four hour treatments represent a standard duration at which transcriptional changes can be observed, whereas 20 minute treatments were used to measure early phosphorylation of SMAD proteins, the magnitude of which may not be accurately captured at 24 hours.

RNA Extraction and cDNA Synthesis

All mitral valve tissue was stored at -80°C prior to RNA extraction. Human mitral valves were pulverized. Human and murine mitral tissue was transferred to RNA lysis buffer (Invitrogen) and

1% 2-mercaptoethanol. Total RNA (30 uL eluted) was extracted from lysates using spin columns (Invitrogen). RNA concentration and quality (260:280 ratio) were evaluated using a NanoDrop2000 spectrophotometer (Thermo Scientific). The 260:280 ratio of all RNA samples approximated 2.0 indicative of minimal-to-no contamination. Synthesis of complementary DNA (cDNA) was carried out using the Superscript VILO cDNA Synthesis Kit (Invitrogen) according to manufacturer instructions and within 24 hours of RNA isolation. All samples were stored at -80°C. A maximum of 2 reverse transcriptase reactions were carried out on each sample of RNA resulting in a maximum of 2 batches of cDNA.

Whole Genome Expression Microarray

Gene expression levels were measured using Affymetrix Human Genome U133 Plus 2.0 expression arrays (Affymetrix, Santa Clara, California). Differential gene expression between myxomatous and non-myxomatous valves was defined as a minimum 1.5 fold-change in gene expression and a p-value <0.05. Please see the statistics section below for further details of data processing and analysis using for the whole genome expression microarrays.

Quantitative Real-Time PCR

In human mitral valve tissue, quantitative real-time PCR (RT-PCR) was used to validate a subset of differentially regulated genes identified by the microarray analysis. We used the residual volume of RNA following high-throughput screening to undertake confirmatory RT-PCR experiments. Due to an insufficient volume of RNA in 1 of the 11 samples of myxomatous tissue, confirmatory RT-PCR was carried out in 10 myxomatous valves (and 11 non-myxomatous valves). Gene expression levels of pro-fibrotic (TGF-β2, BMP and activin membrane-bound inhibitor homolog (Xenopus laevis) [BAMBI], salt-inducible kinase [SIK1]), pro-calcific (BMP4, Runt-related transcription factor 2 [Runx2], Wnt9A, Frizzled [FZD] 8, R-spondin 2 (RSPO2), Wnt-inducible signaling pathway protein 1 [WISP1]), cell growth and proliferation-related (Cyclin-dependent kinase inhibitor 1A [CDKN1A], and Cyclin-dependent kinase 4 inhibitor B [CDKN2B]) and immune-related genes (CD14, CD83, Chemokine (C-X3-C motif) receptor 1 [CX3CR1], and Fc fragment of IgG, high affinity Ib, receptor [FCGR1B]) were measured using TaqMan Gene Expression Assay primers (Life Technologies) and a calibrated Applied Biosystems StepOne Plus unit. Gene expression levels were normalized by hypoxanthine phosphoribosyltransferase 1 (HPRT1), a commonly used housekeeper gene, and expressed using the ∆∆Ct method. The correlation between microarray and qRT-PCR-determined gene expression within individual patient samples, and corresponding R^2 values, are outlined in Table S2.

Differential gene expression levels of TGF-β (TGF-β2, BAMBI, Collagen type I alpha 1 [COL1A1], MMP2), BMP- (BMP4, transducer of erbB2 [TOB2], MSX2, Runx2), Wnt- (Wnt9A, axis-inhibition protein 2 [AXIN2], FZD8, WISP1) and immune-network genes (IL7, CD14, CD83, TLR7) were measured in mitral valve tissue from AngII versus saline-infused C57BL/6 mice. As a negative control and to confirm the absence of significant myocardial contamination in mitral valve tissue isolated from AngII and saline-treated mice, gene expression levels of myocardial specific markers (myosin, light polypeptide 2, regulatory, cardiac, slow [Myl2], and myosin, heavy polypeptide 6, cardiac muscle alpha [Myh6]) were measured in left ventricular and mitral valve tissue. Furthermore, mRNA levels of SIK1, BAMBI, SMURF1, SMURF2, COL1A1, BMP4, Runx2, Wnt9A, WISP1, CD14 and CD83 were measured from MVICs cells receiving *in vitro* treatment with saline, BMP4 or TGF-β2. Guided by results of our microarray analyses, genes for evaluation in cultured MVICs were selected in a manner that would collectively allow the full spectrum of signaling pathways to be probed – from ligand, to intracellular modulators/inhibitors and finally to target genes. In turn this approach would enable commentary on the extent by which BMP4 and/or TGF-β2 treatment is capable of activating various signaling cascades. Separate human-specific and mouse-specific primers were used in the above experiments (Table S1).

Western Blotting

To probe for evidence of canonical TGF-β, BMP and Wnt signaling in cultured MVICs, western blotting was performed for SMAD2, Phospho-SMAD2 (pSMAD2), SMAD1, Phospho-SMAD1/SMAD5/SMAD8 (pSMAD1/5/8), and β-catenin, respectively, following 20 minutes and

24 hour treatments with recombinant TGF-β2, BMP4 or control saline. To evaluate immune cell activation/recruitment, protein levels of CD14 were measured. Protein was obtained from lysed mitral valve cells. Gel electrophoresis was carried out using Bis-Tris gels (Invitrogen), and subsequently transferred to nitrocellulose membranes. Membrane incubation with anti-SMAD2 (Cell Signaling),anti-pSMAD2 (Cell Signaling), anti-SMAD1 (Cell Signaling), anti-pSMAD1/5/8 (Cell Signaling), anti-β-catenin (Cell Signaling) and anti-CD14 (Abcam Inc) antibodies (all monoclonal) was performed at dilutions of 1:1000 and for 18 h at 4°C. Thereafter, membranes were incubated with goat anti-rabbit/mouse HRP-conjugated secondary antibody for 1.5 h at room temperature (1:7500, Fisher Scientific). Following the addition of chemiluminscent substrate (Thermo Scientific), bands were detected by densitometric analysis performed using digital imaging techniques (Fluorochem M) and quantified using Cell Biosystems software. The density of pSMAD2 and pSMAD1/5/8 protein bands was normalized to unphosphorylated SMAD2 and SMAD1, respectively. Density of all other protein bands was normalized to the corresponding HPRT band from the same sample. Quantitation was carried out using AlphaView software (ProteinSimple™).

Immunohistochemistry

To confirm our microarray finding of differential levels of 1) immune cell infiltration and 2) activation of BMP signaling in human myxomatous mitral valves, immunohistochemical staining was performed with anti-CD14 and anti-pSMAD1/5/8 antibodies, respectively. To probe for evidence of increased cellular proliferation in MMVD, immunostaining with cellular proliferation markers anti-KI-67 and anti-proliferation cell nuclear antigen (PCNA) were performed. To evaluate the impact of AngII versus saline infusion on TGF-β, BMP and Wnt signaling, as well as cellular proliferation, immunohistochemical staining for pSMAD2, pSMAD1/5/8, β-catenin, and KI-67 was carried out in mitral valve sections of treated mice.

Both human and murine tissue samples for immunohistochemical study were frozen in OCT compound and serial 10μm thick transverse sections through the mitral valves were obtained using a cryostat and mounted on glass slides[2]. MV sections were fixed with 2%

paraformaldehyde (1:1 of 4% paraformaldehyde:Phosphate-buffered saline) for 10 minutes, All samples were blocked in donkey serum (Invitrogen*)* at room temperature for 1 hour. Thereafter samples were incubated overnight at 4°C; separately in either rabbit anti-CD14 antibodies (Abcam Inc) at a 1:500 dilution[6], a 1:50 dilution of rabbit anti-pSMAD2 (Cell Signaling), 1:100 dilution of rabbit anti-pSMAD1/5/8 antibody (Cell Signaling)[7], a 1:1000 dilution of rabbit anti-KI-67 antibody (Cell Signaling)[8], or a 1:1000 dilution of mouse anti-PCNA antibody (Abcam Inc)[9]. All antibodies were diluted in Tris-buffer (TBS). Samples were then incubated at room temperature for 1 hour in donkey anti-rabbit Alexa Fluor 647 secondary antibody (Life Technologies). All primary antibodies were monoclonal. Thereafter, slides were either 1) incubated for 5 minutes in SYTO-16 Alexa Fluor 488 nuclear counterstain (Life Technologies) followed by application of an anti-fade reagent (ProLong® Gold, Life Technologies), or alternatively 2) ProLong ® Gold antifade reagent with DAPI nuclear counterstain was applied directly to the slides. Negative controls (3 non-myxomatous, 7 myxomatous) for all antibodies were achieved by substituting TBS in place of primary antibody. An LSM780 confocal laser microscope (Carl-Zeiss, Jena, Germany) was used to obtain images at 20x magnification (Excitation 488nm, Emission 647 nm). Image processing was performed using Image J software (version 1.42q; National Institutes of Health, Bethesda). Images were thresholded so that only the mean pixel intensity for punctate, positive staining was measured in mitral valves (i.e. myxomatous vs non-myxomatous human mitral valves, AngII vs Saline-infused murine mitral valves). The difference between these values in groups being compared was used as a measure of relative antibody staining (i.e., relative KI-67 staining).

Immunocytochemistry

To examine the consequence of *in vitro* treatment with saline, BMP4 and TGF-β2 on canonical TGF-β, BMP and Wnt signaling and immune activation in MVICs, immunocytochemical staining was performed on cultured murine cells. Staining with anti-pSMAD2 (Cell Signaling), anti-pSMAD1/5/8 (Cell Signaling), anti-β-catenin (Cell Signaling) and anti-CD14 (Abcam Inc) antibodies was carried out using standard methods[3].

Dissociated cells from cultured murine MVICs were plated on glass cover-slips and fixed with 2% paraformaldehyde for 30 minutes. Thereafter they were blocked with donkey serum at room temperature for 1 hour. Cells were then incubated overnight with rabbit anti-pSMAD2 (1:50) , rabbit anti-pSMAD1/5/8 (1:100), rabbit anti-β-catenin (Cell Signaling; 1:100) and rabbit anti-CD14 (Abcam Inc; 1:500). Primary antibodies were diluted in TBS. Cells were then incubated at room temperature for 1 hour in donkey anti-rabbit Alexa Fluor 647 secondary antibody (Life Technologies). Finally, after the application of anti-fade reagent Prolong ® Gold with DAPI nuclear counterstain, the cover slip harboring the cells was mounted on a glass slide for imaging.

All images were obtained using an LSM780 confocal laser microscope (Carl-Zeiss, Jena, Germany) at 20x or 100x magnification (Excitation 488nm, Emission 647 nm). Images were processed using Image J software (version 1.42q; National Institutes of Health, Bethesda, MD).

Modeling Signaling Interactions

In order to examine potential interactions between signaling pathways that were differentially regulated in human MMVD (i.e. TGF-β pathway, BMP pathway, Wnt/β-catenin pathway, and Immune pathway), we used the PathwayLinker web resource (www.pathwaylinker.org)[10]. PathwayLinker is a service that identifies potential interactions between proteins using data from HPRD, BioGRID, and STRING databases, and places “interactors” into signaling pathways using KEGG, Reactome and SignaLink pathway resources. The network was induced using a list of genes identified by our microarray analyses as differentially expressed in myxomatous versus non-myxomatous valves, and that are depicted in the heat maps of figures 1 – 4 (i.e. TGF-β, BMP, Wnt/β-catenin and immune signaling genes): TGFβ-2, FGF9, HGF, BAMBI, SIK1, MYC, TGIF1, JUN, FOS, DAB2, CREB5, COL1A1, MMP2, MMP16, FN1, FAP, FSCN1, BMP4, TOB2, HEY1, WISP1, RUkNX2, WNT9A, NDP, FZD8, RSPO2, SFRP2, TLE1, HBP1, TCF4, CD14, CD28, CD30, CD39, CD63, CD69, CD71, CD73, CD83, CD93, TLR3, TLR7, FCGR1A, CX3CR1, CX3CL1, IL6 and IL7. Specifically, we entered the list of genes that was differentially expressed but did not account for magnitude or directionality of the changes.

Statistical Analyses

Whole Genome Expression Microarray

Gene expression levels were measured using Affymetrix Human Genome U133 Plus 2.0 expression arrays (Affymetrix, Santa Clara, California). Differential gene expression between myxomatous and non-myxomatous valves was identified by linear modeling using t-test. Please see the statistics section below for further details of data processing and analysis using for the whole genome expression microarrays. Significance thresholds were established a priori as 1) a minimum 1.5 fold-change in gene expression, and 2) a p-value < 0.05. Ingenuity (Ingenuity Systems Inc.) Pathway Analysis systems were used to identify differentially regulated canonical signaling pathways.

Pre-processing and normalization of microarray data.

Pre-processing and normalization of microarray data was done using an in-house built pipeline MAPP. MAPP pre-processes raw intensity files from microarray experiments using Robust Multi-array Analysis (RMA) background subtraction and Loess normalization. The expression values of each probe set were summarized from multiple probe pairs using median polish method. The absent, marginal, and present calls for each probe set were calculated by dChip using the MAS 5.0 algorithm (Affymetrix, Santa Clara, CA).

Differential gene expression analysis.

Transcripts with “absent” calls in all compared samples were excluded from further analysis. We also considered transcripts whose expression in all samples fell below the 50th percentile of all expression values to be not expressed, and were thus excluded. Significantly changed genes obtained from t-testing were prioritized by cut-off values of $p < 0.05$ and a fold-change >1.5 (to interpret statistical and biological significance, respectively).

Secondary analysis to adjust for multiple comparisons was carried out by applying the statistical approach of false discovery rate (FDR). As a result, adjusted p-value, called the q-value, was obtained for individual probes of the whole genome expression microarray. The commonly used significance thresholds of $q < 0.05$ and $q < 0.1$ were applied to control the number of false discoveries.

Pathway analysis.

Pathway analysis was conducted for these changed genes to identify significantly enriched biological processes. Metacore (Thomson Reuters) and Ingenuity (Ingenuity Systems, Inc.) analysis packages were used to identify canonical pathways and functional gene groups.

Functional Validation of Targeted Gene Expression

For qRT-PCR experiments carried out on myxomatous and non-myxomatous human mitral valves, relative change in gene expression was analyzed using the students *t*-test. Quantified results of immunohistochemical staining were also compared between groups using the student's *t*-test.

Comparison of Microarray and qRT-PCR Results

Linear regression analyses were utilized to compare fold-changes in gene expression within individual patient samples, as measured by microarray versus qRT-PCR analyses. This relationship was further summarized by a coefficient of determination (R^2) for each gene analyzed (table S2).

Analysis of In Vivo Angiotensin-II Experiments

Relative gene expression (qRT-PCR) in mitral valves of saline versus AngII treated C57B/6J was compared using the students *t*-test. Quantitation of Immunohistochemical staining results were also compared between groups by the students *t*-test.

Cell Culture Analysis

For cell culture experiments evaluating the relative change in gene (qRT-PCR) and protein (western blot) expression following TGF-β2 or BMP4 treatment versus control saline, Dunnett's test for multiple comparisons was used to compare means. The cut-off used for statistical significance was $p<0.05$.

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SUPPLEMENTAL FIGURES

Figure S1.

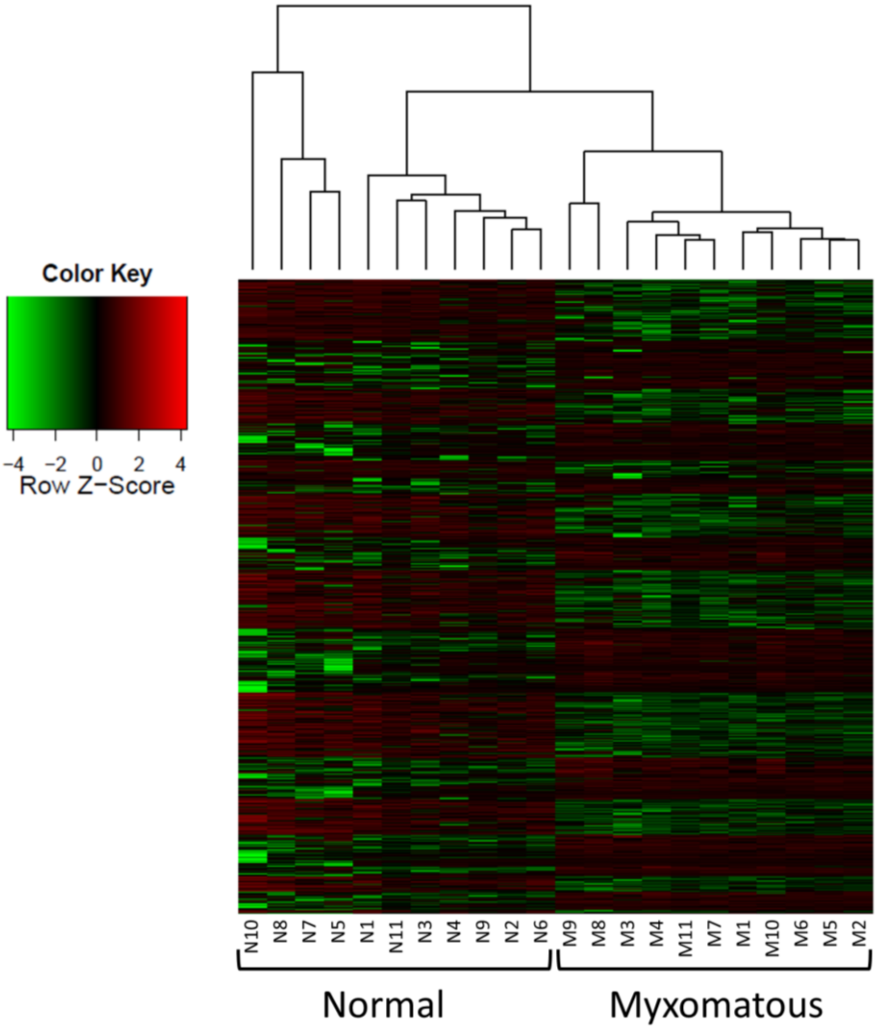

Figure S1. Heat map and hierarchical cluster analysis of differentially expressed genes in human mitral valves. Non-myxomatous and myxomatous human mitral valve samples cluster together within their respective groups. M = myxomatous; N = normal/non-myxomatous samples. For clarity, non-myxomatous control valves are referred to as “normal”.

Figure S2.

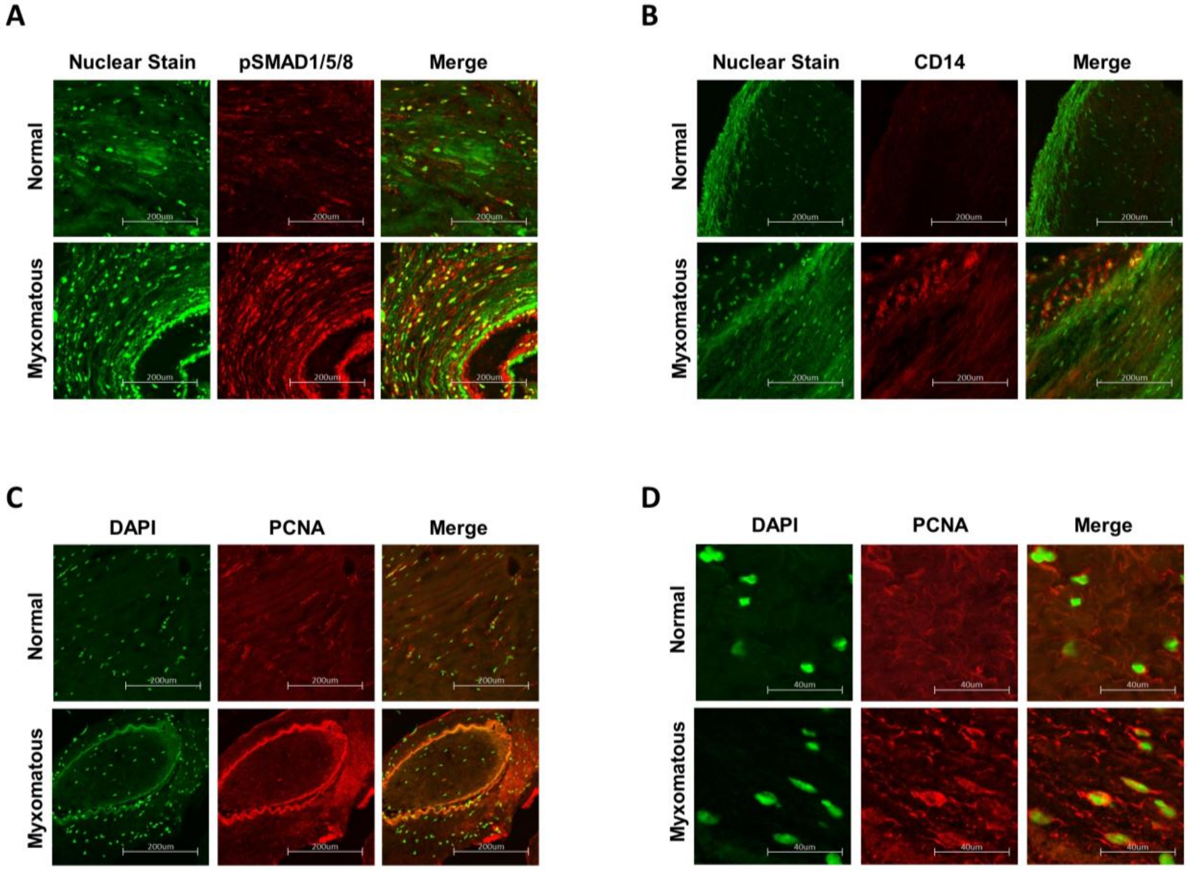

Figure S2. Immunohistochemical analysis of human mitral valve tissue.
Immunofluorescence of A) pSMAD1/5/8 (20x magnification), B) CD14 (20x magnification), and C-D) PCNA (20x and 100x magnification respectively) was increased in myxomatous mitral valve tissue compared to non-myxomatous tissue (representative images from 11 non-myxomatous and 11 myxomatous mitral valves). For clarity, non-myxomatous control valves are referred to as “normal”. CD = Cluster of differentiation; PCNA = Proliferating cell nuclear antigen; SMAD = SMA mothers against decapentaplegic.

Figure S3.

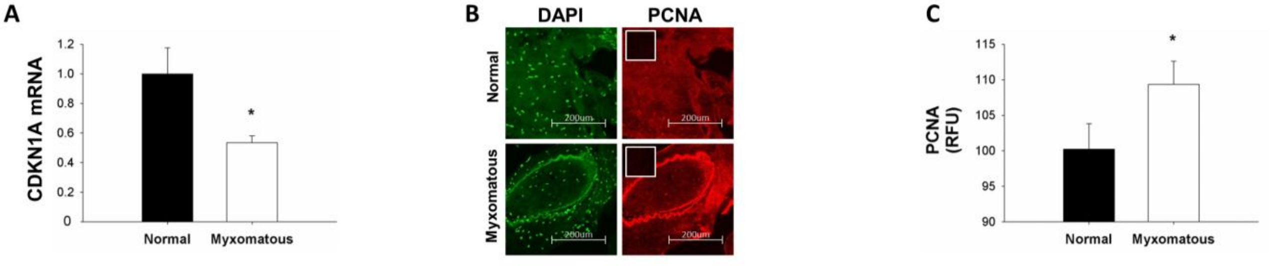

Figure S3. Evidence for increased cellular proliferation in MMVD. A) Gene expression (qRT-PCR) of CDKN1A was reduced in myxomatous versus non-myxomatous human mitral valves. qRT-PCR experiments were performed on the same samples of human mitral valve tissue used for microarray analyses. B) Immunofluorescence of PCNA (20x magnification; inset negative control) was increased in human MMVD tissue (20x magnification; negative controls inset) (n = 11 non-myxomatous valves, n = 10 myxomatous valves). C) Quantitation of PCNA immunofluorescence (* = $p<0.05$). For clarity, non-myxomatous control valves are referred to as “normal”. CDKN1A = Cyclin-dependent kinase 1A; PCNA = Proliferation cell nuclear antigen; RFU = Relative fluorescence units.

Figure S4.

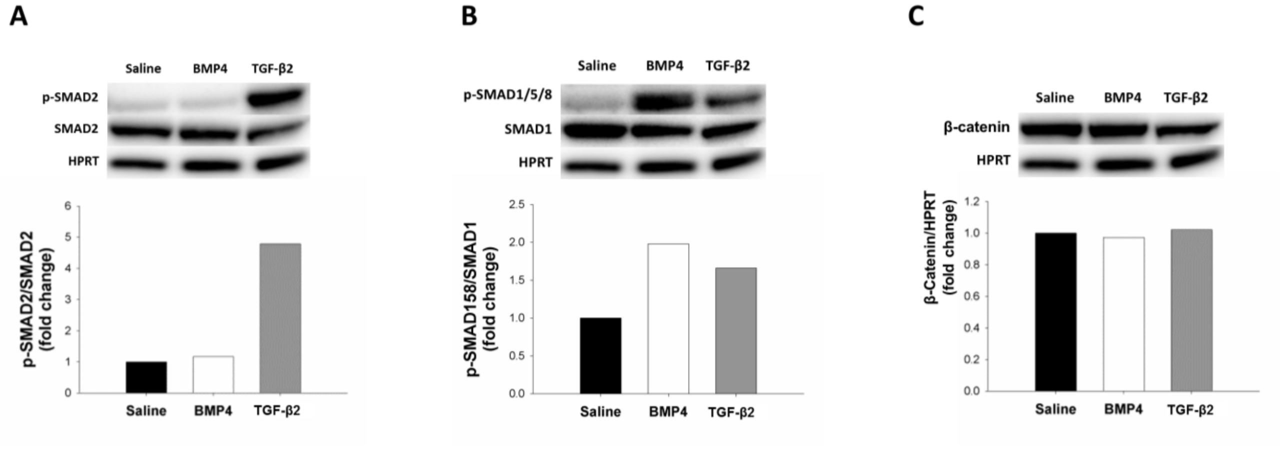

Figure S4. Effects of *in vitro* treatment with BMP4 and TGF-β2 after 20 minutes on protein levels in human mitral valve interstitial cells. A) pSMAD2 protein levels by western blot analysis were increased by TGF-β2 but unaltered by BMP4. B) pSMAD1/5/8 protein expression appeared increased after 20 minutes of BMP4 and TGF-β2 treatment. C) β-catenin levels were unchanged by either treatment condition. BMP = Bone morphogenetic protein; SMAD (SMA mothers against decapentaplegic); TGF-β = Transforming growth factor β.

Figure S5.

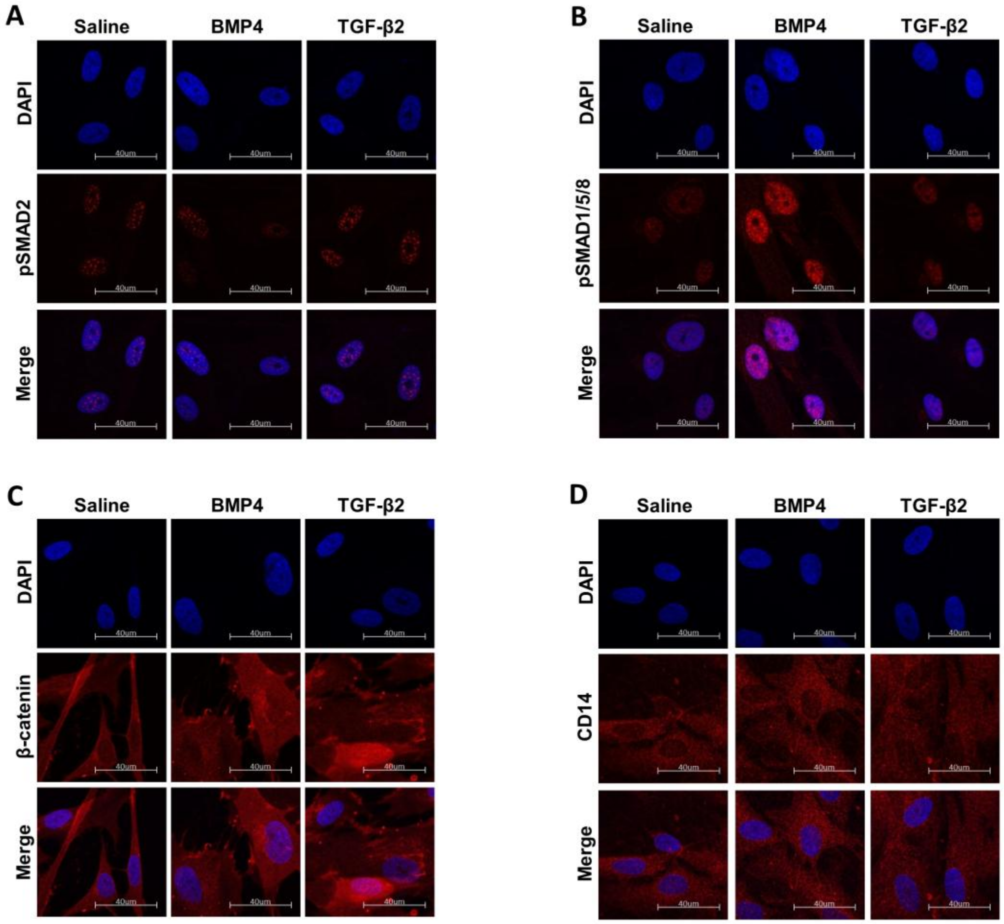

Figure S5. Immunocytochemical analysis of human mitral valve interstitial cells after 24 hours of treatment. A) Immunoctyochemistry could not demonstrate a change in pSMAD2 fluorescence in BMP4 or TGF-β2 treated human MVICs (100x magnification). B) Staining for pSMAD1/5/8 was increased in BMP4 treated cells but was unchanged by TGF-β2 (100x magnification). C) Immunocytochemistry demonstrated increased nuclear β-catenin in human MVICs with TGF-β2 but not BMP4 treatment (100x magnification). D) CD14 was unchanged by BMP4 or TGF-β2 treatment (100x magnification). BMP4 = Bone morphogenetic protein 4; CD = cluster of differentiation; SMAD = SMA mothers against decapentaplegic; TGF-β = Transforming growth factor-beta.

Figure S6.

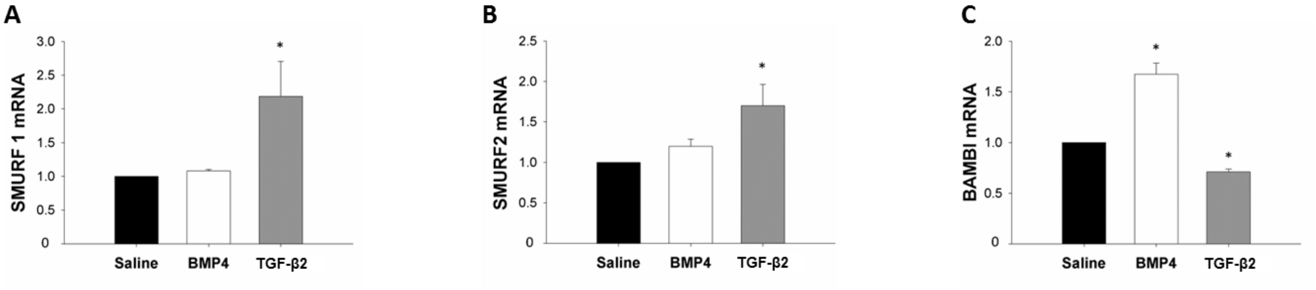

Figure S6. Effects of *in vitro* treatment with BMP4 and TGF-β2 for 24 hours on inhibitors of TGF-β signalling in human mitral valve interstitial cells. Gene expression (RT-PCR) of intracellular inhibitors of canonical TGF-β signalling SMURF1 (A) and SMURF2 (B) was increased in human mitral valve interstitial cells following exogenous TGF-β2, but was unchanged by BMP4 treatment. mRNA levels of BAMBI (C) were increased by BMP4 but decreased by TGF-β2. (* = $p<0.05$). BAMBI = BMP and activin membrane-bound inhibitor homolog (Xenopus laevis); BMP = Bone morphogenetic protein; SMURF = SMAD specific E3 ubiquitin protein ligase; TGF-β = Transforming growth factor-β.

Figure S7.

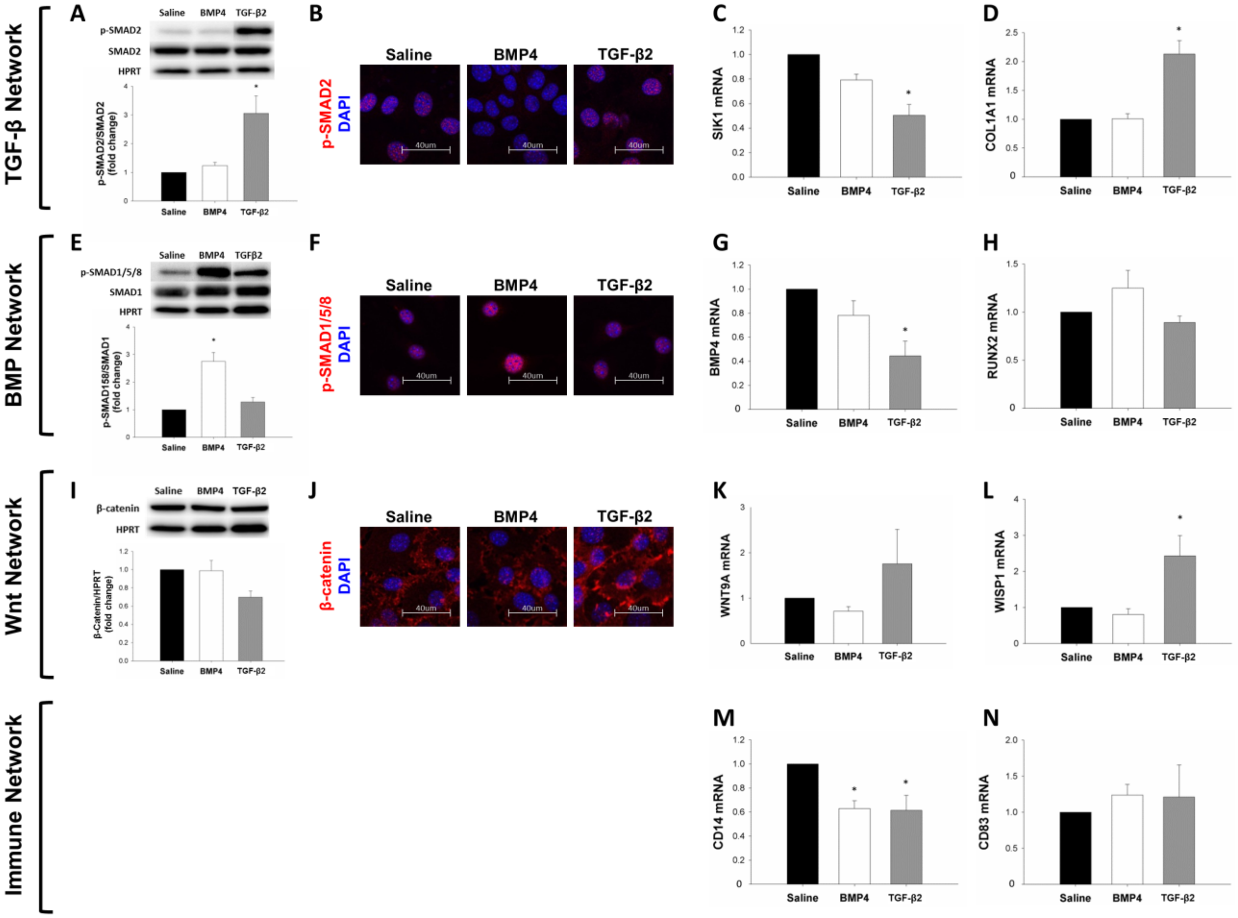

Figure S7. Effects of *in vitro* treatment with BMP4 and TGF-β2 after 24 hours on TGF-β (A-D), BMP (E-H), Wnt/β-catenin (I-L) and immune-signaling (M-N) in murine mitral valve interstitial cells. pSMAD2 protein levels by western blot (A) were increased by TGF-β2 treatment but unchanged by BMP4 (24hr treatment). Immunocytochemistry (B) did not demonstrate a change in pSMAD2 fluorescence (100x magnification) with either treatment condition. SIK1 (C) mRNA expression was reduced and COL1A1 (D) levels increased by TGF-β2 treatment, but both were unchanged following BMP4 treatment. pSMAD1/5/8 protein levels by western blot (E) and immunocytochemistry (F) (100x magnification) were increased by BMP4 treatment, but unaltered by TGF-β2 (24hr treatment). While BMP4 expression (E) was unaltered by exogenous BMP4 treatment, it was reduced by TGF-β2. Runx2 expression (F) was unchanged by either treatment condition. On western blot analysis, total β-catenin (I) was unaltered following BMP4 or TGF-β2 treatment (24hr treatment). Immunocytochemistry (J) (100x magnification) showed increased nuclear β-catenin with TGF-β2 treatment. Gene expression of Wnt9A (K) was not significantly changed, whereas WISP1 (L) mRNA levels increased with TGF-β2 treatment. Gene expression of CD14 by RT-PCR (M) was reduced by BMP4 and TGF-β2, but CD83 (N) was unchanged by either treatment condition (* = $p<0.05$). BMP = Bone morphogenetic protein; CD = Cluster of differentiation; Col1A1 = collagen, type I, alpha I; Runx2 = Runt-related transcription factor 2; SIK1 = Salt-inducible kinase 1; SMAD (SMA mothers against decapentaplegic); TGF-β = Transforming growth factor β; WISP1 = Wnt-inducible signaling pathway protein 1; Wnt9A = Wingless-type MMTV integration site family.

Figure S8.

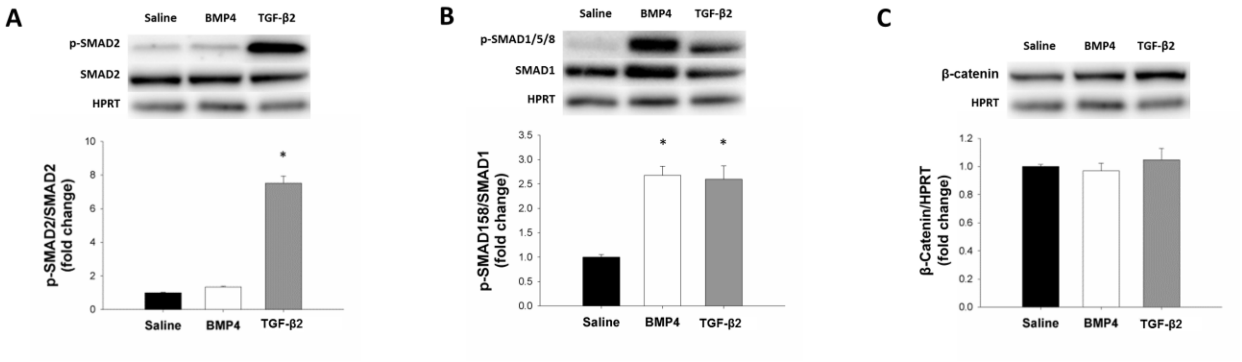

Figure S8. Effects of *in vitro* treatment with BMP4 and TGF-β2 after 20 minutes on protein expression in murine mitral valve interstitial cells. A) Exogenous TGF-β2 treatment increased pSMAD 2 levels by western blot analysis, whereas BMP4 was not associated with a change. B) Both BMP4 and TGF-β2 induced increased pSMAD1/5/8 levels after 20 minutes. C) β-catenin protein levels were unaltered by either treatment. (* = $p<0.05$) BMP = Bone morphogenetic protein; SMAD (SMA mothers against decapentaplegic); TGF-β = Transforming growth factor β.

Figure S9.

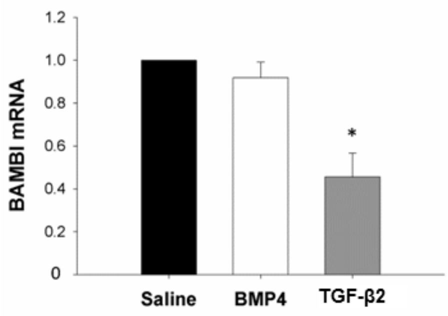

Figure S9. Effects of *in vitro* treatment with BMP4 and TGF-β2 after 24 hours on BAMBI expression in mouse mitral valve interstitial cells. Gene expression (RT-PCR) of BAMBI was unchanged in mouse mitral valve interstitial cells following exogenous BMP4, but decreased by TGF-β2 treatment (*= $p<0.05$). BAMBI = BMP and activin membrane-bound inhibitor homolog (Xenopus laevis); BMP = Bone morphogenetic protein; TGF-β = Transforming growth factor-β.

Figure S10.

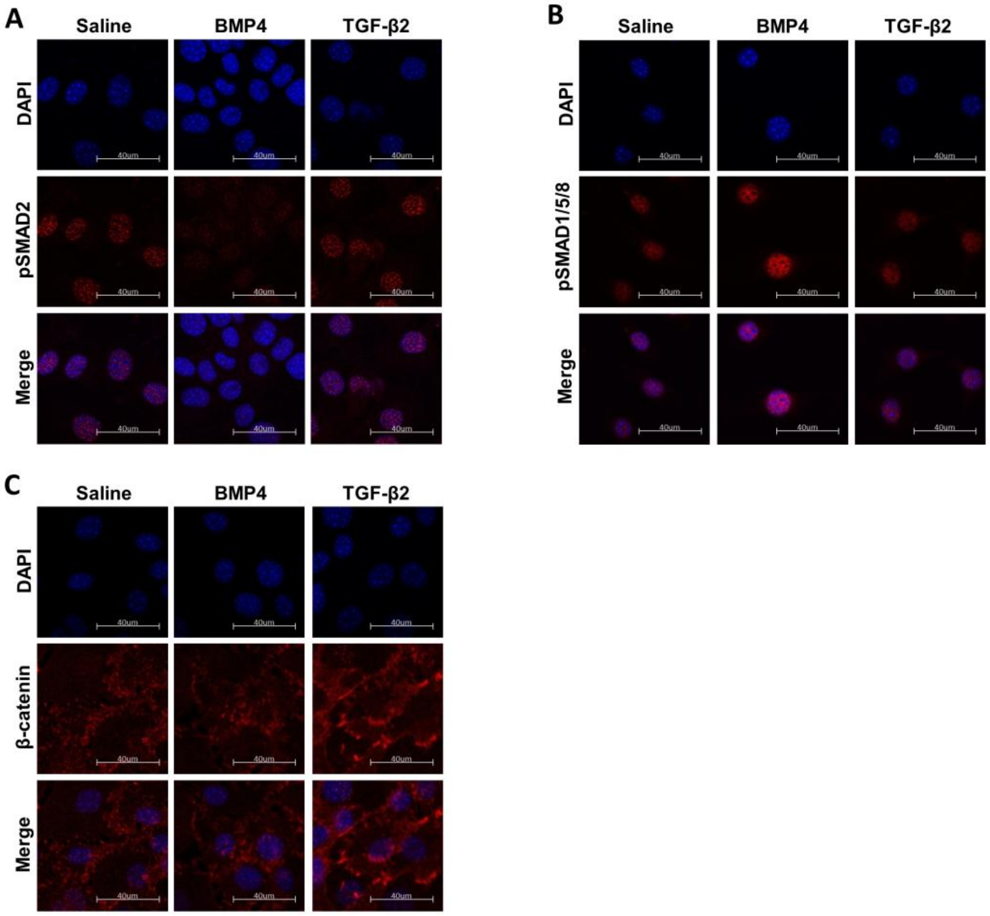

Figure S10. Immunocytochemical analysis of mouse mitral valve interstitial cells after 24 hours of treatment. A) Immunocytochemistry did not show a change in pSMAD2 fluorescence in BMP4 or TGF-β2 treated mouse MVICs (100x magnification). B) Staining for pSMAD1/5/8 was increased in BMP4 treated cells but was not changed by TGF-β2 (100x magnification). C) Immunocytochemistry demonstrated increased nuclear β-catenin in mouse MVICs with TGF-β2 but not BMP4 treatment (100x magnification). BMP4 = Bone morphogenetic protein 4; SMAD = SMA mothers against decapentaplegic; TGF-β = Transforming growth factor-beta.

Figure S11.

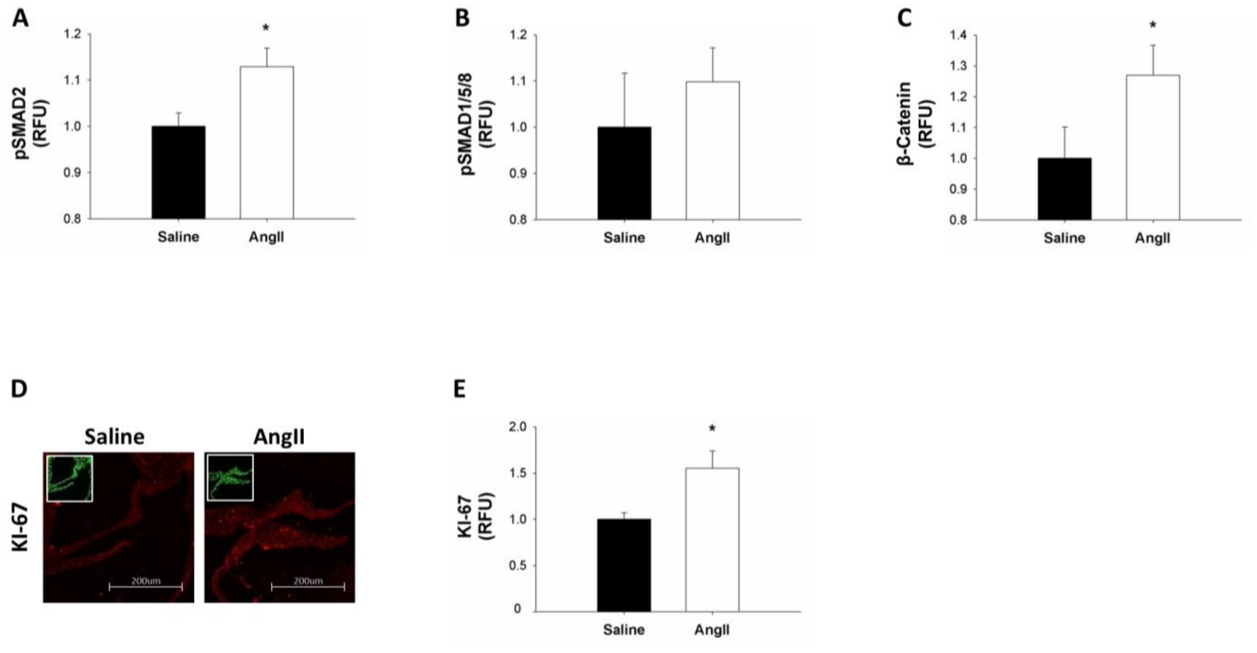

Figure S11. Effects of AngII infusion on canonical TGF-β-, BMP- and Wnt/β-catenin signaling and cellular proliferation in murine mitral valves. Quantitation of pSMAD2 (A), pSMAD1/5/8 (B) and β-catenin (C) immunofluorescence in mitral valves of AngII and saline-infused mice. Immunofluorescence (20x magnification; inset DAPI nuclear stain) of the proliferation marker KI-67 (D-E) was increased in AngII-treated mice. AngII = Angiotensin II; RFU = Relative fluorescence units; SMAD (SMA mothers against decapentaplegic).

Figure S12.

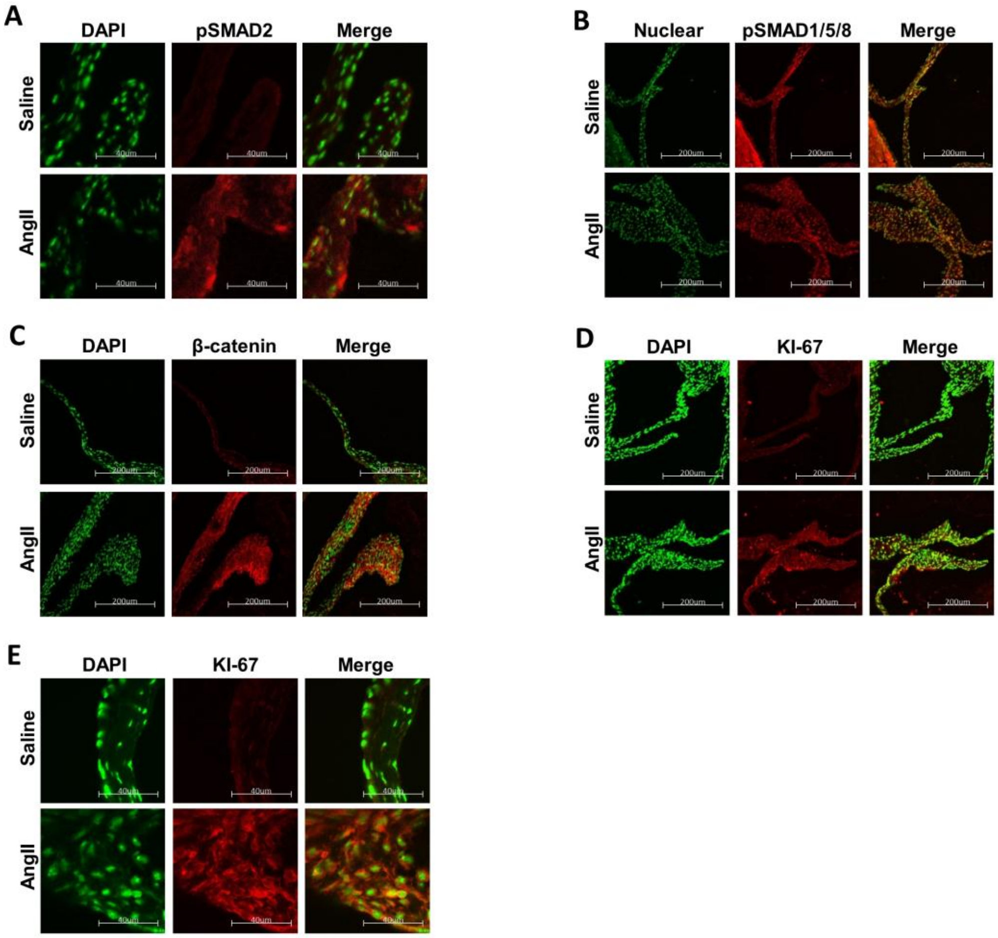

Figure S12. Immunohistochemical analysis of Saline and AngII infused murine mitral valve tissue. Immunofluorescence of A) pSMAD2 (100x magnification) was increased in AngII versus Saline infused mouse mitral valves. B) Staining for pSMAD1/5/8 (20x magnification) was unchanged between groups. Immunofluorescence of C) β-catenin (20x magnification) and D-E) the proliferation marker KI-67 (20x and 100x magnification respectively) was increased in mitral valves of AngII-infused mice (representative images from 8 AngII and 8 Saline-infused mice). AngII = Angiotensin II; SMAD = SMA mothers against decapentaplegic.

Figure S13.

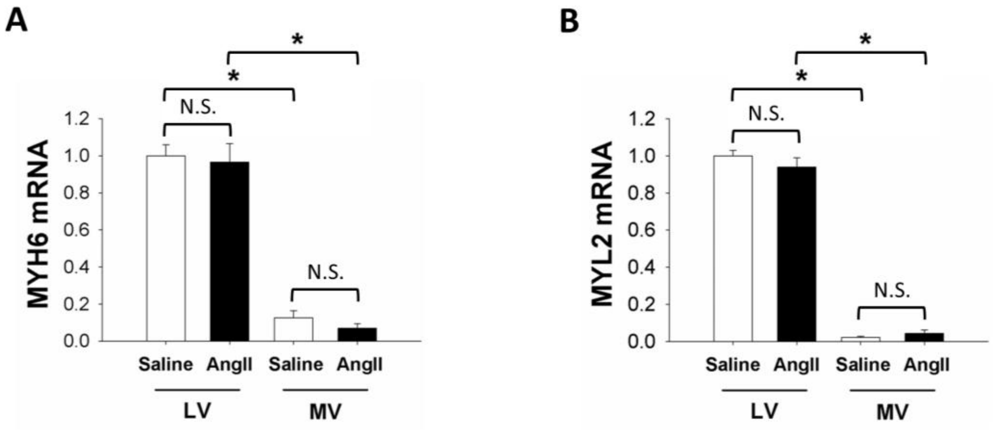

Figure S13. Gene expression levels of myocardium-specific markers in LV and MV tissue of AngII and Saline-infused mice. mRNA levels of MYH6 (A) and MYL2 (B) were significantly greater in LV as compared to MV tissue, irrespective of treatment group. Gene expression levels were comparable between Saline and AngII treated mice within the LV and MV. AngII, angiotensin II; LV, left ventricle; MV, mitral valve; MYL2, myosin light polypeptide 2; MYH6, myosin heavy polypeptide 6; NS, not significant.

Figure S14.

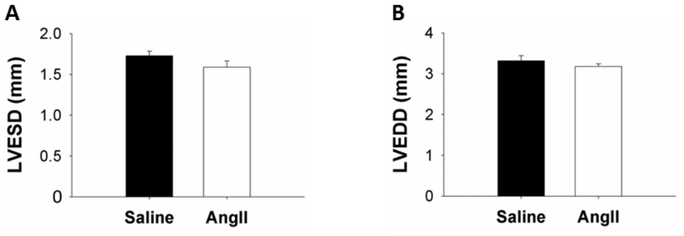

Figure S14. Echocardiographic evaluation of LV dimensions in murine mitral valves. LV end-systolic (A) and end-diastolic (B) dimensions were comparable (p=NS) between AngII and Saline-infused mice on Day 14 post-minipump implantation. AngII = angiotensin II; EDD (end-diastolic dimension); ESD (end-systolic dimension); LV = left ventricle.

SUPPLEMENTAL TABLES

Table S1. Human and Murine-Specific Gene Expression Primers Used for qRT-PCR Experiments

Gene	Human Primer	Murine Primer
AXIN2		Mm00443610_m1
BAMBI	Hs03044164_m1	Mm03053974_s1
BMP4	Hs03676628_s1	Mm00432087_m1
CD14	Hs00259040_s1	Mm00438094_g1
CD83	Hs00188486_m1	Mm00486868_m1
CDKN1A	Hs00355782_m1	
CDKN2B	Hs00793225_m1	
COL1A1	Hs00164004_m1	Mm00801666_g1
CTGF		Mm01192932_g1
CX3CR1	Hs01922583_s1	
FBN1	Hs00171191_m1	
FCGR1B	Hs00417598_m1	
FZD8	Hs00259040_s1	Mm01234717_s1
IL-7		Mm01295803_m1
MMP2		Mm00439498_m1
MSX2		Mm00442992_m1
MYL2		Mm00440384_m1
MYH6		Mm00440359_m1
RSPO2	Hs00379983_m1	
RUNX2	Hs00231692_m1	Mm00501584_m1
SMURF1	Hs00905759_m1	
SMURF2	Hs00224203_m1	
SIK1	Hs00545020_m1	Mm00440317_m1
TGFB2	Hs00234244_m1	Mm00436955_m1
TLR7		Mm00446590_m1
TOB2		Mm00451524_s1
WNT9A	Hs00231692_m1	Mm00460518_m1
WISP1	Hs04234730_m1	Mm01234717_s1

All primers were TaqMan Gene Expression Assay primers (Life Technologies)

Table S2. Differential Gene Expression in Myxomatous vs Non-Myxomatous Mitral Valves: By Microarray and qRT-PCR Analyses

Gene	FC Microarray	FC qRT-PCR	P-value*	R^2
SIK1	0.01	0.05	<0.001	0.85
CDKN1A	0.51	0.53	<0.001	0.86
BAMBI	0.57	0.57	<0.001	0.74
WNT9A	1.93	2.44	0.038	0.21
BMP4	1.96	1.94	0.027	0.23
FBN1	2.05	1.73	<0.001	0.63
FZD8	2.26	1.42	<0.001	0.51
TGFB2	2.42	2.00	<0.001	0.54
RUNX2	2.42	1.81	<0.001	0.74
FCGR1B	3.11	1.62	<0.001	0.57
CD83	3.72	2.23	<0.001	0.57
CDKN2B	4.15	2.29	0.001	0.43
WISP1	4.24	3.81	<0.001	0.90
CD14	4.34	4.17	<0.001	0.91
CX3CR1	7.47	3.71	<0.001	0.87
RSPO2	12.75	4.51	<0.001	0.80

* The p-value of the slope as determined by linear regression analyses. A p-value <0.05 indicates a significant correlation between the fold-change in gene expression measured by microarray analyses as compared to qRT-PCR. The correlation is significant for all genes, many of which had strong R^2 values.

Table S3. Non-Myxomatous Mitral Valves: Patient Data

Patient	Age	Sex	Smoking Status*	Transplant Indication
N1	43	M	0	Restrictive Cardiomyopathy
N2	66	M	1	Ischemic Cardiomyopathy
N3	54	M	0	Ischemic Cardiomyopathy
N4	49	M	0	Restrictive Cardiomyopathy
N5	39	F	0	Restrictive Cardiomyopathy
N6	53	M	0	Ischemic Cardiomyopathy
N7	60	M	1	Dilated Cardiomyopathy
N8	26	F	0	Dilated Cardiomyopathy
N9	64	M	1	Ischemic Cardiomyopathy
N10	22	M	0	Dilated Cardiomyopathy
N11	67	M	0	Ischemic Cardiomyopathy

M = Male; F = Female

*Smoking status: 0 = never smoker, 1 = previous smoker, 2 = current smoker

Table S4. Myxomatous Mitral Valves: Patient Data

Patient	Age	Sex	Smoking Status*	MR Severity	Affected Leaflet	ERO (cm^2)	Regurgitant Volume (cc)
M1	66	F	0	4+	P	0.64	119
M2	78	M	0	3+	B	0.36	62
M3	67	M	1	4+	P	0.51	71
M4	65	M	0	4+	B	0.44	60
M5	57	M	0	4+	P	0.61	85
M6	77	M	1	4+	P	0.31	53
M7	67	F	0	3+	B	0.27	66
M8	56	M	1	4+	B	1.32	148
M9	57	F	0	4+	B	0.71	98
M10	57	M	0	4+	B	0.51	75
M11	85	F	0	4+	P	0.49	75

B = bi-leaflet; ERO = effective regurgitant volume; F = female; M = male; MR = mitral regurgitation; P = posterior leaflet

3+ = moderate-severe, 4+ = severe MR.

*Smoking status: 0 = never smoker, 1 = previous smoker, 2 = current smoker

Table S5. Patient Medications

Drug Class	**Non-Myxomatous (n=11)**	**Myxomatous (n=11)**
Beta-blockers	6	4
ACE-I/ARBs	3	3
Nitrates	1	1
Anticoagulants	4	2
Statins	3	7
5-HT Related*	5	1
Other	11	11

ACE-I = Angiotensin converting-enzyme inhibitors; ARBs = Angiotensin receptor blockers; 5-HT = Serotonin

* Drugs known to alter tissue serotonin levels (Serotonin reuptake inhibitors [SRIs], selective SRIs [SSRIs], monoamine oxidase inhibitors [MAOIs], etc)

Table S6. Full Microarray Dataset

Gene Title	Gene Symbol	Fold Change	*P*	Adjusted P
1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta)	AGPAT4	2.154	0.00011	0.00212
2',5'-oligoadenylate synthetase 1, 40/46kDa	OAS1	3.966	0.00012	0.00221
24-dehydrocholesterol reductase	DHCR24	-1.925	0.01160	0.03843
2'-5'-oligoadenylate synthetase 2, 69/71kDa	OAS2	1.900	0.01630	0.04803
2'-5'-oligoadenylate synthetase 3, 100kDa	OAS3	1.997	0.00445	0.02101
3-oxoacid CoA transferase 2	OXCT2	-1.861	0.02340	0.06090
3'-phosphoadenosine 5'-phosphosulfate synthase 1	PAPSS1	1.628	0.00010	0.00200
4-aminobutyrate aminotransferase	ABAT	-3.250	0.00313	0.01670
5-hydroxytryptamine (serotonin) receptor 2A	HTR2A	1.569	0.04150	0.08763
5-hydroxytryptamine (serotonin) receptor 2B	HTR2B	4.439	0.00003	0.00099
5'-nucleotidase, ecto (CD73)	NT5E	3.162	0.00028	0.00363
A kinase (PRKA) anchor protein 13	AKAP13	-1.703	0.01070	0.03655
abhydrolase domain containing 10	ABHD10	1.613	0.00210	0.01309
abhydrolase domain containing 14A	ABHD14A	1.597	0.00047	0.00511
ABI family, member 3 (NESH) binding protein	ABI3BP	1.735	0.04690	0.09462
absent in melanoma 1	AIM1	2.578	0.00004	0.00102
acid phosphatase-like 2	ACPL2	1.663	0.00008	0.00176
acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	ANP32E	-1.666	0.00818	0.03094
actin filament associated protein 1-like 1	AFAP1L1	-7.525	0.00215	0.01325
actin filament associated protein 1-like 2	AFAP1L2	1.577	0.00083	0.00727
actin, alpha 2, smooth muscle, aorta	ACTA2	-3.945	0.00157	0.01086
actin, alpha, cardiac muscle 1	ACTC1	-18.326	0.03320	0.07640
actin, gamma 2, smooth muscle, enteric	ACTG2	-99.874	0.00110	0.00869
activating signal cointegrator 1 complex subunit 1	ASCC1	-1.696	0.03660	0.08124
activating transcription factor 3	ATF3	-34.981	0.00001	0.00042
activating transcription factor 7	ATF7	-2.104	0.00123	0.00930
activin A receptor, type I	ACVR1	1.739	0.00001	0.00036
activin A receptor, type IB	ACVR1B	-1.748	0.00049	0.00527
acyl-CoA synthetase long-chain family member 1	ACSL1	-2.711	0.00002	0.00063
acyl-CoA synthetase long-chain family member 5	ACSL5	-2.587	0.04260	0.08924
acyl-CoA synthetase medium-chain family member 3	ACSM3	-3.356	0.02820	0.06862
acyl-CoA thioesterase 1 /// acyl-CoA thioesterase 2	ACOT1 /// ACOT2	-1.691	0.01320	0.04188
acyl-CoA thioesterase 4	ACOT4	2.245	0.00012	0.00221
acyl-CoA thioesterase 7	ACOT7	1.542	0.00067	0.00637
acyl-Coenzyme A dehydrogenase, long chain	ACADL	-1.955	0.02670	0.06637
acylphosphatase 2, muscle type	ACYP2	-1.729	0.01960	0.05427
ADAM metallopeptidase domain 12	ADAM12	1.609	0.00207	0.01298
ADAM metallopeptidase with thrombospondin type 1 motif, 1	ADAMTS1	-7.133	0.00000	0.00026
ADAM metallopeptidase with thrombospondin type 1 motif, 19	ADAMTS19	1.763	0.01520	0.04600
ADAM metallopeptidase with thrombospondin type 1 motif, 5	ADAMTS5	-4.906	0.00726	0.02872
ADAM metallopeptidase with thrombospondin type 1 motif, 6	ADAMTS6	2.361	0.00007	0.00161
ADAM metallopeptidase with thrombospondin type 1 motif, 9	ADAMTS9	-11.543	0.04920	0.09753
ADAMTS-like 2	ADAMTSL2	1.810	0.02600	0.06526
adaptor-related protein complex 4, sigma 1 subunit	AP4S1	-1.602	0.02670	0.06637
adducin 3 (gamma)	ADD3	1.782	0.00000	0.00016
adenomatosis polyposis coli down-regulated 1	APCDD1	1.771	0.00592	0.02522
adenosine deaminase, tRNA-specific 1	ADAT1	1.777	0.00008	0.00170
adenosine monophosphate deaminase 2 (isoform L)	AMPD2	1.603	0.00354	0.01818

adenylate cyclase 1 (brain)	ADCY1	-9.237	0.00464	0.02164
adenylate cyclase 2 (brain)	ADCY2	1.746	0.00669	0.02726
adenylate cyclase 5	ADCY5	-2.670	0.04600	0.09346
adenylate cyclase 7	ADCY7	1.995	0.00250	0.01447
ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)	ARFGEF2	-1.797	0.00462	0.02157
ADP-ribosylation factor-like 4A	ARL4A	-1.622	0.02230	0.05907
ADP-ribosylation factor-like 6	ARL6	1.519	0.00948	0.03394
adrenergic, alpha-2C-, receptor	ADRA2C	-3.443	0.02290	0.06004
adrenomedullin	ADM	-6.721	0.00225	0.01360
AE binding protein 1	AEBP1	1.528	0.00175	0.01163
AF4/FMR2 family, member 1	AFF1	-1.744	0.00058	0.00585
AF4/FMR2 family, member 3	AFF3	2.262	0.00127	0.00949
aggrecan	ACAN	-2.409	0.04280	0.08947
AHNAK nucleoprotein 2	AHNAK2	1.776	0.00792	0.03028
akirin 1	AKIRIN1	-1.688	0.00588	0.02516
alcohol dehydrogenase 1B (class I), beta polypeptide	ADH1B	-1.792	0.01850	0.05236
alcohol dehydrogenase, iron containing, 1	ADHFE1	-2.321	0.00018	0.00285
aldehyde dehydrogenase 1 family, member A2	ALDH1A2	-2.524	0.04180	0.08811
aldehyde dehydrogenase 1 family, member A3	ALDH1A3	2.695	0.00282	0.01559
aldehyde dehydrogenase 1 family, member L1	ALDH1L1	-5.103	0.00001	0.00042
aldehyde dehydrogenase 1 family, member L2	ALDH1L2	1.959	0.00019	0.00289
aldehyde dehydrogenase 18 family, member A1	ALDH18A1	2.840	0.00001	0.00034
aldehyde dehydrogenase 3 family, member A2	ALDH3A2	1.811	0.00245	0.01431
aldehyde dehydrogenase 4 family, member A1	ALDH4A1	-1.648	0.01210	0.03950
aldehyde dehydrogenase 5 family, member A1	ALDH5A1	1.518	0.02260	0.05950
aldehyde dehydrogenase 6 family, member A1	ALDH6A1	-1.789	0.00076	0.00685
aldehyde oxidase 1	AOX1	-6.066	0.00551	0.02415
aldo-keto reductase family 1, member B10 (aldose reductase)	AKR1B10	-2.297	0.00941	0.03377
aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)	AKR1C3	1.623	0.00501	0.02271
alkaline ceramidase 3	ACER3	-1.525	0.00839	0.03143
alkB, alkylation repair homolog 8 (E. coli)	ALKBH8	1.715	0.00043	0.00478
alkylglycerone phosphate synthase	AGPS	1.596	0.00001	0.00049
alpha-2-macroglobulin	A2M	-3.115	0.00178	0.01173
alpha-methylacyl-CoA racemase	AMACR	3.286	0.00002	0.00070
alpha-methylacyl-CoA racemase /// C1q and tumor necrosis factor related protein 3	AMACR /// C1QTNF3	2.229	0.04830	0.09639
aminoadipate-semialdehyde synthase	AASS	-2.613	0.00033	0.00411
amphiregulin	AREG	-35.971	0.01760	0.05063
androgen-induced 1	AIG1	1.678	0.00013	0.00236
angiomotin like 2	AMOTL2	-1.723	0.00099	0.00811
angiopoietin 1	ANGPT1	-1.642	0.03550	0.07959
angiopoietin-like 1	ANGPTL1	-1.704	0.02430	0.06242
angiopoietin-like 2	ANGPTL2	3.518	0.00008	0.00173
angiopoietin-like 4	ANGPTL4	-2.486	0.01250	0.04030
angiopoietin-like 7	ANGPTL7	-6.301	0.00198	0.01262
angiotensin II receptor, type 1	AGTR1	-16.810	0.00126	0.00945
ankylosis, progressive homolog (mouse)	ANKH	1.848	0.00204	0.01287
ankyrin 2, neuronal	ANK2	2.219	0.00011	0.00203
ankyrin repeat and KH domain containing 1	ANKHD1	-2.282	0.00551	0.02415
ankyrin repeat and SOCS box-containing 2	ASB2	-16.720	0.03410	0.07762
ankyrin repeat and SOCS box-containing 6	ASB6	1.599	0.00050	0.00533

ankyrin repeat and sterile alpha motif domain containing 1B	ANKS1B	-1.969	0.02980	0.07116
ankyrin repeat domain 10	ANKRD10	1.672	0.02180	0.05821
ankyrin repeat domain 13 family, member D	ANKRD13D	1.769	0.00193	0.01245
ankyrin repeat domain 22	ANKRD22	-1.635	0.01820	0.05188
ankyrin repeat domain 28	ANKRD28	-1.838	0.04840	0.09648
ankyrin repeat domain 35	ANKRD35	1.688	0.01420	0.04393
ankyrin repeat domain 37	ANKRD37	-2.014	0.00001	0.00047
ankyrin repeat domain 43	ANKRD43	2.524	0.00061	0.00603
ankyrin repeat domain 45	ANKRD45	2.236	0.00084	0.00730
ankyrin repeat domain 6	ANKRD6	1.553	0.00310	0.01660
annexin A3	ANXA3	1.798	0.02440	0.06258
annexin A4	ANXA4	1.602	0.00000	0.00007
anoctamin 1, calcium activated chloride channel	ANO1	1.674	0.00757	0.02947
anoctamin 3	ANO3	-2.624	0.04040	0.08636
anoctamin 8	ANO8	1.518	0.00014	0.00241
anthrax toxin receptor 1	ANTXR1	2.172	0.00102	0.00824
antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5	MFI2	1.681	0.00024	0.00335
apolipoprotein B (including Ag(x) antigen)	APOB	-3.760	0.04890	0.09715
apolipoprotein E	APOE	-2.274	0.01710	0.04964
apolipoprotein L domain containing 1	APOLD1	-13.161	0.00041	0.00468
apolipoprotein L, 1	APOL1	1.873	0.00054	0.00556
apolipoprotein L, 3	APOL3	2.332	0.00000	0.00022
apolipoprotein L, 6	APOL6	1.667	0.00121	0.00921
apolipoprotein O-like	APOOL	-1.901	0.01790	0.05126
apoptosis enhancing nuclease	AEN	1.566	0.00018	0.00279
aquaporin 1 (Colton blood group) /// indolethylamine N-methyltransferase	AQP1 /// INMT	1.545	0.04760	0.09557
arachidonate 15-lipoxygenase, type B	ALOX15B	-2.015	0.01390	0.04334
ArfGAP with dual PH domains 1	ADAP1	-1.791	0.00010	0.00193
ArfGAP with dual PH domains 2	ADAP2	1.774	0.02190	0.05840
ArfGAP with GTPase domain, ankyrin repeat and PH domain 1	AGAP1	1.569	0.01170	0.03865
ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1	ARAP1	1.592	0.00233	0.01387
ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2	ARAP2	2.580	0.00147	0.01042
ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3	ARAP3	-2.089	0.03110	0.07326
ArfGAP with SH3 domain, ankyrin repeat and PH domain 1	ASAP1	-1.748	0.03870	0.08415
ArfGAP with SH3 domain, ankyrin repeat and PH domain 3	ASAP3	1.788	0.00008	0.00170
arginine decarboxylase	ADC	1.681	0.00006	0.00149
arginine-glutamic acid dipeptide (RE) repeats	RERE	-1.853	0.00000	0.00022
arginyl aminopeptidase (aminopeptidase B) /// transmembrane protein 189 /// TMEM189-UBE2V1 readthrough transcript /// ubiquitin-conjugating enzyme E2 variant 1	RNPEP /// TMEM189 /// TMEM189-UBE2V1 /// UBE2V1	1.518	0.00013	0.00227
ariadne homolog 2 (Drosophila)	ARIH2	-2.180	0.00000	0.00010
ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila)	ARIH1	-1.706	0.00063	0.00616
armadillo repeat containing 8	ARMC8	-1.990	0.00312	0.01667
armadillo repeat containing 9	ARMC9	2.038	0.00025	0.00339
armadillo repeat containing, X-linked 4	ARMCX4	1.543	0.01380	0.04312
ARP3 actin-related protein 3 homolog (yeast)	ACTR3	-1.585	0.02440	0.06258
arrestin domain containing 2	ARRDC2	-2.814	0.00005	0.00126
arrestin domain containing 3	ARRDC3	-2.051	0.00209	0.01304
aryl hydrocarbon receptor	AHR	1.733	0.00794	0.03031
aryl hydrocarbon receptor nuclear translocator-like	ARNTL	-9.757	0.00010	0.00193

aryl hydrocarbon receptor nuclear translocator-like 2	ARNTL2	1.808	0.00581	0.02495
arylsulfatase E (chondrodysplasia punctata 1)	ARSE	2.210	0.00226	0.01362
arylsulfatase family, member I	ARSI	1.510	0.00026	0.00346
asparagine-linked glycosylation 1, beta-1,4-mannosyltransferase homolog (S. cerevisiae)	ALG1	1.723	0.00687	0.02769
asparagine-linked glycosylation 13 homolog (S. cerevisiae)	ALG13	-1.960	0.00271	0.01520
asparagine-linked glycosylation 6, alpha-1,3-glucosyltransferase homolog (S. cerevisiae)	ALG6	1.691	0.00146	0.01039
aspartoacylase (Canavan disease)	ASPA	2.604	0.00531	0.02353
aspartylglucosaminidase	AGA	1.660	0.00038	0.00446
asteroid homolog 1 (Drosophila)	ASTE1	1.785	0.00002	0.00065
astrotactin 2	ASTN2	-2.686	0.02370	0.06141
AT rich interactive domain 5B (MRF1-like)	ARID5B	-2.318	0.00000	0.00004
Atonal homolog 8 (Drosophila)	ATOH8	-1.885	0.02260	0.05950
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C2 (subunit 9)	ATP5G2	-1.508	0.03290	0.07597
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G	ATP5L	-1.565	0.01240	0.04009
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s (factor B)	ATP5S	-2.455	0.01950	0.05408
ATP/GTP binding protein 1	AGTPBP1	-1.772	0.03540	0.07942
ATP/GTP binding protein-like 3	AGBL3	1.516	0.00473	0.02192
ATPase family, AAA domain containing 2	ATAD2	-2.531	0.00039	0.00455
ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	ATP8A1	1.698	0.00243	0.01426
ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	ATP2A2	-5.229	0.04690	0.09462
ATPase, Ca++ transporting, ubiquitous	ATP2A3	1.845	0.00337	0.01758
ATPase, class V, type 10A	ATP10A	-4.193	0.00004	0.00107
ATPase, H+ transporting V0 subunit e2	ATP6V0E2	1.574	0.01890	0.05309
ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1	ATP6V1C1	-1.978	0.01960	0.05427
ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide	ATP1A2	-12.988	0.00001	0.00032
ATP-binding cassette, sub-family A (ABC1), member 3	ABCA3	1.739	0.00002	0.00083
ATP-binding cassette, sub-family C (CFTR/MRP), member 4	ABCC4	2.150	0.00743	0.02913
ATP-binding cassette, sub-family C (CFTR/MRP), member 9	ABCC9	-1.600	0.01600	0.04748
ATP-binding cassette, sub-family G (WHITE), member 1	ABCG1	2.305	0.03050	0.07232
attractin	ATRN	2.047	0.00101	0.00819
autism susceptibility candidate 2	AUTS2	1.588	0.00123	0.00930
B9 protein domain 1	B9D1	1.746	0.00425	0.02042
BAH domain and coiled-coil containing 1	BAHCC1	2.091	0.00010	0.00193
basal cell adhesion molecule (Lutheran blood group)	BCAM	-2.135	0.02810	0.06847
basic helix-loop-helix domain containing, class B, 9	BHLHB9	1.911	0.00003	0.00086
basic helix-loop-helix family, member e40	BHLHE40	3.159	0.00174	0.01159
basic helix-loop-helix family, member e41	BHLHE41	3.229	0.00030	0.00384
B-cell CLL/lymphoma 3	BCL3	1.525	0.00741	0.02909
B-cell CLL/lymphoma 6	BCL6	-2.066	0.01860	0.05251
B-cell CLL/lymphoma 7A	BCL7A	-1.623	0.00707	0.02824
B-cell linker	BLNK	3.206	0.00093	0.00782
B-cell translocation gene 1, anti-proliferative	BTG1	-2.771	0.00000	0.00004
BCL2/adenovirus E1B 19kDa interacting protein 3	BNIP3	-2.061	0.00976	0.03452
BCL2-associated athanogene 5	BAG5	2.143	0.00023	0.00324
BCL2-associated X protein	BAX	1.766	0.00353	0.01814
BEN domain containing 6	BEND6	2.908	0.00023	0.00328
beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)	B3GALNT1	1.560	0.00423	0.02035
beta-1,3-N-acetylgalactosaminyltransferase 2	B3GALNT2	-1.678	0.00807	0.03068

beta-1,4-N-acetyl-galactosaminyl transferase 3	B4GALNT3	1.910	0.00019	0.00293
betacellulin	BTC	1.742	0.02290	0.06004
beta-site APP-cleaving enzyme 2	BACE2	1.514	0.00510	0.02296
bicaudal D homolog 1 (Drosophila)	BICD1	1.724	0.00299	0.01621
biglycan	BGN	1.520	0.00625	0.02609
biotinidase	BTD	-1.661	0.04880	0.09703
biphenyl hydrolase-like (serine hydrolase)	BPHL	1.573	0.00010	0.00199
block of proliferation 1 /// similar to block of proliferation 1	BOP1 /// LOC727967	1.593	0.00011	0.00209
BMP and activin membrane-bound inhibitor homolog (Xenopus laevis)	BAMBI	-1.757	0.03720	0.08208
BMP binding endothelial regulator	BMPER	3.048	0.00003	0.00087
BMP2 inducible kinase	BMP2K	1.613	0.01220	0.03971
bone marrow stromal cell antigen 1	BST1	1.885	0.01150	0.03823
bone morphogenetic protein 4	BMP4	1.955	0.00090	0.00765
bradykinin receptor B2	BDKRB2	3.701	0.00005	0.00126
brain expressed, associated with Nedd4	BEAN	1.789	0.00497	0.02262
brain expressed, X-linked 1	BEX1	1.818	0.01230	0.03990
brain-derived neurotrophic factor	BDNF	1.512	0.04820	0.09633
branched chain keto acid dehydrogenase E1, beta polypeptide	BCKDHB	-1.717	0.03950	0.08519
BRCA2 and CDKN1A interacting protein	BCCIP	-1.523	0.00009	0.00187
breast cancer 1, early onset	BRCA1	1.550	0.00249	0.01444
breast cancer metastasis-suppressor 1-like	BRMS1L	-1.654	0.00714	0.02839
bromodomain adjacent to zinc finger domain, 1A	BAZ1A	-1.562	0.02610	0.06538
bromodomain and WD repeat domain containing 1	BRWD1	-1.538	0.02230	0.05907
bromodomain containing 4	BRD4	-1.647	0.01800	0.05148
BTB (POZ) domain containing 11	BTBD11	2.520	0.00212	0.01315
BTG family, member 2	BTG2	-18.139	0.00004	0.00103
butyrophilin, subfamily 2, member A2	BTN2A2	1.525	0.00092	0.00777
butyrophilin, subfamily 3, member A1	BTN3A1	1.613	0.00628	0.02618
butyrophilin, subfamily 3, member A3	BTN3A3	2.219	0.00001	0.00044
C1q and tumor necrosis factor related protein 2	C1QTNF2	3.674	0.00008	0.00168
C1q and tumor necrosis factor related protein 9 /// spermatogenesis associated 13	C1QTNF9 /// SPATA13	1.674	0.00057	0.00578
cache domain containing 1	CACHD1	1.555	0.00391	0.01935
cadherin 11, type 2, OB-cadherin (osteoblast)	CDH11	1.662	0.00004	0.00114
cadherin 2, type 1, N-cadherin (neuronal)	CDH2	-2.429	0.01630	0.04803
cadherin 5, type 2 (vascular endothelium)	CDH5	-2.442	0.04720	0.09501
calcineurin-like phosphoesterase domain containing 1	CPPED1	1.577	0.00512	0.02301
calcium binding and coiled-coil domain 2	CALCOCO2	-1.669	0.00000	0.00017
calcium channel, voltage-dependent, alpha 2/delta subunit 2	CACNA2D2	1.633	0.00385	0.01919
calcium channel, voltage-dependent, beta 2 subunit	CACNB2	-12.749	0.02270	0.05971
calcium channel, voltage-dependent, beta 3 subunit	CACNB3	1.912	0.00001	0.00047
calcium channel, voltage-dependent, beta 4 subunit	CACNB4	1.650	0.00008	0.00177
calcium channel, voltage-dependent, L type, alpha 1C subunit	CACNA1C	-3.707	0.00484	0.02228
calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	CACNA1A	1.918	0.00284	0.01565
calcium/calmodulin-dependent protein kinase ID	CAMK1D	2.362	0.00000	0.00005
calcium/calmodulin-dependent protein kinase ID /// hypothetical LOC283070	CAMK1D /// LOC283070	2.762	0.00000	0.00008
calcium/calmodulin-dependent protein kinase kinase 1, alpha	CAMKK1	2.017	0.00014	0.00237
calcium/calmodulin-dependent protein kinase kinase 2, beta	CAMKK2	1.586	0.00074	0.00671
calcium/calmodulin-dependent serine protein kinase (MAGUK family)	CASK	1.515	0.00008	0.00170
caldesmon 1	CALD1	-2.558	0.01300	0.04135
calmin (calponin-like, transmembrane)	CLMN	-1.779	0.01590	0.04727

Calmodulin binding transcription activator 1	CAMTA1	-1.694	0.00741	0.02909
calpain 5	CAPN5	2.424	0.00132	0.00973
calponin 1, basic, smooth muscle	CNN1	-13.422	0.00631	0.02626
calponin 2	CNN2	-1.808	0.00024	0.00329
calsequestrin 2 (cardiac muscle)	CASQ2	-130.216	0.02420	0.06227
cAMP responsive element binding protein 3-like 2	CREB3L2	1.627	0.00000	0.00030
cAMP responsive element binding protein 5	CREB5	2.823	0.00106	0.00846
cannabinoid receptor 1 (brain)	CNR1	3.115	0.00244	0.01428
canopy 4 homolog (zebrafish)	CNPY4	1.915	0.00001	0.00039
CAP-GLY domain containing linker protein 2	CLIP2	2.309	0.00002	0.00069
CAP-GLY domain containing linker protein family, member 4	CLIP4	-1.505	0.02960	0.07084
capping protein (actin filament) muscle Z-line, alpha 2	CAPZA2	-1.623	0.00669	0.02726
capping protein (actin filament), gelsolin-like	CAPG	1.793	0.02740	0.06734
carbamoyl-phosphate synthetase 1, mitochondrial	CPS1	1.560	0.00035	0.00424
Carbohydrate (chondroitin 4) sulfotransferase 11	CHST11	-1.631	0.03180	0.07441
carbohydrate (chondroitin 4) sulfotransferase 12	CHST12	1.614	0.00007	0.00153
carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	CHST1	-2.124	0.02440	0.06258
carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9	CHST9	2.438	0.00466	0.02171
carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 6	CHST6	5.437	0.00001	0.00050
carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	CHST7	-5.650	0.01120	0.03762
carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2	CHST2	5.108	0.00000	0.00009
carbonic anhydrase VB, mitochondrial	CA5B	2.807	0.00038	0.00446
carbonyl reductase 1	CBR1	1.872	0.00037	0.00436
carbonyl reductase 3	CBR3	1.607	0.00046	0.00504
carboxymethylenebutenolidase homolog (Pseudomonas)	CMBL	1.572	0.00008	0.00171
carboxypeptidase D	CPD	-1.532	0.01200	0.03929
carboxypeptidase M	CPM	-2.581	0.03400	0.07748
carnitine O-octanoyltransferase	CROT	1.524	0.00070	0.00652
carnitine palmitoyltransferase 1C	CPT1C	2.402	0.00020	0.00300
cartilage acidic protein 1	CRTAC1	2.110	0.00706	0.02823
Cas-Br-M (murine) ecotropic retroviral transforming sequence b	CBLB	-1.757	0.00383	0.01914
casein kinase 1, alpha 1	CSNK1A1	-1.624	0.04360	0.09034
CASP8 and FADD-like apoptosis regulator	CFLAR	-1.852	0.00247	0.01438
caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	CASP1	2.048	0.00034	0.00414
caspase 2, apoptosis-related cysteine peptidase	CASP2	1.583	0.00007	0.00162
caspase 6, apoptosis-related cysteine peptidase	CASP6	-1.832	0.00099	0.00809
caspase 8, apoptosis-related cysteine peptidase	CASP8	1.844	0.00093	0.00780
castor zinc finger 1	CASZ1	-5.267	0.04030	0.08623
cat eye syndrome chromosome region, candidate 5	CECR5	-1.684	0.00092	0.00779
cathepsin A	CTSA	1.513	0.00059	0.00589
cathepsin C	CTSC	1.987	0.01160	0.03843
cathepsin K	CTSK	1.629	0.00419	0.02022
cathepsin Z	CTSZ	1.702	0.00638	0.02643
caveolin 1, caveolae protein, 22kDa	CAV1	-2.216	0.00258	0.01474
caveolin 2	CAV2	-2.122	0.02400	0.06193
caveolin 3	CAV3	-6.035	0.04240	0.08892
Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	CITED2	-2.608	0.00974	0.03449
CCAAT/enhancer binding protein (C/EBP), beta	CEBPB	-2.597	0.00001	0.00037
CCAAT/enhancer binding protein (C/EBP), delta	CEBPD	-2.615	0.00008	0.00176
CCR4-NOT transcription complex, subunit 3	CNOT3	1.665	0.00025	0.00343

CCR4-NOT transcription complex, subunit 8	CNOT8	-2.005	0.00677	0.02746
CD109 molecule	CD109	1.792	0.00056	0.00573
CD14 molecule	CD14	4.336	0.00000	0.00029
CD163 molecule	CD163	-8.375	0.00670	0.02730
CD163 molecule-like 1	CD163L1	2.315	0.00199	0.01267
CD200 molecule	CD200	1.516	0.00618	0.02593
CD24 molecule	CD24	4.342	0.00065	0.00623
CD276 molecule	CD276	1.732	0.00002	0.00062
CD28 molecule	CD28	3.100	0.00128	0.00954
CD34 molecule	CD34	1.683	0.00072	0.00662
CD38 molecule	CD38	-6.756	0.00617	0.02590
CD44 molecule (Indian blood group)	CD44	1.718	0.00302	0.01633
CD47 molecule	CD47	1.594	0.02170	0.05808
CD69 molecule	CD69	-16.773	0.00432	0.02062
CD83 molecule	CD83	3.720	0.00000	0.00010
CD9 molecule	CD9	-2.677	0.01900	0.05324
CD93 molecule	CD93	-2.706	0.04510	0.09228
CDC28 protein kinase regulatory subunit 2	CKS2	-2.323	0.02100	0.05688
CDC42 effector protein (Rho GTPase binding) 3	CDC42EP3	-2.595	0.00264	0.01496
CDC42 effector protein (Rho GTPase binding) 4	CDC42EP4	1.755	0.00079	0.00703
Cdc42 guanine nucleotide exchange factor (GEF) 9	ARHGEF9	-5.159	0.03200	0.07469
CDC5 cell division cycle 5-like (S. pombe)	CDC5L	-2.058	0.03380	0.07723
Cdk5 and Abl enzyme substrate 1	CABLES1	1.815	0.00052	0.00543
CDK5 regulatory subunit associated protein 2	CDK5RAP2	1.757	0.00556	0.02429
Cdon homolog (mouse)	CDON	3.264	0.00009	0.00187
CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 1	CDS1	3.272	0.04850	0.09659
CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	CDS2	-1.787	0.00311	0.01664
cell adhesion molecule 3	CADM3	1.710	0.02100	0.05688
cell division cycle 37 homolog (S. cerevisiae)-like 1	CDC37L1	-2.600	0.00259	0.01478
cell division cycle associated 7-like	CDCA7L	1.540	0.01590	0.04727
cell growth regulator with EF-hand domain 1	CGREF1	1.636	0.00011	0.00207
cellular retinoic acid binding protein 2	CRABP2	2.113	0.00020	0.00300
centrosomal protein 152kDa	CEP152	1.995	0.00306	0.01646
centrosomal protein 350kDa	CEP350	-1.957	0.03540	0.07942
centrosomal protein 70kDa	CEP70	-1.779	0.01440	0.04432
cerebellar degeneration-related protein 2-like	CDR2L	1.550	0.00008	0.00167
ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation)	CLN8	1.840	0.00063	0.00617
ceruloplasmin (ferroxidase)	CP	1.572	0.01990	0.05490
CGG triplet repeat binding protein 1	CGGBP1	-2.020	0.00009	0.00181
ChaC, cation transport regulator homolog 2 (E. coli)	CHAC2	-2.139	0.00492	0.02251
chaperonin containing TCP1, subunit 2 (beta)	CCT2	-1.622	0.01580	0.04710
chaperonin containing TCP1, subunit 8 (theta)	CCT8	-1.616	0.01050	0.03614
chemokine (C-C motif) ligand 19	CCL19	-10.477	0.00260	0.01480
chemokine (C-C motif) ligand 3 /// chemokine (C-C motif) ligand 3-like 1 /// chemokine (C-C motif) ligand 3-like 3	CCL3 /// CCL3L1 /// CCL3L3	-12.692	0.01760	0.05063
chemokine (C-C motif) ligand 4	CCL4	-5.834	0.01500	0.04561
chemokine (C-C motif) ligand 5	CCL5	-2.706	0.01270	0.04072
chemokine (C-C motif) receptor-like 1	CCRL1	10.850	0.00000	0.00011
chemokine (C-X3-C motif) ligand 1	CX3CL1	2.240	0.00029	0.00374
chemokine (C-X3-C motif) receptor 1	CX3CR1	7.476	0.00057	0.00576
chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	CXCL12	2.305	0.00719	0.02850

chemokine (C-X-C motif) ligand 14	CXCL14	4.378	0.00300	0.01625
chemokine (C-X-C motif) ligand 2	CXCL2	-6.419	0.00574	0.02478
chemokine (C-X-C motif) ligand 9	CXCL9	-9.119	0.01240	0.04009
CHK2 checkpoint homolog (S. pombe)	CHEK2	1.956	0.01080	0.03676
chloride channel 3	CLCN3	1.508	0.00018	0.00280
chloride channel 4	CLCN4	1.675	0.00676	0.02743
chloride channel accessory 2	CLCA2	1.505	0.04760	0.09557
chloride intracellular channel 2	CLIC2	1.863	0.00498	0.02264
chloride intracellular channel 3	CLIC3	3.020	0.00047	0.00507
chloride intracellular channel 6	CLIC6	2.554	0.00098	0.00805
choline dehydrogenase	CHDH	1.961	0.00030	0.00381
choline kinase alpha	CHKA	-1.570	0.02810	0.06847
Choline phosphotransferase 1	CHPT1	-2.588	0.04070	0.08669
cholinergic receptor, nicotinic, alpha 3	CHRNA3	1.769	0.00005	0.00131
chondroadherin-like	CHADL	1.609	0.00238	0.01407
chondroitin polymerizing factor 2	CHPF2	1.560	0.00003	0.00087
chondroitin sulfate synthase 1	CHSY1	1.725	0.00021	0.00306
chondroitin sulfate synthase 3	CHSY3	2.367	0.00001	0.00047
chondrolectin	CHODL	-4.293	0.00130	0.00963
choroideremia-like (Rab escort protein 2)	CHML	-2.220	0.00024	0.00337
chromatin modifying protein 1B	CHMP1B	-1.721	0.00030	0.00383
chromobox homolog 4 (Pc class homolog, Drosophila)	CBX4	1.689	0.00118	0.00907
chromobox homolog 5 (HP1 alpha homolog, Drosophila)	CBX5	1.812	0.00166	0.01125
chromodomain helicase DNA binding protein 1	CHD1	-1.609	0.00128	0.00954
chromosome 1 open reading frame 114	C1orf114	1.711	0.00603	0.02553
chromosome 1 open reading frame 133	C1orf133	3.182	0.00001	0.00039
chromosome 1 open reading frame 144	C1orf144	-2.319	0.03870	0.08415
chromosome 1 open reading frame 156	C1orf156	1.983	0.00005	0.00129
chromosome 1 open reading frame 162	C1orf162	-4.054	0.00011	0.00212
chromosome 1 open reading frame 201	C1orf201	1.620	0.00011	0.00202
chromosome 1 open reading frame 204	C1orf204	1.890	0.00065	0.00626
chromosome 1 open reading frame 212	C1orf212	-1.854	0.00519	0.02322
chromosome 1 open reading frame 230	C1orf230	-1.582	0.03100	0.07314
chromosome 1 open reading frame 43	C1orf43	-1.604	0.02500	0.06357
chromosome 1 open reading frame 71	C1orf71	-1.563	0.00008	0.00170
chromosome 1 open reading frame 85	C1orf85	1.847	0.00107	0.00852
chromosome 1 open reading frame 93	C1orf93	2.010	0.00036	0.00430
chromosome 10 open reading frame 10	C10orf10	-2.614	0.00841	0.03146
chromosome 10 open reading frame 104	C10orf104	-1.631	0.00475	0.02200
chromosome 10 open reading frame 140	C10orf140	1.912	0.00007	0.00166
chromosome 11 open reading frame 1	C11orf1	-1.997	0.04140	0.08751
chromosome 11 open reading frame 24	C11orf24	1.872	0.00001	0.00058
chromosome 11 open reading frame 70	C11orf70	1.650	0.02040	0.05581
chromosome 11 open reading frame 80	C11orf80	4.422	0.00003	0.00092
chromosome 11 open reading frame 83	C11orf83	1.508	0.00006	0.00138
chromosome 11 open reading frame 87	C11orf87	2.215	0.00473	0.02192
chromosome 12 open reading frame 29	C12orf29	-1.615	0.00257	0.01472
chromosome 12 open reading frame 32	C12orf32	1.722	0.00018	0.00281
chromosome 12 open reading frame 62	C12orf62	-1.921	0.04750	0.09543
chromosome 12 open reading frame 73	C12orf73	1.698	0.00001	0.00057
chromosome 12 open reading frame 75	C12orf75	-6.086	0.02440	0.06258

Chromosome 13 open reading frame 15	C13orf15	-7.238	0.01010	0.03532
chromosome 13 open reading frame 18	C13orf18	2.079	0.00949	0.03397
chromosome 13 open reading frame 26	C13orf26	1.583	0.00001	0.00042
Chromosome 13 open reading frame 33	C13orf33	-1.699	0.01130	0.03781
chromosome 14 open reading frame 106	C14orf106	-1.963	0.01450	0.04451
chromosome 14 open reading frame 132	C14orf132	1.845	0.00953	0.03403
chromosome 14 open reading frame 50	C14orf50	2.954	0.00006	0.00144
chromosome 14 open reading frame 64	C14orf64	1.526	0.00233	0.01387
chromosome 14 open reading frame 82	C14orf82	1.657	0.00246	0.01434
chromosome 15 open reading frame 59	C15orf59	1.567	0.04040	0.08636
chromosome 16 open reading frame 61	C16orf61	-2.209	0.03610	0.08054
chromosome 17 open reading frame 57	C17orf57	-2.663	0.03990	0.08571
chromosome 17 open reading frame 76	C17orf76	2.271	0.00001	0.00041
chromosome 17 open reading frame 81	C17orf81	1.728	0.04240	0.08892
chromosome 17 open reading frame 91	C17orf91	-2.892	0.00000	0.00010
chromosome 18 open reading frame 19	C18orf19	-1.896	0.03890	0.08445
chromosome 18 open reading frame 8	C18orf8	-1.569	0.00003	0.00096
chromosome 2 open reading frame 27A	C2orf27A	2.284	0.00306	0.01646
chromosome 2 open reading frame 49	C2orf49	-1.952	0.00546	0.02404
chromosome 2 open reading frame 67	C2orf67	-1.898	0.00042	0.00474
chromosome 2 open reading frame 88	C2orf88	2.091	0.01100	0.03720
chromosome 20 open reading frame 111	C20orf111	-1.576	0.00005	0.00133
chromosome 20 open reading frame 112	C20orf112	2.538	0.00000	0.00018
chromosome 20 open reading frame 199	C20orf199	-1.645	0.00069	0.00648
chromosome 20 open reading frame 7	C20orf7	-2.017	0.01120	0.03762
chromosome 21 open reading frame 62	C21orf62	12.578	0.00192	0.01240
chromosome 22 open reading frame 29	C22orf29	1.609	0.00000	0.00022
chromosome 22 open reading frame 32	C22orf32	-1.632	0.00034	0.00414
chromosome 22 open reading frame 9	C22orf9	2.044	0.00014	0.00243
chromosome 3 open reading frame 14	C3orf14	1.657	0.00000	0.00013
chromosome 3 open reading frame 21	C3orf21	2.181	0.00018	0.00279
chromosome 3 open reading frame 34	C3orf34	1.678	0.00188	0.01220
chromosome 3 open reading frame 64	C3orf64	-1.744	0.00242	0.01423
chromosome 3 open reading frame 67	C3orf67	1.838	0.00005	0.00135
chromosome 4 open reading frame 16	C4orf16	-1.666	0.01780	0.05103
chromosome 4 open reading frame 31	C4orf31	3.174	0.02640	0.06588
chromosome 4 open reading frame 32	C4orf32	-2.482	0.00030	0.00380
chromosome 4 open reading frame 47	C4orf47	1.829	0.00083	0.00724
chromosome 4 open reading frame 48	C4orf48	2.132	0.00003	0.00090
chromosome 4 open reading frame 49	C4orf49	2.393	0.00061	0.00604
chromosome 5 open reading frame 13	C5orf13	3.136	0.00219	0.01340
chromosome 5 open reading frame 23	C5orf23	-6.946	0.00255	0.01464
chromosome 5 open reading frame 26	C5orf26	-1.681	0.00769	0.02972
chromosome 5 open reading frame 33	C5orf33	-1.975	0.00068	0.00646
chromosome 5 open reading frame 46	C5orf46	4.771	0.00071	0.00661
chromosome 5 open reading frame 54	C5orf54	1.820	0.00091	0.00772
chromosome 5 open reading frame 55	C5orf55	1.653	0.00061	0.00604
chromosome 6 open reading frame 105	C6orf105	2.735	0.00158	0.01090
chromosome 6 open reading frame 115	C6orf115	1.919	0.00034	0.00418
chromosome 6 open reading frame 170	C6orf170	1.624	0.00114	0.00890
chromosome 6 open reading frame 226	C6orf226	1.502	0.00002	0.00075

chromosome 6 open reading frame 64	C6orf64	1.864	0.00030	0.00382
chromosome 7 open reading frame 41	C7orf41	-2.083	0.00007	0.00154
chromosome 7 open reading frame 44	C7orf44	3.675	0.00001	0.00032
chromosome 7 open reading frame 55	C7orf55	-1.760	0.00106	0.00846
chromosome 7 open reading frame 58	C7orf58	-2.012	0.01290	0.04114
chromosome 7 open reading frame 68	C7orf68	1.916	0.00136	0.00990
chromosome 8 open reading frame 31	C8orf31	1.561	0.00013	0.00232
chromosome 8 open reading frame 4	C8orf4	-2.007	0.00633	0.02630
chromosome 8 open reading frame 46	C8orf46	-1.794	0.00631	0.02626
chromosome 8 open reading frame 48	C8orf48	1.908	0.00420	0.02026
chromosome 8 open reading frame 49	C8orf49	2.091	0.00685	0.02765
chromosome 8 open reading frame 84	C8orf84	-23.808	0.04170	0.08797
Chromosome 9 open reading frame 3	C9orf3	1.847	0.00757	0.02947
chromosome 9 open reading frame 30	C9orf30	1.545	0.00122	0.00926
chromosome 9 open reading frame 5	C9orf5	-1.888	0.00000	0.00029
chromosome 9 open reading frame 72	C9orf72	-2.093	0.00044	0.00491
chromosome X open reading frame 39	CXorf39	-3.227	0.00078	0.00695
churchill domain containing 1	CHURC1	-1.661	0.00146	0.01039
cingulin-like 1	CGNL1	1.707	0.00151	0.01062
citron (rho-interacting, serine/threonine kinase 21)	CIT	1.551	0.00048	0.00520
CKLF-like MARVEL transmembrane domain containing 5	CMTM5	1.623	0.00321	0.01702
claudin 1	CLDN1	4.269	0.00017	0.00269
claudin 23	CLDN23	1.708	0.01830	0.05201
claudin domain containing 1	CLDND1	-2.352	0.00956	0.03409
cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa	CSTF3	1.561	0.00631	0.02626
clusterin	CLU	1.560	0.00270	0.01517
c-mer proto-oncogene tyrosine kinase	MERTK	-2.842	0.00058	0.00584
CMT1A duplicated region transcript 4 /// family with sequence similarity 18, member B2	CDRT4 /// FAM18B2	1.670	0.00028	0.00362
c-myc binding protein	MYCBP	-1.790	0.04970	0.09810
coagulation factor C homolog, cochlin (Limulus polyphemus)	COCH	-1.631	0.02540	0.06425
coagulation factor II (thrombin) receptor-like 1	F2RL1	1.762	0.02700	0.06680
coagulation factor V (proaccelerin, labile factor)	F5	4.356	0.00016	0.00258
coenzyme Q2 homolog, prenyltransferase (yeast)	COQ2	-1.755	0.03890	0.08445
cofilin 2 (muscle)	CFL2	-3.134	0.01720	0.04983
coiled-coil and C2 domain containing 2A	CC2D2A	1.563	0.00672	0.02735
coiled-coil domain containing 102A	CCDC102A	1.567	0.00330	0.01731
coiled-coil domain containing 113	CCDC113	1.656	0.00134	0.00981
coiled-coil domain containing 121	CCDC121	1.728	0.00115	0.00894
coiled-coil domain containing 141	CCDC141	1.993	0.01150	0.03823
coiled-coil domain containing 142	CCDC142	1.531	0.00316	0.01683
coiled-coil domain containing 151	CCDC151	1.707	0.01490	0.04540
coiled-coil domain containing 28B	CCDC28B	2.008	0.00006	0.00147
coiled-coil domain containing 3	CCDC3	-2.644	0.02670	0.06637
coiled-coil domain containing 34	CCDC34	2.358	0.00042	0.00473
coiled-coil domain containing 68	CCDC68	-1.647	0.01680	0.04903
coiled-coil domain containing 74A /// coiled-coil domain containing 74B	CCDC74A /// CCDC74B	1.640	0.00007	0.00159
coiled-coil domain containing 8	CCDC8	2.440	0.00002	0.00080
coiled-coil domain containing 80	CCDC80	2.428	0.00018	0.00279
coiled-coil domain containing 89	CCDC89	2.339	0.00003	0.00090
coiled-coil domain containing 90B	CCDC90B	1.717	0.00024	0.00335

cold inducible RNA binding protein	CIRBP	1.730	0.02200	0.05858
cold shock domain containing C2, RNA binding	CSDC2	-3.928	0.00619	0.02595
cold shock domain protein A	CSDA	-1.636	0.00445	0.02101
collagen triple helix repeat containing 1	CTHRC1	2.103	0.00245	0.01431
collagen, type I, alpha 1	COL1A1	3.263	0.00033	0.00404
collagen, type I, alpha 2	COL1A2	1.891	0.00167	0.01128
collagen, type III, alpha 1	COL3A1	1.986	0.00038	0.00446
collagen, type IV, alpha 1	COL4A1	-1.734	0.02020	0.05546
collagen, type IV, alpha 2	COL4A2	-4.726	0.03590	0.08028
collagen, type IV, alpha 6	COL4A6	-12.752	0.03070	0.07266
collagen, type IX, alpha 2	COL9A2	2.104	0.00117	0.00904
collagen, type V, alpha 1	COL5A1	3.006	0.00097	0.00800
collagen, type V, alpha 2	COL5A2	1.874	0.00122	0.00926
collagen, type V, alpha 3	COL5A3	-1.523	0.04330	0.09004
collagen, type VI, alpha 1	COL6A1	1.556	0.00081	0.00717
collagen, type VIII, alpha 1	COL8A1	2.635	0.00358	0.01832
collagen, type VIII, alpha 2	COL8A2	1.785	0.00302	0.01633
collagen, type XII, alpha 1	COL12A1	1.657	0.01530	0.04618
collagen, type XIII, alpha 1	COL13A1	1.883	0.02070	0.05639
collagen, type XV, alpha 1	COL15A1	2.475	0.00001	0.00051
collagen, type XXVII, alpha 1	COL27A1	-3.364	0.00599	0.02542
colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	CSF2RA	-1.559	0.00335	0.01752
complement component 2	C2	2.275	0.00099	0.00811
complement component 2 /// complement factor B	C2 /// CFB	1.529	0.03400	0.07748
complement component 7	C7	-1.936	0.01940	0.05399
complement factor I	CFI	2.479	0.02720	0.06705
contactin 4	CNTN4	-4.756	0.03890	0.08445
contactin associated protein 1	CNTNAP1	2.145	0.00000	0.00009
core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1	C1GALT1	2.082	0.00015	0.00250
coronin 6	CORO6	-3.353	0.00005	0.00129
coronin, actin binding protein, 2A	CORO2A	1.643	0.00889	0.03267
coronin, actin binding protein, 2B	CORO2B	3.072	0.00001	0.00059
crystallin, alpha B	CRYAB	-2.341	0.00481	0.02219
CSRP2 binding protein	CSRP2BP	-1.534	0.01350	0.04247
CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	CTDSPL	-1.601	0.00058	0.00580
CTP synthase	CTPS	-9.726	0.00000	0.00006
C-type lectin domain family 11, member A	CLEC11A	1.891	0.00699	0.02804
C-type lectin domain family 2, member B	CLEC2B	3.867	0.00148	0.01047
C-type lectin domain family 4, member E	CLEC4E	-4.289	0.00010	0.00196
CUB and Sushi multiple domains 2	CSMD2	2.213	0.00043	0.00477
cubilin (intrinsic factor-cobalamin receptor)	CUBN	1.805	0.00683	0.02760
CUG triplet repeat, RNA binding protein 2	CUGBP2	-4.718	0.01060	0.03634
Cullin 1	CUL1	-1.738	0.00000	0.00009
cullin 3	CUL3	-1.661	0.00069	0.00648
CXXC finger 5	CXXC5	2.591	0.00016	0.00257
cyclin B1 interacting protein 1	CCNB1IP1	-1.679	0.00303	0.01637
cyclin D1	CCND1	1.811	0.00008	0.00176
cyclin D2	CCND2	1.603	0.01380	0.04312
cyclin D3	CCND3	-2.022	0.00615	0.02588
cyclin E2	CCNE2	-1.826	0.03040	0.07216

cyclin G2	CCNG2	-1.704	0.00042	0.00476
cyclin J-like	CCNJL	1.564	0.00000	0.00008
cyclin L1	CCNL1	-1.848	0.00096	0.00797
cyclin-dependent kinase 2 associated protein 1	CDK2AP1	1.587	0.00000	0.00018
cyclin-dependent kinase 2 associated protein 2	CDK2AP2	-1.588	0.02660	0.06620
cyclin-dependent kinase 6	CDK6	2.121	0.00070	0.00651
cyclin-dependent kinase inhibitor 1A (p21, Cip1)	CDKN1A	-1.952	0.00034	0.00417
cyclin-dependent kinase inhibitor 1C (p57, Kip2)	CDKN1C	-1.542	0.04020	0.08609
cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	CDKN2A	1.726	0.00528	0.02345
cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	CDKN2B	4.153	0.00617	0.02590
cystathionase (cystathionine gamma-lyase)	CTH	-2.860	0.00808	0.03069
cysteine and glycine-rich protein 1	CSRP1	-4.190	0.03170	0.07425
cysteine and glycine-rich protein 2	CSRP2	-5.148	0.00035	0.00420
cysteine and histidine-rich domain (CHORD)-containing 1	CHORDC1	-1.821	0.00027	0.00360
cysteine-rich hydrophobic domain 2	CHIC2	-1.625	0.00753	0.02935
cysteine-rich secretory protein LCCL domain containing 1	CRISPLD1	1.839	0.00057	0.00578
cysteine-rich, angiogenic inducer, 61	CYR61	-2.981	0.00008	0.00167
cysteine-serine-rich nuclear protein 1	CSRNP1	-4.055	0.00000	0.00026
cysteine-serine-rich nuclear protein 3	CSRNP3	1.626	0.00714	0.02839
cystin 1	CYS1	2.498	0.00003	0.00087
cytidine deaminase	CDA	1.654	0.00121	0.00921
cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial	CMPK2	2.242	0.00029	0.00378
cytochrome b-245, beta polypeptide	CYBB	2.133	0.02990	0.07135
cytochrome b-561	CYB561	2.118	0.00000	0.00009
cytochrome b-561 domain containing 2	CYB561D2	1.535	0.00759	0.02950
cytochrome c oxidase subunit VIIc	COX7C	-1.530	0.03040	0.07216
cytochrome c, somatic	CYCS	-3.835	0.00510	0.02296
cytochrome P450, family 1, subfamily B, polypeptide 1	CYP1B1	1.649	0.00653	0.02686
cytochrome P450, family 2, subfamily R, polypeptide 1	CYP2R1	1.607	0.00157	0.01086
cytochrome P450, family 27, subfamily C, polypeptide 1	CYP27C1	2.027	0.02770	0.06779
cytochrome P450, family 39, subfamily A, polypeptide 1	CYP39A1	1.835	0.01720	0.04983
cytochrome P450, family 4, subfamily B, polypeptide 1	CYP4B1	-30.142	0.00522	0.02330
cytochrome P450, family 4, subfamily V, polypeptide 2	CYP4V2	1.582	0.00014	0.00239
cytohesin 1 interacting protein	CYTIP	-3.948	0.00118	0.00907
cytohesin 4	CYTH4	1.641	0.01280	0.04091
cytoplasmic FMR1 interacting protein 2	CYFIP2	-11.394	0.01700	0.04945
cytoplasmic polyadenylation element binding protein 1	CPEB1	3.359	0.00001	0.00055
cytoplasmic polyadenylation element binding protein 4	CPEB4	-3.180	0.00526	0.02340
cytoskeleton-associated protein 4	CKAP4	1.558	0.00014	0.00240
D site of albumin promoter (albumin D-box) binding protein	DBP	4.033	0.00009	0.00181
DAB2 interacting protein	DAB2IP	1.668	0.01300	0.04135
dachsous 1 (Drosophila)	DCHS1	1.612	0.00010	0.00195
DALR anticodon binding domain containing 3	DALRD3	1.754	0.00000	0.00003
damage-specific DNA binding protein 2, 48kDa	DDB2	2.610	0.00034	0.00418
dapper, antagonist of beta-catenin, homolog 2 (Xenopus laevis)	DACT2	3.239	0.00599	0.02542
DCN1, defective in cullin neddylation 1, domain containing 3 (S. cerevisiae)	DCUN1D3	-1.981	0.00130	0.00963
DCP1 decapping enzyme homolog B (S. cerevisiae)	DCP1B	1.548	0.00221	0.01346
D-dopachrome tautomerase	DDT	-2.040	0.00004	0.00104
DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	DDX3X	-1.800	0.01530	0.04618
DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	DDX58	1.813	0.00739	0.02903
death-associated protein	DAP	1.717	0.00002	0.00082

death-associated protein kinase 2	DAPK2	-3.310	0.00769	0.02972
debranching enzyme homolog 1 (S. cerevisiae)	DBR1	1.589	0.00073	0.00668
dedicator of cytokinesis 3	DOCK3	-2.049	0.03580	0.08014
Dedicator of cytokinesis 5	DOCK5	-2.124	0.01620	0.04786
dedicator of cytokinesis 7	DOCK7	1.528	0.00019	0.00289
defective in sister chromatid cohesion 1 homolog (S. cerevisiae)	DSCC1	1.689	0.00031	0.00393
dehydrogenase E1 and transketolase domain containing 1	DHTKD1	-1.919	0.00129	0.00958
dehydrogenase/reductase (SDR family) member 13	DHRS13	1.581	0.00001	0.00047
deiodinase, iodothyronine, type II	DIO2	2.459	0.00000	0.00023
deleted in bladder cancer 1	DBC1	2.536	0.00352	0.01812
deltex 3-like (Drosophila)	DTX3L	1.581	0.00041	0.00471
DENN/MADD domain containing 1B	DENND1B	1.994	0.00040	0.00464
DENN/MADD domain containing 2A	DENND2A	1.965	0.00001	0.00049
deoxythymidylate kinase (thymidylate kinase)	DTYMK	1.512	0.00014	0.00238
DEP domain containing 7	DEPDC7	3.412	0.00002	0.00063
desmin	DES	-94.915	0.01040	0.03593
desmin /// family with sequence similarity 48, member A	DES /// FAM48A	-52.095	0.01090	0.03700
destrin (actin depolymerizing factor)	DSTN	-2.401	0.01100	0.03720
diaphanous homolog 2 (Drosophila)	DIAPH2	-1.816	0.01280	0.04091
dicarbonyl/L-xylulose reductase	DCXR	-2.579	0.00178	0.01173
dihydrofolate reductase	DHFR	1.508	0.01210	0.03950
dihydrofolate reductase-like 1	DHFRL1	1.622	0.00380	0.01904
dihydrolipoamide branched chain transacylase E2	DBT	-1.962	0.00124	0.00936
dihydrolipoamide dehydrogenase	DLD	-1.575	0.00206	0.01294
dihydropyrimidinase-like 3	DPYSL3	2.049	0.00000	0.00025
DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	DIMT1L	-1.682	0.00000	0.00014
dimethylarginine dimethylaminohydrolase 2	DDAH2	1.507	0.00051	0.00537
disabled homolog 1 (Drosophila)	DAB1	-37.200	0.01970	0.05447
disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	DAB2	2.100	0.00002	0.00077
discoidin, CUB and LCCL domain containing 1	DCBLD1	1.707	0.03320	0.07640
discs, large homolog 3 (Drosophila)	DLG3	1.626	0.00163	0.01112
dishevelled associated activator of morphogenesis 2	DAAM2	-1.592	0.02180	0.05821
disrupted in renal carcinoma 2	DIRC2	-1.531	0.04550	0.09277
DIX domain containing 1	DIXDC1	1.558	0.00198	0.01262
DKFZp451A211 protein	DKFZp451A211	-4.236	0.04900	0.09729
Dmx-like 2	DMXL2	1.586	0.00281	0.01557
DNA fragmentation factor, 40kDa, beta polypeptide (caspase-activated DNase)	DFFB	1.688	0.00056	0.00571
DNA-damage-inducible transcript 4	DDIT4	-9.198	0.00000	0.00030
DNA-damage-inducible transcript 4-like	DDIT4L	2.227	0.01690	0.04924
DnaJ (Hsp40) homolog, subfamily A, member 4	DNAJA4	-4.403	0.04740	0.09533
DnaJ (Hsp40) homolog, subfamily B, member 4	DNAJB4	-3.037	0.00007	0.00157
DnaJ (Hsp40) homolog, subfamily B, member 5	DNAJB5	-9.190	0.00792	0.03028
DnaJ (Hsp40) homolog, subfamily B, member 6 /// transmembrane protein 135	DNAJB6 /// TMEM135	-1.682	0.00006	0.00151
DnaJ (Hsp40) homolog, subfamily C, member 10	DNAJC10	1.528	0.00253	0.01458
DnaJ (Hsp40) homolog, subfamily C, member 12	DNAJC12	-1.561	0.01530	0.04618
DnaJ (Hsp40) homolog, subfamily C, member 21	DNAJC21	-1.516	0.02960	0.07084
DnaJ (Hsp40) homolog, subfamily C, member 22	DNAJC22	1.518	0.01430	0.04411
docking protein 4	DOK4	1.559	0.00063	0.00617
docking protein 5	DOK5	2.670	0.00020	0.00296
dolichol kinase	DOLK	1.523	0.00000	0.00009

dopey family member 2	DOPEY2	1.584	0.00003	0.00097
doublecortin-like kinase 1	DCLK1	1.884	0.01850	0.05236
DPH3, KTI11 homolog (S. cerevisiae)	DPH3	-2.271	0.00056	0.00573
drebrin 1	DBN1	2.496	0.00098	0.00805
dual oxidase 1	DUOX1	1.889	0.00081	0.00717
dual specificity phosphatase 1	DUSP1	-3.514	0.00000	0.00002
dual specificity phosphatase 18	DUSP18	1.777	0.00050	0.00534
dual specificity phosphatase 3	DUSP3	-4.941	0.04310	0.08982
dual specificity phosphatase 5	DUSP5	-10.551	0.02390	0.06178
dual specificity phosphatase 7	DUSP7	1.529	0.00018	0.00279
dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	DYRK2	1.713	0.00690	0.02776
dynamin 1	DNM1	2.224	0.00088	0.00753
dynamin 1-like	DNM1L	-1.760	0.00137	0.00994
dynein, axonemal, heavy chain 5	DNAH5	1.610	0.00053	0.00550
dyslexia susceptibility 1 candidate 1	DYX1C1	2.123	0.00162	0.01108
dystrobrevin, alpha	DTNA	-3.134	0.03100	0.07314
E2F transcription factor 3	E2F3	-2.038	0.00325	0.01716
E74-like factor 1 (ets domain transcription factor)	ELF1	-1.844	0.04030	0.08623
early B-cell factor 3	EBF3	2.699	0.00074	0.00672
Early growth response 1	EGR1	-3.482	0.00029	0.00377
early growth response 3	EGR3	-7.280	0.00005	0.00124
echinoderm microtubule associated protein like 1	EML1	2.447	0.00008	0.00174
ectonucleoside triphosphate diphosphohydrolase 1	ENTPD1	-11.764	0.00662	0.02710
EF-hand calcium binding domain 2	EFCAB2	-2.208	0.00126	0.00945
EF-hand domain (C-terminal) containing 1	EFHC1	1.552	0.01600	0.04748
EF-hand domain family, member A2	EFHA2	-1.536	0.00309	0.01657
EF-hand domain family, member D1	EFHD1	-13.945	0.00096	0.00795
EGF-like-domain, multiple 7	EGFL7	-2.082	0.01330	0.04210
elaC homolog 1 (E. coli)	ELAC1	1.506	0.00657	0.02697
elastin microfibril interfacer 3	EMILIN3	2.075	0.00769	0.02972
electron-transfer-flavoprotein, alpha polypeptide	ETFA	-1.607	0.02290	0.06004
electron-transferring-flavoprotein dehydrogenase	ETFDH	-2.046	0.02120	0.05716
ELK1, member of ETS oncogene family	ELK1	-1.655	0.00708	0.02826
ELK3, ETS-domain protein (SRF accessory protein 2)	ELK3	1.657	0.00310	0.01660
Ellis van Creveld syndrome	EVC	1.593	0.00312	0.01667
elongation factor RNA polymerase II-like 3 /// serine incorporator 4	ELL3 /// SERINC4	3.020	0.00000	0.00009
elongation factor, RNA polymerase II, 2	ELL2	-2.223	0.00002	0.00061
elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4	ELOVL4	1.682	0.01070	0.03655
ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)	ELOVL6	1.644	0.00003	0.00097
empty spiracles homeobox 2	EMX2	2.969	0.01220	0.03971
EMX2 opposite strand (non-protein coding)	EMX2OS	1.597	0.02970	0.07100
endothelial cell adhesion molecule	ESAM	-3.898	0.00411	0.01997
endothelin 1	EDN1	-4.750	0.04630	0.09383
endothelin receptor type A	EDNRA	-54.901	0.00868	0.03215
endothelin receptor type B	EDNRB	-5.096	0.00000	0.00032
Enhancer of polycomb homolog 1 (Drosophila)	EPC1	-2.627	0.04330	0.09004
enolase 2 (gamma, neuronal)	ENO2	1.592	0.00282	0.01559
enoyl Coenzyme A hydratase 1, peroxisomal	ECH1	-1.594	0.00269	0.01513
enoyl Coenzyme A hydratase domain containing 3	ECHDC3	-5.566	0.00323	0.01708
ependymin related protein 1 (zebrafish)	EPDR1	1.582	0.00250	0.01447

EPH receptor A3	EPHA3	1.671	0.04120	0.08727
EPH receptor A7	EPHA7	-5.606	0.01860	0.05251
EPH receptor B2	EPHB2	2.376	0.00002	0.00069
ephrin-A4	EFNA4	1.571	0.00001	0.00041
ephrin-A5	EFNA5	1.712	0.02970	0.07100
ephrin-B2	EFNB2	-6.601	0.00027	0.00356
epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	EGFR	-2.686	0.00000	0.00010
epidermal growth factor receptor pathway substrate 8	EPS8	-1.996	0.00000	0.00024
epithelial membrane protein 3	EMP3	2.625	0.00000	0.00029
EPS8-like 2	EPS8L2	2.570	0.00001	0.00036
ERBB receptor feedback inhibitor 1	ERRFI1	-4.905	0.00000	0.00002
ERO1-like (S. cerevisiae)	ERO1L	1.531	0.02240	0.05919
ERO1-like beta (S. cerevisiae)	ERO1LB	-1.725	0.00041	0.00468
erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)	EPB41	1.623	0.00000	0.00018
erythrocyte membrane protein band 4.1 like 4A	EPB41L4A	3.012	0.00007	0.00156
erythrocyte membrane protein band 4.1-like 3	EPB41L3	1.735	0.01210	0.03950
ethanolamine kinase 1	ETNK1	-1.784	0.00195	0.01252
ets variant 1	ETV1	1.681	0.00209	0.01304
Ets2 repressor factor	ERF	2.505	0.00010	0.00197
eukaryotic elongation factor-2 kinase	EEF2K	-1.512	0.01870	0.05269
eukaryotic translation elongation factor 1 alpha 1	EEF1A1	-1.743	0.00086	0.00739
eukaryotic translation elongation factor 1 beta 2	EEF1B2	-1.545	0.00007	0.00158
eukaryotic translation initiation factor 1	EIF1	-4.470	0.02300	0.06018
eukaryotic translation initiation factor 1A domain containing	EIF1AD	-1.596	0.00163	0.01112
eukaryotic translation initiation factor 1B	EIF1B	-1.608	0.00900	0.03290
eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	EIF2S1	-1.569	0.00022	0.00321
eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa	EIF2S3	-1.567	0.00404	0.01978
eukaryotic translation initiation factor 2-alpha kinase 1	EIF2AK1	1.561	0.00471	0.02186
eukaryotic translation initiation factor 2C, 2	EIF2C2	-1.829	0.00073	0.00670
eukaryotic translation initiation factor 3, subunit B	EIF3B	-1.809	0.01100	0.03720
Eukaryotic translation initiation factor 4A, isoform 1	EIF4A1	-3.699	0.02110	0.05698
eukaryotic translation initiation factor 4B	EIF4B	-1.755	0.00000	0.00022
eukaryotic translation initiation factor 5B	EIF5B	-1.546	0.01440	0.04432
excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)	ERCC1	1.551	0.00406	0.01982
exostoses (multiple) 1	EXT1	1.739	0.01700	0.04945
exportin 1 (CRM1 homolog, yeast)	XPO1	2.121	0.00127	0.00949
extracellular matrix protein 1	ECM1	3.148	0.00023	0.00328
ezrin	EZR	-2.411	0.00232	0.01383
family with sequence similarity 100, member B	FAM100B	-2.078	0.00122	0.00926
family with sequence similarity 101, member B	FAM101B	-1.923	0.00364	0.01852
family with sequence similarity 102, member A	FAM102A	1.963	0.00000	0.00018
family with sequence similarity 102, member B	FAM102B	2.299	0.00000	0.00002
family with sequence similarity 108, member B1	FAM108B1	-1.562	0.00037	0.00437
family with sequence similarity 109, member B	FAM109B	1.622	0.00030	0.00383
family with sequence similarity 110, member B	FAM110B	2.027	0.00179	0.01177
family with sequence similarity 110, member C	FAM110C	-3.893	0.01410	0.04372
family with sequence similarity 114, member A1	FAM114A1	1.766	0.00001	0.00040
family with sequence similarity 117, member A	FAM117A	1.531	0.01350	0.04247
family with sequence similarity 118, member B	FAM118B	1.969	0.00003	0.00101
family with sequence similarity 119, member B	FAM119B	2.408	0.00023	0.00326

Family with sequence similarity 124A	FAM124A	1.833	0.00005	0.00132
family with sequence similarity 13, member C	FAM13C	1.959	0.00206	0.01294
family with sequence similarity 131, member A	FAM131A	-1.658	0.00000	0.00020
family with sequence similarity 133, member A	FAM133A	3.820	0.00031	0.00389
family with sequence similarity 133, member B	FAM133B	-1.557	0.00003	0.00101
family with sequence similarity 149, member A	FAM149A	1.878	0.03520	0.07911
family with sequence similarity 150, member B	FAM150B	-2.483	0.00202	0.01279
family with sequence similarity 167, member A	FAM167A	3.453	0.00017	0.00274
family with sequence similarity 171, member A1	FAM171A1	1.880	0.00002	0.00065
family with sequence similarity 171, member B	FAM171B	1.556	0.01630	0.04803
family with sequence similarity 174, member B	FAM174B	1.686	0.00192	0.01240
family with sequence similarity 178, member A	FAM178A	1.535	0.00069	0.00648
family with sequence similarity 181, member B	FAM181B	2.218	0.00656	0.02694
family with sequence similarity 189, member A2	FAM189A2	1.868	0.00061	0.00603
family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	FAM19A5	-4.035	0.02320	0.06052
family with sequence similarity 20, member C	FAM20C	1.587	0.00056	0.00573
family with sequence similarity 3, member B	FAM3B	2.793	0.00001	0.00035
family with sequence similarity 43, member B	FAM43B	3.933	0.00000	0.00012
family with sequence similarity 45, member A /// family with sequence similarity 45, member A pseudogene	FAM45A /// FAM45B	1.668	0.00597	0.02537
family with sequence similarity 46, member C	FAM46C	1.952	0.00002	0.00067
family with sequence similarity 5, member C	FAM5C	4.383	0.00259	0.01478
family with sequence similarity 57, member A	FAM57A	2.581	0.00003	0.00094
family with sequence similarity 65, member B	FAM65B	-4.238	0.01010	0.03532
Family with sequence similarity 7, member A3	FAM7A3	1.666	0.03410	0.07762
family with sequence similarity 70, member A	FAM70A	-3.376	0.01230	0.03990
family with sequence similarity 83, member D	FAM83D	-23.930	0.02450	0.06273
family with sequence similarity 84, member B	FAM84B	1.543	0.04570	0.09307
Family with sequence similarity 98, member A	FAM98A	1.727	0.02260	0.05950
Fanconi anemia, complementation group F	FANCF	2.092	0.00000	0.00024
Far upstream element (FUSE) binding protein 1	FUBP1	1.534	0.00430	0.02058
Fas (TNF receptor superfamily, member 6)	FAS	1.553	0.04430	0.09121
fasciculation and elongation protein zeta 1 (zygin I)	FEZ1	1.615	0.00001	0.00044
fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	FSCN1	3.228	0.00000	0.00003
FAT tumor suppressor homolog 1 (Drosophila)	FAT1	1.892	0.00012	0.00226
FAT tumor suppressor homolog 3 (Drosophila)	FAT3	-41.853	0.01180	0.03884
FAT tumor suppressor homolog 4 (Drosophila)	FAT4	1.788	0.00006	0.00148
fatty acid binding protein 5 (psoriasis-associated)	FABP5	2.740	0.00330	0.01731
Fatty acyl CoA reductase 2	FAR2	-1.517	0.04580	0.09320
FBJ murine osteosarcoma viral oncogene homolog	FOS	-10.786	0.00002	0.00066
FBJ murine osteosarcoma viral oncogene homolog B	FOSB	-60.030	0.00105	0.00840
F-box and leucine-rich repeat protein 14	FBXL14	1.607	0.00089	0.00762
F-box and leucine-rich repeat protein 16	FBXL16	3.785	0.02210	0.05872
F-box and leucine-rich repeat protein 22	FBXL22	-8.710	0.04990	0.09837
F-box and WD repeat domain containing 2	FBXW2	1.516	0.00115	0.00894
F-box protein 2	FBXO2	2.163	0.00172	0.01151
F-box protein 30	FBXO30	-1.737	0.00019	0.00290
F-box protein 32	FBXO32	-7.178	0.00802	0.03055
F-box protein 42	FBXO42	-1.916	0.01260	0.04051
Fc fragment of IgG binding protein	FCGBP	10.323	0.02700	0.06680
Fc fragment of IgG, high affinity Ia, receptor (CD64) /// Fc fragment of	FCGR1A ///	3.110	0.01710	0.04964

IgG, high affinity Ic, receptor (CD64)	FCGR1C			
fem-1 homolog b (C. elegans)	FEM1B	-1.699	0.00882	0.03253
fem-1 homolog c (C. elegans)	FEM1C	-2.193	0.00021	0.00307
FERM domain containing 4B	FRMD4B	2.755	0.00003	0.00099
FERM domain containing 5	FRMD5	4.951	0.00023	0.00323
FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	FARP1	1.529	0.00498	0.02264
fermitin family homolog 1 (Drosophila)	FERMT1	3.110	0.00002	0.00076
fermitin family homolog 2 (Drosophila)	FERMT2	-1.612	0.00003	0.00090
ferredoxin 1	FDX1	-1.598	0.04180	0.08811
ferredoxin reductase	FDXR	2.055	0.00000	0.00008
FGFR1 oncogene partner 2	FGFR1OP2	-1.563	0.00118	0.00907
fibrillin 1	FBN1	2.049	0.00204	0.01287
fibrinogen-like 2	FGL2	1.795	0.00460	0.02152
fibroblast activation protein, alpha	FAP	3.726	0.00025	0.00338
fibroblast growth factor 14	FGF14	3.967	0.00000	0.00021
fibroblast growth factor 18	FGF18	1.649	0.00095	0.00792
fibroblast growth factor 2 (basic)	FGF2	1.876	0.00002	0.00073
fibroblast growth factor 9 (glia-activating factor)	FGF9	9.607	0.00018	0.00285
fibroblast growth factor binding protein 3	FGFBP3	2.642	0.00000	0.00010
fibroblast growth factor receptor 2	FGFR2	1.633	0.02690	0.06663
fibronectin 1	FN1	4.749	0.00043	0.00478
Fibronectin leucine rich transmembrane protein 2	FLRT2	2.625	0.01170	0.03865
fibronectin type III and SPRY domain containing 1-like	FSD1L	1.519	0.00733	0.02889
fibronectin type III domain containing 1	FNDC1	2.611	0.00063	0.00614
fibronectin type III domain containing 7	FNDC7	1.560	0.00449	0.02114
fibulin 2	FBLN2	2.136	0.00039	0.00454
fidgetin-like 1	FIGNL1	1.669	0.00382	0.01912
filamin B, beta	FLNB	-2.010	0.00070	0.00651
filamin binding LIM protein 1	FBLIM1	-8.721	0.00052	0.00548
FK506 binding protein 10, 65 kDa	FKBP10	1.573	0.00876	0.03237
FK506 binding protein 11, 19 kDa	FKBP11	1.612	0.00530	0.02350
FK506 binding protein 14, 22 kDa	FKBP14	3.004	0.00084	0.00731
FK506 binding protein 1B, 12.6 kDa	FKBP1B	1.967	0.00033	0.00409
FK506 binding protein 4, 59kDa	FKBP4	-1.566	0.00989	0.03483
FK506 binding protein 5	FKBP5	-13.777	0.00013	0.00229
FLJ41603 protein	FLJ41603	2.215	0.00006	0.00145
fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	FLT1	-5.870	0.02700	0.06680
folliculin	FLCN	1.595	0.02470	0.06310
forkhead box D1	FOXD1	2.369	0.01650	0.04846
forkhead box F2	FOXF2	1.872	0.00125	0.00941
forkhead box G1	FOXG1	-17.482	0.01530	0.04618
forkhead box N2	FOXN2	-1.870	0.00000	0.00016
forkhead box N3	FOXN3	-1.625	0.00058	0.00585
forkhead box O1	FOXO1	-2.362	0.00399	0.01960
forkhead box O3	FOXO3	-2.443	0.00085	0.00736
forkhead box O3 /// forkhead box O3B pseudogene	FOXO3 /// FOXO3B	-3.272	0.00001	0.00055
forkhead box O6	FOXO6	1.517	0.00048	0.00522
formin-like 2	FMNL2	-3.277	0.04210	0.08854
FOS-like antigen 2	FOSL2	-3.065	0.00000	0.00005
four and a half LIM domains 5	FHL5	-99.781	0.01270	0.04072

four jointed box 1 (Drosophila)	FJX1	3.676	0.00017	0.00270
fragile X mental retardation, autosomal homolog 1	FXR1	-1.520	0.01740	0.05024
FRAS1 related extracellular matrix 1	FREM1	2.034	0.00982	0.03466
Fraser syndrome 1	FRAS1	2.322	0.02090	0.05673
frizzled homolog 10 (Drosophila)	FZD10	2.767	0.00149	0.01052
frizzled homolog 2 (Drosophila)	FZD2	2.916	0.00087	0.00744
frizzled homolog 5 (Drosophila)	FZD5	-2.009	0.00023	0.00328
frizzled homolog 7 (Drosophila)	FZD7	1.582	0.01500	0.04561
frizzled homolog 8 (Drosophila)	FZD8	2.257	0.00061	0.00604
Frizzled-related protein	FRZB	1.719	0.01270	0.04072
FRY-like	FRYL	-3.652	0.01780	0.05103
fucosidase, alpha-L- 2, plasma	FUCA2	1.668	0.00005	0.00120
fucosyltransferase 11 (alpha (1,3) fucosyltransferase)	FUT11	2.060	0.00004	0.00117
fucosyltransferase 8 (alpha (1,6) fucosyltransferase)	FUT8	1.921	0.00033	0.00408
fukutin related protein	FKRP	-2.077	0.00058	0.00583
FXYD domain containing ion transport regulator 5	FXYD5	2.278	0.00102	0.00824
FYVE, RhoGEF and PH domain containing 2	FGD2	-2.045	0.03540	0.07942
FYVE, RhoGEF and PH domain containing 4	FGD4	-2.129	0.00000	0.00009
G protein-coupled estrogen receptor 1	GPER	2.011	0.00003	0.00095
G protein-coupled receptor 116	GPR116	-3.728	0.00638	0.02643
G protein-coupled receptor 125	GPR125	1.590	0.00036	0.00433
G protein-coupled receptor 126	GPR126	-2.815	0.00583	0.02502
G protein-coupled receptor 137C	GPR137C	1.579	0.00898	0.03285
G protein-coupled receptor 153	GPR153	1.712	0.02660	0.06620
G protein-coupled receptor 157	GPR157	2.078	0.00000	0.00004
G protein-coupled receptor 158	GPR158	2.783	0.00835	0.03134
G protein-coupled receptor 162 /// leprecan-like 2	GPR162 /// LEPREL2	2.305	0.00000	0.00010
G protein-coupled receptor 183	GPR183	-14.955	0.00000	0.00025
G protein-coupled receptor 68	GPR68	1.535	0.02830	0.06878
G protein-coupled receptor 83	GPR83	3.422	0.00473	0.02192
G protein-coupled receptor 88	GPR88	-3.381	0.00415	0.02011
G protein-coupled receptor, family C, group 5, member A	GPRC5A	1.505	0.01280	0.04091
G protein-coupled receptor, family C, group 5, member C	GPRC5C	-2.097	0.01240	0.04009
G0/G1switch 2	G0S2	3.583	0.00044	0.00488
G1 to S phase transition 1	GSPT1	-2.080	0.03610	0.08054
GABA(A) receptor-associated protein like 1	GABARAPL1	-2.185	0.00071	0.00658
GABA(A) receptor-associated protein like 1 /// GABA(A) receptors associated protein like 3 (pseudogene)	GABARAPL1 /// GABARAPL3	-1.894	0.00405	0.01981
galactose mutarotase (aldose 1-epimerase)	GALM	2.977	0.00001	0.00046
galactose-3-O-sulfotransferase 4	GAL3ST4	2.036	0.00000	0.00009
gamma-aminobutyric acid (GABA) A receptor, epsilon	GABRE	-1.911	0.00893	0.03275
gamma-glutamyl carboxylase	GGCX	1.775	0.00095	0.00791
gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)	GGH	1.628	0.04240	0.08892
gamma-glutamyltransferase 1	GGT1	2.277	0.00010	0.00193
gamma-glutamyltransferase 1 /// gamma-glutamyltransferase 2 /// gamma-glutamyltransferase 3 pseudogene /// gamma-glutamyltransferase light chain 2 /// gamma-glutamyltransferase light chain 3	GGT1 /// GGT2 /// GGT3P /// GGTLC2 /// GGTLC3	1.786	0.00007	0.00156
gamma-glutamyltransferase 5	GGT5	-3.211	0.00000	0.00018
gap junction protein, alpha 4, 37kDa	GJA4	-2.689	0.00069	0.00648
gap junction protein, alpha 5, 40kDa	GJA5	-1.680	0.04510	0.09228
gap junction protein, gamma 1, 45kDa	GJC1	-2.418	0.01160	0.03843

Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog	FGR	-2.285	0.00747	0.02923
GATA binding protein 3	GATA3	2.043	0.02110	0.05698
GATA binding protein 5	GATA5	2.233	0.00032	0.00403
GATS protein-like 3 /// TBC1 domain family, member 10A	GATSL3 /// TBC1D10A	-1.717	0.03650	0.08111
general transcription factor IIA, 1-like /// stonin 1 /// STON1-GTF2A1L readthrough transcript	GTF2A1L /// STON1 /// STON1-GTF2A1L	-2.254	0.01520	0.04600
general transcription factor IIIA	GTF3A	2.891	0.00001	0.00058
GLI family zinc finger 2	GLI2	3.301	0.00000	0.00002
GLI family zinc finger 3	GLI3	1.777	0.00375	0.01887
GLI pathogenesis-related 2	GLIPR2	1.758	0.00034	0.00413
glia maturation factor, beta	GMFB	-1.840	0.01200	0.03929
glioblastoma amplified sequence	GBAS	-2.167	0.04560	0.09293
GLIS family zinc finger 2	GLIS2	2.594	0.00001	0.00047
GLIS family zinc finger 3	GLIS3	1.745	0.01140	0.03802
glucocorticoid modulatory element binding protein 1	GMEB1	1.578	0.00377	0.01894
glucosaminyl (N-acetyl) transferase 1, core 2 (beta-1,6-N-acetylglucosaminyltransferase)	GCNT1	1.736	0.00500	0.02269
glucose-fructose oxidoreductase domain containing 1	GFOD1	-6.230	0.00000	0.00006
glucosidase, alpha; acid	GAA	1.521	0.00907	0.03304
glucosidase, beta; acid (includes glucosylceramidase) /// glucosidase, beta; acid, pseudogene	GBA /// GBAP	2.040	0.00027	0.00358
glucosidase, beta; acid, pseudogene	GBAP	1.501	0.00018	0.00285
glucuronic acid epimerase	GLCE	2.088	0.00017	0.00273
glucuronidase, beta pseudogene	LOC653188	1.955	0.00464	0.02164
glucuronidase, beta pseudogene /// glucuronidase, beta pseudogene	SMA4 /// SMA5	1.691	0.03810	0.08337
glutamate dehydrogenase 1	GLUD1	2.339	0.00050	0.00532
glutamate receptor, ionotrophic, AMPA 3	GRIA3	1.912	0.00758	0.02948
glutamate-ammonia ligase (glutamine synthetase)	GLUL	-6.102	0.00066	0.00629
glutamate-rich 1	ERICH1	-1.607	0.00053	0.00553
glutamine-fructose-6-phosphate transaminase 2	GFPT2	2.017	0.02270	0.05971
glutamyl aminopeptidase (aminopeptidase A)	ENPEP	-22.483	0.03820	0.08346
glutaredoxin (thioltransferase)	GLRX	-2.397	0.00489	0.02244
glutaryl-Coenzyme A dehydrogenase	GCDH	-2.152	0.00025	0.00339
glutathione peroxidase 3 (plasma)	GPX3	-3.234	0.00005	0.00132
glutathione peroxidase 8 (putative)	GPX8	2.279	0.00001	0.00033
glutathione S-transferase mu 3 (brain)	GSTM3	-2.383	0.00112	0.00881
glycerol-3-phosphate acyltransferase 2, mitochondrial	GPAT2	1.910	0.01840	0.05217
glycerol-3-phosphate acyltransferase, mitochondrial	GPAM	2.405	0.01250	0.04030
glycerophosphodiester phosphodiesterase domain containing 1	GDPD1	2.041	0.00000	0.00018
glycerophosphodiester phosphodiesterase domain containing 5	GDPD5	1.942	0.00807	0.03068
glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzyme A ligase)	GCAT	-2.366	0.00955	0.03406
glycine-N-acyltransferase-like 2	GLYATL2	1.696	0.03040	0.07216
glycogen synthase 1 (muscle)	GYS1	-2.919	0.00681	0.02756
glycoprotein M6A	GPM6A	1.752	0.02640	0.06588
glycoprotein, alpha-galactosyltransferase 1	GGTA1	-1.740	0.00165	0.01120
glycosyltransferase 25 domain containing 2	GLT25D2	3.213	0.00018	0.00282
glyoxylate reductase 1 homolog (Arabidopsis) /// septin 6	GLYR1 /// SEPT6	1.975	0.00003	0.00097
golgi associated, gamma adaptin ear containing, ARF binding protein 2	GGA2	1.580	0.00044	0.00491
golgi autoantigen, golgin subfamily a, 1	GOLGA1	1.599	0.00004	0.00109
golgi autoantigen, golgin subfamily a, 8A	GOLGA8A	-2.883	0.03680	0.08151

golgi autoantigen, golgin subfamily a, 8B	GOLGA8B	-1.835	0.01120	0.03762
golgi membrane protein 1	GOLM1	1.655	0.00948	0.03394
Golgi-localized protein	GOLSYN	-2.117	0.01470	0.04495
golgin, RAB6-interacting	GORAB	1.738	0.00000	0.00013
GPN-loop GTPase 3	GPN3	-1.665	0.00031	0.00394
GRAM domain containing 2	GRAMD2	2.510	0.00013	0.00232
GRAM domain containing 3	GRAMD3	-2.444	0.01570	0.04695
GRAM domain containing 4	GRAMD4	1.827	0.00003	0.00089
granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)	GZMA	-1.722	0.04080	0.08683
granzyme K (granzyme 3; tryptase II)	GZMK	-2.822	0.01370	0.04289
GREB1 protein	GREB1	3.253	0.00000	0.00002
growth arrest and DNA-damage-inducible, alpha	GADD45A	-2.679	0.00000	0.00012
growth arrest and DNA-damage-inducible, beta	GADD45B	-6.548	0.00000	0.00003
growth arrest and DNA-damage-inducible, gamma	GADD45G	-5.552	0.00200	0.01271
Growth arrest-specific 2 like 3	GAS2L3	1.593	0.03640	0.08095
growth arrest-specific 5 (non-protein coding)	GAS5	-2.018	0.00014	0.00242
growth arrest-specific 7	GAS7	1.860	0.00250	0.01447
growth associated protein 43	GAP43	6.782	0.00006	0.00145
growth differentiation factor 1 /// LAG1 homolog, ceramide synthase 1	GDF1 /// LASS1	4.458	0.00000	0.00016
growth differentiation factor 15 /// similar to growth differentiation factor 15	GDF15 /// LOC100292463	1.627	0.00277	0.01539
growth hormone regulated TBC protein 1	GRTP1	1.707	0.00803	0.03057
GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein	GRASP	-1.727	0.00118	0.00907
GrpE-like 1, mitochondrial (E. coli)	GRPEL1	-1.709	0.01120	0.03762
GTF2I repeat domain containing 2	GTF2IRD2	-1.801	0.00126	0.00945
GTP cyclohydrolase 1	GCH1	-5.575	0.00202	0.01279
GTPase, IMAP family member 2	GIMAP2	1.540	0.02970	0.07100
guanine nucleotide binding protein (G protein), alpha 14	GNA14	4.310	0.00000	0.00008
guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O	GNAO1	1.599	0.00902	0.03294
guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type	GNAL	1.744	0.00530	0.02350
guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	GNAI1	-2.642	0.00530	0.02350
guanine nucleotide binding protein (G protein), alpha z polypeptide	GNAZ	3.244	0.00001	0.00051
guanine nucleotide binding protein (G protein), gamma 2	GNG2	2.840	0.00065	0.00626
guanylate binding protein 4	GBP4	2.063	0.00082	0.00720
hairless homolog (mouse)	HR	1.571	0.00207	0.01298
hairy/enhancer-of-split related with YRPW motif 1	HEY1	-7.807	0.02960	0.07084
hairy/enhancer-of-split related with YRPW motif-like	HEYL	-1.972	0.00106	0.00846
haptoglobin	HP	-2.209	0.00854	0.03178
haptoglobin /// haptoglobin-related protein	HP /// HPR	-4.674	0.00012	0.00218
haptoglobin-related protein	HPR	-5.107	0.00106	0.00846
HAUS augmin-like complex, subunit 5	HAUS5	1.592	0.00042	0.00475
HCCA2 protein	HCCA2	-1.919	0.02580	0.06489
hCG1645220	hCG_1645220	2.083	0.00304	0.01640
heat shock 105kDa/110kDa protein 1	HSPH1	-2.348	0.03900	0.08452
heat shock 22kDa protein 8	HSPB8	-6.049	0.00491	0.02249
heat shock 27kDa protein 1	HSPB1	-2.345	0.01830	0.05201
heat shock 27kDa protein 3	HSPB3	-69.738	0.03420	0.07775
heat shock 27kDa protein family, member 7 (cardiovascular)	HSPB7	-20.833	0.01350	0.04247
heat shock 60kDa protein 1 (chaperonin)	HSPD1	-1.794	0.00374	0.01883

heat shock 70kDa protein 12A	HSPA12A	3.494	0.00000	0.00014
heat shock 70kDa protein 1A	HSPA1A	-1.626	0.01690	0.04924
heat shock 70kDa protein 1A /// heat shock 70kDa protein 1B	HSPA1A /// HSPA1B	-1.688	0.02930	0.07040
heat shock 70kDa protein 4-like	HSPA4L	2.112	0.00074	0.00671
heat shock 70kDa protein 9 (mortalin)	HSPA9	-1.579	0.00607	0.02567
heat shock protein, alpha-crystallin-related, B6	HSPB6	-3.431	0.03300	0.07609
heat-responsive protein 12	HRSP12	-1.717	0.02290	0.06004
hect domain and RLD 6	HERC6	1.521	0.02970	0.07100
HECT domain containing 2	HECTD2	1.505	0.01300	0.04135
HEG homolog 1 (zebrafish)	HEG1	1.574	0.03760	0.08263
helicase, lymphoid-specific	HELLS	1.541	0.00426	0.02045
hematopoietic cell-specific Lyn substrate 1	HCLS1	-3.155	0.00057	0.00574
hematopoietic prostaglandin D synthase	HPGDS	4.839	0.00018	0.00285
hematopoietically expressed homeobox	HHEX	2.132	0.02750	0.06753
heme binding protein 2	HEBP2	-1.673	0.00051	0.00538
heme oxygenase (decycling) 2	HMOX2	-1.511	0.03830	0.08355
hemochromatosis	HFE	1.885	0.00301	0.01629
heparan sulfate 2-O-sulfotransferase 1	HS2ST1	2.439	0.00126	0.00945
heparan sulfate 2-O-sulfotransferase 1 /// hypothetical LOC339524	HS2ST1 /// LOC339524	2.220	0.02250	0.05936
heparan-alpha-glucosaminide N-acetyltransferase	HGSNAT	1.797	0.00010	0.00193
heparin-binding EGF-like growth factor	HBEGF	-2.314	0.04140	0.08751
hepatic leukemia factor	HLF	2.339	0.00523	0.02333
hepatocellular carcinoma-related HCRP1	HCRP1	1.604	0.00194	0.01249
hepatocyte growth factor (hepapoietin A; scatter factor)	HGF	2.119	0.00134	0.00981
heterochromatin protein 1, binding protein 3	HP1BP3	-1.534	0.01020	0.03553
heterogeneous nuclear ribonucleoprotein D-like	HNRPDL	-1.612	0.00082	0.00720
heterogeneous nuclear ribonucleoprotein H1 (H)	HNRNPH1	-1.695	0.04130	0.08737
HHIP-like 2	HHIPL2	1.615	0.00090	0.00762
HIG1 hypoxia inducible domain family, member 1A	HIGD1A	-1.677	0.00453	0.02128
high-mobility group box 2	HMGB2	-1.682	0.00090	0.00766
hippocalcin like 4	HPCAL4	-1.782	0.00503	0.02278
histamine receptor H1	HRH1	5.081	0.00002	0.00079
histone cluster 1, H1c	HIST1H1C	-1.884	0.03560	0.07979
histone cluster 1, H2bc	HIST1H2BC	1.543	0.00738	0.02900
histone cluster 1, H2bh	HIST1H2BH	1.538	0.00198	0.01262
histone cluster 2, H2aa3 /// histone cluster 2, H2aa4	HIST2H2AA3 /// HIST2H2AA4	-2.223	0.00096	0.00793
histone cluster 2, H2be	HIST2H2BE	-9.464	0.00220	0.01343
histone deacetylase 4	HDAC4	1.571	0.00003	0.00100
histone deacetylase 8	HDAC8	-1.762	0.00145	0.01036
histone deacetylase 9	HDAC9	-9.433	0.00832	0.03129
HLA complex group 27	HCG27	1.619	0.00058	0.00582
HMG-box transcription factor 1	HBP1	-3.878	0.00587	0.02512
homeodomain interacting protein kinase 2	HIPK2	-3.512	0.00000	0.00006
homer homolog 1 (Drosophila)	HOMER1	-6.965	0.01950	0.05408
homer homolog 3 (Drosophila)	HOMER3	1.652	0.00032	0.00402
homolog of rat pragma of Rnd2	PRAGMIN	1.603	0.00924	0.03338
HOP homeobox	HOPX	-20.058	0.00436	0.02075
hormonally up-regulated Neu-associated kinase	HUNK	1.759	0.00592	0.02522
HtrA serine peptidase 3	HTRA3	3.144	0.00046	0.00506
human immunodeficiency virus type I enhancer binding protein 3	HIVEP3	1.505	0.01540	0.04633

huntingtin interacting protein 1 related /// similar to KIAA0655 protein	HIP1R /// LOC100294412	-1.941	0.00033	0.00405
hyaluronan and proteoglycan link protein 1	HAPLN1	1.947	0.00591	0.02520
hyaluronan synthase 1	HAS1	1.717	0.03360	0.07693
Hyaluronan synthase 2	HAS2	2.497	0.00347	0.01794
hydroxyacyl-Coenzyme A dehydrogenase	HADH	-1.713	0.00462	0.02157
hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	HSD3B7	2.097	0.00001	0.00040
hydroxysteroid (17-beta) dehydrogenase 1	HSD17B1	1.510	0.00176	0.01166
hydroxysteroid dehydrogenase like 2	HSDL2	-1.531	0.04990	0.09837
hyperpolarization activated cyclic nucleotide-gated potassium channel 1	HCN1	1.781	0.04130	0.08737
hypothetical FLJ11235	FLJ11235	3.082	0.00000	0.00003
hypothetical FLJ39739	FLJ39739	1.593	0.00008	0.00170
hypothetical gene supported by AK022396; AK097927	FLJ12334	2.047	0.00244	0.01428
Hypothetical gene supported by AK096370	FLJ39051	1.948	0.00022	0.00315
hypothetical gene supported by AK124342 /// hypothetical LOC100131455	FLJ42351 /// LOC100131455	1.915	0.00000	0.00010
Hypothetical gene supported by BC043549; BX648102	DKFZp686O1327	1.878	0.01630	0.04803
Hypothetical gene supported by BX647608	LOC399959	1.876	0.01030	0.03574
hypothetical LOC100126784	LOC100126784	-2.807	0.00732	0.02887
hypothetical LOC100128239	LOC100128239	2.341	0.00003	0.00091
hypothetical LOC100132707	LOC100132707	1.574	0.01990	0.05490
hypothetical LOC100190986	LOC100190986	-1.723	0.04550	0.09277
hypothetical LOC100216479	LOC100216479	2.780	0.00011	0.00207
hypothetical LOC100216546	LOC100216546	1.758	0.04340	0.09014
hypothetical LOC100271722	hCG_2039027	1.711	0.01220	0.03971
hypothetical LOC100272216	LOC100272216	1.867	0.01550	0.04653
hypothetical LOC100272216 /// hypothetical protein LOC100292101	LOC100272216 /// LOC100292101	2.342	0.00215	0.01325
hypothetical LOC100272217	LOC100272217	1.701	0.00229	0.01371
hypothetical LOC100302650 /// ribokinase	LOC100302650 /// RBKS	-5.366	0.00349	0.01800
hypothetical LOC145788	FLJ27352	1.645	0.00021	0.00303
Hypothetical LOC150538	FLJ32063	2.602	0.00000	0.00018
hypothetical LOC151009	LOC151009	2.494	0.00004	0.00109
hypothetical LOC154761	LOC154761	2.551	0.00029	0.00377
hypothetical LOC253039	LOC253039	2.167	0.00436	0.02075
hypothetical LOC255031	FLJ35390	1.647	0.00197	0.01259
hypothetical LOC25845	LOC25845	1.613	0.00009	0.00179
hypothetical LOC283174	LOC283174	1.813	0.00099	0.00811
hypothetical LOC284297	LOC284297	2.201	0.00013	0.00233
hypothetical LOC284837	LOC284837	1.728	0.00160	0.01100
hypothetical LOC344595	LOC344595	1.798	0.00095	0.00791
hypothetical LOC378805	FLJ43663	-3.068	0.00497	0.02262
hypothetical LOC399753	RP11-144G6.7	1.672	0.01530	0.04618
hypothetical LOC400043	LOC400043	1.861	0.01080	0.03676
hypothetical LOC401093	hCG_1806964	-16.657	0.00627	0.02614
hypothetical LOC440465	FLJ90757	2.034	0.00127	0.00949
hypothetical LOC440944	LOC440944	1.687	0.00028	0.00365
hypothetical LOC441094	FLJ42709	2.725	0.00459	0.02149
hypothetical LOC441461	LOC441461	1.812	0.00007	0.00156
hypothetical LOC541471 /// non-protein coding RNA 152	LOC541471 /// NCRNA00152	1.641	0.01580	0.04710

hypothetical LOC54744	DKFZp566H0824	-1.642	0.02550	0.06439
Hypothetical LOC642477	FLJ39632	2.236	0.00749	0.02927
hypothetical LOC642477 /// hypothetical LOC400879	FLJ39632 /// LOC400879	2.021	0.00521	0.02327
hypothetical LOC642852	LOC642852	1.587	0.02340	0.06090
hypothetical LOC642946	LQK1	2.105	0.00552	0.02418
Hypothetical LOC643517	LOC643517	1.519	0.00282	0.01559
hypothetical LOC643733	LOC643733	1.511	0.03770	0.08278
hypothetical LOC643837	LOC643837	-2.339	0.01920	0.05365
hypothetical LOC645722	LOC645722	-3.473	0.00902	0.03294
hypothetical LOC647115	FLJ36848	-1.546	0.02110	0.05698
hypothetical LOC650669	FLJ41484	8.141	0.00000	0.00007
Hypothetical LOC728264	LOC728264	-15.804	0.01950	0.05408
Hypothetical LOC728431	LOC728431	2.125	0.00000	0.00021
hypothetical LOC729580	LOC729580	-1.659	0.00036	0.00428
Hypothetical LOC730057	LOC730057	-3.257	0.00567	0.02460
hypothetical LOC730101	LOC730101	2.046	0.00028	0.00369
hypothetical LOC730236	LOC730236	1.636	0.00084	0.00733
hypothetical LOC84856	LOC84856	3.683	0.00072	0.00665
hypothetical LOC84989	LOC84989	1.542	0.01940	0.05399
hypothetical protein DKFZp667E0512	DKFZp667E0512	-1.695	0.00914	0.03316
hypothetical protein FLJ10357	FLJ10357	1.942	0.00001	0.00040
hypothetical protein FLJ22167	FLJ22167	2.999	0.00000	0.00017
hypothetical protein FLJ36031	FLJ36031	-1.874	0.00306	0.01646
hypothetical protein LOC100127980	LOC100127980	1.899	0.00000	0.00030
hypothetical protein LOC100127983	LOC100127983	-3.512	0.00006	0.00150
Hypothetical protein LOC100128718	LOC100128718	1.602	0.00933	0.03358
Hypothetical protein LOC100129022	LOC100129022	1.908	0.00000	0.00010
hypothetical protein LOC100129034	LOC100129034	1.627	0.00329	0.01727
Hypothetical protein LOC100129282	LOC100129282	2.426	0.00398	0.01958
hypothetical protein LOC100130468	LOC100130468	2.159	0.01880	0.05288
Hypothetical protein LOC100130837	LOC100130837	-1.731	0.00981	0.03463
hypothetical protein LOC100132884	LOC100132884	1.501	0.00108	0.00857
hypothetical protein LOC100132999	LOC100132999	1.530	0.00424	0.02038
hypothetical protein LOC100287917	LOC100287917	-2.953	0.03630	0.08083
hypothetical protein LOC100288551	LOC100288551	2.029	0.00086	0.00743
hypothetical protein LOC100288911	LOC100288911	1.623	0.03190	0.07458
hypothetical protein LOC100290661	LOC100290661	-7.423	0.03210	0.07482
hypothetical protein LOC100293390	LOC100293390	-4.311	0.03450	0.07817
hypothetical protein LOC144481	LOC144481	-1.983	0.01170	0.03865
hypothetical protein LOC144571	LOC144571	1.881	0.00361	0.01843
Hypothetical protein LOC149478	LOC149478	1.574	0.02850	0.06912
hypothetical protein LOC149832	LOC149832	-1.710	0.01540	0.04633
Hypothetical protein LOC202451	LOC202451	2.723	0.01250	0.04030
hypothetical protein LOC221710	LOC221710	-1.810	0.00004	0.00118
hypothetical protein LOC222070	LOC222070	1.562	0.00020	0.00297
hypothetical protein LOC255480	LOC255480	1.811	0.00275	0.01533
hypothetical protein LOC257396	LOC257396	1.771	0.00113	0.00885
hypothetical protein LOC283143	LOC283143	2.571	0.00001	0.00051
hypothetical protein LOC283278	LOC283278	1.505	0.00517	0.02315
hypothetical protein LOC283508	LOC283508	-1.762	0.00147	0.01042
hypothetical protein LOC284542	LOC284542	-1.624	0.00964	0.03426

hypothetical protein LOC285758	LOC285758	3.888	0.00004	0.00105
hypothetical protein LOC285812	LOC285812	-6.393	0.00000	0.00004
hypothetical protein LOC286052	LOC286052	1.514	0.00138	0.00999
hypothetical protein LOC286071	LOC286071	1.529	0.00000	0.00025
hypothetical protein LOC286272	LOC286272	1.580	0.04170	0.08797
hypothetical protein LOC375295	LOC375295	6.576	0.00000	0.00020
hypothetical protein LOC387763	LOC387763	-4.969	0.00000	0.00010
hypothetical protein LOC440119	FLJ31485	1.639	0.00095	0.00791
Hypothetical protein LOC650392	LOC650392	1.730	0.01020	0.03553
hypothetical protein LOC728392 /// NLR family, pyrin domain containing 1	LOC728392 /// NLRP1	1.844	0.00007	0.00154
hypothetical protein LOC729013	LOC729013	1.649	0.00230	0.01376
hypothetical protein LOC729680	LOC729680	2.597	0.00003	0.00090
hypothetical protein LOC729991	LOC729991	-1.522	0.00321	0.01702
hypothetical protein LOC730102	LOC730102	1.735	0.00017	0.00268
hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	HIF1A	-1.508	0.00161	0.01104
hypoxia inducible factor 3, alpha subunit	HIF3A	-2.794	0.00000	0.00026
IKAROS family zinc finger 1 (Ikaros)	IKZF1	-2.146	0.04700	0.09475
IKK interacting protein	IKIP	1.657	0.00125	0.00941
immediate early response 2	IER2	-2.022	0.02710	0.06693
immediate early response 5-like	IER5L	3.311	0.00005	0.00131
immunoglobulin lambda locus	IGL@	-22.148	0.03220	0.07497
immunoglobulin superfamily containing leucine-rich repeat	ISLR	2.504	0.00018	0.00279
immunoglobulin superfamily, member 11	IGSF11	1.868	0.02350	0.06108
immunoglobulin superfamily, member 3	IGSF3	2.272	0.00042	0.00473
immunoglobulin superfamily, member 6	IGSF6	2.006	0.00574	0.02478
IMP (inosine monophosphate) dehydrogenase 1	IMPDH1	1.732	0.00000	0.00013
IMP1 inner mitochondrial membrane peptidase-like (S. cerevisiae)	IMMP1L	-1.653	0.01640	0.04824
importin 11	IPO11	-1.671	0.00971	0.03439
importin 11 /// leucine rich repeat containing 70	IPO11 /// LRRC70	-1.706	0.00446	0.02104
importin 7	IPO7	-1.700	0.00147	0.01042
indolethylamine N-methyltransferase	INMT	-2.517	0.00040	0.00461
inhibin, beta B	INHBB	-2.248	0.00019	0.00288
inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	ID1	-1.548	0.04680	0.09448
inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	ID4	-1.788	0.03670	0.08139
inhibitor of growth family, member 3	ING3	-1.893	0.00390	0.01931
inositol 1,3,4-triphosphate 5/6 kinase	ITPK1	-1.938	0.00049	0.00524
inositol 1,4,5-triphosphate receptor interacting protein	ITPRIP	-1.959	0.00954	0.03404
inositol 1,4,5-triphosphate receptor, type 1	ITPR1	-6.421	0.00014	0.00243
inositol 1,4,5-triphosphate receptor, type 2	ITPR2	1.594	0.00822	0.03106
inositol 1,4,5-trisphosphate 3-kinase B	ITPKB	2.497	0.00000	0.00009
inositol 1,4,5-trisphosphate 3-kinase C	ITPKC	-1.879	0.00275	0.01533
inositol hexakisphosphate kinase 2	IP6K2	-2.202	0.02530	0.06411
inositol polyphosphate-4-phosphatase, type II, 105kDa	INPP4B	-4.748	0.00843	0.03151
inositol polyphosphate-5-phosphatase F	INPP5F	1.701	0.00001	0.00038
inositol polyphosphate-5-phosphatase, 40kDa	INPP5A	-2.371	0.00554	0.02424
inositol(myo)-1(or 4)-monophosphatase 1	IMPA1	-1.766	0.00009	0.00186
inositol(myo)-1(or 4)-monophosphatase 2	IMPA2	-1.893	0.00258	0.01474
insulin receptor	INSR	-1.869	0.00072	0.00665
insulin receptor substrate 1	IRS1	1.791	0.00209	0.01304
insulin receptor substrate 2	IRS2	-3.286	0.00001	0.00054

insulin-like growth factor 1 (somatomedin C)	IGF1	1.896	0.00770	0.02973
insulin-like growth factor 1 receptor	IGF1R	-1.710	0.02040	0.05581
insulin-like growth factor binding protein 2, 36kDa	IGFBP2	-10.170	0.00046	0.00507
integrator complex subunit 6	INTS6	-2.130	0.00000	0.00008
integrin, alpha 10	ITGA10	-4.642	0.00004	0.00117
integrin, alpha 11	ITGA11	1.860	0.00001	0.00049
integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	ITGA2	3.771	0.00029	0.00372
integrin, alpha 5 (fibronectin receptor, alpha polypeptide)	ITGA5	-3.392	0.00420	0.02026
integrin, alpha 6	ITGA6	1.704	0.00433	0.02066
integrin, alpha 7	ITGA7	-12.854	0.01920	0.05365
integrin, alpha 8	ITGA8	-6.988	0.00120	0.00917
integrin, alpha 9	ITGA9	-1.664	0.00419	0.02022
Integrin, beta-like 1 (with EGF-like repeat domains)	ITGBL1	1.876	0.00051	0.00541
intelectin 1 (galactofuranose binding)	ITLN1	-4.776	0.00565	0.02455
inter-alpha (globulin) inhibitor H3	ITIH3	-53.775	0.02930	0.07040
inter-alpha (globulin) inhibitor H5	ITIH5	2.397	0.00613	0.02584
intercellular adhesion molecule 1	ICAM1	2.598	0.00019	0.00287
intercellular adhesion molecule 2	ICAM2	1.973	0.00132	0.00973
intercellular adhesion molecule 3	ICAM3	1.584	0.00003	0.00090
interferon (alpha, beta and omega) receptor 2	IFNAR2	1.713	0.00024	0.00336
interferon induced with helicase C domain 1	IFIH1	1.672	0.00011	0.00207
interferon regulatory factor 1	IRF1	1.556	0.00034	0.00413
interferon, alpha-inducible protein 27	IFI27	2.152	0.02710	0.06693
interferon-induced protein 35	IFI35	1.611	0.01100	0.03720
Interferon-induced protein 44	IFI44	2.609	0.00009	0.00185
interferon-induced protein with tetratricopeptide repeats 1	IFIT1	2.930	0.00051	0.00537
interferon-induced protein with tetratricopeptide repeats 2	IFIT2	1.546	0.01060	0.03634
interferon-induced protein with tetratricopeptide repeats 3	IFIT3	1.656	0.01830	0.05201
interleukin 1 receptor accessory protein	IL1RAP	1.923	0.03850	0.08384
interleukin 1 receptor, type II	IL1R2	-2.122	0.01870	0.05269
Interleukin 1 receptor-like 1	IL1RL1	-2.278	0.01950	0.05408
interleukin 13 receptor, alpha 2	IL13RA2	5.137	0.00472	0.02190
interleukin 15	IL15	1.813	0.00405	0.01981
interleukin 17 receptor B	IL17RB	1.568	0.00326	0.01718
interleukin 17 receptor D	IL17RD	3.553	0.00000	0.00030
interleukin 17D	IL17D	1.881	0.00179	0.01177
interleukin 6 (interferon, beta 2)	IL6	-16.901	0.01160	0.03843
interleukin 6 receptor	IL6R	-2.390	0.03390	0.07736
interleukin 7	IL7	3.220	0.00268	0.01509
interleukin 7 receptor	IL7R	-5.577	0.00576	0.02481
interleukin 8	IL8	-22.257	0.02770	0.06779
interleukin-1 receptor-associated kinase 2	IRAK2	2.816	0.00000	0.00009
interleukin-1 receptor-associated kinase 3	IRAK3	-1.954	0.02050	0.05603
intermediate filament family orphan 1	IFFO1	2.070	0.00000	0.00016
intraflagellar transport 172 homolog (Chlamydomonas)	IFT172	1.698	0.00119	0.00913
IQ motif and Sec7 domain 1	IQSEC1	1.805	0.00047	0.00511
IQ motif containing E	IQCE	1.701	0.00005	0.00129
IQ motif containing G	IQCG	1.931	0.00014	0.00239
iron-sulfur cluster assembly 1 homolog (S. cerevisiae)	ISCA1	-1.809	0.00297	0.01614
ISG15 ubiquitin-like modifier	ISG15	1.609	0.02030	0.05564
isocitrate dehydrogenase 3 (NAD+) alpha	IDH3A	-1.983	0.00512	0.02301

isopentenyl-diphosphate delta isomerase 1	IDI1	-1.550	0.00621	0.02600
Janus kinase 1	JAK1	-1.870	0.03060	0.07247
Janus kinase 2	JAK2	-3.253	0.00047	0.00511
janus kinase and microtubule interacting protein 2	JAKMIP2	5.692	0.00002	0.00080
jumonji C domain containing histone demethylase 1 homolog D (S. cerevisiae)	JHDM1D	-1.960	0.00466	0.02171
jumonji domain containing 6	JMJD6	-1.911	0.00000	0.00026
jun B proto-oncogene	JUNB	-4.424	0.00023	0.00328
jun oncogene	JUN	-2.685	0.02450	0.06273
junction plakoglobin	JUP	-2.063	0.00005	0.00129
junctophilin 2	JPH2	-29.610	0.02240	0.05919
kalirin, RhoGEF kinase	KALRN	-3.706	0.00036	0.00430
kallikrein B, plasma (Fletcher factor) 1	KLKB1	1.808	0.01790	0.05126
Kallmann syndrome 1 sequence	KAL1	3.123	0.00000	0.00004
karyopherin alpha 4 (importin alpha 3)	KPNA4	-1.630	0.03000	0.07152
kazrin	RP1-21O18.1	1.605	0.00228	0.01368
KDEL (Lys-Asp-Glu-Leu) containing 1	KDELC1	1.854	0.00070	0.00653
KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	KDELR3	2.563	0.00000	0.00010
kelch domain containing 5	KLHDC5	-1.566	0.00196	0.01256
kelch repeat and BTB (POZ) domain containing 6	KBTBD6	1.924	0.00002	0.00063
kelch repeat and BTB (POZ) domain containing 7	KBTBD7	1.764	0.00019	0.00290
kelch-like 13 (Drosophila)	KLHL13	2.490	0.00014	0.00237
kelch-like 22 (Drosophila)	KLHL22	1.822	0.00177	0.01170
kelch-like 23 (Drosophila)	KLHL23	-2.295	0.00522	0.02330
kelch-like 24 (Drosophila)	KLHL24	-2.908	0.00784	0.03010
kelch-like 6 (Drosophila)	KLHL6	-1.567	0.04110	0.08721
kelch-like 8 (Drosophila)	KLHL8	-1.579	0.00008	0.00170
keratin 18	KRT18	-7.466	0.00548	0.02409
KH homology domain containing 1	KHDC1	1.711	0.00302	0.01633
KIAA0040	KIAA0040	2.088	0.00577	0.02484
KIAA0114	KIAA0114	-1.950	0.00620	0.02597
KIAA0141	KIAA0141	-1.708	0.03140	0.07379
KIAA0146	KIAA0146	-6.071	0.00039	0.00459
KIAA0774	KIAA0774	-17.024	0.04260	0.08924
KIAA1305	KIAA1305	3.222	0.00001	0.00033
KIAA1324-like	KIAA1324L	1.947	0.00267	0.01507
KIAA1377	KIAA1377	1.546	0.03910	0.08465
KIAA1429	KIAA1429	-1.709	0.03240	0.07527
KIAA1430	KIAA1430	1.601	0.02420	0.06227
KIAA1618	KIAA1618	1.955	0.00040	0.00464
KIAA1659 protein	KIAA1659	-1.887	0.01650	0.04846
KIAA1737	KIAA1737	-1.953	0.00037	0.00438
KIAA1755	KIAA1755	3.104	0.00075	0.00675
KIAA1797	KIAA1797	1.622	0.00003	0.00092
KIAA1841	KIAA1841	1.569	0.00010	0.00194
kin of IRRE like 3 (Drosophila)	KIRREL3	5.510	0.00010	0.00198
kinase insert domain receptor (a type III receptor tyrosine kinase)	KDR	2.535	0.00001	0.00051
kinesin family member 3C	KIF3C	1.845	0.00775	0.02987
KIT ligand	KITLG	2.057	0.00655	0.02692
klotho	KL	2.575	0.00025	0.00338
KN motif and ankyrin repeat domains 1	KANK1	-3.294	0.01510	0.04579

KN motif and ankyrin repeat domains 3	KANK3	-1.881	0.03820	0.08346
kringle containing transmembrane protein 1	KREMEN1	1.568	0.02290	0.06004
Kruppel-like factor 11	KLF11	-1.510	0.00060	0.00601
Kruppel-like factor 15	KLF15	-4.146	0.00004	0.00109
Kruppel-like factor 2 (lung)	KLF2	-1.794	0.01840	0.05217
Kruppel-like factor 6	KLF6	-1.670	0.01550	0.04653
Kruppel-like factor 7 (ubiquitous)	KLF7	-1.745	0.00418	0.02021
Kruppel-like factor 9	KLF9	-2.296	0.00048	0.00518
kyphoscoliosis peptidase	KY	3.235	0.01030	0.03574
l(3)mbt-like (Drosophila)	L3MBTL	2.247	0.00017	0.00272
La ribonucleoprotein domain family, member 1B	LARP1B	-1.695	0.00087	0.00744
La ribonucleoprotein domain family, member 4	LARP4	-1.938	0.00445	0.02101
lactamase, beta	LACTB	-1.832	0.00516	0.02313
lactate dehydrogenase B	LDHB	-1.740	0.01280	0.04091
LAG1 homolog, ceramide synthase 1	LASS1	2.509	0.00001	0.00033
LAG1 homolog, ceramide synthase 4	LASS4	1.707	0.00015	0.00248
LAG1 homolog, ceramide synthase 6	LASS6	-2.544	0.00060	0.00595
lamin A/C	LMNA	1.571	0.00336	0.01754
lamin B receptor	LBR	-1.523	0.00010	0.00195
laminin, alpha 3	LAMA3	-3.636	0.00242	0.01423
laminin, alpha 4	LAMA4	1.904	0.00017	0.00270
LAS1-like (S. cerevisiae)	LAS1L	-1.769	0.02440	0.06258
latent transforming growth factor beta binding protein 4	LTBP4	1.567	0.00258	0.01474
latrophilin 1	LPHN1	1.702	0.00000	0.00018
latrophilin 2	LPHN2	-1.953	0.00176	0.01166
latrophilin 3	LPHN3	-13.261	0.01220	0.03971
LATS, large tumor suppressor, homolog 2 (Drosophila)	LATS2	-1.651	0.00015	0.00247
lectin, galactoside-binding, soluble, 8	LGALS8	-2.053	0.01770	0.05084
leiomodin 1 (smooth muscle)	LMOD1	-15.716	0.00008	0.00176
leptin receptor overlapping transcript-like 1	LEPROTL1	1.603	0.00352	0.01812
lethal giant larvae homolog 1 (Drosophila)	LLGL1	1.612	0.00001	0.00049
leucine proline-enriched proteoglycan (leprecan) 1	LEPRE1	1.661	0.00136	0.00990
leucine rich repeat (in FLII) interacting protein 2	LRRFIP2	-1.602	0.00467	0.02173
leucine rich repeat and fibronectin type III domain containing 4	LRFN4	1.769	0.00003	0.00090
leucine rich repeat and fibronectin type III domain containing 5	LRFN5	1.923	0.01150	0.03823
leucine rich repeat and Ig domain containing 1	LINGO1	1.874	0.00329	0.01727
leucine rich repeat containing 15	LRRC15	2.491	0.00548	0.02409
leucine rich repeat containing 16A	LRRC16A	-2.501	0.00221	0.01346
leucine rich repeat containing 23	LRRC23	2.163	0.00022	0.00316
leucine rich repeat containing 27	LRRC27	1.689	0.00002	0.00065
leucine rich repeat containing 32	LRRC32	-3.144	0.02210	0.05872
leucine rich repeat containing 34	LRRC34	1.840	0.00168	0.01131
leucine rich repeat containing 4C	LRRC4C	3.490	0.00047	0.00507
leucine rich repeat containing 8 family, member A	LRRC8A	-2.260	0.00101	0.00819
leucine rich repeat neuronal 1	LRRN1	6.932	0.00066	0.00634
leucine rich repeat transmembrane neuronal 4	LRRTM4	2.642	0.01160	0.03843
leucine zipper, putative tumor suppressor 1	LZTS1	2.578	0.00002	0.00066
leucine-rich PPR-motif containing	LRPPRC	-1.715	0.00014	0.00239
leucine-rich repeat LGI family, member 4	LGI4	-1.767	0.00286	0.01573
leucine-rich repeat-containing G protein-coupled receptor 6	LGR6	-9.131	0.02080	0.05655
leucyl/cystinyl aminopeptidase	LNPEP	-1.841	0.00200	0.01271

leukemia inhibitory factor receptor alpha	LIFR	-3.966	0.00000	0.00009
leukocyte receptor tyrosine kinase	LTK	1.909	0.00014	0.00242
leukotriene C4 synthase	LTC4S	1.639	0.01450	0.04451
ligand of numb-protein X 1	LNX1	1.561	0.00001	0.00056
LIM and calponin homology domains 1	LIMCH1	1.512	0.00055	0.00560
LIM and senescent cell antigen-like domains 2	LIMS2	-2.283	0.03630	0.08083
LIM and senescent cell antigen-like domains 3-like	LOC440895	1.572	0.00164	0.01117
LIM domain and actin binding 1	LIMA1	1.691	0.00003	0.00096
LIM domain binding 3	LDB3	-92.996	0.02550	0.06439
LIM domain containing preferred translocation partner in lipoma	LPP	-2.997	0.00354	0.01818
LIM domain only 2 (rhombotin-like 1)	LMO2	2.087	0.00015	0.00251
LIM domain only 4	LMO4	1.826	0.01640	0.04824
LIM homeobox 9	LHX9	2.515	0.04050	0.08643
lin-52 homolog (C. elegans)	LIN52	-1.515	0.00059	0.00592
lin-7 homolog A (C. elegans)	LIN7A	-1.507	0.01850	0.05236
lipase maturation factor 1	LMF1	1.938	0.00011	0.00203
lipoic acid synthetase	LIAS	-1.508	0.04260	0.08924
lipoprotein lipase	LPL	-13.170	0.00171	0.01148
low density lipoprotein receptor	LDLR	-2.387	0.04110	0.08721
low density lipoprotein receptor adaptor protein 1	LDLRAP1	1.865	0.00034	0.00413
low density lipoprotein receptor class A domain containing 3	LDLRAD3	1.651	0.01410	0.04372
low density lipoprotein-related protein 1B (deleted in tumors)	LRP1B	-4.284	0.02200	0.05858
LPS-responsive vesicle trafficking, beach and anchor containing	LRBA	1.591	0.01110	0.03741
LRRN4 C-terminal like	LRRN4CL	4.390	0.00002	0.00065
Ly6/neurotoxin 1	LYNX1	2.242	0.00000	0.00021
lymphocyte-specific protein 1	LSP1	2.014	0.00004	0.00108
lymphocyte-specific protein 1 pseudogene /// lymphocyte-specific protein 1 pseudogene	LOC645166 /// LOC654342	2.475	0.00135	0.00986
lymphoid-restricted membrane protein	LRMP	1.758	0.00121	0.00921
LYR motif containing 1	LYRM1	-1.590	0.00024	0.00331
lysine (K)-specific demethylase 3A	KDM3A	-1.732	0.00033	0.00406
lysine (K)-specific demethylase 4B	KDM4B	-1.702	0.03440	0.07802
lysophosphatidic acid receptor 4	LPAR4	2.459	0.00001	0.00035
lysophosphatidic acid receptor 5	LPAR5	1.837	0.01610	0.04767
lysophosphatidylcholine acyltransferase 1	LPCAT1	1.664	0.00060	0.00597
lysophosphatidylcholine acyltransferase 4	LPCAT4	1.564	0.00085	0.00734
lysyl oxidase-like 1	LOXL1	1.763	0.00152	0.01065
lysyl oxidase-like 2	LOXL2	3.788	0.00183	0.01197
lysyl oxidase-like 3	LOXL3	1.849	0.00051	0.00538
lysyl oxidase-like 4	LOXL4	2.076	0.01340	0.04229
mab-21-like 1 (C. elegans)	MAB21L1	2.997	0.00101	0.00819
macrophage stimulating, pseudogene 9	MSTP9	1.584	0.00166	0.01125
major facilitator superfamily domain containing 5	MFSD5	1.976	0.00005	0.00132
major vault protein	MVP	1.615	0.00005	0.00134
makorin ring finger protein 1	MKRN1	-1.754	0.00173	0.01156
mal, T-cell differentiation protein-like	MALL	1.966	0.00305	0.01644
malonyl-CoA decarboxylase	MLYCD	-2.468	0.00133	0.00977
mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor)	MASP1	1.749	0.03040	0.07216
mannose receptor, C type 2	MRC2	1.594	0.00060	0.00594
mannosidase, alpha, class 1B, member 1	MAN1B1	1.734	0.00237	0.01403
mannosidase, alpha, class 1C, member 1	MAN1C1	2.249	0.00053	0.00550

mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme B	MGAT4B	1.836	0.00466	0.02171
MAP kinase interacting serine/threonine kinase 2	MKNK2	-1.657	0.00004	0.00117
MARVEL domain containing 2	MARVELD2	1.549	0.00066	0.00630
mastermind-like domain containing 1	MAMLD1	1.818	0.00049	0.00526
matrix metallopeptidase 16 (membrane-inserted)	MMP16	4.045	0.00002	0.00074
matrix metallopeptidase 19	MMP19	-2.511	0.04190	0.08827
matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)	MMP2	1.566	0.00773	0.02981
matrix metallopeptidase 3 (stromelysin 1, progelatinase)	MMP3	-9.000	0.04530	0.09251
matrix-remodelling associated 5	MXRA5	3.228	0.00000	0.00024
matrix-remodelling associated 7	MXRA7	1.577	0.00650	0.02679
MAX dimerization protein 1	MXD1	-1.635	0.00525	0.02338
MAX interactor 1	MXI1	-1.566	0.00000	0.00025
MCF.2 cell line derived transforming sequence	MCF2	1.791	0.00714	0.02839
McKusick-Kaufman syndrome	MKKS	-1.981	0.01680	0.04903
MDS1 and EVI1 complex locus	MECOM	1.800	0.00040	0.00460
mediator complex subunit 13-like	MED13L	-1.783	0.03710	0.08195
mediator complex subunit 21	MED21	-1.883	0.00712	0.02836
mediator complex subunit 22	MED22	1.587	0.00007	0.00161
mediator complex subunit 28	MED28	-1.628	0.00035	0.00424
melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)	MC1R	1.531	0.00006	0.00146
melanocortin 2 receptor accessory protein 2	MRAP2	2.290	0.00163	0.01112
melanoma antigen family D, 1	MAGED1	1.626	0.00052	0.00543
melanoma antigen family D, 4 /// melanoma antigen family D, 4B	MAGED4 /// MAGED4B	2.731	0.01340	0.04229
melanoma antigen family E, 1	MAGEE1	2.196	0.00003	0.00089
melanoma antigen family E, 2	MAGEE2	1.932	0.00006	0.00141
melanoma associated antigen (mutated) 1	MUM1	1.549	0.00035	0.00424
melanoma associated antigen (mutated) 1-like 1	MUM1L1	-87.716	0.00008	0.00176
melanoma cell adhesion molecule	MCAM	-25.220	0.00126	0.00945
melanoregulin	MREG	1.851	0.00072	0.00662
membrane associated guanylate kinase, WW and PDZ domain containing 3	MAGI3	1.956	0.00000	0.00002
membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)	MPP5	1.559	0.00195	0.01252
membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	MPP7	-38.123	0.01960	0.05427
membrane-associated ring finger (C3HC4) 5	5-Mar	-1.517	0.01150	0.03823
meningioma (disrupted in balanced translocation) 1	MN1	1.705	0.00729	0.02879
mesenchyme homeobox 1	MEOX1	4.233	0.00004	0.00103
mesoderm specific transcript homolog (mouse)	MEST	2.210	0.01090	0.03700
metallophosphoesterase domain containing 2	MPPED2	1.937	0.00228	0.01368
metallothionein 1 pseudogene 2	MT1P2	-3.472	0.00001	0.00044
metallothionein 1E	MT1E	-3.578	0.00001	0.00036
metallothionein 1E /// metallothionein 1H /// metallothionein 1M	MT1E /// MT1H /// MT1M	-3.667	0.00000	0.00025
metallothionein 1F	MT1F	-4.350	0.00001	0.00051
metallothionein 1G	MT1G	-3.232	0.00007	0.00160
metallothionein 1H	MT1H	-3.558	0.00002	0.00061
metallothionein 1M	MT1M	-3.699	0.00902	0.03294
metallothionein 1X	MT1X	-4.333	0.00000	0.00029
metallothionein 2A	MT2A	-4.179	0.00000	0.00017
metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	MALAT1	-1.709	0.00171	0.01148

methionine adenosyltransferase II, alpha	MAT2A	-1.519	0.00002	0.00069
methionine sulfoxide reductase B3	MSRB3	-1.570	0.01500	0.04561
methionyl aminopeptidase 1	METAP1	-1.691	0.01900	0.05324
methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	MCCC1	-1.602	0.00017	0.00269
methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	MCCC2	-1.663	0.02050	0.05603
methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	MTHFD2	-3.991	0.00000	0.00029
methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	MTHFD2L	-1.995	0.01740	0.05024
methylmalonic aciduria (cobalamin deficiency) cblA type	MMAA	1.644	0.00061	0.00601
methyltransferase like 9	METTL9	-1.512	0.01790	0.05126
mex-3 homolog D (C. elegans)	MEX3D	1.900	0.01100	0.03720
microfibrillar-associated protein 2	MFAP2	2.280	0.00042	0.00473
microfibrillar-associated protein 3-like	MFAP3L	2.003	0.00720	0.02853
microsomal glutathione S-transferase 1	MGST1	-2.248	0.04120	0.08727
microtubule-associated protein 2	MAP2	-1.643	0.04600	0.09346
microtubule-associated protein tau	MAPT	1.713	0.01120	0.03762
minichromosome maintenance complex component 2	MCM2	1.681	0.00003	0.00101
missing oocyte, meiosis regulator, homolog (Drosophila)	MIOS	-1.534	0.00001	0.00061
mitochondrial ribosomal protein L10	MRPL10	-1.593	0.00959	0.03416
mitochondrial ribosomal protein L30	MRPL30	-1.919	0.00395	0.01948
mitochondrial ribosomal protein S15	MRPS15	-1.535	0.03160	0.07408
mitochondrial ribosomal protein S25	MRPS25	-1.677	0.01080	0.03676
mitochondrial ribosomal protein S36	MRPS36	-1.750	0.00663	0.02713
mitochondrial tumor suppressor 1	MTUS1	-2.479	0.03930	0.08491
mitogen-activated protein kinase kinase 6	MAP2K6	-2.767	0.03060	0.07247
mitogen-activated protein kinase kinase kinase 5	MAP3K5	-2.299	0.00078	0.00695
mitogen-activated protein kinase kinase kinase 6	MAP3K6	-1.628	0.00165	0.01120
mitogen-activated protein kinase kinase kinase 8	MAP3K8	-1.705	0.00988	0.03482
mitogen-activated protein kinase kinase kinase kinase 4	MAP4K4	1.597	0.00041	0.00471
mixed lineage kinase domain-like	MLKL	1.615	0.01580	0.04710
MOB1, Mps One Binder kinase activator-like 2B (yeast)	MOBKL2B	-2.576	0.00436	0.02075
modulator of apoptosis 1	MOAP1	-1.606	0.00386	0.01921
mohawk homeobox	MKX	-2.323	0.03840	0.08370
monoamine oxidase A	MAOA	-3.582	0.00000	0.00004
MORC family CW-type zinc finger 4	MORC4	1.536	0.01190	0.03910
Mov10, Moloney leukemia virus 10, homolog (mouse)	MOV10	1.567	0.00077	0.00689
M-phase phosphoprotein 8	MPHOSPH8	-2.141	0.00244	0.01428
msh homeobox 1	MSX1	2.345	0.00140	0.01009
MSTP150	MST150	-1.793	0.00464	0.02164
MTERF domain containing 3	MTERFD3	-2.378	0.00054	0.00555
multimerin 1	MMRN1	-1.839	0.02090	0.05673
multiple EGF-like-domains 10	MEGF10	3.578	0.00065	0.00623
multiple EGF-like-domains 6	MEGF6	1.553	0.00541	0.02388
murine retrovirus integration site 1 homolog	MRVI1	-23.959	0.04520	0.09237
Muscleblind-like (Drosophila)	MBNL1	-2.005	0.02080	0.05655
musculoskeletal, embryonic nuclear protein 1	MUSTN1	-208.066	0.00367	0.01861
muskelin 1, intracellular mediator containing kelch motifs	MKLN1	-1.627	0.00176	0.01166
mutated in colorectal cancers	MCC	1.753	0.00006	0.00146
myc target 1	MYCT1	-3.172	0.04870	0.09691
myelin expression factor 2	MYEF2	1.708	0.04480	0.09192
myeloid cell leukemia sequence 1 (BCL2-related)	MCL1	-2.709	0.00003	0.00099
myeloid cell nuclear differentiation antigen	MNDA	2.257	0.02710	0.06693

myeloid leukemia factor 1	MLF1	-2.709	0.03740	0.08236
myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3	MLLT3	1.718	0.00141	0.01015
myocardin	MYOCD	-149.351	0.00123	0.00930
myosin IE	MYO1E	-2.182	0.00034	0.00415
myosin light chain kinase	MYLK	-5.893	0.00059	0.00589
myosin regulatory light chain interacting protein	MYLIP	1.626	0.00127	0.00949
myosin VB	MYO5B	1.522	0.00791	0.03027
myosin X	MYO10	-6.376	0.00388	0.01926
myosin, heavy chain 11, smooth muscle	MYH11	-33.342	0.00010	0.00193
myosin, light chain 9, regulatory	MYL9	-13.434	0.02720	0.06705
myotilin	MYOT	-7.443	0.02140	0.05743
myotubularin related protein 11	MTMR11	1.918	0.00129	0.00958
myozenin 1	MYOZ1	-3.044	0.03860	0.08403
myozenin 3	MYOZ3	5.062	0.00000	0.00029
myristoylated alanine-rich protein kinase C substrate	MARCKS	1.503	0.00071	0.00661
myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	MX1	1.645	0.01930	0.05384
myxovirus (influenza virus) resistance 2 (mouse)	MX2	1.753	0.01100	0.03720
N-6 adenine-specific DNA methyltransferase 1 (putative)	N6AMT1	-1.635	0.00917	0.03322
N-acetylated alpha-linked acidic dipeptidase 2	NAALAD2	1.677	0.01710	0.04964
N-acetylgalactosaminidase, alpha-	NAGA	1.746	0.00052	0.00547
N-acetyltransferase 11 (GCN5-related, putative)	NAT11	1.859	0.00014	0.00238
N-acetyltransferase 14 (GCN5-related, putative)	NAT14	2.389	0.00001	0.00047
N-acetyltransferase 2 (arylamine N-acetyltransferase)	NAT2	2.142	0.00024	0.00331
N-acylsphingosine amidohydrolase (acid ceramidase) 1	ASAH1	-1.563	0.04520	0.09237
NAD kinase	NADK	-1.967	0.00009	0.00186
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa	NDUFA2	-1.645	0.01140	0.03802
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa	NDUFA4	-1.922	0.02370	0.06141
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 4	NDUFAF4	-2.139	0.02860	0.06929
NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase)	NDUFS2	-1.817	0.01180	0.03884
nanos homolog 1 (Drosophila)	NANOS1	5.268	0.00048	0.00519
natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)	NPR3	-5.620	0.00954	0.03404
NCK interacting protein with SH3 domain	NCKIPSD	-1.521	0.00113	0.00885
NDC80 homolog, kinetochore complex component (S. cerevisiae)	NDC80	1.614	0.04470	0.09177
nephronectin	NPNT	-45.363	0.00000	0.00015
netrin 1	NTN1	1.609	0.00052	0.00543
netrin 4	NTN4	1.601	0.00063	0.00615
neuralized homolog 1B (Drosophila)	NEURL1B	-4.094	0.00057	0.00580
neurexin 2	NRXN2	2.276	0.00114	0.00890
neurexophilin 3	NXPH3	1.926	0.00177	0.01170
neuritin 1	NRN1	-4.026	0.02860	0.06929
neurobeachin-like 1	NBEAL1	-2.030	0.03010	0.07169
neuroblastoma breakpoint family, member 1	NBPF1	2.353	0.00071	0.00661
neuroblastoma breakpoint family, member 1 /// neuroblastoma breakpoint family, member 3 /// neuroblastoma breakpoint family, member 8	NBPF1 /// NBPF3 /// NBPF8	2.154	0.00173	0.01156
neuroblastoma breakpoint family, member 10	NBPF10	1.502	0.04000	0.08582
neuroblastoma breakpoint family, member 3	NBPF3	2.299	0.00000	0.00004
neuroepithelial cell transforming 1	NET1	-1.850	0.00116	0.00899
neurofascin homolog (chicken)	NFASC	-9.221	0.00942	0.03379

neurogranin (protein kinase C substrate, RC3)	NRGN	-1.981	0.02980	0.07116
neuron navigator 1	NAV1	1.996	0.00229	0.01371
neuron navigator 2	NAV2	-2.488	0.00001	0.00059
neuronal growth regulator 1	NEGR1	1.681	0.02770	0.06779
neuronal PAS domain protein 2	NPAS2	-2.295	0.01730	0.05006
neuronal PAS domain protein 3	NPAS3	1.953	0.00683	0.02760
neuro-oncological ventral antigen 1	NOVA1	2.801	0.00120	0.00917
neuropilin (NRP) and tolloid (TLL)-like 2	NETO2	3.732	0.01220	0.03971
neuropilin 1	NRP1	1.503	0.01390	0.04334
neurotrimin	NTM	3.059	0.00541	0.02388
neurotrophic tyrosine kinase, receptor, type 2	NTRK2	1.504	0.01040	0.03593
neurotrophic tyrosine kinase, receptor, type 3	NTRK3	-2.621	0.04560	0.09293
neurotrophin 3	NTF3	-15.594	0.00937	0.03368
nexilin (F actin binding protein)	NEXN	-10.539	0.00002	0.00073
NHL repeat containing 3	NHLRC3	1.654	0.00246	0.01434
NHS-like 1	NHSL1	2.709	0.00301	0.01629
Nicotinamide phosphoribosyltransferase	NAMPT	-5.124	0.01710	0.04964
nidogen 1	NID1	-2.627	0.00005	0.00130
NIMA (never in mitosis gene a)- related kinase 11	NEK11	1.913	0.00065	0.00626
NIMA (never in mitosis gene a)-related kinase 6	NEK6	1.831	0.00446	0.02104
ninein (GSK3B interacting protein)	NIN	1.518	0.00042	0.00475
ninjurin 1	NINJ1	1.913	0.00000	0.00005
Nipped-B homolog (Drosophila)	NIPBL	-1.592	0.01480	0.04516
N-myc (and STAT) interactor	NMI	1.675	0.00027	0.00361
non-metastatic cells 6, protein expressed in (nucleoside-diphosphate kinase)	NME6	1.718	0.00063	0.00616
non-protein coding RNA 117	NCRNA00117	1.755	0.00001	0.00045
non-protein coding RNA 188	NCRNA00188	-1.543	0.00464	0.02164
non-protein coding RNA 94	NCRNA00094	1.610	0.00054	0.00556
non-SMC condensin II complex, subunit G2	NCAPG2	1.514	0.00639	0.02646
NOP16 nucleolar protein homolog (yeast)	NOP16	-3.251	0.00018	0.00281
Norrie disease (pseudoglioma)	NDP	6.771	0.00584	0.02506
Notch homolog 2 (Drosophila)	NOTCH2	1.541	0.00010	0.00195
Notch homolog 3 (Drosophila)	NOTCH3	-3.868	0.02530	0.06411
N-terminal EF-hand calcium binding protein 3	NECAB3	-2.318	0.00738	0.02900
nuclear factor I/B	NFIB	1.607	0.01190	0.03910
nuclear factor I/X (CCAAT-binding transcription factor)	NFIX	1.757	0.00003	0.00088
nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	NFATC1	1.600	0.00382	0.01912
nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	NFKBIA	-2.314	0.00006	0.00140
nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	NFKBIZ	-2.245	0.00276	0.01537
nuclear factor, interleukin 3 regulated	NFIL3	-11.339	0.00000	0.00003
nuclear receptor coactivator 3	NCOA3	-1.703	0.02000	0.05509
nuclear receptor subfamily 1, group D, member 1 /// thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian)	NR1D1 /// THRA	1.851	0.01890	0.05309
nuclear receptor subfamily 1, group D, member 2	NR1D2	2.203	0.00640	0.02649
Nuclear receptor subfamily 2, group F, member 1	NR2F1	2.809	0.00353	0.01814
nuclear receptor subfamily 2, group F, member 2	NR2F2	-2.325	0.02070	0.05639
nuclear receptor subfamily 3, group C, member 2	NR3C2	2.070	0.00039	0.00459
nuclear receptor subfamily 4, group A, member 1	NR4A1	-20.353	0.00001	0.00043
nuclear receptor subfamily 4, group A, member 2	NR4A2	-16.705	0.00226	0.01362

nuclear receptor subfamily 4, group A, member 3	NR4A3	-23.615	0.01500	0.04561
nuclear RNA export factor 3	NXF3	1.568	0.01510	0.04579
nuclear transcription factor Y, beta	NFYB	-1.768	0.00000	0.00008
nucleobindin 2	NUCB2	1.605	0.00014	0.00238
nucleoporin 98kDa	NUP98	-2.114	0.00247	0.01438
nucleoporin like 1	NUPL1	-1.904	0.00001	0.00051
nucleoredoxin	NXN	-1.818	0.04350	0.09019
nucleosome assembly protein 1-like 1	NAP1L1	-1.501	0.00108	0.00857
nudix (nucleoside diphosphate linked moiety X)-type motif 10	NUDT10	-2.941	0.01670	0.04885
nudix (nucleoside diphosphate linked moiety X)-type motif 11	NUDT11	-2.346	0.00117	0.00904
nudix (nucleoside diphosphate linked moiety X)-type motif 16	NUDT16	-2.468	0.00028	0.00369
nudix (nucleoside diphosphate linked moiety X)-type motif 18	NUDT18	1.585	0.00021	0.00313
nudix (nucleoside diphosphate linked moiety X)-type motif 4	NUDT4	-3.200	0.00101	0.00819
nudix (nucleoside diphosphate linked moiety X)-type motif 4 /// nudix (nucleoside diphosphate linked moiety X)-type motif 4 pseudogene 1	NUDT4 /// NUDT4P1	-3.229	0.00001	0.00044
nudix (nucleoside diphosphate linked moiety X)-type motif 6	NUDT6	1.583	0.01400	0.04354
OAF homolog (Drosophila)	OAF	2.383	0.00000	0.00028
occludin/ELL domain containing 1	OCEL1	1.746	0.00000	0.00003
OCIA domain containing 2	OCIAD2	2.262	0.00094	0.00787
odd-skipped related 1 (Drosophila)	OSR1	3.509	0.00191	0.01236
olfactomedin 1	OLFM1	1.573	0.00274	0.01530
olfactomedin-like 1	OLFML1	2.293	0.00027	0.00360
opioid growth factor receptor-like 1	OGFRL1	-2.389	0.00912	0.03313
opioid receptor, kappa 1	OPRK1	4.625	0.02440	0.06258
opsin 3	OPN3	-1.737	0.00165	0.01120
optic atrophy 1 (autosomal dominant)	OPA1	-1.605	0.04910	0.09742
ORAI calcium release-activated calcium modulator 2	ORAI2	2.341	0.00009	0.00180
ornithine decarboxylase 1	ODC1	-2.073	0.00101	0.00819
O-sialoglycoprotein endopeptidase-like 1	OSGEPL1	1.602	0.01310	0.04162
OTU domain containing 7B	OTUD7B	-1.885	0.02910	0.07011
oxidase (cytochrome c) assembly 1-like	OXA1L	-1.501	0.01740	0.05024
oxidative stress induced growth inhibitor family member 2	OSGIN2	2.285	0.00010	0.00195
oxysterol binding protein-like 10	OSBPL10	2.188	0.00053	0.00551
oxysterol binding protein-like 6	OSBPL6	1.641	0.01160	0.03843
p21 protein (Cdc42/Rac)-activated kinase 2	PAK2	-1.952	0.01530	0.04618
paired related homeobox 2	PRRX2	1.639	0.00105	0.00840
palladin, cytoskeletal associated protein	PALLD	-2.091	0.00044	0.00488
palmdelphin	PALMD	2.634	0.00294	0.01603
PAP associated domain containing 5	PAPD5	-1.693	0.00019	0.00290
par-6 partitioning defective 6 homolog beta (C. elegans)	PARD6B	-2.141	0.00076	0.00686
par-6 partitioning defective 6 homolog gamma (C. elegans)	PARD6G	1.597	0.00613	0.02584
Paralemmin-3	PALM3	1.947	0.00144	0.01031
paraneoplastic antigen MA2	PNMA2	1.810	0.00141	0.01015
paraoxonase 2	PON2	-1.541	0.00515	0.02312
parathyroid hormone-like hormone	PTHLH	1.690	0.03140	0.07379
partner of NOB1 homolog (S. cerevisiae)	PNO1	-1.538	0.00748	0.02926
parvin, alpha	PARVA	-1.729	0.02650	0.06607
paternally expressed 3 /// zinc finger, imprinted 2	PEG3 /// ZIM2	1.666	0.00370	0.01870
PBX/knotted 1 homeobox 2	PKNOX2	3.032	0.00000	0.00007
PCF11, cleavage and polyadenylation factor subunit, homolog (S. cerevisiae)	PCF11	-1.569	0.00707	0.02824
PDX1 C-terminal inhibiting factor 1	PCIF1	-1.800	0.00004	0.00113

PDZ and LIM domain 3	PDLIM3	1.725	0.00790	0.03026
PDZ and LIM domain 5	PDLIM5	-3.540	0.00277	0.01539
PDZ and LIM domain 7 (enigma)	PDLIM7	2.143	0.00611	0.02578
PDZ domain containing ring finger 3	PDZRN3	1.588	0.01670	0.04885
pecanex homolog (Drosophila)	PCNX	-1.609	0.00172	0.01151
pellino homolog 2 (Drosophila)	PELI2	-1.568	0.02900	0.06994
Pelota homolog (Drosophila)	PELO	-1.958	0.04430	0.09121
peptidase domain containing associated with muscle regeneration 1	PAMR1	2.440	0.00003	0.00091
peptidylprolyl isomerase (cyclophilin)-like 4 /// zinc finger CCCH-type containing 12D	PPIL4 /// ZC3H12D	-2.361	0.01050	0.03614
peptidylprolyl isomerase C (cyclophilin C)	PPIC	1.572	0.00482	0.02221
perforin 1 (pore forming protein)	PRF1	-1.544	0.00983	0.03469
perilipin 2	PLIN2	-3.823	0.00001	0.00047
period homolog 1 (Drosophila)	PER1	-2.701	0.00167	0.01128
period homolog 2 (Drosophila)	PER2	1.520	0.01780	0.05103
period homolog 3 (Drosophila)	PER3	2.715	0.00042	0.00473
peripherin	PRPH	1.863	0.00249	0.01444
peroxidasin homolog (Drosophila)	PXDN	2.254	0.00012	0.00218
peroxiredoxin 6	PRDX6	-1.745	0.00103	0.00830
peroxisomal membrane protein 2, 22kDa	PXMP2	-1.822	0.00126	0.00945
peroxisome proliferator-activated receptor alpha	PPARA	-1.683	0.01370	0.04289
PHD finger protein 11	PHF11	1.773	0.00212	0.01315
PHD finger protein 17	PHF17	-3.051	0.00001	0.00057
PHD finger protein 20	PHF20	-1.574	0.00032	0.00400
phosducin-like 3 pseudogene /// phosducin-like 3	LOC285359 /// PDCL3	-2.210	0.02350	0.06108
phosphatase and tensin homolog	PTEN	-1.646	0.00197	0.01259
phosphatase and tensin homolog /// phosphatase and tensin homolog pseudogene 1	PTEN /// PTENP1	-1.577	0.00000	0.00009
phosphatase, orphan 2	PHOSPHO2	1.726	0.00342	0.01774
phosphatidic acid phosphatase type 2 domain containing 1A	PPAPDC1A	4.185	0.03140	0.07379
phosphatidic acid phosphatase type 2 domain containing 1B	PPAPDC1B	1.829	0.00104	0.00835
phosphatidic acid phosphatase type 2 domain containing 2	PPAPDC2	1.968	0.00039	0.00454
phosphatidylethanolamine-binding protein 4	PEBP4	-5.014	0.01110	0.03741
phosphatidylinositol glycan anchor biosynthesis, class M	PIGM	1.738	0.00662	0.02710
phosphatidylinositol glycan anchor biosynthesis, class Z	PIGZ	1.782	0.00024	0.00330
phosphatidylinositol transfer protein, cytoplasmic 1	PITPNC1	-1.981	0.01060	0.03634
phosphodiesterase 2A, cGMP-stimulated	PDE2A	-2.490	0.00271	0.01520
phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2 dunce homolog, Drosophila)	PDE4A	1.772	0.00009	0.00179
phosphodiesterase 4D interacting protein	PDE4DIP	-1.726	0.01960	0.05427
phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)	PDE4D	-3.384	0.03200	0.07469
phosphodiesterase 7B	PDE7B	1.833	0.01530	0.04618
phosphoglucomutase 2-like 1	PGM2L1	1.696	0.00967	0.03433
phosphoglucomutase 3	PGM3	1.783	0.00007	0.00159
phosphoinositide-3-kinase, catalytic, alpha polypeptide	PIK3CA	-1.984	0.00000	0.00008
phosphoinositide-3-kinase, class 2, beta polypeptide	PIK3C2B	1.964	0.00039	0.00454
phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	PIK3R1	-2.096	0.00307	0.01650
phosphoinositide-3-kinase, regulatory subunit 2 (beta)	PIK3R2	1.590	0.00004	0.00120
phosphoinositide-interacting regulator of transient receptor potential channels	hCG_1776018	5.458	0.00000	0.00005
phospholamban	PLN	-187.746	0.00158	0.01090
phospholipase A1 member A	PLA1A	-8.034	0.02370	0.06141

phospholipase A2, group IVA (cytosolic, calcium-dependent)	PLA2G4A	1.863	0.00131	0.00967
phospholipase A2, group V	PLA2G5	-5.568	0.00000	0.00003
phospholipase C, beta 1 (phosphoinositide-specific)	PLCB1	1.619	0.03490	0.07869
Phospholipase C, beta 4	PLCB4	1.588	0.00729	0.02879
phospholipase C, delta 4	PLCD4	1.827	0.00001	0.00058
phospholipase C, eta 1	PLCH1	1.850	0.00635	0.02635
phospholipase C-like 1	PLCL1	-2.582	0.00168	0.01131
phosphoprotein enriched in astrocytes 15	PEA15	-1.924	0.00357	0.01828
phosphoribosyl transferase domain containing 1	PRTFDC1	1.613	0.00398	0.01958
phosphorylase kinase, alpha 1 (muscle)	PHKA1	-2.028	0.00260	0.01480
phosphoserine aminotransferase 1	PSAT1	2.678	0.00121	0.00921
phosphoserine phosphatase	PSPH	1.535	0.02240	0.05919
phosphotriesterase related	PTER	1.621	0.01060	0.03634
phytanoyl-CoA dioxygenase domain containing 1	PHYHD1	-1.512	0.00401	0.01969
placenta-specific 9	PLAC9	1.717	0.00495	0.02258
plakophilin 2	PKP2	-9.518	0.00924	0.03338
plasma membrane proteolipid (plasmolipin)	PLLP	-2.470	0.02080	0.05655
plasminogen activator, tissue	PLAT	2.930	0.00144	0.01031
plasminogen activator, urokinase	PLAU	1.986	0.00226	0.01362
plasticity related gene 1	LPPR4	5.497	0.00255	0.01464
platelet endothelial aggregation receptor 1	PEAR1	-3.857	0.00001	0.00047
platelet/endothelial cell adhesion molecule	PECAM1	-4.753	0.03490	0.07869
pleckstrin and Sec7 domain containing 3	PSD3	2.597	0.00001	0.00042
pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 8	PLEKHA8	1.590	0.00001	0.00040
pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 8 /// pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 9	PLEKHA8 /// PLEKHA9	2.887	0.00001	0.00048
pleckstrin homology domain containing, family A member 5	PLEKHA5	1.551	0.00406	0.01982
pleckstrin homology domain containing, family A member 6	PLEKHA6	2.223	0.04000	0.08582
pleckstrin homology domain containing, family A member 7	PLEKHA7	2.103	0.00497	0.02262
pleckstrin homology domain containing, family B (evectins) member 1	PLEKHB1	4.343	0.00023	0.00328
pleckstrin homology domain containing, family G (with RhoGef domain) member 1	PLEKHG1	3.891	0.00203	0.01284
pleckstrin homology domain containing, family G (with RhoGef domain) member 4	PLEKHG4	1.696	0.00165	0.01120
pleckstrin homology domain containing, family O member 2	PLEKHO2	1.879	0.00004	0.00113
pleckstrin homology-like domain, family A, member 2	PHLDA2	2.666	0.00084	0.00728
pleckstrin homology-like domain, family A, member 3	PHLDA3	1.792	0.00001	0.00060
plexin A2	PLXNA2	1.772	0.00116	0.00899
plexin A3	PLXNA3	1.884	0.00000	0.00019
plexin C1	PLXNC1	1.920	0.00043	0.00485
plexin domain containing 1	PLXDC1	4.113	0.00044	0.00487
PNMA-like 1	PNMAL1	1.641	0.01470	0.04495
PNMA-like 2	PNMAL2	1.888	0.00000	0.00020
podocalyxin-like	PODXL	2.378	0.01060	0.03634
podocan	PODN	-1.708	0.04970	0.09810
poly (ADP-ribose) polymerase family, member 9	PARP9	1.903	0.00117	0.00904
poly(A) binding protein interacting protein 2B	PAIP2B	-2.079	0.01860	0.05251
poly(A) binding protein, cytoplasmic 4 (inducible form)	PABPC4	-1.906	0.00066	0.00632
poly(A) binding protein, cytoplasmic 4-like	PABPC4L	2.118	0.00184	0.01201
poly(A) polymerase alpha	PAPOLA	-1.506	0.00225	0.01360
poly(rC) binding protein 2	PCBP2	-1.504	0.04770	0.09571

polycomb group ring finger 2	PCGF2	1.569	0.00000	0.00013
polycomb group ring finger 5	PCGF5	-1.901	0.00970	0.03438
polycystic kidney and hepatic disease 1 (autosomal recessive)-like 1	PKHD1L1	-10.474	0.02130	0.05732
polyhomeotic homolog 2 (Drosophila)	PHC2	-2.232	0.00000	0.00019
polyhomeotic homolog 3 (Drosophila)	PHC3	-1.567	0.00360	0.01839
polymerase (DNA directed), eta	POLH	2.303	0.00001	0.00058
polymerase (DNA-directed), epsilon 4 (p12 subunit)	POLE4	-1.733	0.00002	0.00082
polypyrimidine tract binding protein 2	PTBP2	-1.549	0.00713	0.02837
POM121 membrane glycoprotein-like 9 (rat) pseudogene	POM121L9P	-2.827	0.01090	0.03700
potassium channel tetramerisation domain containing 10	KCTD10	-1.653	0.02100	0.05688
potassium channel tetramerisation domain containing 11	KCTD11	2.021	0.00005	0.00126
potassium channel tetramerisation domain containing 14	KCTD14	1.727	0.00014	0.00243
potassium channel tetramerisation domain containing 4	KCTD4	6.088	0.00000	0.00011
potassium channel tetramerisation domain containing 7	KCTD7	1.582	0.00036	0.00433
potassium channel, subfamily K, member 17	KCNK17	2.304	0.00781	0.03002
potassium channel, subfamily K, member 3	KCNK3	-21.617	0.01850	0.05236
potassium inwardly-rectifying channel, subfamily J, member 12	KCNJ12	2.511	0.00001	0.00049
potassium large conductance calcium-activated channel, subfamily M, beta member 4	KCNMB4	1.594	0.00908	0.03306
potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	KCNS3	3.426	0.00001	0.00053
potassium voltage-gated channel, Isk-related family, member 3	KCNE3	1.796	0.01350	0.04247
potassium voltage-gated channel, Isk-related family, member 4	KCNE4	3.144	0.00013	0.00228
potassium voltage-gated channel, KQT-like subfamily, member 5	KCNQ5	-6.398	0.00863	0.03201
potassium voltage-gated channel, shaker-related subfamily, member 5	KCNA5	-19.180	0.00320	0.01698
POU class 6 homeobox 1	POU6F1	1.699	0.00783	0.03007
PR domain containing 11	PRDM11	-2.341	0.00002	0.00069
PR domain containing 2, with ZNF domain	PRDM2	-1.607	0.00000	0.00004
prenylcysteine oxidase 1 like	PCYOX1L	1.900	0.00004	0.00107
prickle homolog 1 (Drosophila)	PRICKLE1	3.616	0.00019	0.00290
PRKC, apoptosis, WT1, regulator	PAWR	-6.092	0.00221	0.01346
procollagen C-endopeptidase enhancer	PCOLCE	1.584	0.00238	0.01407
procollagen C-endopeptidase enhancer 2	PCOLCE2	1.555	0.01300	0.04135
procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1	PLOD1	1.671	0.00008	0.00171
progestin and adipoQ receptor family member IV	PAQR4	1.709	0.00000	0.00016
programmed cell death 1 ligand 2	PDCD1LG2	1.925	0.00213	0.01319
programmed cell death 4 (neoplastic transformation inhibitor)	PDCD4	-2.067	0.04340	0.09014
programmed cell death 6 pseudogene	LOC728613	-2.264	0.01870	0.05269
programmed cell death 6 pseudogene /// programmed cell death 6	LOC728613 /// PDCD6	-2.280	0.00885	0.03260
proline rich 16	PRR16	-2.414	0.01270	0.04072
proline rich 5 like	PRR5L	9.512	0.00000	0.00003
proline rich Gla (G-carboxyglutamic acid) 1	PRRG1	-2.998	0.00005	0.00124
proline-rich coiled-coil 1	PRRC1	1.775	0.00329	0.01727
proline-rich nuclear receptor coactivator 1	PNRC1	-1.696	0.00000	0.00004
proline-rich transmembrane protein 1	PRRT1	1.731	0.00275	0.01533
proline-rich transmembrane protein 3	PRRT3	1.793	0.00008	0.00174
proline-serine-threonine phosphatase interacting protein 1	PSTPIP1	5.179	0.00000	0.00015
proline-serine-threonine phosphatase interacting protein 2	PSTPIP2	-2.195	0.00389	0.01928
prolyl 4-hydroxylase, alpha polypeptide II	P4HA2	2.069	0.00012	0.00220
proprotein convertase subtilisin/kexin type 6	PCSK6	2.498	0.01030	0.03574
prospero homeobox 1	PROX1	-7.546	0.03990	0.08571
prostaglandin D2 receptor (DP)	PTGDR	1.817	0.02030	0.05564

prostaglandin E synthase	PTGES	3.229	0.00000	0.00002
prostaglandin F receptor (FP)	PTGFR	6.458	0.00010	0.00201
prostaglandin F2 receptor negative regulator	PTGFRN	1.825	0.00114	0.00890
prostaglandin I2 (prostacyclin) receptor (IP)	PTGIR	1.631	0.00288	0.01578
prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	PTGS2	-20.874	0.00213	0.01319
prostate transmembrane protein, androgen induced 1	PMEPA1	1.812	0.00181	0.01187
prostatic androgen-repressed message-1	DKFZP564O0823	-3.591	0.00033	0.00410
proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	PSMD12	-1.511	0.00937	0.03368
proteasome (prosome, macropain) activator subunit 4	PSME4	-1.581	0.00173	0.01156
proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2)	PSMB9	1.682	0.00580	0.02491
protein disulfide isomerase family A, member 2	PDIA2	1.539	0.01630	0.04803
protein disulfide isomerase family A, member 4	PDIA4	1.543	0.00029	0.00373
protein inhibitor of activated STAT, 1	PIAS1	-1.975	0.00000	0.00016
protein kinase C and casein kinase substrate in neurons 2	PACSIN2	-1.846	0.00041	0.00470
protein kinase C, alpha	PRKCA	1.834	0.00021	0.00304
protein kinase C, beta	PRKCB	-4.703	0.00761	0.02955
protein kinase, AMP-activated, alpha 2 catalytic subunit	PRKAA2	-13.622	0.04680	0.09448
protein kinase, AMP-activated, gamma 2 non-catalytic subunit	PRKAG2	-5.076	0.00030	0.00384
protein kinase, cAMP-dependent, regulatory, type II, beta	PRKAR2B	-2.435	0.02950	0.07069
protein kinase-like protein SgK493	SGK493	-1.801	0.00023	0.00324
protein phosphatase 1, regulatory (inhibitor) subunit 12A	PPP1R12A	-1.994	0.03190	0.07458
protein phosphatase 1, regulatory (inhibitor) subunit 12B	PPP1R12B	-15.561	0.00499	0.02265
protein phosphatase 1, regulatory (inhibitor) subunit 12C	PPP1R12C	-1.796	0.00620	0.02597
protein phosphatase 1, regulatory (inhibitor) subunit 14A	PPP1R14A	-8.842	0.00266	0.01503
protein phosphatase 1, regulatory (inhibitor) subunit 15A	PPP1R15A	-2.154	0.00023	0.00328
protein phosphatase 1, regulatory (inhibitor) subunit 16B	PPP1R16B	-1.875	0.01340	0.04229
protein phosphatase 1, regulatory (inhibitor) subunit 3E	PPP1R3E	1.541	0.00307	0.01650
protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform	PPM1A	-1.657	0.01690	0.04924
protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform	PPM1B	-2.857	0.00000	0.00008
protein phosphatase 1F (PP2C domain containing)	PPM1F	1.564	0.00091	0.00772
protein phosphatase 1K (PP2C domain containing)	PPM1K	-2.469	0.00244	0.01428
protein phosphatase 2, regulatory subunit B', alpha isoform	PPP2R5A	-1.535	0.02340	0.06090
protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform	PPP3CC	-1.570	0.00002	0.00067
protein tyrosine phosphatase, receptor type, D	PTPRD	1.574	0.04280	0.08947
protein tyrosine phosphatase, receptor type, F	PTPRF	1.774	0.00120	0.00917
protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2	PPFIA2	-1.513	0.03380	0.07723
protein tyrosine phosphatase, receptor type, G	PTPRG	-2.012	0.00106	0.00846
protein tyrosine phosphatase, receptor type, O	PTPRO	-1.812	0.01460	0.04472
protein tyrosine phosphatase, receptor-type, Z polypeptide 1	PTPRZ1	-2.560	0.00468	0.02176
protein tyrosine phosphatase-like (proline instead of catalytic arginine), member A	PTPLA	-6.465	0.00007	0.00162
protein tyrosine phosphatase-like A domain containing 1	PTPLAD1	1.694	0.00807	0.03068
Protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	PCMTD1	-1.606	0.00676	0.02743
protocadherin 12	PCDH12	1.731	0.01270	0.04072
protocadherin 20	PCDH20	-14.268	0.04910	0.09742
protocadherin 7	PCDH7	-62.480	0.00640	0.02649
protocadherin alpha 1 /// protocadherin alpha 10 /// protocadherin alpha 11 /// protocadherin alpha 12 /// protocadherin alpha 13 /// protocadherin alpha 2 /// protocadherin alpha 3 /// protocadherin alpha	PCDHA1 /// PCDHA10 /// PCDHA11 ///	2.514	0.00062	0.00609

4 /// protocadherin alpha 5 /// protocadherin alpha 6 /// protocadherin alpha 7 /// protocadherin alpha 8 /// protocadherin alpha 9 /// protocadherin alpha subfamily C, 1 /// protocadherin alpha subfamily C, 2	PCDHA12 /// PCDHA13 /// PCDHA2 /// PCDHA3 /// PCDHA4 /// PCDHA5 /// PCDHA6 /// PCDHA7 /// PCDHA8 /// PCDHA9 /// PCDHAC1 /// PCDHAC2			
protocadherin alpha 2	PCDHA2	2.410	0.00014	0.00238
protocadherin beta 10	PCDHB10	1.521	0.02220	0.05890
protocadherin beta 13	PCDHB13	2.529	0.00100	0.00814
protocadherin beta 14	PCDHB14	1.595	0.00688	0.02771
protocadherin beta 16	PCDHB16	1.671	0.00165	0.01120
protocadherin beta 2	PCDHB2	2.024	0.00266	0.01503
protocadherin beta 3	PCDHB3	1.796	0.00503	0.02278
protocadherin beta 6	PCDHB6	2.575	0.00348	0.01797
protocadherin beta 7	PCDHB7	1.811	0.00667	0.02720
PRP4 pre-mRNA processing factor 4 homolog B (yeast)	PRPF4B	-1.639	0.04540	0.09263
prune homolog 2 (Drosophila)	PRUNE2	1.670	0.01440	0.04432
PTC7 protein phosphatase homolog (S. cerevisiae)	PPTC7	-2.145	0.00030	0.00381
PTK7 protein tyrosine kinase 7	PTK7	1.833	0.00000	0.00011
PTPRF interacting protein, binding protein 1 (liprin beta 1)	PPFIBP1	1.638	0.02990	0.07135
purinergic receptor P2X, ligand-gated ion channel, 1	P2RX1	-22.243	0.04450	0.09147
purinergic receptor P2X, ligand-gated ion channel, 4	P2RX4	1.597	0.00630	0.02624
purinergic receptor P2X, ligand-gated ion channel, 7	P2RX7	1.540	0.00041	0.00468
purine-rich element binding protein B	PURB	-1.750	0.02840	0.06897
purine-rich element binding protein G	PURG	1.522	0.01620	0.04786
putative homeodomain transcription factor 1	PHTF1	1.585	0.00000	0.00024
PYD and CARD domain containing	PYCARD	2.717	0.00023	0.00326
pyridoxal (pyridoxine, vitamin B6) phosphatase	PDXP	1.658	0.00209	0.01304
pyroglutamyl-peptidase I	PGPEP1	1.743	0.00000	0.00019
pyrroline-5-carboxylate reductase 1	PYCR1	1.622	0.00023	0.00327
pyruvate dehydrogenase (lipoamide) alpha 1	PDHA1	-2.172	0.01890	0.05309
pyruvate dehydrogenase complex, component X	PDHX	-1.923	0.01990	0.05490
pyruvate dehydrogenase kinase, isozyme 4	PDK4	-64.621	0.00000	0.00002
pyruvate kinase, muscle	PKM2	1.587	0.01040	0.03593
RAB GTPase activating protein 1	RABGAP1	-1.534	0.00327	0.01722
RAB GTPase activating protein 1-like	RABGAP1L	4.595	0.00289	0.01582
RAB, member of RAS oncogene family-like 4	RABL4	2.521	0.00001	0.00051
RAB, member RAS oncogene family-like 5	RABL5	1.714	0.00076	0.00684
RAB11 family interacting protein 1 (class I)	RAB11FIP1	-1.612	0.01050	0.03614
RAB11 family interacting protein 5 (class I)	RAB11FIP5	1.535	0.00006	0.00142
RAB20, member RAS oncogene family	RAB20	-1.787	0.02130	0.05732
RAB21, member RAS oncogene family	RAB21	-1.728	0.00196	0.01256
RAB27A, member RAS oncogene family	RAB27A	-2.073	0.04550	0.09277
RAB30, member RAS oncogene family	RAB30	2.102	0.00000	0.00006
RAB37, member RAS oncogene family	RAB37	1.854	0.00430	0.02058
RAB42, member RAS oncogene family	RAB42	2.235	0.00000	0.00004
RAB4A, member RAS oncogene family	RAB4A	-1.883	0.00169	0.01137
RAB4A, member RAS oncogene family /// S-phase response (cyclin related)	RAB4A /// SPHAR	-1.661	0.00865	0.03207

RAB6B, member RAS oncogene family	RAB6B	2.677	0.00002	0.00074
RAB7, member RAS oncogene family-like 1	RAB7L1	1.702	0.00700	0.02806
RAB7B, member RAS oncogene family	RAB7B	6.416	0.00000	0.00027
RAB8B, member RAS oncogene family	RAB8B	-2.573	0.01050	0.03614
rabphilin 3A-like (without C2 domains)	RPH3AL	1.678	0.01160	0.03843
Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	ARHGEF6	1.503	0.00003	0.00090
RAD54 homolog B (S. cerevisiae)	RAD54B	1.524	0.00115	0.00894
radical S-adenosyl methionine domain containing 2	RSAD2	1.522	0.04960	0.09797
Ral GEF with PH domain and SH3 binding motif 1	RALGPS1	1.709	0.00105	0.00840
RALBP1 associated Eps domain containing 1	REPS1	-1.686	0.01620	0.04786
Rap guanine nucleotide exchange factor (GEF) 3	RAPGEF3	-1.511	0.03820	0.08346
Rap guanine nucleotide exchange factor (GEF) 6	RAPGEF6	-1.513	0.00914	0.03316
RAP1A, member of RAS oncogene family	RAP1A	-1.848	0.00674	0.02739
RAP2A, member of RAS oncogene family	RAP2A	-1.974	0.00026	0.00354
RAP2B, member of RAS oncogene family	RAP2B	1.921	0.00538	0.02379
RAS and EF-hand domain containing	RASEF	1.649	0.00590	0.02518
Ras and Rab interactor 2	RIN2	1.785	0.00000	0.00031
Ras association (RalGDS/AF-6) domain family member 2	RASSF2	-2.112	0.03750	0.08248
RAS guanyl releasing protein 2 (calcium and DAG-regulated)	RASGRP2	-8.054	0.00762	0.02957
Ras homolog enriched in brain	RHEB	-1.511	0.00129	0.00958
ras homolog gene family, member B	RHOB	-2.614	0.00006	0.00138
ras homolog gene family, member J	RHOJ	2.652	0.00182	0.01192
ras homolog gene family, member Q	RHOQ	-1.913	0.00846	0.03158
ras homolog gene family, member U	RHOU	-3.607	0.02900	0.06994
Ras interacting protein 1	RASIP1	-2.561	0.02610	0.06538
RAS p21 protein activator 3	RASA3	1.784	0.00001	0.00040
RAS protein activator like 2	RASAL2	-2.309	0.01670	0.04885
RAS, dexamethasone-induced 1	RASD1	-5.696	0.00046	0.00507
RasGEF domain family, member 1A	RASGEF1A	4.437	0.00044	0.00487
RAS-like, estrogen-regulated, growth inhibitor	RERG	2.229	0.00027	0.00362
RAS-like, family 11, member A	RASL11A	-4.274	0.00869	0.03218
Ras-related associated with diabetes	RRAD	-10.651	0.01140	0.03802
RCAN family member 3	RCAN3	3.042	0.00000	0.00031
RCSD domain containing 1	RCSD1	-4.486	0.00003	0.00086
receptor (chemosensory) transporter protein 4	RTP4	2.932	0.00002	0.00071
receptor (G protein-coupled) activity modifying protein 1	RAMP1	-7.635	0.00136	0.00990
receptor accessory protein 1	REEP1	-50.153	0.00694	0.02790
receptor-interacting serine-threonine kinase 2	RIPK2	1.695	0.00118	0.00907
regulator of calcineurin 2	RCAN2	-4.404	0.01170	0.03865
regulator of G-protein signaling 1	RGS1	-54.211	0.00000	0.00009
regulator of G-protein signaling 10	RGS10	1.583	0.00752	0.02934
regulator of G-protein signaling 12	RGS12	1.566	0.00117	0.00904
regulator of G-protein signaling 19	RGS19	-2.044	0.02740	0.06734
regulator of G-protein signaling 2, 24kDa	RGS2	-2.680	0.00033	0.00405
regulator of G-protein signaling 3	RGS3	2.115	0.00069	0.00648
regulator of G-protein signaling 5	RGS5	-5.364	0.02240	0.05919
regulator of G-protein signaling 7 binding protein	RGS7BP	-6.331	0.00573	0.02477
regulatory factor X, 5 (influences HLA class II expression)	RFX5	1.530	0.00277	0.01539
regulatory factor X, 7	RFX7	1.648	0.00015	0.00248
related RAS viral (r-ras) oncogene homolog 2	RRAS2	-2.228	0.00576	0.02481
replication protein A4, 34kDa	RPA4	-1.554	0.00274	0.01530

reticulocalbin 3, EF-hand calcium binding domain	RCN3	1.656	0.00013	0.00233
retinitis pigmentosa GTPase regulator	RPGR	-2.269	0.00121	0.00921
retinoblastoma binding protein 6	RBBP6	-3.528	0.00016	0.00261
retinoic acid receptor responder (tazarotene induced) 2	RARRES2	-2.108	0.00776	0.02990
retinol binding protein 7, cellular	RBP7	-8.763	0.00182	0.01192
retinol dehydrogenase 13 (all-trans/9-cis)	RDH13	1.618	0.02730	0.06721
reversion-inducing-cysteine-rich protein with kazal motifs	RECK	1.687	0.00047	0.00507
RGM domain family, member A	RGMA	1.609	0.00234	0.01390
Rho family GTPase 2	RND2	1.615	0.00025	0.00338
Rho family GTPase 3	RND3	-1.941	0.00049	0.00524
Rho GTPase activating protein 10	ARHGAP10	-3.504	0.00000	0.00013
Rho GTPase activating protein 12	ARHGAP12	1.611	0.00008	0.00174
Rho GTPase activating protein 15	ARHGAP15	-6.757	0.00457	0.02143
Rho GTPase activating protein 21	ARHGAP21	1.588	0.00003	0.00089
Rho GTPase activating protein 22	ARHGAP22	3.138	0.00015	0.00244
Rho GTPase activating protein 24	ARHGAP24	-1.973	0.04920	0.09753
Rho GTPase activating protein 26	ARHGAP26	-5.183	0.00013	0.00233
Rho GTPase activating protein 28	ARHGAP28	3.382	0.00335	0.01752
Rho GTPase-activating protein	RICS	2.110	0.00229	0.01371
Rho guanine nucleotide exchange factor (GEF) 10	ARHGEF10	1.666	0.00326	0.01718
Rho guanine nucleotide exchange factor (GEF) 12	ARHGEF12	1.676	0.00039	0.00459
Rho guanine nucleotide exchange factor (GEF) 3	ARHGEF3	2.180	0.00000	0.00020
Rho guanine nucleotide exchange factor (GEF) 4	ARHGEF4	1.737	0.00054	0.00558
Rho guanine nucleotide exchange factor (GEF) 7	ARHGEF7	-1.616	0.00298	0.01617
Rho-associated, coiled-coil containing protein kinase 1	ROCK1	-1.903	0.00042	0.00475
rhophilin, Rho GTPase binding protein 2	RHPN2	1.614	0.00980	0.03461
Rho-related BTB domain containing 3	RHOBTB3	-1.925	0.00582	0.02498
rhotekin	RTKN	1.877	0.00249	0.01444
ribonuclease H2, subunit A	RNASEH2A	1.619	0.00079	0.00703
ribonuclease L (2',5'-oligoisoadenylate synthetase-dependent)	RNASEL	1.522	0.00015	0.00249
ribosomal L24 domain containing 1	RSL24D1	-1.573	0.00002	0.00061
ribosomal modification protein rimK-like family member B	RIMKLB	-3.179	0.01350	0.04247
ribosomal protein L13	RPL13	-1.595	0.02200	0.05858
ribosomal protein L13 pseudogene 5	RPL13P5	1.613	0.01520	0.04600
ribosomal protein L14	RPL14	-1.725	0.00201	0.01276
Ribosomal protein L15	RPL15	-1.789	0.01250	0.04030
ribosomal protein L24	RPL24	-1.519	0.00005	0.00129
ribosomal protein L31	RPL31	-1.874	0.00000	0.00031
ribosomal protein L36	RPL36	-1.511	0.00001	0.00048
ribosomal protein L36a	RPL36A	-1.513	0.00017	0.00275
Ribosomal protein L37	RPL37	-1.880	0.00077	0.00692
ribosomal protein L5	RPL5	-1.574	0.00000	0.00003
Ribosomal protein S15a	RPS15A	-1.666	0.00822	0.03106
ribosomal protein S16	RPS16	-1.517	0.00000	0.00018
ribosomal protein S16 pseudogene 5	RPS16P5	-2.934	0.00258	0.01474
ribosomal protein S23	RPS23	-1.921	0.00702	0.02809
ribosomal protein S6 kinase, 90kDa, polypeptide 2	RPS6KA2	-2.061	0.00009	0.00187
ribosome binding protein 1 homolog 180kDa (dog)	RRBP1	1.846	0.00076	0.00686
ring finger and CHY zinc finger domain containing 1	RCHY1	-1.552	0.00309	0.01657
ring finger protein 115	RNF115	-2.960	0.00018	0.00279
ring finger protein 141	RNF141	-1.668	0.00078	0.00695

ring finger protein 144B	RNF144B	-4.355	0.00000	0.00018
ring finger protein 160	RNF160	-1.524	0.01210	0.03950
ring finger protein 19A	RNF19A	-1.867	0.00331	0.01734
ring finger protein 19B	RNF19B	1.601	0.00419	0.02022
ring finger protein 217	RNF217	-1.997	0.00004	0.00107
ring finger protein, transmembrane 2	RNFT2	1.804	0.00505	0.02282
RIO kinase 3 (yeast)	RIOK3	-1.771	0.02560	0.06458
RNA binding motif protein 12B	RBM12B	1.553	0.00462	0.02157
RNA binding motif protein 15	RBM15	1.709	0.01160	0.03843
RNA binding motif protein 43	RBM43	2.179	0.00196	0.01256
RNA binding motif protein 4B	RBM4B	1.789	0.00012	0.00221
RNA binding protein with multiple splicing	RBPMS	-2.680	0.00017	0.00274
RNA binding protein with multiple splicing /// succinate dehydrogenase complex, subunit A, flavoprotein pseudogene 2	RBPMS /// SDHALP2	-4.830	0.01890	0.05309
RNA terminal phosphate cyclase-like 1	RCL1	-2.034	0.00550	0.02412
roundabout, axon guidance receptor, homolog 1 (Drosophila)	ROBO1	1.998	0.00018	0.00285
RPGRIP1-like	RPGRIP1L	1.681	0.01510	0.04579
RPTOR independent companion of MTOR, complex 2	RICTOR	-2.003	0.00633	0.02630
RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	RRS1	-1.568	0.00028	0.00363
R-spondin 2 homolog (Xenopus laevis)	RSPO2	12.759	0.00000	0.00002
RUN and SH3 domain containing 1	RUSC1	1.744	0.00034	0.00418
runt-related transcription factor 1	RUNX1	2.403	0.00020	0.00297
runt-related transcription factor 2	RUNX2	2.428	0.00332	0.01738
RWD domain containing 2A	RWDD2A	1.656	0.00007	0.00161
ryanodine receptor 2 (cardiac)	RYR2	-36.703	0.01850	0.05236
S100 calcium binding protein A10	S100A10	1.778	0.00002	0.00063
S100 calcium binding protein A4	S100A4	1.821	0.00082	0.00720
S100 calcium binding protein A8	S100A8	-12.524	0.01760	0.05063
S100 calcium binding protein B	S100B	1.768	0.01900	0.05324
SAC3 domain containing 1	SAC3D1	1.816	0.00000	0.00013
sal-like 1 (Drosophila)	SALL1	1.826	0.03160	0.07408
sal-like 2 (Drosophila)	SALL2	1.790	0.00272	0.01523
sal-like 3 (Drosophila)	SALL3	1.977	0.01160	0.03843
salt-inducible kinase 1	SIK1	-77.212	0.00000	0.00020
SAM domain and HD domain 1	SAMHD1	-9.781	0.00047	0.00509
SAP domain containing ribonucleoprotein	SARNP	-2.138	0.00023	0.00328
sarcolemma associated protein	SLMAP	-14.760	0.04200	0.08841
SATB homeobox 2	SATB2	2.786	0.00001	0.00059
scavenger receptor class A, member 3	SCARA3	4.584	0.00001	0.00046
scavenger receptor class A, member 5 (putative)	SCARA5	1.935	0.01200	0.03929
scavenger receptor class B, member 1	SCARB1	2.177	0.00000	0.00003
schlafen family member 11	SLFN11	2.444	0.00004	0.00112
schlafen family member 12	SLFN12	1.703	0.00073	0.00667
schlafen family member 13	SLFN13	1.789	0.00910	0.03310
Scm-like with four mbt domains 2	SFMBT2	-1.782	0.03100	0.07314
SCO cytochrome oxidase deficient homolog 2 (yeast)	SCO2	1.834	0.00011	0.00206
SEC16 homolog B (S. cerevisiae)	SEC16B	2.451	0.00001	0.00046
SEC24 family, member D (S. cerevisiae)	SEC24D	1.794	0.00580	0.02491
secretagogin, EF-hand calcium binding protein	SCGN	-7.862	0.00893	0.03275
secreted frizzled-related protein 2	SFRP2	2.978	0.00082	0.00719
secreted protein, acidic, cysteine-rich (osteonectin)	SPARC	1.658	0.00217	0.01334
secretogranin II (chromogranin C)	SCG2	3.595	0.00017	0.00275

selectin L	SELL	2.344	0.00443	0.02098
selectin P (granule membrane protein 140kDa, antigen CD62)	SELP	2.789	0.00048	0.00520
selenoprotein W, 1	SEPW1	-1.796	0.04330	0.09004
selenoprotein X, 1	SEPX1	-2.555	0.00053	0.00553
sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	SEMA3A	1.707	0.03400	0.07748
sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B	SEMA3B	1.947	0.00029	0.00375
sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	SEMA3C	2.471	0.00388	0.01926
sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F	SEMA3F	-4.126	0.00592	0.02522
sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F	SEMA4F	2.040	0.00000	0.00010
sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	SEMA5A	-2.384	0.00226	0.01362
sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	SEMA6D	1.625	0.01840	0.05217
Septin 11	11-Sep	-2.443	0.00494	0.02255
septin 13	13-Sep	-1.830	0.03090	0.07295
septin 6	6-Sep	2.059	0.00014	0.00239
septin 8	8-Sep	2.142	0.00000	0.00009
serglycin	SRGN	-4.830	0.00002	0.00083
serine active site containing 1	SERAC1	1.771	0.00206	0.01294
serine hydroxymethyltransferase 2 (mitochondrial)	SHMT2	1.793	0.01180	0.03884
Serine palmitoyltransferase, long chain base subunit 2	SPTLC2	1.514	0.01450	0.04451
serine palmitoyltransferase, long chain base subunit 3	SPTLC3	1.705	0.00000	0.00027
serine peptidase inhibitor, Kazal type 5	SPINK5	1.802	0.01070	0.03655
serine peptidase inhibitor, Kunitz type, 2	SPINT2	-6.371	0.00196	0.01256
serine racemase	SRR	1.615	0.04910	0.09742
serine/threonine kinase 17a	STK17A	1.741	0.00169	0.01137
serine/threonine kinase 17b	STK17B	-3.616	0.00645	0.02663
serine/threonine kinase 24 (STE20 homolog, yeast)	STK24	-1.638	0.04960	0.09797
serine/threonine-protein kinase NIM1	MGC42105	1.741	0.00008	0.00170
serpin peptidase inhibitor, clade B (ovalbumin), member 9	SERPINB9	-4.978	0.00931	0.03355
serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	SERPINE2	2.149	0.00005	0.00127
serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	SERPINH1	1.941	0.00096	0.00797
SERTA domain containing 4	SERTAD4	7.670	0.00000	0.00002
serum response factor (c-fos serum response element-binding transcription factor)	SRF	-2.275	0.00485	0.02232
serum/glucocorticoid regulated kinase 1	SGK1	-4.519	0.00042	0.00472
sestrin 1	SESN1	-2.026	0.00344	0.01782
SET domain and mariner transposase fusion gene	SETMAR	-1.760	0.00022	0.00317
SET domain containing 4	SETD4	1.837	0.00147	0.01042
seven in absentia homolog 2 (Drosophila)	SIAH2	-1.543	0.01700	0.04945
sex comb on midleg-like 1 (Drosophila)	SCML1	-2.228	0.02950	0.07069
SFRS protein kinase 2	SRPK2	1.501	0.00199	0.01267
SH2 domain containing 4A	SH2D4A	1.592	0.00023	0.00327
SH3 domain containing ring finger 3	SH3RF3	-1.758	0.00003	0.00096
SH3-domain binding protein 5 (BTK-associated)	SH3BP5	-2.345	0.00025	0.00340
SH3-domain GRB2-like (endophilin) interacting protein 1	SGIP1	1.712	0.01040	0.03593
SH3-domain kinase binding protein 1	SH3KBP1	2.038	0.00082	0.00719
short coiled-coil protein	SCOC	-1.677	0.02280	0.05992

short stature homeobox 2	SHOX2	-4.655	0.01670	0.04885
shroom family member 1	SHROOM1	1.720	0.00219	0.01340
shroom family member 4	SHROOM4	1.846	0.00055	0.00567
Shwachman-Bodian-Diamond syndrome /// Shwachman-Bodian-Diamond syndrome pseudogene	SBDS /// SBDSP	-1.636	0.00012	0.00226
sialic acid binding Ig-like lectin 10 /// sialic acid binding Ig-like lectin 12	SIGLEC10 /// SIGLEC12	-2.067	0.00727	0.02876
sidekick homolog 2 (chicken)	SDK2	2.117	0.00001	0.00038
sideroflexin 1	SFXN1	1.767	0.00267	0.01507
sideroflexin 2	SFXN2	-1.546	0.00280	0.01553
sideroflexin 3	SFXN3	1.740	0.00002	0.00067
signal peptide, CUB domain, EGF-like 2	SCUBE2	1.656	0.00419	0.02022
signal peptide, CUB domain, EGF-like 3	SCUBE3	-8.588	0.04540	0.09263
signal-regulatory protein alpha	SIRPA	2.025	0.00009	0.00185
similar to DTW domain containing 2	LOC729839	1.963	0.00011	0.00205
similar to erlectin	LOC100292863	2.185	0.00238	0.01407
Similar to FRAS1 related extracellular matrix protein 2	LOC650794	2.459	0.00894	0.03275
similar to hCG1744891	LOC100289026	2.938	0.00687	0.02769
similar to hCG1747809 /// SHC (Src homology 2 domain containing) transforming protein 2	LOC100291393 /// SHC2	1.653	0.00895	0.03278
similar to hCG1811002	LOC100134361	2.077	0.00012	0.00215
similar to hCG2006445	LOC100287032	-1.770	0.01440	0.04432
Similar to hCG2030186	LOC729070	-15.289	0.03130	0.07364
similar to HSPC047 protein /// similar to HSPC047 protein /// RAS p21 protein activator 4	LOC100286937 /// LOC100287164 /// RASA4	1.852	0.00834	0.03134
similar to hypothetical protein 9630041N07	DKFZp686E2433	1.553	0.00089	0.00758
Similar to LOC166075	LOC401097	4.821	0.00074	0.00672
similar to NADH dehydrogenase subunit 2	LOC100131754	-1.617	0.01880	0.05288
similar to olfactory receptor, family 7, subfamily A, member 17	LOC441453	1.512	0.00050	0.00532
similar to PTPRF interacting protein binding protein 1 /// PTPRF interacting protein, binding protein 1 (liprin beta 1)	LOC729222 /// PPFIBP1	1.821	0.01840	0.05217
similar to R28379_1	LOC390940	1.521	0.00001	0.00047
similar to ribosomal protein S21 /// ribosomal protein S21	LOC100291837 /// RPS21	-1.505	0.00014	0.00243
sine oculis binding protein homolog (Drosophila)	SOBP	1.505	0.00828	0.03117
SIX homeobox 4	SIX4	1.547	0.02230	0.05907
six transmembrane epithelial antigen of the prostate 1	STEAP1	2.710	0.00299	0.01621
SLAIN motif family, member 1	SLAIN1	1.504	0.02090	0.05673
SLC2A4 regulator	SLC2A4RG	1.604	0.00042	0.00474
slingshot homolog 2 (Drosophila)	SSH2	-2.084	0.03920	0.08480
SLIT-ROBO Rho GTPase activating protein 1	SRGAP1	-1.657	0.03270	0.07574
small ArfGAP2	SMAP2	-1.976	0.00014	0.00238
small Cajal body-specific RNA 17	SCARNA17	-2.379	0.00113	0.00885
small G protein signaling modulator 1	SGSM1	1.568	0.02370	0.06141
small G protein signaling modulator 2	SGSM2	1.575	0.00612	0.02581
small nucleolar RNA host gene 8 (non-protein coding)	SNHG8	-1.711	0.00373	0.01880
small nucleolar RNA, C/D box 104	SNORD104	-1.569	0.03660	0.08124
small VCP/p97-interacting protein	SVIP	-1.727	0.00346	0.01790
SMEK homolog 1, suppressor of mek1 (Dictyostelium)	SMEK1	-2.164	0.01270	0.04072
SMEK homolog 2, suppressor of mek1 (Dictyostelium)	SMEK2	-1.690	0.00696	0.02797
smoothelin	SMTN	-5.416	0.04450	0.09147
sodium channel, voltage-gated, type I, beta	SCN1B	1.522	0.00389	0.01928
sodium channel, voltage-gated, type II, alpha subunit	SCN2A	3.784	0.00342	0.01774

sodium channel, voltage-gated, type III, alpha subunit	SCN3A	-8.784	0.02410	0.06209
sodium channel, voltage-gated, type IV, beta	SCN4B	1.832	0.00481	0.02219
sodium channel, voltage-gated, type IX, alpha subunit	SCN9A	1.737	0.00078	0.00698
sodium channel, voltage-gated, type VII, alpha	SCN7A	-3.020	0.04090	0.08696
sodium leak channel, non-selective	NALCN	2.785	0.00006	0.00144
solute carrier family 1 (glial high affinity glutamate transporter), member 2	SLC1A2	2.603	0.00001	0.00033
solute carrier family 1 (glial high affinity glutamate transporter), member 3	SLC1A3	-6.085	0.00625	0.02609
solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	SLC1A4	2.205	0.00002	0.00069
solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	SLC11A1	-1.721	0.01040	0.03593
solute carrier family 12 (potassium/chloride transporters), member 8	SLC12A8	1.874	0.00283	0.01563
solute carrier family 16, member 2 (monocarboxylic acid transporter 8)	SLC16A2	1.574	0.00364	0.01852
solute carrier family 16, member 9 (monocarboxylic acid transporter 9)	SLC16A9	-2.153	0.01860	0.05251
solute carrier family 17 (anion/sugar transporter), member 5	SLC17A5	1.814	0.00578	0.02488
solute carrier family 19 (thiamine transporter), member 2	SLC19A2	-5.923	0.00001	0.00039
solute carrier family 2 (facilitated glucose transporter), member 10	SLC2A10	2.117	0.00002	0.00084
solute carrier family 2 (facilitated glucose transporter), member 6	SLC2A6	2.397	0.00000	0.00017
solute carrier family 20 (phosphate transporter), member 1	SLC20A1	1.508	0.00121	0.00921
solute carrier family 22, member 23	SLC22A23	2.244	0.00566	0.02458
solute carrier family 25 (mitochondrial carrier), member 18	SLC25A18	-1.717	0.00370	0.01870
solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	SLC25A5	-1.659	0.00288	0.01578
solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 25	SLC25A25	-1.832	0.00001	0.00039
solute carrier family 25, member 29	SLC25A29	-1.561	0.00328	0.01725
solute carrier family 25, member 33	SLC25A33	-2.377	0.00003	0.00092
solute carrier family 25, member 45	SLC25A45	1.596	0.00066	0.00630
solute carrier family 26 (sulfate transporter), member 2	SLC26A2	1.653	0.00157	0.01086
solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	SLC3A2	-1.584	0.00490	0.02247
solute carrier family 35, member B2	SLC35B2	1.775	0.00000	0.00029
solute carrier family 35, member B4	SLC35B4	1.700	0.00231	0.01380
solute carrier family 35, member E4	SLC35E4	1.547	0.00003	0.00099
solute carrier family 35, member F1	SLC35F1	-2.096	0.02550	0.06439
solute carrier family 35, member F2	SLC35F2	2.065	0.00781	0.03002
solute carrier family 36 (proton/amino acid symporter), member 4	SLC36A4	-1.868	0.00893	0.03275
solute carrier family 38, member 10	SLC38A10	1.633	0.00570	0.02468
solute carrier family 38, member 2	SLC38A2	-1.917	0.00019	0.00288
solute carrier family 39 (zinc transporter), member 10	SLC39A10	1.745	0.00100	0.00816
solute carrier family 39 (zinc transporter), member 14	SLC39A14	-2.405	0.00022	0.00320
solute carrier family 4, sodium bicarbonate cotransporter, member 4	SLC4A4	2.407	0.02700	0.06680
Solute carrier family 4, sodium bicarbonate cotransporter, member 5	SLC4A5	-1.557	0.01100	0.03720
solute carrier family 46 (folate transporter), member 1	SLC46A1	1.654	0.00087	0.00746
solute carrier family 47, member 1	SLC47A1	1.784	0.01540	0.04633
solute carrier family 6 (neurotransmitter transporter, serotonin), member 4	SLC6A4	-5.117	0.01890	0.05309
Solute carrier family 6, member 16	SLC6A16	-1.971	0.03860	0.08403
solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	SLC7A2	-13.648	0.00298	0.01617
solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	SLC7A7	-1.600	0.00744	0.02916
solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	SLC7A8	-5.100	0.00010	0.00194

solute carrier organic anion transporter family, member 2A1	SLCO2A1	-4.395	0.03110	0.07326
solute carrier organic anion transporter family, member 4A1	SLCO4A1	-10.816	0.00467	0.02173
somatostatin receptor 2	SSTR2	3.129	0.00099	0.00813
son of sevenless homolog 2 (Drosophila)	SOS2	-1.544	0.00026	0.00355
sorbin and SH3 domain containing 1	SORBS1	-2.681	0.00782	0.03004
sorbitol dehydrogenase	SORD	2.260	0.00080	0.00710
sortilin 1	SORT1	-1.710	0.00273	0.01527
sorting nexin 13	SNX13	-1.638	0.00266	0.01503
sorting nexin 16	SNX16	-1.646	0.00517	0.02315
sorting nexin 18	SNX18	1.570	0.00010	0.00194
sorting nexin 25	SNX25	-1.518	0.00303	0.01637
sorting nexin 33	SNX33	1.501	0.01080	0.03676
sorting nexin family member 30	SNX30	1.935	0.00005	0.00131
SPARC related modular calcium binding 1	SMOC1	-4.062	0.04470	0.09177
speckle-type POZ protein-like	SPOPL	-1.684	0.00551	0.02415
spectrin repeat containing, nuclear envelope 2	SYNE2	-3.335	0.03770	0.08278
spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	SPTAN1	1.577	0.01350	0.04247
spectrin, beta, non-erythrocytic 1	SPTBN1	1.596	0.01250	0.04030
spen homolog, transcriptional regulator (Drosophila)	SPEN	-1.859	0.00541	0.02388
sperm associated antigen 1	SPAG1	1.533	0.00521	0.02327
sperm associated antigen 8	SPAG8	1.720	0.00037	0.00439
spermatogenesis associated 18 homolog (rat)	SPATA18	1.963	0.00469	0.02180
S-phase kinase-associated protein 2 (p45)	SKP2	1.616	0.00801	0.03052
sphingosine-1-phosphate receptor 3	S1PR3	-3.598	0.04310	0.08982
spindlin family, member 3	SPIN3	2.047	0.00003	0.00085
splicing factor, arginine/serine-rich 12	SFRS12	-2.081	0.04000	0.08582
splicing factor, arginine/serine-rich 3	SFRS3	-1.502	0.04010	0.08597
spondin 1, extracellular matrix protein	SPON1	-2.192	0.02670	0.06637
spondin 2, extracellular matrix protein	SPON2	2.970	0.00012	0.00221
sprouty homolog 4 (Drosophila)	SPRY4	-1.969	0.00029	0.00375
Src-like-adaptor	SLA	-3.822	0.00326	0.01718
SRY (sex determining region Y)-box 13	SOX13	-1.784	0.00007	0.00163
SRY (sex determining region Y)-box 4	SOX4	1.539	0.00077	0.00688
SRY (sex determining region Y)-box 6	SOX6	1.674	0.00715	0.02841
SRY (sex determining region Y)-box 8	SOX8	3.137	0.00004	0.00104
SRY (sex determining region Y)-box 9	SOX9	1.590	0.02300	0.06018
ST3 beta-galactoside alpha-2,3-sialyltransferase 1	ST3GAL1	-3.104	0.00000	0.00007
ST3 beta-galactoside alpha-2,3-sialyltransferase 4	ST3GAL4	2.199	0.00001	0.00051
ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	ST6GALNAC2	2.667	0.00022	0.00315
ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 3	ST6GALNAC3	-5.162	0.00922	0.03333
ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5	ST6GALNAC5	-30.205	0.03940	0.08504
ST6 beta-galactosamide alpha-2,6-sialyltranferase 2	ST6GAL2	-16.891	0.03800	0.08322
ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1	ST8SIA1	2.590	0.00039	0.00459
STAM binding protein-like 1	STAMBPL1	5.981	0.00000	0.00007
stanniocalcin 2	STC2	-4.474	0.01620	0.04786
STARD3 N-terminal like	STARD3NL	-1.628	0.00003	0.00097
StAR-related lipid transfer (START) domain containing 13	STARD13	-1.548	0.00071	0.00657
StAR-related lipid transfer (START) domain containing 4	STARD4	-7.676	0.04170	0.08797
StAR-related lipid transfer (START) domain containing 8	STARD8	-2.057	0.00296	0.01611
StAR-related lipid transfer (START) domain containing 9	STARD9	1.620	0.00130	0.00963

stathmin-like 3	STMN3	1.761	0.00003	0.00100
STEAP family member 3	STEAP3	3.067	0.00000	0.00005
STEAP family member 4	STEAP4	1.528	0.00943	0.03381
STEAP family protein MGC87042	MGC87042	2.175	0.00070	0.00654
stearoyl-CoA desaturase (delta-9-desaturase)	SCD	4.430	0.00001	0.00051
sterile alpha motif and leucine zipper containing kinase AZK	ZAK	-1.713	0.04680	0.09448
sterile alpha motif domain containing 11	SAMD11	1.520	0.00496	0.02261
sterile alpha motif domain containing 13	SAMD13	3.299	0.00002	0.00075
sterile alpha motif domain containing 5	SAMD5	1.929	0.00626	0.02612
sterile alpha motif domain containing 9	SAMD9	1.546	0.00007	0.00163
sterile alpha motif domain containing 9-like	SAMD9L	1.945	0.00102	0.00824
steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	SRD5A1	1.902	0.00126	0.00945
sterol regulatory element binding transcription factor 1	SREBF1	1.577	0.01620	0.04786
stimulated by retinoic acid gene 6 homolog (mouse)	STRA6	1.521	0.01950	0.05408
stimulator of chondrogenesis 1	SCRG1	1.879	0.00176	0.01166
stonin 1	STON1	-1.601	0.00424	0.02038
stonin 2	STON2	2.428	0.00899	0.03288
stratifin	SFN	3.767	0.02100	0.05688
stromal interaction molecule 1	STIM1	-1.604	0.01800	0.05148
SUB1 homolog (S. cerevisiae)	SUB1	-1.617	0.00223	0.01351
sulfatase 2	SULF2	1.950	0.02770	0.06779
SUMO1/sentrin specific peptidase 5	SENP5	-1.649	0.00013	0.00233
SUMO1/sentrin/SMT3 specific peptidase 2	SENP2	-1.621	0.04380	0.09061
superoxide dismutase 2, mitochondrial	SOD2	-2.318	0.00042	0.00476
suppressor of cancer cell invasion	SCAI	1.901	0.00254	0.01462
suppressor of cytokine signaling 2	SOCS2	-2.383	0.04030	0.08623
suppressor of cytokine signaling 3	SOCS3	-1.845	0.04340	0.09014
survival of motor neuron 1, telomeric /// survival of motor neuron 2, centromeric	SMN1 /// SMN2	-1.501	0.00366	0.01859
sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	SVEP1	-1.671	0.00498	0.02264
sushi-repeat-containing protein, X-linked	SRPX	-1.625	0.00908	0.03306
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	SMARCC1	-1.744	0.03470	0.07845
synaptic vesicle glycoprotein 2A	SV2A	1.985	0.00192	0.01240
synaptogyrin 2	SYNGR2	-2.722	0.02860	0.06929
synaptojanin 2	SYNJ2	1.797	0.00371	0.01874
synaptonemal complex protein SC65	SC65	2.092	0.00002	0.00071
synaptopodin	SYNPO	1.566	0.00215	0.01325
synaptopodin 2	SYNPO2	-3.665	0.00695	0.02793
synaptotagmin XI	SYT11	1.830	0.00011	0.00206
synaptotagmin XVII	SYT17	3.535	0.00003	0.00092
syndecan 3	SDC3	1.547	0.00914	0.03316
synovial sarcoma, X breakpoint 2 interacting protein	SSX2IP	2.842	0.00087	0.00747
syntaphilin	SNPH	1.596	0.00005	0.00121
syntaxin 10	STX10	1.663	0.00024	0.00335
syntaxin 11	STX11	-2.287	0.02540	0.06425
syntrophin, alpha 1 (dystrophin-associated protein A1, 59kDa, acidic component)	SNTA1	-2.627	0.04600	0.09346
syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)	SNTB1	1.767	0.00136	0.00990
synuclein, gamma (breast cancer-specific protein 1)	SNCG	-1.533	0.02410	0.06209
TAF5-like RNA polymerase II, p300/CBP-associated factor (PCAF)-	TAF5L	-2.428	0.00472	0.02190

associated factor, 65kDa				
TAF8 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 43kDa	TAF8	-1.711	0.03270	0.07574
TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa	TAF9	-1.540	0.01050	0.03614
TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	TAF9B	-1.636	0.03370	0.07709
TAR (HIV-1) RNA binding protein 1	TARBP1	1.519	0.01360	0.04266
target of myb1-like 2 (chicken)	TOM1L2	-1.752	0.02100	0.05688
taspase, threonine aspartase, 1	TASP1	-1.677	0.01350	0.04247
TATA box binding protein (TBP)-associated factor, RNA polymerase I, A, 48kDa	TAF1A	1.797	0.00257	0.01472
TATA box binding protein (TBP)-associated factor, RNA polymerase I, B, 63kDa	TAF1B	1.556	0.00379	0.01900
TATA box binding protein (TBP)-associated factor, RNA polymerase I, D, 41kDa	TAF1D	-1.602	0.00007	0.00159
TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	TBC1D1	-2.281	0.00172	0.01151
TBC1 domain family, member 24	TBC1D24	3.146	0.00000	0.00003
TBC1 domain family, member 8B (with GRAM domain)	TBC1D8B	2.278	0.00003	0.00097
T-box 15	TBX15	1.741	0.02000	0.05509
TBP-like 1	TBPL1	-1.565	0.00320	0.01698
TCDD-inducible poly(ADP-ribose) polymerase	TIPARP	-3.350	0.00153	0.01070
T-cell acute lymphocytic leukemia 1	TAL1	-1.874	0.02770	0.06779
T-cell lymphoma invasion and metastasis 2	TIAM2	1.885	0.00477	0.02205
TEA domain family member 3	TEAD3	-2.679	0.00295	0.01606
teashirt zinc finger homeobox 2	TSHZ2	1.943	0.01270	0.04072
teashirt zinc finger homeobox 3	TSHZ3	1.949	0.00000	0.00023
tenascin XA pseudogene /// tenascin XB	TNXA /// TNXB	2.145	0.00037	0.00434
tenascin XB	TNXB	2.313	0.00047	0.00507
tensin 1	TNS1	-2.555	0.00076	0.00687
tensin like C1 domain containing phosphatase (tensin 2)	TENC1	-1.785	0.00003	0.00095
testis expressed 11	TEX11	2.574	0.01480	0.04516
testis specific, 14	TSGA14	1.714	0.00020	0.00297
tet oncogene 1	TET1	1.713	0.00008	0.00177
tetraspanin 14	TSPAN14	-1.535	0.00001	0.00047
tetraspanin 33	TSPAN33	1.767	0.00608	0.02569
tetraspanin 4	TSPAN4	1.727	0.00603	0.02553
tetratricopeptide repeat domain 30A	TTC30A	1.699	0.00014	0.00241
tetratricopeptide repeat domain 30B	TTC30B	2.469	0.00001	0.00047
tetratricopeptide repeat domain 7A	TTC7A	1.520	0.00024	0.00333
tetratricopeptide repeat domain 9C	TTC9C	1.857	0.00038	0.00448
tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	TANC2	2.499	0.00000	0.00013
TGF beta-inducible nuclear protein 1	TINP1	-1.572	0.00084	0.00728
TGFB-induced factor homeobox 1	TGIF1	-8.595	0.00408	0.01990
THAP domain containing, apoptosis associated protein 2	THAP2	2.305	0.00013	0.00228
thioredoxin interacting protein	TXNIP	-4.566	0.00000	0.00020
thioredoxin reductase 1	TXNRD1	-3.298	0.00000	0.00002
thioredoxin-like 4B	TXNL4B	-2.118	0.00185	0.01204
threonine synthase-like 1 (S. cerevisiae)	THNSL1	2.529	0.00000	0.00016
Thrombospondin 1	THBS1	-3.693	0.04380	0.09061
thrombospondin 3	THBS3	1.807	0.00434	0.02068
thrombospondin 4	THBS4	-6.097	0.04250	0.08908
thromboxane A synthase 1 (platelet)	TBXAS1	-1.522	0.01930	0.05384
Thy-1 cell surface antigen	THY1	2.229	0.04020	0.08609

thymic stromal lymphopoietin	TSLP	-2.122	0.02780	0.06797
thymidylate synthetase	TYMS	3.347	0.00016	0.00259
tigger transposable element derived 1	TIGD1	1.766	0.00133	0.00977
tigger transposable element derived 2	TIGD2	1.551	0.02060	0.05620
tight junction protein 2 (zona occludens 2)	TJP2	-1.909	0.00653	0.02686
TIMP metallopeptidase inhibitor 3	TIMP3	1.504	0.00698	0.02801
Tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	TFPI	-2.904	0.02250	0.05936
TLR4 interactor with leucine rich repeats	TRIL	10.025	0.00000	0.00002
TNFAIP3 interacting protein 1	TNIP1	-1.615	0.01580	0.04710
toll-like receptor 1	TLR1	1.542	0.03330	0.07653
toll-like receptor 2	TLR2	-5.470	0.00795	0.03033
toll-like receptor 3	TLR3	3.880	0.00000	0.00013
toll-like receptor 5	TLR5	1.535	0.03200	0.07469
toll-like receptor 7	TLR7	3.765	0.00031	0.00390
toll-like receptor adaptor molecule 2 /// TMED7-TICAM2 read-through transcript	TICAM2 /// TMED7-TICAM2	1.830	0.00348	0.01797
topoisomerase (DNA) I	TOP1	-1.542	0.00000	0.00006
TPTE and PTEN homologous inositol lipid phosphatase pseudogene	LOC374491	1.603	0.00744	0.02916
TPTE pseudogene	psiTPTE22	2.880	0.00659	0.02702
TRAF2 and NCK interacting kinase	TNIK	1.952	0.00829	0.03120
transcription elongation factor A (SII) N-terminal and central domain containing	TCEANC	1.666	0.00135	0.00986
transcription elongation factor A (SII), 3	TCEA3	1.799	0.00212	0.01315
transcription elongation factor A (SII)-like 1	TCEAL1	-2.122	0.00002	0.00084
transcription elongation factor A (SII)-like 3	TCEAL3	-1.510	0.00031	0.00390
transcription elongation factor A (SII)-like 4	TCEAL4	-1.873	0.00002	0.00078
transcription elongation factor A (SII)-like 7	TCEAL7	1.796	0.01120	0.03762
transcription factor 12	TCF12	1.549	0.00051	0.00539
transcription factor 19	TCF19	2.539	0.00000	0.00009
transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	TCF3	1.640	0.00002	0.00067
transcription factor 4	TCF4	1.987	0.00002	0.00071
transcription factor CP2-like 1	TFCP2L1	-1.943	0.00474	0.02196
transcription factor Dp-2 (E2F dimerization partner 2)	TFDP2	-1.655	0.00353	0.01814
transcription factor EC	TFEC	-2.777	0.02750	0.06753
transcriptional regulating factor 1	TRERF1	5.877	0.00000	0.00002
transducer of ERBB2, 2	TOB2	-2.732	0.00585	0.02508
transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)	TLE1	-2.726	0.00008	0.00169
transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)	TLE3	1.588	0.00001	0.00034
transferrin receptor (p90, CD71)	TFRC	-2.123	0.00012	0.00225
transformer 2 beta homolog (Drosophila)	TRA2B	-2.440	0.00175	0.01163
transforming growth factor, beta 2	TGFB2	2.417	0.00177	0.01170
transforming growth factor, beta 3	TGFB3	2.020	0.00028	0.00368
transforming growth factor, beta receptor III	TGFBR3	-1.585	0.02520	0.06393
transforming, acidic coiled-coil containing protein 1	TACC1	-1.869	0.00375	0.01887
transgelin	TAGLN	-5.957	0.00825	0.03111
transgelin 2	TAGLN2	1.787	0.00001	0.00052
transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	TGM2	-2.754	0.02680	0.06645
transient receptor potential cation channel, subfamily C, member 4	TRPC4	-3.320	0.02230	0.05907
transient receptor potential cation channel, subfamily V, member 2	TRPV2	2.180	0.00000	0.00016
translocase of inner mitochondrial membrane 23 homolog (yeast)	TIMM23	-2.417	0.00017	0.00276

translocase of outer mitochondrial membrane 22 homolog (yeast)	TOMM22	-1.571	0.04770	0.09571
translocation associated membrane protein 1-like 1	TRAM1L1	3.641	0.00000	0.00016
translocation associated membrane protein 2	TRAM2	2.460	0.00162	0.01108
transmembrane and coiled-coil domain family 3	TMCC3	-2.466	0.01090	0.03700
transmembrane and tetratricopeptide repeat containing 2	TMTC2	5.610	0.00133	0.00977
transmembrane and tetratricopeptide repeat containing 4	TMTC4	1.921	0.00947	0.03392
transmembrane anterior posterior transformation 1	TAPT1	-1.836	0.00002	0.00076
Transmembrane emp24 protein transport domain containing 5	TMED5	-1.985	0.00222	0.01349
transmembrane protein 106A	TMEM106A	1.897	0.00000	0.00006
transmembrane protein 107	TMEM107	1.957	0.00125	0.00941
transmembrane protein 130	TMEM130	-9.515	0.04310	0.08982
transmembrane protein 132B	TMEM132B	1.547	0.00002	0.00061
transmembrane protein 132E	TMEM132E	2.597	0.00030	0.00384
transmembrane protein 150A	TMEM150A	-1.623	0.00004	0.00111
transmembrane protein 154	TMEM154	1.585	0.03610	0.08054
transmembrane protein 159	TMEM159	-1.767	0.00063	0.00616
transmembrane protein 164	TMEM164	-1.839	0.01040	0.03593
transmembrane protein 17	TMEM17	1.971	0.00003	0.00091
transmembrane protein 18	TMEM18	-1.794	0.00012	0.00218
transmembrane protein 180	TMEM180	1.509	0.00099	0.00809
transmembrane protein 192 /// zinc finger protein 320	TMEM192 /// ZNF320	-1.696	0.00076	0.00687
transmembrane protein 20	TMEM20	1.720	0.00398	0.01958
transmembrane protein 204	TMEM204	-1.900	0.01300	0.04135
transmembrane protein 206	TMEM206	1.809	0.02190	0.05840
transmembrane protein 37	TMEM37	2.058	0.00026	0.00346
transmembrane protein 38B	TMEM38B	-3.049	0.00549	0.02412
transmembrane protein 44	TMEM44	1.742	0.00577	0.02484
transmembrane protein 71	TMEM71	1.623	0.03180	0.07441
transmembrane protein 97	TMEM97	-2.826	0.00808	0.03069
transmembrane protein with EGF-like and two follistatin-like domains 2	TMEFF2	-9.995	0.00480	0.02217
Transportin 1	TNPO1	-2.886	0.04710	0.09487
tribbles homolog 3 (Drosophila)	TRIB3	2.122	0.00033	0.00406
trichoplein, keratin filament binding	TCHP	1.512	0.00000	0.00024
trichorhinophalangeal syndrome I	TRPS1	1.600	0.00205	0.01291
triggering receptor expressed on myeloid cells 2	TREM2	1.655	0.02970	0.07100
tripartite motif-containing 2	TRIM2	1.691	0.00002	0.00080
tripartite motif-containing 25	TRIM25	2.057	0.00386	0.01921
tripartite motif-containing 34 /// TRIM6-TRIM34 readthrough transcript	TRIM34 /// TRIM6-TRIM34	2.860	0.00000	0.00025
tripartite motif-containing 45	TRIM45	1.768	0.00010	0.00198
tripartite motif-containing 47	TRIM47	1.644	0.00590	0.02518
tripartite motif-containing 59	TRIM59	2.381	0.00163	0.01112
tripartite motif-containing 6	TRIM6	3.553	0.00006	0.00145
tripartite motif-containing 61	TRIM61	1.808	0.00111	0.00874
tripartite motif-containing 7	TRIM7	2.260	0.00007	0.00159
tripartite motif-containing 8	TRIM8	1.550	0.00000	0.00019
tRNA-histidine guanylyltransferase 1-like (S. cerevisiae)	THG1L	-1.551	0.00089	0.00758
trophinin	TRO	1.764	0.00010	0.00200
tropomyosin 2 (beta)	TPM2	-5.273	0.00369	0.01867
TSC22 domain family, member 1	TSC22D1	-2.820	0.00252	0.01454
TSC22 domain family, member 3	TSC22D3	-5.016	0.00031	0.00388

TSPY-like 2	TSPYL2	-1.974	0.00000	0.00026
tubby homolog (mouse)	TUB	1.635	0.00691	0.02779
tubulin tyrosine ligase-like family, member 1	TTLL1	1.693	0.00082	0.00718
tubulin, beta 2A	TUBB2A	2.099	0.00000	0.00021
tubulin, beta 2A /// tubulin, beta 2B	TUBB2A /// TUBB2B	1.697	0.00239	0.01411
tubulin, beta 2B	TUBB2B	6.329	0.00009	0.00179
tubulointerstitial nephritis antigen-like 1	TINAGL1	-2.090	0.00772	0.02978
tudor domain containing 9	TDRD9	-1.938	0.02110	0.05698
tumor necrosis factor (ligand) superfamily, member 10	TNFSF10	2.605	0.00162	0.01108
tumor necrosis factor (ligand) superfamily, member 13b	TNFSF13B	6.244	0.00002	0.00073
tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain	TNFRSF10C	2.412	0.00001	0.00041
tumor necrosis factor receptor superfamily, member 21	TNFRSF21	2.338	0.00685	0.02765
tumor necrosis factor receptor superfamily, member 25	TNFRSF25	2.684	0.00130	0.00963
tumor necrosis factor receptor superfamily, member 8	TNFRSF8	1.625	0.00008	0.00167
tumor necrosis factor, alpha-induced protein 2	TNFAIP2	1.766	0.00519	0.02322
tumor necrosis factor, alpha-induced protein 6	TNFAIP6	5.420	0.00003	0.00091
tumor protein p53 inducible nuclear protein 2	TP53INP2	-2.503	0.02560	0.06458
tumor protein p53 inducible protein 3	TP53I3	2.263	0.00161	0.01104
tumor protein p63	TP63	1.897	0.00001	0.00033
tyrosylprotein sulfotransferase 1	TPST1	2.052	0.00066	0.00634
ubiquinol-cytochrome c reductase binding protein	UQCRB	-1.948	0.02730	0.06721
ubiquinol-cytochrome c reductase hinge protein	UQCRH	-1.893	0.03980	0.08562
ubiquitin protein ligase E3A	UBE3A	-1.686	0.00266	0.01503
ubiquitin protein ligase E3B	UBE3B	-2.142	0.02970	0.07100
ubiquitin specific peptidase 10	USP10	-1.649	0.03930	0.08491
ubiquitin specific peptidase 15	USP15	-1.889	0.00001	0.00033
ubiquitin specific peptidase 18	USP18	1.682	0.01010	0.03532
ubiquitin specific peptidase 25	USP25	-2.274	0.00035	0.00422
ubiquitin specific peptidase 31	USP31	-1.680	0.01540	0.04633
ubiquitin specific peptidase 33	USP33	-2.113	0.02250	0.05936
ubiquitin specific peptidase 53	USP53	-2.244	0.00250	0.01447
ubiquitin-conjugating enzyme E2B (RAD6 homolog)	UBE2B	-1.509	0.04830	0.09639
ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast)	UBE2D1	-1.850	0.01400	0.04354
ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, yeast)	UBE2G1	-1.592	0.00053	0.00553
ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast)	UBE2N	-1.880	0.00493	0.02252
ubiquitin-conjugating enzyme E2S	UBE2S	-1.712	0.00297	0.01614
ubiquitin-conjugating enzyme E2W (putative)	UBE2W	-1.586	0.00041	0.00471
ubiquitin-like modifier activating enzyme 2	UBA2	-1.796	0.00120	0.00917
ubiquitin-like modifier activating enzyme 7	UBA7	1.664	0.00404	0.01978
UBX domain protein 7	UBXN7	-1.603	0.01240	0.04009
UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4	B3GALT4	1.735	0.00000	0.00007
UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	B4GALT1	-5.979	0.00065	0.00626
UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 2	B4GALT2	2.510	0.00000	0.00029
UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	B3GNT2	-1.914	0.00028	0.00362
UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	B3GNT7	2.535	0.00025	0.00338
UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9	B3GNT9	1.555	0.00000	0.00006
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 12 (GalNAc-T12)	GALNT12	3.257	0.00006	0.00152
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 5 (GalNAc-T5)	GALNT5	3.562	0.00028	0.00366
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-	GALNTL1	3.466	0.00016	0.00264

acetylgalactosaminyltransferase-like 1				
UDP-N-acteylglucosamine pyrophosphorylase 1-like 1	UAP1L1	1.861	0.00045	0.00492
UL16 binding protein 2	ULBP2	1.901	0.00036	0.00429
Unc-5 homolog B (C. elegans)	UNC5B	1.794	0.00001	0.00061
unc-5 homolog C (C. elegans)	UNC5C	2.219	0.00712	0.02836
Uncharacterized protein LOC100131897	LOC100131897	4.643	0.00288	0.01578
uncharacterized serine/threonine-protein kinase SgK494	FLJ25006	1.682	0.00273	0.01527
uncoupling protein 2 (mitochondrial, proton carrier)	UCP2	1.702	0.01160	0.03843
unkempt homolog (Drosophila)	UNK	1.550	0.00027	0.00360
up-regulated during skeletal muscle growth 5 homolog (mouse)	USMG5	-1.527	0.01420	0.04393
uridine-cytidine kinase 2	UCK2	2.018	0.00066	0.00629
uveal autoantigen with coiled-coil domains and ankyrin repeats	UACA	1.504	0.03340	0.07666
vacuolar protein sorting 37 homolog A (S. cerevisiae)	VPS37A	-1.898	0.01170	0.03865
v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	AKT3	-1.703	0.00717	0.02847
vang-like 1 (van gogh, Drosophila)	VANGL1	2.429	0.00010	0.00199
vasodilator-stimulated phosphoprotein	VASP	-2.429	0.02250	0.05936
vav 2 guanine nucleotide exchange factor	VAV2	1.627	0.00000	0.00003
vav 3 guanine nucleotide exchange factor	VAV3	2.146	0.00357	0.01828
v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	ERBB4	1.867	0.02520	0.06393
versican	VCAN	1.505	0.04060	0.08656
vesicle amine transport protein 1 homolog (T. californica)	VAT1	1.719	0.00000	0.00009
vesicular, overexpressed in cancer, prosurvival protein 1	VOPP1	1.598	0.00000	0.00013
vestigial like 3 (Drosophila)	VGLL3	-5.040	0.00000	0.00016
v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	ETS2	1.675	0.00005	0.00126
vezatin, adherens junctions transmembrane protein	VEZT	-2.119	0.00014	0.00238
villin-like	VILL	2.011	0.00325	0.01716
vinculin	VCL	-4.349	0.04510	0.09228
vitamin D (1,25- dihydroxyvitamin D3) receptor	VDR	1.626	0.01960	0.05427
vitrin	VIT	-3.355	0.02080	0.05655
v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	MAF	1.983	0.00642	0.02654
v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	MAFF	-3.253	0.00004	0.00108
v-maf musculoaponeurotic fibrosarcoma oncogene homolog K (avian)	MAFK	-1.500	0.00079	0.00703
v-myb myeloblastosis viral oncogene homolog (avian)-like 1	MYBL1	-8.493	0.00025	0.00339
v-myc myelocytomatosis viral oncogene homolog (avian)	MYC	-2.732	0.00123	0.00930
voltage-dependent anion channel 1	VDAC1	-1.623	0.02630	0.06575
voltage-dependent anion channel 2	VDAC2	-1.602	0.01390	0.04334
von Hippel-Lindau tumor suppressor	VHL	1.630	0.00039	0.00458
von Willebrand factor A domain containing 5A	VWA5A	3.395	0.00034	0.00415
v-raf murine sarcoma viral oncogene homolog B1	BRAF	-1.856	0.00840	0.03145
WAP four-disulfide core domain 1	WFDC1	-74.326	0.00518	0.02319
WAS protein family, member 1	WASF1	-2.354	0.00023	0.00328
WAS protein family, member 3	WASF3	-1.540	0.03040	0.07216
WAS protein homolog associated with actin, golgi membranes and microtubules	WHAMM	-1.674	0.00000	0.00024
WD repeat and FYVE domain containing 2	WDFY2	-1.716	0.00738	0.02900
WD repeat domain 1	WDR1	-2.214	0.04110	0.08721
WD repeat domain 17	WDR17	1.694	0.00563	0.02447
WD repeat domain 33	WDR33	-1.516	0.00943	0.03381
WD repeat domain 51B	WDR51B	-1.532	0.00399	0.01960
WD repeat domain 54	WDR54	1.507	0.00202	0.01279
WD repeat domain 5B	WDR5B	1.623	0.00063	0.00616

WEE1 homolog (S. pombe)	WEE1	-5.926	0.00065	0.00623
Wilms tumor 1 associated protein	WTAP	-1.885	0.00061	0.00601
Wilms tumor 1 interacting protein	WTIP	-2.093	0.01860	0.05251
wingless-type MMTV integration site family, member 3	WNT3	1.645	0.00871	0.03223
wingless-type MMTV integration site family, member 5A	WNT5A	-6.090	0.04050	0.08643
wingless-type MMTV integration site family, member 5B	WNT5B	1.790	0.03530	0.07928
wingless-type MMTV integration site family, member 9A	WNT9A	1.932	0.00093	0.00783
WNK lysine deficient protein kinase 3	WNK3	-15.929	0.00012	0.00226
WNT1 inducible signaling pathway protein 1	WISP1	4.249	0.00008	0.00170
Wolf-Hirschhorn syndrome candidate 1-like 1	WHSC1L1	1.594	0.00207	0.01298
WW and C2 domain containing 2	WWC2	-1.560	0.03210	0.07482
WW domain containing E3 ubiquitin protein ligase 2	WWP2	2.567	0.00000	0.00013
xenotropic and polytropic retrovirus receptor	XPR1	-1.678	0.02830	0.06878
Xg blood group	XG	2.549	0.00043	0.00477
XIAP associated factor 1	XAF1	1.533	0.00184	0.01201
X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	XPNPEP1	1.581	0.00268	0.01509
xylosyltransferase I	XYLT1	2.256	0.00002	0.00077
xylosyltransferase II	XYLT2	1.514	0.00001	0.00049
Y box binding protein 1	YBX1	-1.850	0.00128	0.00954
Yes-associated protein 1, 65kDa	YAP1	-2.722	0.00697	0.02800
yippee-like 4 (Drosophila)	YPEL4	1.733	0.03010	0.07169
yrdC domain containing (E. coli)	YRDC	-1.765	0.00018	0.00285
YTH domain containing 1	YTHDC1	-1.505	0.02850	0.06912
YY1 associated factor 2	YAF2	-2.933	0.00314	0.01674
zinc and ring finger 3	ZNRF3	-1.659	0.00246	0.01434
zinc finger and BTB domain containing 16	ZBTB16	-7.632	0.00000	0.00004
zinc finger and BTB domain containing 46	ZBTB46	1.548	0.00812	0.03080
zinc finger and BTB domain containing 7C	ZBTB7C	3.476	0.00000	0.00004
zinc finger and SCAN domain containing 2	ZSCAN2	1.579	0.00016	0.00265
zinc finger CCCH-type containing 12B	ZC3H12B	1.599	0.00558	0.02433
zinc finger CCCH-type containing 12C	ZC3H12C	-1.775	0.00004	0.00110
zinc finger CCCH-type, antiviral 1-like	ZC3HAV1L	1.688	0.00001	0.00049
zinc finger protein 114	ZNF114	3.076	0.00000	0.00020
zinc finger protein 135	ZNF135	1.565	0.00040	0.00463
zinc finger protein 161 homolog (mouse)	ZFP161	1.847	0.00062	0.00609
zinc finger protein 167	ZNF167	1.706	0.00051	0.00537
zinc finger protein 180	ZNF180	1.733	0.00089	0.00760
zinc finger protein 184	ZNF184	1.645	0.00062	0.00609
zinc finger protein 20 /// zinc finger protein 625	ZNF20 /// ZNF625	1.652	0.00057	0.00578
zinc finger protein 233	ZNF233	1.838	0.00109	0.00863
zinc finger protein 250	ZNF250	1.517	0.00012	0.00226
zinc finger protein 252	ZNF252	1.565	0.00626	0.02612
zinc finger protein 273	ZNF273	1.526	0.00779	0.02998
zinc finger protein 285A	ZNF285A	1.796	0.00042	0.00476
zinc finger protein 30	ZNF30	1.680	0.00023	0.00328
Zinc finger protein 302	ZNF302	1.616	0.01900	0.05324
zinc finger protein 326	ZNF326	-2.405	0.01930	0.05384
zinc finger protein 33B	ZNF33B	-2.144	0.00122	0.00926
zinc finger protein 36, C3H type, homolog (mouse)	ZFP36	-4.776	0.00000	0.00005
zinc finger protein 36, C3H type-like 2	ZFP36L2	-2.209	0.00128	0.00954
zinc finger protein 365	ZNF365	2.758	0.00004	0.00119

zinc finger protein 367	ZNF367	-1.779	0.00639	0.02646
zinc finger protein 382	ZNF382	1.546	0.00003	0.00091
zinc finger protein 385B	ZNF385B	-12.011	0.01480	0.04516
zinc finger protein 396	ZNF396	1.778	0.04210	0.08854
zinc finger protein 397 opposite strand	ZNF397OS	1.517	0.00395	0.01948
zinc finger protein 398	ZNF398	1.527	0.02210	0.05872
zinc finger protein 423	ZNF423	2.166	0.00025	0.00338
zinc finger protein 436	ZNF436	1.955	0.00002	0.00061
zinc finger protein 441	ZNF441	1.611	0.00802	0.03055
zinc finger protein 443	ZNF443	1.576	0.00013	0.00228
zinc finger protein 469	ZNF469	1.974	0.00045	0.00492
zinc finger protein 512B	ZNF512B	1.594	0.00005	0.00125
zinc finger protein 518B	ZNF518B	-2.243	0.03940	0.08504
zinc finger protein 519	ZNF519	2.211	0.00001	0.00041
zinc finger protein 521	ZNF521	2.137	0.00041	0.00471
zinc finger protein 540	ZNF540	1.718	0.00818	0.03094
zinc finger protein 571	ZNF571	1.611	0.00403	0.01976
zinc finger protein 575	ZNF575	1.663	0.00004	0.00113
zinc finger protein 599	ZNF599	1.780	0.00887	0.03264
zinc finger protein 605	ZNF605	1.612	0.00002	0.00075
zinc finger protein 606	ZNF606	1.785	0.00008	0.00171
zinc finger protein 610	ZNF610	1.606	0.00104	0.00835
zinc finger protein 624	ZNF624	2.545	0.00000	0.00018
zinc finger protein 64 homolog (mouse)	ZFP64	1.598	0.00002	0.00072
zinc finger protein 642	ZNF642	2.182	0.00172	0.01151
zinc finger protein 655	ZNF655	-1.723	0.00968	0.03435
zinc finger protein 667	ZNF667	1.808	0.00200	0.01271
zinc finger protein 668	ZNF668	1.573	0.00006	0.00145
zinc finger protein 671	ZNF671	1.907	0.00026	0.00350
zinc finger protein 678	ZNF678	1.644	0.01960	0.05427
Zinc finger protein 70	ZNF70	2.182	0.00001	0.00050
zinc finger protein 703	ZNF703	-1.750	0.00664	0.02715
zinc finger protein 709	ZNF709	1.663	0.00116	0.00899
zinc finger protein 780A	ZNF780A	1.558	0.00049	0.00523
zinc finger protein 785	ZNF785	1.780	0.00001	0.00059
zinc finger protein 786	ZNF786	1.658	0.00014	0.00243
zinc finger protein 79	ZNF79	1.722	0.00005	0.00121
zinc finger protein 82 homolog (mouse)	ZFP82	2.353	0.00001	0.00039
zinc finger protein 821	ZNF821	1.676	0.00000	0.00020
zinc finger protein 826	ZNF826	1.951	0.01160	0.03843
Zinc finger protein 827	ZNF827	1.804	0.00615	0.02588
zinc finger protein 850 pseudogene	ZNF850P	2.900	0.00001	0.00047
zinc finger RNA binding protein	ZFR	-1.621	0.00935	0.03363
zinc finger with KRAB and SCAN domains 4	ZKSCAN4	2.119	0.00000	0.00009
zinc finger, AN1-type domain 5	ZFAND5	-5.880	0.00000	0.00027
zinc finger, CCHC domain containing 2	ZCCHC2	-1.978	0.01860	0.05251
zinc finger, CCHC domain containing 24	ZCCHC24	1.504	0.00016	0.00267
zinc finger, DHHC-type containing 15	ZDHHC15	1.771	0.00028	0.00369
zinc finger, DHHC-type containing 9	ZDHHC9	1.584	0.00129	0.00958
zinc finger, FYVE domain containing 16	ZFYVE16	2.517	0.00000	0.00018
zinc finger, matrin type 3	ZMAT3	2.210	0.00004	0.00112

zinc finger, MIZ-type containing 1	ZMIZ1	1.558	0.00051	0.00538
zinc finger, MYND-type containing 8	ZMYND8	-1.534	0.00134	0.00981
zinc finger, SWIM-type containing 5	ZSWIM5	1.618	0.00041	0.00471