SUPPLEMENTAL MATERIAL

Supplemental Methods

METHODS

Cardiac-targeted *Trpm7* knock out mice

All animal procedures have been reviewed and approved by the Institutional Animal Care and Use Committee at Children's Hospital Boston. Animals were housed under standard conditions and allowed access to food and water *ad libitum*. Cardiac-targeted knockout mice were generated by crossing *Trpm7*$^{fl/fl}$ and *Trpm7*$^{-/fl}$ mice described previously[1] with *TnT-Cre*, *Isl1-Cre* mouse lines (provided by Dr. W. Pu) and α*MHC-Cre* (provided by Dr. M. Schneider). For simplicity, *Trpm7*$^{fl/fl}$ x (*TnT-Cre*) is denoted as ***Trpm7***$^{TnT/fl}$, *Trpm7*$^{+/fl}$ x (*TnT-Cre*) as ***Trpm7***$^{TnT/+}$, *Trpm7*$^{fl/fl}$ x (*Isl1-Cre*) as ***Trpm7***$^{Isl1/fl}$, *Trpm7*$^{fl/fl}$ x (α*MHC-Cre)* as ***Trpm7*** $^{\alpha MHC/fl}$, and *Trpm7*$^{-/fl}$ x (α*MHC-Cre)* as ***Trpm7*** $^{\alpha MHC/-}$**.** Mice were maintained on 129/SvEvTac mixed genetic background. *Cre* recombinase expression and function was assessed by crossing the above cardiac *Cre* lines with *ROSA26*^{mTmG} reporter mice[2] and imaging isolated cardiomyocytes using an FV1000 confocal microscope (Olympus). Mice/embryos were genotyped from tail tip or yolk sac DNA using: αMHC-Cre-specific primers (αMHC-Cre-F: 5'-ATG ACA GAC AGA TCC CTC CTA TCT CC-3'; αMHC-Cre-R: 5'-CTC ATC ACT CGT TGC ATC ATC GAC-3'), TnT-Cre-specific primers (TnT-Cre-F: 5'-GCG GGA GAA CGA GAG ATT TGG C-3'; TnT-Cre -R: 5'-ACG-GAC-AGA-AGC-ATT-TTC-CAG-GTA-TG-3'), Isl1-Cre primers (Isl1-Cre-F: 5'-ACT ATT TGC CAC CTA GCC ACA GCA-3'; Isl1-Cre-R: 5'-TCC CTG AAC ATG TCC ATC AGG TTC-3') and primers flanking Exon 17 of *Trpm7*[1] (M7-exon17-F: 5'-GCC ATC TCT CCT CTG GTT TT-3'; M7-exon17-R: 5'-GAT AGA CTA TAT ACT AGG TAC ATG G-3'). Transnetyx Inc performed some of the genotyping. To assess for deletion of *Trpm7* at the level of genomic DNA, DNA was isolated using Purelink Genomic DNA Mini kit (Invitrogen) and PCR performed using primers flanking Exon 17 (above).

Embryology

Embryo gestational age was determined from timed matings, with noon of the day of the vaginal plug defined as day 0.5. Embryos were removed from pregnant females euthanized by cervical dislocation between E9-12. Yolk sacs were removed for genotyping (Transnetyx Inc.) and embryos were fixed in 4% formalin overnight at 4^{o}C. Embryos were then embedded in paraffin, sectioned and stained with hematoxylin and eosin. For fluorescence imaging of *TnT-Cre/ROSA26*^{mTmG} crosses and immunostaining of *Trpm7*$^{TnT/+}$ and *Trpm7*$^{TnT/fl}$ hearts, fixed embryos were washed with phosphate buffered saline (PBS) and then treated sequentially with 15% and 30% sucrose/PBS until the tissue was fully penetrated. They were then embedded in optimal cutting temperature (OCT) medium and snap-frozen. Cryosections (6-10 μM) were collected on microscope slides (Colorfrost Plus, Fisher) and imaged using an FV1000 confocal microscope (Olympus). For bromodeoxyuridine (BrdU) labeling, pregnant mice were injected intraperitoneally with BrdU (100 μg/g body weight) 1 h before sacrifice and embryo extraction/fixation.

Echocardiography

Echocardiography was performed on conscious mice. Fur was cleared from the chest with depilatory gel and animals were restrained in a supine position on a table warmed to 37°C. Warmed gel was applied to the animal and 2D and M-mode images were recorded at the level of the papillary muscle using the Vevo 2100 equipped with either a 30 MHz or 40 MHz ultrasound probe (Visual Sonics). Electroconductive gel applied to the limbs and underlying electrode pads allowed for simultaneous ECG during the echocardiogram.

In Vivo Hemodynamics

Mice were anesthetized with 2,2,2-tribromoethanol (250 mg/kg IP for induction with a maintenance infusion of 150 mg/kg/hour via intraperitoneal catheter using a purpose-built infusion system). Anesthetic was stored refrigerated and protected from light until time of administration. Tracheostomy or orotracheal intubation under direct visualization was performed and mice were ventilated (V_T 300 μL, 130 breaths/minute) via a 20 gauge plastic cannula using a small animal ventilator (Harvard Apparatus) connected to humidified supplemental oxygen. Temperature of the animal was maintained at 37º for the duration of the procedure. The superior epigastric artery and vein were occluded by ligation with suture prior to surgery to maintain hemostasis. A subdiaphragmatic incision was made and hearts were accessed via diaphragmotomy. A 1.2F pressure catheter (Scisense, Inc.) was placed in the left ventricle via apical cardiac puncture. Catheter was allowed to equilibrate for 10 minutes before obtaining pressure measurements. Data was collected using Clampex 9.2 software (Axon Instruments), and analysis was performed using Microcal Origin.

Immunostaining ventricular myocytes and frozen embryonic sections

Freshly dissociated ventricular myocytes in KB solution were plated on polylysine coated Colorfrost Plus microscope slides (Fisher) for 30 minutes, then fixed with 4% PFA for 20 min. Fixed embryonic cryosections were soaked for 5 minutes in PBS at RT to remove OCT. Slides were washed 3x in PBS and then permeabilized with 0.5% Triton in PBS for 10 min. For BrdU staining, embryonic cryosections were soaked in 1% Triton in 2M HCl for 1 h. After washing 3x in PBS, slides were blocked in 10% goat serum for 20 min, then incubated overnight at 4ºC in rabbit anti-Troponin-I polyclonal antibody (Santa Cruz, 1:1000 of 200 μg/ml) in 10% goat serum. Embryonic cryosections were incubated overnight at 4ºC in rabbit anti-Troponin-I polyclonal antibody (Santa Cruz, 1:1000 of 200 μg/ml) and rat anti-Brdu monoclonal antibody (Abcam 1:1000 of 1 mg/ml) in 10% goat serum. After 3x PBS wash, slides were incubated for 1-2 h at RT with Alexa Fluor 546 goat anti-rabbit secondary antibody, and stained with DAPI. Slides were then mounted with coverslips and imaged using an FV1000 confocal microscope (Olympus). Quantification of adult ventricular myocyte dimensions and surface area, as well as embryonic myocardium wall thickness was performed using analysis software included with the FV1000 confocal microscope.

Apoptosis Assay

Frozen embryo sections were washed for 30 minutes in PBS and permeabilized for 15 minutes in a solution of 0.1% Triton X and 0.1M Sodium Citrate. A terminal deoxynucleotidyl transferase dUTP nick end labeling (TUNEL)-based cell death assay was used to label apoptotic cells (Roche Applied Science). Samples for positive control were incubated with DNase I (400 U/mL; New England Biolabs) at 37 °C for 30 minutes before TUNEL labeling. For internal positive control, samples were examined for apoptosis in the region of the rostral neural tube. Epifluorescence images were obtained on an Eclipse 90i microscope (Nikon) using a Photometrics CoolSnapHQ2 CCD camera. Data was analyzed using ImageJ.

Electrocardiography (ECG)

ECGs were performed in supine mice sedated using Avertin anesthesia. Dissection pins were placed subcutaneously in the right arm and left leg. The ECG signal was amplified using a speaker amplifier/mixer and then digitized using a Digidata 1320 board (Molecular Devices) acquired with Clampex (pClamp9, Molecular Devices) and analyzed with Clampfit (Molecular Devices) and Origin software (OriginLab Corporation, Northampton, MA).

Ventricular cardiomyocyte isolation

Hearts were excised from Avertin-anesthetized, heparin-anticoagulated mice and aortas cannulated with an 18-gauge needle connected to a peristaltic pump. Hearts were then retrograde perfused for 8-10 minutes at a perfusion pressure of 70-100 mm Hg with either a solution of 0.066 mg/ml Liberase Blendzyme (Roche Diagnostics) or a mixture of 0.4 mg/ml Collagenase B (Roche), 0.3 mg/ml Collagenase D (Roche) and 0.025-0.05 mg/ml Protease XVI (Sigma), in nominally calcium-free Tyrode’s solution (in mM: 140 NaCl, 5.4 KCl, 10 HEPES, 10 Glucose, 1 $MgCl_2$, pH 7.4 with NaOH) warmed to 36° C. Following digestion, hearts were perfused with high [K^+] solution (KB, in mM: 120 K^+ glutamate, 20 KCl, 10 HEPES, 1 $MgCl_2$ and 0.3 EGTA, 10 Glucose; pH 7.4 with KOH), minced with scissors, suspended in KB solution by gentle pipetting and filtered with a >100 micron mesh cell strainer. Freshly dissociated cardiomyocytes were then used for electrophysiological studies within 6-8 h.

Atrioventricular node cell isolation

Hearts were excised from Avertin-anesthetized, heparin-anticoagulated mice and atrioventricular node (AVN) micro-dissected and AVN cells isolated as previously described [3]. Briefly, the dissected AVN was washed in 2.5 ml nominally Ca^{2+}/ Mg^{2+} free Tyrode's solution (pH 6.9) for 4 minutes x 3. The AVN tissue was then transferred to 5 ml of low Ca^{2+}/low Mg^{2+} Tyrode's solution with added $CaCl_2$ 0.066 mM, Glucose 18.5 mM, BSA 1mg/ml, and taurine 50 mM, 1.2 mg elastase (Worthington) and 150 μl Liberase TH Research Grade (Roche) and incubated at 37^oC for 20-30 min. The tissue was transferred to 2.5 ml KB solution and washed 4x. AVN cells were then dispersed by triturating for 1 min in KB and then readapted to Ca^{2+} over 15 minutes by addition of Tyrode's solution with 1.8 mM $CaCl_2$.

Cellular Electrophysiology

TRPM7 current was measured in isolated cardiomyocytes in the whole-cell configuration as previously described[1]. Extracellular solution composition was (in mM): 135 NaCl, 5.4 CsCl, 10 HEPES, 10 Glucose, 0.1 $CdCl_2$ and 1 $CaCl_2$; pH 4.0 to 7.4 with NaOH. To measure Mg^{2+}-inhibited current, 10 mM $MgCl_2$ was added to the solution and perfused onto cells. Pipette solution composition (in mM): 120 L-aspartic acid, 20 CsCl, 2.5 EGTA or BAPTA, 2.5 EDTA, 10 HEPES, 120 CsOH, 5 Na_2ATP, 0.5 Na_2GTP; pH 7.2 in CsOH. The voltage protocol (shown in figure insets) held the myocytes at 0 mV, stepped to +100 mV for 40 ms and then ramped down to -80 mV over 500 ms, holding at -80 mV for 40 ms before stepping back up to 0 mV. This protocol was repeated every 4-6 s and recordings continued for 10-15 min per cell until a steady-state TRPM7 current was obtained. For EDTA-AM experiments, myocytes were loaded with 30 μM EDTA-AM (Invitrogen, custom synthesis) for 30 min in KB solution prior to electrophysiological recording. For measurement of action potentials and potassium currents the extracellular solution composition was (in mM): 140 NaCl, 4 KCl, 10 HEPES, 10 Glucose, 1.2 $CaCl_2$; pH 4.0 to 7.4 with NaOH. Pipette solution composition (in mM): 120 potassium aspartate, 20 KCl, 5 EGTA, 10 HEPES, 1 $MgCl_2$, 5 MgATP, pH 7.2 in KOH. After establishing whole-cell configuration, cell capacitance transients were recorded by applying 40 ms voltage steps from 0 mV to 10 mV, and cell capacitance was calculated offline. Action potentials were recorded in current-clamp mode at 23°C in response to 2 ms, 5-7 mV stimulus steps at a frequency of 0.17-0.25 Hz. Action potential durations (APD) are reported in ms at 30%, 50%, 70% and 90% repolarization and measured from the peak of the action potential to X% repolarization. After recording action potentials, voltage-clamp mode was re-established and potassium currents measured. The voltage protocols (shown in Figure 6) held myocytes at -80 mV, stepped to -40 mV for 50 ms to inactivate voltage-gated sodium channels, then stepped to +60 mV for 2.5 s to activate voltage-gated potassium currents. The transient outward current (I_{to}) was defined at the peak current (I_{peak}) minus the sustained current (I_{sus}) after 2.5 s, and would include both fast ($I_{to, fast}$) and slow ($I_{to, slow}$) components of ($I_{to,}$)[4]. For measuring the 'funny' current in AVN cells, I_f, the extracellular solution was standard Tyrode's solution with 2 mM $BaCl_2$ added to block I_{K1}: (in mM) 140 NaCl, 4 KCl, 10 HEPES, 10 Glucose, 1.2 $CaCl_2$; pH 4.0 to 7.4 with NaOH. The pipette solution contained (in mM): 135 KCl, 1 MgCl2, 0.1 CaCl2, 10 EGTA, 10 HEPES, 5 MgATP, 0.3 NaGTP, 6.6 phosphocreatine, pH 7.2 with KOH. All currents were recorded using an Axopatch 200B amplifier (Molecular Devices), acquired with Clampex (pClamp9, Molecular Devices) and analyzed with Origin software (OriginLab Corporation, Northampton, MA). Signals were low-pass filtered at 5 kHz and sampled at 10 kHz.

Supplemental Table 1: Ventricular morphometry and function		
Ventricular Morphometry		
	WT	***Trpm7***$^{\alpha MHC/fl}$
HW:BW ratio (mg/g)	6.0 ± 0.3	7.2 ± 0.7
n	15	5
Conscious Transthoracic Echocardiographic Parameters		
	WT	***Trpm7***$^{\alpha MHC/fl}$
Interventricular septum diameter (mm)	0.91 ± 0.04	0.94 ± 0.04
Posterior wall (mm)	0.80 ± 0.06	0.83 ± 0.03
Left ventricle (LV) in diastole, d (mm)	3.18 ± 0.13	3.24 ± 0.09
Fractional shortening (%)	54.4 ± 4.1	48.1 ± 2.4
Heart Rate (bpm)	515 ± 23	531 ± 12
n	9	20
Sedated Left Ventricular Invasive Hemodynamic Parameters		
	WT	***Trpm7***$^{\alpha MHC/fl}$
LVP$_{max}$ (mmHg)	86.3 ± 5.1	83.6 ± 3.0
LVEDP (mmHg)	2.5 ± 0.7	2.6 ± 0.6
LVDP (mmHg)	83.8 ± 4.7	81.0 ± 2.7
LV dP/dt$_{Max}$ (mmHg/s)	5946 ± 387	6137 ± 677
LV dP/dt$_{Min}$ (mmHg/s)	-6489 ± 720	-6063 ± 588
Heart Rate (bpm)	546 ± 18	555 ± 30
n	5	5

Supplemental Table 1: Ventricular morphometry and function of *WT* and *Trpm7*$^{\alpha MHC/fl}$ mice

Heart weight (HW) to body weight (BW) ratio, Conscious-restrained transthoracic echocardiographic parameters and sedated invasive left ventricular invasive hemodynamic parameters. LVP$_{max}$: peak left ventricular pressure. LVEDP: left ventricular end-diastolic pressure. LVDP: left ventricular developed pressure. LV dP/dt$_{Max}$: maximum rate of LV pressure development over time. LV dP/dt$_{Min}$: maximum rate of LV pressure relaxation over time.

Supplemental Table 2. Differentially expressed genes from microarray analysis (> 1.3-fold change, p < 0.05)

ID	Fold Change	Ave Expr	Pvalue	adj Pvalue	B	Symbol	Name
10492021	7.289	10.403	9.08E-08	1.86E-04	8.297	Postn	periostin, osteoblast specific factor
10565434	6.705	5.905	1.77E-06	9.61E-04	5.697	Rps13	similar to ribosomal protein S13; predicted gene 12270; predicted gene 6834; predicted gene 15483; predicted gene 6573; ribosomal protein S13; predicted gene 10159
10474129	5.951	6.954	6.22E-09	5.17E-05	10.284	Pamr1	peptidase domain containing associated with muscle regeneration 1
10411082	5.659	8.947	7.45E-05	6.34E-03	2.049	Thbs4	thrombospondin 4
10485711	5.398	7.426	9.97E-06	2.19E-03	4.05	Fibin	fin bud initiation factor homolog (zebrafish)
10492798	5.281	8.079	1.10E-06	6.82E-04	6.139	Sfrp2	secreted frizzled-related protein 2
10518526	5.157	7.63	1.58E-04	9.25E-03	1.285	Angptl7	angiopoietin-like 7
10349968	5.091	7.036	6.85E-06	1.75E-03	4.414	Chi3l1	chitinase 3-like 1
10440091	5.007	8.835	3.56E-08	1.03E-04	9.035	Col8a1	collagen, type VIII, alpha 1
10417212	4.833	8.043	2.37E-07	3.55E-04	7.499	Itgbl1	integrin, beta-like 1
10574023	4.305	11.485	6.89E-09	5.17E-05	10.216	Mt2	metallothionein 2
10541496	4.264	9.903	4.51E-08	1.21E-04	8.853	Mfap5	microfibrillar associated protein 5
10506714	4.207	7.058	3.14E-05	3.84E-03	2.918	Lrp8	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor
10598976	4.126	7.73	3.02E-05	3.82E-03	2.955	Timp1	tissue inhibitor of metalloproteinase 1
10571399	4.115	7.682	8.71E-06	2.03E-03	4.182	Zdhhc2	zinc finger, DHHC domain containing 2
10598085	4.079	6.04	7.04E-05	6.12E-03	2.106	Gdf2/BMP9	growth differentiation factor 2
10470392	4.068	8.003	3.12E-07	3.62E-04	7.26	Adamtsl2	ADAMTS-like 2
10405047	4.019	9.827	6.15E-06	1.66E-03	4.518	Aspn	asporin
10567010	3.896	7.202	6.46E-09	5.17E-05	10.258	Dkk3	dickkopf homolog 3 (Xenopus laevis)
10406176	3.862	5.936	8.86E-07	6.26E-04	6.335	Slc9a3	solute carrier family 9 (sodium/hydrogen exchanger), member 3
10598083	3.621	9.798	6.63E-05	5.90E-03	2.166	LOC100504272	ENSMUSG00000064352
10554752	3.609	6.025	1.89E-05	2.95E-03	3.419	Nox4	NADPH oxidase 4
10598087	3.605	6.484	1.28E-03	3.17E-02	-0.86	ND6	similar to Unknown (protein for IMAGE:4910858); predicted gene 4076
10363455	3.57	7.266	6.11E-06	1.66E-03	4.525	Pcbd1	pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 1
10586357	3.494	6.813	1.02E-07	1.96E-04	8.205	Cilp	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase
10599348	3.493	6.744	6.28E-07	5.45E-04	6.645	Gria3	glutamate receptor, ionotropic, AMPA3 (alpha 3)
10582592	3.432	11.651	5.08E-07	4.88E-04	6.833	Acta1	actin, alpha 1, skeletal muscle
10376778	3.423	9.286	5.32E-06	1.56E-03	4.658	Mfap4	microfibrillar-associated protein 4
10438753	3.408	8.409	7.70E-08	1.67E-04	8.43	Leprel1	leprecan-like 1
10434689	3.252	6.876	1.67E-05	2.74E-03	3.544	Ahsg	alpha-2-HS-glycoprotein
10381798	3.228	9.437	2.66E-04	1.26E-02	0.755	Myl4	myosin, light polypeptide 4
10578045	3.187	6.898	1.80E-06	9.61E-04	5.685	Nrg1	neuregulin 1

10510265	3.134	12.925	3.08E-08	1.01E-04	9.144	Nppa	natriuretic peptide precursor type A
10362201	3.114	11.635	3.41E-07	3.82E-04	7.184	Ctgf	connective tissue growth factor
10595211	3.048	6.351	7.70E-05	6.34E-03	2.015	Col12a1	collagen, type XII, alpha 1
10604853	3.041	7.301	1.74E-06	9.61E-04	5.716	Slitrk4	SLIT and NTRK-like family, member 4
10360235	3.005	9.998	1.17E-04	7.87E-03	1.592	Casq1	calsequestrin 1
10534343	2.928	8.787	1.89E-04	1.03E-02	1.105	Eln	elastin
10573979	2.915	8.978	7.44E-09	5.17E-05	10.164	Gnao1	guanine nucleotide binding protein, alpha O
10401527	2.893	6.875	1.26E-05	2.45E-03	3.823	Ltbp2	latent transforming growth factor beta binding protein 2
10401841	2.843	6.235	1.34E-05	2.57E-03	3.757	Dio2	deiodinase, iodothyronine, type II
10540275	2.816	7.424	9.79E-07	6.54E-04	6.244	Gxylt2	glycosyltransferase 8 domain containing 4
10424140	2.775	8.627	6.57E-08	1.52E-04	8.557	Col14a1	collagen, type XIV, alpha 1
10571715	2.671	6.792	2.25E-06	1.07E-03	5.475	Enpp6	ectonucleotide pyrophosphatase/phosphodiesterase 6
10481627	2.652	8.248	2.23E-06	1.07E-03	5.484	Lcn2	lipocalin 2
10375751	2.641	9.042	2.41E-05	3.39E-03	3.182	Adamts2	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 2; similar to A disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 2
10601648	2.641	5.311	1.66E-03	3.69E-02	-1.128	Tnmd	tenomodulin
10428698	2.632	8.96	8.04E-06	1.92E-03	4.259	Sntb1	syntrophin, basic 1
10410931	2.628	8.9	1.72E-05	2.78E-03	3.513	Vcan	versican
10350438	2.607	7.222	5.65E-08	1.40E-04	8.676	Kcnt2	potassium channel, subfamily T, member 2
10360920	2.588	8.127	2.21E-06	1.07E-03	5.494	Tgfb2	transforming growth factor, beta 2
10469151	2.545	7.75	5.78E-06	1.62E-03	4.578	Itih5	inter-alpha (globulin) inhibitor H5
10449452	2.538	7.812	6.72E-04	2.19E-02	-0.198	Fkbp5	FK506 binding protein 5
10391504	2.529	6.824	5.20E-04	1.88E-02	0.066	Meox1	mesenchyme homeobox 1
10484307	2.516	7.145	2.62E-08	1.01E-04	9.268	Frzb	frizzled-related protein
10458663	2.499	8.942	3.20E-08	1.01E-04	9.115	Dpysl3	dihydropyrimidinase-like 3
10435961	2.488	6.698	7.89E-06	1.92E-03	4.278	Gm10808	ENSMUSG00000075047
10564207	2.477	7.362	1.57E-03	3.59E-02	-1.071	Snord116	small nucleolar RNA, C/D box 116 cluster
10435641	2.466	10.587	1.17E-05	2.37E-03	3.892	Fstl1	follistatin-like 1

10559883	2.458	5.959	2.71E-03	4.89E-02	-1.629	Vmn2r39	vomeronasal 2, receptor, pseudogene 44; vomeronasal 2, receptor 34; vomeronasal 2, receptor 35; vomeronasal 2, receptor 32; vomeronasal 2, receptor, pseudogene 42; vomeronasal 2, receptor 38; vomeronasal 2, receptor, pseudogene 46; vomeronasal 2, receptor 36; vomeronasal 2, receptor 37; predicted gene 3675; predicted gene 3962; predicted gene 7025; vomeronasal 2, receptor 42; vomeronasal 2, receptor 41; vomeronasal 2, receptor 40; predicted gene 5583; similar to EC2-V2R pheromone receptor; predicted gene 4033; vomeronasal 2, receptor33; predicted gene 3978; predicted gene 4073; predicted gene 3991; vomeronasal 2, receptor 48; vomeronasal 2, receptor 29; vomeronasal 2, receptor 47; predicted gene 3972; vomeronasal 2, receptor 49; vomeronasal 2, receptor 44; vomeronasal 2, receptor 43; vomeronasal 2, receptor 46; vomeronasal 2, receptor 45; vomeronasal 2, receptor 51; predicted gene 3607; predicted gene 7648; predicted gene 3956; vomeronasal 2, receptor 31; predicted gene 10302; vomeronasal 2, receptor 30
10351056	2.431	6.315	1.17E-05	2.37E-03	3.893	Ankrd45	ankyrin repeat domain 45
10363541	2.419	5.943	1.59E-04	9.26E-03	1.28	Ass1	argininosuccinate synthetase 1
10478415	2.417	7.77	5.44E-06	1.56E-03	4.638	Wisp2	WNT1 inducible signaling pathway protein 2
10488029	2.398	7.008	1.01E-04	7.29E-03	1.737	Zfand1	zinc finger, AN1-type domain 1
10477920	2.395	9.957	1.14E-03	2.96E-02	-0.737	Myl9	myosin, light polypeptide 9, regulatory
10466606	2.383	7.837	2.24E-04	1.14E-02	0.929	Anxa1	annexin A1
10479165	2.381	6.386	5.28E-04	1.90E-02	0.05	Edn3	endothelin 3
10513208	2.37	8.138	7.24E-06	1.82E-03	4.361	Svep1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1
10433445	2.351	8.248	1.78E-08	1.01E-04	9.552	Abat	4-aminobutyrate aminotransferase
10349947	2.344	7.306	5.64E-05	5.30E-03	2.329	Fmod	fibromodulin
10485405	2.34	7.075	7.85E-07	6.06E-04	6.444	Cd44	CD44 antigen
10420957	2.338	7.164	3.48E-05	3.99E-03	2.814	Ptk2b	PTK2 protein tyrosine kinase 2 beta
10399540	2.337	7.962	3.87E-05	4.25E-03	2.707	Pqlc3	PQ loop repeat containing
10456545	2.31	5.592	5.71E-06	1.61E-03	4.59	Ccdc68	coiled-coil domain containing 68
10393106	2.31	7.92	1.21E-04	8.05E-03	1.559	Trim47	tripartite motif-containing 47
10495306	2.303	6.406	7.58E-05	6.34E-03	2.031	Mybphl	myosin binding protein H-like
10528804	2.292	5.694	6.34E-04	2.12E-02	-0.138	Gm5862	hypothetical protein LOC100046568; predicted gene 1979; predicted gene 10220; spermatogenesis associated glutamate (E)-rich protein 4d; predicted gene 7347; similar to RIKEN cDNA 5031410I06; RIKEN cDNA 5031410I06 gene; predicted gene 5862; predicted gene 7361; spermatogenesis associated glutamate (E)-rich protein 4a
10467191	2.287	12.59	4.75E-07	4.72E-04	6.892	Ankrd1	ankyrin repeat domain 1 (cardiac muscle)
10436623	2.278	5.193	2.26E-05	3.27E-03	3.246	Chodl	chondrolectin
10510260	2.269	11.537	9.45E-05	7.10E-03	1.808	Nppb	natriuretic peptide precursor type B
10354309	2.263	6.902	3.03E-06	1.24E-03	5.196	Col5a2	collagen, type V, alpha 2

10355403	2.26	9.729	6.46E-05	5.77E-03	2.192	Fn1	fibronectin 1
10375956	2.251	6.946	2.13E-05	3.17E-03	3.303	Fstl4	follistatin-like 4
10556528	2.241	6.597	1.41E-04	8.67E-03	1.401	Pde3b	similar to phosphodiesterase 3B; phosphodiesterase 3B, cGMP-inhibited
10380419	2.21	9.329	2.12E-04	1.11E-02	0.984	Col1a1	collagen, type I, alpha 1
10358339	2.204	10.697	1.01E-06	6.63E-04	6.215	Cfh	complement component factor h; similar to complement component factor H
10478048	2.204	7.898	7.36E-07	5.81E-04	6.503	Lbp	lipopolysaccharide binding protein
10453057	2.192	6.66	6.44E-06	1.70E-03	4.475	Cyp1b1	cytochrome P450, family 1, subfamily b, polypeptide 1
10381962	2.185	9.236	3.13E-04	1.40E-02	0.585	Ace	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1
10448182	2.142	8.487	3.51E-05	4.00E-03	2.805	---	ENSMUSG00000076137
10598077	2.129	10.269	2.13E-03	4.24E-02	-1.383	---	ENSMUSG00000064350
10489878	2.123	8.506	4.00E-06	1.41E-03	4.931	Ptgis	prostaglandin I2 (prostacyclin) synthase
10514088	2.111	5.497	5.37E-06	1.56E-03	4.648	Frem1	Fras1 related extracellular matrix protein 1
10473494	2.096	7.181	8.57E-04	2.54E-02	-0.448	Olfr1034	olfactory receptor 1034
10555389	2.083	10.544	8.02E-07	6.06E-04	6.425	Ucp2	uncoupling protein 2 (mitochondrial, proton carrier)
10517677	2.081	7.903	1.71E-07	2.97E-04	7.775	Nbl1	neuroblastoma, suppression of tumorigenicity 1
10572378	2.076	6.449	8.24E-04	2.49E-02	-0.408	Comp	cartilage oligomeric matrix protein
10519983	2.075	9.598	6.12E-05	5.64E-03	2.248	Fgl2	fibrinogen-like protein 2
10494655	2.073	7.047	4.01E-04	1.63E-02	0.332	Zfp697	zinc finger protein 697
10478949	2.05	5.686	1.62E-03	3.63E-02	-1.102	Dok5	docking protein 5
10435948	2.047	10.723	4.62E-05	4.71E-03	2.53	Ccdc80	coiled-coil domain containing 80
10456492	2.042	8.565	2.13E-07	3.37E-04	7.588	D18Ertd653e	DNA segment, Chr 18, ERATO Doi 653, expressed
10407792	2.035	6.578	1.39E-05	2.61E-03	3.724	Gpr137b-ps	similar to Gpr137b protein; G protein-coupled receptor 137B
10536220	2.027	9.414	6.30E-05	5.71E-03	2.219	Col1a2	collagen, type I, alpha 2
10542885	2.015	8.242	2.77E-05	3.64E-03	3.043	2810474O19Rik	RIKEN cDNA 2810474O19 gene
10605711	2.008	6.851	9.90E-06	2.19E-03	4.057	Pdk3	pyruvate dehydrogenase kinase, isoenzyme 3
10598073	2.007	11.129	4.38E-05	4.58E-03	2.584	---	ENSMUSG00000064343
10447056	1.998	6.499	1.98E-07	3.27E-04	7.652	Qpct	glutaminyl-peptide cyclotransferase (glutaminyl cyclase)
10415806	1.997	7.629	3.05E-05	3.82E-03	2.947	Fam124a	family with sequence similarity 124, member A
10368289	1.985	8.946	2.87E-07	3.58E-04	7.332	Enpp1	ectonucleotide pyrophosphatase/phosphodiesterase 1
10416215	1.981	8	4.34E-05	4.56E-03	2.592	Loxl2	lysyl oxidase-like 2
10595404	1.973	9.016	2.58E-04	1.24E-02	0.786	Fam46a	family with sequence similarity 46, member A
10441610	1.973	8.405	3.46E-05	3.99E-03	2.82	Rsph3b	similar to Unknown (protein for MGC:117841); radial spokehead-like 2A; radial spokehead-like 2B
10492682	1.972	10.065	3.17E-04	1.40E-02	0.574	Fam198b	RIKEN cDNA 1110032E23 gene
10475314	1.972	6.286	2.82E-04	1.30E-02	0.692	Mtap1a	microtubule-associated protein 1 A
10344990	1.965	6.425	2.55E-06	1.11E-03	5.359	Crispld1	cysteine-rich secretory protein LCCL domain containing 1
10494262	1.961	6.93	1.94E-05	2.98E-03	3.395	Ctsk	cathepsin K
10544036	1.959	5.399	2.26E-05	3.27E-03	3.244	Atp6v0a4	ATPase, H+ transporting, lysosomal V0 subunit A4
10571467	1.959	6.446	5.80E-05	5.39E-03	2.302	Pdgfrl	platelet-derived growth factor receptor-like
10344897	1.952	8.414	1.06E-05	2.24E-03	3.992	Sulf1	sulfatase 1
10430358	1.945	6.589	1.75E-03	3.80E-02	-1.183	C1qtnf6	C1q and tumor necrosis factor related protein 6
10503259	1.937	8.975	2.29E-04	1.15E-02	0.908	Trp53inp1	transformation related protein 53 inducible nuclear protein 1

10368638	1.933	6.997	9.87E-05	7.19E-03	1.763	Fam26e	family with sequence similarity 26, member E
10396952	1.923	6.361	5.47E-06	1.56E-03	4.632	Ttc9	tetratricopeptide repeat domain 9
10600169	1.919	12.082	3.70E-07	4.02E-04	7.112	Bgn	biglycan
10425287	1.918	8.424	7.02E-04	2.25E-02	-0.242	Kdelr3	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3
10596222	1.917	7.659	4.22E-06	1.43E-03	4.88	Ccrl1	ENSMUSG00000041748
10358476	1.913	6.565	2.23E-03	4.33E-02	-1.428	Prg4	proteoglycan 4 (megakaryocyte stimulating factor, articular superficial zone protein)
10585703	1.911	7.461	4.09E-05	4.44E-03	2.652	Rpp25	ribonuclease P 25 subunit (human)
10434934	1.898	8.041	3.60E-05	4.02E-03	2.78	Bdh1	3-hydroxybutyrate dehydrogenase, type 1
10401673	1.895	8.928	4.05E-06	1.41E-03	4.92	Tgfb3	transforming growth factor, beta 3
10519140	1.892	7.118	2.04E-04	1.08E-02	1.022	Mmp23	matrix metallopeptidase 23
10487040	1.884	9.834	9.35E-04	2.65E-02	-0.538	Fbn1	fibrillin 1
10508829	1.878	6.927	4.15E-05	4.47E-03	2.639	Map3k6	mitogen-activated protein kinase kinase kinase 6
10346015	1.877	8.981	7.62E-04	2.38E-02	-0.327	Col3a1	collagen, type III, alpha 1
10353775	1.874	7.473	9.10E-04	2.62E-02	-0.51	Bend6	BEN domain containing 6
10508879	1.872	7.697	8.01E-05	6.45E-03	1.975	Fam46b	family with sequence similarity 46, member B
10562784	1.87	8.102	8.02E-06	1.92E-03	4.262	Mybpc2	myosin binding protein C, fast-type
10389617	1.869	8.114	4.32E-05	4.56E-03	2.598	Ppm1e	protein phosphatase 1E (PP2C domain containing)
10351041	1.866	5.589	1.61E-03	3.63E-02	-1.097	---	ENSMUSG00000065735
10388430	1.866	9.189	9.71E-07	6.54E-04	6.252	Serpinf1	serine (or cysteine) peptidase inhibitor, clade F, member 1
10356712	1.855	5.878	1.24E-06	7.54E-04	6.031	Kif1a	kinesin family member 1A
10555323	1.85	5.876	1.18E-04	7.90E-03	1.587	P4ha3	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide III
10543939	1.848	5.814	4.60E-05	4.70E-03	2.534	Fam180a	cDNA sequence BC064033
10540085	1.836	9.522	3.01E-06	1.24E-03	5.203	Fbln2	fibulin 2
10424779	1.834	6.193	9.65E-04	2.69E-02	-0.57	Cks2	similar to Cyclin-dependent kinases regulatory subunit 2 (CKS-2); CDC28 protein kinase regulatory subunit 2; predicted gene 15452
10522585	1.832	4.04	7.80E-04	2.41E-02	-0.351	LOC625240	predicted gene, EG620551; predicted gene 6468; predicted gene 6502; predicted gene, EG620639; predicted gene 7918; predicted gene 6509; predicted gene, EG665031; predicted gene 6346; similar to D5Ertd577e protein; predicted gene 6348; hypothetical protein LOC632173
10584883	1.825	9.476	3.88E-06	1.41E-03	4.96	Fxyd6	FXYD domain-containing ion transport regulator 6
10604620	1.818	7.015	5.71E-04	1.99E-02	-0.031	Fam122b	family with sequence similarity 122, member B
10567995	1.817	7.275	3.54E-06	1.35E-03	5.048	Nupr1	nuclear protein 1
10405058	1.816	4.747	8.08E-06	1.92E-03	4.255	Omd	osteomodulin
10492864	1.815	8.093	2.15E-05	3.18E-03	3.293	Sh3d19	SH3 domain protein D19
10542355	1.808	11.249	5.93E-06	1.64E-03	4.554	Emp1	epithelial membrane protein 1
10475625	1.805	7.217	9.20E-05	6.97E-03	1.835	Eid1	EP300 interacting inhibitor of differentiation 1
10587639	1.804	8.887	7.54E-04	2.37E-02	-0.316	Nt5e	5' nucleotidase, ecto
10471909	1.801	10.383	2.64E-05	3.54E-03	3.09	---	ENSMUSG00000082536
10438708	1.801	7.415	3.57E-05	4.01E-03	2.787	Masp1	mannan-binding lectin serine peptidase 1
10403980	1.8	9.565	2.21E-03	4.32E-02	-1.422	Hist1h2bk	histone cluster 1, H2bb

10357043	1.797	9.021	9.71E-06	2.16E-03	4.076	Bcl2	predicted gene 3655; B-cell leukemia/lymphoma 2
10567297	1.794	7.648	1.20E-04	8.03E-03	1.564	Itpripl2	inositol 1,4,5-triphosphate receptor interacting protein-like 2
10585976	1.793	6.929	8.99E-04	2.61E-02	-0.498	Myo9a	myosin IXa
10364494	1.787	7.926	3.57E-05	4.01E-03	2.789	Fstl3	follistatin-like 3
10467258	1.787	7.101	2.29E-04	1.15E-02	0.905	Myof	myoferlin
10607116	1.783	9.14	3.29E-05	3.93E-03	2.869	Ammecr1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1 homolog (human)
10466210	1.783	6.722	1.04E-04	7.41E-03	1.715	Ms4a6d	membrane-spanning 4-domains, subfamily A, member 6D
10606989	1.781	9.527	2.46E-05	3.42E-03	3.161	Tsc22d3	TSC22 domain family, member 3
10473491	1.78	5.572	1.54E-04	9.14E-03	1.31	Olfr1033	olfactory receptor 1033
10398075	1.78	10.241	1.85E-04	1.01E-02	1.123	Serpina3n	serine (or cysteine) peptidase inhibitor, clade A, member 3N
10381603	1.779	7.519	4.45E-06	1.44E-03	4.83	Fzd2	frizzled homolog 2 (Drosophila)
10402783	1.775	6.352	1.81E-03	3.87E-02	-1.218	Ahnak2	AHNAK nucleoprotein 2; similar to Unknown (protein for IMAGE:3599271)
10462613	1.769	7.17	7.50E-05	6.34E-03	2.041	Ifit2	interferon-induced protein with tetratricopeptide repeats 2
10376885	1.769	9.664	3.86E-05	4.25E-03	2.71	Snord49b	RIKEN cDNA 2410006H16 gene
10543004	1.768	8.664	7.52E-05	6.34E-03	2.038	Pon2	paraoxonase 2
10523451	1.767	9.126	2.69E-04	1.27E-02	0.742	Anxa3	similar to Anxa3; annexin A3
10437590	1.758	7.652	7.60E-04	2.38E-02	-0.324	Carhsp1	calcium regulated heat stable protein 1; predicted gene 9791
10573747	1.755	7.353	7.45E-06	1.86E-03	4.334	Adcy7	adenylate cyclase 7
10510167	1.753	4.826	1.54E-05	2.67E-03	3.625	Gm13212	carnitine deficiency-associated gene expressed in ventricle 3; predicted gene 7236
10419261	1.75	8.567	3.57E-04	1.52E-02	0.453	Bmp4	bone morphogenetic protein 4
10404422	1.746	10.895	8.44E-06	1.98E-03	4.212	Serpinb6b	serine (or cysteine) peptidase inhibitor, clade B, member 6b
10505517	1.746	7.904	4.99E-05	4.89E-03	2.453	Tlr4	toll-like receptor 4
10532741	1.745	7.868	1.67E-05	2.74E-03	3.543	Tmem119	transmembrane protein 119
10598075	1.744	11.29	1.40E-03	3.35E-02	-0.951	---	ENSMUSG00000064348
10571601	1.744	9.621	2.16E-05	3.18E-03	3.291	Pdlim3	PDZ and LIM domain 3
10590031	1.742	9.526	1.30E-04	8.31E-03	1.488	Itga9	integrin alpha 9
10539263	1.74	6.799	1.46E-03	3.44E-02	-0.993	Loxl3	lysyl oxidase-like 3
10408280	1.738	6.46	2.73E-04	1.28E-02	0.726	Lrrc16a	leucine rich repeat containing 16A
10410547	1.736	6.12	5.83E-06	1.62E-03	4.571	Nkd2	naked cuticle 2 homolog (Drosophila)
10439891	1.735	9.942	6.45E-06	1.70E-03	4.473	Eef1a1	predicted gene 5869; predicted gene 7161; predicted gene 7105; predicted gene 5822; similar to eukaryotic translation elongation factor 1 alpha 1; predicted gene 6192; predicted gene 6392; predicted gene 6767; predicted gene 6170; predicted gene 6548; predicted gene 6789; eukaryotic translation elongation factor 1 alpha 1
10399208	1.731	5.265	1.30E-05	2.51E-03	3.79	Tmem196	transmembrane protein 196
10434668	1.731	8.258	1.31E-04	8.35E-03	1.473	Tmem97	transmembrane protein 97; predicted gene 5809
10467730	1.73	7.167	6.62E-06	1.72E-03	4.447	Morn4	MORN repeat containing 4
10358434	1.73	6.606	1.52E-05	2.67E-03	3.639	Pla2g4a	phospholipase A2, group IVA (cytosolic, calcium-dependent)
10604961	1.727	7.285	2.37E-05	3.36E-03	3.197	Gabra3	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 3

10600324	1.722	10.433	1.44E-04	8.83E-03	1.378	Rpl3l	predicted gene 5879; similar to 60S ribosomal protein L3 (J1 protein); predicted gene 4959; predicted gene 6035; predicted gene 12816; ribosomal protein L3; predicted gene 5851; predicted gene 16468; predicted gene 5850
10416974	1.716	8.546	6.39E-06	1.70E-03	4.481	Gpc6	predicted gene 4672; glypican 6; similar to Glypican 6
10571840	1.716	8.369	1.76E-04	9.89E-03	1.175	Hpgd	hydroxyprostaglandin dehydrogenase 15 (NAD)
10366541	1.715	11.236	3.36E-05	3.93E-03	2.849	Lrrc10	leucine rich repeat containing 10
10538356	1.707	7.238	1.05E-05	2.24E-03	4	Chn2	chimerin (chimaerin) 2
10386197	1.705	5.023	4.34E-05	4.56E-03	2.593	2210407C18Rik	RIKEN cDNA 2210407C18 gene
10543145	1.704	7.727	5.45E-05	5.21E-03	2.363	Thsd7a	thrombospondin, type I, domain containing 7A
10519693	1.703	6.53	3.46E-04	1.50E-02	0.485	Sema3d	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D; hypothetical protein LOC100044160
10354418	1.701	9.783	4.31E-06	1.43E-03	4.86	Obfc2a	oligonucleotide/oligosaccharide-binding fold containing 2A
10340492	1.701	6.257	5.64E-04	1.97E-02	-0.017	Tbl3	transducin (beta)-like 3
10427796	1.7	8.656	4.56E-06	1.46E-03	4.805	Npr3	natriuretic peptide receptor 3
10443494	1.7	8.718	1.07E-05	2.24E-03	3.981	Pi16	peptidase inhibitor 16
10366293	1.697	9.062	7.65E-05	6.34E-03	2.021	Csrp2	cysteine and glycine-rich protein 2
10548879	1.695	9.675	2.56E-06	1.11E-03	5.355	Mgp	matrix Gla protein
10396936	1.692	6.621	4.20E-07	4.42E-04	7.002	Smoc1	SPARC related modular calcium binding 1
10504775	1.686	8.998	5.37E-04	1.92E-02	0.033	Col15a1	collagen, type XV, alpha 1
10581266	1.686	9.571	2.09E-04	1.09E-02	0.999	Tppp3	tubulin polymerization-promoting protein family member 3
10579799	1.682	9.902	1.44E-05	2.64E-03	3.689	Tmem184c	transmembrane protein 184C
10371770	1.679	6.558	9.67E-05	7.13E-03	1.784	Gas2l3	similar to growth arrest-specific 2 like 3; growth arrest-specific 2 like 3
10595402	1.676	7.372	1.69E-03	3.72E-02	-1.147	Fam46a	family with sequence similarity 46, member A
10401244	1.669	8.678	9.17E-06	2.10E-03	4.131	Actn1	actinin, alpha 1
10393379	1.668	8.037	7.60E-05	6.34E-03	2.028	Mxra7	matrix-remodelling associated 7
10366346	1.668	8.341	2.11E-03	4.21E-02	-1.373	Phlda1	pleckstrin homology-like domain, family A, member 1
10491106	1.668	7.702	4.93E-06	1.49E-03	4.732	Pld1	phospholipase D1
10594044	1.666	9.852	2.57E-04	1.24E-02	0.787	Islr	immunoglobulin superfamily containing leucine-rich repeat
10453555	1.665	6.466	3.35E-04	1.46E-02	0.518	2610044O15Rik	predicted gene 1976
10388880	1.662	6.484	8.26E-04	2.49E-02	-0.409	Tmem97	transmembrane protein 97; predicted gene 5809
10598091	1.661	9.483	1.67E-03	3.70E-02	-1.135	---	ENSMUSG00000064372
10578649	1.661	6.62	1.38E-04	8.55E-03	1.423	Odz3	odd Oz/ten-m homolog 3 (Drosophila)
10350146	1.659	8.075	9.60E-05	7.10E-03	1.792	Phlda3	pleckstrin homology-like domain, family A, member 3
10539135	1.658	7.049	2.05E-04	1.08E-02	1.021	Capg	capping protein (actin filament), gelsolin-like
10594066	1.658	8.808	1.16E-03	2.99E-02	-0.76	Loxl1	lysyl oxidase-like 1
10402211	1.657	8.883	3.61E-05	4.02E-03	2.777	Fbln5	fibulin 5
10577782	1.657	8.367	7.28E-04	2.31E-02	-0.28	Htra4	HtrA serine peptidase 4
10588037	1.654	7.601	9.59E-05	7.10E-03	1.793	Rbp1	retinol binding protein 1, cellular
10522208	1.652	6.825	9.80E-05	7.18E-03	1.771	Uchl1	ubiquitin carboxy-terminal hydrolase L1
10471154	1.65	6.883	8.55E-05	6.68E-03	1.909	Ass1	argininosuccinate synthetase 1
10371082	1.65	7.203	5.80E-04	2.01E-02	-0.046	Itgb1bp3	integrin beta 1 binding protein 3
10590983	1.648	6.05	6.59E-06	1.72E-03	4.453	Panx1	pannexin 1

10583008	1.647	7.332	1.07E-03	2.88E-02	-0.676	Casp12	caspase 12; hypothetical protein LOC100044205
10527233	1.646	10.039	7.11E-07	5.81E-04	6.534	Cyth3	cytohesin 3
10501456	1.646	7.834	8.74E-05	6.74E-03	1.887	Fam102b	family with sequence similarity 102, member B
10555027	1.643	9.197	1.28E-05	2.48E-03	3.809	Gab2	growth factor receptor bound protein 2-associated protein 2
10352143	1.642	6.299	1.23E-05	2.45E-03	3.841	Kif26b	kinesin family member 26B
10392056	1.64	6.828	1.26E-04	8.23E-03	1.514	Cyb561	cytochrome b-561
10387170	1.639	8.699	1.57E-05	2.67E-03	3.607	Ntn1	similar to Netrin-1 precursor; netrin 1
10531610	1.639	7.017	6.40E-05	5.75E-03	2.203	Rasgef1b	RasGEF domain family, member 1B; hypothetical protein LOC100044232
10349876	1.638	8.927	1.77E-04	9.90E-03	1.171	Plekha6	pleckstrin homology domain containing, family A member 6

10564043	1.637	3.77	2.69E-03	4.88E-02	-1.624	---	ENSMUSG00000075898; ENSMUSG00000075756; ENSMUSG00000075757; ENSMUSG00000075947; ENSMUSG00000075800; ENSMUSG00000075801; ENSMUSG00000075803; ENSMUSG00000075808; ENSMUSG00000075940; ENSMUSG00000075809; ENSMUSG00000075941; ENSMUSG00000075751; ENSMUSG00000075805; ENSMUSG00000075944; ENSMUSG00000075891; ENSMUSG00000075750; ENSMUSG00000075894; ENSMUSG00000075886; ENSMUSG00000077645; ENSMUSG00000075742; ENSMUSG00000075884; ENSMUSG00000075743; ENSMUSG00000075885; ENSMUSG00000075888; ENSMUSG00000075748; ENSMUSG00000075812; ENSMUSG00000075810; ENSMUSG00000075953; ENSMUSG00000075819; ENSMUSG00000075950; ENSMUSG00000075883; ENSMUSG00000075956; ENSMUSG00000075882; ENSMUSG00000075881; ENSMUSG00000075954; ENSMUSG00000075816; ENSMUSG00000075734; ENSMUSG00000075733; ENSMUSG00000075730; ENSMUSG00000077225; ENSMUSG00000075738; ENSMUSG00000075739; ENSMUSG00000075821; ENSMUSG00000075925; ENSMUSG00000075823; ENSMUSG00000075926; ENSMUSG00000075824; ENSMUSG00000075927; ENSMUSG00000075827; ENSMUSG00000075922; ENSMUSG00000075828; ENSMUSG00000075920; ENSMUSG00000075726; ENSMUSG00000075721; ENSMUSG00000075722; ENSMUSG00000075831; ENSMUSG00000075830; ENSMUSG00000075835; ENSMUSG00000075939; ENSMUSG00000075834; ENSMUSG00000075935; ENSMUSG00000075932; ENSMUSG00000075933; ENSMUSG00000075783; ENSMUSG00000075781; ENSMUSG00000075717; ENSMUSG00000075716; ENSMUSG00000075782; ENSMUSG00000075901; ENSMUSG00000075715; ENSMUSG00000075909; ENSMUSG00000075714; ENSMUSG00000075981; ENSMUSG00000077615; ENSMUSG00000075713; ENSMUSG00000075982;
10359034	1.636	8.449	1.63E-04	9.37E-03	1.256	Qsox1	quiescin Q6 sulfhydryl oxidase 1
10523001	1.635	9.263	4.33E-06	1.43E-03	4.857	Mobkl1a	MOB1, Mps One Binder kinase activator-like 1A (yeast)
10405755	1.631	6.679	2.01E-03	4.12E-02	-1.325	---	ENSMUSG00000077057
10490302	1.631	6.361	9.19E-04	2.63E-02	-0.519	2810021G02Rik	RIKEN cDNA 2810021G02 gene
10492558	1.63	8.319	2.29E-04	1.15E-02	0.907	Smc4	structural maintenance of chromosomes 4
10595636	1.628	8.434	1.19E-04	7.97E-03	1.576	---	ENSMUSG00000075724; ENSMUSG00000075725; ENSMUSG00000075972; ENSMUSG00000075818; ENSMUSG00000075945

10503833	1.627	10.103	4.82E-06	1.48E-03	4.753	Rplp1	predicted gene 11942; predicted gene 13777; predicted gene 10073; ribosomal protein, large, P1
10526838	1.626	9.36	1.09E-03	2.91E-02	-0.696	Gm10874	ENSMUSG00000075591
10577190	1.626	8.683	1.36E-04	8.50E-03	1.438	Rasa3	RAS p21 protein activator 3
10571530	1.623	8.42	1.58E-05	2.67E-03	3.596	Fat1	FAT tumor suppressor homolog 1 (Drosophila)
10370180	1.622	8.996	1.10E-04	7.62E-03	1.653	Col6a2	collagen, type VI, alpha 2
10527649	1.621	7.881	4.05E-04	1.64E-02	0.321	6330406I15Rik	RIKEN cDNA 6330406I15 gene
10423498	1.62	9.169	5.06E-06	1.52E-03	4.706	Dap	death-associated protein
10556381	1.62	9.525	3.13E-05	3.84E-03	2.919	Mical2	microtubule associated monoxygenase, calponin and LIM domain containing 2
10586744	1.619	9.458	6.93E-05	6.09E-03	2.121	Anxa2	similar to Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (Chromobindin-8) (p36) (Protein I) (Placental anticoagulant protein IV) (PAP-IV); annexin A2
10433114	1.619	9.354	8.46E-04	2.53E-02	-0.434	Itga5	integrin alpha 5 (fibronectin receptor alpha)
10475378	1.616	7.859	1.42E-05	2.62E-03	3.7	Casc4	cancer susceptibility candidate 4
10376201	1.615	11.029	4.76E-06	1.48E-03	4.766	Gpx3	glutathione peroxidase 3
10411229	1.614	9.175	6.09E-05	5.63E-03	2.253	F2r	coagulation factor II (thrombin) receptor
10439009	1.613	7.389	1.31E-03	3.21E-02	-0.883	Apod	apolipoprotein D
10594762	1.611	8.744	2.11E-04	1.10E-02	0.99	Fam81a	family with sequence similarity 81, member A
10399691	1.61	9.535	1.25E-04	8.21E-03	1.521	Id2	inhibitor of DNA binding 2
10528332	1.61	8.491	8.82E-05	6.76E-03	1.877	Napepld	N-acyl phosphatidylethanolamine phospholipase D
10504817	1.606	8.316	4.63E-04	1.77E-02	0.186	Tgfbr1	transforming growth factor, beta receptor I
10498775	1.601	7.562	3.57E-04	1.52E-02	0.452	Golim4	golgi integral membrane protein 4
10522060	1.599	7.836	2.26E-04	1.14E-02	0.919	Fam114a1	family with sequence similarity 114, member A1
10467979	1.594	8.88	1.57E-03	3.59E-02	-1.069	Scd1	stearoyl-Coenzyme A desaturase 1
10523595	1.589	6.029	1.55E-05	2.67E-03	3.62	Ptpn13	protein tyrosine phosphatase, non-receptor type 13
10514240	1.588	5.401	9.96E-04	2.76E-02	-0.603	Slc24a2	solute carrier family 24 (sodium/potassium/calcium exchanger), member 2
10467470	1.587	7.525	4.48E-04	1.74E-02	0.218	Aldh18a1	aldehyde dehydrogenase 18 family, member A1
10489891	1.583	8.01	1.13E-04	7.70E-03	1.626	B4galt5	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5
10478572	1.583	6.211	4.99E-04	1.83E-02	0.107	Ube2c	ubiquitin-conjugating enzyme E2C; predicted gene 8956
10467768	1.582	6.135	1.92E-03	4.03E-02	-1.278	Loxl4	lysyl oxidase-like 4
10534085	1.582	7.735	1.70E-03	3.72E-02	-1.151	Phkg1	phosphorylase kinase gamma 1
10464761	1.577	5.249	5.55E-04	1.95E-02	-0.001	Syt12	synaptotagmin XII
10450920	1.575	8.364	2.48E-03	4.65E-02	-1.541	AY036118	ENSMUSG00000045999
10599736	1.574	11.23	8.19E-05	6.53E-03	1.952	Fhl1	four and a half LIM domains 1
10593293	1.574	8.165	5.65E-05	5.30E-03	2.327	Ncam1	neural cell adhesion molecule 1
10601854	1.574	7.036	1.80E-04	1.00E-02	1.154	Wbp5	WW domain binding protein 5
10518069	1.573	8.961	1.78E-05	2.81E-03	3.483	Efhd2	similar to EF hand domain containing 2; EF hand domain containing 2
10427075	1.573	6.522	2.09E-03	4.19E-02	-1.362	Krt18	keratin 18
10461614	1.573	7.748	2.17E-03	4.28E-02	-1.402	Ms4a6c	membrane-spanning 4-domains, subfamily A, member 6C
10575799	1.572	7.409	2.53E-04	1.22E-02	0.806	Plcg2	phospholipase C, gamma 2
10437210	1.571	7.562	1.67E-04	9.55E-03	1.228	Bace2	beta-site APP-cleaving enzyme 2

10601659	1.571	7.607	2.97E-04	1.35E-02	0.64	Srpx2	sushi-repeat-containing protein, X-linked 2
10447619	1.57	9.348	2.16E-04	1.11E-02	0.966	Rsph3b	similar to Unknown (protein for MGC:117841); radial spokehead-like 2A; radial spokehead-like 2B
10459620	1.567	5.715	1.67E-04	9.55E-03	1.23	Rab27b	RAB27b, member RAS oncogene family
10365983	1.563	9.809	1.00E-05	2.20E-03	4.043	Lum	lumican
10517053	1.563	7.833	1.93E-03	4.03E-02	-1.281	Trnp1	TMF1-regulated nuclear protein 1
10565456	1.562	7.633	3.42E-04	1.49E-02	0.495	Prss23	protease, serine, 23
10489484	1.56	8.03	4.85E-05	4.81E-03	2.482	Sdc4	syndecan 4
10385391	1.557	8.408	4.42E-04	1.73E-02	0.232	Cyfip2	cytoplasmic FMR1 interacting protein 2
10408200	1.557	6.048	1.54E-03	3.55E-02	-1.047	Hist1h4f	histone cluster 1, H4k; histone cluster 1, H4m; histone cluster 4, H4; similar to germinal histone H4 gene; histone cluster 1, H4h; histone cluster 1, H4j; histone cluster 1, H4i; histone cluster 1, H4d; histone cluster 1, H4c; histone cluster 1, H4f; histone cluster 1, H4b; histone cluster 1, H4a; histone cluster 2, H4; similar to histone H4
10411519	1.556	8.422	6.08E-04	2.06E-02	-0.096	Mtap1b	microtubule-associated protein 1B
10522467	1.553	8.726	6.53E-05	5.82E-03	2.182	Rasl11b	RAS-like, family 11, member B
10457640	1.553	9.988	1.27E-03	3.17E-02	-0.856	S100a11	predicted gene 7665; S100 calcium binding protein A11 (calgizzarin); predicted gene 5068
10370210	1.551	9.304	1.26E-04	8.21E-03	1.518	Col6a1	collagen, type VI, alpha 1
10452978	1.55	6.267	9.34E-04	2.65E-02	-0.537	Gm6548	predicted gene 5869; predicted gene 7161; predicted gene 7105; predicted gene 5822; similar to eukaryotic translation elongation factor 1 alpha 1; predicted gene 6192; predicted gene 6392; predicted gene 6767; predicted gene 6170; predicted gene 6548; predicted gene 6789; eukaryotic translation elongation factor 1 alpha 1
10435266	1.55	9.546	1.56E-05	2.67E-03	3.609	Heg1	ENSMUSG00000035500
10480003	1.548	5.062	3.06E-05	3.82E-03	2.942	Itih2	inter-alpha trypsin inhibitor, heavy chain 2
10598721	1.546	11.075	6.87E-04	2.22E-02	-0.221	Rpl3l	predicted gene 5879; similar to 60S ribosomal protein L3 (J1 protein); predicted gene 4959; predicted gene 6035; predicted gene 12816; ribosomal protein L3; predicted gene 5851; predicted gene 16468; predicted gene 5850
10456184	1.545	7.04	1.37E-04	8.51E-03	1.431	Apcdd1	adenomatosis polyposis coli down-regulated 1
10481186	1.543	6.726	8.25E-04	2.49E-02	-0.409	Sardh	sarcosine dehydrogenase
10545974	1.541	8.104	9.27E-04	2.64E-02	-0.528	Antxr1	anthrax toxin receptor 1
10501762	1.54	7.141	4.94E-04	1.82E-02	0.119	Snx7	sorting nexin 7
10453604	1.538	7.944	8.52E-04	2.53E-02	-0.441	Bambi	BMP and activin membrane-bound inhibitor, homolog (Xenopus laevis)
10502949	1.536	10.042	1.13E-03	2.95E-02	-0.733	---	ENSMUSG00000065463; ENSMUSG00000065738; ENSMUSG00000064731
10492428	1.535	7.947	1.57E-04	9.23E-03	1.289	4931440P22Rik	TCDD-inducible poly(ADP-ribose) polymerase
10538640	1.535	7.568	1.04E-04	7.44E-03	1.707	Abcg2	ATP-binding cassette, sub-family G (WHITE), member 2
10493990	1.534	10.667	1.31E-04	8.35E-03	1.475	S100a11	predicted gene 7665; S100 calcium binding protein A11 (calgizzarin); predicted gene 5068
10494672	1.534	4.991	1.14E-04	7.72E-03	1.622	Tbx15	T-box 15

10442219	1.534	5.552	5.21E-04	1.88E-02	0.064	Zfp52	hypothetical protein LOC100044274; zinc finger protein 52
10476106	1.533	11.791	1.79E-03	3.85E-02	-1.207	Snord57	ENSMUSG00000065272
10440491	1.532	10.64	3.02E-06	1.24E-03	5.198	App	amyloid beta (A4) precursor protein
10407319	1.531	9.991	2.90E-05	3.74E-03	2.994	Gm10154	ribosomal protein L34; predicted gene 10154; similar to ribosomal protein L34; predicted gene 7800; predicted gene 4705
10457686	1.53	8.875	5.57E-05	5.28E-03	2.341	Dsc2	desmocollin 2
10590909	1.53	6.904	1.81E-04	1.00E-02	1.146	Endod1	endonuclease domain containing 1
10407040	1.528	8.558	7.18E-04	2.29E-02	-0.267	Esco1	predicted gene 7054; establishment of cohesion 1 homolog 1 (S. cerevisiae)
10363901	1.527	7.898	2.19E-03	4.30E-02	-1.413	Etv5	ets variant gene 5
10561212	1.527	10.478	5.13E-05	4.96E-03	2.425	Ltbp4	latent transforming growth factor beta binding protein 4
10397002	1.526	7.429	1.83E-06	9.63E-04	5.669	Sipa1l1	signal-induced proliferation-associated 1 like 1
10421924	1.523	6.844	6.82E-05	6.00E-03	2.138	Pcdh9	protocadherin 9
10502196	1.523	9.309	1.24E-03	3.11E-02	-0.83	Rpl34	ribosomal protein L34; predicted gene 10154; similar to ribosomal protein L34; predicted gene 7800; predicted gene 4705
10369388	1.523	7.62	3.53E-05	4.00E-03	2.799	Unc5b	unc-5 homolog B (C. elegans)
10360764	1.522	10.3	1.05E-04	7.45E-03	1.703	Enah	enabled homolog (Drosophila)
10439710	1.522	8.622	3.48E-06	1.35E-03	5.064	Phldb2	pleckstrin homology-like domain, family B, member 2
10582275	1.522	7.566	1.54E-04	9.14E-03	1.313	Slc7a5	similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 5; similar to Solute carrier family 7 (cationic amino acid transporter, y+ system), member 5; solute carrier family 7 (cationic amino acid transporter, y+ system), member 5
10374908	1.521	7.857	8.65E-04	2.56E-02	-0.458	Rtn4	reticulon 4
10587880	1.52	9.34	2.56E-05	3.51E-03	3.12	Pcolce2	procollagen C-endopeptidase enhancer 2
10490159	1.52	9.517	1.11E-05	2.29E-03	3.943	Pmepa1	prostate transmembrane protein, androgen induced 1; similar to Nedd4 WW binding protein 4
10590830	1.518	5.679	4.35E-04	1.71E-02	0.248	AK129341	similar to CDNA sequence AK129341; cDNA sequence AK129341
10514275	1.517	7.62	1.55E-04	9.18E-03	1.302	Ptplad2	protein tyrosine phosphatase-like A domain containing 2
10604393	1.515	7.388	1.01E-03	2.77E-02	-0.613	Elf4	predicted gene 9907
10515090	1.514	7.364	2.14E-04	1.11E-02	0.976	Cdkn2c	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)
10476648	1.514	10.879	7.93E-04	2.43E-02	-0.368	Dstn	destrin
10398211	1.514	5.833	2.34E-04	1.16E-02	0.886	Hhipl1	hedgehog interacting protein-like 1
10567564	1.513	8.023	2.74E-03	4.92E-02	-1.641	Cdr2	cerebellar degeneration-related 2
10493820	1.513	6.752	4.48E-04	1.74E-02	0.22	S100a6	S100 calcium binding protein A6 (calcyclin)
10523727	1.511	8.591	1.25E-05	2.45E-03	3.826	Pkd2	polycystic kidney disease 2
10405033	1.507	8.892	8.00E-05	6.45E-03	1.977	Ecm2	extracellular matrix protein 2, female organ and adipocyte specific
10427125	1.507	8.623	2.46E-05	3.42E-03	3.159	Igfbp6	insulin-like growth factor binding protein 6
10407481	1.507	9.184	2.65E-04	1.26E-02	0.757	Pfkp	phosphofructokinase, platelet
10590438	1.506	6.136	3.76E-04	1.57E-02	0.399	Fam198a	RIKEN cDNA C730027P07 gene
10592471	1.506	8.377	4.54E-04	1.75E-02	0.205	Gramd1b	GRAM domain containing 1B
10442495	1.506	8.39	1.35E-04	8.48E-03	1.444	Pkd1	polycystic kidney disease 1 homolog

10373223	1.505	9.801	4.18E-06	1.43E-03	4.89	Lrp1	low density lipoprotein receptor-related protein 1
10424404	1.505	5.837	4.59E-04	1.76E-02	0.194	Pvt1	plasmacytoma variant translocation 1
10408210	1.5	9.754	1.44E-03	3.42E-02	-0.984	Gm13646	similar to Hist1h2bj protein; histone cluster 1, H2bl; predicted gene, OTTMUSG00000013203; histone cluster 1, H2bj; histone cluster 1, H2bf; H2b histone family member; histone cluster 1, H2bn
10454097	1.5	9.047	3.35E-04	1.46E-02	0.518	Gm7589	predicted gene 10288; predicted gene 7589; ribosomal protein L11; predicted gene 10036; predicted gene 7384; predicted gene 6745; predicted gene 5093
10467784	1.5	7.005	1.12E-04	7.68E-03	1.636	Pyroxd2	pyridine nucleotide-disulphide oxidoreductase domain 2
10438445	1.499	6.991	3.48E-04	1.50E-02	0.477	Klhl6	kelch-like 6 (Drosophila)
10586246	1.498	6.971	6.05E-04	2.06E-02	-0.09	Dennd4a	DENN/MADD domain containing 4A
10554094	1.498	8.704	9.38E-06	2.12E-03	4.109	Igf1r	insulin-like growth factor I receptor
10579331	1.497	5.932	1.42E-03	3.37E-02	-0.965	Gdf15	growth differentiation factor 15
10530666	1.497	6.315	8.32E-07	6.08E-04	6.391	Lnx1	ligand of numb-protein X 1
10404606	1.497	8.006	1.34E-03	3.26E-02	-0.907	Ly86	lymphocyte antigen 86
10345704	1.497	7.785	3.09E-04	1.39E-02	0.599	Snord3a	U3B small nuclear RNA 4; U3B small nuclear RNA 3; U3A small nuclear RNA; U3B small nuclear RNA 1
10340406	1.494	7.539	8.75E-04	2.57E-02	-0.469	Fryl	furry homolog-like (Drosophila)
10562192	1.493	10.468	1.58E-05	2.67E-03	3.597	Fxyd5	FXYD domain-containing ion transport regulator 5
10511180	1.493	9.794	2.13E-04	1.11E-02	0.979	Mxra8	matrix-remodelling associated 8
10459084	1.491	6.825	7.19E-04	2.29E-02	-0.267	Synpo	synaptopodin
10358565	1.49	7.608	8.03E-05	6.45E-03	1.973	Hmcn1	hemicentin 1
10386058	1.489	12.584	2.31E-04	1.15E-02	0.897	Sparc	secreted acidic cysteine rich glycoprotein; similar to Secreted acidic cysteine rich glycoprotein
10538150	1.488	7.959	2.25E-05	3.27E-03	3.25	Tmem176a	transmembrane protein 176A
10493995	1.487	11.363	7.63E-05	6.34E-03	2.024	S100a10	S100 calcium binding protein A10 (calpactin)
10592535	1.487	8.052	1.10E-03	2.92E-02	-0.706	Sorl1	similar to sortilin-related receptor, LDLR class A repeats-containing; sortilin-related receptor, LDLR class A repeats-containing
10534889	1.486	7.759	7.43E-05	6.34E-03	2.051	Agfg2	ArfGAP with FG repeats 2
10457614	1.486	6.753	7.91E-04	2.43E-02	-0.365	Aqp4	aquaporin 4
10443949	1.485	7.942	6.31E-05	5.72E-03	2.216	Adamts10	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 10
10360684	1.484	9.203	2.40E-04	1.18E-02	0.857	Ephx1	epoxide hydrolase 1, microsomal
10583343	1.483	5.511	4.14E-04	1.66E-02	0.299	---	predicted gene 4977
10350113	1.482	9.202	4.76E-04	1.79E-02	0.156	Arl8a	ADP-ribosylation factor-like 8A
10604564	1.482	9.044	1.96E-03	4.05E-02	-1.296	Gpc4	glypican 4; similar to Glypican 4
10435305	1.482	10.345	6.73E-06	1.73E-03	4.432	Itgb5	integrin beta 5
10571567	1.479	11.472	6.38E-05	5.74E-03	2.206	Sorbs2	sorbin and SH3 domain containing 2
10548128	1.478	8.927	8.20E-04	2.49E-02	-0.403	Tspan9	tetraspanin 9
10444658	1.475	8.904	5.58E-04	1.96E-02	-0.007	Clic1	chloride intracellular channel 1
10357488	1.474	6.369	8.96E-04	2.60E-02	-0.494	Cd55	CD55 antigen
10459747	1.474	6.239	8.62E-05	6.69E-03	1.9	Mapk4	mitogen-activated protein kinase 4
10523260	1.474	8.334	1.06E-04	7.49E-03	1.691	Shroom3	shroom family member 3

10543959	1.473	6.008	1.10E-03	2.92E-02	-0.703	Ptn	pleiotrophin
10411373	1.472	8.337	2.10E-03	4.21E-02	-1.368	Hexb	hexosaminidase B
10505073	1.472	7.225	2.04E-04	1.08E-02	1.024	Zfp462	zinc finger protein 462
10530841	1.47	12.593	1.35E-05	2.57E-03	3.752	Igfbp7	insulin-like growth factor binding protein 7
10556076	1.469	6.422	8.98E-05	6.85E-03	1.859	Olfml1	olfactomedin-like 1
10452633	1.468	6.858	5.02E-04	1.83E-02	0.102	Tgif1	TGFB-induced factor homeobox 1
10437272	1.467	5.901	8.41E-05	6.66E-03	1.926	Nlrc3	NLR family, CARD domain containing 3
10428310	1.465	9.022	8.08E-05	6.46E-03	1.966	Azin1	antizyme inhibitor 1
10431874	1.465	9.384	5.19E-04	1.88E-02	0.069	Slc38a1	solute carrier family 38, member 1
10407420	1.464	6.923	1.62E-03	3.63E-02	-1.099	Net1	predicted gene 8990; neuroepithelial cell transforming gene 1
10478847	1.463	7.765	2.66E-04	1.26E-02	0.753	Znfx1	RIKEN cDNA 1500012F01 gene
10531887	1.462	7.18	2.42E-04	1.19E-02	0.849	Slc10a6	solute carrier family 10 (sodium/bile acid cotransporter family), member 6
10489219	1.454	6.359	6.62E-04	2.17E-02	-0.182	D630003M21Rik	RIKEN cDNA D630003M21 gene
10491721	1.454	8.878	8.70E-05	6.73E-03	1.892	Spry1	sprouty homolog 1 (Drosophila); similar to sprouty 1
10505143	1.453	9.224	6.09E-04	2.06E-02	-0.096	Akap2	A kinase (PRKA) anchor protein 2; paralemmin 2
10510700	1.453	7.258	2.13E-03	4.24E-02	-1.383	Gpr153	G protein-coupled receptor 153
10466587	1.452	5.399	1.96E-03	4.06E-02	-1.3	Rorb	hypothetical protein LOC100047843; RAR-related orphan receptor beta
10378253	1.451	5.888	1.57E-05	2.67E-03	3.606	Camkk1	calcium/calmodulin-dependent protein kinase kinase 1, alpha
10439732	1.451	5.619	2.19E-04	1.13E-02	0.952	Phldb2	phosphatidylinositol-specific phospholipase C, X domain containing 2
10479925	1.449	7.01	3.45E-04	1.50E-02	0.487	5430407P10Rik	RIKEN cDNA 5430407P10 gene
10602105	1.449	6.969	2.95E-05	3.77E-03	2.98	Col4a5	collagen, type IV, alpha 5
10490212	1.449	9.363	1.09E-04	7.57E-03	1.668	Ctsz	cathepsin Z
10452419	1.449	8.639	5.10E-05	4.95E-03	2.431	Efna5	ephrin A5
10500183	1.448	8.454	6.70E-04	2.19E-02	-0.195	Adamtsl4	ADAMTS-like 4
10357705	1.448	6.139	3.98E-04	1.62E-02	0.341	Cntn2	contactin 2
10548105	1.447	11.17	1.10E-05	2.28E-03	3.954	Ccnd2	cyclin D2
10364593	1.447	8.864	2.57E-03	4.75E-02	-1.577	Cnn2	calponin 2
10498771	1.447	5.017	1.12E-03	2.95E-02	-0.723	Pdcd10	programmed cell death 10
10462005	1.447	7.166	2.85E-05	3.70E-03	3.014	Tmem2	transmembrane protein 2
10582997	1.444	4.836	2.23E-04	1.14E-02	0.933	Casp4	caspase 4, apoptosis-related cysteine peptidase; hypothetical protein LOC100044206
10358299	1.443	4.719	6.61E-04	2.17E-02	-0.181	Cfhr1	predicted gene, EG214403
10381898	1.442	7.616	5.87E-04	2.02E-02	-0.058	Mrc2	mannose receptor, C type 2
10551852	1.441	7.693	4.52E-05	4.67E-03	2.551	Clip3	CAP-GLY domain containing linker protein 3
10460666	1.441	8.629	2.57E-05	3.51E-03	3.115	Ltbp3	latent transforming growth factor beta binding protein 3
10563077	1.441	9.371	1.14E-03	2.97E-02	-0.745	Rcn3	reticulocalbin 3, EF-hand calcium binding domain
10586227	1.44	7.595	1.50E-03	3.51E-02	-1.026	Dennd4a	RIKEN cDNA F730015K02 gene
10574027	1.44	10.966	4.25E-04	1.68E-02	0.274	Mt1	metallothionein 1
10505132	1.439	8.897	1.41E-03	3.37E-02	-0.96	Akap2	A kinase (PRKA) anchor protein 2; paralemmin 2
10421932	1.439	6.92	8.81E-05	6.76E-03	1.878	Pcdh9	protocadherin 9
10342447	1.439	6.507	1.87E-03	3.95E-02	-1.251	Cic	capicua homolog (Drosophila)

10441497	1.437	10.152	1.11E-04	7.66E-03	1.642	Tulp4	similar to mKIAA1397 protein; tubby like protein 4
10354111	1.436	6.209	8.03E-05	6.45E-03	1.973	Aff3	AF4/FMR2 family, member 3; similar to AF4/FMR2 family member 3 (LAF-4 protein) (Lymphoid nuclear protein related to AF4)
10544002	1.436	8.689	1.02E-04	7.35E-03	1.727	Creb3l2	cAMP responsive element binding protein 3-like 2
10356968	1.436	11.856	3.24E-05	3.91E-03	2.885	Pam	peptidylglycine alpha-amidating monooxygenase
10596200	1.436	6.724	6.50E-04	2.16E-02	-0.163	Tmem108	transmembrane protein 108
10408741	1.436	8.485	2.07E-03	4.17E-02	-1.353	Txndc5	thioredoxin domain containing 5
10357870	1.435	9.973	6.16E-05	5.65E-03	2.241	Prelp	proline arginine-rich end leucine-rich repeat
10491780	1.434	8.867	1.12E-03	2.95E-02	-0.723	Hspa4l	heat shock protein 4 like
10409464	1.433	8.031	4.12E-04	1.66E-02	0.305	Dbn1	drebrin 1
10547869	1.433	7.834	1.11E-04	7.65E-03	1.646	Leprel2	leprecan-like 2
10455826	1.433	5.965	2.67E-04	1.27E-02	0.749	Megf10	multiple EGF-like-domains 10
10522024	1.433	7.557	1.73E-04	9.73E-03	1.196	Tbc1d1	TBC1 domain family, member 1; similar to TBC1 domain family member 1
10406852	1.432	8.368	1.94E-03	4.04E-02	-1.288	Cnn3	similar to calponin 3, acidic; predicted gene 4815; calponin 3, acidic
10441494	1.432	8.1	4.81E-04	1.80E-02	0.146	Tulp4	ENSMUSG00000073472
10416057	1.431	11.104	1.42E-03	3.37E-02	-0.964	Clu	similar to clusterin; clusterin
10553773	1.43	6.357	8.03E-04	2.46E-02	-0.381	Gabrb3	gamma-aminobutyric acid (GABA) A receptor, subunit beta 3
10467139	1.43	8.66	1.76E-03	3.80E-02	-1.188	Lipa	lysosomal acid lipase A
10513256	1.43	8.052	1.62E-04	9.37E-03	1.257	Lpar1	lysophosphatidic acid receptor 1
10425808	1.43	8.837	1.39E-03	3.35E-02	-0.948	Tspo	translocator protein
10470027	1.427	7.375	6.28E-04	2.11E-02	-0.128	Npdc1	neural proliferation, differentiation and control gene 1
10433885	1.426	6.801	9.64E-04	2.69E-02	-0.569	Cebpd	CCAAT/enhancer binding protein (C/EBP), delta
10357115	1.426	7.091	5.07E-04	1.84E-02	0.091	Dsel	dermatan sulfate epimerase-like
10413398	1.425	7.129	2.67E-04	1.27E-02	0.749	Il17rd	interleukin 17 receptor D
10440019	1.425	7.202	1.40E-03	3.35E-02	-0.954	Tmem45a	transmembrane protein 45a
10496837	1.425	6.16	6.99E-05	6.10E-03	2.113	Ttll7	tubulin tyrosine ligase-like family, member 7
10347807	1.424	6.294	1.27E-04	8.26E-03	1.509	Col4a3	collagen, type IV, alpha 3
10399005	1.424	11.347	7.74E-05	6.35E-03	2.009	Crip1	cysteine-rich protein 1 (intestinal)
10501827	1.423	6.966	7.70E-05	6.34E-03	2.016	A730020M07Rik	RIKEN cDNA A730020M07 gene
10432682	1.422	6.636	1.52E-03	3.53E-02	-1.037	Krt80	keratin 80
10534862	1.422	10.111	2.13E-03	4.25E-02	-1.385	Pcolce	procollagen C-endopeptidase enhancer protein
10453747	1.42	9.036	2.01E-03	4.11E-02	-1.321	Colec12	collectin sub-family member 12
10526853	1.419	7.205	4.09E-04	1.65E-02	0.313	Fam20c	family with sequence similarity 20, member C
10421361	1.418	8.963	7.05E-05	6.12E-03	2.104	Bmp1	bone morphogenetic protein 1
10446376	1.418	9.203	1.19E-04	7.98E-03	1.572	Man2a1	mannosidase 2, alpha 1
10535559	1.417	8.241	2.10E-05	3.15E-03	3.319	Baiap2l1	BAI1-associated protein 2-like 1
10567735	1.416	6.161	1.24E-04	8.18E-03	1.529	---	RIKEN cDNA 3110040M04 gene
10452485	1.416	9.22	1.67E-03	3.69E-02	-1.131	Rab31	RAB31, member RAS oncogene family
10410092	1.416	8.427	7.59E-05	6.34E-03	2.03	Zfp367	zinc finger protein 367
10553788	1.415	6.174	2.31E-04	1.15E-02	0.898	Atp10a	ATPase, class V, type 10A
10523255	1.415	4.87	1.43E-03	3.39E-02	-0.972	Stbd1	starch binding domain 1

10577757	1.414	9.918	4.32E-05	4.56E-03	2.598	Adam9	a disintegrin and metallopeptidase domain 9 (meltrin gamma)
10604694	1.414	5.191	1.33E-03	3.25E-02	-0.9	Mtap7d3	MAP7 domain containing 3
10437180	1.414	8.764	4.01E-05	4.38E-03	2.673	Sh3bgr	similar to putative SH3BGR protein; SH3-binding domain glutamic acid-rich protein
10362968	1.413	11.209	1.56E-04	9.18E-03	1.299	Bves	blood vessel epicardial substance
10393364	1.413	10.61	1.47E-03	3.46E-02	-1.001	Cygb	cytoglobin
10436372	1.413	8.391	1.23E-03	3.09E-02	-0.82	Dcbld2	discoidin, CUB and LCCL domain containing 2
10592719	1.413	7.779	7.92E-04	2.43E-02	-0.367	Oaf	OAF homolog (Drosophila)
10339446	1.413	10.086	4.66E-04	1.77E-02	0.178	Snrnp27	small nuclear ribonucleoprotein 27 (U4/U6.U5)
10369844	1.412	8.335	1.70E-04	9.62E-03	1.211	Bicc1	bicaudal C homolog 1 (Drosophila)
10432236	1.412	5.462	4.17E-04	1.66E-02	0.292	Rnd1	Rho family GTPase 1
10384579	1.41	10.393	2.22E-03	4.33E-02	-1.425	Ugp2	UDP-glucose pyrophosphorylase 2
10416302	1.409	7.353	2.94E-04	1.35E-02	0.65	Hr	hairless
10374012	1.408	6.37	1.47E-03	3.46E-02	-1.001	Rasl10a	RAS-like, family 10, member A
10436402	1.407	10.351	1.13E-03	2.95E-02	-0.728	Cldnd1	claudin domain containing 1
10476314	1.407	10.029	9.17E-04	2.63E-02	-0.518	Prnd	prion protein
10386211	1.406	5.031	3.43E-04	1.49E-02	0.494	Fam183b	RIKEN cDNA 3100002J23 gene
10544875	1.406	7.946	1.30E-04	8.31E-03	1.488	Scrn1	secernin 1
10394914	1.405	7.249	5.35E-04	1.92E-02	0.037	Iah1	isoamyl acetate-hydrolyzing esterase 1 homolog (S. cerevisiae)
10420988	1.404	10.526	1.29E-04	8.31E-03	1.49	Dpysl2	dihydropyrimidinase-like 2
10606235	1.404	6.393	5.75E-04	2.00E-02	-0.038	Zdhhc15	zinc finger, DHHC domain containing 15
10339988	1.404	7.897	1.06E-03	2.86E-02	-0.669	Anapc2	anaphase promoting complex subunit 2
10365716	1.402	7.579	7.99E-05	6.45E-03	1.978	Ikbip	RIKEN cDNA 1200009F10 gene
10537146	1.401	6.458	2.21E-03	4.31E-02	-1.419	Akr1b8	aldo-keto reductase family 1, member B8
10393559	1.401	10.178	6.51E-04	2.16E-02	-0.165	Timp2	tissue inhibitor of metalloproteinase 2
10341518	1.401	4.627	2.58E-03	4.75E-02	-1.579	Zranb1	zinc finger, RAN-binding domain containing 1
10368888	1.4	8.73	2.19E-03	4.30E-02	-1.412	Foxo3	forkhead box O3
10354598	1.4	7.954	4.81E-05	4.81E-03	2.49	Hecw2	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2
10497149	1.4	9.423	1.05E-03	2.84E-02	-0.658	Wls	G protein-coupled receptor 177
10402708	1.399	10.126	1.10E-04	7.62E-03	1.655	Ckb	similar to creatine kinase, brain; predicted gene 12892; creatine kinase, brain
10595183	1.399	12.532	7.10E-06	1.80E-03	4.38	Eef1a1	predicted gene 5869; predicted gene 7161; predicted gene 7105; predicted gene 5822; similar to eukaryotic translation elongation factor 1 alpha 1; predicted gene 6192; predicted gene 6392; predicted gene 6767; predicted gene 6170; predicted gene 6548; predicted gene 6789; eukaryotic translation elongation factor 1 alpha 1
10572097	1.399	7.033	1.40E-03	3.35E-02	-0.951	Sh2d4a	SH2 domain containing 4A
10601616	1.398	8.594	4.67E-04	1.77E-02	0.175	Diap2	diaphanous homolog 2 (Drosophila)
10482301	1.398	7.138	2.57E-03	4.75E-02	-1.578	Scai	RIKEN cDNA A930041I02 gene
10504606	1.397	7.717	1.19E-03	3.03E-02	-0.786	Aldh1b1	aldehyde dehydrogenase 1 family, member B1
10595298	1.397	9.758	1.06E-03	2.86E-02	-0.665	Filip1	filamin A interacting protein 1
10425161	1.397	11.991	7.38E-05	6.33E-03	2.058	Lgals1	lectin, galactose binding, soluble 1
10567043	1.397	9.799	2.07E-04	1.09E-02	1.011	Rras2	related RAS viral (r-ras) oncogene homolog 2

10347481	1.396	8.518	1.28E-03	3.17E-02	-0.859	Cyp27a1	cytochrome P450, family 27, subfamily a, polypeptide 1
10480414	1.396	4.484	4.71E-04	1.78E-02	0.168	Enkur	enkurin, TRPC channel interacting protein
10467013	1.396	7.555	1.91E-04	1.03E-02	1.092	Prkg1	protein kinase, cGMP-dependent, type I
10358717	1.395	11.531	8.75E-05	6.74E-03	1.886	1700025G04Rik	RIKEN cDNA 1700025G04 gene
10360506	1.395	9.735	1.57E-04	9.20E-03	1.293	Akt3	thymoma viral proto-oncogene 3
10484283	1.394	6.951	1.65E-03	3.68E-02	-1.12	Pde1a	phosphodiesterase 1A, calmodulin-dependent
10397853	1.394	7.442	3.36E-04	1.47E-02	0.513	Rin3	Ras and Rab interactor 3
10564290	1.391	7.698	4.50E-05	4.67E-03	2.557	Klf13	Kruppel-like factor 13
10391454	1.391	8.65	2.57E-05	3.51E-03	3.116	Vat1	vesicle amine transport protein 1 homolog (T californica)
10455294	1.39	5.614	2.69E-03	4.88E-02	-1.624	Kctd16	potassium channel tetramerisation domain containing 16
10577164	1.389	10.088	9.91E-05	7.21E-03	1.759	Gas6	growth arrest specific 6
10587829	1.389	8.553	9.84E-05	7.19E-03	1.766	Plod2	procollagen lysine, 2-oxoglutarate 5-dioxygenase 2
10493449	1.389	6.208	6.24E-04	2.10E-02	-0.121	Thbs3	thrombospondin 3
10521616	1.388	7.348	6.76E-04	2.19E-02	-0.204	C1qtnf7	C1q and tumor necrosis factor related protein 7
10412207	1.387	10.326	2.11E-04	1.10E-02	0.99	Gpx8	glutathione peroxidase 8 (putative)
10547386	1.385	9.742	1.75E-03	3.79E-02	-1.18	Adipor2	adiponectin receptor 2
10490802	1.385	8.101	8.16E-04	2.48E-02	-0.397	Fam164a	family with sequence similarity 164, member A
10472436	1.384	5.356	1.46E-04	8.83E-03	1.369	B3galt1	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1
10487392	1.384	6.285	3.95E-04	1.62E-02	0.349	Kcnip3	Kv channel interacting protein 3, calsenilin
10499394	1.384	8.839	1.09E-04	7.59E-03	1.661	Lmna	lamin A
10480347	1.384	8.743	3.53E-04	1.52E-02	0.464	Pip4k2a	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha
10338709	1.383	8.893	4.93E-04	1.82E-02	0.121	Itch	itchy, E3 ubiquitin protein ligase
10431935	1.382	6.414	1.02E-03	2.80E-02	-0.631	Amigo2	adhesion molecule with Ig like domain 2
10428192	1.381	11.391	1.77E-04	9.90E-03	1.17	Pabpc1	poly(A) binding protein, cytoplasmic 1
10549733	1.379	7.205	4.15E-04	1.66E-02	0.297	A430110N23Rik	RIKEN cDNA A430110N23 gene
10446777	1.379	7.566	8.35E-04	2.51E-02	-0.421	Ehd3	EH-domain containing 3
10435271	1.378	11.059	6.24E-05	5.71E-03	2.227	Heg1	HEG homolog 1 (zebrafish)
10500666	1.378	8.328	4.91E-04	1.82E-02	0.124	Ptgfrn	prostaglandin F2 receptor negative regulator

10416923	1.377	6.241	1.09E-03	2.92E-02	-0.698	---	ENSMUSG00000075949; ENSMUSG00000070225; ENSMUSG00000075942; ENSMUSG00000075804; ENSMUSG00000077556; ENSMUSG00000077350; ENSMUSG00000065107; ENSMUSG00000084595; ENSMUSG00000077743; ENSMUSG00000075814; ENSMUSG00000075811; ENSMUSG00000084599; ENSMUSG00000065102; ENSMUSG00000064631; ENSMUSG00000075817; ENSMUSG00000070219; ENSMUSG00000064635; ENSMUSG00000075955; ENSMUSG00000064467; ENSMUSG00000064521; ENSMUSG00000075820; ENSMUSG00000064770; ENSMUSG00000075822; ENSMUSG00000070201; ENSMUSG00000075921; ENSMUSG00000064906; ENSMUSG00000070209; ENSMUSG00000064903; ENSMUSG00000064455; ENSMUSG00000077437; ENSMUSG00000065719; ENSMUSG00000065311; ENSMUSG00000075836; ENSMUSG00000064515; ENSMUSG00000077620; ENSMUSG00000075838; ENSMUSG00000064519; ENSMUSG00000075931; ENSMUSG00000064409; ENSMUSG00000065823; ENSMUSG00000064798; ENSMUSG00000070192; ENSMUSG00000084612; ENSMUSG00000077309; ENSMUSG00000084613; ENSMUSG00000070199; ENSMUSG00000075846; ENSMUSG00000064588; ENSMUSG00000075788; ENSMUSG00000075792; ENSMUSG00000077705; ENSMUSG00000075794; ENSMUSG00000065005; ENSMUSG00000077706; ENSMUSG00000075790; ENSMUSG00000084498; ENSMUSG00000077313; ENSMUSG00000065149; ENSMUSG00000084624; ENSMUSG00000084623; ENSMUSG00000084492; ENSMUSG00000084491; ENSMUSG00000084494; ENSMUSG00000075999; ENSMUSG00000075859; ENSMUSG00000077316; ENSMUSG00000075858; ENSMUSG00000075856; ENSMUSG00000075799; ENSMUSG00000065691; ENSMUSG00000065806; ENSMUSG00000075965; ENSMUSG00000075962; ENSMUSG00000084480; ENSMUSG00000075863; ENSMUSG00000075765;
10352928	1.377	4.732	6.71E-04	2.19E-02	-0.197	Rp1	retinitis pigmentosa 1 (human)
10343078	1.377	8.985	1.62E-03	3.64E-02	-1.104	Tmem165	transmembrane protein 165
10340193	1.377	9.41	1.58E-03	3.59E-02	-1.075		ENSMUSG00000081429
10436304	1.376	7.943	1.56E-03	3.58E-02	-1.061	Abi3bp	ABI gene family, member 3 (NESH) binding protein
10505030	1.376	8.34	2.49E-03	4.66E-02	-1.544	Fsd1l	fibronectin type III and SPRY domain containing 1-like
10462702	1.376	5.452	7.73E-04	2.40E-02	-0.341	Hectd2	HECT domain containing 2
10376950	1.376	11.414	2.20E-04	1.13E-02	0.946	Pmp22	peripheral myelin protein 22
10548030	1.375	7.687	1.12E-03	2.95E-02	-0.725	Cd9	CD9 antigen
10500808	1.375	10.169	2.16E-04	1.11E-02	0.968	Olfml3	olfactomedin-like 3

10569714	1.374	6.792	1.81E-03	3.87E-02	-1.216	Cacng7	calcium channel, voltage-dependent, gamma subunit 7
10489053	1.373	5.497	1.96E-03	4.05E-02	-1.296	4930518I15Rik	RIKEN cDNA 4930518I15 gene
10350838	1.37	6.141	6.77E-04	2.19E-02	-0.205	2810417H13Rik	ENSMUSG00000080804
10492860	1.37	8.139	2.73E-03	4.91E-02	-1.637	Higd1a	similar to hypoxia induced gene 1; predicted gene 9790
10599530	1.37	4.513	5.51E-05	5.23E-03	2.354	Rab33a	RAB33A, member of RAS oncogene family
10532711	1.369	7.905	4.70E-04	1.78E-02	0.169	Cmklr1	chemokine-like receptor 1
10459353	1.367	5.507	1.57E-03	3.59E-02	-1.071	Fam38b	family with sequence similarity 38, member B2
10526113	1.366	7.538	1.68E-03	3.70E-02	-1.137	Crcp	calcitonin gene-related peptide-receptor component protein
10443021	1.365	9.539	5.08E-05	4.95E-03	2.434	Atp6v0e	ATPase, H+ transporting, lysosomal V0 subunit E
10567355	1.365	7.751	2.46E-03	4.62E-02	-1.53	Gprc5b	G protein-coupled receptor, family C, group 5, member B
10381371	1.364	7.15	1.03E-03	2.81E-02	-0.634	Aoc3	amine oxidase, copper containing 3
10472095	1.362	7.228	1.38E-04	8.55E-03	1.425	Bloc1s2	biogenesis of lysosome-related organelles complex-1, subunit 2; predicted gene 13540
10551336	1.361	7.372	7.97E-04	2.44E-02	-0.374	Numbl	numb-like
10541114	1.361	5.725	2.96E-04	1.35E-02	0.642	Rasgef1a	RasGEF domain family, member 1A
10498620	1.361	4.438	1.54E-03	3.56E-02	-1.053	Trim59	similar to mouse RING finger 1; tripartite motif-containing 59
10396440	1.36	5.792	4.64E-04	1.77E-02	0.184	Gm5068	predicted gene 7665; S100 calcium binding protein A11 (calgizzarin); predicted gene 5068
10475350	1.36	8.438	8.85E-04	2.58E-02	-0.481	Serf2	small EDRK-rich factor 2
10485048	1.359	9.937	1.40E-04	8.60E-03	1.412	Atg13	DNA segment, Chr 2, ERATO Doi 391, expressed
10504349	1.359	8.956	5.37E-04	1.92E-02	0.033	Creb3	cAMP responsive element binding protein 3
10350630	1.359	8.162	2.18E-03	4.29E-02	-1.409	Fam129a	family with sequence similarity 129, member A
10371321	1.359	6.182	1.73E-03	3.77E-02	-1.17	Slc41a2	solute carrier family 41, member 2
10590060	1.358	7.472	2.59E-04	1.24E-02	0.781	Ctdspl	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like
10511617	1.357	6.989	1.12E-03	2.95E-02	-0.719	Fam92a	family with sequence similarity 92, member A
10576661	1.357	11.062	9.71E-04	2.70E-02	-0.576	Itgb1	integrin beta 1 (fibronectin receptor beta)
10364702	1.357	10.11	8.09E-04	2.47E-02	-0.389	Midn	midnolin
10601449	1.357	10.447	4.91E-05	4.83E-03	2.469	Sh3bgrl	SH3-binding domain glutamic acid-rich protein like
10459335	1.356	5.222	1.45E-04	8.83E-03	1.374	Fam38b	family with sequence similarity 38, member B
10382243	1.355	9.921	4.07E-04	1.65E-02	0.316	Gna13	guanine nucleotide binding protein, alpha 13
10575120	1.355	8.065	1.21E-03	3.06E-02	-0.804	Sntb2	similar to beta-2-syntrophin; syntrophin, basic 2
10556598	1.355	7.011	2.88E-04	1.32E-02	0.672	Xylt1	xylosyltransferase 1
10384795	1.354	9.342	2.66E-04	1.26E-02	0.754	Cyb5d1	cytochrome b5 domain containing 1; predicted gene 6685
10573924	1.354	11.095	2.02E-03	4.12E-02	-1.327	Mmp2	matrix metallopeptidase 2
10486396	1.353	12.042	2.43E-04	1.19E-02	0.844	Ehd4	EH-domain containing 4
10570982	1.353	8.901	1.54E-03	3.55E-02	-1.047	Fgfr1	fibroblast growth factor receptor 1
10528702	1.353	8.266	1.80E-03	3.86E-02	-1.213	Prkag2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit
10469322	1.353	12.554	3.04E-05	3.82E-03	2.95	Vim	vimentin
10389522	1.353	10.183	3.73E-04	1.56E-02	0.408	Rpl13a	similar to 60S ribosomal protein L13a (Transplantation antigen P198) (Tum-P198 antigen); ribosomal protein L13A; similar to 60S ribosomal protein L13a; predicted gene 6533
10583809	1.352	6.774	1.47E-04	8.83E-03	1.36	Cnn1	calponin 1
10498160	1.352	9.575	2.21E-04	1.13E-02	0.945	Ufm1	ubiquitin-fold modifier 1

10498064	1.351	8.963	5.33E-04	1.91E-02	0.039	Setd7	SET domain containing (lysine methyltransferase) 7
10459643	1.349	6.204	1.05E-03	2.84E-02	-0.655	4930503L19Rik	RIKEN cDNA 4930503L19 gene
10477090	1.349	9.455	3.97E-04	1.62E-02	0.344	Tbc1d20	TBC1 domain family, member 20
10476443	1.348	10.183	5.46E-04	1.94E-02	0.015	Plcb4	phospholipase C, beta 4
10521824	1.348	7.393	7.34E-04	2.32E-02	-0.289	Sod3	superoxide dismutase 3, extracellular
10549536	1.347	7.31	4.06E-04	1.64E-02	0.319	Amn1	antagonist of mitotic exit network 1 homolog (S. cerevisiae)
10406934	1.347	8.47	1.15E-03	2.98E-02	-0.752	Gm5454	ets variant gene 1
10385941	1.347	7.295	9.27E-04	2.64E-02	-0.529	Tnip1	TNFAIP3 interacting protein 1
10473190	1.346	7.87	3.80E-04	1.57E-02	0.389	Dnajc10	DnaJ (Hsp40) homolog, subfamily C, member 10
10529375	1.345	9.304	7.95E-05	6.45E-03	1.982	Mxd4	Max dimerization protein 4
10384233	1.345	7.753	1.87E-04	1.02E-02	1.113	Tns3	tensin 3
10530612	1.344	9.025	1.62E-04	9.37E-03	1.263	Fryl	furry homolog-like (Drosophila)
10409994	1.343	4.361	1.40E-03	3.35E-02	-0.954	Gm5665	predicted gene 5665
10561178	1.342	8.235	1.09E-03	2.91E-02	-0.691	Rab4b	RAB4B, member RAS oncogene family
10578623	1.342	8.799	6.26E-04	2.10E-02	-0.125	Wwc2	WW, C2 and coiled-coil domain containing 2
10570201	1.341	9.907	5.67E-05	5.30E-03	2.324	Atp11a	ENSMUSG00000079149
10499666	1.34	7.623	1.42E-03	3.38E-02	-0.968	Atp8b2	ATPase, class I, type 8B, member 2
10467766	1.339	4.62	1.74E-03	3.79E-02	-1.177	Loxl4	ENSMUSG00000055590
10543921	1.338	5.947	2.24E-03	4.35E-02	-1.434	Slc13a4	solute carrier family 13 (sodium/sulfate symporters), member 4
10561104	1.337	9.945	8.58E-05	6.69E-03	1.906	Axl	AXL receptor tyrosine kinase
10491877	1.337	6.781	9.20E-04	2.64E-02	-0.521	D3Ertd751e	predicted gene 9529; DNA segment, Chr 3, ERATO Doi 751, expressed
10409978	1.336	6.322	2.06E-03	4.16E-02	-1.351	6720457D02Rik	predicted gene 3325; predicted gene 7036
10378319	1.335	7.83	1.66E-03	3.69E-02	-1.128	P2rx5	purinergic receptor P2X, ligand-gated ion channel, 5
10602198	1.335	4.895	9.49E-05	7.10E-03	1.803	Pak3	p21 protein (Cdc42/Rac)-activated kinase 3
10356088	1.334	6.473	1.01E-03	2.78E-02	-0.62	Col4a4	collagen, type IV, alpha 4
10404407	1.333	5.983	1.41E-03	3.36E-02	-0.958	Foxc1	forkhead box C1
10457273	1.333	10.961	1.00E-03	2.76E-02	-0.606	Kif5b	kinesin family member 5B
10606876	1.333	7.795	2.05E-03	4.14E-02	-1.342	Morf4l2	predicted gene 5521; similar to mortality factor 4 like 2; mortality factor 4 like 2
10452147	1.333	8.201	2.70E-03	4.88E-02	-1.627	Nrtn	neurturin
10564646	1.333	4.925	1.83E-04	1.01E-02	1.136	Sv2b	synaptic vesicle glycoprotein 2 b
10499431	1.333	7.255	2.34E-03	4.47E-02	-1.482	Syt11	synaptotagmin XI; similar to synaptotagmin XI
10590427	1.332	6.146	2.30E-03	4.44E-02	-1.461	Ccbp2	chemokine binding protein 2
10341507	1.332	9.346	3.25E-04	1.43E-02	0.548	Tmem165	transmembrane protein 165
10425852	1.331	9.138	3.05E-04	1.38E-02	0.613	Parvb	parvin, beta; similar to parvin, beta
10599377	1.331	8.546	1.18E-03	3.02E-02	-0.777	Stag2	stromal antigen 2
10568988	1.33	7.365	8.32E-04	2.50E-02	-0.417	Bet1l	blocked early in transport 1 homolog (S. cerevisiae)-like
10361186	1.33	6.512	1.70E-03	3.72E-02	-1.151	Sertad4	SERTA domain containing 4
10455919	1.329	6.029	2.41E-03	4.56E-02	-1.512	Adamts19	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 19
10554166	1.328	8.405	6.95E-04	2.23E-02	-0.233	Akap13	A kinase (PRKA) anchor protein 13
10420532	1.328	6.692	9.26E-04	2.64E-02	-0.527	Atp8a2	ATPase, aminophospholipid transporter-like, class I, type 8A, member 2

10542200	1.328	10.088	3.86E-04	1.60E-02	0.371	Gabarapl1	gamma-aminobutyric acid (GABA) A receptor-associated protein-like 1
10534102	1.328	7.349	6.42E-04	2.14E-02	-0.15	Gusb	glucuronidase, beta
10403229	1.328	6.305	7.52E-04	2.36E-02	-0.314	Itgb8	integrin beta 8
10478692	1.328	5.381	1.94E-03	4.04E-02	-1.287	Slc2a10	solute carrier family 2 (facilitated glucose transporter), member 10
10447517	1.327	7.079	6.00E-04	2.05E-02	-0.081	Pisd-ps2	phosphatidylserine decarboxylase, pseudogene 2
10512739	1.326	7.417	4.19E-04	1.67E-02	0.288	Xpa	xeroderma pigmentosum, complementation group A
10500928	1.326	10.564	4.81E-04	1.80E-02	0.145	Capza1	capping protein (actin filament) muscle Z-line, alpha 1; similar to capping protein (actin filament) muscle Z-line, alpha 1; predicted gene 3608; predicted gene 5920
10473281	1.325	9.021	3.54E-04	1.52E-02	0.46	Itgav	integrin alpha V
10363786	1.324	8.832	6.06E-04	2.06E-02	-0.091	Ank3	ankyrin 3, epithelial
10381601	1.324	6.922	5.74E-04	1.99E-02	-0.035	Mdk	midkine pseudogene 1
10603896	1.323	8.879	1.11E-03	2.94E-02	-0.712	Klhl13	kelch-like 13 (Drosophila)
10394837	1.322	6.776	1.49E-03	3.49E-02	-1.019	LOC100043371	predicted gene 9187; predicted gene 9306
10541910	1.322	8.4	1.66E-03	3.69E-02	-1.13	Vwf	Von Willebrand factor homolog
10404686	1.321	9.111	6.52E-04	2.16E-02	-0.167	Bmp6	bone morphogenetic protein 6
10450374	1.321	6.024	7.91E-05	6.44E-03	1.988	D17H6S56E-5	DNA segment, Chr 17, human D6S56E 5
10378893	1.32	6.126	3.16E-05	3.84E-03	2.91	Abhd15	RIKEN cDNA 1300007F04 gene
10352815	1.32	6.045	2.13E-04	1.11E-02	0.982	Irf6	interferon regulatory factor 6
10371271	1.32	7.431	4.24E-04	1.68E-02	0.276	Zfp781	zinc finger protein 781
10430974	1.319	7.848	7.69E-04	2.39E-02	-0.337	Arfgap3	ADP-ribosylation factor GTPase activating protein 3
10366848	1.319	6.222	1.56E-04	9.18E-03	1.299	B4galnt1	beta-1,4-N-acetyl-galactosaminyl transferase 1
10349401	1.319	4.675	2.43E-03	4.58E-02	-1.519	Gpr39	G protein-coupled receptor 39
10352661	1.319	8.806	1.19E-03	3.03E-02	-0.784	Ptpn14	protein tyrosine phosphatase, non-receptor type 14
10597531	1.319	8.128	2.46E-03	4.62E-02	-1.531	Rbms3	RNA binding motif, single stranded interacting protein
10591867	1.318	12.304	2.45E-04	1.19E-02	0.838	Rpl41	ribosomal protein L41; predicted gene 3699
10468893	1.317	8.448	1.84E-04	1.01E-02	1.131	Csf2ra	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)
10405587	1.317	8.703	2.49E-03	4.65E-02	-1.542	Tgfbi	transforming growth factor, beta induced
10518346	1.316	10.092	3.46E-04	1.50E-02	0.485	Gm13051	predicted gene 13251; predicted gene, OTTMUSG00000010657; RIKEN cDNA 1700029I01 gene
10373662	1.315	3.952	4.49E-04	1.74E-02	0.216	Olfr819	olfactory receptor 247
10457853	1.314	9.501	1.88E-03	3.96E-02	-1.253	Ino80c	INO80 complex subunit C
10343221	1.313	8.586	7.43E-04	2.34E-02	-0.3	Anapc2	anaphase promoting complex subunit 2
10584435	1.312	8.765	4.95E-04	1.82E-02	0.116	Vwa5a	von Willebrand factor A domain containing 5A
10599032	1.312	6.753	6.40E-04	2.14E-02	-0.148	Wdr44	WD repeat domain 44
10408629	1.311	7.226	1.11E-03	2.94E-02	-0.713	1300014I06Rik	RIKEN cDNA 1300014I06 gene
10513776	1.311	6.708	8.98E-04	2.61E-02	-0.496	Astn2	astrotactin 2
10491970	1.311	9.854	4.76E-04	1.79E-02	0.156	Lhfp	lipoma HMGIC fusion partner
10588263	1.311	7.312	1.84E-03	3.92E-02	-1.236	Slco2a1	solute carrier organic anion transporter family, member 2a1

10591208	1.309	10.082	1.33E-03	3.24E-02	-0.897	Gm5239	predicted gene 5928; predicted gene 12617; predicted gene 4802; similar to ribosomal protein S27a; predicted gene 13215; predicted gene 6111; predicted gene 7808; predicted gene 6014; predicted gene 8317; ubiquitin C; ubiquitin B; similar to fusion protein: ubiquitin (bases 43_513); ribosomal protein S27a (bases 217_532); similar to ubiquitin B; predicted gene 8649; ribosomal protein S27A; predicted gene 11517; predicted gene 11808; predicted gene 8430; RIKEN cDNA 2810422J05 gene; similar to Ubc protein; predicted gene 13815; ubiquitin A-52 residue ribosomal protein fusion product 1; predicted gene 8797; predicted gene 1821; predicted gene 11759; predicted gene 5239; predicted gene 6438
10552824	1.309	11.524	6.80E-04	2.20E-02	-0.209	Rras	Harvey rat sarcoma oncogene, subgroup R
10537102	1.308	9.311	9.13E-04	2.63E-02	-0.513	Exoc4	exocyst complex component 4
10583992	1.308	7.006	1.93E-03	4.03E-02	-1.282	Igsf9b	immunoglobulin superfamily, member 9B
10447341	1.308	9.965	2.22E-04	1.14E-02	0.937	Rhoq	ras homolog gene family, member Q
10408600	1.308	8.724	1.19E-03	3.03E-02	-0.788	Serpinb6a	serine (or cysteine) peptidase inhibitor, clade B, member 6a
10392943	1.307	9.958	6.03E-04	2.06E-02	-0.087	Hn1	hematological and neurological expressed sequence 1; predicted gene 3687
10574096	1.305	8.022	1.15E-03	2.97E-02	-0.746	Ap3s1	predicted gene 7603; adaptor-related protein complex 3, sigma 1 subunit; predicted gene 5610
10469066	1.305	6.577	2.72E-04	1.28E-02	0.73	Ccdc3	coiled-coil domain containing 3
10371846	1.304	7.074	7.61E-04	2.38E-02	-0.326	Apaf1	apoptotic peptidase activating factor 1
10536444	1.304	6.401	1.75E-04	9.86E-03	1.181	Foxp2	forkhead box P2
10438358	1.304	6.539	8.28E-05	6.58E-03	1.941	Gp1bb	similar to CDCrel-1AI; septin 5
10567299	1.304	7.838	2.20E-03	4.30E-02	-1.416	Itpripl2	inositol 1,4,5-triphosphate receptor interacting protein-like 2
10434806	1.304	9.842	9.45E-04	2.66E-02	-0.548	Lpp	ENSMUSG00000057796
10530558	1.304	8.532	6.09E-04	2.06E-02	-0.097	Slain2	ENSMUSG00000052154
10595013	1.304	6.519	2.32E-03	4.45E-02	-1.472	Tmod2	tropomodulin 2
10408111	1.303	9.94	2.40E-03	4.54E-02	-1.505	Hist1h2ai	histone cluster 1, H2ad; histone cluster 1, H2ae; histone cluster 1, H2ag; histone cluster 1, H2ah; histone cluster 1, H2ai; similar to histone 2a; histone cluster 1, H2an; histone cluster 1, H2ao; histone cluster 1, H2ac; histone cluster 1, H2ab
10597900	1.303	9.242	6.90E-04	2.22E-02	-0.225	Zfp445	zinc finger protein 445
10604230	1.302	8.556	1.12E-03	2.95E-02	-0.718	Ap3s1	predicted gene 7603; adaptor-related protein complex 3, sigma 1 subunit; predicted gene 5610
10550332	1.301	8.15	1.79E-03	3.85E-02	-1.208	Slc1a5	solute carrier family 1 (neutral amino acid transporter), member 5
10444459	1.301	8.172	7.69E-05	6.34E-03	2.017	Tnxb	tenascin XB
10585588	1.299	7.821	5.27E-04	1.89E-02	0.052	Cspg4	chondroitin sulfate proteoglycan 4
10567106	1.299	6.649	2.54E-03	4.72E-02	-1.564	Gm6816	predicted gene 6816; ribosomal protein S4, Y-linked 2

10576246	1.299	8.139	1.94E-03	4.04E-02	-1.288	Rps12	predicted gene 16422; predicted gene 6646; ribosomal protein S12; predicted gene 12334; predicted gene 5642; predicted gene 14059; predicted gene 5462; predicted gene 7698; predicted gene 7586; similar to ribosomal protein S12; predicted gene 14958; predicted gene 15887; predicted gene 10063; predicted gene 7601; predicted gene 9153; predicted gene 7671; predicted gene 9122; similar to 40S ribosomal protein S12; predicted gene 7711; predicted gene 7567; predicted gene 7643
10585974	1.297	6.945	1.75E-03	3.79E-02	-1.179	Myo9a	myosin IXa
10461636	1.296	4.218	1.94E-03	4.04E-02	-1.287	---	ENSMUSG00000067555
10529485	1.296	9.192	3.91E-04	1.61E-02	0.357	Htra3	HtrA serine peptidase 3
10434291	1.295	5.146	8.77E-05	6.75E-03	1.883	B3gnt5	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5
10529252	1.295	8.695	8.02E-04	2.45E-02	-0.38	C330019G07Rik	hypothetical protein LOC100045758; similar to EMO2; RIKEN cDNA C330019G07 gene; similar to CG6004-PB
10458340	1.295	9.149	1.47E-03	3.46E-02	-1.002	Hbegf	heparin-binding EGF-like growth factor
10570236	1.294	7.614	5.37E-04	1.92E-02	0.032	Mcf2l	mcf.2 transforming sequence-like
10445898	1.294	9.149	2.15E-03	4.26E-02	-1.395	Rab5a	RAB5A, member RAS oncogene family; similar to small GTP-binding protein rab5
10603009	1.292	12.349	1.55E-03	3.57E-02	-1.058	Gm5239	predicted gene 5928; predicted gene 12617; predicted gene 4802; similar to ribosomal protein S27a; predicted gene 13215; predicted gene 6111; predicted gene 7808; predicted gene 6014; predicted gene 8317; ubiquitin C; ubiquitin B; similar to fusion protein: ubiquitin (bases 43_513); ribosomal protein S27a (bases 217_532); similar to ubiquitin B; predicted gene 8649; ribosomal protein S27A; predicted gene 11517; predicted gene 11808; predicted gene 8430; RIKEN cDNA 2810422J05 gene; similar to Ubc protein; predicted gene 13815; ubiquitin A-52 residue ribosomal protein fusion product 1; predicted gene 8797; predicted gene 1821; predicted gene 11759; predicted gene 5239; predicted gene 6438
10436519	1.291	6.48	4.77E-04	1.79E-02	0.153	Robo1	roundabout homolog 1 (Drosophila)
10447100	1.29	8.635	1.09E-03	2.92E-02	-0.699	Dhx57	MORN repeat containing 2
10409833	1.29	9.063	1.14E-03	2.97E-02	-0.743	Gas1	growth arrest specific 1
10351013	1.29	7.902	2.00E-03	4.11E-02	-1.316	Rc3h1	ENSMUSG00000073520
10561004	1.289	7.31	1.71E-03	3.74E-02	-1.157	Erf	Ets2 repressor factor
10348817	1.289	11.316	1.26E-03	3.14E-02	-0.841	Sept2	septin 2
10529636	1.289	4.92	1.57E-03	3.59E-02	-1.07	Stk32b	serine/threonine kinase 32B; predicted gene 3080
10455292	1.288	4.857	1.46E-03	3.44E-02	-0.995	2900055J20Rik	RIKEN cDNA 2900055J20 gene
10359339	1.288	8.766	1.37E-03	3.31E-02	-0.931	Rabgap1l	RAB GTPase activating protein 1-like
10581395	1.287	8.139	1.57E-03	3.59E-02	-1.071	Slc12a4	solute carrier family 12, member 4
10406854	1.287	3.918	1.12E-03	2.95E-02	-0.727	Rpl27a	predicted gene 14439; predicted gene 8213; predicted gene 13981; predicted gene 8451; predicted gene 6378; predicted gene 8667; predicted gene 4923; predicted gene 5908; ribosomal protein L27a; predicted gene 14044; predicted gene 7536; predicted gene 14407

10460196	1.285	7.968	2.55E-03	4.73E-02	-1.568	1810055G02Rik	RIKEN cDNA 1810055G02 gene
10470462	1.285	7.425	1.28E-03	3.18E-02	-0.863	Col5a1	collagen, type V, alpha 1
10418410	1.285	8.127	2.28E-03	4.42E-02	-1.455	Prkcd	protein kinase C, delta
10471967	1.284	7.369	2.31E-03	4.45E-02	-1.468	Mbd5	methyl-CpG binding domain protein 5
10405918	1.284	6.387	1.61E-03	3.63E-02	-1.098	Rsl1	regulator of sex limited protein 1
10346668	1.283	8.539	1.80E-03	3.86E-02	-1.213	Fam117b	hypothetical protein LOC100045775; family with sequence similarity 117, member B
10473496	1.283	4.666	4.86E-04	1.81E-02	0.135	Olfr1036	olfactory receptor 1036
10355115	1.283	10.084	2.15E-03	4.26E-02	-1.395	Prelid1	predicted gene 12565
10602756	1.283	11.686	1.08E-03	2.88E-02	-0.681	Smpx	small muscle protein, X-linked
10501608	1.283	8.16	1.57E-03	3.59E-02	-1.071	Vcam1	vascular cell adhesion molecule 1
10497817	1.282	11.596	2.52E-03	4.70E-02	-1.555	Anxa5	annexin A5
10497842	1.282	6.365	1.74E-03	3.79E-02	-1.177	Bbs7	Bardet-Biedl syndrome 7 (human)
10439766	1.282	7.54	2.74E-03	4.93E-02	-1.642	Pvrl3	poliovirus receptor-related 3
10577808	1.282	8.187	6.63E-04	2.17E-02	-0.184	Tacc1	transforming, acidic coiled-coil containing protein 1
10577048	1.281	7.68	1.32E-03	3.22E-02	-0.888	Ankrd10	ankyrin repeat domain 10
10550383	1.281	7.495	4.44E-04	1.73E-02	0.229	Dact3	dapper homolog 3, antagonist of beta-catenin (xenopus)
10588899	1.281	10.063	3.96E-04	1.62E-02	0.346	Gpx1	glutathione peroxidase 1
10405063	1.281	10.911	1.80E-03	3.86E-02	-1.213	Ogn	osteoglycin
10510178	1.281	6.142	9.44E-04	2.66E-02	-0.547	Zfp534	predicted gene 13251; predicted gene, OTTMUSG00000010657; RIKEN cDNA 1700029I01 gene
10373448	1.28	12.753	2.30E-03	4.44E-02	-1.46	Rpl41	ribosomal protein L41; predicted gene 3699
10355050	1.28	10.157	1.38E-03	3.32E-02	-0.934	Raph1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1

10569996	1.279	8.757	2.43E-03	4.57E-02	-1.518	Rpl21-ps14	predicted gene 12618; predicted gene 8724; predicted gene 10155; predicted gene 3355; predicted gene 3713; predicted gene 3201; predicted gene 13641; similar to ribosomal protein L21; predicted gene 12411; predicted gene 5445; predicted gene 5495; predicted gene 13604; predicted gene 10045; predicted gene 14648; predicted gene 15150; predicted gene 8252; predicted gene 8157; predicted gene 8880; predicted gene 6813; predicted gene 15312; predicted gene 5534; predicted gene 8054; predicted gene 10095; predicted gene 5857; predicted gene 8195; predicted gene 8840; predicted gene 10240; predicted gene 5810; predicted gene 11975; predicted gene 5816; predicted gene 7547; predicted gene 7702; predicted gene 8012; predicted gene 8557; predicted gene 12760; predicted gene 2815; predicted gene 14336; predicted gene 7806; predicted gene 7799; predicted gene 5042; predicted gene 7062; similar to 60S ribosomal protein L21; predicted gene 8397; predicted gene 5528; ribosomal protein L21; predicted gene 11703; predicted gene 12944; predicted gene 5502; predicted gene 10163; predicted gene 7218; predicted gene 15309; ribosomal protein L21 pseudogene; predicted gene 8915; predicted gene 16060; predicted gene 13653; predicted gene 6689; predicted gene 8101; predicted gene 9130
10484927	1.279	9.421	3.05E-04	1.38E-02	0.612	Slc39a13	solute carrier family 39 (metal ion transporter), member 13
10500204	1.278	8.802	1.58E-03	3.59E-02	-1.077	Ecm1	extracellular matrix protein 1
10357878	1.277	7.833	2.35E-03	4.47E-02	-1.484	Adora1	adenosine A1 receptor
10584358	1.277	4.348	3.21E-04	1.42E-02	0.56	Olfr877	olfactory receptor 877
10462535	1.277	5.365	2.19E-03	4.30E-02	-1.411	Pten	RIKEN cDNA B430203M17 gene
10472440	1.277	10.957	9.89E-04	2.74E-02	-0.596	Tax1bp3	Tax1 (human T-cell leukemia virus type I) binding protein 3; predicted gene 13597; similar to Tax1 (human T-cell leukemia virus type I) binding protein 3
10595831	1.277	9.63	1.76E-03	3.80E-02	-1.187	Zbtb38	zinc finger and BTB domain containing 38
10370072	1.276	7.063	2.02E-03	4.12E-02	-1.329	Prmt2	protein arginine N-methyltransferase 2
10362959	1.275	8.603	1.29E-03	3.18E-02	-0.865	Popdc3	popeye domain containing 3
10410124	1.274	11.115	1.83E-04	1.01E-02	1.135	Ctsl	cathepsin L
10368409	1.273	10.457	1.42E-03	3.38E-02	-0.969	Lama2	laminin, alpha 2
10504398	1.273	10.591	1.03E-03	2.80E-02	-0.632	Serf2	RIKEN cDNA 2310003F16 gene
10533145	1.273	8.272	1.87E-03	3.95E-02	-1.251	Tpcn1	two pore channel 1
10521537	1.272	8.891	7.76E-04	2.41E-02	-0.346	Cytl1	cytokine-like 1
10572722	1.271	8.422	2.42E-03	4.57E-02	-1.515	---	predicted gene 3771
10564377	1.271	7.706	4.13E-04	1.66E-02	0.301	Lrrk1	leucine-rich repeat kinase 1
10591853	1.271	10.935	1.78E-03	3.83E-02	-1.197	Tbx20	T-box 20
10421758	1.269	8.57	2.56E-03	4.74E-02	-1.573	Akap11	A kinase (PRKA) anchor protein 11
10491279	1.269	8.375	1.33E-04	8.42E-03	1.459	Prkci	protein kinase C, iota
10394862	1.268	7.661	7.64E-04	2.38E-02	-0.33	Asap2	development and differentiation enhancing factor 2

10542156	1.268	8.678	2.17E-03	4.28E-02	-1.402	Clec2d	C-type lectin domain family 2, member d
10555197	1.268	6.013	2.22E-03	4.33E-02	-1.427	Mtap6	microtubule-associated protein 6
10569513	1.268	7.922	3.13E-04	1.40E-02	0.586	Osbpl5	oxysterol binding protein-like 5
10384152	1.268	8.347	1.67E-04	9.55E-03	1.226	Purb	purine rich element binding protein B
10405216	1.268	7.294	2.38E-03	4.52E-02	-1.498	Sykb	spleen tyrosine kinase
10483667	1.266	6.812	2.54E-03	4.72E-02	-1.563	Cir1	RIKEN cDNA 1700023B02 gene; predicted gene 5605; similar to CBF1 interacting corepressor; predicted gene 13803; predicted gene 2810
10453797	1.266	4.842	7.60E-04	2.38E-02	-0.324	Greb1l	cDNA sequence AK220484
10435704	1.265	5.715	9.06E-04	2.62E-02	-0.505	Cd80	CD80 antigen
10464877	1.265	7.886	2.78E-03	4.97E-02	-1.656	Dpp3	dipeptidylpeptidase 3
10386628	1.265	6.568	8.83E-04	2.58E-02	-0.479	Gm16515	gene trap locus F3b
10562260	1.265	8.066	1.76E-03	3.80E-02	-1.188	Gramd1a	GRAM domain containing 1A
10475890	1.264	7.123	1.15E-04	7.77E-03	1.611	Mertk	c-mer proto-oncogene tyrosine kinase
10348424	1.263	7.32	8.51E-04	2.53E-02	-0.44	Sh3bp4	SH3-domain binding protein 4
10510225	1.262	4.436	1.04E-03	2.82E-02	-0.643	---	ENSMUSG00000078500
10516027	1.262	7.989	2.17E-03	4.28E-02	-1.4	Rlf	rearranged L-myc fusion sequence
10535095	1.262	10.144	4.55E-04	1.75E-02	0.202	Zfand2a	zinc finger, AN1-type domain 2A
10606581	1.261	9.306	2.00E-03	4.11E-02	-1.319	Rps12-ps2	predicted gene 16422; predicted gene 6646; ribosomal protein S12; predicted gene 12334; predicted gene 5642; predicted gene 14059; predicted gene 5462; predicted gene 7698; predicted gene 7586; similar to ribosomal protein S12; predicted gene 14958; predicted gene 15887; predicted gene 10063; predicted gene 7601; predicted gene 9153; predicted gene 7671; predicted gene 9122; similar to 40S ribosomal protein S12; predicted gene 7711; predicted gene 7567; predicted gene 7643
10586604	1.26	10.452	5.48E-04	1.94E-02	0.013	Rps27l	ribosomal protein S27-like
10408266	1.259	5.681	2.04E-03	4.14E-02	-1.341	Hist1h2ba	histone cluster 1, H2ba
10593421	1.258	8.296	1.30E-03	3.20E-02	-0.876	1110032A03Rik	RIKEN cDNA 1110032A03 gene; hypothetical protein LOC100048251
10505120	1.258	7.137	6.30E-04	2.11E-02	-0.132	Palm2	A kinase (PRKA) anchor protein 2; paralemmin 2
10490824	1.257	8.576	1.30E-03	3.20E-02	-0.876	Rpl29	similar to ribosomal protein; predicted gene 6344; predicted gene 11449; predicted gene 13841; predicted gene 8210; hypothetical protein LOC675793; ribosomal protein L29; predicted gene 12704; predicted gene 7252; predicted gene 8965; predicted gene 13213; predicted gene 8580; predicted gene 15526; predicted gene 7934; predicted gene 5218; predicted gene 5561; predicted gene 8548; predicted gene 12447; predicted gene 8852; predicted gene 12508; predicted gene 6010; predicted gene 13921; predicted gene 8860; predicted gene 13545; predicted gene 9405; predicted gene 6862; predicted gene 13141; predicted gene 10709
10473384	1.257	11.142	2.24E-04	1.14E-02	0.927	Slc43a3	solute carrier family 43, member 3
10406877	1.256	7.265	9.02E-04	2.61E-02	-0.501	Serf1	small EDRK-rich factor 1

10550406	1.255	6.407	2.47E-03	4.63E-02	-1.534	Ccdc8	coiled-coil domain containing 8
10495659	1.254	9.497	1.10E-03	2.93E-02	-0.708	Cnn3	similar to calponin 3, acidic; predicted gene 4815; calponin 3, acidic
10506939	1.254	9.278	1.04E-03	2.83E-02	-0.649	Eps15	epidermal growth factor receptor pathway substrate 15
10570975	1.254	9.861	3.13E-04	1.40E-02	0.588	Tm2d2	TM2 domain containing 2
10555425	1.253	8.147	8.77E-04	2.57E-02	-0.472	Fam168a	family with sequence similarity 168, member A
10508651	1.253	8.784	2.31E-03	4.45E-02	-1.468	Sdc3	syndecan 3
10345074	1.252	4.159	2.77E-04	1.29E-02	0.71	Cetn4	ENSMUSG00000046847
10533023	1.252	12.763	8.79E-04	2.57E-02	-0.473	Gm3550	similar to ribosomal protein; predicted gene 6344; predicted gene 11449; predicted gene 13841; predicted gene 8210; hypothetical protein LOC675793; ribosomal protein L29; predicted gene 12704; predicted gene 7252; predicted gene 8965; predicted gene 13213; predicted gene 8580; predicted gene 15526; predicted gene 7934; predicted gene 5218; predicted gene 5561; predicted gene 8548; predicted gene 12447; predicted gene 8852; predicted gene 12508; predicted gene 6010; predicted gene 13921; predicted gene 8860; predicted gene 13545; predicted gene 9405; predicted gene 6862; predicted gene 13141; predicted gene 10709
10485745	1.25	4.355	4.67E-04	1.77E-02	0.176	Ano3	anoctamin 3
10502469	1.25	11.791	1.15E-03	2.98E-02	-0.752	Pdlim5	PDZ and LIM domain 5
10514158	1.25	6.892	1.14E-03	2.97E-02	-0.745	Psip1	PC4 and SFRS1 interacting protein 1
10427744	1.25	7.094	1.58E-03	3.59E-02	-1.075	Rai14	retinoic acid induced 14
10382136	0.769	6.553	9.51E-04	2.67E-02	-0.555	1810010H24Rik	RIKEN cDNA 1810010H24 gene
10582390	0.769	7.784	3.43E-04	1.49E-02	0.492	Aprt	adenine phosphoribosyl transferase
10479938	0.769	7.845	7.26E-04	2.31E-02	-0.278	Echdc3	enoyl Coenzyme A hydratase domain containing 3
10365408	0.769	9.051	2.19E-03	4.30E-02	-1.413	Ric8b	resistance to inhibitors of cholinesterase 8 homolog B (C. elegans)
10457475	0.768	6.796	1.10E-03	2.92E-02	-0.7	Abhd3	abhydrolase domain containing 3
10422822	0.768	8.737	5.99E-04	2.05E-02	-0.08	Lifr	leukemia inhibitory factor receptor
10572130	0.768	12.687	3.71E-04	1.56E-02	0.411	Lpl	lipoprotein lipase; similar to Lipoprotein lipase precursor (LPL)
10387222	0.768	6.611	5.62E-04	1.97E-02	-0.014	Pfas	phosphoribosylformylglycinamidine synthase (FGAR amidotransferase)
10343572	0.768	12.172	6.06E-04	2.06E-02	-0.091	Canx	calnexin
10600341	0.767	10.076	2.73E-04	1.28E-02	0.727	Emd	emerin
10503856	0.767	6.121	1.10E-03	2.92E-02	-0.7	Gabrr2	gamma-aminobutyric acid (GABA) C receptor, subunit rho 2
10476740	0.767	6.24	1.27E-03	3.16E-02	-0.854	Slc24a3	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3
10545697	0.766	9.516	3.18E-04	1.41E-02	0.569	Dguok	deoxyguanosine kinase
10571321	0.766	6.535	9.33E-04	2.65E-02	-0.535	Ppp1r3b	protein phosphatase 1, regulatory (inhibitor) subunit 3B
10423030	0.766	5.285	2.15E-04	1.11E-02	0.971	Prlr	prolactin receptor
10468533	0.766	9.972	2.80E-03	5.00E-02	-1.663	Gpam	glycerol-3-phosphate acyltransferase, mitochondrial
10533360	0.765	7.734	9.39E-04	2.66E-02	-0.542	9330129D05Rik	RIKEN cDNA 9330129D05 gene
10568735	0.765	7.631	2.27E-03	4.40E-02	-1.449	Ebf3	early B-cell factor 3
10364072	0.765	6.403	4.94E-04	1.82E-02	0.118	Ggt5	gamma-glutamyltransferase 5

10370000	0.765	7.989	2.49E-04	1.21E-02	0.823	Gstt1	glutathione S-transferase, theta 1
10562096	0.765	9.793	1.83E-03	3.90E-02	-1.228	Tmem147	transmembrane protein 147
10362490	0.765	6.581	1.09E-04	7.59E-03	1.662	Tspyl4	TSPY-like 4
10575961	0.765	8.995	1.37E-04	8.51E-03	1.433	Usp10	ubiquitin specific peptidase 10
10519988	0.764	8.034	2.11E-03	4.22E-02	-1.375	Fam185a	expressed sequence AI847670
10370999	0.764	8.425	1.20E-03	3.05E-02	-0.795	Lingo3	leucine rich repeat and Ig domain containing 3
10490794	0.764	10.045	4.27E-04	1.69E-02	0.268	Pkia	protein kinase inhibitor, alpha
10471337	0.764	7.967	3.14E-04	1.40E-02	0.584	Pomt1	protein-O-mannosyltransferase 1
10388310	0.764	9.009	6.97E-05	6.10E-03	2.116	Rap1gap2	GTPase activating RANGAP domain-like 4
10488472	0.763	7.608	1.82E-03	3.89E-02	-1.222	2310001A20Rik	RIKEN cDNA 2310001A20 gene
10364601	0.763	6.458	1.17E-03	3.00E-02	-0.766	Abca7	ATP-binding cassette, sub-family A (ABC1), member 7
10554076	0.763	6.827	1.95E-03	4.04E-02	-1.292	Lysmd4	LysM, putative peptidoglycan-binding, domain containing 4
10592330	0.763	6.165	5.85E-04	2.02E-02	-0.055	Nrgn	neurogranin
10569069	0.763	10.012	1.60E-03	3.62E-02	-1.092	Rps9	ribosomal protein S9; predicted gene 5905
10395058	0.762	8.887	2.00E-03	4.11E-02	-1.32	Adi1	acireductone dioxygenase 1
10603116	0.762	10.627	1.91E-03	4.01E-02	-1.269	Asb11	ankyrin repeat and SOCS box-containing 11
10361754	0.762	7.837	1.90E-04	1.03E-02	1.098	Epm2a	epilepsy, progressive myoclonic epilepsy, type 2 gene alpha
10506301	0.762	5.369	9.23E-05	6.98E-03	1.831	Lepr	leptin receptor
10419532	0.762	9.152	9.30E-05	7.02E-03	1.823	Osgep	O-sialoglycoprotein endopeptidase
10566529	0.762	9.911	4.14E-04	1.66E-02	0.3	Tpp1	tripeptidyl peptidase I
10427997	0.761	7.73	1.31E-03	3.21E-02	-0.881	Ankrd33b	ankyrin repeat domain 33B
10538658	0.761	8.681	2.32E-03	4.45E-02	-1.471	Herc3	hect domain and RLD 3
10602592	0.761	11.676	7.26E-05	6.26E-03	2.075	Hsd17b10	hydroxysteroid (17-beta) dehydrogenase 10
10451953	0.761	8.597	2.97E-04	1.35E-02	0.64	Lrg1	leucine-rich alpha-2-glycoprotein 1
10348277	0.76	8.372	9.97E-05	7.21E-03	1.754	Atg16l1	autophagy-related 16-like 1 (yeast)
10495625	0.76	5.955	1.99E-03	4.11E-02	-1.316	Dpyd	dihydropyrimidine dehydrogenase
10574944	0.76	6.946	1.37E-04	8.51E-03	1.433	Dus2l	dihydrouridine synthase 2-like (SMM1, S. cerevisiae)
10579925	0.76	9.856	1.13E-03	2.95E-02	-0.734	Gab1	growth factor receptor bound protein 2-associated protein 1
10564857	0.76	12.555	1.39E-04	8.59E-03	1.416	Idh2	isocitrate dehydrogenase 2 (NADP+), mitochondrial
10362876	0.76	7.699	1.94E-03	4.04E-02	-1.286	Pdss2	prenyl (solanesyl) diphosphate synthase, subunit 2
10422028	0.76	8.863	8.29E-05	6.58E-03	1.94	Tbc1d4	TBC1 domain family, member 4
10539907	0.76	9.167	1.11E-03	2.94E-02	-0.713	Tpra1	G protein-coupled receptor 175
10491613	0.759	8.897	2.33E-03	4.46E-02	-1.477	4932438A13Rik	RIKEN cDNA 4932438A13 gene
10585834	0.759	6.888	1.15E-03	2.98E-02	-0.751	6030419C18Rik	RIKEN cDNA 6030419C18 gene; hypothetical protein LOC100048292
10524460	0.759	9.746	1.44E-04	8.82E-03	1.382	Acacb	acetyl-Coenzyme A carboxylase beta
10592816	0.759	9.059	2.77E-03	4.96E-02	-1.652	Hmbs	hydroxymethylbilane synthase
10542824	0.759	8.206	2.22E-03	4.33E-02	-1.427	Mrps35	mitochondrial ribosomal protein S35
10404763	0.759	8.527	8.53E-04	2.53E-02	-0.443	Tmem170b	transmembrane protein 170B
10339754	0.759	8.841	9.65E-04	2.69E-02	-0.57	Anapc1	anaphase promoting complex subunit 1
10484203	0.758	11.13	2.25E-03	4.36E-02	-1.438	Ccdc141	RIKEN cDNA 2610301F02 gene
10460312	0.758	8.525	1.34E-04	8.45E-03	1.453	Cdk2ap2	CDK2-associated protein 2
10420935	0.757	10.319	5.12E-04	1.86E-02	0.081	Ephx2	epoxide hydrolase 2, cytoplasmic

10382435	0.757	7.001	3.98E-04	1.62E-02	0.34	Gprc5c	G protein-coupled receptor, family C, group 5, member C; similar to G protein-coupled receptor, family C, group 5, member C
10587315	0.757	9.657	2.05E-04	1.08E-02	1.021	Gsta4	glutathione S-transferase, alpha 4
10502780	0.757	10.776	2.14E-03	4.25E-02	-1.387	Lphn2	latrophilin 2
10347564	0.756	8.614	1.16E-04	7.83E-03	1.599	Dnajb2	DnaJ (Hsp40) homolog, subfamily B, member 2
10550400	0.756	5.606	1.81E-04	1.00E-02	1.147	Pnmal2	PNMA-like 2
10342369	0.756	9.89	3.55E-04	1.52E-02	0.458	Copa	coatomer protein complex subunit alpha
10528622	0.755	8.287	2.19E-03	4.30E-02	-1.411	Asb10	ankyrin repeat and SOCS box-containing 10
10550915	0.755	6.078	1.02E-03	2.80E-02	-0.629	Cadm4	cell adhesion molecule 4
10548815	0.755	8.51	8.40E-04	2.51E-02	-0.427	Coq2	coenzyme Q2 homolog, prenyltransferase (yeast); predicted gene 6728
10483150	0.755	6.972	8.43E-04	2.52E-02	-0.43	Fign	fidgetin
10406865	0.755	8.188	9.82E-04	2.73E-02	-0.588	Mrps27	mitochondrial ribosomal protein S27
10360349	0.754	5.623	2.09E-05	3.15E-03	3.319	Cadm3	cell adhesion molecule 3
10370413	0.754	10.534	1.01E-04	7.25E-03	1.745	D10Jhu81e	similar to es1 protein; DNA segment, Chr 10, Johns Hopkins University 81 expressed
10475144	0.754	6.606	3.71E-05	4.10E-03	2.749	Ganc	calpain 3
10393628	0.754	8.349	1.23E-03	3.09E-02	-0.822	Tbc1d16	TBC1 domain family, member 16
10392098	0.753	7.421	7.83E-04	2.41E-02	-0.356	Ftsj3	FtsJ homolog 3 (E. coli)
10520506	0.753	9.522	8.06E-04	2.46E-02	-0.384	Kcnk3	potassium channel, subfamily K, member 3
10373157	0.753	8.532	1.49E-04	8.94E-03	1.342	Mars	methionine-tRNA synthetase
10364542	0.752	5.63	9.36E-04	2.65E-02	-0.539	Cfd	complement factor D (adipsin)
10539894	0.752	9.719	2.11E-03	4.22E-02	-1.374	Mgll	monoglyceride lipase
10477673	0.752	7.397	1.07E-03	2.88E-02	-0.679	Myh7b	myosin, heavy chain 7B, cardiac muscle, beta
10574404	0.752	7.444	1.90E-03	4.00E-02	-1.264	Setd6	SET domain containing 6
10510509	0.752	8.362	2.39E-03	4.53E-02	-1.5	Gpr157	similar to G protein-coupled receptor 157; G protein-coupled receptor 157
10577030	0.751	8.668	2.07E-04	1.09E-02	1.008	Cars2	cysteinyl-tRNA synthetase 2 (mitochondrial)(putative)
10394735	0.751	8.611	5.23E-04	1.88E-02	0.059	Pdia6	similar to Protein disulfide isomerase associated 6; protein disulfide isomerase associated 6
10448459	0.751	6.958	6.12E-04	2.06E-02	-0.101	Tbc1d24	TBC1 domain family, member 24
10470427	0.751	7.881	1.60E-03	3.62E-02	-1.088	Wdr5	WD repeat domain 5
10443482	0.75	9.586	6.64E-04	2.17E-02	-0.185	BC004004	cDNA sequence BC004004
10547789	0.75	10.064	4.85E-05	4.81E-03	2.482	Grcc10	gene rich cluster, C10 gene
10358726	0.75	7.757	1.27E-03	3.15E-02	-0.848	Tsen15	tRNA splicing endonuclease 15 homolog (S. cerevisiae)
10415132	0.749	5.629	3.77E-04	1.57E-02	0.396	Cmtm5	CKLF-like MARVEL transmembrane domain containing 5
10597470	0.749	7.363	1.61E-03	3.63E-02	-1.097	Cmtm8	CKLF-like MARVEL transmembrane domain containing 8
10530819	0.749	10.266	1.18E-03	3.01E-02	-0.773	Hopx	HOP homeobox
10383389	0.749	9.919	2.86E-04	1.32E-02	0.679	Mrpl12	mitochondrial ribosomal protein L12
10509002	0.749	6.724	2.41E-04	1.18E-02	0.855	Rhd	Rh blood group, D antigen
10445338	0.748	8.092	1.94E-03	4.04E-02	-1.29	Enpp5	ectonucleotide pyrophosphatase/phosphodiesterase 5
10431030	0.748	7.855	2.59E-04	1.24E-02	0.78	Mcat	similar to mitochondrial malonyltransferase isoform b precursor; malonyl CoA:ACP acyltransferase (mitochondrial)
10467162	0.748	9.983	2.77E-03	4.96E-02	-1.652	Pank1	pantothenate kinase 1
10606102	0.748	8.727	3.51E-05	4.00E-03	2.804	Phka1	phosphorylase kinase alpha 1

10502982	0.748	10.687	6.32E-04	2.12E-02	-0.135	Tnni3k	TNNI3 interacting kinase
10542592	0.747	6.073	1.54E-04	9.14E-03	1.312	Gm10400	predicted gene 10400
10559478	0.747	4.764	2.11E-03	4.21E-02	-1.372	Gm14548	hypothetical protein LOC100038909; similar to PIRA2; hypothetical protein LOC100038908; predicted gene 15448; paired-Ig-like receptor A11; paired-Ig-like receptor A5; paired-Ig-like receptor A6; paired-Ig-like receptor A4; paired-Ig-like receptor A7; predicted gene 15930; paired-Ig-like receptor A1; paired-Ig-like receptor A2; predicted gene 10693
10522749	0.747	5.714	4.09E-04	1.65E-02	0.312	Lphn3	latrophilin 3
10518679	0.747	9.546	2.07E-03	4.17E-02	-1.352	Nmnat1	nicotinamide nucleotide adenylyltransferase 1
10534152	0.747	6.447	2.02E-04	1.08E-02	1.034	Wbscr17	Williams-Beuren syndrome chromosome region 17 homolog (human); similar to UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase-like 3
10442625	0.746	5.915	4.62E-04	1.76E-02	0.188	Igfals	insulin-like growth factor binding protein, acid labile subunit
10567657	0.746	8.894	3.59E-04	1.53E-02	0.445	Ndufab1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1; predicted gene 4459
10450226	0.746	8.427	1.55E-04	9.18E-03	1.303	Ppt2	palmitoyl-protein thioesterase 2
10465844	0.745	8.23	6.73E-04	2.19E-02	-0.2	Asrgl1	asparaginase like 1
10423505	0.745	8.702	8.55E-04	2.54E-02	-0.446	Cmbl	carboxymethylenebutenolidase-like (Pseudomonas)
10573082	0.745	8.056	1.87E-03	3.95E-02	-1.25	Inpp4b	inositol polyphosphate-4-phosphatase, type II
10515536	0.745	9.067	3.54E-05	4.00E-03	2.797	Ipo13	importin 13
10445430	0.745	8.718	1.61E-03	3.63E-02	-1.099	Mrpl14	mitochondrial ribosomal protein L14
10349834	0.745	8.718	1.83E-03	3.90E-02	-1.229	Pik3c2b	phosphoinositide-3-kinase, class 2, beta polypeptide
10412882	0.745	7.194	6.68E-04	2.18E-02	-0.192	Thrb	thyroid hormone receptor beta
10472794	0.745	7.858	5.86E-04	2.02E-02	-0.058	Metap1	methionine aminopeptidase-like 1
10382573	0.744	10.099	4.60E-04	1.76E-02	0.191	2310067B10Rik	RIKEN cDNA 2310067B10 gene
10580771	0.744	9.796	5.21E-04	1.88E-02	0.064	Ciapin1	cytokine induced apoptosis inhibitor 1
10431226	0.744	5.189	5.85E-04	2.02E-02	-0.055	Pkdrej	polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homolog)-like
10375608	0.744	6.81	2.17E-03	4.28E-02	-1.403	Scgb3a1	secretoglobin, family 3A, member 1
10339814	0.744	9.851	2.57E-03	4.74E-02	-1.575	Dhrs1	dehydrogenase/reductase (SDR family) member 1
10362513	0.743	5.6	4.39E-04	1.72E-02	0.241	Hs3st5	heparan sulfate (glucosamine) 3-O-sulfotransferase 5
10567171	0.743	5.44	2.08E-03	4.19E-02	-1.361	Rps13	ENSMUSG00000064741; ENSMUSG00000075876; ENSMUSG00000075924; ENSMUSG00000064791
10600357	0.743	9.433	4.53E-04	1.75E-02	0.206	Taz	tafazzin
10385542	0.742	8.553	1.12E-03	2.95E-02	-0.724	Btnl9	butyrophilin-like 9
10346783	0.742	6.134	6.50E-04	2.16E-02	-0.164	Cd28	CD28 antigen; similar to CD28 antigen
10544913	0.742	8.208	6.28E-05	5.71E-03	2.221	Crhr2	corticotropin releasing hormone receptor 2
10381708	0.742	7.54	1.35E-04	8.48E-03	1.444	Fmnl1	formin-like 1
10500329	0.742	10.611	1.57E-03	3.59E-02	-1.073	Hist2h3c1	histone cluster 2, H3b; histone cluster 1, H3f; histone cluster 1, H3e; histone cluster 2, H3c1; histone cluster 1, H3d; histone cluster 1, H3c; histone cluster 1, H3b; histone cluster 2, H3c2; histone cluster 2, H2aa1; histone cluster 2, H2aa2
10477637	0.742	10.068	1.66E-03	3.69E-02	-1.128	Map1lc3a	microtubule-associated protein 1 light chain 3 alpha
10515242	0.742	8.325	1.44E-04	8.82E-03	1.381	Nsun4	NOL1/NOP2/Sun domain family, member 4

10510162	0.742	10.433	1.30E-04	8.31E-03	1.486	Ppp2r5a	predicted gene 3353; predicted gene 13142; predicted gene 13169; similar to protein phosphatase 2, regulatory subunit B (B56), alpha isoform; predicted gene 13244; predicted gene 13233; protein phosphatase 2, regulatory subunit B (B56), alpha isoform
10364571	0.742	8.693	3.25E-04	1.43E-02	0.548	Wdr18	WD repeat domain 18
10554819	0.741	8.869	2.04E-04	1.08E-02	1.023	Me3	malic enzyme 3, NADP(+)-dependent, mitochondrial
10368935	0.741	8.54	2.20E-03	4.31E-02	-1.417	Qrsl1	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1
10410995	0.741	6.296	2.51E-03	4.68E-02	-1.551	Rasgrf2	RAS protein-specific guanine nucleotide-releasing factor 2
10446553	0.741	6.009	1.08E-03	2.89E-02	-0.683	Epb41l1	erythrocyte protein band 4.1-like 3
10537157	0.74	10.106	1.51E-03	3.52E-02	-1.033	Akr1b10	RIKEN cDNA 2310005E10 gene
10473754	0.74	7.708	8.20E-04	2.49E-02	-0.402	Kbtbd4	kelch repeat and BTB (POZ) domain containing 4
10587748	0.739	7.556	1.00E-03	2.77E-02	-0.611	Adamts7	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 7
10434224	0.739	5.542	1.40E-03	3.35E-02	-0.953	Gnb1l	guanine nucleotide binding protein (G protein), beta polypeptide 1-like; similar to mKIAA1645 protein
10435752	0.739	5.958	1.93E-03	4.03E-02	-1.283	Lsamp	limbic system-associated membrane protein
10381462	0.739	7.886	2.30E-03	4.44E-02	-1.462	Rdm1	RAD52 motif 1
10408616	0.739	7.406	1.69E-04	9.60E-03	1.215	Slc22a23	solute carrier family 22, member 23
10474241	0.738	5.728	3.62E-04	1.53E-02	0.437	---	ENSMUSG00000082379
10502951	0.738	12.789	1.24E-04	8.18E-03	1.53	Acadm	acyl-Coenzyme A dehydrogenase, medium chain
10424979	0.738	6.381	1.37E-03	3.31E-02	-0.929	Gpt	glutamic pyruvic transaminase, soluble
10434664	0.738	11.693	2.32E-03	4.45E-02	-1.473	Ndufa11	predicted gene 4943
10588028	0.737	6.737	6.16E-04	2.08E-02	-0.109	Nmnat3	nicotinamide nucleotide adenylyltransferase 3
10565819	0.737	6.892	3.71E-04	1.56E-02	0.413	Slco2b1	solute carrier organic anion transporter family, member 2b1
10593842	0.737	10.384	4.77E-04	1.79E-02	0.154	Tspan3	tetraspanin 3
10573566	0.736	7.274	1.80E-04	1.00E-02	1.152	Dhps	deoxyhypusine synthase
10475643	0.736	5.033	2.01E-03	4.12E-02	-1.326	Fgf7	fibroblast growth factor 7
10480921	0.736	7.522	6.83E-04	2.21E-02	-0.214	Qsox2	quiescin Q6 sulfhydryl oxidase 2
10569456	0.735	8.101	9.45E-04	2.66E-02	-0.548	---	ENSMUSG00000065118
10400030	0.735	10.493	1.61E-05	2.71E-03	3.577	Bzw2	basic leucine zipper and W2 domains 2
10458731	0.735	8.418	5.67E-04	1.98E-02	-0.024	Mcc	mutated in colorectal cancers
10445607	0.735	7.576	1.84E-04	1.01E-02	1.129	Pex6	peroxisomal biogenesis factor 6
10426180	0.735	9.032	5.88E-04	2.02E-02	-0.061	Ppp6r2	SAPS domain family, member 2
10572730	0.735	6.691	2.55E-03	4.73E-02	-1.568	Zfp617	zinc finger protein 617
10497481	0.734	9.37	2.68E-03	4.87E-02	-1.618	2810416G20Rik	hypothetical protein LOC100046169; RIKEN cDNA 2810416G20 gene
10538459	0.734	10.782	3.45E-04	1.50E-02	0.487	Aqp1	aquaporin 1
10502335	0.734	5.62	1.05E-03	2.85E-02	-0.66	Bank1	B-cell scaffold protein with ankyrin repeats 1
10404132	0.734	6.785	5.87E-04	2.02E-02	-0.059	Cmah	cytidine monophospho-N-acetylneuraminic acid hydroxylase
10566026	0.734	7.991	8.53E-05	6.68E-03	1.912	Folr2	folate receptor 2 (fetal)
10466771	0.734	7.212	3.15E-04	1.40E-02	0.581	Fxn	frataxin
10462281	0.734	11.25	6.14E-05	5.65E-03	2.244	Vldlr	very low density lipoprotein receptor
10390780	0.733	8.832	1.46E-04	8.83E-03	1.366	Krt222	keratin 222

10529895	0.733	9.137	1.17E-03	3.01E-02	-0.771	Qdpr	quinoid dihydropteridine reductase; similar to Quinoid dihydropteridine reductase
10410695	0.733	8.481	7.05E-04	2.26E-02	-0.247	Rhobtb3	Rho-related BTB domain containing 3
10442435	0.733	9.158	1.65E-03	3.67E-02	-1.12	Rnps1	hypothetical protein LOC100044797; ribonucleic acid binding protein S1; predicted gene 9825
10511416	0.733	5.579	1.30E-04	8.31E-03	1.484	Tox	thymocyte selection-associated high mobility group box; similar to thymus high mobility group box protein TOX
10387201	0.732	7.865	2.34E-04	1.16E-02	0.884	Arhgef15	Rho guanine nucleotide exchange factor (GEF) 15
10361152	0.732	7.217	3.59E-04	1.53E-02	0.447	Gstp2	glutathione S-transferase, pi 2; glutathione S-transferase, pi 1; similar to glutathione S-transferase pi class A; predicted gene 3934
10577882	0.732	8.627	3.47E-05	3.99E-03	2.818	Hgsnat	heparan-alpha-glucosaminide N-acetyltransferase
10488322	0.732	9.384	4.57E-05	4.69E-03	2.54	Ralgapa2	RIKEN cDNA A230067G21 gene
10546538	0.732	8.87	7.68E-04	2.39E-02	-0.335	Suclg2	succinate-Coenzyme A ligase, GDP-forming, beta subunit
10342892	0.732	9.387	1.62E-04	9.37E-03	1.258	C19orf42	RIKEN cDNA 9130011J15 gene
10586110	0.731	8.94	4.52E-05	4.67E-03	2.552	Cln6	ceroid-lipofuscinosis, neuronal 6
10427496	0.731	6.682	1.49E-04	8.90E-03	1.348	Egflam	EGF-like, fibronectin type III and laminin G domains
10373367	0.731	11.147	3.19E-04	1.41E-02	0.568	Coq10A	coenzyme Q10 homolog A (yeast)
10519527	0.73	7.781	1.37E-03	3.31E-02	-0.932	Abcb1a	ATP-binding cassette, sub-family B (MDR/TAP), member 1A
10564698	0.73	7.428	1.21E-03	3.06E-02	-0.802	Det1	de-etiolated homolog 1 (Arabidopsis)
10566564	0.73	8.266	5.46E-04	1.94E-02	0.015	Mrpl17	mitochondrial ribosomal protein L17
10412385	0.73	6.958	9.96E-04	2.76E-02	-0.603	Mrps30	mitochondrial ribosomal protein S30
10395807	0.729	8.661	4.76E-05	4.79E-03	2.501	1110008L16Rik	RIKEN cDNA 1110008L16 gene
10571657	0.729	12.053	1.69E-04	9.58E-03	1.218	Acsl1	acyl-CoA synthetase long-chain family member 1
10597627	0.729	9.504	1.31E-04	8.35E-03	1.473	Oxsr1	oxidative-stress responsive 1
10587871	0.729	8.937	7.35E-04	2.33E-02	-0.29	Paqr9	progestin and adipoQ receptor family member IX
10575102	0.728	8.82	8.44E-05	6.67E-03	1.922	Cirh1a	cirrhosis, autosomal recessive 1A (human)
10481574	0.728	8.029	2.10E-03	4.21E-02	-1.37	Fam78a	family with sequence similarity 78, member A; hypothetical protein LOC100047386
10402808	0.728	8.059	6.87E-04	2.22E-02	-0.22	Jag2	jagged 2
10410393	0.728	7.595	1.82E-04	1.00E-02	1.144	Mtrr	5-methyltetrahydrofolate-homocysteine methyltransferase reductase
10361023	0.728	9.094	1.94E-03	4.04E-02	-1.29	Prox1	prospero-related homeobox 1
10357220	0.728	7.87	5.32E-05	5.13E-03	2.388	Tmem177	transmembrane protein 177
10484207	0.727	9.914	7.11E-05	6.14E-03	2.096	Ccdc141	RIKEN cDNA 2610301F02 gene
10347351	0.727	9.828	3.33E-04	1.46E-02	0.524	Ctdsp1	similar to golli-interacting protein; CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1
10348889	0.727	7.669	1.23E-03	3.09E-02	-0.816	D2hgdh	similar to D-2-hydroxyglutarate dehydrogenase; D-2-hydroxyglutarate dehydrogenase
10440926	0.727	8.044	1.95E-03	4.05E-02	-1.294	Dnajc28	DnaJ (Hsp40) homolog, subfamily C, member 28
10583634	0.727	7.793	4.72E-04	1.78E-02	0.165	Qtrt1	queuine tRNA-ribosyltransferase 1
10446235	0.727	9.289	1.63E-04	9.38E-03	1.253	Trip10	thyroid hormone receptor interactor 10
10375240	0.726	11.39	2.36E-04	1.17E-02	0.875	Hspd1	predicted gene 12141; heat shock protein 1 (chaperonin)
10491621	0.725	8.787	5.63E-04	1.97E-02	-0.016	4932438A13Rik	RIKEN cDNA 4932438A13 gene
10376596	0.725	10.315	1.13E-03	2.95E-02	-0.728	4933439F18Rik	RIKEN cDNA 4933439F18 gene

10483679	0.725	8.484	8.51E-05	6.68E-03	1.913	Gpr155	G protein-coupled receptor 155
10548047	0.725	5.635	1.19E-03	3.03E-02	-0.786	Kcna1	potassium voltage-gated channel, shaker-related subfamily, member 1
10344011	0.725	10.871	7.81E-04	2.41E-02	-0.353	Psapl1	prosaposin
10565935	0.724	8.409	4.90E-04	1.82E-02	0.126	Arhgef17	Rho guanine nucleotide exchange factor (GEF) 17
10467842	0.724	12.838	1.47E-04	8.83E-03	1.359	Got1	similar to Aspartate aminotransferase, cytoplasmic (Transaminase A) (Glutamate oxaloacetate transaminase 1); glutamate oxaloacetate transaminase 1, soluble
10420385	0.724	8.197	7.45E-05	6.34E-03	2.049	N6amt2	N-6 adenine-specific DNA methyltransferase 2 (putative)
10571302	0.724	9.535	8.29E-06	1.96E-03	4.229	Tmem66	transmembrane protein 66
10341992	0.724	8.773	1.55E-03	3.58E-02	-1.06	Hdac5	histone deacetylase 5
10590972	0.724	10.965	9.61E-05	7.10E-03	1.791	Mst1	predicted gene 6097; macrophage migration inhibitory factor; similar to macrophage migration inhibitory factor; predicted gene 8762; predicted gene 10169; macrophage migration inhibitory factor-like
10503584	0.723	10.621	2.12E-03	4.23E-02	-1.38	Coq3	coenzyme Q3 homolog, methyltransferase (yeast)
10481474	0.723	11.97	2.29E-05	3.29E-03	3.23	Crat	carnitine acetyltransferase
10367440	0.723	9.639	5.94E-04	2.04E-02	-0.072	Itga7	integrin alpha 7
10437364	0.722	8.076	2.27E-05	3.27E-03	3.242	Adcy9	adenylate cyclase 9
10412773	0.722	7.623	2.94E-05	3.77E-03	2.982	Slc4a7	solute carrier family 4, sodium bicarbonate cotransporter, member 7
10430319	0.722	7.565	1.15E-03	2.97E-02	-0.747	Tst	thiosulfate sulfurtransferase, mitochondrial
10559568	0.721	6.282	2.53E-05	3.49E-03	3.133	6030429G01Rik	RIKEN cDNA 6030429G01 gene
10358389	0.721	9.07	1.60E-04	9.29E-03	1.275	Rgs2	regulator of G-protein signaling 2
10341699	0.721	11.702	1.24E-04	8.18E-03	1.531	Canx	calnexin
10604637	0.72	9.681	2.66E-04	1.26E-02	0.753	Cxx1c	CAAX box 1 homolog A (human); CAAX box 1 homolog B (human); similar to mammalian retrotransposon derived 8b
10456727	0.72	10.215	3.34E-05	3.93E-03	2.854	Dym	dymeclin
10565152	0.72	7.702	4.28E-04	1.69E-02	0.265	Homer2	RIKEN cDNA 9330120H11 gene
10582330	0.72	8.684	4.85E-04	1.81E-02	0.137	Rnf166	ring finger protein 166
10569870	0.719	5.301	2.87E-05	3.70E-03	3.008	Retn	resistin
10387791	0.719	7.144	4.58E-04	1.76E-02	0.197	Slc16a13	solute carrier family 16 (monocarboxylic acid transporters), member 13
10488482	0.718	11.833	3.17E-04	1.40E-02	0.574	Acss1	acyl-CoA synthetase short-chain family member 1
10553015	0.718	9.585	1.23E-05	2.45E-03	3.846	Bcat2	branched chain aminotransferase 2, mitochondrial
10581865	0.718	7.855	4.23E-04	1.68E-02	0.278	Ldhd	lactate dehydrogenase D
10541695	0.718	9.874	4.29E-05	4.56E-03	2.604	Lpcat3	lysophosphatidylcholine acyltransferase 3
10443391	0.717	9.442	1.47E-04	8.83E-03	1.361	Mapk14	mitogen-activated protein kinase 14
10420216	0.717	9.711	9.54E-05	7.10E-03	1.798	Sdr39u1	short chain dehydrogenase/reductase family 39U, member 1
10530319	0.716	9.092	1.29E-04	8.31E-03	1.49	Atp8a1	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1
10517600	0.715	11.183	2.04E-04	1.08E-02	1.025	Pink1	PTEN induced putative kinase 1
10535369	0.715	9.767	1.83E-04	1.01E-02	1.134	Gm15770	predicted gene 15770
10469581	0.714	8.079	2.71E-03	4.89E-02	-1.63	Etl4	enhancer trap locus 4

10558910	0.714	9.29	1.62E-03	3.63E-02	-1.1	Rangrf	predicted gene 7791; similar to Ran-interacting protein MOG1; predicted gene 15711; RAN guanine nucleotide release factor; predicted gene 4535; predicted gene 8572
10589166	0.714	6.973	2.47E-04	1.20E-02	0.827	Slc26a6	solute carrier family 26, member 6
10431282	0.713	8.554	3.14E-04	1.40E-02	0.583	2810001A02Rik	RIKEN cDNA 2810001A02 gene
10354732	0.713	10.737	2.32E-04	1.16E-02	0.894	Hspd1	predicted gene 12141; heat shock protein 1 (chaperonin)
10544660	0.713	8.467	8.84E-04	2.58E-02	-0.48	Osbpl3	oxysterol binding protein-like 3
10506188	0.713	10.19	9.66E-06	2.16E-03	4.08	Pgm2	phosphoglucomutase 2
10524659	0.713	6.061	9.98E-05	7.21E-03	1.753	Pop5	processing of precursor 5, ribonuclease P/MRP family (S. cerevisiae)
10571128	0.713	8.987	3.49E-04	1.50E-02	0.476	Prosc	proline synthetase co-transcribed
10342913	0.713	7.602	1.11E-04	7.65E-03	1.645	Gbf1	golgi-specific brefeldin A-resistance factor 1
10438517	0.712	9.333	2.67E-03	4.86E-02	-1.615	Alg3	asparagine-linked glycosylation 3 homolog (yeast, alpha-1,3-mannosyltransferase)
10484197	0.712	10.558	4.83E-05	4.81E-03	2.486	Ccdc141	RIKEN cDNA 2610301F02 gene
10351347	0.712	10.939	3.70E-04	1.56E-02	0.414	Creg1	cellular repressor of E1A-stimulated genes 1
10600936	0.712	8.015	3.90E-04	1.60E-02	0.362	Efnb1	ephrin B1
10502205	0.712	12.699	1.74E-05	2.79E-03	3.501	Hadh	hydroxyacyl-Coenzyme A dehydrogenase
10575685	0.712	9.376	6.88E-04	2.22E-02	-0.221	Nudt7	nudix (nucleoside diphosphate linked moiety X)-type motif 7
10608676	0.712	7.782	1.56E-04	9.19E-03	1.297	L2hgdh	L-2-hydroxyglutarate dehydrogenase; predicted gene 7842
10574232	0.711	11.678	5.67E-05	5.30E-03	2.325	Coq9	coenzyme Q9 homolog (yeast)
10474836	0.71	10.794	4.89E-05	4.83E-03	2.472	Ivd	isovaleryl coenzyme A dehydrogenase
10531191	0.709	6.795	1.63E-03	3.64E-02	-1.108	Adamts3	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 3
10446207	0.709	9.856	2.40E-05	3.38E-03	3.186	Clpp	caseinolytic peptidase, ATP-dependent, proteolytic subunit homolog (E. coli)
10411107	0.709	10.355	6.77E-05	5.98E-03	2.145	Cmya5	cardiomyopathy associated 5
10494423	0.709	11.466	1.73E-05	2.79E-03	3.507	Hfe2	hemochromatosis type 2 (juvenile) (human homolog)
10507833	0.709	7.904	8.77E-04	2.57E-02	-0.472	Nt5c1a	5'-nucleotidase, cytosolic IA
10491603	0.708	8.225	2.82E-04	1.30E-02	0.693	4932438A13Rik	RIKEN cDNA 4932438A13 gene
10498837	0.708	11.51	7.70E-05	6.34E-03	2.015	Etfdh	electron transferring flavoprotein, dehydrogenase
10359908	0.708	7.35	2.32E-03	4.45E-02	-1.473	Rgs4	regulator of G-protein signaling 4
10491623	0.707	9.418	1.58E-03	3.59E-02	-1.074	4932438A13Rik	RIKEN cDNA 4932438A13 gene
10537742	0.707	5.145	3.91E-04	1.61E-02	0.359	Clcn1	chloride channel 1
10513162	0.707	8.774	3.73E-04	1.56E-02	0.406	Ptpn3	protein tyrosine phosphatase, non-receptor type 3
10575917	0.707	8.741	9.60E-04	2.69E-02	-0.564	Wfdc1	WAP four-disulfide core domain 1
10465388	0.706	9.831	1.52E-05	2.67E-03	3.639	Arl2	ADP-ribosylation factor-like 2
10387743	0.706	11.284	5.47E-05	5.21E-03	2.36	Slc2a4	solute carrier family 2 (facilitated glucose transporter), member 4
10561063	0.705	9.452	3.53E-05	4.00E-03	2.8	Bckdha	branched chain ketoacid dehydrogenase E1, alpha polypeptide
10370021	0.705	9.395	2.69E-05	3.59E-03	3.07	Mif	predicted gene 6097; macrophage migration inhibitory factor; similar to macrophage migration inhibitory factor; predicted gene 8762; predicted gene 10169; macrophage migration inhibitory factor-like
10497209	0.705	7.947	7.32E-05	6.30E-03	2.066	Mrps28	mitochondrial ribosomal protein S28

10453373	0.705	10.74	8.52E-05	6.68E-03	1.912	Prepl	prolyl endopeptidase-like
10599719	0.705	8.902	7.61E-05	6.34E-03	2.027	Slc9a6	solute carrier family 9 (sodium/hydrogen exchanger), member 6
10389701	0.704	8.608	9.45E-05	7.10E-03	1.808	Akap1	A kinase (PRKA) anchor protein 1
10496605	0.704	7.567	1.21E-05	2.44E-03	3.859	Ccbl2	cysteine conjugate-beta lyase 2
10436841	0.704	10.758	4.42E-04	1.73E-02	0.232	Il10rb	interleukin 10 receptor, beta
10550250	0.704	8.104	1.87E-05	2.94E-03	3.429	Kptn	kaptin
10413047	0.704	5.755	3.78E-04	1.57E-02	0.393	Plau	plasminogen activator, urokinase
10587534	0.703	10.02	3.69E-05	4.10E-03	2.755	Bckdhb	branched chain ketoacid dehydrogenase E1, beta polypeptide; similar to 3-methyl-2-oxobutanoate dehydrogenase
10456021	0.703	6.773	8.93E-06	2.07E-03	4.157	Camk2a	calcium/calmodulin-dependent protein kinase II alpha
10601350	0.703	9.343	1.47E-04	8.83E-03	1.362	Fgf16	fibroblast growth factor 16
10464583	0.703	10.592	5.40E-04	1.93E-02	0.027	Gstp1	glutathione S-transferase, pi 2; glutathione S-transferase, pi 1; similar to glutathione S-transferase pi class A; predicted gene 3934
10531869	0.703	9.352	5.50E-04	1.95E-02	0.007	Mapk10	mitogen-activated protein kinase 10
10531729	0.702	9.878	2.65E-05	3.54E-03	3.086	Coq2	coenzyme Q2 homolog, prenyltransferase (yeast); predicted gene 6728
10461782	0.702	8.361	2.32E-03	4.45E-02	-1.469	Rmnd1	required for meiotic nuclear division 1 homolog (S. cerevisiae); predicted gene 5512
10342754	0.702	7.319	1.58E-03	3.59E-02	-1.077	Cic	capicua homolog (Drosophila)
10555550	0.701	8.596	3.99E-06	1.41E-03	4.933	Clpb	ClpB caseinolytic peptidase B homolog (E. coli)
10492590	0.701	8.201	2.23E-04	1.14E-02	0.934	Ppm1l	protein phosphatase 1 (formerly 2C)-like
10423049	0.701	4.667	7.63E-04	2.38E-02	-0.328	Prlr	prolactin receptor
10359861	0.7	10.119	1.05E-04	7.45E-03	1.7	Mgst3	microsomal glutathione S-transferase 3
10553140	0.7	9.146	1.40E-05	2.61E-03	3.714	Tmem143	transmembrane protein 143
10549990	0.699	6.669	1.60E-03	3.62E-02	-1.088	Gm4741	predicted gene 9807; similar to vomeronasal receptor V1RG10; vomeronasal 1 receptor, G10; vomeronasal 1 receptor, G10-like
10545588	0.699	9.613	4.25E-05	4.54E-03	2.614	Hk2	hexokinase 2
10399121	0.699	6.271	3.11E-05	3.84E-03	2.927	Ptprn2	protein tyrosine phosphatase, receptor type, N polypeptide 2; similar to Protein tyrosine phosphatase, receptor type, N polypeptide 2
10380751	0.698	8.374	9.54E-05	7.10E-03	1.798	Mrpl45	mitochondrial ribosomal protein L45
10412394	0.698	11.755	2.30E-04	1.15E-02	0.9	Nnt	nicotinamide nucleotide transhydrogenase
10473783	0.698	7.253	2.73E-04	1.28E-02	0.728	Rapsn	receptor-associated protein of the synapse
10561031	0.697	8.711	6.46E-04	2.15E-02	-0.158	Lipe	lipase, hormone sensitive
10524955	0.697	9.301	1.06E-04	7.49E-03	1.691	Tesc	tescalcin; similar to Tescalcin

10523843	0.696	7.28	2.56E-03	4.74E-02	-1.572	---	ENSMUSG00000075949; ENSMUSG00000070225; ENSMUSG00000075942; ENSMUSG00000075804; ENSMUSG00000077556; ENSMUSG00000077350; ENSMUSG00000065107; ENSMUSG00000084595; ENSMUSG00000077743; ENSMUSG00000075814; ENSMUSG00000075811; ENSMUSG00000084599; ENSMUSG00000065102; ENSMUSG00000064631; ENSMUSG00000075817; ENSMUSG00000070219; ENSMUSG00000064635; ENSMUSG00000075955; ENSMUSG00000064467; ENSMUSG00000064521; ENSMUSG00000075820; ENSMUSG00000064770; ENSMUSG00000075822; ENSMUSG00000070201; ENSMUSG00000075921; ENSMUSG00000064906; ENSMUSG00000070209; ENSMUSG00000064903; ENSMUSG00000064455; ENSMUSG00000077437; ENSMUSG00000065719; ENSMUSG00000065311; ENSMUSG00000075836; ENSMUSG00000064515; ENSMUSG00000077620; ENSMUSG00000075838; ENSMUSG00000064519; ENSMUSG00000075931; ENSMUSG00000064409; ENSMUSG00000065823; ENSMUSG00000064798; ENSMUSG00000070192; ENSMUSG00000084612; ENSMUSG00000077309; ENSMUSG00000084613; ENSMUSG00000070199; ENSMUSG00000075846; ENSMUSG00000064588; ENSMUSG00000075788; ENSMUSG00000075792; ENSMUSG00000077705; ENSMUSG00000075794; ENSMUSG00000065005; ENSMUSG00000077706; ENSMUSG00000075790; ENSMUSG00000084498; ENSMUSG00000077313; ENSMUSG00000065149; ENSMUSG00000084624; ENSMUSG00000084623; ENSMUSG00000084492; ENSMUSG00000084491; ENSMUSG00000084494; ENSMUSG00000075999; ENSMUSG00000075859; ENSMUSG00000077316; ENSMUSG00000075858; ENSMUSG00000075856; ENSMUSG00000075799; ENSMUSG00000065691; ENSMUSG00000065806; ENSMUSG00000075965; ENSMUSG00000075962; ENSMUSG00000084480; ENSMUSG00000075863; ENSMUSG00000075765;
10593418	0.696	9.253	3.30E-06	1.33E-03	5.115	Cryab	heat shock protein 2
10501229	0.696	10.829	1.38E-03	3.33E-02	-0.94	Gstm1	similar to Glutathione S-transferase Mu 1 (GST class-mu 1) (Glutathione S-transferase GT8.7) (pmGT10) (GST 1-1); predicted gene 5562; glutathione S-transferase, mu 1
10531653	0.696	6.094	2.79E-03	5.00E-02	-1.662	Tmem150c	cDNA sequence BC062109
10556962	0.696	6.195	9.97E-05	7.21E-03	1.754	Vwa3a	von Willebrand factor A domain containing 3A
10440513	0.695	9.53	4.22E-04	1.68E-02	0.28	Cyyr1	cysteine and tyrosine-rich protein 1
10606301	0.694	9.132	2.07E-04	1.09E-02	1.011	Magt1	magnesium transporter 1
10471586	0.693	11.666	1.03E-05	2.22E-03	4.019	Hspa5	heat shock protein 5

10517173	0.691	7.058	7.74E-05	6.35E-03	2.01	Ccdc21	coiled-coil domain containing 21
10577144	0.691	9.427	1.62E-04	9.37E-03	1.259	Dcun1d2	DCN1, defective in cullin neddylation 1, domain containing 2 (S. cerevisiae)
10345855	0.691	6.348	4.16E-05	4.47E-03	2.636	Slc9a2	solute carrier family 9 (sodium/hydrogen exchanger), member 2
10502655	0.689	9.226	1.35E-03	3.27E-02	-0.913	Cyr61	cysteine rich protein 61
10450640	0.689	9.2	5.18E-04	1.88E-02	0.07	Mrps18b	mitochondrial ribosomal protein S18B
10517655	0.689	9.753	9.07E-04	2.62E-02	-0.506	Pla2g5	phospholipase A2, group V; similar to phospholipase A2, group V
10344216	0.689	9.507	1.23E-03	3.09E-02	-0.816	Rfk	riboflavin kinase
10561008	0.688	8.421	1.68E-03	3.70E-02	-1.14	Ceacam1	carcinoembryonic antigen-related cell adhesion molecule 1; carcinoembryonic antigen-related cell adhesion molecule 2
10374020	0.688	8.341	1.39E-04	8.60E-03	1.414	Rhbdd3	rhomboid domain containing 3
10521415	0.687	7.622	4.95E-04	1.82E-02	0.117	Ablim2	actin-binding LIM protein 2
10540269	0.687	7.327	1.55E-03	3.57E-02	-1.056	Gpr27	G protein-coupled receptor 27
10401564	0.686	9.856	6.80E-04	2.20E-02	-0.209	1110018G07Rik	RIKEN cDNA 1110018G07 gene
10361104	0.686	10.236	3.31E-05	3.93E-03	2.864	Ppp2r5a	predicted gene 3353; predicted gene 13142; predicted gene 13169; similar to protein phosphatase 2, regulatory subunit B (B56), alpha isoform; predicted gene 13244; predicted gene 13233; protein phosphatase 2, regulatory subunit B (B56), alpha isoform
10537394	0.685	9.381	5.41E-05	5.18E-03	2.371	1110001J03Rik	formation of mitochondrial complexes 1 homolog (S. cerevisiae)
10574480	0.685	7.759	1.46E-03	3.45E-02	-0.996	Car7	carbonic anhydrase 7
10584712	0.685	8.108	3.31E-05	3.93E-03	2.865	Hyou1	hypoxia up-regulated 1
10505200	0.684	10.716	2.49E-04	1.21E-02	0.82	Hsdl2	hydroxysteroid dehydrogenase like 2
10376074	0.684	7.397	2.38E-04	1.17E-02	0.866	P4ha2	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha II polypeptide
10408656	0.684	9.785	9.11E-05	6.93E-03	1.845	Peci	peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase
10355343	0.683	5.442	1.92E-05	2.96E-03	3.407	Abca12	ATP-binding cassette, sub-family A (ABC1), member 12
10541075	0.683	9.082	4.68E-05	4.76E-03	2.517	Cxcl12	chemokine (C-X-C motif) ligand 12
10491609	0.682	9.438	3.56E-04	1.52E-02	0.456	4932438A13Rik	RIKEN cDNA 4932438A13 gene
10396079	0.682	8.628	5.88E-04	2.02E-02	-0.061	Klhdc1	kelch domain containing 1
10601888	0.682	6.974	2.83E-05	3.70E-03	3.019	Plp1	proteolipid protein (myelin) 1
10490221	0.681	9.61	1.75E-05	2.79E-03	3.498	Atp5e	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit
10548194	0.681	9.697	1.32E-04	8.39E-03	1.466	Fkbp4	FK506 binding protein 4
10354247	0.679	12.133	1.73E-03	3.77E-02	-1.167	Fhl2	four and a half LIM domains 2
10374197	0.678	6.953	1.64E-03	3.65E-02	-1.113	Ramp3	receptor (calcitonin) activity modifying protein 3; similar to receptor activity modifying protein 3
10509858	0.678	11.798	2.04E-05	3.11E-03	3.346	Sdhb	succinate dehydrogenase complex, subunit B, iron sulfur (Ip); similar to succinate dehydrogenase Ip subunit
10463704	0.677	9.319	1.26E-03	3.15E-02	-0.848	As3mt	arsenic (+3 oxidation state) methyltransferase
10408335	0.676	7.759	1.22E-03	3.08E-02	-0.812	Aldh5a1	aldhehyde dehydrogenase family 5, subfamily A1
10389300	0.676	10.816	4.29E-05	4.56E-03	2.603	Dhrs11	dehydrogenase/reductase (SDR family) member 11
10592926	0.676	8.01	4.06E-05	4.43E-03	2.659	Tmem25	transmembrane protein 25
10534493	0.675	5.25	1.40E-05	2.61E-03	3.72	Ccl24	chemokine (C-C motif) ligand 24
10565815	0.675	7.735	2.73E-05	3.61E-03	3.056	Gm4980	predicted gene 4980

10393898	0.675	8.226	8.98E-06	2.07E-03	4.152	Myadml2	myeloid-associated differentiation marker-like 2
10489569	0.675	9.003	1.84E-03	3.91E-02	-1.234	Pltp	phospholipid transfer protein
10377782	0.674	5.542	9.08E-04	2.62E-02	-0.507	Clec10a	macrophage galactose N-acetyl-galactosamine specific lectin 1
10435617	0.674	8.359	7.89E-05	6.44E-03	1.99	Rabl3	RAB, member of RAS oncogene family-like 3
10520467	0.673	12.089	1.03E-05	2.22E-03	4.014	Hadhb	predicted gene 13910; similar to Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit; hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit; predicted gene 9108
10379524	0.672	6.082	2.31E-03	4.44E-02	-1.466	Ccl11	chemokine (C-C motif) ligand 11
10557738	0.672	6.847	1.07E-04	7.57E-03	1.678	Ctf1	cardiotrophin 1
10343934	0.671	7.456	2.05E-03	4.16E-02	-1.346	Trappc4	trafficking protein particle complex 4
10466903	0.668	6.97	5.33E-05	5.13E-03	2.385	4430402I18Rik	RIKEN cDNA 4430402I18 gene
10371916	0.667	5.818	1.51E-05	2.67E-03	3.643	4930485B16Rik	RIKEN cDNA 4930485B16 gene
10512251	0.667	6.744	8.23E-04	2.49E-02	-0.406	AI464131	expressed sequence AI464131
10399478	0.667	9.827	3.04E-05	3.82E-03	2.949	Lpin1	lipin 1
10411171	0.667	5.698	5.01E-05	4.89E-03	2.449	Pde8b	phosphodiesterase 8B
10491611	0.666	8.209	9.01E-04	2.61E-02	-0.499	4932438A13Rik	RIKEN cDNA 4932438A13 gene
10392834	0.666	8.284	8.61E-05	6.69E-03	1.902	Clm3	predicted gene 11710; predicted gene, OTTMUSG00000003606
10369704	0.666	9.215	3.61E-04	1.53E-02	0.44	Hnrnph3	heterogeneous nuclear ribonucleoprotein H3
10461391	0.666	9.651	2.76E-03	4.95E-02	-1.649	Pcna	proliferating cell nuclear antigen; similar to proliferating cell nuclear antigen (DNA polymerase delta auxiliary protein)
10418921	0.666	7.374	2.70E-03	4.88E-02	-1.626	Sncg	synuclein, gamma
10559406	0.666	8.479	1.63E-05	2.72E-03	3.569	Tfpt	TCF3 (E2A) fusion partner
10377841	0.666	6.078	5.95E-04	2.04E-02	-0.072	Tm4sf5	transmembrane 4 superfamily member 5
10568939	0.665	11.692	9.68E-05	7.13E-03	1.783	Echs1	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial
10572786	0.664	9.791	1.21E-04	8.06E-03	1.557	Ap1m1	adaptor-related protein complex AP-1, mu subunit 1
10528929	0.663	12.211	1.54E-05	2.67E-03	3.623	Hadha	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit
10569168	0.663	7.401	2.85E-05	3.70E-03	3.014	Slc25a22	solute carrier family 25 (mitochondrial carrier, glutamate), member 22
10558600	0.662	6.852	2.20E-04	1.13E-02	0.945	Mtg1	mitochondrial GTPase 1 homolog (S. cerevisiae)
10567134	0.662	6.77	3.46E-05	3.99E-03	2.82	Plekha7	pleckstrin homology domain containing, family A member 7
10484389	0.662	10.292	2.31E-04	1.15E-02	0.898	Tfpi	tissue factor pathway inhibitor
10437205	0.661	6.222	2.05E-06	1.05E-03	5.561	Pcp4	Purkinje cell protein 4; immunoglobulin superfamily, member 5
10368947	0.66	5.49	6.45E-05	5.77E-03	2.193	Aim1	absent in melanoma 1
10490818	0.66	7.68	5.66E-05	5.30E-03	2.326	Stmn2	stathmin-like 2
10476952	0.659	7.59	2.03E-06	1.05E-03	5.572	Entpd6	ectonucleoside triphosphate diphosphohydrolase 6
10451943	0.659	8.485	1.26E-04	8.21E-03	1.518	Plin5	RIKEN cDNA 2310076L09 gene
10450038	0.658	6.096	1.17E-03	3.00E-02	-0.766	Angptl4	angiopoietin-like 4
10511429	0.657	7.864	1.30E-03	3.20E-02	-0.878	Car8	carbonic anhydrase 8; similar to Carbonic anhydrase-related protein (CARP) (CA-VIII)
10363146	0.657	5.623	4.87E-05	4.82E-03	2.477	Slc35f1	solute carrier family 35, member F1

10408074	0.656	6.68	3.63E-04	1.53E-02	0.435	Hist1h4m	histone cluster 1, H4k; histone cluster 1, H4m; histone cluster 4, H4; similar to germinal histone H4 gene; histone cluster 1, H4h; histone cluster 1, H4j; histone cluster 1, H4i; histone cluster 1, H4d; histone cluster 1, H4c; histone cluster 1, H4f; histone cluster 1, H4b; histone cluster 1, H4a; histone cluster 2, H4; similar to histone H4
10415742	0.656	9.503	3.91E-06	1.41E-03	4.954	Mipep	mitochondrial intermediate peptidase; similar to Mipep protein
10384725	0.656	8.926	1.43E-03	3.40E-02	-0.976	Rel	reticuloendotheliosis oncogene
10466087	0.656	9.9	1.91E-05	2.96E-03	3.41	Tmem109	transmembrane protein 109
10385353	0.654	8.244	3.32E-05	3.93E-03	2.86	Adra1b	adrenergic receptor, alpha 1b
10401473	0.654	10.495	2.87E-06	1.23E-03	5.247	Aldh6a1	aldehyde dehydrogenase family 6, subfamily A1
10475502	0.654	6.567	2.07E-04	1.09E-02	1.012	Gm14085	similar to purine-selective Na+ nucleoside cotransporter; novel protein similar to solute carrier family 28 (sodium-coupled nucleoside transporter) member 2 (Slc28a2)
10575867	0.654	8.102	2.12E-04	1.11E-02	0.984	Mlycd	malonyl-CoA decarboxylase
10449741	0.654	9.396	2.53E-03	4.72E-02	-1.562	Sik1	salt inducible kinase 1
10550638	0.653	9.561	5.93E-05	5.50E-03	2.279	Rtn2	reticulon 2 (Z-band associated protein)
10364030	0.652	6.955	3.00E-04	1.36E-02	0.631	Adora2a	adenosine A2a receptor
10449142	0.652	9.46	6.50E-04	2.16E-02	-0.163	Fam195a	WD repeat domain 90
10373054	0.651	7.661	1.34E-03	3.26E-02	-0.907	Slc26a10	solute carrier family 26, member 10
10359826	0.651	10.464	4.47E-05	4.67E-03	2.562	Uqcr11	ubiquinol-cytochrome c reductase (6.4kD) subunit; similar to ubiquinol-cytochrome c reductase subunit
10522666	0.65	9.623	1.73E-03	3.78E-02	-1.172	---	RIKEN cDNA 2310040G07 gene
10536697	0.65	9.682	1.17E-03	3.00E-02	-0.764	Asb15	ankyrin repeat and SOCS box-containing 15
10595480	0.648	10.161	2.14E-04	1.11E-02	0.978	Me1	predicted gene 7049; similar to NADP-dependent malic enzyme (NADP-ME) (Malic enzyme 1); malic enzyme 1, NADP(+)-dependent, cytosolic
10513608	0.647	10.808	1.42E-05	2.62E-03	3.701	Alad	aminolevulinate, delta-, dehydratase
10536324	0.647	6.523	2.38E-03	4.52E-02	-1.499	Asb4	ankyrin repeat and SOCS box-containing 4
10515201	0.646	8.139	1.23E-04	8.18E-03	1.537	Cyp4b1	predicted gene 12839; cytochrome P450, family 4, subfamily b, polypeptide 1
10339071	0.645	10.412	3.37E-05	3.94E-03	2.845	Cox18	COX18 cytochrome c oxidase assembly homolog (S. cerevisiae)
10446763	0.645	11.21	3.43E-06	1.35E-03	5.077	Lbh	limb-bud and heart
10509577	0.645	6.5	1.17E-05	2.37E-03	3.892	Pla2g2d	phospholipase A2, group IID
10447521	0.645	8.708	4.52E-04	1.75E-02	0.209	Tfb1m	transcription factor B1, mitochondrial
10450103	0.644	9.019	1.08E-06	6.80E-04	6.159	H2-Ke6	H2-K region expressed gene 6
10433403	0.644	9.038	5.99E-04	2.05E-02	-0.08	Rbfox1	ataxin 2 binding protein 1
10557439	0.643	7.722	2.36E-05	3.36E-03	3.201	Ccdc101	coiled-coil domain containing 101
10584024	0.643	6.444	2.60E-05	3.53E-03	3.106	Opcml	opioid binding protein/cell adhesion molecule-like
10455647	0.643	7.445	1.12E-04	7.68E-03	1.636	Tnfaip8	tumor necrosis factor, alpha-induced protein 8
10491605	0.642	9.31	8.51E-05	6.68E-03	1.913	4932438A13Rik	RIKEN cDNA 4932438A13 gene
10387768	0.642	10.444	1.78E-05	2.81E-03	3.482	Acadvl	acyl-Coenzyme A dehydrogenase, very long chain
10554789	0.642	9.183	7.15E-04	2.28E-02	-0.261	Ctsc	cathepsin C
10447084	0.642	8.368	1.68E-04	9.55E-03	1.223	Galm	galactose mutarotase
10581069	0.642	6.824	2.80E-04	1.30E-02	0.699	Gm9853	ENSMUSG00000051554

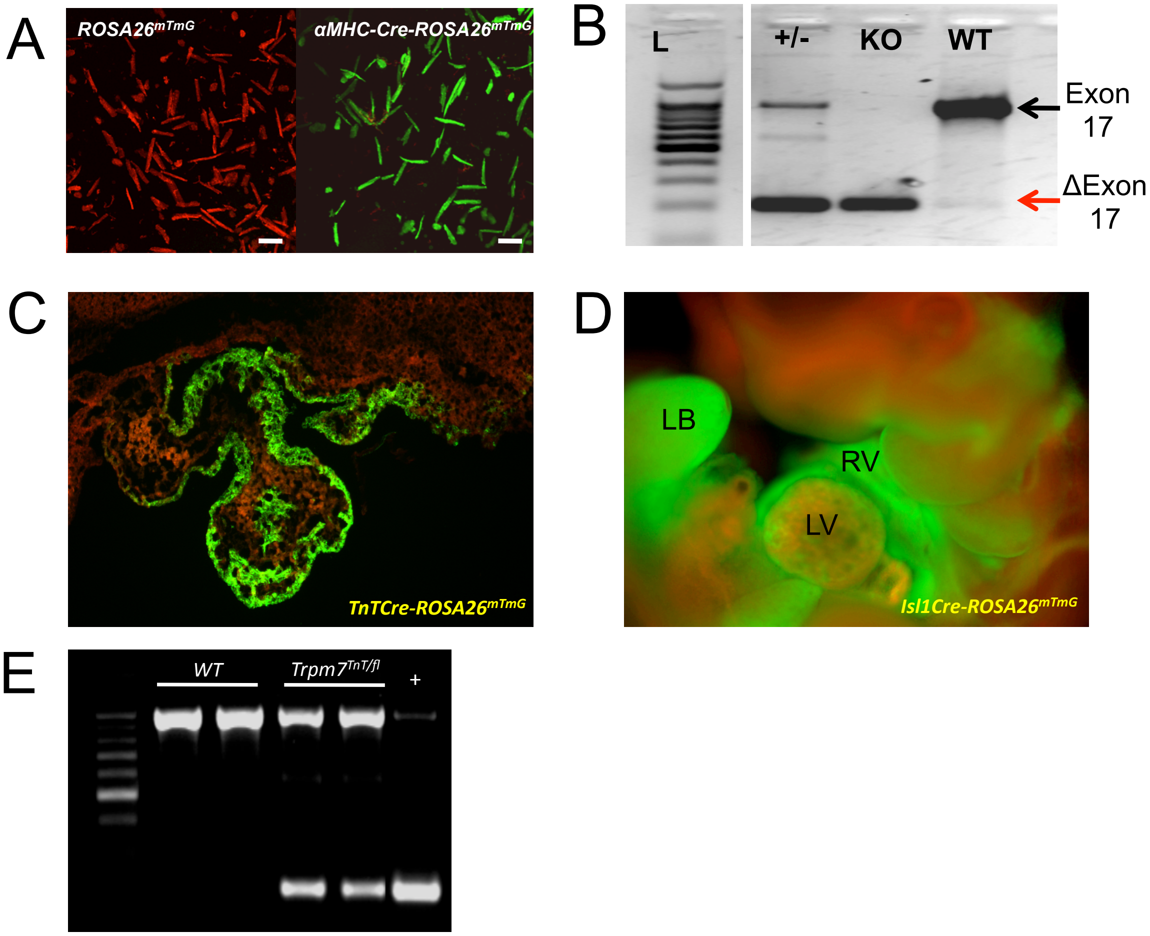
10470959	0.641	9.617	1.47E-04	8.83E-03	1.36	Phyhd1	phytanoyl-CoA dioxygenase domain containing 1
10469255	0.641	6.06	2.43E-05	3.41E-03	3.171	Prkcq	protein kinase C, theta
10493335	0.64	7.731	2.04E-03	4.14E-02	-1.34	5830417I10Rik	RIKEN cDNA 5830417I10 gene; similar to GON-4-like protein (GON-4 homolog); similar to Dingo protein isoform 2
10585233	0.639	8.347	3.71E-04	1.56E-02	0.411	Alg9	asparagine-linked glycosylation 9 homolog (yeast, alpha 1,2 mannosyltransferase)
10390519	0.639	7.343	1.08E-04	7.57E-03	1.668	Plxdc1	plexin domain containing 1
10482030	0.639	9.904	1.46E-05	2.66E-03	3.674	Stom	stomatin
10572928	0.638	5.987	3.13E-04	1.40E-02	0.587	Rasd2	RASD family, member 2
10464586	0.637	9.009	1.08E-04	7.57E-03	1.673	Gstp2	glutathione S-transferase, pi 2; glutathione S-transferase, pi 1; similar to glutathione S-transferase pi class A; predicted gene 3934
10519497	0.637	8.361	6.72E-04	2.19E-02	-0.198	Steap4	STEAP family member 4
10565775	0.635	11.04	1.19E-03	3.03E-02	-0.786	Dgat2	diacylglycerol O-acyltransferase 2
10530371	0.635	10.167	3.34E-05	3.93E-03	2.855	Yipf7	Yip1 domain family, member 7
10397148	0.634	5.528	1.84E-05	2.89E-03	3.449	Acot1	acyl-CoA thioesterase 1
10461459	0.633	7.095	4.73E-06	1.48E-03	4.771	Syt7	synaptotagmin VII
10579996	0.632	12.022	2.37E-06	1.07E-03	5.428	Tecr	predicted gene 4948; glycoprotein, synaptic 2; RIKEN cDNA 1600014K23 gene
10552919	0.631	10.259	1.70E-06	9.61E-04	5.737	Hrc	histidine rich calcium binding protein
10409265	0.63	10.005	7.73E-06	1.92E-03	4.298	Auh	AU RNA binding protein/enoyl-coenzyme A hydratase
10426081	0.63	6.081	1.09E-04	7.57E-03	1.668	Fam19a5	family with sequence similarity 19, member A5
10600502	0.629	8.951	3.01E-04	1.37E-02	0.626	2810453I06Rik	predicted gene 12579; RIKEN cDNA 2810453I06 gene; hypothetical LOC674122; predicted gene 6036
10352448	0.627	7.676	9.12E-04	2.63E-02	-0.511	Dusp10	dual specificity phosphatase 10
10394990	0.627	8.311	1.58E-04	9.25E-03	1.283	Mboat2	membrane bound O-acyltransferase domain containing 2
10415651	0.626	7.314	5.18E-06	1.54E-03	4.685	Fgf9	fibroblast growth factor 9
10533504	0.626	7.875	2.33E-04	1.16E-02	0.889	Ift81	intraflagellar transport 81 homolog (Chlamydomonas)
10422585	0.624	5.52	1.72E-04	9.73E-03	1.198	Fgf14	fibroblast growth factor 14
10580233	0.624	9.306	2.37E-05	3.36E-03	3.197	Gcdh	glutaryl-Coenzyme A dehydrogenase
10494023	0.624	8.477	3.29E-05	3.93E-03	2.87	Rorc	RAR-related orphan receptor gamma
10377662	0.624	7.511	4.41E-06	1.44E-03	4.837	Ybx2	similar to Y box protein 2; Y box protein 2
10514933	0.622	10.96	1.66E-06	9.60E-04	5.76	Cpt2	carnitine palmitoyltransferase 2
10449575	0.622	7.549	2.30E-03	4.44E-02	-1.461	Ppil1	similar to peptidylprolyl isomerase-like 1; peptidylprolyl isomerase (cyclophilin)-like 1
10589368	0.62	7.87	1.72E-05	2.78E-03	3.517	Plxnb1	plexin B1
10399973	0.62	8.97	1.90E-04	1.03E-02	1.096	Hdac9	histone deacetylase 9
10459768	0.619	9.479	1.85E-04	1.01E-02	1.125	---	ENSMUSG00000077346; ENSMUSG00000077335; ENSMUSG00000077754
10338615	0.619	6.739	2.60E-04	1.25E-02	0.777	Tbl3	transducin (beta)-like 3
10422962	0.618	8.806	1.66E-05	2.74E-03	3.549	1110020G09Rik	RIKEN cDNA 1110020G09 gene
10419416	0.618	6.159	7.79E-04	2.41E-02	-0.35	3632451O06Rik	RIKEN cDNA 3632451O06 gene
10563085	0.618	10.339	2.90E-04	1.33E-02	0.664	Fcgrt	Fc receptor, IgG, alpha chain transporter
10572647	0.618	10.543	2.50E-03	4.66E-02	-1.546	Slc27a1	solute carrier family 27 (fatty acid transporter), member 1

10370833	0.617	11.282	1.04E-04	7.41E-03	1.712	Uqcr11	ubiquinol-cytochrome c reductase (6.4kD) subunit; similar to ubiquinol-cytochrome c reductase subunit
10413932	0.616	8.263	2.23E-03	4.33E-02	-1.429	E130203B14Rik	RIKEN cDNA E130203B14 gene
10461038	0.615	8.347	3.51E-06	1.35E-03	5.055	Macrod1	MACRO domain containing 1
10506415	0.615	8.415	3.16E-05	3.84E-03	2.91	Oma1	OMA1 homolog, zinc metallopeptidase (S. cerevisiae)
10556487	0.614	5.281	2.25E-04	1.14E-02	0.924	---	RIKEN cDNA A630005I04 gene
10536611	0.614	9.364	2.15E-06	1.07E-03	5.519	Kcnd2	potassium voltage-gated channel, Shal-related family, member 2
10456699	0.613	12.815	4.49E-05	4.67E-03	2.56	Acaa2	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)
10608715	0.61	10.518	8.07E-05	6.46E-03	1.968	C1orf170	RIKEN cDNA 2310042D19 gene
10608709	0.61	8.158	2.72E-03	4.91E-02	-1.635	Nkain1	Na+/K+ transporting ATPase interacting 1
10387821	0.609	6.453	3.79E-04	1.57E-02	0.39	Alox12	arachidonate 12-lipoxygenase
10434516	0.608	7.405	1.91E-04	1.04E-02	1.089	Fam131a	family with sequence similarity 131, member A
10513945	0.604	8.243	4.75E-05	4.79E-03	2.502	2310002L09Rik	RIKEN cDNA 2310002L09 gene
10525989	0.604	7.61	1.51E-04	9.04E-03	1.329	Gpr133	G protein-coupled receptor 133
10416023	0.604	6.621	1.47E-04	8.84E-03	1.357	Scara5	scavenger receptor class A, member 5 (putative)
10475487	0.604	7.367	6.28E-05	5.71E-03	2.222	Slc28a2	solute carrier family 28 (sodium-coupled nucleoside transporter), member 2
10552668	0.603	9.122	6.64E-04	2.17E-02	-0.185	Lrrc4b	leucine rich repeat containing 4B; similar to Leucine rich repeat containing 4B
10355456	0.603	7.714	1.34E-05	2.57E-03	3.76	Mreg	melanoregulin
10441718	0.603	8.093	6.11E-04	2.06E-02	-0.1	Park2	Parkinson disease (autosomal recessive, juvenile) 2, parkin
10363860	0.602	7.404	3.13E-04	1.40E-02	0.585	Slc16a9	solute carrier family 16 (monocarboxylic acid transporters), member 9
10555460	0.601	9.08	8.91E-04	2.59E-02	-0.488	Stard10	START domain containing 10
10523547	0.6	7.284	1.50E-05	2.67E-03	3.65	Agpat9	1-acylglycerol-3-phosphate O-acyltransferase 9
10476886	0.599	6.255	4.31E-04	1.70E-02	0.259	Sstr4	somatostatin receptor 4
10490384	0.598	7.994	4.02E-06	1.41E-03	4.926	Lama5	laminin, alpha 5
10475866	0.596	6.884	8.63E-04	2.56E-02	-0.456	Bcl2l11	BCL2-like 11 (apoptosis facilitator)
10452404	0.595	8.319	2.90E-06	1.23E-03	5.237	Nudt12	nudix (nucleoside diphosphate linked moiety X)-type motif 12
10454683	0.595	5.733	3.98E-04	1.62E-02	0.339	Pkd2l2	polycystic kidney disease 2-like 2
10350159	0.594	5.835	5.05E-04	1.84E-02	0.096	Lad1	ladinin
10578222	0.593	8.894	2.68E-04	1.27E-02	0.746	Dlc1	deleted in liver cancer 1
10552857	0.592	6.664	1.13E-03	2.95E-02	-0.731	Slc17a7	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7
10460285	0.591	8.955	2.18E-06	1.07E-03	5.507	Nudt8	nudix (nucleoside diphosphate linked moiety X)-type motif 8
10463361	0.591	6.163	9.83E-05	7.19E-03	1.767	Scd4	stearoyl-coenzyme A desaturase 4
10530100	0.589	7.244	1.83E-04	1.01E-02	1.136	Arap2	predicted gene 336; ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2
10412231	0.589	7.733	1.28E-04	8.31E-03	1.496	Hspb3	heat shock protein 3
10351430	0.589	10.385	2.36E-04	1.17E-02	0.877	Rxrg	retinoid X receptor gamma
10529515	0.589	7.386	4.53E-04	1.75E-02	0.207	Sorcs2	sortilin-related VPS10 domain containing receptor 2
10446771	0.588	11.299	1.13E-04	7.70E-03	1.63	Lclat1	lysocardiolipin acyltransferase 1
10460556	0.586	8.302	4.87E-06	1.49E-03	4.743	Gal3st3	galactose-3-O-sulfotransferase 3
10500283	0.584	10.554	2.37E-06	1.07E-03	5.425	Car14	carbonic anhydrase 14

10434229	0.584	8.913	2.02E-03	4.12E-02	-1.328	Cldn5	claudin 5
10578241	0.584	8.446	1.40E-05	2.61E-03	3.714	Dlc1	RIKEN cDNA A730069N07 gene
10494551	0.582	9.038	2.71E-05	3.60E-03	3.063	Acp6	acid phosphatase 6, lysophosphatidic
10511679	0.578	11.018	2.12E-05	3.17E-03	3.307	Decr1	2,4-dienoyl CoA reductase 1, mitochondrial
10566457	0.576	7.411	1.03E-05	2.22E-03	4.02	Apbb1	amyloid beta (A4) precursor protein-binding, family B, member 1
10420730	0.575	9.384	1.29E-06	7.71E-04	5.994	Fdft1	predicted gene 6781; farnesyl diphosphate farnesyl transferase 1
10589076	0.573	10.463	7.78E-06	1.92E-03	4.292	Slc25a20	solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase), member 20
10551614	0.572	11.971	3.16E-05	3.84E-03	2.91	Ech1	enoyl coenzyme A hydratase 1, peroxisomal
10539143	0.571	9.05	2.29E-04	1.15E-02	0.905	Retsat	retinol saturase (all trans retinol 13,14 reductase)
10600597	0.571	9.836	1.29E-04	8.31E-03	1.491	Tmem47	transmembrane protein 47
10586865	0.57	7.04	2.21E-03	4.32E-02	-1.423	Aldh1a2	aldehyde dehydrogenase family 1, subfamily A2
10397145	0.567	11.761	1.13E-04	7.70E-03	1.627	Acot2	acyl-CoA thioesterase 2
10585851	0.567	6.841	2.60E-04	1.25E-02	0.775	Hcn4	hyperpolarization-activated, cyclic nucleotide-gated K+ 4
10582322	0.567	5.441	1.03E-03	2.81E-02	-0.64	Snai3	snail homolog 3 (Drosophila)
10397440	0.565	7.36	2.13E-05	3.17E-03	3.302	Esrrb	estrogen related receptor, beta
10467989	0.562	6.623	1.22E-04	8.13E-03	1.545	Sec31b	Sec31 homolog B (S. cerevisiae)
10472155	0.558	8.807	3.08E-04	1.38E-02	0.602	Kcnj3	potassium inwardly-rectifying channel, subfamily J, member 3
10354374	0.558	7.579	1.75E-06	9.61E-04	5.71	Slc40a1	solute carrier family 40 (iron-regulated transporter), member 1
10385540	0.556	6.226	8.15E-04	2.48E-02	-0.397	Olfr1396	olfactory receptor 1396
10345065	0.554	6.914	1.21E-03	3.06E-02	-0.805	Gsta3	glutathione S-transferase, alpha 3
10492330	0.553	8.505	3.89E-06	1.41E-03	4.958	P2ry1	purinergic receptor P2Y, G-protein coupled 1
10369806	0.551	9.123	1.16E-03	2.99E-02	-0.758	1700040L02Rik	RIKEN cDNA 1700040L02 gene
10361234	0.551	6.366	2.31E-06	1.07E-03	5.452	Hsd11b1	hydroxysteroid 11-beta dehydrogenase 1
10520304	0.55	8.233	4.10E-05	4.44E-03	2.65	Actr3b	ARP3 actin-related protein 3 homolog B (yeast)
10537712	0.55	11.373	4.56E-05	4.69E-03	2.544	Gstk1	glutathione S-transferase kappa 1
10491825	0.548	9.83	1.08E-05	2.24E-03	3.975	3110057O12Rik	RIKEN cDNA 3110057O12 gene; predicted gene 2011
10548038	0.548	7.658	9.00E-04	2.61E-02	-0.498	Ntf3	neurotrophin 3
10442445	0.542	10.757	9.32E-06	2.12E-03	4.115	Dci	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase)
10491820	0.542	8.871	3.44E-05	3.99E-03	2.826	Gm2011	RIKEN cDNA 3110057O12 gene; predicted gene 2011
10383813	0.536	9.456	4.56E-06	1.46E-03	4.805	1700020C11Rik	RIKEN cDNA 1700020C11 gene
10497399	0.533	8.507	3.20E-05	3.87E-03	2.899	Pde7a	phosphodiesterase 7A
10412909	0.526	9.317	6.06E-06	1.66E-03	4.532	Fdft1	predicted gene 6781; farnesyl diphosphate farnesyl transferase 1
10360745	0.525	8.544	3.70E-05	4.10E-03	2.753	Lbr	lamin B receptor
10435019	0.522	7.699	7.65E-05	6.34E-03	2.021	2310010M20Rik	RIKEN cDNA 2310010M20 gene
10404376	0.52	9.428	2.05E-05	3.12E-03	3.34	Agtr1a	angiotensin II receptor, type 1a
10583920	0.52	7.405	5.00E-04	1.83E-02	0.106	Eepd1	endonuclease/exonuclease/phosphatase family domain containing 1
10506269	0.519	6.924	4.22E-06	1.43E-03	4.881	Ak4	predicted gene 13639; similar to adenylate kinase 4; adenylate kinase 3-like 1
10379866	0.519	9.298	6.36E-05	5.74E-03	2.209	Car4	carbonic anhydrase 4
10397346	0.518	6.121	4.50E-07	4.61E-04	6.94	Fos	FBJ osteosarcoma oncogene
10547153	0.517	7.148	1.70E-05	2.78E-03	3.524	Alox5	arachidonate 5-lipoxygenase

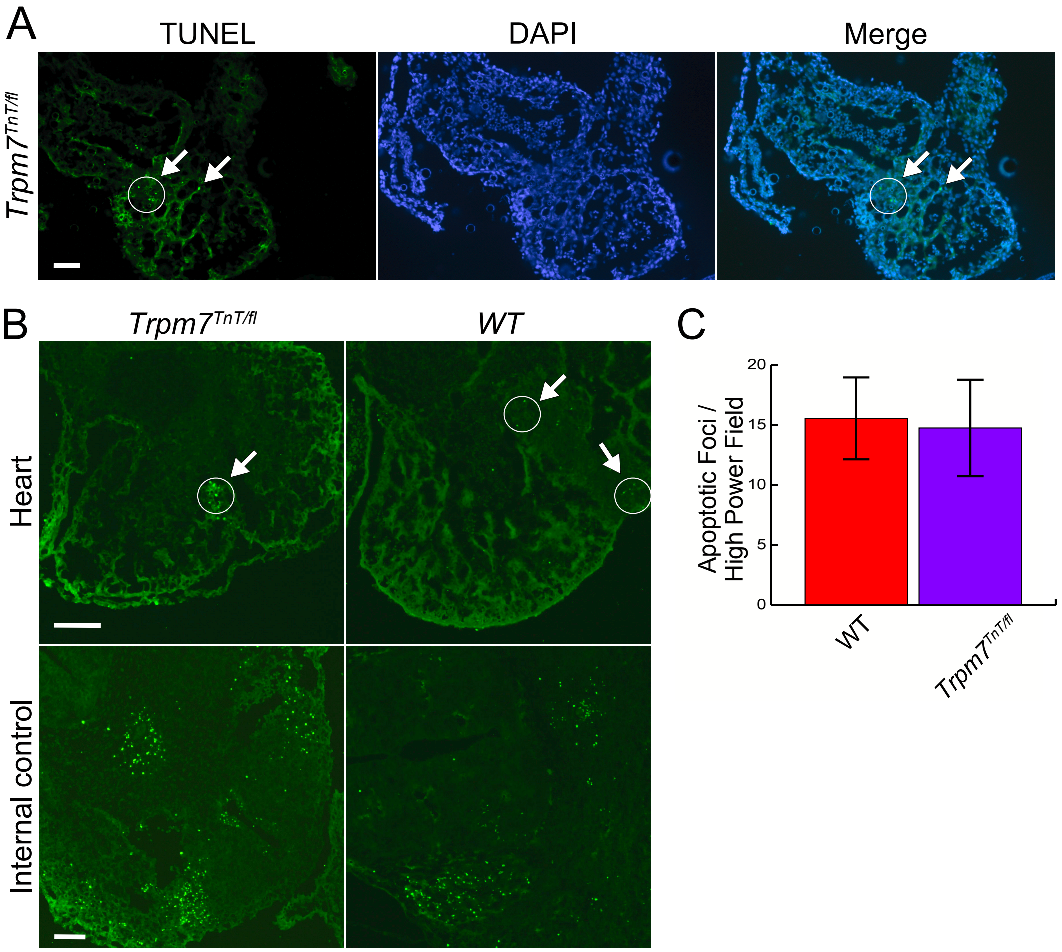
10512145	0.517	10.247	7.58E-04	2.38E-02	-0.322	Aqp7	aquaporin 7
10596718	0.516	9.415	1.52E-05	2.67E-03	3.635	Slc38a3	solute carrier family 38, member 3
10386020	0.515	8.098	5.34E-07	4.88E-04	6.79	Slc36a2	solute carrier family 36 (proton/amino acid symporter), member 2
10564805	0.513	7.588	3.07E-05	3.82E-03	2.939	Pex11a	peroxisomal biogenesis factor 11 alpha
10502105	0.508	6.428	2.48E-05	3.44E-03	3.15	Egf	epidermal growth factor
10413381	0.506	9.89	1.55E-05	2.67E-03	3.619	Asb14	ankyrin repeat and SOCS box-containing 14
10355998	0.502	5.874	2.88E-04	1.32E-02	0.671	Fam124b	family with sequence similarity 124, member B
10584870	0.501	6.319	5.71E-04	1.99E-02	-0.03	Tmprss13	transmembrane protease, serine 13
10357875	0.498	9.33	1.76E-04	9.89E-03	1.177	Btg2	B-cell translocation gene 2, anti-proliferative
10456383	0.498	7.588	1.04E-06	6.68E-04	6.191	Impa2	inositol (myo)-1(or 4)-monophosphatase 2
10455299	0.497	9.573	3.65E-06	1.37E-03	5.017	Sh3rf2	SH3 domain containing ring finger 2
10387483	0.496	8.689	3.28E-05	3.93E-03	2.872	Efnb3	ephrin B3
10400304	0.496	10.292	1.14E-04	7.77E-03	1.613	Egln3	EGL nine homolog 3 (C. elegans)
10452648	0.493	7.984	1.68E-04	9.55E-03	1.224	Emilin2	elastin microfibril interfacer 2
10602385	0.49	6.052	2.56E-04	1.24E-02	0.792	Pfkfb1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1
10472923	0.488	9.462	2.53E-08	1.01E-04	9.293	Ak4	predicted gene 13639; similar to adenylate kinase 4; adenylate kinase 3-like 1
10461642	0.485	10.314	2.84E-05	3.70E-03	3.019	Scarna17	ENSMUSG00000077346; ENSMUSG00000077335; ENSMUSG00000077754
10374777	0.481	7.575	7.82E-05	6.40E-03	1.999	Efemp1	epidermal growth factor-containing fibulin-like extracellular matrix protein 1
10398824	0.478	8.706	5.72E-05	5.33E-03	2.316	A530016L24Rik	hypothetical protein LOC100047653; RIKEN cDNA A530016L24 gene
10377774	0.471	7.383	3.03E-05	3.82E-03	2.952	Mgl2	macrophage galactose N-acetyl-galactosamine specific lectin 2
10408543	0.469	10.339	2.17E-05	3.18E-03	3.286	Mylk4	myosin light chain kinase family, member 4
10350473	0.456	7.514	9.00E-07	6.26E-04	6.32	B3galt2	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2
10454782	0.455	7.876	1.18E-03	3.02E-02	-0.779	Egr1	early growth response 1
10399892	0.455	8.262	2.55E-07	3.55E-04	7.435	Gpr22	G protein-coupled receptor 22
10365769	0.446	6.757	1.56E-03	3.59E-02	-1.065	Hal	histidine ammonia lyase
10462303	0.439	6.524	1.26E-05	2.45E-03	3.823	Kcnv2	potassium channel, subfamily V, member 2
10581151	0.438	9.743	2.64E-03	4.83E-02	-1.605	Rrad	Ras-related associated with diabetes
10402512	0.437	8.783	8.39E-07	6.08E-04	6.384	Scarna13	ENSMUSG00000077583; ENSMUSG00000077781
10581538	0.424	8.38	1.67E-05	2.74E-03	3.544	Nqo1	NAD(P)H dehydrogenase, quinone 1
10355893	0.417	8.318	9.77E-05	7.18E-03	1.773	Epha4	Eph receptor A4
10502081	0.414	7.47	2.27E-06	1.07E-03	5.466	Enpep	glutamyl aminopeptidase
10483000	0.413	8.639	1.08E-04	7.57E-03	1.671	Itgb6	integrin beta 6
10427035	0.413	9.289	7.18E-04	2.29E-02	-0.265	Nr4a1	nuclear receptor subfamily 4, group A, member 1
10547227	0.406	6.564	5.00E-05	4.89E-03	2.451	Ret	ret proto-oncogene
10428376	0.405	8.264	1.98E-04	1.06E-02	1.058	Angpt1	angiopoietin 1
10441794	0.404	8.325	6.82E-04	2.21E-02	-0.214	Mrgprh	MAS-related GPR, member H
10360406	0.401	7.596	1.37E-03	3.31E-02	-0.929	Ifi205	interferon activated gene 205
10413874	0.399	6.079	1.67E-03	3.70E-02	-1.135	Ogdhl	oxoglutarate dehydrogenase-like
10571797	0.396	8.332	2.49E-07	3.55E-04	7.455	Asb5	ankyrin repeat and SOCs box-containing 5

10585068	0.394	6.536	1.44E-03	3.41E-02	-0.98	Fam55d	family with sequence similarity 55, member D
10405179	0.387	8.938	4.92E-04	1.82E-02	0.122	S1pr3	sphingosine-1-phosphate receptor 3
10540059	0.361	9.485	8.51E-04	2.53E-02	-0.441	Slc41a3	solute carrier family 41, member 3
10409999	0.357	6.461	2.62E-05	3.54E-03	3.099	Fbp2	fructose bisphosphatase 2
10447773	0.351	6.629	1.64E-07	2.97E-04	7.809	Slc22a3	solute carrier family 22 (organic cation transporter), member 3
10428619	0.349	6.879	2.43E-06	1.08E-03	5.403	Enpp2	ectonucleotide pyrophosphatase/phosphodiesterase 2
10409278	0.349	7.12	7.85E-06	1.92E-03	4.283	Nfil3	similar to NFIL3/E4BP4 transcription factor; nuclear factor, interleukin 3, regulated
10556463	0.346	6.444	6.04E-04	2.06E-02	-0.088	Arntl	aryl hydrocarbon receptor nuclear translocator-like
10413492	0.34	11.138	2.99E-07	3.58E-04	7.299	Lrtm1	leucine-rich repeats and transmembrane domains 1
10494160	0.333	8.882	7.11E-07	5.81E-04	6.533	Tmod4	tropomodulin 4
10457038	0.332	7.528	3.63E-04	1.53E-02	0.435	Gm10524	ENSMUSG00000073519
10442584	0.332	9.653	4.72E-06	1.48E-03	4.774	Rpl3l	ribosomal protein L3-like
10416099	0.319	6.681	1.51E-05	2.67E-03	3.643	Adra1a	adrenergic receptor, alpha 1a
10603746	0.307	9.254	5.50E-07	4.90E-04	6.762	Maob	monoamine oxidase B
10580635	0.305	9.3	1.97E-05	3.01E-03	3.381	Ces1d	carboxylesterase 3
10407707	0.289	8.411	4.41E-10	1.53E-05	11.832	Gm10336	ENSMUSG00000071543
10548817	0.268	8.304	7.24E-07	5.81E-04	6.517	Plbd1	phospholipase B domain containing 1; similar to RIKEN cDNA 1100001H23 gene
10392152	0.254	6.546	2.71E-07	3.58E-04	7.381	Scn4a	sodium channel, voltage-gated, type IV, alpha
10492355	0.239	6.385	2.42E-08	1.01E-04	9.325	Mme	membrane metallo endopeptidase
10409579	0.231	7.032	1.48E-06	8.71E-04	5.866	Cxcl14	chemokine (C-X-C motif) ligand 14
10511363	0.151	6.89	5.31E-07	4.88E-04	6.795	Penk	preproenkephalin
10490913	0.141	6.4	5.39E-06	1.56E-03	4.645	Car3	carbonic anhydrase 3
10436095	0.136	5.907	3.66E-06	1.37E-03	5.016	Retnla	resistin like alpha
10462912	0.102	6.433	2.99E-07	3.58E-04	7.299	Lgi1	leucine-rich repeat LGI family, member 1; predicted gene 3888

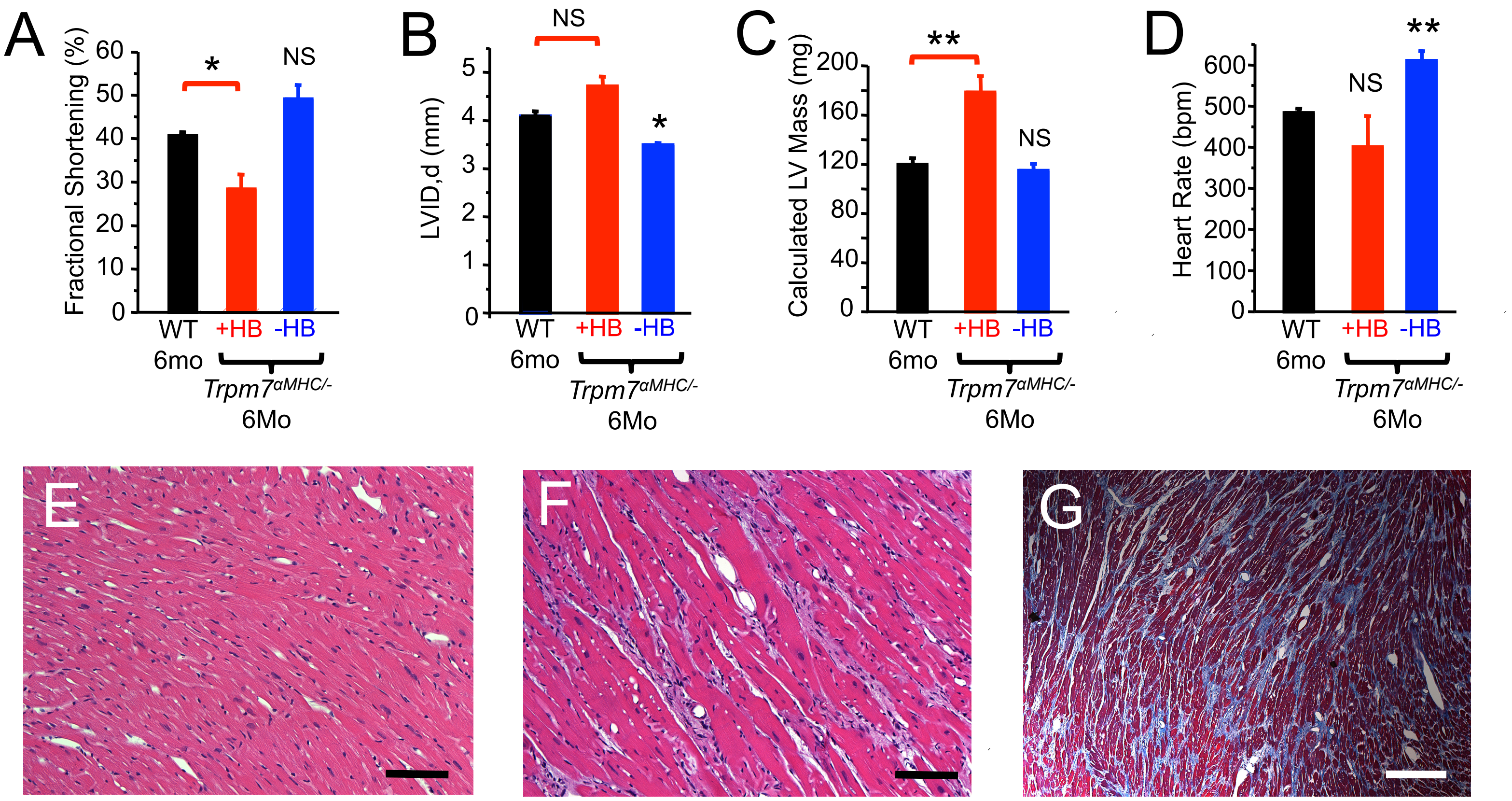


Supplemental Figure 1. *Cre*-mediated recombination and *Trpm7* deletion by *TnT-Cre*/*Isl1-Cre* and *αMHC-Cre*

(**A**) Confocal images of isolated cardiomyocytes from *WT ROSA26*^{mTmG} hearts and α*MHC-Cre-ROSA26*^{mTmG} hearts. EGFP expressed in 100% of myocytes when *ROSA26*^{mTmG} was crossed with α*MHC-Cre*, confirming *Cre* expression in all ventricular myocytes. Scale bars, 100 μm. **(B)** PCR across exon 17 from genomic DNA isolated from P1 *Trpm7*$^{\alpha MHC/fl}$ heart (*KO*), WT heart (*WT*) and from tail DNA of *Trpm7*$^{+/-}$ mouse (**+/-**). Deletion of exon 17 is present selectively in *KO* heart (200 bp amplicon, *red arrow*) as compared to WT heart (1 Kb amplicon, *black arrow*). (**C**) Fluorescence image of *TnT-Cre*-ROSA26^{mTmG} heart at E9 shows cardiac-restricted Cre expression. (**D**) *Isl1-Cre*-ROSA26^{mTmG} is predominantly restricted to the right ventricle (RV), but is also more widely expressed in the embryo (i.e. limb bud, LB). (**E**) Deletion of *Trpm7* exon 17 from genomic DNA of E9 *Trpm7*$^{TnT/fl}$ hearts compared to *Trpm7*$^{fl/fl}$ (*WT*) controls.

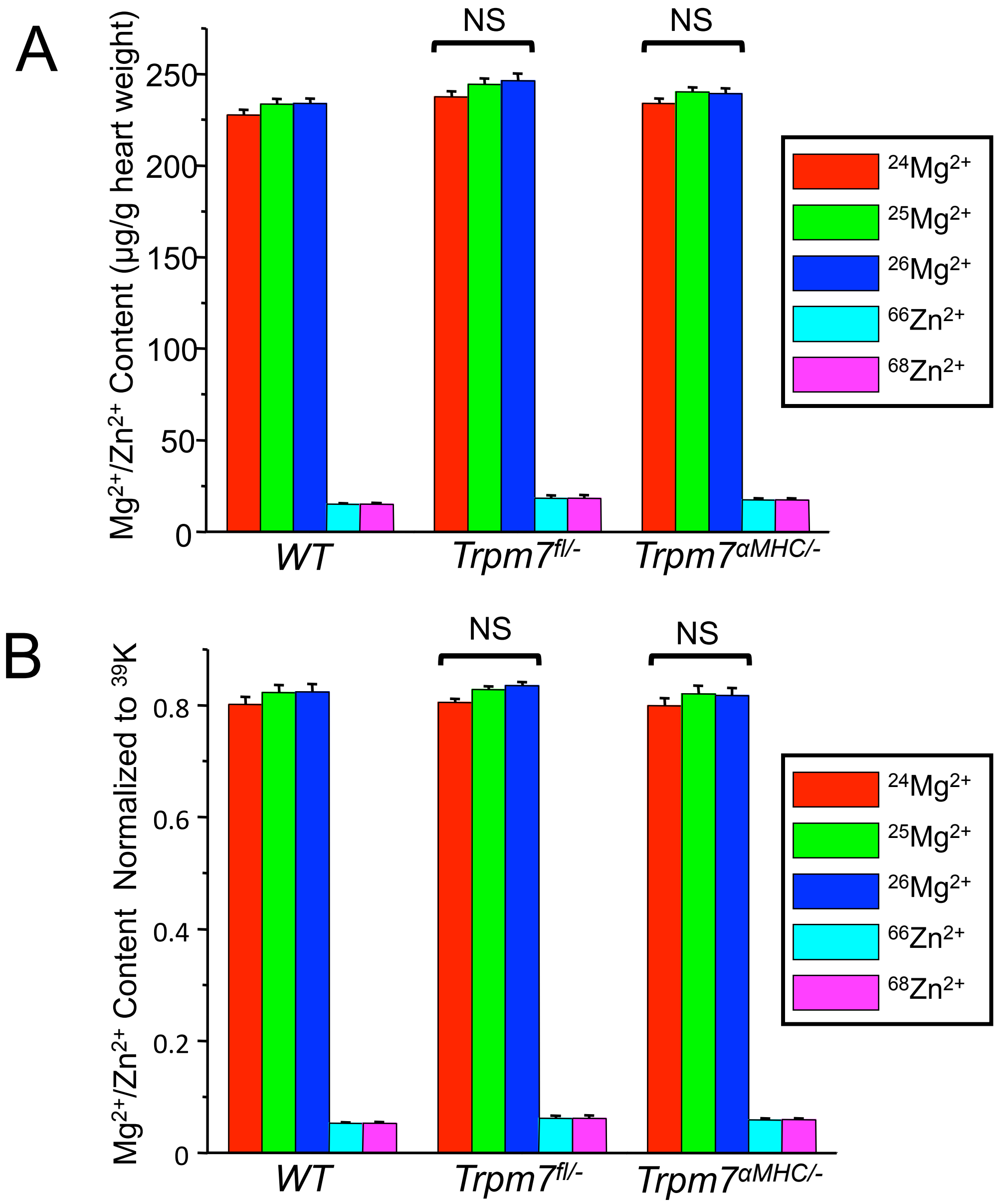


Supplemental Figure 2. Apoptosis in the compact myocardium is unchanged in *Trpm7*$^{TnT/fl}$ mice. A TUNEL-based cell assay was used to assess rates of apoptosis in the developing heart at E10**. (A)** TUNEL-based fluorescein labelling of *Trpm7*$^{TnT/fl}$ hearts shows nuclear localization (center panel, DAPI; right panel, merged image). **(B)** Distribution and density of apoptotic foci appears similar in control (*WT*) and *Trpm7*$^{TnT/fl}$ hearts**;** dense apoptosis was consistently observed in the rostral lateral plate, and paraxial mesoderm **(Internal control). (C)** Quantitative analysis demonstrates similar rates of apoptosis in *WT* and *Trpm7*$^{TnT/fl}$ hearts (P=0.87). Scale bar, 100 µm. Error bars represent SEM.



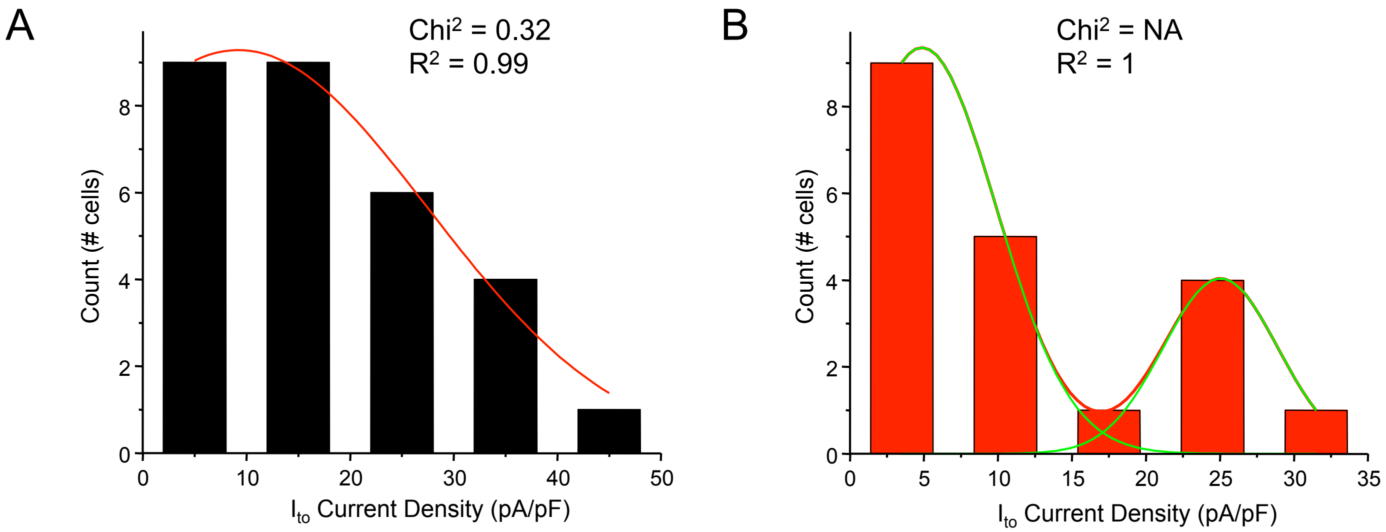
Supplementary Figure 3. Functional assessment and histological examination of ventricular tissue from 6 month old *Trpm7$^{\alpha MHC/-}$* mice

(A) Fractional shortening, (B) Left ventricular internal dimension (LVID), (C) Calculated left ventricular mass, (D) Heart rate in WT (black bar, n = 13), *Trpm7$^{\alpha MHC/-}$* with heart block (+HB, red bar, n = 3) and without heart block (-HB, blue bar, n = 5). Hematoxylin-eosin stain of 6 month-old *WT* **(E)** compared with *Trpm7$^{\alpha MHC/-}$* ventricular myocardium **(F)** shows myocyte enlargement and interstitial extracellular matrix deposition in the latter. Scale bar, 100 μm. **(G)** Masson-Trichrome stain shows diffuse interstitial fibrosis (blue stain) in *Trpm7$^{\alpha MHC/-}$* myocardium consistent with extensive collagen deposition. Scale bar, 400 μm. * $p < 0.05$, ** $p < 0.01$.



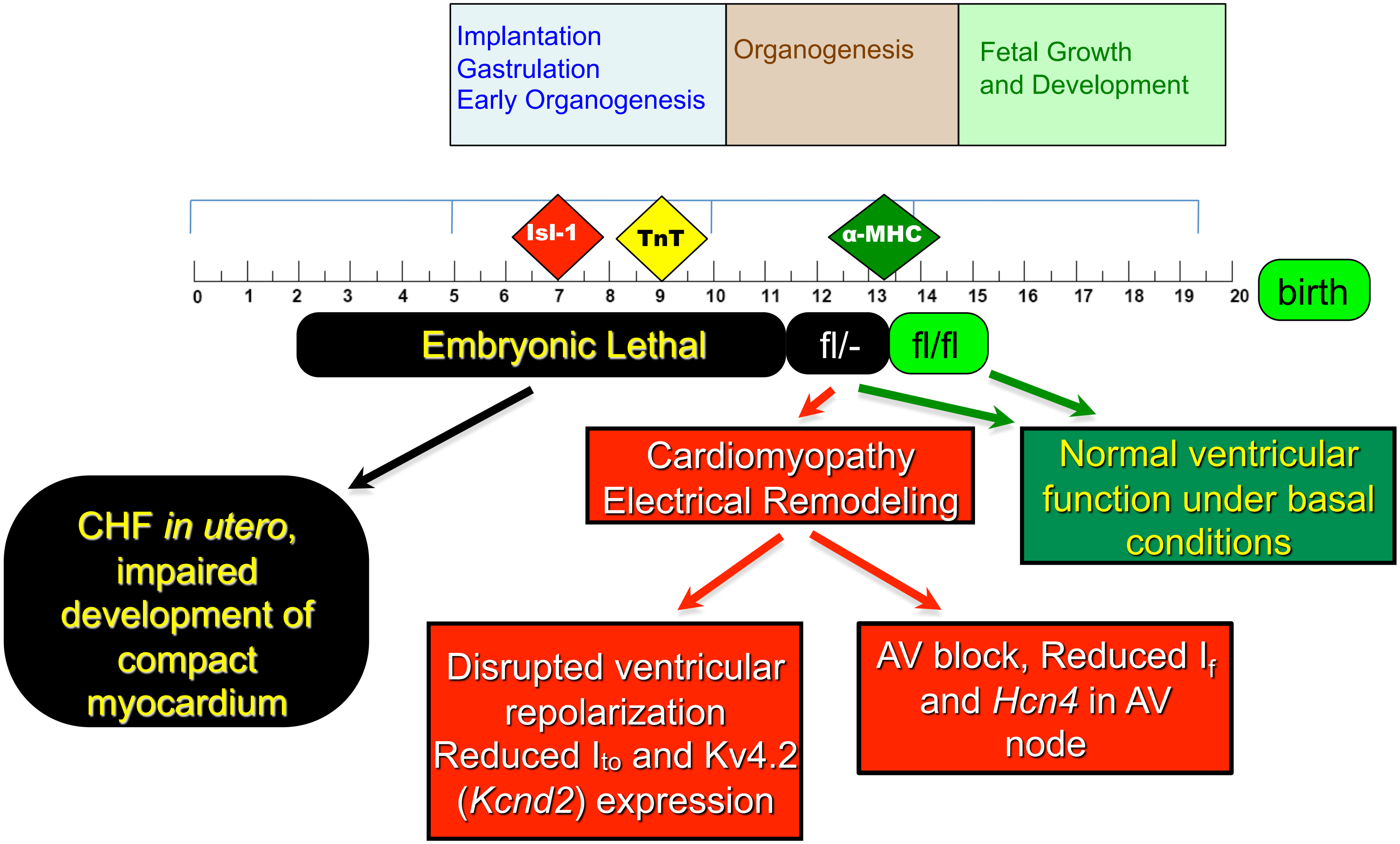
Supplemental Figure 4. Total myocardial magnesium and zinc content is unchanged in *Trpm7*$^{\alpha MHC/-}$ hearts

Total myocardial levels of isotopes $^{24}Mg^{2+}$, $^{25}Mg^{2+}$, $^{26}Mg^{2+}$, $^{66}Zn^{2+}$ and $^{68}Zn^{2+}$ in *WT, Trpm7*$^{fl/-}$ and *Trpm7*$^{\alpha MHC/-}$ myocardium per gram heart (**A**) and normalized to total ^{39}K (**B**), measured by Inductively Coupled Plasma Mass Spectrometry (ICP-MS). NS, not statistically significant compared to *WT*.



Supplemental Figure 5. Distribution of I_{to} current density in *WT* and *Trpm7*$^{\alpha MHC/-}$ *-HB* myocytes

(A) I_{to} current density distribution in cardiomyocytes from *WT* left ventricle is best fit to a single gaussian distribution. (B) I_{to} current density distribution from *Trpm7*$^{\alpha MHC/-}$ *-HB* left ventricle is best fit to by two gaussian distributions suggesting the presence of a mosaic consisting of two populations of cells.



Supplemental Figure 6. Cardiac phenotypes depend on timing of *Trpm7* deletion during myocardial development

Videos

Movie 1. 2D transthoracic echocardiogram of *Trpm7* $^{\alpha MHC/-}$ mouse with heart block

Severely impaired left-ventricular (LV) systolic function; the left ventricle is dilated. The green tracing (below) shows the simultaneously recorded ECG demonstrating high-grade atrioventricular block. Yellow trace (below) shows respirophasic changes in respiratory impedance. Heart rate in green (right) reflects QRS complex per minute (BPM). Respiration rate (RR) is shown in yellow.

Movie 2. Severe biventricular dysfunction in cardiac-targeted *Trpm7* $^{\alpha MHC/-}$ mouse with heart block

Severe biventricular dilation and dysfunction in a *Trpm7* $^{\alpha MHC/-}$ *+HB* mouse. The simultaneously recorded ECG (green trace) shows high-grade atrioventricular block. Respirophasic changes (yellow trace) reports respiratory impedance. Heart rate in green (right) is calculated from the number of QRS complexes per minute (BPM). Respiration rate (RR) is shown in yellow.

Movie 3. 2D transthoracic echocardiogram of cardiac-targeted *Trpm7* $^{\alpha MHC/-}$ mouse without heart block

Normal LV size and function in *Trpm7* $^{\alpha MHC/-}$ *-HB* mice. The simultaneously recorded ECG (green trace) is a normal sinus rhythm. Respirophasic changes in respiratory impedance are in yellow. Heart rate in green (right) is calculated from the number of QRS complexes per minute (BPM). Respiration rate (RR) is shown in yellow.