Supplemental Materials

TWEAK-Fn14 activates myofibroblasts to drive progression of fibrotic disease of the kidney

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Supplemental Methods

Pericyte and myofibroblast isolation and culture

Myofibroblasts were purified from single cell suspensions from d21 post IRI mouse *Col1a1-GFP*^{Tg} kidneys by separation of GFP+, CD45-, EpCAM-, LTL- cells with fluorescence-activated cell sorting . Pericytes were isolated from wildtype or *CollGFP*^{Tg} mice by magnetic-activated cell sorting (MACS) column, selecting PDGFRβ+ cells as described [1]. Cell cultures were screened for the absence of epithelial, leukocyte, and endothelial markers as described [1]. Other mouse and human primary cell cultures were purified and characterized as reported [2, 3]. Purity of pericyte and myofibroblast populations in culture was ascertained by flow cytometry. Purified cells were >98% PDGFRβ+, CD45-, EpCAM-, CD31- by flow cytometry. Additional immunostaining for PDGFRβ confirmed >99% positivity. Cells were cultured on plastic coated with 0.2% gelatin from porcine skin (Sigma-Aldrich) and maintained in DMEM-F12 with 10% FBS, 1% Insulin-Transferrin-Seleniuum, and 1% Penicillin-Streptomycin (Life Technologies). All *in vitro* experiments were performed at or before passage 5.

In vitro experiments

<u>Migration assays:</u> For wound-healing assays, monolayers of confluent cells were scratched with a 20μL pipette tip. The monolayer "wounds" were visualized under phase contrast light microscopy at 24 h, and the area between wound edges was measured using ImageJ software, as described [4]. Recombinant soluble TWEAK (Genbank accession number AF030099) containing amino acid residues A106-H249) prepared by Biogen or vehicle was applied at 100ng/mL in the presence of an IκKβ inhibitor (ACHP) [5], a NIK small molecule inhibitor, [6], or a P42/44 ERK inhibitor (U0126). For transmigration assays, transwell filters with 8μm pores across a polycarbonate membrane were used (Corning). Cells were seeded at a density of 1000/well. Growth factors, cytokines, and inhibitors (TWEAK [1-100ng/]), PDGF-BB (Peprotech, 50ng/mL), TGFβ1 (Peprotech, [1-10ng/mL]), Ultrapure LPS (E. coli 0111:B4) (Invivogen [10ng/mL]) were added to the

bottom chamber of the transwell apparatus. At 16 or 24 h, cells were gently removed from the upper surface of the filter. The cells that had migrated to the underside were visualized with phase contrast microscopy and/or immunofluorescence.

Proliferation assay: Pericytes or myofibroblasts were seeded onto gelatin-coated glass 1.5-cm diameter cover slips (n=9 cover slips/group). BrdU (Sigma) (10 μM/mL) was applied to the medium and incubated for 3 hours. Cells were fixed in acid ethanol, washed, and incubated with 2M HCL, then 0.1M sodium borate, and then 0.2% Triton in 3% BSA. After additional washing, cells were incubated with an anti-BrdU FITC antibody (1:200; eBioscience) in 3% BSA and mounted with Vectashield and 4',6-diamidino-2-phenylindole (DAPI) (Vector Laboratories), and BrdU+ nuclei were quantified in 15 random fields per coverslip.

Stress Fiber assay: Cells were treated with TWEAK (100ng/mL) or TGFβ1 (10ng/mL) for 24h hours in serum free conditions, and treated with vehicle, anti-Fn14 antibodies (clone mP4a8), or IgG control (10 μg/mL). After staining with phalloidin (see below) to detect stress fibers, cells were counted in a blinded fashion for cells with stress fibers in random fields.

Cytokine stimulation assays: Subconfluent myofibroblasts were plated at P4 in 6 well-plates pre-coated with gelatin (Corning), washed X5, then cultured in medium without serum for 16h followed by treatment with vehicle, TWEAK (100 ng/mL), TGFβ1 (10 ng/mL), PDGF-BB (50 ng/mL), IL-1β (10 ng/mL), or LPS for 6 or 16 h, comparing the effect of TWEAK to other stimuli. Cells were harvested in RLT buffer and RNA prepared using the RNeasy Mini Kit (Qiagen).

Cytokine quantification: Briefly, cells were seeded 10^4 per well onto gelatin coated 6-well plates. After attachment, cells were washed X5 with PBS and cultured in medium without serum for 16h. Cells were then treated as indicated, and supernatants were collected at 24h. MCP-1 and IL-6 secretions were detected by ELISA (BioLegend), as recommended by the manufacturer. Other cytokines were detected by Luminex quantification using an xMap kit (Millipore).

Quantitative RT-PCR

Total RNA was extracted using RNeasy Mini Kit (Qiagen). cDNA was synthesized using iScript cDNA Synthesis Kit (Bio-Rad). Quantitative RT-PCR (qRT-PCR) assay was performed either using the ABI7900HT (Applied Biosystems) and iTaq SYBR Green Supermix with ROX (Bio-Rad) or using the QuantStudio™ 7 Flex Real-Time PCR System (Life Technologies) and TaqMan® Gene Expression Assays, as recommended by the manufacturer (Life Technologies). The specific primer pairs or Taqman probe sets are described (Table S3).

Western blotting

Cultured cells were lysed on ice with RIPA buffer containing leupeptin, pepstatin A, PMSF, and EDTA as described [4]. Whole kidneys were homogenized in ice-cold RIPA Buffer (Boston BioProducts), including 1 mM PMSF (Sigma-Aldrich) and 1X Halt™ Combined Protease and Phosphatase Inhibitor Cocktail (Thermo Scientific), using the Omni Bead Ruptor Homogenizer. All samples were centrifuged for 10 min at 14000 x g, and the supernatant was taken for protein determination. Cell or kidney extracts containing 15-50 μg of protein were prepared in 4X NuPAGE® LDS Sample Buffer (Life Technologies) and reduced with 10X NuPAGE® Sample Reducing Agent (Life Technologies), then subjected to SDS-PAGE. Proteins were transferred onto nitrocellulose paper, blocked in SuperBlock T20 (TBS) Blocking Buffer for 40 min (RT), then incubated O/N (4°C) with primary antibody in blocking buffer: Fn14 (1:500, Epitomics or Biolegend), α-SMA (1:500, Abcam), Laminin (1:1000, Abcam), Collagen VI (1:1000, Novus Biologicals), phospho-IRF-3 (Ser396), IRF-4, p44/42 MAPK (Erk1/2), phospho-p44/42 MAPK (Erk1/2) (Thr202/Tyr204), p38 MAPK, Phospho-p38 MAPK (Thr180/Tyr182), Akt (pan), Phospho-Akt (Ser473), Phospho-IκBα (Ser32/36), NF-κB p65, Phospho-NF-κB p65 (Ser536), NF-κB2 p100/p52, Phospho-NF-κB2 p100 (Ser866/870), and NIK (1:1000, Cell Signaling Technology). Following washing with Tris Buffered Saline with Tween 20 (Cell Signaling Technology), blots were detected with HRP-linked secondary antibodies (GE Healthcare Life Sciences, 1:1000-1:3000 in blocking buffer). SuperSignal West Dura Extended Duration Substrate (Thermo

Scientific) was used for visualization, and the luminescence was captured by the ChemiDoc MP Imaging System (Bio-Rad). Blots were stripped with Restore Western Blot Stripping Buffer (Life Technologies), and then re-incubated with either anti-Actin (C-11)-R (1:1000, Santa Cruz Biotechnology) or anti-GAPDH (1:1000, Life Technologies) as a loading control.

Immunofluorescence and histological quantification in tissue sections

Mouse and human tissues were prepared and stained as described [2]. Briefly, tissues were fixed in PLP solution for 2h and washed in 18% sucrose solution overnight prior to cryopreservation and cryosectioning (7µm). For fluorescence labeling, primary antibodies against the following proteins were used: Collagen VI (1:10, Novus Biologicals), CD45 (1:50, BioLegend), and CD31 (1:100, Abcam). Primary antibodies were detected with fluorescence-conjugated affinity purified secondary antibody labeling (1:200-1:800, Jackson ImmunoResearch). Anti-Fn14 antibodies (1:100, BioLegend) were pre-conjugated to Alexa Fluor® 647 using an Antibody Labeling Kit (Life Technologies), as recommended by the manufacturer. Anti-Fn14 and Alpha-Smooth Muscle Actin FITC (1:400, Sigma-Aldrich) or Alpha-Smooth Muscle Actin Cy3 (1:400, Sigma-Aldrich) conjugated antibodies were applied directly in 10% horse or mouse serum, respectively. In other experiments anti-CD34 (Q-bend) (1:400) or anti-CD45 antibodies (1:200) were applied. Sections were post-fixed with 1% paraformaldehyde and mounted with Prolong Gold with DAPI (Life Technologies). For F-actin visualization, treated cells were washed PBS then fixed with PLP solution. They were then washed a X3 and incubated at RT, 20 mins with Phalloidin-TRITC (100 nM, Sigma-Aldrich) and 1:2000 v/v Hoechst 33342 for nuclear counter-staining. Cells were then washed X3, dried, and mounted. Images were obtained with an A1 Nikon confocal microscope and a Zeiss LSM 710. Tubular injury was determined by a scoring method on blinded tissue sections as described [7]. Glomerulosclerosis was determined by blinded scoring of glomeruli (30 sequential glomeruli per kidney section) as described [2]. Live rat kidney slices were incubated with Alexa Fluor 488-conjugated isolectin B4 (IB4) (Invitrogen Ltd) to identify the vasa recta capillaries [8]. IB4 (50 μg/mL) was prepared in PSS bubbled with 95% O2/5% CO2; slices

were incubated with IB4 for 45 min, washed with PSS and subsequently fixed using 4% paraformaldehyde. Fixed kidney slices were then incubated for 16 h with the anti-Fn14 antibody and probed with an Alexa Fluor 555-conjugated donkey anti-rabbit secondary antibody (Invitrogen Ltd). Kidney slices were mounted using Citiflour (Agar Scientific Ltd, Stanstead, Essex, UK) and the medulla of fixed slices were imaged using a Zeiss LSM 510 laser scanning confocal microscope (Carl Zeiss Ltd). Alexa 488-conjugated was excited at 488 nm and Alexa Fluor 555-conjugated secondary antibody excited at 543 nm. Emitted light was collected with the following filters: long-pass 560 nm (Alexa Fluor 555) and band-pass 505–550 nm (FITC and IB4).

Kidney Functional Analysis

Urine albumin concentration was measured using Albuwell M kit (Exocell, Philadelphia). Urine creatinine was measured using Creatinine Liquid Reagents Assay (DIAZYME, San Diego). Urea and nitrogen levels in the serum were detected by BUN reagent set (Pointe Scientific).

Microarray Sample labeling, Hybridization and Scanning

Cultured myofibroblasts were treated in triplicate with vehicle, 100ng/mL TWEAK, 10ng/mL IL1b, 10ng/mL TGFb1, or 50ng/mL PDGFBB for 16h. RNA was isolated. Automated sample amplifications and biotin labelings were carried out using the NuGEN Ovation RNA Amplification system V2 (Cat # 3100), Ovation WB reagent (Cat # 1300) and Encore Biotin module (Cat # 4200) (NuGEN Technologies, Inc, San Carlos, CA) according to manufacturer's recommendations using an Arrayplex automated liquid handler (Beckman Coulter, Indianapolis, IN). Two μg of biotin labeled sscDNA probe were hybridized to Affymetrix GeneChip HT_MG-430_PM plate arrays with modified conditions as described in Allaire *et al*. Washing and staining of the hybridized arrays were completed as described in the GeneChip Expression analysis technical manual for HT plate arrays using the Genechip® Array Station (Affymetrix, Santa Clara, CA) with

modifications as described [9]. The processed GeneChip® plate arrays were scanned using GeneTitan scanner (Affymetrix, Santa Clara, CA).

Analysis of Affymetrix data

Affymetrix scans were subject to quality control (QC) measures. These tests included a visual inspection of the distribution of raw signal intensities and an assessment of RNA degradation, relative log expression (RLE), and normalized unscaled standard error (NUSE). All sample scans passed these QC metrics. CEL files were subjected to GC-content-based Robust Multi-array Average (GCRMA) normalization [10, 11]. Expression levels were log (base 2) transformed. All calculations and analyses were carried out using R and Bioconductor computational tools [12]. Analyses were applied to discover genes that were differentially expressed (DEGs) between cell types of interest. To identify differentially expressed genes between groups of samples, we applied the linear modeling approach (Bioconductor limma package) to fit gene expression levels ($\log_2$ transformed) according to the defined groups of samples and Bayesian posterior error analysis as implemented by Smyth [13]. Genes that exhibited a log-odds score (lods) greater than zero, absolute fold change greater than 1.5, and average normalized intensity greater than four were considered significantly different.

Statistics

All data are presented as mean ± SEM. Significance of difference between groups was evaluated by one-way ANOVA with Bonferroni post-hoc analysis and survival determined by the Mantel-Cox Test using GraphPad Prism (GraphPad Software). For *in situ* experiments, statistical significance was calculated using Student's t test. Values are expressed as mean ± SE. P values <0.05 considered to be significant.

Supplemental References

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FIGURE S1

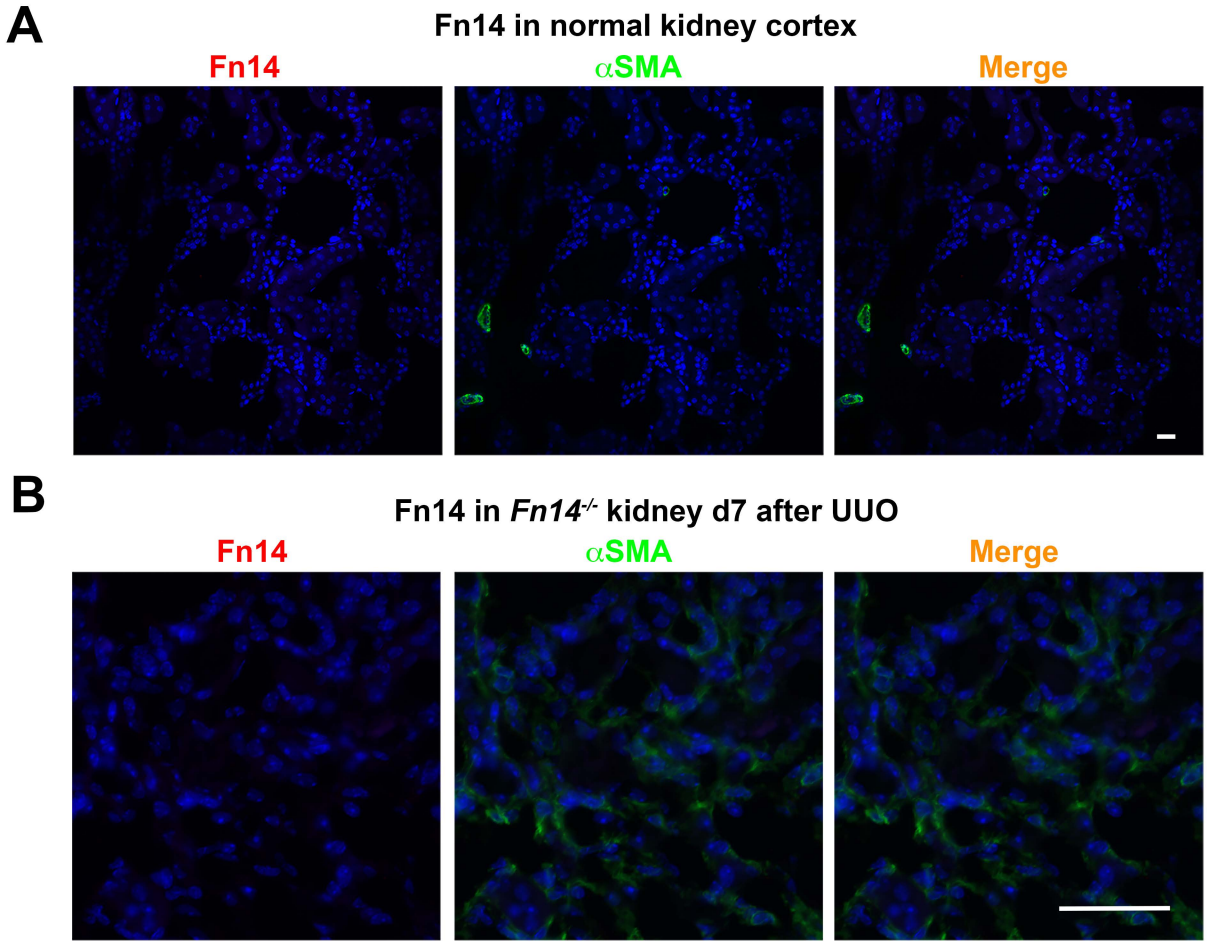

Fig. S1. Photomicrographs showing immuodetection of Fn14 healthy kidney and in UUO kidney in the Fn14-/- mouse. Lack of staining indicates specificity of antibody to detect Fn14.

FIGURE S2

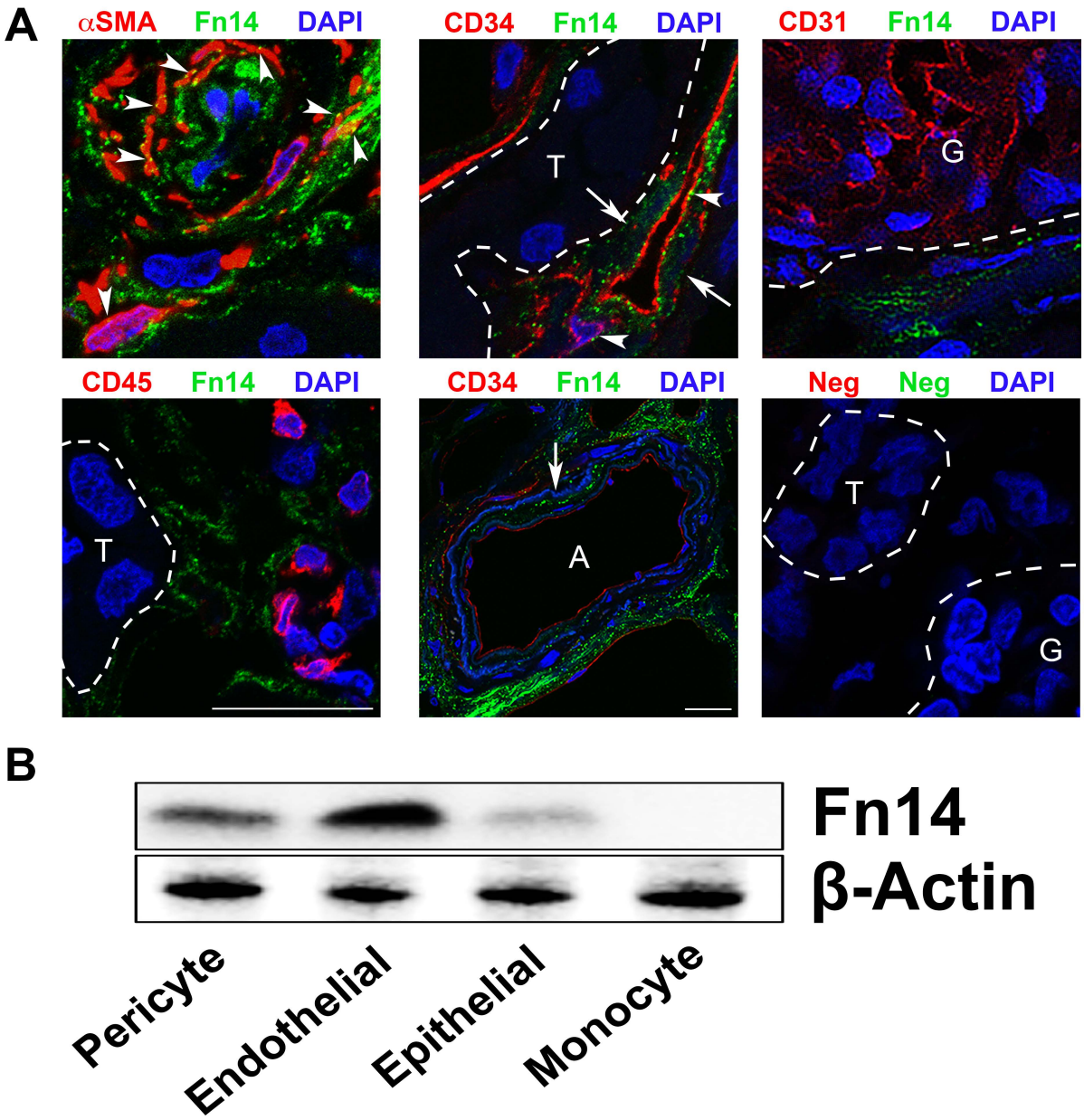

Fig S2. Detection of Fn14 in human kidney (A) Fluorescence images showing immunodetection of Fn14 in a patient with diabetic kidney disease. Note expression of Fn14 in the interstitium of the kidney (arrows, upper middle panel) but not the glomerulus (upper right panel). Note also co-expression with αSMA+ myofibroblasts (arrowheads, upper left panel), and CD34+ endothelium (arrowheads, upper middle panel) but not CD45+ leukocytes (lower left panel). Note expression of Fn14 in arterial adventitia (arrow, lower middle panel). (B) Western blots of protein lysates from primary human kidney cell cultures showing a single band detecting Fn14.

FIGURE S3

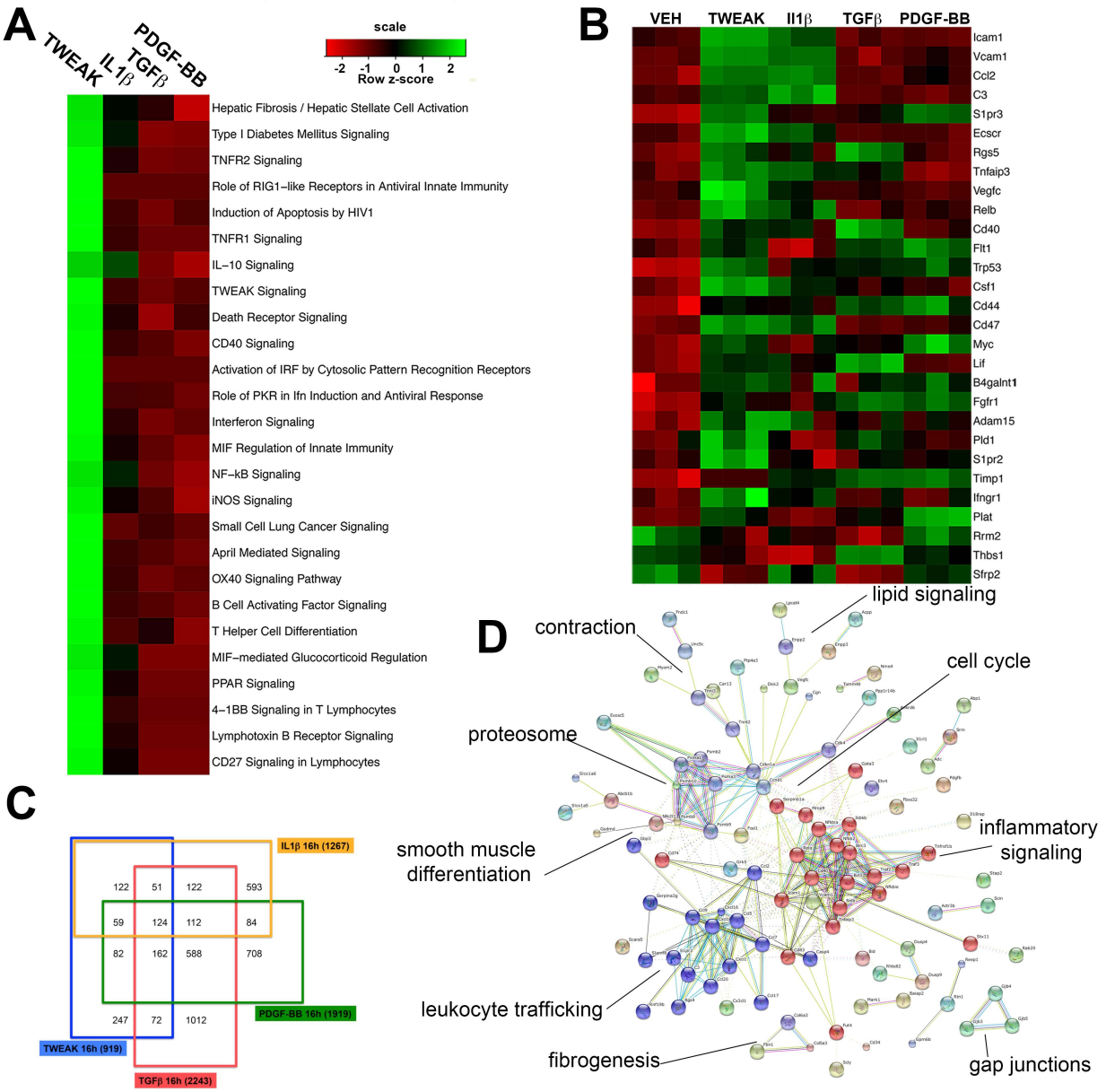

Fig. S3. Effect of TWEAK on myofibroblasts (A) Heatmap showing Ingenuity pathways enriched specifically in response to TWEAK treatment at 16h but not by treatment with other cytokines. (B) Heatmap showing the transcriptional intensity of individual genes involved in vascular pathways in response to cytokines at 16h. Each sample was performed in triplicate. (C) Venn diagram showing the total number (brackets) of genes regulated by each of the cytokines on primary myofibroblasts, and showing the overlap of these regulated genes. Note, TWEAK regulated genes overlap predominantly with each of the other cytokines, but that TGFβ regulates most genes in myofibroblasts. (D) String analysis showing known and predicted protein-protein interactions from the 200 most upregulated genes by TWEAK, showing different types of evidence denoted by the color of the connecting lines, where green = neighborhood, r ed = gene fusion, blue = co-occurrence, black = co-expression, purple = experiments, cyan = databases, yellow = text mining, and lilac = homology.

FIGURE S4

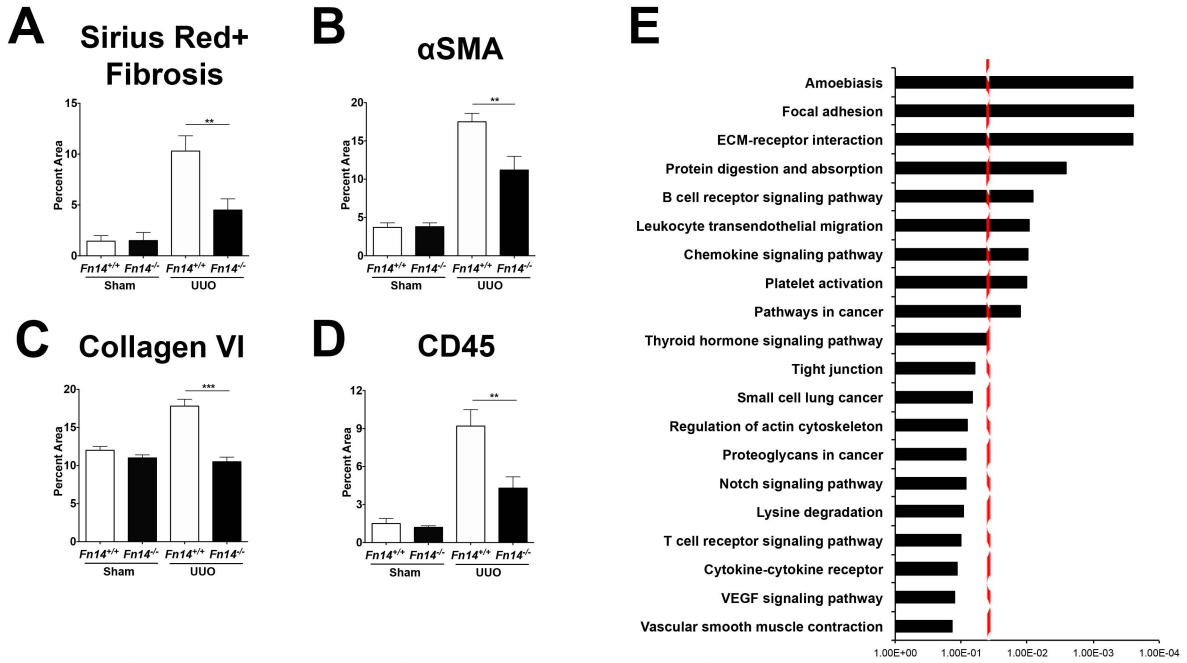

Fig. S4. Highlighted pathways inhibited by the absence of Fn14 in UUO kidney (A-D) Graphs quantifying fibrosis, αSMA+ myofibroblasts, Collagen type VI and CD45+ cells in the UUO disease and normal kidneys comparing Fn14+/+ to Fn14-/- (* $p < 0.05$, ** $p < 0.01$, n = 7/group) (E) Kegg pathways analysis of genes enriched in the UUO d10 diseased kidney from Fn14+/+ kidney compared to Fn14-/- kidney subjected to the same insult. X-axis shows significance on a Log scale and red line indicates significance after Boneferroni correction.

FIGURE S5

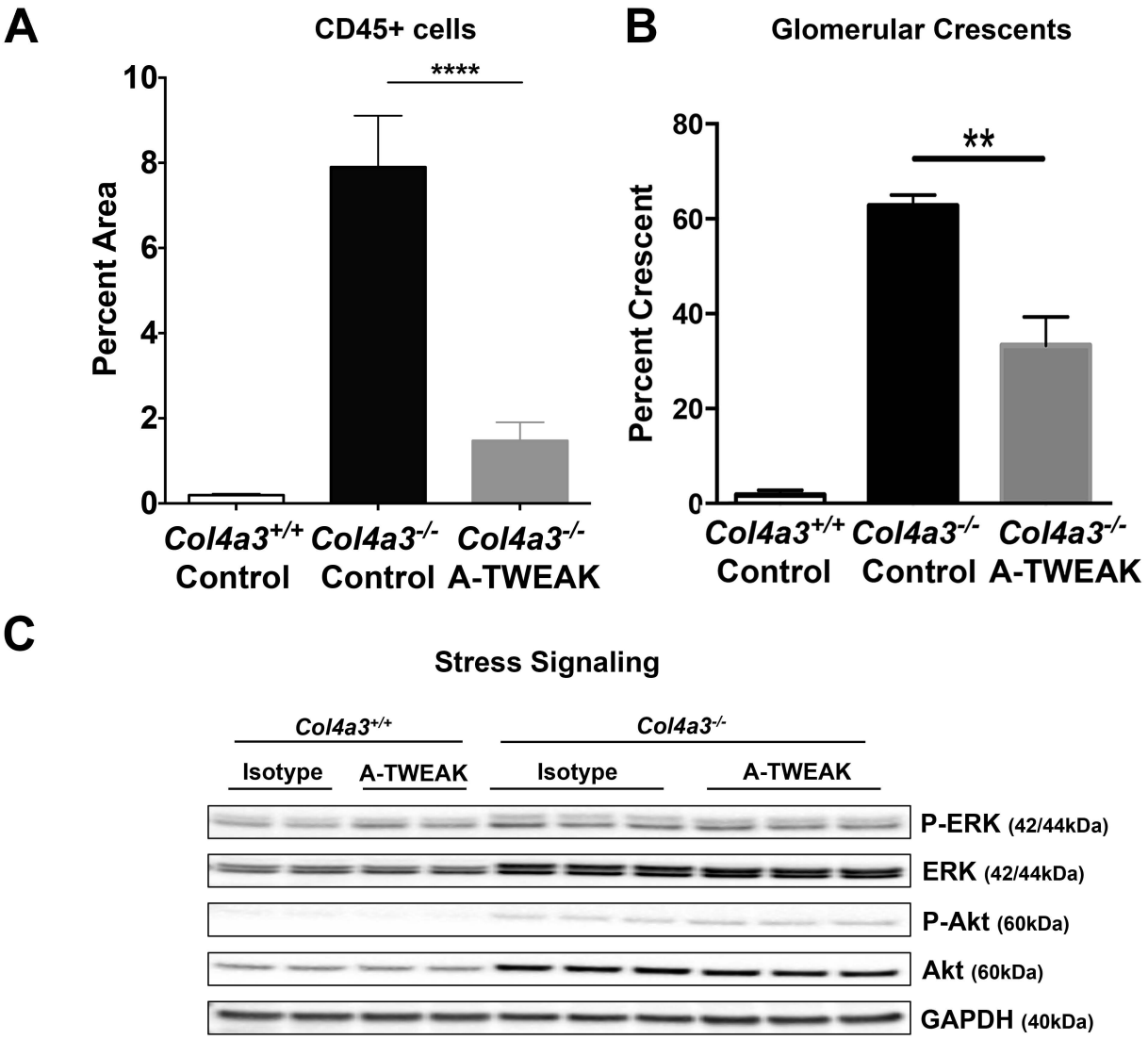

Fig. S5. Anti-TWEAK antibodies protect against kidney disease in mice with Alport nephropathy. (A-B) Graphs quantifying CD45+ cells and the proportion of glomeruli with cellular crescents (C) Representative blots from whole kidney showing the effect of anti-TWEAK antibodies on P-ERK and P-AKT levels at 8 weeks of age. (*$p < 0.05$, ** $p < 0.01$ n=8-14/group)

Table S1. Genes regulated by TWEAK in myofibroblasts

					x100ng_per_ml_TWEAK_16h-vs-Vehicle		
	Gene Title	Gene Symbol	Entrez Gene	AvgNormInt	Fold Change	p.value	lods
1425145_PM_at	interleukin 1 receptor-like 1	Il1rl1	17082	7.04461899	18.36777096	1.07358E-11	16.9936159
1418930_PM_at	chemokine (C-X-C motif) ligand 10	Cxcl10	15945	7.8074335	14.71959357	1.72869E-09	11.9044633
1424067_PM_at	intercellular adhesion molecule 1	Icam1	15894	7.02992121	13.25111054	1.18869E-13	21.41406
1417936_PM_at	chemokine (C-C motif) ligand 9	Ccl9	20308	7.25918006	11.88582545	4.86974E-08	8.52975259
1422317_PM_a_at	interleukin 1 receptor-like 1	Il1rl1	17082	10.091026	11.6242342	7.4003E-13	19.6323529
1444242_PM_at	Solute carrier organic anion transporter family, member 2a1	Slco2a1	24059	6.54887106	11.35897362	2.08315E-10	14.0330982
1421228_PM_at	chemokine (C-C motif) ligand 7	Ccl7	20306	10.3097116	9.303724074	4.22439E-11	15.6298857
1449195_PM_s_at	chemokine (C-X-C motif) ligand 16	Cxcl16	66102	8.05183008	9.206211196	5.31035E-12	17.691395
1415989_PM_at	vascular cell adhesion molecule 1	Vcam1	22329	8.55994758	8.56817546	4.26807E-10	13.3127966
1448162_PM_at	vascular cell adhesion molecule 1	Vcam1	22329	10.0924737	8.333160857	5.06843E-11	15.4480175
1451314_PM_a_at	vascular cell adhesion molecule 1	Vcam1	22329	6.83186776	8.18707264	6.36169E-11	15.2209515
1451204_PM_at	scavenger receptor class A, member 5 (putative)	Scara5	71145	4.93600374	7.5005273	7.13642E-07	5.81007539
1425681_PM_a_at	prion protein dublet	Prnd	26434	5.33413512	7.300039084	2.57945E-07	6.84090452
1418718_PM_at	chemokine (C-X-C motif) ligand 16	Cxcl16	66102	6.8740799	6.927590888	3.03967E-12	18.2428397
1457644_PM_s_at	chemokine (C-X-C motif) ligand 1	Cxcl1	14825	9.34764274	6.247252936	2.05563E-08	9.40291193
1420380_PM_at	chemokine (C-C motif) ligand 2	Ccl2	20296	12.1180912	6.001379442	1.06471E-10	14.7057668
1441855_PM_x_at	chemokine (C-X-C motif) ligand 1	Cxcl1	14825	8.65938949	5.652160737	1.71087E-08	9.58868561
1423954_PM_at	complement component 3	C3	12266	10.2667681	5.492313491	6.04396E-10	12.9629494
1425519_PM_a_at	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)	Cd74	16149	5.14374024	4.901163443	1.38435E-08	9.80294202
1438658_PM_a_at	sphingosine-1-phosphate receptor 3	S1pr3	13610	8.20940216	4.843976411	2.14046E-13	20.8432453
1439758_PM_at	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 12 (human)	Als2cr12	108812	5.09312767	4.647671141	3.54379E-05	1.86665795
1420914_PM_at	solute carrier organic anion transporter family, member 2a1	Slco2a1	24059	7.60210123	4.594897653	6.85192E-10	12.8367032
1449591_PM_at	caspase 4, apoptosis-related cysteine peptidase	Casp4	12363	7.5723068	4.558973484	2.34342E-08	9.27029583
1434470_PM_at	synaptotagmin XIII	Syt13	80976	6.4913133	4.498473847	2.51684E-08	9.19803235
1437173_PM_at	sphingosine-1-phosphate receptor 3	S1pr3	13610	7.50449303	4.437232979	3.6559E-10	13.4683853
1428834_PM_at	dual specificity phosphatase 4	Dusp4	319520	9.84819416	4.386818094	2.40044E-08	9.24596248
1450414_PM_at	platelet derived growth factor, B polypeptide	Pdgfb	18591	8.5043098	4.241440709	2.11172E-07	7.04360973
1422029_PM_at	chemokine (C-C motif) ligand 20	Ccl20	20297	4.62632721	4.088542327	2.63923E-05	2.16298693
1420913_PM_at	solute carrier organic anion transporter family, member 2a1	Slco2a1	24059	9.07839557	4.065424058	4.07423E-11	15.6660087
1419209_PM_at	chemokine (C-X-C motif) ligand 1	Cxcl1	14825	8.35799643	4.064990853	1.18157E-06	5.29954044
1421392_PM_a_at	baculoviral IAP repeat-containing 3	Birc3	11796	8.63168268	4.046544379	7.01154E-11	15.1237204
1436365_PM_at	zinc finger and BTB domain containing 7C	Zbtb7c	207259	6.66539413	3.97247569	7.96517E-11	14.9961915
1442819_PM_at	rhomboid, veinlet-like 2 (Drosophila)	Rhbdl2	230726	6.23909443	3.924758594	1.23263E-08	9.92036412
1450413_PM_at	platelet derived growth factor, B polypeptide	Pdgfb	18591	6.25695126	3.922055636	5.04345E-07	6.16164734
1424923_PM_at	serine (or cysteine) peptidase inhibitor, clade A, member 3G	Serpina3g	20715	10.7947791	3.856044328	3.94575E-10	13.3917176
1423947_PM_at	RIKEN cDNA 1110008P14 gene	1110008P14Rik	73737	5.33351046	3.83383379	3.68111E-07	6.48061206
1429946_PM_at	coiled-coil domain containing 141	Ccdc141	545428	4.31440646	3.792325489	5.94079E-06	3.66634778
1458299_PM_s_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	Nfkbie	18037	9.49981694	3.784579354	8.1896E-10	12.6572012
1423232_PM_at	ets variant gene 4 (E1A enhancer binding protein, E1AF)	Etv4	18612	5.86116056	3.768986356	1.17823E-07	7.63476035
1431843_PM_a_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	Nfkbie	18037	9.25787994	3.743400622	6.9049E-09	10.5063033
1434716_PM_at	hepatitis A virus cellular receptor 1	Havcr1	171283	8.57130949	3.736105598	2.16514E-06	4.68664761
1417520_PM_at	nuclear factor, erythroid derived 2, like 3	Nfe2l3	18025	4.89134997	3.72694617	3.6206E-06	4.16670552
1450276_PM_a_at	scinderin	Scin	20259	8.86252522	3.690575933	6.74448E-11	15.162544
1450364_PM_a_at	hepatitis A virus cellular receptor 1	Havcr1	171283	6.74286881	3.62178603	7.22732E-07	5.79725816
1447564_PM_x_at	piwi-like homolog 4 (Drosophila)	Piwil4	330890	6.10375737	3.555355562	4.88914E-08	8.52572731
1437451_PM_at	endothelial cell-specific chemotaxis regulator	Ecscr	68545	7.70575098	3.540056075	2.10454E-09	11.7060481
1424758_PM_s_at	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 10	Serpina10	217847	5.7868216	3.434196044	2.29059E-05	2.30554765
1441975_PM_at	acid phosphatase, prostate	Acpp	56318	5.00046181	3.402573953	3.43333E-06	4.22039558
1425902_PM_a_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2, p49/p100	Nfkb2	18034	8.34889071	3.389065809	1.03151E-10	14.7374802
1460125_PM_at	coiled-coil domain containing 141	Ccdc141	545428	9.78709585	3.352761544	2.198E-09	11.6622184
1457681_PM_at	coiled-coil domain containing 141	Ccdc141	545428	5.89088142	3.349714713	1.01517E-09	12.4409218
1448306_PM_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	Nfkbia	18035	9.96298682	3.319379603	1.32107E-07	7.51883325
1415803_PM_at	chemokine (C-X3-C motif) ligand 1	Cx3cl1	20312	9.12844285	3.23785601	1.13485E-09	12.3286557
1437967_PM_at	coiled-coil domain containing 141	Ccdc141	545428	4.38210629	3.208933779	1.01179E-06	5.45658395
1452889_PM_at	phospholysine phosphohistidine inorganic pyrophosphate phosphatase	Lhpp	76429	4.79439772	3.156210869	1.51272E-05	2.72338996
1454659_PM_at	dCMP deaminase	Dctd	320685	7.632567	3.127530388	5.48885E-14	22.1604478
1447251_PM_x_at	coiled-coil domain containing 141	Ccdc141	545428	5.66001788	3.108346849	4.68056E-09	10.899172
1422962_PM_a_at	proteasome (prosome, macropain) subunit, beta type 8 (large multifunctional peptidase 7)	Psmb8	16913	6.56408557	3.025574735	3.28285E-10	13.576513
1449514_PM_at	G protein-coupled receptor kinase 5	Grk5	14773	6.79629555	2.983398315	3.89563E-10	13.4045627
1418133_PM_at	B-cell leukemia/lymphoma 3	Bcl3	12051	6.72195808	2.977582795	5.33205E-07	6.10528511
1455197_PM_at	Rho family GTPase 1	Rnd1	223881	7.91273346	2.956397788	7.4328E-09	10.4318382
1417466_PM_at	regulator of G-protein signaling 5	Rgs5	19737	7.88379111	2.932863317	3.05619E-07	6.66908876
1449586_PM_at	plakophilin 1	Pkp1	18772	8.2091347	2.922682815	1.05688E-05	3.08491881
1436094_PM_at	VGF nerve growth factor inducible	Vgf	381677	6.9659039	2.854294674	2.22142E-05	2.33640965
1429012_PM_at	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	Arhgef6	73341	4.80259533	2.836940772	5.90879E-06	3.67180246
1434777_PM_at	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)	Mycl1	16918	8.19323272	2.819437575	5.67898E-08	8.37405839
1444086_PM_at	NCK-associated protein 5	Nckap5	210356	5.82959592	2.812501135	1.95495E-08	9.45373331
1453102_PM_at	fibronectin leucine rich transmembrane protein 3	Flrt3	71436	7.79910813	2.807247169	8.54136E-08	7.96063996
1422758_PM_at	carbohydrate sulfotransferase 2	Chst2	54371	7.81264195	2.786361693	6.21764E-08	8.28227713
1424148_PM_a_at	signal transducing adaptor family member 2	Stap2	106766	5.31579484	2.771822928	3.18787E-07	6.6263532
1419413_PM_at	chemokine (C-C motif) ligand 17	Ccl17	20295	10.008768	2.763396611	2.48349E-05	2.22417909
1417928_PM_at	PDZ and LIM domain 4	Pdlim4	30794	9.11215037	2.761295936	4.82439E-09	10.8685974
1417419_PM_at	cyclin D1	Ccnd1	12443	6.78567677	2.691251806	2.21356E-08	9.32799705
1447250_PM_a_at	coiled-coil domain containing 141	Ccdc141	545428	7.219139	2.688092819	1.39841E-07	7.46119017
1453321_PM_at	fibronectin type III domain containing 1	Fndc1	68655	6.25557401	2.682473438	7.68894E-07	5.73455792
1433699_PM_at	tumor necrosis factor, alpha-induced protein 3	Tnfaip3	21929	9.8091735	2.654670941	1.43771E-08	9.76467923
1416286_PM_at	regulator of G-protein signaling 4	Rgs4	19736	9.39529277	2.650959981	3.27824E-07	6.5980339
1423091_PM_a_at	glycoprotein m6b	Gpm6b	14758	8.23515936	2.632679986	1.61908E-08	9.64447837
1448698_PM_at	cyclin D1	Ccnd1	12443	11.3935588	2.621045861	3.71127E-10	13.4532796
1439766_PM_x_at	vascular endothelial growth factor C	Vegfc	22341	8.32200884	2.620234592	6.85377E-07	5.85100268
1417420_PM_at	cyclin D1	Ccnd1	12443	8.69701184	2.614419712	4.42364E-07	6.2944731
1422179_PM_at	gap junction protein, beta 4	Gjb4	14621	7.07339554	2.61198263	3.51622E-08	8.85951573
1420512_PM_at	dickkopf homolog 2 (Xenopus laevis)	Dkk2	56811	4.75724402	2.607436182	1.07086E-07	7.73156403
1449204_PM_at	gap junction protein, beta 5	Gjb5	14622	6.41112911	2.602596103	4.52105E-12	17.8505936
1438157_PM_s_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	Nfkbia	18035	10.8157331	2.601230342	9.28468E-08	7.87610777
1418296_PM_at	FXYD domain-containing ion transport regulator 5	Fxyd5	18301	8.03952031	2.593038568	4.81069E-06	3.87949051
1416287_PM_at	regulator of G-protein signaling 4	Rgs4	19736	8.01257163	2.570036865	9.24518E-06	3.21989943
1421923_PM_at	SH3-domain binding protein 5 (BTK-associated)	Sh3bp5	24056	6.67201406	2.564049336	9.34135E-07	5.53743894
1450085_PM_at	angiopoietin-like 2	Angptl2	26360	5.52672502	2.54843839	9.09107E-07	5.56493732
1436672_PM_at	G protein-coupled receptor kinase 5	Grk5	14773	7.2119909	2.517280365	1.42868E-11	16.7097583
1418099_PM_at	tumor necrosis factor receptor superfamily, member 1b	Tnfrsf1b	21938	7.53432499	2.517237551	3.60505E-07	6.50176318
1440739_PM_at	vascular endothelial growth factor C	Vegfc	22341	4.73817004	2.516454812	3.04743E-07	6.67199807

1424131_PM_at	collagen, type VI, alpha 3	Col6a3	12835	7.47183885	2.502791566	2.80496E-05	2.10172528
1420088_PM_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	Nfkbia	18035	11.923042	2.499456418	1.33479E-09	12.165144
1449508_PM_at	interleukin 27 receptor, alpha	Il27ra	50931	5.2611804	2.494440284	4.6276E-06	3.91869542
1438097_PM_at	RAB20, member RAS oncogene family	Rab20	19332	5.84044766	2.48502949	1.2376E-06	5.2526406
1429310_PM_at	fibronectin leucine rich transmembrane protein 3	Flrt3	71436	5.73078097	2.477011189	1.37805E-05	2.81736274
1447707_PM_s_at	phosphodiesterase 2A, cGMP-stimulated	Pde2a	207728	6.26284522	2.474974242	1.42249E-06	5.1117106
1425025_PM_at	transmembrane protein 106A	Tmem106a	217203	5.05770235	2.469229971	6.36282E-07	5.9262797
1419417_PM_at	vascular endothelial growth factor C	Vegfc	22341	7.89106106	2.465209269	1.75065E-06	4.90164222
1435265_PM_at	---	---	---	9.96247894	2.455264952	1.07495E-08	10.0587937
1438699_PM_at	steroid 5 alpha-reductase 1	Srd5a1	78925	7.82562373	2.454744636	6.01425E-05	1.33562921
1437820_PM_at	forkhead box S1	Foxs1	14239	8.25448105	2.447073601	2.51595E-09	11.5259057
1440207_PM_at	lysophosphatidylcholine acyltransferase 4	Lpcat4	99010	6.15563642	2.444494894	9.81001E-10	12.4754072
1417856_PM_at	avian reticuloendotheliosis viral (v-rel) oncogene related B	Relb	19698	6.76770891	2.436965558	3.58873E-07	6.50635949
1450696_PM_at	proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2)	Psmb9	16912	4.90861931	2.422990903	2.5769E-07	6.84190918
1457780_PM_at	syntaxin 11	Stx11	74732	8.44852754	2.421248433	4.81626E-08	8.54093779
1435605_PM_at	ARP3 actin-related protein 3 homolog B (yeast)	Actr3b	242894	5.07121605	2.414228934	1.25991E-05	2.90771647
1448632_PM_at	proteasome (prosome, macropain) subunit, beta type 10	Psmb10	19171	10.00892	2.396855559	2.21261E-10	13.9726069
1425223_PM_at	baculoviral IAP repeat-containing 3	Birc3	11796	5.14221609	2.387376879	1.9432E-05	2.47112873
1453556_PM_x_at	CD99 antigen	Cd99	673094	6.6844775	2.385144242	2.14298E-05	2.37259906
1419703_PM_at	collagen, type V, alpha 3	Col5a3	53867	8.07906089	2.352671587	1.23175E-05	2.93051107
1436716_PM_at	Protein phosphatase 1, regulatory (inhibitor) subunit 14B	Ppp1r14b	18938	9.79412374	2.349648689	0.000164593	0.32836253
1449203_PM_at	solute carrier organic anion transporter family, member 1a5	Slco1a5	108096	7.83098818	2.337640833	1.25646E-07	7.5696348
1460570_PM_at	piggyBac transposable element derived 5	Pgbd5	209966	5.46936094	2.334937545	0.000125488	0.59926112
1426118_PM_a_at	translocase of outer mitochondrial membrane 40 homolog (yeast)	Tomm40	53333	6.95866232	2.32009714	2.2608E-06	4.64291034
1416002_PM_x_at	coactosin-like 1 (Dictyostelium)	Cotl1	72042	7.91253489	2.319678841	4.07366E-05	1.72665559
1436237_PM_at	tetratricopeptide repeat domain 9	Ttc9	69480	9.77001705	2.293770247	3.10735E-08	8.98467145
1421308_PM_at	carbonic anhydrase 13	Car13	71934	5.04529989	2.288490413	0.000137313	0.50928699
1418872_PM_at	ATP-binding cassette, sub-family B (MDR/TAP), member 1B	Abcb1b	18669	7.12567965	2.286325561	2.09646E-09	11.7099299
1442093_PM_at	arginine decarboxylase	Adc	242669	4.07365329	2.266647195	2.22515E-06	4.6589895
1418186_PM_at	glutathione S-transferase, theta 1	Gstt1	14871	8.73140731	2.247649415	2.30846E-07	6.95336176
1432478_PM_a_at	ring finger protein 19B	Rnf19b	75234	7.78436964	2.242153842	1.71975E-06	4.91965955
1417167_PM_at	exosome component 5	Exosc5	27998	6.97540212	2.236099375	1.20949E-07	7.60823691
1453228_PM_at	syntaxin 11	Stx11	74732	8.39032492	2.233013282	6.31657E-06	3.60440783
1426734_PM_at	family with sequence similarity 43, member A	Fam43a	224093	4.86825858	2.232441876	1.62701E-05	2.65000614
1455843_PM_at	fucosyltransferase 4	Fut4	14345	6.34919888	2.210230518	1.96669E-06	4.783903
1423891_PM_at	glutathione S-transferase, theta 3	Gstt3	103140	4.38227937	2.207696455	4.29194E-05	1.67423183
1425296_PM_a_at	regulator of G-protein signaling 3	Rgs3	50780	7.54811184	2.202792161	5.64488E-08	8.38015989
1416845_PM_at	transmembrane protein 132A	Tmem132a	98170	9.36923484	2.200187383	5.08504E-08	8.48593957
1434786_PM_at	protein phosphatase 1, regulatory (inhibitor) subunit 12B	Ppp1r12b	329251	8.56453253	2.198271384	9.81482E-08	7.81985645
1440618_PM_at	rhomboid, veinlet-like 2 (Drosophila)	Rhbdl2	230726	4.11393391	2.196298629	0.00017576	0.26286973
1451293_PM_at	RRP9, small subunit (SSU) processome component, homolog (yeast)	Rrp9	27966	6.09996576	2.195823898	4.48891E-07	6.27963597
1422528_PM_a_at	zinc finger protein 36, C3H type-like 1	Zfp36l1	12192	6.15659594	2.194952509	2.51247E-06	4.5361521
1448886_PM_at	GATA binding protein 3	Gata3	14462	5.54003991	2.170427167	1.29266E-05	2.88184541
1435226_PM_at	ring finger protein 19B	Rnf19b	75234	8.06402972	2.167233759	2.02735E-07	7.08491704
1455881_PM_at	immediate early response 5-like	Ier5l	72500	6.0769704	2.166655408	8.95103E-05	0.93719667
1434153_PM_at	src homology 2 domain-containing transforming protein B	Shb	230126	6.48291815	2.160253602	7.92804E-09	10.3666339
1416798_PM_a_at	non-metastatic cells 4, protein expressed in	Nme4	56520	7.7098959	2.157642265	5.86635E-07	6.00855834
1448747_PM_at	F-box protein 32	Fbxo32	67731	9.84234372	2.154916752	1.03036E-07	7.7706177
1416318_PM_at	serine (or cysteine) peptidase inhibitor, clade B, member 1a	Serpinb1a	66222	5.71472787	2.154798148	1.24852E-05	2.91687427
1418746_PM_at	paroxysmal nonkinesiogenic dyskinesia	Pnkd	56695	6.47370617	2.153565474	0.000112046	0.71252264
1433509_PM_s_at	receptor accessory protein 1	Reep1	52250	4.8614213	2.151676358	0.000174552	0.26975175
1425656_PM_a_at	brain-specific angiogenesis inhibitor 1-associated protein 2	Baiap2	108100	5.70896011	2.143798263	7.03208E-06	3.49605992
1448560_PM_at	BH3 interacting domain death agonist	Bid	12122	6.00924593	2.143546169	8.04213E-07	5.68907939
1448550_PM_at	lipopolysaccharide binding protein	Lbp	16803	8.25945269	2.140048197	2.21188E-08	9.32876746
1448618_PM_at	major vault protein	Mvp	78388	8.93863769	2.13447694	1.92203E-08	9.47091813
1421307_PM_at	carbonic anhydrase 13	Car13	71934	8.09231442	2.133090981	3.93407E-06	4.08277667
1417110_PM_at	mannosidase 1, alpha	Man1a	17155	5.95729512	2.130184155	1.39785E-09	12.1186192
1416715_PM_at	gap junction protein, beta 3	Gjb3	14620	8.37554224	2.121363342	1.28387E-05	2.88872615
1418181_PM_at	protein tyrosine phosphatase 4a3	Ptp4a3	19245	7.89880844	2.119249687	7.68611E-05	1.08977031
1419496_PM_at	solute carrier organic anion transporter family, member 1a6	Slco1a6	28254	4.76841696	2.11315221	1.44124E-05	2.77217159
1449473_PM_s_at	CD40 antigen	Cd40	21939	6.41033409	2.107364528	9.63866E-06	3.17784812
1421260_PM_a_at	spermidine synthase	Srm	20810	10.0720573	2.105929228	5.96751E-09	10.6537527
1451261_PM_s_at	signal transducing adaptor family member 2	Stap2	106766	6.80620529	2.09576511	4.58456E-08	8.59086728
1416503_PM_at	latexin	Lxn	17035	11.8056531	2.093555771	7.22128E-11	15.0942482
1456605_PM_at	CCAAT/enhancer binding protein (C/EBP), delta	Cebpd	12609	6.63312951	2.091074469	7.95274E-05	1.05561019
1428767_PM_at	gasdermin D	Gsdmd	69146	7.22064503	2.087323524	7.48634E-08	8.09419046
1417785_PM_at	phospholipase A1 member A	Pla1a	85031	6.13734558	2.082384786	2.75588E-07	6.77387791
1417671_PM_at	selenocysteine lyase	Scly	50880	6.23124708	2.078117408	4.67084E-08	8.57198483
1438452_PM_at	nebulette	Nebl	74103	6.92304257	2.075515211	7.23328E-05	1.15061073
1441894_PM_s_at	GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein	Grasp	56149	8.51970252	2.072696733	7.25796E-08	8.12557359
1419592_PM_at	unc-5 homolog C (C. elegans)	Unc5c	22253	5.19371789	2.072558373	0.000101275	0.81361172
1429154_PM_at	similar to Solute carrier family 35, member F2 /// solute carrier family 35, member F2	LOC100048307 100048307 /		5.37490242	2.065199589	6.7233E-06	3.54139609
1417522_PM_at	F-box protein 32	Fbxo32	67731	8.82689487	2.063791208	3.34423E-08	8.91029179
1449522_PM_at	unc-5 homolog C (C. elegans)	Unc5c	22253	7.45772538	2.063487297	1.31444E-06	5.19167345
1423358_PM_at	endothelin converting enzyme 2	Ece2	107522	8.03489257	2.061990753	6.22112E-05	1.30171559
1420089_PM_at	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	Nfkbia	18035	12.4874332	2.060220971	5.00043E-08	8.50293298
1424312_PM_at	adiponectin receptor 1	Adipor1	72674	6.9261804	2.059354425	8.87598E-05	0.94562599
1415804_PM_at	chemokine (C-X3-C motif) ligand 1	Cx3cl1	20312	5.79072032	2.046615663	2.13653E-05	2.37563259
1436002_PM_at	signal peptide, CUB domain, EGF-like 3	Scube3	268935	9.23280139	2.045504842	8.81003E-05	0.95309289
1448472_PM_at	valyl-tRNA synthetase	Vars	22321	6.5783151	2.041693834	6.57884E-06	3.56332842
1451564_PM_at	poly (ADP-ribose) polymerase family, member 14	Parp14	547253	7.46787019	2.038047741	1.82573E-09	11.8493865
1449226_PM_at	hypermethylated in cancer 1	Hic1	15248	6.83362155	2.036355742	3.71269E-05	1.81987052
1441931_PM_x_at	glutathione synthetase	Gss	14854	6.63087491	2.031193125	0.000107717	0.7519303
1419477_PM_at	C-type lectin domain family 2, member d	Clec2d	93694	9.79461545	2.031175554	2.32057E-06	4.6165165
1425545_PM_x_at	histocompatibility 2, D region locus 1	H2-D1	14964	9.88668952	2.015681582	2.07546E-07	7.06115784
1451756_PM_at	FMS-like tyrosine kinase 1	Flt1	14254	7.95607649	2.006636591	7.61914E-05	1.09853852
1427348_PM_at	zinc finger CCCH type containing 12A	Zc3h12a	230738	6.96207657	2.003394299	0.000210309	0.08395913
1456586_PM_x_at	major vault protein	Mvp	78388	7.63256918	2.002298503	1.02121E-08	10.1106598
1426538_PM_a_at	transformation related protein 53	Trp53	22059	9.29492091	2.002224379	3.00885E-09	11.345347
1449731_PM_s_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	Nfkbia	18035	11.7624646	1.995242368	7.33915E-08	8.11430443
1435460_PM_at	protein kinase, cGMP-dependent, type II	Prkg2	19092	9.57490507	1.991589554	7.85082E-05	1.0685298
1425336_PM_x_at	histocompatibility 2, K1, K region	H2-K1	14972	9.24545838	1.991346713	7.45095E-07	5.76639827
1456874_PM_at	fibronectin leucine rich transmembrane protein 2	Flrt2	399558	8.5820009	1.988993651	0.000116561	0.67302207
1428384_PM_at	DNA segment, Chr 4, Brigham & Women's Genetics 0951 expressed	D4Bwg0951e	52829	10.483669	1.986408581	1.53788E-08	9.69653962
1451784_PM_x_at	histocompatibility 2, D region locus 1	H2-D1	14964	9.25089461	1.983605232	2.48631E-07	6.87816762
1424587_PM_at	gem (nuclear organelle) associated protein 8	Gemin8	237221	6.28469861	1.978093041	1.14377E-06	5.33245822
1419080_PM_at	glial cell line derived neurotrophic factor	Gdnf	14573	7.22739736	1.967368897	9.02448E-06	3.24427813

1452178_PM_at	poly (ADP-ribose) polymerase family, member 10 /// plectin	Parp10 /// Plec	18810 /// 67	7.29263199	1.96050693	1.18661E-08	9.95884481
1428705_PM_at	RIKEN cDNA 1700007K13 gene	1700007K13Rik	69327	6.42099079	1.954273963	1.52305E-05	2.71653633
1460742_PM_at	asparagine-linked glycosylation 3 homolog (yeast, alpha-1,3-mannosyltransferase)	Alg3	208624	7.73033525	1.951827532	6.10437E-06	3.63891599
1421266_PM_s_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta	Nfkbib	18036	7.1681669	1.949601362	5.77163E-06	3.6955239
1423557_PM_at	interferon gamma receptor 2	Ifngr2	15980	9.83503584	1.948973815	2.46824E-10	13.8628867
1448742_PM_at	snail homolog 1 (Drosophila)	Snai1	20613	5.92787963	1.947324184	0.000211767	0.0770748
1452599_PM_s_at	expressed sequence AI413582	AI413582	106672	6.09126115	1.945794103	3.99729E-05	1.74566645
1447181_PM_s_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	Slc7a7	20540	6.01813035	1.943768777	0.000129736	0.56599239
1431035_PM_at	dishevelled associated activator of morphogenesis 1	Daam1	208846	6.0882745	1.941688597	2.15105E-06	4.69325041
1444062_PM_at	RIKEN cDNA 2900056L01 gene	2900056L01Rik	73050	7.54733236	1.939935228	4.54401E-06	3.93711613
1418869_PM_a_at	pseudouridine synthase 1	Pus1	56361	7.76969188	1.939004416	3.91148E-08	8.75165027
1435066_PM_at	phosphatidylinositol transfer protein, cytoplasmic 1	Pitpnc1	71795	7.77565019	1.934458555	2.8356E-05	2.09080031
1421296_PM_at	tumor necrosis factor receptor superfamily, member 10b	Tnfrsf10b	21933	7.96358294	1.933648609	4.55701E-05	1.61405451
1436562_PM_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	Ddx58	230073	7.25005512	1.931061073	1.89733E-10	14.1268205
1436304_PM_at	transmembrane protein 200A	Tmem200a	77220	6.38600447	1.927118762	0.000130698	0.55860916
1437828_PM_s_at	WD repeat domain 46	Wdr46	57315	7.7294648	1.924308771	7.86295E-06	3.38332358
1449390_PM_at	G patch domain containing 4	Gpatch4	66614	8.46853559	1.918182187	4.39266E-08	8.63416848
1440489_PM_at	zinc finger and BTB domain containing 46	Zbtb46	72147	5.87442246	1.913800857	0.000110201	0.72912884
1426834_PM_s_at	RIKEN cDNA D930015E06 gene	D930015E06Rik	229473	6.76107626	1.91276816	7.31898E-06	3.45569023
1448914_PM_a_at	colony stimulating factor 1 (macrophage)	Csf1	12977	8.51670978	1.912127046	3.51186E-08	8.86077387
1437373_PM_at	apoptosis enhancing nuclease	Aen	68048	8.25966987	1.911736991	1.94658E-11	16.4021088
1452483_PM_a_at	CD44 antigen	Cd44	12505	9.87528041	1.907436088	1.44562E-05	2.76911686
1451931_PM_x_at	histocompatibility 2, D region	H2-L	14980	9.00992459	1.907256821	1.82934E-07	7.18904206
1448950_PM_at	interleukin 1 receptor, type I	Il1r1	16177	10.2823378	1.89878755	4.68086E-05	1.5871337
1450506_PM_a_at	apoptosis enhancing nuclease	Aen	68048	8.83042359	1.898535084	1.42663E-08	9.77250863
1416012_PM_at	EH-domain containing 1	Ehd1	13660	5.90826499	1.897575714	8.58251E-05	0.97928868
1425801_PM_x_at	coactosin-like 1 (Dictyostelium)	Cotl1	72042	8.10027311	1.89491627	4.5945E-05	1.60582881
1447946_PM_at	a disintegrin and metallopeptidase domain 23	Adam23	23792	7.43305302	1.893863994	7.18244E-07	5.80356659
1431920_PM_a_at	interleukin 34	Il34	76527	4.93932854	1.890756271	5.87196E-07	6.00759072
1427103_PM_at	pleckstrin homology domain containing, family O member 2	Plekho2	102595	6.84857508	1.890511613	1.38896E-08	9.79957912
1451186_PM_at	apoptosis enhancing nuclease	Aen	68048	6.67897675	1.888605391	2.32017E-05	2.29263422
1443007_PM_at	---	---	---	5.56532276	1.887565756	8.80732E-06	3.26885668
1423233_PM_at	CCAAT/enhancer binding protein (C/EBP), delta	Cebpd	12609	8.05578223	1.886263909	0.000168471	0.30512369
1456475_PM_s_at	protein kinase, cAMP dependent regulatory, type II beta	Prkar2b	19088	9.76560341	1.88215556	5.06729E-05	1.50751037
1453598_PM_at	RIKEN cDNA 3110082D06 gene	3110082D06Rik	627626	6.47177225	1.878551821	6.24116E-05	1.29849118
1428635_PM_at	catechol-O-methyltransferase domain containing 1	Comtd1	69156	7.50683105	1.87854183	8.11905E-06	3.35097377
1417726_PM_at	Sjogren's syndrome/scleroderma autoantigen 1 homolog (human)	Sssca1	56390	8.12791227	1.876723091	6.36343E-07	5.92618243
1428025_PM_s_at	phosphatidylinositol transfer protein, cytoplasmic 1	Pitpnc1	71795	7.92822846	1.870656266	1.68149E-08	9.60621206
1455649_PM_at	tetratricopeptide repeat domain 9	Ttc9	69480	8.71321374	1.870305129	9.29853E-08	7.87459787
1425701_PM_a_at	regulator of G-protein signaling 3	Rgs3	50780	4.90216861	1.870195497	1.03136E-05	3.1095739
1426324_PM_at	histocompatibility 2, D region locus 1	H2-D1	14964	7.2281525	1.868898558	8.59263E-06	3.29375968
1434322_PM_at	MICAL-like 2	Micall2	231830	8.95022607	1.861172118	1.48913E-05	2.73923392
1438664_PM_at	protein kinase, cAMP dependent regulatory, type II beta	Prkar2b	19088	9.41962433	1.856828018	1.59702E-05	2.66875132
1428743_PM_at	Bri3 binding protein	Bri3bp	76809	7.25011177	1.856591179	1.87953E-07	7.16162139
1444312_PM_at	solute carrier family 22 (organic anion/cation transporter), member 15	Slc22a15	242126	8.02367428	1.855518173	5.31969E-08	8.44025183
1427665_PM_a_at	nuclear factor I/C	Nfic	18029	6.86138432	1.848870633	7.78732E-05	1.07666541
1457092_PM_at	family with sequence similarity 19, member A1	Fam19a1	320265	8.04771973	1.843419693	1.20095E-05	2.95603702
1434364_PM_at	mitogen-activated protein kinase kinase kinase 14	Map3k14	53859	6.92716285	1.842136139	1.39799E-06	5.12929858
1446894_PM_at	---	---	---	5.74053828	1.842005294	3.89075E-05	1.77280295
1449009_PM_at	T-cell specific GTPase 1 /// T-cell specific GTPase 2	Tgtp1 /// Tgtp2	100039796 /	9.43356625	1.840298339	2.9608E-05	2.04734554
1439790_PM_at	serine (or cysteine) peptidase inhibitor, clade B, member 9	Serpinb9	20723	8.37074833	1.836895656	3.40489E-06	4.22880342
1453103_PM_at	actin-binding LIM protein 1	Ablim1	226251	8.08824569	1.835942347	1.26738E-05	2.9017581
1426784_PM_at	tripartite motif-containing 47	Trim47	217333	7.68785354	1.83493433	1.02079E-05	3.11996112
1422482_PM_at	RuvB-like protein 2	Ruvbl2	20174	9.36467668	1.826865424	2.92856E-08	9.04466395
1419554_PM_at	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	Cd47	16423	9.91603257	1.822893807	8.75762E-10	12.5896842
1418304_PM_at	cadherin-related family member 1	Cdhr1	170677	7.26855814	1.820971569	5.82742E-05	1.36727929
1451400_PM_at	gem (nuclear organelle) associated protein 8	Gemin8	237221	7.82803439	1.820684011	1.2822E-08	9.88047799
1423315_PM_at	BCL2 binding component 3	Bbc3	170770	6.60214346	1.819337345	1.44726E-05	2.76797655
1417035_PM_at	SAC3 domain containing 1	Sac3d1	66406	6.90694507	1.818398132	9.40582E-08	7.8629763
1423673_PM_at	leucine zipper, down-regulated in cancer 1-like	Ldoc1l	223732	4.14560303	1.81802846	0.000107223	0.75652292
1415899_PM_at	Jun-B oncogene	Junb	16477	5.52637022	1.816775798	2.07794E-05	2.40362387
1424150_PM_at	glycerophosphodiester phosphodiesterase domain containing 5	Gdpd5	233552	8.60646342	1.813164601	1.28163E-06	5.21725877
1426260_PM_a_at	UDP glucuronosyltransferase 1 family, polypeptide A1 /// UDP glycosyltransferase 1 family, polypeptide A10 ///	Ugt1a1 /// Ugt	22236 /// 39	8.82043637	1.812554866	5.52774E-06	3.7391321
1450944_PM_at	chondroitin sulfate proteoglycan 4	Cspg4	121021	5.78451945	1.80984301	5.32971E-05	1.4568446
1424031_PM_at	sorting nexin 11	Snx11	74479	5.61990282	1.809722817	1.54451E-05	2.70243456
1449507_PM_a_at	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	Cd47	16423	10.7451088	1.804175823	6.21883E-11	15.2436519
1417397_PM_at	solute carrier family 9 (sodium/hydrogen exchanger), member 1	Slc9a1	20544	6.68072909	1.801059422	1.24928E-05	2.91626041
1418712_PM_at	CDC42 effector protein (Rho GTPase binding) 5	Cdc42ep5	58804	7.34871229	1.798629099	1.41397E-06	5.11779106
1449420_PM_at	phosphodiesterase 1B, Ca2+-calmodulin dependent	Pde1b	18574	4.33350854	1.792964639	7.59872E-05	1.10122605
1430153_PM_at	tropomodulin 2	Tmod2	50876	7.06791776	1.79184716	4.82293E-05	1.5571173
1416942_PM_at	endoplasmic reticulum aminopeptidase 1	Erap1	80898	7.34964888	1.790356928	7.77137E-05	1.07871993
1449424_PM_at	pleckstrin 2	Plek2	27260	4.42598413	1.790125689	1.25608E-05	2.91078936
1435431_PM_at	proteasome (prosome, macropain) assembly chaperone 4	Psmg4	69666	7.31885505	1.789614639	5.87085E-08	8.3404048
1447860_PM_x_at	component of oligomeric golgi complex 8	Cog8	97484	7.61917937	1.786012388	1.10054E-05	3.04408646
1427578_PM_a_at	eukaryotic translation initiation factor 6	Eif6	16418	10.9660221	1.785265948	3.0612E-10	13.6467227
1418153_PM_at	laminin, alpha 1	Lama1	16772	5.94145579	1.784864528	0.000106362	0.76459138
1424942_PM_a_at	myelocytomatosis oncogene	Myc	17869	10.226418	1.78327472	1.51288E-06	5.04936188
1417292_PM_at	interferon gamma inducible protein 47	Ifi47	15953	10.6985457	1.779833772	2.25198E-08	9.31058368
1431284_PM_a_at	spinster homolog 1 (Drosophila)	Spns1	73658	9.86322247	1.779806564	3.85152E-06	4.10421004
1419456_PM_at	dicarbonyl L-xylulose reductase	Dcxr	67880	8.92262219	1.779300718	7.76934E-09	10.3870756
1416439_PM_at	dCTP pyrophosphatase 1	Dctpp1	66422	9.23369361	1.777433024	9.58592E-06	3.18338377
1455330_PM_at	nucleolar protein 9	Nol9	74035	6.43547988	1.776569959	2.79493E-07	6.75962399
1431582_PM_at	eukaryotic translation initiation factor 6	Eif6	16418	7.33807666	1.776336314	1.87823E-06	4.8304674
1427746_PM_x_at	histocompatibility 2, K1, K region	H2-K1	14972	8.30644464	1.775248761	8.15775E-06	3.34617496
1417045_PM_at	BH3 interacting domain death agonist	Bid	12122	9.57043429	1.773752739	4.0233E-10	13.3721572
1417147_PM_at	family with sequence similarity 69, member B	Fam69b	56279	6.28118263	1.771768709	2.00172E-05	2.44125038
1427739_PM_a_at	transformation related protein 53	Trp53	22059	9.75779781	1.771634657	3.69322E-10	13.4581796
1460206_PM_at	GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein	Grasp	56149	7.96492979	1.768715478	1.49808E-07	7.39143928
1420998_PM_at	ets variant gene 5	Etv5	104156	6.07799185	1.767679866	3.04578E-05	2.01889284
1430997_PM_at	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	Cd47	16423	4.85619206	1.766022598	0.000204343	0.112634
1426932_PM_at	DNA segment, Chr 19, Brigham & Women's Genetics 1357 expressed	D19Bwg1357e	52874	7.70045578	1.762513208	8.07976E-07	5.68435224
1426261_PM_s_at	UDP glucuronosyltransferase 1 family, polypeptide A1 /// UDP glycosyltransferase 1 family, polypeptide A10 ///	Ugt1a1 /// Ugt	22236 /// 39	6.46718437	1.759291616	8.46251E-06	3.30915949
1421319_PM_at	prostaglandin F2 receptor negative regulator	Ptgfrn	19221	5.7562281	1.75779173	3.89882E-05	1.77072131
1419460_PM_at	ribonuclease P 14 subunit (human)	Rpp14	67053	10.1234326	1.756439945	1.33054E-05	2.85272841
1416819_PM_at	cell division cycle 37 homolog (S. cerevisiae)	Cdc37	12539	9.82409285	1.753624477	2.3507E-08	9.26715649
1460617_PM_s_at	RAB6B, member RAS oncogene family	Rab6b	270192	6.48131316	1.751422977	5.93813E-06	3.66680029
1424490_PM_at	zinc finger protein 428	Zfp428	232969	7.84372135	1.751275999	5.76399E-05	1.37825727

1459890_PM_s_at	RIKEN cDNA 1110008P14 gene	1110008P14Rik	73737	8.85850985	1.750188327	1.11282E-06	5.36022789
1430293_PM_a_at	ferredoxin 1-like /// zinc finger, GATA-like protein 1	Fdx1l /// Zglp1	100009600 /	8.94286209	1.748831713	7.54144E-05	1.10880693
1434270_PM_at	Cbx6-Nptxr readthrough transcripts /// neuronal pentraxin receptor	Cbx6-Nptxr ///	504193 /// 7	6.9880134	1.748317153	7.85035E-05	1.06859057
1448273_PM_at	glutathione synthetase	Gss	14854	6.89156561	1.748019918	1.15429E-06	5.32319131
1415694_PM_at	tryptophanyl-tRNA synthetase	Wars	22375	8.39006819	1.744224165	2.54367E-06	4.52366896
1419455_PM_at	interleukin 10 receptor, beta	Il10rb	16155	7.50752357	1.744173565	4.76471E-07	6.21923617
1421207_PM_at	leukemia inhibitory factor	Lif	16878	8.92932977	1.742390201	4.04209E-05	1.73447089
1433909_PM_at	synaptotagmin XVII	Syt17	110058	8.58969778	1.741985288	3.70798E-05	1.82114598
1447783_PM_x_at	solute carrier family 25, member 39	Slc25a39	68066	6.55222357	1.740380039	7.18191E-05	1.15775273
1417096_PM_at	ribosomal RNA processing 15 homolog (S. cerevisiae)	Rrp15	67223	8.48191799	1.739331016	8.17594E-05	1.0278875
1449440_PM_at	lipin 3	Lpin3	64899	5.67018943	1.737696199	0.000100307	0.82322638
1416588_PM_at	protein tyrosine phosphatase, receptor type, N	Ptprn	19275	6.24331674	1.736409751	0.000213259	0.07007915
1455390_PM_at	alkB, alkylation repair homolog 6 (E. coli)	Alkbh6	233065	7.55550819	1.735015498	7.49428E-05	1.11509174
1426821_PM_at	component of oligomeric golgi complex 8	Cog8	97484	6.11536702	1.734370722	4.08618E-05	1.7235737
1429138_PM_at	neuronal PAS domain protein 3	Npas3	27386	7.34155561	1.733599447	5.39887E-08	8.42528941
1416695_PM_at	translocator protein	Tspo	12257	9.62496922	1.733469977	0.000105819	0.76971153
1447961_PM_s_at	mitochondrial ribosomal protein L38	Mrpl38	60441	8.6361937	1.732188663	2.68182E-09	11.4614798
1436524_PM_at	RIKEN cDNA 4833438C02 gene	4833438C02Rik	107243	5.58952739	1.731870797	0.000205132	0.10879254
1417212_PM_at	family with sequence similarity 195, member A	Fam195a	68241	4.46850416	1.729795348	3.99549E-05	1.74611694
1419652_PM_s_at	Na+/K+ transporting ATPase interacting 1	Nkain1	67149	7.18268228	1.729767196	7.04512E-10	12.808721
1434813_PM_x_at	tryptophanyl-tRNA synthetase	Wars	22375	9.2702267	1.729373401	2.92125E-08	9.04719643
1438488_PM_at	esterase D/formylglutathione hydrolase	Esd	13885	7.97744616	1.726921702	0.000137199	0.51011497
1451167_PM_at	coiled-coil domain containing 101 /// similar to coiled-coil domain containing 101	Ccdc101 /// LO	100047712 /	7.83396719	1.726097724	1.62719E-07	7.30768488
1425155_PM_x_at	colony stimulating factor 1 (macrophage)	Csf1	12977	7.67855781	1.724932872	2.38688E-05	2.26410792
1417470_PM_at	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 3	Apobec3	80287	9.66219316	1.721128185	2.79622E-06	4.4279365
1450672_PM_a_at	three prime repair exonuclease 1	Trex1	22040	7.10685806	1.719086329	2.03219E-05	2.42603929
1426568_PM_at	solute carrier family 2 (facilitated glucose transporter), member 9	Slc2a9	117591	4.66976666	1.717905193	4.84905E-05	1.55169634
1434015_PM_at	solute carrier family 2 (facilitated glucose transporter), member 6	Slc2a6	227659	6.12606876	1.7177089	0.000171181	0.289204
1424203_PM_at	nicalin homolog (zebrafish)	Ncln	103425	6.99504291	1.717378308	1.29451E-05	2.88040284
1426897_PM_at	regulator of chromosome condensation 2	Rcc2	108911	10.0504524	1.716461628	1.39187E-06	5.13373685
1416335_PM_at	macrophage migration inhibitory factor	Mif	17319	11.5676845	1.714212308	7.82742E-06	3.38789509
1417111_PM_at	mannosidase 1, alpha	Man1a	17155	8.66348156	1.71373559	6.0542E-06	3.64725055
1423543_PM_at	SWA-70 protein	Swap70	20947	9.01368071	1.713490507	3.67846E-08	8.81384307
1456516_PM_x_at	similar to UDP-N-acetylhexosamine pyrophosphorylase /// UDP-N-acetylglucosamine pyrophosphorylase 1	LOC640502 ///	107652 /// 6	11.5219766	1.709714947	3.917E-05	1.76604898
1453745_PM_at	RIKEN cDNA 2700038G22 gene	2700038G22Rik	67194	6.74264191	1.709117408	0.000107597	0.75304197
1422789_PM_at	aldehyde dehydrogenase family 1, subfamily A2	Aldh1a2	19378	10.0862137	1.707792682	2.87307E-06	4.40051801
1455841_PM_s_at	glutamate-rich WD repeat containing 1	Grwd1	101612	8.59907684	1.707779729	3.70634E-06	4.14304772
1418061_PM_at	latent transforming growth factor beta binding protein 2	Ltbp2	16997	10.7722858	1.706206461	3.44306E-07	6.54833891
1437078_PM_at	H2A histone family, member B3 /// vacuolar protein sorting 52 (yeast)	H2afb3 /// Vps	224705 /// 6	6.35976323	1.705535511	1.13256E-05	3.01516662
1423430_PM_at	MYB binding protein (P160) 1a	Mybbp1a	18432	9.12015272	1.703257215	2.67313E-07	6.80476308
1451544_PM_at	TAP binding protein-like	Tapbpl	213233	7.2008488	1.703144569	7.68392E-07	5.73521961
1453855_PM_at	matrix-remodelling associated 7	Mxra7	67622	6.02708483	1.701880609	4.42749E-05	1.64300653
1437385_PM_at	collagen and calcium binding EGF domains 1	Ccbe1	320924	10.1465875	1.701098744	0.000187127	0.20037193
1437490_PM_x_at	similar to UDP-N-acetylhexosamine pyrophosphorylase /// UDP-N-acetylglucosamine pyrophosphorylase 1	LOC640502 ///	107652 /// 6	11.4193281	1.701069211	3.5324E-05	1.86989221
1429104_PM_at	LIM domain containing 2	Limd2	67803	7.70371243	1.700411219	1.1954E-06	5.28776752
1440447_PM_at	abhydrolase domain containing 2	Abhd2	54608	5.55486339	1.699663711	6.46444E-05	1.26324729
1427574_PM_s_at	SH3 domain protein D19	Sh3d19	27059	8.60783505	1.699581214	2.87992E-05	2.07519997
1424921_PM_at	bone marrow stromal cell antigen 2	Bst2	69550	7.0872055	1.699567442	1.85366E-05	2.51863541
1438165_PM_x_at	vesicle amine transport protein 1 homolog (T californica)	Vat1	26949	8.65516393	1.699223229	3.76731E-05	1.80519629
1453129_PM_a_at	regulator of G-protein signaling 12	Rgs12	71729	7.15061911	1.69733106	3.65879E-06	4.15610055
1416016_PM_at	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	Tap1	21354	7.67174805	1.68916814	8.97371E-07	5.57809382
1438728_PM_at	Ngg1 interacting factor 3-like 1 (S. pombe)	Nif3l1	65102	8.87294512	1.687726052	6.96439E-07	5.83478818
1455450_PM_at	protein tyrosine phosphatase, non-receptor type 3	Ptpn3	545622	6.94075601	1.687580867	3.16531E-05	1.98018816
1429716_PM_at	zinc finger, CCHC domain containing 4	Zcchc4	78796	7.85827561	1.687558209	4.15506E-05	1.70678381
1448436_PM_a_at	interferon regulatory factor 1	Irf1	16362	9.46003059	1.687236853	2.23005E-08	9.32048721
1442077_PM_at	RIKEN cDNA 2310076G05 gene	2310076G05Rik	76963	9.94684707	1.687205078	1.04677E-06	5.4221769
1424948_PM_x_at	histocompatibility 2, D region locus 1 /// histocompatibility 2, K1, K region /// similar to H-2K(d) antigen	H2-D1 /// H2-K	100044874 /	5.96967189	1.686094846	2.51831E-05	2.2101726
1460642_PM_at	TNF receptor associated factor 4	Traf4	22032	7.48763782	1.685799024	5.56398E-09	10.7245009
1451233_PM_at	TNF receptor-associated factor 2	Traf2	22030	6.68389955	1.684932182	2.32265E-07	6.94715253
1455204_PM_at	phosphatidylinositol transfer protein, cytoplasmic 1	Pitpnc1	71795	8.02878783	1.684543446	0.000113717	0.69771969
1417311_PM_at	cysteine rich protein 2	Crip2	68337	8.13490214	1.6811511	3.06036E-05	2.01409064
1418655_PM_at	beta-1,4-N-acetyl-galactosaminyl transferase 1	B4galnt1	14421	7.08324	1.681005436	0.000185135	0.21104159
1421034_PM_a_at	interleukin 4 receptor, alpha	Il4ra	16190	7.08197074	1.680481189	4.5177E-07	6.27315968
1419552_PM_at	enoyl Coenzyme A hydratase domain containing 1	Echdc1	52665	7.92674174	1.679381704	5.24031E-05	1.47381739
1421153_PM_at	lysyl oxidase-like 4	Loxl4	67573	7.27164125	1.676775239	2.67924E-05	2.14785241
1454786_PM_at	RIKEN cDNA 5031439G07 gene	5031439G07Rik	223739	7.43524752	1.676711513	0.000116143	0.67661591
1417584_PM_at	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	Slc11a2	18174	6.89719235	1.673455262	1.32422E-06	5.18416981
1451067_PM_at	small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha	Sgta	52551	8.73615582	1.67245732	1.63347E-06	4.97174827
1435208_PM_at	deltex 3-like (Drosophila)	Dtx3l	209200	10.6555958	1.67104533	0.000108973	0.74033122
1426757_PM_at	adenosine monophosphate deaminase 2	Ampd2	109674	6.84475126	1.670048318	3.59663E-05	1.85178277
1449480_PM_at	Sin3-associated polypeptide 18	Sap18	20220	7.86070681	1.667066693	5.04735E-05	1.51146825
1421002_PM_at	angiopoietin-like 2	Angptl2	26360	6.48670973	1.666346837	3.7257E-05	1.81635478
1452415_PM_at	actinin, alpha 1	Actn1	109711	8.63221158	1.666069491	4.70096E-06	3.90280479
1421103_PM_at	BMP2 inducible kinase	Bmp2k	140780	5.66882218	1.664849854	0.00021532	0.06049616
1424726_PM_at	transmembrane protein 150A	Tmem150a	232086	8.23941467	1.664472413	1.35166E-07	7.49563861
1429620_PM_at	RIKEN cDNA 8430406I07 gene	8430406I07Rik	74528	4.52800326	1.664164336	0.000125939	0.59567527
1421926_PM_at	mitogen-activated protein kinase 11	Mapk11	19094	7.24616082	1.663415291	4.44793E-08	8.6215049
1416750_PM_at	sigma non-opioid intracellular receptor 1	Sigmar1	18391	7.10334539	1.663327351	8.58774E-07	5.62260941
1455277_PM_at	Hedgehog-interacting protein	Hhip	15245	5.82461911	1.661287139	0.000193292	0.16805534
1454674_PM_at	fasciculation and elongation protein zeta 1 (zygin I)	Fez1	235180	6.89186054	1.66100149	5.66312E-05	1.39596769
1439601_PM_at	HEAT repeat containing 6	Heatr6	217026	7.61507553	1.660029709	1.41761E-05	2.78883488
1430332_PM_a_at	glucuronidase, beta	Gusb	110006	7.02566407	1.659335837	8.29462E-05	1.01345423
1431351_PM_at	plasmacytoma variant translocation 1	Pvt1	19296	7.00650193	1.658351447	4.88645E-05	1.54398417
1424617_PM_at	interferon-induced protein 35	Ifi35	70110	7.33054061	1.65821778	3.14527E-06	4.3089901
1452226_PM_at	hypothetical protein LOC100047340 /// regulator of chromosome condensation 2	LOC100047340	100047340 /	8.44909709	1.657799027	2.20908E-07	6.99794372
1434754_PM_at	RAP1 GTPase activating protein 2	Rap1gap2	380711	9.78357182	1.656682667	5.34207E-06	3.77364446
1448132_PM_at	solute carrier family 19 (sodium/hydrogen exchanger), member 1	Slc19a1	20509	6.66103647	1.656205975	3.22808E-08	8.94608229
1459898_PM_at	suprabasin	Sbsn	282619	5.54732194	1.656153284	7.88591E-05	1.06406336
1419205_PM_x_at	G patch domain containing 4	Gpatch4	66614	8.16045674	1.655654377	1.84193E-05	2.52502462
1415976_PM_a_at	calcium regulated heat stable protein 1	Carhsp1	52502	8.42214545	1.653717601	1.67691E-05	2.61956998
1459718_PM_x_at	Kruppel-like factor 6	Klf6	23849	5.93166355	1.652987421	1.2616E-06	5.23320063
1423878_PM_at	glycophorin C	Gypc	71683	9.22244908	1.652924853	2.68836E-07	6.799008
1430421_PM_a_at	transmembrane protein 205	Tmem205	235043	8.72234428	1.651294489	2.34452E-05	2.28212836
1416013_PM_at	phospholipase D family, member 3	Pld3	18807	9.18124312	1.650446672	3.02045E-08	9.01338735
1443493_PM_at	DEAH (Asp-Glu-Ala-His) box polypeptide 37	Dhx37	208144	7.73252614	1.649982472	3.21811E-05	1.96355685
1425911_PM_a_at	fibroblast growth factor receptor 1	Fgfr1	14182	7.36107386	1.649486564	6.846E-07	5.85215215
1429322_PM_at	exosome component 6	Exosc6	72544	8.13383583	1.649017346	4.44356E-05	1.63936909

1428365_PM_a_at	lon peptidase 1, mitochondrial	Lonp1	74142	8.32020611	1.648524286	6.06561E-07	5.97472729
1450387_PM_s_at	adenylate kinase 3-like 1 /// similar to adenylate kinase 4	Ak3l1 /// LOC1(	100047616 /	8.8670732	1.64672835	7.76187E-06	3.39638282
1449556_PM_at	RIKEN cDNA C920025E04 gene /// histocompatibility 2, T region locus 23	C920025E04Rik	15040 /// 66	9.18933927	1.645067969	1.25655E-05	2.91040867
1448175_PM_at	EH-domain containing 1	Ehd1	13660	8.49383125	1.644438073	7.90984E-07	5.70587523
1432372_PM_a_at	sepiapterin reductase	Spr	20751	8.6651044	1.643880222	7.64731E-07	5.74005533
1452171_PM_at	glutamate-rich WD repeat containing 1	Grwd1	101612	7.49042053	1.643824307	2.3643E-07	6.92914347
1423823_PM_at	MRT4, mRNA turnover 4, homolog (S. cerevisiae)	Mrto4	69902	10.1619869	1.642603929	5.33752E-07	6.10424634
1435195_PM_at	vasohibin 1	Vash1	238328	8.22715394	1.640220875	5.11703E-05	1.49770874
1451079_PM_at	ADP-dependent glucokinase	Adpgk	72141	10.3240273	1.639318573	2.17279E-05	2.35869309
1419173_PM_at	aminoacylase 1	Acy1	109652	6.21571484	1.638451219	8.43371E-05	0.99680151
1425170_PM_a_at	a disintegrin and metallopeptidase domain 15 (metargidin)	Adam15	11490	4.63717893	1.635792578	0.000115267	0.6841871
1452830_PM_s_at	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	Cad	69719	8.26740323	1.634893683	2.65947E-05	2.15530291
1456738_PM_s_at	brain protein 16	Brp16	59053	8.62656806	1.634362177	2.45794E-07	6.88979372
1447856_PM_x_at	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25	Slc25a25	227731	7.98978907	1.634052761	0.000183557	0.21957732
1416358_PM_at	major facilitator superfamily domain containing 10	Mfsd10	68294	7.26061001	1.633584698	0.000177558	0.25271901
1416743_PM_at	similar to UDP-N-acetylhexosamine pyrophosphorylase /// UDP-N-acetylglucosamine pyrophosphorylase 1	LOC640502 ///	107652 /// 6	10.7710668	1.633434855	1.08602E-05	3.05748737
1430062_PM_at	hedgehog interacting protein-like 1	Hhipl1	214305	6.00140396	1.632666026	0.000142408	0.47289655
1430172_PM_a_at	cytochrome P450, family 4, subfamily f, polypeptide 16 /// predicted gene 9705	Cyp4f16 /// Gm	677156 /// 7	5.75473377	1.630080867	1.45408E-05	2.7632376
1449109_PM_at	suppressor of cytokine signaling 2	Socs2	216233	7.92158691	1.629625842	1.28718E-06	5.21288249
1450023_PM_at	GTP binding protein 1	Gtpbp1	14904	7.89866607	1.628315996	2.59455E-07	6.83499262
1423754_PM_at	interferon induced transmembrane protein 3	Ifitm3	66141	12.2010923	1.627832948	8.64969E-10	12.6021706
1448266_PM_at	endothelial differentiation-related factor 1	Edf1	59022	11.0336944	1.627689638	5.30307E-06	3.78104602
1452139_PM_at	solute carrier family 35, member C1	Slc35c1	228368	6.20917453	1.627285194	5.9862E-05	1.34031719
1444049_PM_at	adenosine deaminase, tRNA-specific 1	Adat1	30947	6.67303343	1.626232602	0.000187231	0.19981922
1430018_PM_at	CDC42 effector protein (Rho GTPase binding) 5	Cdc42ep5	58804	6.41606349	1.625943398	1.49989E-07	7.39021723
1431352_PM_s_at	plasmacytoma variant translocation 1	Pvt1	19296	9.14229252	1.624513499	9.82293E-07	5.4865416
1416730_PM_at	RNA terminal phosphate cyclase-like 1	Rcl1	59028	8.53656451	1.623847912	1.77932E-08	9.54899139
1424259_PM_at	lipase maturation factor 1	Lmf1	76483	8.37809495	1.623334195	2.24605E-05	2.32531221
1449183_PM_at	catechol-O-methyltransferase 1	Comt1	12846	9.50245558	1.622840947	4.81062E-09	10.8714849
1423801_PM_a_at	adenine phosphoribosyl transferase	Aprt	11821	10.3570712	1.621707743	1.45361E-05	2.7635622
1451365_PM_at	RNA binding motif protein 19	Rbm19	74111	6.62671929	1.621422169	1.35832E-05	2.83190145
1417481_PM_at	receptor (calcitonin) activity modifying protein 1	Ramp1	51801	4.2539889	1.621126121	9.71047E-08	7.83068468
1433635_PM_at	WD repeat domain 18	Wdr18	216156	5.71070888	1.620454476	0.000109881	0.73203472
1425154_PM_a_at	colony stimulating factor 1 (macrophage)	Csf1	12977	8.2050294	1.620409445	7.82816E-05	1.07142609
1448563_PM_at	prohibitin	Phb	18673	8.66278075	1.619961727	1.68763E-07	7.27073512
1426479_PM_a_at	canopy 3 homolog (zebrafish)	Cnpy3	72029	7.98317861	1.619950756	0.000180928	0.23396691
1456890_PM_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	Ddx58	230073	7.14667025	1.619596185	1.72528E-05	2.59092248
1448417_PM_at	ninjurin 1	Ninj1	18081	6.08706359	1.619200032	3.11382E-05	1.99667891
1451782_PM_a_at	solute carrier family 29 (nucleoside transporters), member 1	Slc29a1	63959	6.6277164	1.618695411	3.59762E-05	1.85150724
1426975_PM_at	amplified in osteosarcoma	Os9	216440	7.54621724	1.617321043	9.96642E-06	3.14411331
1429128_PM_x_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2, p49/p100	Nfkb2	18034	7.08228847	1.616933028	2.40094E-06	4.58207469
1421074_PM_at	cytochrome P450, family 7, subfamily b, polypeptide 1	Cyp7b1	13123	9.10631315	1.61516852	5.06115E-09	10.8201994
1448095_PM_at	---	---	---	8.59224321	1.614168671	0.000138912	0.49772019
1422500_PM_at	isocitrate dehydrogenase 3 (NAD+) alpha	Idh3a	67834	8.95331007	1.613830716	1.29463E-05	2.88031192
1451085_PM_at	RIKEN cDNA C030006K11 gene	C030006K11Rik	223665	7.0248717	1.612170137	0.000202938	0.11951272
1417732_PM_at	annexin A8	Anxa8	11752	8.88455678	1.611928226	2.28404E-05	2.30842855
1451180_PM_a_at	5'-nucleotidase, cytosolic III-like	Nt5c3l	68106	7.44559804	1.611824186	2.91813E-05	2.06194691
1433273_PM_at	Na+/K+ transporting ATPase interacting 1	Nkain1	67149	7.23979839	1.611394081	1.54302E-06	5.02939446
1434774_PM_at	rhomboid 5 homolog 2 (Drosophila)	Rhbdf2	217344	7.37489965	1.609952248	5.40545E-06	3.76173072
1455932_PM_at	Metadherin	Mtdh	67154	6.45895261	1.609867382	8.06302E-05	1.04181655
1448679_PM_at	hyaluronoglucosaminidase 2	Hyal2	15587	7.5530553	1.609399343	3.91622E-07	6.41789264
1449002_PM_at	pleckstrin homology-like domain, family A, member 3	Phlda3	27280	11.1936447	1.60917774	2.43047E-08	9.23337943
1418092_PM_s_at	thyroid hormone receptor interactor 10	Trip10	106628	7.65808299	1.608050524	4.37068E-07	6.30667291
1453111_PM_a_at	solute carrier family 25, member 39	Slc25a39	68066	9.31663239	1.608037701	1.09215E-05	3.05180563
1421378_PM_s_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	Abcc1	17250	8.88574799	1.607905973	1.68279E-06	4.94164366
1455096_PM_at	fibronectin leucine rich transmembrane protein 2	Flrt2	399558	10.8872571	1.607621736	0.000190498	0.18256803
1418507_PM_s_at	suppressor of cytokine signaling 2	Socs2	216233	10.7052113	1.607100254	1.27594E-09	12.2105872
1432826_PM_a_at	CD80 antigen	Cd80	12519	5.99408814	1.60693111	1.7881E-05	2.55489907
1455711_PM_at	deltex 4 homolog (Drosophila)	Dtx4	207521	7.61016662	1.605743053	3.04757E-05	2.01830017
1416954_PM_at	solute carrier family 25 (mitochondrial carrier, dicarboxylate transporter), member 10	Slc25a10	27376	6.4322442	1.605497468	5.66159E-05	1.3962383
1424735_PM_at	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25	Slc25a25	227731	5.22639713	1.605447926	2.20565E-05	2.34358339
1417053_PM_at	prohibitin	Phb	18673	10.4769264	1.605008073	7.87137E-05	1.06591202
1435932_PM_at	Hermansky-Pudlak syndrome 6	Hps6	20170	6.57223776	1.6016653	8.42535E-06	3.31360044
1417130_PM_s_at	angiopoietin-like 4	Angptl4	57875	9.68759781	1.601345104	0.00022691	0.00827324
1424522_PM_at	HEAT repeat containing 1	Heatr1	217995	8.56127248	1.598650199	1.85099E-08	9.50903203
1452076_PM_at	SPRY domain containing 4	Spryd4	66701	7.671617	1.598323074	1.52464E-05	2.71548059
1417392_PM_a_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	Slc7a7	20540	8.61817727	1.597951753	2.42474E-05	2.24827254
1437832_PM_x_at	similar to Wars protein /// tryptophanyl-tRNA synthetase	LOC100046672	100046672 /	8.07194897	1.597154536	1.32976E-08	9.84363638
1437159_PM_at	galactosidase, beta 1	Glb1	12091	6.11784157	1.594871694	1.41194E-05	2.79287307
1455456_PM_a_at	translocase of inner mitochondrial membrane 50 homolog (yeast)	Timm50	66525	8.66191239	1.594809861	5.14107E-05	1.49300475
1428330_PM_at	dopey family member 2	Dopey2	70028	7.81888715	1.594326067	0.000123338	0.61653223
1434762_PM_at	ORAI calcium release-activated calcium modulator 2	Orai2	269717	7.37862496	1.590871371	7.23287E-05	1.1506673
1416684_PM_at	fibrillarin	Fbl	14113	10.2004082	1.590848745	3.86811E-08	8.76294172
1434522_PM_at	WD repeat domain 4	Wdr4	57773	7.12492082	1.590821633	0.00012726	0.58524704
1419179_PM_at	thioredoxin-like 4A	Txnl4a	27366	7.29253198	1.590108801	1.09747E-07	7.70669592
1422709_PM_a_at	WD repeat domain 46	Wdr46	57315	7.41566351	1.588606161	2.81125E-05	2.09947416
1434552_PM_at	WD repeat domain 77	Wdr77	70465	7.74482882	1.588580575	0.000145291	0.45287742
1436431_PM_at	RIKEN cDNA 1700025G04 gene	1700025G04Rik	69399	6.87621448	1.587989818	1.81925E-05	2.53750486
1434879_PM_at	cell division cycle 34 homolog (S. cerevisiae) /// similar to Cell division cycle 34 homolog (S. cerevisiae)	Cdc34 /// LOC1	100046898 /	9.14878811	1.586377651	1.17148E-05	2.98109547
1418587_PM_at	TNF receptor-associated factor 3	Traf3	22031	9.91663614	1.585015598	4.86995E-07	6.19710737
1449553_PM_at	Na+/K+ transporting ATPase interacting 1	Nkain1	67149	9.27544409	1.584931336	8.11154E-09	10.3435027
1427449_PM_a_at	ADP-ribosylhydrolase like 2	Adprhl2	100206	6.95999422	1.58472383	1.06105E-05	3.08094144
1419213_PM_at	N-acetyltransferase 6	Nat6	56441	7.66075581	1.584207014	3.39333E-05	1.91026184
1418167_PM_at	transcription factor AP4	Tcfap4	83383	4.85246519	1.583729762	3.11967E-06	4.31725407
1428669_PM_at	brain expressed myelocytomatosis oncogene	Bmyc	107771	7.4467066	1.583316804	5.44846E-05	1.43473355
1418377_PM_a_at	SIVA1, apoptosis-inducing factor	Siva1	30954	8.73919061	1.583167262	5.20591E-05	1.48042712
1424760_PM_a_at	SET and MYND domain containing 2	Smyd2	226830	9.70660815	1.581103144	9.26911E-06	3.21729085
1417103_PM_at	D-dopachrome tautomerase	Ddt	13202	10.3618345	1.580782949	1.76261E-06	4.89474993
1425416_PM_s_at	proline/serine-rich coiled-coil 1	Psrc1	56742	9.1273033	1.580467856	3.102E-06	4.3229969
1416383_PM_a_at	pyruvate carboxylase	Pcx	18563	6.02023098	1.580430605	8.96837E-05	0.93525956
1429475_PM_at	similar to RIKEN cDNA 2810457I06 /// ubiquitin associated and SH3 domain containing, B	LOC677224 ///	677224 /// 7	6.97850301	1.58042504	5.2184E-05	1.47802144
1425106_PM_a_at	tryptophanyl-tRNA synthetase	Wars	22375	6.90981387	1.580106293	3.11556E-05	1.9961163
1428744_PM_s_at	Bri3 binding protein	Bri3bp	76809	9.69561331	1.580002874	3.11159E-06	4.31987682
1419046_PM_at	brain protein 16	Brp16	59053	7.83309837	1.579292471	3.64524E-07	6.49053292
1417725_PM_a_at	Sjogren's syndrome/scleroderma autoantigen 1 homolog (human)	Sssca1	56390	8.55644237	1.579087515	8.96426E-05	0.93571837
1422787_PM_at	FK506 binding protein-like	Fkbpl	56299	7.07560794	1.576955058	1.01819E-05	3.1225342
1438498_PM_at	zinc finger, MYND-type containing 15	Zmynd15	574428	4.2496521	1.574176816	0.000103285	0.79395126

1422767_PM_at	bystin-like	Bysl	53414	9.04468684	1.573914403	1.44839E-06	5.09345295
1426529_PM_a_at	transgelin 2	Tagln2	21346	10.7073561	1.57373539	6.29925E-06	3.60718029
1443750_PM_s_at	ribonuclease P 40 subunit (human)	Rpp40	208366	7.23446183	1.573302921	2.77631E-05	2.11205166
1438178_PM_x_at	ATPase family, AAA domain containing 3A	Atad3a	108888	7.26820514	1.57292333	5.07198E-07	6.15593358
1425300_PM_at	dihydroxyacetone kinase 2 homolog (yeast)	Dak	225913	6.21581362	1.570517006	8.54049E-05	0.98420304
1422601_PM_at	serine (or cysteine) peptidase inhibitor, clade B, member 9	Serpinb9	20723	9.3296232	1.569578308	0.00014548	0.45157994
1416436_PM_a_at	ubiquinol-cytochrome c reductase complex chaperone, CBP3 homolog (yeast)	Uqcc	56046	6.66259962	1.569229003	9.23253E-05	0.90620113
1437112_PM_at	phospholipase D1	Pld1	18805	6.45138595	1.568813461	3.052E-05	2.01684106
1438962_PM_s_at	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 31	Ddx31	227674	7.46263494	1.568407194	5.84028E-05	1.36506987
1417897_PM_at	breast cancer metastasis-suppressor 1	Brms1	107392	7.82405509	1.568124004	3.12371E-05	1.99348893
1452811_PM_at	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	Atic	108147	9.32589846	1.567569202	4.5207E-06	3.94231219
1429097_PM_at	ring finger protein 150	Rnf150	330812	9.39366815	1.565572976	9.30849E-05	0.89800012
1417226_PM_at	F-box and WD-40 domain protein 4	Fbxw4	30838	7.41559415	1.565174424	1.50243E-05	2.73027186
1421679_PM_a_at	cyclin-dependent kinase inhibitor 1A (P21)	Cdkn1a	12575	10.4374805	1.564381781	5.23586E-07	6.12372395
1450997_PM_at	serine/threonine kinase 17b (apoptosis-inducing)	Stk17b	98267	9.67521859	1.564268681	0.0002097	0.086846
1450971_PM_at	growth arrest and DNA-damage-inducible 45 beta	Gadd45b	17873	11.2359015	1.561446948	6.07209E-05	1.32603115
1436897_PM_at	malignant fibrous histiocytoma amplified sequence 1	Mfhas1	52065	7.35632742	1.559373524	0.000187505	0.19835823
1454667_PM_at	sorting nexin 8	Snx8	231834	8.60995995	1.558381801	6.73351E-06	3.53986428
1454708_PM_at	actin-binding LIM protein 1	Ablim1	226251	11.5802767	1.554991417	0.000108734	0.74252777
1440152_PM_x_at	endothelial differentiation-related factor 1 /// predicted gene 11964	Edf1 /// Gm11	59022 /// 66	11.8169021	1.554700617	2.446E-07	6.89472697
1460396_PM_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	Ddx54	71990	7.93061898	1.554295663	2.68924E-05	2.14410256
1448164_PM_at	kelch domain containing 3	Klhdc3	71765	5.86360494	1.554233916	0.000118712	0.65473875
1448817_PM_at	OTU domain, ubiquitin aldehyde binding 1	Otub1	107260	10.4133085	1.552454997	4.76727E-06	3.88865101
1451248_PM_at	protein arginine N-methyltransferase 7	Prmt7	214572	9.0755734	1.551944358	5.0242E-07	6.16552033
1460633_PM_at	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	Prpf19	28000	9.37154046	1.551351605	1.8481E-07	7.17870751
1428395_PM_at	SMAD specific E3 ubiquitin protein ligase 1	Smurf1	75788	9.40802655	1.550823248	1.8242E-06	4.86000135
1451016_PM_at	interferon-related developmental regulator 2	Ifrd2	15983	5.15654329	1.550517029	1.19761E-05	2.9588476
1428290_PM_at	similar to Mipep protein /// mitochondrial intermediate peptidase	LOC100047713	100047713 /	7.15943622	1.549599223	0.00015539	0.38578784
1450111_PM_a_at	nudix (nucleoside diphosphate linked moiety X)-type motif 8	Nudt8	66387	7.34620883	1.5494407	0.000137305	0.5093391
1446499_PM_at	Fas (TNFRSF6)-associated via death domain	Fadd	14082	7.03940075	1.54908444	1.99626E-05	2.44400116
1451278_PM_a_at	methyltransferase like 11A	Mettl11a	66617	7.4589154	1.548958757	1.03974E-05	3.10140496
1433843_PM_at	HCLS1 binding protein 3	Hs1bp3	58240	9.15186464	1.548361105	7.17527E-05	1.1586795
1415795_PM_at	similar to Spindlin 1 /// spindlin 1	LOC100046080	100046080 /	8.22386919	1.547453264	0.000192579	0.17173607
1429380_PM_at	regulator of G-protein signaling 12	Rgs12	71729	5.20238132	1.545957133	0.000104117	0.78592901
1435031_PM_at	transmembrane protein 120A	Tmem120a	215210	8.86160455	1.544833961	0.000223869	0.02170849
1417675_PM_a_at	midasin homolog (yeast)	Mdn1	100019	8.93859859	1.544702613	1.39692E-06	5.13007371
1424859_PM_at	homer homolog 3 (Drosophila)	Homer3	26558	9.46752825	1.54334132	1.87839E-07	7.16223463
1434560_PM_at	WD and tetratricopeptide repeats 1	Wdtc1	230796	7.06140839	1.543160842	1.85182E-05	2.51963138
1449189_PM_at	cDNA sequence BC003266	BC003266	80284	8.39317557	1.542536097	0.000101986	0.80661443
1426843_PM_at	ATG2 autophagy related 2 homolog A (S. cerevisiae)	Atg2a	329015	7.39153432	1.542384155	6.25449E-06	3.61438206
1428605_PM_at	coiled-coil domain containing 124	Ccdc124	234388	7.51714375	1.542211968	6.92979E-05	1.19356645
1435402_PM_at	GRAM domain containing 1B	Gramd1b	235283	7.22999514	1.541415439	1.06079E-05	3.08119212
1416964_PM_at	eukaryotic elongation factor, selenocysteine-tRNA-specific	Eefsec	65967	7.14180524	1.540831865	2.23579E-05	2.32991941
1424577_PM_at	misato homolog 1 (Drosophila)	Msto1	229524	8.72964501	1.538867351	4.81751E-06	3.87805905
1438422_PM_at	leucine rich repeat containing 20	Lrrc20	216011	6.07127167	1.538475298	6.47858E-06	3.57883419
1418288_PM_at	lipin 1	Lpin1	14245	7.3409433	1.536997514	8.52011E-05	0.98659575
1436651_PM_at	PR domain containing 11	Prdm11	100042784	4.23855326	1.536732284	7.54587E-05	1.10821904
1452099_PM_at	expressed sequence AA408296	AA408296	215193	7.67714745	1.536562606	1.40991E-07	7.45289841
1451243_PM_at	arginyl aminopeptidase (aminopeptidase B)	Rnpep	215615	8.52239301	1.536266953	9.38688E-06	3.20455278
1417977_PM_at	eukaryotic translation initiation factor 4E member 3	Eif4e3	66892	8.15342836	1.536171377	2.20641E-06	4.6675456
1423413_PM_at	N-myc downstream regulated gene 1	Ndrg1	17988	7.11106229	1.535976091	0.000147391	0.43855075
1434586_PM_a_at	phosphatidylserine synthase 2	Ptdss2	27388	7.36220267	1.535845986	0.000172624	0.28082751
1422945_PM_a_at	kinesin family member 5C	Kif5c	16574	7.41149194	1.5356806	0.000198369	0.14220711
1416172_PM_at	pescadillo homolog 1, containing BRCT domain (zebrafish)	Pes1	64934	9.55492748	1.534812796	4.02135E-08	8.72359936
1438928_PM_x_at	ninjurin 1	Ninj1	18081	8.65802241	1.533346591	8.30053E-05	1.01274191
1428678_PM_s_at	WD repeat domain 73	Wdr73	71968	6.83665076	1.533328442	5.63398E-05	1.40114245
1425531_PM_at	zinc finger, HIT domain containing 1	Znhit1	70103	9.10976497	1.533218947	5.13164E-05	1.49484724
1438485_PM_at	RIKEN cDNA E130112L23 gene	E130112L23Rik	268739	7.74482578	1.532726885	3.14526E-05	1.98657608
1421784_PM_a_at	ephrin A4	Efna4	13639	6.49137139	1.530387482	6.39579E-05	1.27395206
1424728_PM_at	cDNA sequence BC011248	BC011248	224823	9.01710872	1.529277195	1.83422E-07	7.18634544
1460220_PM_a_at	colony stimulating factor 1 (macrophage)	Csf1	12977	10.5433415	1.528375238	9.3446E-06	3.20910762
1416126_PM_at	polymerase (RNA) I polypeptide B	Polr1b	20017	6.4868849	1.52775937	1.14072E-05	3.00792579
1424212_PM_at	RIKEN cDNA 9430023L20 gene	9430023L20Rik	68118	8.70124661	1.527665192	7.4905E-05	1.11559758
1423668_PM_at	zinc finger, DHHC domain containing 14	Zdhhc14	224454	7.14218486	1.527056847	4.88827E-05	1.54361053
1441513_PM_at	TRAF family member-associated Nf-kappa B activator	Tank	21353	5.85790007	1.5265724	8.40647E-05	1.000041
1455752_PM_a_at	transmembrane protein 134	Tmem134	66990	8.82948421	1.526074568	6.82453E-06	3.52630833
1416379_PM_at	pannexin 1	Panx1	55991	8.62963673	1.525945658	2.75014E-06	4.4447385
1416898_PM_a_at	interferon regulatory factor 3	Irf3	54131	8.26411887	1.525785557	3.99922E-05	1.74518138
1424887_PM_at	kelch domain containing 4	Klhdc4	234825	8.71357145	1.524691732	1.12656E-05	3.02051757
1418540_PM_a_at	protein tyrosine phosphatase, receptor type, E	Ptpre	19267	6.59639808	1.523544854	0.000227724	0.00470566
1422572_PM_at	ras homolog gene family, member G	Rhog	56212	7.8379012	1.522959759	3.45063E-05	1.89343069
1434619_PM_at	regulatory associated protein of MTOR, complex 1	Rptor	74370	6.76917417	1.522081995	4.4315E-05	1.64209656
1428176_PM_at	sphingosine-1-phosphate receptor 2	S1pr2	14739	9.12015639	1.519692137	3.9071E-05	1.76859122
1448414_PM_at	RAD1 homolog (S. pombe)	Rad1	19355	9.20129612	1.519137419	7.82343E-05	1.07203078
1441788_PM_s_at	dyskeratosis congenita 1, dyskerin homolog (human)	Dkc1	245474	10.4402012	1.519097239	5.78144E-06	3.69380805
1447864_PM_s_at	pogo transposable element with KRAB domain	Pogk	71592	9.13021229	1.518989547	3.46864E-05	1.88819814
1420138_PM_at	solute carrier family 19 (sodium/hydrogen exchanger), member 1	Slc19a1	20509	8.35904436	1.517746431	4.94941E-06	3.85077042
1419471_PM_a_at	nuclear distribution gene C homolog (Aspergillus)	Nudc	18221	9.14806991	1.516685978	4.43148E-05	1.64210193
1448590_PM_at	collagen, type VI, alpha 1	Col6a1	12833	10.7716321	1.516319484	0.000219321	0.04215389
1460227_PM_at	tissue inhibitor of metalloproteinase 1	Timp1	21857	12.5283206	1.516026928	5.33972E-06	3.77408885
1455768_PM_at	Niemann Pick type C2	Npc2	67963	7.48485748	1.515516806	7.48041E-06	3.43366642
1417692_PM_at	developmentally regulated GTP binding protein 2	Drg2	13495	8.78174705	1.514713098	2.24772E-05	2.3245654
1421172_PM_at	a disintegrin and metalloproteinase domain 12 (meltrin alpha)	Adam12	11489	11.6896355	1.514660256	0.000116691	0.67190981
1424837_PM_at	ring finger protein 113A1	Rnf113a1	69942	5.7553105	1.513894374	4.53552E-05	1.61880149
1424685_PM_at	exosome component 4	Exosc4	109075	8.16490671	1.512977397	1.42131E-05	2.78620768
1428135_PM_a_at	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	Eef1d	66656	8.37422491	1.512627583	5.77762E-05	1.375889
1455211_PM_a_at	translocase of inner mitochondrial membrane 13 homolog (yeast)	Timm13	30055	9.19053378	1.511289561	0.000116178	0.67631089
1427065_PM_at	RIKEN cDNA 4933439F18 gene	4933439F18Rik	66771	6.29417244	1.510970355	6.34076E-05	1.2826168
1431569_PM_a_at	Ly6/Plaur domain containing 1	Lypd1	72585	6.16673071	1.510866884	0.000144	0.46178957
1447683_PM_x_at	methyltransferase like 1	Mettl1	17299	6.88485857	1.510812018	1.08775E-05	3.05587811
1456524_PM_at	neuregulin 1	Nrg1	211323	10.0891812	1.510113178	8.48892E-06	3.30601462
1418522_PM_at	metaxin 1	Mtx1	17827	7.55881439	1.509115869	6.54534E-05	1.25077997
1424472_PM_at	nucleolar protein family 6 (RNA-associated)	Nol6	230082	7.75152444	1.509007652	0.000115755	0.67996042
1422620_PM_s_at	phosphatidic acid phosphatase type 2A	Ppap2a	19012	10.9948305	1.508959051	2.35855E-06	4.60009468
1416135_PM_at	apurinic/apyrimidinic endonuclease 1	Apex1	11792	10.7042504	1.508862271	1.47173E-07	7.40941844
1452324_PM_at	plasmacytoma variant translocation 1	Pvt1	19296	10.009215	1.508649895	8.56952E-06	3.29647828
1421989_PM_s_at	3'-phosphoadenosine 5'-phosphosulfate synthase 2	Papss2	23972	8.68726504	1.507754947	0.000129507	0.56775422

1448167_PM_at	interferon gamma receptor 1	Ifngr1	15979	8.96281677	1.506650489	9.2529E-06	3.2190574
1448450_PM_at	adenylate kinase 2 /// similar to adenylate kinase 2	Ak2 /// LOC100	100047005 /	10.0667437	1.506327553	1.43076E-07	7.43802221
1455992_PM_at	vestigial like 4 (Drosophila)	Vgll4	232334	8.13152161	1.50605347	1.04654E-05	3.0948325
1450854_PM_at	proliferation-associated 2G4	Pa2g4	18813	9.58605579	1.505975891	9.38813E-07	5.53238114
1450863_PM_a_at	doublecortin-like kinase 1	Dclk1	13175	10.0471385	1.505675681	9.21985E-06	3.22266759
1415806_PM_at	plasminogen activator, tissue	Plat	18791	10.8821647	1.505635556	5.51309E-08	8.40408467
1416362_PM_a_at	FK506 binding protein 4	Fkbp4	14228	9.37164988	1.504683569	6.29637E-06	3.60764166
1419058_PM_at	polymerase (RNA) I polypeptide E	Polr1e	64424	8.23768393	1.504190328	7.66233E-05	1.09287505
1456079_PM_x_at	apurinic/apyrimidinic endonuclease 1	Apex1	11792	11.1045795	1.503572869	2.01654E-07	7.09033546
1451735_PM_at	ADP-ribosylation factor related protein 1	Arfrp1	76688	9.31017287	1.50336272	0.000108387	0.74572517
1450630_PM_at	queuine tRNA-ribosyltransferase 1	Qtrt1	60507	7.86504276	1.502121635	0.000160045	0.356325
1424529_PM_s_at	cell growth regulator with EF hand domain 1	Cgref1	68567	8.81577644	1.501316797	2.27277E-05	2.31340982
1419122_PM_at	methyltransferase like 1	Mettl1	17299	6.7113639	1.501080614	4.24141E-05	1.68612528
1441315_PM_s_at	solute carrier family 19 (thiamine transporter), member 2	Slc19a2	116914	10.3026693	1.500950531	9.95866E-05	0.83043508
1415792_PM_at	RanBP-type and C3HC4-type zinc finger containing 1	Rbck1	24105	7.98713627	1.500299151	4.09888E-05	1.72045684
1437010_PM_a_at	ornithine decarboxylase antizyme 3	Oaz3	53814	7.93633468	1.500110111	4.22248E-05	1.69061583
1423675_PM_at	ubiquitin specific peptidase 1	Usp1	230484	7.40840807	-1.50601572	0.000169623	0.29832956
1440764_PM_at	v-raf murine sarcoma 3611 viral oncogene homolog	Araf	11836	6.85049446	-1.50674328	0.000205105	0.10892629
1426993_PM_at	xenotropic and polytropic retrovirus receptor 1	Xpr1	19775	9.75457435	-1.50774065	5.25187E-05	1.47160683
1453771_PM_at	GULP, engulfment adaptor PTB domain containing 1	Gulp1	70676	10.5652039	-1.50786507	0.000160007	0.35656468
1449871_PM_at	T-box18	Tbx18	76365	7.14851357	-1.50923293	9.63283E-05	0.86372254
1455104_PM_at	MAX dimerization protein 1	Mxd1	17119	9.03578648	-1.50958232	3.96412E-05	1.75403692
1432195_PM_s_at	cyclin L2	Ccnl2	56036	10.0272489	-1.51231441	1.31407E-05	2.86528562
1424156_PM_at	retinoblastoma-like 1 (p107)	Rbl1	19650	8.64278293	-1.51247733	0.000164189	0.33081338
1457424_PM_at	eyes absent 1 homolog (Drosophila)	Eya1	14048	7.49969206	-1.51957963	1.88373E-05	2.50242985
1455195_PM_at	ribosomal protein S24	Rps24	20088	9.52396566	-1.52023838	4.16889E-05	1.70344464
1460431_PM_at	glucosaminyl (N-acetyl) transferase 1, core 2	Gcnt1	14537	9.59111551	-1.52187889	2.12711E-06	4.70457087
1434960_PM_at	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor	Taf9b	407786	9.44944368	-1.52279821	7.8713E-06	3.38225164
1417216_PM_at	proviral integration site 2	Pim2	18715	7.50611084	-1.52281922	7.64446E-05	1.09521393
1459838_PM_s_at	BTB (POZ) domain containing 11	Btbd11	74007	9.71196566	-1.52368003	0.000101301	0.81336102
1429361_PM_at	pro-melanin-concentrating hormone	Pmch	110312	6.97339547	-1.52415203	0.000215641	0.0590114
1435654_PM_at	coiled-coil domain containing 14	Ccdc14	239839	7.59267891	-1.52508744	0.000111225	0.7198742
1455095_PM_at	histone cluster 2, H2be	Hist2h2be	319190	8.33585732	-1.52719017	7.8368E-05	1.07032122
1419089_PM_at	tissue inhibitor of metalloproteinase 3	Timp3	21859	11.5135934	-1.52990312	2.25235E-10	13.9547452
1426832_PM_at	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B	Ddx26b	236790	8.56620255	-1.53005258	4.76335E-05	1.56959613
1428562_PM_at	RIKEN cDNA 2210403K04 gene	2210403K04Rik	100042498	9.68932546	-1.53147907	7.76848E-05	1.07909153
1459467_PM_at	expressed sequence AA986715	AA986715	105449	4.83880278	-1.53265683	2.48375E-05	2.22407578
1429166_PM_s_at	calmin	Clmn	94040	10.4452416	-1.5328748	0.000143792	0.46323482
1419111_PM_at	inhibitor of growth family, member 2	Ing2	69260	8.77942198	-1.53308797	1.67584E-05	2.62021407
1456674_PM_at	RAD54 homolog B (S. cerevisiae)	Rad54b	623474	7.01250381	-1.53328409	2.66469E-05	2.1533298
1456048_PM_at	cytoplasmic polyadenylation element binding protein 3	Cpeb3	208922	4.90353512	-1.53646537	5.2385E-05	1.47416511
1448048_PM_at	cDNA sequence BC016495	BC016495	225994	5.26724323	-1.53782554	0.000167968	0.30810986
1424252_PM_at	heterogeneous nuclear ribonucleoprotein D-like	Hnrpdl	50926	10.5708934	-1.54211555	4.50698E-08	8.60815064
1451131_PM_at	ADP-ribosylation factor-like 6 interacting protein 1	Arl6ip1	54208	9.61335679	-1.54342012	7.78448E-05	1.07703057
1454070_PM_a_at	DDHD domain containing 1	Ddhd1	114874	8.86550176	-1.54508329	3.44132E-07	6.54885012
1418293_PM_at	interferon-induced protein with tetratricopeptide repeats 2	Ifit2	15958	7.47134505	-1.54851201	4.51504E-05	1.62334573
1432360_PM_a_at	transmembrane and tetratricopeptide repeat containing 4	Tmtc4	70551	7.29181728	-1.55145625	2.94481E-05	2.05279419
1431861_PM_a_at	outer dense fiber of sperm tails 2-like	Odf2l	52184	6.30579281	-1.55594079	4.58602E-05	1.60768332
1426218_PM_at	glucocorticoid induced transcript 1	Glcci1	170772	7.65432213	-1.556261	0.000218081	0.04780347
1447640_PM_s_at	pre B-cell leukemia transcription factor 3	Pbx3	18516	9.67770087	-1.55791767	3.29719E-06	4.26129809
1434917_PM_at	cordon-bleu	Cobl	12808	9.61842074	-1.55796135	0.000112239	0.71080565
1429144_PM_at	glycerophosphocholine phosphodiesterase GDE1 homolog (S. cerevisiae)	Gpcpd1	74182	8.51601903	-1.55857287	9.59876E-09	10.1732945
1426082_PM_a_at	solute carrier family 16 (monocarboxylic acid transporters), member 4	Slc16a4	229699	6.25185456	-1.559261	4.43671E-06	3.96126175
1448049_PM_at	jumonji domain containing 1C	Jmjd1c	108829	7.47323751	-1.56006523	6.81931E-06	3.52707999
1421346_PM_a_at	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	Slc6a6	21366	12.7552308	-1.56801883	5.75818E-06	3.69787985
1434945_PM_at	lysophosphatidylcholine acyltransferase 2	Lpcat2	270084	10.1620619	-1.57241611	1.43349E-07	7.43609504
1421471_PM_at	neuropeptide Y receptor Y1	Npy1r	18166	7.26974724	-1.57461573	6.2669E-05	1.29436368
1455388_PM_at	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	Pcmtd1	319263	10.9208124	-1.57464739	5.25689E-07	6.11966401
1416950_PM_at	tumor necrosis factor, alpha-induced protein 8	Tnfaip8	106869	8.7983906	-1.57617285	6.45048E-05	1.26541535
1418780_PM_at	cytochrome P450, family 39, subfamily a, polypeptide 1	Cyp39a1	56050	8.52793909	-1.58559941	5.94903E-05	1.34656562
1427254_PM_at	zinc finger protein 445	Zfp445	235682	10.055167	-1.58642563	0.000223163	0.02485838
1437872_PM_at	N-acyl phosphatidylethanolamine phospholipase D	Napepld	242864	8.12687616	-1.58770041	2.72575E-05	2.1305385
1429649_PM_at	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member 3	Slc35a3	229782	7.85063793	-1.59387699	2.8887E-05	2.07213881
1429345_PM_at	tubulin, gamma complex associated protein 4	Tubgcp4	51885	7.36182814	-1.59426858	0.000106243	0.76570835
1436299_PM_at	glutaminase	Gls	14660	10.5810699	-1.59500831	5.85416E-05	1.36268812
1448007_PM_at	bromodomain adjacent to zinc finger domain, 2B	Baz2b	407823	9.24490284	-1.59682857	6.83967E-07	5.85308867
1439107_PM_a_at	myeloid/lymphoid or mixed-lineage leukemia 5	Mll5	69188	7.92006862	-1.598711	3.60553E-05	1.84929961
1453360_PM_a_at	testis expressed gene 9	Tex9	21778	8.75858587	-1.59927004	2.12812E-06	4.70409464
1452991_PM_at	chromodomain helicase DNA binding protein 2	Chd2	244059	6.88069973	-1.60185817	0.000143928	0.46228938
1434630_PM_at	ankyrin repeat domain 28	Ankrd28	105522	9.33803837	-1.60322749	1.52952E-05	2.71226417
1438809_PM_at	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	Atp5c1	11949	7.18226871	-1.6057816	1.66845E-05	2.62466911
1423854_PM_a_at	RAS-like, family 11, member B	Rasl11b	68939	9.81299448	-1.60621784	5.77449E-07	6.02454392
1453004_PM_at	solute carrier family 22, member 23	Slc22a23	73102	10.0402219	-1.60727743	3.58251E-07	6.50811715
1449198_PM_a_at	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	St3gal5	20454	11.2749386	-1.61187049	1.32046E-10	14.4901574
1460062_PM_at	pleckstrin homology domain containing, family H (with MyTH4 domain) member 2	Plekhh2	213556	7.69383218	-1.61197902	2.64549E-05	2.1606039
1454149_PM_a_at	cyclin L2	Ccnl2	56036	9.14403686	-1.61282091	5.27049E-08	8.44966256
1422886_PM_a_at	CDC like kinase 4	Clk4	12750	10.4371411	-1.61313113	2.85933E-07	6.73654406
1451738_PM_at	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosamin	Ogt	108155	7.23803047	-1.61938135	1.82968E-05	2.53174862
1421193_PM_a_at	pre B-cell leukemia transcription factor 3	Pbx3	18516	8.06860136	-1.6214087	8.20376E-07	5.66892886
1446915_PM_at	DNA segment, Chr 7, ERATO Doi 316, expressed	D7Ertd316e	52275	5.9761066	-1.62152748	8.22267E-06	3.33817423
1440444_PM_at	fatty acid desaturase 1	Fads1	76267	7.33434349	-1.62409896	1.03619E-05	3.10485558
1422540_PM_at	fibulin 1	Fbln1	14114	6.88191935	-1.62479772	0.00010178	0.80864285
1426635_PM_at	acyl-Coenzyme A binding domain containing 3	Acbd3	170760	7.06808419	-1.62595597	1.13932E-06	5.33640144
1460335_PM_at	LysM, putative peptidoglycan-binding, domain containing 3	Lysmd3	80289	7.00728479	-1.62998184	8.33857E-05	1.00816223
1458021_PM_at	---	---	---	4.71929316	-1.63205615	7.39935E-05	1.12786522
1435917_PM_at	OCIA domain containing 2	Ociad2	433904	5.13777013	-1.6324524	4.56972E-05	1.61125956
1429811_PM_at	RIKEN cDNA 4933424B01 gene	4933424B01Rik	71177	5.88893803	-1.6401845	9.03646E-06	3.24293963
1433825_PM_at	neurotrophic tyrosine kinase, receptor, type 3	Ntrk3	18213	9.07739491	-1.64099951	8.47929E-05	0.99140481
1436872_PM_at	transforming, acidic coiled-coil containing protein 3	Tacc3	21335	4.65059139	-1.6437909	2.70501E-05	2.13822123
1433685_PM_a_at	RIKEN cDNA 6430706D22 gene /// Holliday junction recognition protein	6430706D22Rik	381280 /// 7	10.3928034	-1.64399038	4.74511E-08	8.55600856
1459420_PM_at	---	---	---	7.19364316	-1.64572729	1.72668E-05	2.59010785
1427084_PM_a_at	mitogen-activated protein kinase kinase kinase kinase 5	Map4k5	399510	10.086978	-1.64581816	0.000157824	0.37027597
1444677_PM_at	expressed sequence C77673	C77673	97696	6.65807563	-1.64718048	0.000189784	0.18631092
1433485_PM_x_at	G protein-coupled receptor 56	Gpr56	14766	8.52472788	-1.65288597	1.4666E-05	2.75459614
1440854_PM_at	RIKEN cDNA 2810403A07 gene	2810403A07Rik	74200	8.17639693	-1.65297125	6.1707E-06	3.62800118
1426301_PM_at	activated leukocyte cell adhesion molecule	Alcam	11658	10.5133562	-1.65478372	8.25712E-06	3.33395533
1429089_PM_s_at	RIKEN cDNA 2900026A02 gene	2900026A02Rik	243219	9.7130059	-1.65683215	4.82294E-06	3.87692235

1424393_PM_s_at	alcohol dehydrogenase, iron containing, 1	Adhfe1	76187	4.30872952	-1.65765473	7.48933E-05	1.11575474
1431042_PM_at	progestin and adipoQ receptor family member VIII	Paqr8	74229	6.52728949	-1.6586327	0.000114903	0.68734825
1454686_PM_at	RIKEN cDNA 6430706D22 gene /// Holliday junction recognition protein	6430706D22Ri	381280 /// 7	7.59312534	-1.66203126	1.17022E-05	2.98217916
1428377_PM_at	BTB (POZ) domain containing 11	Btbd11	74007	9.88947031	-1.66315003	0.000165155	0.32496154
1426208_PM_x_at	pleiomorphic adenoma gene-like 1	Plagl1	22634	9.848021	-1.66339794	7.12079E-05	1.1663172
1429247_PM_at	annexin A6	Anxa6	11749	6.76923983	-1.66374004	0.000111134	0.72069306
1456908_PM_at	cDNA sequence BC023202	BC023202	407816	6.43416983	-1.66669406	5.40726E-05	1.44234866
1416332_PM_at	cold inducible RNA binding protein	Cirbp	12696	6.52672895	-1.67108221	3.00642E-05	2.03197013
1435240_PM_at	bromodomain adjacent to zinc finger domain, 2B	Baz2b	407823	10.4735487	-1.6731451	3.52995E-05	1.87059098
1426421_PM_s_at	RNA binding motif protein 26	Rbm26	74213	8.36976246	-1.67471276	1.29769E-05	2.87793205
1433757_PM_a_at	nischarin	Nisch	64652	9.31980165	-1.6749868	0.000146743	0.4429513
1440984_PM_at	bromodomain adjacent to zinc finger domain, 2B	Baz2b	407823	8.02147673	-1.68147041	1.9146E-06	4.81106196
1418877_PM_at	Forkhead box D1	Foxd1	15229	4.97478281	-1.6836732	4.47699E-05	1.63184334
1459627_PM_at	Sterol-C4-methyl oxidase-like	Sc4mol	66234	9.61492276	-1.68588015	3.49529E-05	1.88050657
1438256_PM_at	eukaryotic translation initiation factor 5A2	Eif5a2	208691	7.13580996	-1.68726408	0.000196452	0.15188611
1426758_PM_s_at	maternally expressed 3	Meg3	17263	7.53695445	-1.69082497	4.59943E-05	1.6047513
1440668_PM_at	ADAMTS-like 3	Adamtsl3	269959	7.71889679	-1.69127782	1.73597E-07	7.24212149
1428646_PM_at	region containing RIKEN cDNA 2310056B04 gene; pre B-cell leukemia transcription factor 1 /// pre B-cell leukem	LOC676870 /// 18514 /// 67		10.0734704	-1.69257052	0.00022586	0.01289138
1449455_PM_at	hemopoietic cell kinase	Hck	15162	7.31666421	-1.69344446	0.000207046	0.09953901
1452125_PM_at	thyroid hormone receptor associated protein 3	Thrap3	230753	8.2846241	-1.69466663	0.000153108	0.40055749
1417214_PM_at	RAB27b, member RAS oncogene family	Rab27b	80718	9.81634864	-1.69490788	1.83694E-06	4.85295616
1423775_PM_s_at	protein regulator of cytokinesis 1	Prc1	233406	10.5625128	-1.6987905	6.73234E-05	1.22254078
1417384_PM_at	ectonucleoside triphosphate diphosphohydrolase 5	Entpd5	12499	8.35223019	-1.69884133	9.484E-06	3.19416728
1436544_PM_at	ATPase, class V, type 10D	Atp10d	231287	7.23455919	-1.69960601	0.000151725	0.40961414
1416034_PM_at	CD24a antigen	Cd24a	12484	10.9734644	-1.70716798	1.09069E-05	3.05316017
1423249_PM_at	natural killer tumor recognition sequence	Nktr	18087	9.41352429	-1.70776634	0.000212911	0.07170738
1456407_PM_a_at	similar to tousled-like kinase 1 /// tousled-like kinase 1	LOC100046241	100046241 /	7.61543094	-1.71395048	0.000147667	0.43668363
1419486_PM_at	forkhead box C1	Foxc1	17300	8.87656208	-1.71935442	1.5555E-05	2.69529453
1438065_PM_at	regulation of nuclear pre-mRNA domain containing 1A	Rprd1a	225283	7.55116156	-1.72110188	5.3495E-07	6.10197519
1451538_PM_at	SRY-box containing gene 9	Sox9	20682	10.4750311	-1.72333594	0.000203166	0.11839118
1455771_PM_at	benzodiazapine receptor associated protein 1	Bzrap1	207777	4.24457997	-1.72488585	4.4756E-06	3.95244337
1425768_PM_at	diablo homolog (Drosophila)	Diablo	66593	5.0135737	-1.72546746	0.000140522	0.48621029
1429538_PM_a_at	splicing factor, arginine/serine-rich 18	Sfrs18	66625	8.76545496	-1.7339752	6.43081E-06	3.58630881
1460241_PM_a_at	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	St3gal5	20454	7.36516513	-1.73535428	8.83888E-06	3.26524705
1438713_PM_at	Ras association (RalGDS/AF-6) domain family (N-terminal) member 8	Rassf8	71323	9.45388721	-1.73560022	2.15492E-06	4.69143444
1439109_PM_at	coiled-coil domain containing 68	Ccdc68	381175	6.88688467	-1.73606517	6.4927E-05	1.25887412
1442542_PM_at	eyes absent 4 homolog (Drosophila)	Eya4	14051	10.1331806	-1.7362547	1.04686E-05	3.09452484
1439151_PM_at	methionine sulfoxide reductase B3	Msrb3	320183	6.70865412	-1.73633904	7.28289E-05	1.1437617
1440038_PM_at	RIKEN cDNA B430007K19 gene	B430007K19Rik	320708	7.26059318	-1.74079147	0.000204217	0.11324855
1445298_PM_at	---	---	---	7.95531759	-1.74529789	8.76223E-05	0.95853966
1450512_PM_at	netrin 4	Ntn4	57764	6.57573972	-1.75874212	0.000108458	0.74506837
1438403_PM_s_at	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	Malat1	72289	11.3173048	-1.76129763	3.05929E-05	2.01444164
1420938_PM_at	heparan sulfate 6-O-sulfotransferase 2	Hs6st2	50786	9.289702	-1.76240571	7.50699E-06	3.43008564
1423774_PM_a_at	protein regulator of cytokinesis 1	Prc1	233406	10.769547	-1.76272121	1.02285E-05	3.11792642
1453285_PM_at	transmembrane protein 88	Tmem88	67020	7.07638272	-1.764688	1.2079E-05	2.95022342
1453395_PM_at	RIKEN cDNA 5330403D14 gene	5330403D14Rik	76675	5.03755284	-1.77117574	0.000202961	0.11939782
1429313_PM_at	receptor tyrosine kinase-like orphan receptor 1	Ror1	26563	7.57902151	-1.77233377	6.64533E-06	3.55317419
1429256_PM_at	maternally expressed 3	Meg3	17263	5.36523958	-1.77651541	8.88643E-06	3.25983377
1457809_PM_at	K(lysine) acetyltransferase 2B	Kat2b	18519	4.40727361	-1.77780535	0.000160019	0.3564889
1422837_PM_at	sciellin	Scel	64929	10.1377218	-1.78389652	6.89854E-07	5.84440822
1450090_PM_at	zinc finger protein 101	Zfp101	22643	6.84964255	-1.78435215	7.28998E-05	1.14278666
1437184_PM_at	GUF1 GTPase homolog (S. cerevisiae)	Guf1	231279	7.55517924	-1.79213079	5.32875E-06	3.77616704
1442365_PM_at	---	---	---	4.20079658	-1.793951	3.01129E-05	2.03034236
1447951_PM_at	---	---	---	8.55844578	-1.79454403	0.000159056	0.36251294
1430133_PM_at	TBC1 domain family, member 8B	Tbc1d8b	245638	9.48265817	-1.79802978	4.09776E-05	1.72073138
1439153_PM_at	ring finger protein 144B	Rnf144b	218215	7.92183202	-1.79810643	0.000222558	0.02756195
1439495_PM_at	RIKEN cDNA 4933407H18 gene	4933407H18Rik	71101	9.19239492	-1.80222431	1.98804E-06	4.77297886
1417450_PM_a_at	transforming, acidic coiled-coil containing protein 3	Tacc3	21335	9.0680359	-1.80277154	0.000101864	0.80781192
1458873_PM_at	asp (abnormal spindle)-like, microcephaly associated (Drosophila)	Aspm	12316	4.86518652	-1.80527545	0.000222785	0.02654616
1459750_PM_s_at	G protein-coupled receptor 123	Gpr123	52389	7.78790925	-1.80531835	0.000169047	0.30172069
1418037_PM_at	complement component 4 binding protein	C4bp	12269	7.82078276	-1.80735375	9.48071E-07	5.52244544
1440935_PM_at	---	---	---	8.98175438	-1.8108042	0.000149719	0.42290217
1452183_PM_a_at	maternally expressed 3	Meg3	17263	8.17409391	-1.81391922	3.74383E-07	6.46349652
1448752_PM_at	carbonic anhydrase 2	Car2	12349	8.95327698	-1.8183168	1.42262E-05	2.78528284
1449530_PM_at	trichorhinophalangeal syndrome I (human)	Trps1	83925	7.97912505	-1.81976117	1.66235E-05	2.62835611
1440402_PM_at	RIKEN cDNA 4831426I19 gene	4831426I19Rik	212073	6.93394542	-1.82460203	1.30302E-05	2.87380133
1417355_PM_at	paternally expressed 3	Peg3	18616	10.3820245	-1.82819802	1.97238E-08	9.44475128
1442335_PM_at	---	---	---	7.18556935	-1.8282766	8.47231E-05	0.9922291
1452954_PM_at	ubiquitin-conjugating enzyme E2C	Ube2c	68612	9.55150977	-1.82896245	0.000123224	0.61745135
1433763_PM_at	ectonucleoside triphosphate diphosphohydrolase 5	Entpd5	12499	8.79338578	-1.83021057	4.37896E-06	3.97450149
1435438_PM_at	SRY-box containing gene 8	Sox8	20681	10.9926162	-1.83088308	2.06377E-07	7.06687731
1452413_PM_at	RIKEN cDNA C230081A13 gene	C230081A13Rik	244895	5.58749551	-1.8309921	1.23983E-05	2.92391201
1455238_PM_at	melanoma associated antigen (mutated) 1-like 1	Mum1l1	245631	8.03671374	-1.833226	3.54215E-05	1.86712337
1453583_PM_at	zinc finger, ZZ-type with EF hand domain 1	Zzef1	195018	8.47299019	-1.83357578	4.15097E-06	4.02853589
1433893_PM_s_at	sperm associated antigen 5	Spag5	54141	7.47637568	-1.8346647	3.56788E-05	1.8598484
1451322_PM_at	carboxymethylenebutenolidase-like (Pseudomonas)	Cmbl	69574	7.23733684	-1.83575291	0.000107128	0.75741078
1452160_PM_at	TCDD-inducible poly(ADP-ribose) polymerase	Tiparp	99929	8.09450991	-1.84533784	2.82894E-05	2.09316509
1449967_PM_at	single-minded homolog 1 (Drosophila)	Sim1	20464	4.33500142	-1.84712232	0.000211772	0.07705077
1452040_PM_a_at	cell division cycle associated 3	Cdca3	14793	9.38307821	-1.84831579	0.000190397	0.18309901
1456096_PM_at	RIKEN cDNA 6430573F11 gene	6430573F11Rik	319582	4.69793346	-1.85024534	4.54893E-05	1.6158364
1455917_PM_at	neurotrophic tyrosine kinase, receptor, type 3	Ntrk3	18213	7.00370702	-1.85157078	0.000112962	0.70438359
1442594_PM_at	Ttk protein kinase	Ttk	22137	5.46458334	-1.85158619	7.57216E-05	1.10473417
1433743_PM_at	dachshund 1 (Drosophila)	Dach1	13134	6.81058414	-1.85440776	0.000196023	0.15406876
1428765_PM_at	maternally expressed 3	Meg3	17263	6.94512303	-1.85890669	6.98999E-05	1.18489761
1445048_PM_at	bromodomain adjacent to zinc finger domain, 2B	Baz2b	407823	4.99251335	-1.86191535	2.03377E-05	2.42525935
1419088_PM_at	tissue inhibitor of metalloproteinase 3	Timp3	21859	9.1856662	-1.86237299	1.74209E-10	14.2124199
1420416_PM_at	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	Sema3a	20346	8.48302591	-1.86553321	1.9274E-05	2.4793507
1438420_PM_at	RNA binding motif protein 39	Rbm39	170791	9.53290837	-1.8689376	3.19488E-05	1.97083857
1429658_PM_a_at	structural maintenance of chromosomes 2	Smc2	14211	7.88842765	-1.87002526	0.000160597	0.35288815
1455859_PM_at	RIKEN cDNA A330021E22 gene	A330021E22Rik	207686	9.55223779	-1.87497239	0.000148585	0.43049184
1422941_PM_at	wingless-related MMTV integration site 16	Wnt16	93735	9.17398863	-1.87833136	0.00012658	0.59060134
1458601_PM_at	RIKEN cDNA 8030447M02 gene	8030447M02Ri	399578	5.64567229	-1.87839027	5.76454E-05	1.37816249
1423100_PM_at	FBJ osteosarcoma oncogene	Fos	14281	9.5464759	-1.8817637	1.65222E-07	7.29221685
1432591_PM_at	pregnancy-associated plasma protein A	Pappa	18491	6.72948451	-1.88353969	1.12671E-05	3.02038939
1440693_PM_at	---	---	---	7.33003388	-1.88450222	1.18468E-05	2.9697921
1435744_PM_at	RIKEN cDNA 6720401G13 gene	6720401G13Rik	103012	9.00194677	-1.88589327	1.46306E-05	2.75703412
1437765_PM_at	cytoplasmic polyadenylation element binding protein 3	Cpeb3	208922	8.11500496	-1.8865636	1.92096E-05	2.48271769

1423963_PM_at	WD repeat domain 26	Wdr26	226757	6.19254449	-1.89143218	8.50668E-05	0.98817574
1426013_PM_s_at	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 4	Plekha4	69217	6.66466161	-1.89191743	3.41225E-06	4.22662026
1450098_PM_at	dihydrodipicolinate synthase-like, mitochondrial	Dhdpsl	67432	8.06104222	-1.89280343	3.07328E-05	2.00985354
1431204_PM_at	RIKEN cDNA 4930578N16 gene	4930578N16Ril	75051	6.10798876	-1.89336876	0.000121246	0.63363202
1455834_PM_x_at	transforming, acidic coiled-coil containing protein 3	Tacc3	21335	5.94680113	-1.8939133	4.11441E-06	4.03747659
1427663_PM_a_at	CDC like kinase 4	Clk4	12750	10.0434435	-1.89443711	7.89749E-05	1.06259363
1445537_PM_at	RIKEN cDNA 2310039F13 gene	2310039F13Rik	76754	7.22657636	-1.89528301	0.000199204	0.13802063
1439922_PM_at	proline-rich coiled-coil 1	Prrc1	73137	6.66784116	-1.89798983	9.11319E-05	0.91922414
1427550_PM_at	paternally expressed 10	Peg10	170676	12.6102119	-1.89892212	0.000125043	0.60280696
1427133_PM_s_at	low density lipoprotein receptor-related protein 2	Lrp2	14725	7.20721358	-1.89974707	2.69215E-06	4.46629101
1456665_PM_at	eyes absent 4 homolog (Drosophila)	Eya4	14051	9.07360066	-1.90658026	9.86473E-06	3.15445893
1452320_PM_at	low density lipoprotein receptor-related protein 2	Lrp2	14725	7.39564549	-1.9086848	1.9119E-05	2.48747856
1433939_PM_at	AF4/FMR2 family, member 3	Aff3	16764	8.7605135	-1.91154724	2.27304E-07	6.96902579
1417673_PM_at	growth factor receptor bound protein 14	Grb14	50915	7.58469171	-1.91880702	7.13799E-07	5.80985356
1428083_PM_at	nuclear paraspeckle assembly transcript 1 (non-protein coding)	Neat1	66961	9.11713693	-1.91913964	4.3225E-08	8.65047362
1439380_PM_x_at	maternally expressed 3	Meg3	17263	8.82494833	-1.92541832	8.65505E-07	5.61470396
1435306_PM_a_at	kinesin family member 11	Kif11	16551	7.68623156	-1.92987664	0.000188554	0.1927945
1423092_PM_at	inner centromere protein	Incenp	16319	5.80649155	-1.93405388	9.29799E-05	0.89913007
1438558_PM_x_at	forkhead box Q1	Foxq1	15220	7.23979636	-1.93681147	6.23251E-05	1.29988266
1429129_PM_at	leucine rich repeat and coiled-coil domain containing 1	Lrrcc1	71710	7.452197	-1.93879787	4.41982E-06	3.9651169
1427551_PM_at	ubiquitin specific peptidase 29	Usp29	57775	7.22645616	-1.9412685	1.50299E-05	2.72989601
1449558_PM_at	coagulation factor VIII	F8	14069	4.97892076	-1.94253115	1.23075E-05	2.93132839
1444232_PM_at	protein kinase, cGMP-dependent, type I	Prkg1	19091	8.50178923	-1.94561863	3.40648E-06	4.22833021
1459560_PM_at	speckle-type POZ protein-like	Spopl	76857	5.57171366	-1.94984468	3.35217E-05	1.92252941
1453769_PM_at	cytoskeleton associated protein 2-like	Ckap2l	70466	8.88316445	-1.95442875	0.000106076	0.76728214
1427516_PM_a_at	biregional cell adhesion molecule-related/down-regulated by oncogenes (Cdon) binding protein	Boc	117606	5.54014523	-1.95705458	4.05967E-05	1.7301104
1440796_PM_at	RIKEN cDNA A330021E22 gene	A330021E22Rik	207686	7.39714265	-1.96052458	0.000188038	0.19552925
1424950_PM_at	SRY-box containing gene 9	Sox9	20682	8.53427185	-1.96335453	8.87206E-06	3.26146637
1454694_PM_a_at	topoisomerase (DNA) II alpha	Top2a	21973	9.3346267	-1.96541722	2.38599E-05	2.26448138
1437251_PM_at	cell division cycle associated 2	Cdca2	108912	5.77820198	-1.97075186	1.39094E-05	2.80797556
1420178_PM_at	---	---	---	6.48205793	-1.98395904	0.000106116	0.76690418
1460448_PM_s_at	tetratricopeptide repeat domain 14	Ttc14	67120	9.39477072	-1.98656927	3.25865E-05	1.95096995
1441491_PM_at	RIKEN cDNA A330068G13 gene	A330068G13Ril	414087	7.89003762	-1.9875966	8.16037E-05	1.02979667
1435741_PM_at	phosphodiesterase 8B	Pde8b	218461	6.54318499	-1.99929742	1.46277E-05	2.75723393
1459256_PM_at	---	---	---	5.50516947	-2.00029343	7.92311E-05	1.05934939
1452197_PM_at	structural maintenance of chromosomes 4	Smc4	70099	9.90481244	-2.00092087	3.388E-06	4.2338292
1455786_PM_at	zinc finger protein 820	Zfp820	75424	4.43817721	-2.00169788	0.000182086	0.22760446
1460121_PM_at	RIKEN cDNA 9630010G10 gene	9630010G10Ril	399612	8.38498052	-2.00451649	3.77646E-06	4.12410403
1419153_PM_at	RIKEN cDNA 2810417H13 gene	2810417H13Ril	68026	9.73976702	-2.01381348	8.18882E-05	1.02631147
1427275_PM_at	structural maintenance of chromosomes 4	Smc4	70099	10.2589553	-2.0179698	5.6889E-06	3.71010673
1435938_PM_at	cytoskeleton associated protein 2-like	Ckap2l	70466	9.21782493	-2.02682079	0.000144196	0.46043477
1455990_PM_at	kinesin family member 23	Kif23	71819	8.08489815	-2.03858798	9.77262E-05	0.84930481
1426420_PM_at	RNA binding motif protein 26	Rbm26	74213	7.23107844	-2.04149842	8.9126E-05	0.94150456
1452905_PM_at	maternally expressed 3	Meg3	17263	9.32100395	-2.04476679	7.62319E-07	5.74325479
1438030_PM_at	RAS, guanyl releasing protein 3	Rasgrp3	240168	8.09505023	-2.05418348	4.50397E-05	1.62580904
1417445_PM_at	NDC80 homolog, kinetochore complex component (S. cerevisiae)	Ndc80	67052	6.82845626	-2.06030627	0.000121449	0.63196037
1459322_PM_at	---	---	---	4.89708016	-2.08808363	5.70177E-06	3.70782296
1439691_PM_at	DNA segment, Chr 5, ERATO Doi 579, expressed	D5Ertd579e	320661	5.49323409	-2.08990221	0.000171446	0.28766082
1434974_PM_at	pyruvate dehydrogenase kinase, isoenzyme 1	Pdk1	228026	6.28340166	-2.09454687	1.81684E-05	2.53883941
1416846_PM_a_at	PDZ domain containing RING finger 3	Pdzrn3	55983	8.91244465	-2.09698151	6.54073E-05	1.25148632
1451456_PM_at	Holliday junction recognition protein	Hjurp	381280	8.13936783	-2.10147134	1.78103E-06	4.88423265
1448226_PM_at	ribonucleotide reductase M2	Rrm2	20135	7.99848899	-2.1076953	7.11836E-05	1.16665917
1418979_PM_at	aldo-keto reductase family 1, member C14	Akr1c14	105387	5.71108859	-2.11277945	2.68604E-05	2.14530028
1426283_PM_at	neurotrimin	Ntm	235106	6.61427833	-2.11607435	5.97722E-05	1.34182276
1425321_PM_a_at	calmin	Clmn	94040	8.04486701	-2.11687544	1.38193E-05	2.81452734
1419717_PM_at	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E	Sema3e	20349	8.23467086	-2.15802398	0.000135998	0.51889417
1427763_PM_a_at	calcium/calmodulin-dependent protein kinase II, delta	Camk2d	108058	7.79046	-2.1609475	2.99369E-11	15.9733853
1427141_PM_at	NDC80 homolog, kinetochore complex component pseudogene	2700099C18Rik	77022	6.44799436	-2.16222885	4.43563E-06	3.96150777
1446906_PM_at	expressed sequence C81615	C81615	97548	4.11894287	-2.18594754	2.33869E-05	2.28463291
1442063_PM_at	ADAMTS-like 1	Adamtsl1	77739	4.27168162	-2.18651811	1.68829E-05	2.61276031
1417215_PM_at	RAB27b, member RAS oncogene family	Rab27b	80718	6.6954019	-2.2008996	1.89242E-06	4.82284846
1449171_PM_at	Ttk protein kinase	Ttk	22137	6.82576937	-2.20503007	3.41662E-05	1.90338607
1425847_PM_a_at	RIKEN cDNA B230120H23 gene	B230120H23Ril	65964	6.57491576	-2.21361356	1.99844E-05	2.44290359
1446613_PM_at	---	---	---	6.72682425	-2.2192314	0.000173048	0.27838374
1421035_PM_a_at	membrane associated guanylate kinase, WW and PDZ domain containing 3	Magi3	99470	6.1077486	-2.22219602	2.47855E-07	6.88133442
1456658_PM_at	actin, alpha 2, smooth muscle, aorta	Acta2	11475	6.62506153	-2.22399021	8.21726E-06	3.33883854
1428837_PM_at	kelch-like 14 (Drosophila)	Klhl14	225266	6.76465409	-2.23120216	0.000114706	0.68906208
1429857_PM_at	RIKEN cDNA 2900092D14 gene	2900092D14Ril	73100	8.26003293	-2.23413603	0.00021728	0.05146985
1427673_PM_a_at	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E	Sema3e	20349	9.34464088	-2.25251488	5.28941E-06	3.7836517
1453416_PM_at	growth arrest-specific 2 like 3	Gas2l3	237436	8.65580022	-2.26720714	2.67723E-05	2.14860512
1449865_PM_at	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	Sema3a	20346	7.74659834	-2.26871461	1.14763E-06	5.32904823
1416203_PM_at	aquaporin 1	Aqp1	11826	6.36389593	-2.27185632	1.2076E-06	5.27748734
1441466_PM_at	transformer 2 beta homolog (Drosophila)	Tra2b	20462	7.42840233	-2.31412886	9.76178E-05	0.85041544
1419152_PM_at	RIKEN cDNA 2810417H13 gene	2810417H13Ril	68026	9.13437135	-2.31429864	8.8887E-05	0.94419277
1456623_PM_at	tropomyosin 1, alpha	Tpm1	22003	9.37113747	-2.32356871	5.2385E-08	8.45582855
1427276_PM_at	structural maintenance of chromosomes 4	Smc4	70099	9.50016174	-2.3279703	3.59964E-06	4.17257649
1437989_PM_at	phosphodiesterase 8B	Pde8b	218461	6.88959244	-2.3332098	1.12929E-05	3.01808425
1433302_PM_at	cadherin 10	Cdh10	320873	4.14954352	-2.33765072	0.000101747	0.80896723
1429171_PM_a_at	non-SMC condensin I complex, subunit G	Ncapg	54392	9.59265967	-2.34658614	2.63811E-05	2.1634149
1428055_PM_at	RNA imprinted and accumulated in nucleus	Rian	75745	8.23461629	-2.34701599	8.8812E-06	3.26042759
1447096_PM_at	---	---	---	4.65529452	-2.38036716	6.41107E-05	1.27155909
1417356_PM_at	paternally expressed 3	Peg3	18616	10.9115166	-2.3965072	9.86586E-05	0.83980303
1438234_PM_at	WD repeat domain 26	Wdr26	226757	4.79385076	-2.39778408	3.94941E-05	1.7577712
1420388_PM_at	protease, serine, 12 neurotrypsin (motopsin)	Prss12	19142	4.50804766	-2.40180632	2.21824E-06	4.66213366
1449751_PM_at	Solute carrier family 6 (neurotransmitter transporter, taurine), member 6	Slc6a6	21366	6.33600678	-2.40983709	0.0001166	0.6726904
1427298_PM_at	dynamin 3, opposite strand	Dnm3os	474332	11.2882928	-2.41523901	2.68568E-05	2.1454368
1436713_PM_s_at	maternally expressed 3	Meg3	17263	7.97610304	-2.46499463	0.000115484	0.68230122
1459687_PM_x_at	---	---	---	5.05361797	-2.47174045	9.5145E-07	5.5188427
1451800_PM_at	GRIP and coiled-coil domain containing 2	Gcc2	70297	5.98519354	-2.50163534	2.26097E-06	4.64283639
1423294_PM_at	mesoderm specific transcript	Mest	17294	7.86917933	-2.53307388	2.11544E-07	7.04182737
1450377_PM_at	similar to thrombospondin 1 /// thrombospondin 1	LOC640441 /// 21825 /// 64		9.4074281	-2.58557425	9.61643E-05	0.86542715
1440462_PM_at	RIKEN cDNA B930068K11 gene	B930068K11Rik	320622	5.05642731	-2.59372483	0.000145835	0.44914918
1448201_PM_at	secreted frizzled-related protein 2	Sfrp2	20319	10.4605518	-2.62751358	1.46244E-05	2.75745804
1449025_PM_at	interferon-induced protein with tetratricopeptide repeats 3	Ifit3	15959	8.32330146	-2.6305955	1.17428E-06	5.30580464
1439168_PM_at	calcium/calmodulin-dependent protein kinase II, delta	Camk2d	108058	8.21985005	-2.65813817	4.49022E-05	1.62887916
1438169_PM_a_at	FERM domain containing 4B	Frmd4b	232288	6.60604297	-2.6591243	3.39791E-06	4.23087704
1421225_PM_a_at	solute carrier family 4 (anion exchanger), member 4	Slc4a4	54403	5.70346859	-2.67571282	1.68315E-05	2.61582837

1420417_PM_at	predicted gene 2521 /// sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin)	Gm2521 /// Se	100039963 /	5.86940384	-2.68647447	3.51897E-06	4.19548689
1458374_PM_at	expressed sequence C79407	C79407	217653	6.25997766	-2.73293261	0.000139131	0.49614288
1431248_PM_at	RIKEN cDNA 5031426D15 gene	5031426D15Rik	68144	5.64601385	-2.73885077	0.000130022	0.56379341
1442903_PM_at	RIKEN cDNA 4732423E21 gene	4732423E21Rik	106967	6.77080184	-2.7671206	0.000214383	0.06484063
1448729_PM_a_at	septin 4	41886	18952	7.84135488	-2.77407426	3.20429E-08	8.9535698
1435185_PM_at	leucine rich repeat and coiled-coil domain containing 1	Lrrcc1	71710	8.04670641	-2.77823495	6.37425E-05	1.27733494
1439058_PM_at	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	Sfpq	71514	6.51744666	-2.80278727	3.62625E-06	4.16513133
1436287_PM_at	predicted gene 10664	Gm10664	100038489	5.86281564	-2.82958294	1.64482E-05	2.63903586
1420148_PM_at	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	Slc6a6	21366	7.9825805	-2.8498278	1.792E-05	2.55270828
1432592_PM_at	pregnancy-associated plasma protein A	Pappa	18491	6.53052255	-2.85923452	1.41094E-06	5.11996179
1455258_PM_at	potassium voltage gated channel, Shaw-related subfamily, member 2	Kcnc2	268345	6.7223197	-2.87779358	1.64421E-06	4.9651171
1459120_PM_at	erythrocyte protein band 4.1-like 5	Epb4.1l5	226352	4.44916302	-2.8834847	1.49595E-05	2.73462816
1440587_PM_at	---	---	---	6.13015339	-2.88690881	0.000166784	0.31516669
1456647_PM_a_at	eyes absent 4 homolog (Drosophila)	Eya4	14051	7.76333029	-2.90437298	1.40652E-06	5.12313682
1439095_PM_at	splicing factor, arginine/serine-rich 11	Sfrs11	69207	7.48475339	-2.90633073	2.79219E-05	2.10631519
1445397_PM_at	---	---	---	4.01879123	-2.91419474	1.28638E-05	2.88675805
1449528_PM_at	c-fos induced growth factor	Figf	14205	5.65111031	-2.91485985	8.79479E-10	12.5854192
1427482_PM_a_at	carbonic anhydrase 8	Car8	12319	5.91849376	-2.92309921	7.61535E-07	5.74429666
1438954_PM_x_at	c-fos induced growth factor	Figf	14205	6.84574626	-2.96632838	8.41009E-07	5.6437761
1445412_PM_at	coiled-coil domain containing 73	Ccdc73	211936	6.32392067	-2.99710323	2.36959E-05	2.2714238
1438953_PM_at	c-fos induced growth factor /// similar to FIGF	Figf /// LOC100	100047108 /	6.68483174	-3.00309877	5.25271E-07	6.12046955
1452161_PM_at	TCDD-inducible poly(ADP-ribose) polymerase	Tiparp	99929	6.368027	-3.02618185	2.014E-06	4.75985435
1445387_PM_at	SUMO/sentrin specific peptidase 6	Senp6	215351	5.23047953	-3.04989041	0.000150342	0.41875424
1453683_PM_a_at	centrosomal protein 55	Cep55	74107	5.52116915	-3.07552539	2.31247E-05	2.2959782
1428304_PM_at	establishment of cohesion 1 homolog 2 (S. cerevisiae)	Esco2	71988	7.08661855	-3.09607708	2.05881E-06	4.73758897
1459457_PM_at	calcium/calmodulin-dependent protein kinase II, delta	Camk2d	108058	8.65095188	-3.11101692	6.5208E-05	1.25454456
1440765_PM_at	Fraser syndrome 1 homolog (human)	Fras1	231470	5.83950627	-3.11402772	0.000203879	0.11489849
1426594_PM_at	FERM domain containing 4B	Frmd4b	232288	6.29942765	-3.14420703	1.90113E-07	7.15004692
1440924_PM_at	kinesin family member 20B	Kif20b	240641	6.65806879	-3.19196975	3.17685E-05	1.97653025
1459444_PM_at	zinc finger protein 91	Zfp91	109910	5.81842752	-3.19508896	3.59406E-05	1.85250298
1441333_PM_at	---	---	---	6.40531708	-3.20853082	0.000192114	0.17414569
1447381_PM_at	---	---	---	4.9470666	-3.22597715	1.09725E-07	7.70689943
1438833_PM_at	cancer susceptibility candidate 5	Casc5	76464	5.37892056	-3.27096691	2.00003E-05	2.44210093
1441656_PM_at	RIKEN cDNA B930068K11 gene	B930068K11Rik	320622	6.02010186	-3.32461707	0.000147898	0.43511831
1452123_PM_s_at	FERM domain containing 4B	Frmd4b	232288	6.1504027	-3.3953295	2.44605E-07	6.89470726
1441677_PM_at	---	---	---	5.38219002	-3.4204763	0.000145665	0.45031384
1416761_PM_at	hydroxysteroid 11-beta dehydrogenase 2	Hsd11b2	15484	5.69804711	-3.469713	8.3293E-08	7.98610724
1426817_PM_at	antigen identified by monoclonal antibody Ki 67	Mki67	17345	9.10548933	-3.55537819	3.35994E-07	6.57309609
1435005_PM_at	centromere protein E	Cenpe	229841	7.84042779	-3.57824161	1.59071E-06	4.99859222
1442226_PM_at	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E	Sema3e	20349	4.30866473	-3.63921856	0.000150947	0.41474758
1457339_PM_at	---	---	---	4.64585928	-3.68734719	3.74278E-05	1.81175995
1458447_PM_at	centromere protein F	Cenpf	108000	5.6132918	-3.72891935	7.75357E-05	1.08101713
1439040_PM_at	centromere protein E	Cenpe	229841	6.82572203	-3.78129284	1.73744E-06	4.90930468
1439695_PM_a_at	kinesin family member 20B	Kif20b	240641	5.76836868	-3.8005412	1.10722E-06	5.36534001
1455422_PM_x_at	septin 4	41886	18952	7.5515459	-3.85104999	1.50671E-09	12.0430259
1443264_PM_at	membrane-spanning 4-domains, subfamily A, member 2	Ms4a2	14126	7.43909944	-3.90495498	8.64418E-05	0.97211994
1430193_PM_at	cancer susceptibility candidate 5	Casc5	76464	4.30121321	-3.92568022	7.03312E-06	3.4959109
1444432_PM_at	RIKEN cDNA D330040H18 gene	D330040H18Ri	320847	5.16732008	-4.67139459	1.72864E-05	2.58896346
1427161_PM_at	centromere protein F	Cenpf	108000	5.89659376	-4.69424003	7.86732E-05	1.0664276
1421475_PM_at	membrane-spanning 4-domains, subfamily A, member 2	Ms4a2	14126	4.48883217	-5.04299745	1.84518E-06	4.84842874

Table S2. Genes under-represented in kidneys 10d after UUO from Tnfrsf12-/- compared to WT

				x10day_DISEASED_WT-vs-x10day_DISEASED_Fn14_KO		
	Gene Title	GeneSymbol	AvgNormInt	Fold Change	p.value	lods
1437128_PM_a_at	RIKEN cDNA A630033E08 gene	.630033E08Ri	4.55	49.18	0.00	55.60
1418571_PM_at	tumor necrosis factor receptor superfamily, member 12a	Tnfrsf12a	5.02	14.37	0.00	43.99
1418572_PM_x_at	tumor necrosis factor receptor superfamily, member 12a	Tnfrsf12a	4.94	11.31	0.00	43.00
1424631_PM_a_at	Immunoglobulin heavy chain (gamma polypeptide)	Ighg	4.99	6.39	0.00	-2.82
1444589_PM_at	predicted gene 4944	Gm4944	4.54	4.17	0.00	22.72
1425738_PM_at	similar to anti-glycoprotein-B of human Cytomegalovirus immunoglobulin Vl chain /// similar to Ig kappa chain V-III region PC 6684	47222 /// LO	3.08	3.71	0.00	-0.90
1427329_PM_a_at	immunoglobulin heavy chain 6 (heavy chain of IgM)	Igh-6	5.11	3.61	0.01	-3.88
1427351_PM_s_at	immunoglobulin heavy chain 6 (heavy chain of IgM)	Igh-6	6.85	3.56	0.05	-4.98
1416957_PM_at	POU domain, class 2, associating factor 1	Pou2af1	2.91	3.31	0.00	1.26
1420466_PM_at	mucin-like 1	Mucl1	3.58	3.23	0.00	4.40
1426174_PM_s_at	immunoglobulin heavy chain 3 (serum IgG2b) /// Immunoglobulin heavy chain (gamma polypeptide)	Igh-3 /// Ighg	2.53	3.20	0.01	-3.28
1417851_PM_at	chemokine (C-X-C motif) ligand 13	Cxcl13	4.29	3.00	0.00	-2.67
1449846_PM_at	eosinophil-associated, ribonuclease A family, member 2	Ear2	6.07	2.85	0.01	-3.03
1422412_PM_x_at	eosinophil-associated, ribonuclease A family, member 3	Ear3	3.62	2.85	0.00	2.37
1457685_PM_at	zinc finger protein 81	Zfp81	3.92	2.56	0.00	-0.92
1422411_PM_s_at	eosinophil-associated, ribonuclease A family, member 1 /// eosinophil-associated, ribonuclease A family, member 12 /// eosinophil-associated, rib	Ear12 /// Ear2	4.57	2.51	0.00	-1.06
1449015_PM_at	resistin like alpha	Retnla	4.49	2.48	0.00	2.24
1448028_PM_at	TBC1 domain family, member 24	Tbc1d24	5.66	2.46	0.00	12.68
1435331_PM_at	pyrin and HIN domain family, member 1	Pyhin1	3.76	2.42	0.00	4.28
1443816_PM_s_at	phosphoinositide-3-kinase, regulatory subunit 6	Pik3r6	4.69	2.39	0.00	3.10
1425385_PM_a_at	Immunoglobulin heavy chain 6 (heavy chain of IgM)	Igh-6	4.96	2.38	0.16	-5.95
1451513_PM_x_at	serine (or cysteine) peptidase inhibitor, clade A, member 1A /// serine (or cysteine) preptidase inhibitor, clade A, member 1B	na1a /// Serp	5.92	2.37	0.00	-0.35
1425471_PM_x_at	---	---	2.92	2.37	0.00	5.03
1435984_PM_at	Zinc finger protein 40	Zfp40	6.11	2.32	0.00	9.78
1458462_PM_at	Rho GTPase activating protein 30	Arhgap30	3.19	2.31	0.00	2.00
1418282_PM_x_at	serine (or cysteine) preptidase inhibitor, clade A, member 1B	Serpina1b	7.01	2.30	0.00	-0.71
1425470_PM_at	---	---	3.57	2.28	0.00	6.12
1437217_PM_at	ankyrin repeat domain 6	Ankrd6	5.34	2.26	0.00	-1.44
1442350_PM_at	---	---	3.41	2.24	0.00	5.55
1425151_PM_a_at	NADPH oxidase organizer 1	Noxo1	4.40	2.22	0.00	7.46
1422831_PM_at	fibrillin 2	Fbn2	5.08	2.20	0.00	-0.36
1427859_PM_at	immunoglobulin kappa chain variable 19 (V19)-15	Igk-V19-15	3.21	2.19	0.00	-1.42
1455426_PM_at	Eph receptor A3	Epha3	4.08	2.16	0.00	2.19
1421228_PM_at	chemokine (C-C motif) ligand 7	Ccl7	4.68	2.14	0.00	-2.82
1434873_PM_a_at	ArfGAP with coiled-coil, ankyrin repeat and PH domains 1 /// similar to Centaurin, beta 1	/// LOC1000	3.67	2.14	0.00	5.23
1451289_PM_at	doublecortin-like kinase 1	Dclk1	2.64	2.13	0.00	0.14
1427892_PM_at	myosin IG	Myo1g	4.22	2.11	0.00	3.27
1434152_PM_at	apolipoprotein L 7c /// apolipoprotein L, 3-like	ol7c /// Gm82	3.52	2.10	0.00	0.21
1426159_PM_x_at	T-cell receptor beta, joining region	Tcrb-J	4.74	2.09	0.00	-0.42
1448575_PM_at	interleukin 7 receptor	Il7r	3.75	2.08	0.00	3.44
1428720_PM_s_at	RIKEN cDNA 2010309G21 gene /// immunoglobulin lambda chain, constant region 2 /// immunoglobulin lambda chain, constant region 3	21Rik /// Igl-C	5.17	2.07	0.03	-4.66
1425374_PM_at	2'-5' oligoadenylate synthetase 3	Oas3	3.13	2.06	0.00	-0.31
1418776_PM_at	guanylate-binding protein 8	Gbp8	3.65	2.06	0.00	1.48
1454830_PM_at	fibrillin 2	Fbn2	5.13	2.00	0.00	-1.02
1438467_PM_at	macrophage galactose N-acetyl-galactosamine specific lectin 2	Mgl2	4.71	1.99	0.00	-0.46
1423602_PM_at	TNF receptor-associated factor 1	Traf1	5.43	1.99	0.00	6.40
1422632_PM_at	cathepsin W	Ctsw	4.61	1.99	0.00	-1.82
1427860_PM_at	similar to immunoglobulin kappa-chain /// similar to Ig kappa chain V-V region MPC11 precursor	47162 /// LO	2.47	1.98	0.00	-2.33
1437578_PM_at	chloride channel calcium activated 2	Clca2	2.61	1.95	0.01	-3.61
1453321_PM_at	fibronectin type III domain containing 1	Fndc1	4.98	1.94	0.01	-3.28
1422723_PM_at	stimulated by retinoic acid gene 6	Stra6	5.68	1.94	0.00	-0.94
1424546_PM_at	cDNA sequence BC003965	BC003965	4.61	1.92	0.00	15.21
1430523_PM_s_at	immunoglobulin lambda chain, variable 1	Igl-V1	3.79	1.90	0.13	-5.78
1428947_PM_at	RIKEN cDNA 2010001M09 gene	010001M09R	3.08	1.87	0.01	-3.85
1455656_PM_at	B and T lymphocyte associated	Btla	3.77	1.86	0.00	0.57
1455627_PM_at	collagen, type VIII, alpha 1	Col8a1	6.05	1.86	0.01	-3.38
1437911_PM_at	RIKEN cDNA 6330416L07 gene	330416L07Ri	4.96	1.86	0.00	7.33
1454838_PM_s_at	protein kinase domain containing, cytoplasmic	Pkdcc	3.21	1.86	0.00	7.97
1426168_PM_a_at	RIKEN cDNA A130082M07 gene /// T-cell receptor alpha chain	82M07Rik //	4.33	1.86	0.00	-2.40
1426471_PM_at	zinc finger protein 52	Zfp52	3.93	1.85	0.00	4.96
1427858_PM_at	immunoglobulin kappa chain variable 1-117	Igkv1-117	3.79	1.84	0.13	-5.80
1418061_PM_at	latent transforming growth factor beta binding protein 2	Ltbp2	4.88	1.84	0.05	-4.94
1427792_PM_at	---	---	2.90	1.84	0.16	-5.95
1437636_PM_at	RIKEN cDNA E030037K03 gene	030037K03Ri	3.99	1.83	0.01	-3.36
1436598_PM_at	inducible T-cell co-stimulator	Icos	3.42	1.83	0.00	-1.77
1435710_PM_at	expressed sequence AI661384	AI661384	2.63	1.82	0.00	0.90
1435582_PM_at	WD repeat and FYVE domain containing 4	Wdfy4	5.94	1.81	0.00	-1.64
1460134_PM_at	RIKEN cDNA 9330175E14 gene	330175E14Ri	4.70	1.81	0.00	-2.72
1425294_PM_at	SLAM family member 8	Slamf8	3.92	1.81	0.00	-0.63
1448749_PM_at	pleckstrin	Plek	2.99	1.79	0.00	0.54
1428735_PM_at	CD69 antigen	Cd69	2.98	1.79	0.00	-1.12
1447927_PM_at	macrophage activation 2 like	Mpa2l	6.94	1.79	0.02	-3.98
1434767_PM_at	expressed sequence C79407	C79407	2.70	1.79	0.00	-0.46
1457973_PM_at	---	---	3.74	1.79	0.00	0.66
1434130_PM_at	lipoma HMGIC fusion partner-like 2	Lhfpl2	3.79	1.78	0.00	3.07
1450639_PM_at	predicted gene 14085 /// solute carrier family 28 (sodium-coupled nucleoside transporter), member 2	14085 /// Slc2	2.94	1.78	0.00	-2.83
1425510_PM_at	MAP/microtubule affinity-regulating kinase 1	Mark1	3.87	1.77	0.00	5.43
1427503_PM_at	expressed sequence AI324046	AI324046	3.14	1.76	0.18	-6.02
1419192_PM_at	interleukin 4 induced 1 /// Nup62-Il4i1 protein	1 /// Nup62-il	4.12	1.75	0.00	4.19
1450936_PM_a_at	deoxyribonuclease 1-like 2	Dnase1l2	3.41	1.75	0.00	1.81
1421194_PM_at	integrin alpha 4	Itga4	2.32	1.75	0.00	1.62
1460259_PM_s_at	chloride channel calcium activated 1 /// chloride channel calcium activated 2	Clca1 /// Clca2	5.27	1.75	0.06	-5.21
1423937_PM_at	potassium channel tetramerisation domain containing 5	Kctd5	3.68	1.75	0.00	1.75
1424931_PM_s_at	immunoglobulin lambda chain complex /// immunoglobulin lambda chain, constant region 1 /// immunoglobulin lambda chain, variable 1 /// simil	/// Igl-V1 ///	5.50	1.74	0.32	-6.44
1417852_PM_x_at	chloride channel calcium activated 1	Clca1	5.04	1.74	0.05	-4.95
1418612_PM_at	schlafen 1	Slfn1	3.02	1.74	0.00	3.48
1446780_PM_at	---	---	4.20	1.73	0.00	1.30
1423495_PM_at	2-4-dienoyl-Coenzyme A reductase 2, peroxisomal	Decr2	5.42	1.73	0.13	-5.75
1436649_PM_at	IKAROS family zinc finger 3	Ikzf3	3.92	1.73	0.01	-3.40
1443937_PM_at	---	---	3.09	1.73	0.00	0.41
1420534_PM_at	guanylate cyclase 1, soluble, alpha 3	Gucy1a3	4.08	1.72	0.01	-3.50
1417845_PM_at	claudin 6	Cldn6	5.33	1.72	0.00	-1.70
1438532_PM_at	hemicentin 1	Hmcn1	2.93	1.72	0.00	0.60
1450227_PM_at	ankyrin repeat domain 6	Ankrd6	3.72	1.71	0.00	-1.43
1419128_PM_at	integrin alpha X	Itgax	6.21	1.71	0.00	1.77
1433543_PM_at	anillin, actin binding protein	Anln	4.34	1.71	0.00	-1.69
1440695_PM_at	---	---	2.67	1.71	0.00	-2.47
1460423_PM_x_at	predicted gene 5571 /// immunoglobulin kappa chain variable 1 (V1)	n5571 /// Igk-	2.67	1.70	0.18	-6.02
1455719_PM_at	tubulin, beta 5	Tubb5	8.50	1.70	0.00	3.35
1429672_PM_at	RIKEN cDNA 5830407E08 gene	830407E08Ri	3.14	1.70	0.02	-4.33
1418675_PM_at	oncostatin M receptor	Osmr	3.75	1.70	0.02	-4.05
1452067_PM_at	N-acylethanolamine acid amidase	Naaa	5.89	1.70	0.00	-1.13
1427434_PM_at	NLR family, apoptosis inhibitory protein 6	Naip6	3.84	1.70	0.00	1.98
1419178_PM_at	CD3 antigen, gamma polypeptide	Cd3g	4.79	1.69	0.03	-4.52
1452272_PM_a_at	growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)	Gfer	5.92	1.69	0.00	8.37
1419043_PM_a_at	interferon inducible GTPase 1	Iigp1	5.38	1.69	0.07	-5.31
1456494_PM_a_at	expressed sequence AI451617 /// tripartite motif-containing 30	51617 /// Trir	2.99	1.69	0.01	-3.08
1433471_PM_at	transcription factor 7, T-cell specific	Tcf7	3.82	1.69	0.00	-2.84
1455299_PM_at	vestigial like 3 (Drosophila)	Vgll3	4.65	1.68	0.01	-3.80
1453147_PM_at	polymerase (RNA) III (DNA directed) polypeptide E	Polr3e	5.25	1.68	0.11	-5.67
1429215_PM_at	RIKEN cDNA 2310058N22 gene	310058N22Ri	6.43	1.68	0.01	-3.07
1424647_PM_at	gamma-aminobutyric acid (GABA) A receptor, pi	Gabrp	3.68	1.68	0.05	-4.95
1421694_PM_a_at	versican	Vcan	3.92	1.67	0.07	-5.27
1431843_PM_a_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	Nfkbie	6.34	1.67	0.01	-2.96

1419413_PM_at	chemokine (C-C motif) ligand 17	Ccl17	7.59	1.67	0.00	-0.83
1422317_PM_a_at	interleukin 1 receptor-like 1	Il1rl1	4.21	1.67	0.00	-0.77
1458634_PM_at	---	---	4.79	1.66	0.01	-3.77
1458589_PM_at	---	---	4.49	1.66	0.00	-2.89
1436003_PM_at	Vascular cell adhesion molecule 1	Vcam1	5.43	1.66	0.05	-5.05
1449009_PM_at	T-cell specific GTPase 1 /// T-cell specific GTPase 2	gtp1 /// Tgtp	8.94	1.66	0.01	-3.25
1419762_PM_at	ubiquitin D	Ubd	7.42	1.66	0.03	-4.43
1460628_PM_at	essential meiotic endonuclease 1 homolog 2 (S. pombe)	Eme2	3.46	1.66	0.00	-1.26
1418652_PM_at	chemokine (C-X-C motif) ligand 9	Cxcl9	4.95	1.65	0.18	-6.04
1419297_PM_at	histocompatibility 2, O region alpha locus	H2-Oa	4.26	1.65	0.00	-2.21
1417455_PM_at	transforming growth factor, beta 3	Tgfb3	4.11	1.65	0.02	-4.31
1443349_PM_at	---	---	4.58	1.65	0.01	-3.90
1440363_PM_at	---	---	3.51	1.64	0.00	-2.18
1419834_PM_x_at	MAP/microtubule affinity-regulating kinase 1	Mark1	4.25	1.64	0.00	1.79
1444878_PM_at	---	---	3.91	1.64	0.00	-2.61
1425832_PM_a_at	chemokine (C-X-C motif) receptor 6	Cxcr6	2.67	1.63	0.00	-0.65
1440481_PM_at	signal transducer and activator of transcription 1	Stat1	2.57	1.63	0.00	0.81
1442741_PM_at	mutated in colorectal cancers	Mcc	2.68	1.62	0.00	5.60
1434734_PM_at	RAD54 homolog B (S. cerevisiae)	Rad54b	2.60	1.62	0.00	2.19
1416871_PM_at	a disintegrin and metallopeptidase domain 8	Adam8	4.78	1.62	0.01	-3.56
1460138_PM_at	---	---	5.27	1.62	0.11	-5.67
1438676_PM_at	macrophage activation 2 like	Mpa2l	5.60	1.62	0.05	-4.94
1427837_PM_at	immunoglobulin kappa chain variable 32 (V32)	Igk-V32	2.48	1.62	0.01	-3.22
1423213_PM_at	plexin C1	Plxnc1	5.34	1.61	0.00	-1.97
1439795_PM_at	G protein-coupled receptor 64	Gpr64	4.65	1.61	0.02	-4.15
1429293_PM_at	glypican 2 (cerebroglycan)	Gpc2	4.58	1.61	0.00	-2.31
1438239_PM_at	midline 1	Mid1	4.77	1.61	0.11	-5.65
1435343_PM_at	dedicator of cytokinesis 10	Dock10	7.13	1.61	0.00	-2.49
1460407_PM_at	Spi-B transcription factor (Spi-1/PU.1 related)	Spib	4.04	1.61	0.00	5.17
1418842_PM_at	hematopoietic cell specific Lyn substrate 1	Hcls1	4.54	1.61	0.02	-4.34
1435792_PM_at	component of Sp100-rs /// predicted gene 7582	prs /// Gm75	6.33	1.60	0.01	-3.45
1436037_PM_at	integrin alpha 4	Itga4	5.81	1.60	0.02	-4.20
1449420_PM_at	phosphodiesterase 1B, Ca2+-calmodulin dependent	Pde1b	3.99	1.59	0.00	-0.82
1430593_PM_at	coiled-coil domain containing 30	Ccdc30	3.14	1.59	0.04	-4.85
1415989_PM_at	vascular cell adhesion molecule 1	Vcam1	6.48	1.59	0.03	-4.55
1455161_PM_at	expressed sequence AI504432	AI504432	4.53	1.59	0.01	-3.03
1424305_PM_at	immunoglobulin joining chain	Igj	6.93	1.59	0.33	-6.47
1449414_PM_at	zinc finger protein 53	Zfp53	2.78	1.58	0.00	1.82
1452417_PM_x_at	RIKEN cDNA 2010205A11 gene /// predicted gene 10883 /// predicted gene 1420 /// predicted gene 7202 /// immunoglobulin kappa chain comple	7202 /// Igk	6.09	1.58	0.53	-6.76
1417141_PM_at	interferon gamma induced GTPase	Igtp	7.80	1.58	0.01	-3.05
1439744_PM_at	---	---	4.82	1.58	0.00	-2.27
1425145_PM_at	interleukin 1 receptor-like 1	Il1rl1	3.13	1.58	0.01	-3.38
1427007_PM_at	SAM and SH3 domain containing 3	Sash3	4.83	1.58	0.00	-1.89
1420380_PM_at	chemokine (C-C motif) ligand 2	Ccl2	7.14	1.58	0.02	-4.16
1456993_PM_at	DNA segment, Chr 2, ERATO Doi 640, expressed	D2Ertd640e	5.42	1.58	0.17	-6.00
1451902_PM_at	zinc finger protein 758	Zfp758	3.05	1.58	0.00	2.22
1449640_PM_at	toll-like receptor 7	Tlr7	2.81	1.58	0.00	-1.39
1434280_PM_at	---	---	3.45	1.57	0.01	-3.76
1418945_PM_at	matrix metallopeptidase 3	Mmp3	5.66	1.57	0.07	-5.26
1447258_PM_at	---	---	3.44	1.57	0.28	-6.35
1418930_PM_at	chemokine (C-X-C motif) ligand 10	Cxcl10	7.11	1.57	0.01	-3.16
1425291_PM_at	forkhead box J1	Foxj1	2.92	1.57	0.00	8.55
1424010_PM_at	microfibrillar-associated protein 4	Mfap4	5.73	1.56	0.04	-4.81
1434625_PM_at	RIKEN cDNA 4930432O21 gene	930432O21Ri	4.61	1.56	0.00	3.94
1445031_PM_at	---	---	3.03	1.56	0.00	-2.89
1418126_PM_at	chemokine (C-C motif) ligand 5	Ccl5	5.89	1.56	0.00	-0.27
1434929_PM_at	cDNA sequence BC035044	BC035044	3.20	1.56	0.00	0.44
1426161_PM_at	---	---	2.34	1.56	0.02	-3.96
1447213_PM_at	---	---	4.71	1.55	0.07	-5.28
1454694_PM_a_at	topoisomerase (DNA) II alpha	Top2a	5.63	1.55	0.03	-4.63
1434788_PM_at	frizzled homolog 3 (Drosophila)	Fzd3	4.15	1.55	0.00	-1.60
1438953_PM_at	c-fos induced growth factor /// similar to FIGF	/// LOC10004	6.85	1.55	0.01	-3.45
1460210_PM_at	polycystic kidney disease 1 homolog	Pkd1	3.75	1.55	0.00	12.17
1448859_PM_at	chemokine (C-X-C motif) ligand 13	Cxcl13	2.45	1.55	0.01	-3.38
1448759_PM_at	interleukin 2 receptor, beta chain	Il2rb	3.28	1.55	0.00	4.29
1455132_PM_at	RAS protein activator like 3	Rasal3	4.07	1.55	0.00	5.06
1417853_PM_at	chloride channel calcium activated 1	Clca1	5.39	1.55	0.17	-5.99
1427306_PM_at	ryanodine receptor 1, skeletal muscle	Ryr1	3.42	1.55	0.00	-0.43
1453593_PM_at	vestigial like 3 (Drosophila)	Vgll3	5.84	1.54	0.09	-5.45
1450033_PM_a_at	signal transducer and activator of transcription 1	Stat1	5.87	1.54	0.00	-2.90
1427325_PM_s_at	AT-hook transcription factor	Akna	3.80	1.54	0.00	-0.85
1444235_PM_at	RIKEN cDNA 1700025G04 gene	700025G04Ri	4.12	1.54	0.00	4.16
1417333_PM_at	RAS p21 protein activator 4	Rasa4	4.43	1.54	0.00	-2.60
1417160_PM_s_at	extracellular proteinase inhibitor	Expi	5.06	1.54	0.03	-4.45
1419152_PM_at	RIKEN cDNA 2810417H13 gene	810417H13Ri	3.11	1.54	0.10	-5.53
1426947_PM_x_at	collagen, type VI, alpha 2	Col6a2	5.14	1.54	0.03	-4.59
1440087_PM_at	---	---	3.85	1.54	0.00	-2.63
1438954_PM_x_at	c-fos induced growth factor	Figf	7.30	1.53	0.00	-2.43
1436625_PM_at	Fc receptor, IgG, high affinity I	Fcgr1	4.28	1.53	0.00	-2.24
1450495_PM_a_at	killer cell lectin-like receptor subfamily K, member 1	Klrk1	2.53	1.53	0.00	0.81
1458057_PM_at	---	---	3.50	1.53	0.01	-3.70
1450912_PM_at	membrane-spanning 4-domains, subfamily A, member 1	Ms4a1	2.57	1.53	0.00	1.11
1420970_PM_at	adenylate cyclase 7	Adcy7	4.87	1.53	0.00	-1.08
1419358_PM_at	sortilin-related VPS10 domain containing receptor 2	Sorcs2	3.82	1.53	0.01	-3.02
1423887_PM_a_at	TEL2, telomere maintenance 2, homolog (S. cerevisiae)	Telo2	5.33	1.53	0.00	2.38
1460440_PM_at	latrophilin 3	Lphn3	3.22	1.53	0.00	-1.76
1421173_PM_at	interferon regulatory factor 4	Irf4	5.85	1.52	0.02	-4.36
1426966_PM_at	axin 1 /// similar to Axin	/// LOC1000	4.77	1.52	0.00	-1.93
1452728_PM_at	kin of IRRE like 3 (Drosophila)	Kirrel3	4.29	1.52	0.00	0.21
1427660_PM_x_at	predicted gene 10883 /// predicted gene 1420 /// predicted gene 7202 /// immunoglobulin kappa chain complex /// immunoglobulin kappa chain	Jgk /// Igk-C /	7.15	1.52	0.46	-6.68
1458299_PM_s_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	Nfkbie	6.46	1.52	0.01	-2.96
1454850_PM_at	TBC1 domain family, member 10c	Tbc1d10c	2.77	1.52	0.00	6.31
1416558_PM_at	maternal embryonic leucine zipper kinase	Melk	4.19	1.52	0.00	-2.01
1433716_PM_x_at	glial cell line derived neurotrophic factor family receptor alpha 2	Gfra2	2.87	1.52	0.02	-4.01
1440837_PM_at	histocompatibility 2, O region beta locus	H2-Ob	3.42	1.52	0.00	-1.33
1444851_PM_at	---	---	3.67	1.51	0.00	-2.03
1458704_PM_at	---	---	4.27	1.51	0.01	-3.23
1418269_PM_at	lysyl oxidase-like 3	Loxl3	5.52	1.51	0.00	-2.71
1449220_PM_at	GTPase, IMAP family member 3 /// similar to immunity-associated nucleotide 4	3 /// LOC100	6.24	1.51	0.00	-1.86
1459872_PM_x_at	histocompatibility 2, class II, locus DMa	H2-DMa	2.74	1.51	0.01	-3.48
1445186_PM_at	stanniocalcin 2	Stc2	5.23	1.51	0.01	-3.25
1417793_PM_at	immunity-related GTPase family M member 2	Irgm2	8.01	1.51	0.01	-2.92
1433828_PM_at	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	Atp8a1	4.46	1.51	0.00	-0.03
1453352_PM_at	ATPase, class V, type 10B	Atp10b	4.73	1.51	0.15	-5.91
1420704_PM_at	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage) /// similar to granulocyte-macrophage colony stimulating factor	/// LOC1000	4.50	1.51	0.00	3.01
1440208_PM_at	RAS-related C3 botulinum substrate 2	Rac2	3.87	1.51	0.04	-4.74
1445422_PM_at	hypothetical protein LOC621549	LOC621549	6.11	1.51	0.00	-2.14
1454701_PM_at	RIKEN cDNA 4930503L19 gene	930503L19Ri	2.39	1.51	0.00	-1.19
1419627_PM_s_at	C-type lectin domain family 4, member n	Clec4n	4.19	1.51	0.18	-6.05
1427855_PM_at	Immunoglobulin kappa chain variable 38(V38)	Igk-V38	3.36	1.51	0.09	-5.50
1444765_PM_at	RNA binding protein gene with multiple splicing	Rbpms	3.64	1.51	0.01	-3.01

Table S3. **Taqman probe sets and specific primer pairs**

Gene	Vendor	Format	Assay ID
Tnfrsf12a	Life Technologies	TaqMan® Gene Expression Assays	Mm01302476_g1
Tnfsf12	Life Technologies	TaqMan® Gene Expression Assays	Mm02583406_s1

Gene	Forward Sequence	Reverse Sequence
Acta2	CTGACAGAGGCACCACTGAA	CATCTCCAGAGTCCAGCACA