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p90 Ribosomal S6 kinases play a significant role in early gene regulation in the cardiomyocyte response to G_q-protein-coupled receptor stimuli, endothelin-1 and α_1-adrenergic receptor agonists

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ERK1/2 (extracellular-signal-regulated kinase 1/2) and their substrates RSKs (p90 ribosomal S6 kinases) phosphorylate different transcription factors, contributing differentially to transcriptomic profiles. In cardiomyocytes ERK1/2 are required for >70 % of the transcriptomic response to endothelin-1. In the present study we investigated the role of RSKs in the transcriptomic responses to the G_q-protein-coupled receptor agonists endothelin-1, phenylephrine (a generic α_1-adrenergic receptor agonist) and A61603 (α_{1A}-adrenergic receptor selective). Phospho-ERK1/2 and phospho-RSKs appeared in cardiomyocyte nuclei within 2–3 min of stimulation (endothelin-1>A61603≈phenylephrine). All agonists increased nuclear RSK2, but only endothelin-1 increased the nuclear RSK1 content. PD184352 (inhibits ERK1/2 activation) and BI-D1870 (inhibits RSKs) were used to dissect the contribution of RSKs to the endothelin-1-responsive transcriptome. Of the 213 RNAs up-regulated after 1 h, 51 % required RSKs for their up-regulation, whereas 29 % required ERK1/2 but not RSKs. The transcriptomic response to phenylephrine overlapped with, but was not identical with, endothelin-1. As with endothelin-1, PD184352 inhibited the up-regulation of most phenylephrine-responsive transcripts, but the greater variation in the effects of BI-D1870 suggests that differential RSK signalling influences global gene expression. A61603 induced similar changes in RNA expression in cardiomyocytes as phenylephrine, indicating that the signal was mediated largely through α_{1A}-adrenergic receptors. A61603 also increased expression of immediate early genes in perfused adult rat hearts and, as in cardiomyocytes, up-regulation of the majority of genes was inhibited by PD184352. PD184352 or BI-D1870 prevented the increased surface area induced by endothelin-1 in cardiomyocytes. Thus RSKs play a significant role in regulating cardiomyocyte gene expression and hypertrophy in response to G_q-protein-coupled receptor stimulation.

Key words: α_1-adrenergic receptor, cardiomyocyte, endothelin, mitogen-activated protein kinase (MAPK), p90 ribosomal S6 kinase (p90 RSK), transcriptomics.

INTRODUCTION

The ERK1/2 (extracellular-signal-regulated kinase 1/2) cascade plays a major role in the global regulation of gene expression [1]. ERK1/2, the prototypic MAPKs (mitogen-activated protein kinases), are activated by dual phosphorylation of threonine and tyrosine residues within a T-E-Y motif, and they then phosphorylate substrates in both the cytoplasmic and nuclear compartments [2]. In the nucleus ERK1/2 phosphorylate nuclear-localized transcription factors (e.g. Elk1) to regulate their transactivating activities and/or association with other transcription factors, thus directly influencing the transcription of specific genes. ERK1/2 also phosphorylate downstream protein kinases including RSKs (p90 ribosomal S6 kinases) [3,4]. RSKs are ubiquitously expressed and are generally localized in the cytoplasm in unstimulated cells, but mitogenic stimulation results in the nuclear translocation of three of the four RSK isoforms (RSK1, RSK2 and RSK3). Like ERK1/2, RSKs phosphorylate cytoplasmic and nuclear substrates. However, the preferred phosphorylation motifs for ERK1/2 (proline-directed kinases) and RSKs (which phosphorylate serine/threonine residues within an R-X-R-X-X-S/T motif) differ and they phosphorylate different substrates. ERK1/2 also activate MSKs (mitogen- and stress-activated protein kinases), kinases related to RSKs [3]. MSKs are predominantly nuclear-localized and are involved in transcriptional regulation. A third family of downstream kinase substrates of ERK1/2 are MNKs (MAPK-interacting kinases) [3]. Although MNK1/2 may traffic into the nucleus they primarily target components of the translational apparatus.

Mammalian cardiomyocytes, the contractile cells of the heart, are terminally differentiated, withdrawing from the cell cycle around the time of birth. In response to a demand for increased power output (e.g. following the death of adjacent cells as a result of myocardial infarction or in hypertensive states), cardiomyocytes increase in size and myofibrillar content, adapting the components of the contractile apparatus and modulating their

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Abbreviations used: AMPKα, AMP-activated protein kinase α; AR, adrenergic receptor; Areg, amphiregulin; Atf3, activating transcription factor 3; BH-MTC, Benjamini and Hochberg multiple testing correction; CREB, cAMP-response-element-binding protein; Dusp, dual-specificity phosphatase; Egr, early growth response; ERK1/2, extracellular-signal-regulated kinase 1/2; ET-1, endothelin-1; FDR, false discovery rate; Fosb, FBJ murine osteosarcoma viral oncogene homologue B; Gapdh, glyceraldehyde 3-phosphate dehydrogenase; GSK3α/β, glycogen synthase kinase 3α/β; Has, hyaluronan synthase; IL11, interleukin 11; Klf, Krüppel-like factor; Lif, leukaemia inhibitory factor; MAPK, mitogen-activated protein kinase; MKK, MAPK kinase; MNK, MAPK-interacting protein kinase; MSK, mitogen- and stress-activated protein kinase; NPE, nuclear protein-enriched; Nr4a, nuclear receptor subfamily 4, group A; Olr1, oxidized low-density lipoprotein (lectin-like) receptor 1; PE, phenylephrine; PKB, protein kinase B; Plk2, polo-like kinase 2; Ptgs2, prostaglandin-endoperoxide synthase 2, qPCR, quantitative PCR; Rgs2, regulator of G-protein signalling 2, 24 kDa; RSK, ribosomal S6 kinase; Sik1, salt-inducible kinase 1; SNK, Student–Newman–Keuls.

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metabolism (i.e. they undergo hypertrophic growth). ERK1/2 signalling is associated with cardiomyocyte hypertrophy. Thus hypertrophic stimuli, such as ET-1 (endothelin-1) and α_1-AR (adrenergic receptor) agonists, activate the ERK1/2 cascade in cardiomyocytes, and overexpression of constitutively activated components of the cascade induce aspects of the response in isolated cardiomyocytes [5]. Furthermore, small-molecule or genetic inhibition of the cascade prevents hypertrophy [6–8]. *In vivo* studies in genetically modified mice highlight further the importance of ERK1/2 signalling in the heart [9–11]. However, none of these studies clearly establishes how ERK1/2 elicit their effects.

Biochemical studies in neonatal rat cardiomyocytes, place dually phosphorylated (i.e. activated) ERK1/2 in the nucleus within 2 min of stimulation with ET-1 [12]. ERK1/2 phosphorylate DNA-binding transcription factors, including GATA4 (GATA-binding protein 4) and Elk1 [5], consistent with a role in direct transcriptional regulation [2]. Small-molecule inhibitors of ERK1/2 signalling inhibit the increases in expression of >70 % of the mRNAs up-regulated by ET-1 [13–15]. Presumably, activation of other signalling pathways by ET-1 (e.g. c-Jun N-terminal kinases and p38 MAPKs [2]) contributes to the transcriptional changes, but the data suggest that the ERK1/2 cascade plays a major role in regulating cardiomyocyte gene expression [2,5,12–15]. ET-1 is particularly potent at activating ERK1/2. Other stimuli such as PE (phenylephrine; an α_1-AR agonist) do not activate ERK1/2 to the same degree [16] and also activate other MAPKs [2]. It is unclear whether (although they signal through a similar G_q-protein-coupled receptor system [17]) ERK1/2 play as significant a role in this context. Even if they do, since different degrees/duration of ERK1/2 signalling can elicit profoundly different cellular responses in other cells, the transcriptional responses to PE compared with ET-1 may still be qualitatively different. In cardiomyocytes, as in other cells, activated ERK1/2 in the cytoplasm phosphorylate and activate RSKs, but the importance of RSKs in regulating cardiomyocyte gene expression has not been explored. In the present study we demonstrate that RSKs contribute to the changes in expression of >50 % of the RNAs up-regulated by ET-1 within 1 h (when most changes in immediate early gene expression are detected [14]), whereas 29 % required ERK1/2, but not RSKs, for up-regulation. We also demonstrate that the gene expression response to α_1-AR stimulation (signalling primarily through α_{1A}-ARs) is not identical with that of ET-1, although the signal is still predominantly mediated by the ERK1/2 cascade. The contribution of RSKs differs according to stimulus and this probably reflects differential signalling to specific RSK isoforms.

EXPERIMENTAL

Cardiomyocyte cultures

Ventricles were dissected from neonatal (2–4-day-old) Sprague–Dawley rat hearts (Harlan) and the cardiomyocytes were prepared and plated as described previously [15]. After 18 h in medium containing 15 % (v/v) fetal bovine serum, the medium was changed to serum-free maintenance medium for a further 24 h. Stock solutions of agonists/inhibitors were prepared at 1000× the working concentration and added directly to the tissue culture medium. PD184352 (Alexis Biochemicals, Enzo Life Sciences) and BI-D1870 (Division of Signal Transduction Therapy Unit, University of Dundee, Dundee, U.K. and Enzo Life Sciences) were prepared in DMSO. ET-1 (Bachem), PE (Sigma–Aldrich) and A61603 (Tocris Bioscience) were dissolved in water.

Adult rat heart perfusions

Male 275–300 g Sprague–Dawley rats were housed and work was undertaken in accordance with local institutional animal care committee procedures and the U.K. Animals (Scientific Procedures) Act 1986. Hearts were perfused retrogradely (37 °C at 70 mmHg) as described previously [18]. For the experiments with PD184352, the drug was added to the perfusate during the 15 min equilibration period. A61603 was added at the end of the equilibration period and all perfusions were continued for 1 h. Hearts were 'freeze-clamped' between aluminium tongs cooled in liquid nitrogen and were pulverized under liquid nitrogen in a pestle and mortar. The powders were stored at − 80 °C.

Immunoblotting

Total cardiomyocyte extracts were prepared as described previously [15]. Cytosolic and NPE (nuclear protein-enriched) extracts were prepared as described in [19] with the addition of 4 μM microcystin-LR in all buffers. Samples were stored at − 20 °C. Proteins were separated by SDS/PAGE (10 % gels). For ERK1/2, volumes equivalent to 2×10^5 or 5.3×10^5 cells were used for analysis of the cytosolic or NPE fractions respectively. For RSKs, volumes equivalent to 3×10^5 or 8×10^5 cells were used for analysis of the cytosolic or NPE fractions respectively. For RSK1 and RSK2, volumes equivalent to 1×10^6 cells were used for analysis of the NPE fractions. Immunoblotting was performed as described previously [15] (primary antibodies are listed in Supplementary Table S1A at http://www.biochemj.org/bj/450/bj4500351add.htm). Secondary antibodies conjugated to horseradish peroxidase were from Dako (1:5000 dilution). Bands were detected using ECL reagent and X-ray film ECL Prime and an Imagequant 350 system or a LAS4000 mini system (GE Healthcare). Quantification was performed using Imagequant software. To determine relative amounts of total ERK1/2 or total RSKs in the cytosol compared with the NPE fractions, cytosol samples (control and 5 min ET-1 treatment) were analysed on the same blots as the NPE fractions.

Microarray hybridizations, data analysis and qPCR (quantitative PCR) validations

The additions of inhibitors/agonists were staggered and cells were harvested simultaneously. To minimize variation from different cardiomyocyte preparations, equal amounts of RNA from three separate myocyte preparations were pooled to generate a single sample set and three such sets were hybridized to separate microarrays. For changes in RNA expression induced by PE or ET-1 at 2, 4 or 24 h, RNA was extracted, labelled cRNA was prepared and hybridization to Affymetrix rat genome 230 2.0 arrays was performed as described previously [14]. For studies using Affymetrix rat exon 1.0 ST arrays, cardiomyocytes were unstimulated (controls), exposed to 2 μM PD184352 or 10 μM BI-D1870 for 70 min, exposed to PE or ET-1 for 0.5 or 1 h, or exposed to PD184352 or BI-D1870 for 10 min before the addition of ET-1 for a further 1 h. Total RNA was provided to the NASC (Nottingham *Arabidopsis* Stock Centre) for preparation and hybridization according to their protocols (http://affymetrix.arabidopsis.info). The data were deposited in ArrayExpress (accession numbers E-MIMR-3, E-MIMR-37, E-MEXP-3393, E-MEXP-3394, E-MEXP-3678 and E-MEXP-3679).

Microarray data (.CEL files) were imported into GeneSpring 12.0 (Agilent Technologies). For the Affymetrix rat genome 230 2.0 microarrays, PE and ET-1 data were imported, normalized and analysed as described previously [15]. Probesets were selected with minimum raw values of 50 in all of any condition, with >1.5-fold change at any time relative to controls and statistically significant changes [FDR (false discovery rate)<0.05] identified by one-way ANOVA with an SNK (Student–Newman–Keuls) post-test, applying a BH-MTC (Benjamini and Hochberg multiple testing correction). The data for PE and ET-1 at 24 h were co-analysed, selecting probesets according to the same criteria. Heatmaps were generated by hierarchical clustering on entities using a Euclidean similarity measure and centroid linkage rule. For the Affymetrix exon 1.0 ST microarrays, the data for PE and ET-1 (0.5 and 1 h) with their corresponding controls were summarized and normalized as described previously [20], selecting probesets according to the criteria listed above. For analysis of the effects of PD184352 or BI-D1870 on RNA responses to ET-1, samples were imported and summarized as for the time course analysis. For the baseline effects of the inhibitors, probesets were selected with >1.5-fold change with PD184352 or BI-D1870 relative to the controls. Statistically significant changes (FDR<0.05) were identified by unpaired Student's *t* test with a BH-MTC. To identify effects of PD184352 or BI-D1870 on the response to ET-1, probesets were selected with >1.5-fold change with ET-1 relative to the controls (unpaired Student's *t* test with a BH-MTC). For the up-regulated RNAs, the significant effects of PD184352 or BI-D1870 were then identified by one-way ANOVA with an SNK post-test, applying a BH-MTC. PE data were analysed by *k*-means clustering of entities using a Euclidean similarity measure.

Validations were performed using different RNA preparations from those used for microarray analysis. Total RNA and cDNAs were prepared and qPCR performed as described previously [15]. The primers designed for qPCR are listed in Supplementary Table S1(B). Values were normalized to Gapdh (glyceraldehyde 3-phosphate dehydrogenase) expression and then to the controls.

Immunostaining and planimetry

Cardiomyocytes were unstimulated (controls) or exposed to inhibitors with and without ET-1 (24 h at 37 °C). Immunostaining was performed as described previously [15] using mouse primary monoclonal antibodies to cardiac troponin T. Cardiomyocytes were viewed with a Zeiss Axioskop fluorescence microscope using a ×40 objective. Digital images captured using a Canon PowerShot G3 camera were converted into greyscale using Adobe Photoshop 7.0. Planimetry was performed using ImageJ (http://rsbweb.nih.gov/ij/). Cardiomyocyte surface area was measured for an average of 51 cells per condition. The experiment was performed four times. Mean values were taken for each experiment and used as a single observation.

Data interpretation and statistical analysis

Graphs were constructed and statistical analysis performed with GraphPad Prism 4.0. Unless otherwise stated, statistical testing used one-way ANOVA with an SNK post-test.

RESULTS

Nuclear localization of activated ERK1/2 and RSKs in cardiomyocytes

Activated ERK1/2 and RSKs translocate to the nucleus to modulate transcription [2,4]. To examine the subcellular localization of activated (i.e. dually phosphorylated) ERK1/2 and RSKs, cardiomyocytes were exposed to 100 nM ET-1, 100 μM PE (a generic α_1-AR agonist activating α_{1A}-ARs and α_{1B}-ARs, both being expressed in cardiomyocytes [21]) or 50 nM A61603 (selective for α_{1A}-ARs). The concentrations were selected on the basis of the EC$_{50}$ values for activation of protein kinase Cε (acting upstream of the ERK1/2 cascade) in cardiomyocytes (~1 nM and 1 μM for ET-1 and PE respectively [16]) and the EC$_{50}$ value for activation of ERK1/2 by ET-1 (~10 nM [22]). The reported EC$_{50}$ value for A61603 stimulation of α_{1A}-ARs and α_{1B}-ARs is ~6 and ~380 nM respectively [23]. We therefore selected 50 nM A61603 for activation of α_{1A}-ARs. Propranolol (20 μM), a β-AR antagonist, did not enhance the stimulation of MKK (MAPK kinase) 1/2 or ERK1/2 by PE, but inhibited the activation of ERK1/2 signalling by 50 μM isoprenaline (Figure 1A). There is, therefore, no inhibitory input from β-AR signalling into the activation of ERK1/2 by PE.

Soluble cytosolic proteins (e.g. GAPDH) were separated from an NPE fraction containing transcription factors [e.g. CREB (cAMP-response-element-binding protein); Figure 1B] and the levels of activated or total ERK1/2 were determined by immunoblotting. Phospho-ERK1/2 were detected in the cytosolic and NPE fractions following stimulation with each agonist (Figures 1C–1E). ET-1 promoted maximal phosphorylation of ERK1/2 within 2–3 min with similar profiles of activation in the cytosolic or NPE fractions (Figures 1C and 1D). Since MKK1/2 (the upstream kinases for ERK1/2) localize to the cytoplasm [24], this suggests that trafficking of activated ERK1/2 between compartments is rapid. Quantitative assessment indicated that 24 ± 2% (mean ± S.E.M., $n = 3$) of the total cellular ERK1/2 protein was present in the NPE fractions of unstimulated cells and this did not change significantly following stimulation (Figure 1C). The time course for activation of ERK1/2 by A61603 or PE was delayed relative to and was less than that induced by ET-1 (Figures 1C–1E). A61603 and PE induced similar responses, indicating that PE signals predominantly through α_{1A}-ARs to ERK1/2.

ERK1/2 activate RSKs by phosphorylation of Thr^{573} in the C-terminal kinase domain with additional phosphorylation of Thr^{359}/Ser^{363} [4]. The C-terminal kinase causes autophosphorylation of Ser^{380} (residue numbers relate to RSK1). ET-1 and A61603 promoted phosphorylation of all of these sites with maximal phosphorylation at ~5 min (Figures 2A and 2B). The profiles for phosphorylation were similar with both agonists. Although the degree of phosphorylation of Thr^{573} started to decline from ~10 min, phosphorylation of Thr^{359}/Ser^{363} and Ser^{380} was sustained over at least 20 min. As with phospho-ERK1/2, phospho-RSKs [assessed by immunoblotting with antibodies against phospho-RSK(Thr^{573})] were detected in the cytosolic and NPE fractions following stimulation with ET-1, PE or A61603. The time course indicated that phosphorylation of RSKs (Figures 2C and 2D) was delayed relative to ERK1/2 (Figures 1C and 1D) as expected. Only 4–8 % of the total RSKs were present in the NPE fractions of unstimulated cells (Figure 2D). This increased to 34 ± 2% following stimulation with ET-1 with a lesser increase induced by A61603 (18 ± 7%) or PE (15 ± 2%). The time course for translocation of total RSKs to the nucleus coincided with RSK phosphorylation, suggesting that the events are associated. ET-1 promoted greater activation of RSKs than A61603 or PE (Figure 2E). RSK1 and RSK2 are the preponderant isoforms in cardiomyocytes [25]. Although all three agonists stimulated nuclear accumulation of RSK2, only ET-1 increased nuclear localization of RSK1 (Figures 2E–2H). Thus differential signalling through RSKs may influence gene expression profiles.

Signalling to gene expression via RSKs

To determine the contribution of RSKs to the changes in gene expression that occur in cardiomyocytes, we focused on ET-1

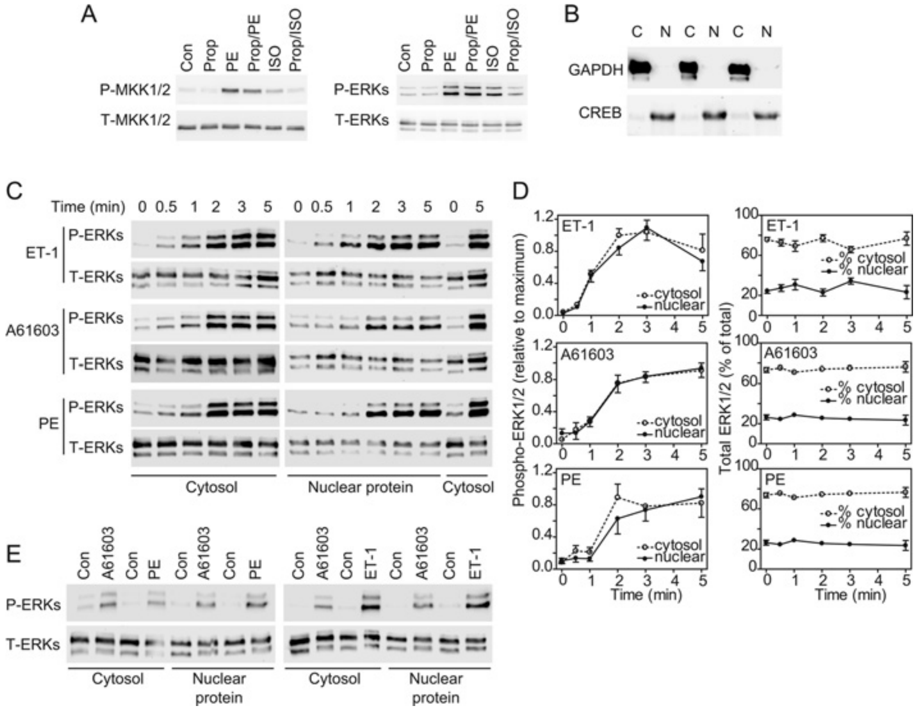

Figure 1 Nuclear signalling of ERK1/2 in cardiomyocytes

(**A**) Cardiomyocytes were unstimulated (Con), exposed to 100 μM PE, 50 μM isoprenaline (ISO; 5 min) or to 20 μM propranolol (Prop; 15 min), or exposed to propranolol (10 min) before addition of PE (Prop/PE) or isoprenaline (Prop/ISO) (5 min). Samples were immunoblotted for phospho-MKK1/2 (P-MKK1/2), total MKK1/2 (T-MKK1/2), phospho-ERK1/2 (P-ERKs) and total ERK1/2 (T-ERKs). The experiment was repeated with similar results. (**B**) Immunoblots of GAPDH or CREB in cytosolic (C) and NPE (N) fractions from cardiomyocytes. (**C** and **E**) Cardiomyocytes were unstimulated (Con), or exposed to 100 nM ET-1, 100 μM PE or 50 nM A61603 for the times indicated (**C**) or for 5 min (**E**). Fractions were immunoblotted for phospho-ERK1/2 or total ERK1/2. Blots are representative of at least three experiments with different cardiomyocyte preparations. (**D**) Densitometric analysis of the blots in (**C**). The graphs on the left-hand side show data normalized to maximum values. The graphs on the right-hand show the relative percentage in each fraction. Results are means ± S.E.M. for three independent myocyte preparations.

and compared the effects of 2 μM PD184352 (which inhibits ERK1/2 activation [26]) with 10 μM BI-D1870, a selective inhibitor of RSKs [27]. The effects of BI-D1870 on the phosphorylation of GSK3α/β (glycogen synthase kinase 3α/β; established RSK substrates [27]) demonstrated that 10 μM was the lowest effective concentration for inhibition of RSKs in cardiomyocytes (Figure 3A). BI-D1870 did not affect activation of ERK1/2 by ET-1, but (as in other cells [27]) BI-D1870 alone activated ERK1/2, albeit to a lesser degree than ET-1 (Figure 3B). Others report that BI-D1870 partially inhibits the activation of PKB (protein kinase B) in the context of insulin signalling in some cells [28]. However, PKB is not activated to any significant extent by ET-1 [7] or α_1-AR agonists (results not shown) in cardiomyocytes. Cardiomyocytes were exposed to inhibitors alone or ET-1 for 1 h in the absence or presence of inhibitors. Transcriptomic changes were determined using Affymetrix rat exon 1.0 ST arrays. PD184352 alone promoted the down-regulation of 42 RNAs (clusters i, iii and v) and up-regulation of eight RNAs (clusters ii and iv) (Figure 3C and Supplementary Table S2 at http://www.biochemj.org/bj/450/bj4500351add.htm). BI-D1870 had a greater effect promoting the down-regulation of 155 RNAs (clusters i and vi) and the up-regulation of 76 RNAs (clusters ii, iii and vii).

To determine the role of RSKs in regulating the ET-1-responsive transcriptome, we selected 213 RNAs up-regulated by ET-1 after 1 h (excluding six with >3-fold change with BI-D1870 alone). The effects of PD184352 or BI-D1870 on the change induced by ET-1 was determined statistically (FDR<0.05) and on the condition of $\geqslant$20 % modulation of the response allowing for inhibitor baseline effects (Supplementary Table S3 at http://www.biochemj.org/bj/450/bj4500351add.htm). The microarray data were validated by qPCR for selected mRNAs studying the effects of inhibitors over 0.5, 1, 1.5 and 2 h. The largest cluster (111 RNAs, cluster 1) contained RNAs whose up-regulation was inhibited by PD184352 or BI-D1870 (Figure 3D), indicating that the signal from ERK1/2 to RNA expression is mediated by RSKs. For the 11 mRNAs we validated, up-regulation by ET-1 was consistently inhibited by either drug at all times [Figure 3E and results not shown for *Areg* (amphiregulin), *Dusp* (dual-specificity phosphatase) 4, *Dusp10*, *Ets1* (v-ets erythroblastosis virus E26 oncogene homologue 1), *Has* (hyaluronan synthase) 2, *Hmgcr* (3-hydroxy-3-methylglutaryl-CoA reductase), *Klf* (Krüppel-like factor) 5 and *Ripk* (receptor-interacting serine-threonine kinase)]. The second largest group (40 RNAs, cluster 2) contained RNAs inhibited by PD184352 with no significant effect of BI-D1870 (Figure 3F). For the seven mRNAs selected for validation, up-regulation by ET-1 was consistently inhibited by PD184352 and there was no significant change with BI-D1870 at 1 h [Figure 3G and results not shown for *Fosb* (FBJ murine osteosarcoma viral oncogene homologue B), *Klf4*, *Rnd3* (Rho family GTPase 3) and *Plk2* (polo-like kinase 2)]. However, for most [e.g. *Egr* (early growth response) 3 and *Ptgs2* (prostaglandin-endoperoxide synthase 2)], there was enhancement of the ET-1 response with BI-D1870 at the later times. For these RNAs, the primary signal for up-regulation is mediated by ERK1/2 independently of RSKs, although RSKs may negatively influence the response at the later times. The third significant group (22 RNAs, cluster 3)

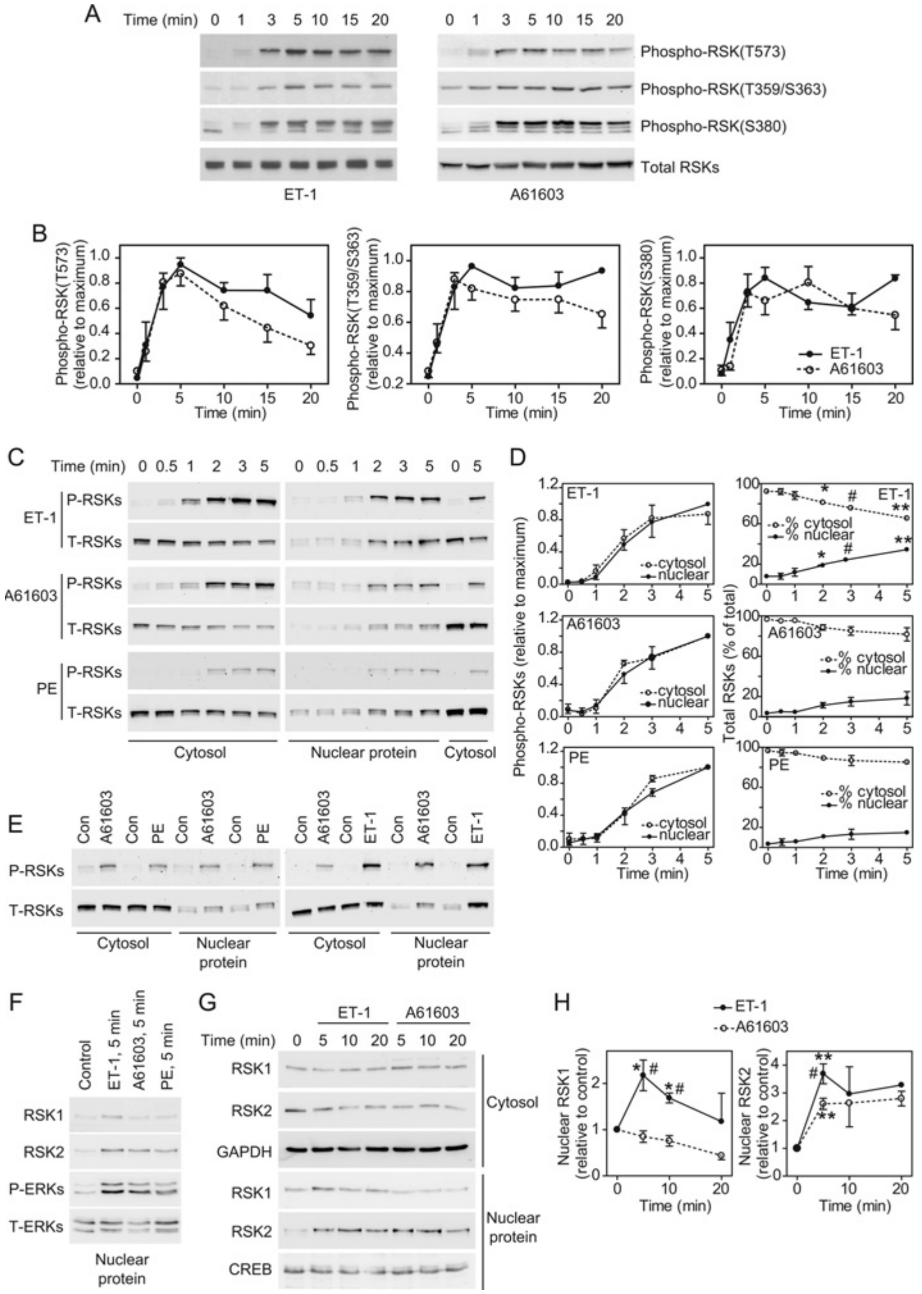

Figure 2 Phosphorylation and nuclear signalling of RSKs in cardiomyocytes

(**A**) Cardiomyocytes were exposed to ET-1 or A61603 for the times indicated. Total extracts were immunoblotted with antibodies against total RSKs or RSKs phosphorylated on Thr^{573}, $\mathrm{Thr}^{359}/\mathrm{Ser}^{363}$ or Ser^{380}. Blots are representative of at least three experiments with independent myocyte preparations. (**B**) Densitometric analysis of the blots in (**A**). Data were normalized to the maximum values. Results are means ± S.E.M. for three (ET-1) or five (A61603) experiments with different cardiomyocyte preparations. (**C** and **E**) Cardiomyocytes were unstimulated (Con), or exposed to ET-1, PE or A61603 for the times indicated (**C**) or for 5 min (**E**). Cysotolic and nuclear proteins were immunoblotted with antibodies against phospho-RSK(Thr^{573}) (P-RSKs) or total RSKs (T-RSKs). Blots are representative of at least three experiments with different cardiomyocyte preparations. (**D**) Densitometric analysis of the blots in (**C**). The graphs on the left-hand side show data normalized to the maximum values. The graphs on the right-hand side show the relative percentage in each fraction. Results are means ± S.E.M. for three experiments with different cardiomyocyte preparations. $^{*}P < 0.05$, $\#P < 0.01$ and $^{**}P < 0.001$ relative to zero time. (**F**) Immunoblots of nuclear proteins following stimulation with ET-1, A61603 or PE (5 min) using goat polyclonal antibodies against RSK1 (sc-231) or RSK2 (sc-1430), or antibodies against phospho-ERK1/2 (P-ERKs) or total ERK1/2 (T-ERKs). The experiment was repeated twice with different cardiomyocyte preparations with similar results. (**G**) Immunoblots of nuclear proteins following stimulation with ET-1 or A61603 using rabbit polyclonal antibodies against RSK1 (#9333) or RSK2 (#9340) or antibodies against GAPDH or CREB. The experiment was repeated twice with different cardiomyocyte preparations with similar results. (**H**) Densitometric analysis of the data from (**F**) and (**G**). Results are means ± S.E.M. for at least three observations with different cardiomyocyte preparations. $^{*}P < 0.01$ and $^{**}P < 0.001$ relative to zero time; $\#P < 0.01$ relative to A61603 at the same time.

contained RNAs for which BI-D1870 enhanced the response to ET-1, whereas PD184352 inhibited the response (Figure 3H, cluster 3). For the six mRNAs validated from cluster 3, up-regulation by ET-1 was consistently inhibited by PD184352 and BI-D1870 enhanced the response [Figure 3I and results not shown for *Egr2*, *Lif* (leukaemia inhibitory factor) and *Nr4a* (nuclear receptor subfamily 4, group A)3]. Other RNAs did not cluster into significant groups. Overall, ~51 % of the mRNAs up-regulated by ET-1 required RSKs for up-regulation, whereas ~29 % required ERK1/2, but not RSKs, for up-regulation. Approximately half of

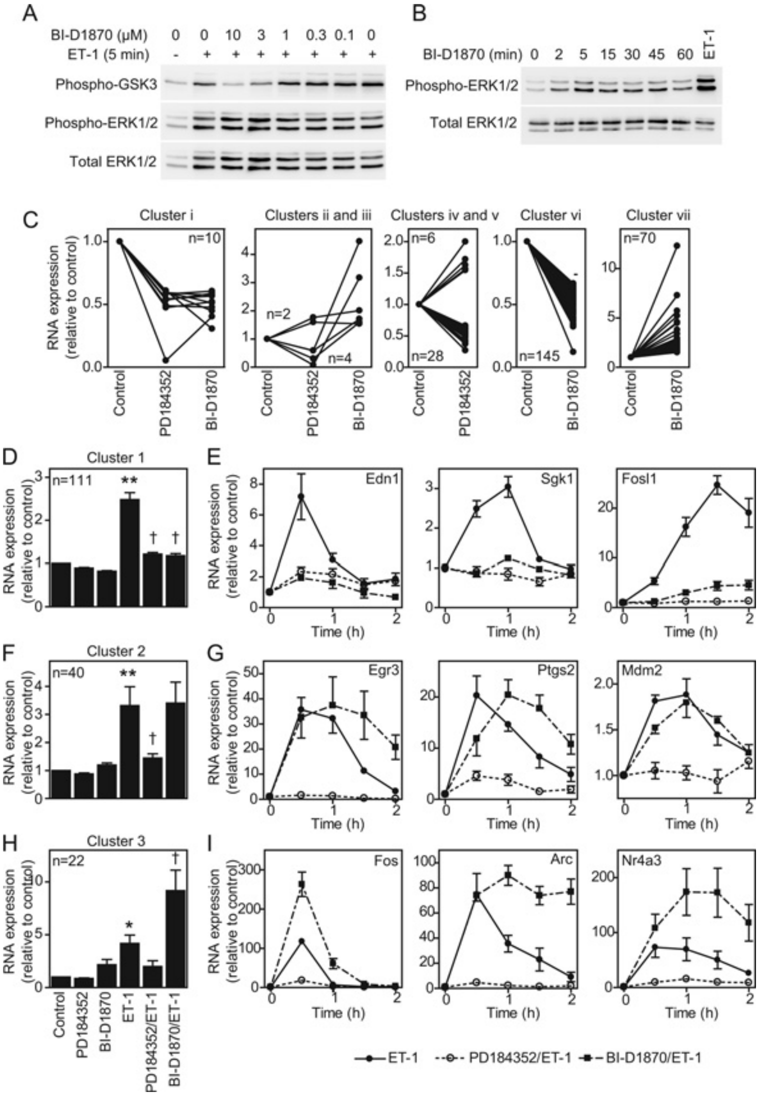

Figure 3 Regulation of cardiomyocyte gene expression by ERK1/2 compared with RSKs

(**A**) Cardiomyocytes were exposed to ET-1 (5 min) in the presence of indicated concentrations of BI-D1870. Samples were immunoblotted for phospho-GSK3α/β, phospho-ERK1/2 or total ERK1/2. The experiment was repeated with similar results. (**B**) Cardiomyocytes were exposed to 10 μM BI-D1870 for the times indicated or ET-1 (5 min). Samples were immunoblotted for phospho- or total ERK1/2. The experiment was repeated with similar results. (**C**) Cardiomyocytes were unstimulated (control), or exposed to PD184352 or BI-D1870 (70 min). RNA expression was determined using Affymetrix rat exon 1.0 ST arrays. RNAs regulated by PD184352 and/or BI-D1870 alone were clustered according to inhibition or enhancement. Mean expression ($n=3$) relative to the controls is shown for each RNA (numbers in each cluster are indicated). (**D**, **F** and **H**) Cardiomyocytes were unstimulated (control), exposed to PD184352, BI-D1870 or ET-1 alone (1 h), or exposed to ET-1 in the presence of PD184352 or BI-D1870. RNA expression was determined using Affymetrix rat exon 1.0 ST arrays. RNAs up-regulated by ET-1 were clustered according to effects of each inhibitor (numbers in each cluster are shown). Results are means $\pm$ S.E.M. for RNAs in each cluster relative to controls. $^*P < 0.001$ and $^{**}P < 0.01$ relative to the control; $^\dagger P < 0.001$ relative to ET-1. (**E**, **G** and **I**) Cardiomyocytes were exposed to ET-1 in the absence/presence of PD184352 or BI-D1870 and mRNA expression for selected transcripts analysed by qPCR. Results are means $\pm$ S.E.M. ($n=4$).

the latter mRNAs showed enhanced expression following RSK inhibition.

Regulation of cardiomyocyte RNA expression by α_1-AR agonists

Our previous studies of the regulation of gene expression in cardiomyocytes focused on ET-1. However, α_1-AR agonists also promote cardiomyocyte growth [17] whilst activating ERK1/2 to a lesser degree than ET-1 (Figure 1). To compare the effects of α_1-AR stimulation with ET-1, we initially used Affymetrix rat expression 230 2.0 arrays for transcriptomic profiling of the response to PE over a prolonged time course (2, 4 and 24 h). We identified 385 and 120 RNAs as significantly up- or down-regulated respectively (Supplementary Table S4 at http://www.biochemj.org/bj/450/bj4500351add.htm), substantially less than the response to ET-1 (827 RNAs up-regulated and 598 RNAs down-regulated; Supplementary Table S5 at http://www.biochemj.org/bj/450/bj4500351add.htm; the previously reported data for ET-1 [14] were reanalysed in the present study in parallel with the data for PE). After 24 h, 178 RNAs were significantly and similarly changed by either agonist, 156 RNAs exhibited significantly different responses to the two agonists, 23 RNAs were significantly changed only with PE, and 206 RNAs were significantly changed with ET-1 (Figure 4A and Supplementary Table S6 at http://

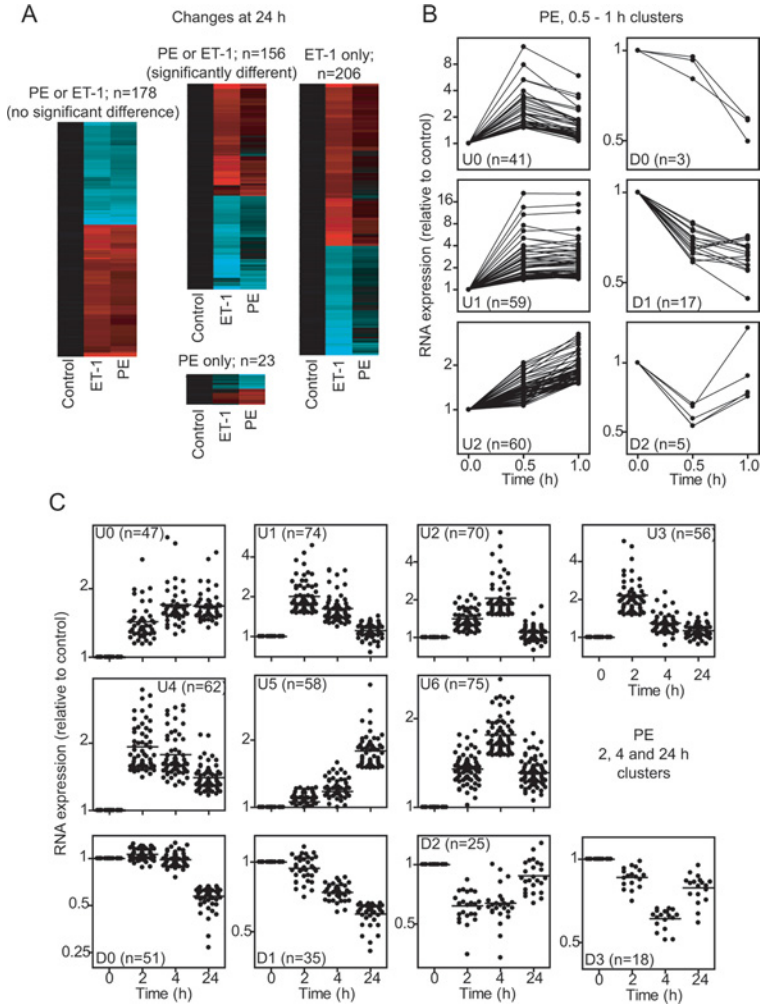

Figure 4 Regulation of the cardiomyocyte transcriptome by PE

Cardiomyocytes were exposed to PE or ET-1 for the times indicated. RNA expression profiling was performed using Affymetrix rat 230 2.0 microarrays (**A** and **C**) or Affymetrix rat exon 1.0 ST arrays (**B**). (**A**) Heatmaps for transcriptional changes at 24 h clustered according to similarity of response to PE compared with ET-1 (range: cyan = − 2.5; black = 0; red = 2.5; $\log_2$ scale). Results are means for $n = 3$ independent hybridizations of different samples each prepared from three cardiomyocyte preparations. (**B**) *k*-Means clustering of mRNAs regulated by PE at 0.5 or 1 h. (**C**) *k*-Means clustering of RNAs regulated by PE at 2, 4 or 24 h. (**B** and **C**) Results (means for $n = 3$ hybridizations) are shown for each RNA. Numbers of transcripts in each cluster are in parentheses.

www.biochemj.org/bj/450/bj4500351add.htm). Thus, although there is overlap in response, cardiomyocyte hypertrophy induced by ET-1 or PE is associated with different gene expression profiles. This presumably reflects variation in the early phase gene expression. We therefore examined the earliest phase of gene expression (0.5 and 1 h) induced by PE compared with ET-1 using more comprehensive Affymetrix rat exon 1.0 ST arrays. The overall response to PE at 0.5–1 h was less than that induced by ET-1 with up-regulation of 159 (compare with 285 for ET-1) RNAs and down-regulation of 25 (compare with 93 for ET-1) RNAs (Supplementary Tables S7 and S8 at http://www.biochemj.org/bj/450/bj4500351add.htm). As for ET-1 [14], PE-responsive RNAs were temporally regulated (Figures 4B and 4C).

We selected 34 mRNAs (~25 % of protein-encoding transcripts significantly up-regulated by PE over 0.5–1 h) for validation experiments and further study by qPCR (Table 1). Overall, the correlation between microarray and qPCR data was high with a linear regression coefficient of 0.98 (Figure 5A). We used 2 μM PD184352 to determine the role of ERK1/2 activation in the response to PE at 1 h. In some, although not all, cells PD184352 may alter the energy balance and activate AMP kinase [29,30]. In cardiomyocytes we did not detect phosphorylation (i.e. activation) of AMPKα (AMP-activated protein kinase α) by 2 μM PD184352, although AMPKα phosphorylation was increased by 0.5 mM H_2O_2 (Figure 5B). As expected, PD184352 reduced the degree of ERK1/2 phosphorylation below basal levels. Of the 31 mRNAs significantly up-regulated by PE at 1 h, only *Has1* and *Klf4* were insensitive to PD184352 and *Atf3* (activating transcription factor 3) was inhibited to a small non-significant degree (Figure 5C), whereas increased expression of 28 was significantly inhibited by PD184352 (Figures 5D, i and 5D, ii). Thus ERK1/2 signalling plays a significant role in the PE-responsive cardiomyocyte transcriptome. We compared the effects of PD184352 or BI-D1870 on the up-regulation of selected mRNAs by PE with ET-1 (Figures 5E–5H). For all mRNAs studied the inhibition of the response by PD184352 was similar with either stimulus, whereas the relative effect of BI-D1870 varied. For some the relative inhibition (e.g. *Areg*, *Fosl1*, *Dusp10* and *Dusp4*; Figure 5E) or enhancement (e.g. *Egr1*, *Fos*, *Nr4a1* and *FosB*; Figure 5F) by BI-D1870 was similar. However, for seven of the 28 RNAs the effects of the inhibitors were

Table 1 RNA expression data for PE and A61603

Cardiomyocytes were exposed to PE or A61603 for 0.5 or 1 h. RNA was extracted and analysed using Affymetrix microarrays or by qPCR. Results are expressed relative to the controls. Microarray results are means for $n = 3$. The qPCR data are means $\pm$ S.E.M. ($n = 3$). Gene symbols are provided; accession numbers are provided in Supplementary Table S1(B) at http://www.biochemj.org/bj/450/bj4500351add.htm *Arc*, activity-regulated cytoskeleton-associated protein; *Ch25h*, cholesterol 25-hydroxylase; *Clcf1*, cardiotrophin-like cytokine factor 1; *Edn1*, endothelin 1; *Gclc*, glutamate-cysteine ligase, catalytic subunit; *Gpr3*, G-protein-coupled receptor 3; *Rasd1*, RAS, dexamethasone-induced 1; *Rasl11b*, RAS-like, family 11, member B.

	PE (microarrays)		PE (qPCR)		A61603 (qPCR)			
	0.5 h	1 h	1 h		0.5 h		1 h	
Gene symbol	Mean	Mean	Mean	S.E.M.	Mean	S.E.M.	Mean	S.E.M.
Arc	2.67	2.76	6.05	1.38	24.50	4.16	28.25	2.14
Areg	1.33	1.79	5.36	0.48	1.62	0.14	6.67	0.92
Atf3	3.30	3.45	4.96	0.81	9.04	1.12	13.96	2.49
Ch25h	3.44	2.31	3.44	0.35	4.32	0.43	1.84	0.07
Clcf1	1.63	1.63	2.68	0.11	2.42	0.23	3.36	0.69
Dusp10	1.16	1.61	1.79	0.24	1.03	0.02	2.30	0.18
Dusp4	1.53	2.04	2.91	0.32	1.40	0.02	2.16	0.24
Dusp5	2.35	2.51	3.90	0.89	3.05	0.33	2.82	0.32
Edn1	2.22	1.38	2.11	0.38	2.66	0.16	2.04	0.21
Egr1	3.17	2.29	4.87	0.87	16.59	1.99	7.30	0.74
Egr2	5.15	3.45	6.08	0.73	14.46	1.77	6.47	0.90
Egr3	6.46	6.82	11.93	1.42	33.12	2.82	27.44	1.37
Fos	7.34	2.51	7.29	1.41	44.57	3.62	6.43	0.18
FosB	3.49	2.64	16.99	3.23	22.34	4.43	17.29	4.54
Fosl1	2.08	2.98	5.58	0.46	4.69	0.14	9.60	0.61
Gclc	1.45	1.99	2.91	0.41	1.40	0.10	2.26	0.27
Gpr3	1.36	1.83	2.89	0.72	1.91	0.03	5.79	0.90
Has1	3.37	3.42	7.05	1.10	4.19	0.42	2.78	0.21
Has2	3.84	4.77	8.35	1.37	2.10	0.21	4.76	0.78
IL11	2.15	2.25	8.29	0.42	4.37	0.61	5.50	1.35
Klf4	2.19	2.28	3.03	0.47	1.78	0.04	1.93	0.16
Lif	7.45	5.07	11.49	2.38	9.61	0.33	7.93	0.60
Myc	1.35	1.59	2.15	0.14	2.07	0.07	2.69	0.07
Nr4a1	19.17	19.23	34.94	4.81	29.73	1.93	24.18	2.20
Nr4a2	13.16	14.77	25.77	3.11	2.70	0.26	2.23	0.35
Nr4a3	10.40	11.64	73.74	16.49	19.66	2.38	28.59	3.88
Olr1	1.55	1.90	2.79	0.34	1.60	0.07	2.30	0.20
Pim1	1.75	1.21	1.38	0.19	2.00	0.12	0.98	0.07
Plk2	1.64	1.50	1.91	0.17	2.10	0.11	2.50	0.17
Ptgs2	5.23	3.38	4.70	0.43	5.86	0.68	4.15	0.54
Rasd1	2.41	1.24	1.47	0.15	1.55	0.24	0.86	0.13
Rasl11b	1.62	1.32	1.46	0.18	1.99	0.19	1.78	0.07
Rgs2	4.93	4.09	6.87	0.88	2.95	0.23	4.62	0.36
Sik1	3.43	4.05	7.33	0.74	2.35	0.05	2.69	0.13

qualitatively different for the two agonists. For *Egr2*, *Lif*, *Olr1* [oxidized low-density lipoprotein (lectin-like) receptor 1], *Nr4a3* and *Nr4a2*, up-regulation of mRNA expression by ET-1 was enhanced by BI-D1870 with no significant effect of BI-D1870 on the response to PE (Figure 5G and results not shown for *Nr4a2*). For *Rgs2* (regulator of G-protein signalling 2, 24 kDa) and Klf4, up-regulation of mRNA expression by PE, but not ET-1 was enhanced by BI-D1870 (Figure 5H). These data indicate that differential activation of RSKs contributes to the different RNA expression profiles induced in cardiomyocytes by ET-1 compared with α_1-ARs and are consistent with differential regulation of nuclear RSKs, either because of the different relative degrees of stimulation (Figure 2E) or selective nuclear translocation of RSK2, but not RSK1, by α_1-AR agonists (Figures 2F–2H).

To determine the specific role of α_{1A}-ARs in regulating cardiomyocyte gene expression, cardiomyocytes were exposed to A61603 (50 nM) and expression of the panel of 34 mRNAs studied for validation of the PE response was examined by qPCR. All were up-regulated by A61603 over 0.5–1 h (Figures 6A–6D and Table 1). The relative increases in expression of four were significantly greater and five were significantly less than PE. However, the increase in expression of the remaining 25 mRNAs was within 1.5-fold that induced by PE. Thus the principal effect of PE on cardiomyocyte gene expression is mediated through α_{1A}-ARs, although other receptors may modulate the response of selected mRNAs. As with PE and ET-1, there was temporal regulation of gene expression by A61603 with some mRNAs showing maximal stimulation at 0.5 h (Figure 6A), some at 0.5–1 h (Figure 6B) and some over 0.5–1.5 h (Figure 6C), whereas other mRNAs were not up-regulated until later times (Figure 6D). To confirm the extent to which the response in neonatal cardiomyocytes is representative of the intact heart, we perfused adult rat hearts *ex vivo* with A61603 in the absence or presence of PD184352 and examined the mRNA expression of a subset of 25 mRNAs (for reasons unknown, but possibly because of effects on the sinoatrial node or because of effects on the vasculature, 5 or 10 μM BI-D1870 had a significant adverse effect on cardiac contractility in the perfused heart system, so we were unable to study its effects on mRNA expression). As expected with a mixed population of unsynchronized cells, the degree of up-regulation of all mRNAs in perfused hearts was less, but 17 were significantly up-regulated (four showed a small non-significant increase), the response of 13 of which

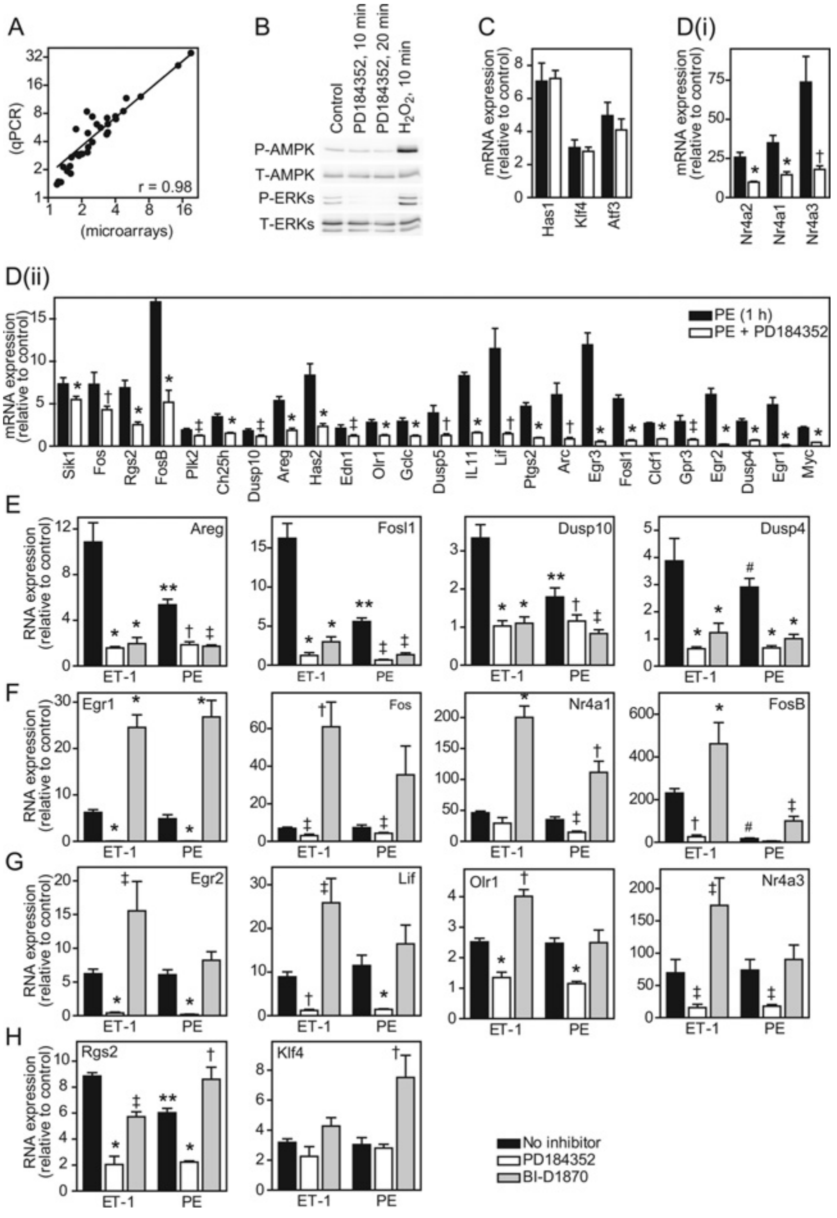

Figure 5 Role of ERK1/2 compared with RSK signalling in the RNA expression response to PE

(**A**) Cardiomyocytes were exposed to PE (1 h). RNA expression was determined by qPCR or microarrays. Linear regression analysis was performed to compare mRNA expression determined by qPCR (ordinate) compared with microarrays (abscissa) (axes are on a $\log_2$ scale). The regression coefficient (*r*) is 0.98. Results are means (relative to controls) for $n = 3$ different cardiomyocyte preparations. (**B**) Cardiomyocytes were unstimulated, or exposed to 2 μM PD184352 or 0.5 mM H_2O_2 for the times indicated. Total extracts were immunoblotted with antibodies against phospho-AMPKα (P-AMPK), total AMPKα (T-AMPK), phospho-ERK1/2 (P-ERKs) or total ERK1/2 (T-ERKs). The experiment was repeated with similar results. (**C** and **D**) Cardiomyocytes were exposed to PE in the absence (closed bars) or presence (open bars) of PD184352 for 1 h. RNA expression was determined by qPCR. Data were normalized to GAPDH and then to the controls. Results are means ± S.E.M. ($n = 3$). $*P < 0.001$, $\dagger P < 0.01$ and $\ddagger P < 0.05$ relative to PE alone. (**E**–**H**) Cardiomyocytes were exposed to ET-1 or PE (1 h) in the absence (black bars) or presence of PD184352 (white bars) or BI-D1870 (grey bars). Expression of selected mRNAs was measured by qPCR. Results are means ± S.E.M. for three (*Rgs2* and *Olr1*) or four (other mRNAs) experiments with different cardiomyocyte preparations. mRNAs are grouped according to relative effects of the inhibitors with each agonist. $*P < 0.001$, $\dagger P < 0.01$ and $\ddagger P < 0.05$ relative to the respective agonist alone; $**P < 0.001$ and $\#P < 0.05$ relative to ET-1.

was inhibited by PD184352 (Figure 6E) consistent with the cardiomyocyte response to PE (Figures 5C and 5D). Five were not sensitive to PD184352 (Figure 6F), the greatest anomalies being *Lif* and *Ptgs2* that were sensitive to PD184352 inhibition in cardiomyocytes exposed to PE (Figure 5C). Three showed no change in expression in perfused hearts (Figure 6G), but these are delayed and/or low level responses and the lack of synchronization of the cells may be a factor. Overall the early gene expression response to α_{1A}-AR stimulation in adult intact rat hearts is largely representative of that of neonatal rat cardiomyocytes in primary culture.

RSKs are required for the increase in surface area induced by ET-1 in cardiomyocytes

In neonatal cardiomyocytes, ET-1 increases myofibrillar organization and content, in addition to increasing cell surface

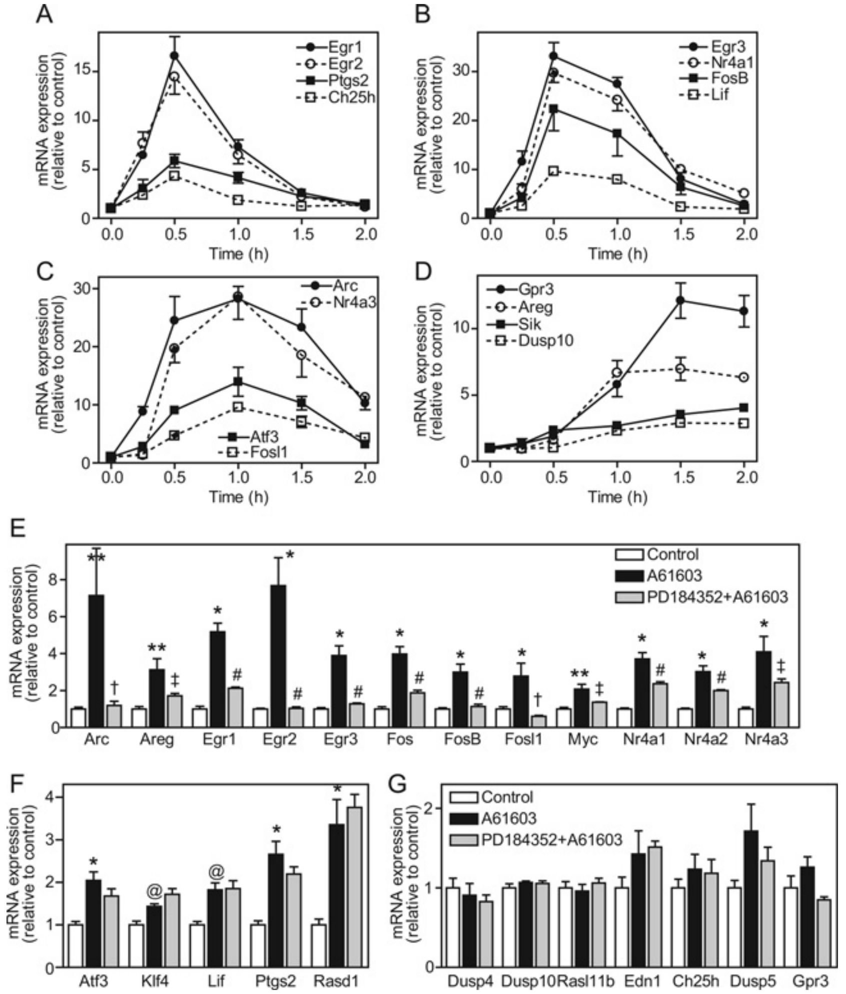

Figure 6 Regulation of cardiomyocyte and cardiac mRNA expression by A61603

(**A**–**D**) Cardiomyocytes were exposed to A61603 for the times indicated and mRNA expression was measured by qPCR. Results expressed relative to controls are means ± S.E.M. for four independent experiments. Expression profiles are grouped according to temporal regulation. (**E**–**G**) Adult rat hearts were perfused retrogradely under control conditions (white bars), with A61603 alone (black bars) or with A61603 in the presence of PD184352 (grey bars). (**E**) mRNAs significantly up-regulated by A61603 with significant inhibition by PD184352. (**F**) mRNAs significantly up-regulated by A61603 without significant inhibition by PD184352. (**G**) mRNAs not significantly up-regulated by A61603. Results are means ± S.E.M. for at least four hearts per condition. *$P < 0.001$, **$P < 0.01$ and @$P < 0.05$ relative to control; #$P < 0.001$, †$P < 0.01$ and ‡$P < 0.05$ relative to A61603 alone.

area. We compared the effects of PD184352 with BI-D1870 on cardiomyocyte morphology by immunostaining with antibodies against troponin T, a component of the myofibrillar apparatus (Figure 7). PD184352 alone increased disruption of myofibrillar organization compared with the unstimulated cells, whereas BI-D1870 appeared to enhance myofibrillar organization to some degree. Neither drug alone significantly affected the cell surface area. ET-1 increased cardiomyocyte surface area, a response that was reduced by PD184352 and inhibited by BI-D1870. Notably, PD184352 particularly disrupted the myofibrillar organization induced by ET-1.

DISCUSSION

Regulation of cardiomyocyte gene expression by ET-1 compared with α_1-ARs

Our previous transcriptomics studies focused on ET-1 and the role of ERK1/2 signalling [13–15,20] because maximally effective concentrations activate the entire pool of ERK1/2 in cardiomyocytes (thus a maximal transcriptomics response should be obtained), and rapid (within 2 min) nuclear localization of phosphorylated ERK1/2 was detectable by immunostaining [12]. In contrast, α_1-AR agonists such as PE do not activate the entire pool of ERK1/2 and we could not detect a significant nuclear signal for phospho-ERK1/2 using immunostaining (results not shown). We now attribute this latter issue to the lower signal being below the threshold for detection by immunostaining, since nuclear phospho-ERK1/2 is detected in response to PE or A61603 by immunoblotting (Figure 1). Additional concerns for studies with PE related to possible contradictory signals between different α_1-AR subtypes and even whether there may be interaction with β-ARs. However, the β-AR antagonist propranolol did not enhance the activation of ERK1/2 by PE (Figure 1A), indicating that the reduced level of activation did not result from an inhibitory input from β-ARs. Furthermore, activation profiles for ERK1/2 and RSKs by PE and A61603 (highly selective for α_{1A}-ARs) were similar (Figures 1 and 2), and mRNA expression studies conducted with PE and A61603 were largely consistent (Figures 5 and 6, and Table 1). We therefore

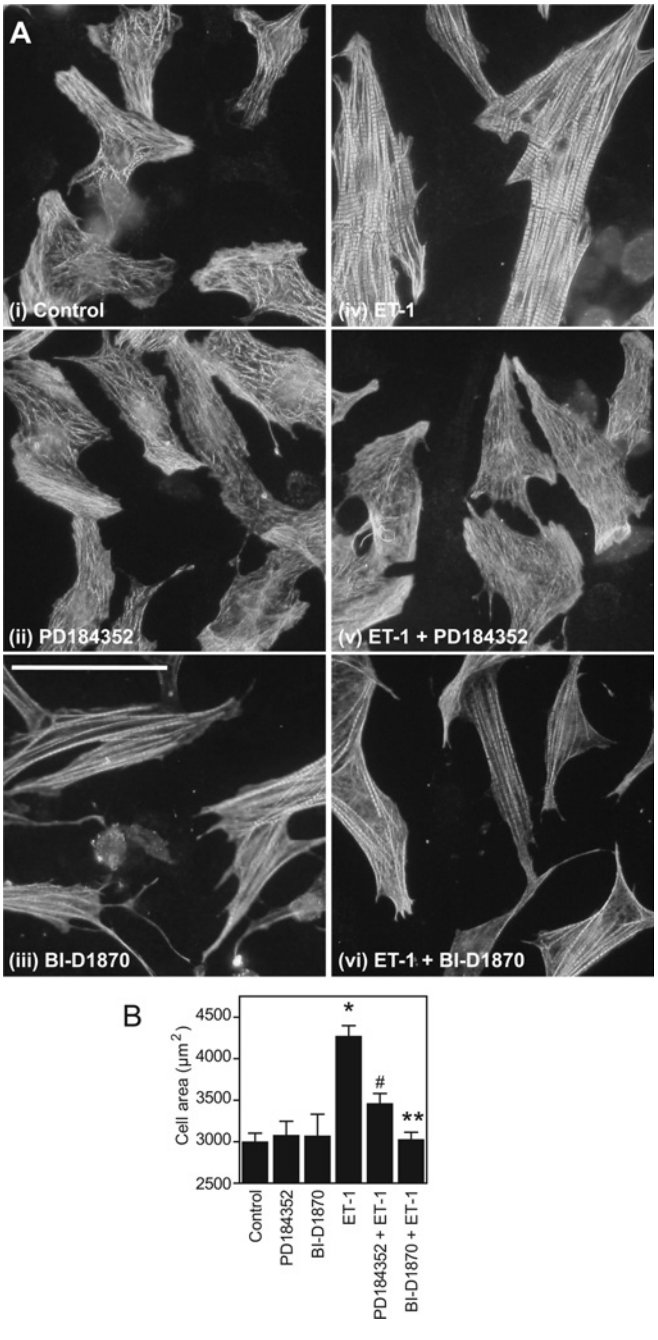

Figure 7 RSKs are required for the increase in size induced by ET-1

(**A**) Representative images of cardiomyocytes that were unstimulated (i, Control), or exposed (24 h) to PD184352 (ii), BI-D1870 (iii), ET-1 (iv), or ET-1 plus PD184352 (v) or BI-D1870 (vi). Cells were immunostained for troponin T. The experiment was performed four times with similar results. Scale bar = 100 μm. (**B**) Cardiomyocyte surface area was measured for each condition, the average values being taken from each experiment as a single observation. Results are means ± S.E.M. ($n = 4$). $^{*}P < 0.001$ relative to the control, $^{**}P < 0.001$ relative to ET-1 and $\#P < 0.01$ relative to ET-1.

conclude that the responses to PE are mediated primarily through α_{1A}-ARs.

ET-1 and α_{1A}-AR agonists each activate G_q-protein-coupled receptors, signalling through protein kinase C and Ras to the ERK1/2 cascade [17]. It is not clear, therefore, why gene expression profiles induced by the two agonists, although overlapping, are quite distinct (Figure 4 and Supplementary Tables S4–S8). Our data indicate that this does not result from differential ERK1/2 signalling in the cytoplasmic and nuclear fractions (Figures 1C and 1D). Instead, with RSKs playing such a prominent role in the transcriptomic response to ET-1 (Figure 3 and Supplementary Table S3), differential regulation of nuclear RSK1 by ET-1 and α_1-AR agonists (Figures 2F–2H) seems the most likely reason for the divergent profiles (Figure 8). Further studies are necessary to dissect the downstream events and identify the specific transcriptional regulators involved in each response. The reason why PE and A61603 fail to stimulate nuclear translocation of RSK1 also remains to be investigated. One tantalizing observation is that ET-1 promotes accumulation of catalytically active monophosphothreonyl-ERK1/2 in addition to the classical dually phosphorylated form [12]. Since the phosphotyrosine residue is important in substrate recognition, the substrate specificity of monophosphothreonyl-ERK1/2 may differ from the dually phosphorylated form. Alternatively or additionally, constraints with respect to location within the cytoplasm may influence signalling specificity. Finally, it is possible that a threshold effect might operate whereby lower levels of ERK1/2 activation are sufficient to activate RSK2, but an increased level of activity is required for RSK1.

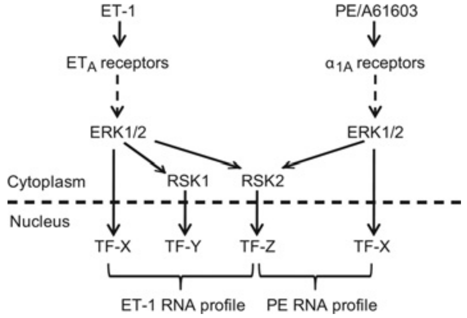

Figure 8 Schematic diagram of the signal from ET-1 or PE/A61603 via ERK1/2 to cardiomyocyte gene expression

ET-1, signalling through ET_A (endothelin receptor type A) receptors, activates ERK1/2. The nuclear signal is propagated via ERK1/2, RSK1 and RSK2 which phosphorylate and regulate different panels of transcription factors (TFs). PE or A61603 signal through α_{1A}-ARs to activate ERK1/2 and the nuclear signal is propagated via ERK1/2 and RSK2, but not RSK1. This divergence contributes to the overlapping, although distinct, transcriptomic profiles induced in cardiomyocytes by these stimuli.

Nuclear trafficking of ERK1/2 and RSKs

In other cells, activation of ERK1/2 is associated with net nuclear accumulation. ERK1/2 do not possess a classic nuclear localization signal, and it is still unclear how ERK1/2 migrate into the nucleus. Passive constitutive flux clearly plays a role [24], potentially modulated by dimerization and/or scaffolding proteins that retain inactive ERK1/2 in the cytoplasm [31]. Phosphorylation of ERK1/2 on additional sites may also be important [32] and, in the heart, autophosphorylation of ERK2(Thr^{188}) may promote nuclear localization [33]. Unexpectedly, our immunoblotting experiments failed to reveal a net translocation of total ERK1/2 to the nuclear compartment in response to ET-1 or α_1-AR agonists, despite accumulation of phosphorylated ERK1/2 (Figures 1C–1E). This is unlikely to result from poor quality preparations either of cardiomyocytes or of nuclear proteins since we detect nuclear accumulation of RSKs (Figure 2). Thus our data are consistent with a model of constitutive, rapid and passive flux of ERK1/2 in and out of the nucleus and there could be separate pools of ERK1/2, one of which is directed to the nucleus, whereas another is anchored in the cytoplasm. We propose that the difference between cardiomyocytes and other cells most likely reflects the relative concentrations and precise components of the anchoring and shuttling machinery, all of which remain to be defined. Unlike ERK1/2, we detected very low levels of RSKs in the nuclear compartment of unstimulated cells, with net translocation of total RSKs to the nucleus following stimulation (Figures 2C–2E). This is consistent with a model of cytoplasmic ERK1/2 phosphorylating cytoplasmic RSKs, enhancing their nuclear translocation. Our observations are in agreement with recent studies in other cells which indicate that activation of RSKs reveals a bipartite nuclear localization signal resulting in nuclear translocation [34].

The significant role of nuclear RSKs in regulating gene expression

Although activated RSKs were shown to translocate to the nucleus in proliferating cells over 20 years ago [35], their contribution to the transcriptomic effects of the ERK1/2 cascade has still not yet been fully evaluated. In the heart, the focus has been almost exclusively on their cytoplasmic role. Thus RSKs are implicated in phosphorylation of Na^+/H^+ exchanger 1 in the plasma membrane and they phosphorylate cardiac myosin-binding protein C, a regulatory component of the myofibrillar apparatus [36,37]. Other cytoplasmic RSK substrates in cardiomyocytes include the pro-apoptotic protein BAD (Bcl-2/Bcl-xL-antagonist, causing cell death) [25] and GSK3α/β (Figure 3A). To our knowledge, ours is the first study to demonstrate that RSKs play a significant role in the nucleus and in regulating cardiomyocyte gene expression. Interestingly, although the largest proportion of mRNAs up-regulated by ET-1 required RSKs for up-regulation, many other up-regulated mRNAs showed an enhanced response in the presence of BI-D1870. An obvious explanation (since BI-D1870 activates ERK1/2, Figure 3B) is that it is a consequence of enhanced ERK1/2 activity. We think this unlikely because all RNAs in this group should then exhibit similar profiles and this is not the case (Figures 3G and 3I). Secondly, BI-D1870 did not enhance activation of ERK1/2 by ET-1 nor increase the duration of the response (Figure 3A and results not shown). Therefore, although enhanced ERK1/2 signalling induced by BI-D1870 could stimulate RNA expression independently of agonist stimulation (consistent with data in Figure 3C, cluster vii), it cannot account for the enhanced stimulation induced by ET-1. More probably, for some mRNAs, RSKs exert a negative effect on expression, potentially via activation of inhibitory transcriptional regulators, stimulation of microRNAs or enhancement of mRNA degradation.

The role of RSKs in regulating gene expression has been explored in a global context previously in cancer cells in relation to cell migration [38]. That study used artificial and constitutive activation of ERK1/2 over 24 h. The benefits of this approach lie in the highly selective nature of the signal; however, although this occurs in cancer cells, such high level constitutive activation of the pathway is less common in other cells and tissues. In cardiomyocytes exposed to ET-1 [14] or α_1-AR agonists (Figures 4 and 6), regulation of early gene expression occurs according to temporal profiles with many RNAs exhibiting only transient expression. This occurs in other systems including (as recent examples) skeletal muscle exposed to insulin [39] and macrophages exposed to pro-inflammatory stimuli [40]. Given the difference in time point studied in our experiments (1 h) and in the cancer cell system (24 h), and the nature of the two cell types, it is perhaps not surprising that there is little overlap in the RSK-responsive genes. However, in both systems and irrespective of the degree of ERK1/2 signalling (i.e. potent activation of the ERK1/2 cascade by ET-1 or lesser activation by α_1-AR agonists), RSKs clearly play a major role in regulating gene expression.

Despite the major contribution from RSKs to the transcriptomic changes resulting from ERK1/2 activation, they are not the sole means by which ERK1/2 promote gene expression and there is a divergence, therefore, in the signal immediately after ERK1/2 activation. This appears to be functionally relevant given that inhibition of RSKs with BI-D1870 inhibited the increase in cell surface area induced by ET-1, but not the increase in myofibrillar organization, whereas inhibiting the cascade with PD184352 caused myofibrillar disarray (Figure 7).

Influence of changes in immediate early gene expression on the cardiomyocyte hypertrophic response

The principal aim of the present study was to gain insight into the degree to which RSKs contribute to changes in mRNA expression in cardiomyocyte hypertrophy. However, the genes themselves are of prime importance. With an emphasis on early times following stimulation, we identified different types of modulator that are likely to propagate the hypertrophic response. Thus, within the first few hours, classic immediate early genes encoding transcription factors (e.g. Fos and Egr family members, *Atf3* and *Myc*) were up-regulated, in addition to orphan nuclear receptors whose function remains to be established (e.g. Nr4a family members). Some of these will regulate downstream gene expression, whereas others are required to terminate immediate early gene expression (e.g. *Atf3* operates in a negative-feedback loop with *Egr1* [20]). We also identified changes in expression of protein kinases [e.g. *Sik1* (salt-inducible kinase 1) and *Plk2*] and phosphatases (e.g. Dusps) indicating that innate signalling networks are undergoing modification. Changes in the expression of secreted growth factors [e.g. *Areg*, *Lif* and *IL11* (interleukin 11)] and cell surface receptors (e.g. *Olr1*) are indicative of changes in intercellular signalling. There were also changes in the expression of channels and transporters, in addition to metabolic enzymes, even at early times. Notably, many RNAs encoded hypothetical proteins and proteins of no known function, and the contribution of these to the overall hypertrophic response may be immense.

Clearly it will be necessary to verify the degree to which changes in mRNA expression are recapitulated at the protein level. Nevertheless our data paint a picture of great flux and dynamic change for the cardiomyocyte in this initial phase of the response. This is presumably on-going *in vivo*, suggesting that there are opportunities for modulating the response. Identifying the optimum points for intervention will require a systems biology approach to develop our understanding of the signalling and gene expression networks within cardiomyocytes and other cardiac cells, in addition to the communication networks that operate between them. In the present study we take the first steps by generating the data required for such an approach.

AUTHOR CONTRIBUTION

The present study was conceived, directed and supervised by Angela Clerk and Peter Sugden. Emre Amirak conducted the RNA experiments with support from Stephen Fuller. Angela Clerk conducted the immunoblotting experiments with support from Emre Amirak and Stephen Fuller. Angela Clerk analysed the microarray data.

FUNDING

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Supplemental Table S1A Antibodies used for immunoblotting

CST, Cell Signaling Technologies Inc.; SCBT, Santa Cruz Biotechnology Inc.

Primary Antibodies	**Source(Cat. no.)**	**Species**	**Dilution**
Total ERK1/2	CST (#9102)	Rabbit	1/1000
Phospho-ERK1(Thr^{203}/Tyr^{205})/ Phospho-ERK2(Thr^{183}/Tyr^{185})	CST (#4377)	Rabbit	1/1000
RSK1/RSK2/RSK3 (32D7) (Total RSKs)	CST (#9355)	Rabbit	1/750
RSK1	CST (#9333)	Rabbit	1/750
RSK2	CST (#9340)	Rabbit	1/750
Phospho-p90RSK(Thr^{573})	CST (#9346)	Rabbit	1/750
Phospho-p90RSK (Thr^{359}/Ser^{363})	CST (#9340)	Rabbit	1/750
Phospho-p90RSK (Ser^{380})	CST (#9341)	Rabbit	1/750
Total MKK1/2	CST (#9122)	Rabbit	1/1000
Phospho-MKK1/2(Ser$^{217/221}$)	CST (#9121)	Rabbit	1/1000
Total AMPK	CST (#2603)	Rabbit	1/1000
Phospho-AMPK(Thr^{172})	CST (#2535)	Rabbit	1/1000
RSK1(C-21)	SCBT (sc-231)	Goat	1/200
RSK2(C-19)	SCBT (sc-1430)	Goat	1/200

Supplemental Table S1B Primers used for qPCR

mRNA sequences were from the Rat Genome Database viewed at http://www.ncbi.nlm.nih.gov/entrez (gene symbols are given with accession numbers).

Gene Symbol, Accession no.	Size (bp)	Position	Forward primer	Reverse primer
Arc, NM_019361.1	85	2207-2291	CCGTCCCCTCCTCTCTTGA	CACCTCCTCTTTGTAATCCTATTTTCTC
Areg, NM_017123.1	58	222-279	TGGTCTTAGGCTCAGGCCATT	CCAGAGCTGGTCCCATTG
Atf3, NM_012912.1	108	302-409	TCGCCATCCAGAACAAGCA	GGGCCACCTCAGACTTGGT
Ch25h, NM_001025415.1	100	404-503	GCTCTTCGACACCGAGATCTTC	GGAGGACGAGTTCTGGTGATG
Clcf1, NM_207615.2	99	373-471	AACCTATGACCTCACCCGCTAC	TTGAAGTCAGGCTCGTTGAAAGG
Dusp10, NM_001105734	137	1279-1415	GCCACAGACAGCAACAAGCAGAAC	ATGACAATGGTGGCAGAACGGGAC
Dusp4, NM_022199	114	783-896	GGAAGCCATCGAATACATAGACGCAG	TTCATCATCAGGTAGGCCAGGCAG
Dusp5, NM_133578.1	72	882-953	CGACATTAGCTCCCACTTTCAA	AGGACCTTGCCTCCCTCTTC
Edn1, NM_012548	92	520-611	CAGTGTGCTCACCAAAAAGACAAGA	TTTACGCCTTTCTGCATGGTACTT
Egr1, NM_012551.2	84	198-281	ACAACCCTACGAGCACCTG	GGATAACTTGTCTCCACCAG
Egr2, NM_053633.1	102	507-608	CTGGAGATGGCATGATCAACA	TCTGGTTTCTAGGCGCAGAGA
Egr3, NM_017086.1	96	66-161	CAATCTGTACCCCGAGGAGATC	ACATTCTCTGTAGCCATCTGAGTGTAA
Ets1, NM_012555	94	443-536	GTTTCACAAAAGAGCAGCAGCGAC	TTCACAGCCCACATCACCCAATCC
Fos, NM_022197	111	226-336	ACAGCCTTTCCTACTACCATTCCC	GGATAAAGTTGGCACTAGAGACGG
Fosb, NM_001256509.1	70	847-916	CGTCGGAGGGAGCTGACA	CCAGCTCTGCCTTTTCCTCTT
Fosl1, NM_012953.1	71	324-394	GCAGCAGAAGTTCCACCTTGT	GCACCATCCACTGCAATTCC
Gclc, NM_012815.2	78	882-957	TGCCCAATTGTTATGGCTTTG	TCCCCACGCACAATCAAT
Gapdh, NM_017008.3	93	552-644	CCAAGGTCATCCATGACAACTT	AGGGGCCATCCACAGTCTT
Gpr3, NM_153727.1	81	789-869	CGCCAACTCTCCTCCTCTCTAC	GCGTAAATGACCGGGTTGAT
Has1, NM_172323	119	1059-1177	CACATTTGGGGATGACAGGCAC	TCAGCCAACGAAGGAAAGAGGAG
Has2, NM_013153	147	1086-1232	ATGTACACCGCCTTCAGAGCAC	AACATCTCCCCCAACACCTCC
Hbegf, NM_012945.1	101	538-638	ACTGTCATCTGTCTGTCTTCTTGTC	CCAACTTCACTTTCTCCTCACTTTC
Hmgcr, NM_013134.2	65	2301-2365	CATGCTGCCAACATCGTCA	CCCACATTCTGTGCTGCATC
IL11, NM_133519.4	80	209-288	CTTCAGACCCTCGTGCAGATC	TGCAGCTAGTTGCCGTGTGT
Klf4, NM_053713.1	138	1159-1296	GCAAGTCCCCTCTCTCCATTATC	CCACAGCCTGCATAGTCACAAG
Klf5, NM_053394.2	153	442-594	TTCCCCGGAGACGATCTGAAAC	TGAAATTATCGGAACTGGAGGAAGC
Lif, NM_022196	139	170-308	GCAGTGCCAATGCCCTCTTTATTTC	ACCAACTTGGTCTTCTCTGTCCC
Mdm2, NM_001108099.1	69	211-279	TCCGACCACCGTGCTTCT	TCGGTAGACACAGACATGTTGGTA
Myc, NM_012603	117	516-632	GCTCCTCGCGTTATTTGAAGCCTG	CGAGTCGTAGTCGAGGTCATAGTTCC
Nr4a1, NM_024388	146	1190-1335	TACCAATCTCCTCACGTCCCTC	GCAAGTCATAAAATTGCTGCACGTC
Nr4a2, NM_019328	114	1452-1565	TGTTCTACGCTTAGCATACAGGTCC	GAATCAATCCATTCCCCAAAGCCAC
Nr4a3, NM_031628.1, NM_017352	81	1770-1850, 1557-1637	CGGGATGGTGAAGGAAGTTGTG	AGTGGGCTCTTTGGTTTGGAAG
Olr1, NM_133306	115	852-966	ACTGGGAAAAAAGTCGGGAGAATTG	AATGGGGAGGTGGAATGGGAAG
Pim1, NM_017034	112	712-823	TGCGGAGATATTCCATTTGAGCAC	TCAGGGACAGGCACCATCTAATAAG
Plk2, NM_031821.1	92	1046-1137	GCACTTGATAGCCAGCATGCT	TGAAGCCCTGCAGAAAGAAGTC
Ptgs2, NM_017232.3	90	1393-1482	GAAGAACTTACAGGAGAGAAAGAAATGG	CAGCAGGGCGGGATACAGT
Rasd1, XM_340809.4	94	314-407	GCGGCGAAGTCTACCAGTTG	AAAACGTCTCCTGTGAGGATAGAGA
Rasl11b, NM_001002830.2	82	344-425	GAACGAAATGCAGGTAACCTCTACA	CTGGAGTGTCCTGGACCTGAA
Rgs2, NM_053453.2	90	209-298	TCAAGCCTTCTCCTGAGGAAGC	ACGCTCTGAATGCAGCAAGC
Ripk2, NM_001191865	142	666-807	TCACGGAGCTACAAATCTGCAC	TGGACAACACTTCCCACATGATAAC
Rnd3, NM_001007641.1	117	411-527	CTGTGGGACACTTCAGGTTC	GACACTGTCCAGAGTTTCTG
Sgk1, NM_001193568, NM_001193569, NM_019232.3	80	883-862, 821-900, 795-874	GGAGAACATCGAGCACAATGGGACAAC	GCTTATGGAGAACCTCAGGAGCGAGATAC
Sik1, NM_021693	94	493-586	ACAACCATCACATCGTCCACCG	TTCCCAAATCCAAAATCTGCCAGC

Supplemental Table S2 Changes in transcript expression induced by PD184352 or BI-D1870

Cardiomyocytes were exposed to 2 µM PD184352 or 10 µM BI-D1870 for 70 min or were unstimulated (Control). RNA expression analysis was performed using Affymetrix rat exon 1.0 ST arrays and GeneSpring 12.0. The raw data for controls are given and results are the mean fold change relative to the controls (n=3). Statistical analysis was performed by one-way ANOVA with SNK post-test using a Benjamini and Hochberg false discovery rate correction (FDR<0.05) * PD184352 vs control; # BI-D1870 vs control.

Probeset ID	**Gene Symbol**	**Gene Title**	**Raw data (Control)**	**PD184352**	**BI-D1870**	
7091079	Adamts1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	1011	0.787	0.496	#
7343686	Adamts15	ADAM metallopeptidase with thrombospondin type 1 motif, 15	451	1.323	0.610	#
7035427	Adm	Adrenomedullin	440	1.097	0.374	#
7221853	Adora2a	Adenosine A2a receptor	325	0.945	0.612	#
7068434	Adora2b	Adenosine A2B receptor	342	0.995	0.606	#
7339834	Amotl2	Angiomotin like 2	248	1.025	0.662	#
7229539	Aplnr	Apelin receptor	422	0.798	0.460	#
7328919	Arc	Activity-regulated cytoskeleton-associated protein	67	1.010	2.254	#
7218259	Arid5b	AT rich interactive domain 5B (Mrf1 like)	671	0.948	0.639	#
7224825	Arrdc3	Arrestin domain containing 3	1403	0.789	0.571	#
7115455	Atf3	Activating transcription factor 3	599	1.161	2.728	#
7318949	Atf4	Activating transcription factor 4 (tax-responsive enhancer element B67)	1343	1.103	1.551	#
7105894	B3galt2	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	332	0.958	0.594	#
7346390	Bbs4	Bardet-Biedl syndrome 4	186	1.099	1.579	#
7246720	Bcl2l1	Bcl2-like 1	102	0.795	0.636	#
7048723	Bcl3	B-cell CLL/lymphoma 3	423	1.229	0.501	#
7271485	Bhlhe41	Basic helix-loop-helix family, member e41	206	1.273	0.536	#
7341999	Birc3	Baculoviral IAP repeat-containing 3	181	1.068	0.653	#
7137201	Bmp4	Bone morphogenetic protein 4	259	0.969	0.658	#
7111272	Btg2	BTG family, member 2	448	0.740	1.918	#
7204662	Card6	Caspase recruitment domain family, member 6	651	0.855	0.658	#
7041913	Ccnj	Cyclin J	356	1.008	0.654	#
7113283	Cct6a	Chaperonin containing Tcp1, subunit 6A (zeta 1)	1150	1.008	0.121	#
7059858	Cdc42ep2	CDC42 effector protein (Rho GTPase binding) 2	403	0.913	0.455	#
7145493	Cdkn2aip	CDKN2A interacting protein	212	1.117	2.218	#
7231595	Chac1	ChaC, cation transport regulator homolog 1 (E. coli)	450	1.089	1.668	#
7258873	Clec2g	C-type lectin domain family 2, member g	602	0.906	0.395	#
7353440	Cnnm4	Cyclin M4	188	1.072	1.730	#
7350918	Csrnp1	Cysteine-serine-rich nuclear protein 1	269	1.140	1.658	#
7331805	Csrnp2	Cysteine-serine-rich nuclear protein 2	158	1.191	1.691	#
7235787	Cstf1	Cleavage stimulation factor, 3' pre-RNA, subunit 1	495	0.940	0.636	#
7110790	Cxcr4	Chemokine (C-X-C motif) receptor 4	759	0.693	0.628	#
7357534	Cxcr7	Chemokine (C-X-C motif) receptor 7	2808	1.095	0.583	#
7299086	Dact1	Dapper, antagonist of beta-catenin, homolog 1 (Xenopus laevis)	416	1.116	0.509	#

7315869	Ddit3	DNA-damage inducible transcript 3	328	1.139	2.427	#
7212476	Ddx20	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	339	1.087	0.633	#
7146093	Dlc1	Deleted in liver cancer 1	472	0.804	0.655	#
7107035	Dnm3	Dynamin 3	253	1.043	0.347	#
7108644	Dusp10	Dual specificity phosphatase 10	374	1.097	0.626	#
7163221	Edn1	Endothelin 1	180	0.826	0.653	#
7188693	Enc1	Ectodermal-neural cortex 1	570	0.900	0.543	#
7198615	F3	Coagulation factor III (thromboplastin, tissue factor)	158	1.090	0.638	#
7297136	Fam110c	Family with sequence similarity 110, member C	140	1.092	0.595	#
7348271	Fam46a	Family with sequence similarity 46, member A	926	0.903	0.339	#
7045890	Fbxo5	F-box protein 5	98	1.089	0.665	#
7376314	Fgf16	Fibroblast growth factor 16	264	0.889	0.569	#
7279359	Fhl3	Four and a half LIM domains 3	677	0.672	0.658	#
7300295	Fos	FBJ osteosarcoma oncogene	175	0.815	2.153	#
7048605	Fosb	FBJ osteosarcoma oncogene B	95	1.346	2.295	#
7246735	Foxs1	Forkhead box S1	343	0.745	0.444	#
7158860	Fzd8	Frizzled homolog 8 (Drosophila)	417	0.918	0.658	#
7115625	G0s2	G0/G1switch 2	508	0.998	0.577	#
7163357	Gcnt2	Glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	135	0.904	0.612	#
7335470	H2afx	H2A histone family, member X	1202	1.079	1.831	#
7084517	H3f3b	H3 histone, family 3B	2359	1.137	1.869	#
7157777	Hist1h1t	Histone cluster 1, H1t	57	1.133	7.278	#
7157872	Hist1h4b	Histone cluster 1, H4b	568	1.139	2.373	#
7197073	Hist2h2be	Histone cluster 2, H2be	137	1.105	2.320	#
7157786	Hist2h3c	Histone cluster 2, H3c	52	1.032	4.485	#
7269087	Hsn2	Hereditary sensory neuropathy, type II	109	1.020	1.741	#
7133438	Htr2a	5-hydroxytryptamine (serotonin) receptor 2A	778	0.701	0.559	#
7333461	Icam4	Intercellular adhesion molecule 4, Landsteiner-Wiener blood group	86	1.000	1.783	#
7194929	Il12a	Interleukin 12a	99	0.710	0.585	#
7199369	Ints12	integrator complex subunit 12	543	1.006	0.625	#
7364446	Irs1	Insulin receptor substrate 1	432	0.871	0.658	#
7311391	Itgb8	Integrin, beta 8	332	0.918	0.615	#
7041047	Jak2	Janus kinase 2	160	0.710	0.455	#
7288744	Jun	Jun proto-oncogene	440	1.116	3.392	#
7179739	Junb	Jun B proto-oncogene	295	0.980	1.781	#
7356519	Kcne4	Potassium voltage-gated channel, Isk-related subfamily, gene 4	546	1.177	0.550	#
7073296	Kcnj2	Potassium inwardly-rectifying channel, subfamily J, member 2	490	0.427	0.427	#
7149521	Klf2	Kruppel-like factor 2 (lung)	173	1.371	4.566	#
7286480	Klf4	Kruppel-like factor 4 (gut)	275	1.079	1.599	#
7327859	Klhl38	Kelch-like 38 (Drosophila)	151	1.142	0.642	#
7057647	LOC100360446	Zinc finger and SCAN domain containing 2-like	147	0.990	0.632	#
7157787	LOC502940	Pro-histogranin	45	0.990	5.205	#
7177292	LOC679129	Similar to Peroxisomal biogenesis factor 19 (Peroxin-19) (Peroxisomal farnesylated protein)	169	1.046	0.551	#
7263342	LOC688916	Hypothetical protein LOC688916	154	1.027	0.579	#
7133360	Lpar6	Lysophosphatidic acid receptor 6	799	0.985	0.560	#

7088871	Lrrc33	Leucine rich repeat containing 33	360	0.669	0.611	#
7118006	Lrrc66	Leucine rich repeat containing 66	52	1.050	1.816	#
7216760	Ly6g5b	Lymphocyte antigen 6 complex, locus G5B	67	1.342	2.063	#
7374315	MGC95208	Similar to 4930453N24Rik protein	694	0.958	0.600	#
7070818	Mir301a	MicroRNA mir-301a	158	0.989	0.661	#
7290692	Mir30c-1 /// Mir30e	MicroRNA mir-30c-1 /// MicroRNA mir-30e	98	1.110	0.622	#
7250666	Mterf	Mitochondrial transcription termination factor	139	1.000	0.609	#
7304727	Mycn	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	181	0.713	0.638	#
7156535	Nedd9	Neural precursor cell expressed, developmentally down-regulated 9	472	1.314	0.574	#
7197523	Ngf	Nerve growth factor (beta polypeptide)	104	0.834	0.624	#
7320920	Nr4a1	Nuclear receptor subfamily 4, group A, member 1	234	1.150	12.279	#
7239111	Nr4a2	Nuclear receptor subfamily 4, group A, member 2	155	1.267	2.867	#
7274931	Nr4a3	Nuclear receptor subfamily 4, group A, member 3	141	0.869	1.955	#
7104982	Nuak2	NUAK family, SNF1-like kinase, 2	202	1.212	0.566	#
7354355	Obfc2a	Oligonucleotide/oligosaccharide-binding fold containing 2A	592	0.959	0.600	#
7286860	Olr854	Olfactory receptor 854	28	1.099	1.639	#
7296159	Osr1	Odd-skipped related 1 (Drosophila)	452	1.330	0.420	#
7208307	Pcdh18	Protocadherin 18	535	1.018	0.512	#
7255389	Pcgf1	Polycomb group ring finger 1	362	1.085	0.557	#
7159665	Pfkfb3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	271	1.341	0.584	#
7308833	Pgf	Placental growth factor	356	1.449	0.660	#
7042529	Pprc1	Peroxisome proliferator-activated receptor gamma, coactivator-related 1	292	0.904	0.635	#
7308969	Pqcp	Polyglutamine-containing protein	553	1.025	0.566	#
7152038	Pragmin	Pragma of Rnd2	224	0.793	0.648	#
7204681	Ptger4	Prostaglandin E receptor 4 (subtype EP4)	306	0.673	0.442	#
7061758	Ranbp6	RAN binding protein 6	333	0.984	0.499	#
7329428	Rbm9	RNA binding motif protein 9	251	1.006	0.646	#
7057923	RGD1305014	Similar to RIKEN cDNA 2310057M21	222	0.977	0.532	#
7280458	RGD1359529	Similar to chromosome 1 open reading frame 63	737	1.068	1.581	#
7197076	RGD1563516	Similar to histone protein Hist2h3c1	135	1.094	2.337	#
7157785	RGD1564767	Histone H2a	104	1.131	2.040	#
7113758	Rgs4	Regulator of G-protein signaling 4	468	1.423	0.510	#
7304448	Rhob	Ras homolog gene family, member B	575	1.280	5.709	#
7075385	Rnf151	Ring finger protein 151	91	0.851	1.832	#
7141425	Rnf219	Ring finger protein 219	187	0.905	0.666	#
7160191	Rpp38	Ribonuclease P/MRP 38 subunit (human)	172	0.902	0.635	#
7178179	Rrad	Ras-related associated with diabetes	471	0.939	0.400	#
7055461	Rrp8	Ribosomal RNA processing 8, methyltransferase, homolog (yeast)	235	0.864	0.636	#
7342926	S1pr2	Sphingosine-1-phosphate receptor 2	727	0.983	0.631	#
7137751	Sall2	Sal-like 2 (Drosophila)	138	0.995	0.614	#
7232029	Sema6d	Sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	285	0.787	0.661	#

7106913	Serpinc1	Serine (or cysteine) peptidase inhibitor, clade C (antithrombin), member 1	58	0.883	1.621	#
7101220	Serpine1	Serine (or cysteine) peptidase inhibitor, clade E, member 1	944	0.719	1.582	#
7029999	Sertad1	SERTA domain containing 1	191	1.080	1.513	#
7045121	Sgk1	Serum/glucocorticoid regulated kinase 1	909	0.836	0.563	#
7226284	Sh2d3c	SH2 domain containing 3C	318	0.792	0.654	#
7157791	Slc17a2|Slc17a3	Solute carrier family 17 (sodium phosphate), member 2 | solute carrier family 17 (sodium phosphate), member 3	65	0.985	1.549	#
7053013	Slco3a1	Solute carrier organic anion transporter family, member 3a1	152	0.820	0.525	#
7191852	Snx16	Sorting nexin 16	126	0.976	0.595	#
7084788	Socs3	Suppressor of cytokine signaling 3	827	1.175	0.478	#
7132725	Sox7	SRY (sex determining region Y)-box 7	175	0.829	0.598	#
7193228	Spry1	Sprouty homolog 1, antagonist of FGF signaling (Drosophila)	528	0.699	0.618	#
7258354	Spsb2	SplA/ryanodine receptor domain and SOCS box containing 2	129	1.046	0.597	#
7233921	Srxn1	Sulfiredoxin 1 homolog (S. cerevisiae)	120	1.039	1.871	#
7133039	Stc1	Stanniocalcin 1	1359	1.048	0.606	#
7232526	Stk35	Serine/threonine kinase 35	390	1.086	0.644	#
7025936	Tcf21	Transcription factor 21	583	0.924	0.385	#
7366702	Tgif1	TGFB-induced factor homeobox 1	1578	0.774	0.372	#
7276021	Tlr4	Toll-like receptor 4	403	0.683	0.591	#
7202800	Tmem171	Transmembrane protein 171	132	1.048	0.636	#
7292877	Tnfrsf1b	Tumor necrosis factor receptor superfamily, member 1b	604	0.934	0.652	#
7071308	Tob1	Transducer of ErbB-2.1	608	1.254	1.587	#
7054758	Tsku	Tsukushin	494	1.067	0.648	#
7197113	Txnip	Thioredoxin interacting protein	1972	1.425	1.812	#
7113823	Uap1	UDP-N-acteylglucosamine pyrophosphorylase 1	347	0.904	1.591	#
7034150	Unknown	Unknown	432	0.811	0.632	#
7040414	Unknown	Unknown	120	0.655	0.606	#
7043386	Unknown	Unknown	121	1.057	0.608	#
7054400	Unknown	Unknown	410	0.960	0.572	#
7077262	Unknown	Unknown	195	1.018	1.834	#
7080234	Unknown	Unknown	76	0.958	3.794	#
7081328	Unknown	Unknown	104	1.107	0.559	#
7083509	Unknown	Unknown	69	1.005	1.673	#
7088940	Unknown	Unknown	71	1.037	2.718	#
7091841	Unknown	Unknown	88	1.163	0.629	#
7092568	Unknown	Unknown	55	0.848	2.562	#
7105681	Unknown	Unknown	180	0.598	0.340	#
7109374	Unknown	Unknown	133	0.685	0.513	#
7113691	Unknown	Unknown	214	1.244	0.590	#
7113707	Unknown	Unknown	620	1.030	0.323	#
7145048	Unknown	Unknown	481	0.979	0.365	#
7152220	Unknown	Unknown	37	1.512	1.716	#
7157921	Unknown	Unknown	144	0.945	2.935	#
7158264	Unknown	Unknown	35	1.035	1.505	#
7159984	Unknown	Unknown	64	1.191	2.182	#
7164765	Unknown	Unknown	108	0.949	1.564	#

7173133	Unknown	Unknown	403	0.870	0.433	#
7173511	Unknown	Unknown	172	1.035	0.661	#
7187974	Unknown	Unknown	57	0.890	0.578	#
7194002	Unknown	Unknown	158	0.860	0.480	#
7205580	Unknown	Unknown	254	1.014	0.599	#
7209283	Unknown	Unknown	72	0.924	1.643	#
7209914	Unknown	Unknown	169	0.871	0.562	#
7228743	Unknown	Unknown	98	0.804	0.655	#
7229859	Unknown	Unknown	106	1.151	1.553	#
7252783	Unknown	Unknown	63	1.144	1.871	#
7259007	Unknown	Unknown	93	0.879	0.525	#
7270654	Unknown	Unknown	77	0.930	0.645	#
7277650	Unknown	Unknown	101	1.091	0.619	#
7287843	Unknown	Unknown	71	0.838	0.601	#
7288050	Unknown	Unknown	307	0.986	0.457	#
7292063	Unknown	Unknown	47	1.165	1.649	#
7292143	Unknown	Unknown	59	1.033	1.633	#
7315377	Unknown	Unknown	53	1.066	1.508	#
7318841	Unknown	Unknown	46	0.834	1.696	#
7319177	Unknown	Unknown	445	1.175	0.479	#
7327300	Unknown	Unknown	184	0.899	0.332	#
7327468	Unknown	Unknown	398	0.768	0.503	#
7327469	Unknown	Unknown	206	0.744	0.600	#
7328512	Unknown	Unknown	238	0.801	0.539	#
7335235	Unknown	Unknown	1138	0.691	0.425	#
7343801	Unknown	Unknown	111	0.749	0.618	#
7350634	Unknown	Unknown	156	0.820	0.589	#
7355170	Unknown	Unknown	134	1.008	0.607	#
7356789	Unknown	Unknown	80	0.905	2.098	#
7361426	Unknown	Unknown	107	0.972	2.151	#
7361747	Unknown	Unknown	158	1.004	0.446	#
7364445	Unknown	Unknown	109	0.757	0.477	#
7366359	Unknown	Unknown	202	0.950	0.584	#
7368920	Unknown	Unknown	46	1.059	1.760	#
7370451	Unknown	Unknown	118	1.414	1.696	#
7370467	Unknown	Unknown	234	0.997	2.787	#
7372037	Unknown	Unknown	78	1.042	2.810	#
7375683	Unknown	Unknown	54	1.165	1.839	#
7268578	Vgll4	Vestigial like 4 (Drosophila)	635	0.965	0.666	#
7335234	Vof16	Ischemia related factor vof-16	672	0.688	0.427	#
7035407	Wee1	Wee 1 homolog (S. pombe)	334	1.017	0.626	#
7349142	Zbtb38	Zinc finger and BTB domain containing 38	336	1.078	0.605	#
7290942	Zc3h12a	Zinc finger CCCH type containing 12A	346	0.769	0.637	#
7168453	Zfp35	Zinc finger protein 35	185	0.965	0.592	#
7049312	Zfp36	Zinc finger protein 36	574	0.961	2.441	#
7191656	Zfp455	Zinc finger protein 455	264	1.005	0.544	#

7220309	Zfp57	Zinc finger protein 57	276	0.963	0.496	#
7153504	Zfp828	Zinc finger protein 828	281	0.881	0.590	#
7041917	Znf518a	Zinc finger protein 518A	131	0.967	0.580	#
7175874	Znf608	Zinc finger protein 608	257	0.774	0.598	#
7080749	Ccl3	Chemokine (C-C motif) ligand 3	842	0.610	0.721	*
7222772	Chst3	Carbohydrate (chondroitin 6) sulfotransferase 3	104	1.560	1.194	*
7071906	Csf3	Colony stimulating factor 3 (granulocyte)	139	0.661	0.706	*
7044959	Ctgf	Connective tissue growth factor	2178	0.614	0.682	*
7123885	Cxcl1	Chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	1582	0.576	1.205	*
7123883	Cxcl2	Chemokine (C-X-C motif) ligand 2	233	0.608	0.817	*
7302739	Cyp1b1	Cytochrome P450, family 1, subfamily b, polypeptide 1	1349	1.563	0.853	*
7215359	Cyr61	Cysteine-rich, angiogenic inducer, 61	2677	0.606	1.544	*
7231589	Dll4	Delta-like 4 (Drosophila)	381	0.369	0.840	*
7043230	Dusp5	Dual specificity phosphatase 5	480	0.509	1.374	*
7222466	Egr2	Early growth response 2	216	0.471	1.392	*
7133143	Egr3	Early growth response 3	252	0.399	1.117	*
7281135	Epha2	Eph receptor A2	187	0.549	0.678	*
7281719	Errfi1	ERBB receptor feedback inhibitor 1	2644	0.659	0.737	*
7260080	Il6	Interleukin 6	162	0.412	0.716	*
7147838	Irs2	Insulin receptor substrate 2	288	0.621	0.817	*
7073296	Kcnj2	Potassium inwardly-rectifying channel, subfamily J, member 2	490	0.427	0.427	*
7166280	Klf6	Kruppel-like factor 6	755	0.616	1.314	*
7105681	Mir181b-1	MicroRNA mir-181b-1	180	0.598	0.340	*
7225165	Nrarp	Notch-regulated ankyrin repeat protein	187	0.605	0.826	*
7120384	Pik3ip1	Phosphoinositide-3-kinase interacting protein 1	445	1.625	0.892	*
7290290	Plk3	Polo-like kinase 3 (Drosophila)	244	0.492	1.145	*
7224182	Prdm1	PR domain containing 1, with ZNF domain	90	0.644	0.917	*
7106132	Ptgs2	Prostaglandin-endoperoxide synthase 2	368	0.648	1.545	*
7294961	RGD1565310	Similar to RIKEN cDNA 1110018J12	105	1.998	0.600	*
7112009	Rgs2	Regulator of G-protein signaling 2	421	0.537	0.954	*
7141508	Spry2	Sprouty homolog 2 (Drosophila)	793	0.269	0.827	*
7216733	Tnf	Tumor necrosis factor (TNF superfamily, member 2)	121	0.663	0.786	*
7317342	Trib1	Tribbles homolog 1 (Drosophila)	269	0.525	0.850	*
7031802	Unknown	Unknown	113	0.564	0.815	*
7225362	Unknown	Unknown	100	0.619	1.069	*
7294269	Unknown	Unknown	55	1.718	1.026	*
7369143	Unknown	Unknown	105	0.628	1.262	*
7384266	Unknown	Unknown	68	1.543	1.311	*
7070340	Ccl7	Chemokine (C-C motif) ligand 7	1575	0.597	0.512	*#
7062006	Ch25h	Cholesterol 25-hydroxylase	163	0.490	0.476	*#
7152119	Dusp4	Dual specificity phosphatase 4	398	0.544	0.566	*#
7314286	Dusp6	Dual specificity phosphatase 6	1599	0.053	0.403	*#
7169197	Egr1	Early growth response 1	3468	0.077	3.172	*#
7322066	Gadd45b	Growth arrest and DNA-damage-inducible, beta	593	1.761	2.005	*#
7327675	Has2	Hyaluronan synthase 2	633	0.609	0.306	*#
7179800	Ier2	Immediate early response 2	204	0.592	4.463	*#

7244755	Il1a	Interleukin 1 alpha	170	0.534	0.588	*#
7120521	Lif	Leukemia inhibitory factor (cholinergic differentiation factor)	325	0.585	1.710	*#
7317471	Myc	Myelocytomatosis oncogene	236	0.474	0.520	*#
7261911	Pdk4	Pyruvate dehydrogenase kinase, isozyme 4	215	1.595	1.539	*#
7314872	Phlda1	Pleckstrin homology-like domain, family A, member 1	863	0.303	1.591	*#
7189518	Plk2	Polo-like kinase 2 (Drosophila)	1934	0.583	0.605	*#
7106414	Rgs16	Regulator of G-protein signaling 16	603	0.598	0.448	*#
7244657	Unknown	Unknown	217	0.594	0.572	*#

Supplemental Table S3 Effects of PD184352 or BI-D1870 on expression of RNAs induced by ET-1

Analysis was performed using Affymetrix rat exon 1.0 ST microarrays and GeneSpring 12.0, identifying transcripts that were significantly changed by ET-1 at 1 h and then establishing the effects of PD184352 or BI-D1870. The raw data for controls are given and results at each time are the mean fold change relative to the controls (n=3). Statistical analysis for ET-1-responsive transcripts was performed by Student's T-test using a Benjamini and Hochberg false discovery rate correction (FDR<0.05). Identification of significant difference in the presence of PD184352 or BI-D1870 was performed with one-way ANOVA with SNK post-test using a Benjamini and Hochberg false discovery rate correction (FDR<0.05). RNAs were clustered according to effects of inhibitors (cluster 1, inhibited by either PD184352 or BI-D1870; cluster 2, inhibited by PD184352 and not inhibited by BI-D1870; cluster 3, inhibited by PD184352 and enhanced by BI-D1870). *FDR<0.05 for ET-1 vs ET-1+PD184352; # FDR<0.05 for ET-1 vs ET-1+BI-D1870

Trasncript cluster ID	Gene Symbol	Gene Title	Raw data (Control)	PD184352	BI-D1870	ET-1	PD184352 + ET-1	BI-D1870 + ET-1	% inhibition PD184352	% inhibition BI-D1870	Cluster	
7091079	Adamts1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	1011	0.787	0.496	2.329	1.646	0.878	35.36	71.27	1	*#
7123129	Agpat9	1-acylglycerol-3-phosphate O-acyltransferase 9	107	1.005	0.934	2.069	1.022	1.202	98.47	74.95	1	*#
7275485	Akap2	A kinase (PRKA) anchor protein 2	1087	0.924	0.936	1.767	1.251	1.091	57.43	79.67	1	*#
7213945	Alpk1	Alpha-kinase 1	161	1.070	0.926	1.581	1.322	0.920	56.57	101.07	1	*#
7060990	Anxa1	Annexin A1	978	1.056	0.958	2.287	1.267	1.195	83.59	81.61	1	*#
7123848	Areg	Amphiregulin	156	0.855	0.976	2.968	1.160	1.135	84.50	91.92	1	*#
7142915	Arhgef3	Rho guanine nucleotide exchange factor (GEF) 3	197	0.918	0.927	2.851	1.231	0.985	83.10	96.86	1	*#
7218259	Arid5b	AT rich interactive domain 5B (Mrf1 like)	671	0.948	0.639	1.781	1.270	0.836	58.79	74.79	1	*#
7105894	B3galt2	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	332	0.958	0.594	1.588	1.076	0.567	79.83	104.61	1	*#
7232862	Bmp2	Bone morphogenetic protein 2	255	0.911	0.728	2.462	1.188	1.599	81.04	40.44	1	*#
7193902	Ccrn4l	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	222	0.871	1.059	6.898	2.202	2.719	77.43	71.86	1	*#
7242411	Cd44	Cd44 antigen	443	0.931	1.063	2.269	1.158	1.571	82.05	59.95	1	*#
7110888	Cd55	Cd55 antigen	245	0.970	0.924	1.633	0.885	1.057	113.48	78.91	1	*#
7025269	Cited2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	1997	0.905	0.763	3.119	1.993	2.389	48.61	23.28	1	*#
7045969	Cnksr3	Cnksr family member 3	316	0.933	0.775	1.524	1.274	0.897	35.02	76.70	1	*#
7077481	Csf2	Colony stimulating factor 2 (granulocyte-macrophage)	35	0.985	1.049	1.611	1.044	1.106	90.35	90.65	1	*#
7108644	Dusp10	Dual specificity phosphatase 10	374	1.097	0.626	3.478	1.160	1.241	97.45	75.17	1	*#
7152119	Dusp4	Dual specificity phosphatase 4	398	0.544	0.566	1.957	0.766	0.796	76.78	75.96	1	*#
7314286	Dusp6	Dual specificity phosphatase 6	1599	0.053	0.403	2.142	0.147	0.841	91.72	61.65	1	*#
7163221	Edn1	Endothelin 1	180	0.826	0.653	2.927	1.526	1.302	63.65	66.33	1	*#
7147985	Efnb2	Ephrin B2	232	1.055	0.939	1.563	1.061	1.129	98.88	66.30	1	*#
7259141	Emp1	Epithelial membrane protein 1	2218	0.961	0.985	2.134	1.083	1.059	89.22	93.49	1	*#
7281135	Epha2	Eph receptor A2	187	0.549	0.678	2.111	0.767	1.493	80.36	26.67	1	*#
7123853	Ereg	Epiregulin	222	0.789	1.309	4.888	1.444	3.611	83.14	40.80	1	*#
7281719	Errfi1	ERBB receptor feedback inhibitor 1	2644	0.659	0.737	3.615	1.776	2.728	57.27	23.89	1	*#

7334452	Ets1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	946	0.888	0.763	1.738	0.996	1.056	85.42	60.37	1	*#
7198615	F3	Coagulation factor III (thromboplastin, tissue factor)	158	1.090	0.638	3.488	2.236	1.086	53.96	82.00	1	*#
7297136	Fam110c	Family with sequence similarity 110, member C	140	1.092	0.595	3.770	2.502	0.857	49.09	90.53	1	*#
7260805	Fgl2	Fibrinogen-like 2	317	1.040	0.927	1.932	1.200	1.171	82.92	73.81	1	*#
7039170	Fosl1	Fos-like antigen 1	279	0.672	0.699	6.216	1.139	1.189	91.04	90.60	1	*#
7299050	Frmd6	FERM domain containing 6	243	0.957	1.072	1.596	1.079	1.361	79.43	51.65	1	*#
7204090	Fst	Follistatin	263	0.796	0.823	4.306	1.091	0.930	91.08	96.76	1	*#
7163357	Gcnt2	Glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	135	0.904	0.612	1.743	1.422	0.806	30.30	73.86	1	*#
7187674	Glrx1	Glutaredoxin 1	328	1.101	1.063	1.782	1.008	1.070	111.94	99.04	1	*#
7248966	Gmeb2	Glucocorticoid modulatory element binding protein 2	245	1.023	0.835	1.568	1.147	0.942	78.22	81.12	1	*#
7280238	Gpr3	G protein-coupled receptor 3	126	0.978	0.798	2.046	1.167	1.439	81.92	38.69	1	*#
7243216	Grem1	Gremlin 1, cysteine knot superfamily, homolog (Xenopus laevis)	91	0.902	0.842	1.861	1.380	0.944	44.48	88.17	1	*#
7327675	Has2	Hyaluronan synthase 2	633	0.609	0.306	8.374	3.782	0.651	56.97	95.32	1	*#
7174562	Hbegf	Heparin-binding EGF-like growth factor	488	0.798	0.774	3.676	1.662	2.573	67.68	32.75	1	*#
7266497	Hk2	Hexokinase 2	541	0.850	0.804	1.719	0.915	0.930	91.00	82.53	1	*#
7202670	Hmgcr	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	713	0.952	0.940	1.691	1.235	1.186	59.12	64.50	1	*#
7150903	Hpgd	ydroxyprostaglandin dehydrogenase 15 (NAD)	51	1.137	0.934	1.571	1.086	0.943	109.07	98.45	1	*#
7216806	Hspa1b|Hspa1a|Hspa1l	Heat shock 70kD protein 1B (mapped) | heat shock 70kD protein 1A | heat shock protein 1-like	86	1.045	1.090	2.629	1.795	1.704	53.98	62.27	1	*#
7133438	Htr2a	5-hydroxytryptamine (serotonin) receptor 2A	778	0.701	0.559	1.622	0.885	0.764	70.34	67.12	1	*#
7194929	Il12a	Interleukin 12a	99	0.710	0.585	1.528	0.892	0.692	65.63	79.85	1	*#
7353844	Il1rl1	Interleukin 1 receptor-like 1	428	1.065	1.003	2.991	1.098	1.655	98.36	67.25	1	*#
7192049	Il7	Interleukin 7	75	0.959	0.917	1.558	0.937	0.987	104.03	87.52	1	*#
7165193	Inhba	Inhibin beta-A	310	0.694	0.706	6.472	2.227	1.489	71.99	85.68	1	*#
7134502	Klf5	Kruppel-like factor 5	334	1.059	0.853	2.308	1.157	0.955	92.50	92.17	1	*#
7210664	Lmna	Lamin A	802	1.074	0.997	1.609	1.285	1.149	65.36	75.03	1	*#
7352509	LOC688459	Hypothetical protein LOC688459	51	0.974	0.892	2.968	1.190	1.085	89.05	90.18	1	*#
7318753	Maff	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	151	0.859	0.946	2.073	1.050	1.558	82.18	42.96	1	*#
7100653	Mafk	v-maf musculoaponeurotic fibrosarcoma oncogene homolog K (avian)	729	0.739	0.916	1.745	1.108	1.123	50.32	72.23	1	*#
7067118	Mgat1	Mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	363	1.019	0.938	1.976	1.382	0.949	62.80	98.92	1	*#
7070060	Mir193	MicroRNA mir-193	118	0.993	0.642	2.329	1.370	0.760	71.56	91.13	1	*#
7135292	Mir19b-1	MicroRNA mir-19b-1	41	0.845	0.901	1.506	1.043	0.751	60.88	129.57	1	*#
7373217	Mir222	MicroRNA mir-222	37	1.039	1.007	2.970	0.979	1.603	103.07	69.76	1	*#
7288447	Mir31	MicroRNA mir-31	102	0.680	0.602	2.354	1.140	0.827	66.06	83.41	1	*#
7211447	Mllt11	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11	506	0.955	0.665	1.608	1.142	0.734	69.27	88.67	1	*#
7274970	Murc	Muscle-related coiled-coil protein	145	1.014	0.972	1.684	1.048	0.929	95.02	106.29	1	*#
7317471	Myc	Myelocytomatosis oncogene	236	0.474	0.520	2.908	1.056	1.498	69.47	48.76	1	*#
7297245	Nampt	Nicotinamide phosphoribosyltransferase	535	1.045	1.007	1.536	0.948	1.191	117.94	65.89	1	*#
7197523	Ngf	Nerve growth factor (beta polypeptide)	104	0.834	0.624	1.716	0.831	0.891	100.36	62.73	1	*#
7235566	Pard6b	Par-6 (partitioning defective 6) homolog beta (C. elegans)	103	1.110	1.100	3.545	1.136	1.631	98.97	79.10	1	*#
7283909	Pdp1	Pyruvate dehyrogenase phosphatase catalytic	603	0.928	0.761	1.701	0.759	0.687	124.00	110.49	1	*#

		subunit 1										
7121583	Peli1	Pellino 1	115	0.970	1.139	1.611	1.303	1.363	45.52	63.41	1	*#
7068987	Per1	Period homolog 1 (Drosophila)	175	1.035	0.966	1.506	1.277	1.070	52.28	79.52	1	*#
7278671	Pik3r3	Phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	352	1.088	0.885	1.545	1.130	1.021	92.41	75.09	1	*#
7152038	Pragmin	Pragma of Rnd2	224	0.793	0.648	1.969	0.826	0.704	96.55	94.27	1	*#
7048738	PVR	Poliovirus receptor	1193	0.843	1.040	1.858	1.088	1.603	71.44	34.33	1	*#
7064324	RGD1308127	Similar to 2700078E11Rik protein	472	0.967	0.891	1.649	1.028	1.140	90.59	61.53	1	*#
7284153	Ripk2	Receptor-interacting serine-threonine kinase 2	437	0.923	0.855	2.704	0.945	1.038	98.72	89.30	1	*#
7220337	Rnf39	Ring finger protein 39	161	0.882	0.763	1.548	0.991	0.775	80.02	97.76	1	*#
7196707	S100a10	S100 calcium binding protein A10	865	1.154	1.176	1.744	1.188	1.474	95.55	60.00	1	*#
7144691	Sc4mol	Sterol-C4-methyl oxidase-like	1802	0.997	0.856	1.534	1.058	1.080	88.52	58.25	1	*#
7103916	Serpinb2	Serine (or cysteine) peptidase inhibitor, clade B, member 2	224	0.777	1.122	14.648	1.463	4.071	94.97	78.39	1	*#
7045121	Sgk1	Serum/glucocorticoid regulated kinase 1	909	0.836	0.563	3.087	0.905	1.287	96.68	65.31	1	*#
7170785	Slc12a2	Solute carrier family 12 (sodium/potassium/chloride transporters), member 2	370	0.971	0.974	1.924	1.289	1.048	65.58	91.97	1	*#
7232493	Slc20a1	Solute carrier family 20 (phosphate transporter), member 1	1253	0.845	0.784	1.640	0.949	1.022	83.80	62.81	1	*#
7269356	Slc2a3	Solute carrier family 2 (facilitated glucose transporter), member 3	230	0.871	1.002	1.565	0.879	1.113	98.46	80.38	1	*#
7136592	Slc4a7	Solute carrier family 4, sodium bicarbonate cotransporter, member 7	147	0.994	1.180	1.795	1.162	1.363	78.81	76.92	1	*#
7096358	Slc7a1	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	767	0.984	0.838	1.603	1.261	0.979	54.12	76.58	1	*#
7187663	Snrpd1|Ell2	Small nuclear ribonucleoprotein D1 | elongation factor RNA polymerase II 2	254	1.009	1.037	2.330	1.264	1.657	80.83	53.37	1	*#
7141508	Spry2	Sprouty homolog 2 (Drosophila)	793	0.269	0.827	2.108	0.804	1.267	51.70	60.27	1	*#
7265169	Spty2d1	SPT2, Suppressor of Ty, domain containing 1 (S. cerevisiae)	175	1.001	0.983	1.504	1.100	1.168	80.22	63.33	1	*#
7308910	Tgfb3	Transforming growth factor, beta 3	444	1.027	0.949	2.085	1.280	0.937	76.69	101.09	1	*#
7246265	Thbd	Thrombomodulin	83	0.911	0.750	1.796	1.123	0.892	73.40	82.28	1	*#
7287386	Tnfsf15	Tumor necrosis factor (ligand) superfamily, member 15	189	0.901	0.841	1.903	1.345	0.793	50.89	105.34	1	*#
7106964	Tnfsf18	Tumor necrosis factor (ligand) superfamily, member 18	91	0.897	0.957	7.906	1.598	1.436	89.85	93.07	1	*#
7297329	Twist1	Twist homolog 1 (Drosophila)	282	0.985	0.813	3.588	1.217	1.059	91.05	90.49	1	*#
7061626	Unknown	Unknown	56	0.862	0.703	1.557	0.931	0.714	87.65	98.05	1	*#
7085832	Unknown	Unknown	121	0.650	0.587	1.531	0.762	0.752	78.94	68.91	1	*#
7105586	Unknown	Unknown	327	0.918	0.694	2.623	1.058	0.837	91.40	91.14	1	*#
7111633	Unknown	Unknown	104	0.863	0.914	1.961	1.197	0.891	65.25	102.34	1	*#
7212310	Unknown	Unknown	246	1.251	0.713	2.197	1.317	1.022	94.45	74.15	1	*#
7235911	Unknown	Unknown	176	0.954	0.817	1.646	1.110	0.723	75.88	114.49	1	*#
7244657	Unknown	Unknown	217	0.594	0.572	2.127	0.810	0.808	80.81	79.04	1	*#
7268354	Unknown	Unknown	67	0.939	0.889	2.116	1.222	1.305	74.70	62.73	1	*#
7270654	Unknown	Unknown	77	0.930	0.645	1.516	0.835	0.595	118.26	109.67	1	*#
7297222	Unknown	Unknown	177	0.958	0.751	2.738	0.962	0.772	99.79	98.82	1	*#
7297247	Unknown	Unknown	173	1.017	0.909	2.978	1.020	1.728	99.85	58.60	1	*#
7327468	Unknown	Unknown	398	0.768	0.503	1.527	1.022	0.887	51.86	27.19	1	*#
7327469	Unknown	Unknown	206	0.744	0.600	1.551	1.037	0.855	46.79	53.71	1	*#
7335235	Unknown	Unknown	1138	0.691	0.425	2.664	1.014	0.604	80.62	89.20	1	*#
7361747	Unknown	Unknown	158	1.004	0.446	1.688	1.339	0.774	51.16	52.32	1	*#

7136062	Vcl	Vinculin	1093	0.997	1.018	1.783	1.443	1.259	43.01	69.15	1	*#
7151046	Vegfc	vascular endothelial growth factor C	169	1.014	0.965	1.564	1.274	0.894	53.87	112.63	1	*#
7085544	Vgll3	Vestigial like 3 (Drosophila)	651	0.969	0.913	2.358	1.760	1.090	41.76	87.01	1	*#
7128932	Rel	Rel v-rel reticuloendotheliosis viral oncogene homolog (avian)	206	1.078	0.951	2.022	1.520	1.109	56.71	84.57	1	*#
7105589	Zfp281	Zinc finger protein 281	659	0.763	0.707	2.166	1.082	0.937	72.67	80.27	1	*#
7197294	Znf697	Zinc finger protein 697	263	0.781	0.956	2.076	1.132	1.420	67.35	56.91	1	*#
7370009	Ankrd57	Ankyrin repeat domain 57	149	0.876	0.998	1.636	1.168	1.401	54.12	36.67	2	*
7160453	Arl5b	ADP-ribosylation factor-like 5B	375	0.875	0.983	1.813	1.165	1.516	64.34	34.41	2	*
7024628	Atp13a3|LOC678704|LOC292449	ATPase type 13A3 | hypothetical protein LOC678704 | similar to hypothetical protein	268	0.908	1.047	1.591	0.918	1.217	98.36	71.18	2	*
7145493	Cdkn2aip	CDKN2A interacting protein	212	1.117	2.218	1.525	1.239	2.766	76.75	-4.42	2	*#
7039008	Clcf1	Cardiotrophin-like cytokine factor 1	152	0.869	0.906	1.535	0.919	1.369	90.61	13.64	2	*
7354636	Coq10b	Coenzyme Q10 homolog B (S. cerevisiae)	316	0.939	1.399	2.261	1.592	2.588	48.18	5.76	2	*
7350918	Csrnp1	Cysteine-serine-rich nuclear protein 1	269	1.140	1.658	4.430	2.264	5.023	67.23	1.90	2	*#
7133143	Egr3	Early growth response 3	252	0.399	1.117	17.163	1.398	13.662	93.82	22.38	2	*
7345585	Fdx1	Ferredoxin 1	198	0.918	1.038	3.649	1.087	5.210	93.61	-57.49	2	*
7252051	Flnc	Filamin C, gamma	1068	0.989	0.959	1.564	0.943	1.416	108.19	18.99	2	*
7048605	Fosb	FBJ osteosarcoma oncogene B	95	1.346	2.295	24.665	6.815	29.434	76.89	-14.68	2	*
7333460	Icam1	Intercellular adhesion molecule 1	1512	0.833	1.169	1.756	1.269	1.759	42.30	21.97	2	*
7112556	Ier5	Immediate early response 5	342	0.910	1.054	1.800	1.235	1.908	59.33	-6.74	2	*
7028549	Il11	Interleukin 11	184	0.862	1.312	2.013	1.158	2.179	70.74	14.36	2	*
7260080	Il6	Interleukin 6	162	0.412	0.716	4.749	2.562	4.670	42.67	-5.44	2	*
7147838	Irs2	Insulin receptor substrate 2	288	0.621	0.817	1.728	1.164	1.315	25.54	31.52	2	*
7286480	Klf4	Kruppel-like factor 4 (gut)	275	1.079	1.599	3.635	2.551	4.224	44.15	0.38	2	*#
7257290	Lmcd1	LIM and cysteine-rich domains 1	683	0.910	0.805	3.072	1.831	2.661	55.53	10.41	2	*
7335998	LOC363060	Similar to RIKEN cDNA 1600029D21	168	0.885	1.096	1.718	1.043	1.650	77.96	22.80	2	*
7325416	Mdm2	Mdm2 p53 binding protein homolog (mouse)	250	1.056	0.978	1.644	1.082	1.692	95.95	-10.86	2	*
7194351	Mei1|Tsc22d2	Meiosis inhibitor 1 | TSC22 domain family, member 2	326	0.948	1.041	2.165	1.237	2.472	75.18	-22.82	2	*
7185182	Nqo1	NAD(P)H dehydrogenase, quinone 1	278	1.143	1.090	1.515	1.234	1.231	82.32	72.78	2	*
7270053	Olr1	Oxidized low density lipoprotein (lectin-like) receptor 1	1942	0.816	1.247	1.536	1.051	1.955	56.09	-32.19	2	*
7189518	Plk2	Polo-like kinase 2 (Drosophila)	1934	0.583	0.605	2.925	1.700	2.358	41.94	8.94	2	*
7106132	Ptgs2	Prostaglandin-endoperoxide synthase 2	368	0.648	1.545	8.007	2.554	10.021	72.80	-20.96	2	*
7112009	Rgs2	Regulator of G-protein signaling 2	421	0.537	0.954	5.498	1.966	4.588	68.23	19.19	2	*
7331581	Rnd1	Rho family GTPase 1	622	0.948	0.938	2.207	1.454	1.739	58.04	33.59	2	*
7238766	Rnd3	Rho family GTPase 3	885	0.825	0.778	1.830	0.940	1.642	86.11	-4.10	2	*
7029999	Sertad1	SERTA domain containing 1	191	1.080	1.513	1.590	1.088	1.890	98.68	36.07	2	*
7214260	Sgms2	Sphingomyelin synthase 2	125	0.988	0.970	1.777	0.953	1.428	104.45	41.06	2	*
7221460	Sik1	Salt-inducible kinase 1	727	0.941	1.047	2.044	1.245	2.154	70.83	-6.05	2	*
7261795	Tfpi2	Tissue factor pathway inhibitor 2	154	0.713	0.826	2.044	0.838	2.198	88.05	-31.41	2	*
7075088	Tnfrsf12a	Tumor necrosis factor receptor superfamily, member 12a	1569	0.917	1.177	1.767	1.263	1.594	54.94	45.57	2	*
7272734	Tp53inp1	Tumor protein p53 inducible nuclear protein 1	978	1.058	0.960	1.532	1.177	1.013	77.61	89.99	2	*
7113823	Uap1	UDP-N-acteylglucosamine pyrophosphorylase 1	347	0.904	1.591	3.229	1.237	3.030	85.04	35.42	2	*
7118521	Ugdh	UDP-glucose dehydrogenase	815	1.025	1.013	1.552	1.205	1.452	67.34	20.50	2	*
7135004	Unknown	Unknown	41	0.850	1.401	1.503	0.904	1.416	89.19	96.95	2	*
7194194	Unknown	Unknown	93	1.225	0.740	2.485	1.334	1.785	92.68	29.61	2	*
7350922	Xirp1	Xin actin-binding repeat containing 1	857	0.820	0.981	1.929	0.997	2.334	80.89	-45.62	2	*
7096947	Zfand2a	Zinc finger, AN1-type domain 2A	710	0.969	1.181	1.709	1.172	1.584	71.31	43.07	2	*

7259100	Apold1	Apolipoprotein L domain containing 1	198	1.027	1.185	2.040	1.460	2.967	58.43	-71.30	3	*#
7328919	Arc	Activity-regulated cytoskeleton-associated protein	67	1.010	2.254	7.297	1.464	25.754	92.79	-273.17	3	*#
7111272	Btg2	BTG family, member 2	448	0.740	1.918	5.348	2.093	9.128	68.87	-65.85	3	*#
7043230	Dusp5	Dual specificity phosphatase 5	480	0.509	1.374	4.689	0.821	7.689	91.53	-71.15	3	*#
7222466	Egr2	Early growth response 2	216	0.471	1.392	5.083	0.736	7.508	93.49	-49.81	3	*#
7300295	Fos	FBJ osteosarcoma oncogene	175	0.815	2.153	2.896	2.083	13.849	33.16	-516.92	3	*#
7265600	Gadd45a	Growth arrest and DNA-damage-inducible, alpha	617	0.989	1.303	1.815	0.928	2.475	107.39	-43.87	3	*#
7338247	Gclc	Glutamate-cysteine ligase, catalytic subunit	989	0.982	1.118	1.651	1.000	2.476	97.31	-108.58	3	*#
7120521	Lif	Leukemia inhibitory factor (cholinergic differentiation factor)	325	0.585	1.710	4.964	1.107	7.272	86.85	-40.32	3	*#
7239111	Nr4a2	Nuclear receptor subfamily 4, group A, member 2	155	1.267	2.867	9.338	3.863	30.993	68.86	-237.31	3	*#
7274931	Nr4a3	Nuclear receptor subfamily 4, group A, member 3	141	0.869	1.955	7.160	3.525	15.172	56.88	-114.58	3	*#
7314872	Phlda1	Pleckstrin homology-like domain, family A, member 1	863	0.303	1.591	4.220	0.621	5.931	90.11	-34.79	3	*#
7217331	Pim1	Pim-1 oncogene	1911	1.198	0.832	1.653	1.462	2.180	59.58	-106.37	3	*#
7051029	Ppp1r15a	Protein phosphatase 1, regulatory (inhibitor) subunit 15A	368	0.884	1.395	2.040	1.676	2.849	23.83	-39.89	3	*#
7354851	Ptp4a1	Protein tyrosine phosphatase 4a1	921	1.044	1.138	1.827	1.027	2.572	102.11	-73.37	3	*#
7308679	RGD1306119	Similar to transcriptional regulating protein 132	223	0.996	1.308	1.529	0.934	2.198	111.74	-68.35	3	*#
7375057	Sat1	Spermidine/spermine N1-acetyl transferase 1	463	0.989	1.452	2.466	1.208	3.413	85.08	-33.71	3	*#
7233921	Srxn1	Sulfiredoxin 1 homolog (S. cerevisiae)	120	1.039	1.871	2.154	1.313	6.781	76.23	-325.59	3	*#
7323040	Timp3	TIMP metallopeptidase inhibitor 3	1753	0.971	0.973	1.669	1.300	2.188	50.89	-81.41	3	*#
7317342	Trib1	Tribbles homolog 1 (Drosophila)	269	0.525	0.850	2.721	0.878	4.552	79.45	-115.10	3	*#
7049312	Zfp36	Zinc finger protein 36	574	0.961	2.441	2.569	1.792	5.794	47.02	-113.77	3	*#
7327038	Abra	Actin-binding Rho activating protein	87	0.948	0.800	1.798	1.268	0.972	59.95	78.38	None	#
7160892	Apbb1ip	Amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein	103	0.998	0.856	1.509	1.285	0.842	43.78	102.72	None	#
7353382	Arid5a	AT rich interactive domain 5A (Mrf1 like)	374	0.832	1.121	1.545	1.431	1.994	-9.91	-60.31	None	#
7115455	Atf3	Activating transcription factor 3	599	1.161	2.728	7.194	4.575	15.559	44.89	-107.15	None	#
7301401	Bdkrb1	Bradykinin receptor B1	47	1.062	0.997	1.506	1.311	1.061	50.96	87.33	None	#
7070340	Ccl7	Chemokine (C-C motif) ligand 7	1575	0.597	0.512	1.530	1.041	0.803	16.09	45.17	None	*#
7209338	Ccnl1	Cyclin L1	785	1.072	1.373	1.885	1.761	3.176	22.20	-103.75	None	#
7062006	Ch25h	Cholesterol 25-hydroxylase	163	0.490	0.476	6.261	5.967	1.552	-4.10	79.55	None	#
7231595	Chac1	ChaC, cation transport regulator homolog 1 (E. coli)	450	1.089	1.668	2.106	2.194	3.815	0.02	-94.24	None	#
7044959	Ctgf	Connective tissue growth factor	2178	0.614	0.682	2.556	2.252	1.474	-5.30	49.10	None	#
7215359	Cyr61	Cysteine-rich, angiogenic inducer, 61	2677	0.606	1.544	3.667	3.512	4.367	-8.97	-5.85	None	#
7066011	Dusp1	Dual specificity phosphatase 1	1479	0.694	0.840	2.686	2.151	2.976	13.62	-26.70	None	*
7169197	Egr1	Early growth response 1	3468	0.077	3.172	2.984	0.164	3.929	95.61	61.83	None	*
7202562	F2rl1	Coagulation factor II (thrombin) receptor-like 1	226	0.965	0.783	1.567	1.452	0.854	14.02	87.44	None	#
7024951	Fbxo30	F-box protein 30	305	0.941	0.792	1.508	1.349	1.066	19.67	45.86	None	#
7162363	Gadd45g	Growth arrest and DNA-damage-inducible, gamma	946	1.038	1.480	2.381	1.885	3.891	38.62	-74.63	None	#
7137256	Gch1	GTP cyclohydrolase 1	58	0.998	1.039	1.537	1.358	1.228	32.89	64.66	None	#
7324926	Glipr1	GLI pathogenesis-related 1	281	1.113	1.020	1.537	1.385	1.081	49.35	88.60	None	#
7047218	Has1	Hyaluronan synthase 1	76	1.482	0.811	2.461	2.637	1.452	20.88	56.09	None	#
7166170	Idi1	Isopentenyl-diphosphate delta isomerase 1	623	1.070	1.102	1.663	1.239	1.791	74.47	-4.04	None	#
7179800	Ier2	Immediate early response 2	204	0.592	4.463	2.451	0.900	12.749	78.75	-471.11	None	*#
7353831	Il1rl2	Interleukin 1 receptor-like 2	107	0.926	0.950	1.584	1.422	1.028	15.06	86.63	None	#
7229388	Itgav	Integrin, alpha V	124	1.156	0.971	1.749	1.477	1.125	57.16	79.40	None	#

7288744	Jun	Jun proto-oncogene	440	1.116	3.392	2.349	3.374	8.345	-67.37	-267.23	None	*#
7149521	Klf2	Kruppel-like factor 2 (lung)	173	1.371	4.566	2.083	3.537	5.917	-100.13	-24.85	None	*#
7166280	Klf6	Kruppel-like factor 6	755	0.616	1.314	3.005	2.246	3.038	18.70	14.00	None	*
7187867	Lysmd3	LysM, putative peptidoglycan-binding, domain containing 3	251	1.177	0.910	1.559	1.369	0.954	65.59	92.03	None	#
7266023	Mat2a	Methionine adenosyltransferase II, alpha	2389	1.113	0.844	1.589	1.363	1.501	57.72	-11.46	None	#
7383823	Morc4	MORC family CW-type zinc finger 4	215	1.121	0.902	1.661	1.432	0.992	53.00	86.31	None	#
7155813	Nfil3	Nuclear factor, interleukin 3 regulated	114	1.278	1.160	2.798	2.767	1.937	17.22	56.81	None	#
7059690	Npas4	Neuronal PAS domain protein 4	65	0.936	0.920	2.020	2.453	0.964	-48.75	95.69	None	#
7320920	Nr4a1	Nuclear receptor subfamily 4, group A, member 1	234	1.150	12.279	18.433	13.496	34.449	29.18	-27.17	None	*#
7365259	Per2	Period homolog 2 (Drosophila)	199	0.927	0.824	1.836	1.671	0.857	11.05	96.04	None	#
7290290	Plk3	Polo-like kinase 3 (Drosophila)	244	0.492	1.145	1.533	1.156	2.275	-24.53	-111.80	None	*#
7197221	Prkab2	Protein kinase, AMP-activated, beta 2 non-catalytic subunit	147	1.113	1.308	1.755	1.721	1.427	19.49	84.26	None	#
7124933	Rasl11b	RAS-like family 11 member B	1201	0.983	0.895	1.850	2.106	1.341	-32.10	47.49	None	#
7304448	Rhob	Ras homolog gene family, member B	575	1.280	5.709	2.561	4.382	9.829	-98.69	-163.91	None	*#
7101220	Serpine1	Serine (or cysteine) peptidase inhibitor, clade E, member 1	944	0.719	1.582	7.690	5.122	6.892	34.17	20.62	None	#
7237652	Slc25a25	Solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25	140	0.929	0.972	1.752	2.005	1.653	-43.20	9.38	None	*
7351949	Srf	Serum response factor (c-fos serum response element-binding transcription factor)	1479	0.958	1.023	1.644	1.553	1.459	7.64	32.34	None	#
7133039	Stc1	Stanniocalcin 1	1359	1.048	0.606	1.581	1.606	0.821	4.02	63.06	None	#
7345054	Tagln	Transgelin	2599	1.118	1.053	1.602	1.487	1.248	38.59	67.64	None	#
7327525	Tnfrsf11b	Tumor necrosis factor receptor superfamily, member 11b	1719	0.936	0.830	1.802	1.700	0.873	4.76	94.63	None	#
7184926	Tppp3	Tubulin polymerization-promoting protein family member 3	257	1.148	0.906	1.561	2.021	0.939	-55.55	94.03	None	#
7200422	Unknown	Unknown	128	1.052	1.204	2.236	2.023	1.776	21.42	53.75	None	#
7205580	Unknown	Unknown	254	1.014	0.599	1.701	1.686	0.942	4.17	50.97	None	#
7335234	Vof16	Ischemia related factor vof-16	672	0.688	0.427	2.880	1.106	0.540	77.81	93.98	None	#

Supplemental Table S4 Changes in transcript expression induced by PE at 2, 4 and 24 h

RNA expression analysis was performed using Affymetrix rat expression 230 2.0 microarrays and GeneSpring 12.0. The raw data for controls are given and results at each time are the mean fold change relative to the controls (n=3). K-means clustering was performed to identify upregulated (U0-U7) and downregulated (D0-D3) groups. Statistical analysis was performed by one-way ANOVA with SNK post-test using a Benjamini and Hochberg false discovery rate correction (FDR<0.05) * 2 h vs control; # 4 h vs control; † 24 h v control

Probeset ID	Gene Symbol	Gene Title	Raw data (Control)	2 h	4 h	24 h	Statistical significance	Cluster
1369027_at	A4galt	Alpha 1,4-galactosyltransferase	144	1.143	1.603	1.249	#	U6
1390783_at	Abca8a	ATP-binding cassette, sub-family A (ABC1), member 8a	173	1.133	1.012	0.654	†	D0
1390455_at	Abhd2	Abhydrolase domain containing 2	180	1.981	2.211	1.888	*#†	U0
1387101_at	Acsl4	Acyl-CoA synthetase long-chain family member 4	607	1.550	1.343	1.446	---	U4
1389189_at	Actn1	Actinin, alpha 1	1561	1.268	1.565	1.639	---	U0
1393730_at	Adamts4	ADAM metallopeptidase with thrombospondin type 1 motif, 4	185	1.653	1.080	0.880	*	U3
1394483_at	Adamts5	A disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5	269	0.726	0.572	0.938	---	D2
1376481_at	Adamts9	A disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9	176	2.010	1.898	1.148	*#	U1
1374677_at	Adssl1	Adenylosuccinate synthase like 1	409	1.189	1.103	0.611	†	D0
1384022_at	Agfg1	ArfGAP with FG repeats 1	558	1.181	1.565	1.324	*#†	U6
1395414_at	Agl	Amylo-1,6-glucosidase, 4-alpha-glucanotransferase	100	0.983	0.603	0.712	#	D3
1372276_at	Agpat3	1-acylglycerol-3-phosphate O-acyltransferase 3	86	1.442	2.398	0.981	*#	U2
1382041_at	Agpat3	1-acylglycerol-3-phosphate O-acyltransferase 3	401	1.280	1.713	1.129	#	U6
1382227_at	Agpat3	1-acylglycerol-3-phosphate O-acyltransferase 3	173	1.413	2.262	1.099	*#	U6
1369291_at	Agtr1a	Angiotensin II receptor, type 1a	84	0.926	0.646	0.820	#	D3
1369146_a_at	Ahr	Aryl hydrocarbon receptor	78	1.018	0.992	1.506	†	U5
1371824_at	Ak3l1	Adenylate kinase 3-like 1	84	1.452	1.936	1.345	#	U6
1388070_a_at	Akap1	A kinase (PRKA) anchor protein 1	288	0.774	0.629	0.828	#	D3
1386764_at	Akap2	A kinase (PRKA) anchor protein 2	109	2.000	1.581	1.175	*	U1
1386998_at	Aldoc	Aldolase C, fructose-bisphosphate	663	1.025	0.992	0.604	†	D0
1368342_at	Ampd3	Adenosine monophosphate deaminase 3	237	0.869	0.608	0.533	#†	D1
1388924_at	Angptl4	Angiopoietin-like 4	165	1.900	1.168	1.028	*	U3
1389398_at	Ank1	Ankyrin 1, erythrocytic	223	1.013	0.800	0.638	#†	D1
1373250_at	Anln	Anillin, actin binding protein	231	1.075	1.153	1.506	†	U5
1367974_at	Anxa3	Annexin A3	100	1.149	1.511	1.053	#	U6
1387376_at	Aox1	Aldehyde oxidase 1	225	1.151	0.879	0.556	†	D0
1398616_at	Ap1s2	Adaptor-related protein complex 1, sigma 2 subunit	633	1.151	1.071	0.603	†	D0
1377750_at	Arhgef3	Rho guanine nucleotide exchange factor (GEF) 3	136	2.198	1.820	1.344	*#†	U4
1379311_at	Arid5a	AT rich interactive domain 5A (Mrf1 like)	95	1.858	1.322	1.001	*	U3
1397437_at	Arid5a	AT rich interactive domain 5A (Mrf1 like)	53	1.721	1.315	1.086	*	U3
1369268_at	Atf3	Activating transcription factor 3	50	2.747	1.537	1.221	*	U3
1373287_at	Atoh8	Atonal homolog 8 (Drosophila)	294	0.646	0.940	0.962	*	D2
1385361_at	Atp10a	ATPase, class V, type 10A	48	1.589	1.170	1.282	*#†	U3
1368701_at	Atp1a3	ATPase, Na+/K+ transporting, alpha 3 polypeptide	219	0.986	0.889	0.606	†	D0
1379906_at	Atp1b2	ATPase, Na+/K+ transporting, beta 2 polypeptide	376	1.010	0.878	0.632	†	D0

1370050_at	Atp2b1	ATPase, Ca++ transporting, plasma membrane 1	407	1.826	1.560	1.105	*#	U1
1386426_at	Atp2b1	ATPase, Ca++ transporting, plasma membrane 1	431	1.963	1.624	1.207	*	U1
1381382_at	Atp6ap1l	ATPase, H+ transporting, lysosomal accessory protein 1-like	227	1.011	0.907	0.626	†	D0
1378134_at	Atp8b1	ATPase, Class I, type 8B, member 1	75	2.389	1.328	1.191	*	U3
1391693_at	Atp8b1	ATPase, Class I, type 8B, member 1	73	2.479	1.190	0.955	*	U3
1370252_at	Avpi1	arginine vasopressin-induced 1	1017	1.146	1.345	1.518	---	U0
1389402_at	Axud1	AXIN1 up-regulated 1	145	2.414	1.732	1.321	*#	U1
1387206_at	B4galt6	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6	452	1.148	1.512	1.346	#	U0
1387938_at	Baalc	Brain and acute leukemia, cytoplasmic	49	1.458	1.982	0.962	*#	U2
1389047_at	Bag2	Bcl2-associated athanogene 2	386	1.428	1.656	1.366	#	U6
1374113_at	Baz1a	Bromodomain adjacent to zinc finger domain, 1A	163	1.741	1.533	1.176	*#	U1
1370869_at	Bcat1	Branched chain aminotransferase 1, cytosolic	856	1.434	1.529	1.657	†	U0
1373494_at	Bcr	Breakpoint cluster region	384	2.329	2.232	1.314	*#	U4
1372613_at	Bdh2	3-hydroxybutyrate dehydrogenase, type 2	333	1.047	0.981	0.630	†	D0
1370649_at	Bdkrb2 /// RGD1308470	Bradykinin receptor B2 /// similar to RIKEN cDNA 4933433P14 gene	106	1.670	1.793	1.218	*#†	U2
1370650_s_at	Bdkrb2 /// RGD1308470	Bradykinin receptor B2 /// similar to RIKEN cDNA 4933433P14 gene	60	2.440	2.793	1.545	*#	U4
1371120_s_at	Bdkrb2 /// RGD1308470	Bradykinin receptor B2 /// similar to RIKEN cDNA 4933433P14 gene	44	1.751	1.575	1.215	*#	U4
1398270_at	Bmp2	Bone morphogenetic protein 2	106	2.134	2.264	1.586	*#†	U4
1389403_at	Bmp7	Bone morphogenetic protein 7	182	1.348	1.654	1.689	#†	U0
1386994_at	Btg2	B-cell translocation gene 2, anti-proliferative	361	1.865	1.845	1.281	*#	U4
1386995_at	Btg2	B-cell translocation gene 2, anti-proliferative	252	2.606	1.977	1.239	*#	U1
1374654_at	Btrc	Beta-transducin repeat containing	254	1.621	1.260	0.985	*	U1
1389569_at	Bxdc2	Brix domain containing 2	350	1.529	1.528	1.235	---	U4
1395479_at	Bxdc2	Brix domain containing 2	159	1.194	1.570	1.224	#	U6
1372293_at	C2cd4d	C2 calcium-dependent domain containing 4D	3633	1.069	1.185	1.836	†	U5
1372536_at	Cabc1	Chaperone, ABC1 activity of bc1 complex homolog (S. pombe)	286	0.922	0.783	0.590	†	D1
1370178_at	Cacnb2	Calcium channel, voltage-dependent, beta 2 subunit	378	1.581	1.295	1.183	*	U3
1391030_at	Camta1	Calmodulin-binding transcription activator 1	443	1.532	2.269	1.683	#	U6
1397536_at	Camta1	Calmodulin-binding transcription activator 1	234	1.369	1.948	1.586	*#†	U6
1368131_at	Capn6	Calpain 6	282	1.172	1.115	0.661	†	D0
1371027_at	Cblb	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	356	1.635	1.283	1.059	*	U1
1368037_at	Cbr1	Carbonyl reductase 1	571	1.502	1.545	1.011	*#	U2
1373085_at	Cbr3	Carbonyl reductase 3	126	2.302	1.492	1.119	*#	U3
1390101_at	Ccdc107	Coiled-coil domain containing 107	343	1.194	1.155	1.602	†	U5
1376104_at	Ccdc165	Coiled-coil domain containing 165	80	1.748	1.613	1.185	*#	U1
1376850_a_at	Ccl27	Chemokine (C-C motif) ligand 27	95	1.092	1.225	1.830	†	U5
1384268_at	Ccnyl1	Cyclin Y-like 1	216	1.323	1.659	1.305	#	U6
1377869_at	Ccrn4l	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	137	4.884	2.921	1.297	*#	U1
1369953_a_at	Cd24	CD24 molecule	190	1.913	1.630	1.273	*#†	U4
1367689_a_at	Cd36	CD36 molecule (thrombospondin receptor)	1102	1.096	0.816	0.607	†	D1
1386901_at	Cd36	CD36 molecule (thrombospondin receptor)	1798	0.992	0.962	0.651	†	D0
1376866_at	Cd3eap	CD3E antigen, epsilon polypeptide-associated protein	91	1.349	1.608	1.306	#	U6
1368921_a_at	Cd44	Cd44 molecule	400	1.501	1.787	1.257	*#†	U6
1387952_a_at	Cd44	Cd44 molecule	437	1.667	1.704	1.328	*#	U4
1375910_at	Cdc42ep3	CDC42 effector protein (Rho GTPase binding) 3	885	1.503	1.687	1.202	*#	U2
1374139_at	Cdr2	Cerebellar degeneration-related 2	237	1.371	1.554	1.468	---	U0
1380063_at	Ch25h	Cholesterol 25-hydroxylase	84	2.394	2.732	1.121	*#	U2
1379300_at	Chst2	Carbohydrate sulfotransferase 2	102	1.536	1.622	1.206	*#	U2
1386615_at	Chst2	Carbohydrate sulfotransferase 2	182	1.598	1.733	1.131	*#	U2

1367601_at	Cited2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	343	2.499	2.471	1.155	*#	U2
1367602_at	Cited2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	453	2.627	2.024	1.172	*#	U1
1370225_at	Cited4	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4	361	0.508	0.600	0.745	*#†	D2
1367626_at	Ckm	Creatine kinase, muscle	1760	1.068	1.019	0.641	†	D0
1373182_at	Cldn12	Claudin 12	229	1.504	1.220	1.059	*#	U3
1370254_at	Clic5	Chloride intracellular channel 5	155	1.117	1.635	0.971	#	U6
1383219_at	Clip4	CAP-GLY domain containing linker protein family, member 4	338	0.913	0.815	0.620	#†	D1
1393619_at	Cnot6l	CCR4-NOT transcription complex, subunit 6-like	70	1.594	1.065	1.046	*	U3
1370927_at	Col12a1	Collagen, type XII, alpha 1	253	1.215	1.345	1.960	*#†	U5
1395580_at	Col12a1	Collagen, type XII, alpha 1	104	1.098	0.940	1.619	†	U5
1376955_at	Col4a4	Procollagen, type IV, alpha 4	72	1.165	0.933	1.528	†	U5
1393891_at	Col8a1	Collagen, type VIII, alpha 1	174	1.060	1.151	1.569	†	U5
1373866_at	Coq10b	Coenzyme Q10 homolog B (S. cerevisiae)	297	2.239	1.864	1.434	*#†	U4
1372223_at	Cpeb4	Cytoplasmic polyadenylation element binding protein 4	459	2.220	1.436	1.328	*	U3
1393294_at	Cpeb4	Cytoplasmic polyadenylation element binding protein 4	285	1.622	1.179	1.067	*	U3
1367742_at	Cpt1b	Carnitine palmitoyltransferase 1b, muscle	907	1.074	0.899	0.596	†	D0
1390420_at	Cpxm1	Carboxypeptidase X (M14 family), member 1	970	1.203	0.961	0.624	†	D0
1369737_at	Crem	cAMP responsive element modulator	35	4.165	1.868	1.029	*#	U3
1369738_s_at	Crem	cAMP responsive element modulator	176	2.433	1.657	1.080	*#	U1
1378925_at	Crem	cAMP responsive element modulator	116	5.232	1.965	1.080	*#	U3
1393550_at	Crem	cAMP responsive element modulator	38	3.093	1.117	1.020	*	U3
1376799_a_at	Crlf1	Cytokine receptor-like factor 1	200	1.172	1.475	2.435	*#†	U5
1395512_at	Crlf1	Cytokine receptor-like factor 1	130	1.001	1.216	2.388	†	U5
1392640_at	Cry1	Cryptochrome 1 (photolyase-like)	114	1.476	1.582	0.994	*#	U2
1368685_at	Cspg4	Chondroitin sulfate proteoglycan 4	229	1.490	1.770	1.541	#	U0
1370057_at	Csrp1	Cysteine and glycine-rich protein 1	2358	1.055	1.141	1.502	†	U5
1391635_at	Ctdspl	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	137	1.201	1.546	1.133	#	U6
1398354_at	Ctnnal1	Catenin (cadherin associated protein), alpha-like 1	87	1.480	1.609	0.792	*#	U2
1379365_at	Cxcl11	Chemokine (C-X-C motif) ligand 11	408	1.111	0.941	0.317	†	D0
1387655_at	Cxcl12	Chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	412	0.937	0.583	0.693	#	D3
1398383_at	Cyb561	Cytochrome b-561	253	1.120	1.047	0.644	†	D0
1376788_at	Dapk1	Death associated protein kinase 1	818	0.964	0.977	0.612	†	D0
1379911_at	Dapk1	Death associated protein kinase 1	407	0.974	0.988	0.655	†	D0
1387111_at	Ddah1	Dimethylarginine dimethylaminohydrolase 1	755	1.041	1.143	1.885	†	U5
1389079_at	Dhrs7c	Dehydrogenase/reductase (SDR family) member 7C	93	1.040	0.845	0.509	†	D0
1370328_at	Dkk3	Dickkopf homolog 3 (Xenopus laevis)	1498	0.971	0.859	0.635	†	D1
1374651_at	Dopey2	Dopey family member 2	139	1.575	1.761	1.016	*#	U2
1389155_at	Dos	Downstream of Stk11	183	2.409	1.667	1.304	*#	U1
1388589_at	Dot1l	DOT1-like, histone H3 methyltransferase (S. cerevisiae)	266	1.937	2.053	1.022	---	U2
1368146_at	Dusp1	Dual specificity phosphatase 1	240	1.510	1.906	1.102	*#	U2
1368147_at	Dusp1	Dual specificity phosphatase 1	57	1.347	1.569	1.091	#	U2
1373324_at	Dusp14	Dual specificity phosphatase 14	121	1.570	1.478	1.240	*#†	U4
1377023_at	Dusp2	Dual specificity phosphatase 2	100	1.983	1.441	1.293	*#†	U3
1368124_at	Dusp5	Dual specificity phosphatase 5	212	2.956	1.843	1.007	*#	U1
1377064_at	Dusp6	Dual specificity phosphatase 6	339	1.237	1.929	1.500	#†	U6
1387146_a_at	Ednrb	Endothelin receptor type B	85	1.359	1.815	1.035	#	U2
1390112_at	Efemp1	EGF-containing fibulin-like extracellular matrix protein 1	288	1.080	0.999	0.437	†	D0
1372844_at	Efna1	Ephrin A1	105	1.542	1.091	0.978	*	U3

1387306_a_at	Egr2	Early growth response 2	113	1.721	2.354	1.393	#	U6
1368867_at	Eif2c2	Eukaryotic translation initiation factor 2C, 2	204	1.750	1.649	1.125	*#	U1
1389680_at	Ell2	Elongation factor RNA polymerase II 2	122	2.142	1.434	1.172	*#	U3
1386907_at	Eno3	Enolase 3, beta, muscle	133	1.065	1.227	2.106	†	U5
1370047_at	Enpp1	Ectonucleotide pyrophosphatase/phosphodiesterase 1	465	1.211	1.123	1.851	†	U5
1374143_at	Epha2	Eph receptor A2	128	2.512	2.066	1.376	*#	U4
1373093_at	Errfi1	ERBB receptor feedback inhibitor 1	603	1.735	1.535	1.079	*#	U1
1371710_at	Etnk1	Ethanolamine kinase 1	533	2.003	1.595	1.210	*#†	U1
1393151_at	Etnk1	Ethanolamine kinase 1	224	2.034	1.475	1.162	*	U1
1388342_at	Etv3	Ets variant 3	206	1.739	1.419	1.109	*#	U1
1367899_at	F2r	Coagulation factor II (thrombin) receptor	846	1.179	1.385	1.543	#†	U0
1369182_at	F3	Coagulation factor III (thromboplastin, tissue factor)	106	1.593	1.400	1.220	*	U4
1392510_at	Fam180a	Family with sequence similarity 180, member A	363	0.633	0.600	0.825	*#	D2
1391944_at	Fam184a /// RGD1560557	Family with sequence similarity 184, member A /// similar to minichromosome maintenance protein 8 isoform 1	63	1.253	1.819	1.114	*#	U6
1389533_at	Fbln2	Fibulin 2	964	1.103	1.239	1.749	†	U5
1368336_at	Fdx1	Ferredoxin 1	857	2.643	3.028	1.108	*#	U2
1387301_at	Fgf1	Fibroblast growth factor 1	172	0.910	0.539	0.798	#	D3
1368114_at	Fgf13	Fibroblast growth factor 13	391	1.026	0.767	0.627	#†	D1
1383516_at	Fgl2	Fibrinogen-like 2	87	1.948	1.192	1.067	*	U3
1386637_at	Fgl2	Fibrinogen-like 2	197	1.566	1.062	0.986	*	U3
1392894_at	Fgl2	Fibrinogen-like 2	506	1.779	1.497	1.162	*	U1
1376937_at	Filipl	Filamin A interacting protein 1-like	223	1.323	1.654	1.382	#	U6
1389449_at	Fit1	Fat-inducing transcript 1	197	0.877	0.865	0.558	†	D0
1375043_at	Fos	FBJ osteosarcoma oncogene	51	1.616	2.370	1.243	*#	U6
1368489_at	Fosl1	Fos-like antigen 1	76	2.018	1.757	1.328	*#†	U4
1383860_at	Fosl2	Fos-like antigen 2	77	1.759	1.195	1.126	*	U3
1387843_at	Fst	Follistatin	82	1.403	1.506	1.540	*#†	U0
1379440_at	Fstl3	Follistatin-like 3 (secreted glycoprotein)	170	0.993	1.353	1.604	#†	U5
1368207_at	Fxyd5	FXYD domain-containing ion transport regulator 5	499	1.094	1.181	1.545	#†	U5
1392818_at	Gas5	Growth arrest specific 5	248	1.307	1.550	1.150	*#	U6
1374125_at	Gata5	GATA binding protein 5	134	0.529	0.656	0.851	*	D2
1387221_at	Gch1	GTP cyclohydrolase 1	55	1.585	1.739	1.232	*#	U2
1370688_at	Gclc	Glutamate-cysteine ligase, catalytic subunit	265	1.968	1.122	1.159	*	U3
1372523_at	Gclc	Glutamate-cysteine ligase, catalytic subunit	267	2.166	1.281	1.142	*#	U3
1387659_at	Gda	Guanine deaminase	1156	1.823	1.971	1.026	*#	U2
1382351_at	Gem	GTP binding protein (gene overexpressed in skeletal muscle)	82	2.167	1.560	0.910	*	U1
1377761_at	Gfpt2	Glutamine-fructose-6-phosphate transaminase 2	1455	2.367	1.874	1.303	*#†	U1
1367852_s_at	Gp1bb /// Sept5	Glycoprotein Ib (platelet), beta polypeptide /// septin 5	49	1.144	1.383	1.522	#†	U0
1369666_at	Gpd2	Glycerol-3-phosphate dehydrogenase 2, mitochondrial	116	1.512	1.096	1.124	*	U3
1387241_at	Gpr88	G-protein coupled receptor 88	99	0.778	0.662	0.621	*#†	D1
1376828_at	Gprc5a	G protein-coupled receptor, family C, group 5, member A	112	1.809	2.341	1.777	*#†	U6
1378163_at	Grem2	Gremlin 2, cysteine knot superfamily, homolog (Xenopus laevis)	110	1.192	1.137	0.662	†	D0
1389890_at	Gse1	Genetic suppressor element 1	88	1.505	1.219	1.162	*	U3
1371942_at	Gstt3	Glutathione S-transferase, theta 3	211	1.154	0.900	0.548	†	D0
1387396_at	Hamp	Hepcidin antimicrobial peptide	720	1.186	1.254	0.510	†	D0
1371819_at	Hdac5	Histone deacetylase 5	406	1.690	1.581	1.000	*#	U1
1373381_at	Herc4	Hect domain and RLD 4	204	1.609	1.435	1.069	*#	U1
1391429_at	Hfe2	Hemochromatosis type 2 (juvenile) (human homolog)	129	1.037	0.793	0.562	#†	D1
1374105_at	Higd1a	HIG1 domain family, member 1A	185	1.338	1.746	1.327	#	U6
1376692_at	Hipk2	Homeodomain interacting protein kinase 2	141	1.396	1.541	1.245	---	U6
1368546_at	Hivep2	Human immunodeficiency virus type I enhancer binding protein 2	245	2.071	1.447	1.319	*#	U3

1369006_at	Hk2	Hexokinase 2	241	1.601	1.484	1.122	*#	U1
1383519_at	Hk2	Hexokinase 2	582	1.447	1.538	0.984	*#	U2
1387233_at	Hsd17b7	Hydroxysteroid (17-beta) dehydrogenase 7	159	1.318	1.259	1.558	*#†	U0
1370912_at	Hspa1b	Heat shock 70kD protein 1B (mapped)	129	1.299	1.565	1.400	#	U0
1369841_at	Hspa2	Heat shock protein 2	41	1.367	1.679	1.239	#	U6
1385620_at	Hsph1	Heat shock 105kDa/110kDa protein 1	315	1.574	1.635	1.430	*#†	U4
1387202_at	Icam1	Intercellular adhesion molecule 1	763	1.514	1.347	0.968	*#	U1
1375120_at	Id4	Inhibitor of DNA binding 4	91	1.592	1.691	1.371	---	U4
1375183_at	Id4	Inhibitor of DNA binding 4	57	1.391	1.801	1.237	---	U6
1394022_at	Id4	Inhibitor of DNA binding 4	106	1.999	2.152	1.485	*#†	U4
1368878_at	Idi1	Isopentenyl-diphosphate delta isomerase 1	1117	1.070	1.114	1.555	†	U5
1372389_at	Ier2	Immediate early response 2	283	1.780	1.612	1.350	*#	U4
1388587_at	Ier3	Immediate early response 3	821	1.631	1.769	1.444	*#†	U4
1389355_at	Ier5	Immediate early response 5	509	1.360	1.626	1.107	*#	U2
1367795_at	Ifrd1	Interferon-related developmental regulator 1	377	1.773	1.526	1.500	*#†	U4
1370960_at	Igfbp5	Insulin-like growth factor binding protein 5	700	1.003	0.893	0.444	†	D0
1387348_at	Igfbp5	Insulin-like growth factor binding protein 5	421	0.954	0.685	0.477	#†	D1
1396152_s_at	Igfbp5	Insulin-like growth factor binding protein 5	315	1.163	0.677	0.479	†	D1
1387273_at	Il1rl1	Interleukin 1 receptor-like 1	229	2.003	2.135	2.150	---	U0
1387124_at	Inha	Inhibin alpha	145	1.162	1.586	3.527	#†	U5
1377379_at	Irf6	Interferon regulatory factor 6	56	1.327	1.569	1.135	#	U2
1371091_at	Irs2	Insulin receptor substrate 2	266	1.999	2.187	1.158	*#	U2
1392981_at	Irx4	Iroquois homeobox 4	521	0.549	0.575	0.690	*#†	D2
1373049_at	Itprip	Inositol 1,4,5-trisphosphate receptor interacting protein	117	1.841	1.683	1.331	*#	U4
1373122_at	Jub	jJb, ajuba homolog (Xenopus laevis)	375	1.152	1.556	1.234	#	U6
1390473_at	Kcng2	Potassium voltage-gated channel, subfamily G, member 2	453	0.843	0.644	0.818	#	D3
1370773_a_at	Kcnip2	Kv channel-interacting protein 2	130	1.203	0.757	0.409	†	D0
1373987_at	Kcnip2	Kv channel-interacting protein 2	351	0.984	0.843	0.269	†	D0
1387698_at	Kcnj11	Potassium inwardly rectifying channel, subfamily J, member 11	147	0.600	0.622	0.783	#	D2
1391007_s_at	Kcnj11	Potassium inwardly rectifying channel, subfamily J, member 11	186	0.571	0.623	0.710	*#†	D2
1397764_at	Kctd5	Potassium channel tetramerisation domain containing 5	425	1.574	1.449	1.167	*#	U4
1368249_at	Klf15	Kruppel-like factor 15	314	0.752	0.729	0.662	*#†	D1
1381396_s_at	Klf15	Kruppel-like factor 15	215	0.705	0.624	0.634	*#†	D3
1387260_at	Klf4	Kruppel-like factor 4 (gut)	513	1.813	1.304	1.211	*#†	U3
1368363_at	Klf5	Kruppel-like factor 5	83	3.356	1.348	1.167	*	U3
1394039_at	Klf5	Kruppel-like factor 5	37	2.804	1.289	1.005	*	U3
1388155_at	Krt18	Keratin 18	41	1.016	1.304	1.570	†	U5
1376632_at	Lmcd1	LIM and cysteine-rich domains 1	236	4.051	4.595	1.342	*#	U2
1375726_at	Lmo7	LIM domain 7	615	1.396	1.758	1.164	#	U6
1381190_at	Lmo7	LIM domain 7	941	1.381	1.794	1.213	*#	U6
1389464_at	Lnx1	Ligand of numb-protein X 1	112	0.957	0.771	0.634	#†	D1
1374932_at	LOC100361444	rCG31799-like	50	0.941	1.423	1.688	#†	U5
1389018_at	LOC100362331	rCG59612-like	228	1.049	0.964	1.601	†	U5
1372213_at	LOC500300	Similar to hypothetical protein MGC6835	489	1.418	1.684	1.497	*#†	U0
1383675_at	LOC679127	Similar to Protein KIAA0690	150	1.343	1.767	1.361	#	U6
1386669_at	LOC679127	Similar to Protein KIAA0690	165	1.072	1.518	1.281	#†	U6
1383382_at	LOC681740	Similar to jumonji protein	287	1.993	1.155	1.066	*#	U3
1384390_at	LOC681740	Similar to jumonji protein	189	2.284	1.132	1.166	*	U3
1389984_at	LOC681740	Similar to jumonji protein	391	2.132	1.057	1.007	*	U3
1373659_at	LOC689926	Hypothetical protein LOC689926	81	0.558	0.499	0.714	*#	D2
1368171_at	Lox	Lysyl oxidase	638	1.171	1.281	1.913	#†	U5
1368172_a_at	Lox	Lysyl oxidase	392	1.036	1.198	1.804	†	U5

1393177_at	Lrch1	Leucine-rich repeats and calponin homology (CH) domain containing 1	81	1.548	1.369	1.106	*#	U1
1389727_at	Lrrc10	Leucine-rich repeat-containing 10	440	0.524	0.337	0.828	*#	D2
1373755_at	Lrrc39	Leucine rich repeat containing 39	235	0.921	0.786	0.610	†	D1
1384178_at	Lrrc4b	Leucine rich repeat containing 4B	279	0.837	0.829	1.801	†	U5
1389351_at	Lrrfip1	Leucine rich repeat (in FLII) interacting protein 1	282	1.454	1.658	1.309	*#†	U6
1367912_at	Ltbp1	Latent transforming growth factor beta binding protein 1	79	1.358	2.220	1.574	#	U6
1380229_at	Maff	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	86	1.654	1.395	1.244	*#†	U4
1372211_at	Mafk	v-maf musculoaponeurotic fibrosarcoma oncogene homolog K (avian)	338	1.746	1.631	1.284	---	U4
1387753_s_at	Magi3	Membrane associated guanylate kinase, WW and PDZ domain containing 3	269	1.567	1.640	1.044	---	U2
1398866_at	Magi3	mMmbrane associated guanylate kinase, WW and PDZ domain containing 3	135	1.720	1.989	1.160	*#†	U2
1388858_at	Map2k3	Mitogen activated protein kinase kinase 3	929	1.716	1.838	1.214	*#†	U2
1378552_at	Map3k6	Mitogen-activated protein kinase kinase kinase 6	135	1.298	1.537	1.186	#	U6
1389543_at	Masp1	Mannan-binding lectin serine peptidase 1	173	0.930	0.993	0.596	†	D0
1391474_at	Med14	Mediator complex subunit 14	130	1.352	1.474	1.552	---	U0
1371479_at	Mettl7a	Methyltransferase like 7A	302	0.816	0.747	0.660	†	D1
1392547_at	MGC105649	Hypothetical LOC302884	70	1.230	1.643	1.501	#†	U0
1379059_at	Micall2	MICAL-like 2	106	1.593	1.354	1.026	*#	U1
1383668_at	Mmp15	Matrix metallopeptidase 15	252	0.901	0.614	0.776	#†	D3
1372117_at	Mtmr10	Myotubularin related protein 10	80	1.310	1.569	1.227	#	U6
1373032_at	Mustn1	Musculoskeletal, embryonic nuclear protein 1	92	1.365	1.629	1.442	*#†	U0
1368308_at	Myc	Myelocytomatosis oncogene	275	2.313	1.684	1.679	*#†	U4
1393639_at	Myo10	Myosin X	46	1.508	1.605	1.123	*#	U2
1374088_at	Mypn	Myopalladin	145	2.651	3.440	0.908	*#	U2
1389014_at	Nampt	Nicotinamide phosphoribosyltransferase	344	1.634	1.449	1.135	*#	U1
1375861_at	Nap1l5	Nucleosome assembly protein 1-like 5	89	1.897	1.682	1.975	*#†	U0
1375436_at	Naprt1	Nicotinate phosphoribosyltransferase domain containing 1	611	1.054	1.005	0.660	†	D0
1372953_at	Ncald	Neurocalcin delta	138	1.315	1.515	1.298	*#†	U6
1371360_at	Ndrg1	N-myc downstream regulated gene 1	358	1.269	1.692	1.136	#	U6
1368488_at	Nfil3	Nuclear factor, interleukin 3 regulated	196	2.310	1.767	1.037	*#	U1
1370968_at	Nfkb1	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1	928	1.683	1.309	0.957	*#	U1
1370408_at	Nid67	Putative small membrane protein NID67	179	1.965	1.763	1.576	*#†	U4
1374857_at	Nola1	Nucleolar protein family A, member 1 (H/ACA small nucleolar RNPs)	294	1.323	1.500	1.293	#	U6
1376362_at	Nptxr	Neuronal pentraxin receptor	69	1.375	1.632	1.491	*#†	U0
1368376_at	Nr0b2	Nuclear receptor subfamily 0, group B, member 2	77	0.622	0.622	0.801	*#	D2
1386935_at	Nr4a1	Nuclear receptor subfamily 4, group A, member 1	156	4.283	3.152	1.345	*#†	U1
1369007_at	Nr4a2	Nuclear receptor subfamily 4, group A, member 2	58	1.871	1.278	1.189	*	U3
1369067_at	Nr4a3	Nuclear receptor subfamily 4, group A, member 3	25	34.779	7.564	1.587	*#	U1
1393389_at	Nr4a3	Nuclear receptor subfamily 4, group A, member 3	92	5.767	2.277	1.184	*#	U3
1379982_at	Nrip1	Nuclear receptor interacting protein 1	64	1.598	0.968	0.928	*	U3
1369200_at	Nt5e	5' nucleotidase, ecto	357	1.433	1.859	1.825	*#†	U0
1384112_at	Nt5e	5' nucleotidase, ecto	194	1.264	1.659	1.678	#†	U0
1387267_at	Ntf3	Neurotrophin 3	94	0.826	0.744	0.609	#†	D1
1376128_at	Ntn1	Netrin 1	313	1.178	1.005	0.540	†	D0
1383614_at	Nuak2	NUAK family, SNF1-like kinase, 2	112	1.593	1.186	0.839	*	U1
1382134_at	Olfml1	Olfactomedin-like 1	401	1.083	0.739	0.665	#†	D1
1368683_at	Olr1	Oxidized low density lipoprotein (lectin-like) receptor 1	176	3.524	3.142	1.425	*#	U1
1384254_at	Otud1	OTU domain containing 1	385	3.067	3.230	1.539	*#	U2
1376924_a_at	Palmd	Palmdelphin	62	1.324	1.862	1.277	#	U6
1394966_at	Pap2d	Phosphatidic acid phosphatase type 2	76	0.933	0.839	1.662	†	U5
1375625_at	Paqr8	Progestin and adipoQ receptor family member VIII	148	0.862	0.628	0.893	#	D3
1383224_at	Pard6b	Par-6 (partitioning defective 6) homolog beta (C. elegans)	118	3.352	1.593	1.101	*	U3
1390227_at	Pcp4l1	Purkinje cell protein 4-like 1	199	0.886	0.945	0.620	†	D0

1368438_at	Pde10a	Phosphodiesterase 10A	187	2.557	2.428	1.240	*#	U2
1370669_a_at	Pde10a	Phosphodiesterase 10A	81	2.975	2.344	1.195	*#	U1
1369044_a_at	Pde4b	Phosphodiesterase 4B, cAMP specific	256	1.349	1.618	1.326	*#†	U6
1374157_at	Pde4b	Phosphodiesterase 4B, cAMP specific	448	1.271	1.660	1.460	*#†	U0
1367892_at	Pdk2	Pyruvate dehydrogenase kinase, isozyme 2	780	0.946	0.738	0.653	#†	D1
1390942_at	Peli2	Pellino 2	142	1.701	0.867	0.889	*	U3
1371684_at	Pelo	Pelota homolog (Drosophila)	777	1.624	1.675	1.078	*#	U2
1367949_at	Penk1	Proenkephalin 1	3855	1.597	1.651	1.090	*#	U2
1386961_at	Pfkm	Phosphofructokinase, muscle	600	0.926	0.680	0.665	#†	D1
1367951_at	Pgam2	Phosphoglycerate mutase 2 (muscle)	273	1.080	1.063	0.612	†	D0
1375223_at	Phactr1	Phosphatase and actin regulator 1	138	0.878	0.619	0.534	#†	D1
1368860_at	Phlda1	Pleckstrin homology-like domain, family A, member 1	185	2.886	1.764	1.529	*#†	U3
1388525_at	Pik3ip1	Phosphoinositide-3-kinase interacting protein 1	369	0.350	0.433	0.670	*#†	D2
1372199_at	Pink1	PTEN induced putative kinase 1	338	1.025	0.951	0.544	†	D0
1372475_at	Pink1	PTEN induced putative kinase 1	1465	1.078	0.966	0.607	†	D0
1387566_at	Pla2g4a	Phospholipase A2, group IVA (cytosolic, calcium-dependent)	122	1.330	1.500	1.281	*#†	U6
1387122_at	Plagl1	Pleiomorphic adenoma gene-like 1	285	1.776	1.795	0.939	*#	U2
1387269_s_at	Plaur	Plasminogen activator, urokinase receptor	109	2.033	1.622	1.345	*#	U4
1372897_at	Plod2	Procollagen lysine, 2-oxoglutarate 5-dioxygenase 2	1549	1.103	1.202	1.538	#†	U5
1369029_at	Plscr1	Phospholipid scramblase 1	118	2.602	2.441	1.750	*#†	U4
1391435_at	Pltp	Phospholipid transfer protein	768	1.083	0.942	0.577	†	D0
1389809_at	Pmepa1	Prostate transmembrane protein, androgen induced 1	889	1.227	1.449	1.528	#†	U0
1392534_at	Pmepa1	Prostate transmembrane protein, androgen induced 1	940	1.181	1.573	1.581	#†	U0
1387142_at	Polb	Polymerase (DNA directed), beta	140	1.301	1.552	0.917	*#	U2
1370950_at	Ppap2b	Phosphatidic acid phosphatase type 2B	370	1.666	1.273	0.757	---	U1
1372531_at	Ppfibp2	PTPRF interacting protein, binding protein 2 (liprin beta 2)	102	0.705	0.681	0.590	*#†	D1
1373108_at	Ppp1r3c	Protein phosphatase 1, regulatory (inhibitor) subunit 3C	470	1.752	1.642	1.082	*#	U1
1395236_at	Ppp1r3c	Protein phosphatase 1, regulatory (inhibitor) subunit 3C	83	1.657	1.350	1.134	*	U1
1387803_at	Ppp2r2b	Protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform	291	1.172	1.518	0.958	#	U2
1368277_at	Ppp3ca	Protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform	642	1.184	1.514	1.309	#	U6
1391121_at	Pragmin	Pragma of Rnd2	81	2.399	1.636	1.072	*#	U1
1373152_at	Prss23	Protease, serine, 23	1556	1.451	1.704	1.516	*#†	U0
1367851_at	Ptgds	Prostaglandin D2 synthase (brain)	197	1.097	0.999	0.562	†	D0
1368014_at	Ptges	Prostaglandin E synthase	81	2.037	1.391	0.898	*#	U1
1370012_at	Ptgis	Prostaglandin I2 (prostacyclin) synthase	1004	1.075	1.326	2.189	†	U5
1370193_at	Ptp4a1	Protein tyrosine phosphatase 4a1	1065	1.530	1.455	1.132	*#	U1
1382154_at	Ptpn12	Protein tyrosine phosphatase, non-receptor type 12	445	1.748	1.428	1.195	*#	U1
1370362_at	Ptprn	Protein tyrosine phosphatase, receptor type, N	540	1.479	1.614	1.212	*#†	U2
1370177_at	PVR	Poliovirus receptor	206	2.936	2.792	1.595	*#†	U4
1389873_at	Pycard	PYD and CARD domain containing	243	0.938	0.851	0.641	†	D1
1379606_at	Rab30	RAB30, member RAS oncogene family	298	1.659	1.315	1.021	*	U1
1370061_at	Rab3b	RAB3B, member RAS oncogene family	182	1.003	0.921	0.561	†	D0
1384528_at	Rai14	Retinoic acid induced 14	81	1.319	1.357	1.654	†	U0
1389263_at	Rai14	Retinoic acid induced 14	687	1.291	1.566	1.623	---	U0
1373666_at	Rapgef5	Rap guanine nucleotide exchange factor (GEF) 5	69	1.470	1.543	0.950	*#	U2
1383322_at	Rasl11b	RAS-like family 11 member B	527	1.759	2.268	1.663	#	U6
1373923_at	Rdh10	Retinol dehydrogenase 10 (all-trans)	88	1.554	1.539	0.939	*#	U2
1384391_at	Rdh10	Retinol dehydrogenase 10 (all-trans)	84	1.678	1.381	1.114	*	U1
1393351_at	Rdh10	Retinol dehydrogenase 10 (all-trans)	42	2.067	1.355	1.064	*	U3
1374448_at	Reck	Reversion-inducing-cysteine-rich protein with kazal motifs	490	1.420	1.879	1.240	#	U6
1368238_at	Reg3b	Regenerating islet-derived 3 beta	5202	0.946	0.954	0.478	†	D0

1373957_at	Reln	Reelin	149	1.245	1.541	1.174	#	U6
1376645_at	RGD1307396	Similar to RIKEN cDNA 6330406I15	248	2.794	2.682	1.496	*#†	U4
1395765_at	RGD1307396	Similar to RIKEN cDNA 6330406I15	75	1.822	1.582	1.172	*#	U1
1397848_at	RGD1307396	Similar to RIKEN cDNA 6330406I15	33	2.563	2.073	1.459	*#†	U4
1398485_at	RGD1307396	Similar to RIKEN cDNA 6330406I15	50	1.607	1.443	1.187	*#	U4
1383258_at	RGD1310587	Similar to hypothetical protein FLJ14146	41	1.248	1.536	0.911	#	U2
1367495_at	RGD1560211	Similar to prefoldin 4	499	1.351	1.537	1.348	#	U6
1383874_at	RGD1560812	RGD1560812	114	1.531	1.227	1.027	*#	U3
1390051_at	RGD1562533	Similar to mKIAA0774 protein	191	1.658	1.916	1.034	#	U2
1367998_at	RGD1563818 /// Slpi	Similar to secretory leukocyte protease inhibitor /// secretory leukocyte peptidase inhibitor	378	1.490	1.834	1.145	*#	U2
1384943_at	RGD1563888	Similar to DNA segment, Chr 16, ERATO Doi 472, expressed	61	1.552	1.359	1.086	*	U1
1390443_at	RGD1563888	Similar to DNA segment, Chr 16, ERATO Doi 472, expressed	128	1.575	1.502	1.056	*#	U1
1389639_at	RGD1565350	Similar to Shb protein	333	1.533	1.810	1.426	#	U6
1371731_at	RGD1566215	Similar to Coatomer gamma-2 subunit (Gamma-2 coat protein) (Gamma-2 COP)	1319	1.074	1.058	0.647	†	D0
1395145_at	Rgl1	Ral guanine nucleotide dissociation stimulator,-like 1	358	0.855	0.663	0.826	#	D3
1368144_at	Rgs2	Regulator of G-protein signaling 2	268	3.163	2.440	2.158	*#†	U4
1387074_at	Rgs2	Regulator of G-protein signaling 2	661	3.261	2.882	2.178	*#†	U4
1379517_at	Rgs6	Regulator of G protein signaling 6	152	1.093	0.926	0.623	†	D0
1381279_at	Ripk2	Receptor-interacting serine-threonine kinase 2	188	1.615	1.339	1.295	*	U4
1367544_at	Rnf111	Ring finger protein 111	131	1.642	1.690	1.201	*#†	U2
1373456_at	Rnf111	Ring finger protein 111	485	1.765	1.610	1.320	*#	U4
1393045_at	Rock2	Rho-associated coiled-coil containing protein kinase 2	384	1.577	1.581	1.292	*#	U4
1398732_at	Rpl7a	60S ribosomal protein L7a	128	0.978	1.032	1.823	†	U5
1367862_at	Rrad	Ras-related associated with diabetes	854	0.762	0.705	0.412	†	D1
1373427_at	Rragd	Ras-related GTP binding D	131	1.079	0.829	0.590	†	D1
1376065_at	Rrs1	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	143	1.262	1.595	1.362	#	U6
1371840_at	S1pr1	Sphingosine-1-phosphate receptor 1	945	1.784	1.875	1.097	*#	U2
1376150_at	S1pr3	Sphingosine-1-phosphate receptor 3	607	1.552	1.512	0.948	*#	U2
1371774_at	Sat1	Spermidine/spermine N1-acetyl transferase 1	1049	1.484	1.537	1.118	*#	U2
1387926_at	Sc5dl	Sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, S. cerevisiae)-like	430	1.100	1.067	1.558	†	U5
1370355_at	Scd1	Stearoyl-Coenzyme A desaturase 1	339	1.060	1.088	2.027	†	U5
1367721_at	Sdc4	Syndecan 4	1315	1.589	1.617	1.171	*#	U2
1376319_at	Sema3c	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	577	1.225	1.428	2.703	†	U5
1368519_at	Serpine1	Serine (or cysteine) peptidase inhibitor, clade E, member 1	131	1.931	1.629	2.155	*†	U0
1392264_s_at	Serpine1	Serine (or cysteine) peptidase inhibitor, clade E, member 1	70	1.590	1.553	1.700	---	U0
1391537_at	Sertad4	SERTA domain containing 4	324	0.636	1.003	1.282	*	D2
1395809_at	Sesn1	Sestrin 1	130	0.819	0.663	0.868	#	D3
1382878_at	Sfrp1	Secreted frizzled-related protein 1	233	1.263	1.758	1.681	---	U0
1383266_at	Sfrp1	Secreted frizzled-related protein 1	65	1.247	1.931	2.064	#†	U0
1389203_at	Sh3bp5l	SH3 binding domain protein 5 like	209	1.392	1.519	1.051	*#	U2
1368965_at	Slc16a3	Solute carrier family 16, member 3 (monocarboxylic acid transporter 4)	483	1.059	1.471	2.057	#†	U5
1370314_at	Slc20a1	Solute carrier family 20 (phosphate transporter), member 1	766	1.581	1.484	1.286	*#	U4
1372326_at	Slc2a3	Solute carrier family 2 (facilitated glucose transporter), member 3	66	2.009	1.716	1.499	*#†	U4
1387130_at	Slc40a1	Solute carrier family 39 (iron-regulated transporter), member 1	444	0.868	0.612	0.838	#	D3
1373953_at	Slc4a1ap	Solute carrier family 4 (anion exchanger), member 1, adaptor protein	639	0.994	0.974	0.504	†	D0
1368391_at	Slc7a1	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	419	1.439	1.626	1.455	*#†	U0
1377916_at	Slfn2	Schlafen 2	460	1.579	1.435	0.902	*#	U1
1387134_at	Slfn3	Schlafen 3	145	1.589	1.459	0.916	*#	U1

1384246_at	Smarca5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	121	1.324	1.579	1.366	#	U6
1392965_a_at	Smoc2	SPARC related modular calcium binding 2	267	0.962	1.187	0.459	†	D0
1373699_at	Sned1	Sushi, nidogen and EGF-like domains 1	452	1.240	1.217	0.506	†	D0
1380250_at	Sned1	Sushi, nidogen and EGF-like domains 1	440	1.151	1.150	0.570	†	D0
1368596_at	Snf1lk	SNF1-like kinase	277	3.464	2.944	1.720	*#†	U4
1368597_at	Snf1lk	SNF1-like kinase	83	2.313	1.710	1.295	*	U1
1390298_at	Snx18	Sorting nexin 18	728	1.610	1.292	1.150	*	U3
1374168_at	Sphkap	SPHK1 interactor, AKAP domain containing	507	0.996	0.761	0.532	#†	D1
1384243_at	Spsb4	splA/ryanodine receptor domain and SOCS box containing 4	109	1.462	2.712	1.443	#	U6
1372510_at	Srxn1	Sulfiredoxin 1 homolog (S. cerevisiae)	285	2.000	1.304	1.432	*#†	U3
1384331_at	Srxn1	Sulfiredoxin 1 homolog (S. cerevisiae)	197	1.963	1.203	1.528	*†	U3
1370714_a_at	St6gal1	ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	69	0.837	0.662	1.018	#	D2
1385397_at	Steap4	STEAP family member 4	238	1.051	0.678	0.448	†	D1
1390489_at	Syncrip	Synaptotagmin binding, cytoplasmic RNA interacting protein	226	1.537	1.488	1.217	*#	U4
1390107_at	Sytl2	synaptotagmin-like 2	99	1.445	1.587	0.990	*#	U2
1383401_at	Tes	Testis derived transcript	192	1.365	1.665	1.308	#	U6
1367859_at	Tgfb3	Transforming growth factor, beta 3	412	1.435	1.856	1.420	#	U6
1368900_at	Thbd	Thrombomodulin	67	2.672	2.613	0.991	*#	U2
1368901_at	Thbd	Thrombomodulin	55	3.942	4.009	0.848	*#	U2
1375951_at	Thbd	Thrombomodulin	52	4.546	5.304	1.050	*#	U2
1388497_at	Them2	Thioesterase superfamily member 2	425	1.009	0.923	0.648	†	D0
1367650_at	Tinagl1	Tubulointerstitial nephritis antigen-like 1	190	1.047	1.214	1.690	---	U5
1390832_at	Tmcc3	Transmembrane and coiled-coil domain family 3	222	0.558	0.817	1.189	*#	D2
1377772_at	Tmeff1	Transmembrane protein with EGF-like and two follistatin-like domains 1	170	1.271	2.081	1.518	#†	U6
1387850_at	Tmeff1	Transmembrane protein with EGF-like and two follistatin-like domains 1	78	1.511	1.958	1.654	*#†	U0
1373204_at	Tmem176a	Transmembrane protein 176A	885	1.063	0.966	0.632	†	D0
1394160_at	Tmem2	Transmembrane protein 2	187	1.669	1.452	1.135	*	U1
1383314_at	Tmem51	Transmembrane protein 51	396	0.737	1.096	1.583	---	U5
1389583_at	Tmem82	Transmembrane protein 82	117	0.914	0.677	0.607	†	D1
1372156_at	Tmem97	Transmembrane protein 97	748	1.204	1.303	1.527	*#†	U0
1370442_at	Tmsbl1	Thymosin beta-like protein 1	333	1.265	1.515	1.428	*#†	U0
1373401_at	Tnc	Tenascin C	262	1.657	1.536	1.341	*#†	U4
1371194_at	Tnfaip6	Tumor necrosis factor alpha induced protein 6	246	2.540	1.576	1.264	*	U3
1388145_at	Tnxa /// Tnxb	Tenascin XA /// tenascin XB	251	1.058	0.996	0.654	†	D0
1370198_at	Trdn	Triadin	118	1.200	1.127	0.594	†	D0
1373578_at	Trim2	Tripartite motif-containing 2	235	0.792	0.627	0.747	#	D3
1384238_at	Ttyh2	Tweety homolog 2 (Drosophila)	328	1.935	1.534	1.042	*#	U1
1371618_s_at	Tubb3	Tubulin, beta 3	181	1.100	0.845	1.534	#†	U5
1372403_at	Uaca	Uveal autoantigen with coiled-coil domains and ankyrin repeats	322	1.337	1.586	1.194	#	U6
1379910_at	Uap1	UDP-N-acteylglucosamine pyrophosphorylase 1	226	6.023	6.867	1.764	*#†	U2
1383945_at	Uck2	Uridine-cytidine kinase 2	272	1.468	1.645	1.394	*#†	U6
1367938_at	Ugdh	UDP-glucose dehydrogenase	1318	1.754	1.850	1.253	*#†	U2
1369235_at	Unc5b	Unc-5 homolog B (C. elegans)	530	0.983	1.219	1.618	†	U5
1393799_at	Unc5b	Unc-5 homolog B (C. elegans)	784	0.910	1.168	1.519	†	U5
1371595_at	Unknown	Unknown	1154	1.596	1.429	1.133	*#	U1
1371699_at	Unknown	Unknown	532	1.622	2.336	1.457	*#†	U6
1371861_at	Unknown	Unknown	344	1.321	2.028	1.596	*#†	U6
1372011_at	Unknown	Unknown	650	1.716	2.021	1.109	*#	U2
1372095_at	Unknown	Unknown	170	0.814	0.717	0.646	†	D1
1372347_at	Unknown	Unknown	456	1.451	1.695	1.688	*#†	U0
1372371_at	Unknown	Unknown	296	1.363	1.516	1.146	*#	U2

1372583_at	Unknown	Unknown	78	0.871	1.001	1.652	†	U5
1372642_at	Unknown	Unknown	274	1.489	1.513	1.257	*#†	U4
1372750_at	Unknown	Unknown	127	1.478	1.528	1.757	*#†	U0
1372964_at	Unknown	Unknown	426	1.500	1.237	1.048	*	U1
1373035_at	Unknown	Unknown	473	1.708	1.617	1.307	*#	U4
1373298_at	Unknown	Unknown	56	1.490	1.733	1.293	*#†	U6
1373628_at	Unknown	Unknown	110	1.019	1.018	2.027	†	U5
1373676_at	Unknown	Unknown	236	1.506	1.586	1.330	*#†	U4
1373701_at	Unknown	Unknown	542	0.909	1.162	1.550	†	U5
1373843_at	Unknown	Unknown	961	1.440	1.573	1.201	*#†	U2
1374529_at	Unknown	Unknown	2561	1.935	1.608	1.458	*#†	U4
1374610_at	Unknown	Unknown	127	3.764	3.195	1.120	*#	U1
1374702_at	Unknown	Unknown	469	1.531	1.694	1.254	*#	U2
1374710_at	Unknown	Unknown	589	1.592	1.923	1.494	#	U6
1374758_at	Unknown	Unknown	174	1.235	1.508	1.326	---	U6
1374814_at	Unknown	Unknown	458	0.879	0.657	0.834	#	D3
1374893_at	Unknown	Unknown	346	1.253	1.956	1.259	#	U6
1374916_at	Unknown	Unknown	119	1.365	1.621	1.260	#	U6
1374934_at	Unknown	Unknown	221	1.027	0.870	0.641	†	D0
1375904_at	Unknown	Unknown	160	1.406	1.515	1.214	*#†	U4
1376021_at	Unknown	Unknown	646	1.491	1.580	1.147	*#	U2
1376076_at	Unknown	Unknown	276	1.504	1.476	1.253	*#	U4
1376275_at	Unknown	Unknown	189	1.669	1.327	1.095	*	U1
1376282_at	Unknown	Unknown	359	1.275	1.682	1.215	#	U6
1376395_at	Unknown	Unknown	53	1.572	1.132	0.986	*	U3
1376435_at	Unknown	Unknown	48	1.377	1.743	1.002	#	U2
1376513_a_at	Unknown	Unknown	247	1.108	1.311	1.508	†	U5
1376627_at	Unknown	Unknown	214	1.581	1.394	1.303	---	U4
1376848_at	Unknown	Unknown	254	1.627	1.433	1.152	*	U1
1376869_at	Unknown	Unknown	196	1.508	1.277	1.069	*#	U1
1377240_at	Unknown	Unknown	83	1.347	2.017	1.792	*#†	U0
1377328_at	Unknown	Unknown	100	0.727	0.633	0.863	#	D2
1377469_at	Unknown	Unknown	55	1.222	1.531	1.163	#	U6
1377636_at	Unknown	Unknown	156	1.249	1.645	1.245	*#†	U6
1377705_at	Unknown	Unknown	1294	1.134	1.125	1.878	†	U5
1377706_x_at	Unknown	Unknown	1131	1.211	1.174	2.035	†	U5
1377789_at	Unknown	Unknown	46	2.354	2.184	1.355	*#	U4
1377994_at	Unknown	Unknown	42	1.112	1.251	1.852	†	U5
1378074_at	Unknown	Unknown	70	0.875	0.558	0.801	*#†	D3
1378413_at	Unknown	Unknown	455	1.030	0.806	0.647	†	D1
1378414_at	Unknown	Unknown	254	1.016	1.590	1.245	#	U6
1378467_at	Unknown	Unknown	57	1.688	1.293	1.379	*	U4
1378556_at	Unknown	Unknown	313	1.183	1.229	1.892	*#†	U5
1379332_at	Unknown	Unknown	78	1.511	1.514	1.190	*#	U4
1379534_at	Unknown	Unknown	129	0.765	0.511	0.589	#†	D3
1379598_at	Unknown	Unknown	176	1.441	2.161	1.776	#†	U0
1379607_at	Unknown	Unknown	64	3.034	2.578	1.141	*#	U1
1379733_at	Unknown	Unknown	78	0.738	0.641	1.018	*#	D2
1379799_at	Unknown	Unknown	121	0.818	1.376	1.634	†	U5
1380306_at	Unknown	Unknown	34	1.724	1.144	0.921	*	U3
1380318_at	Unknown	Unknown	312	0.812	0.512	0.950	#	D3
1380494_at	Unknown	Unknown	272	0.973	1.012	0.524	†	D0

1380831_at	Unknown	Unknown	58	1.503	1.852	1.200	#	U2
1381016_at	Unknown	Unknown	149	1.603	1.236	1.111	*	U3
1381163_at	Unknown	Unknown	110	1.238	1.531	1.328	#	U6
1381431_at	Unknown	Unknown	42	1.554	1.364	1.077	*	U1
1382296_at	Unknown	Unknown	138	0.736	0.601	1.047	#	D2
1382512_at	Unknown	Unknown	183	1.514	1.585	1.218	*#†	U4
1382647_at	Unknown	Unknown	57	1.685	1.908	1.127	*#	U2
1382651_at	Unknown	Unknown	59	1.328	1.974	1.058	*#	U2
1382882_x_at	Unknown	Unknown	32	2.636	1.787	1.298	*#	U1
1382914_at	Unknown	Unknown	151	1.222	1.421	1.888	†	U5
1383058_at	Unknown	Unknown	494	0.560	0.582	0.998	*#	D2
1383169_at	Unknown	Unknown	610	0.818	0.676	0.587	#†	D1
1383210_at	Unknown	Unknown	67	1.809	1.192	1.197	*	U3
1383222_at	Unknown	Unknown	331	1.642	1.419	1.086	*#	U1
1383486_at	Unknown	Unknown	108	2.681	3.353	2.880	*#†	U0
1383744_at	Unknown	Unknown	644	1.354	1.526	1.159	#	U2
1383852_at	Unknown	Unknown	87	1.385	1.948	1.498	#	U6
1383939_at	Unknown	Unknown	462	1.437	1.651	1.420	*#†	U6
1384051_at	Unknown	Unknown	132	0.952	1.217	1.747	#†	U5
1384188_at	Unknown	Unknown	134	0.872	0.752	0.644	#†	D1
1384882_at	Unknown	Unknown	88	1.575	1.547	1.391	*#†	U4
1384899_at	Unknown	Unknown	68	1.607	1.233	1.093	*	U3
1385053_at	Unknown	Unknown	88	1.049	0.742	0.606	#†	D1
1385082_at	Unknown	Unknown	111	1.051	0.718	0.573	†	D1
1385132_at	Unknown	Unknown	44	1.760	3.153	2.689	*#†	U0
1385869_at	Unknown	Unknown	143	1.500	1.397	1.130	*#	U1
1385925_at	Unknown	Unknown	460	1.133	1.233	1.548	†	U5
1385948_at	Unknown	Unknown	188	1.407	1.609	0.884	*#	U2
1388872_at	Unknown	Unknown	808	1.159	1.113	1.535	†	U5
1389127_at	Unknown	Unknown	329	1.703	1.411	1.044	*#	U1
1389194_at	Unknown	Unknown	629	1.578	1.955	1.380	*#†	U6
1389206_at	Unknown	Unknown	51	2.050	1.178	1.075	*	U3
1389412_at	Unknown	Unknown	300	1.872	1.481	0.963	*#	U1
1389465_at	Unknown	Unknown	332	1.335	1.586	1.105	#	U2
1389565_at	Unknown	Unknown	129	1.653	1.320	1.026	*#	U1
1389586_at	Unknown	Unknown	312	1.686	1.915	1.251	*#†	U2
1389618_at	Unknown	Unknown	290	0.492	0.541	0.636	*#†	D2
1389700_at	Unknown	Unknown	87	1.867	1.523	1.245	*#†	U1
1390117_at	Unknown	Unknown	454	1.529	1.266	0.874	*#	U1
1390515_at	Unknown	Unknown	210	1.163	1.509	1.186	#	U6
1390645_at	Unknown	Unknown	57	1.409	1.673	1.015	#	U2
1390659_at	Unknown	Unknown	293	2.273	2.577	1.679	*#†	U4
1391481_at	Unknown	Unknown	117	1.219	1.549	1.524	#†	U0
1391582_at	Unknown	Unknown	116	1.530	1.364	1.025	*#	U1
1391758_at	Unknown	Unknown	363	0.949	0.649	0.745	---	D3
1392627_x_at	Unknown	Unknown	348	0.943	0.960	1.525	†	U5
1393003_at	Unknown	Unknown	261	1.455	1.507	1.371	*#†	U4
1393119_at	Unknown	Unknown	256	1.767	1.625	1.737	*#†	U0
1393262_at	Unknown	Unknown	141	0.625	0.867	0.852	*	D2
1393478_at	Unknown	Unknown	294	1.933	1.369	1.185	*	U3
1393728_at	Unknown	Unknown	76	1.277	1.659	1.543	---	U0
1393743_at	Unknown	Unknown	120	0.674	0.609	0.818	---	D2

1394047_at	Unknown	Unknown	43	1.554	1.499	1.068	*#	U1
1394109_at	Unknown	Unknown	738	2.788	2.079	1.795	*#†	U4
1395119_at	Unknown	Unknown	95	2.173	3.227	1.274	*#	U2
1395362_at	Unknown	Unknown	372	1.181	1.330	1.577	#†	U5
1395442_at	Unknown	Unknown	49	1.590	1.585	1.571	*#†	U0
1395518_at	Unknown	Unknown	242	0.628	0.560	0.716	*#†	D2
1395557_at	Unknown	Unknown	157	1.618	1.315	1.472	*†	U4
1395645_at	Unknown	Unknown	198	1.493	1.653	1.179	*#	U2
1396539_at	Unknown	Unknown	88	1.782	1.340	1.152	*	U3
1397164_at	Unknown	Unknown	308	1.860	1.500	1.198	*	U1
1397540_at	Unknown	Unknown	309	0.877	0.721	0.649	#†	D1
1397750_at	Unknown	Unknown	155	1.235	1.502	1.168	#	U6
1397766_at	Unknown	Unknown	32	2.109	1.250	1.109	*	U3
1398348_at	Unknown	Unknown	511	1.071	1.130	1.967	†	U5
1398597_at	Unknown	Unknown	239	0.645	0.689	1.060	*#	D2
1373510_at	Vamp1	Vesicle-associated membrane protein 1	147	0.968	0.889	0.625	†	D0
1368474_at	Vcam1	Vascular cell adhesion molecule 1	933	1.089	0.789	0.624	#†	D1
1371232_a_at	Vcan	Versican	594	1.539	1.468	1.218	---	U4
1388054_a_at	Vcan	Versican	674	1.579	1.515	1.212	---	U4
1388142_at	Vcan	Versican	499	1.606	1.641	1.463	*#†	U4
1387873_at	Wfdc1	WAP four-disulfide core domain 1	177	1.034	1.101	1.899	†	U5
1369484_at	Wisp2	WNT1 inducible signaling pathway protein 2	569	0.871	0.899	1.505	*#†	U5
1372791_at	Wnk1	WNK lysine deficient protein kinase 1	953	1.251	1.662	1.208	*#†	U6
1387072_at	Wnk1	WNK lysine deficient protein kinase 1	460	1.399	1.684	1.245	*#†	U6
1377223_at	Wt1	Wilms tumor 1	111	1.557	1.203	1.328	*†	U3
1392670_at	Wwc2	WW and C2 domain containing 2	216	1.107	1.323	1.541	#†	U5
1389119_at	Xirp1	Xin actin-binding repeat containing 1	583	2.904	2.461	1.168	*#	U1
1375846_at	Xpr1	Xenotropic and polytropic retrovirus receptor 1	555	1.312	1.412	1.580	*#†	U0
1385883_at	Zbtb11	Zinc finger and BTB domain containing 11	123	1.363	1.608	1.256	*#	U6
1386106_at	Zcchc24	Zinc finger, CCHC domain containing 24	266	0.745	0.634	0.920	#	D2

Supplemental Table S5 Changes in transcript expression induced by ET-1 at 2, 4 and 24 h

RNA expression analysis was performed using Affymetrix rat expression 230 2.0 microarrays and GeneSpring 12.0. The raw data for controls are given and results at each time are the mean fold change relative to the controls (n=3). Statistical analysis was performed by one-way ANOVA with SNK post-test using a Benjamini and Hochberg false discovery rate correction (FDR<0.05) * 2 h vs control; # 4 h vs control; † 24 h vs control

Probeset ID	Gene Symbol	Gene Title	Raw data (control)	2 h	4 h	24 h	Statistical significance
1370561_at	A3galt2	Alpha 1,3-galactosyltransferase 2	182	1.325	1.807	1.456	*#†
1369027_at	A4galt	Alpha 1,4-galactosyltransferase	204	1.083	1.736	1.112	#
1383355_at	Abca1	ATP-binding cassette, sub-family A (ABC1), member 1	273	0.793	0.587	0.667	*#†
1394490_at	Abca1	ATP-binding cassette, sub-family A (ABC1), member 1	101	0.658	0.490	0.672	*#†
1390783_at	Abca8a	ATP-binding cassette, sub-family A (ABC1), member 8a	172	0.816	0.706	0.494	#†
1379402_at	Abcc4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	190	0.864	0.702	0.593	*#†
1398265_at	Abcc9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	466	0.921	0.803	0.535	#†
1368103_at	Abcg1	ATP-binding cassette, sub-family G (WHITE), member 1	342	0.648	0.706	1.177	*#
1390455_at	Abhd2	Abhydrolase domain containing 2	219	2.092	3.092	1.471	*#†
1398109_at	Abhd2	Abhydrolase domain containing 2	157	1.325	1.673	1.116	*#
1390881_at	Abra	Actin-binding Rho activating protein	200	2.669	1.253	0.879	*
1373302_at	Acer2	Alkaline ceramidase 2	122	0.577	0.723	0.952	*#
1391791_at	Acer2	Alkaline ceramidase 2	146	0.639	0.821	0.855	*
1388153_at	Acsl1	Acyl-CoA synthetase long-chain family member 1	1233	0.832	0.780	0.631	†
1397375_at	Acsl5	Acyl-CoA synthetase long-chain family member 5	236	1.122	1.337	1.533	#†
1370857_at	Acta2	Smooth muscle alpha-actin	4515	1.054	1.178	2.218	†
1386869_at	Actg2	Actin, gamma 2, smooth muscle, enteric	199	1.297	1.214	3.092	†
1389189_at	Actn1	Actinin, alpha 1	2246	1.629	2.128	1.845	*#†
1398294_at	Actn1	Actinin, alpha 1	1392	1.687	2.387	1.813	*#†
1369942_at	Actn4	Actinin, alpha 4	1947	1.105	1.331	1.748	#†
1390931_at	Adamts15	ADAM metallopeptidase with thrombospondin type 1 motif, 15	406	0.488	0.618	0.760	*#†
1393730_at	Adamts4	ADAM metallopeptidase with thrombospondin type 1 motif, 4	207	1.013	0.927	0.564	†
1394483_at	Adamts5	ADAM metallopeptidase with thrombospondin type 1 motif, 5	282	0.729	0.569	1.377	*#†
1379022_at	Adamts8	ADAM metallopeptidase with thrombospondin type 1 motif, 8	146	1.024	1.226	1.854	†
1391139_at	Adamtsl1	ADAMTS-like 1	99	1.090	1.685	0.933	#
1398370_at	Adarb1	Adenosine deaminase, RNA-specific, B1	149	0.955	1.002	1.556	†
1399096_at	Add3	Adducin 3 (gamma)	1571	0.746	0.613	0.794	*#†
1390383_at	Adfp	Adipose differentiation related protein	2681	1.564	1.637	0.866	*#
1390850_at	Adfp	Adipose differentiation related protein	92	1.782	1.195	1.604	---
1370584_a_at	Adora1	Adenosine A1 receptor	85	0.837	0.631	0.700	#†
1368300_at	Adora2a	Adenosine A2a receptor	104	0.776	0.861	0.495	†
1387395_at	Adora2b	Adenosine A2B receptor	381	0.596	0.564	0.584	*#†
1368574_at	Adra1b	Adrenergic, alpha-1B-, receptor	573	0.732	0.548	0.556	*#†
1369806_at	Adrb1	Adrenergic, beta-1-, receptor	142	0.612	0.685	0.890	*#
1383848_at	Adrb1	Adrenergic, beta-1-, receptor	349	0.455	0.575	0.918	*#
1382533_at	Agfg1	ArfGAP with FG repeats 1	677	1.156	1.618	1.269	#†
1384022_at	Agfg1	ArfGAP with FG repeats 1	758	1.247	1.629	1.351	*#†
1372736_at	Agl	Amylo-1,6-glucosidase, 4-alpha-glucanotransferase	759	0.790	0.632	0.785	*#
1395414_at	Agl	Amylo-1,6-glucosidase, 4-alpha-glucanotransferase	143	0.703	0.596	0.838	*#

1369291_at	Agtr1a	Angiotensin II receptor, type 1a	100	0.769	0.651	1.038	*#
1384240_at	Agtr1a	Angiotensin II receptor, type 1a	109	0.650	0.389	1.506	*#†
1369146_a_at	Ahr	Aryl hydrocarbon receptor	87	1.079	1.488	1.783	#†
1375845_at	Aig1	Androgen-induced 1	492	1.083	1.325	1.642	#†
1382206_a_at	Akap2	A kinase (PRKA) anchor protein 2	274	2.134	2.048	1.229	*#
1385566_at	Akap2	A kinase (PRKA) anchor protein 2	212	2.511	2.271	1.357	*#
1386764_at	Akap2	A kinase (PRKA) anchor protein 2	126	2.161	1.953	1.312	*#
1392079_at	Akap7	A kinase (PRKA) anchor protein 7	134	0.828	0.832	1.805	†
1385713_at	Akap8l	A kinase (PRKA) anchor protein 8-like	489	0.756	0.621	0.867	#
1396933_s_at	Akr1c14	Aldo-keto reductase family 1, member C14	106	0.821	0.528	0.533	*#†
1394681_at	Akr1cl1	Aldo-keto reductase family 1, member C-like 1	741	0.801	0.576	0.607	*#†
1370043_at	Alcam	Activated leukocyte cell adhesion molecule	508	1.214	1.512	1.186	#
1368003_at	Aldh1a2	Aldehyde dehydrogenase 1 family, member A2	213	1.045	1.097	1.786	†
1386998_at	Aldoc	Aldolase C, fructose-bisphosphate	1055	0.930	0.885	0.511	†
1389546_at	Amotl2	Angiomotin like 2	1044	1.468	1.547	1.647	*#†
1368342_at	Ampd3	Adenosine monophosphate deaminase 3	385	0.720	0.669	0.536	*#†
1374207_at	Angpt2	Angiopoietin 2	363	0.961	0.965	0.523	†
1388924_at	Angptl4	Angiopoietin-like 4	139	1.535	1.238	0.679	*†
1389398_at	Ank1	Ankyrin 1, erythrocytic	362	0.848	0.754	0.424	†
1372742_at	Ankmy2	Ankyrin repeat and MYND domain containing 2	658	0.716	0.639	0.950	*#
1371927_at	Ankrd23	Ankyrin repeat domain 23	56	1.131	1.851	1.289	#
1398432_at	Ankrd28	Ankyrin repeat domain 28	428	1.314	1.596	1.131	*#
1389264_at	Ankrd54	Ankyrin repeat domain 54	186	0.580	1.016	0.987	*
1377587_at	Ankrd60	Ankyrin repeat domain 60	75	0.989	0.962	1.560	†
1377949_s_at	Anks1a	Ankyrin repeat and sterile alpha motif domain containing 1A	261	0.584	0.643	0.894	*#
1397634_at	Anks1a	Ankyrin repeat and sterile alpha motif domain containing 1A	200	0.477	0.561	0.759	*#
1386938_at	Anpep	Alanyl (membrane) aminopeptidase	424	0.836	0.809	0.653	*#†
1367614_at	Anxa1	Annexin A1	2459	1.863	2.039	1.210	*#†
1394451_at	Anxa1	Annexin A1	186	1.432	1.513	1.064	*#
1367974_at	Anxa3	Annexin A3	132	2.278	3.561	1.024	*#
1387376_at	Aox1	Aldehyde oxidase 1	178	0.878	0.752	0.316	#†
1397579_x_at	Apc2	Adenomatosis polyposis coli 2	367	0.404	0.436	0.732	*#†
1372390_at	Apeg3	Antisense paternally expressed gene 3	831	0.798	0.616	0.744	*#†
1389651_at	Apln	Apelin	513	0.908	0.882	0.496	†
1379772_at	Aplnr	Apelin receptor	131	0.828	1.015	0.588	*†
1370862_at	Apoe	Apolipoprotein E	3890	0.842	0.846	0.483	†
1387068_at	Arc	Activity-regulated cytoskeleton-associated protein	79	2.125	1.133	0.871	*
1369871_at	Areg	Amphiregulin	22	8.274	1.748	1.115	*#
1368946_at	Arf2	ADP-ribosylation factor 2	227	1.534	1.437	1.132	*#
1380383_at	Arf4l	ADP-ribosylation factor 4-like	143	1.584	1.164	0.911	*
1398361_at	Arhgap10	Rho GTPase activating protein 10	336	1.170	1.512	1.088	#
1391083_at	Arhgap22	Rho GTPase activating protein 22	59	1.353	2.007	1.371	#
1392590_at	Arhgap24	Rho GTPase activating protein 24	276	0.786	0.660	0.872	#
1373541_at	Arhgef17	Rho guanine nucleotide exchange factor (GEF) 17	329	1.097	1.614	1.077	#
1377750_at	Arhgef3	Rho guanine nucleotide exchange factor (GEF) 3	185	3.364	2.378	1.732	*#†
1379311_at	Arid5a	AT rich interactive domain 5A (Mrf1 like)	142	1.760	1.181	1.144	*
1397437_at	Arid5a	AT rich interactive domain 5A (Mrf1 like)	69	1.685	1.392	1.286	*#†
1382312_at	Arid5b	AT rich interactive domain 5B (Mrf1 like)	140	1.630	1.237	1.230	*
1370510_a_at	Arntl	Aryl hydrocarbon receptor nuclear translocator-like	179	1.490	1.808	1.079	*#
1369268_at	Atf3	Activating transcription factor 3	130	3.562	1.001	0.968	*
1377939_at	Atg4c	ATG4 autophagy related 4 homolog C (S. cerevisiae)	108	0.640	0.617	0.830	*#
1373287_at	Atoh8	Atonal homolog 8 (Drosophila)	298	0.442	0.801	0.706	*#†

1385361_at	Atp10a	ATPase, class V, type 10A	96	1.291	1.436	1.643	*#†
1369798_at	Atp1b2	ATPase, Na+/K+ transporting, beta 2 polypeptide	105	0.884	0.773	0.586	†
1379906_at	Atp1b2	ATPase, Na+/K+ transporting, beta 2 polypeptide	445	0.931	0.799	0.467	#†
1370050_at	Atp2b1	ATPase, Ca++ transporting, plasma membrane 1	478	1.918	1.856	1.145	*#†
1386426_at	Atp2b1	ATPase, Ca++ transporting, plasma membrane 1	561	1.795	1.810	1.229	*#
1394714_at	Atp2b1	ATPase, Ca++ transporting, plasma membrane 1	91	1.859	1.217	1.021	*
1397224_at	Atp2b1	ATPase, Ca++ transporting, plasma membrane 1	73	1.664	1.537	1.084	*#
1378134_at	Atp8b1	ATPase, Class I, type 8B, member 1	88	3.740	2.112	1.966	*#†
1391693_at	Atp8b1	ATPase, Class I, type 8B, member 1	79	2.915	1.969	1.439	*#†
1390294_at	Atxn7l4	Ataxin 7-like 4	206	0.967	1.084	1.539	†
1398347_at	Axl /// LOC687188	Axl receptor tyrosine kinase /// similar to AXL receptor tyrosine kinase	971	1.414	1.870	1.864	*#†
1389402_at	Axud1	AXIN1 up-regulated 1	180	4.427	2.063	1.357	*#†
1398373_at	B3galnt1	Beta-1,3-N-acetylgalactosaminyltransferase 1	381	1.843	1.740	0.975	*#
1371073_at	B4galt1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	607	1.295	1.546	1.056	*#
1389047_at	Bag2	Bcl2-associated athanogene 2	625	1.374	1.651	1.579	*#†
1370074_at	Baiap2	BAI1-associated protein 2	125	1.314	1.560	0.948	*#
1373081_at	Baiap2	BAI1-associated protein 2	172	1.474	1.716	1.081	*#
1370823_at	Bambi	BMP and activin membrane-bound inhibitor, homolog (Xenopus laevis)	581	0.401	0.888	1.037	*
1374113_at	Baz1a	Bromodomain adjacent to zinc finger domain, 1A	180	1.621	1.129	1.203	*
1377727_at	Baz1a	Bromodomain adjacent to zinc finger domain, 1A	89	1.549	1.089	1.005	*
1367752_at	Bcar1	Breast cancer anti-estrogen resistance 1	549	1.476	1.572	1.132	*#†
1369520_a_at	Bcat1	Branched chain aminotransferase 1, cytosolic	505	1.144	1.665	1.561	#†
1370869_at	Bcat1	Branched chain aminotransferase 1, cytosolic	1162	1.229	1.553	1.572	#†
1370897_at	Bckdha	Branched chain ketoacid dehydrogenase E1, alpha polypeptide	220	0.941	0.919	0.574	†
1368118_at	Bcl10	B-cell CLL/lymphoma 10	620	1.586	1.427	1.117	*#†
1385627_at	Bcl3	B-cell CLL/lymphoma 3	347	0.976	0.890	0.659	†
1398482_at	Bcl3	B-cell CLL/lymphoma 3	257	0.841	0.714	0.600	*#†
1384335_at	Bcl9l	B-cell CLL/lymphoma 9-like	678	0.536	0.715	1.015	*#
1373494_at	Bcr	Breakpoint cluster region	531	2.425	2.493	1.075	*#
1370649_at	Bdkrb2 /// RGD1308470	Bradykinin receptor B2 /// similar to RIKEN cDNA 4933433P14 gene	99	1.700	1.705	1.093	*#
1370650_s_at	Bdkrb2 /// RGD1308470	Bradykinin receptor B2 /// similar to RIKEN cDNA 4933433P14 gene	82	2.740	3.217	1.156	*#
1371120_s_at	Bdkrb2 /// RGD1308470	Bradykinin receptor B2 /// similar to RIKEN cDNA 4933433P14 gene	58	1.582	1.888	1.170	*#
1368677_at	Bdnf	Brain derived neurotrophic factor	63	2.148	1.788	1.485	*#†
1377814_at	Bean	Brain expressed, associated with Nedd4	166	1.426	2.052	1.256	*#†
1370113_at	Birc3	Baculoviral IAP repeat-containing 3	149	0.938	1.016	0.643	†
1368945_at	Bmp2	Bone morphogenetic protein 2	47	2.520	2.043	1.155	*#
1398270_at	Bmp2	Bone morphogenetic protein 2	154	2.841	2.555	1.349	*#
1379659_at	Bmp2k	BMP-2 inducible kinase	66	1.727	1.664	1.238	*#†
1387232_at	Bmp4	Bone morphogenetic protein 4	181	0.902	1.203	2.092	†
1388920_at	Bmp6	Bone morphogenetic protein 6	369	0.937	0.862	1.539	†
1389403_at	Bmp7	Bone morphogenetic protein 7	285	1.146	1.644	1.177	#
1386994_at	Btg2	B-cell translocation gene 2, anti-proliferative	442	2.400	1.522	1.161	*#
1386995_at	Btg2	B-cell translocation gene 2, anti-proliferative	372	3.390	2.177	1.117	*#
1382185_at	C1qtnf2	C1q and tumor necrosis factor related protein 2	153	0.584	0.610	1.381	*#†
1393632_at	C1qtnf7	C1q and tumor necrosis factor related protein 7	182	0.652	0.605	1.046	#
1393632_at	C1qtnf7	C1q and tumor necrosis factor related protein 7	182	0.652	0.605	1.046	*#
1368000_at	C3	Complement component 3	331	0.981	1.021	0.352	†
1370892_at	C4-2 /// C4b	Complement component 4, gene 2 /// complement component 4B (Childo blood group)	698	0.948	0.872	0.326	†

1384580_at	C6	Complement component 6	101	0.986	0.912	0.476	†
1383291_at	C7 /// Tubb2c	Complement component 7 /// tubulin, beta 2c	3051	0.893	0.874	0.496	†
1388557_at	C7 /// Tubb2c	Complement component 7 /// tubulin, beta 2c	3204	0.877	0.818	0.539	†
1372536_at	Cabc1	Chaperone, ABC1 activity of bc1 complex homolog (S. pombe)	407	0.764	0.540	0.680	*#†
1376657_at	Cadm1	Cell adhesion molecule 1	69	0.944	1.003	1.940	†
1384132_at	Cadm1	Cell adhesion molecule 1	108	0.932	1.081	1.986	†
1368824_at	Cald1	Caldesmon 1	450	1.360	1.557	1.958	#†
1368131_at	Capn6	Calpain 6	342	0.865	0.902	0.561	†
1367733_at	Car2	Carbonic anhydrase II	139	0.938	0.837	0.631	†
1386922_at	Car2	Carbonic anhydrase II	133	0.943	0.946	0.642	†
1387605_at	Casp12	Caspase 12	229	1.068	0.961	1.503	†
1388604_at	Casq1	Calsequestrin 1 (fast-twitch, skeletal muscle)	859	0.968	0.941	1.833	†
1370131_at	Cav1	Caveolin 1, caveolae protein	638	2.093	2.865	1.521	*#†
1372111_at	Cav1	Caveolin 1, caveolae protein	1511	1.798	2.063	1.415	*#†
1393281_at	Cav1	Caveolin 1, caveolae protein	1273	1.899	2.317	1.504	*#†
1370135_at	Cav2	Caveolin 2	60	1.341	1.572	1.041	*#
1377642_at	Cav2	Caveolin 2	100	1.656	1.618	1.192	*#
1390101_at	Ccdc107	Coiled-coil domain containing 107	650	1.001	1.046	1.740	†
1385426_at	Ccdc109b	Coiled-coil domain containing 109B	147	1.381	1.555	1.846	*#†
1367973_at	Ccl2	Chemokine (C-C motif) ligand 2	3430	1.137	1.285	0.598	*#†
1369814_at	Ccl20	Chemokine (C-C motif) ligand 20	101	1.365	1.567	1.075	*#
1379935_at	Ccl7	Chemokine (C-C motif) ligand 7	857	1.030	1.085	0.533	†
1371150_at	Ccnd1	Cyclin D1	392	1.067	1.576	1.224	#
1371953_at	Ccng2	Cyclin G2	418	0.486	0.534	0.751	*#†
1384268_at	Ccnyl1	Cyclin Y-like 1	292	1.751	1.989	1.329	*#†
1377869_at	Ccrn4l	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	211	5.397	2.452	1.155	*#
1387745_at	Cd200r1	CD200 receptor 1	197	0.515	0.853	1.282	*†
1374061_at	Cd302	CD302 molecule	641	0.843	0.682	0.570	†
1367689_a_at	Cd36	CD36 molecule (thrombospondin receptor)	1728	0.897	0.962	0.531	†
1386901_at	Cd36	CD36 molecule (thrombospondin receptor)	2663	0.970	0.938	0.560	†
1368975_at	Cd38	CD38 molecule	79	0.915	1.078	1.552	†
1376866_at	Cd3eap	CD3E antigen, epsilon polypeptide-associated protein	115	1.822	1.899	1.321	*#†
1368921_a_at	Cd44	Cd44 molecule	486	2.552	2.985	1.243	*#†
1387952_a_at	Cd44	Cd44 molecule	519	2.609	3.184	1.470	*#†
1370406_a_at	Cd55	Cd55 molecule	48	1.733	1.791	1.354	*#†
1387951_at	Cd55	Cd55 molecule	45	1.518	2.031	1.177	*#†
1375910_at	Cdc42ep3	CDC42 effector protein (Rho GTPase binding) 3	1360	1.665	1.629	1.355	*#†
1388730_at	Cdc42ep4	CDC42 effector protein (Rho GTPase binding) 4	459	1.512	1.113	0.876	*#†
1388530_at	Cdc42se1	CDC42 small effector 1	505	1.506	1.613	0.955	*#
1389255_at	Cdh5	Cadherin 5	795	0.969	0.997	0.643	†
1373812_at	Cdkn1b	Cyclin-dependent kinase inhibitor 1B	1153	0.661	0.702	0.989	*#
1372299_at	Cdkn1c	Cyclin-dependent kinase inhibitor 1C (P57)	324	0.975	0.939	0.637	†
1369193_at	Cdkn2b	Cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	154	1.142	1.715	1.155	#
1372685_at	Cdkn3	Cyclin-dependent kinase inhibitor 3	364	1.011	0.957	1.536	†
1374139_at	Cdr2	Cerebellar degeneration-related 2	312	1.920	1.775	1.400	*#†
1368480_at	Cdw92	CDW92 antigen	600	0.950	0.912	0.612	†
1373054_at	Cdw92	CDW92 antigen	1334	1.052	1.017	0.596	†
1375950_a_at	Cep164	Centrosomal protein 164kDa	210	0.774	0.643	0.995	*#
1377829_at	Cep57	Centrosomal protein 57kDa	139	0.532	0.634	1.186	*#
1389470_at	Cfb	Complement factor B	102	0.920	0.955	0.613	†
1392171_at	Chi3l1	Chitinase 3-like 1	422	0.875	0.747	0.328	†
1386615_at	Chst2	Carbohydrate sulfotransferase 2	175	1.129	1.551	1.484	#†

1389179_at	Cidea	Cell death-inducing DNA fragmentation factor, alpha subunit-like effector A	1765	0.886	0.862	0.632	†
1367601_at	Cited2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	560	2.895	2.357	1.852	*#†
1367602_at	Cited2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	816	2.562	2.123	1.781	*#†
1370225_at	Cited4	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4	545	0.489	0.515	0.759	*#†
1395342_at	Ckap4	Cytoskeleton-associated protein 4	325	1.013	1.337	1.514	#†
1367626_at	Ckm	Creatine kinase, muscle	2579	0.916	0.909	0.500	†
1373823_at	Cks2	CDC28 protein kinase regulatory subunit 2	403	0.905	0.914	1.583	†
1374104_at	Cldn5	Claudin 5	161	0.910	0.910	0.489	†
1389368_at	Cnksr3	Cnksr family member 3	446	1.698	1.353	1.300	*#†
1367785_at	Cnn1	Calponin 1, basic, smooth muscle	423	1.263	1.218	2.083	†
1393619_at	Cnot6l	CCR4-NOT transcription complex, subunit 6-like	108	1.674	1.255	1.338	*
1387897_at	Cnp	2',3'-cyclic nucleotide 3' phosphodiesterase	551	0.771	0.655	1.155	*#†
1370185_at	Cntnap1	Contactin associated protein 1	189	0.884	0.798	0.626	†
1377254_a_at	Cohh1	Cohen syndrome homolog 1	88	0.917	0.630	1.092	#
1392915_at	Col11a1	Collagen, type XI, alpha 1	75	1.037	0.897	1.771	†
1370927_at	Col12a1	Collagen, type XII, alpha 1	379	1.268	1.304	3.138	†
1395580_at	Col12a1	Collagen, type XII, alpha 1	116	1.156	1.356	2.308	†
1398321_a_at	Col12a1	Collagen, type XII, alpha 1	179	1.262	1.352	2.868	†
1368347_at	Col5a3	Collagen, type V, alpha 3	557	1.157	1.501	1.064	*#
1393891_at	Col8a1	Collagen, type VIII, alpha 1	277	1.232	1.225	3.162	†
1373866_at	Coq10b	Coenzyme Q10 homolog B (S. cerevisiae)	466	1.772	1.537	1.439	*#†
1396250_at	Coro1c	Coronin, actin binding protein 1C	116	1.107	1.061	1.772	†
1372223_at	Cpeb4	Cytoplasmic polyadenylation element binding protein 4	681	1.535	1.306	1.246	*
1393294_at	Cpeb4	Cytoplasmic polyadenylation element binding protein 4	359	1.544	1.414	0.966	*#
1374474_at	Cpne8	Copine VIII	809	0.769	0.634	0.770	*#†
1386946_at	Cpt1a	Carnitine palmitoyltransferase 1a, liver	587	0.718	0.600	0.866	*#
1367742_at	Cpt1b	Carnitine palmitoyltransferase 1b, muscle	1369	0.919	0.867	0.539	†
1390420_at	Cpxm1	Carboxypeptidase X (M14 family), member 1	845	0.828	0.826	0.288	†
1375428_at	Creg1	Cellular repressor of E1A-stimulated genes 1	143	0.830	0.790	0.638	*#†
1382037_at	Crim1	Cysteine rich transmembrane BMP regulator 1 (chordin like)	201	1.502	1.561	1.782	*#†
1391448_at	Crim1	Cysteine rich transmembrane BMP regulator 1 (chordin like)	399	1.593	1.632	1.509	*#†
1398622_at	Crim1	Cysteine rich transmembrane BMP regulator 1 (chordin like)	1113	1.381	1.379	1.706	*#†
1376799_a_at	Crlf1	Cytokine receptor-like factor 1	227	1.108	1.365	3.374	#†
1395512_at	Crlf1	Cytokine receptor-like factor 1	164	1.002	1.309	3.493	#†
1368426_at	Crot	Carnitine O-octanoyltransferase	334	0.729	0.567	0.957	*#
1368059_at	Crym	Crystallin, mu	278	1.010	1.100	1.526	†
1383590_at	Csgalnact1	Chondroitin sulfate N-acetylgalactosaminyltransferase 1	112	1.406	1.515	0.865	*#†
1373184_at	Csgalnact2	Chondroitin sulfate N-acetylgalactosaminyltransferase 2	360	1.169	1.188	1.540	*#†
1368685_at	Cspg4	Chondroitin sulfate proteoglycan 4	255	1.706	2.571	1.632	*#†
1368704_a_at	Cspg5	Chondroitin sulfate proteoglycan 5	110	0.875	0.976	0.652	†
1384162_at	Csrnp2	Cysteine-serine-rich nuclear protein 2	125	1.801	1.221	1.047	*
1398243_at	Csrp3	Cysteine and glycine-rich protein 3	6383	1.404	1.510	1.203	---
1367631_at	Ctgf	Connective tissue growth factor	4345	1.980	1.918	2.394	*#†
1367838_at	Cth	Cystathionase (cystathionine gamma-lyase)	67	1.066	0.873	2.209	†
1384063_at	Cthrc1	Collagen triple helix repeat containing 1	1802	1.005	1.181	1.593	†
1398354_at	Ctnnal1	Catenin (cadherin associated protein), alpha-like 1	138	1.585	1.755	0.825	*#†
1368280_at	Ctsc	Cathepsin C	1104	0.873	0.785	0.536	#†
1374778_at	Ctsc	Cathepsin C	925	0.916	0.771	0.598	#†
1379450_at	Cttnbp2nl	CTTNBP2 N-terminal like	499	1.561	1.385	1.158	*#†
1382873_at	Cttnbp2nl	CTTNBP2 N-terminal like	229	1.482	1.521	1.188	*#†
1387316_at	Cxcl1	Chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	1897	0.421	0.460	0.413	*#†
1379365_at	Cxcl11	Chemokine (C-X-C motif) ligand 11	519	0.885	0.884	0.422	†

1388583_at	Cxcl12	Chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	789	0.725	0.621	0.769	*#†
1387648_at	Cxcl6	Chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)	612	0.764	0.394	0.223	#†
1370097_a_at	Cxcr4	Chemokine (C-X-C motif) receptor 4	514	0.839	0.933	0.469	†
1373661_a_at	Cxcr4	Chemokine (C-X-C motif) receptor 4	523	0.861	0.950	0.548	†
1389244_x_at	Cxcr4	Chemokine (C-X-C motif) receptor 4	652	0.868	0.938	0.570	†
1367940_at	Cxcr7	Chemokine (C-X-C motif) receptor 7	399	0.591	0.813	0.943	*
1398383_at	Cyb561	Cytochrome b-561	265	0.988	0.859	0.647	†
1377738_a_at	Cyhr1	Cysteine and histidine rich 1	201	0.679	0.486	0.827	*#†
1379287_at	Cyld	Cylindromatosis (turban tumor syndrome)	171	1.316	1.659	1.134	*#
1392958_at	Cyld	Cylindromatosis (turban tumor syndrome)	173	1.457	1.626	1.179	*#†
1398710_at	Cyp2u1	Cytochrome P450, family 2, subfamily u, polypeptide 1	322	0.578	0.774	0.812	*#†
1368290_at	Cyr61	Cysteine-rich, angiogenic inducer, 61	67	2.985	2.332	3.113	*#†
1387513_at	Cyth3	Cytohesin 3	151	1.125	2.013	1.243	#
1388712_at	Cyth3	Cytohesin 3	602	1.142	1.797	1.389	#†
1368202_a_at	Dab2	Disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	1815	1.471	1.524	0.990	*#
1383205_at	Dact2	Dapper, antagonist of beta-catenin, homolog 2 (Xenopus laevis)	115	2.467	2.673	1.128	*#
1376788_at	Dapk1	Death associated protein kinase 1	876	0.464	0.437	0.383	*#†
1379911_at	Dapk1	Death associated protein kinase 1	384	0.556	0.501	0.446	*#†
1387874_at	Dbp	D site of albumin promoter (albumin D-box) binding protein	255	0.591	0.513	0.662	*#†
1387111_at	Ddah1	Dimethylarginine dimethylaminohydrolase 1	1535	1.075	1.312	1.859	#†
1369590_a_at	Ddit3	DNA-damage inducible transcript 3	752	0.666	0.721	1.081	*#
1368025_at	Ddit4	DNA-damage-inducible transcript 4	1147	0.315	0.498	0.871	*#
1367793_at	Ddt	D-dopachrome tautomerase	1676	0.894	0.829	0.630	†
1371615_at	Dgat2	Diacylglycerol O-acyltransferase homolog 2 (mouse)	343	1.002	0.792	0.653	#†
1373240_at	Dhrs3	Dehydrogenase/reductase (SDR family) member 3	306	0.650	0.629	1.144	*#†
1389079_at	Dhrs7c	Dehydrogenase/reductase (SDR family) member 7C	90	0.922	1.038	0.620	†
1390172_at	Dhtkd1	Dehydrogenase E1 and transketolase domain containing 1	157	0.837	0.635	0.771	#
1368944_at	Dlg1	Discs, large homolog 1 (Drosophila)	223	1.286	1.514	1.024	#
1388816_at	Dlg1	Discs, large homolog 1 (Drosophila)	614	1.215	1.508	1.071	#
1372144_at	Dnajb5	DnaJ (Hsp40) homolog, subfamily B, member 5	339	1.509	1.484	1.138	*#
1375762_at	Dnajb5	DnaJ (Hsp40) homolog, subfamily B, member 5	139	1.350	1.555	1.067	---
1377835_at	Dock8	Dedicator of cytokinesis 8	208	0.947	0.995	1.591	†
1388589_at	Dot1l	DOT1-like, histone H3 methyltransferase (S. cerevisiae)	289	3.343	2.614	1.040	*#
1395910_at	Dot1l	DOT1-like, histone H3 methyltransferase (S. cerevisiae)	40	1.490	1.688	1.066	*#
1371732_at	Dpt	Dermatopontin	2034	0.916	0.871	0.592	†
1373947_at	Dpt	Dermatopontin	1833	0.838	0.956	0.611	†
1380964_at	Dtna	Dystrobrevin alpha	90	0.934	0.830	1.566	#†
1376612_at	Dtwd1	DTW domain containing 1	135	0.524	0.822	1.085	*#
1374718_at	Dtx3l	Deltex 3-like (Drosophila)	135	0.703	0.588	0.786	#
1368146_at	Dusp1	Dual specificity phosphatase 1	648	1.891	1.791	1.507	*#†
1368147_at	Dusp1	Dual specificity phosphatase 1	93	2.135	2.087	1.308	*#
1394028_at	Dusp10	Dual specificity phosphatase 10	76	2.662	1.908	1.003	*#
1373324_at	Dusp14	Dual specificity phosphatase 14	203	2.036	2.033	1.523	*#†
1377023_at	Dusp2	Dual specificity phosphatase 2	181	2.980	1.680	0.976	*#
1368124_at	Dusp5	Dual specificity phosphatase 5	343	2.737	1.032	1.100	*
1377064_at	Dusp6	Dual specificity phosphatase 6	442	1.927	2.154	1.687	*#†
1382778_at	Dusp6	Dual specificity phosphatase 6	277	1.894	2.098	1.362	*
1387024_at	Dusp6	Dual specificity phosphatase 6	744	1.902	2.164	1.343	*#†
1389712_at	Ebf3	Early B-cell factor 3	207	0.523	0.912	1.068	*
1383747_at	Ect2	Epithelial cell transforming sequence 2 oncogene	120	1.020	0.795	1.536	†
1369511_at	Ednra	Endothelin receptor type A	418	0.630	0.595	0.632	*#†
1378342_at	Ednra	Endothelin receptor type A	401	0.588	0.467	0.617	*#†

1383641_at	Ednra	Endothelin receptor type A	586	0.497	0.441	0.604	*#†
1393415_at	Ednra	Endothelin receptor type A	720	0.585	0.519	0.705	*#†
1387146_a_at	Ednrb	Endothelin receptor type B	103	1.282	1.255	1.701	†
1390112_at	Efemp1	EGF-containing fibulin-like extracellular matrix protein 1	285	0.898	0.874	0.192	†
1374388_at	Efhd2	EF-hand domain family, member D2	715	1.622	2.271	1.201	*#
1372844_at	Efna1	Ephrin A1	112	2.606	1.141	0.769	*†
1398273_at	Efna1	Ephrin A1	113	2.385	1.137	0.764	*†
1383078_at	Efnb3	Ephrin B3	757	0.876	0.804	0.530	#†
1387306_a_at	Egr2	Early growth response 2	132	1.853	2.317	1.429	*#†
1398266_a_at	Egr2	Early growth response 2	64	1.347	1.603	1.151	*#
1368967_at	Eif2b3	Eukaryotic translation initiation factor 2B, subunit 3 gamma	314	1.124	1.313	1.524	#†
1368866_at	Eif2c2	Eukaryotic translation initiation factor 2C, 2	195	1.356	1.519	0.989	*#
1368867_at	Eif2c2	Eukaryotic translation initiation factor 2C, 2	183	1.405	1.706	0.963	*#
1383867_at	Eif5a2	Eukaryotic translation initiation factor 5A2	169	1.020	1.172	1.516	†
1389680_at	Ell2	Elongation factor RNA polymerase II 2	183	1.915	1.433	1.223	*#†
1372587_at	Emcn	Endomucin	477	0.951	0.980	0.406	†
1369736_at	Emp1	Epithelial membrane protein 1	1160	2.182	2.729	1.494	*#†
1371527_at	Emp1	Epithelial membrane protein 1	2394	1.771	1.843	1.605	*#†
1373535_at	Enah	Enabled homolog (Drosophila)	1080	1.519	1.890	1.518	---
1396450_at	Enah	Enabled homolog (Drosophila)	301	1.479	1.837	1.308	---
1370047_at	Enpp1	Ectonucleotide pyrophosphatase/phosphodiesterase 1	706	1.192	1.344	2.410	---
1370047_at	Enpp1	Ectonucleotide pyrophosphatase/phosphodiesterase 1	706	1.192	1.344	2.410	#†
1370047_at	Enpp1	Ectonucleotide pyrophosphatase/phosphodiesterase 1	706	1.192	1.344	2.410	†
1368536_at	Enpp2	Ectonucleotide pyrophosphatase/phosphodiesterase 2	135	1.001	0.921	0.478	†
1370845_at	Entpd2	Ectonucleoside triphosphate diphosphohydrolase 2	118	0.990	0.960	0.666	†
1374143_at	Epha2	Eph receptor A2	130	4.311	2.530	1.417	*#†
1375729_at	Epha4	Eph receptor A4	84	0.641	0.698	0.604	*#†
1390638_at	Epha4	Eph receptor A4	101	0.455	0.462	0.632	*#†
1382317_at	Eps8	Epidermal growth factor receptor pathway substrate 8	178	1.651	1.954	1.261	*#†
1383213_at	Eps8	Epidermal growth factor receptor pathway substrate 8	221	1.681	1.965	1.212	*#
1387813_at	Erbb2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	187	1.322	1.637	1.015	*#
1373093_at	Errfi1	ERBB receptor feedback inhibitor 1	739	2.312	1.683	0.935	*#
1368851_at	Ets1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	712	2.200	1.596	1.314	*#†
1388342_at	Etv3	Ets variant 3	283	1.577	1.183	1.239	*#†
1386739_at	Etv4	Ets variant 4	63	1.020	1.114	1.526	†
1373393_at	Ext1	Exostoses (multiple) 1	1059	1.408	1.657	1.311	*#†
1373290_at	Ezh2	Enhancer of zeste homolog 2 (Drosophila)	107	0.809	0.654	1.078	*#
1367899_at	F2r	Coagulation factor II (thrombin) receptor	1169	1.184	1.282	2.256	*#†
1387596_at	F2rl1	Coagulation factor II (thrombin) receptor-like 1	109	1.738	1.760	1.170	*#
1369182_at	F3	Coagulation factor III (thromboplastin, tissue factor)	119	1.198	0.993	1.673	†
1368271_a_at	Fabp4	Fatty acid binding protein 4, adipocyte	250	0.977	0.917	0.311	†
1367857_at	Fads1	Fatty acid desaturase 1	2063	0.798	0.655	1.143	*#†
1377938_at	Fam100a	Family with sequence similarity 100, member A	337	1.567	1.352	1.024	*#
1379356_at	Fam102b	Family with sequence similarity 102, member B	299	1.711	1.454	1.457	*#†
1380696_at	Fam102b	Family with sequence similarity 102, member B	151	1.864	1.701	1.118	*#
1385251_at	Fam110c	Family with sequence similarity 110, member C	29	3.335	2.230	1.213	*#†
1371970_at	Fam111a	Family with sequence similarity 111, member A	130	0.788	0.651	1.182	*#
1388482_at	Fam129b	Family with sequence similarity 129, member B	1475	1.435	1.754	1.283	*#†
1379625_at	Fam164a	Family with sequence similarity 164, member A	56	0.955	0.900	1.559	†
1391944_at	Fam184a /// RGD1560557	Family with sequence similarity 184, member A /// similar to minichromosome maintenance protein 8 isoform 1	87	1.465	2.628	1.225	*#†

1389695_at	Fam20c	Fmily with sequence similarity 20, member C	429	1.162	1.608	1.417	#†
1391780_at	Fam46b	fFmily with sequence similarity 46, member B	104	1.146	1.565	1.115	#
1382629_at	Far1	fFtty acyl CoA reductase 1	201	1.322	1.528	1.143	*#
1382143_at	Farp1	FERM, RhoGEF (Arhgef) and pleckstrin domain protein 1 (chondrocyte-derived)	434	0.964	1.257	1.599	#†
1367654_at	Fat1	FAT tumor suppressor homolog 1 (Drosophila)	1159	0.941	0.969	1.535	†
1372518_at	Fbln1	FIbulin 1	1197	0.844	0.833	0.595	†
1389533_at	Fbln2	Fibulin 2	1009	0.951	1.026	2.044	†
1387351_at	Fbn1	Fibrillin 1	1310	0.884	0.870	1.530	†
1369972_at	Fbxo21	F-box protein 21	196	0.720	0.657	1.082	*#
1368336_at	Fdx1	Ferredoxin 1	1202	1.664	1.493	1.090	*
1384182_at	Fermt2	Fermitin family homolog 2 (Drosophila)	272	1.235	1.565	1.122	#
1370623_at	Fgl2	Fibrinogen-like 2	382	2.201	2.370	1.186	*#†
1383516_at	Fgl2	Fibrinogen-like 2	126	2.889	2.753	1.290	*#
1386637_at	Fgl2	Fibrinogen-like 2	212	2.550	2.740	1.135	*#
1392894_at	Fgl2	Fibrinogen-like 2	581	2.278	2.540	1.352	*#†
1390049_at	Fhl1	Four and a half LIM domains 1	2588	1.299	1.729	1.573	---
1394750_at	Fhl1	Four and a half LIM domains 1	48	2.019	2.471	1.141	*#
1373727_at	Fibin	Fin bud initiation factor homolog (zebrafish)	452	0.898	1.304	2.243	†
1393696_at	Fibin	Fin bud initiation factor homolog (zebrafish)	170	0.816	1.254	2.669	†
1373882_at	Figf	c-fos induced growth factor	1084	0.837	0.609	1.075	*#
1389449_at	Fit1	Fat-inducing transcript 1	312	0.903	0.816	0.599	†
1380611_at	Fkbp5	FK506 binding protein 5	117	1.296	1.540	1.022	*#
1388901_at	Fkbp5	FK506 binding protein 5	111	1.115	1.550	1.031	#
1372526_at	Flcn	Folliculin	1383	0.530	0.770	0.850	*#†
1371382_at	Flna	Filamin, alpha	2260	1.183	1.233	1.711	†
1388401_at	Flnb	Filamin, beta	376	1.285	1.579	1.488	*#†
1391827_at	Flnb	Filamin, beta	261	1.177	1.539	1.389	*#†
1388496_at	Flnc	Filamin C, gamma (actin binding protein 280)	785	1.985	1.917	1.113	*#
1396085_at	Flnc	Filamin C, gamma (actin binding protein 280)	887	1.706	1.828	1.082	*#
1378057_at	Flrt3	Fibronectin leucine rich transmembrane protein 3	86	0.907	0.756	0.637	#†
1370492_a_at	Flt1	Fms-related tyrosine kinase 1	76	1.265	1.703	1.300	#
1369216_a_at	Flt4	Fms-related tyrosine kinase 4	103	0.925	1.113	1.692	†
1395404_at	Fn3krp	Fructosamine-3-kinase-related protein	125	0.789	0.561	0.902	---
1387530_a_at	Fosb /// Fosl2	FBJ osteosarcoma oncogene B /// fos-like antigen 2	141	1.584	0.981	0.867	*
1368489_at	Fosl1	Fos-like antigen 1	89	6.631	2.842	1.306	*#
1383860_at	Fosl2	Fos-like antigen 2	109	2.113	1.061	1.011	*
1370795_at	Foxc2	Forkhead box C2	41	1.545	1.612	1.340	*#†
1375607_at	Foxc2	Forkhead box C2	88	1.599	1.536	1.333	*#†
1376779_at	Foxo1	Forkhead box O1	66	1.024	0.975	0.659	†
1379651_at	Foxp1	Forkhead box P1	364	1.276	1.523	1.758	*#†
1380387_at	Foxp2	Forkhead box P2	68	0.900	0.586	1.010	#
1389404_at	Foxs1	Forkhead box S1	144	1.564	1.700	1.448	*#†
1376753_at	Fpgt	Fucose-1-phosphate guanylyltransferase	64	0.615	0.995	1.077	*
1387843_at	Fst	Follistatin	90	5.246	3.875	3.498	*#†
1368821_at	Fstl1	Follistatin-like 1	1888	0.913	1.037	1.627	†
1368822_at	Fstl1	Follistatin-like 1	2792	0.994	1.044	1.651	†
1371331_at	Fstl1	Follistatin-like 1	3049	0.969	1.030	1.554	†
1370120_at	Fstl3	Follistatin-like 3 (secreted glycoprotein)	122	1.328	1.927	2.121	#†
1379440_at	Fstl3	Follistatin-like 3 (secreted glycoprotein)	433	1.243	1.679	2.191	#†
1368207_at	Fxyd5	FXYD domain-containing ion transport regulator 5	807	1.151	1.526	2.214	*#†
1370256_at	Fzd1	Frizzled homolog 1 (Drosophila)	2560	0.513	0.728	1.001	*#
1398304_at	Fzd2	Frizzled homolog 2 (Drosophila)	695	0.890	1.539	1.406	#†

1374530_at	Fzd7	Frizzled homolog 7 (Drosophila)	180	0.639	1.044	1.516	*†
1388395_at	G0s2	G0/G1switch 2	2705	0.249	0.570	0.595	*#†
1368947_at	Gadd45a	Growth arrest and DNA-damage-inducible, alpha	1505	1.521	1.243	0.955	*
1372016_at	Gadd45b	Growth arrest and DNA-damage-inducible, beta	302	1.998	1.401	1.410	*#†
1388792_at	Gadd45g	Growth arrest and DNA-damage-inducible, gamma	968	2.510	2.295	1.039	*#
1374759_at	Galntl1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 1	111	1.022	1.062	1.745	†
1370293_at	Gata4	GATA binding protein 4	457	0.838	1.528	1.087	#
1374125_at	Gata5	GATA binding protein 5	246	0.369	0.556	0.674	*#†
1387221_at	Gch1	GTP cyclohydrolase 1	108	1.596	1.595	1.139	*#†
1374903_at	Gcnt2	Glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	77	1.701	1.533	1.528	*#†
1374816_at	Gcom1	GRINL1A complex locus	2545	0.797	0.651	0.992	*#
1382351_at	Gem	GTP binding protein (gene overexpressed in skeletal muscle)	146	2.221	1.459	0.865	*
1367954_at	Gfra1	GDNF family receptor alpha 1	65	1.046	1.502	0.960	#
1387007_at	Gfra1	GDNF family receptor alpha 1	128	1.052	1.539	0.953	#
1368924_at	Ghr	Growth hormone receptor	336	0.898	0.674	0.642	#†
1373803_a_at	Ghr	Growth hormone receptor	565	0.935	0.902	0.652	†
1394095_at	Gin1	Gypsy retrotransposon integrase 1	60	0.650	0.860	0.969	*
1373504_at	Glipr1	GLI pathogenesis-related 1	87	1.633	1.515	2.432	*#†
1390121_at	Glis2	GLIS family zinc finger 2	989	1.230	1.643	1.111	*#†
1398724_at	Glis2	GLIS family zinc finger 2	101	1.147	1.571	0.878	#
1382521_at	Gls	Glutaminase	363	1.501	1.434	1.493	*#†
1382616_at	Gls	Glutaminase	158	1.406	1.563	1.567	*#†
1367632_at	Glul	Glutamate-ammonia ligase (glutamine synthetase)	949	1.215	1.015	0.615	†
1367633_at	Glul	Glutamate-ammonia ligase (glutamine synthetase)	956	1.069	1.041	0.562	†
1386870_at	Glul	Glutamate-ammonia ligase (glutamine synthetase)	1436	1.105	1.068	0.564	†
1369560_at	Gpd1	Glycerol-3-phosphate dehydrogenase 1 (soluble)	159	1.033	0.994	0.513	†
1371363_at	Gpd1	Glycerol-3-phosphate dehydrogenase 1 (soluble)	311	0.957	0.913	0.429	†
1373773_at	Gpm6a	Glycoprotein m6a	182	0.922	0.663	1.022	#
1388109_at	Gpr116	G protein-coupled receptor 116	186	0.945	1.030	0.649	†
1373158_at	Gpr146	G protein-coupled receptor 146	886	0.688	0.535	0.753	*#†
1388243_at	Gpr176	G protein-coupled receptor 176	474	1.700	1.639	1.718	*#†
1376828_at	Gprc5a	G protein-coupled receptor, family C, group 5, member A	180	2.619	3.671	1.532	*#†
1371671_at	Gprc5b	G protein-coupled receptor, family C, group 5, member B	247	1.445	1.940	0.818	*#
1373336_at	Gprc5b	G protein-coupled receptor, family C, group 5, member B	96	1.763	1.642	0.806	*#†
1369113_at	Grem1	Gremlin 1, cysteine knot superfamily, homolog (Xenopus laevis)	56	3.329	8.520	7.525	*#†
1378163_at	Grem2	Gremlin 2, cysteine knot superfamily, homolog (Xenopus laevis)	101	0.870	0.831	0.452	†
1387954_a_at	Grip2	Glutamate receptor interacting protein 2	86	1.454	2.706	1.281	*#†
1388016_a_at	Grip2	Glutamate receptor interacting protein 2	75	1.067	1.548	1.078	#
1389890_at	Gse1	Genetic suppressor element 1	109	1.823	1.381	0.715	*#†
1370365_at	Gss	Glutathione synthetase	323	1.428	1.897	1.101	*#
1368354_at	Gstt1	Glutathione S-transferase theta 1	186	0.961	0.937	0.525	†
1371942_at	Gstt3	Glutathione S-transferase, theta 3	197	1.024	0.899	0.203	†
1368154_at	Gucy1a3	Guanylate cyclase 1, soluble, alpha 3	341	0.592	0.409	0.777	*#†
1369097_s_at	Gucy1b3	Guanylate cyclase 1, soluble, beta 3	178	0.719	0.555	1.554	*#†
1374389_at	Gucy1b3	Guanylate cyclase 1, soluble, beta 3	145	0.759	0.543	1.113	#
1371298_at	H19	H19 fetal liver mRNA	989	0.886	0.941	0.566	†
1388164_at	H2-T23	Histocompatibility 2, T region locus 23	125	1.395	1.716	0.992	*#
1371123_x_at	H2-T23 /// H2-T24	Histocompatibility 2, T region locus 23 /// histocompatibility 2, T region locus 24	120	1.577	1.997	0.933	*#†
1388212_a_at	H2-T23 /// H2-T24	Histocompatibility 2, T region locus 23 /// histocompatibility 2, T region locus 24	185	1.653	2.008	1.085	*#

1388213_a_at	H2-T23 /// H2-T24	Histocompatibility 2, T region locus 23 /// histocompatibility 2, T region locus 24	95	1.633	2.099	0.981	*#
1387396_at	Hamp	Hepcidin antimicrobial peptide	1110	0.951	1.099	0.550	†
1387548_at	Has2	Hyaluronan synthase 2	119	1.730	1.161	0.734	*†
1368983_at	Hbegf	Heparin-binding EGF-like growth factor	158	5.568	3.308	1.253	*#
1371819_at	Hdac5	Histone deacetylase 5	563	1.596	1.754	1.175	*#
1374625_at	Hes6	Hairy and enhancer of split 6 (Drosophila)	635	0.697	0.591	0.993	*#
1386080_at	Hey1	Hairy/enhancer-of-split related with YRPW motif 1	114	0.731	0.822	0.540	*†
1384515_at	Hey2	Hairy/enhancer-of-split related with YRPW motif 2	323	0.625	0.576	1.018	*#
1391429_at	Hfe2	Hemochromatosis type 2 (juvenile) (human homolog)	165	0.871	0.784	0.534	#†
1388193_at	Hip1	Huntingtin interacting protein 1	584	0.866	1.027	1.683	†
1392941_at	Hip1	Huntingtin interacting protein 1	469	0.912	0.978	1.653	†
1370994_at	Hip1r	Huntingtin interacting protein 1 related	183	1.229	1.522	1.083	*#
1390876_at	Hisppd2a	Histidine acid phosphatase domain containing 2A	112	1.246	1.409	1.646	†
1391560_at	Hivep1	Human immunodeficiency virus type I enhancer binding protein 1	57	1.550	1.496	1.065	*#
1368546_at	Hivep2	Human immunodeficiency virus type I enhancer binding protein 2	217	2.072	1.522	1.113	*#
1388309_at	Hmga1	High mobility group AT-hook 1	1696	1.606	2.016	1.011	*#
1370080_at	Hmox1	Heme oxygenase (decycling) 1	1759	0.661	0.577	0.692	*#†
1372693_at	Hnrnpa1	Heterogeneous nuclear ribonucleoprotein A1	430	0.652	0.797	0.998	*#
1370454_at	Homer1	Homer homolog 1 (Drosophila)	44	3.698	1.225	0.996	*
1367816_at	Hopx	HOP homeobox	985	0.814	0.655	0.605	*#†
1393790_at	Hrasls	HRAS-like suppressor	139	1.048	1.241	1.721	#†
1372467_at	Hs6st1	Heparan sulfate 6-O-sulfotransferase 1	273	1.536	1.445	1.882	†
1380138_at	Hs6st2	Heparan sulfate 6-O-sulfotransferase 2	57	0.971	0.846	1.810	†
1368247_at	Hspa1a /// Hspa1b	Heat shock 70kD protein 1A /// heat shock 70kD protein 1B (mapped)	117	3.449	2.149	1.909	*#†
1370912_at	Hspa1b	Heat shock 70kD protein 1B (mapped)	188	2.419	1.980	2.048	*#†
1373515_at	Hspc159	Galectin-related protein	459	0.847	0.938	1.990	†
1376867_at	Hspc159	Galectin-related protein	237	0.774	1.035	2.134	†
1372565_at	Htra3	HtrA serine peptidase 3	1325	0.904	0.868	0.519	†
1375306_at	Htra3	HtrA serine peptidase 3	452	0.945	0.979	0.621	†
1387202_at	Icam1	Intercellular adhesion molecule 1	1101	2.306	1.614	1.158	*#
1389235_at	Icam2	Intercellular adhesion molecule 2	194	0.943	0.938	0.602	†
1387028_a_at	Id1	Inhibitor of DNA binding 1	1120	1.540	1.412	0.816	*#†
1368870_at	Id2	Inhibitor of DNA binding 2	545	0.468	0.828	0.791	*
1375120_at	Id4	Inhibitor of DNA binding 4	108	1.957	1.387	0.955	*#
1375183_at	Id4	Inhibitor of DNA binding 4	82	1.942	1.412	1.031	*#
1394022_at	Id4	Inhibitor of DNA binding 4	127	2.082	1.581	1.107	*#
1369954_at	Idh1	Isocitrate dehydrogenase 1 (NADP+), soluble	2379	0.818	0.655	1.052	*#
1372389_at	Ier2	Immediate early response 2	362	1.697	1.422	1.424	*#†
1388587_at	Ier3	Immediate early response 3	1518	1.565	1.444	1.402	*#†
1389355_at	Ier5	Immediate early response 5	738	2.120	1.834	1.162	*#†
1389882_at	Ier5	Immediate early response 5	149	1.964	1.816	0.937	*#
1391026_at	Ier5l	Immediate early response 5-like	689	0.621	0.722	0.883	*#
1385702_at	Ifi204	Interferon activated gene 204	547	1.722	0.940	0.785	*
1384180_at	Ifit2	Interferon-induced protein with tetratricopeptide repeats 2	276	0.720	0.651	1.252	*#
1367795_at	Ifrd1	Interferon-related developmental regulator 1	813	2.099	1.337	1.435	*#†
1394038_at	Ift81	Intraflagellar transport 81 homolog (Chlamydomonas)	270	0.682	0.549	1.094	*#
1371462_at	Igfbp4	Insulin-like growth factor binding protein 4	1119	0.899	0.915	0.540	†
1370960_at	Igfbp5	Insulin-like growth factor binding protein 5	854	0.752	0.646	0.329	*#†
1387347_at	Igfbp5	Insulin-like growth factor binding protein 5	249	0.911	1.026	0.656	†
1387348_at	Igfbp5	Insulin-like growth factor binding protein 5	424	0.909	0.830	0.398	†

1396152_s_at	Igfbp5	Insulin-like growth factor binding protein 5	310	0.835	0.778	0.348	†
1397830_at	Igfbp5	Insulin-like growth factor binding protein 5	191	0.875	0.874	0.601	†
1390901_at	Igsf10	Immunoglobulin superfamily, member 10	734	0.841	0.617	0.517	#†
1368424_at	Ikbkb	Inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta	240	1.062	1.512	1.024	#
1369266_at	Il13ra2	Interleukin 13 receptor, alpha 2	48	1.622	1.861	1.254	*#†
1368375_a_at	Il15	Interleukin 15	67	0.716	0.851	1.680	*†
1370692_at	Il1rl1	Interleukin 1 receptor-like 1	104	1.957	2.949	1.161	*#
1387273_at	Il1rl1	Interleukin 1 receptor-like 1	326	11.010	13.013	5.149	*#†
1373140_at	Il6st	Interleukin 6 signal transducer	1639	0.740	0.645	0.825	*#†
1383489_at	Il6st	Interleukin 6 signal transducer	1057	0.716	0.622	0.831	*#†
1369208_at	Il7	Interleukin 7	48	1.662	1.491	0.934	*#†
1387124_at	Inha	Inhibin alpha	237	1.069	1.298	1.739	†
1369012_at	Inhba	Inhibin beta-A	74	1.913	1.899	0.994	*#
1377163_at	Inhbb	Inhibin beta-B	43	1.249	1.362	1.825	*#†
1373955_at	Ipo5	Importin 5	1536	1.470	1.670	1.141	*#
1396742_at	Ipo5	Importin 5	357	1.404	1.759	1.188	*#†
1388762_at	Iqgap1	IQ motif containing GTPase activating protein 1	642	1.163	1.370	1.502	#†
1368073_at	Irf1	Interferon regulatory factor 1	434	0.544	0.611	0.718	*#†
1377379_at	Irf6	Interferon regulatory factor 6	102	1.350	1.696	0.734	*#†
1383448_at	Irf9	Interferon regulatory factor 9	275	0.591	0.680	0.956	*#
1391489_at	Irgm	Immunity-related GTPase family, M	142	0.928	0.791	0.665	†
1371091_at	Irs2	Insulin receptor substrate 2	359	1.411	1.560	1.128	*#
1390776_at	Irx3	Iroquois homeobox 3	627	0.636	0.746	1.098	*
1392981_at	Irx4	Iroquois homeobox 4	841	0.388	0.414	0.707	*#†
1387144_at	Itga1	Integrin alpha 1	373	1.248	1.409	1.648	*#†
1394824_at	Itga11	Integrin, alpha 11	43	0.896	0.847	2.134	†
1385649_at	Itga5	Integrin alpha 5 (fibronectin receptor alpha)	532	1.839	1.861	1.174	*#
1371186_at	Itga6	Integrin, alpha 6	235	1.254	1.778	1.060	#
1393558_at	Itga6	Integrin, alpha 6	185	1.286	1.865	1.196	#
1383880_at	Itgav	Integrin alpha V	341	1.391	1.457	1.656	*#†
1370802_at	Itgb5	Integrin, beta 5	213	0.866	1.193	1.511	†
1398358_a_at	Itgb5	Integrin, beta 5	863	1.009	1.159	1.594	†
1387907_at	Itpr1	Inositol 1,4,5-triphosphate receptor, type 1	205	0.914	0.710	1.536	#†
1368725_at	Jag1	Jagged 1	139	0.868	0.700	1.528	*#†
1373122_at	Jub	Jub, ajuba homolog (Xenopus laevis)	518	1.476	1.861	1.546	*#†
1388230_at	Jub	Jub, ajuba homolog (Xenopus laevis)	209	1.380	1.765	1.300	#
1387788_at	Junb	Jun B proto-oncogene	986	1.615	1.283	0.993	*#
1395851_at	Kbtbd5	Kelch repeat and BTB (POZ) domain containing 5	249	2.351	2.841	1.163	*#
1387160_at	Kcne3	Potassium voltage-gated channel, Isk-related subfamily, gene 3	524	0.850	1.047	0.554	*†
1370773_a_at	Kcnip2	Kv channel-interacting protein 2	164	0.884	0.979	0.447	†
1373987_at	Kcnip2	Kv channel-interacting protein 2	422	0.956	0.947	0.417	†
1387698_at	Kcnj11	Potassium inwardly rectifying channel, subfamily J, member 11	199	0.566	0.704	0.764	*#†
1391007_s_at	Kcnj11	Potassium inwardly rectifying channel, subfamily J, member 11	279	0.598	0.678	0.753	*#†
1368911_at	Kcnj8	Potassium inwardly-rectifying channel, subfamily J, member 8	177	0.516	0.446	0.488	*#†
1387441_at	Kcnk3	Potassium channel, subfamily K, member 3	409	1.064	1.197	0.562	#†
1371857_at	Kctd10	Potassium channel tetramerization domain containing 10	806	1.410	1.555	1.252	*#†
1385226_at	Kctd11	Potassium channel tetramerisation domain containing 11	283	1.758	1.315	1.391	*#†
1397764_at	Kctd5	Potassium channel tetramerisation domain containing 5	566	1.630	1.614	0.979	*#
1367948_a_at	Kdr	Kinase insert domain protein receptor	858	0.835	0.723	0.546	#†
1391526_at	Kif16b	Kinesin family member 16B	107	0.892	0.655	0.824	---
1391063_at	Kif23	Kinesin family member 23	122	0.863	0.938	1.660	†
1378197_at	KIFC2	Kinesin family member C2	111	0.817	0.761	0.651	*#†

1389374_at	Kifc3	Kinesin family member C3	181	2.197	2.687	1.225	*#†
1388856_at	Kitlg	KIT ligand	147	2.071	2.136	1.161	*#†
1396214_at	Kitlg	KIT ligand	41	1.962	2.462	1.396	*#†
1368650_at	Klf10	Kruppel-like factor 10	461	2.031	1.347	0.964	*#
1368249_at	Klf15	Kruppel-like factor 15	379	0.291	0.430	0.599	*#†
1381396_s_at	Klf15	Kruppel-like factor 15	250	0.346	0.450	0.596	*#†
1378332_at	Klf3	Kruppel-like factor 3 (basic)	640	0.586	1.039	0.797	*†
1389479_at	Klf3	Kruppel-like factor 3 (basic)	763	0.532	0.968	0.940	*
1393150_at	Klf3	Kruppel-like factor 3 (basic)	527	0.636	1.062	0.859	*
1387260_at	Klf4	Kruppel-like factor 4 (gut)	722	2.362	1.538	1.303	*#†
1368363_at	Klf5	Kruppel-like factor 5	102	5.859	1.917	1.395	*#†
1385961_at	Klf5	Kruppel-like factor 5	29	4.884	1.281	1.203	*#†
1394039_at	Klf5	Kruppel-like factor 5	61	5.712	1.438	1.372	*#†
1387060_at	Klf6	Kruppel-like factor 6	566	1.960	1.669	1.151	*#
1370209_at	Klf9	Kruppel-like factor 9	626	1.599	1.208	1.388	*#†
1388799_at	Klhl7	Kelch-like 7 (Drosophila)	303	0.667	0.588	1.283	*#†
1370035_at	Kras	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	445	1.561	1.420	1.347	*#†
1388155_at	Krt18	Keratin 18	72	1.218	2.274	1.646	#†
1388433_at	Krt19	Keratin 19	60	1.162	1.555	0.695	#†
1379462_at	Ksr1	Kinase suppressor of ras 1	109	0.628	0.805	1.002	*
1390851_at	Lactb2	Lactamase, beta 2	354	0.795	0.653	0.994	#
1372884_at	Large	Like-glycosyltransferase	292	0.882	1.115	1.514	†
1390207_at	Lats2	Large tumor suppressor 2	994	1.338	1.425	1.586	*#†
1387868_at	Lbp	Lipopolysaccharide binding protein	672	0.883	0.896	0.656	†
1387011_at	Lcn2	Lipocalin 2	3877	0.949	0.925	0.616	†
1373233_at	Lhfpl2	Lipoma HMGIC fusion partner-like 2	461	0.725	0.709	0.557	*#†
1378179_a_at	Lhfpl2	Lipoma HMGIC fusion partner-like 2	319	0.737	0.695	0.612	*#†
1376700_at	Lima1	LIM domain and actin binding 1	409	1.409	1.023	1.558	*†
1376632_at	Lmcd1	LIM and cysteine-rich domains 1	489	5.688	6.271	2.698	*#†
1368054_at	Lmna	Lamin A	752	1.445	1.669	1.180	*#
1368055_a_at	Lmna	Lamin A	1822	1.467	1.651	1.142	*#
1375726_at	Lmo7	LIM domain 7	941	1.255	1.527	1.011	#
1377610_at	Lmod2	Leiomodin 2 (cardiac)	1550	2.013	1.618	1.256	*#
1389464_at	Lnx1	Ligand of numb-protein X 1	118	0.719	0.582	0.538	*#†
1374171_at	LOC100360403	ATP-binding cassette, sub-family C, member 9-like	1173	0.825	0.724	0.565	*#†
1388985_at	LOC100361467	Hypothetical LOC100361467	1139	2.382	1.035	2.437	---
1375706_at	LOC100361913	rCG54286-like	517	1.098	1.261	1.557	#†
1376056_at	LOC100362108	Poly (ADP-ribose) polymerase family, member 10	137	0.790	0.630	0.759	*#†
1372647_at	LOC100363743	Proline arginine-rich end leucine-rich repeat protein-like	240	1.456	1.907	2.479	*#†
1376151_a_at	LOC100365106	rCG32755-like	229	0.716	0.770	0.608	*#†
1374029_at	LOC100365118	rCG54747-like	253	0.930	1.125	1.762	†
1393210_at	LOC100365207	Extracellular matrix protein 2-like	192	0.954	0.855	0.602	†
1389918_at	LOC290704	Similar to palladin	237	2.232	1.188	1.059	*
1398593_at	LOC298139	Similar to RIKEN cDNA 2310003M01	45	1.298	1.804	1.177	*#
1373232_at	LOC302022	Similar to nidogen 2 protein	344	1.666	1.796	1.278	*#†
1381434_s_at	LOC302022	Similar to nidogen 2 protein	246	1.899	1.803	1.386	*#†
1372856_at	LOC363331	Similar to plasma membrane associated protein, S3-12	305	0.771	0.718	0.650	*#†
1381065_at	LOC499120	Hypothetical protein LOC499120	350	0.572	0.710	0.899	*#
1391030_at	LOC500591	Similar to calmodulin-binding transcription activator 1	837	1.082	1.679	1.905	#†
1397536_at	LOC500591	Similar to calmodulin-binding transcription activator 1	322	1.244	1.569	1.919	#†
1393309_at	LOC503192	Zinc finger protein ZFP	173	0.658	0.775	0.910	*#
1385503_at	LOC678772	Similar to O-acetyltransferase	139	0.776	0.650	1.053	*#

1375988_at	LOC680262	Hypothetical protein LOC680262	112	0.628	0.697	1.132	*#
1385777_at	LOC681647	Similar to F43G9.2	106	0.577	0.630	0.753	*#†
1383649_a_at	LOC681665	Similar to integrator complex subunit 6 isoform a	93	0.771	0.581	1.072	#
1384390_at	LOC681740	Similar to jumonji protein	228	1.544	0.940	0.840	*
1385659_at	LOC682861	Similar to adenomatosis polyposis coli down-regulated 1	151	0.790	0.542	0.741	*#†
1383149_at	LOC684122	Similar to development and differentiation enhancing factor-like 1	223	0.500	0.594	0.958	*#
1377169_at	LOC684173	Similar to TNF receptor-associated factor 5	145	1.604	1.591	0.968	*#
1388384_at	LOC684259	Similar to RUN and SH3 domain-containing protein 2	216	1.076	1.542	1.155	#
1374677_at	LOC684425	Similar to Adenylosuccinate synthetase isozyme 1 (Adenylosuccinate synthetase, muscle isozyme) (IMP--aspartate ligase 1) (AdSS 1) (AMPSase 1)	593	0.881	0.963	0.638	†
1373921_at	LOC684538	Similar to enoyl Coenzyme A hydratase domain containing 3	102	0.690	0.615	0.970	*#†
1373403_at	LOC684871	Similar to Protein C8orf4 (Thyroid cancer protein 1) (TC-1)	36	1.541	1.691	1.389	*#†
1376219_at	LOC685152	Similar to Probable phospholipid-transporting ATPase ID (ATPase class I type 8B member 2)	796	1.438	1.522	1.350	*#†
1384406_at	LOC685243	Similar to C-C chemokine receptor type 11 (C-C CKR-11) (CC-CKR-11) (CCR-11) (Chemokine receptor-like 1) (CCRL1) (CCX CKR)	127	0.982	1.204	1.839	†
1374377_at	LOC686781	Similar to NFkB interacting protein 1	219	1.581	1.564	1.158	*#
1384035_at	LOC686794	Similar to liver-specific bHLH-Zip transcription factor	102	1.376	1.729	1.939	---
1380486_at	LOC687022	Similar to SEC22 vesicle trafficking protein-like 3	116	0.631	0.767	0.986	*#
1371554_at	LOC688173	Similar to Telethonin (Titin cap protein)	337	2.129	2.257	1.560	*#
1393691_at	LOC688273	Hypothetical protein LOC688273	55	0.702	0.911	1.689	*†
1398732_at	LOC688273	Hypothetical protein LOC688273	119	0.733	0.812	2.056	*#†
1373659_at	LOC689926	Hypothetical protein LOC689926	236	0.435	0.494	0.934	*#
1389365_at	LOC690000	Similar to CG3740-PA	476	0.631	0.652	0.860	*#†
1375198_at	LOC690139	Similar to RNA binding motif protein 24	183	0.606	0.756	0.802	*
1376441_at	LOC690217 /// RGD1566114	Similar to B0511.12 /// similar to chromosome 14 open reading frame 135	102	0.692	0.605	1.041	*#
1395614_at	LOC690372 /// U2af2	Similar to U2 (RNU2) small nuclear RNA auxiliary factor 2 isoform b /// U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 2	85	0.896	0.975	0.608	---
1388763_at	LOC690976	Similar to Calponin-2 (Calponin H2, smooth muscle) (Neutral calponin)	1497	1.423	1.039	1.667	†
1390907_at	LOC691170	Similar to zinc finger protein 84 (HPF2)	88	0.658	0.753	0.914	*#
1375148_at	LOC691504	Similar to Zinc finger protein ZFPM1 (Zinc finger protein multitype 1) (Friend of GATA protein 1) (Friend of GATA-1) (FOG-1)	175	0.945	1.538	0.932	#
1373172_at	LOC691777	Hypothetical protein LOC691777	256	0.517	0.880	1.162	*
1368171_at	Lox	Lysyl oxidase	922	1.068	1.157	2.263	†
1368172_a_at	Lox	Lysyl oxidase	525	1.111	1.117	2.107	†
1388902_at	Loxl1	Lysyl oxidase-like 1	1184	0.964	1.071	1.706	†
1393177_at	Lrch1	Leucine-rich repeats and calponin homology (CH) domain containing 1	88	0.931	1.201	1.557	#†
1374626_at	Lrg1	Leucine-rich alpha-2-glycoprotein 1	107	0.948	1.006	0.577	†
1375531_at	Lrig3	Leucine-rich repeats and immunoglobulin-like domains 3	59	0.655	0.892	1.105	*#
1389727_at	Lrrc10	Leucine-rich repeat-containing 10	660	0.431	0.365	0.939	*#
1395472_at	Lrrc17	Leucine rich repeat containing 17	1339	0.622	0.430	0.570	*#†
1382941_at	Lrrc32	Leucine rich repeat containing 32	415	1.196	1.502	1.424	#†
1393460_at	Lrrc33	Leucine rich repeat containing 33	180	1.011	0.965	0.612	†
1385155_at	Lrrfip1	Leucine rich repeat (in FLII) interacting protein 1	92	1.344	1.836	1.305	#
1389351_at	Lrrfip1	Leucine rich repeat (in FLII) interacting protein 1	521	1.599	2.256	1.665	*#†
1367912_at	Ltbp1	Latent transforming growth factor beta binding protein 1	175	1.188	1.525	2.776	#†
1368448_at	Ltbp2	Latent transforming growth factor beta binding protein 2	417	1.095	1.206	2.574	*#†
1369325_at	Lyst	Lysosomal trafficking regulator	103	1.195	1.609	0.989	#
1382192_at	Lyve1	Lymphatic vessel endothelial hyaluronan receptor 1	237	0.986	0.913	0.514	†
1382732_at	Lyve1	Lymphatic vessel endothelial hyaluronan receptor 1	153	0.878	0.912	0.578	†
1387165_at	Maf	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	122	0.800	0.816	0.518	†

1380229_at	Maff	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	127	2.479	1.674	1.075	*#
1372211_at	Mafk	v-maf musculoaponeurotic fibrosarcoma oncogene homolog K (avian)	470	2.444	1.958	1.295	*#
1387753_s_at	Magi3	Membrane associated guanylate kinase, WW and PDZ domain containing 3	363	1.515	2.202	1.016	*#
1398866_at	Magi3	Membrane associated guanylate kinase, WW and PDZ domain containing 3	253	1.635	2.275	1.295	*#†
1371988_at	Man1a1	Mannosidase, alpha, class 1A, member 1	518	0.684	0.659	0.901	*#
1368514_at	Maob	Monoamine oxidase B	119	0.997	0.824	0.581	†
1371003_at	Map1b	Microtubule-associated protein 1B	70	1.334	1.618	1.701	*#†
1373363_at	Map1b	Microtubule-associated protein 1B	874	1.205	1.406	1.551	#†
1395357_at	Map1b	Microtubule-associated protein 1B	213	1.248	1.533	1.874	#†
1388858_at	Map2k3	Mitogen activated protein kinase kinase 3	1427	2.080	2.236	0.983	*#
1368871_at	Map3k1	Mitogen activated protein kinase kinase kinase 1	332	0.708	0.784	0.617	*#†
1378552_at	Map3k6	Mitogen-activated protein kinase kinase kinase 6	153	1.284	1.532	1.171	#
1372912_at	Map3k7ip1	Mitogen-activated protein kinase kinase kinase 7 interacting protein 1	441	0.659	0.816	0.885	*#†
1371087_a_at	Map6	Microtubule-associated protein 6	140	1.407	1.996	1.573	*#†
1389543_at	Masp1	Mannan-binding lectin serine peptidase 1	281	0.910	0.834	0.561	#†
1372520_at	Mcl1	Myeloid cell leukemia sequence 1	1710	1.582	1.287	1.014	*#
1367682_at	Mdk	Midkine	1153	0.941	0.959	0.606	†
1379567_at	Med13	Mediator complex subunit 13	48	2.374	1.032	1.055	*
1386156_at	Med13	Mediator complex subunit 13	51	1.864	1.011	0.880	*
1376690_at	Med21	Mediator complex subunit 21	388	1.267	1.327	1.544	*#†
1373410_at	Mef2c	Myocyte enhancer factor 2C	339	1.264	1.718	1.503	*#†
1377696_at	Mesdc1	Mesoderm development candidate 1	603	1.504	1.498	1.065	*#
1389911_at	Metrnl	Meteorin, glial cell differentiation regulator-like	821	1.928	2.031	1.071	*#
1371479_at	Mettl7a	Methyltransferase like 7A	336	0.710	0.480	0.527	*#†
1380682_at	Mex3b	Mex3 homolog B (C. elegans)	101	0.682	0.728	1.626	*#†
1371815_at	Mfap2	Microfibrillar-associated protein 2	242	0.975	0.929	0.439	†
1373674_at	Mfap5	Microfibrillar associated protein 5	81	1.105	1.087	3.194	†
1367796_at	Mgat1	Mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	491	1.552	1.487	1.506	*#†
1392547_at	MGC105649	Hypothetical LOC302884	125	1.485	1.873	1.268	*#†
1373333_at	MGC109340	SImilar to Microsomal signal peptidase 23 kDa subunit (SPase 22 kDa subunit) (SPC22/23)	48	0.841	0.749	1.602	#†
1376200_at	MGC72974	Hypothetical LOC316976	72	0.625	0.648	0.996	*#
1367612_at	Mgst1	Microsomal glutathione S-transferase 1	4162	0.832	0.747	0.581	*#†
1389096_at	Mical2	Microtubule associated monoxygenase, calponin and LIM domain containing 2	866	1.124	1.622	1.381	#†
1374775_at	Mki67	Antigen identified by monoclonal antibody Ki-67	163	0.660	0.580	1.301	*#†
1385953_at	Mllt3	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3	88	0.781	0.645	0.829	#
1371883_at	Mmd	Monocyte to macrophage differentiation-associated	852	1.535	1.868	1.326	*#†
1383668_at	Mmp15	Matrix metallopeptidase 15	402	0.742	0.578	0.645	*#†
1368590_at	Mmp16	Matrix metallopeptidase 16	130	1.233	1.453	1.577	#†
1372904_at	Mobkl2a	MOB1, Mps One Binder kinase activator-like 2A (yeast)	308	1.972	1.330	1.183	*#
1384900_at	Mobkl2a	MOB1, Mps One Binder kinase activator-like 2A (yeast)	84	1.992	1.427	1.087	*#
1382190_at	Mrgprf	MAS-related GPR, member F	305	1.624	1.894	0.789	*#†
1371237_a_at	Mt1a	Metallothionein 1a	6763	1.143	0.770	0.665	#†
1397644_at	Mtap	Methylthioadenosine phosphorylase	260	0.991	1.130	1.643	†
1388661_at	Mtp18	Mitochondrial protein 18 kDa	233	0.731	0.637	0.978	*#
1388874_at	Mtss1	Metastasis suppressor 1	1138	0.631	1.001	0.905	*
1378765_at	Mul1	Mitochondrial ubiquitin ligase activator of NFKB 1	165	0.599	0.702	0.716	*#†
1373032_at	Mustn1	Musculoskeletal, embryonic nuclear protein 1	120	1.573	2.390	2.215	*#†
1382748_at	Mut	Methylmalonyl-Coenzyme A mutase	144	0.852	0.665	0.813	#
1368308_at	Myc	Myelocytomatosis oncogene	498	1.751	1.439	1.763	*#†
1370896_a_at	Myh11	Myosin, heavy chain 11, smooth muscle	143	1.027	0.935	1.812	†

1387049_at	Myh6	Myosin, heavy chain 6, cardiac muscle, alpha	4281	0.849	0.872	0.622	*#†
1396165_at	Myh6	Myosin, heavy chain 6, cardiac muscle, alpha	1159	0.851	0.846	0.626	†
1367928_at	Myh7	Myosin, heavy chain 7, cardiac muscle, beta	3085	0.875	0.954	1.634	†
1371725_at	Myh9	Myosin, heavy chain 9, non-muscle	1960	1.200	1.326	1.648	†
1387402_at	Myh9	Myosin, heavy chain 9, non-muscle	719	1.242	1.531	1.717	#†
1389474_at	Mylip	Myosin regulatory light chain interacting protein	111	0.460	0.713	1.079	*#
1388917_at	Myo1d	Myosin ID	249	0.911	1.077	2.012	†
1375857_at	Myof	Myoferlin	827	1.030	1.338	1.730	#†
1374088_at	Mypn	Myopalladin	270	1.619	2.191	0.842	*#
1372295_at	Narf	Nuclear prelamin A recognition factor	426	0.700	0.602	0.850	*#
1384009_at	Narf	Nuclear prelamin A recognition factor	169	0.704	0.634	0.600	*#†
1374799_at	Ncapd2	Non-SMC condensin I complex, subunit D2	81	0.656	0.695	1.068	*#
1383166_at	Ncoa1	Nuclear receptor coactivator 1	457	0.767	0.638	0.807	*#†
1390010_at	Ncoa1	Nuclear receptor coactivator 1	209	0.771	0.651	0.814	*#†
1392385_at	Ncoa3	Nuclear receptor coactivator 3	65	0.633	0.807	0.833	*†
1383938_at	Ncoa7	Nuclear receptor coactivator 7	367	0.634	0.626	0.655	*#†
1374650_at	Nedd9	Neural precursor cell expressed, developmentally down-regulated 9	343	1.027	1.527	1.756	#†
1396053_at	Nedd9	Neural precursor cell expressed, developmentally down-regulated 9	147	1.005	1.667	1.879	#†
1386948_at	Nes	Nestin	170	1.260	1.545	1.259	*#†
1372000_at	Net1	Neuroepithelial cell transforming 1	217	0.590	0.461	1.053	*#
1369679_a_at	Nfia	Nuclear factor I/A	769	0.961	0.636	1.006	#
1368488_at	Nfil3	Nuclear factor, interleukin 3 regulated	316	1.961	1.703	1.192	*#
1389538_at	Nfkbia	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	768	0.845	0.904	0.582	†
1392686_at	Nkd2	Naked cuticle homolog 2 (Drosophila)	77	0.961	0.936	2.212	†
1372236_at	Nod1	Nucleotide-binding oligomerization domain containing 1	450	0.648	0.754	0.740	*#†
1373839_at	Nope	Neighbor of Punc E11	697	0.751	0.485	0.585	*#†
1371166_at	Nos3	Nitric oxide synthase 3, endothelial cell	161	0.872	0.884	0.590	†
1371491_at	Notch1	Notch homolog 1, translocation-associated (Drosophila)	98	1.081	1.114	0.651	†
1368883_at	Nov	Nephroblastoma overexpressed gene	346	1.108	1.160	2.895	†
1382874_at	Npl	N-acetylneuraminate pyruvate lyase	65	0.762	0.667	0.823	#
1370517_at	Nptx1	Neuronal pentraxin 1	46	1.097	1.875	0.669	#†
1376362_at	Nptxr	Neuronal pentraxin receptor	73	1.276	1.735	2.097	#†
1391059_at	Npw	Neuropeptide W	81	1.397	1.596	1.410	*#†
1387154_at	Npy	Neuropeptide Y	1109	0.805	0.663	0.581	*#
1368376_at	Nr0b2	Nuclear receptor subfamily 0, group B, member 2	132	0.447	0.451	0.819	*#
1370541_at	Nr1d2	Nuclear receptor subfamily 1, group D, member 2	395	0.673	0.618	0.969	*#
1386935_at	Nr4a1	Nuclear receptor subfamily 4, group A, member 1	215	3.778	2.047	1.580	*#†
1369067_at	Nr4a3	Nuclear receptor subfamily 4, group A, member 3	29	10.843	3.006	2.105	*#†
1393389_at	Nr4a3	Nuclear receptor subfamily 4, group A, member 3	95	2.025	1.486	1.386	*#†
1387267_at	Ntf3	Neurotrophin 3	93	0.526	0.522	0.655	*#†
1383614_at	Nuak2	NUAK family, SNF1-like kinase, 2	188	2.289	1.453	1.577	*#†
1370000_at	Nucb2	Nucleobindin 2	959	0.964	1.016	1.523	†
1388198_at	Nupl1	Nucleoporin like 1	41	1.755	1.249	1.198	*#†
1391749_a_at	Nxnl2	Nucleoredoxin-like 2	208	1.172	1.559	1.278	#
1368962_at	Nxph3	Neurexophilin 3	45	1.316	1.948	0.966	*#
1374818_at	Nxph3	Neurexophilin 3	101	1.456	1.852	0.903	*#
1392579_at	Obfc2a	Oligonucleotide/oligosaccharide-binding fold containing 2A	327	0.898	0.866	0.648	†
1369008_a_at	Olfm1	Olfactomedin 1	102	1.180	1.289	2.253	†
1382134_at	Olfml1	Olfactomedin-like 1	370	0.865	0.750	0.548	*#†
1383453_at	Olfml1	Olfactomedin-like 1	437	0.804	0.622	0.573	*#†
1368683_at	Olr1	Oxidized low density lipoprotein (lectin-like) receptor 1	319	2.394	2.888	2.262	*#†
1384136_at	Osbpl3	Oxysterol binding protein-like 3	172	1.313	1.569	1.062	*#

1384254_at	Otud1	OTU domain containing 1	743	4.625	2.813	1.573	*#†
1391530_a_at	Oxsm	3-oxoacyl-ACP synthase, mitochondrial	145	0.581	0.721	1.023	*#
1369673_at	P2rx5	Purinergic receptor P2X, ligand-gated ion channel, 5	55	1.402	1.672	1.244	*#
1369674_at	P2rx5	Purinergic receptor P2X, ligand-gated ion channel, 5	60	1.523	2.395	1.316	*#†
1393129_at	P4ha3	Procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide III	275	1.072	1.074	2.458	†
1389093_at	Pak1	P21 (CDKN1A)-activated kinase 1	82	1.098	1.070	1.618	†
1376924_a_at	Palmd	Palmdelphin	191	0.670	0.521	1.078	*#
1382864_at	Palmd	Palmdelphin	174	0.797	0.603	0.768	*#†
1395734_at	Palmd	Palmdelphin	164	0.708	0.633	0.826	*#
1394966_at	Pap2d	Phosphatidic acid phosphatase type 2	222	0.953	0.755	1.552	#†
1383224_at	Pard6b	Par-6 (partitioning defective 6) homolog beta (C. elegans)	155	5.334	1.707	1.007	*#
1368702_at	Pawr	PRKC, apoptosis, WT1, regulator	262	0.978	1.106	1.834	†
1384824_at	Pcdh18	Protocadherin 18	358	0.624	1.010	1.325	*†
1385229_at	Pcdh20	Protocadherin 20	52	1.569	0.993	1.622	*†
1388962_at	Pcgf2	Polycomb group ring finger 2	153	0.614	0.739	0.971	*#
1377042_at	Pcgf5	Polycomb group ring finger 5	611	1.195	1.527	1.395	*#†
1374454_at	Pcmtd2	Protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	208	0.830	0.625	0.979	#
1375916_at	Pcmtd2	Protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	445	0.828	0.666	0.790	#
1373368_at	PCOLCE2	Procollagen C-endopeptidase enhancer 2	82	1.137	1.705	1.871	#†
1392773_at	Pcsk5	Proprotein convertase subtilisin/kexin type 5	122	1.082	0.874	0.587	†
1382345_at	Pctk2	PCTAIRE protein kinase 2	407	1.981	1.471	1.167	*#†
1383326_a_at	Pdcd4	Programmed cell death 4	154	0.698	0.479	0.830	---
1383327_at	Pdcd4	Programmed cell death 4	231	0.749	0.614	0.821	*#
1383328_x_at	Pdcd4	Programmed cell death 4	322	0.756	0.636	0.759	#†
1370427_at	Pdgfa	Platelet-derived growth factor alpha polypeptide	339	1.612	1.917	1.586	*#†
1379375_at	Pdgfa	Platelet-derived growth factor alpha polypeptide	373	1.707	1.943	1.359	*#†
1370941_at	Pdgfra	Platelet derived growth factor receptor, alpha polypeptide	2234	0.671	0.819	0.609	*#†
1367892_at	Pdk2	Pyruvate dehydrogenase kinase, isozyme 2	1181	0.827	0.766	0.645	*#†
1367946_at	Pdlim1	PDZ and LIM domain 1	1439	0.996	1.031	1.535	†
1368703_at	Pdlim5	PDZ and LIM domain 5	1161	1.098	1.475	1.623	---
1372745_at	Pdlim5	PDZ and LIM domain 5	1431	1.508	1.705	1.154	*#
1370347_at	Pdlim7	PDZ and LIM domain 7	504	1.428	1.546	1.904	*#†
1371441_at	Pea15a	Phosphoprotein enriched in astrocytes 15A	800	1.082	1.268	1.548	#†
1388339_at	Pea15a	Phosphoprotein enriched in astrocytes 15A	702	1.175	1.386	1.502	#†
1371545_at	Pecam1	Platelet/endothelial cell adhesion molecule 1	214	0.971	0.940	0.612	†
1371684_at	Pelo	Pelota homolog (Drosophila)	1129	1.896	1.759	0.967	*#
1367949_at	Penk1	Proenkephalin 1	3520	1.089	1.102	0.420	†
1386961_at	Pfkm	Phosphofructokinase, muscle	913	0.853	0.781	0.602	†
1367951_at	Pgam2	Phosphoglycerate mutase 2 (muscle)	352	0.931	1.014	0.604	†
1382303_at	Phactr1	Phosphatase and actin regulator 1	114	0.863	0.658	0.685	#†
1368860_at	Phlda1	Pleckstrin homology-like domain, family A, member 1	292	2.497	1.778	1.289	*#†
1375224_at	Phlda3	Pleckstrin homology-like domain, family A, member 3	873	1.093	1.606	1.278	#†
1387271_at	Phyh	Phytanoyl-CoA 2-hydroxylase	1424	0.885	0.868	0.661	†
1393245_at	Phyh	Phytanoyl-CoA 2-hydroxylase	1096	0.895	0.829	0.635	#†
1370196_at	Pias3	Protein inhibitor of activated STAT, 3	326	0.666	0.725	0.936	*#
1388525_at	Pik3ip1	Phosphoinositide-3-kinase interacting protein 1	537	0.281	0.450	0.837	*#
1369862_at	Pim1	Pim-1 oncogene	42	1.529	1.127	0.894	*
1367725_at	Pim3	Pim-3 oncogene	585	1.585	1.186	0.908	*†
1372199_at	Pink1	PTEN induced putative kinase 1	539	0.941	0.920	0.659	†
1371600_at	Pkig	Protein kinase inhibitor, gamma	1331	1.077	1.309	1.639	#†
1385182_at	Pkp1	Plakophilin 1	90	1.199	1.541	1.583	*#†

1370445_at	Pla1a	Phospholipase A1 member A	305	1.055	1.147	1.538	†
1370202_at	Pla2g16	Phospholipase A2, group XVI	412	1.014	1.040	0.601	†
1368128_at	Pla2g2a	Phospholipase A2, group IIA (platelets, synovial fluid)	2885	0.914	0.848	0.295	†
1384558_at	Plac9	Placenta-specific 9	297	0.989	1.120	2.315	†
1387122_at	Plagl1	Pleiomorphic adenoma gene-like 1	379	1.831	2.138	0.955	*#
1387675_at	Plau	Plasminogen activator, urokinase	254	1.011	0.986	0.601	†
1398287_at	Plau	Plasminogen activator, urokinase	108	0.926	1.018	0.513	†
1387269_s_at	Plaur	Plasminogen activator, urokinase receptor	162	4.663	3.139	1.534	*#†
1367916_at	Plcd1	Phospholipase C, delta 1	343	1.351	1.629	0.980	*#†
1376137_at	Plekhb2	Pleckstrin homology domain containing, family B (evectins) member 2	351	1.198	1.536	1.120	#
1368106_at	Plk2	Polo-like kinase 2 (Drosophila)	842	1.904	1.611	1.041	*#
1372897_at	Plod2	Procollagen lysine, 2-oxoglutarate 5-dioxygenase 2	1817	1.046	1.264	1.926	#†
1369029_at	Plscr1	Phospholipid scramblase 1	126	2.334	2.075	2.072	*#†
1391435_at	Pltp	Phospholipid transfer protein	623	0.970	0.860	0.364	†
1389341_at	Plxnd1	Plexin D1	402	0.897	0.934	0.656	†
1389809_at	Pmepa1	Prostate transmembrane protein, androgen induced 1	1010	1.326	1.902	2.068	#†
1392534_at	Pmepa1	Prostate transmembrane protein, androgen induced 1	1543	1.262	1.795	2.205	#†
1384523_at	Pms1	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)	119	0.641	0.798	1.062	*#
1373312_at	Pnkd	Paroxysmal nonkinesiogenic dyskinesia	362	0.775	0.609	0.853	*#†
1370381_at	Pnrc1	Proline-rich nuclear receptor coactivator 1	1024	0.675	0.635	0.756	*#†
1368341_at	Polb	Polymerase (DNA directed), beta	289	1.232	1.531	1.070	*#
1370950_at	Ppap2b	Phosphatidic acid phosphatase type 2B	341	1.326	1.209	0.606	*
1372531_at	Ppfibp2	PTPRF interacting protein, binding protein 2 (liprin beta 2)	86	0.727	0.668	0.572	*#†
1391187_at	Ppl	Periplakin	102	2.181	3.618	0.718	*#†
1368910_at	Ppm2c	Protein phosphatase 2C, magnesium dependent, catalytic subunit	414	1.731	1.234	1.089	*#
1386971_at	Ppp1r10	Protein phosphatase 1, regulatory subunit 10	390	0.541	1.116	0.840	*
1367813_at	Ppp1r14a	Protein phosphatase 1, regulatory (inhibitor) subunit 14A	132	0.869	0.907	2.321	†
1397559_at	Ppp1r3a	Protein phosphatase 1, regulatory (inhibitor) subunit 3A	123	0.747	0.490	0.754	#
1371161_at	Ppp1r3b	Protein phosphatase 1, regulatory (inhibitor) subunit 3B	92	0.460	0.616	0.715	*#†
1384262_at	Ppp1r3b	Protein phosphatase 1, regulatory (inhibitor) subunit 3B	198	0.331	0.397	0.550	*#†
1390839_at	Pqlc3	PQ loop repeat containing 3	644	0.962	1.281	2.204	#†
1391121_at	Pragmin	Pragma of Rnd2	105	2.915	1.873	0.930	*#
1387886_at	Prelp	Proline arginine-rich end leucine-rich repeat protein	282	1.318	1.830	1.877	#†
1379369_at	Prickle1	Prickle homolog 1 (Drosophila)	859	1.089	1.313	1.512	#†
1386653_at	Prickle2	Prickle homolog 2 (Drosophila)	308	0.423	0.833	0.846	*#†
1390156_a_at	Prickle2	Prickle homolog 2 (Drosophila)	297	0.349	0.758	0.875	*
1372176_at	Prkca	Protein kinase C, alpha	129	1.166	1.602	1.173	#
1378978_a_at	Prr12	Proline rich 12	99	0.526	0.702	1.177	*#
1392593_a_at	Prr12	Proline rich 12	128	0.600	0.763	1.126	*#
1373152_at	Prss23	Protease, serine, 23	2076	1.465	1.701	1.606	*#†
1379747_at	Prss35	Protease, serine, 35	96	2.348	3.245	4.688	#†
1386073_at	Psmd14	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	214	1.189	1.098	1.538	---
1367851_at	Ptgds	Prostaglandin D2 synthase (brain)	423	0.893	0.897	0.641	†
1368014_at	Ptges	Prostaglandin E synthase	81	0.896	0.953	0.657	†
1370012_at	Ptgis	Prostaglandin I2 (prostacyclin) synthase	1407	1.049	1.355	2.168	†
1368259_at	Ptgs1	Prostaglandin-endoperoxide synthase 1	85	1.029	1.202	1.904	†
1368527_at	Ptgs2	Prostaglandin-endoperoxide synthase 2	48	4.378	2.761	1.736	*#†
1369968_at	Ptn	Pleiotrophin	1280	0.954	0.885	0.646	†
1368645_at	Ptpn1	Protein tyrosine phosphatase, non-receptor type 1	319	1.406	1.503	0.735	*#†
1369496_at	Ptpn12	Protein tyrosine phosphatase, non-receptor type 12	203	1.544	1.507	1.139	*#†
1382154_at	Ptpn12	Protein tyrosine phosphatase, non-receptor type 12	643	1.711	1.517	1.118	*#
1389362_at	Ptpn3	Protein tyrosine phosphatase, non-receptor type 3	996	0.733	0.652	1.046	*#

1370362_at	Ptprn	Protein tyrosine phosphatase, receptor type, N	624	1.300	1.634	1.339	*#†
1370214_at	Pvalb	Parvalbumin	348	0.880	1.110	0.286	†
1370177_at	PVR	Poliovirus receptor	312	3.828	2.916	1.447	*#†
1397363_at	Pvrl3	Poliovirus receptor-related 3	118	1.834	1.552	1.334	*#†
1390422_at	Pxk	PX domain containing serine/threonine kinase	282	0.640	0.811	0.926	*#
1383831_at	Qrsl1	Glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	144	0.605	0.592	0.859	*#†
1373646_at	Rab15	RAB15, member RAS oncogene family	63	1.227	1.524	1.267	*#†
1396716_at	Rab23	RAB23, member RAS oncogene family	157	1.402	1.633	1.615	*#†
1370414_at	Rab38	RAB38, member RAS oncogene family	298	0.660	0.524	0.624	*#†
1370061_at	Rab3b	RAB3B, member RAS oncogene family	193	1.036	0.907	0.532	†
1374502_at	Rab3gap2	RAB3 GTPase activating protein subunit 2	318	1.453	1.810	1.383	*#†
1377902_a_at	Rad52	RAD52 homolog (S. cerevisiae)	81	0.646	0.714	0.749	*#†
1384528_at	Rai14	Retinoic acid induced 14	109	1.601	2.470	1.825	*#†
1389263_at	Rai14	Retinoic acid induced 14	889	1.690	2.464	1.886	*#†
1367825_at	Ralgds	Ral guanine nucleotide dissociation stimulator	362	0.917	0.868	0.663	#†
1383571_at	Rapgefl1	Rap guanine nucleotide exchange factor (GEF)-like 1	88	1.303	1.660	0.814	*#
1376755_at	Rarb	Retinoic acid receptor, beta	239	0.552	0.517	0.648	*#†
1370085_at	Rasa1	RAS p21 protein activator (GTPase activating protein) 1	516	1.338	1.570	1.336	*#†
1384386_at	Rasa2	RAS p21 protein activator 2	88	1.463	1.725	1.201	*#
1370942_at	Rasa3	RAS p21 protein activator 3	497	0.847	1.097	0.541	†
1390159_at	Rasgrp3	RAS guanyl releasing protein 3 (calcium and DAG-regulated)	948	1.538	1.968	1.076	*#
1388970_at	Rasip1	Ras interacting protein 1	169	0.990	0.908	0.642	†
1383322_at	Rasl11b	RAS-like family 11 member B	837	2.225	2.693	1.804	*#†
1378484_at	Rasl12	RAS-like, family 12	156	0.485	0.606	0.952	*#
1382749_at	Rbm5	RNA binding motif protein 5	500	0.663	0.764	0.738	*#†
1395523_at	Rbmx	RNA binding motif protein, X-linked	282	0.598	0.647	0.896	*#
1388686_at	Rcan1	Regulator of calcineurin 1	2232	1.387	1.507	0.973	*#
1379714_at	rCG_43687	Hypothetical protein LOC688459	44	1.742	1.198	1.180	*#†
1381341_at	rCG_43687	Hypothetical protein LOC688459	104	4.858	1.905	1.618	*#†
1389607_at	Rcor2	REST corepressor 2	371	0.565	0.678	0.904	*#
1382179_at	Rdh14	Retinol dehydrogenase 14 (all-trans/9-cis/11-cis)	257	0.619	0.728	0.953	*#
1368238_at	Reg3b	Regenerating islet-derived 3 beta	6909	0.960	0.916	0.477	†
1371890_at	Rere	Arginine-glutamic acid dipeptide (RE) repeats	1611	0.611	0.619	0.837	*#†
1390812_a_at	Rerg	RAS-like, estrogen-regulated, growth-inhibitor	365	0.810	0.838	1.511	*#†
1372266_at	Rev3l	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)	183	0.734	0.533	0.880	#
1368080_at	Rgc32	Response gene to complement 32	150	1.559	2.035	2.301	*#†
1378802_at	RGD1303232	Phytn_dehydro and Pyr_redox domain containing protein RGD1303232	123	0.875	0.788	0.651	*#†
1391817_at	RGD1304595	Similar to RIKEN cDNA 6330416G13 gene	177	0.627	0.821	1.046	*#
1375756_at	RGD1305081	Similar to ionized calcium binding adapter molecule 2 (Iba2)	406	1.133	1.612	1.138	---
1392597_at	RGD1305081	Similar to ionized calcium binding adapter molecule 2 (Iba2)	1793	1.202	1.513	1.312	#
1371438_at	RGD1305422	Similar to mKIAA0226 protein	477	1.630	1.976	1.261	*#†
1380619_at	RGD1305537	Similar to RIKEN cDNA 3110001I22	52	1.700	1.278	1.049	*
1373321_at	RGD1306622	Similar to KIAA0954 protein	222	1.089	1.356	1.541	#†
1382235_at	RGD1306809	Similar to hypothetical protein FLJ30596	84	0.629	0.560	0.758	*#†
1377011_at	RGD1307034	Similar to hypothetical protein CG003	430	0.821	0.814	1.717	*#†
1376645_at	RGD1307396	Similar to RIKEN cDNA 6330406I15	285	2.577	2.528	1.851	*#†
1395765_at	RGD1307396	Similar to RIKEN cDNA 6330406I15	81	2.164	1.897	1.391	*#
1397848_at	RGD1307396	Similar to RIKEN cDNA 6330406I15	39	2.594	2.193	1.632	*#†
1389007_at	RGD1307524	Similar to Friedreich ataxia region gene X123	500	1.500	1.818	1.316	*#†
1374278_at	RGD1307696	Similar to dJ881L22.2 (novel protein)	380	0.878	0.660	0.661	#†
1374067_at	RGD1308127	Similar to 2700078E11Rik protein	861	1.512	1.184	1.131	*#†
1383774_at	RGD1308179	Similar to RIKEN cDNA 2010316F05	96	0.620	0.686	1.048	*#

1379367_at	RGD1308251	Similar to RIKEN cDNA 2810405K02	421	0.926	0.880	0.653	†
1376104_at	RGD1308319	Similar to KIAA0802 protein	73	1.116	1.551	1.585	#†
1376654_at	RGD1308448	Similar to RIKEN cDNA B130016O10 gene	79	0.784	0.461	0.595	#†
1390937_at	RGD1309051	Similar to chromosome 14 open reading frame 50	194	0.945	0.989	1.546	†
1383726_at	RGD1309360	Hypothetical LOC294715	59	1.572	1.645	1.406	*#†
1373262_at	RGD1309543	Similar to 2310014H01Rik protein	419	1.581	1.687	1.194	*#†
1388824_at	RGD1309707	Similar to RIKEN cDNA 4930431E10	234	1.298	1.573	1.268	*#†
1392802_at	RGD1309707	Similar to RIKEN cDNA 4930431E10	112	1.248	1.520	1.128	#
1372848_at	RGD1310269	Hypothetical LOC314472	431	0.840	0.760	0.563	*#†
1373596_at	RGD1310423	Similar to hypothetical protein FLJ31737	272	0.748	0.639	1.233	*#
1372805_at	RGD1310444	LOC363015	209	0.950	1.330	1.685	#†
1393015_at	RGD1310587	Similar to hypothetical protein FLJ14146	239	0.996	0.927	0.667	†
1377250_at	RGD1310799	Similar to RIKEN cDNA A930008G19	130	0.620	0.811	0.780	*
1382813_at	RGD1310810	Similar to RIKEN cDNA 4930444A02	310	0.656	0.624	0.967	*#
1388945_at	RGD1311307	Similar to 1300014I06Rik protein	212	2.861	2.650	1.653	*#†
1375997_at	RGD1311756	Similar to hypothetical protein FLJ20950	254	0.896	0.762	0.659	#†
1390232_at	RGD1311946	Similar to RIKEN cDNA 1810055G02	336	1.241	1.536	1.374	*#†
1390928_at	RGD1559612	Similar to tigger transposable element derived 2	140	0.413	0.719	0.818	*#†
1393004_at	RGD1559864	Similar to mKIAA1045 protein	106	1.340	2.029	1.270	#
1372403_at	RGD1560011	Similar to Nuclear membrane binding protein NUCLING	408	1.495	1.546	1.101	*#
1367495_at	RGD1560211	Similar to prefoldin 4	491	1.353	1.503	1.404	*#†
1377674_at	RGD1560612	Similar to PHF21A protein	207	0.585	0.626	0.900	*#
1383001_at	RGD1560812	RGD1560812	106	1.696	1.276	0.948	*#
1383874_at	RGD1560812	RGD1560812	157	3.044	1.584	1.126	*#
1394278_at	RGD1560812	RGD1560812	184	1.838	1.430	1.063	*#
1374874_at	RGD1561042	Similar to RIKEN cDNA 5730509K17 gene	113	0.590	0.703	1.043	*#
1373485_at	RGD1561238	Similar to ring finger protein 122 homolog	330	0.608	0.597	0.880	*#
1372293_at	RGD1562059	Similar to RIKEN cDNA 1110038F21	3569	1.046	1.038	1.934	†
1373049_at	RGD1562136	Similar to D1Ertd622e protein	171	1.956	1.502	1.266	*#†
1377867_at	RGD1562284	Similar to Glutaminyl-peptide cyclotransferase precursor (QC)	227	1.041	0.972	1.586	†
1383846_at	RGD1562846	Similar to Docking protein 5 (Downstream of tyrosine kinase 5) (Protein dok-5)	160	1.695	2.770	1.398	*#†
1396206_at	RGD1562846	Similar to Docking protein 5 (Downstream of tyrosine kinase 5) (Protein dok-5)	53	1.579	3.372	1.234	*#
1383398_at	RGD1564327	Similar to integrin alpha 8	302	0.955	0.874	1.747	†
1385354_at	RGD1564327	Similar to integrin alpha 8	143	0.907	0.907	1.647	†
1373696_at	RGD1564859	RGD1564859	229	0.716	0.620	0.717	*#†
1395064_at	RGD1564943	Similar to 4930429A08Rik protein	187	0.615	0.888	0.989	*
1376927_at	RGD1564978	Similar to LOC432779 protein	114	0.453	0.494	0.765	*#
1389639_at	RGD1565350	Similar to Shb protein	511	1.185	1.827	1.324	#
1391837_at	RGD1565705	Similar to chr2 synaptotagmin	479	1.158	1.379	1.555	*#†
1373248_at	RGD1565800	Similar to hypothetical protein FLJ20674	350	1.065	1.205	1.500	†
1376937_at	RGD1565927	Similar to 4631422O05Rik protein	348	1.327	1.623	2.065	*#†
1380287_at	RGD1566107	Similar to cAMP responsive element binding protein 5	47	3.274	1.813	1.326	*#
1371731_at	RGD1566215	Similar to Coatomer gamma-2 subunit (Gamma-2 coat protein) (Gamma-2 COP)	1823	0.969	0.942	0.448	†
1382436_at	RGD1566265	Similar to RIKEN cDNA 2610002M06	95	1.017	1.075	1.518	†
1394472_at	Rgl1	Ral guanine nucleotide dissociation stimulator,-like 1	372	0.725	0.651	0.753	*#†
1395145_at	Rgl1	Ral guanine nucleotide dissociation stimulator,-like 1	485	0.755	0.652	0.711	*#†
1368144_at	Rgs2	Regulator of G-protein signaling 2	395	3.692	2.178	2.291	*#†
1387074_at	Rgs2	Regulator of G-protein signaling 2	699	3.308	2.139	2.126	*#†
1368505_at	Rgs4	Regulator of G-protein signaling 4	371	0.515	0.621	1.828	*#†
1368506_at	Rgs4	Regulator of G-protein signaling 4	230	0.545	0.681	1.765	*#†
1389003_at	Rhobtb3	Rho-related BTB domain containing 3	335	0.792	0.638	1.027	*#
1387153_at	Ril	Reversion induced LIM gene	114	2.167	3.825	1.085	*#

1375020_at	Rin3	Ras and Rab interactor 3	160	0.943	1.610	1.175	#
1381279_at	Ripk2	Receptor-interacting serine-threonine kinase 2	232	2.481	1.548	1.570	*#†
1374545_at	Rkhd2	Ring finger and KH domain containing 2	667	1.578	1.711	1.174	*#†
1381533_at	Rnd1	Rho family GTPase 1	292	5.204	3.848	1.255	*#
1377663_at	Rnd3	Rho family GTPase 3	455	1.481	1.712	1.272	*#†
1394077_at	Rnd3	Rho family GTPase 3	577	1.379	1.555	1.447	*#†
1389525_at	Rnf149	Ring finger protein 149	680	1.195	1.290	1.512	*#†
1384416_at	Rnf168	Ring finger protein 168	87	0.652	0.804	0.904	*#
1374311_at	Rnf207	Ring finger protein 207	259	0.785	0.666	0.806	*#†
1387379_at	Rock2	Rho-associated coiled-coil containing protein kinase 2	187	1.592	1.939	1.323	*#†
1393045_at	Rock2	Rho-associated coiled-coil containing protein kinase 2	524	1.574	1.915	1.427	*#†
1393097_at	Rprd1a	Regulation of nuclear pre-mRNA domain containing 1A	51	1.555	0.953	1.217	*†
1372133_at	Rras2	Related RAS viral (r-ras) oncogene homolog 2	1216	1.577	1.780	1.130	*#
1382058_at	Rras2	Related RAS viral (r-ras) oncogene homolog 2	1093	1.436	1.644	1.197	*#
1388710_at	Rreb1	Ras responsive element binding protein 1	497	0.405	0.664	0.824	*#
1372690_at	Rtn4rl1	Reticulon 4 receptor-like 1	90	0.814	0.659	0.890	#
1393404_at	Rtn4rl1	Reticulon 4 receptor-like 1	106	0.610	0.412	0.636	*#†
1368914_at	Runx1	Runt related transcription factor 1	144	2.252	2.337	2.103	*#†
1370981_at	Rxrg	Retinoid X receptor gamma	101	0.948	0.742	0.665	#†
1386890_at	S100a10	S100 calcium binding protein A10	2469	1.639	1.824	1.295	*#†
1367661_at	S100a6	S100 calcium binding protein A6	4405	1.209	1.365	1.726	*#†
1371840_at	S1pr1	Sphingosine-1-phosphate receptor 1	1472	2.119	2.177	1.005	*#
1376150_at	S1pr3	Sphingosine-1-phosphate receptor 3	723	1.217	1.535	0.589	*#†
1379358_at	Samd4a	Sterile alpha motif domain containing 4A	91	1.552	1.687	1.167	*#†
1398620_at	Samd4a	Sterile alpha motif domain containing 4A	162	1.813	2.027	1.177	*#
1371774_at	Sat1	Spermidine/spermine N1-acetyl transferase 1	1623	1.543	1.501	1.089	*#
1388462_at	Sbk1	SH3-binding domain kinase 1	242	0.726	0.658	0.831	*#
1384707_at	Scara5	Scavenger receptor class A, member 5 (putative)	44	1.027	0.896	1.595	†
1370355_at	Scd1	Stearoyl-Coenzyme A desaturase 1	840	0.855	0.791	1.920	#†
1389367_at	Schip1	Schwannomin interacting protein 1	699	1.129	1.549	1.458	#†
1374524_at	Scly	Selenocysteine lyase	346	0.669	0.574	0.729	*#†
1367849_at	Sdc1	Syndecan 1	356	3.281	4.200	1.203	*#†
1376062_at	Sdc1	Syndecan 1	90	2.109	2.978	1.064	*#
1370166_at	Sdc2	Syndecan 2	594	1.096	1.277	1.520	#†
1382189_at	Sdc2	Syndecan 2	569	1.125	1.248	1.507	#†
1367721_at	Sdc4	Syndecan 4	1495	2.127	2.138	1.200	*#†
1376319_at	Sema3c	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	768	1.297	1.702	2.664	†
1390437_at	Sema5a	Sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	248	0.801	0.645	1.132	*#
1389353_at	Sema6d	Sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	320	0.754	0.758	0.560	#†
1394086_at	Senp7	SUMO1/sentrin specific protease 7	108	0.534	0.510	0.760	*#
1368806_at	Sepp1	Selenoprotein P, plasma, 1	1811	0.852	0.797	0.649	#†
1398986_at	Serinc3	Serine incorporator 3	1821	1.206	1.271	1.525	*#†
1368487_at	Serpinb2	Serine (or cysteine) peptidase inhibitor, clade B, member 2	30	43.389	14.690	0.950	*#
1368519_at	Serpine1	Serine (or cysteine) peptidase inhibitor, clade E, member 1	190	13.378	10.548	6.810	*#†
1392264_s_at	Serpine1	Serine (or cysteine) peptidase inhibitor, clade E, member 1	171	10.470	7.299	4.116	*#†
1372254_at	Serping1	Serine (or cysteine) peptidase inhibitor, clade G, member 1	2654	0.936	0.885	0.622	†
1372417_at	Sertad1	SERTA domain containing 1	579	1.961	1.467	0.987	*#
1375279_at	Sertad2	SERTA domain containing 2	499	1.861	1.454	1.030	*#†
1391537_at	Sertad4	SERTA domain containing 4	484	0.424	0.743	1.570	*#†
1372248_at	Sesn1	Sestrin 1	314	0.451	0.509	0.731	*#†

1395809_at	Sesn1	Sestrin 1	148	0.609	0.711	0.759	*#
1396614_at	Sfrp2	Secreted frizzled-related protein 2	639	0.955	1.074	0.637	†
1367723_a_at	Sh2b3	SH2B adaptor protein 3	407	1.222	1.522	0.931	*#
1389203_at	Sh3bp5l	SH3 binding domain protein 5 like	296	2.159	1.923	1.158	*#
1370419_a_at	Sh3kbp1	SH3-domain kinase binding protein 1	1799	0.928	0.880	0.509	#†
1387957_a_at	Sh3kbp1	SH3-domain kinase binding protein 1	2582	0.901	0.863	0.549	#†
1387408_at	Siah2	Seven in absentia 2	143	1.612	1.539	1.164	*#
1391498_at	Sin3a	SIN3 homolog A, transcription regulator (yeast)	193	0.656	0.647	0.918	*#
1384037_at	Sipa1l2	Signal-induced proliferation-associated 1 like 2	207	0.932	1.532	1.195	#
1367853_at	Slc12a2	Solute carrier family 12 (sodium/potassium/chloride transporters), member 2	407	1.547	1.505	1.251	*#
1368565_at	Slc1a3	Solute carrier family 1 (glial high affinity glutamate transporter), member 3	295	0.853	1.187	1.628	†
1370314_at	Slc20a1	Solute carrier family 20 (phosphate transporter), member 1	1291	1.520	1.427	1.218	*#†
1376165_at	Slc24a3	Solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	114	1.002	1.063	1.654	†
1398295_at	Slc29a1	Solute carrier family 29 (nucleoside transporters), member 1	235	0.863	0.980	1.762	*†
1387585_at	Slc29a2	Solute carrier family 29 (nucleoside transporters), member 2	130	1.212	1.507	1.148	#
1372326_at	Slc2a3	Solute carrier family 2 (facilitated glucose transporter), member 3	96	1.881	2.333	1.514	*#†
1387707_at	Slc2a3	Solute carrier family 2 (facilitated glucose transporter), member 3	70	1.650	1.940	1.188	*#
1367989_at	Slc2a4	Solute carrier family 2 (facilitated glucose transporter), member 4	342	0.799	0.624	0.871	*#
1369099_at	Slc30a1	Solute carrier family 30 (zinc transporter), member 1	159	1.515	0.926	1.053	*
1387942_at	Slc35e4	Solute carrier family 35, member E4	217	1.585	2.003	1.209	*#
1382076_at	Slc37a1	Solute carrier family 37 (glycerol-3-phosphate transporter), member 1	144	1.163	1.994	1.184	#
1370286_at	Slc38a2	Solute carrier family 38, member 2	1889	0.649	0.826	1.087	*#
1369074_at	Slc38a4	Solute carrier family 38, member 4	130	0.992	0.945	1.787	†
1390412_at	Slc40a1	Solute carrier family 39 (iron-regulated transporter), member 1	227	0.829	0.666	0.888	#
1379805_at	Slc41a2	Solute carrier family 41, member 2	189	1.617	1.807	1.144	*#
1384934_at	Slc41a2	Solute carrier family 41, member 2	400	1.449	1.861	1.158	*#
1384302_at	Slc6a17	Solute carrier family 6 (neurotransmitter transporter), member 17	405	0.777	0.597	0.547	#†
1368391_at	Slc7a1	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	588	1.664	1.448	1.357	*#†
1368392_at	Slc7a1	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	511	1.570	1.528	1.225	*#†
1387167_at	Slc7a1	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	68	1.295	1.617	1.385	#
1368582_at	Slc7a3	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 3	270	1.038	1.027	1.799	†
1368296_at	Slco2b1	Solute carrier organic anion transporter family, member 2b1	70	1.016	0.993	0.662	---
1377916_at	Slfn2	Schlafen 2	534	1.713	1.361	0.911	*#
1369528_at	Smad3	SMAD family member 3	71	1.253	1.578	1.022	#
1394025_at	Smad6	SMAD family member 6	200	0.434	0.944	0.905	*
1390350_at	Smap2	Small ArfGAP2	180	1.216	1.507	1.044	#
1373706_at	Smarcal1	Swi/SNF related matrix associated, actin dependent regulator of chromatin, subfamily a-like 1	207	0.625	0.727	0.779	*#†
1392965_a_at	Smoc2	SPARC related modular calcium binding 2	375	0.938	1.042	0.611	†
1377695_at	Smtnl2	Smoothelin-like 2	225	0.729	0.572	0.732	*#†
1373865_at	Snap91	Synaptosomal-associated protein 91	519	0.978	1.112	2.570	†
1381205_at	Snapc5	Small nuclear RNA activating complex, polypeptide 5	78	0.641	0.821	1.163	*
1380250_at	Sned1	Sushi, nidogen and EGF-like domains 1	379	0.946	0.846	0.203	†
1368596_at	Snf1lk	SNF1-like kinase	328	2.387	1.889	1.189	*#
1368597_at	Snf1lk	SNF1-like kinase	97	2.181	1.958	1.029	*#
1370898_at	Snn	Stannin	473	1.087	0.973	0.653	†
1371066_at	Snrk	SNF related kinase	239	0.651	0.897	0.760	*†
1386762_at	Snx18	Sorting nexin 18	153	1.341	1.515	1.087	*#
1373239_at	Snx33	Sorting nexin 33	663	0.569	0.661	0.831	*#†
1383742_at	Snx7	Sorting nexin 7	327	1.510	1.725	1.160	*#†
1379271_at	Socs5	Suppressor of cytokine signaling 5	1273	1.576	1.406	1.478	*#†
1390555_at	Socs5	Suppressor of cytokine signaling 5	1114	1.676	1.709	1.432	*#†

1387275_at	Sox11	SRY (sex determining region Y)-box 11	45	2.450	2.395	1.405	*#†
1381971_at	Sox18	SRY (sex determining region Y)-box 18	442	0.842	0.959	0.454	†
1373860_at	Sox4	SRY (sex determining region Y)-box 4	1007	0.406	0.568	0.757	*#†
1375123_at	Sox4	SRY (sex determining region Y)-box 4	686	0.339	0.518	0.741	*#†
1383137_at	Sox4	SRY (sex determining region Y)-box 4	1647	0.433	0.551	0.858	*#
1384000_at	Sox4	SRY (sex determining region Y)-box 4	187	0.525	0.679	0.882	*
1382020_at	Spag9	Sperm associated antigen 9	91	1.622	1.026	1.459	*
1397618_at	Spag9	Sperm associated antigen 9	259	1.224	1.522	1.293	#
1386865_at	Sparcl1	SPARC-like 1 (hevin)	424	0.943	0.868	0.514	†
1368254_a_at	Sphk1	Sphingosine kinase 1	1025	1.713	1.505	0.707	*#†
1374168_at	Sphkap	SPHK1 interactor, AKAP domain containing	701	0.750	0.498	0.447	*#†
1396081_at	Spire1	Spire homolog 1 (Drosophila)	106	1.342	1.706	1.092	*#
1398601_at	Spire1	Spire homolog 1 (Drosophila)	180	1.461	1.898	1.258	*#
1370847_at	Spon2	Spondin 2, extracellular matrix protein	575	0.962	0.945	0.548	†
1379380_at	Spry1	Sprouty homolog 1, antagonist of FGF signaling (Drosophila)	388	0.792	1.053	1.835	†
1374864_at	Spry2	Sprouty homolog 2 (Drosophila)	401	2.025	1.617	1.328	*#†
1373018_at	Spryd3	SPRY domain containing 3	349	1.350	1.548	1.245	*#†
1371104_at	Srebf1	Sterol regulatory element binding transcription factor 1	475	0.633	0.546	1.078	*#
1388426_at	Srebf1	Sterol regulatory element binding transcription factor 1	812	0.666	0.551	1.043	*#
1374829_at	Srf	Serum response factor (c-fos serum response element-binding transcription factor)	203	1.597	1.277	1.018	*#
1388842_at	Srf	Serum response factor (c-fos serum response element-binding transcription factor)	1199	1.756	1.506	1.003	*#
1395378_at	Srf	Serum response factor (c-fos serum response element-binding transcription factor)	97	1.768	1.557	1.046	*#
1370228_at	Srprb /// Tf	Signal recognition particle receptor, B subunit /// transferrin	91	1.011	0.972	0.605	†
1373000_at	Srpx2	Sushi-repeat-containing protein, X-linked 2	446	1.136	1.377	2.677	†
1372510_at	Srxn1	Sulfiredoxin 1 homolog (S. cerevisiae)	437	2.588	1.114	1.208	*†
1384331_at	Srxn1	Sulfiredoxin 1 homolog (S. cerevisiae)	275	2.730	1.151	1.086	*
1377595_at	Ssfa2	Sperm specific antigen 2	466	1.586	1.079	0.885	*
1369732_a_at	St3gal2	ST3 beta-galactoside alpha-2,3-sialyltransferase 2	890	1.063	1.335	1.583	#†
1373288_at	St5	Suppression of tumorigenicity 5	292	0.658	0.873	1.276	*#†
1387174_a_at	Star	Steroidogenic acute regulatory protein	53	1.078	1.072	1.631	†
1391871_at	Stard13	StAR-related lipid transfer (START) domain containing 13	238	2.585	1.470	1.087	*#
1393183_at	Stard5	StAR-related lipid transfer (START) domain containing 5	212	1.508	1.537	0.854	*#
1368835_at	Stat1	Signal transducer and activator of transcription 1	639	0.743	0.610	0.784	*#†
1372757_at	Stat1	Signal transducer and activator of transcription 1	481	0.804	0.603	0.970	*#
1373670_at	Stat2	Signal transducer and activator of transcription 2	318	0.716	0.592	0.868	*#
1396101_at	Stc1	Stanniocalcin 1	396	1.291	1.308	1.628	†
1393706_at	Steap1	Six transmembrane epithelial antigen of the prostate 1	332	1.346	1.563	1.523	*#†
1372955_at	Stk38l	Serine/threonine kinase 38 like	406	1.772	2.288	1.752	#
1371943_at	Stk40	Serine/threonine kinase 40	165	1.537	1.325	1.075	*#
1379732_at	Stx11	Syntaxin 11	186	1.780	1.506	1.419	*#†
1390489_at	Syncrip	Synaptotagmin binding, cytoplasmic RNA interacting protein	350	1.524	1.407	1.129	*#†
1371679_at	Synpo2	Synaptopodin 2	1773	1.474	1.840	1.301	#
1384160_at	Synpo2	Synaptopodin 2	831	1.507	1.986	1.279	#
1390107_at	Sytl2	Synaptotagmin-like 2	162	0.931	1.373	2.020	†
1387138_at	Tac2	Tachykinin 2	187	1.002	0.952	0.480	†
1367570_at	Tagln	Transgelin	2097	1.530	1.743	4.374	†
1388679_at	Tbc1d14	TBC1 domain family, member 14	501	0.579	0.619	0.643	*#†
1377139_at	Tbx5	T-box 5	110	0.550	0.866	1.000	*
1388782_at	Tcf21	Transcription factor 21	887	0.591	0.671	0.970	*#
1379914_at	Tcfcp2l2	Transcription factor CP2-like 2	111	0.669	0.559	0.833	*#
1367765_at	Tcn2	Transcobalamin 2	1343	0.964	0.930	0.666	†
1390819_at	Tef	Thyrotrophic embryonic factor	447	0.719	0.613	0.885	*#

1371356_at	Tenc1	Tensin like C1 domain containing phosphatase (tensin 2)	419	0.661	0.874	0.970	*
1383401_at	Tes	Testis derived transcript	305	2.047	2.488	1.939	*#†
1389409_at	Tes	Testis derived transcript	96	2.368	3.220	1.599	*#†
1385174_at	Tessp6	Testis-specific serine protease-6	63	0.993	1.061	1.536	†
1377340_at	Tfpi2	Tissue factor pathway inhibitor 2	33	2.154	1.657	1.157	*#
1376425_at	Tgfb2	Transforming growth factor, beta 2	614	1.289	1.793	1.590	---
1387172_a_at	Tgfb2	Transforming growth factor, beta 2	709	1.534	2.172	1.451	#
1388011_a_at	Tgfb2	Transforming growth factor, beta 2	579	1.415	2.146	1.455	#
1392382_at	Tgfb2	Transforming growth factor, beta 2	87	1.361	1.914	1.391	#
1367859_at	Tgfb3	Transforming growth factor, beta 3	530	1.979	2.406	2.067	*#†
1371913_at	Tgfbi	Transforming growth factor, beta induced	507	0.995	1.709	1.348	#
1369653_at	Tgfbr2	Transforming growth factor, beta receptor II	532	0.887	0.937	0.613	†
1383282_at	Thap11	THAP domain containing 11	403	0.655	0.814	1.018	*#
1368900_at	Thbd	Thrombomodulin	61	1.671	1.318	0.861	*#
1368901_at	Thbd	Thrombomodulin	55	1.844	1.310	0.778	*#†
1375951_at	Thbd	Thrombomodulin	58	1.779	1.324	0.804	*#†
1388497_at	Them2	Thioesterase superfamily member 2	693	0.878	0.794	0.648	*#†
1369652_at	Thy1	Thy-1 cell surface antigen	78	1.064	0.957	1.630	†
1389324_at	Tie1	Tyrosine kinase with immunoglobulin-like and EGF-like domains 1	210	0.994	0.968	0.661	†
1367712_at	Timp1	TIMP metallopeptidase inhibitor 1	2610	1.481	1.594	1.487	*#†
1368989_at	Timp3	TIMP metallopeptidase inhibitor 3	209	2.290	2.907	1.549	*#†
1372926_at	Timp3	TIMP metallopeptidase inhibitor 3	144	2.764	3.097	1.647	*#†
1375138_at	Timp3	TIMP metallopeptidase inhibitor 3	549	2.129	2.392	1.793	*#†
1389836_a_at	Timp3	TIMP metallopeptidase inhibitor 3	1148	2.104	2.331	1.200	*#†
1367650_at	Tinagl1	Tubulointerstitial nephritis antigen-like 1	336	1.020	1.173	1.793	†
1370940_at	Tjp2	Tight junction protein 2	215	2.002	2.144	1.190	*#†
1387495_at	Tle4	Transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	65	1.597	1.059	0.930	*
1384319_at	Tlk2	Tousled-like kinase 2	68	1.878	1.249	1.143	*
1392280_at	Tlr2	Toll-like receptor 2	287	0.803	0.865	0.580	*†
1390832_at	Tmcc3	Transmembrane and coiled-coil domain family 3	284	0.351	0.453	1.183	*#†
1393822_at	Tmcc3	Transmembrane and coiled-coil domain family 3	97	0.498	0.625	1.266	*#†
1387850_at	Tmeff1	Transmembrane protein with EGF-like and two follistatin-like domains 1	197	1.154	1.633	1.037	#
1390042_at	Tmem140	Transmembrane protein 140	186	0.699	0.622	0.619	*#†
1373204_at	Tmem176a	Transmembrane protein 176A	994	0.928	0.916	0.368	†
1368840_at	Tmem176b	Transmembrane protein 176B	2415	0.850	0.843	0.478	†
1376106_at	Tmem178	Transmembrane protein 178	381	0.792	0.647	0.390	#†
1376623_at	Tmem204	Transmembrane protein 204	157	0.763	1.045	1.547	*†
1373595_at	Tmem43	Transmembrane protein 43	882	1.466	1.741	1.290	*#†
1383314_at	Tmem51	Transmembrane protein 51	431	0.514	0.945	1.363	*†
1389583_at	Tmem82	Transmembrane protein 82	129	0.817	0.656	0.690	#†
1373309_at	Tmem86a	Transmembrane protein 86A	132	0.809	0.660	0.943	*#
1373401_at	Tnc	Tenascin C	316	4.000	4.518	2.449	*#†
1371194_at	Tnfaip6	Tumor necrosis factor alpha induced protein 6	209	2.825	0.721	0.861	*
1369407_at	Tnfrsf11b	Tumor necrosis factor receptor superfamily, member 11b	329	2.902	2.697	2.608	*#†
1371785_at	Tnfrsf12a	Tumor necrosis factor receptor superfamily, member 12a	1296	2.954	3.418	1.887	*#†
1391190_at	Tnrc6a	Trinucleotide repeat containing 6a	388	0.883	1.032	1.531	†
1376982_at	Tnrc6b	Trinucleotide repeat containing 6B	270	0.802	0.655	0.866	#
1371361_at	Tns1	Tensin 1	515	1.166	1.600	1.373	#†
1385704_at	Tns1	Tensin 1	394	1.042	1.560	1.338	#†
1388145_at	Tnxa /// Tnxb	Tenascin XA /// tenascin XB	230	0.927	0.827	0.295	†
1378572_at	Tollip	Toll interacting protein	260	1.475	1.528	0.943	*#
1380808_at	Tollip	Toll interacting protein	290	1.393	1.508	0.872	*#

1379751_at	Tox3	TOX high mobility group box family member 3	138	1.532	1.347	1.217	*
1382579_at	Tox3	TOX high mobility group box family member 3	173	1.756	1.558	1.511	*#†
1383981_at	Tp53bp2	Tumor protein p53 binding protein, 2	69	0.792	0.666	0.870	---
1370287_a_at	Tpm1	Tropomyosin 1, alpha	1023	1.549	1.636	2.628	*#†
1372219_at	Tpm2	Tropomyosin 2	2126	1.085	1.122	2.255	†
1368838_at	Tpm4	Tropomyosin 4	2240	1.294	1.496	1.637	*#†
1371653_at	Tpm4	Tropomyosin 4	3603	1.250	1.403	1.639	*#†
1383321_at	Tpst1	Tyrosylprotein sulfotransferase 1	342	0.890	0.646	1.013	#
1390077_at	Tram1	Translocation associated membrane protein 1	101	1.575	1.193	1.708	---
1370198_at	Trdn	Triadin	150	0.982	0.988	0.630	†
1371019_at	Trib1	Tribbles homolog 1 (Drosophila)	148	1.920	1.495	0.742	*#†
1385124_at	Trib2	Tribbles homolog 2 (Drosophila)	362	1.054	1.557	1.188	#
1370694_at	Trib3	Tribbles homolog 3 (Drosophila)	375	0.638	0.658	1.402	*#†
1370695_s_at	Trib3	Tribbles homolog 3 (Drosophila)	512	0.641	0.818	1.461	*#†
1385899_at	Trim16	Tripartite motif-containing 16	180	1.316	1.302	1.591	*#†
1373578_at	Trim2	Tripartite motif-containing 2	276	0.611	0.388	0.613	*#†
1375278_at	Trim2	Tripartite motif-containing 2	382	0.699	0.499	0.620	*#†
1397596_at	Trim2	Tripartite motif-containing 2	131	0.729	0.572	0.898	*#
1385252_at	Trim6	Tripartite motif-containing 6	96	0.600	0.618	0.943	*#†
1377651_at	Trio	Triple functional domain (PTPRF interacting)	164	1.520	1.901	1.255	*#
1390709_at	Trio	Triple functional domain (PTPRF interacting)	437	1.166	1.696	1.308	*#†
1392972_at	Trio	Triple functional domain (PTPRF interacting)	583	1.325	1.934	1.142	*#
1370139_a_at	Trpc6	Transient receptor potential cation channel, subfamily C, member 6	38	1.587	1.979	2.730	*#†
1382171_at	Tsc22d2	TSC22 domain family, member 2	403	2.490	1.522	1.275	*#
1371550_at	Tsc22d4	TSC22 domain family, member 4	1423	0.885	0.904	0.666	*#†
1377089_a_at	Tspan5	Tetraspanin 5	263	2.610	3.238	1.173	*#
1380725_at	Tspan5	Tetraspanin 5	86	3.007	4.244	1.393	*#†
1394316_a_at	Tspan5	Tetraspanin 5	183	2.365	2.844	1.245	*#†
1372286_at	Tspan6	Tetraspanin 6	1677	1.022	1.071	1.538	†
1371702_at	Tspan7	Tetraspanin 7	1216	0.952	0.943	0.623	†
1370881_at	Tst	Thiosulfate sulfurtransferase, mitochondrial	594	0.941	0.896	0.657	†
1392531_at	Ttpal	Tocopherol (alpha) transfer protein-like	286	1.598	1.499	1.147	*#
1371618_s_at	Tubb3	Tubulin, beta 3	208	0.890	0.841	1.935	†
1376100_at	Tubb6	Tubulin, beta 6	2257	1.624	1.804	1.207	*#†
1378165_at	Twist1	Twist homolog 1 (Drosophila)	162	2.603	1.754	1.455	*#†
1387750_at	Twist1	Twist homolog 1 (Drosophila)	82	2.203	1.708	1.185	*#
1375221_at	Txndc13	Thioredoxin domain containing 13	2013	1.018	1.115	1.500	†
1397194_at	Txndc13	Thioredoxin domain containing 13	235	1.093	1.360	1.515	---
1379910_at	Uap1	UDP-N-acteylglucosamine pyrophosphorylase 1	337	5.311	4.011	2.037	*#†
1388387_at	Ubac1	UBA domain containing 1	623	0.711	0.661	0.761	*#†
1379284_at	Ubash3b	Ubiquitin associated and SH3 domain containing, B	51	1.212	1.769	1.145	#
1393126_at	Ubtd1	Ubiquitin domain containing 1	422	1.272	1.576	1.108	*#
1383945_at	Uck2	Uridine-cytidine kinase 2	427	1.573	1.927	1.507	*#†
1387975_at	Ugcg	UDP-glucose ceramide glucosyltransferase	273	1.731	1.746	1.006	*#
1367938_at	Ugdh	UDP-glucose dehydrogenase	1394	1.601	1.686	1.390	*#†
1375869_at	Ulk1	Unc-51 like kinase 1 (C. elegans)	424	0.708	0.498	0.861	*#
1382402_at	Ulk1	Unc-51 like kinase 1 (C. elegans)	269	0.800	0.645	0.896	*#
1369235_at	Unc5b	Unc-5 homolog B (C. elegans)	632	0.852	1.422	1.594	#†
1370141_at	Unknown	Unknown	1195	1.566	1.489	1.087	*#
1371450_at	Unknown	Unknown	123	1.340	1.527	1.240	*#
1371595_at	Unknown	Unknown	1235	1.745	1.271	1.234	*
1371699_at	Unknown	Unknown	547	1.728	2.342	1.277	*#†

1371795_at	Unknown	Unknown	542	0.680	0.635	0.854	*#
1371864_at	Unknown	Unknown	827	1.530	1.151	1.292	*#†
1371969_at	Unknown	Unknown	1295	1.240	1.281	2.483	*#†
1372060_at	Unknown	Unknown	198	0.516	0.643	0.893	*#
1372095_at	Unknown	Unknown	176	0.705	0.616	0.592	*#†
1372347_at	Unknown	Unknown	831	1.245	1.455	1.639	*#†
1372371_at	Unknown	Unknown	537	1.369	1.576	1.263	*#†
1372414_at	Unknown	Unknown	620	0.585	0.822	0.924	*#
1372479_at	Unknown	Unknown	150	1.002	0.766	0.645	#†
1372583_at	Unknown	Unknown	179	0.758	0.884	2.892	*†
1372681_at	Unknown	Unknown	368	0.870	0.555	1.034	#
1372696_at	Unknown	Unknown	189	0.570	0.841	0.880	*
1372722_at	Unknown	Unknown	908	1.621	1.740	1.398	*#†
1372750_at	Unknown	Unknown	140	6.918	4.951	4.013	*#†
1372761_at	Unknown	Unknown	88	0.964	0.948	0.562	†
1372889_at	Unknown	Unknown	131	1.015	1.283	1.594	†
1372957_at	Unknown	Unknown	202	0.638	0.766	0.939	*
1372964_at	Unknown	Unknown	662	1.775	1.333	1.337	*#†
1373092_at	Unknown	Unknown	1428	0.689	0.558	0.655	*#†
1373165_at	Unknown	Unknown	101	0.777	0.628	1.090	#
1373178_at	Unknown	Unknown	441	0.517	0.417	0.509	*#†
1373298_at	Unknown	Unknown	76	1.237	1.904	0.898	*#
1373478_at	Unknown	Unknown	105	0.747	0.611	0.773	#
1373487_at	Unknown	Unknown	501	0.945	0.843	0.643	†
1373525_at	Unknown	Unknown	229	1.821	1.287	1.155	*#
1373558_at	Unknown	Unknown	92	0.915	1.226	1.675	†
1373624_at	Unknown	Unknown	506	1.829	1.866	1.889	*#†
1373628_at	Unknown	Unknown	255	1.174	1.124	5.775	†
1373651_at	Unknown	Unknown	138	1.496	1.802	1.561	*#†
1373680_at	Unknown	Unknown	251	2.869	1.880	1.138	*#
1373691_at	Unknown	Unknown	163	0.665	0.691	0.822	*#†
1373699_at	Unknown	Unknown	257	0.877	0.889	0.150	†
1373751_at	Unknown	Unknown	121	0.485	0.670	1.038	*#
1373759_at	Unknown	Unknown	27	2.536	1.047	1.076	*
1373776_at	Unknown	Unknown	150	0.577	0.826	1.164	*
1374023_at	Unknown	Unknown	289	0.627	0.807	0.958	*#
1374030_at	Unknown	Unknown	295	0.936	0.658	0.911	#
1374038_at	Unknown	Unknown	517	0.819	0.644	0.753	*#†
1374060_at	Unknown	Unknown	688	0.636	0.870	1.037	*
1374166_at	Unknown	Unknown	383	1.514	1.815	1.149	---
1374172_at	Unknown	Unknown	100	0.788	0.878	3.307	†
1374276_at	Unknown	Unknown	182	1.535	2.185	1.337	#
1374298_at	Unknown	Unknown	82	0.698	0.543	0.648	*#†
1374325_at	Unknown	Unknown	416	0.955	1.103	1.549	†
1374350_at	Unknown	Unknown	290	0.781	0.652	0.710	*#†
1374410_at	Unknown	Unknown	80	1.234	1.706	1.541	#†
1374493_at	Unknown	Unknown	169	0.537	0.680	0.736	*#†
1374514_at	Unknown	Unknown	349	1.533	0.949	0.922	*
1374529_at	Unknown	Unknown	3100	2.885	2.371	2.020	*#†
1374609_at	Unknown	Unknown	493	1.365	1.646	1.192	*#†
1374610_at	Unknown	Unknown	165	5.234	3.783	1.171	*#
1374627_at	Unknown	Unknown	152	0.535	0.755	0.835	*#†

1374685_at	Unknown	Unknown	343	0.783	0.647	0.993	*#
1374702_at	Unknown	Unknown	540	1.701	1.663	1.363	*#†
1374710_at	Unknown	Unknown	1054	1.560	1.927	1.115	*#
1374742_at	Unknown	Unknown	381	1.324	1.762	1.264	*#†
1374868_at	Unknown	Unknown	51	0.885	0.936	1.552	†
1374893_at	Unknown	Unknown	469	1.437	1.626	1.260	*#†
1374934_at	Unknown	Unknown	161	0.928	0.754	0.368	†
1375184_at	Unknown	Unknown	129	2.857	3.974	1.524	*#†
1375199_at	Unknown	Unknown	135	1.073	1.522	1.302	#†
1375223_at	Unknown	Unknown	208	0.831	0.561	0.555	#†
1375532_at	Unknown	Unknown	1079	0.656	0.964	0.797	---
1375561_at	Unknown	Unknown	298	1.534	1.016	0.995	*
1375658_at	Unknown	Unknown	850	0.612	0.706	0.863	*#†
1375667_at	Unknown	Unknown	113	0.653	0.752	0.776	*#†
1375886_at	Unknown	Unknown	121	0.580	0.643	0.934	*#
1375925_at	Unknown	Unknown	144	1.404	2.130	1.278	*#
1375986_at	Unknown	Unknown	56	1.506	1.407	1.101	*#
1376045_at	Unknown	Unknown	782	0.912	0.937	1.522	†
1376071_at	Unknown	Unknown	691	1.275	1.357	1.612	*#†
1376109_at	Unknown	Unknown	262	1.234	1.743	1.405	*#†
1376152_at	Unknown	Unknown	348	1.073	1.739	1.435	#†
1376178_at	Unknown	Unknown	66	0.645	0.724	1.028	*#
1376267_at	Unknown	Unknown	69	1.770	1.550	0.758	---
1376282_at	Unknown	Unknown	550	1.207	1.837	1.749	#†
1376435_at	Unknown	Unknown	80	1.865	2.882	1.089	*#
1376513_a_at	Unknown	Unknown	300	1.709	1.958	1.716	*#†
1376522_at	Unknown	Unknown	95	0.654	0.841	0.824	*
1376574_at	Unknown	Unknown	639	1.022	1.021	0.596	†
1376593_at	Unknown	Unknown	893	0.471	0.798	0.883	*#†
1376617_at	Unknown	Unknown	273	0.728	0.598	0.738	*#†
1376624_at	Unknown	Unknown	190	0.983	0.800	0.516	†
1376672_at	Unknown	Unknown	212	0.455	0.553	0.838	*#
1376734_at	Unknown	Unknown	298	1.104	1.247	2.894	#†
1376848_at	Unknown	Unknown	304	2.335	2.127	1.469	*#†
1376869_at	Unknown	Unknown	223	1.654	1.097	0.994	*
1376891_at	Unknown	Unknown	369	0.697	0.638	0.658	*#†
1376907_at	Unknown	Unknown	499	1.388	1.762	1.348	*#†
1376946_at	Unknown	Unknown	186	0.609	0.663	1.191	*#
1377032_at	Unknown	Unknown	116	0.761	0.596	0.926	*#
1377092_at	Unknown	Unknown	794	1.149	0.545	0.707	#†
1377113_at	Unknown	Unknown	50	1.506	1.881	1.269	*#†
1377151_at	Unknown	Unknown	282	1.549	2.460	1.144	*#
1377240_at	Unknown	Unknown	107	0.952	1.497	2.070	#†
1377263_at	Unknown	Unknown	258	1.332	1.486	1.503	*#†
1377328_at	Unknown	Unknown	207	0.616	0.414	0.752	*#†
1377452_at	Unknown	Unknown	154	1.050	0.898	0.666	†
1377517_at	Unknown	Unknown	81	0.665	0.745	1.043	*#
1377673_at	Unknown	Unknown	244	0.809	0.697	0.658	*#†
1377705_at	Unknown	Unknown	1469	1.044	1.133	2.117	†
1377706_x_at	Unknown	Unknown	1283	1.031	1.124	2.371	†
1377789_at	Unknown	Unknown	55	0.963	1.468	1.759	#†
1377795_at	Unknown	Unknown	601	0.820	0.620	0.778	*#†

1377799_at	Unknown	Unknown	51	1.326	1.511	1.062	*#
1377823_at	Unknown	Unknown	130	1.410	1.625	1.107	*#
1377994_at	Unknown	Unknown	101	1.322	1.301	2.584	†
1378009_at	Unknown	Unknown	220	1.229	1.250	1.508	---
1378074_at	Unknown	Unknown	140	0.604	0.501	0.828	*#†
1378093_at	Unknown	Unknown	142	1.017	1.023	1.580	†
1378098_at	Unknown	Unknown	330	1.511	1.528	1.206	*#
1378109_at	Unknown	Unknown	111	0.850	0.641	0.744	#
1378113_at	Unknown	Unknown	337	1.797	1.643	1.431	*#†
1378171_at	Unknown	Unknown	333	1.073	0.961	1.882	†
1378205_at	Unknown	Unknown	157	1.026	0.852	0.644	†
1378241_at	Unknown	Unknown	299	0.615	0.744	0.937	*#
1378311_at	Unknown	Unknown	1070	1.385	1.560	1.038	*#
1378413_at	Unknown	Unknown	541	0.749	0.552	0.590	*#†
1378447_at	Unknown	Unknown	35	2.969	1.424	1.190	*#
1378467_at	Unknown	Unknown	89	1.041	1.301	1.540	#†
1378556_at	Unknown	Unknown	555	1.149	1.193	2.273	*#†
1378754_at	Unknown	Unknown	119	3.666	3.112	1.307	*#
1378808_at	Unknown	Unknown	153	0.350	0.466	0.886	*#
1378927_at	Unknown	Unknown	570	0.610	0.494	0.911	*#
1379089_at	Unknown	Unknown	92	1.515	1.367	1.444	*#†
1379236_at	Unknown	Unknown	133	1.062	1.506	1.058	#
1379252_at	Unknown	Unknown	145	0.900	0.982	2.324	†
1379310_at	Unknown	Unknown	127	1.532	1.426	1.288	*#†
1379534_at	Unknown	Unknown	137	0.751	0.525	0.754	#
1379573_at	Unknown	Unknown	44	1.621	1.570	0.951	*#
1379598_at	Unknown	Unknown	239	1.037	1.614	2.395	#†
1379605_at	Unknown	Unknown	113	0.634	0.491	1.047	*#
1379629_at	Unknown	Unknown	64	1.805	1.343	1.177	*#†
1379662_a_at	Unknown	Unknown	677	0.644	0.861	0.806	*†
1379666_at	Unknown	Unknown	155	1.701	1.170	1.313	*†
1379739_at	Unknown	Unknown	151	1.739	1.068	1.096	*
1379768_at	Unknown	Unknown	355	0.723	0.552	0.630	*#†
1379785_at	Unknown	Unknown	316	1.134	1.062	1.520	†
1379799_at	Unknown	Unknown	292	0.526	0.776	2.249	*†
1379912_at	Unknown	Unknown	81	1.686	1.188	1.239	*#†
1379934_at	Unknown	Unknown	168	1.219	1.835	1.039	#
1379996_at	Unknown	Unknown	89	0.989	0.880	1.548	†
1380057_at	Unknown	Unknown	357	0.743	0.472	0.765	*#†
1380143_at	Unknown	Unknown	195	1.576	1.345	1.306	---
1380195_at	Unknown	Unknown	110	1.538	0.965	1.012	*
1380306_at	Unknown	Unknown	45	1.577	1.023	0.972	*
1380318_at	Unknown	Unknown	288	1.065	1.028	1.722	†
1380376_at	Unknown	Unknown	89	0.786	0.654	1.020	*#
1380410_at	Unknown	Unknown	357	1.309	1.180	1.870	†
1380494_at	Unknown	Unknown	446	0.970	0.941	0.611	†
1380544_at	Unknown	Unknown	335	1.171	1.430	1.643	#†
1380741_at	Unknown	Unknown	238	0.822	0.644	1.119	*#†
1380831_at	Unknown	Unknown	82	1.640	1.915	1.521	*#†
1380855_at	Unknown	Unknown	282	0.665	0.972	0.898	*
1381016_at	Unknown	Unknown	218	1.711	1.296	1.056	*#
1381100_at	Unknown	Unknown	388	1.235	1.145	0.661	†

1381127_at	Unknown	Unknown	47	1.432	1.606	1.209	*#
1381269_at	Unknown	Unknown	111	0.577	0.488	1.126	*#
1381334_at	Unknown	Unknown	67	1.376	1.559	1.043	*#
1381461_at	Unknown	Unknown	245	1.586	1.415	0.926	*#
1382017_at	Unknown	Unknown	188	1.557	1.805	1.591	*#†
1382050_at	Unknown	Unknown	183	0.964	0.882	1.571	†
1382054_at	Unknown	Unknown	112	1.513	1.655	2.564	*#†
1382108_at	Unknown	Unknown	249	0.490	0.383	0.460	*#†
1382199_at	Unknown	Unknown	493	0.599	0.836	0.891	*
1382225_at	Unknown	Unknown	296	1.498	1.571	1.058	*#
1382291_at	Unknown	Unknown	183	1.693	1.423	0.914	*#
1382294_at	Unknown	Unknown	81	1.235	1.546	1.275	#
1382296_at	Unknown	Unknown	117	0.734	0.661	1.498	*#†
1382375_at	Unknown	Unknown	263	0.851	0.884	0.660	*†
1382431_at	Unknown	Unknown	388	0.607	0.501	0.714	*#†
1382438_at	Unknown	Unknown	69	0.729	0.512	0.677	*#†
1382482_at	Unknown	Unknown	144	1.240	1.560	0.906	*#
1382512_at	Unknown	Unknown	319	1.482	1.708	1.479	*#†
1382567_at	Unknown	Unknown	145	1.406	1.519	1.455	*#†
1382599_at	Unknown	Unknown	702	0.738	0.635	0.636	*#†
1382603_at	Unknown	Unknown	81	1.506	1.243	0.744	*#†
1382631_at	Unknown	Unknown	93	1.279	1.707	1.432	#
1382682_at	Unknown	Unknown	149	1.584	1.967	1.201	*#
1382705_at	Unknown	Unknown	90	0.748	0.665	0.971	---
1382746_s_at	Unknown	Unknown	118	0.811	0.538	0.943	*#
1382835_at	Unknown	Unknown	310	0.783	0.654	0.826	#
1382882_x_at	Unknown	Unknown	36	2.186	1.749	1.522	*#†
1382914_at	Unknown	Unknown	215	0.915	1.350	1.952	#†
1382950_at	Unknown	Unknown	215	0.833	0.633	0.586	#†
1382995_at	Unknown	Unknown	235	0.982	1.096	2.071	†
1383058_at	Unknown	Unknown	875	0.560	0.545	0.971	*#
1383063_a_at	Unknown	Unknown	973	0.839	0.640	1.001	#
1383169_at	Unknown	Unknown	654	0.395	0.355	0.378	*#†
1383173_at	Unknown	Unknown	608	0.817	0.608	0.914	*#
1383185_at	Unknown	Unknown	59	1.104	1.542	1.417	#†
1383194_a_at	Unknown	Unknown	180	0.900	0.623	0.915	#
1383210_at	Unknown	Unknown	66	3.094	2.399	1.261	*#
1383222_at	Unknown	Unknown	391	2.626	1.691	1.133	*#
1383228_at	Unknown	Unknown	144	1.062	1.512	1.013	#
1383240_at	Unknown	Unknown	300	1.392	1.809	1.339	*#†
1383253_at	Unknown	Unknown	368	1.619	0.975	0.978	*
1383299_at	Unknown	Unknown	262	1.383	2.128	1.660	#†
1383353_at	Unknown	Unknown	323	1.864	1.891	2.001	*#†
1383486_at	Unknown	Unknown	187	7.522	6.700	5.937	*#†
1383527_at	Unknown	Unknown	42	1.718	1.666	0.877	*#
1383533_at	Unknown	Unknown	265	0.627	0.793	0.968	*#
1383557_at	Unknown	Unknown	146	1.471	1.354	1.879	†
1383565_at	Unknown	Unknown	27	1.000	3.075	0.981	#
1383589_at	Unknown	Unknown	520	0.477	0.537	0.797	*#†
1383632_at	Unknown	Unknown	311	1.692	0.911	0.969	*
1383688_at	Unknown	Unknown	351	0.645	0.668	0.875	*#
1383744_at	Unknown	Unknown	950	1.248	1.510	1.334	*#†

1383757_at	Unknown	Unknown	166	0.541	0.474	0.951	*#
1383784_at	Unknown	Unknown	152	0.763	0.652	0.846	*#†
1383852_at	Unknown	Unknown	147	1.148	1.643	1.148	#
1383939_at	Unknown	Unknown	574	1.486	1.706	1.521	*#†
1383987_at	Unknown	Unknown	272	1.484	1.726	1.400	#
1384051_at	Unknown	Unknown	208	1.263	1.999	3.875	#†
1384081_at	Unknown	Unknown	50	1.341	1.988	1.393	#
1384135_at	Unknown	Unknown	193	0.569	0.733	0.964	*#
1384228_at	Unknown	Unknown	193	1.495	1.387	1.525	*#†
1384286_at	Unknown	Unknown	124	1.029	1.074	1.815	†
1384449_at	Unknown	Unknown	329	1.196	1.108	1.539	†
1384508_at	Unknown	Unknown	87	0.696	0.646	0.968	*#
1384605_at	Unknown	Unknown	581	1.203	1.599	1.314	#†
1384709_at	Unknown	Unknown	79	1.686	1.745	2.390	*#†
1384724_at	Unknown	Unknown	269	0.802	0.653	1.292	*#†
1384743_at	Unknown	Unknown	117	1.518	1.380	2.121	*†
1384841_at	Unknown	Unknown	202	0.630	0.379	0.395	*#†
1384882_at	Unknown	Unknown	214	1.693	1.441	1.327	*#†
1384899_at	Unknown	Unknown	113	1.795	1.032	1.222	*
1384901_at	Unknown	Unknown	89	1.510	1.065	0.794	*
1384916_at	Unknown	Unknown	169	0.663	0.678	1.043	*#
1385029_at	Unknown	Unknown	313	1.110	1.005	1.503	†
1385053_at	Unknown	Unknown	136	0.894	0.456	0.811	#
1385082_at	Unknown	Unknown	143	0.814	0.412	0.809	#
1385110_at	Unknown	Unknown	71	1.516	1.235	1.116	*
1385132_at	Unknown	Unknown	75	1.397	3.387	2.267	#†
1385138_at	Unknown	Unknown	497	0.752	0.578	0.918	*#
1385166_at	Unknown	Unknown	45	1.149	1.565	1.076	#
1385180_at	Unknown	Unknown	68	1.782	1.252	0.934	*#
1385243_at	Unknown	Unknown	542	0.793	0.759	0.520	†
1385393_at	Unknown	Unknown	125	0.511	0.551	1.110	*#
1385505_at	Unknown	Unknown	90	0.791	0.530	0.685	#†
1385569_at	Unknown	Unknown	120	1.793	1.734	1.258	*#
1385641_at	Unknown	Unknown	187	1.829	1.023	0.609	*†
1385798_at	Unknown	Unknown	49	0.925	1.156	1.725	†
1385869_at	Unknown	Unknown	225	1.693	1.333	1.167	*#†
1385924_at	Unknown	Unknown	80	0.689	0.662	0.903	*#
1385925_at	Unknown	Unknown	491	1.239	1.511	1.497	#†
1385926_at	Unknown	Unknown	239	1.225	1.143	1.857	†
1386026_at	Unknown	Unknown	75	0.736	0.646	0.807	*#
1388742_at	Unknown	Unknown	525	0.574	0.418	0.469	*#†
1388786_at	Unknown	Unknown	844	0.471	0.879	1.229	*†
1388804_at	Unknown	Unknown	148	0.541	0.830	1.422	*#†
1388825_at	Unknown	Unknown	328	0.915	1.623	1.179	#†
1388880_at	Unknown	Unknown	522	0.746	0.619	0.644	*#†
1388986_at	Unknown	Unknown	726	1.702	1.500	1.539	*#†
1389039_at	Unknown	Unknown	290	0.904	0.927	1.885	†
1389082_at	Unknown	Unknown	197	0.807	0.647	0.925	#
1389159_at	Unknown	Unknown	209	0.867	0.581	0.989	#
1389186_at	Unknown	Unknown	393	0.820	0.922	0.656	*†
1389206_at	Unknown	Unknown	59	1.232	1.865	0.908	*#
1389230_at	Unknown	Unknown	1069	0.651	0.545	0.721	*#†

1389256_at	Unknown	Unknown	420	0.782	0.630	0.917	*#
1389284_at	Unknown	Unknown	236	0.918	0.636	0.580	#†
1389394_at	Unknown	Unknown	1149	1.027	1.168	1.746	†
1389419_at	Unknown	Unknown	160	0.470	0.691	0.997	*#
1389460_at	Unknown	Unknown	103	0.437	0.565	0.956	*#
1389465_at	Unknown	Unknown	397	1.392	1.506	1.071	*#
1389500_at	Unknown	Unknown	374	0.833	0.842	0.422	†
1389554_at	Unknown	Unknown	302	0.599	0.827	1.154	*
1389586_at	Unknown	Unknown	354	1.134	1.341	1.865	#†
1389612_at	Unknown	Unknown	78	0.889	0.651	0.790	#
1389618_at	Unknown	Unknown	673	0.347	0.415	0.691	*#†
1389700_at	Unknown	Unknown	146	2.001	1.902	1.165	*#
1389707_at	Unknown	Unknown	128	0.955	1.507	1.210	#
1389726_at	Unknown	Unknown	122	0.660	0.729	0.836	*#
1389748_at	Unknown	Unknown	288	0.625	0.617	0.831	*#
1389761_at	Unknown	Unknown	76	1.653	1.094	1.230	*
1389986_at	Unknown	Unknown	745	1.234	1.075	0.576	†
1390109_at	Unknown	Unknown	985	0.591	0.641	1.174	*#
1390136_at	Unknown	Unknown	110	1.447	2.094	1.165	*#
1390364_at	Unknown	Unknown	98	1.732	1.857	1.874	*#†
1390427_at	Unknown	Unknown	105	0.617	0.635	1.052	*#
1390430_at	Unknown	Unknown	320	0.648	0.586	1.109	*#
1390436_at	Unknown	Unknown	680	1.354	1.352	0.566	*#†
1390457_at	Unknown	Unknown	81	0.887	0.661	0.926	#
1390508_at	Unknown	Unknown	319	0.768	0.632	0.871	*#†
1390515_at	Unknown	Unknown	242	1.407	2.095	1.217	*#
1390536_at	Unknown	Unknown	542	0.600	0.692	0.743	*#†
1390645_at	Unknown	Unknown	85	1.142	1.627	1.071	#
1390659_at	Unknown	Unknown	454	3.179	3.321	1.709	*#†
1390902_at	Unknown	Unknown	77	1.357	1.802	1.125	*#
1390969_at	Unknown	Unknown	883	0.353	0.509	1.136	*#
1391071_at	Unknown	Unknown	35	1.054	1.124	1.844	†
1391171_at	Unknown	Unknown	92	0.969	0.864	0.655	†
1391256_at	Unknown	Unknown	107	1.353	1.370	1.616	†
1391418_at	Unknown	Unknown	104	1.344	1.418	1.605	*#†
1391428_at	Unknown	Unknown	140	0.725	0.514	1.801	*#†
1391447_at	Unknown	Unknown	185	0.695	0.645	0.853	*#
1391460_at	Unknown	Unknown	618	0.730	0.659	0.932	*#
1391466_at	Unknown	Unknown	95	1.070	1.047	1.618	†
1391551_at	Unknown	Unknown	106	1.049	1.028	1.528	†
1391553_at	Unknown	Unknown	304	0.667	0.496	1.002	*#
1391643_at	Unknown	Unknown	360	1.606	1.205	0.736	*#†
1391744_at	Unknown	Unknown	82	0.625	0.728	0.956	*
1391753_at	Unknown	Unknown	247	2.134	2.283	1.401	*#
1391812_at	Unknown	Unknown	174	0.865	0.910	0.313	†
1391939_at	Unknown	Unknown	151	1.708	1.377	1.095	*#
1392492_at	Unknown	Unknown	377	1.060	1.511	1.146	#
1392501_at	Unknown	Unknown	117	0.885	0.565	0.741	#†
1392566_at	Unknown	Unknown	186	0.907	0.866	0.573	---
1392618_at	Unknown	Unknown	501	1.127	1.826	1.409	#†
1392627_x_at	Unknown	Unknown	1143	0.945	1.011	2.153	†
1392791_at	Unknown	Unknown	37	12.431	1.693	1.145	*#

1392842_at	Unknown	Unknown	307	0.774	0.656	0.668	*#†
1392893_a_at	Unknown	Unknown	122	0.733	0.702	0.633	*†
1392933_a_at	Unknown	Unknown	65	0.704	0.622	0.748	*#†
1392935_at	Unknown	Unknown	349	0.542	0.719	1.609	*#†
1393003_at	Unknown	Unknown	326	1.408	2.134	1.450	*#†
1393119_at	Unknown	Unknown	469	1.783	1.538	1.704	*#†
1393120_at	Unknown	Unknown	208	0.653	0.744	1.009	*#
1393262_at	Unknown	Unknown	202	0.448	0.710	0.733	*#†
1393302_at	Unknown	Unknown	107	0.966	0.751	0.646	†
1393492_at	Unknown	Unknown	133	1.061	1.529	1.529	#†
1393494_at	Unknown	Unknown	98	1.745	1.650	1.492	*#†
1393516_at	Unknown	Unknown	122	0.840	0.650	0.979	#
1393522_at	Unknown	Unknown	291	1.526	1.922	1.216	*#
1393559_at	Unknown	Unknown	319	1.391	1.212	1.717	---
1393648_at	Unknown	Unknown	56	2.023	1.404	1.024	*#
1393653_at	Unknown	Unknown	222	0.936	0.970	2.313	†
1393728_at	Unknown	Unknown	102	3.375	1.954	1.702	*#†
1393743_at	Unknown	Unknown	313	0.439	0.452	0.990	*#
1393782_at	Unknown	Unknown	51	1.564	1.102	0.950	*#
1393793_at	Unknown	Unknown	339	0.503	0.560	0.718	*#
1393860_at	Unknown	Unknown	203	1.414	1.929	1.282	*#†
1393883_at	Unknown	Unknown	123	1.100	1.276	1.761	†
1394047_at	Unknown	Unknown	89	1.189	1.599	0.975	#
1394109_at	Unknown	Unknown	1102	5.554	4.044	2.774	*#†
1394456_at	Unknown	Unknown	198	0.791	0.622	0.860	#
1394517_at	Unknown	Unknown	572	0.563	0.516	0.937	*#
1394527_at	Unknown	Unknown	71	1.593	1.284	1.092	*
1394727_at	Unknown	Unknown	36	1.039	1.113	1.508	†
1394907_at	Unknown	Unknown	271	0.621	1.048	1.214	*
1394932_at	Unknown	Unknown	291	1.327	1.510	0.937	*#
1394948_at	Unknown	Unknown	383	0.650	0.570	0.697	*#†
1395119_at	Unknown	Unknown	138	2.410	3.446	1.101	*#
1395197_at	Unknown	Unknown	164	1.274	1.599	1.054	*#
1395350_at	Unknown	Unknown	80	1.582	1.607	1.166	*#
1395355_at	Unknown	Unknown	136	1.499	1.593	1.054	*#
1395362_at	Unknown	Unknown	540	0.984	1.357	1.517	#†
1395442_at	Unknown	Unknown	61	1.533	1.983	1.993	*#†
1395518_at	Unknown	Unknown	458	0.538	0.593	0.985	*#
1395557_at	Unknown	Unknown	238	1.960	1.850	1.754	*#†
1395615_at	Unknown	Unknown	65	1.916	2.270	1.416	*#†
1395704_at	Unknown	Unknown	96	0.869	0.664	0.975	#
1395814_at	Unknown	Unknown	131	1.712	2.001	0.924	*#
1396057_at	Unknown	Unknown	163	0.780	0.577	1.033	#
1396263_at	Unknown	Unknown	209	1.119	1.673	1.273	#†
1396539_at	Unknown	Unknown	79	2.009	1.664	1.518	*#†
1396799_at	Unknown	Unknown	57	0.957	1.099	1.521	†
1397164_at	Unknown	Unknown	412	1.792	1.329	1.153	*#
1397204_s_at	Unknown	Unknown	63	0.928	1.096	1.553	---
1397215_at	Unknown	Unknown	75	1.593	1.061	0.958	*
1397300_at	Unknown	Unknown	318	0.799	0.663	0.785	*#†
1397449_at	Unknown	Unknown	49	1.378	1.545	1.000	#
1397470_at	Unknown	Unknown	176	0.673	0.476	0.965	*#

1397540_at	Unknown	Unknown	454	0.627	0.476	0.663	*#†
1397766_at	Unknown	Unknown	54	6.323	1.797	1.502	*#†
1397808_at	Unknown	Unknown	963	0.554	0.298	0.417	*#†
1397851_at	Unknown	Unknown	261	1.196	1.525	1.256	#
1397897_x_at	Unknown	Unknown	153	1.042	1.235	1.577	†
1397944_at	Unknown	Unknown	104	1.517	1.986	1.347	*#†
1398348_at	Unknown	Unknown	818	1.045	1.201	1.942	†
1398394_at	Unknown	Unknown	50	1.704	1.386	0.883	*#
1398493_at	Unknown	Unknown	193	0.690	0.660	0.897	---
1398597_at	Unknown	Unknown	194	0.591	0.820	1.493	*#†
1398727_at	Unknown	Unknown	442	0.691	0.468	0.684	*#†
1399071_at	Unknown	Unknown	569	1.836	1.438	1.186	*#†
1399113_at	Unknown	Unknown	674	1.185	1.423	1.631	#†
1389091_at	Usp3	Ubiquitin specific peptidase 3	529	0.662	0.725	0.867	*#†
1373510_at	Vamp1	Vesicle-associated membrane protein 1	241	0.848	0.797	0.590	*#†
1389689_at	Vars2	Valyl-tRNA synthetase 2, mitochondrial (putative)	83	0.662	0.727	1.135	*#
1389271_at	Vasn	Vasorin	671	2.238	1.837	1.333	*#†
1368474_at	Vcam1	Vascular cell adhesion molecule 1	1083	0.855	0.604	0.331	#†
1372905_at	Vcl	Vinculin	1656	1.688	1.410	1.903	*†
1375538_at	Vcl	Vinculin	1968	1.683	1.527	1.342	*#
1398476_at	Vcl	Vinculin	760	1.767	2.029	1.665	*#†
1368463_at	Vegfc	Vascular endothelial growth factor C	253	1.957	1.896	1.939	*#†
1377778_at	Vof16	Ischemia related factor vof-16	103	1.751	1.936	1.107	*#
1385449_s_at	Vps37b	Vacuolar protein sorting 37 homolog B (S. cerevisiae)	151	1.365	1.896	1.172	*#
1373399_at	Wdr6	WD repeat domain 6	969	0.798	0.649	0.810	#
1389644_at	Wdr67	WD repeat domain 67	84	0.825	0.634	0.937	#
1373746_at	Wdr91	WD repeat domain 91	117	0.662	0.748	0.744	*#†
1387873_at	Wfdc1	WAP four-disulfide core domain 1	217	0.990	1.172	1.760	†
1382283_at	Wipf1	WAS/WASL interacting protein family, member 1	174	0.664	0.892	0.961	*
1370221_at	Wisp1	WNT1 inducible signaling pathway protein 1	123	1.226	1.732	2.214	#†
1369484_at	Wisp2	WNT1 inducible signaling pathway protein 2	572	0.892	1.157	2.378	†
1377223_at	Wt1	Wilms tumor 1	193	0.480	0.810	1.367	*†
1385783_at	Wwc2	WW and C2 domain containing 2	492	0.979	1.063	1.543	†
1392670_at	Wwc2	WW and C2 domain containing 2	367	0.904	0.979	1.789	†
1395525_at	Wwc2	WW and C2 domain containing 2	512	0.957	0.982	1.543	†
1369973_at	Xdh	Xanthine dehydrogenase	377	0.895	0.750	0.534	#†
1389119_at	Xirp1	Xin actin-binding repeat containing 1	942	3.011	2.767	1.205	*#
1384029_at	Xpa	Xeroderma pigmentosum, complementation group A	121	0.610	0.511	0.909	*#
1375846_at	Xpr1	Xenotropic and polytropic retrovirus receptor 1	834	1.134	1.590	1.541	#†
1371729_at	Ypel5	Yippee-like 5 (Drosophila)	578	0.691	0.663	1.020	*#†
1377687_at	Zc4h2	Zinc finger, C4H2 domain containing	137	0.789	0.598	1.145	*#
1390820_at	Zcchc11	Zinc finger, CCHC domain containing 11	124	0.624	0.669	1.033	*#
1378948_at	Zcchc24	Zinc finger, CCHC domain containing 24	207	0.659	0.763	0.819	*
1386106_at	Zcchc24	Zinc finger, CCHC domain containing 24	318	0.457	0.553	0.824	*#
1388672_at	Zcchc24	Zinc finger, CCHC domain containing 24	771	0.611	0.579	0.808	*#†
1372989_at	Zdhhc14	Zinc finger, DHHC-type containing 14	64	0.923	1.359	1.507	#†
1372205_at	Zfp278	Zinc finger protein 278	286	0.527	0.980	0.921	*
1382642_at	Zfp281	Zinc finger protein 281	316	1.661	1.352	1.342	*#†
1392699_at	Zfp346	Zinc finger protein 346	63	0.726	0.641	0.968	*#
1387870_at	Zfp36	Zinc finger protein 36	629	1.661	1.335	1.020	*#
1378049_at	Zfp362 /// Zscan20	Zinc finger protein 362 /// Zinc finger and SCAN domain containing 20	327	0.659	0.872	0.960	*#

1372865_at	Zfp364	Zinc finger protein 364	1412	1.332	1.511	1.149	*#†
1379967_at	Zfp367	Zinc finger protein 367	88	2.007	1.295	1.189	*
1369959_at	Zfp36l1	Zinc finger protein 36, C3H type-like 1	2790	0.615	0.696	0.894	*#
1373106_at	Zfp36l2	Zinc finger protein 36, C3H type-like 2	904	1.818	1.600	1.001	*#
1389851_at	Zfp36l2	Zinc finger protein 36, C3H type-like 2	56	1.657	1.563	0.973	*#
1368542_at	Zfp423	Zinc finger protein 423	168	0.618	0.499	0.762	*#†
1393360_at	Zfp426l	Zinc finger protein 426-like	701	0.564	0.726	0.993	*#
1394654_at	Zfp451	Zinc finger protein 451	58	1.518	1.408	0.966	*#
1370984_at	Zfp46	Zinc finger protein 46	369	0.652	0.899	0.949	*
1367540_at	Zfyve26	Zinc finger, FYVE domain containing 26	263	0.639	0.736	0.919	*#
1382744_at	Zkscan3	Zinc finger with KRAB and SCAN domains 3	242	0.549	0.865	1.003	*
1398573_at	Zkscan3	Zinc finger with KRAB and SCAN domains 3	238	0.583	0.809	1.037	*
1377701_at	Zmym6	Zinc finger, MYM-type 6	155	0.627	0.712	0.872	*#
1390945_at	Znf292	Zinc finger protein 292	145	0.646	0.836	0.869	*
1391507_at	Znf467	Zinc finger protein 467	172	0.500	0.512	0.963	*#
1386721_at	Znf503	Zinc finger protein 503	295	0.770	0.904	0.663	*†
1393944_at	Znf521	Zinc finger protein 521	259	0.653	0.689	0.989	*#
1389445_at	Znf688	Zinc finger protein 688	139	0.600	0.844	0.932	*
1372699_at	Znf775	Zinc finger protein 775	68	0.599	0.798	0.957	*
1374664_at	Znf787	Zinc finger protein 787	286	0.634	0.815	0.864	*#†
1391972_a_at	Zswim4	Zinc finger, SWIM-type containing 4	170	1.975	1.457	0.946	*#

Supplemental Table S6 Changes in transcript expression induced by PE and/or ET-1 at 24 h

RNA analysis was performed using Affymetrix rat expression 230 2.0 microarrays and GeneSpring 12.0. The raw data for controls are given and results at each time are the mean fold change relative to the controls (n=3). Statistical analysis was performed by one-way ANOVA with SNK post-test using a Benjamini and Hochberg false discovery rate correction (FDR<0.05) * PE vs control; # ET-1 vs control; † PE vs ET-1

Probeset ID	Gene Symbol	Gene Title	Raw data (Control)	ET-1	PE	Statistical significance
1383355_at	Abca1	ATP-binding cassette, sub-family A (ABC1), member 1	316.04	0.655	0.869	#
1394490_at	Abca1	ATP-binding cassette, sub-family A (ABC1), member 1	137.60	0.626	0.762	---
1390783_at	Abca8a	ATP-binding cassette, sub-family A (ABC1), member 8a	195.54	0.507	0.661	*#
1379402_at	Abcc4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	158.63	0.615	0.781	*#†
1390455_at	Abhd2	Abhydrolase domain containing 2	197.76	1.451	1.822	*
1388153_at	Acsl1	Acyl-CoA synthetase long-chain family member 1	820.86	0.611	0.761	#
1397375_at	Acsl5	Acyl-CoA synthetase long-chain family member 5	212.17	1.602	1.364	*#
1370857_at	Acta2	Smooth muscle alpha-actin	2482.46	2.241	1.408	#
1386869_at	Actg2	Actin, gamma 2, smooth muscle, enteric	85.81	2.699	1.288	#†
1389189_at	Actn1	Actinin, alpha 1	1716.26	1.868	1.630	---
1398294_at	Actn1	Actinin, alpha 1	1193.36	1.758	1.443	#
1369942_at	Actn4	Actinin alpha 4	1499.44	1.798	1.367	*#
1393730_at	Adamts4	ADAM metallopeptidase with thrombospondin type 1 motif, 4	222.08	0.590	0.812	*#†
1379022_at	Adamts8	ADAM metallopeptidase with thrombospondin type 1 motif, 8	103.57	1.763	1.299	#
1398370_at	Adarb1	Adenosine deaminase, RNA-specific, B1	112.15	1.617	1.239	#
1368300_at	Adora2a	Adenosine A2a receptor	122.79	0.496	0.761	#†
1387395_at	Adora2b	Adenosine A2B receptor	403.34	0.603	0.827	*#†
1368574_at	Adra1b	Adrenergic, alpha-1B-, receptor	391.97	0.567	0.694	*#
1369146_a_at	Ahr	Aryl hydrocarbon receptor	89.28	1.613	1.493	*#
1375845_at	Aig1	Androgen-induced 1	399.75	1.634	1.474	*#
1389496_at	Akap7	A kinase (PRKA) anchor protein 7	404.03	1.511	1.210	#
1392079_at	Akap7	A kinase (PRKA) anchor protein 7	105.30	1.765	1.201	#†
1370563_at	Akr1c14	Aldo-keto reductase family 1, member C14	117.82	0.643	0.819	*#†
1396933_s_at	Akr1c14	Aldo-keto reductase family 1, member C14	108.87	0.585	0.727	*#
1394681_at	Akr1cl1	Aldo-keto reductase family 1, member C-like 1	672.43	0.590	0.703	*#
1368003_at	Aldh1a2	Aldehyde dehydrogenase 1 family, member A2	258.13	1.653	1.282	#
1386998_at	Aldoc	Aldolase C, fructose-bisphosphate	734.22	0.510	0.609	*#†
1389546_at	Amotl2	Angiomotin like 2	649.40	1.552	1.191	#
1368342_at	Ampd3	Adenosine monophosphate deaminase 3	259.88	0.542	0.538	#
1374207_at	Angpt2	Angiopoietin 2	231.92	0.545	0.982	#†
1389398_at	Ank1	Ankyrin 1, erythrocytic	240.79	0.425	0.608	*#†
1372069_at	Ankrd15	Ankyrin repeat domain 15	574.66	1.507	1.432	*#
1373250_at	Anln	Anillin, actin binding protein	249.58	1.406	1.518	*#
1372615_at	Aoc3	Amine oxidase, copper containing 3 (vascular adhesion protein 1)	96.04	0.772	0.654	*#
1387376_at	Aox1	Aldehyde oxidase 1	228.40	0.311	0.554	*#†
1398616_at	Ap1s2	Adaptor-related protein complex 1, sigma 2 subunit	663.27	0.721	0.621	*#
1389651_at	Apln	Apelin	315.12	0.478	0.989	#†
1379772_at	Aplnr	Apelin receptor	131.76	0.590	0.928	#†
1370862_at	Apoe	Apolipoprotein E	4175.70	0.489	0.809	#†

1377750_at	Arhgef3	Rho guanine nucleotide exchange factor (GEF) 3	144.31	1.630	1.427	*#
1385361_at	Atp10a	ATPase, class V, type 10A	61.69	1.963	1.214	*#†
1368701_at	Atp1a3	ATPase, Na+/K+ transporting, alpha 3 polypeptide	236.06	0.854	0.658	*
1369798_at	Atp1b2	ATPase, Na+/K+ transporting, beta 2 polypeptide	85.91	0.597	0.709	*#
1379906_at	Atp1b2	ATPase, Na+/K+ transporting, beta 2 polypeptide	419.01	0.485	0.618	*#†
1378134_at	Atp8b1	ATPase, Class I, type 8B, member 1	83.29	1.964	1.215	#†
1390294_at	Atxn7l4	Ataxin 7-like 4	164.84	1.549	1.218	*#†
1398347_at	Axl /// LOC687188	Axl receptor tyrosine kinase /// similar to AXL receptor tyrosine kinase	1002.00	1.788	1.334	*#†
1389047_at	Bag2	Bcl2-associated athanogene 2	468.42	1.516	1.324	---
1370869_at	Bcat1	Branched chain aminotransferase 1, cytosolic	989.27	1.629	1.616	---
1370897_at	Bckdha	Branched chain ketoacid dehydrogenase E1, alpha polypeptide	170.23	0.589	0.707	*#
1398482_at	Bcl3	B-cell CLL/lymphoma 3	272.66	0.599	0.755	*#†
1372613_at	Bdh2	3-hydroxybutyrate dehydrogenase, type 2	371.30	0.730	0.647	*#
1370113_at	Birc3	Baculoviral IAP repeat-containing 3	141.30	0.657	0.808	*#†
1398270_at	Bmp2	Bone morphogenetic protein 2	125.58	1.384	1.724	*
1387232_at	Bmp4	Bone morphogenetic protein 4	123.42	2.093	1.261	#†
1368000_at	C3	Complement component 3	282.30	0.353	0.725	#†
1370892_at	C4-2 /// C4b	Complement component 4, gene 2 /// Complement component 4B (Childo blood group)	760.11	0.341	0.669	*#†
1384580_at	C6	Complement component 6	92.00	0.545	0.835	#†
1383291_at	C7 /// Tubb2c	Complement component 7 /// tubulin, beta 2c	3306.12	0.493	0.929	#†
1388557_at	C7 /// Tubb2c	Complement component 7 /// tubulin, beta 2c	2740.97	0.539	0.982	#†
1372536_at	Cabc1	Chaperone, ABC1 activity of bc1 complex homolog (S. pombe)	305.24	0.724	0.568	*
1376657_at	Cadm1	Cell adhesion molecule 1	48.58	1.945	1.150	#†
1384132_at	Cadm1	Cell adhesion molecule 1	81.77	1.872	1.254	*#†
1368824_at	Cald1	Caldesmon 1	429.75	1.920	1.318	#
1368131_at	Capn6	Calpain 6	322.90	0.538	0.689	*#†
1386922_at	Car2	Carbonic anhydrase II	133.22	0.666	0.844	#
1388604_at	Casq1	Calsequestrin 1 (fast-twitch, skeletal muscle)	298.38	1.780	1.702	---
1393281_at	Cav1	Caveolin 1, caveolae protein	799.76	1.504	1.136	#†
1390101_at	Ccdc107	Coiled-coil domain containing 107	383.47	1.866	1.551	*#
1385426_at	Ccdc109b	Coiled-coil domain containing 109B	115.18	1.730	1.226	#
1367973_at	Ccl2	Chemokine (C-C motif) ligand 2	3386.98	0.602	0.885	*#†
1376850_a_at	Ccl27	Chemokine (C-C motif) ligand 27	91.23	1.473	1.820	*#
1379935_at	Ccl7	Chemokine (C-C motif) ligand 7	956.78	0.516	0.749	*#†
1389566_at	Ccnb2	Cyclin B2	350.82	1.510	1.214	#
1367689_a_at	Cd36	CD36 molecule (thrombospondin receptor)	1285.88	0.576	0.588	*#
1386901_at	Cd36	CD36 molecule (thrombospondin receptor)	1823.52	0.595	0.647	*#
1368975_at	Cd38	CD38 molecule	38.55	1.601	1.533	*#
1372299_at	Cdkn1c	Cyclin-dependent kinase inhibitor 1C (P57)	294.59	0.637	0.725	*#
1368480_at	Cdw92	CDW92 antigen	619.31	0.648	0.865	*#†
1373054_at	Cdw92	CDW92 antigen	1554.93	0.621	0.960	#†
1389470_at	Cfb	Complement factor B	110.23	0.629	0.741	*#
1392171_at	Chi3l1	Chitinase 3-like 1	516.66	0.340	0.697	*#†
1389179_at	Cidea	Cell death-inducing DNA fragmentation factor, alpha subunit-like effector A	1244.61	0.664	0.796	#
1367601_at	Cited2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	371.31	1.934	1.255	*#†
1367602_at	Cited2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	518.76	1.725	1.184	#†
1367626_at	Ckm	Creatine kinase, muscle	1888.66	0.505	0.641	*#
1374104_at	Cldn5	Claudin 5	129.40	0.543	0.846	#†
1383219_at	Clip4	CAP-GLY domain containing linker protein family, member 4	379.06	0.632	0.612	*#
1382269_at	Cnnm2	Cyclin M2	80.97	1.660	0.802	*#†
1392915_at	Col11a1	Collagen, type XI, alpha 1	63.53	1.742	0.998	#†

1370927_at	Col12a1	Collagen, type XII, alpha 1	282.20	2.852	1.919	*#†
1395580_at	Col12a1	Collagen, type XII, alpha 1	120.23	2.322	1.721	*#
1398321_a_at	Col12a1	Collagen, type XII, alpha 1	203.52	2.549	1.694	#
1376955_at	Col4a4	Procollagen, type IV, alpha 4	81.99	1.431	1.553	---
1393891_at	Col8a1	Collagen, type VIII, alpha 1	215.46	3.070	1.538	*#†
1368648_at	Cox4i2	Cytochrome c oxidase subunit IV isoform 2	184.55	1.056	1.501	*†
1367742_at	Cpt1b	Carnitine palmitoyltransferase 1b, muscle	1017.49	0.563	0.595	*#
1390420_at	Cpxm1	Carboxypeptidase X (M14 family), member 1	1065.87	0.291	0.607	*#†
1375428_at	Creg1	Cellular repressor of E1A-stimulated genes 1	147.19	0.655	0.685	*#
1382037_at	Crim1	Cysteine rich transmembrane BMP regulator 1 (chordin like)	169.38	1.861	1.190	#†
1398622_at	Crim1	Cysteine rich transmembrane BMP regulator 1 (chordin like)	709.30	1.838	1.192	#†
1376799_a_at	Crlf1	Cytokine receptor-like factor 1	226.34	3.155	2.354	*#†
1395512_at	Crlf1	Cytokine receptor-like factor 1	165.16	3.169	2.449	*#
1368685_at	Cspg4	Chondroitin sulfate proteoglycan 4	279.93	1.611	1.542	---
1367838_at	Cth	Cystathionase (cystathionine gamma-lyase)	42.85	2.103	1.548	#
1384063_at	Cthrc1	Collagen triple helix repeat containing 1	2049.93	1.639	1.456	*#
1368280_at	Ctsc	Cathepsin C	1225.27	0.569	0.788	*#†
1374778_at	Ctsc	Cathepsin C	920.97	0.604	0.829	#†
1387316_at	Cxcl1	Chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	2114.59	0.409	0.781	*#†
1379365_at	Cxcl11	Chemokine (C-X-C motif) ligand 11	456.69	0.401	0.303	*#
1387648_at	Cxcl6	Chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)	755.62	0.206	0.625	*#†
1370097_a_at	Cxcr4	Chemokine (C-X-C motif) receptor 4	340.53	0.499	0.942	#†
1373661_a_at	Cxcr4	Chemokine (C-X-C motif) receptor 4	388.53	0.600	1.060	#†
1389244_x_at	Cxcr4	Chemokine (C-X-C motif) receptor 4	481.65	0.595	1.002	#†
1376788_at	Dapk1	Death associated protein kinase 1	944.54	0.394	0.607	*#†
1379911_at	Dapk1	Death associated protein kinase 1	451.84	0.436	0.663	*#†
1387874_at	Dbp	D site of albumin promoter (albumin D-box) binding protein	209.58	0.667	0.804	*#
1387111_at	Ddah1	Dimethylarginine dimethylaminohydrolase 1	862.65	1.769	1.864	*#
1367793_at	Ddt	D-dopachrome tautomerase	1640.15	0.642	0.778	*#†
1389079_at	Dhrs7c	Dehydrogenase/reductase (SDR family) member 7C	93.25	0.647	0.513	*#
1370328_at	Dkk3	Dickkopf homolog 3 (Xenopus laevis)	1670.14	0.874	0.631	*†
1377835_at	Dock8	Dedicator of cytokinesis 8	201.10	1.712	1.222	*#†
1371732_at	Dpt	Dermatopontin	2281.00	0.595	0.770	*#†
1373947_at	Dpt	Dermatopontin	2454.83	0.583	0.767	*#†
1380964_at	Dtna	Dystrobrevin alpha	51.63	1.553	1.407	*#
1373324_at	Dusp14	Dual specificity phosphatase 14	148.54	1.502	1.261	*#
1377064_at	Dusp6	Dual specificity phosphatase 6	409.45	1.591	1.491	*#
1383747_at	Ect2	Epithelial cell transforming sequence 2 oncogene	109.99	1.531	1.215	#†
1378342_at	Ednra	Endothelin receptor type A	435.94	0.586	0.739	*#†
1383641_at	Ednra	Endothelin receptor type A	532.91	0.576	0.746	*#†
1387146_a_at	Ednrb	Endothelin receptor type B	100.95	1.719	1.097	#†
1390112_at	Efemp1	EGF-containing fibulin-like extracellular matrix protein 1	356.55	0.185	0.435	*#†
1376770_at	Efhd1	EF-hand domain family, member D1	72.03	0.740	0.665	*#
1383078_at	Efnb3	Ephrin B3	579.01	0.538	0.746	*#†
1368967_at	Eif2b3	Eukaryotic translation initiation factor 2B, subunit 3 gamma	195.30	1.511	1.376	#
1372587_at	Emcn	Endomucin	437.84	0.423	0.841	#†
1371527_at	Emp1	Epithelial membrane protein 1	1739.35	1.608	1.346	*#†
1386907_at	Eno3	Enolase 3, beta, muscle	126.47	0.908	2.101	*†
1370047_at	Enpp1	Ectonucleotide pyrophosphatase/phosphodiesterase 1	532.84	2.289	1.784	*#
1368536_at	Enpp2	Ectonucleotide pyrophosphatase/phosphodiesterase 2	160.41	0.497	0.860	#†
1370845_at	Entpd2	Ectonucleoside triphosphate diphosphohydrolase 2	130.66	0.647	0.906	#†
1375729_at	Epha4	Eph receptor A4	80.77	0.603	0.833	#†

1367899_at	F2r	Coagulation factor II (thrombin) receptor	933.73	2.318	1.497	*#†
1369182_at	F3	Coagulation factor III (thromboplastin, tissue factor)	140.14	1.622	1.211	#
1368271_a_at	Fabp4	Fatty acid binding protein 4, adipocyte	215.98	0.327	0.752	#†
1379625_at	Fam164a	Family with sequence similarity 164, member A	51.64	1.600	1.098	#†
1382143_at	Farp1	FERM, RhoGEF (Arhgef) and pleckstrin domain protein 1 (chondrocyte-derived)	421.37	1.502	1.273	*#
1372518_at	Fbln1	Fibulin 1	1408.58	0.586	0.870	#†
1389533_at	Fbln2	Fibulin 2	1068.43	1.978	1.737	*#
1387351_at	Fbn1	Fibrillin 1	1629.69	1.523	1.364	*#
1368114_at	Fgf13	Fibroblast growth factor 13	410.09	0.851	0.665	*†
1373727_at	Fibin	Fin bud initiation factor homolog (zebrafish)	359.67	2.134	1.384	#
1393696_at	Fibin	Fin bud initiation factor homolog (zebrafish)	138.42	2.336	1.390	#†
1389449_at	Fit1	Fat-inducing transcript 1	226.94	0.577	0.559	*#
1371382_at	Flna	Filamin, alpha	2243.95	1.728	1.296	#
1388401_at	Flnb	Filamin, beta	301.11	1.512	1.235	*#†
1376779_at	Foxo1	Forkhead box O1	70.77	0.664	0.784	*#
1379651_at	Foxp1	Forkhead box P1	309.88	1.749	1.236	*#†
1387843_at	Fst	Follistatin	88.55	3.289	1.553	*#†
1368821_at	Fstl1	Follistatin-like 1	1740.97	1.638	1.208	*#†
1368822_at	Fstl1	Follistatin-like 1	2373.34	1.623	1.283	*#†
1371331_at	Fstl1	Follistatin-like 1	2404.92	1.584	1.241	*#†
1379440_at	Fstl3	Follistatin-like 3 (secreted glycoprotein)	249.99	1.831	1.549	*#
1368207_at	Fxyd5	FXYD domain-containing ion transport regulator 5	565.20	2.175	1.496	*#†
1374530_at	Fzd7	Frizzled homolog 7 (Drosophila)	203.06	1.507	1.375	*#
1388395_at	G0s2	G0/G1switch 2	2270.78	0.587	0.910	#†
1374759_at	Galntl1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 1	97.59	1.635	1.320	#
1374903_at	Gcnt2	Glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	58.99	1.520	1.039	#†
1373504_at	Glipr1	GLI pathogenesis-related 1	87.26	2.550	1.318	#†
1382616_at	Gls	Glutaminase	151.00	1.523	1.330	*#
1367632_at	Glul	Glutamate-ammonia ligase (glutamine synthetase)	977.64	0.637	0.735	*#
1367633_at	Glul	Glutamate-ammonia ligase (glutamine synthetase)	931.58	0.536	0.701	*#†
1386870_at	Glul	Glutamate-ammonia ligase (glutamine synthetase)	1566.09	0.572	0.692	*#†
1369560_at	Gpd1	Glycerol-3-phosphate dehydrogenase 1 (soluble)	162.95	0.551	0.834	#†
1371363_at	Gpd1	Glycerol-3-phosphate dehydrogenase 1 (soluble)	303.76	0.434	0.830	#†
1388243_at	Gpr176	G protein-coupled receptor 176	417.43	1.761	1.075	#†
1387241_at	Gpr88	G-protein coupled receptor 88	97.89	0.489	0.611	*#†
1376828_at	Gprc5a	G protein-coupled receptor, family C, group 5, member A	132.32	1.583	1.629	*#
1369113_at	Grem1	Gremlin 1, cysteine knot superfamily, homolog (Xenopus laevis)	38.65	8.186	1.296	#†
1378163_at	Grem2	Gremlin 2, cysteine knot superfamily, homolog (Xenopus laevis)	127.62	0.454	0.632	*#†
1368354_at	Gstt1	Glutathione S-transferase theta 1	275.41	0.512	0.790	*#†
1371942_at	Gstt3	Glutathione S-transferase, theta 3	215.93	0.206	0.522	*#†
1371298_at	H19	H19 fetal liver mRNA	894.51	0.578	0.893	#†
1387396_at	Hamp	Hepcidin antimicrobial peptide	803.58	0.560	0.510	*#
1386080_at	Hey1	Hairy/enhancer-of-split related with YRPW motif 1	175.48	0.558	0.800	#†
1391429_at	Hfe2	Hemochromatosis type 2 (juvenile) (human homolog)	148.25	0.486	0.574	*#
1388193_at	Hip1	Huntingtin interacting protein 1	462.27	1.660	1.506	*#
1390082_at	Hip1	Huntingtin interacting protein 1	458.44	1.500	1.348	*#
1392941_at	Hip1	Huntingtin interacting protein 1	414.06	1.537	1.430	*#
1367816_at	Hopx	HOP homeobox	555.07	0.637	0.797	#
1372179_at	Hpcal1	Hippocalcin-like 1	730.50	1.560	1.149	#†
1393790_at	Hrasls	HRAS-like suppressor	105.25	1.722	1.080	#†
1387233_at	Hsd17b7	Hydroxysteroid (17-beta) dehydrogenase 7	161.76	1.203	1.561	*#†

1368247_at	Hspa1a /// Hspa1b	Heat shock 70kD protein 1A /// heat shock 70kD protein 1B (mapped)	100.39	2.016	1.198	#†
1370912_at	Hspa1b	Heat shock 70kD protein 1B (mapped)	139.62	2.122	1.467	#
1373515_at	Hspc159	Galectin-related protein	304.23	1.968	1.188	#†
1376867_at	Hspc159	Galectin-related protein	138.33	2.164	1.362	*#†
1372565_at	Htra3	HtrA serine peptidase 3	1367.83	0.532	0.791	*#†
1375306_at	Htra3	HtrA serine peptidase 3	575.80	0.621	0.770	*#
1389235_at	Icam2	Intercellular adhesion molecule 2	206.63	0.644	0.937	#†
1368878_at	Idi1	Isopentenyl-diphosphate delta isomerase 1	1179.32	1.382	1.542	*#
1367795_at	Ifrd1	Interferon-related developmental regulator 1	440.19	1.514	1.505	---
1371462_at	Igfbp4	Insulin-like growth factor binding protein 4	1332.63	0.558	0.945	#†
1370960_at	Igfbp5	Insulin-like growth factor binding protein 5	821.30	0.347	0.457	*#
1387347_at	Igfbp5	Insulin-like growth factor binding protein 5	260.75	0.638	0.699	*#
1387348_at	Igfbp5	Insulin-like growth factor binding protein 5	486.01	0.382	0.473	*#
1396152_s_at	Igfbp5	Insulin-like growth factor binding protein 5	382.04	0.348	0.474	*#
1390901_at	Igsf10	Immunoglobulin superfamily, member 10	771.36	0.524	0.850	#†
1368375_a_at	Il15	Interleukin 15	55.16	1.664	1.042	#†
1387273_at	Il1rl1	Interleukin 1 receptor-like 1	262.30	4.661	2.124	*#†
1380055_at	Il34	Interleukin 34	116.35	0.654	0.911	#†
1387124_at	Inha	Inhibin alpha	171.36	1.725	3.466	*#†
1391489_at	Irgm	Immunity-related GTPase family, M	150.26	0.651	0.720	---
1387144_at	Itga1	Integrin alpha 1	437.52	1.613	1.412	*#
1383880_at	Itgav	Integrin alpha V	278.03	1.557	1.285	#
1398358_a_at	Itgb5	Integrin, beta 5	717.99	1.653	1.377	---
1387160_at	Kcne3	potassium voltage-gated channel, Isk-related subfamily, gene 3	387.21	0.596	0.948	#†
1370773_a_at	Kcnip2	Kv channel-interacting protein 2	126.70	0.498	0.401	*#
1373987_at	Kcnip2	Kv channel-interacting protein 2	320.03	0.428	0.265	*#
1368911_at	Kcnj8	Potassium inwardly-rectifying channel, subfamily J, member 8	161.79	0.467	1.016	#†
1367948_a_at	Kdr	Kinase insert domain protein receptor	616.75	0.518	0.848	#†
1391063_at	Kif23	Kinesin family member 23	112.02	1.567	1.222	#†
1378197_at	KIFC2	Kinesin family member C2	127.03	0.644	0.749	*#
1381396_s_at	Klf15	Kruppel-like factor 15	232.62	0.624	0.673	*#
1383300_at	Klhl24	Kelch-like 24 (Drosophila)	576.21	0.661	0.704	*#
1388155_at	Krt18	Keratin 18	54.13	1.637	1.526	---
1379340_at	Lamc2	Laminin, gamma 2	212.79	1.353	1.835	*
1390207_at	Lats2	Large tumor suppressor 2	675.35	1.546	1.268	*#†
1387011_at	Lcn2	Lipocalin 2	4187.32	0.613	0.947	#†
1373233_at	Lhfpl2	Lipoma HMGIC fusion partner-like 2	436.54	0.581	0.752	*#†
1378179_a_at	Lhfpl2	Lipoma HMGIC fusion partner-like 2	288.89	0.638	0.813	#†
1376700_at	Lima1	LIM domain and actin binding 1	425.88	1.504	1.298	*#
1389464_at	Lnx1	Ligand of numb-protein X 1	133.36	0.531	0.583	*#
1374171_at	LOC100360403	ATP-binding cassette, sub-family C, member 9-like	810.28	0.598	0.771	*#†
1374932_at	LOC100361444	rCG31799-like	52.80	0.967	1.692	*†
1375706_at	LOC100361913	rCG54286-like	470.44	1.540	1.196	#†
1372647_at	LOC100363743	Proline arginine-rich end leucine-rich repeat protein-like	326.06	2.254	1.161	#†
1376151_a_at	LOC100365106	rCG32755-like	205.36	0.646	0.810	*#†
1374029_at	LOC100365118	rCG54747-like	183.46	1.831	1.264	#†
1393210_at	LOC100365207	Extracellular matrix protein 2-like	210.70	0.631	0.684	*#
1372856_at	LOC363331	Similar to plasma membrane associated protein, S3-12	266.69	0.661	0.774	*#
1391030_at	LOC500591	Similar to calmodulin-binding transcription activator 1	513.92	1.913	1.685	---
1397536_at	LOC500591	Similar to calmodulin-binding transcription activator 1	268.81	1.723	1.551	*#
1374677_at	LOC684425	Similar to Adenylosuccinate synthetase isozyme 1 (Adenylosuccinate synthetase,	456.14	0.624	0.602	*#

		muscle isozyme) (IMP--aspartate ligase 1) (AdSS 1) (AMPSase 1)				
1384406_at	LOC685243	Similar to C-C chemokine receptor type 11 (C-C CKR-11) (CC-CKR-11) (CCR-11) (Chemokine receptor-like 1) (CCRL1) (CCX CKR)	111.86	1.758	1.228	#†
1398732_at	LOC688273	Hypothetical protein LOC688273	143.39	1.932	1.786	*#
1388763_at	LOC690976	Similar to Calponin-2 (Calponin H2, smooth muscle) (Neutral calponin)	1667.88	1.529	1.310	#
1368171_at	Lox	Lysyl oxidase	754.14	2.225	1.860	*#
1368172_a_at	Lox	Lysyl oxidase	425.13	2.155	1.698	*#†
1388902_at	Loxl1	Lysyl oxidase-like 1	1323.05	1.621	1.490	---
1374626_at	Lrg1	Leucine rich alpha-2-glycoprotein 1	100.42	0.590	0.903	#†
1395472_at	Lrrc17	Leucine rich repeat containing 17	1438.28	0.561	0.714	*#†
1393460_at	Lrrc33	Leucine rich repeat containing 33	155.80	0.615	0.813	*#†
1373755_at	Lrrc39	Leucine rich repeat containing 39	294.91	0.775	0.617	*
1396140_at	Lrrc39	Leucine rich repeat containing 39	176.03	0.691	0.664	*#
1384178_at	Lrrc4b	Leucine rich repeat containing 4B	337.07	1.376	1.734	*#†
1389351_at	Lrrfip1	Leucine rich repeat (in FLII) interacting protein 1	333.83	1.798	1.346	*#†
1367912_at	Ltbp1	Latent transforming growth factor beta binding protein 1	82.40	2.850	1.610	*#†
1368448_at	Ltbp2	Latent transforming growth factor beta binding protein 2	379.11	2.203	1.404	*#†
1382192_at	Lyve1	Lymphatic vessel endothelial hyaluronan receptor 1	163.60	0.569	0.984	#†
1382732_at	Lyve1	Lymphatic vessel endothelial hyaluronan receptor 1	135.80	0.571	0.870	#†
1387165_at	Maf	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	176.23	0.530	0.762	#†
1368514_at	Maob	Monoamine oxidase B	118.79	0.586	0.718	*#
1371003_at	Map1b	Microtubule-associated protein 1B	62.74	1.625	1.402	---
1373363_at	Map1b	Microtubule-associated protein 1B	778.94	1.558	1.460	---
1395357_at	Map1b	Microtubule-associated protein 1B	204.36	1.959	1.802	*#
1368871_at	Map3k1	Mitogen activated protein kinase kinase kinase 1	388.50	0.584	0.740	*#†
1371087_a_at	Map6	Microtubule-associated protein 6	149.98	1.515	1.402	---
1389543_at	Masp1	Mannan-binding lectin serine peptidase 1	207.17	0.643	0.572	*#
1367682_at	Mdk	Midkine	1181.61	0.623	0.776	#
1371479_at	Mettl7a	Methyltransferase like 7A	337.97	0.542	0.693	*#
1371815_at	Mfap2	Microfibrillar-associated protein 2	266.85	0.446	0.704	*#†
1373674_at	Mfap5	Microfibrillar associated protein 5	62.55	3.116	1.376	*#†
1392547_at	MGC105649	Hypothetical LOC302884	67.52	1.228	1.504	*
1373333_at	MGC109340	Similar to Microsomal signal peptidase 23 kDa subunit (SPase 22 kDa subunit) (SPC22/23)	48.05	1.516	1.250	#
1367612_at	Mgst1	Microsomal glutathione S-transferase 1	4440.09	0.560	0.739	*#†
1368590_at	Mmp16	Matrix metallopeptidase 16	133.69	1.604	1.276	#
1371237_a_at	Mt1a	Metallothionein 1a	7838.12	0.644	0.818	*#†
1397644_at	Mtap	Methylthioadenosine phosphorylase	230.46	1.629	1.389	*#
1373032_at	Mustn1	Musculoskeletal, embryonic nuclear protein 1	115.09	2.112	1.419	*#†
1368308_at	Myc	Myelocytomatosis oncogene	327.47	1.684	1.644	*#
1370158_at	Myh10	Myosin, heavy chain 10, non-muscle	1505.17	1.512	1.081	#†
1370896_a_at	Myh11	Myosin, heavy chain 11, smooth muscle	133.94	1.736	1.018	#†
1387049_at	Myh6	Myosin, heavy chain 6, cardiac muscle, alpha	3805.14	0.618	0.796	*#†
1396165_at	Myh6	Myosin, heavy chain 6, cardiac muscle, alpha	1202.01	0.626	0.811	#
1371725_at	Myh9	Myosin, heavy chain 9, non-muscle	1805.22	1.683	1.275	#
1387402_at	Myh9	Myosin, heavy chain 9, non-muscle	760.96	1.723	1.311	#
1388917_at	Myo1d	Myosin ID	163.54	2.013	1.211	#†
1375857_at	Myof	Myoferlin	806.34	1.788	1.368	*#†
1375861_at	Nap1l5	Nucleosome assembly protein 1-like 5	96.54	1.222	1.894	*#†
1384009_at	Narf	Nuclear prelamin A recognition factor	129.38	0.627	0.891	#†
1383938_at	Ncoa7	Nuclear receptor coactivator 7	371.76	0.659	0.914	#†
1374650_at	Nedd9	Neural precursor cell expressed, developmentally down-regulated 9	293.37	1.726	1.136	#†

1396053_at	Nedd9	Neural precursor cell expressed, developmentally down-regulated 9	106.72	1.873	1.218	#†
1389538_at	Nfkbia	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	766.87	0.587	0.844	#†
1370408_at	Nid67	Putative small membrane protein NID67	196.48	1.266	1.528	*
1392686_at	Nkd2	Naked cuticle homolog 2 (Drosophila)	60.67	2.247	1.059	#†
1373839_at	Nope	Neighbor of Punc E11	772.10	0.576	0.818	*#†
1371166_at	Nos3	Nitric oxide synthase 3, endothelial cell	139.16	0.589	0.896	#†
1368883_at	Nov	Nephroblastoma overexpressed gene	331.81	2.737	1.062	#†
1376362_at	Nptxr	Neuronal pentraxin receptor	75.57	2.035	1.493	*#†
1387154_at	Npy	Neuropeptide Y	1004.02	0.580	0.726	*#†
1386935_at	Nr4a1	Nuclear receptor subfamily 4, group A, member 1	149.72	1.612	1.289	#
1369200_at	Nt5e	5' nucleotidase, ecto	400.52	1.390	1.830	*#†
1384112_at	Nt5e	5' nucleotidase, ecto	210.27	1.392	1.724	*#†
1387267_at	Ntf3	Neurotrophin 3	107.82	0.681	0.618	*#
1383614_at	Nuak2	NUAK family, SNF1-like kinase, 2	130.27	1.502	0.819	#†
1370000_at	Nucb2	Nucleobindin 2	940.77	1.596	1.333	#
1392579_at	Obfc2a	Oligonucleotide/oligosaccharide-binding fold containing 2A	373.63	0.593	0.733	*#†
1369008_a_at	Olfm1	Olfactomedin 1	111.15	2.030	1.386	#†
1382134_at	Olfml1	Olfactomedin-like 1	428.92	0.578	0.659	*#†
1383453_at	Olfml1	Olfactomedin-like 1	482.60	0.575	0.671	*#
1382072_at	Olfml2a	Olfactomedin-like 2A	106.73	0.487	0.832	#†
1368683_at	Olr1	Oxidized low density lipoprotein (lectin-like) receptor 1	192.02	2.164	1.363	#†
1393129_at	P4ha3	Procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide III	249.93	2.361	1.387	*#†
1389093_at	Pak1	P21 (CDKN1A)-activated kinase 1	87.42	1.722	1.378	*#
1394966_at	Pap2d	Phosphatidic acid phosphatase type 2	91.44	1.814	1.837	*#
1368702_at	Pawr	PRKC, apoptosis, WT1, regulator	162.05	1.654	0.918	#†
1385229_at	Pcdh20	Protocadherin 20	41.27	1.712	1.123	#†
1373368_at	PCOLCE2	Procollagen C-endopeptidase enhancer 2	69.23	1.813	1.358	*#†
1390912_at	Pcp4l1	Purkinje cell protein 4-like 1	155.54	0.678	0.660	*#
1392773_at	Pcsk5	Proprotein convertase subtilisin/kexin type 5	125.19	0.629	0.728	*#
1393467_at	Pcsk5	Proprotein convertase subtilisin/kexin type 5	120.77	0.448	0.730	*#†
1370427_at	Pdgfa	Platelet-derived growth factor alpha polypeptide	253.53	1.528	1.240	#
1370941_at	Pdgfra	Platelet derived growth factor receptor, alpha polypeptide	2710.11	0.583	0.800	*#†
1367892_at	Pdk2	Pyruvate dehydrogenase kinase, isozyme 2	870.82	0.625	0.658	*#
1367946_at	Pdlim1	PDZ and LIM domain 1	1105.55	1.516	1.187	---
1370347_at	Pdlim7	PDZ and LIM domain 7	390.52	1.797	1.436	*#
1371441_at	Pea15a	PhosPhoprotein enriched in astrocytes 15A	572.09	1.503	1.410	*#
1371545_at	Pecam1	Platelet/endothelial cell adhesion molecule 1	176.04	0.629	0.845	*#†
1367949_at	Penk1	Proenkephalin 1	3911.72	0.419	1.088	#†
1386961_at	Pfkm	Phosphofructokinase, muscle	655.02	0.625	0.663	*#
1367951_at	Pgam2	Phosphoglycerate mutase 2 (muscle)	288.20	0.613	0.623	*#
1382303_at	Phactr1	Phosphatase and actin regulator 1	104.45	0.690	0.640	---
1368860_at	Phlda1	Pleckstrin homology-like domain, family A, member 1	241.84	1.224	1.500	*#†
1383749_at	Phospho1	Phosphatase, orphan 1	260.77	0.657	0.743	*#
1388525_at	Pik3ip1	Phosphoinositide-3-kinase interacting protein 1	390.00	0.822	0.647	*
1372199_at	Pink1	PTEN induced putative kinase 1	413.24	0.660	0.543	*#†
1372475_at	Pink1	PTEN induced putative kinase 1	1640.96	0.700	0.605	*#†
1371600_at	Pkig	Protein kinase inhibitor, gamma	1399.16	1.666	0.941	#†
1385182_at	Pkp1	Plakophilin 1	78.00	1.591	1.332	*#†
1368128_at	Pla2g2a	Phospholipase A2, group IIA (platelets, synovial fluid)	2864.70	0.288	0.848	#†
1384558_at	Plac9	Placenta-specific 9	193.00	2.346	1.221	#†
1387675_at	Plau	Plasminogen activator, urokinase	225.38	0.612	1.068	#†

1398287_at	Plau	Plasminogen activator, urokinase	101.67	0.550	0.948	#†
1372897_at	Plod2	Procollagen lysine, 2-oxoglutarate 5-dioxygenase 2	1693.85	1.908	1.519	*#†
1369029_at	Plscr1	Phospholipid scramblase 1	137.69	2.067	1.728	*#
1391435_at	Pltp	Phospholipid transfer protein	744.65	0.381	0.583	*#†
1389809_at	Pmepa1	Prostate transmembrane Protein, androgen induced 1	985.70	2.019	1.524	*#
1392534_at	Pmepa1	Prostate transmembrane Protein, androgen induced 1	1075.58	2.116	1.580	*#
1370950_at	Ppap2b	Phosphatidic acid phosphatase type 2B	374.32	0.605	0.738	*#†
1372531_at	Ppfibp2	PTPRF interacting Protein, binding Protein 2 (liprin beta 2)	102.95	0.579	0.592	*#
1367813_at	Ppp1r14a	Protein phosphatase 1, regulatory (inhibitor) subunit 14A	114.32	2.228	1.075	#†
1390839_at	Pqlc3	PQ loop repeat containing 3	511.15	2.196	1.330	*#†
1387886_at	Prelp	Proline arginine-rich end leucine-rich repeat Protein	334.17	1.863	1.105	#†
1379369_at	Prickle1	Prickle homolog 1 (Drosophila)	779.48	1.528	1.367	*#
1373152_at	Prss23	Protease, serine, 23	1464.80	1.623	1.485	*#
1367851_at	Ptgds	Prostaglandin D2 synthase (brain)	217.69	0.619	0.572	*#
1368014_at	Ptges	Prostaglandin E synthase	97.80	0.643	0.833	#†
1368259_at	Ptgs1	Prostaglandin-endoperoxide synthase 1	67.35	1.942	1.155	#†
1370214_at	Pvalb	Parvalbumin	415.60	0.293	0.663	#†
1370177_at	PVR	Poliovirus receptor	231.60	1.442	1.597	*
1389873_at	Pycard	PYD and CARD domain containing	267.68	0.962	0.658	*†
1370061_at	Rab3b	RAB3B, member RAS oncogene family	163.53	0.519	0.500	*#
1384528_at	Rai14	Retinoic acid induced 14	98.18	2.027	1.619	*#
1389263_at	Rai14	Retinoic acid induced 14	748.35	1.859	1.612	*#
1367791_at	Ramp1	Receptor (G protein-coupled) activity modifying protein 1	225.90	1.515	0.922	#†
1370942_at	Rasa3	RAS p21 protein activator 3	555.39	0.570	0.741	*#†
1388970_at	Rasip1	Ras interacting protein 1	147.18	0.630	0.751	*#
1381341_at	rCG_43687	Hypothetical protein LOC688459	87.95	1.730	1.360	*#
1374448_at	Reck	Reversion-inducing-cysteine-rich protein with kazal motifs	545.13	1.502	1.230	#
1368238_at	Reg3b	Regenerating islet-derived 3 beta	5435.06	0.461	0.486	*#
1368080_at	Rgc32	Response gene to complement 32	132.10	2.200	1.255	*#†
1377011_at	RGD1307034	Similar to hypothetical protein CG003	271.51	1.638	1.424	*#
1376645_at	RGD1307396	Similar to RIKEN cDNA 6330406I15	290.78	1.827	1.438	#
1372848_at	RGD1310269	Hypothetical LOC314472	275.28	0.542	0.763	*#†
1372805_at	RGD1310444	LOC363015	180.75	1.609	1.306	*#
1393015_at	RGD1310587	Similar to hypothetical protein FLJ14146	223.83	0.662	0.843	*#†
1372293_at	RGD1562059	Similar to RIKEN cDNA 1110038F21	4050.12	1.979	1.797	---
1377867_at	RGD1562284	Similar to Glutaminyl-peptide cyclotransferase precursor (QC)	144.01	1.647	1.477	*#
1389241_at	RGD1562326	Similar to ubiquitin-protein ligase E3-alpha	236.82	1.509	1.289	#
1383398_at	RGD1564327	Similar to integrin alpha 8	267.80	1.502	1.065	#†
1385354_at	RGD1564327	Similar to integrin alpha 8	141.38	1.706	1.122	#†
1393171_at	RGD1564799	Similar to transmembrane 4 superfamily member 10	240.47	1.530	1.257	*#†
1376937_at	RGD1565927	Similar to 4631422O05Rik protein	248.31	2.063	1.377	#†
1371731_at	RGD1566215	Similar to Coatomer gamma-2 subunit (Gamma-2 coat protein) (Gamma-2 COP)	1589.68	0.449	0.662	*#†
1368144_at	Rgs2	Regulator of G-protein signaling 2	319.43	2.043	2.129	*#
1387074_at	Rgs2	Regulator of G-protein signaling 2	745.16	2.062	2.136	*#
1368505_at	Rgs4	Regulator of G-protein signaling 4	168.67	2.019	1.180	#†
1368506_at	Rgs4	Regulator of G-protein signaling 4	118.13	1.830	1.150	#†
1381279_at	Ripk2	Receptor-interacting serine-threonine kinase 2	216.58	1.536	1.310	#
1394077_at	Rnd3	Rho family GTPase 3	467.99	1.534	1.436	---
1367862_at	Rrad	Ras-related associated with diabetes	1028.00	0.886	0.408	*†
1373427_at	Rragd	Ras-related GTP binding D	150.62	0.742	0.576	*
1368914_at	Runx1	Runt related transcription factor 1	118.15	1.864	1.349	*#†
1367661_at	S100a6	S100 calcium binding protein A6	3796.99	1.698	1.286	#†

1376150_at	S1pr3	Sphingosine-1-phosphate receptor 3	631.72	0.647	0.925	#†
1384707_at	Scara5	Scavenger receptor class A, member 5 (putative)	55.64	1.756	1.343	*#†
1370355_at	Scd1	Stearoyl-Coenzyme A desaturase 1	379.13	1.809	2.071	*#
1376319_at	Sema3c	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	655.02	2.546	2.638	*#
1389353_at	Sema6d	Sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	332.47	0.538	0.821	#†
1398986_at	Serinc3	Serine incorporator 3	1442.63	1.519	1.070	#†
1368224_at	Serpina3n	Serine (or cysteine) peptidase inhibitor, clade A, member 3N	135.49	0.455	1.176	#†
1368519_at	Serpine1	Serine (or cysteine) peptidase inhibitor, clade E, member 1	131.30	6.782	2.265	*#†
1392264_s_at	Serpine1	Serine (or cysteine) peptidase inhibitor, clade E, member 1	78.74	3.997	1.700	#†
1372254_at	Serping1	Serine (or cysteine) peptidase inhibitor, clade G, member 1	2494.00	0.624	0.838	#†
1391537_at	Sertad4	SERTA domain containing 4	366.52	1.648	1.244	*#†
1382878_at	Sfrp1	Secreted frizzled-related protein 1	273.88	1.267	1.644	---
1383266_at	Sfrp1	Secreted frizzled-related protein 1	65.71	1.635	1.995	*#
1396614_at	Sfrp2	Secreted frizzled-related protein 2	715.83	0.655	0.822	#
1370419_a_at	Sh3kbp1	SH3-domain kinase binding protein 1	1288.11	0.519	0.817	*#†
1387957_a_at	Sh3kbp1	SH3-domain kinase binding protein 1	1766.62	0.552	0.907	#†
1373521_at	Sh3tc2	SH3 domain and tetratricopeptide repeats 2	98.16	1.519	1.233	*#†
1368965_at	Slc16a3	Solute carrier family 16, member 3 (monocarboxylic acid transporter 4)	579.54	1.411	2.080	*†
1368565_at	Slc1a3	Solute carrier family 1 (glial high affinity glutamate transporter), member 3	231.06	1.580	1.125	#†
1398295_at	Slc29a1	Solute carrier family 29 (nucleoside transporters), member 1	206.01	1.793	1.442	*#†
1372326_at	Slc2a3	Solute carrier family 2 (facilitated glucose transporter), member 3	67.87	1.524	1.512	*#
1369074_at	Slc38a4	Solute carrier family 38, member 4	102.49	1.776	1.152	#†
1373953_at	Slc4a1ap	Solute carrier family 4 (anion exchanger), member 1, adaptor protein	714.19	0.763	0.500	*†
1384302_at	Slc6a17	Solute carrier family 6 (neurotransmitter transporter), member 17	194.82	0.549	0.683	*#
1368582_at	Slc7a3	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 3	162.91	1.766	1.385	*#
1392965_a_at	Smoc2	SPARC related modular calcium binding 2	286.32	0.680	0.487	*#†
1373865_at	Snap91	Synaptosomal-associated protein 91	280.71	2.536	1.565	#
1380250_at	Sned1	Sushi, nidogen and EGF-like domains 1	482.62	0.215	0.546	*#†
1368596_at	Snf1lk	SNF1-like kinase	267.02	1.038	1.587	*†
1379271_at	Socs5	Suppressor of cytokine signaling 5	967.78	1.510	1.313	*#†
1381971_at	Sox18	SRY (sex determining region Y)-box 18	292.74	0.485	0.908	#†
1386865_at	Sparcl1	SPARC-like 1 (hevin)	314.25	0.535	0.906	#†
1374168_at	Sphkap	SPHK1 interactor, AKAP domain containing	525.13	0.458	0.551	*#
1370847_at	Spon2	Spondin 2, extracellular matrix protein	632.00	0.555	0.682	*#
1379380_at	Spry1	Sprouty homolog 1, antagonist of FGF signaling (Drosophila)	325.43	1.737	1.224	#†
1370228_at	Srprb /// Tf	Signal recognition particle receptor, B subunit /// transferrin	96.58	0.650	0.916	#†
1373000_at	Srpx2	Sushi-repeat-containing protein, X-linked 2	416.04	2.562	1.301	#†
1396101_at	Stc1	Stanniocalcin 1	251.64	1.569	0.855	#†
1393706_at	Steap1	Six transmembrane epithelial antigen of the prostate 1	387.18	1.515	1.405	---
1385397_at	Steap4	STEAP family member 4	239.69	0.225	0.463	#
1390107_at	Sytl2	Synaptotagmin-like 2	129.52	1.926	0.963	#†
1387138_at	Tac2	Tachykinin 2	226.21	0.458	1.052	#†
1367570_at	Tagln	Transgelin	1122.23	4.336	1.951	#
1383401_at	Tes	Testis derived transcript	219.21	1.859	1.306	#†
1389409_at	Tes	Testis derived transcript	52.23	1.547	1.310	---
1367859_at	Tgfb3	Transforming growth factor, beta 3	453.97	2.000	1.356	#
1369653_at	Tgfbr2	Transforming growth factor, beta receptor II	627.68	0.621	0.717	*#
1388497_at	Them2	Thioesterase superfamily member 2	494.69	0.655	0.661	*#
1369652_at	Thy1	Thy-1 cell surface antigen	58.17	1.511	1.109	#†
1372926_at	Timp3	TIMP metallopeptidase inhibitor 3	103.30	1.943	1.529	*#
1375138_at	Timp3	TIMP metallopeptidase inhibitor 3	433.86	1.796	1.322	*#†

1367650_at	Tinagl1	Tubulointerstitial nephritis antigen-like 1	223.25	1.733	1.702	---
1392280_at	Tlr2	Toll-like receptor 2	224.70	0.620	0.712	*#
1390042_at	Tmem140	Transmembrane protein 140	193.57	0.615	0.725	*#†
1373204_at	Tmem176a	Transmembrane protein 176A	914.46	0.373	0.624	*#†
1368840_at	Tmem176b	Transmembrane protein 176B	2155.28	0.479	0.669	*#
1376106_at	Tmem178	Transmembrane protein 178	572.08	0.418	0.793	*#†
1376623_at	Tmem204	Transmembrane protein 204	90.50	1.511	0.996	#†
1377448_at	Tmem38a	Transmembrane protein 38a	248.17	0.651	0.837	*#†
1389583_at	Tmem82	Transmembrane protein 82	126.92	0.695	0.596	---
1372156_at	Tmem97	Transmembrane protein 97	762.23	1.357	1.530	*#
1373401_at	Tnc	Tenascin C	289.54	2.387	1.364	#†
1369407_at	Tnfrsf11b	Tumor necrosis factor receptor superfamily, member 11b	287.92	2.589	1.410	#
1388145_at	Tnxa /// Tnxb	Tenascin XA /// tenascin XB	296.62	0.297	0.691	*#†
1370287_a_at	Tpm1	tTopomyosin 1, alpha	702.33	2.505	1.497	*#†
1372219_at	Tpm2	Tropomyosin 2	1632.63	2.257	1.271	#†
1368838_at	Tpm4	Tropomyosin 4	1828.01	1.557	1.305	*#
1371653_at	Tpm4	Tropomyosin 4	3012.89	1.713	1.451	*#
1385899_at	Trim16	Tripartite motif-containing 16	68.61	1.685	1.424	#
1375278_at	Trim2	Tripartite motif-containing 2	345.55	0.642	0.731	*#
1370139_a_at	Trpc6	Transient receptor potential cation channel, subfamily C, member 6	23.28	2.997	1.123	#†
1372286_at	Tspan6	Tetraspanin 6	1285.92	1.522	1.279	*#
1371702_at	Tspan7	Tetraspanin 7	1171.27	0.625	0.782	*#†
1370881_at	Tst	Thiosulfate sulfurtransferase, mitochondrial	554.95	0.656	0.779	*#†
1371618_s_at	Tubb3	Tubulin, beta 3	183.88	1.765	1.546	*#
1378165_at	Twist1	Twist homolog 1 (Drosophila)	137.80	1.528	1.238	#
1375221_at	Txndc13	Thioredoxin domain containing 13	1368.77	1.538	1.039	#†
1379910_at	Uap1	UDP-N-acteylglucosamine pyrophosphorylase 1	248.14	2.104	1.819	*#
1383945_at	Uck2	Uridine-cytidine kinase 2	305.54	1.511	1.373	*#
1369235_at	Unc5b	Uunc-5 homolog B (C. elegans)	625.94	1.552	1.610	---
1393799_at	Unc5b	Unc-5 homolog B (C. elegans)	835.71	1.522	1.531	*#
1371861_at	Unknown	Unknown	387.88	1.310	1.588	*#
1371969_at	Unknown	Unknown	851.03	2.368	1.370	*#†
1372095_at	Unknown	Unknown	189.58	0.587	0.665	*#
1372347_at	Unknown	Unknown	529.83	1.624	1.690	*#
1372583_at	Unknown	Unknown	95.98	2.646	1.638	*#†
1372750_at	Unknown	Unknown	139.11	3.966	1.759	*#†
1372761_at	Unknown	Unknown	81.54	0.608	0.900	#†
1373092_at	Unknown	Unknown	1494.77	0.650	0.743	*#
1373178_at	Unknown	Unknown	390.25	0.492	0.688	#
1373487_at	Unknown	Unknown	744.36	0.656	0.791	#
1373558_at	Unknown	Unknown	60.51	1.617	1.388	---
1373624_at	Unknown	Unknown	398.38	1.865	1.364	*#†
1373628_at	Unknown	Unknown	121.00	4.960	2.000	*#†
1373651_at	Unknown	Unknown	115.16	1.634	1.201	*#†
1373699_at	Unknown	Unknown	468.79	0.149	0.507	*#†
1374172_at	Unknown	Unknown	103.81	2.908	1.579	*#†
1374298_at	Unknown	Unknown	74.72	0.648	0.776	#
1374325_at	Unknown	Unknown	389.22	1.563	1.400	*#
1374410_at	Unknown	Unknown	63.34	1.536	1.261	*#
1374529_at	Unknown	Unknown	2639.64	2.030	1.462	*#†
1374749_at	Unknown	Unknown	183.25	1.503	1.414	*#
1374934_at	Unknown	Unknown	220.35	0.395	0.625	*#†

1375223_at	Unknown	Unknown	166.71	0.611	0.532	*#
1376071_at	Unknown	Unknown	510.71	1.565	1.318	*#
1376128_at	Unknown	Unknown	369.20	0.669	0.522	*#†
1376208_at	Unknown	Unknown	78.95	0.654	0.697	*#
1376282_at	Unknown	Unknown	412.92	1.670	1.226	#†
1376513_a_at	Unknown	Unknown	282.36	1.687	1.525	*#
1376574_at	Unknown	Unknown	530.84	0.626	1.026	#†
1376624_at	Unknown	Unknown	186.80	0.542	0.953	#†
1376734_at	Unknown	Unknown	238.81	2.749	1.200	#†
1376891_at	Unknown	Unknown	376.99	0.649	0.862	#†
1377240_at	Unknown	Unknown	92.38	2.044	1.897	*#
1377705_at	Unknown	Unknown	1438.05	2.139	1.830	*#
1377706_x_at	Unknown	Unknown	1254.27	2.364	2.012	*#
1377789_at	Unknown	Unknown	50.02	1.666	1.351	#
1377994_at	Unknown	Unknown	50.81	2.634	1.713	*#†
1378093_at	Unknown	Unknown	107.24	1.508	1.055	#†
1378171_at	Unknown	Unknown	335.48	1.719	1.120	#†
1378413_at	Unknown	Unknown	521.24	0.616	0.638	*#
1378467_at	Unknown	Unknown	66.62	1.570	1.363	#
1378556_at	Unknown	Unknown	398.24	2.265	1.817	*#†
1379252_at	Unknown	Unknown	137.32	2.436	1.382	*#†
1379517_at	Unknown	Unknown	161.45	0.696	0.609	*#
1379598_at	Unknown	Unknown	200.01	2.319	1.826	*#
1379785_at	Unknown	Unknown	221.25	1.619	1.406	*#
1379799_at	Unknown	Unknown	136.62	2.298	1.628	*#
1380318_at	Unknown	Unknown	294.00	1.880	1.041	#†
1380494_at	Unknown	Unknown	324.69	0.606	0.542	*#
1380544_at	Unknown	Unknown	220.60	1.739	1.402	*#
1380626_at	Unknown	Unknown	72.32	1.466	1.541	---
1380831_at	Unknown	Unknown	64.40	1.537	1.221	---
1382054_at	Unknown	Unknown	79.49	2.197	1.400	#
1382108_at	Unknown	Unknown	167.26	0.432	0.620	#
1382375_at	Unknown	Unknown	202.80	0.665	0.861	*#†
1382914_at	Unknown	Unknown	169.32	1.814	1.801	*#
1382950_at	Unknown	Unknown	197.64	0.552	0.754	*#†
1382995_at	Unknown	Unknown	264.28	1.991	1.184	#†
1383169_at	Unknown	Unknown	665.87	0.392	0.594	*#†
1383353_at	Unknown	Unknown	246.50	1.851	1.449	*#
1383486_at	Unknown	Unknown	110.87	5.750	2.947	*#†
1383939_at	Unknown	Unknown	460.62	1.518	1.361	*#
1384051_at	Unknown	Unknown	143.67	3.750	1.813	*#†
1384188_at	Unknown	Unknown	143.63	0.691	0.651	*#
1384228_at	Unknown	Unknown	166.22	1.535	1.498	*#
1384286_at	Unknown	Unknown	116.41	1.574	1.085	#†
1384709_at	Unknown	Unknown	70.42	2.456	1.163	#†
1384841_at	Unknown	Unknown	213.40	0.401	0.725	*#†
1385053_at	Unknown	Unknown	98.21	0.832	0.583	*†
1385128_at	Unknown	Unknown	83.87	0.480	0.793	#†
1385132_at	Unknown	Unknown	49.77	2.324	2.605	*#
1385181_at	Unknown	Unknown	46.22	1.582	1.313	---
1386186_s_at	Unknown	Unknown	110.49	1.541	1.116	#†
1388742_at	Unknown	Unknown	458.25	0.487	0.673	*#†

1388872_at	Unknown	Unknown	946.13	1.273	1.546	*#†
1388880_at	Unknown	Unknown	537.65	0.602	0.740	*#
1388986_at	Unknown	Unknown	507.54	1.516	1.326	*#
1389039_at	Unknown	Unknown	253.41	1.779	1.251	#†
1389186_at	Unknown	Unknown	443.25	0.621	0.963	#†
1389284_at	Unknown	Unknown	262.04	0.592	0.930	#†
1389394_at	Unknown	Unknown	1017.80	1.681	1.411	*#
1389500_at	Unknown	Unknown	404.49	0.421	0.914	#†
1389586_at	Unknown	Unknown	335.56	1.884	1.198	*#†
1390364_at	Unknown	Unknown	86.04	1.807	1.372	*#
1390436_at	Unknown	Unknown	763.06	0.583	0.707	*#
1390659_at	Unknown	Unknown	355.52	1.771	1.564	*#
1390885_at	Unknown	Unknown	271.63	1.538	1.191	*#†
1391071_at	Unknown	Unknown	36.99	1.803	1.119	#†
1391418_at	Unknown	Unknown	112.29	1.667	1.228	#†
1391428_at	Unknown	Unknown	123.39	1.666	1.066	#†
1391481_at	Unknown	Unknown	124.94	1.309	1.586	*
1391812_at	Unknown	Unknown	195.72	0.345	0.807	#†
1392627_x_at	Unknown	Unknown	401.84	1.503	1.428	*#
1392863_at	Unknown	Unknown	67.88	0.645	0.706	*#
1393119_at	Unknown	Unknown	254.52	1.620	1.754	*#
1393492_at	Unknown	Unknown	72.65	1.545	1.240	#
1393559_at	Unknown	Unknown	137.04	1.519	0.699	†
1393653_at	Unknown	Unknown	192.33	2.120	1.241	*#†
1393728_at	Unknown	Unknown	88.73	1.535	1.487	---
1394109_at	Unknown	Unknown	841.50	2.689	1.771	*#
1395362_at	Unknown	Unknown	384.04	1.533	1.607	*#
1395442_at	Unknown	Unknown	58.15	2.026	1.429	*#†
1395557_at	Unknown	Unknown	173.22	1.720	1.447	*#
1397540_at	Unknown	Unknown	306.77	0.641	0.658	*#
1397808_at	Unknown	Unknown	850.98	0.434	0.754	#†
1397851_at	Unknown	Unknown	186.84	1.304	1.531	---
1397897_x_at	Unknown	Unknown	94.33	1.566	1.252	*#†
1398348_at	Unknown	Unknown	618.84	1.851	1.953	---
1373510_at	Vamp1	Vesicle-associated membrane protein 1	173.46	0.600	0.634	*#
1368474_at	Vcam1	Vascular cell adhesion molecule 1	1165.17	0.330	0.626	*#†
1388142_at	Vcan	Versican	660.54	1.343	1.513	---
1372905_at	Vcl	Vinculin	1928.79	1.840	1.431	---
1368463_at	Vegfc	Vascular endothelial growth factor C	240.90	1.942	1.244	*#†
1387873_at	Wfdc1	WAP four-disulfide core domain 1	185.54	1.765	1.956	*#
1370221_at	Wisp1	WNT1 inducible signaling pathway protein 1	110.34	2.242	1.413	#†
1369484_at	Wisp2	WNT1 inducible signaling pathway protein 2	678.10	2.375	1.480	*#†
1392670_at	Wwc2	WW and C2 domain containing 2	245.54	1.750	1.521	*#
1395525_at	Wwc2	WW and C2 domain containing 2	305.76	1.551	1.305	#
1369973_at	Xdh	Xanthine dehydrogenase	458.12	0.540	0.690	*#†
1375846_at	Xpr1	Xenotropic and polytropic retrovirus receptor 1	569.88	1.504	1.607	*#

Supplemental Table S7 Changes in transcript expression induced by PE at 0.5 and 1 h

RNA expression analysis was performed using Affymetrix rat exon 1.0 ST microarrays and GeneSpring 12.0, identifying transcripts that were significantly changed by PE at 0.5 or 1 h. Data are provided for PE and ET-1 for the same transcripts for comparison. The raw data for controls are given and results at each time are the mean fold change relative to the controls (n=3). K-means clustering was performed to identify upregulated (U0-U2) and downregulated (D0-D2) groups. Statistical analysis was performed by one-way ANOVA with SNK post-test using a Benjamini and Hochberg false discovery rate correction (FDR<0.05) * 0.5 h vs control; # 1 h vs control; † 0.5 vs 1 h.

Transcript cluster ID	Gene Symbol	Gene Title	Raw data (Control)	ET-1, 0.5 h	ET-1, 1 h	PE, 0.5 h	PE, 1 h	Statistical significance (PE)	Cluster
7091079	Adamts1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	757	1.981	2.291	1.459	1.520	*#	U1
7370009	Ankrd57	Ankyrin repeat domain 57	141	1.456	1.643	1.683	1.616	*#	U1
7259100	Apold1	Apolipoprotein L domain containing 1	487	1.681	1.843	1.527	1.432	*#	U1
7328919	Arc	Activity-regulated cytoskeleton-associated protein	66	1.887	6.367	2.711	2.649	*#	U1
7123848	Areg	Amphiregulin	163	1.862	2.880	1.414	1.900	*#†	U2
7142915	Arhgef3	Rho guanine nucleotide exchange factor (GEF) 3	199	1.054	2.763	1.220	2.068	*#†	U2
7160453	Arl5b	ADP-ribosylation factor-like 5B	445	1.525	1.820	2.384	2.732	*#†	U1
7224825	Arrdc3	Arrestin domain containing 3	1760	1.150	0.694	2.787	2.214	*#†	U1
7135004	AS to Spry2	Antisense to Sprouty 2	214	1.416	1.601	1.357	1.683	*#	U2
7115455	Atf3	Activating transcription factor 3	480	2.141	7.189	3.286	3.487	*#	U1
7249102	Bdnf	Brain derived neurotrophic factor	161	1.009	1.311	1.347	1.530	*#†	U2
7257144	Bhlhe40	Basic helix-loop-helix family, member e40	2190	1.117	1.107	1.770	1.718	*#	U1
7111272	Btg2	BTG family, member 2	421	5.329	5.287	5.059	3.802	*#†	U1
7086934	Cbr1	Carbonyl reductase 1	1107	0.812	0.935	1.738	2.366	*#†	U2
7086951	Cbr1	Carbonyl reductase 1	811	0.914	0.977	1.952	2.872	*#†	U2
7086964	Cbr3	Carbonyl reductase 3	109	0.975	1.017	1.725	2.191	*#†	U2
7070340	Ccl7	Chemokine (C-C motif) ligand 7	2024	1.385	1.548	1.516	1.068	*†	U0
7209338	Ccnl1	Cyclin L1	597	2.904	1.917	1.683	1.455	*#	U0
7350504	Ccr4	Chemokine (C-C motif) receptor 4	43	1.320	1.230	1.555	1.174	*†	U0
7193902	Ccrn4l	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	186	1.812	6.278	1.271	2.209	*#†	U2
7219866	Cd24	CD24 molecule	739	0.896	0.943	1.404	1.688	*#†	U2
7062006	Ch25h	Cholesterol 25-hydroxylase	420	3.704	5.685	3.463	2.519	*#†	U0
7025269	Cited2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	1277	1.934	3.206	1.493	1.969	*#†	U2
7039008	Clcf1	Cardiotrophin-like cytokine factor 1	184	1.082	1.347	1.603	1.648	*#	U1
7153439	Cln8	Claudin 8	288	0.961	1.007	1.380	1.502	*#†	U1
7354636	Coq10b	Coenzyme Q10 homolog B (S. cerevisiae)	580	1.421	2.253	2.049	2.393	*#	U1
7158671	Crem	cAMP responsive element modulator	239	1.207	1.301	1.509	1.535	*#	U1
7071906	Csf3	Colony stimulating factor 3 (granulocyte)	274	1.416	0.894	1.597	1.222	*#†	U0
7350918	Csrnp1	Cysteine-serine-rich nuclear protein 1	257	2.066	4.191	2.613	2.400	*#†	U1
7044959	Ctgf	cCnnective tissue growth factor	1305	3.006	2.566	1.743	1.819	*#	U1
7123885	Cxcl1	Chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	2563	1.585	1.257	2.044	1.085	*†	U0
7123883	Cxcl2	Chemokine (C-X-C motif) ligand 2	762	1.164	1.318	1.471	1.651	*#	U1
7357534	Cxcr7	Chemokine (C-X-C motif) receptor 7	1370	1.291	1.220	1.567	1.557	*#	U1
7302739	Cyp1b1	Cytochrome P450, family 1, subfamily B, polypeptide 1	948	1.362	1.080	1.450	1.510	*#	U1
7215359	Cyr61	Cysteine-rich, angiogenic inducer, 61	1616	5.414	3.769	2.591	1.826	*#†	U0
7107035	Dnm3	Dynamin 3	379	0.481	0.566	0.530	0.743	*#†	D2

7312560	Dos	Downstream of Stk11	92	1.078	1.059	1.385	1.691	*#†	U2
7066011	Dusp1	Dual specificity phosphatase 1	1462	3.605	2.695	2.469	1.607	*#†	U0
7108644	Dusp10	Dual specificity phosphatase 10	281	1.063	3.725	1.131	1.675	*#†	U2
7152119	Dusp4	Dual specificity phosphatase 4	306	1.299	1.849	1.504	2.019	*#†	U2
7043230	Dusp5	Dual specificity phosphatase 5	377	1.996	4.501	2.310	2.540	*#	U1
7314286	Dusp6	Dual specificity phosphatase 6	1813	1.953	2.184	1.368	1.737	*#†	U2
7163221	Edn1	Endothelin 1	121	2.475	2.745	2.191	1.351	*#†	U0
7169197	Egr1	Early growth response 1	1804	6.774	3.158	3.421	2.388	*#†	U0
7222466	Egr2	Early growth response 2	159	5.112	4.856	5.306	3.579	*#†	U0
7133143	Egr3	Early growth response 3	142	4.254	16.346	6.353	6.743	*#	U1
7188693	Enc1	Ectodermal-neural cortex 1	380	1.109	1.299	1.508	1.644	*#†	U1
7123853	Ereg	Epiregulin	139	2.137	4.518	2.968	3.572	*#†	U1
7281719	Errfi1	ERBB receptor feedback inhibitor 1	1669	3.142	3.706	2.673	2.988	*#†	U1
7297136	Fam110c	Family with sequence similarity 110, member C	111	1.979	3.760	1.875	2.537	*#†	U2
7212002	Fam46c	Family with sequence similarity 46, member C	163	1.235	1.126	1.432	1.781	*#†	U2
7345585	Fdx1	Ferredoxin 1	494	1.553	3.480	2.676	3.197	*#†	U1
7300295	Fos	FBJ osteosarcoma oncogene	178	15.214	2.952	7.867	2.566	*#†	U0
7048605	Fosb	FBJ osteosarcoma oncogene B	94	25.477	23.168	3.508	2.739	*#†	U1
7039170	Fosl1	Fos-like antigen 1	184	1.456	5.980	2.073	3.088	*#†	U2
7162363	Gadd45g	Growth arrest and DNA-damage-inducible, gamma	748	3.560	2.381	1.741	1.893	*#	U1
7338247	Gclc	Glutamate-cysteine ligase, catalytic subunit	798	1.412	1.668	1.451	2.034	*#†	U2
7144218	Gdf15	Growth differentiation factor 15	291	1.583	1.143	1.804	1.158	*#†	U0
7067195	Gfpt2	Glutamine-fructose-6-phosphate transaminase 2	2413	1.025	1.186	1.424	1.820	*#†	U2
7280238	Gpr3	G protein-coupled receptor 3	128	1.085	1.942	1.359	1.790	*#†	U2
7047218	Has1	Hyaluronan synthase 1	71	2.021	2.452	3.319	3.324	*#	U1
7327675	Has2	Hyaluronan synthase 2	552	3.069	8.143	3.862	4.896	*#†	U1
7055290	Hbb	Hemoglobin subunit beta-1	4634	0.912	0.600	0.646	0.714	*#	D1
7174562	Hbegf	Heparin-binding EGF-like growth factor	304	1.503	3.592	1.285	1.610	*#†	U2
7266497	Hk2	Hexokinase 2	305	1.034	1.712	1.098	1.551	*#†	U2
7179800	Ier2	Immediate early response 2	435	5.475	2.463	3.344	1.871	*#†	U0
7220503	Ier3	Immediate early response 3	1963	1.766	1.347	2.924	1.871	*#†	U0
7104832	Il10	Interleukin 10	43	4.331	1.479	3.948	1.642	*#†	U0
7028549	Il11	Interleukin 11	222	1.769	1.920	2.061	2.115	*#	U1
7036726	Il4ra	Interleukin 4 receptor, alpha	645	1.173	0.937	1.319	1.537	*#†	U2
7260080	Il6	Interleukin 6	229	6.140	4.611	12.595	5.897	*#†	U0
7165193	Inhba	Inhibin beta-A	213	1.950	6.251	1.713	2.519	*#†	U2
7147829	Intron to Col14a1	Intron to Col14a1	180	1.198	1.332	1.564	1.314	*#	U0
7135534	Intron to Mbn12	Intron to Mbn12	186	1.352	1.315	1.303	1.531	*#	U2
7091841	Intron to Runx1	Intron to Runx1	68	1.216	1.593	1.154	1.779	*#†	U2
7147838	Irs2	Insulin receptor substrate 2	209	1.610	1.707	2.157	2.436	*#†	U1
7049112	Itpkc	Inositol 1,4,5-trisphosphate 3-kinase C	132	1.180	1.291	2.151	2.412	*#†	U1
7041047	Jak2	Janus kinase 2	379	2.151	0.673	0.658	0.705	*#	D1
7179739	Junb	Jun B proto-oncogene	392	3.287	1.443	2.713	1.781	*#†	U0
7326749	Klf10	Kruppel like factor 10	227	0.783	1.088	1.296	1.518	*#†	U2
7149521	Klf2	Kruppel-like factor 2 (lung)	178	2.282	1.931	1.591	1.199	*#†	U0
7286480	Klf4	Kruppel-like factor 4 (gut)	234	2.580	3.458	2.153	2.242	*#	U1
7120521	Lif	Leukemia inhibitory factor (cholinergic differentiation factor)	204	4.823	4.712	7.569	5.317	*#†	U1
7257290	Lmcd1	LIM and cysteine-rich domains 1	523	1.751	2.929	1.181	1.714	*#†	U2
7335998	LOC363060	Similar to RIKEN cDNA 1600029D21	120	1.053	1.704	1.153	2.123	*#†	U2
7318753	Maff	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	147	1.553	1.957	1.360	1.510	*#	U1

7266023	Mat2a	Methionine adenosyltransferase II, alpha	2888	1.468	1.620	1.547	1.678	*#	U1
7173133	Mir1-2/Mir133a-1	MicroRNA Mir1-2/Mir133a-1	791	1.184	0.492	0.927	0.498	#†	D0
7335235	Mir125b-1	MicroRNA Mir125b-1	580	1.268	2.624	1.184	1.640	#†	U2
7105681	Mir181b-1	MicroRNA mir-181b-1	112	0.849	0.723	0.645	1.418	*†	D2
7384266	Mir351/542	MicroRNA Mir351/542	232	1.447	1.005	1.690	1.115	*†	U0
7211447	Mllt1	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1	335	1.675	1.681	1.402	1.552	*#	U1
7317471	Myc	Myelocytomatosis oncogene	212	1.830	2.602	1.323	1.554	*#†	U2
7326308	Nab2	Ngfi-A binding protein 2	580	1.025	1.012	1.530	1.403	*#†	U1
7297245	Nampt	Nicotinamide phosphoribosyltransferase	352	0.848	1.570	1.242	1.710	*#†	U2
7155813	Nfil3	Nuclear factor, interleukin 3 regulated	107	1.584	2.735	1.968	2.369	*#	U1
7320920	Nr4a1	Nuclear receptor subfamily 4, group A, member 1	163	8.505	18.929	20.769	20.607	*#	U1
7239111	Nr4a2	Nuclear receptor subfamily 4, group A, member 2	106	2.381	8.923	13.409	14.626	*#	U1
7274931	Nr4a3	Nuclear receptor subfamily 4, group A, member 3	121	2.813	7.361	10.615	11.601	*#	U1
7270053	Olr1	Oxidized low density lipoprotein (lectin-like) receptor 1	1893	1.290	1.585	1.639	1.998	*#†	U2
7034940	Olr148	Olfactory receptor 148	53	1.099	1.202	1.587	1.206	*†	U0
7241464	Olr704	olfactory receptor 704	40	1.049	1.402	1.530	1.191	*#†	U0
7296159	Osr1	Odd-skipped related 1 (Drosophila)	259	0.857	0.964	0.952	0.592	#†	D0
7235566	Pard6b	Par-6 (partitioning defective 6) homolog beta (C. elegans)	98	1.230	3.622	1.104	1.838	#†	U2
7277759	Pde4b	Phosphodiesterase 4b	474	0.910	1.110	1.410	1.516	*#†	U1
7189455	Pde4d	Phosphodiesterase 4d	385	1.012	1.048	1.250	1.500	*#†	U2
7204067	Pelo	Pelota homolog (Drosophila)	1185	1.079	1.419	1.241	1.520	*#†	U2
7283288	Penk	Proenkephalin	2246	1.258	1.101	1.360	1.524	*#†	U1
7068987	Per1	Period homolog 1 (Drosophila)	131	1.368	1.467	1.631	2.210	*#†	U2
7314872	Phlda1	Pleckstrin homology-like domain, family A, member 1	520	3.517	4.155	3.994	3.388	*#†	U1
7120384	Pik3ip1	Phosphoinositide-3-kinase interacting protein 1	485	0.696	0.544	0.803	0.585	*#†	D0
7217331	Pim1	Pim-1 oncogene	1687	1.610	1.703	1.772	1.208	*#†	U0
7189518	Plk2	Polo-like kinase 2 (Drosophila)	1947	2.445	3.030	1.707	1.559	*#	U1
7290290	Plk3	Polo-like kinase 3 (Drosophila)	179	1.449	1.508	1.678	1.308	*#†	U0
7339147	Plscr1	Phospholipid scramblase 1	169	0.997	1.408	1.464	1.833	*	U2
7237508	Ptges	Prostaglandin E synthase	427	0.979	0.902	1.276	1.862	*#†	U2
7106132	Ptgs2	Prostaglandin-endoperoxide synthase 2	258	7.005	7.981	5.272	3.312	*#†	U0
7354851	Ptp4a1	Protein tyrosine phosphatase 4a1	544	1.346	1.779	1.431	1.575	*#	U1
7078129	Rasd1	RAS, dexamethasone-induced 1	419	2.249	0.875	2.179	1.236	*#†	U0
7124933	Rasl11b	RAS-like family 11 member B	855	2.304	1.841	1.643	1.362	*#†	U0
7128932	Rel	v-rel reticuloendotheliosis viral oncogene homolog gene	203	1.532	1.951	1.581	2.022	*#†	U2
7030172	RGD1563982	Similar to F-box only protein 27	192	1.060	1.071	1.431	1.592	*#†	U1
7294961	RGD1565310	Similar to RIKEN cDNA 1110018J12	83	0.771	0.878	0.588	0.614	*#	D1
7112009	Rgs2	Regulator of G-protein signaling 2	613	3.146	5.494	5.024	4.199	*#†	U1
7304448	Rhob	Ras homolog gene family, member B	799	2.595	2.593	2.209	1.786	*#†	U0
7284153	Ripk2	Receptor-interacting serine-threonine kinase 2	397	0.936	2.663	1.105	1.535	#†	U2
7331581	Rnd1	Rho family GTPase 1	421	1.595	2.215	1.173	1.519	*#†	U2
7178179	Rrad	Ras-related associated with diabetes	443	0.856	0.894	0.658	0.553	*#	D1
7103916	Serpinb2	Serine (or cysteine) peptidase inhibitor, clade B, member 2	284	3.388	14.086	1.826	3.231	*#†	U2
7101220	Serpine1	Serine (or cysteine) peptidase inhibitor, clade E, member 1	601	6.428	8.141	1.773	2.001	*#	U1
7221460	Sik1	Salt-inducible kinase 1	415	1.889	2.039	3.478	4.112	*#†	U1
7237652	Slc25a25	Solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25	148	2.662	1.748	1.561	1.257	*#†	U0
7269356	Slc2a3	Solute carrier family 2 (facilitated glucose transporter), member 3	435	0.833	1.571	2.040	2.752	*#†	U2
7187663	Snrpd1|Ell2	Small nuclear ribonucleoprotein D1 | elongation factor RNA polymerase II 2	148	1.285	2.281	1.239	2.557	*#†	U2

7073409	Sox9	SRY box-containing gene 9	351	1.006	0.974	1.568	1.826	*#†	U1
7382102	Spin4	Spindlin family, member 4	248	0.921	1.323	1.433	1.785	*#†	U2
7141508	Spry2	Sprouty 2	795	1.720	2.261	1.523	1.221	*#†	U0
7233921	Srxn1	Sulfiredoxin 1 homolog (S. cerevisiae)	119	1.802	2.171	1.553	1.812	*#	U1
7152722	Star	Steroidogenic acute regulatory protein	159	1.125	1.143	1.494	1.753	*#†	U2
7261795	Tfpi2	Tissue factor pathway inhibitor 2	294	1.040	2.020	1.314	1.781	*#†	U2
7308910	Tgfb3	Transforming growth factor beta 3	299	1.297	2.044	1.240	1.505	*#†	U2
7246265	Thbd	Thrombomodulin	110	1.756	1.588	1.218	1.642	#†	U2
7106964	Tnfsf18	Tumor necrosis factor (ligand) superfamily, member 18	129	2.348	7.480	1.578	1.602	*#	U1
7317342	Trib1	Tribbles homolog 1 (Drosophila)	183	2.805	2.680	1.427	1.726	*#†	U2
7297329	Twist1	Twist homolog 1 (Drosophila)	215	1.259	3.797	1.477	1.707	*#	U1
7197113	Txnip	Thioredoxin interacting protein	2271	1.149	0.671	0.599	0.571	*#	D1
7113823	Uap1	UDP-N-acteylglucosamine pyrophosphorylase 1	430	1.172	3.186	1.701	3.032	*#†	U2
7118521	Ugdh	UDP-glucose 6-dehydrogenase	1143	1.054	1.566	1.415	1.548	*#†	U1
7043686	Unknown	Unknown	50	1.150	1.022	1.507	1.063	*†	U0
7057552	Unknown	Unknown	134	0.807	0.698	0.646	0.697	*#	D1
7061626	Unknown	Unknown	57	0.892	1.503	1.116	1.702	#†	U2
7071496	Unknown	Unknown	96	0.587	0.789	0.662	0.877	*†	D2
7085388	Unknown	Unknown	85	1.385	0.962	1.802	1.370	*#†	U0
7085832	Unknown	Unknown	98	0.872	1.411	2.165	1.680	*#	U0
7096304	Unknown	Unknown	90	0.795	0.625	0.692	0.620	*#†	D1
7145048	Unknown	Unknown	283	0.930	0.615	0.624	0.594	*#	D1
7146009	Unknown	Unknown	124	1.329	1.192	1.486	1.651	*#	U1
7174327	Unknown	Unknown	85	1.568	1.400	1.756	1.600	*#	U1
7200422	Unknown	Unknown	124	2.974	2.049	1.590	1.447	*#†	U1
7203844	Unknown	Unknown	65	1.016	1.099	1.563	1.278	*	U0
7209914	Unknown	Unknown	103	1.107	0.601	0.703	0.665	*#	D1
7212310	Unknown	Unknown	155	1.077	2.227	1.429	1.869	*#†	U2
7224482	Unknown	Unknown	540	0.354	0.504	0.532	0.712	*#†	D2
7243539	Unknown	Unknown	62	0.858	1.310	1.381	1.607	*#	U2
7256305	Unknown	Unknown	70	1.403	1.519	2.035	2.238	*#	U1
7288050	Unknown	Unknown	182	1.014	0.619	0.792	0.651	*#†	D1
7297222	Unknown	Unknown	267	1.827	2.360	1.210	1.539	*#†	U2
7297247	Unknown	Unknown	194	1.399	2.808	2.224	1.575	*#†	U0
7305661	Unknown	Unknown	86	0.886	1.334	1.063	1.530	#†	U2
7341409	Unknown	Unknown	46	1.461	1.073	1.553	1.149	*†	U0
7367172	Unknown	Unknown	450	0.966	0.925	0.782	0.654	*#†	D1
7368431	Unknown	Unknown	99	1.099	0.692	0.709	0.632	*#	D1
7368915	Unknown	Unknown	98	1.222	0.712	0.637	0.548	*#	D1
7369143	Unknown	Unknown	153	0.854	0.876	0.585	0.442	*#	D1
7369253	Unknown	Unknown	91	1.034	1.004	0.751	0.660	*#	D1
7370000	Unknown	Unknown	166	0.671	1.112	1.831	1.176	*†	U0
7370355	Unknown	Unknown	1984	0.906	1.432	1.582	1.326	*	U0
7370666	Unknown	Unknown	466	0.829	0.824	0.743	0.651	#	D1
7370806	Unknown	Unknown	360	0.785	0.788	0.571	0.734	*	D2
7371629	Unknown	Unknown	72	0.909	0.891	0.676	0.571	*#	D1
7335234	Vof16	Ischemia related factor vof-16	410	1.443	2.856	1.080	1.616	#†	U2
7350922	Xirp1	Xin actin-binding repeat containing 1	520	1.323	1.997	1.132	1.644	#†	U2
7290942	Zc3h12a	Zinc finger CCCH type containing 12A	264	0.980	0.981	1.805	1.467	*#†	U0
7096947	Zfand2a	Zinc finger, AN1-type domain 2A	555	1.204	1.714	1.217	1.513	*#†	U2
7049312	Zfp36	Zinc finger protein 36	302	3.606	2.516	3.204	1.845	*#†	U0

Supplemental Table S8 Changes in transcript expression induced by ET-1 at 0.5 and 1 h

RNA expression analysis was performed using Affymetrix rat exon 1.0 ST microarrays, identifying transcripts that were significantly changed by ET-1 at 0.5 or 1 h. Data are provided for PE and ET-1 for the same transcripts for comparison. The raw data for controls are given and results at each time are the mean fold change relative to the controls (n=3). Statistical analysis for ET-1-responsive transcripts was performed by one-way ANOVA with SNK post-test using a Benjamini and Hochberg false discovery rate correction (FDR<0.05) * 0.5 h vs control; # 1 h vs control; † 0.5 vs 1 h.

Transcript cluster ID	Gene Symbol	Gene Title	Raw data (Control)	ET-1, 0.5 h	ET-1, 1 h	PE, 0.5 h	PE, 1 h	Statistical significance (ET-1)
7327038	Abra	Actin-binding Rho activating protein	86	1.249	1.775	1.033	1.295	#†
7091079	Adamts1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	757	1.981	2.291	1.459	1.520	*#†
7343686	Adamts15	ADAM metallopeptidase with thrombospondin type 1 motif, 15	318	0.822	0.590	0.839	0.726	*#†
7123129	Agpat9	1-acylglycerol-3-phosphate O-acyltransferase 9	109	0.952	2.054	0.995	1.404	#†
7275485	Akap2	A kinase (PRKA) anchor protein 2	829	1.395	1.783	1.224	1.356	*#†
7213945	Alpk1	Alpha-kinase 1	130	1.014	1.608	0.940	0.996	#†
7322881	Angptl4	Angiopoietin-like 4	303	0.889	0.664	0.775	0.869	#†
7370009	Ankrd57	Ankyrin repeat domain 57	141	1.456	1.643	1.683	1.616	*#
7060990	Anxa1	Annexin A1	2440	1.322	2.344	0.993	1.031	#†
7160892	Apbb1ip	Amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein	81	1.085	1.556	0.973	0.854	*#†
7259100	Apold1	Apolipoprotein L domain containing 1	487	1.681	1.843	1.527	1.432	*#
7328919	Arc	Activity-regulated cytoskeleton-associated protein	66	1.887	6.367	2.711	2.649	*#†
7123848	Areg	Amphiregulin	163	1.862	2.880	1.414	1.900	*#†
7142915	Arhgef3	Rho guanine nucleotide exchange factor (GEF) 3	199	1.054	2.763	1.220	2.068	#†
7353382	Arid5a	AT rich interactive domain 5A (Mrf1 like)	246	1.457	1.547	1.069	1.311	*#
7218259	Arid5b	AT rich interactive domain 5B (Mrf1 like)	397	1.266	1.684	1.099	1.326	*#†
7160453	Arl5b	ADP-ribosylation factor-like 5B	445	1.525	1.820	2.384	2.732	*#
7115455	Atf3	Activating transcription factor 3	480	2.141	7.189	3.286	3.487	*#†
7024628	Atp13a3|LOC678704|LOC292449	ATPase type 13A3 | hypothetical protein LOC678704 | similar to hypothetical protein	347	1.017	1.616	1.055	1.173	#†
7105894	B3galt2	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	394	1.220	1.515	1.144	1.271	*#†
7048723	Bcl3	B-cell CLL/lymphoma 3	289	0.855	0.583	1.007	0.825	*#†
7301401	Bdkrb1	Bradykinin receptor B1	52	1.677	1.445	1.148	1.240	*#
7271485	Bhlhe41	Basic helix-loop-helix family, member e41	274	0.667	0.952	1.088	1.324	*†
7232862	Bmp2	Bone morphogenetic protein 2	139	1.821	2.443	1.141	1.393	*#
7111272	Btg2	BTG family, member 2	421	5.329	5.287	5.059	3.802	*#
7159536	Calml3	Calmodulin-like 3	114	1.538	0.991	1.038	1.004	*†
7251397	Cav1	Caveolin 1, caveolae protein	2474	0.979	1.551	1.007	1.073	#†
7070340	Ccl7	Chemokine (C-C motif) ligand 7	2024	1.385	1.548	1.516	1.068	*#†
7209338	Ccnl1	Cyclin L1	597	2.904	1.917	1.683	1.455	*#†
7193902	Ccrn4l	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	186	1.812	6.278	1.271	2.209	*#†
7113283	Cct6a	Chaperonin containing Tcp1, subunit 6A (zeta 1)	678	0.736	0.551	1.182	0.883	#
7242411	Cd44	Cd44 molecule	402	1.175	2.327	1.071	1.421	*#†
7110888	Cd55	Cd55 molecule	193	1.014	1.632	1.120	1.335	#†
7059858	Cdc42ep2	CDC42 effector protein (Rho GTPase binding) 2	310	1.020	0.626	0.972	0.795	#†
7062006	Ch25h	Cholesterol 25-hydroxylase	420	3.704	5.685	3.463	2.519	*#
7231595	Chac1	ChaC, cation transport regulator homolog 1 (E. coli)	315	1.344	2.368	1.461	1.078	*#†

7025269	Cited2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	1277	1.934	3.206	1.493	1.969	*#†
7279127	Cited4	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4	365	0.695	0.641	0.865	0.631	---
7045969	Cnksr3	Cnksr family member 3	289	0.988	1.544	0.975	1.115	#†
7250799	Col1a2	Collagen, type I, alpha 2	2538	1.583	0.935	0.951	1.003	*#†
7354636	Coq10b	Coenzyme Q10 homolog B (S. cerevisiae)	580	1.421	2.253	2.049	2.393	*#†
7077481	Csf2	Colony stimulating factor 2 (granulocyte-macrophage)	37	1.008	1.694	1.163	1.168	#†
7350918	Csrnp1	Cysteine-serine-rich nuclear protein 1	257	2.066	4.191	2.613	2.400	*#†
7051386	Csrp3	Cysteine and glycine-rich protein 3	2662	1.040	1.512	1.234	1.245	#†
7044959	Ctgf	Connective tissue growth factor	1305	3.006	2.566	1.743	1.819	*#
7333046	Cwc15|LOC310177	CWC15 spliceosome-associated protein homolog (S. cerevisiae) | similar to RIKEN cDNA 0610040D20	425	0.664	1.135	1.016	1.196	*†
7123885	Cxcl1	Chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	2563	1.585	1.257	2.044	1.085	*#†
7214253	Cyp2u1	Cytochrome P450, family 2, subfamily u, polypeptide 1	362	0.856	0.599	0.927	0.868	#
7215359	Cyr61	Cysteine-rich, angiogenic inducer, 61	1616	5.414	3.769	2.591	1.826	*#†
7222734	Ddit4	DNA-damage-inducible transcript 4	1221	0.941	0.483	1.147	1.013	#†
7107035	Dnm3	Dynamin 3	379	0.481	0.566	0.530	0.743	*#
7060585	Dtx4	Deltex homolog 4 (Drosophila)	455	0.851	0.643	0.785	0.738	*#†
7066011	Dusp1	Dual specificity phosphatase 1	1462	3.605	2.695	2.469	1.607	*#†
7108644	Dusp10	Dual specificity phosphatase 10	281	1.063	3.725	1.131	1.675	#†
7152119	Dusp4	Dual specificity phosphatase 4	306	1.299	1.849	1.504	2.019	*#†
7043230	Dusp5	Dual specificity phosphatase 5	377	1.996	4.501	2.310	2.540	*#†
7314286	Dusp6	Dual specificity phosphatase 6	1813	1.953	2.184	1.368	1.737	*#
7163221	Edn1	Endothelin 1	121	2.475	2.745	2.191	1.351	*#
7147985	Efnb2	Ephrin B2	154	0.933	1.537	1.075	1.221	#†
7169197	Egr1	Early growth response 1	1804	6.774	3.158	3.421	2.388	*#†
7222466	Egr2	Early growth response 2	159	5.112	4.856	5.306	3.579	*#
7133143	Egr3	Early growth response 3	142	4.254	16.346	6.353	6.743	*#†
7259141	Emp1	Epithelial membrane protein 1	1724	1.265	2.128	1.060	1.101	#†
7114850	Enah	Enabled homolog (Drosophila)	1485	1.817	1.339	1.050	1.066	*#†
7281135	Epha2	Eph receptor A2	163	1.169	2.020	1.101	1.328	*#†
7123853	Ereg	Epiregulin	139	2.137	4.518	2.968	3.572	*#†
7281719	Errfi1	ERBB receptor feedback inhibitor 1	1669	3.142	3.706	2.673	2.988	*#†
7334452	Ets1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	712	0.895	1.755	1.044	1.276	#†
7198615	F3	Coagulation factor III (thromboplastin, tissue factor)	165	1.466	3.580	1.073	0.958	*#†
7065178	Fam100a	Family with sequence similarity 100, member A	352	1.570	1.342	1.082	1.152	*#†
7297136	Fam110c	Family with sequence similarity 110, member C	111	1.979	3.760	1.875	2.537	*#†
7327842	Fbxo32	F-box protein 32	731	0.592	0.690	0.876	0.713	---
7345585	Fdx1	Ferredoxin 1	494	1.553	3.480	2.676	3.197	*#†
7260805	Fgl2	Fibrinogen-like 2	349	1.542	1.808	1.178	1.403	*#
7252051	Flnc	Filamin C, gamma	559	1.735	1.583	0.917	1.051	*#
7300295	Fos	FBJ osteosarcoma oncogene	178	15.214	2.952	7.867	2.566	*#†
7048605	Fosb	FBJ osteosarcoma oncogene B	94	25.477	23.168	3.508	2.739	*#
7039170	Fosl1	Fos-like antigen 1	184	1.456	5.980	2.073	3.088	*#†
7299050	Frmd6	FERM domain containing 6	200	1.039	1.606	1.035	1.205	#†
7204090	Fst	Follistatin	195	1.377	4.347	1.103	1.274	*#†
7115625	G0s2	G0/G1switch 2	2879	0.994	0.635	0.819	0.762	#†
7265600	Gadd45a	Growth arrest and DNA-damage-inducible, alpha	951	1.094	1.842	0.927	1.218	*#†
7162363	Gadd45g	Growth arrest and DNA-damage-inducible, gamma	748	3.560	2.381	1.741	1.893	*#†
7248808	Gata5	GATA binding protein 5	426	0.965	0.664	0.914	0.719	#†

7338247	Gclc	Glutamate-cysteine ligase, catalytic subunit	798	1.412	1.668	1.451	2.034	*#†
7163357	Gcnt2	Glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	109	1.094	1.670	1.079	1.100	#†
7144218	Gdf15	Growth differentiation factor 15	291	1.583	1.143	1.804	1.158	*†
7324926	Glipr1	GLI pathogenesis-related 1	232	1.318	1.555	1.142	1.134	*#
7187674	Glrx1	Glutaredoxin 1	302	0.995	1.793	1.062	1.256	#†
7248966	Gmeb2	Glucocorticoid modulatory element binding protein 2	188	1.202	1.541	1.096	1.311	*#†
7364791	Gpr55	G protein-coupled receptor 55	47	1.705	1.186	1.331	1.064	*†
7243216	Grem1	Gremlin 1, cysteine knot superfamily, homolog (Xenopus laevis)	70	1.010	1.834	1.103	1.122	#†
7077710	Hand1	Heart and neural crest derivatives expressed 1	176	1.680	0.856	0.955	1.046	*†
7047218	Has1	Hyaluronan synthase 1	71	2.021	2.452	3.319	3.324	*#†
7327675	Has2	Hyaluronan synthase 2	552	3.069	8.143	3.862	4.896	*#†
7055290	Hbb|LOC689064|LOC100134871	Hemoglobin, beta | beta-globin | beta globin minor gene	4634	0.912	0.600	0.646	0.714	#†
7174562	Hbegf	Heparin-binding EGF-like growth factor	304	1.503	3.592	1.285	1.610	*#†
7164850	Hist1h2ak	Histone cluster 1, H2ak	211	0.625	0.743	0.852	0.900	*
7163227	Hivep1	Human immunodeficiency virus type I enhancer binding protein 1	216	1.011	1.508	0.973	1.392	#†
7266497	Hk2	Hexokinase 2	305	1.034	1.712	1.098	1.551	#†
7202670	Hmgcr	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	676	1.417	1.703	1.339	1.447	*#†
7150903	Hpgd	Hydroxyprostaglandin dehydrogenase 15 (NAD)	48	0.996	1.524	1.090	1.040	#†
7216806	Hspa1b|Hspa1a|Hspa1l	Heat shock 70kD protein 1B (mapped) | heat shock 70kD protein 1A | heat shock protein 1-like	73	1.672	2.460	1.044	1.057	*#†
7133438	Htr2a	5-hydroxytryptamine (serotonin) receptor 2A	652	1.224	1.598	1.271	1.042	*#†
7364798	Htr2b	5-hydroxytryptamine (serotonin) receptor 2B	131	0.653	0.982	0.963	0.861	*†
7333460	Icam1	Intercellular adhesion molecule 1	813	2.330	1.748	1.221	1.350	*#†
7166170	Idi1	Isopentenyl-diphosphate delta isomerase 1	1158	1.060	1.647	1.383	1.297	#†
7179800	Ier2	Immediate early response 2	435	5.475	2.463	3.344	1.871	*#†
7220503	Ier3	Immediate early response 3	1963	1.766	1.347	2.924	1.871	*#†
7112556	Ier5	Immediate early response 5	411	2.056	1.741	1.287	1.148	*#
7237488	Ier5l	Immediate early response 5-like	512	0.998	0.646	0.994	0.949	#†
7104832	Il10	Interleukin 10	43	4.331	1.479	3.948	1.642	*†
7028549	Il11	Interleukin 11	222	1.769	1.920	2.061	2.115	*#
7353844	Il1rl1	Interleukin 1 receptor-like 1	525	1.069	2.842	1.178	1.257	#†
7353831	Il1rl2	Interleukin 1 receptor-like 2	91	1.136	1.600	1.097	1.100	#†
7260080	Il6	Interleukin 6	229	6.140	4.611	12.595	5.897	*#
7165193	Inhba	Inhibin beta-A	213	1.950	6.251	1.713	2.519	*#†
7067595	Irf1	Interferon regulatory factor 1	298	0.784	0.459	0.823	0.667	*#†
7147838	Irs2	Insulin receptor substrate 2	209	1.610	1.707	2.157	2.436	*#
7229388	Itgav	Integrin, alpha V	140	1.723	1.631	1.062	1.118	*#
7041047	Jak2	Janus kinase 2	379	2.151	0.673	0.658	0.705	*#†
7288744	Jun	Jun proto-oncogene	587	3.052	2.252	1.410	1.074	*#
7179739	Junb	Jun B proto-oncogene	392	3.287	1.443	2.713	1.781	*#†
7197866	Kcna3	Potassium voltage-gated channel, shaker-related subfamily, member 3	128	0.618	0.852	0.928	1.171	*†
7091804	Kcne1	Potassium voltage-gated channel, Isk-related subfamily, member 1	86	1.538	1.149	1.121	1.099	*
7356519	Kcne4	Potassium voltage-gated channel, Isk-related subfamily, gene 4	1027	0.977	0.563	1.190	0.963	#†
7073296	Kcnj2	Potassium inwardly-rectifying channel, subfamily J, member 2	367	0.998	0.530	0.765	0.885	#†
7149521	Klf2	Kruppel-like factor 2 (lung)	178	2.282	1.931	1.591	1.199	*#†
7286480	Klf4	Kruppel-like factor 4 (gut)	234	2.580	3.458	2.153	2.242	*#†
7134502	Klf5	Kruppel-like factor 5	206	1.274	2.239	0.954	1.436	*#†
7166280	Klf6	Kruppel-like factor 6	970	2.538	3.016	1.433	1.419	*#†
7120521	Lif	Leukemia inhibitory factor (cholinergic differentiation factor)	204	4.823	4.712	7.569	5.317	*#
7331757	Lima1|LOC100361502	LIM domain and actin binding 1 | hypothetical protein LOC100361502	188	1.577	1.374	0.971	0.939	*#†
7257290	Lmcd1	LIM and cysteine-rich domains 1	523	1.751	2.929	1.181	1.714	*#†

7210664	Lmna	Lamin A	909	1.429	1.588	0.985	0.995	*#
7057647	LOC100360446	Zinc finger and SCAN domain containing 2-like	105	0.726	0.650	0.761	0.727	*#
7335998	LOC363060	Similar to RIKEN cDNA 1600029D21	120	1.053	1.704	1.153	2.123	#†
7368381	LOC367515	Similar to RIKEN cDNA 1700081O22	163	0.608	0.919	0.959	1.021	*†
7369922	LOC501092|LOC501091|LOC687464|LOC367381|RGD1565423|LOC498374|LOC100360712|LOC501222|LOC690398|LOC691575|LOC691487|LOC690576|LOC690672|LOC363433|LOC363306|LOC691626|LOC501224	Hypothetical LOC501092 | similar to Discs large homolog 5 (Placenta and prostate DLG) (Discs large protein P-dlg) | similar to similar to RIKEN cDNA 1700001E04 | similar to RIKEN cDNA 4930555G01 | similar to cDNA sequence AY358078 | rCG43589-like | Hypothetical protein LOC690398 | Hypothetical LOC363433 | Hypothetical protein LOC363306 | Hypothetical protein LOC691626 | similar to RIKEN cDNA 2610042L04	70	0.637	0.923	1.002	1.070	*†
7352509	LOC688459	Hypothetical protein LOC688459	59	2.175	2.969	1.157	1.360	*#†
7369926	LOC690672	Similar to Discs large homolog 5 (Placenta and prostate DLG) (Discs large protein P-dlg)	548	1.504	1.647	1.233	1.098	*#
7187867	Lysmd3	LysM, putative peptidoglycan-binding, domain containing 3	302	1.120	1.572	1.426	1.411	*#†
7318753	Maff	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	147	1.553	1.957	1.360	1.510	*#
7100653	Mafk	v-maf musculoaponeurotic fibrosarcoma oncogene homolog K (avian)	498	1.439	1.742	1.145	1.417	*#†
7068314	Map2k3	Mitogen activated protein kinase kinase 3	404	1.090	1.500	1.117	1.421	#†
7266023	Mat2a	Methionine adenosyltransferase II, alpha	2888	1.468	1.620	1.547	1.678	*#
7325416	Mdm2	Mdm2 p53 binding protein homolog (mouse)	637	1.460	1.622	1.213	1.035	*#
7194351	Mei1|Tsc22d2	Meiosis inhibitor 1 | TSC22 domain family, member 2	263	1.497	2.219	1.182	1.346	*#†
7067118	Mgat1	Mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	468	0.933	1.978	1.066	1.132	#†
7055296	MGC72973	Beta-glo	2197	0.912	0.615	0.668	0.717	#†
7173783	Mir187	MicroRNA mir-187	103	0.666	1.077	1.211	1.238	*†
7340376	Mir191	MicroRNA mir-191	260	0.619	0.846	1.066	0.913	*†
7070060	Mir193	MicroRNA mir-193	95	1.196	2.283	1.085	1.208	#†
7069220	Mir195	MicroRNA mir-195	56	1.807	0.837	0.841	0.972	*†
7069688	Mir212	MicroRNA mir-212	95	2.231	1.214	1.409	1.341	*†
7069718	Mir22	MicroRNA mir-22	360	1.505	1.332	1.079	1.212	*#
7373217	Mir222	MicroRNA mir-222	40	1.472	2.856	1.089	1.247	*#†
7184116	Mir27a	MicroRNA mir-27a	79	2.616	1.287	1.194	1.482	*†
7288447	Mir31	MicroRNA mir-31	66	1.611	2.298	1.024	1.175	*#
7345523	Mir34b	MicroRNA mir-34b	87	0.570	1.238	0.997	1.000	*†
7211447	Mllt11	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11	335	1.675	1.681	1.402	1.552	*#
7383823	Morc4	MORC family CW-type zinc finger 4	200	1.567	1.672	0.994	0.960	*#†
7274970	Murc	Muscle-related coiled-coil protein	98	0.847	1.634	0.976	1.217	*#†
7317471	Myc	Myelocytomatosis oncogene	212	1.830	2.602	1.323	1.554	*#†
7297245	Nampt	Nicotinamide phosphoribosyltransferase	352	0.848	1.570	1.242	1.710	#†
7155813	Nfil3	Nuclear factor, interleukin 3 regulated	107	1.584	2.735	1.968	2.369	*#†
7197523	Ngf	Nerve growth factor (beta polypeptide)	110	0.935	1.720	1.184	1.238	#†
7029445	Nkpd1	NTPase, KAP family P-loop domain containing 1	126	0.583	1.167	1.364	0.989	*†
7059690	Npas4	Neuronal PAS domain protein 4	64	1.215	2.004	1.004	1.059	*#†
7218756	Npffr1	Neuropeptide FF receptor 1	73	1.524	1.008	1.003	0.941	*†
7194492	Npy2r	Neuropeptide Y receptor Y2	55	1.705	0.668	0.803	0.754	*#†
7185182	Nqo1	NAD(P)H dehydrogenase, quinone 1	286	1.052	1.504	1.164	1.321	#†
7082318	Nr1d1	Nuclear receptor subfamily 1, group D, member 1	361	0.974	0.641	0.872	0.773	#†
7320920	Nr4a1	Nuclear receptor subfamily 4, group A, member 1	163	8.505	18.929	20.769	20.607	*#†
7239111	Nr4a2	Nuclear receptor subfamily 4, group A, member 2	106	2.381	8.923	13.409	14.626	*#†

7274931	Nr4a3	Nuclear receptor subfamily 4, group A, member 3	121	2.813	7.361	10.615	11.601	*#†
7057283	Nupr1	Nuclear protein, transcriptional regulator, 1	573	0.899	1.534	1.023	0.905	#†
7371735	Odz3|LOC100361541	Odz, odd Oz/ten-m homolog 3 (Drosophila) | odz, odd Oz/ten-m homolog 3-like	163	0.647	1.000	0.992	1.051	*†
7270053	Olr1	Oxidized low density lipoprotein (lectin-like) receptor 1	1893	1.290	1.585	1.639	1.998	*#
7078087	Olr1463	Olfactory receptor 1463	66	1.811	0.828	1.029	1.155	*†
7034974	Olr152	Olfactory receptor 152	54	1.620	1.012	1.253	1.073	*†
7131237	Olr1614	Olfactory receptor 1614	82	1.682	0.848	1.022	0.906	*†
7216279	Olr1730	Olfactory receptor 1730	68	1.903	1.020	1.081	0.974	*†
7055382	Olr175	Olfactory receptor 175	56	1.591	0.855	0.874	1.187	*†
7055527	Olr217	Olfactory receptor 217	89	1.668	0.976	1.023	1.005	*†
7241229	Olr496	Olfactory receptor 496	54	1.740	0.816	0.952	0.890	*#†
7241352	Olr602	Olfactory receptor 602	98	0.594	0.993	1.074	0.984	*†
7241406	Olr661	Olfactory receptor 661	40	1.644	1.163	1.135	0.923	*†
7235566	Pard6b	Par-6 (partitioning defective 6) homolog beta (C. elegans)	98	1.230	3.622	1.104	1.838	*#†
7208307	Pcdh18	Protocadherin 18	531	0.612	0.797	0.828	0.761	*†
7133759	Pcdh8	Protocadherin 8	68	0.650	1.081	1.267	1.297	*†
7283909	Pdp1	Pyruvate dehyrogenase phosphatase catalytic subunit 1	705	0.836	1.668	0.960	1.075	#†
7121583	Peli1	Pellino 1	102	1.537	1.422	1.363	1.411	*#†
7365259	Per2	Period homolog 2 (Drosophila)	140	1.417	1.820	1.020	1.090	*#†
7314872	Phlda1	Pleckstrin homology-like domain, family A, member 1	520	3.517	4.155	3.994	3.388	*#†
7120384	Pik3ip1	Phosphoinositide-3-kinase interacting protein 1	485	0.696	0.544	0.803	0.585	*#†
7217331	Pim1	Pim-1 oncogene	1687	1.610	1.703	1.772	1.208	*#
7189518	Plk2	Polo-like kinase 2 (Drosophila)	1947	2.445	3.030	1.707	1.559	*#†
7290290	Plk3	Polo-like kinase 3 (Drosophila)	179	1.449	1.508	1.678	1.308	*#
7051029	Ppp1r15a	Protein phosphatase 1, regulatory (inhibitor) subunit 15A	241	1.729	2.059	1.402	1.307	*#†
7152038	Pragmin	Pragma of Rnd2	148	1.113	1.887	1.100	1.422	*#†
7375047	Prdx4	Peroxiredoxin 4	916	0.657	1.065	1.008	1.024	*†
7197221	Prkab2	Protein kinase, AMP-activated, beta 2 non-catalytic subunit	148	1.541	1.691	1.062	1.131	*#
7106132	Ptgs2	Prostaglandin-endoperoxide synthase 2	258	7.005	7.981	5.272	3.312	*#
7360736	Ptp4a1	Protein tyrosine phosphatase 4a1	1189	1.542	1.629	1.408	1.422	*#
7048738	PVR	Poliovirus receptor	916	1.054	1.853	1.149	1.442	#†
7346979	Rab8b	RAB8B, member RAS oncogene family	892	0.648	1.178	1.065	1.071	*†
7089813	Ranbp1	RAN binding protein 1	1954	0.486	1.016	1.005	1.025	*†
7078129	Rasd1	RAS, dexamethasone-induced 1	419	2.249	0.875	2.179	1.236	*#†
7124933	Rasl11b	RAS-like family 11 member B	855	2.304	1.841	1.643	1.362	*#†
7128932	Rel	v-rel reticuloendotheliosis viral oncogene homolog (avian)	203	1.532	1.951	1.581	2.022	*#†
7346143	RGD1305464	Similar to human chromosome 15 open reading frame 39	266	1.050	0.634	1.194	1.056	#†
7064324	RGD1308127	Similar to 2700078E11Rik protein	486	0.932	1.645	1.055	1.110	#†
7349995	RGD1560778	Similar to RIKEN cDNA 6530418L21	136	0.584	0.776	0.880	1.122	*#†
7157785	RGD1564767	Histone H2a	165	0.663	0.856	0.923	0.964	*
7112009	Rgs2	Regulator of G-protein signaling 2	613	3.146	5.494	5.024	4.199	*#†
7304448	Rhob	Ras homolog gene family, member B	799	2.595	2.593	2.209	1.786	*#
7284153	Ripk2	Receptor-interacting serine-threonine kinase 2	397	0.936	2.663	1.105	1.535	#†
7331581	Rnd1	Rho family GTPase 1	421	1.595	2.215	1.173	1.519	*#†
7072329	Rnd2	Rho family GTPase 2	173	1.509	0.950	0.932	0.996	*†
7238766	Rnd3	Rho family GTPase 3	604	1.767	1.793	1.238	1.013	*#
7220337	Rnf39	Ring finger protein 39	133	1.031	1.587	0.945	1.147	#†
7266888	Rpl22	Ribosomal protein L22	661	0.550	1.168	1.161	1.150	*†
7162921	Rpl27|RGD1563835	Ribosomal protein L27 | similar to Ribosomal protein L27	1217	0.490	1.072	1.421	1.191	*†
7204692	Rps15a	Ribosomal protein S15a	349	0.637	1.091	0.998	1.137	*†
7110777	Rps26	Ribosomal protein S26	2062	0.631	1.009	0.977	1.056	---

7062166	Rps27a	Ribosomal protein S27a	596	0.667	1.050	1.180	1.180	*†
7196707	S100a10	S100 calcium binding protein A10	1623	0.919	1.812	1.127	1.156	#†
7375057	Sat1	Spermidine/spermine N1-acetyl transferase 1	641	2.226	2.550	1.471	1.497	*#
7144691	Sc4mol	Sterol-C4-methyl oxidase-like	1985	0.910	1.520	1.137	1.137	#†
7103916	Serpinb2	Serine (or cysteine) peptidase inhibitor, clade B, member 2	284	3.388	14.086	1.826	3.231	*#†
7101220	Serpine1	Serine (or cysteine) peptidase inhibitor, clade E, member 1	601	6.428	8.141	1.773	2.001	*#
7029999	Sertad1	SERTA domain containing 1	299	1.776	1.622	1.275	1.324	*#
7045121	Sgk1	Serum/glucocorticoid regulated kinase 1	1072	1.779	3.202	0.962	0.910	*#†
7214260	Sgms2	Sphingomyelin synthase 2	126	1.003	1.720	0.955	1.319	#†
7221460	Sik1	Salt-inducible kinase 1	415	1.889	2.039	3.478	4.112	*#†
7170785	Slc12a2	Solute carrier family 12 (sodium/potassium/chloride transporters), member 2	333	1.484	1.934	0.945	1.008	*#†
7232493	Slc20a1	Solute carrier family 20 (phosphate transporter), member 1	1144	1.288	1.665	1.256	1.453	*#†
7237652	Slc25a25	Solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25	148	2.662	1.748	1.561	1.257	*#†
7269356	Slc2a3	Solute carrier family 2 (facilitated glucose transporter), member 3	435	0.833	1.571	2.040	2.752	*#†
7136592	Slc4a7	Solute carrier family 4, sodium bicarbonate cotransporter, member 7	156	1.027	1.742	1.014	1.297	#†
7096358	Slc7a1	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	410	0.963	1.594	1.014	1.186	#†
7053013	Slco3a1	Solute carrier organic anion transporter family, member 3a1	101	1.861	1.615	0.767	1.003	*#
7346730	Smad6	SMAD family member 6	353	0.819	0.617	1.039	0.811	*#†
7235533	Snai1	Snail homolog 1 (Drosophila)	178	0.973	0.511	1.205	1.109	#†
7187663	Snrpd1|Ell2	Small nuclear ribonucleoprotein D1 | elongation factor RNA polymerase II 2	148	1.285	2.281	1.239	2.557	*#†
7084788	Socs3	Suppressor of cytokine signaling 3	588	1.280	0.614	1.039	1.258	*#†
7141508	Spry2	Sprouty homolog 2 (Drosophila)	795	1.720	2.261	1.523	1.221	*#†
7351949	Srf	Serum response factor (c-fos serum response element-binding transcription factor)	732	1.775	1.663	1.100	1.143	*#
7233921	Srxn1	Sulfiredoxin 1 homolog (S. cerevisiae)	119	1.802	2.171	1.553	1.812	*#†
7298488	Sstr1	Somatostatin receptor 1	125	1.792	1.123	1.202	1.237	*†
7133039	Stc1	Stanniocalcin 1	1016	1.162	1.568	0.968	1.049	#†
7345054	Tagln	Transgelin	2486	1.124	1.651	1.183	1.214	*#†
7261795	Tfpi2	Tissue factor pathway inhibitor 2	294	1.040	2.020	1.314	1.781	#†
7308910	Tgfb3	Transforming growth factor, beta 3	299	1.297	2.044	1.240	1.505	*#†
7246265	Thbd	Thrombomodulin	110	1.756	1.588	1.218	1.642	*#
7323040	Timp3	TIMP metallopeptidase inhibitor 3	960	1.374	1.717	1.022	1.171	*#†
7210192	Tlr2	Toll-like receptor 2	336	0.545	0.952	0.978	0.986	*†
7313905	Tmcc3	transmembrane and coiled-coil domain family 3	190	1.011	0.638	0.889	0.749	#†
7327525	Tnfrsf11b	Tumor necrosis factor receptor superfamily, member 11b	1541	1.213	1.818	1.167	1.106	*#†
7075088	Tnfrsf12a	Tumor necrosis factor receptor superfamily, member 12a	1263	1.519	1.830	1.164	1.419	*#†
7287386	Tnfsf15	Tumor necrosis factor (ligand) superfamily, member 15	220	1.370	1.813	0.986	0.862	*#†
7106964	Tnfsf18	Tumor necrosis factor (ligand) superfamily, member 18	129	2.348	7.480	1.578	1.602	*#†
7272734	Tp53inp1	Tumor protein p53 inducible nuclear protein 1	1029	1.078	1.554	1.077	1.122	#†
7317342	Trib1	Tribbles homolog 1 (Drosophila)	183	2.805	2.680	1.427	1.726	*#
7054758	Tsku	Tsukushin	427	0.666	0.890	0.824	0.830	*#†
7297329	Twist1	Twist homolog 1 (Drosophila)	215	1.259	3.797	1.477	1.707	#†
7113823	Uap1	UDP-N-acteylglucosamine pyrophosphorylase 1	430	1.172	3.186	1.701	3.032	*#†
7118521	Ugdh	UDP-glucose dehydrogenase	1143	1.054	1.566	1.415	1.548	#†
7030810	Unknown	Unknown	35	1.573	1.116	1.157	1.118	*†
7031418	Unknown	Unknown	170	0.600	0.643	0.930	0.931	*#
7034150	Unknown	Unknown	392	0.886	0.665	0.696	0.887	#†
7040909	Unknown	Unknown	227	0.650	0.764	0.884	1.019	---
7041453	Unknown	Unknown	52	2.208	1.430	1.387	1.158	*†
7054779	Unknown	Unknown	38	1.935	1.100	0.989	0.953	*†

7067733	Unknown	Unknown	41	1.515	0.888	0.944	0.930	*†
7068430	Unknown	Unknown	80	0.621	0.860	0.955	1.196	*
7068912	Unknown	Unknown	94	1.547	0.983	1.121	1.125	*†
7071496	Unknown	Unknown	96	0.587	0.789	0.662	0.877	*
7072840	Unknown	Unknown	85	1.621	1.027	1.105	1.105	*†
7075049	Unknown	Unknown	138	1.514	0.986	1.014	1.110	*†
7076649	Unknown	Unknown	41	1.644	1.126	1.223	1.300	*
7077802	Unknown	Unknown	96	0.568	0.751	0.789	0.726	*#
7083146	Unknown	Unknown	67	1.563	0.995	1.007	0.936	*†
7083509	Unknown	Unknown	67	2.010	1.119	1.299	1.028	*†
7091841	Unknown	Unknown	68	1.216	1.593	1.154	1.779	#†
7096304	Unknown	Unknown	90	0.795	0.625	0.692	0.620	*#†
7098954	Unknown	Unknown	76	0.619	0.906	1.022	0.919	*†
7105586	Unknown	Unknown	457	1.248	2.543	1.221	1.412	#†
7108686	Unknown	Unknown	58	1.616	0.940	0.920	0.955	*†
7111633	Unknown	Unknown	112	1.896	1.984	1.434	1.512	*#
7113707	Unknown	Unknown	373	0.904	0.585	0.768	0.724	#†
7113780	Unknown	Unknown	63	1.743	0.967	1.079	1.158	*†
7118707	Unknown	Unknown	57	1.547	0.975	1.085	1.009	*†
7147988	Unknown	Unknown	68	0.918	1.676	1.094	1.174	#†
7150788	Unknown	Unknown	70	0.472	1.135	0.980	0.979	*†
7153410	Unknown	Unknown	139	1.173	0.631	0.826	0.834	*#†
7164849	Unknown	Unknown	942	0.584	0.891	0.843	0.871	*†
7167845	Unknown	Unknown	342	0.561	0.747	1.035	0.976	*
7170361	Unknown	Unknown	78	0.606	0.878	0.875	0.939	*†
7173133	Unknown	Unknown	791	1.184	0.492	0.927	0.498	#†
7174327	Unknown	Unknown	85	1.568	1.400	1.756	1.600	---
7194194	Unknown	Unknown	75	1.136	2.320	0.859	1.213	#†
7200422	Unknown	Unknown	124	2.974	2.049	1.590	1.447	*#†
7205580	Unknown	Unknown	185	1.920	1.774	1.298	0.900	*#
7207860	Unknown	Unknown	395	0.659	1.204	1.051	1.042	*†
7209914	Unknown	Unknown	103	1.107	0.601	0.703	0.665	#†
7212310	Unknown	Unknown	155	1.077	2.227	1.429	1.869	#†
7224482	Unknown	Unknown	540	0.354	0.504	0.532	0.712	*#
7239047	Unknown	Unknown	37	1.514	1.059	1.094	1.086	*†
7239847	Unknown	Unknown	35	1.659	0.892	1.079	1.020	*†
7244036	Unknown	Unknown	124	0.624	0.894	1.036	0.936	*†
7244657	Unknown	Unknown	290	0.921	2.037	1.166	1.343	#†
7252930	Unknown	Unknown	41	2.276	0.916	1.123	1.076	*†
7256305	Unknown	Unknown	70	1.403	1.519	2.035	2.238	*#
7259197	Unknown	Unknown	78	1.594	1.070	1.263	1.179	*†
7264249	Unknown	Unknown	57	1.502	0.971	1.040	0.954	*†
7267783	Unknown	Unknown	60	1.531	1.092	1.136	1.024	*†
7268354	Unknown	Unknown	63	1.665	1.842	1.119	1.373	*#
7288050	Unknown	Unknown	182	1.014	0.619	0.792	0.651	#†
7290857	Unknown	Unknown	111	0.595	0.881	0.816	0.691	*#†
7294779	Unknown	Unknown	90	1.518	0.938	1.026	0.960	*†
7297222	Unknown	Unknown	267	1.827	2.360	1.210	1.539	*#†
7297247	Unknown	Unknown	194	1.399	2.808	2.224	1.575	*#†
7300423	Unknown	Unknown	134	0.561	0.935	1.084	0.999	*†
7306804	Unknown	Unknown	54	1.808	1.019	1.031	1.062	*†
7310849	Unknown	Unknown	132	0.518	0.622	0.784	0.761	*#

7316664	Unknown	Unknown	43	1.513	0.988	1.069	1.012	*†
7318523	Unknown	Unknown	59	1.603	1.408	1.111	1.107	*#
7324225	Unknown	Unknown	51	1.506	0.907	0.943	1.013	*†
7327468	Unknown	Unknown	188	1.083	1.626	0.990	1.191	#†
7327469	Unknown	Unknown	120	1.231	1.688	1.023	1.280	*#†
7330257	Unknown	Unknown	126	0.632	0.932	1.103	1.073	*†
7335235	Unknown	Unknown	580	1.268	2.624	1.184	1.640	#†
7340113	Unknown	Unknown	113	0.546	0.911	0.980	0.952	*†
7351669	Unknown	Unknown	40	1.845	1.059	1.101	1.115	*†
7361747	Unknown	Unknown	95	2.246	1.756	0.847	0.825	*#†
7367065	Unknown	Unknown	305	0.663	1.402	0.942	0.983	†
7367480	Unknown	Unknown	242	0.553	1.158	0.728	0.996	*†
7367576	Unknown	Unknown	105	0.548	0.943	0.931	0.921	*†
7368026	Unknown	Unknown	107	0.465	1.027	1.066	0.985	*†
7368095	Unknown	Unknown	112	1.810	0.840	0.821	0.810	*†
7368449	Unknown	Unknown	86	0.658	1.168	0.988	0.913	*†
7368483	Unknown	Unknown	224	1.029	2.519	0.923	1.490	#†
7368677	Unknown	Unknown	87	1.643	1.079	1.075	0.964	*†
7368735	Unknown	Unknown	131	1.628	1.272	1.150	0.935	*
7369075	Unknown	Unknown	48	1.556	1.206	0.984	0.820	*#†
7369324	Unknown	Unknown	86	2.336	1.133	1.100	1.289	*†
7369358	Unknown	Unknown	968	0.605	0.941	0.972	1.002	*†
7369500	Unknown	Unknown	124	0.623	0.980	0.752	0.876	*†
7369845	Unknown	Unknown	165	0.663	1.053	0.916	0.742	*†
7370018	Unknown	Unknown	371	1.600	1.002	0.910	0.742	*†
7370023	Unknown	Unknown	888	1.076	1.500	1.312	1.168	#†
7370343	Unknown	Unknown	402	0.589	1.383	1.229	0.824	*†
7370444	Unknown	Unknown	70	1.631	1.253	0.777	0.766	*#†
7370452	Unknown	Unknown	77	0.799	0.653	0.823	0.732	#
7370879	Unknown	Unknown	94	0.602	1.049	1.050	0.928	*†
7370997	Unknown	Unknown	761	0.913	2.179	0.836	1.376	#†
7370998	Unknown	Unknown	912	1.013	1.550	0.847	1.066	#†
7371014	Unknown	Unknown	82	1.564	0.907	0.720	0.726	*†
7371233	Unknown	Unknown	38	2.207	1.055	1.093	0.972	*†
7371555	Unknown	Unknown	172	1.117	2.645	1.117	1.572	#†
7371731	Unknown	Unknown	624	0.611	0.755	0.862	0.790	*#
7381687	Unknown	Unknown	128	1.648	0.941	0.990	1.252	*†
7384598	Unknown	Unknown	49	1.823	0.951	0.985	0.904	*†
7136062	Vcl	Vinculin	669	1.437	1.821	1.023	1.060	*#†
7151046	Vegfc	Vascular endothelial growth factor C	182	0.996	1.537	0.979	0.942	#†
7085544	Vgll3	Vestigial like 3 (Drosophila)	417	1.101	2.416	1.033	1.036	#†
7335234	Vof16	Ischemia related factor vof-16	410	1.443	2.856	1.080	1.616	#†
7095316	Vpreb1|Vpreb2	Pre-B lymphocyte 1 | pre-B lymphocyte gene 2	61	1.514	1.067	1.072	1.100	*†
7350922	Xirp1	Xin actin-binding repeat containing 1	520	1.323	1.997	1.132	1.644	*#†
7228236	Xirp2	Xin actin-binding repeat containing 2	586	1.267	1.810	1.172	1.264	#
7096947	Zfand2a	Zinc finger, AN1-type domain 2A	555	1.204	1.714	1.217	1.513	*#†
7105589	Zfp281	Zinc finger protein 281	462	1.817	2.214	1.326	1.439	*#†
7049312	Zfp36	Zinc finger protein 36	302	3.606	2.516	3.204	1.845	*#†
7149612	Zfp709	Zinc finger protein 709	129	0.659	0.752	0.945	0.879	*#
7284912	Znf292	Zinc finger protein 292	235	1.024	0.638	0.938	0.690	#†
7197294	Znf697	Zinc finger protein 697	183	1.047	2.216	1.041	1.412	#†