Circulation
Cardiovascular Genetics
JOURNAL OF THE AMERICAN HEART ASSOCIATION

American Heart Association
Learn and Live

Time-Warped Comparison of Gene Expression in Adaptive and Maladaptive Cardiac Hypertrophy

Sean P. Sheehy, Sui Huang and Kevin Kit Parker

Circ Cardiovasc Genet 2009;2;116-124; originally published online Feb 18, 2009;
DOI: 10.1161/CIRCGENETICS.108.806935
Circulation: Cardiovascular Genetics is published by the American Heart Association. 7272 Greenville Avenue, Dallas, TX 72514

Time-Warped Comparison of Gene Expression in Adaptive and Maladaptive Cardiac Hypertrophy

Sean P. Sheehy, ALM; Sui Huang, MD, PhD; Kevin Kit Parker, PhD

Background**—**Cardiac hypertrophy is classically regarded as a compensatory response, yet the active tissue remodeling processes triggered by various types of mechanical stress can enhance or diminish the function of the heart. Despite the disparity in outcomes, there are similarities in the hypertrophic responses. We hypothesized that a generic genetic response that is not dependent on the particular nature of the hypertrophic stimulus exists. To test our hypothesis, we compared the temporal evolution of transcriptomes measured in hearts subjected to either adaptive (exercise-induced) or maladaptive (aortic banding–induced) hypertrophy.

Methods and Results**—**Generic hypertrophy-associated genes were identified and distinguished from stimulus-dependent transcripts by coupling a metric of cardiac growth with a dynamic time-warping algorithm to align transcriptome changes with respect to the hypertrophy response. The major differences in expression between the adaptive and maladaptive hypertrophy models were centered around the genes involved in metabolism, fibrosis, and immune response. Conversely, transcripts with common expression patterns in both hypertrophy models were associated with signal transduction, cytoskeletal development, and muscle contraction. Thus, despite the apparent differences in the expression response of the heart to either athletic conditioning or pressure overload, there is a set of genes that displays similar expression profiles.

Conclusions**—**This finding lends support to the notion of a generalized cardiac growth mechanism that is activated in response to mechanical perturbation. The common and unique genetic signatures of adaptive and maladaptive hypertrophy may be useful in the diagnosis and treatment of pathological myocardial remodeling. **(*Circ Cardiovasc Genet*. 2009;2:116-124.)**

Key Words: heart ■ hypertrophy ■ gene expression ■ self-organizing map ■ GEDI ■ time warp

Many risk factors associated with cardiovascular disease, such as high blood pressure, diabetes, and obesity, increase the workload on the heart and can lead to gross and microscale morphological changes associated with a decrease in overall cardiac performance.[1] Athletic conditioning also intensifies demand on the heart, but cardiac function is usually sustained or enhanced by this form of hypertrophic growth.[2] At the microanatomical level, adaptive and maladaptive cardiac hypertrophy elicits distinct morphological changes in the cardiac tissue. Maladaptive cardiac remodeling is characterized by alterations in myocyte size, rarefaction in the myocardial vasculature, expression of fetal genes, and apoptotic loss of myocytes that leads to fibrosis.[3] In contrast, adaptive hypertrophy entails sustained or increased capillary density in the myocardium, and an enhanced metabolic profile with no fetal gene expression and no sign of fibrosis.[4] Nevertheless, the relative magnitude of overall myocardial growth observed in adaptive and maladaptive remodeling is remarkably similar.[3] This suggests that at its core, cardiac growth may be driven in part by a generic mechanism, regardless of the nature of the hypertrophy stimulus.

Clinical Perspective see p 124

Genome-scale analyses have provided snapshots of differential gene expression between normal and hypertrophied myocardium.[5,6] In a detailed study, Izumo and colleagues[7] looked at gene expression in mice subjected to either swim training as a model for exercise or transverse constriction of the aorta ("banding") as a model for hemodynamic stress due to pressure overload. Mice subjected to regular bouts of swim exercise of increasing intensity over a period of 4 weeks experienced an increase in heart mass of up to 45%. Resting heart rate in these mice decreased with respect to nonexercised mice, and no apoptosis or fibrosis was observed in the myocardium.[7] Thus, changes in gene expression in these conditioned hearts were considered an "adaptive" hypertrophic re-

Received July 13, 2008; accepted February 12, 2009.

From the Disease Biophysics Group, School of Engineering and Applied Sciences (S.P.S., K.K.P), Harvard University, Cambridge, Mass; and the Department of Biological Sciences (S.H.), Institute for Biocomplexity and Informatics, University of Calgary, Calgary, Alberta, Canada.

Guest Editor for this article was Martin M. LeWinter, MD.

The online-only Data Supplement is available at http://circgenetics.ahajournals.org/cgi/content/full/CIRCGENETICS.108.806935/DC1.

Correspondence to Kevin Kit Parker, PhD, Harvard University, SEAS, Pierce Hall 321, 29 Oxford St, Cambridge, MA 02138. E-mail kkparker@seas.harvard.edu

***Circ Cardiovasc Genet* is available at http://circgenetics.ahajournals.org** **DOI: 10.1161/CIRCGENETICS.108.806935**

sponse. In the same study, transverse aortic constriction induced pressure overload in the left ventricle that resulted in a subset of mice progressing to heart failure. Therefore, the changes in gene expression in this model represent a "maladaptive" hypertrophy response.

We hypothesized that a comparison of the respective gene expression patterns would differentiate genes whose expression was associated with a decrease in cardiac function from those associated with enhancement of cardiac performance, as well as identify nonspecific transcriptional activity intrinsic to cardiac remodeling. The comparative dynamics of such an endeavor is complicated by the differences in the time courses of the different hypertrophy processes, in which it is inappropriate to simply match up expression values collected at equal measurement intervals.[8] However, a commonly varying feature between the 2 response profiles may serve as a reference frame for comparisons despite the differing time scales. Therefore, instead of the chronological time elapsed after stress application, we used the change in relative cardiac mass to register the genomic profiles of adaptive and maladaptive hypertrophy. This was achieved by using dynamic time warping, an algorithm commonly used in studies of speech pattern recognition.[9] In fact, the expression patterns of many genes activated in response to pressure overload hypertrophy were recently shown to exhibit a strong correlation to gross parameters of cardiac growth.[10] Thus, we compared the 2 hypertrophy gene expression time courses based on heart weight to body weight (HW/BW) ratio as a surrogate time line. Despite the differences in the transcriptomes of these 2 hypertrophy responses, we uncovered several transcripts associated with cytoskeletal development and regulation of muscle contraction that displayed similar expression profiles when the profile data were compared relative to cardiac mass. In contrast, several fibrosis and immune response-related transcripts demonstrated significant changes in expression level only in the pressure overload model. Expression levels of transcripts associated with metabolism were significantly changed in the swim training model representing the adaptive response but not in the pressure overload model representing the maladaptive response.

Methods

Selection of Hypertrophy Model Datasets

A query of the Gene Expression Omnibus revealed a pair of time course microarray gene expression datasets published by the CardioGenomics Program for Genomic Applications by Izumo and colleagues[7] collected on mice subjected to swim training (Gene Expression Omnibus series GSE77), and pressure overload induced by transverse aortic constriction (Gene Expression Omnibus series GSE76) is suitable for this study. In their study, FVB wild-type mice were subjected to a modified version of a previously described swim training protocol[11] to stimulate cardiac hypertrophy with enhanced cardiac function and pressure overload was induced using a published transverse aortic constriction surgical procedure[12] to represent cardiac hypertrophy associated with diminished cardiac function. Sedentary mice served as a control for exercise-induced hypertrophy. Mice that underwent a sham operation without aortic constriction served as the control condition for the pressure overload–induced hypertrophy model. Affymetrix mgu74A GeneChips were used to measure gene expression levels in ventricular tissues isolated at 10 minutes, 2 days, 1 week, 2 weeks, 3 weeks, and 4 weeks posttraining in the exercise-induced hypertrophy model and 1 hour, 4 hours, 1 day, 2 days, 1 week, and 8 weeks postsurgery in the pressure overload–induced hypertrophy model. Gene expression measurements were collected in triplicate at each time point sampled in both models. To analyze this data, we downloaded normalized signal values and probe set "detection calls" computed by Affymetrix Microarray Suite 5.0 software, as well as HW and BW values made by the investigators and available from the CardioGenomics web site.[7]

Preprocessing of Gene Expression Data

Preprocessing of the data requires for both hypertrophy models to be evaluated relative to the sham and sedentary control conditions. Detection calls calculated by the Affymetrix Microarray Suite 5.0 software at the default cutoff of $P<0.05$ were used to eliminate transcripts that were judged not significantly expressed at all time points in either of the time series being compared. Specifically, detection call scores from the 3 replicate arrays for each time point were evaluated and probe sets whose detection call was "marginal" or "absent" in 2 of the 3 replicate measurements at all time points were excluded from analysis. This resulted in a dataset with 5153 transcripts. The Microarray Suite 5.0 signal values for these genes were averaged, $\log_2$-transformed, and analyzed with Significance Analysis of Microarrays (SAM) 3.00 software[13] to identify the sets of these genes that demonstrated statistically different expression values between the band and sham (control) conditions in the banding model and between the exercise and sedentary conditions in the exercise model. The 2-class, paired-response format was used for the SAM analysis. The δ value for determining the false discovery rate cutoff was set at 0.379 for the exercise-induced hypertrophy model, resulting in a dataset of 511 genes with a false discovery rate of 0.96%. For the banding-induced hypertrophy model, the δ value was set at 0.119, yielding 544 significant genes with a false discovery rate of 31.63%. The δ values were chosen to create symmetrical data sets for the Gene Warp program, where the symmetry is defined by the same set of genes for both sets of experiments. In further analyses, the 511 significant genes from the exercise model and the 544 significant genes from the banding model were combined into a dataset consisting of 963 genes that were present in the SAM results for both hypertrophy models. The remaining 92 transcripts consisted of genes that were present in the SAM results for the maladaptive hypertrophy model, but not the adaptive model, and vice versa.

Analysis of Cardiac Growth

Postmortem HW and BW values for the set of mice used at each measurement interval in the time series were averaged and used to compute the HW/BW ratio representative of each time point. Linear regression analysis was used to compare the HW/BW ratios calculated for the adaptive and maladaptive time courses.

Alignment of Time Course Expression Data

Log_2-transformed signal ratios (SLRs) were calculated for the transcripts whose expression levels were significantly changed in response to the adaptive and maladaptive hypertrophy stimuli. The time course expression data for the adaptive and maladaptive models were then aligned based on the similarity of the HW/BW ratio associated with each time point. Finally, the aligned expression data were input into genewarp, a program implementing the classic dynamic time-warping algorithm modified for analyzing global gene expression,[9] to assess the alignment. The quality of the alignment was determined by measuring the weighted Euclidean distance D(a,b) along the warping path between the global expression profiles of the 2 models. For comparison, the hypertrophy expression data were also evaluated with the gene-warp program with the expression data aligned with respect to the order of the measurement intervals rather than HW/BW ratio. All analyses were conducted with the parameters of the program set to their default values.

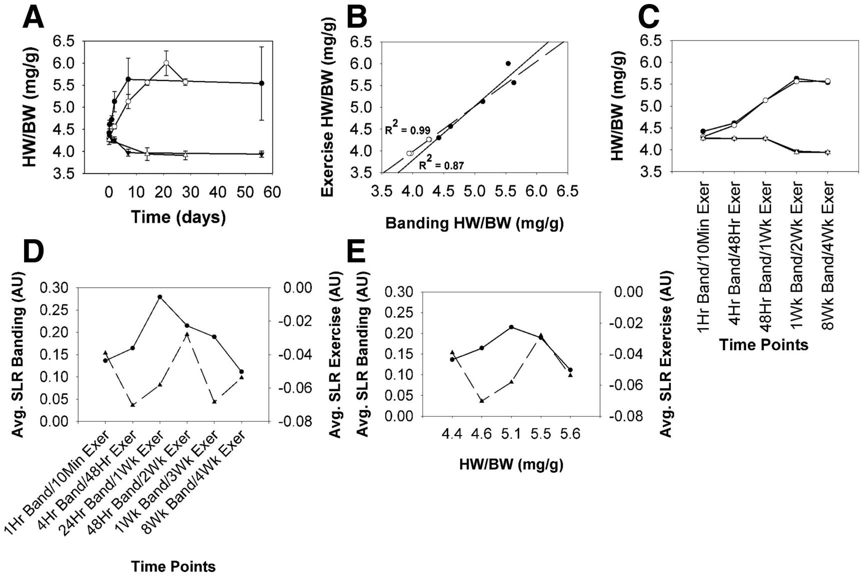

Figure 1. A, Average HW/BW ratios for the adaptive hypertrophy experimental (exercise, ○) and control (sedentary, △) conditions and the maladaptive hypertrophy experimental (banding, ●) and control (sham, ▲) conditions plotted against time. Error bars represent SEM. B, HW/BW ratio for the adaptive and maladaptive hypertrophy experimental (●) and control (○) conditions were plotted against each other and subjected to Pearson correlation analysis. C, HW/BW ratio from selected time points in the adaptive and maladaptive hypertrophy models were plotted to visualize their similarity over the time courses. D, Average SLRs for the distinct set of significantly expressed genes from the adaptive (▲) and maladaptive (●) models were calculated at each time point in the time series and aligned based on the order of the measurement intervals or (E) based on HW/BW ratio. AU indicates arbitrary units.

Global Analysis of Differences in Gene Expression

The adaptive and maladaptive models were evaluated relative to each other to identify their differences. We used SAM to identify the set of transcripts among the 963 transcripts that were found to be significantly expressed in both the exercise and banding hypertrophy models whose expression significantly differed between the exercise and banding hypertrophy models. For this analysis, the SLR values from the exercise and banding datasets were input into SAM, and the 2-class, unpaired-response format was used. The δ threshold was set at 0.424, yielding a false discovery rate of 5.28%. This analysis resulted in a list of 314 genes with significantly different expression between the exercise and banding models. The expression values for these differentially expressed genes were then subjected to cluster analysis and visualization using Gene Expression Dynamics Inspector (GEDI) 2.1 software.[14] SLR values for these transcripts aligned, based on change in HW/BW ratio, were input into GEDI. Grid size was set to 9×8, and all other parameters were set to their default values.

Global Analysis of Commonalities in Gene Expression

The adaptive and maladaptive models were evaluated relative to each other to identify their commonalities. Transcripts with similar expression profiles in the adaptive and maladaptive hypertrophy models were identified with a novel analysis program designated Statistical Investigator of Transcriptional Homology. This software uses a modified form of the dynamic time-warping algorithm used in the global analysis to identify individual genes within a pair of genes in the expression datasets that exhibit comparable temporal expression patterns. A score (d_i) for gene i is computed by summing the Euclidean distances calculated for the expression measures taken at each pair of aligned time points multiplied by a time weight that adjusts for the length of the path through the distance table. This distance score indicates how closely the temporal expression profiles of gene i in the 2 experiments match. A cutoff value can then be set to limit the range of distance scores that represent similarly expressed transcripts. The distance score d_i was set to 0.45 in this study, meaning those transcripts that received distance scores ≤0.45 were considered to have matching temporal expression profiles. Transcripts determined to have matching expression profiles were visualized using Cluster and Treeview software.[15] Functional classification and enrichment analysis of the set of commonly expressed genes was conducted using the web-based DAVID bioinformatics resources.[16] Enrichment was assessed using a "heuristic fuzzy multiple linkage" algorithm that assigns enrichment scores to functional groups based on the geometric mean of a modified Fisher Exact statistical test.[16]

Statistics

Data are presented as mean±SEM. Pearson product moment correlation was used to test for similarity between the HW/BW values observed over time in the adaptive and maladaptive models. Significant differences were revealed to exist at $P<0.05$.

Results

Exercise and Banding Stimuli Elicit a Similar Magnitude of Myocardial Growth

To achieve time warping based on relative progression of hypertrophy, we first plotted the average HW/BW ratio for each time point in the exercise and aortic banding hypertrophy data sets to compare the changes in cardiac mass over time (Figure 1A). Although the rate of change in cardiac mass differed between the 2 hypertrophy models, the magnitude of overall growth seemed to be similar. This was compared quantitatively with linear correlation analysis of the change in HW/BW ratio observed in the adaptive (exercise) and maladaptive (aortic-banding) models (Figure 1B), which showed a strong correlation between the control (r^2=0.97, $P<0.01$) and hypertrophy (r^2=0.87, $P<0.01$) conditions. This analysis indicated that the exercise training and aortic banding stimuli elicited an analogous increase in cardiac mass albeit with disparate characteristic time scales. Closer inspection of the temporal evolution of HW/BW ratio in response to the hypertrophy stimuli identified the time points in the adaptive and maladaptive hypertrophy models with nearly identical HW/BW values (Figure 1C). Because alignment of these time points via HW/BW ratio could be achieved without violating their temporal order, it was postulated that this metric of cardiac growth might serve as a common feature to facilitate comparison between the time series gene expression data of the adaptive and maladaptive hypertrophy models. In other words, the gene expression values could be mapped from the time space into the cardiac growth (HW/BW) domain, or mass space, as a new reference system for comparing the hypertrophy models. When the data sets are examined in

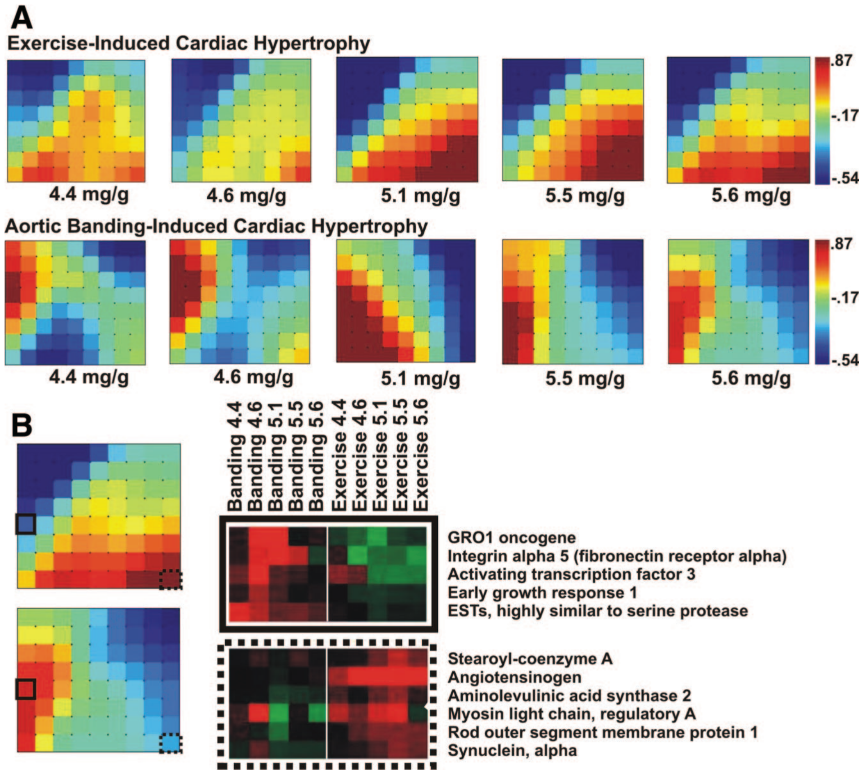

Figure 2. A, Genes expressed primarily in either the adaptive or maladaptive model were input into GEDI to produce mosaics of global gene expression with respect to HW/BW ratio. Scale bars indicate the centroid SLR value associated with each tile color in the mosaics. B, Inspection of the gene clusters comprising the GEDI mosaics reveals the identities of genes differentially expressed in the hypertrophy models. Heat maps of gene clusters from mosaic tiles with solid and dashed outlines provide examples of genes demonstrating this expression pattern.

mass space, this registration results in 5 different mass points versus the 6 time points in the traditional comparison. This does not imply a loss of fidelity but rather a shift of the data points over a defined mass range for comparison.

Alignment of Hypertrophy Gene Expression Time Series Using HW/BW

Gene expression data sets downloaded from the Cardiogenomics web site[7] were subjected to low-level processing to remove genes that were not considered to be expressed significantly above noise (see Methods section). This produced a dataset of 963 genes that were present in both hypertrophy models after the SAM analyses. To assess the benefit of using HW/BW ratio as an alignment system to study the gene expression profiles, we compared the distance scores D(a,b) (=a high-dimensional distance in gene expression space between 2 profiles at [warped] time t) between the profiles of adaptive and maladaptive hypertrophy time series microarray data aligned based on temporal progression alone to that computed for time series data aligned based on HW/BW ratio. The alignment based solely on temporal progression resulted in a high distance score of 1001.25, indicating that the global expression profiles were not well aligned between the hypertrophy model datasets (Figure 1D). In contrast, the alignment that used HW/BW ratio rather than time as an alignment parameter produced a much lower distance score of 31.34, demonstrating a markedly better alignment of the datasets (Figure 1E). Thus, the alignment based on the common feature of HW/BW ratio drastically reduced the distance between gene expression profiles and hence removed noise in gene expression differences because of the disparity of the characteristic time scales.

Differential Gene Expression Between Exercise and Banding Models

The mass aligned hypertrophy gene expression data were subjected to SAM[13] analysis to identify transcripts that exhibited differential expression between the adaptive and maladaptive hypertrophy models. This yielded 314 significantly differentially expressed genes. To assess global patterns in the transcriptome, this set of differentially expressed genes was analyzed and visualized using the program GEDI.[14] The GEDI mosaics representing these transcripts indicate that as the HW/BW ratio surpasses 5 mg/g, the global expression profiles in each hypertrophy model approach a steady state. They also reveal that these transcripts cluster into 2 large, oppositely regulated groups over the course of the growth processes initiated in the compared hypertrophy models (Figure 2A). Closer inspection of the most distinctive miniclusters in the GEDI mosaics showed that transcripts upregulated in response to aortic banding pertain primarily to cell adhesion, immune response, and transcriptional regulation processes (Figure 2B). In contrast, genes that were upregulated primarily in response to the exercise stimulus were associated with metabolism and regulation of muscle contraction.

Commonalities in Gene Expression Between Exercise and Banding Models

To identify genes that may be involved in a generic hypertrophy, we next examined the HW/BW ratio aligned exercise and banding gene expression data to find individual genes that exhibited similar expression profiles in both datasets after application of the dynamic time-warping algorithm (Figure 3). The similarity of the temporal

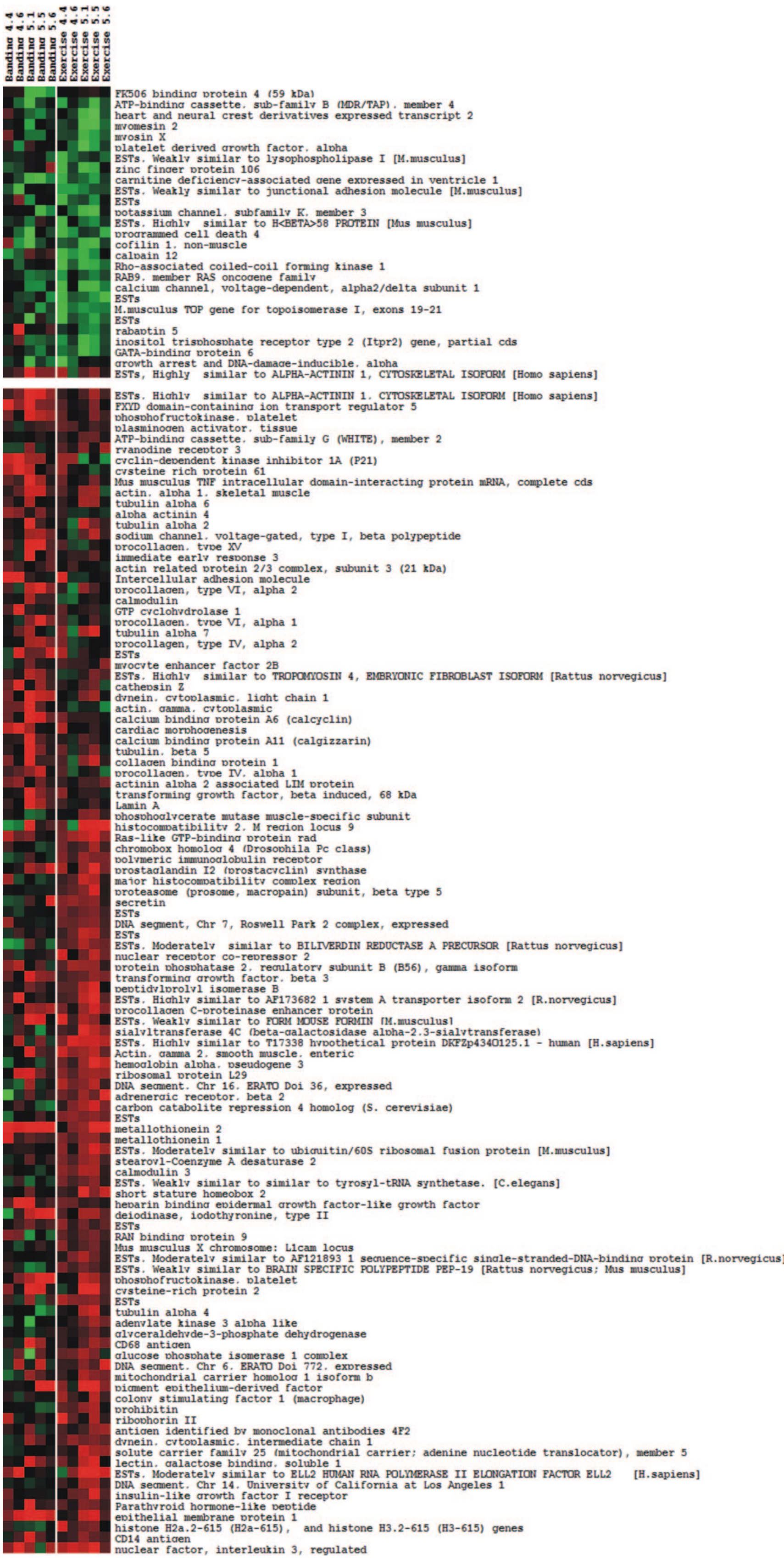

Figure 3. Transcripts with comparable expression profiles between the adaptive and maladaptive hypertrophy models were subjected to 2-group K-means clustering and their expression profiles visualized using a heat map.

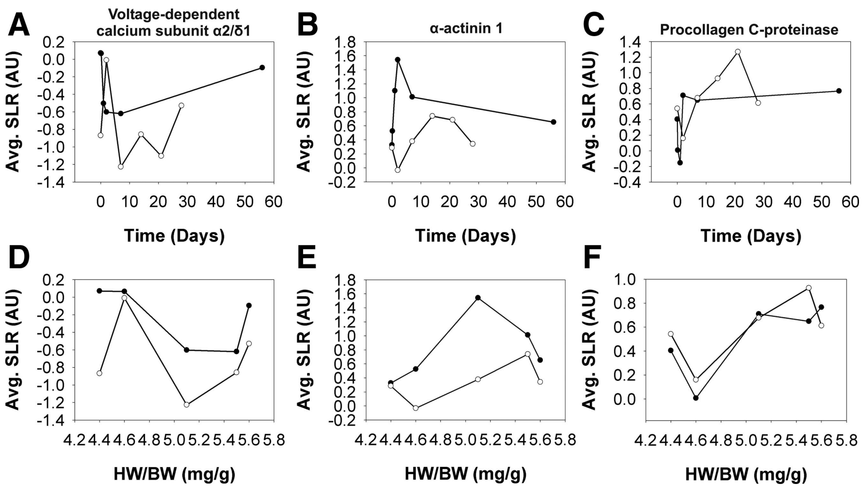

Figure 4. Average SLRs were plotted against time (A through C) and HW/BW ratio (D through F) for the adaptive (exercise, ○) and maladaptive (banding, ●) hypertrophy experimental conditions to compare the gene-expression profiles for voltage-dependent calcium channel $\alpha 2/\delta 1$ (A, D), α-actinin 1 (B and E), and procollagen C-proteinase enhancer (C and F) before and after mass alignment. AU indicates arbitrary units.

expression patterns of individual transcripts in the 2 mass-aligned profiles was determined using Statistical Investigator of Transcriptional Homology (see Methods section), which computes a distance scores d_i for gene i. Values for d_i ranged from d_i 0.089 for i=tubulin α6 to 2.65 for i=connective tissue growth factor, with lower scores d_i representing a greater degree of similarity between the temporal expression profiles of a gene i observed in the hypertrophy models. A cutoff score of 0.45 was chosen to distinguish transcripts with similar expression profiles in the exercise and banding time courses. That is, all genes with $d_i<0.45$ were considered to have similar temporal patterns of expression in both types of hypertrophy. Between the HW/BW aligned hypertrophy models, 136 transcripts (14.5%) displayed distance scores <0.45. The vastly different expression profiles for the connective tissue growth factor gene observed in the adaptive and maladaptive responses, coupled with the previous association of increased connective tissue growth factor expression with heart failure,[17] suggest that the Statistical Investigator of Transcriptional Homology analysis correctly distinguished transcripts with common expression patterns in response to the adaptive and maladaptive stimuli from those that embody a stimulus-specific response. Additionally, comparison of the time- and mass-aligned profiles for genes with distance scores less than the selected cutoff value, such as voltage-gated calcium channel subunit $\alpha 2/\delta 1$ (Figure 4A and 4D), α-actinin 1 (Figure 4B and 4E), and procollagen C-proteinase (Figure 4C and 4F), showed that the similarities in the expression profiles revealed by the Statistical Investigator of Transcriptional Homology analysis for the mass-aligned hypertrophy models was not evident when they were aligned based on time. The transcripts identified as having common temporal expression profiles (low d_i) were subjected to functional enrichment analysis to identify the cellular processes they participate in (Figure 5). The results suggest that the functional categories to which the generic hypertrophy associated genes belong include primarily cytoskeletal organization, extracellular matrix, metabolism, ion transport, cell adhesion, proteolysis, and regulation of transcription.

Discussion

Previous studies have used expression profiling to identify genes contributing to hypertrophic growth. Friddle et al[18], did expression profiling of pharmacological models of cardiac hypertrophy in mice and reported groups of known and novel genes whose expression was transiently regulated distinctly during induction and regression of hypertrophy. Several models of experimentally induced hypertrophy in rats have identified a group of 139 genes with consistent differential expression, suggesting a common genetic program that underlies pathogenic hypertrophic growth.[19] Zhao et al[20], used aortic constriction to induce hypertrophic growth in the hearts

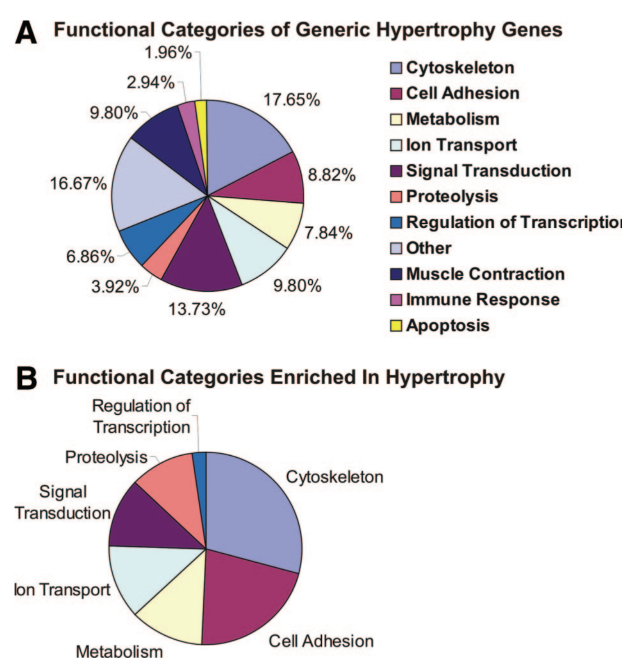

Figure 5. A, Gene ontology biological process terms were used to identify the cellular processes represented in the list of similarly expressed genes, and the proportion of genes that fell into each category was plotted. B, Functional enrichment analysis provided by the National Institutes of Health's DAVID Bioinformatics Resources (see Methods section) identified the biological processes terms that were overrepresented in the list of similarly expressed genes. Segment sizes represent the enrichment scores with geometric means >0.05, with larger segments indicating higher enrichment.

of mice to identify individual genes that were either uniquely upregulated or downregulated over the course of days at 3 unique time points. In an examination of adaptive and maladaptive hypertrophy, Kong et al[21], conducted microarray profiling of physiological and pathological hypertrophic growth in Dahl salt-sensitive rats. This study reported increases in stress response and inflammation-related genes in pathological processes but not in physiological hypertrophy. In the case of the latter, differential expression of genes associated with metabolic function and protein synthesis were observed. These studies are important, because they documented changes in expression in a variety of experimentally induced cardiac hypertrophy; however, they illustrate the lack of analytic strategies and tools for looking at hypertrophic growth as a dynamic event and the means of comparing and contrasting adaptive versus maladaptive growth.

Our study differed from previous work because our comparison of adaptive and maladaptive hypertrophic growth was in mass space, thus allowing us to compare disparate timescales of different studies as the growth occurred. We hypothesized that the concordant change in cardiac mass observed in mouse models of these hypertrophic stimuli was in part the product of a generic tissue-remodeling program that is activated regardless of the nature of the inciting stimulus. The average HW/BW values associated with each time point in the hypertrophy time courses revealed that certain time points exhibited similar values, and hence could be used to align the time courses without violating the temporal order of the time points. We postulated that it may be possible to use this metric of cardiac growth as a common feature between these dissimilar hypertrophy models to facilitate comparison of the gene expression changes associated with each. This comparison allowed us to distinguish between stimulus-dependent and -independent hypertrophic gene expression.

Despite the pronounced differences in the stimulus-dependent responses of the heart to adaptive and maladaptive stimuli, several transcripts had similar expression profiles between the contrasting hypertrophy models. Functional enrichment analysis revealed that transcripts coding for components of the sarcomere, such as α-actinin, were observed to have similar expression patterns in response to the adaptive and maladaptive stimuli. Likewise, transcripts coding for ion transport-related transcripts, particularly one associated with L-type calcium channels, were also commonly expressed in the adaptive and maladaptive models. Also of note, an enrichment of proteolysis-related transcripts was also observed in the list of commonly expressed genes, such as the transcript for procollagen C-proteinase enhancer protein. Taken together, the cellular processes represented in the list of genes found to have similar expression patterns in the exercise and banding hypertrophy models suggest that a baseline level of remodeling occurs in the myocytes and extracellular matrix comprising the myocardium to enhance its performance in response to hypertrophic stimuli.

Genes whose expression was perturbed primarily by the exercise stimulus were transcripts associated with metabolic processes and muscle contraction. Notably the expression of myosin light chain, regulatory 7, and angiotensinogen transcripts were significantly upregulated in response to exercise training. Angiotensinogen plays a role in the renin-angiotensin system as the substrate that angiotensin converting enzyme converts into angiotensin I during the process of blood pressure regulation. Studies have shown that the heart possesses an intracardiac renin-angiotensin system associated with various initiators of cardiac hypertrophy.[22] Additionally, enhanced expression of transcripts coding for proteins involved in lipid and glucose metabolism observed in the adaptive hypertrophy model corresponded well to those reported in the literature.[4,23] As expected, these transcripts expressed specifically in response to the adaptive stimulus contrast sharply with the genes expressed exclusively in response to the maladaptive stimulus.

Fibrosis and immune response-related transcripts dominated the list of genes whose expression was explicitly modulated in response to the maladaptive stimulus, consistent with previous reports.[20,24,25] Among the transcripts that were highly expressed only in response to aortic banding were several well-characterized clinical biomarkers for heart failure, such as brain-derived neutrophic factor, natriuretic peptide precursor type A, and natriuretic peptide precursor type B.[26] Several isoforms of collagen, such as procollagen type I, $\alpha 1$ and procollagen type III, $\alpha 1$, as well as the genes for secreted phosphoprotein 1 (ie, osteopontin), fibronectin 1, and the fibronectin receptor integrin $\alpha 5$, were also highly upregulated exclusively in response to the maladaptive stimulus. It is not surprising that the expression of these particular transcripts is significantly altered exclusively in response to the maladaptive stimulus because they are involved in augmenting the extracellular matrix of the myocardium, a hallmark of fibrosis.[3] The cell surface antigen CD44 and the fibronectin receptor integrin $\alpha 5$ were both highly expressed with similar expression profiles in response to the maladaptive stimulus and are associated with osteopontin. It has been hypothesized that osteonpontin is a component of the mechanism that regulates the cardiac response to increased pressure or volume load on the heart because cardiac fibroblasts and/or cardiac myocytes demonstrate radically increased osteopontin expression in response to angiotensin II stimulation associated with the onset of heart failure.[27] As shown in this study and widely reported in the literature, fibrosis plays a major role in the heart's response to maladaptive, but not adaptive stimuli.

Traditionally, the genetic differences between the diseased and healthy heart are mined for therapeutic opportunities. In this study, we have identified similarities between the expression profiles of adaptive and maladaptive hypertrophy that may be generally involved in cardiac growth. Most of these commonly expressed genes code for proteins, which support the structure and function of cardiomyocytes; yet, the architectural differences between the conditions are profound. This suggests that overlapping molecular signatures in the responses to beneficial and pathological stimuli may result in disparate outcomes. This offers a starting point to investigate the cause of the divergent development to better understand the disease course and how it might be reversed.

Limitations of This Study

Although most gene expression studies focus on finding genes differentially expressed in various pathological situations, we used a new analysis technique to identify common elements in 2 distinct models of cardiac hypertrophy, for commonalities can provide a deeper understanding of fundamental processes that do not depend on specific mechanistic aspects.

In doing so, we first uncovered a relationship between HW/BW ratio and the gene expression profiles in adaptive or maladaptive hypertrophy. However, HW/BW ratio may not be the best physiological indicator of cardiac hypertrophy. HW/BW ratio was chosen for this study because the values for these physiological parameters are commonly reported in studies of cardiac hypertrophy. Nonetheless, BW can fluctuate independently of HW because of perturbations in diet and/or exercise, leading to false-positive or false-negative reporting of hypertrophy. A more stable parameter, such as tibia length instead of BW may provide a more reliable comparison against HW for determining the incidence of cardiac hypertrophy.

In addition, artifactual differences in the experimental protocols often hard to avoid when comparing physiological and pathological manifestations of the same process. The sham operation and sedentary control groups against which the aortic banding– and exercise-induced hypertrophy groups were compared consisted of mice with slight differences in age, weight, and the manner in which they were treated. This may introduce unspecific differences in the transcriptomes of the mice. However, because our emphasis is on the characterization of commonalities between 2 hypertrophy models, technical (nonrelevant) differences will not have affected the specificity of our findings albeit the sensitivity could have been reduced (omission of interesting, commonly altered genes).

Finally, the analysis algorithms used in this study required that the gene expression datasets be "symmetrical," that is, for every transcript in the banding dataset, the same transcript had to be present in the exercise dataset as well. This symmetry was created by using different stringency criteria in the SAM analyses initially conducted on the banding- and exercise-induced hypertrophy expression datasets. Although we attempted to account for this discrepancy by applying more restrictive standards in our characterization of the differences and similarities between the banding and exercise datasets, the criteria used for the selection of the genes were established subjectively. Therefore, the results presented in this study provide what we feel is a representative, but incomplete, sampling of the differences and commonalities in gene expression between these models of hypertrophy.

Sources of Funding

Funding for this work was provided by the Harvard University Joseph H. Clark research support fund and National Institutes of Health R01 grant HL079126-01A2 (K.K.P.).

Disclosures

None.

References

1. Levy D, Garrison RJ, Savage DD, Kannel WB, Castelli WP. Prognostic implications of echocardiographically determined left ventricular mass in the Framingham Heart Study. *N Eng J Med*. 1990;322:1561–1566.
2. Fagard RH. Impact of different sports and training on cardiac structure and function. *Cardiol. Clin*. 1997;15:397–412.
3. Wakatsuki T, Schlessinger J, Elson EL. The biochemical response of the heart to hypertension and exercise. *TRENDS Biochem Sci.* 2004;29:609–617.
4. Strom CC, Aplin M, Ploug T, Christoffersen TEH, Langfort J, Viese M, Galbo H, Haunso S, Sheikh SP. Expression profiling reveals differences in metabolic gene expression between exercise-induced cardiac effects and maladaptive cardiac hypertrophy. *FEBS Journal*. 2005;272:2684–2695.
5. MacLellan WR, Schneider MD. Genetic dissection of cardiac growth control pathways. *Annu Rev Physiol.* 2000;62:289–319.
6. Mirotsou M, Watanabe CMH, Schultz PG, Pratt RE, Dzau VJ. Elucidating the molecular mechanism of cardiac remodeling using a comparative genomic approach. *Physiol Genomics*. 2003;15:115–126.
7. Genomics of Cardiovascular Development, Adaptation, and Remodeling. NHLBI Program for Genomic Applications, Harvard Medical School. Available at http://www.cardiogenomics.org. Accessed October 2006.
8. Bar-Joseph Z. Analyzing time series gene expression data. *Bioinformatics*. 2004;20:2493–2503.
9. Aach J, Church GM. Aligning gene expression time series with time warping algorithms. *Bioinformatics*. 2001;17:495–508.
10. Mirotsou M, Dzau VJ, Pratt RE, Weinberg EO. Physiological genomics of cardiac disease: quantitative relationships between gene expression and left ventricular hypertrophy. *Physiol Genomics*. 2006;27:86–94.
11. Kaplan ML, Cheslow Y, Vikstrom K, Malhotra A, Geenen DL, Nakouzi A, Leinwand LA, Buttrick PM. Cardiac adaptations to chronic exercise in mice. *Am J Physiol*. 1994;267:H1167–H1173.
12. Tarnavski O, McMullen JR, Schinke M, Nie Q, Kong S, Izumo S. Mouse cardiac surgery: comprehensive techniques for the generation of mouse models of human diseases and their application for genomic studies. *Physiol Genomics*. 2004;16:349–360.
13. Tusher VG, Tibshirani R, Chu G. Significance analysis of microarrays applied to the ionizing radiation response. *Proc Natl Acad Sci USA*. 2001;98:5116–5121.
14. Eichler GS, Huang S, Ingber DE. Gene Expression Dynamics Inspector (GEDI): for integrative analysis of expression profiles. *Bioinformatics*. 2003;19:2321–2322.
15. Eisen MB, Spellman PT, Brown PO, Botstein D. Cluster analysis and display of genome-wide expression patterns. *Proc Natl Acad Sci USA*. 1998;95:14863–14868.
16. Dennis G Jr, Sherman BT, Hosack DA, Yang J, Gao W, Lane HC, Lempicki RA. DAVID: database for annotation, visualization, and integrated discovery. *Genome Biol*. 2003;4:R60.
17. Weinberg EO, Mirotsou M, Gannon J, Dzau VJ, Lee RT, Pratt RT. Sex dependence and temporal dependence of the left ventricular genomic response to pressure overload. *Physiol Genomics*. 2003;12:113–127.
18. Friddle CJ, Koga T, Rubin EM, Bristow J. Expression profiling reveals distinct sets of genes altered during induction and regression of cardiac hypertrophy. *Proc Natl Acad Sci USA*. 2000;97:6745–6750.
19. Strøm CC, Kruhøffer M, Knudsen S, Stensgaard-Hansen F, Jonassen TE, Orntoft TF, Haunsø S, Sheikh SP. Identification of a core set of genes that signifies pathways underlying cardiac hypertrophy. *Comp Funct Genomics*. 2004;5:459–470.
20. Zhao M, Chow A, Powers J, Fajardo G, Bernstein D. Microarray analysis of gene expression after transverse aortic constriction in mice. *Physiol Genomics*. 2004;19:93–105.
21. Kong SW, Bodyak N, Yue P, Liu Z, Brown J, Izumo S, Kang PM. Genetic expression profiles during physiological and pathological cardiac hypertrophy and heart failure in rats. *Physiol Genomics*. 2005;21:34–42.
22. Raman VK, Lee YA, Lindpaintner K. The cardiac rennin-angiotensin-aldosterone system and hypertensive cardiac hypertrophy. *Am J Cardiol.* 1995;76:18D–23D.
23. Selvetella G, Hirsch E, Notte A, Tarone G, Lembo G. Adaptive and maladaptive hypertrophic pathways: points of convergence and divergence. *Cardiovasc Res.* 2004;63:373–380.
24. Johnatty SE, Dyck JRB, Michael LH, Olsen EN, Abdellatif M. Identification of genes regulated during mechanical load-induced cardiac hypertrophy. *J Mol Cell Cardiol*. 2000;32:805–815.
25. Van den Bosch BJC, Lindsey PJ, Van den Burg CMM, Van der Vlies SA, Lips DJ, Van der Vusse GJ, Ayoubi TA, Doevendans PA, Smeets HJM. Early and transient gene expression changes in pressure

overload-induced cardiac hypertrophy in mice. *Genomics.* 2006;88: 480–488.

26. Maisel AS, Bhalla V, Braunwald E. Cardiac biomarkers: a contemporary status report. *Nat Clin Pract Cardiovasc Med.* 2006;3:24–34.

27. Graf K, Do YS, Ashizawa N, Meehan WP, Giachelli CM, Marboe CC, Fleck E, Hsueh WH. Myocardial osteopontin expression is associated with left ventricular hypertrophy. *Circulation.* 1997;96:3063-3071.

CLINICAL PERSPECTIVE

The genes identified in this study as having similar expression profiles between adaptive and maladaptive stimuli of cardiac hypertrophy, which may have been overseen without the time-warping alignment to the state of hypertrophy, may be generically involved in profound mechanisms for the development of hypertrophy. They offer a starting point for understanding the mechanisms of mechanically induced cardiac remodeling, which could in turn lead to the development of diagnostic and treatment strategies for preventing the progression from cardiac hypertrophy to heart failure. Peptides, such as cardiac troponin I, have long been used to evaluate patients for the diagnosis of myocardial infarction. However, these peptides are not released from cardiac myocytes until late in the disease process after cell destruction has occurred. Using gene microarray expression studies, we may be able to identify proteins that are secreted early in the pathological response to stress before cell death occurs; these proteins could serve as biomarkers for the onset of maladaptive remodeling. Additionally, understanding the mechanisms underlying myocardial remodeling could yield insight for the development of therapeutic strategies that take advantage of these common processes to normalize stress in the myocardium before pathological remodeling mechanisms, such as fibrosis, are initiated.

Table 1: Genes Expressed in Both Hypertrophy Models

Table 1 contains the set of 963 genes identified to be significantly expressed in both the exercise and banding hypertrophy models in the Significance Analaysis of Microarrays (SAM) analysis of the exercise and banding gene expression profiles relative to their respective control conditions. The table is organized such that the name of each gene is associated with its corresponding Affymetrix probe identification number and its Log2-transformed signal ratios (SLR) for each measurement interval in both hypertrophy models.

Gene Name	Affymetrix Probe ID	Banding HW/BW (mg/g)					Exercise HW/BW (mg/g)				
		4.4	4.6	5.1	5.5	5.6	4.4	4.6	5.1	5.5	5.6
Angiotensinogen	101887_at	0.120064	0.244256	-0.38109	0.125446	0.661892	2.437013	4.763328	5.193975	5.259772	4.670396
aminolevulinic acid synthase 2, erythroid	92768_s_at	-0.114533	-0.127398	-0.841593	-0.63878	-0.477823	1.086838	0.394718	1.488336	2.192093	0.863324
synuclein, alpha	93273_at	-0.465075	1.434054	-0.752238	-0.619051	-0.591144	0.461032	0.720032	1.259002	2.048864	1.572019
rod outer segment membrane protein 1	93453_at	0.74255	-0.396273	-1.53741	0.312552	0.144343	0.325863	1.359997	1.911574	1.920967	1.717913
Stearoyl-coenzyme A desaturase 1	94057_g_at	0.303912	0.950794	-0.31627	1.041261	0.404316	0.409511	0.587308	1.619581	2.817202	1.689801
2,3-bisphosphoglycerate mutase	94815_at	0.316791	0.5688	-1.133031	-0.17446	-0.013107	0.670335	0.397163	0.848301	1.620777	0.840095
nuclear factor, interleukin 3, regulated	102955_at	0.611749	1.346668	0.684929	-0.402479	0.731082	0.784484	0.915171	0.834618	1.246376	0.446849
Ras-like GTP-binding protein rad	97319_at	0.822493	0.477628	0.582404	0.186688	0.035864	0.529122	0.716672	0.849754	0.978337	0.607456
ESTs	104477_at	-0.518849	0.123603	-1.179513	-0.843824	-0.184904	0.629928	0.738434	1.192906	1.764174	0.295539
ESTs, Highly similar to T17338 hypothetical protein DKFZp434O125.1 - human [H.sapiens]	96732_at	0.093802	0.782961	-0.205488	0.5513	-0.239396	0.574507	1.033997	0.905436	0.919203	0.812219
rat generating islet-derived, mouse homolog 3 alpha	103954_at	0.260148	-1.123932	0.370256	0.06876	0.415668	1.64631	1.035998	0.921129	0.434267	0.820876
Actin, gamma 2, smooth muscle, enteric	93102_f_at	-0.101096	0.048649	1.038172	0.399721	0.295699	0.910385	0.641388	0.707258	0.845138	0.446691
hemoglobin, beta adult minor chain	103534_at	-0.483358	0.128236	-0.560019	-0.602821	-0.343598	0.637128	0.24838	1.079649	1.362802	0.655472
alkaline phosphatase 2, liver	92796_at	0.270208	-0.080681	-0.088502	-0.261378	0.174737	0.544234	0.341738	0.824991	0.949607	0.770377
ESTs, Highly similar to cytosolic acyl coenzyme A thioester hydrolase [R.norvegicus]	100539_at	-0.044096	0.219342	-0.89662	-0.465755	-0.047246	0.451542	0.395504	1.156508	1.450592	0.484081
hemoglobin alpha, pseudogene 3	101703_at	-0.476836	-0.039781	0.162977	-0.337403	0.291865	0.501029	0.285358	0.697138	1.180277	0.870824
small proline-rich protein 1B	100446_r_at	-0.167534	-0.251298	-0.339813	-0.140874	-0.124924	0.798436	0.150935	0.921183	1.096446	0.750815
ribosomal protein L29	95418_at	0.004752	0.926028	0.974628	0.512772	0.258695	0.609671	0.398621	0.67018	0.724894	0.678116
aminolevulinic acid synthase 1	93500_at	0.014282	-0.017693	-0.409172	-0.322348	-0.140137	0.483826	0.330428	0.793311	0.791057	0.596449
CD8beta opposite strand	101903_at	1.012713	0.123791	-1.519877	-0.431301	0.103749	0.117542	0.498584	1.877824	1.430526	0.81922
DNA segment, Chr 16, ERATO Doi 36, expressed	103790_at	-0.233533	-0.447007	0.727108	-0.188015	0.180315	0.795472	0.512592	0.612853	0.830898	0.293319
receptor (calcitonin) activity modifying protein 1	104680_at	-0.437845	-0.19105	0.235436	-0.183027	-0.236408	0.345924	0.386545	1.131491	0.777503	0.751673
sialyltransferase 4C (beta-galactosidase alpha-2,3-sialytransferase)	95599_at	-0.240047	0.376114	0.226181	-0.621955	0.184963	0.367968	0.286034	1.177878	0.838189	0.597794
carbon catabolite repression 4 homolog (S. cerevisiae)	99535_at	-0.078362	0.366227	0.156727	-0.390537	-0.527448	0.264118	0.574426	0.748691	0.928506	0.556767
lectin, galactose binding, soluble 3	95706_at	-0.081454	-1.173296	3.759924	2.038551	2.154041	0.044555	1.653407	1.178634	1.2975	0.514573
ESTs	95905_at	-0.53532	0.38738	-0.504969	0.501309	-0.552174	0.514265	0.591902	0.483466	0.615413	0.449929
adrenergic receptor, beta 2	93193_at	-1.064519	-0.216789	0.47569	-0.128186	0.293896	0.507309	0.377819	0.698666	0.490612	1.101583
Stearoyl-coenzyme A desaturase 1	94056_at	0.55294	0.203639	-0.105981	-0.119576	0.170509	0.176501	0.281519	1.004728	1.949333	0.876711
metallothionein 2	101561_at	1.283515	0.97877	1.111424	1.554173	1.24287	0.117861	0.567167	0.674328	1.228729	1.148309
metallothionein 1	93573_at	1.016799	0.30002	0.457689	0.371623	0.311366	0.571081	0.372389	0.648265	0.672944	0.345293
ESTs, Moderately similar to ubiquitin/60S ribosomal fusion protein [M.musculus]	102841_at	0.177131	0.238495	0.232694	-0.00343	0.00465	0.632553	0.155686	0.685143	0.967928	0.715195
stearoyl-Coenzyme A desaturase 2	95758_at	-0.193501	-0.073342	0.448344	0.095219	0.288721	0.56702	0.375961	0.654558	0.74217	0.351873
adipocyte complement related protein of 30 kDa	99104_at	0.647922	-0.666915	-0.482971	-1.264254	-0.695212	0.220795	0.302804	0.981871	1.064706	1.227426
ESTs, Moderately similar to G3P_MOUSE GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE [M.musculus]	97751_f_at	-0.07676	0.015786	-0.596267	-0.053294	0.150866	0.522401	0.196499	0.680541	1.028169	0.59471
calmodulin 3	92631_f_at	0.231029	0.020312	-0.05858	-0.25244	-0.022185	0.636053	0.494501	0.784486	0.764194	0.255523
ESTs	95374_f_at	-0.458697	-0.038745	-0.033292	0.368918	0.096177	0.581045	0.650628	0.558107	0.64104	0.498318
procollagen C-proteinase enhancer protein	93349_at	0.404126	0.00671	0.709088	0.647922	0.765432	0.541174	0.159169	0.676661	0.926224	0.610821
ESTs	104267_at	-0.208187	0.347125	0.145297	0.277737	-0.06196	0.304951	0.489228	0.867127	0.810709	0.37221
myosin light chain, regulatory A	100403_at	0.98121	3.891829	-2.457717	0.584858	-2.102374	2.7936	1.633966	3.134263	3.631305	-0.636409
ESTs	100828_at	-0.196147	0.497839	0.641566	0.342429	-0.004691	1.224778	0.439224	1.202952	1.147402	0.066472
melanocortin 5 receptor	99896_at	-0.324242	-0.907935	0.746899	-0.237524	-0.069612	0.443162	0.44412	0.900949	0.447932	1.004471
ESTs, Highly similar to AF173682_1 system A transporter isoform 2 [R.norvegicus]	94433_at	0.319699	1.505071	0.141937	0.286635	0.119004	0.343218	0.397126	0.858493	1.292391	0.424033
microfibrillar associated protein 5	99518_at	-0.137764	0.115988	1.639713	1.935403	1.419716	0.735536	0.47974	0.435273	1.001378	0.241008
ESTs, Moderately similar to CYANELLE 30S RIBOSOMAL PROTEIN S11 [Cyanophora paradoxa]	97884_at	-0.002225	-0.336638	-0.002581	-0.208957	-0.272214	0.468748	0.448208	0.565457	0.847498	0.255869
polymeric immunoglobulin receptor	99926_at	-0.366794	-0.211988	0.383322	-0.004187	-0.188495	0.58776	0.325607	0.697186	0.57763	0.55644
ESTs, Highly similar to HYPOTHETICAL 27.6 KD PROTEIN IN PDX1-SNG1 INTERGENIC REGION [Saccharomyces c	97517_at	-0.449975	-0.86399	0.607654	-0.610314	-0.073578	0.665694	0.330415	0.548409	0.49991	0.338142
prostaglandin I2 (prostacyclin) synthase	104538_at	0.015677	0.207459	0.751279	0.573554	0.961261	0.740019	-0.03487	0.67565	1.336286	0.53179
Down syndrome critical region homolog 1 (human)	100555_at	0.262719	1.55471	1.682119	1.526422	1.077439	0.651701	0.384798	0.495632	0.50948	0.343741
ESTs	104342_i_at	1.323621	0.047786	-0.854379	-0.320162	-0.447166	0.036025	0.75882	0.699708	1.143213	0.65893
major histocompatibility complex region	102343_at	0.718705	-0.301673	-0.021452	-0.275018	-0.137707	0.304013	0.41813	0.887077	0.791754	0.233413
proteasome (prosome, macropain) subunit, beta type 5	101558_s_at	0.123749	0.082462	-0.114974	-0.106944	-0.12194	0.349507	0.445931	0.614592	0.983355	0.214369
secretin	92756_r_at	-0.346155	-0.274964	0.359848	-0.059086	1.034361	0.599292	0.672147	0.578753	0.64254	0.227812
chromobox homolog 4 (Drosophila Pc class)	93697_at	0.360534	-0.005263	-0.028649	-0.30578	-0.182933	0.53399	0.301059	0.421546	0.751245	0.324248
DNA segment, Chr 7, Roswell Park 2 complex, expressed	96629_at	0.691051	0.161196	-0.080879	-0.129264	-0.086724	0.49728	0.46625	0.568915	0.632887	0.336654
ESTs	96546_r_at	-0.12335	-0.25648	0.112743	0.107868	0.02647	0.550246	0.392602	0.503544	0.577413	0.318402
Mus musculus TNF intracellular domain-interacting protein mRNA, complete cds	95151_at	1.461187	1.041727	1.616745	0.479077	2.05716	0.656064	0.360321	0.182214	0.791802	0.390564
M.musculus mRNA for transferrin receptor	103958_g_at	-0.788028	-0.659128	1.420099	-0.256958	0.588281	0.179594	0.593265	0.928473	0.784515	0.724955
ESTs, Moderately similar to BILIVERDIN REDUCTASE A PRECURSOR [Rattus norvegicus]	104124_at	-0.716295	-0.607093	0.458849	-0.126674	-0.444165	0.383058	0.463505	0.795372	0.584603	0.49796
nuclear receptor co-repressor 2	95129_at	0.324858	-0.243875	0.152691	0.186575	0.297545	0.950399	0.017789	0.510709	0.855454	0.499084
protein phosphatase 2, regulatory subunit B (B56), gamma isoform	98993_at	0.610955	0.818874	-0.061075	0.439685	-0.24091	0.422696	0.732613	0.679433	0.670852	0.262922
transforming growth factor, beta 3	102751_at	0.467826	0.069792	0.989126	0.643304	0.578364	0.316121	0.420078	0.473775	0.658264	0.552751
DNA segment, Chr 15, ERATO Doi 55, expressed	95861_at	-0.102393	-0.22924	1.276463	-0.0942	-0.196864	0.423317	0.323339	0.606111	0.397859	0.799037
peptidylprolyl isomerase B	94915_at	0.206986	0.137207	0.52677	0.35793	0.158573	0.431751	0.427431	0.797785	1.02217	0.046114

ESTs	104179_at	1.456302	1.005275	0.985436	0.688765	-0.214717	0.30964	0.46784	1.052561	0.710348	0.759763
EST	102136_r_at	-0.292945	-0.048727	1.465646	1.023789	-0.092823	1.130968	0.410173	0.939747	0.534392	0.613664
ESTs, Weakly similar to similar to tyrosyl-tRNA synthetase. [C.elegans]	101023_f_at	-0.31019	0.311545	-0.457779	-0.055173	-0.235905	0.554257	0.345661	0.491331	0.626045	0.23153
ESTs, Weakly similar to FORM_MOUSE FORMIN [M.musculus]	103424_at	-0.223367	0.347444	1.312015	0.968863	0.061095	1.046069	0.325315	0.789158	0.640524	0.069623
ESTs	96924_at	-0.423435	0.192538	-0.581944	-0.141593	-0.130407	0.365515	0.075448	0.874939	0.839028	0.555873
ATPase, H? transporting, alpha polypeptide	94163_at	-0.484206	-0.571884	0.59184	-0.201233	-0.077226	0.938217	0.321928	0.601585	0.210968	0.725008
short stature homeobox 2	99042_s_at	-0.070764	0.050006	0.484228	-0.057103	0.068837	0.319309	0.234886	1.180783	0.600674	0.885051
pigment epithelium-derived factor	93574_at	0.164177	0.189517	0.020319	1.314065	1.335979	0.610782	-0.156958	1.139759	1.107598	0.615749
prohibitin	94855_at	-0.019928	0.089314	-0.049368	-0.396291	-0.347387	0.456094	0.3888	0.647932	0.78181	0.117076
ribophorin II	94076_i_at	0.82423	-0.145272	-0.042568	0.273394	0.021059	1.14768	0.44753	0.156009	0.76929	0.269207
clone BPS3.23 germline Ig variable region heavy chain precursor gene, partial cds	93927_f_at	-1.313652	-0.530486	2.110619	0.425808	-0.428433	1.835343	0.812172	0.871462	-0.499444	1.398423
DNA segment, Chr X, Wayne State University 72, expressed	104201_at	-0.386538	0.024411	0.578914	-0.408948	-0.049137	0.222261	-0.023436	0.932851	1.252454	1.187707
G-protein-coupled receptor 50	101763_at	-0.458375	-0.21683	0.761328	0.322622	0.056636	0.434561	0.368875	0.81421	0.369743	0.470868
fatty acid synthase	98575_at	0.246513	0.653538	-0.008894	0.211301	-0.318951	0.612507	-0.181308	0.729606	1.382319	0.647077
antigen identified by monoclonal antibodies 4F2	99133_at	0.279496	-0.025765	0.560269	-0.235022	-0.111364	0.377015	0.167161	0.342595	0.657086	0.719407
dynein, cytoplasmic, intermediate chain 1	103809_r_at	-0.237703	-0.123207	0.703034	0.414375	-0.017443	0.404354	0.651086	0.497461	0.570217	0.445407
solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	100618_f_at	-0.21292	-0.144876	0.034182	0.035123	0.148333	0.278908	0.161891	0.919688	0.744185	0.664199
RAN guanine nucleotide release factor	100562_at	-0.1071	0.186825	-0.273477	-0.643526	-0.087407	0.014583	0.705374	0.708939	0.514264	0.67407
ESTs, Highly similar to PHOSPHORYLASE B KINASE GAMMA CATALYTIC CHAIN, TESTIS ISOFORM [Homo sapiens	97971_at	1.167091	-0.19904	-0.225688	-0.185006	0.136093	0.601515	0.5025	0.182071	0.489063	0.357045
colony stimulating factor 1 (macrophage)	101450_at	0.253229	-0.266024	0.269777	-0.072709	-0.079614	0.727336	0.329277	0.130368	0.836214	0.313979
eukaryotic translation initiation factor 1A	94745_f_at	-0.975185	0.321602	1.450434	0.214157	-0.274341	0.697612	0.115881	1.257798	1.176878	1.409663
5-hydroxytryptamine (serotonin) receptor 5A	101152_at	-0.296176	0.397615	0.728033	-0.519789	0.141104	0.598241	0.539111	0.59168	0.465604	0.694754
ESTs, Moderately similar to ELL2_HUMAN RNA POLYMERASE II ELONGATION FACTOR ELL2 [H.sapiens]	103891_i_at	0.574097	1.438238	0.084519	0.219799	-0.078985	-0.481097	0.607936	1.511261	1.37214	0.927131
lectin, galactose binding, soluble 1	99669_at	0.190113	0.09443	0.995931	0.58854	0.296481	0.542392	0.214705	0.844703	1.006153	-0.002183
tubulin alpha 1	100342_i_at	-0.998138	-0.580662	1.043946	0.594664	0.323089	0.167772	-0.105599	1.631962	1.624276	0.465956
insulin-like growth factor I receptor	102224_at	0.507825	0.049458	0.147273	0.154856	-0.099634	0.013501	0.467634	0.517663	1.045258	0.396009
zinc finger protein 30	104437_at	0.238573	-0.26815	-0.223786	-0.125241	-0.352604	-0.053541	0.418067	0.945405	0.729516	1.108443
Parathyroid hormone-like peptide	104262_at	0.423805	0.129687	1.191815	0.26289	0.306398	0.438992	0.198196	0.595567	0.534751	0.292143
eyes absent 1 homolog (Drosophila)	94706_s_at	-0.841508	-0.276614	1.013004	0.103642	0.146354	0.310579	0.38868	0.536317	0.611615	0.608998
ESTs, Highly similar to NIFU PROTEIN [Anabaena pcc7120]	95645_at	0.105169	0.105326	0.864887	-0.085885	0.004571	0.837065	0.704409	0.73816	-0.029069	0.585686
epithelial membrane protein 1	97426_at	0.563736	0.956743	1.39164	1.199544	0.890644	0.147161	0.243843	0.870148	0.977058	0.366206
ESTs, Moderately similar to AF126743_1 DNAJ domain-containing protein MCJ [H.sapiens]	97204_s_at	0.395396	0.178196	-0.43995	-0.475554	-0.290305	0.102313	0.24099	0.894108	0.87295	0.430125
aquaporin 4	102704_at	0.291792	-0.036725	-0.11355	-1.312854	-0.966292	-0.129683	0.985159	1.316672	0.956207	0.321578
angiopoietin 2	92210_at	-0.840159	0.266481	0.137559	0.056883	0.62967	0.073968	0.335872	0.49597	0.724311	0.993408
histone H2a.2-615 (H2a-615), and histone H3.2-615 (H3-615) genes	93068_r_at	0.320665	-0.231647	-0.276499	-0.407592	0.101045	0.964413	0.320938	0.511717	0.57375	-0.014672
Mus musculus domesticus partial mRNA for oxystyrol-binding protein homologue 1 (Obph1 gene)	103311_at	0.236998	-0.088981	-0.09619	-0.10307	0.349837	0.278283	0.197913	0.619105	0.493614	0.439731
S100 calcium-binding protein A4	99051_at	0.825071	-1.190508	2.320032	0.541792	0.728751	0.38396	0.1847	0.394325	0.62818	0.773207
CD14 antigen	98088_at	-0.14526	0.370904	0.99766	0.422279	0.136068	0.242628	0.321288	0.64387	0.448227	0.333788
DNA segment, Chr 14, University of California at Los Angeles 1	102356_at	-0.149765	-0.05661	-0.215418	-0.108664	0.02756	0.333144	0.120775	0.742628	0.770069	0.274661
ryanodine receptor 3	97126_at	0.795999	-0.330001	-0.086333	-0.820748	0.410402	0.188021	0.819069	0.642918	0.34231	0.626866
mitochondrial carrier homolog 1 isoform b	95689_at	-0.456106	-0.201273	0.682001	0.424371	0.180021	0.309515	0.08943	0.783884	0.615169	0.522109
ESTs	104160_at	0.331081	-0.241278	0.68841	-0.398872	0.337148	0.76977	0.60495	0.578143	0.638392	0.353424
polynucleotide kinase 3'- phosphatase	97332_at	0.244662	0.096784	0.008889	-0.5695	-0.080076	0.515293	0.494525	0.252067	0.603579	0.246545
cDNA sequence AF180471	98892_at	0.317662	0.003131	-0.694863	-0.394658	-0.237085	0.139913	0.170679	0.472201	0.828345	0.837097
DNA segment, Chr 6, ERATO Doi 772, expressed	96875_r_at	-0.237215	0.805654	-0.128298	0.885872	-0.19202	0.298449	0.28392	0.614999	0.392606	0.993409
ESTs	98837_at	-0.788393	-0.380932	0.75415	0.342632	-0.183402	0.804461	1.11392	0.039778	0.24159	0.625558
ESTs	94430_at	-0.661094	-0.071407	0.176267	-0.271017	0.004963	0.844099	0.03964	0.50749	0.600303	0.184772
Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	101973_at	-0.019551	0.35638	-0.615176	-0.23536	-0.141203	0.132954	0.174509	0.627011	0.829206	0.677716
ESTs	97933_at	0.106147	0.33281	0.536642	0.289265	0.393686	0.649395	0.256878	0.528669	0.300434	0.456589
ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE PDSW SUBUNIT [Bos taurus]	101525_at	0.074498	0.035168	-0.676922	-0.474797	-0.033193	0.241689	0.206448	0.552353	0.616765	0.261448
myelin and lymphocyte protein; T-cell differentiation protein	99089_at	0.300032	-0.019883	0.054784	-0.117076	-0.641382	0.786547	0.40919	0.315729	0.249914	0.461207
transducer of ErbB-2.1	99532_at	0.485808	0.371126	-0.675675	-0.366125	-0.076697	-0.004044	0.138391	0.901118	0.919523	0.648796
Lamin A	98060_at	-0.200159	0.154225	0.819227	0.168588	0.231932	0.677677	0.178868	0.181825	0.513611	0.447988
ESTs, Highly similar to Ror2 [M.musculus]	93724_at	-1.197939	-0.2409	1.13237	0.285272	-0.194356	0.378328	-0.295094	0.882049	1.050347	0.983729
RAN binding protein 9	97812_at	0.60251	0.536175	-0.669528	0.079155	-0.415803	0.45734	0.269609	0.472329	0.552403	0.324241
growth arrest specific 1	94813_at	-0.107812	-0.058521	-0.880582	0.156361	0.241797	0.526053	0.377371	0.673838	0.515702	0.048075
ESTs, Weakly similar to AF113615_1 FH1/FH2 domain-containing protein FHOS [H.sapiens]	104255_at	0.128762	0.098414	-0.554763	-0.394578	-0.414032	0.309013	0.164201	0.320533	0.582246	0.596191
Mus musculus X chromosome: L1cam locus	96154_at	0.150049	-0.327523	0.142278	0.305172	0.150186	0.620426	0.244508	0.416094	0.53283	0.265528
ESTs, Moderately similar to AF121893_1 sequence-specific single-stranded-DNA-binding protein [R.norvegicus]	103504_at	0.198943	0.036829	0.015919	-0.033101	0.132953	0.222882	0.550234	0.774916	0.502932	0.255106
ESTs, Weakly similar to BRAIN SPECIFIC POLYPEPTIDE PEP-19 [Rattus norvegicus; Mus musculus]	97297_at	0.312493	-0.158118	-0.572514	-0.440724	-0.082069	0.563057	0.331991	0.527407	0.404912	0.230898
ESTs, Highly similar to unnamed protein product [H.sapiens]	93992_at	0.248528	0.180062	-0.111824	0.002238	-0.071278	0.562261	0.208765	0.198564	0.758115	0.277558
ESTs	100965_at	-0.547697	-0.397736	0.705244	0.223137	0.038639	0.646412	0.355615	0.657053	0.24652	0.431248
Mus musculus clone BAC126c8 Rsp29-like protein (Rsp29)	95730_at	-0.068187	0.081403	-0.195974	-0.313257	0.263395	0.262665	0.362138	0.532562	0.701456	0.074153
prion protein	100606_at	0.888484	0.629374	-0.540046	0.404399	0.5655	-0.060463	0.476628	0.566779	0.763453	0.786648
glucose-6-phosphate dehydrogenase X-linked	94966_at	0.986442	0.829247	1.042004	0.077494	0.284729	1.143807	0.678143	-0.058717	0.792898	0.136734
outer dense fiber of sperm tails 1	101968_at	-0.648547	-0.216152	0.278893	-0.537827	0.267397	0.819865	0.288674	0.666074	0.051511	0.56863
ESTs	95937_at	-0.526229	-0.171026	0.168018	-0.137056	-0.063765	0.211423	0.251254	0.33609	0.449596	0.529642
Myxovirus (influenza virus) resistance 2	102699_at	0.025491	-0.559342	0.082088	0.298275	0.071174	0.538807	0.198154	0.65975	0.425822	0.242219
Hydroxymethylbilane synthase	93258_at	0.894705	-0.19645	0.148768	-0.103066	0.119425	0.67433	0.270873	0.165205	0.592084	0.269615
M.musculus mRNA for transferrin receptor	103957_at	-1.346625	0.067496	0.912969	-0.203098	0.747244	-0.305312	0.053854	1.741897	1.337977	0.763937
Mus musculus DAZ-associated protein 1 (Dazap1) mRNA, complete cds	97372_at	-0.724978	-0.793283	0.650104	0.400943	-0.185995	0.172871	0.45214	0.694296	0.471686	0.603122
deiodinase, iodothyronine, type II	103438_at	-0.723496	0.299577	0.859024	1.046199	1.228104	0.390629	-0.015553	0.743032	0.74922	0.441665
ESTs	96864_at	0.439223	0.402404	-0.182565	-0.121564	-0.405931	0.162581	0.128988	0.574943	0.7082	0.366411

deoxyguanosine kinase	99544_at	-0.276101	-0.143413	-0.669041	-0.600292	0.191863	0.195655	0.072044	0.752219	0.598633	0.323105
haptoglobin	96092_at	0.0031	0.220257	0.684386	0.077933	-0.08006	0.256002	0.037723	0.456423	0.681078	0.823753
cell death-inducing DNA fragmentation factor, alpha subunit-like effector A	99994_at	0.791863	0.07159	0.365562	-0.058662	0.155845	0.108252	0.455539	0.832549	0.428792	0.221471
ESTs, Moderately similar to unnamed protein product [H.sapiens]	96621_at	-0.042263	0.089917	-0.144613	0.192826	0.515978	0.305343	0.252129	0.528277	0.780193	0.042461
epithelial membrane protein 3	93593_f_at	0.048574	-0.225363	0.902783	0.372408	0.398339	0.607614	-0.113233	0.515893	0.675334	0.524479
nuclear receptor subfamily 1, group I, member 3	102171_r_at	-0.280339	-0.363109	0.053669	-0.157751	-0.206993	0.582702	0.167945	0.249016	0.477566	0.505764
solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	102642_at	-0.219324	-0.128147	0.682089	0.331992	-0.126833	0.246213	0.351013	0.694279	0.433334	0.324164
cysteine-rich protein 2	93550_at	0.621156	0.15514	1.320989	1.002607	0.21532	-0.271646	0.142708	1.414784	1.357556	0.401334
C5a anaphylatoxin receptor=peptidergic G-protein-coupled receptor [mice, BALB/C, Genomic, 1114 nt 2 segments]	101728_at	0.269142	0.002121	0.598816	0.010221	0.273196	0.199579	0.094059	0.548226	0.833859	0.428612
ESTs	104076_at	0.31351	0.221816	-0.689206	-0.513082	-0.442927	0.275976	0.400147	0.419036	0.710977	0.088078
ESTs, Moderately similar to BIOTIN CARBOXYLASE [Anabaena pcc7120]	95674_r_at	-0.010415	-0.066355	0.146305	0.267927	0.016207	0.643383	0.564907	0.251279	0.336198	0.366482
ESTs, Moderately similar to ELL2_HUMAN RNA POLYMERASE II ELONGATION FACTOR ELL2 [H.sapiens]	103892_r_at	0.315679	2.02318	-0.047923	0.253033	-0.007629	-0.112981	0.444096	1.072981	0.739267	0.483591
Mouse (AKR/J) endogenous retrovirus, clone A-12, pol-env region	97197_r_at	0.340752	0.58724	-0.644941	1.010752	0.850326	1.577519	1.158286	0.077194	0.749343	0.25912
proteasome (prosome, macropain) subunit, beta type 5, pseudogene	101741_at	-0.144253	-0.306213	0.419597	-0.0454	0.154782	0.236313	0.119584	0.546864	0.6687	0.286893
ESTs, Highly similar to MITOCHONDRIAL PROCESSING PROTEASE BETA SUBUNIT PRECURSOR [Rattus norvegic	94005_at	0.302348	0.437039	-0.847128	-0.044914	-0.275063	0.200517	0.275907	0.45917	0.521801	0.390115
fractured callus expressed transcript 1	99123_s_at	0.280918	-0.016256	-0.157038	-0.143671	-0.044935	0.145271	0.220601	0.509286	0.498881	0.397796
endoglin	100134_at	0.649121	0.027618	-0.246884	0.110326	0.164958	0.404686	0.061898	0.626622	0.516534	0.22171
elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2	94393_r_at	-0.264929	-0.374174	0.86185	1.077583	-0.738562	0.171009	-0.241718	1.255945	0.819428	1.309427
phosphofructokinase, platelet	97834_g_at	0.045333	0.555881	0.793003	1.260084	1.079061	0.062068	0.121925	0.864174	0.741286	0.383323
EST	101229_at	0.013785	-0.109197	0.465894	0.392815	0.026633	0.251154	-0.18687	1.028029	0.405697	1.408225
tubulin alpha 4	92635_at	-0.08508	-0.011793	0.052911	-0.692051	-0.427382	0.197304	0.043217	0.808731	0.919489	0.207449
adenylate kinase 3 alpha like	92492_at	-0.330142	0.049376	-0.821627	0.049423	0.094204	0.060317	0.227361	0.487739	0.739135	0.509605
lymphotoxin B receptor	97980_at	-0.631165	-0.017418	0.504066	0.599379	0.195929	0.587146	-0.154049	0.73624	0.908462	0.186078
ESTs, Moderately similar to KIAA0943 protein [H.sapiens]	94551_at	-0.318148	0.018471	0.316078	0.201429	0.368075	0.222108	0.260774	0.216987	0.475592	0.741585
hexokinase 2	94375_at	0.181305	0.122136	-0.583401	-0.480609	-0.28466	0.059766	0.099517	0.727122	0.698373	0.64174
ESTs, Moderately similar to phosphoenolpyruvate carboxykinase [M.musculus]	95449_at	-0.158466	-0.474798	-0.00507	-0.388482	-0.284292	0.506302	0.511325	0.372398	0.335651	0.140116
ESTs, Highly similar to AF112204_1 Vacuolar proton pump subunit SFD alpha isoform [H.sapiens]	96610_at	-0.05331	0.006469	0.24449	0.317512	0.411418	-0.033139	0.264138	0.689377	0.733765	0.468506
glyceraldehyde-3-phosphate dehydrogenase	101214_f_at	0.144326	-0.031954	-0.360311	-0.115587	0.231729	0.289367	0.195231	0.34398	0.527781	0.247247
sialyltransferase 4A (beta-galactosidase alpha-2,3-sialytransferase)	99847_at	0.077777	0.478416	0.70852	0.426591	0.126545	0.498623	0.321761	0.147527	0.300141	0.419555
ganglioside-induced differentiation-associated-protein 2	104134_at	0.749777	-0.611146	0.801362	0.647621	0.561766	0.499414	0.529283	0.396327	0.147954	0.256375
ESTs, Highly similar to RSP-1 PROTEIN [Mus musculus]	104523_at	-1.248149	0.244854	-0.044169	-0.74848	-0.732823	0.113595	0.511343	0.31018	0.398097	0.461783
ESTs, Highly similar to mediator [H.sapiens]	95616_at	0.546814	-0.019977	0.118446	-0.247043	-0.245403	0.491745	0.24121	0.242471	0.221543	0.42186
ESTs	104451_at	0.118137	0.280739	0.633242	0.283051	-0.255364	0.200216	0.269463	0.506039	0.627368	0.234782
CD68 antigen	103016_s_at	0.269903	-0.153363	1.467172	0.684512	0.09452	0.301453	-0.037794	0.411495	0.723017	0.556151
carbonic anhydrase 14	98079_at	-0.208865	0.008501	-0.467358	-0.577925	-1.028422	-0.120495	0.372542	0.64226	0.560116	0.470824
glucose phosphate isomerase 1 complex	100573_f_at	-0.226027	0.489746	-0.949169	0.470626	-0.056413	0.453984	0.496012	0.758983	0.561408	-0.189035
DNA segment, Chr 15, Wayne State University 97, expressed	97132_at	-0.187592	-0.215144	0.532223	0.107513	-0.199919	0.473838	0.469557	0.329419	0.378275	0.335855
ESTs, Moderately similar to unnamed protein product [H.sapiens]	104767_f_at	0.207327	-0.140288	-0.118352	-0.022089	-0.401551	0.50768	0.35315	0.275846	0.41893	0.129299
heparin binding epidermal growth factor-like growth factor	92730_at	0.411571	2.029934	1.063759	0.255168	0.392311	0.517991	0.488085	0.262804	0.317117	0.186183
cytochrome c oxidase, subunit VIIa 1	102749_at	-0.047552	0.125932	-0.743128	-0.470424	-0.422606	0.342437	0.194172	0.223033	0.514069	0.39412
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	97060_at	0.68321	-0.079689	-0.180755	0.008783	0.371084	0.258856	-0.065488	0.867833	0.884926	0.921793
Friedreich ataxia	101407_at	1.145335	0.605732	-0.678426	-0.361223	-0.168298	0.248009	0.029445	0.799721	0.783833	0.185281
karyopherin (importin) alpha 2	92790_at	0.250818	0.523936	-0.151953	0.064084	-0.176864	0.497613	0.252517	0.461964	0.58635	0.157519
ESTs	101665_at	-0.550504	-0.397307	0.855528	0.120337	-0.058308	0.322862	0.2429	0.42471	0.344652	0.554829
complement component 3a receptor 1	103707_at	0.254455	-0.194668	1.554194	0.934784	0.37098	0.219241	0.036464	0.648919	0.601916	0.516174
ESTs	95707_at	-0.020517	0.088117	-0.546453	-0.39278	-0.320594	0.122097	0.203476	0.839593	0.764645	0.058394
putative TNF-resistance related protein	100717_at	-0.331223	-0.334007	0.647981	-0.198925	-0.146079	0.516533	0.360456	0.401853	0.405227	0.367421
ESTs, Weakly similar to CG7979 gene product [D.melanogaster]	102423_at	0.38077	-0.255202	0.33688	-0.192932	0.421275	0.051581	-0.777399	2.597684	1.749457	1.993014
S100 calcium binding protein A11	98600_at	1.320167	0.462946	1.747314	1.52111	0.815531	0.528771	-0.331392	0.730608	1.14559	0.371082
ESTs	103467_g_at	-0.085643	1.560563	-0.560913	-0.227558	-0.000335	0.44443	0.194029	0.157821	0.476236	0.270597
pleiotropic regulator 1, PRL1 homolog (Arabidopsis)	101064_at	0.149941	0.178149	-0.147342	0.069592	-0.201411	0.197654	0.403912	0.579744	0.574162	0.026151
ESTs	103935_at	-0.223624	0.093666	-0.310826	-0.120414	0.035901	0.37098	0.025537	0.556259	0.506668	0.340899
apolipoprotein B editing complex 2	97235_f_at	0.05718	0.440243	-0.859672	-0.277626	-0.266348	0.935586	0.285711	0.544344	0.569452	0.36306
histocompatibility 2, M region locus 9	101341_at	-0.653283	-0.524998	1.217394	0.237272	0.393868	0.487339	-0.621582	1.024763	1.067153	1.333241
suppressor of Ty 4 homolog (S. cerevisiae)	100587_f_at	0.227726	0.385978	-0.78568	-0.637303	-0.505942	0.428358	0.395765	0.264058	0.489686	0.142046
utrophin	92507_at	0.65342	-0.140988	-0.297915	-0.196032	-0.453173	0.103477	0.50098	0.237039	0.798373	0.515131
hemoglobin, beta adult major chain	101869_s_at	-0.228087	-0.290147	0.024163	-0.161093	0.139829	0.215491	-0.012456	0.602127	0.647139	0.363533
solute carrier family 16 (monocarboxylic acid transporters), member 1	101588_at	0.596915	0.613867	-0.16229	0.098043	-0.307896	0.480538	0.319531	0.486199	0.753124	0.031474
DNA segment, Chr 15, Wayne State University 75, expressed	104141_at	-0.055023	-0.468844	0.434232	0.63975	-0.039478	0.324722	0.092942	0.474016	0.35393	0.491695
ATP synthase, H transporting, mitochondrial F0 complex, subunit f, isoform 2	93114_at	0.174373	-0.237953	0.450015	-0.459083	-0.185505	0.776412	0.220945	0.446631	0.206845	0.391331
olfactory receptor 71	97004_at	-0.244427	0.001639	0.528975	-0.345214	0.035122	0.59513	0.547981	0.319595	0.364598	0.227741
DNA segment, Chr 16, ERATO Doi 779, expressed	95137_at	-0.691441	-0.50422	0.778027	0.712652	-0.011198	0.585039	0.161332	0.335741	0.561973	0.065447
ESTs, Highly similar to HYPOTHETICAL PROTEIN C22G7.01C IN CHROMOSOME I [Schizosaccharomyces pombe]	101591_at	-0.075718	0.146185	-0.094223	-0.11946	0.273555	0.162996	0.379892	0.266271	0.584177	0.453277
ESTs, Highly similar to sarcosine dehydrogenase [R.norvegicus]	96763_at	-0.540883	-0.055556	-0.109343	-0.11433	0.202719	0.365624	0.069301	0.493612	0.567612	0.565875
myocyte enhancer factor 2B	93417_at	-0.289987	-0.119525	0.527494	0.230941	0.166346	0.390012	0.293612	0.283198	0.145603	0.633687
ESTs, Weakly similar to HYPOTHETICAL 40.4 KD PROTEIN R06F6.5 IN CHROMOSOME II [Caenorhabditis elegans]	95075_at	-1.570881	0.672232	0.792819	0.180305	-0.379695	0.399905	0.660563	0.169826	0.309281	0.2823
interleukin 10 receptor, beta	99491_at	0.254044	0.283457	-0.981466	-0.380045	-0.285265	-0.00414	0.237568	0.565642	0.637048	0.305492
SH3-domain GRB2-like B1 (endophilin)	98945_at	0.030465	0.302247	-0.555207	-0.281028	-0.176472	0.171981	0.14765	0.860634	0.962841	0.269407
phosphoglycerate mutase muscle-specific subunit	92599_at	0.21076	-0.026581	-0.479796	-0.392076	-0.07431	0.107627	0.085324	0.579052	0.652336	0.289662
ESTs	100306_at	0.883355	-0.524441	0.547895	-0.752724	0.245054	-0.088108	0.106136	0.783643	0.599639	0.880571
glucose phosphate isomerase 1 complex	100574_f_at	0.240575	0.297388	-0.807631	-0.028278	0.093983	0.153931	-0.052842	0.871288	0.849984	0.248023
odd Oz/ten-m homolog 4 (Drosophila)	97581_at	0.337076	-0.202205	0.516485	0.356087	0.059059	0.372163	0.046305	0.836255	0.271884	1.029197
seven in absentia 2	97906_at	-0.482676	0.063295	0.306616	-0.203303	0.160065	0.716618	0.548197	0.449125	0.402024	-0.163779

Mus musculus Bat-4 gene, complete cds	101416_f_at	0.258046	-0.10311	0.149362	-0.127094	0.007574	0.539158	0.54448	0.334963	0.353441	0.072058
ESTs	101426_at	2.217651	0.304855	0.509455	-0.835385	0.351226	0.392773	0.33719	0.520461	0.375952	0.029936
neoplastic progression 3	102780_at	2.345964	1.786719	1.168726	0.929163	0.229411	0.620296	0.525738	0.080905	0.361547	0.570218
ESTs, Highly similar to unnamed protein product [H.sapiens]	97356_at	-0.108277	-0.134283	-0.218044	-0.14217	-0.2852	0.174493	-0.012705	0.963433	0.592739	0.244695
homeo box B8	96418_r_at	-0.361575	-0.569338	0.94954	0.442069	0.274937	0.251113	0.220462	0.600709	0.226414	0.514044
annexin A3	101393_at	-0.323908	0.3253	0.479143	1.034107	0.499249	0.130671	0.199426	0.363678	0.618104	0.492413
cathepsin B	95608_at	0.427905	0.347734	-0.530242	0.275819	-0.113505	0.549262	0.310788	0.431174	0.620502	0.060737
plasminogen activator, tissue	93981_at	0.288956	-0.237521	0.261306	0.332937	0.386632	0.48737	0.39651	0.159131	0.357619	0.251902
ATP-binding cassette, sub-family G (WHITE), member 2	95023_at	0.105668	-0.078096	0.065329	0.24019	-0.031492	0.30885	0.108415	0.456863	0.492811	0.189602
ESTs	104034_at	0.355576	-0.534956	0.03472	-0.101802	-0.268641	0.436455	0.12807	0.200994	0.453659	0.441107
ESTs	103927_at	0.206713	0.292622	0.043178	-0.074469	0.169783	0.435667	0.601538	0.357664	0.615645	0.207906
ESTs, Highly similar to KIAA0095 gene is related to S.cerevisiae NIC96 gene. [H.sapiens]	98975_at	0.010559	0.681513	-0.210045	0.89847	0.301971	0.357974	-0.113358	0.504853	0.553095	0.488407
ESTs, Highly similar to HYPOTHETICAL 13.6 KD PROTEIN IN NUP170-ILS1 INTERGENIC REGION [Saccharomyces	97447_at	0.18411	0.000451	-0.095156	-0.265408	-0.275184	0.246815	-0.226998	0.720479	0.889825	0.455494
glutathione S-transferase, mu 3	97681_f_at	0.113111	-0.134143	-0.522623	-0.314562	-0.088201	0.580283	0.278147	0.238143	0.32486	0.157848
DNA segment, Chr 12, ERATO Doi 771, expressed	98061_at	-0.183376	0.407093	0.333243	-0.080267	-0.038007	0.350555	0.150021	0.240553	0.41919	0.300962
ESTs, Weakly similar to polymerase I-transcript release factor [M.musculus]	97496_f_at	0.435771	0.294387	0.0896	0.67111	-0.04234	0.89665	0.401837	0.553281	0.336198	-0.208906
ryanodine receptor 3	101830_at	-0.295261	-0.2864	0.613657	-0.184294	0.1254	0.410192	0.211294	0.616997	0.156596	0.727579
disabled homolog 2 (Drosophila)	98045_s_at	1.316096	0.921596	0.400442	0.674153	0.299055	0.284457	0.062837	0.570798	0.762064	0.414806
ESTs, Weakly similar to T17344 hypothetical protein DKFZp586L2024.1 - human [H.sapiens]	93443_at	0.078639	-0.141055	0.336414	0.932489	0.168291	0.360967	-0.409472	0.835883	0.832462	0.819387
interferon gamma inducing factor binding protein	92689_at	-0.76187	-0.257326	0.5288	-0.64457	-0.243401	0.107405	0.218551	0.378061	0.533959	0.418611
cytochrome c oxidase, subunit Vb	93119_at	0.145317	0.026424	-0.380616	-0.511927	-0.160763	0.16424	0.147824	0.505643	0.645275	0.154937
protease (prosome, macropain) 28 subunit, alpha	101510_at	0.059649	0.086163	-0.36651	-0.602293	-0.647524	0.368137	0.363386	0.266359	0.380352	0.146723
ESTs, Moderately similar to Y110_HUMAN HYPOTHETICAL PROTEIN KIAA0110 [H.sapiens]	95565_at	0.267385	0.130226	-0.177323	-0.100433	0.059314	0.3752	0.458568	0.478442	0.293194	0.102019
glycophorin A	102770_at	-0.347396	0.134109	0.485689	0.275601	-0.032638	-0.166838	-0.191265	1.161247	0.910909	1.090701
transgene insert site 737, insertional mutation, polycystic kidney disease	100404_at	-0.452418	-0.233127	0.389696	-0.053399	-0.074202	0.221964	0.209887	0.524925	0.380108	0.551934
Mus musculus eukaryotic translation elongation factor 1-delta mRNA, complete cds	99142_at	-0.585266	-0.517468	0.784365	0.130786	0.139302	0.338395	-0.08693	0.567676	0.471037	0.420079
S100 calcium binding protein A3	101051_at	-0.165984	-0.179053	0.790396	-0.135426	0.130094	-0.00255	0.039754	0.54668	0.648744	0.773533
peptidase 4	101042_f_at	-0.210646	0.117247	-0.408224	0.037927	-0.287277	0.211771	0.20856	0.56373	0.553607	0.120714
histocompatibility 2, K region locus 2	97173_f_at	-0.990031	-1.199259	1.170179	0.900369	-0.001464	-0.661484	-1.323068	-1.783031	-1.614189	-1.011842
ESTs	95936_at	-0.805263	-0.612278	1.712933	0.267052	0.285665	-0.981772	-0.387604	-1.533076	-1.563783	-2.194
ceruloplasmin	92851_at	0.575824	0.302653	-0.100169	0.426425	0.637221	-0.696925	-0.740481	-1.394221	-0.918781	-0.918578
Myelocytomatosis oncogene	104712_at	1.577575	2.534677	1.138772	-0.209638	-0.293766	-1.06253	-1.71793	-1.288818	-0.671883	-1.808596
B-cell translocation gene 2, anti-proliferative	101583_at	1.418129	1.332521	0.633509	0.753403	0.200547	-0.609097	-0.522826	-1.868078	-1.670861	-1.682387
brain derived neurotrophic factor	102727_at	0.446273	0.906665	0.223145	0.242823	0.204441	-1.265285	-0.419086	-1.550686	-1.272251	-1.041794
ESTs, Highly similar to G33_RAT GENE 33 POLYPEPTIDE [R.norvegicus]	93975_at	1.239925	0.771514	-0.33169	0.697538	-0.199134	-0.7046	-0.602684	-0.953952	-1.428724	-1.070462
Kruppel-like factor 9	93527_at	0.012326	0.021881	-1.225507	-0.397492	-0.217086	-1.309108	-0.783106	-0.943431	-0.875286	-0.441822
nuclear receptor subfamily 4, group A, member 1	102371_at	0.640059	0.876154	0.29729	0.457674	0.431653	-0.600302	-0.825437	-1.328757	-1.285266	-1.118296
insulin-like growth factor binding protein 3	95082_at	0.752805	1.410179	-0.862872	0.237746	0.62527	-0.492732	-0.78419	-1.172401	-1.209323	-0.734178
fibrinogen/angiopoietin-related protein	96119_s_at	0.089476	0.369039	-0.11308	0.241713	-0.248051	-0.841392	-0.608794	-0.598921	-1.006845	-0.928733
CD2-associated proten	103281_at	-0.508535	0.166347	-0.215796	1.897686	0.672505	-1.239678	-0.62595	-0.959937	-0.573033	-1.403625
interferon-inducible GTPase	103963_f_at	-0.255095	-0.05178	-0.470125	-0.171918	-1.557164	-0.774541	-0.524391	-0.841174	-0.980417	-0.586812
T-cell specific GTPase	102906_at	-0.634376	-0.327445	-0.383082	0.368448	-0.496175	-0.475886	-0.202025	-2.053788	-2.501192	-2.292985
interferon-inducible GTPase	96764_at	-0.095965	-0.135528	-0.708251	0.319743	-1.534714	-0.743164	-0.467764	-1.23267	-0.704255	-0.832167
ESTs	97711_at	-0.737999	-0.269242	-0.341921	-0.079828	0.317869	-1.405187	-0.389042	-0.798559	-1.071337	-0.916391
potassium voltage gated channel, shaker related subfamily, member 5	102295_at	-0.142355	0.226288	-0.412945	-0.099601	-0.377337	-0.663504	-0.972847	-0.928905	-1.18948	-0.950909
ESTs, Highly similar to KIAA0824 protein [H.sapiens]	99923_at	-0.48796	-0.71595	-0.479522	-0.031441	-0.83376	-1.045554	-0.380502	-0.87478	-0.996586	-0.53879
interferon activated gene 204	98465_f_at	-0.060637	0.285102	-0.249329	0.304224	0.263923	-0.898823	-0.543771	-0.834181	-0.650824	-0.631108
Mus musculus putative RNA helicase RCK mRNA, partial cds	93965_r_at	-0.388647	0.307963	0.509872	-0.334641	0.244889	-0.604957	-0.630245	-1.909886	-1.807722	-0.282829
catechol-O-methyltransferase	98535_at	0.749591	-0.337036	-0.259713	0.433461	0.689908	-0.302562	-0.726902	-1.062032	-1.104422	-1.020944
purine-nucleoside phosphorylase	93290_at	0.376475	0.089334	0.249957	0.137007	0.127045	-0.778239	-0.434746	-1.062518	-0.972865	-0.838777
ESTs	97710_f_at	0.896899	0.66426	-0.655934	-0.36754	-0.125818	-0.653377	-0.697576	-0.807272	-0.527608	-0.727713
RPB5-mediating protein	103682_at	0.153246	0.396076	-0.36937	-0.038856	0.035827	-0.618036	-0.813487	-1.083699	-0.710111	-0.367628
ESTs, Highly similar to G33_RAT GENE 33 POLYPEPTIDE [R.norvegicus]	93974_at	0.526634	0.677281	-0.05341	0.065337	0.370903	-0.67475	-0.426328	-0.735964	-1.024853	-1.059645
ESTs, Highly similar to TENSIN [Gallus gallus]	96825_at	0.042019	-0.523478	-0.436672	-0.764241	0.13837	-0.221298	-1.156432	-1.246362	-1.426771	-0.74331
malic enzyme, supernatant	101082_at	0.278369	-0.101507	-0.558939	-0.42564	0.075209	-0.597913	-0.685117	-0.5812	-0.98761	-0.498692
Rho-associated coiled-coil forming kinase 1	100980_at	0.148353	-0.422497	-0.088807	-0.013681	0.120769	-1.078349	-0.384768	-0.828837	-0.776092	-0.451214
early B-cell factor	92535_at	-0.217835	0.108755	0.852404	-0.981211	-0.276776	-0.691803	-0.392439	-0.692764	-0.705663	-0.843199
connective tissue growth factor	93294_at	-0.044479	1.781996	1.878405	2.136207	1.424384	-0.368089	-0.202687	-1.989831	-1.777713	-2.196326
ESTs	92971_at	0.122626	-0.009444	0.041625	0.425236	-0.168396	-0.36808	-0.901889	-0.713856	-1.013353	-0.648564
high mobility group box 1	93095_at	-0.035037	0.083992	-0.080176	-0.143091	0.251183	-0.96025	-0.290556	-0.837741	-0.96662	-0.597186
Mus musculus major histocompatibility locus class III region: complement C4 and cytochrome P450 hydroxylase A	97429_at	-0.077019	-0.435571	-0.894026	-0.162331	-0.117398	-0.992813	-0.245223	-1.127974	-0.85966	-0.563994
esterase 1	101538_i_at	-0.345884	-0.033332	-2.261793	-2.991669	-2.142128	-0.35615	-0.293012	-1.086018	-1.739677	-1.291133
ESTs	93569_f_at	-1.203266	-0.416281	1.170666	0.265025	-0.680236	-0.97009	-1.028919	-0.681935	-0.461464	-0.681935
ESTs	102936_at	0.393205	0.315821	0.767481	0.258828	0.307418	-0.672114	-0.393535	-1.11744	-0.99363	-0.367873
proteosome (prosome, macropain) subunit, beta type 9 (large multifunctional protease 2)	93085_at	-0.297271	-1.405292	-0.278692	-0.029041	-0.588444	-0.166851	-0.607448	-0.945662	-1.69087	-1.642201
serine racemase	93488_at	0.187804	0.037086	0.483525	-0.00536	0.197497	-0.521914	-0.440078	-0.812542	-0.972114	-0.650085
ESTs	93568_i_at	-1.015052	-0.469314	1.241093	0.264424	-0.56744	-0.540168	-0.890179	-0.77512	-0.518538	-0.617827
ESTs, Moderately similar to unnamed protein product [H.sapiens]	103460_at	-0.016793	-0.072917	-1.363095	0.694703	-0.495736	-0.25486	-0.378662	-0.956252	-2.214394	-2.237481
GRO1 oncogene	95349_g_at	0.502175	3.026377	2.615156	-0.137658	0.474437	-0.503885	-0.895555	-1.577828	-0.608656	-0.399455
ESTs	96534_at	0.481271	0.26664	-1.183949	-0.231964	-0.739933	-0.588366	-0.16286	-1.679218	-1.244329	-0.688324
ESTs	102370_at	0.278839	0.028312	-0.834802	-0.310949	-0.150912	-0.327187	-0.306443	-1.262794	-1.353357	-1.125921
ESTs	95883_at	0.332115	-0.380838	-0.18509	-0.008736	-0.163405	-0.717006	-0.572662	-1.166297	-0.7688	-0.227245
ESTs	98083_at	0.222878	1.142074	-0.146457	0.400893	-0.119596	-0.714063	-0.459327	-0.4834	-0.812718	-0.948612

ESTs	103427_at	-0.413475	0.032645	-0.465217	-0.426333	-0.037167	-0.766944	-0.240559	-0.834389	-1.162521	-0.58555
DNA segment, Chr 6, ERATO Doi 313, expressed	96674_at	0.020374	0.56183	-0.530591	0.071938	0.14918	-0.622071	-0.699396	-0.825444	-0.523962	-0.485632
Kruppel-like factor 4 (gut)	99622_at	0.198592	0.257738	-0.067635	0.143293	0.339493	-0.4862	-0.38044	-0.936203	-0.756475	-0.959613
acyl-CoA thioesterase 1, cytosolic	103581_at	0.934362	0.352821	-0.443284	-0.762453	-0.857208	-0.133299	-0.047451	-2.073964	-2.258488	-2.499895
ESTs	96526_at	-0.016545	-0.262264	-0.318742	0.159672	-0.624083	-1.204388	-0.349339	-0.44127	-0.680478	-0.883867
cathepsin L	104480_at	0.548549	0.007757	-0.355909	-0.497562	-0.878802	-0.470668	-0.400882	-0.778408	-0.796344	-0.762245
cathepsin L	101963_at	0.090405	-0.395348	-0.144347	0.303612	0.161402	-0.681759	-0.312195	-0.861996	-0.685553	-0.640707
TATA box binding protein (Tbp)-associated factor, RNA polymerase I, A	92339_at	0.702125	-0.340346	-0.773253	-0.624005	0.470369	-0.546182	-0.412733	-0.756796	-1.013364	-0.394052
ESTs	93240_f_at	0.135619	0.22247	0.304688	-0.530804	0.171689	-0.649386	-0.407084	-0.477799	-0.882965	-0.780985
ESTs	93439_f_at	-0.356	0.249237	-0.037434	0.565416	-0.016933	-0.642733	-1.972401	-0.511731	-0.552742	-0.6794
M.musculus TOP gene for topoisomerase I, exons 19-21	95694_at	0.238455	-0.242457	0.201052	-0.663408	-0.251143	-1.090468	-0.49191	-0.66966	-0.594655	-0.533001
ESTs	104228_at	-1.006715	-0.97683	4.145182	-1.117394	-1.112938	-0.303781	-0.243857	-1.451746	-1.063897	-1.576426
fibrinogen/angiopoietin-related protein	102114_f_at	1.017435	1.091726	-0.044427	0.920417	-0.375786	-1.696979	0.032723	-0.78695	-0.929495	-1.471748
histocompatibility 2, D region locus 1	97540_f_at	0.323642	0.101587	0.35669	0.714064	0.035385	-0.254096	-0.791767	-0.929943	-1.040528	-1.048976
ESTs	104661_at	-0.003081	-0.265253	-0.088509	-0.010922	-0.265059	-0.59536	-0.15351	-1.119583	-1.104426	-0.628811
pericentriolar material 1 (Pcm1) gene, partial cds	96140_at	0.052842	-0.778784	-0.627814	0.031244	-0.168098	-0.743438	-0.348985	-0.787819	-0.839811	-0.394129
ESTs, Weakly similar to JC4899 proline rich protein - rat [R.norvegicus]	95059_at	-0.103418	-0.310567	-0.419008	0.103478	-0.013369	-0.582578	-0.348183	-0.57826	-1.104247	-0.636584
AI837905:UI-M-AL0-abq-c-01-0-UI.s1 Mus musculus cDNA, 3' end	100379_f_at	-0.079528	-0.068658	-0.686782	-0.359435	-0.20878	-0.404282	-0.32643	-1.160885	-1.112824	-0.510306
ESTs	92272_at	0.402856	0.596278	-0.739164	-0.100947	0.23167	-0.509489	-0.560615	-0.717761	-0.753982	-0.588073
ESTs, Moderately similar to KIAA0007 [H.sapiens]	98973_at	-0.302616	-0.030131	0.096834	0.603402	-0.023785	-0.514452	-0.255868	-0.821819	-1.100805	-0.546895
glycerol-3-phosphate acyltransferase gene, nuclear gene encoding mitochondrial protein, 5 region and partial cds	101867_at	0.411087	-0.183641	-0.878163	-0.23685	-0.235413	-0.579196	-0.329081	-0.556669	-0.966003	-0.727093
retinoblastoma-like 2	95617_at	-0.503202	-0.073296	-0.106357	-0.161699	-0.228644	-0.557756	-0.456627	-0.586145	-0.505261	-0.577105
ESTs, Weakly similar to envelope protein [M.musculus]	94027_at	-1.884923	-1.34596	3.655669	0.394293	0.274775	-0.634911	-0.620251	-0.670959	-0.871267	-0.192315
acid phosphatase 1, soluble	93219_at	0.710928	-0.199878	0.295178	0.434782	-0.266358	-1.126935	0.0392	-0.903852	-1.421149	-0.83357
hemoglobin alpha, adult chain 1	101524_at	0.155197	0.445203	-0.108639	-0.031581	-0.680668	-0.917578	-0.381073	-0.542906	-0.602506	-0.395993
ESTs, Weakly similar to Ig heavy chain precursor [M.musculus]	103456_at	0.014656	-0.382763	0.025932	0.019329	-0.180929	-0.351592	-0.777927	-1.095322	-0.503667	-0.49804
gene for protein phosphatase 2C beta, exon 8 and complete cds	101838_r_at	-1.429658	-0.322219	-0.233618	0.169526	0.310494	-1.108258	-0.344518	-0.653438	-1.012751	-0.27235
fructose bisphosphatase 2	97379_at	0.496158	-1.043318	-0.315808	-0.821454	-1.469625	-0.095157	-0.367078	-1.053828	-0.840789	-1.58966
ESTs	103739_at	-0.692325	-0.055194	-0.066915	-0.025437	0.210388	-0.514962	-0.187366	-0.929289	-1.080221	-0.535056
esterase 1	101539_f_at	0.35799	0.120281	-1.811902	-1.447229	-1.414146	-0.447726	-0.269408	-0.498157	-1.138463	-0.784551
ESTs	100988_at	-0.950235	-0.547149	-0.909326	-0.014388	-0.410121	-0.771676	-0.192156	-0.572013	-0.960273	-0.839426
nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha	101554_at	0.524071	0.042925	-0.269734	0.174735	-0.142489	-0.188354	-0.305915	-1.184254	-1.199728	-1.03878
translocase of inner mitochondrial membrane 10 homolog (yeast)	96760_at	-1.095369	-0.663509	0.032215	-0.248489	0.165372	-0.335361	-0.465573	-0.844661	-1.035718	-0.457581
ESTs, Moderately similar to KIAA1155 protein [H.sapiens]	96158_at	-0.092289	-0.032204	-0.567866	-0.102968	0.197063	-0.795208	-0.534708	-0.417163	-0.517182	-0.396824
ESTs	104193_at	-0.164407	-0.118138	-0.940656	0.243944	-0.316757	-1.085039	-0.307016	-0.504701	-0.747043	-0.39234
thioether S-methyltransferase	97402_at	-0.674038	-0.551009	-2.118003	-0.848398	-0.724556	-0.599135	0.320604	-2.220213	-2.71861	-1.720088
RNA binding motif protein, X chromosome	97848_at	0.727765	0.163936	-0.459386	-0.5895	-0.800084	-0.663343	-0.27411	-0.349131	-0.814235	-0.717815
DNA segment, Chr 5, ERATO Doi 135, expressed	103786_at	0.963331	-0.075764	0.297582	0.034676	-0.410199	-0.334215	-0.393164	-0.769899	-0.660244	-0.642563
desmoglein 2	98319_at	0.790077	-1.266461	0.103016	0.210276	-1.934629	-0.628003	-0.413995	-0.835783	-1.191432	-0.112636
ESTs	96207_at	0.602558	0.147577	0.282465	0.153196	0.108512	-0.868062	-0.203732	-0.846096	-0.47582	-0.530432
CDC-like kinase	93274_at	-0.272362	0.05771	-0.308091	0.090859	-0.175915	-0.971708	-0.105788	-0.662569	-1.014315	-0.556042
ESTs, Highly similar to hypothetical protein [H.sapiens]	93985_at	-1.724397	1.427881	-0.841752	0.85195	0.823565	-0.666235	0.033741	-1.465721	-1.397601	-0.666864
ESTs, Weakly similar to PLASMOLIPIN [Rattus norvegicus]	104626_at	-0.033446	-0.110081	-0.872781	-0.849819	-0.477559	-0.283953	-0.43151	-0.842137	-0.813233	-0.539507
ring finger protein 2	93164_at	0.561651	1.129994	0.136057	-1.147931	0.869865	-0.95417	0.066008	-1.235653	-1.068172	-0.951881
inositol trisphosphate receptor type 2 (Itpr2) gene, partial cds	101441_i_at	-0.184443	0.494752	-0.500835	-0.417068	-0.275811	-0.638091	-0.214002	-1.197606	-0.746942	-0.278425
nuclear factor I/B	99440_at	0.285698	-0.388629	-0.399292	-0.117501	-0.013084	-0.573507	-0.316972	-0.867039	-0.682972	-0.28312
ESTs, Highly similar to HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K [Homo sapiens; Rattus norvegicus]	94041_at	0.066287	0.211023	-0.173327	0.069445	-0.322923	-0.285978	-0.421968	-0.825991	-0.87521	-0.465769
serum/glucocorticoid regulated kinase	97890_at	0.455552	0.528946	-0.457575	0.716644	-0.106056	-0.211261	-0.394499	-0.674787	-0.907588	-1.399471
WW domain binding protein 5	100522_s_at	-0.331484	0.029457	0.009768	0.488735	0.232079	-0.632715	-0.517872	-0.608388	-0.581839	-0.24211
GATA-binding protein 6	104698_at	0.241575	0.096598	-0.238541	-0.546438	-0.136336	-0.512397	-0.361178	-1.094349	-0.738466	-0.246391
Kruppel-like factor 9	93528_s_at	0.407503	-0.011487	-0.615695	-0.345476	-0.254707	-0.284906	-0.249551	-1.380409	-0.75813	-0.530237
calcium channel, voltage-dependent, alpha2/delta subunit 1	104510_at	0.069954	0.064987	-0.603	-0.620611	-0.09678	-0.869514	-0.01084	-1.226966	-0.858563	-0.530258
ESTs, Moderately similar to 1905361A AKR Qa protein [M.musculus]	93714_f_at	1.623767	-0.145171	-0.003673	0.70429	0.282607	-0.198651	-1.023174	-0.684848	-1.288861	-0.674475
aldehyde oxidase 1	104011_at	0.066055	0.062461	-1.625914	0.578467	0.007336	-0.41087	-0.082025	-1.313037	-1.079979	-0.648109
CCAAT/enhancer binding protein (C/EBP), gamma	92195_at	-0.443761	0.586565	0.590179	-0.030935	0.19132	-0.522098	-0.168108	-1.234706	-0.980075	-0.263852
nuclear factor I/C	93006_at	-1.532659	-0.003127	0.188662	0.144287	-0.000143	0.073428	-0.203341	-2.607539	-1.753928	-0.457694
ESTs	95978_at	0.637703	0.801205	1.171061	1.104682	0.193823	-0.613852	0.01026	-1.008301	-1.569215	-0.621959
CCAAT/enhancer binding protein (C/EBP), beta	92925_at	-0.040556	0.545521	-0.310201	0.28437	-0.23952	-0.557627	-1.155077	-0.615739	-0.76714	-0.995232
ESTs, Weakly similar to A57514 RNA helicase HEL117 - rat [R.norvegicus]	94261_at	-0.087257	-0.059317	-0.699639	-0.155064	-0.229538	-0.499233	-0.361346	-0.431665	-0.737443	-0.481302
formin	92953_at	0.465512	0.436335	-0.903284	0.356392	0.345638	-0.681648	-0.379752	-0.560824	-0.762377	-0.667574
SIK similar protein	92569_f_at	0.034484	0.46903	0.760041	0.331372	0.284066	-0.569187	-0.41025	-0.547555	-0.730154	-0.215144
nucleolin	100144_at	0.041781	0.036714	0.134448	0.120049	-0.12675	-0.825621	-0.161324	-0.598717	-0.539071	-0.659183
regulator of G-protein signaling 2	97844_at	0.84477	0.085465	-1.279575	-0.694041	-0.729384	-0.70044	-0.120873	-0.387012	-0.668612	-1.159748
histocompatibility 2, L region	101886_f_at	0.173966	-0.085449	0.418325	0.43705	0.164246	-0.270418	-0.825632	-0.898297	-0.666309	-0.428304
calpain 12	95093_at	-0.697655	-0.399471	0.445978	0.221293	0.346475	-1.19665	-0.648388	-0.813824	-0.611712	0.028853
fibroblast growth factor 9	100346_at	-0.392696	-0.077591	-0.283065	0.198727	0.028818	-0.562062	-0.366698	-0.96199	-0.33194	-0.312216
pre-B-cell colony-enhancing factor	94461_at	-0.163636	0.188487	-0.848119	-0.382894	-0.082171	-0.984577	-0.053438	-0.663366	-0.855467	-0.448717
ESTs	93155_at	-0.12492	0.366527	-0.840996	-0.248787	-0.302873	-0.362612	-0.296401	-0.63568	-0.579205	-0.479549
growth arrest specific 5	98531_g_at	0.143384	0.307885	-0.320135	0.407317	0.237709	-0.724533	0.007232	-0.843119	-0.847011	-0.612142
interleukin 1 receptor, type I	93914_at	-0.118161	0.300489	0.394599	-0.423204	-0.320891	-0.690158	-0.726712	-0.385375	-0.446893	-0.320891
methyl-CpG binding domain protein 1	104340_at	0.230448	0.746173	-0.191231	0.356333	-0.259886	-0.344494	-0.336434	-0.788911	-0.593112	-0.679429
cofilin 1, non-muscle	93667_at	0.59444	-0.660665	-1.049373	-0.32822	-0.056749	-0.399708	-0.292932	-0.827896	-0.8766	-0.238506
Mus musculus putative RNA helicase RCK mRNA, partial cds	93964_s_at	-1.482125	1.072594	0.116611	-0.410421	-0.022163	-0.596985	0.064584	-2.149346	-1.392552	-0.248616

Mus musculus mRNA for slow myosin heavy chain-beta, partial	98616_f_at	0.271896	-0.2777	0.689039	1.30535	0.843434	0.251473	-0.066327	-1.930316	-2.046316	-1.797255
ESTs, Highly similar to PIM-1 PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE [Homo sapiens]	96841_at	0.004972	-0.200166	-0.269467	-0.169315	-0.597093	-0.544548	-0.536462	-0.748599	-0.910036	-0.797794
ESTs	94415_at	0.407365	0.350599	-0.856813	0.148228	-0.30903	-0.900883	-0.329951	-0.318708	-0.527328	-0.822454
ESTs, Moderately similar to GAR1 PROTEIN [Saccharomyces cerevisiae]	104766_at	0.081636	0.505396	0.316839	0.031591	0.063889	-0.452869	-0.474304	-0.340227	-0.672713	-0.407515
zinc finger protein 36	92830_s_at	0.422397	0.021728	0.76266	0.408129	-0.129207	0.193067	-0.437821	-0.95842	-1.609696	-1.17099
uncoupling protein 3, mitochondrial	93392_at	0.131135	0.08755	-0.733236	0.272676	-0.441661	-0.993745	-0.019341	-0.874346	-0.682689	-0.738944
Mus musculus mRNA for erythroid differentiation regulator, partial	96215_f_at	0.330571	0.067669	-0.528969	-0.315113	0.013433	-0.393942	-0.445472	-0.592551	-0.926872	-0.135415
ESTs, Moderately similar to unknown [H.sapiens]	94983_at	-0.724393	-0.045493	-0.141892	0.547332	0.002951	-0.662326	-0.203282	-0.550605	-0.446314	-0.427646
carnitine deficiency-associated gene expressed in ventricle 1	102215_at	0.096325	-0.306493	-1.122399	-0.909055	-0.56371	-0.797838	-0.29349	-0.457995	-0.707466	-0.225662
insulin-like growth factor binding protein 5	100566_at	0.042442	-0.180882	-0.198135	0.404025	0.728058	-0.081592	-0.39169	-0.79852	-0.75816	-0.659699
ESTs	95020_at	0.015641	-0.147961	-0.6703	-0.16419	-0.004627	-0.297418	-0.624248	-0.536539	-0.604353	-0.26748
ESTs	104513_at	0.237121	0.599496	-1.321856	0.144126	-0.388001	-0.448692	-0.179505	-0.668496	-0.641192	-0.500349
Mus musculus HSP40-like protein mRNA, partial sequence	93853_at	-0.266975	1.542998	-0.263807	0.136804	-0.151254	-0.810725	0.165788	-0.931019	-1.040442	-0.645932
acid phosphatase 1, soluble	96054_f_at	0.292234	-0.642798	0.217628	-0.25818	0.603072	-0.629532	-0.283699	-0.414325	-0.537229	-0.319231
multidrug-resistance protein (MDR1) gene, exons 1 and 2	93414_at	0.182641	1.429261	0.330129	0.442222	-0.518623	-0.55049	-0.22616	-0.775278	-0.529337	-0.846855
desmocollin 2	97768_at	-0.208516	-0.164444	-0.305169	-0.885523	-1.28252	-0.794746	-0.039949	-0.620693	-0.533488	-0.704188
glioblastoma amplified sequence	102402_at	-1.101341	-0.272307	-0.376346	-0.162494	-0.268338	-0.245515	-0.744576	-1.112565	-1.091043	-0.122764
ESTs, Weakly similar to HYPOTHETICAL 51.6 KD PROTEIN ZK353.8 IN CHROMOSOME III [Caenorhabditis elegans]	104311_at	0.323032	0.613009	0.055251	0.377452	0.167733	-0.656685	-0.146701	-0.89584	-0.496333	-0.306738
ectonucleotide pyrophosphatase/phosphodiesterase 2	97317_at	0.451465	-0.032757	-0.518352	-0.576011	-0.769609	-0.58864	-0.19422	-0.542393	-0.337008	-0.669696
ESTs	101217_at	-0.712649	0.533627	1.071415	0.346194	0.186413	-0.291172	-0.47955	-0.753385	-0.948847	-0.143151
silent mating type information regulation 2, (S.cerevisiae, homolog)-like	95502_at	0.23065	-0.017497	-0.196427	0.113416	0.278408	-0.294563	-0.375017	-0.676642	-0.842781	-0.230318
tumor protein D52-like 1	101446_at	1.97408	0.226435	-1.048419	0.369971	0.961111	-0.23499	-0.618716	-0.570824	-0.888222	-0.352296
inactive X specific transcripts	99126_at	-0.646952	0.892065	0.798625	-0.528928	-0.465898	-0.569975	-0.018575	-0.869994	-0.931178	-0.241181
DNA segment, Chr 1, ERATO Doi 654, expressed	101914_at	-0.237091	0.224388	0.177078	-0.165948	-0.065674	-0.610497	-0.294323	-0.433165	-0.655963	-0.295854
ESTs, Moderately similar to AF132964_1 CGI-30 protein [H.sapiens]	100912_at	0.146625	0.183657	0.229205	-0.260609	-0.064193	-0.869043	0.008351	-0.621755	-0.81516	-0.860506
ESTs, Weakly similar to cartilage-associated protein [M.musculus]	100471_at	0.0341	1.106123	-0.080905	0.439794	-0.522249	-0.242998	-0.412701	-0.475263	-0.833536	-0.352009
histocompatibility 2, K region	93120_f_at	0.213879	0.064853	0.161848	0.736366	0.194788	-0.038832	-0.737545	-0.708329	-0.637456	-0.821356
excision repair cross-complementing rodent repair deficiency,complementation group 5	103483_at	-0.599077	0.569061	-1.323013	0.746997	0.145469	-0.865239	-0.309446	-0.359863	-0.36474	-0.38041
amylase 1, salivary	101058_at	0.533364	0.414232	-0.159551	-1.686319	-0.162044	-1.427067	0.889328	-2.230157	-1.510213	-1.188459
ESTs	104396_at	-0.078702	0.088103	-0.631032	-0.263647	-0.02379	-0.308666	-0.036199	-0.663015	-0.882542	-0.705215
programmed cell death 4	103029_at	0.067019	-0.454271	-0.938966	0.043965	-0.294704	-1.182625	-0.635722	-0.187212	-0.276288	-0.783302
peroxisomal biogenesis factor 11a	103660_at	0.198917	0.138221	-0.604194	-1.213944	-0.212638	-0.231603	-0.146337	-0.897619	-0.521692	-0.760044
ESTs	95848_at	-0.076989	0.342921	0.256143	0.153662	0.086098	-0.640687	-0.480181	-0.583204	-0.525244	-0.090352
Q4 class I MHC gene (exon 5)	98438_f_at	0.065945	-0.09301	0.231884	0.292148	0.195795	-0.054414	-0.580631	-0.741203	-0.691448	-0.703251
ESTs, Highly similar to RAS-RELATED PROTEIN RAP-1A [Homo sapiens; Rattus norvegicus; Bos taurus]	100048_at	0.002402	-0.037171	0.066997	-0.404921	0.360063	-0.655611	-0.182548	-0.511507	-0.557858	-0.299762
Xlr-related, meiosis regulated	102818_at	-0.936105	-0.401018	2.99796	-1.427171	0.06772	-1.581767	-1.988318	-0.227623	-1.00523	-0.114028
heart and neural crest derivatives expressed transcript 2	99914_at	0.422507	-0.089602	-0.417212	-0.591852	-0.208779	0.013896	-0.251532	-1.637194	-0.957589	-0.319136
myomesin 2	102041_at	-0.110574	-0.032352	-0.74487	0.026355	-0.135276	-0.292083	-0.155964	-0.907315	-0.92101	-0.450076
myosin X	100923_at	0.505186	-0.035504	-0.496283	-0.502974	0.00912	-0.287188	-0.25741	-0.84665	-0.721112	-0.367412
ESTs	95530_at	0.275194	0.149234	0.103966	-0.118745	0.200436	-0.911604	-0.407686	-0.322866	-0.399715	-0.344755
ESTs, Highly similar to EUKARYOTIC INITIATION FACTOR 4 GAMMA [Homo sapiens]	96850_at	-0.13311	0.53217	-0.263635	0.237682	0.137562	-0.34875	-0.519371	-0.616838	-0.546645	-0.320967
platelet derived growth factor, alpha	94932_at	0.277178	-0.611914	0.30974	0.044924	-0.042088	-0.01624	-0.464622	-1.043022	-0.726882	-0.232219
ESTs, Weakly similar to AF145613_1 BcDNA.GH03108 [D.melanogaster]	93478_at	0.248316	0.17717	0.021851	-0.144733	-0.12538	-0.775011	-0.154274	-0.881449	-0.356362	-0.289743
exostoses (multiple) 1	102811_at	0.301813	-0.053036	0.935066	0.101798	-0.48247	-0.432099	-0.182637	-0.482893	-0.504944	-0.485177
heat shock protein 40	96254_at	1.803552	1.672396	0.177733	-0.124581	0.024392	-0.421576	-0.432897	-0.579378	-0.333666	-0.342451
a disintegrin and metalloproteinase domain 19 (meltrin beta)	103554_at	1.126538	0.263959	0.43866	1.12276	1.101566	-0.002606	-0.171453	-1.282697	-0.805158	-1.367586
ESTs	93829_at	-0.141863	0.768844	-0.663498	0.749014	0.021609	-0.792481	-0.51795	-0.357971	-0.056636	-0.552529
Ewing sarcoma homolog	94810_at	-0.047848	0.047339	0.076583	0.369416	-0.390499	-0.345035	-0.396888	-0.575665	-0.637073	-0.2705
thyroid hormone receptor alpha	99077_at	0.154652	-0.401795	-0.377504	0.721635	-0.389057	0.250274	-0.866084	-1.229224	-0.542898	-0.419224
ESTs	95021_at	0.180802	-0.456879	-0.234114	0.073458	0.041598	-0.84332	-0.83001	-0.161158	-0.636978	-0.30574
trans-golgi network protein 1	99144_s_at	-0.103155	-0.190664	-0.360283	0.13661	0.264338	-0.446617	-0.135554	-0.765916	-0.787264	-0.348637
cofilin 1, non-muscle	99120_f_at	0.313011	-0.020226	-0.913583	-0.037	-0.028477	-0.185412	-0.01906	-1.200382	-0.949544	-0.767858
ESTs, Weakly similar to trg [R.norvegicus]	103356_at	-0.859357	-0.307584	-0.346228	-0.135603	0.682976	-1.119172	-0.315638	0.02287	-0.770217	-0.332694
ESTs, Highly similar to HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II [Caenorhabditis elegans]	92831_at	0.007554	0.291205	0.422597	0.399947	-0.030933	-0.754345	-0.668777	-0.261738	-0.475983	-0.205454
histocompatibility 2, class II antigen A, alpha	92866_at	-0.822233	0.253242	0.040923	0.131483	-0.240621	0.44407	-0.426388	-0.964875	-1.658969	-1.846522
profilin 2	93567_at	0.751884	0.290403	-0.648661	-0.393927	-0.176703	-0.628335	-0.228965	-0.354643	-0.657449	-0.45416
ESTs, Moderately similar to I52722 TCTA protein - human [H.sapiens]	104739_at	-0.181455	-0.283292	-0.453969	-0.16749	0.333667	-0.297554	-0.210197	-0.697109	-0.795989	-0.274058
ESTs, Highly similar to KIAA0370 [H.sapiens]	104105_at	-0.473373	-0.369855	0.432084	-0.121887	0.000978	-0.166085	-0.324827	-0.631848	-0.836578	-0.331611
ESTs, Highly similar to KIAA0710 protein [H.sapiens]	94397_at	0.474509	-0.206418	0.320721	-0.650082	-0.239083	-0.412692	-0.423984	-0.356538	-0.850344	-0.213133
RuvB-like protein 1	99537_at	1.253614	1.260953	-0.01154	0.097933	-0.463437	-0.126403	-0.565593	-0.818664	-0.959269	-0.208493
ATP-binding cassette, sub-family B (MDR/TAP), member 4	102910_at	0.045833	-0.458802	-1.085255	-0.279141	-0.045112	-0.745158	-0.088589	-0.362152	-0.864914	-0.309853
EST AI115388	104605_at	-0.026673	0.075448	-0.507825	-0.055512	-0.292049	-0.374697	-0.135422	-0.522347	-0.798773	-0.511737
protein tyrosine phosphatase 4a2	100595_at	0.086922	0.069517	-0.242826	-0.062304	-0.214462	-0.688604	-0.504537	-0.267002	-0.48358	-0.201061
tumor differentially expressed 1	100151_at	0.015166	0.199354	-0.341637	0.188008	-0.244252	-0.6154	-0.318607	-0.297057	-0.511254	-0.372763
zinc finger protein 106	101456_at	-0.381288	-0.25765	0.166594	-0.054803	0.642665	-1.129859	-0.239167	-0.880565	-0.786918	0.090219
cyclin T1	93712_at	-0.065668	-0.650369	-0.534061	0.172204	0.017102	-0.310669	-0.80207	-0.61642	-0.667776	-0.087348
ESTs	94395_at	0.506655	0.314442	-0.126163	-0.283868	-0.138182	-0.585664	-0.50977	-0.06853	-0.799777	-0.23296
DNA j protein b9	96679_at	0.751425	0.240825	0.061099	-0.35677	0.15632	-1.107048	-0.255868	-1.125909	-1.18918	0.238657
geranylgeranyl diphosphate synthase 1	98970_at	0.350639	-0.283089	-0.026162	-0.181951	0.221682	-0.454189	-0.190544	-0.717829	-0.851742	-0.237993
ESTs	104206_at	-0.076611	-0.440722	-0.469371	-0.26487	-0.088493	-0.320286	-0.243426	-0.728955	-0.676661	-0.302762
integrin-associated protein	103611_at	0.460609	0.032855	-0.549662	0.069897	0.031428	-0.355753	0.029287	-0.730311	-0.740172	-0.704072
lymphocyte antigen 57	100772_g_at	0.710735	1.179494	0.747661	1.26278	-0.50166	-0.054725	-0.846688	-0.44435	-0.320333	-1.042401
nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha	104149_at	0.249419	0.273665	-0.238589	-0.001633	-0.306721	-0.352951	-0.415651	-0.4675	-0.642113	-0.375003

diacylglycerol kinase, alpha (80 kDa)	103596_at	-0.981228	0.099081	-0.280083	0.06151	-0.394974	-0.319813	-0.513019	-0.606613	-0.636518	-0.112942
nucleosome assembly protein 1-like 1	98587_at	0.175104	-0.454316	-0.075022	0.006336	-0.044178	-0.512158	-0.592711	-0.266053	-0.611655	-0.368173
leptin receptor	93600_at	-0.10167	0.289826	0.577778	0.485215	0.229282	-0.622116	-0.198655	-0.490562	-0.565272	-0.243773
SH3-domain binding protein 5 (BTK-associated)	98766_at	0.768184	-0.21698	0.118914	-0.119127	0.033475	-0.377172	-0.133862	-1.067923	-0.883498	-0.193667
endogenous retroviral sequence 4 (with leucine t-RNA primer)	98577_f_at	-2.33115	-0.604658	4.174125	0.588235	-0.213035	-0.549416	-0.627935	-0.301188	-0.665435	-0.106427
WSB-1	98946_at	-0.027086	0.888895	0.340096	0.65305	-0.044894	-0.314103	-0.080682	-0.540358	-1.062938	-0.587125
protein kinase, interferon inducible double stranded RNA dependent inhibitor	102414_i_at	-0.675051	0.370345	0.662752	-0.719925	0.202126	-0.766933	-0.33669	-1.031292	-0.454386	-0.045566
ESTs	96532_at	0.420121	-0.01192	-0.024507	0.114578	0.617263	-0.294206	-1.367422	-0.393637	-0.464205	-1.028188
gene trap ROSA 26 antisense, Philippe Soriano	101444_at	-0.205787	-0.332698	0.289844	0.4705	0.163325	-0.355346	-0.084465	-0.836859	-0.676866	-0.515022
ESTs, Weakly similar to lysophospholipase I [M.musculus]	100880_at	-0.152734	-0.179543	0.164111	0.103996	-0.438802	-1.43246	-0.46253	-0.266749	-0.149246	-0.451437
procollagen, type III, alpha 1	102990_at	3.276422	-0.71594	2.636518	1.019916	0.661023	0.24761	-0.831371	-1.314762	-0.138353	-1.629397
DNA segment, Chr 5, ERATO Doi 189, expressed	103538_at	0.825456	1.110371	-0.317574	0.65594	0.001852	-0.489271	-0.067255	-0.589661	-0.586343	-1.113639
ESTs, Weakly similar to junctional adhesion molecule [M.musculus]	98957_at	-0.347923	-1.096353	-0.063604	-0.021089	-0.080766	-0.714721	-0.719459	-0.560982	-0.337795	-0.290554
protein tyrosine phosphatase, non-receptor type 2	101996_at	-0.083398	0.678225	0.124531	0.402995	0.383736	-0.525334	-0.27913	-0.687345	-0.342766	-0.2352
solute carrier family 4 (anion exchanger), member 4	98457_at	-0.442266	-0.951857	-0.707833	-0.241423	0.240212	-0.892052	0.117372	-1.288771	-0.586066	-0.660148
thrombospondin 2	94930_at	0.592545	-0.165863	-0.07992	0.281504	-0.151408	0.043745	-0.015342	-1.156206	-1.187117	-0.589312
serine protease inhibitor 2-2	104374_at	0.899723	0.615667	1.343104	1.078329	0.834082	-0.281425	-0.202577	-0.552999	-0.72277	-0.57701
Mus musculus ORF1 for hypothetical protein, clone 424981	94289_r_at	0.508702	-0.272526	0.363702	0.18302	-0.217467	0.129993	-0.757666	-0.819189	-0.749512	-0.594602
ESTs, Weakly similar to HSPC035 protein [H.sapiens]	95146_at	0.111964	-0.053496	-0.215177	-0.376519	-0.258746	-0.36747	-0.059657	-0.59963	-0.77221	-0.599597
ESTs, Weakly similar to female sterile homeotic-related protein Frg-1 [M.musculus]	97892_at	0.464128	0.357867	0.127522	0.505361	0.008125	-0.702174	-0.497331	-0.575186	-0.372312	-0.159105
karyopherin (importin) alpha 4	100320_at	-0.72105	0.551647	1.075639	-0.154706	0.184288	-0.92917	-0.108226	-0.936463	-0.879116	0.055418
ribosomal protein L22	92857_at	0.456556	-0.090129	-0.340561	-0.127274	-0.02595	-0.543019	-0.145326	-0.714111	-0.580256	-0.203564
beta-galactoside alpha-2,3-sialyltransferase	98596_s_at	-0.378031	-0.071173	-0.153452	-0.388148	0.415353	-0.978436	-0.651115	-0.657338	-0.234445	-0.073567
untitled	92475_g_at	1.068794	-0.129894	0.158311	0.319042	0.168003	-0.267104	-0.427671	-0.484052	-0.448898	-0.338701
ESTs, Highly similar to unnamed protein product [H.sapiens]	100895_at	-0.905864	0.139133	0.609678	0.10781	0.028503	-0.16889	-0.662251	-0.45543	-0.573226	-0.382028
ESTs	103552_at	-0.117605	0.558119	-0.628791	-0.039456	0.015039	-1.258445	-0.366293	-0.267735	-0.64239	-0.073989
zinc finger protein, autosomal	95800_s_at	-0.42855	-0.892244	0.548225	0.391747	0.122354	-0.323855	-0.067799	-0.558904	-0.918486	-0.270016
phosphodiesterase 7A	100489_at	0.134022	0.268884	-0.901927	-0.367981	-0.33006	-0.616799	-0.60853	-0.392276	-0.452186	-0.19727
ESTs	95457_at	0.37423	0.16881	-0.207941	-0.29465	0.238363	-0.860308	-0.338052	-0.285638	-0.387941	-0.29668
ESTs, Highly similar to sorting nexin 4 [H.sapiens]	97818_at	-0.204942	-0.180499	0.096005	0.060906	-0.06638	-0.497525	-0.09288	-0.311134	-0.773391	-0.61249
Tial1 cytotoxic granule-associated RNA-binding protein-like 1	99947_at	-0.041433	0.354763	0.310625	-0.056697	0.253233	-0.5012	-0.125408	-0.582295	-0.424837	-0.44823
Mouse MHC class I D-region cell surface antigen (D2d) gene, complete cds	99379_f_at	-0.348713	-0.254058	0.541815	0.373028	-0.089565	0.035755	-0.50172	-1.010838	-0.675778	-0.471526
ESTs	102207_at	-0.280097	-0.207848	-0.016283	0.116524	-0.059055	-0.193018	-0.100171	-0.707509	-0.691922	-0.601487
LIM only 2	93666_at	-0.342876	0.130685	0.014068	0.102255	0.177429	-0.396502	-0.297533	-0.532135	-0.364015	-0.286546
ESTs, Highly similar to POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L1 [Homo sapiens]	93701_at	0.054055	0.153988	0.269274	0.259987	0.456886	-0.433301	-0.3747	-0.739116	-0.816786	-0.070076
DNA segment, Chr 1, Lubeck 1	103517_at	-0.891309	-0.37577	4.078373	-0.979253	-0.068242	-0.289045	-0.332883	0.125443	-1.78169	-0.715981
heterogeneous nuclear ribonucleoprotein D-like	96084_at	-0.131166	-0.155972	-0.004252	0.030709	-0.311236	-0.483914	-0.120674	-0.603783	-0.491652	-0.316833
ESTs	103895_at	0.647728	0.120185	-0.691484	0.174849	-0.287568	-0.623085	-0.250148	-0.151848	-0.596133	-0.394445
myristoylated alanine rich protein kinase C substrate	96865_at	-0.235072	0.182454	-0.183446	0.69865	0.750472	-0.196841	-0.289382	-0.63462	-0.424805	-0.605411
potassium channel, subfamily K, member 3	102020_at	0.045839	-0.035619	0.037176	-1.240051	-0.574148	-0.01678	-0.465258	-1.40284	-0.913172	-0.096245
glycosylation dependent cell adhesion molecule 1	100977_at	0.067108	-0.163977	0.031385	0.097757	0.367823	-0.454927	-0.217707	-0.68155	-0.537835	-0.160541
ESTs	99196_at	0.18293	0.128233	-0.358862	0.146885	0.345161	-0.393953	-0.550185	-0.317334	-0.322257	-0.291835
DNA segment, Chr 18, Wayne State University 181, expressed	97449_at	-0.564912	0.059634	0.271924	-0.222048	0.07779	-0.133303	-0.273144	-0.615381	-0.705036	-0.346903
ESTs, Moderately similar to ERYTHROID KRUEPPEL-LIKE TRANSCRIPTION FACTOR [Mus musculus]	104645_at	0.217892	1.001051	-0.165966	0.1036	0.193445	-0.392772	-0.210524	-0.691878	-0.536787	-0.167319
hydroxysteroid 11-beta dehydrogenase 1	97867_at	0.131484	-0.116392	-0.46104	-0.442246	-0.723623	-0.091222	-0.043758	-0.97019	-0.95608	-0.47269
protein kinase, cAMP dependent regulatory, type II alpha	97096_at	-0.07506	-0.197599	0.41134	-0.112917	0.193968	-0.644741	-0.302203	-1.214814	-0.546569	0.090462
Sjogren syndrome antigen A2	92265_f_at	-0.457132	0.090307	0.378173	-0.08425	-0.208551	-0.247023	-0.110301	-1.075728	-1.099985	-0.09441
ESTs	92653_at	-1.062695	0.555605	-0.908188	-0.543979	0.495157	-0.104261	-0.356888	-0.636738	-0.364817	-0.470147
trans-golgi network protein 2	93882_f_at	0.324362	0.424336	-0.357125	0.102964	0.378005	-0.628819	-0.062699	-0.562972	-0.710763	-0.184929
ubiquitously transcribed tetratricopeptide repeat gene, X chromosome	102222_at	-0.101152	-0.237381	-0.335555	-0.182173	-0.149025	-0.366462	-0.02237	-0.543887	-0.495313	-0.562136
Ia-associated invariant chain	101054_at	-0.139184	0.199087	0.613631	-0.100452	0.011242	0.366366	-0.849983	-0.496979	-0.839171	-0.993499
splicing factor, arginine/serine-rich 2 (SC-35)	94017_s_at	0.125636	-0.040683	-0.102281	-0.032039	-0.282809	-0.321273	-0.156662	-0.542257	-0.689659	-0.284558
hypoxia inducible factor 1, alpha subunit	98628_f_at	0.029741	0.372682	0.262345	0.52295	0.180805	-0.594653	-0.022603	-0.358543	-0.631278	-0.649152
Mus musculus strain C3H/HeN mRNA preferentially expressed in LPS-normoresponsive macrophages	101520_at	0.073051	-0.201783	0.413652	0.431751	0.13353	-0.333298	-0.229107	-0.269138	-0.734897	-0.462749
guanylate nucleotide binding protein 3	103202_at	-0.316336	-0.450531	-0.206961	0.434843	-0.329965	-0.325792	-0.10714	-0.542282	-0.665186	-0.610377
DNA segment, Chr 18, Wayne State University 181, expressed	97450_s_at	-0.270694	-0.082789	0.069048	-0.162068	0.078198	-0.253999	-0.15313	-0.881847	-0.678466	-0.354017
transforming growth factor, beta 2	93300_at	-1.100131	-0.472081	1.285293	0.419223	1.080628	-0.414746	-0.270411	-0.698399	-1.383454	0.12219
ESTs, Highly similar to KIAA0160 gene product is novel. [H.sapiens]	103746_at	1.276632	-0.116814	-0.09072	0.552706	-0.076019	-1.060581	-0.208385	-0.538597	-0.400504	-0.064827
ESTs, Highly similar to SEC14L [H.sapiens]	95665_at	-0.269855	-0.244586	-0.436046	-0.142237	-0.018609	0.073138	-0.146754	-0.868289	-0.85602	-0.624967
ESTs	104296_at	-0.471822	-0.176532	-0.124129	-0.509008	-0.241593	-0.176188	-0.299626	-0.133823	-0.620215	-0.578216
major histocompatibility complex region NG27, NG28, RPS28	96785_at	-0.318557	0.165053	-1.181172	-0.203737	-0.193285	-0.284673	-0.374719	-0.581609	-0.536237	-0.513188
ESTs, Moderately similar to RAS-LIKE PROTEIN TC10 [Homo sapiens]	104697_at	-0.012733	0.729946	-0.13774	0.318925	-0.301065	-0.132847	-0.225771	-1.032073	-0.481458	-0.568242
ESTs	103321_at	-0.776539	-0.097813	-0.024388	0.101165	0.094159	-0.319895	-0.148698	-0.224856	-0.962331	-0.487677
ESTs	103736_at	-0.29956	0.147851	-0.242942	-0.146724	-0.024766	-0.203623	-0.203114	-1.035293	-0.476612	-0.600748
ESTs, Weakly similar to polycomb-group proteins [M.musculus]	94352_at	0.301618	-0.390613	-0.471994	0.035961	-0.093172	-0.450916	-0.332363	-0.660863	-0.358711	-0.17829
ESTs, Weakly similar to AF186469_1 TM6P1 [R.norvegicus]	96688_at	0.211285	0.174747	-0.497512	-0.093094	-0.448702	-0.658053	-0.486027	-0.170193	-0.337815	-0.219989
ESTs, Highly similar to MDM2-like p53-binding protein [M.musculus]	93339_at	-0.52755	-0.097056	-0.489934	-0.033405	-0.369567	-0.765466	-0.265064	-0.125003	-0.703949	-0.143514
syntaxin 4A (placental)	103781_at	0.50057	-0.09303	-0.188532	-0.252163	0.3224	-0.495712	-0.229172	-0.385088	-0.268554	-0.337016
ESTs, Highly similar to H<BETA>58 PROTEIN [Mus musculus]	96665_at	-0.211906	-0.115137	-0.515257	0.297083	-0.084548	-1.131073	-0.042612	-0.464752	-0.629377	-0.191904
splicing factor, arginine/serine-rich 5 (SRp40, HRS)	99628_at	-0.429399	0.234147	-0.945619	0.285898	-0.057457	-0.684889	0.19405	-0.722608	-0.784314	-0.525998
retinoid X receptor interacting protein 110	99464_at	0.769241	-0.063695	0.304855	0.228394	-0.191837	-0.297097	-0.569024	-0.222942	-0.452534	-0.21591
menage a trois 1	98979_at	0.790778	0.304744	-0.743275	-0.010643	-0.016945	-0.416075	0.040806	-0.8078	-0.585407	-0.437662
ESTs, Weakly similar to TRANSCRIPTION REGULATORY PROTEIN SNF2 [Saccharomyces cerevisiae]	92703_at	1.90642	0.701172	-1.004107	0.373673	0.291671	-0.420644	0.310421	-1.138348	-1.194419	-0.521353

heterogeneous nuclear ribonucleoprotein H1	93990_at	0.173768	0.142153	-0.074752	-0.255705	-0.226942	-0.631184	-0.354388	-0.173972	-0.430667	-0.174616
regulator of G-protein signaling 5	103294_at	0.050993	0.35306	-1.26487	0.061869	0.004051	-0.322025	-0.031604	-0.729432	-0.448153	-0.964468
caspase 6	94458_at	0.218543	0.16446	-0.336753	0.899836	-0.528002	-0.650291	0.144609	-0.857981	-0.80292	-0.746473
microtubule-associated protein tau	102743_at	0.240175	-0.191165	-0.150992	0.528868	0.194538	0.105126	0.023279	-1.222174	-0.96854	-0.505475
DNA segment, Chr 13, ERATO Doi 275, expressed	103314_at	0.022026	-0.24394	-0.445534	0.74632	0.524941	-0.32925	-0.216338	-1.210178	-0.270312	-0.263639
serine/threonine kinase 2	101437_at	-0.21676	0.636424	0.371792	0.335133	0.511164	-0.189003	-0.115654	-0.884378	-1.046217	-0.097619
proteosome (prosome, macropain) subunit, beta type 8 (large multifunctional protease 7)	102791_at	0.246575	-0.201596	0.02053	0.526744	-0.343579	0.065922	-0.249738	-0.907332	-0.835406	-0.552696
DNA segment, Chr 6, Wayne State University 176, expressed	95541_at	-0.466533	0.304992	1.053965	0.800286	1.048915	-0.411056	-0.259451	-0.346731	-0.163073	-0.636013
ESTs	102645_at	0.155474	-0.04007	-0.668619	0.084294	0.070546	-0.620679	0.116373	-0.370729	-0.542024	-0.691653
receptor (calcitonin) activity modifying protein 2	99444_at	-0.084767	-0.341634	-0.272281	-0.091211	-0.021994	0.038723	-0.560387	-0.572687	-0.635112	-0.744679
enabled homolog (Drosophila)	93864_s_at	1.423037	2.425833	2.990955	1.149261	1.632775	-0.346902	0.0165	-0.676596	-0.265445	-0.008183
natriuretic peptide precursor type B	104184_at	0.693059	1.668498	1.986334	1.095484	0.747987	0.346947	0.077078	-0.646241	-0.013869	-0.264797
Fibrinogen-like protein 2	97949_at	0.975569	1.484109	0.903138	1.142259	0.948865	-0.217875	-0.45116	0.258493	-0.006776	-0.091549
ESTs, Moderately similar to URIDINE KINASE [Escherichia coli]	94367_at	0.763204	0.93516	2.267056	1.69587	0.471282	-0.004261	-0.215721	-0.296323	-0.277501	-0.228421
small inducible cytokine A2	102736_at	2.343038	3.634905	4.437081	1.088562	0.087433	0.409769	-0.667716	0.396726	1.195944	0.27264
four and a half LIM domains 1	97500_g_at	0.361903	0.89596	2.282789	1.377623	1.311755	0.136614	0.46512	0.293299	0.04591	0.405263
CD44 antigen	103005_s_at	0.646466	1.244165	2.783508	1.187047	0.386487	0.178506	0.082328	-1.847697	-0.706269	-0.301987
four and a half LIM domains 1	97498_at	0.376959	0.932753	2.095301	1.385084	0.646247	0.135858	0.424339	0.341829	0.199456	0.235578
FXYD domain-containing ion transport regulator 5	103394_at	2.319813	0.630208	1.266871	0.572288	0.542671	0.417786	0.130123	0.221048	0.574704	0.038341
ESTs, Highly similar to serine protease [H.sapiens]	94238_at	2.34843	1.817072	0.974275	1.135736	0.807167	0.354835	-0.025668	-0.425348	-0.211427	-0.2464
P lysozyme structural	101753_s_at	0.737929	0.634211	2.581448	0.987521	0.368265	-0.407042	-0.034241	-0.011068	0.062616	0.620003
interleukin 4 receptor, alpha	102021_at	1.301467	0.53187	1.526064	1.148166	0.264522	0.510931	-1.026274	-0.810766	-0.326661	-0.251214
CD53 antigen	94939_at	0.320359	1.64322	1.36486	0.992152	0.38688	-1.008136	-0.454416	0.130312	0.277266	0.52526
natriuretic peptide precursor type A	103593_at	0.290039	0.743007	0.894518	2.009901	1.423113	0.273546	0.203117	-0.045966	0.019481	0.236562
secreted phosphoprotein 1	97519_at	0.079727	0.011195	6.266377	2.525576	2.414031	0.009238	-0.64811	-0.170764	0.14055	1.908232
NPC derived proline rich protein 1	100472_at	0.6634	0.817798	0.442064	0.732315	0.758508	-0.07625	-0.108555	-0.731627	-0.367302	-0.192401
ESTs, Highly similar to ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM [Homo sapiens]	104578_f_at	0.324987	0.524777	1.540381	1.011281	0.651005	0.283708	-0.034351	0.377251	0.738648	0.341089
lysozyme M gene	100611_at	0.475986	0.595901	1.840523	0.695202	0.404211	-0.347884	-0.267476	0.20815	0.398389	0.494224
activating transcription factor 3	104155_f_at	1.053722	2.892277	0.874443	0.639912	0.161055	1.332704	1.013668	-1.149394	-1.225832	-1.148836
follistatin-like	94833_at	0.479773	0.177143	1.845953	1.17469	1.135799	-0.116848	-0.527781	-0.274744	0.015007	0.027774
glycoprotein 49 A	100325_at	1.173738	0.958188	1.13401	1.040512	0.022076	-0.531575	-0.463552	0.689093	0.629799	0.170784
tubulin, beta 2	94835_f_at	0.40112	0.194603	1.393911	0.92128	0.607577	0.352092	-0.251973	0.082584	0.173599	-0.346456
MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70t, and smRNP genes; G7A ge	100946_at	0.281986	3.264022	0.74086	0.853577	0.168039	-0.025003	-0.295787	1.188775	0.990236	0.404167
heat shock protein, 86 kDa 1	95282_at	0.736183	1.29054	0.175655	0.434455	0.588474	-0.893606	-0.667188	-0.30577	0.300229	-0.216842
Early growth response 1	98579_at	0.551939	1.633444	0.77457	0.240172	0.417716	0.114092	-0.422896	-0.474119	-0.395193	-0.347941
insulin receptor substrate 1	98824_at	1.417668	0.658361	0.831902	0.184959	2.954708	-1.133966	-0.465642	0.184139	0.068347	0.398155
ESTs, Highly similar to ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM [Homo sapiens]	104579_r_at	0.266193	0.396659	1.064664	0.588147	0.595583	0.766457	-0.415386	0.422228	0.623009	0.226235
plasminogen activator inhibitor, type I	94147_at	-0.371289	0.980606	2.187135	1.708013	0.835098	-0.220213	0.059802	-0.61818	-1.028148	-0.960082
cyclin-dependent kinase inhibitor 1A (P21)	94881_at	0.896864	1.197141	0.720501	0.686639	0.041632	0.68175	0.686842	-0.647415	0.07645	-0.62711
expressed in non-metastatic cells 1, protein (NM23A) (nucleoside diphosphate kinase)	92794_f_at	0.645378	0.81187	0.777325	0.322257	0.630962	-0.818474	-0.486675	0.384764	0.519557	0.03479
C85523:C85523 Mus musculus cDNA, 3' end	99849_at	0.63248	0.39584	0.673011	0.532001	0.300716	0.06067	0.592672	0.331822	0.375013	0.366302
procollagen, type I, alpha 1	94305_at	0.662495	-0.133044	2.169968	1.858587	1.530609	0.467567	-0.341869	0.214176	0.719356	-0.109667
RAN GTPase activating protein 1	98603_s_at	0.743077	0.321181	0.231787	1.752149	1.423976	-0.249741	-0.904094	-1.041865	0.38882	0.610545
osteoblast specific factor 2 (fasciclin I-like)	92593_at	-0.194561	0.103874	3.14774	3.031569	2.496345	-0.1552	-0.45937	0.185706	0.362278	-0.02272
phosphofructokinase, platelet	97833_at	0.513542	0.127196	1.015957	0.823648	0.700993	0.462135	0.056214	0.162992	0.585607	0.315657
DNA segment, Chr 2, ERATO Doi 198, expressed	104639_i_at	0.504805	0.934593	1.407047	0.803608	0.576469	-0.430634	-0.017068	-0.4303	-0.692643	-0.242905
Mus musculus TNF intracellular domain-interacting protein mRNA, complete cds	95152_g_at	0.455091	0.32978	1.111826	0.727923	0.19864	0.49742	0.014732	0.19513	0.538648	0.1737
procollagen, type V, alpha 2	92567_at	0.113551	-0.099944	2.706678	2.940866	1.549529	0.394485	-0.426404	0.383278	0.809787	-0.30947
actin, alpha 1, skeletal muscle	100381_at	0.245005	0.450645	0.93033	0.911128	0.334738	0.422998	0.163627	0.688193	0.739672	-0.343721
cysteine rich protein 61	92777_at	0.796322	1.824274	0.859545	-0.003005	0.324082	0.683352	0.174506	0.107009	-0.375304	-0.107701
pleckstrin homology, Sec7 and coiled/coil domains 3	103434_at	0.525091	0.914889	0.250478	0.143158	2.004785	0.140093	-0.375733	-1.105517	-0.535884	-0.688431
lymphocyte specific 1	104093_at	0.39491	0.330081	1.553131	0.901134	0.196052	0.051289	-0.467766	-0.106478	0.072545	-0.1394
Lipocortin 1	93037_i_at	2.098505	1.015322	0.321144	0.651037	0.228094	-0.47059	-0.530958	0.662052	0.364976	0.281128
oncostatin receptor	102255_at	0.321156	0.652422	0.697026	0.452498	0.269866	-0.052609	0.010436	-0.170819	0.00143	-0.384844
matrix gamma-carboxyglutamate (gla) protein	93866_s_at	0.286192	0.304696	0.778516	0.947017	0.862129	0.026724	-0.162457	0.602387	0.646094	0.132481
ornithine decarboxylase antizyme inhibitor	101002_at	0.571224	0.867218	0.474787	0.333233	0.227198	-0.28841	0.104459	-0.092689	-0.118641	-0.21332
a disintegrin and metalloproteinase domain 9 (meltrin gamma)	96738_at	0.156527	0.818033	0.75709	1.021869	0.353601	-0.466213	-0.061016	0.023008	-0.167209	-0.011425
solute carrier family 20, member 1	103065_at	1.177405	1.011167	0.771586	0.278213	0.178597	-0.187282	-0.110769	-0.614202	-0.523277	-0.298486
small inducible cytokine A9	104388_at	1.061167	1.389657	1.764198	0.105284	-0.01128	-0.30898	-0.582817	1.154209	1.22675	0.574313
ESTs, Highly similar to U05334_1 rap7a [R.norvegicus]	93842_at	1.147571	0.054968	1.038009	0.823368	0.733905	0.275157	-0.158379	-0.211963	0.021414	-0.268768
procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide	104139_at	0.345604	0.549282	0.378522	0.525059	0.623625	-0.226181	-0.54706	0.039484	0.412695	-0.325414
TYRO protein tyrosine kinase binding protein	100397_at	0.580196	0.732743	1.26046	0.462556	0.160661	-0.058882	-0.585173	0.457408	0.432575	0.541513
cathepsin Z	92633_at	0.477369	1.086035	0.154236	0.694196	0.330906	0.264133	-0.046904	0.371773	0.516492	-0.318787
cathepsin S	98543_at	0.403588	0.200128	2.141695	1.168404	0.207606	-0.410754	-0.097475	0.108238	-0.072772	-0.289507
GRO1 oncogene	95348_at	1.613054	1.845626	1.28651	-0.166214	0.307815	-0.005241	-0.05769	0.146425	0.310371	-0.388548
ESTs, Moderately similar to AF120206_1 XY body protein [M.musculus]	103563_at	0.979866	1.330913	0.133375	0.183061	0.367493	0.341003	-0.088799	0.056236	0.300528	0.300977
integrin alpha 5 (fibronectin receptor alpha)	103039_at	0.515697	2.279611	3.220285	1.912429	-0.556933	0.56539	-1.656924	-1.004694	-0.912503	-1.456433
ESTs, Highly similar to PROTEIN HI1715 [Haemophilus influenzae]	94034_at	0.680351	0.771941	0.182422	0.398335	0.276314	0.159278	0.245085	0.458733	0.483745	0.173634
v-maf musculoaponeurotic fibrosarcoma oncogene family, protein K (avian)	102919_at	0.873737	0.377558	0.398526	0.214821	0.551807	0.369516	0.327435	0.211628	0.436278	0.077888
ESTs, Weakly similar to DIA1_MOUSE DIAPHANOUS PROTEIN HOMOLOG 1 [M.musculus]	96278_at	0.604706	0.073852	1.055509	0.387902	0.430417	0.498137	0.259799	-0.168188	-0.198533	0.019047
dynein, cytoplasmic, light chain 1	96298_f_at	0.550596	-0.013757	1.135388	0.880408	0.810417	0.030851	-0.12078	0.557494	0.735175	0.129382
procollagen, type III, alpha 1	98331_at	0.186059	-0.094864	1.999963	1.897202	1.043648	0.441607	-0.871836	0.409393	0.567532	0.106031
transgelin	93541_at	0.33113	0.257686	1.085604	0.941015	0.294552	0.047834	0.039451	0.223208	0.313779	0.285907

DNA segment, Chr 5, ERATO Doi 287, expressed	100024_at	0.293242	0.295019	0.495369	0.828562	0.349396	0.089317	-0.023852	0.041206	0.281116	-0.525814
ninjurin 1	93318_at	0.647152	0.527188	0.335876	0.571936	0.236604	0.601052	0.384437	-0.094491	0.547587	0.048687
actin, gamma, cytoplasmic	96573_at	0.494114	0.504194	1.143136	0.432997	0.053542	0.180243	-0.337411	-0.118308	-0.128295	-0.592902
small inducible cytokine A7	94761_at	1.080993	0.966018	2.553028	-0.091182	0.030312	0.231202	-0.695225	0.550405	0.383755	-1.866901
transforming growth factor, beta 1	101918_at	0.309502	0.842319	0.872297	0.446495	0.222783	0.505262	-1.707786	-0.173753	-0.094805	-0.127608
Mus musculus TNF intracellular domain-interacting protein mRNA, complete cds	95150_at	0.533404	0.335557	0.175939	0.437646	0.537191	0.120697	-0.012281	0.394342	0.594274	0.397102
ESTs, Highly similar to HYPOTHETICAL 13.5 KD PROTEIN C45G9.7 IN CHROMOSOME III [Caenorhabditis elegans]	93327_at	1.177395	0.217846	0.16904	0.640318	0.593677	0.209694	-0.019308	-0.106339	0.198698	-0.09736
DNA segment, Chr 15, ERATO Doi 621, expressed	98013_at	2.427299	1.544017	-0.079475	0.427717	0.686175	0.14566	0.198448	-0.415407	-0.719176	-0.50763
calcium binding protein A6 (calcyclin)	92770_at	0.474969	-0.072682	1.285171	0.967211	0.490838	0.543418	0.267586	0.278098	0.279284	-0.086075
A kinase anchor protein 2	101435_at	0.367411	0.42223	0.493582	0.376023	0.49531	-0.519502	-0.129799	0.664377	0.230453	0.749631
synaptobrevin like 1	102885_at	2.349661	1.000309	-0.757851	0.536512	0.961821	-0.458377	-0.637686	-0.05854	-0.120941	0.096955
cardiac morphogenesis	102213_at	0.834963	1.680522	0.726925	0.144607	-0.019137	0.792622	0.043138	0.076835	0.287985	0.078477
amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein	102710_at	0.043985	0.385138	0.963401	0.804475	0.425082	0.360505	-0.082221	0.08272	0.335621	0.053399
ESTs, Highly similar to TROPOMYOSIN 4, EMBRYONIC FIBROBLAST ISOFORM [Rattus norvegicus]	95542_at	0.324474	0.187186	0.833252	0.664631	0.303909	-0.261714	-0.20714	0.238612	0.557426	0.387586
UDP-glucose dehydrogenase	102322_at	0.022067	0.393117	0.885657	0.586568	0.5423	-0.033545	0.38763	0.415232	0.304208	-0.011713
calcium binding protein A11 (calgizzarin)	92539_at	0.221298	0.25752	1.616015	0.426204	0.229879	0.236432	-0.16765	0.431607	0.314159	-0.021378
collagen binding protein 1	94817_at	0.559572	0.117189	1.077142	0.314848	0.328858	0.372573	-0.424948	0.620443	0.905967	0.249186
fibrillin 1	101090_at	-0.416862	0.432223	1.681274	1.781112	0.882968	0.549394	-0.228386	-0.707837	-0.290198	-0.86097
complement component 1, q subcomponent, beta polypeptide	96020_at	0.673836	0.350745	0.956865	0.507525	0.223822	0.233831	-0.290681	0.829606	1.030296	0.263812
ESTs, Highly similar to THRR_MOUSE THROMBIN RECEPTOR PRECURSOR [M.musculus]	95474_at	0.176824	0.244909	0.858809	0.957478	0.584058	-0.041139	-0.080909	0.188271	0.423949	0.018871
spinocerebellar ataxia 10 homolog (human)	99127_at	0.254165	0.08161	0.800672	0.722427	0.444787	0.166608	0.184695	0.099723	0.145459	0.031449
procollagen, type IV, alpha 1	101093_at	0.316278	0.439054	0.630936	0.898303	0.122271	0.420172	-0.377638	-0.081647	0.245686	-0.472475
fibulin 2	100928_at	0.126889	0.011596	1.294428	1.203166	0.894727	0.195468	0.008428	-0.52545	-0.065243	-0.516877
ESTs, Highly similar to ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM [Homo sapiens]	92280_at	0.70974	-0.460943	2.275436	0.296493	1.75756	0.097638	-0.013796	-0.426831	-1.474312	0.858993
ESTs, Moderately similar to GOLIATH PROTEIN [Drosophila melanogaster]	98915_at	0.798718	-0.0129	1.263653	0.89215	0.060101	-0.045057	0.492482	-0.246106	-0.712934	-0.337956
actinin alpha 2 associated LIM protein	101089_at	0.525031	0.653099	0.095821	0.503694	0.226588	0.300175	0.13199	0.362511	0.346268	0.528035
ESTs, Moderately similar to KIAA1029 protein [H.sapiens]	94991_at	-0.077739	0.365471	0.891129	0.966554	0.687795	0.474072	-0.053771	-0.06087	0.47327	0.214471
drebrin-like	95529_at	0.567154	0.181202	0.083361	0.793693	0.843998	0.657633	-0.399045	-0.025217	-0.032002	-0.222017
ESTs, Weakly similar to CA11_RAT COLLAGEN ALPHA 1(I) CHAIN [R.norvegicus]	95035_at	0.677278	0.097621	0.675931	0.403241	0.272136	0.925793	0.153453	-0.592076	-0.246216	-0.202031
peptidylprolyl isomerase C-associated protein	97507_at	0.422217	0.556753	0.671072	0.930062	0.210552	0.609538	-0.354288	-0.642893	-0.164931	-0.068199
ESTs, Highly similar to MYOSIN HEAVY CHAIN, NONMUSCLE [Gallus gallus]	100915_at	0.445596	0.566757	0.466992	0.655125	0.187065	0.445087	-0.481283	-0.176949	0.657361	0.139738
procollagen, type VIII, alpha 1	100308_at	-0.054925	-0.044483	1.788599	1.833656	0.663274	-0.100881	-0.216485	0.047248	0.381326	0.365336
cytotoxic T lymphocyte-associated protein 2 alpha	96912_s_at	0.300694	0.209717	0.699715	0.419956	0.309683	-0.406095	0.138119	0.587121	0.544981	0.824156
growth arrest and DNA-damage-inducible, gamma	101979_at	0.182439	0.514449	1.665014	0.030317	0.264634	0.228289	0.354166	0.079514	-0.411786	-0.631459
ADP-ribosylation-like 6	101439_at	0.901273	0.335652	0.468109	0.543619	0.120844	-0.36913	0.334333	-0.198553	-0.085256	-0.018622
transforming growth factor, beta induced, 68 kDa	92877_at	0.127121	0.192596	1.256435	0.609513	0.379241	0.628109	-0.029583	0.269797	0.276881	-0.128648
Lamin A	98059_s_at	0.293237	-0.003353	1.063849	0.74308	0.372693	0.337976	-0.105274	0.164749	0.365985	0.137587
actin, gamma, cytoplasmic	97904_at	0.295154	0.22118	0.627082	0.442121	0.243514	-0.35907	-0.138674	-0.001583	-0.247795	-0.154523
aryl hydrocarbon receptor nuclear translocator-like	102382_at	1.226771	0.590975	1.303786	-0.131257	0.555265	0.642467	0.669817	-0.32577	-0.970154	-0.269511
Lipocortin 1	93038_f_at	0.426302	-0.040862	0.965597	0.987381	0.717629	-0.218688	0.064907	0.239162	0.172461	-0.011432
major histocompatibility locus class III regions Hsc70t gene	95654_at	-0.113918	0.336644	1.284168	0.855705	0.239584	0.364141	-0.002951	0.313622	0.32618	0.332041
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	97535_at	0.302008	0.384939	0.476398	0.349827	0.221979	0.088825	0.148804	0.412186	0.469937	0.190323
serine protease inhibitor 4	97487_at	0.33889	0.292053	0.219739	0.803388	0.8107	-0.059258	0.025328	-0.030235	0.417378	0.37943
Mus musculus p53-variant (p53) mRNA, partial cds	101617_s_at	0.144213	0.350941	0.956784	0.947424	0.394723	0.062471	-0.352815	-0.368265	0.206272	-0.321146
ESTs	103667_at	0.176496	0.375513	0.286307	0.562168	0.276081	-0.630084	-0.414216	-0.163157	-0.106936	-0.060103
calpain 2	101040_at	0.353431	0.295473	0.917075	0.321776	0.134775	-0.107666	-0.043013	-0.464507	-0.230406	0.038799
steroid dehydrogenase	94276_at	0.156247	0.893691	0.448484	-0.035369	0.755661	-0.488392	-0.15437	0.447858	0.22894	-0.018541
protein tyrosine phosphatase, receptor type, C	101048_at	0.650023	-0.155486	0.406173	0.983442	0.300678	-0.467838	-0.588693	0.17814	-0.408696	-0.45877
ESTs, Weakly similar to DYNA_RAT DYNACTIN, 150 KD ISOFORM [R.norvegicus]	97276_at	1.346355	0.520655	0.224705	0.208177	0.287909	-0.220253	-0.241935	-0.443939	-0.53883	-0.286605
ESTs	97838_at	0.356987	0.44651	0.419927	0.309553	0.142846	-0.484629	-0.287556	-0.359527	-0.229796	-0.155043
heat shock protein, 70 kDa 3	93875_at	0.31081	2.754836	0.98182	0.723276	-0.416273	-0.383689	-0.767388	0.143075	0.205517	-0.26254
tubulin, beta 5	94788_f_at	0.268954	0.017928	1.472174	0.56238	0.212916	0.486959	-0.19581	0.346319	0.618233	-0.12996
ESTs, Highly similar to THRR_MOUSE THROMBIN RECEPTOR PRECURSOR [M.musculus]	95313_at	-0.361344	0.940294	0.855935	0.916731	0.405385	-0.528431	-0.417594	0.12827	0.322181	0.635938
insulin-like growth factor binding protein 6	103904_at	0.299549	0.516101	0.097936	0.592468	1.075313	0.570729	0.367951	-0.193604	-0.128316	-1.038787
secreted acidic cysteine rich glycoprotein	97160_at	0.212281	-0.144643	0.746349	1.292225	0.478303	0.031298	-0.828255	0.231717	0.301704	-0.044476
ESTs, Highly similar to G02273 LIV-1 protein - human [H.sapiens]	103459_at	0.018905	0.61485	1.288161	1.21124	-0.051637	0.205702	-0.038078	0.304698	0.112738	-0.023913
nuclear receptor-binding SET-domain protein 1	92827_at	0.660364	-0.244622	1.273882	0.897956	0.231824	-1.033457	0.126572	-0.367446	-0.51253	0.11773
ESTs, Weakly similar to INTERFERON-INDUCED PROTEIN 6-16 PRECURSOR [Homo sapiens]	92718_at	0.498083	0.672261	1.068318	0.283704	0.387871	0.38901	0.168842	0.396625	0.305033	0.058744
annexin A2	100569_at	-0.222788	0.060258	1.682275	0.943186	0.432832	0.161873	-0.152279	0.644167	0.402842	0.381612
eukaryotic translation initiation factor 1A	93058_at	0.720777	0.61503	0.847194	1.061615	-0.270254	-0.213677	0.503857	-0.129555	-0.088006	-0.117415
protein tyrosine phosphatase, receptor type, A	100908_at	0.515327	0.913433	-0.290512	0.424073	1.01141	-0.224358	-0.58543	0.065569	-0.286816	-0.227342
WD repeat domain 1	96075_at	0.430511	0.11607	0.740107	0.474212	0.105366	-0.021336	-0.236905	0.315097	0.336967	0.037162
FK506 binding protein 5 (51 kDa)	94297_at	-0.262835	0.414603	0.924336	1.306302	0.292918	-0.241311	0.714965	-0.092703	-0.2019	-0.31001
ESTs	102056_f_at	0.702499	0.435402	0.28224	0.685865	0.074298	0.404398	0.069486	0.155335	0.112171	-0.108262
5' nucleotidase	93202_at	-0.054751	0.458777	0.647406	1.376546	0.185282	0.038323	0.048094	0.184608	-0.277167	0.266846
thioredoxin reductase 1	99985_at	0.200314	0.369993	0.568476	0.116334	0.321838	0.381518	0.235995	-0.188693	-0.358173	0.194097
ESTs	98346_at	-0.298955	1.041677	0.474802	0.485865	0.933109	0.788779	-0.284729	0.299086	-0.018654	0.172497
ESTs	95404_at	0.630255	0.241136	0.504197	0.462706	0.188798	-0.108681	-0.063976	-0.245372	-0.193514	-0.124086
Rho interacting protein 2	92710_at	0.660176	0.162377	0.375069	0.608879	0.483634	0.072286	-0.080869	0.246345	0.277528	0.29577
nidogen 2	93563_s_at	-0.016575	0.956402	0.315619	1.050273	0.456036	0.081491	-0.329353	-0.339241	-0.232688	-0.437428
ESTs	98594_at	0.465112	1.170591	-0.176861	0.29864	0.365056	-0.483642	0.297439	-0.357818	-0.385932	-0.359527
tumor necrosis factor receptor superfamily, member 1a	92793_at	0.086402	0.358107	0.396221	0.441495	0.270742	0.359562	0.014082	0.030545	0.182203	-0.249112
neoplastic progression 1	101168_at	0.189057	0.339232	0.349831	0.487069	0.422151	-0.108339	0.012715	0.102204	-0.424989	0.167587

Intercellular adhesion molecule	96752_at	1.1134	1.335823	0.294069	0.154769	-0.117336	1.032653	-0.190495	-0.219524	0.086995	0.15879
biglycan	96049_at	-0.042858	-0.129856	1.576702	1.496142	1.438945	0.196357	-0.162442	-0.025184	0.264697	-0.057889
glutamine fructose-6-phosphate transaminase 2	103737_at	0.481368	1.179765	0.932746	0.288679	0.28898	-0.068757	-0.05145	0.1142	0.140663	0.181241
mitogen-activated protein kinase kinase kinase kinase 4	102195_at	1.235088	0.607551	0.050437	0.198787	0.271479	0.003152	-0.147954	0.058635	-0.030573	-0.187954
suppressor of clear, C. elegans, homolog of	104216_at	1.172464	0.822123	0.017984	0.027546	0.318848	-0.289948	0.051809	-0.243379	0.083637	-0.677166
secreted frizzled-related sequence protein 3	104672_at	0.790686	-0.33989	1.67533	1.971734	1.305057	0.23785	-0.574523	-0.27675	-0.312628	-0.522134
procollagen, type I, alpha 2	101130_at	0.15623	-0.139725	1.444894	1.874827	1.112612	0.559211	-0.589601	-0.174927	0.604866	0.044843
ESTs, Weakly similar to AF234765_1 serine-arginine-rich splicing regulatory protein SRRP86 [R.norvegicus]	98948_at	0.658609	0.800372	0.429277	-0.033402	0.058543	-0.367932	0.067819	-0.44597	-0.303333	-0.168506
procollagen, type IV, alpha 2	101039_at	-0.046107	0.110588	0.74361	0.801582	0.544584	0.56576	-0.294996	-0.162261	0.063329	0.061536
ESTs, Highly similar to TRAM PROTEIN [Canis familiaris]	98956_at	0.418903	0.198245	0.220369	0.365934	0.228267	-0.026013	0.31769	0.466363	0.270533	0.248672
mannose receptor, C type 1	103226_at	0.301472	0.476385	0.344195	0.513798	0.358536	-0.46277	-0.321872	-0.110539	-0.04696	-0.232227
alpha actinin 4	96343_at	0.680848	0.592559	0.217558	0.574832	0.224138	0.302276	-0.184547	-0.206922	-0.088776	-0.204823
ESTs	93458_at	-0.271481	0.966588	0.41528	0.891284	0.252892	0.680283	-0.291278	-0.341661	-0.173879	-0.347604
Mus musculus chromosome 10 popeye protein 3 (Pop3) mRNA, complete cds	103484_at	0.209386	0.525018	0.435826	0.119971	0.263019	0.144109	0.08461	0.438281	0.764737	0.259264
E26 avian leukemia oncogene 1, 5' domain	94720_at	0.846825	0.2553	0.688665	0.225581	0.301753	-0.151985	0.452595	-0.467169	0.059744	0.165191
ESTs, Highly similar to RIBONUCLEASE INHIBITOR [Rattus norvegicus]	100621_at	1.166647	-0.313662	0.935004	0.687273	0.190026	0.044715	-0.02174	-0.231413	-0.295384	-0.361487
solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein, 34 kDa), member 17	97473_at	0.351238	-0.076526	0.637229	0.518465	0.273099	0.020603	-0.256362	-0.502637	-0.018142	0.012254
tubulin alpha 2	98759_f_at	0.212911	0.127285	1.219979	0.345907	0.1102	0.24649	-0.482547	0.901031	0.551637	0.280601
ESTs, Highly similar to TRANSLOCON-ASSOCIATED PROTEIN, BETA SUBUNIT PRECURSOR [Homo sapiens]	101061_at	0.79391	0.314865	0.069572	0.484207	0.193601	0.324744	-0.079821	0.112915	0.002708	0.118474
ESTs	93187_at	0.368157	-0.022147	0.720096	0.345186	0.512074	0.414873	-0.229408	-0.129694	0.169523	-0.040494
clusterin	95286_at	0.22662	0.130588	0.821711	0.925807	0.071836	0.279245	-0.024518	-0.511602	-0.400513	-0.380258
immediate early response 2	99109_at	0.481628	0.838363	0.206683	0.191851	0.048969	0.23787	-0.280458	-0.349769	-0.091757	-0.580997
serum amyloid A 3	102712_at	-0.924018	0.708052	2.379979	2.285736	0.147122	-0.423916	-0.851542	0.62684	0.806487	0.367732
ESTs, Moderately similar to 60S RIBOSOMAL PROTEIN L39 [Rattus norvegicus]	94844_at	0.116802	0.229217	0.813871	0.256723	0.256473	0.498138	-0.640933	0.25013	0.392499	0.119571
actin, alpha, vascular smooth muscle	93100_at	0.91492	0.05983	0.574016	0.521389	0.221227	0.584484	-0.090852	0.079421	0.475172	0.060549
hematological and neurological expressed sequence 1	93276_at	0.473767	-0.06749	0.513023	0.659304	0.380337	0.368569	0.178137	0.11272	0.548909	0.271984
ferritin light chain 1	99872_s_at	0.477258	0.280446	0.423243	0.516709	0.170711	0.057007	-0.167215	-0.245777	0.144908	-0.081981
ESTs, Weakly similar to nuclear protein ZAP [M.musculus]	96288_at	0.272864	0.232787	0.625592	0.120245	0.501661	0.401726	-0.072949	-0.368702	-0.134574	-0.323998
ESTs, Highly similar to ER23_HUMAN ER LUMEN PROTEIN RETAINING RECEPTOR 3 [H.sapiens]	104464_s_at	0.218993	-0.325886	1.382523	1.211213	0.345941	0.770966	-0.004731	0.131027	0.159498	-0.193736
latent transforming growth factor beta binding protein 2	92335_at	0.526675	-0.10468	2.519514	2.049431	1.605186	0.035709	-1.110404	0.733815	0.705146	0.776986
aortic preferentially expressed gene 1	99331_at	0.190657	0.156868	0.736655	0.215533	0.258453	0.644015	-0.141548	0.253172	0.70434	0.287881
ESTs, Weakly similar to AF154120_1 sorting nexin 1 [M.musculus]	96331_at	0.323884	0.818136	0.176841	0.432923	0.110342	-0.061183	0.44059	-0.163059	-0.38112	-0.322279
mitogen activated protein kinase 3	101834_at	0.517143	0.279038	0.630417	0.365407	0.015294	-0.047146	-0.463837	-0.272473	-0.493223	0.203211
G protein-coupled receptor kinase 5	102217_at	-0.136872	0.170014	0.604811	0.43431	0.805529	0.486734	-0.025469	-0.571927	-0.508339	-0.378705
ESTs, Weakly similar to CA11_RAT COLLAGEN ALPHA 1(I) CHAIN [R.norvegicus]	95034_f_at	0.378995	0.539565	-0.152899	0.639726	0.310845	0.331992	-0.318176	0.284203	0.643162	-0.563355
B-cell translocation gene 3	96146_at	0.619808	0.509852	-0.098071	0.603099	0.205549	-0.167923	0.295443	0.255833	0.53375	0.511186
keratin-associated protein 14	92246_at	0.53477	0.386038	0.603605	0.517733	0.087617	-0.397529	-0.715981	0.051544	-0.11188	0.153237
chromobox homolog 1 (Drosophila HP1 beta)	96775_at	0.748023	0.801293	0.693699	0.208009	0.709479	-0.126119	-0.318159	0.136915	-0.964639	0.117168
cholesterol 25-hydroxylase	104509_at	0.146903	1.014224	1.86853	0.574424	-0.001599	0.204604	-0.271527	0.064007	0.4467	0.690997
ESTs, Highly similar to POSSIBLE GUSTATORY RECEPTOR TYPE B [Bos taurus]	97383_at	0.39528	0.25442	0.617664	-0.088479	0.380121	0.144751	0.284043	-0.323351	0.099067	0.078032
Mus musculus collagenous repeat-containing sequence of 26kDa protein (CORS26) mRNA, complete cds	103570_at	-0.231677	0.063209	1.896222	2.048282	0.711508	-0.121883	-0.34262	-0.560752	-0.513517	-0.486315
TGFB inducible early growth response	99603_g_at	0.013268	0.580838	0.379459	0.008012	0.906948	-0.564327	-0.138369	-0.040396	-0.27136	-0.41628
ribosomal protein L3	100734_at	0.130729	0.044027	1.144895	0.296403	0.21057	-0.021784	-0.052666	0.108155	-0.268278	-0.206657
DNA segment, Chr 11, ERATO Doi 175, expressed	97824_at	-0.038905	0.644808	0.691484	0.14188	0.225784	-0.231815	-0.03711	-0.479939	-0.461765	-0.593226
DNA segment, Chr 11, KL Mohlke 35	98635_at	0.657573	-0.111057	0.265789	0.525837	0.272064	0.114185	-0.24474	0.020245	-0.392089	-0.143187
ESTs, Moderately similar to PLSL_MOUSE L-PLASTIN [M.musculus]	94445_at	-0.299506	0.456656	0.352636	0.883169	0.395466	-0.093601	0.122714	-0.080492	0.213626	0.059316
membrane-spanning 4-domains, subfamily A, member 11	102104_f_at	-0.293563	0.965182	1.06965	1.283233	-0.107912	-0.202027	-0.354922	0.280172	0.161553	0.215532
vasodilator-stimulated phosphoprotein	101982_at	0.402119	0.035957	0.403638	0.293649	0.31878	0.31301	-0.506951	-0.127426	0.158052	-0.104064
SEC23B (S. cerevisiae)	98944_at	1.608496	0.098276	0.050495	0.443524	0.057207	0.600164	0.24972	0.087157	0.167499	-0.090734
heat shock protein, 110 kDa	92571_at	0.244325	0.820261	0.126915	0.355528	0.024038	-0.346762	0.082721	-0.152109	-0.128695	-0.16532
cathepsin C	101019_at	0.212847	0.824643	0.948045	1.001345	-0.269778	0.263613	0.266706	0.241662	0.072204	-0.216471
sodium channel, voltage-gated, type I, beta polypeptide	102808_at	0.25586	-0.081711	0.724866	0.77293	0.490301	0.088128	-0.364848	0.432925	0.841756	0.291954
ESTs, Highly similar to KINESIN-II 85 KD SUBUNIT [Strongylocentrotus purpuratus]	95118_r_at	0.272404	0.08313	1.650936	1.147889	0.124441	-0.019669	-0.899826	-0.341257	-0.059857	0.294303
ESTs, Weakly similar to AF164793_1 protein x 013 [H.sapiens]	98615_at	0.136255	0.679958	0.4304	0.173217	0.111947	-0.197613	0.029915	0.667661	0.760911	0.099561
proteolipid protein 2	93323_at	0.007002	-0.009389	0.981451	0.753216	0.667173	0.110814	0.161535	0.179938	0.112278	0.113721
procollagen, type XV	99637_at	0.391513	-0.162265	1.044238	1.102739	0.401082	0.403017	-0.254686	-0.35669	0.216715	-0.01153
peripheral myelin protein, 22 kDa	102395_at	0.186049	0.575266	0.211473	0.46419	0.303425	0.378729	0.021751	0.354348	0.702053	-0.11046
NF-YB-like protein	100408_at	-0.384912	0.757282	1.02715	0.82026	0.578551	0.604917	0.313868	0.021374	0.005799	0.025745
tubulin alpha 1	100343_f_at	0.006812	0.184888	1.06606	0.156206	0.647153	0.268687	-0.766704	1.138372	0.699416	-0.182977
ESTs	103709_at	-0.467796	-0.082076	2.031433	1.282214	0.645392	0.720352	-0.338096	0.168156	0.548826	0.012245
origin recognition complex subunit 6	95712_at	0.187585	1.036324	0.136162	0.510041	0.491898	-0.167665	-0.11115	-0.000227	-0.318182	-0.52017
ESTs	103423_at	0.300556	0.18139	0.355395	0.366858	0.157285	0.107792	0.087297	0.156498	0.670036	0.081366
DNA segment, Chr 3, University of California at Los Angeles 1	95708_at	-0.007045	0.180491	0.638269	0.421329	0.273846	-0.107883	0.012763	0.055173	0.085259	-0.217148
annexin A4	100584_at	0.351537	0.124203	0.505645	0.677164	0.606313	0.115577	0.00649	0.336658	0.15958	-0.257485
pleckstrin homology, Sec7 and coiled/coil domains 3	103433_at	0.800444	0.348523	0.272732	0.208315	0.430555	0.439592	0.237741	-0.23395	-0.229764	-0.364023
MORF-related gene X	96632_at	-0.152314	-0.013304	1.054946	0.59151	0.420612	-0.612387	-0.215569	0.119295	-0.329099	-0.097148
DNA segment, Chr 2, ERATO Doi 93, expressed	97165_r_at	1.191502	0.018532	0.352473	0.726304	-0.119718	-0.52167	-1.029671	0.547414	0.270055	0.786494
glutathione peroxidase 3	101676_at	0.522328	0.048124	-0.027724	1.09492	0.55393	-0.006304	-0.819686	-0.935203	-0.437939	-0.332215
karyopherin (importin) alpha 3	93857_at	0.823122	0.336777	-0.522019	0.506996	0.887369	-0.316712	0.041536	-0.20524	-0.583214	0.091796
nucleoplasmin 3	102796_at	1.045385	1.525396	0.240543	0.228136	-0.006578	0.068536	0.001085	0.547894	0.210868	0.129386
ESTs, Highly similar to KIAA0456 protein [H.sapiens]	96516_at	0.461565	-0.013436	0.324261	0.446987	0.087605	-0.159884	-0.527715	-0.467409	-0.267896	-0.323531
MARCKS-like protein	97203_at	0.106239	0.137441	0.818454	0.312889	0.078397	0.21069	-0.828012	0.340474	0.482605	0.52408
platelet/endothelial cell adhesion molecule	97830_at	-0.154358	0.216574	0.936397	0.445232	0.343453	0.686497	-0.185959	0.562355	0.38149	0.418722

DNA segment, Chr 6, ERATO Doi 746, expressed	104168_at	1.07502	0.424375	-0.322081	1.017215	0.44909	-0.919787	-0.074526	0.107475	-0.028648	0.174688
ubiquitin-like 1 (sentrin) activating enzyme subunit 2	96701_at	0.118914	0.423361	0.668266	0.389029	-0.031097	-0.117819	-0.268849	0.123488	-0.301702	0.075499
fibroblast growth factor receptor 1	97509_f_at	0.433489	-0.062096	0.393039	0.51627	0.206425	0.263069	-0.044375	-0.32486	-0.495344	-0.183745
cyclin-dependent kinase 4	101017_at	0.555491	0.414274	-0.205771	0.679227	0.148859	-0.042137	-0.542671	0.059763	0.325337	0.35324
ESTs, Weakly similar to HYPOTHETICAL 39.2 KD PROTEIN IN EGT2-KRE1 INTERGENIC REGION [Saccharomyces c	104582_g_at	0.85207	0.592793	0.542467	0.733185	-0.447431	-0.069826	-0.149604	-0.508141	-0.503016	-0.149284
ESTs, Moderately similar to quiescin [H.sapiens]	96603_at	0.898181	-0.604366	1.403711	0.263487	0.318292	0.154775	-0.545622	0.278363	0.207719	0.317941
immediate early response 3	94384_at	0.23705	-0.1763	1.167892	0.054257	0.447563	0.151535	0.287016	0.281759	0.46541	0.054902
ESTs, Weakly similar to ADP-RIBOSYLATION FACTOR 2 [Saccharomyces cerevisiae]	98491_at	0.228896	0.623719	-0.137155	0.309102	0.444408	-0.114809	-0.167032	0.199727	0.090537	0.188743
RAS p21 protein activator 3	93319_at	0.390234	0.186424	0.114342	0.167925	0.279106	0.649932	0.273447	0.025901	0.334073	-0.458205
capping protein alpha 1	93499_at	0.040646	0.353923	0.364578	0.425689	0.093905	-0.246067	0.064584	0.06743	0.040823	-0.068169
ERG-associated protein	98129_at	0.47585	-0.171437	0.784812	0.676672	0.218198	0.448891	-0.313166	0.177175	0.735654	-0.388398
endothelin 1	102737_at	0.590232	1.242994	0.520908	-0.029255	0.038501	-0.240439	-0.345614	0.130289	0.050613	-0.288329
ESTs, Highly similar to ARGINYL-TRNA SYNTHETASE [Cricetulus longicaudatus]	96693_at	0.224169	0.224526	0.1589	0.275176	0.454005	-0.492245	0.104381	-0.104762	0.03847	-0.046491
ESTs	99366_at	-0.363388	0.307587	0.560258	0.720906	0.989371	0.217186	-0.09617	0.215507	0.296628	0.199395
glycogenin 1	100597_at	0.01298	0.400203	0.155523	0.208357	0.395673	0.305943	-0.173567	0.020608	0.250371	0.141923
tenascin C	101993_at	-0.148779	0.304232	3.464742	0.305185	-0.054858	0.353747	-0.161109	0.388155	-0.527692	-0.006199
ESTs, Highly similar to HYPOTHETICAL 45.3 KD PROTEIN ZK370.5 IN CHROMOSOME III [Caenorhabditis elegans]	92810_at	0.555163	-0.651802	0.457063	1.196623	0.285388	0.345878	0.131973	-0.136573	0.31009	0.374329
fragile X mental retardation syndrome 1 homolog	98441_at	-0.350743	0.43085	0.395413	0.867643	0.367692	-0.832797	-0.460498	-0.239686	-0.515266	-0.025795
rabaptin 5	101381_at	0.066447	1.218102	0.107432	0.110974	0.38247	-0.222123	0.106019	-0.526258	-0.641235	-0.254441
cystatin B	100581_at	0.206297	0.058423	0.639899	0.390248	0.191196	0.122409	-0.208185	0.465059	0.513893	-0.06235
ESTs, Moderately similar to I53908 major vault protein - rat [R.norvegicus]	103793_at	0.802173	-0.057157	0.486615	0.275815	0.167507	0.094974	-0.120019	-0.68112	-0.551329	-0.524078
interferon concensus sequence binding protein	98002_at	0.404856	0.641081	0.988438	0.749286	0.135094	0.339034	-0.500539	0.022624	-0.174527	0.228941
calponin 2	94004_at	0.790527	-0.261843	0.699299	0.214323	0.310786	0.198015	-0.690209	0.151769	0.464324	0.234775
ESTs, Weakly similar to ZINC FINGER PROTEIN ZFP-27 [Mus musculus]	103631_at	1.199859	1.241214	-0.116191	0.190817	0.013123	0.090104	0.185509	-0.21507	0.152755	0.12577
annexin A5	93083_at	0.27845	-0.048771	0.552537	0.443716	0.359364	0.282966	0.046606	-0.056099	0.046521	-0.166845
spermidine/spermine N1-acetyl transferase	96657_at	0.342029	0.69248	0.036127	0.395603	0.191661	0.340643	0.437229	-0.4362	0.163994	0.150788
interferon (alpha and beta) receptor 2	101015_s_at	-0.281629	0.379077	-0.048502	0.66494	1.097896	0.481484	0.174476	0.370502	0.657406	-0.415912
NCK-associated protein 1	95508_at	0.062815	0.461638	0.175487	0.442648	0.189157	-0.338465	0.057674	-0.317885	-0.244788	-0.214767
ESTs	94362_at	0.135253	0.352522	-0.000287	0.325252	0.293301	-0.750796	-0.485117	0.106154	0.137218	-0.199848
cytokine inducible SH2-containing protein 2	99475_at	0.954158	0.112511	-0.085823	0.218852	0.478667	-0.472186	-0.194258	-0.677989	-0.145476	0.265966
mesenchyme homeobox 1	98419_at	-0.140829	-0.281821	1.630842	0.838387	0.889152	0.098205	-0.595144	-0.139837	0.326172	0.254136
centrin 3	92789_r_at	0.295884	0.889572	0.133214	0.102281	0.009844	-0.294471	-0.536239	0.074371	-0.322925	-0.278035
apolipoprotein D	93592_at	0.916739	0.107312	0.244732	0.319357	0.686825	-0.058	1.426389	0.078763	0.423326	-0.904904
pre B-cell leukemia transcription factor 3	93615_at	0.67299	0.276407	0.314252	0.139436	-0.111603	0.29956	-0.004116	-0.986048	-0.225521	-0.316407
deoxycytidine kinase	98071_f_at	0.068542	-0.309727	1.189571	1.169697	0.279224	-0.083277	-0.136273	0.526884	0.329275	0.102877
SH3-binding domain glutamic acid-rich protein like	93806_at	-0.002081	0.213697	0.199339	0.587334	0.492422	-0.807071	-0.34369	0.01047	-0.054522	-0.341411
ESTs	95284_at	1.184425	-0.536462	2.983485	0.361219	0.113159	-0.311851	-0.47468	0.050753	-0.303824	0.398804
Sid394p	93818_g_at	0.46678	0.630029	0.116841	0.081507	0.126641	-0.332665	-0.060389	0.061559	-0.045687	-0.027177
phospholipase A2, group IV	99513_at	0.219005	-0.249607	1.215913	0.339223	1.126079	-0.24383	-0.584963	0.246209	-0.239945	-0.190623
tubulin alpha 6	101543_f_at	0.374882	0.145942	0.79231	-0.033118	0.120353	0.281654	0.071464	0.754047	0.702142	-0.083208
retinol binding protein 1, cellular	104716_at	-0.341787	0.114469	1.270614	1.403133	0.997345	0.192097	-0.06798	-0.189329	-0.245766	-0.796068
growth associated protein 43	102389_s_at	-0.220783	0.193457	0.571906	1.039211	0.271513	0.009497	-1.351609	1.10803	0.657874	0.250914
DNA segment, Chr 6, ERATO Doi 109, expressed	98608_at	0.193251	0.182053	0.079598	0.363199	0.237926	-0.518367	0.407391	0.022286	-0.485158	-0.112783
DNA segment, Chr 19, ERATO Doi 721, expressed	97241_at	0.383807	0.178027	-0.047295	0.191935	0.351989	0.114979	0.037552	-0.004272	0.371107	0.092322
actin related protein 2/3 complex, subunit 3 (21 kDa)	95434_at	0.543139	0.356395	-0.028976	0.277969	0.466749	0.089632	0.345631	0.043594	0.102171	-0.13301
Mus musculus mRNA for MAIL, complete cds	98988_at	0.526646	0.176472	0.964683	0.095312	-0.046399	0.277061	-0.29192	0.055648	-0.154369	0.126965
interferon activated gene 202A	94774_at	0.937785	0.117021	0.435043	0.022515	0.093892	-0.75738	-0.376416	-0.414427	-0.118383	0.288923
procollagen, type VI, alpha 2	93517_at	0.386882	-0.289732	0.865564	1.222689	0.593479	0.267766	-0.579264	0.650253	0.373278	0.000871
OCTN3	92486_at	0.283736	0.442258	0.311095	0.854809	-0.164378	-0.343887	-1.300298	0.05242	0.035591	-0.057865
kidney cell line derived transcript 1	102644_at	0.12421	0.388388	0.148161	0.322113	0.184133	-0.291498	0.178706	-0.324222	-0.410282	-0.296639
fascin homolog 1 (actin bundling protein, Strongylocentrotus purpuratus)	92838_at	0.041171	-0.168806	1.049274	0.487602	0.482611	0.109423	0.146914	0.500747	0.395365	0.374486
ESTs, Highly similar to AF161530_1 HSPC182 [H.sapiens]	93533_at	0.627028	0.165213	-0.095679	0.541843	0.049381	0.258516	-0.067953	0.399187	0.506183	0.148822
Eph receptor B4	98446_s_at	0.345938	-0.086317	1.179913	0.048663	0.081637	0.07427	-0.341147	-0.052063	0.035689	-0.119273
ESTs, Weakly similar to AF114379_1 cypher2 [M.musculus]	102845_at	0.064711	-0.355686	0.751674	0.819991	0.479101	0.539189	0.346588	0.11235	0.489424	-0.149501
ATP-binding cassette, sub-family A (ABC1), member 1	97198_at	0.226338	0.041006	0.70209	0.110934	0.680442	-0.46196	-0.125369	-0.486595	-0.219476	0.430958
calmodulin	96522_at	0.194291	-0.082504	0.762351	0.321272	0.3235	-0.344334	-0.458556	0.131698	0.2309	0.010419
ESTs, Weakly similar to Edp1 protein [M.musculus]	102099_f_at	0.548001	0.234506	0.918007	0.066475	0.121775	0.67713	-0.12146	0.061169	0.319787	0.116497
heat shock 70 kDa protein 4	100353_g_at	0.189264	0.084343	-0.033603	0.617211	0.334623	0.295747	0.724728	-0.139255	-0.1162	-0.033094
GTP cyclohydrolase 1	102313_at	0.367012	1.663663	0.295522	-0.113518	0.234106	0.444737	-0.074793	0.234968	0.309656	-0.145866
ESTs, Weakly similar to unknown [S.cerevisiae]	103853_at	0.101595	0.539667	-0.052419	0.167316	0.111483	0.278185	-0.178627	0.159049	0.306936	-0.055551
ESTs	92836_at	-0.053184	-0.3872	0.906823	1.859313	0.305337	0.675893	0.282977	0.152729	0.340164	-0.228227
Tumor necrosis factor induced protein 1	93215_at	0.481441	0.130881	0.293217	-0.000993	0.20589	-0.000139	-0.194615	-0.661397	-0.320187	-0.148449
vascular cell adhesion molecule 1	92559_at	0.15976	0.922117	-0.14389	0.253099	0.092052	-0.635257	-0.200215	-0.276659	-0.057126	0.016123
serine protease inhibitor 3	96060_at	-0.1149	0.105907	0.704471	0.51598	0.243607	-0.171611	0.011259	0.261642	0.146795	0.068531
H2A histone family, member Z	101954_at	0.659509	0.279069	0.5634	0.455641	-0.249178	-0.314952	-0.021406	0.36532	0.373573	0.242264
LIM and SH3 protein 1	93793_at	0.638188	0.618962	0.303879	0.290006	0.180075	0.573146	-0.151393	-0.06479	0.264351	-0.164695
ESTs, Moderately similar to CLATHRIN LIGHT CHAIN B [Bos taurus]	98560_at	0.011214	0.151074	0.343781	0.290803	0.37096	0.153733	0.202178	0.198014	0.306193	0.367886
ESTs, Weakly similar to A57514 RNA helicase HEL117 - rat [R.norvegicus]	94262_at	0.673917	0.088006	0.002481	0.377211	0.113569	-0.203984	0.244905	-0.622656	-0.504033	-0.286674
claudin 5	104516_at	0.703511	-0.097526	0.24354	1.553236	-0.081718	0.092122	-0.133334	-0.535384	-0.144401	-0.708159
purinergic receptor P2X, ligand-gated ion channel 4	95586_at	0.592462	0.515	-0.460356	0.689595	0.255272	0.002376	-0.001189	-0.035348	-0.235624	-0.111588
enhancer of rudimentary homolog (Drosophila)	94040_at	0.294267	0.046761	0.425676	0.213538	0.13314	-0.442207	-0.245774	0.314302	0.117746	0.03601
calpain 3	99812_at	0.550244	-0.354185	0.80203	0.893571	0.306193	0.054422	0.002805	0.030652	0.078781	0.464352
ESTs, Weakly similar to hepatoma-derived growth factor [M.musculus]	97853_at	0.157151	0.321443	0.311188	0.401657	0.470418	-0.823757	-0.719129	0.059876	-0.144895	0.459595

ESTs, Weakly similar to AF144731_1 putative splicing factor YT521-B [R.norvegicus]	94895_at	0.420233	0.062847	0.248787	0.060151	0.207926	0.197685	-0.094456	0.29669	0.325183	0.106754
DNA segment, Chr 4, ERATO Doi 314, expressed	99621_s_at	0.346397	0.438618	-0.137095	-0.000941	0.258235	-0.331934	-0.386458	0.219451	-0.019187	0.234286
ESTs, Moderately similar to ZINC FINGER PROTEIN ZFMSA12A [Micropterus salmoides]	103989_at	0.817249	0.570266	-0.032216	0.167368	0.040445	-0.213651	0.039709	-0.511529	-0.460554	-0.316563
ESTs, Highly similar to JC2472 brain and reproductive organ-expressed protein - human [H.sapiens]	104348_at	0.563373	0.041284	0.173544	0.24038	0.225996	0.607114	0.081189	0.130046	0.028033	0.006268
ESTs, Highly similar to TRANSLATIONAL INITIATION FACTOR 2 ALPHA SUBUNIT [Rattus norvegicus; Bos taurus]	94253_at	0.089145	0.491992	0.354412	-0.063286	0.309796	-0.794472	-0.159925	-0.257465	-0.329134	-0.277703
cytochrome c oxidase, subunit VIIc	99661_r_at	0.329845	-1.220486	2.161999	0.209762	1.424173	-0.461184	-0.139684	0.034854	-0.40376	-0.06937
nuclear receptor coactivator 1	103229_at	0.196873	0.139011	0.318954	-0.059354	0.660301	0.101066	-0.416985	0.104518	0.369186	0.058683
DNA segment, Chr 6, ERATO Doi 32, expressed	95618_at	-0.001595	0.374087	0.183996	0.295788	0.250442	0.77494	0.211132	-0.366326	0.049899	-0.235936
ESTs, Moderately similar to APB3_RAT AMYLOID BETA A4 PRECURSOR PROTEIN-BINDING FAMILY A MEMBER 3	95102_at	-0.020848	0.005067	0.901024	0.451116	0.40324	0.336135	-0.218218	0.080404	0.072077	0.088891
ESTs, Highly similar to U83194_1 TRAF4-associated factor 2 [H.sapiens]	97839_at	0.189092	0.197749	0.045638	0.394865	0.221541	-0.275184	0.049621	0.175616	-0.08376	0.031386
TATA box binding protein-like protein	97893_at	2.850909	2.916964	-1.125345	0.099195	1.032421	0.159478	0.041885	0.260941	0.186861	0.225719
MORF-related gene X	96633_s_at	0.220751	-0.053569	0.734994	0.476476	0.067057	-0.248051	-0.019513	0.040017	0.103671	-0.044706
ESTs	97242_at	0.203977	0.030796	0.297755	0.46122	0.215849	0.029307	0.217877	0.705871	0.333299	0.384879
IQ motif containing GTPase activating protein 1	100561_at	-0.015832	0.151518	0.338428	0.709439	0.388196	0.050424	-0.326278	-0.058477	0.418784	0.046406
SRY-box containing gene 6	92726_at	0.930649	-0.097599	1.357889	0.13394	0.489563	-0.578794	-0.527405	0.263883	0.123619	0.231341
ESTs, Highly similar to TRANSCRIPTION FACTOR IIIA [Xenopus laevis]	94557_at	-0.138023	-0.23595	0.670048	0.76184	1.050588	0.112619	-0.507095	0.023834	0.030468	0.298151
ESTs	99080_at	0.499575	0.159347	0.430942	0.129518	0.155049	0.065021	-0.134433	-0.460425	-0.183797	-0.361206
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	97061_g_at	0.484176	0.132197	0.039281	0.381808	0.251124	0.101104	-0.259215	0.17343	0.189731	-0.007408
hypoxia inducible factor 1, alpha subunit	98629_f_at	0.093342	0.197143	0.098342	0.539395	0.164697	-0.522432	-0.037836	-0.219578	-0.54645	-0.559358
ESTs	104325_at	0.442721	0.140507	0.105681	0.371986	0.053727	-0.072202	0.059721	0.413295	0.550432	0.657256
MAD homolog 1 (Drosophila)	102984_g_at	0.289803	0.368201	0.348604	0.150751	0.123377	0.088936	-0.368496	-0.372591	-0.346736	-0.502779
ESTs, Moderately similar to AF161518_1 HSPC169 [H.sapiens]	95501_at	0.363456	1.880387	0.257461	-0.359034	0.053206	0.365405	-0.185642	-0.111975	-0.047787	-0.042157
ESTs, Highly similar to Unknown [H.sapiens]	96886_at	0.460383	0.059391	0.445109	0.404018	0.168386	0.163275	-0.588332	0.174593	0.3884	0.438053
fibronectin 1	92852_at	-1.008249	0.121306	1.179839	0.870627	0.869725	0.523052	0.153777	-0.006857	0.014308	-0.056514
ESTs, Highly similar to SPECTRIN ALPHA CHAIN, NON-ERYTHROID [Rattus norvegicus]	103345_at	0.556431	0.495006	-0.386758	0.177802	0.518598	0.270863	-0.246664	-0.079028	0.537322	-0.075677
developmentally regulated GTP-binding protein 1	98020_at	0.200682	0.154434	0.618143	0.143941	0.121018	0.12163	-0.112592	0.659234	0.522705	-0.183502
protein tyrosine phosphatase, non-receptor type 1	94929_at	0.785442	0.100081	0.16565	0.32795	-0.04241	0.281805	0.203055	-0.229723	0.200419	-0.239602
ESTs, Highly similar to G10 PROTEIN [Xenopus laevis]	96305_at	0.990131	0.364328	0.137756	0.347767	-0.27926	0.292831	0.042463	-0.019052	0.534423	-0.008961
ESTs, Weakly similar to AF069992_1 LIM domain interacting RING finger protein [M.musculus]	99574_at	0.373994	-0.216085	0.650238	0.217449	0.181997	-0.436705	-0.254437	-0.34509	-0.392388	-0.215538
chloride intracellular channel 4 (mitochondrial)	94255_g_at	0.084121	0.270455	0.61378	0.076381	0.035782	0.014402	-0.398818	0.400991	0.376027	0.127464
Mouse complement factor H-related protein mRNA, complete cds, clone 9C4	94743_f_at	0.700154	0.526673	-0.889142	0.419553	0.679131	-0.051819	0.280555	0.479434	0.571766	0.392709
fibroblast growth factor 6	97121_at	0.735187	1.027286	-0.13328	0.253211	0.533606	0.206699	0.187748	0.020831	0.124789	-0.098673
ESTs	96491_at	0.319675	0.050948	0.041383	0.750007	0.092846	0.054374	0.318714	0.064287	0.006469	-0.035926
Mus musculus mRNA for proliferation related acidic leucine rich protein PAL31, complete cds	96891_at	0.155366	-0.012989	0.447825	0.185716	0.375002	-0.364888	-0.265316	-0.363727	-0.386965	-0.179344
hemoglobin alpha, adult chain 1	101523_at	0.284852	0.22948	0.077899	0.35673	0.010104	-0.580987	-0.241557	0.200358	0.137508	0.10797
Messenger RNA fragment for mouse interferon beta (type 1) coding for the c-terminal part	101464_at	-0.601968	-0.192892	3.891357	1.343807	-0.006131	0.488777	-0.037061	0.914658	0.034267	0.068081
ESTs, Highly similar to ALPHA-1,6-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFER/	95417_at	-0.168169	0.655021	0.067632	0.221661	0.474879	0.192687	-0.01048	0.504503	0.428212	-0.162063
fibroblast growth factor inducible 14	93309_at	0.171513	0.23893	-0.049762	0.057946	0.297137	-0.461672	-0.096831	0.339459	0.340934	0.070366
RAB11a, member RAS oncogene family	92854_at	0.090478	0.252213	0.133966	0.333499	0.162174	-0.256289	-0.129939	-0.027226	-0.001767	-0.159189
ESTs, Moderately similar to T08694 hypothetical protein DKFZp564O092.1 - human [H.sapiens]	93776_at	1.634531	1.115776	0.208665	-0.368044	0.049573	-0.615284	-0.195564	0.175367	-0.510673	-0.772809
protective protein for beta-galactosidase	101055_at	0.455914	0.152378	-0.044916	0.385138	0.228199	0.279568	-0.019429	0.281443	0.30968	-0.028652
ESTs, Highly similar to PRE-MRNA SPLICING FACTOR SF2, P33 SUBUNIT [Homo sapiens]	96834_at	0.289286	0.686725	0.043496	0.094659	0.025113	-0.348396	-0.328761	0.328554	0.469068	-0.050458
MAD2 (mitotic arrest deficient, homolog)-like 1 (yeast)	99632_at	0.964486	0.427842	0.767358	0.674844	0.174858	0.091601	-0.309441	0.217365	0.117671	0.19388
glycoprotein 38	104469_at	-0.402157	0.430681	0.871789	0.25019	0.11097	0.072535	-0.573064	-0.312792	-0.039429	-0.73786
programmed cell death 4	95520_at	0.383533	-0.523405	0.266674	0.391559	0.711127	0.312872	-0.265258	0.053923	0.274565	-0.226878
complement component 1, q subcomponent, alpha polypeptide	98562_at	0.239563	0.00438	0.633366	0.447412	0.240019	0.007327	-0.263657	0.092085	0.444942	0.071638
Pak3 binding protein	98434_at	0.481017	0.09198	-0.013865	0.335936	0.159096	0.019085	-0.147353	0.28022	-0.077415	0.036664
Mus musculus sarcolemmal associated protein 1 mRNA, complete cds, alternatively spliced	98553_at	0.920192	1.351894	-0.443623	-0.018848	0.178531	-0.360886	0.313617	-0.307643	-0.126101	-0.347482
lymphocyte antigen 68	93454_at	0.258641	0.533318	-0.209247	0.491988	0.165593	0.081983	-0.482502	-0.226141	0.122776	0.042702
ESTs	97960_at	0.019465	0.166731	-0.466542	1.043599	0.497362	0.709525	-0.010355	-0.794119	0.076257	-0.319725
ESTs, Moderately similar to unnamed protein product [H.sapiens]	95647_f_at	0.21606	0.982738	0.044211	0.208034	0.107078	-0.209133	0.106741	-0.133744	-0.118075	-0.136234
DNA segment, Chr 2, ERATO Doi 391, expressed	98875_at	0.542388	0.111351	-0.14225	0.261207	0.239296	0.318788	0.304142	-0.465278	-0.127771	-0.069774
LIM only 4	95069_at	-0.022529	0.26024	0.215896	0.2819	0.262101	-0.069589	0.238608	-0.31136	-0.81358	-0.195266
esterase 10	92553_at	-0.139131	0.342879	0.64325	0.05547	0.483798	0.026727	0.778343	-0.088832	-0.000298	-0.276671
ESTs, Highly similar to RABPHILIN-3A [Rattus norvegicus]	99949_at	0.419564	0.892875	0.433264	-0.270983	0.270405	0.315632	-0.012518	-0.131362	0.25459	0.255417
housekeeping DXS253E (P3) and DXS254E (GdX) genes, 3 end, and complete cds	103218_at	-0.208881	0.046619	1.23015	0.662523	0.211021	0.243863	0.072912	-0.065009	0.319951	0.261076
ESTs, Weakly similar to LIS1_MOUSE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB ALPHA SUBUNIT		96654_at	-0.043223	0.391862	0.196253	0.080638	0.370424	-0.571583	-0.442473	-0.134274	0.015157	0.284735
ESTs	103491_at	-0.888807	0.903905	0.825585	0.387778	0.2629	0.432759	0.110831	-0.863651	-0.07313	-0.315721
ESTs, Weakly similar to T17295 hypothetical protein DKFZp434H132.1 - human [H.sapiens]	104389_at	-0.251227	0.758086	0.339889	0.933934	-0.020498	0.043643	-0.444716	-0.020175	0.174153	-0.458289
ELK3, member of ETS oncogene family	99984_at	0.779267	-0.132546	-0.188141	0.180854	0.623954	0.412964	0.353307	-0.076826	-0.212232	0.093639
HISTONE H3.4	101781_f_at	0.52321	0.1413	-0.032964	0.14978	0.157591	-0.360808	-0.279939	-0.171873	-0.080046	-0.149092
glycolipid transfer protein	104524_at	0.010205	0.219066	0.475721	0.206213	0.240978	0.053114	-0.768968	-0.444744	0.010768	0.025829
Sid23p	94492_at	0.146344	0.388181	-0.14477	0.576702	0.173727	-0.072536	0.308281	0.117429	0.01605	-0.134641
septin 7	98905_at	0.191239	0.147137	0.148477	0.160759	0.31259	-1.100873	-0.452255	-0.111928	-0.407735	-0.178497
circadian locomoter output cycles kaput	92257_at	0.353514	0.200585	0.234711	0.414462	0.112628	-0.478544	-0.026298	-0.251045	-0.32752	-0.440373
ESTs, Weakly similar to GDIS_MOUSE RHO GDP-DISSOCIATION INHIBITOR 2 [M.musculus]	96360_at	0.260872	-0.191819	0.956931	0.288236	0.108685	0.196814	-0.319709	0.525123	0.640271	-0.024544
DNA segment, Chr 7, ERATO Doi 373, expressed	103871_at	0.145851	0.217699	1.160499	0.01977	0.556005	0.143753	0.009878	-0.714593	-0.542644	-0.495459
ESTs, Weakly similar to similar to molybdoterin biosynthesis MOEB proteins [C.elegans]	102812_i_at	0.407035	-0.037385	0.070414	0.328954	0.358647	-0.261842	-0.240433	-0.107205	-0.024941	0.182706
S100 calcium-binding protein A13	100959_at	0.039256	0.249224	0.215407	0.42649	0.323131	0.180475	0.085276	0.47065	0.393786	-0.209396
cell adhesion kinase	100155_at	0.360774	0.218471	0.117571	0.362596	0.034911	0.512635	0.0692	0.204834	0.704196	-0.274603
RNA binding motif protein 3	96041_at	-0.062869	0.252408	0.42444	0.843576	-0.143844	-0.474817	0.314873	0.184955	0.134041	0.050491
ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 BETA SUBUNIT [Homo sapiens; Canis familiaris]	93548_at	-0.129194	-0.001387	0.902036	0.39961	0.182996	-0.485958	-0.062553	-0.127789	-0.380136	-0.160648
procollagen, type VI, alpha 1	95493_at	0.125848	-0.219055	0.600584	1.077328	0.565205	0.402758	-0.310874	0.095112	0.393766	-0.122525

U14 snRNA (intron 5 of hsc70 gene)	96564_at	0.459633	0.350137	0.115146	-0.090563	0.073888	0.033552	-0.028384	0.209109	0.547551	0.093295
guanine nucleotide binding protein, beta 1	94853_at	0.06981	0.369193	0.118159	0.247728	0.176124	0.259187	-0.130085	0.423082	0.791081	0.314393
ESTs, Moderately similar to unknown [R.norvegicus]	94019_at	0.684498	0.186586	-0.038098	0.410801	-0.008171	-0.43952	-0.171562	0.258962	0.329328	-0.102327
midline 2	103967_at	0.187138	0.403553	0.505843	0.329594	0.218205	-0.257981	0.266737	-0.177902	-0.069753	0.019594
expressed sequence tag mouse EST 25	93491_f_at	0.331891	0.680818	-0.580346	0.288323	0.191475	0.125107	-0.435754	0.4293	0.393231	0.403715
TBX1 protein	93753_at	-0.256249	0.707172	0.345696	1.069774	0.205434	0.447433	0.029739	-0.123662	0.133313	-0.136955
DNA segment, Chr 16, Wayne State University 109, expressed	95431_at	0.220089	0.235687	0.063155	0.06268	0.158845	-0.469829	0.030684	0.04684	0.096225	0.021006
Zinc transporter 4	95571_at	-0.494355	0.031012	0.461391	0.952802	0.442237	-0.021603	0.317826	-0.406438	-0.556624	-0.276584
rho, GDP dissociation inhibitor (GDI) beta	94258_at	0.002185	0.219103	0.716841	0.283132	0.189104	0.164912	-0.283585	0.129854	-0.029879	0.15122
ESTs	97154_f_at	-0.298922	1.200819	0.181974	-0.019538	0.99347	-1.418091	-1.115308	-0.892258	-0.077253	0.309531
vascular cell adhesion molecule 1	92560_g_at	0.081928	0.242326	0.141662	0.057724	0.641563	-0.1792	-0.08735	0.002114	0.089463	0.211224
Fc receptor, IgG, high affinity I	102879_s_at	0.152756	-0.179843	1.540611	0.719804	0.024366	-0.15206	-0.404936	0.174552	-0.260333	-0.052734
ribosomal protein, mitochondrial, L26	100040_at	0.345261	0.299332	0.237553	0.10537	-0.046582	0.336206	-0.242892	0.162961	0.60941	0.714796
ESTs	97918_at	-0.151958	0.941172	-0.128457	0.696613	0.17517	-0.613005	-0.3382	0.045888	0.232014	0.142103
ESTs, Moderately similar to RIBOSOMAL PROTEIN S6 KINASE [Homo sapiens]	104503_at	0.03791	0.264827	-0.074255	0.631744	0.153071	0.310628	0.365941	-0.064551	-0.504588	-0.212041
ESTs, Highly similar to GLYCYL-TRNA SYNTHETASE [Homo sapiens]	93270_at	0.345054	0.196383	0.129929	0.16138	0.183471	0.237419	0.029848	0.094668	0.277976	-0.023039
hypothetical protein MNCb-0091	93011_at	0.241989	0.499591	-0.300838	0.161578	0.422515	-0.291492	-0.015153	-0.382083	-0.279107	-0.12926
RAS-like, family 2, locus 9	102821_s_at	0.220975	0.085424	0.742921	-0.000664	0.082021	-0.054821	0.036432	-0.285181	-0.363505	-0.220853
ESTs, Highly similar to PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG [Anopheles gambiae]	95531_at	0.198162	-0.08951	0.334374	0.693997	0.24618	0.091686	-0.086881	-0.355431	-0.020525	-0.25423
ESTs	100929_at	0.508443	0.223885	0.044627	0.421221	0.305528	0.054196	-0.59263	-0.111364	-0.127156	0.006218
ras-GTPase-activating protein (GAP<120>) SH3-domain-binding protein 2	94913_at	-0.104265	0.309054	0.483172	0.261185	0.027788	0.183242	0.081881	0.258894	-0.033508	0.265825
procollagen, type IV, alpha 5	93220_at	-0.301096	-0.20554	0.709858	0.702399	0.457242	0.001427	-0.351786	-0.296138	-0.042247	0.126606
Mus musculus 15 kDa selenoprotein (Sep15) mRNA, complete cds	96249_at	0.059278	0.147992	0.29416	0.230076	0.492441	-0.294422	0.112623	-0.151832	-0.160968	0.268319
spindlin	99528_at	0.603495	0.102738	0.178168	-0.031718	0.128578	0.111552	-0.002206	0.014511	0.285896	0.164665
3-monooxgenase/tryptophan 5-monooxgenase activation protein, gamma polypeptide	95716_at	0.258478	0.352436	-0.529526	0.351681	0.274372	0.557054	-0.12004	0.490043	0.40665	0.154209
cytochrome P450, 1a1, aromatic compound inducible	94715_at	0.19183	0.27011	0.340191	0.897415	0.226077	1.090177	-0.099936	-0.337748	-0.769824	-0.609203
tubulin alpha 7	93924_f_at	0.132951	0.471513	0.740143	0.072511	-0.18001	0.616488	-0.537446	0.759258	1.042636	0.07834
Rho-associated coiled-coil forming kinase 2	98504_at	-0.062505	0.453922	-0.049168	0.011982	0.459459	-0.817466	0.053611	-0.158004	-0.137546	-0.095822
tissue-type vomeronasal neurons putative pheromone receptor V2R1	99700_at	0.467029	0.169498	1.739223	-0.114982	0.035552	0.05196	-0.369867	0.593447	0.32612	0.774484
vascular cell adhesion molecule 1	92558_at	0.02656	0.084043	0.927945	0.237767	0.491703	-0.528694	-0.329385	0.233637	-0.155785	-0.120323
laminin, beta 3	92759_at	-0.844308	-0.794703	-1.026064	-0.578658	-0.481212	0.022684	0.255877	-0.482693	-0.501039	-0.076028
DNA segment, Chr 5, ERATO Doi 708, expressed	103884_at	-1.357964	-0.952733	-1.275922	-1.010515	-0.216471	-0.698939	-0.152647	-0.300556	-0.627729	-0.12543
ESTs, Highly similar to THERMOSENSITIVE GLUCONOKINASE [Escherichia coli]	97324_at	-1.106413	-0.421507	-1.071131	-0.412783	-0.349297	0.681824	0.788031	-0.082297	-0.192511	-0.538781
ESTs, Moderately similar to A54691 octamer-binding protein NonO - mouse [M.musculus]	103393_at	-1.623901	-0.680204	-0.824596	-0.425244	-0.158924	-0.797304	-0.183127	-0.587904	-0.229342	-0.143938
potassium inwardly-rectifying channel, subfamily J, member 5	99376_at	-1.240959	-1.463194	-0.292121	-1.791845	-2.232536	-1.229386	0.194214	-0.81419	-0.417087	0.373532
ganglioside-induced differentiation-associated-protein 10	94192_at	-0.787022	-0.42991	-1.299454	-0.344691	-0.224624	-0.763387	-0.219311	0.044004	-0.305902	-0.232241
signal transducer and activator of transcription 5B	92199_at	-1.727969	-0.725572	-0.929119	-0.40237	-0.21173	0.160919	0.196895	-0.163266	0.018714	0.282214
granzyme G	102876_at	-0.596218	-0.97455	-0.025746	-0.675015	-0.353072	-0.063108	-0.306859	-0.231761	-0.346015	-0.070214
nuclear autoantigenic sperm protein (histone-binding)	101108_at	-1.822046	-1.776622	-0.429601	-1.24283	-1.288735	0.328881	0.583568	-0.290754	-0.213641	-0.524102
fibronectin 1	101531_at	-0.871542	-0.248158	-0.521541	-1.243383	-0.398914	-0.034603	-0.142117	-0.031632	0.31457	0.7409
protein that interacts with C kinase 1	97684_at	-1.226564	-0.089037	0.093047	-1.10677	-1.066712	-0.464224	0.117138	-0.509801	-0.149316	-0.040062
phospholipase A2, group V	94665_at	-0.285186	-0.368608	-0.396478	-1.042287	-0.615423	-0.505013	-0.165564	-0.322406	-0.250052	0.103042
ESTs	94113_at	-0.531969	-2.165399	-1.254444	-0.633815	0.007211	-0.208064	-0.174394	0.664247	0.378687	-0.441688
CBFA2T3 identified gene homolog (human)	102397_at	-0.254152	-0.739559	-0.56024	-0.503923	-0.321096	0.331183	0.306177	-0.011025	-0.028244	-0.429756
ESTs	97265_at	-0.192132	-0.278882	-1.113801	-0.59564	-0.142592	-0.104381	-0.15959	-0.094143	-0.208592	-0.063948
ESTs, Highly similar to EFB3_MOUSE EPHRIN-B3 PRECURSOR [M.musculus]	103692_at	0.125706	-0.189346	-0.875706	-1.05787	-0.966944	0.095866	0.377567	-0.057011	0.117171	0.073794
growth arrest and DNA-damage-inducible, alpha	102292_at	-0.242245	-0.08768	-1.535559	-0.228088	-0.509692	-1.002098	-0.466973	-0.041719	-0.106981	0.099249
integral membrane protein 2 B	104033_at	-0.495946	-0.057692	-1.415459	-0.354648	-0.490695	-0.608994	0.101463	0.005787	-0.016839	-0.027747
ubiquitin specific protease 23	95027_at	-0.055194	-0.689881	-0.940688	-0.401336	-0.138965	0.049472	-0.181719	-0.336596	0.249489	-0.349926
sulfotransferase family 1A, phenol-preferring, member 1	103087_at	-0.560103	-0.018753	-1.175987	-0.500074	-0.419548	-0.127477	-0.031863	-0.599213	-0.122385	-0.511731
eukaryotic translation elongation factor 1 alpha 1	93838_at	-0.49202	-0.780439	-0.28625	-0.557982	-0.117923	0.360701	0.270323	0.173526	-0.081113	0.030073
ESTs	92281_at	-0.906549	-0.175941	-0.452081	-0.29221	-0.575075	-0.188726	0.301664	-0.203029	-0.294926	0.065709
superoxide dismutase 1, soluble	100538_at	-0.667375	-0.248969	-0.573058	-0.137719	-0.32685	-0.260498	-1.134345	-0.563822	-0.42793	0.092432
CCCTC-binding factor	100148_at	-1.131281	-1.201982	-1.885453	0.238894	0.033929	-0.469697	-0.061041	0.061538	0.062653	-0.294539
myeloid leukemia factor 1	102061_at	0.072441	0.066475	-1.473741	-0.639887	-0.826099	-0.528515	-0.337399	1.497503	0.906074	0.446169
ESTs	96572_at	-0.531423	-0.408329	-0.517428	-0.477941	-1.298774	0.239651	0.584327	0.553991	0.054012	-0.12229
phospholipase A2, group V	101328_at	-1.968817	0.204163	0.14254	-0.861847	-0.907252	-0.043467	0.210394	-0.256964	-0.109673	0.287662
Nsp-like 1 protein (Nspl1) gene; tRNA-Sec gene, complete sequence; and FosB protein (Fosb) gene	104607_at	-0.042628	-0.097752	-0.940553	-0.573274	-0.619393	-0.007426	-0.069467	0.065315	0.302033	0.085254
heat-responsive protein 12	96048_at	0.349449	-0.059178	-0.784083	-1.249499	-0.884772	-0.923397	-0.897898	-0.200573	-0.11237	0.461886
ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE 9 KD SUBUNIT PRECURSOR [Bos taurus]	97874_at	-0.073632	-0.024833	-1.252833	-0.812443	-0.374397	0.228398	-0.009569	0.204639	0.325966	0.17065
dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase)	98527_at	-0.007289	-0.152035	-0.91242	-0.832103	-0.59156	-0.440135	0.127215	-0.284785	-0.411783	-0.36862
CD1d1 antigen	103422_at	-1.106616	-0.117224	-1.093292	0.154604	-0.533767	-0.486587	0.220642	0.248508	-0.367092	-0.34452
farnesyl diphosphate farnesyl transferase 1	97518_at	-0.064616	-0.259777	-0.406621	-0.348414	-0.457751	0.222088	0.446269	-0.172478	-0.116399	-0.542774
matrix metalloproteinase 11	100016_at	-1.058549	-0.389963	-0.847003	-0.300183	-0.205376	0.122002	-0.334566	-0.167077	0.306972	0.387771
Rhesus blood group-like	103340_at	-0.323108	-0.09188	-0.767476	-0.560572	-0.283867	-0.445897	-0.126391	-0.262144	-0.213557	0.146452
copper chaperone for superoxide dismutase	103909_at	0.147038	-0.223338	-0.460695	-1.204849	-0.865884	-0.294081	0.015224	-0.140586	-0.432401	0.089907
3-hydroxy-3-methylglutaryl-coenzyme A lyase	94324_f_at	-0.241511	-0.265637	-0.608921	-0.203941	-0.265444	0.376066	0.747175	-1.515371	-1.199788	-0.562648
ESTs, Highly similar to sodium-dependent multi-vitamin transporter [R.norvegicus]	104200_at	-0.540346	-0.739755	-0.457067	-0.413387	0.030244	0.007489	0.00533	0.35365	-0.095984	0.284736
ESTs	97260_at	-0.226026	-0.546319	-1.13397	-0.401332	0.098959	0.13845	0.393249	-0.143875	-0.191072	0.114199
ESTs, Weakly similar to CG13922 gene product [D.melanogaster]	104567_at	-1.004751	-0.380613	0.224955	-0.647247	-0.342203	-0.086057	0.292828	-0.059826	-0.326499	0.04193
ESTs	102922_at	-0.144563	-0.180477	-1.077644	-0.314259	-0.267669	-0.218101	-0.119955	-0.348268	-0.090743	-0.192944
Preproenkephalin 2	94516_f_at	0.357869	-0.054472	-1.011143	-0.914419	-0.687331	0.006177	0.257201	-0.67848	-0.875464	-0.8026
ESTs, Weakly similar to PROBABLE PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE FAB1 [Saccharomyces cer	92182_at	0.117626	-0.412833	-0.882706	-0.493829	-0.30298	-0.314145	-0.038124	-0.016654	-0.026688	-0.266875

tryptophanyl-tRNA synthetase	98605_at	-0.103854	-0.15818	-0.186105	-0.697497	-0.47075	0.093146	-0.057893	-0.390705	-0.373919	0.083324
ESTs, Highly similar to 40S RIBOSOMAL PROTEIN S25 [Homo sapiens; Rattus norvegicus]	96071_at	-0.84412	-0.642656	-0.165794	-0.424748	-0.068517	0.393369	0.473426	0.174113	0.493048	0.206633
phosphorylase kinase gamma	97094_at	0.581717	-0.229367	-1.268537	-0.658835	-0.983549	-0.383857	-0.41173	-0.132434	-0.161951	-0.025189
proteasome (prosome, macropain) subunit, alpha type 6	97247_at	1.099659	-0.828065	-0.974218	-1.663632	-0.543758	-0.865909	0.331126	-0.967558	-0.775293	0.254524
ESTs	92958_at	-0.33707	0.012631	-1.004507	-0.288844	-0.15369	-0.419059	-0.51	-0.239895	-0.59663	-0.501147
RAB9, member RAS oncogene family	95516_at	-0.103664	-0.134246	-0.534003	-0.431326	-0.318162	-0.662898	0.044825	-0.337076	-0.571363	-0.270508
mutS homolog 2 (E. coli)	100033_at	-0.920116	-0.708121	-0.377905	-0.866202	0.321973	-0.063042	0.197453	-0.364886	-0.294234	-0.004591
zinc finger protein X-linked	101919_at	-0.227108	-0.242614	-1.122049	-0.219542	-0.522554	-0.124848	0.302266	0.103087	-0.162104	-0.066606
ESTs, Moderately similar to dolichol-phosphate-mannose synthase [H.sapiens]	101084_f_at	-0.056399	-0.773576	-0.357492	-0.552745	-0.13331	0.172785	0.179829	0.182428	-0.040851	-0.353171
DNA segment, Chr 15, ERATO Doi 221, expressed	100948_at	0.048373	-0.110981	-0.823099	-0.522067	-0.275813	0.051276	0.157203	0.490941	0.254523	0.207042
ESTs	103697_at	-0.547121	-0.037998	-0.505175	-0.345998	-0.551837	0.4845	0.744884	0.124461	0.434705	0.278899
ESTs	95517_i_at	0.225008	-0.203384	-0.891375	-0.626268	-0.430066	0.106364	0.202749	-0.360231	-0.400359	-0.180415
origin recognition complex, subunit 5 homolog (S. cerevisiae)	100894_at	-0.302927	-0.590834	0.278634	-0.346118	-0.316668	-0.361609	-0.177221	0.381346	-0.166124	0.001463
ESTs, Highly similar to 2118318A promyelocyte leukemia Zn finger protein [M.musculus]	92202_g_at	-0.505942	0.185528	-1.196727	-0.260844	-0.725279	-0.104591	-0.320897	0.182144	0.215408	-0.579442
aquaporin 1	93330_at	-0.143584	0.163867	-1.328985	-1.008356	-0.241992	-0.117193	0.371719	0.189344	0.048427	0.015046
FK506 binding protein 4 (59 kDa)	92808_f_at	0.202558	0.221267	-1.203009	-0.856501	-0.650225	0.078149	0.037438	0.202838	0.267112	-0.066041
RNA polymerase 1-4 (194 kDa subunit)	93620_at	-0.247194	-0.716056	-0.115034	-0.561253	-0.195857	-0.10008	-0.18297	-0.304067	-0.072176	-0.120695
Zinc finger protein 35	98032_at	-0.744743	0.158886	-0.197567	-0.591606	-0.665807	0.257751	0.315364	0.467155	0.116353	0.697809
ESTs, Weakly similar to unknown [S.cerevisiae]	96122_at	0.085884	0.158636	-1.152241	-1.205262	-0.575317	-0.339072	0.154952	0.452976	0.195967	0.173135
peroxisomal membrane protein 2, 22 kDa	104098_at	-0.060581	-0.118424	-0.699239	-0.726005	-0.349553	-0.029052	0.332567	0.132069	0.043588	0.067945
vesicle-associated membrane protein 2	98926_at	-0.377819	-0.158984	-0.662848	-0.26504	-0.449824	0.212929	-0.444098	-0.053884	0.163767	0.270121
peroxisome proliferator activated receptor alpha	102668_at	0.137021	-0.357493	-0.913808	-0.563959	-0.104907	-0.184894	0.310348	0.487798	0.313879	0.01316
RNA polymerase I associated factor, 53 kD	96096_f_at	-0.012492	0.098965	-0.885724	-0.738081	-0.643336	-0.804199	0.288435	-0.036151	-0.41603	-0.638194
DNA segment, Chr 4, Wayne State University 53, expressed	92542_at	-0.287824	-0.181775	-0.753565	-0.257202	-0.284946	-0.283743	0.312456	-0.291735	-0.518374	-0.108672

Table 2: Genes With Differential Expression Profiles

Table 2 contains the set of 314 genes identified to be significantly differentially expressed between the exercise and banding hypertrophy models in the Significance Analaysis of Microarrays (SAM) analysis of the Log2-transformed signal ratios (SLR) computed for the transcripts in the exercise and banding hypertrophy models identified in Table 1. The table is organized such that the name of each gene is associated with its corresponding Affymetrix probe identification number and its for each measurement interval in both hypertrophy models.

Gene Name	Affymetrix Probe ID	Banding HW/BW (mg/g)					Exercise HW/BW (mg/g)				
		4.4	4.6	5.1	5.5	5.6	4.4	4.6	5.1	5.5	5.6
Angiotensinogen	101887_at	0.120064	0.244256	-0.38109	0.125446	0.661892	2.437013	4.763328	5.193975	5.259772	4.670396
aminolevulinic acid synthase 2, erythroid	92768_s_at	-0.114533	-0.127398	-0.841593	-0.63878	-0.477823	1.086838	0.394718	1.488336	2.192093	0.863324
ESTs	104477_at	-0.518849	0.123603	-1.179513	-0.843824	-0.184904	0.629928	0.738434	1.192906	1.764174	0.295539
hemoglobin, beta adult minor chain	103534_at	-0.483358	0.128236	-0.560019	-0.602821	-0.343598	0.637128	0.24838	1.079649	1.362802	0.655472
small proline-rich protein 1B	100446_r_at	-0.167534	-0.251298	-0.339813	-0.140874	-0.124924	0.798436	0.150935	0.921183	1.096446	0.750815
nuclear autoantigenic sperm protein (histone-binding)	101108_at	-1.822046	-1.776622	-0.429601	-1.24283	-1.288735	0.328881	0.583568	-0.290754	-0.213641	-0.524102
rod outer segment membrane protein 1	93453_at	0.74255	-0.396273	-1.53741	0.312552	0.144343	0.325863	1.359997	1.911574	1.920967	1.717913
adipocyte complement related protein of 30 kDa	99104_at	0.647922	-0.666915	-0.482971	-1.264254	-0.695212	0.220795	0.302804	0.981871	1.064706	1.227426
aminolevulinic acid synthase 1	93500_at	0.014282	-0.017693	-0.409172	-0.322348	-0.140137	0.483826	0.330428	0.793311	0.791057	0.596449
ESTs	103697_at	-0.547121	-0.037998	-0.505175	-0.345998	-0.551837	0.4845	0.744884	0.124461	0.434705	0.278899
ESTs	96572_at	-0.531423	-0.408329	-0.517428	-0.477941	-1.298774	0.239651	0.584327	0.553991	0.054012	-0.12229
synuclein, alpha	93273_at	-0.465075	1.434054	-0.752238	-0.619051	-0.591144	0.461032	0.720032	1.259002	2.048864	1.572019
receptor (calcitonin) activity modifying protein 1	104680_at	-0.437845	-0.19105	0.235436	-0.183027	-0.236408	0.345924	0.386545	1.131491	0.777503	0.751673
ESTs, Highly similar to cytosolic acyl coenzyme A thioester hydrolase [R.norvegicus]	100539_at	-0.044096	0.219342	-0.89662	-0.465755	-0.047246	0.451542	0.395504	1.156508	1.450592	0.484081
ESTs, Highly similar to 40S RIBOSOMAL PROTEIN S25 [Homo sapiens; Rattus norvegicus]	96071_at	-0.84412	-0.642656	-0.165794	-0.424748	-0.068517	0.393369	0.473426	0.174113	0.493048	0.206633
ESTs, Moderately similar to CYANELLE 30S RIBOSOMAL PROTEIN S11 [Cyanophora paradoxa]	97884_at	-0.002225	-0.336638	-0.002581	-0.208957	-0.272214	0.468748	0.448208	0.565457	0.847498	0.255869
ESTs, Moderately similar to BILIVERDIN REDUCTASE A PRECURSOR [Rattus norvegicus]	104124_at	-0.716295	-0.607093	0.458849	-0.126674	-0.444165	0.383058	0.463505	0.795372	0.584603	0.49796
carbonic anhydrase 14	98079_at	-0.208865	0.008501	-0.467358	-0.577925	-1.028422	-0.120495	0.372542	0.64226	0.560116	0.470824
aquaporin 4	102704_at	0.291792	-0.036725	-0.11355	-1.312854	-0.966292	-0.129683	0.985159	1.316672	0.956207	0.321578
ESTs, Moderately similar to phosphoenolpyruvate carboxykinase [M.musculus]	95449_at	-0.158466	-0.474798	-0.00507	-0.388482	-0.284292	0.506302	0.511325	0.372398	0.335651	0.140116
signal transducer and activator of transcription 5B	92199_at	-1.727969	-0.725572	-0.929119	-0.40237	-0.21173	0.160919	0.196895	-0.163266	0.018714	0.282214
alkaline phosphatase 2, liver	92796_at	0.270208	-0.080681	-0.088502	-0.261378	0.174737	0.544234	0.341738	0.824991	0.949607	0.770377
hemoglobin alpha, pseudogene 3	101703_at	-0.476836	-0.039781	0.162977	-0.337403	0.291865	0.501029	0.285358	0.697138	1.180277	0.870824
Zinc finger protein 35	98032_at	-0.744743	0.158886	-0.197567	-0.591606	-0.665807	0.257751	0.315364	0.467155	0.116353	0.697809
ESTs	96924_at	-0.423435	0.192538	-0.581944	-0.141593	-0.130407	0.365515	0.075448	0.874939	0.839028	0.555873
rat generating islet-derived, mouse homolog 3 alpha	103954_at	0.260148	-1.123932	0.370256	0.06876	0.415668	1.64631	1.035998	0.921129	0.434267	0.820876
nuclear receptor subfamily 1, group I, member 3	102171_r_at	-0.280339	-0.363109	0.053669	-0.157751	-0.206993	0.582702	0.167945	0.249016	0.477566	0.505764
ESTs, Moderately similar to G3P_MOUSE GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE [M.musculus]	97751_f_at	-0.07676	0.015786	-0.596267	-0.053294	0.150866	0.522401	0.196499	0.680541	1.028169	0.59471
fibronectin 1	101531_at	-0.871542	-0.248158	-0.521541	-1.243383	-0.398914	-0.034603	-0.142117	-0.031632	0.31457	0.7409
ESTs, Highly similar to RSP-1 PROTEIN [Mus musculus]	104523_at	-1.248149	0.244854	-0.044169	-0.74848	-0.732823	0.113595	0.511343	0.31018	0.398097	0.461783
2,3-bisphosphoglycerate mutase	94815_at	0.316791	0.5688	-1.133031	-0.17446	-0.013107	0.670335	0.397163	0.848301	1.620777	0.840095
zinc finger protein 30	104437_at	0.238573	-0.26815	-0.223786	-0.125241	-0.352604	-0.053541	0.418067	0.945405	0.729516	1.108443
polymeric immunoglobulin receptor	99926_at	-0.366794	-0.211988	0.383322	-0.004187	-0.188495	0.58776	0.325607	0.697186	0.57763	0.55644
calmodulin 3	92631_f_at	0.231029	0.020312	-0.05858	-0.25244	-0.022185	0.636053	0.494501	0.784486	0.764194	0.255523
carbon catabolite repression 4 homolog (S. cerevisiae)	99535_at	-0.078362	0.366227	0.156727	-0.390537	-0.527448	0.264118	0.574426	0.748691	0.928506	0.556767
prohibitin	94855_at	-0.019928	0.089314	-0.049368	-0.396291	-0.347387	0.456094	0.3888	0.647932	0.78181	0.117076

RAN guanine nucleotide release factor	100562_at	-0.1071	0.186825	-0.273477	-0.643526	-0.087407	0.014583	0.705374	0.708939	0.514264	0.67407
ESTs	95374_f_at	-0.458697	-0.038745	-0.033292	0.368918	0.096177	0.581045	0.650628	0.558107	0.64104	0.498318
cytochrome c oxidase, subunit VIIa 1	102749_at	-0.047552	0.125932	-0.743128	-0.470424	-0.422606	0.342437	0.194172	0.223033	0.514069	0.39412
deoxyguanosine kinase	99544_at	-0.276101	-0.143413	-0.669041	-0.600292	0.191863	0.195655	0.072044	0.752219	0.598633	0.323105
eukaryotic translation elongation factor 1 alpha 1	93838_at	-0.49202	-0.780439	-0.28625	-0.557982	-0.117923	0.360701	0.270323	0.173526	-0.081113	0.030073
melanocortin 5 receptor	99896_at	-0.324242	-0.907935	0.746899	-0.237524	-0.069612	0.443162	0.44412	0.900949	0.447932	1.004471
potassium inwardly-rectifying channel, subfamily J, member 5	99376_at	-1.240959	-1.463194	-0.292121	-1.791845	-2.232536	-1.229386	0.194214	-0.81419	-0.417087	0.373532
ESTs	96546_r_at	-0.12335	-0.25648	0.112743	0.107868	0.02647	0.550246	0.392602	0.503544	0.577413	0.318402
ESTs, Highly similar to HYPOTHETICAL 27.6 KD PROTEIN IN PDX1-SNG1 INTERGENIC REGION [Saccharomyces c	97517_at	-0.449975	-0.86399	0.607654	-0.610314	-0.073578	0.665694	0.330415	0.548409	0.49991	0.338142
ESTs, Weakly similar to similar to tyrosyl-tRNA synthetase. [C.elegans]	101023_f_at	-0.31019	0.311545	-0.457779	-0.055173	-0.235905	0.554257	0.345661	0.491331	0.626045	0.23153
ESTs, Weakly similar to AF113615_1 FH1/FH2 domain-containing protein FHOS [H.sapiens]	104255_at	0.128762	0.098414	-0.554763	-0.394578	-0.414032	0.309013	0.164201	0.320533	0.582246	0.596191
ESTs	94113_at	-0.531969	-2.165399	-1.254444	-0.633815	0.007211	-0.208064	-0.174394	0.664247	0.378687	-0.441688
apolipoprotein B editing complex 2	97235_f_at	0.05718	0.440243	-0.859672	-0.277626	-0.266348	0.935586	0.285711	0.544344	0.569452	0.36306
ATPase, H? transporting, alpha polypeptide	94163_at	-0.484206	-0.571884	0.59184	-0.201233	-0.077226	0.938217	0.321928	0.601585	0.210968	0.725008
CD8beta opposite strand	101903_at	1.012713	0.123791	-1.519877	-0.431301	0.103749	0.117542	0.498584	1.877824	1.430526	0.81922
ESTs, Highly similar to THERMOSENSITIVE GLUCONOKINASE [Escherichia coli]	97324_at	-1.106413	-0.421507	-1.071131	-0.412783	-0.349297	0.681824	0.788031	-0.082297	-0.192511	-0.538781
cDNA sequence AF180471	98892_at	0.317662	0.003131	-0.694863	-0.394658	-0.237085	0.139913	0.170679	0.472201	0.828345	0.837097
solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	100618_f_at	-0.21292	-0.144876	0.034182	0.035123	0.148333	0.278908	0.161891	0.919688	0.744185	0.664199
ESTs, Weakly similar to BRAIN SPECIFIC POLYPEPTIDE PEP-19 [Rattus norvegicus; Mus musculus]	97297_at	0.312493	-0.158118	-0.572514	-0.440724	-0.082069	0.563057	0.331991	0.527407	0.404912	0.230898
DNA segment, Chr 14, University of California at Los Angeles 1	102356_at	-0.149765	-0.05661	-0.215418	-0.108664	0.02756	0.333144	0.120775	0.742628	0.770069	0.274661
protease (prosome, macropain) 28 subunit, alpha	101510_at	0.059649	0.086163	-0.36651	-0.602293	-0.647524	0.368137	0.363386	0.266359	0.380352	0.146723
ESTs, Highly similar to EFB3_MOUSE EPHRIN-B3 PRECURSOR [M.musculus]	103692_at	0.125706	-0.189346	-0.875706	-1.05787	-0.966944	0.095866	0.377567	-0.057011	0.117171	0.073794
tubulin alpha 4	92635_at	-0.08508	-0.011793	0.052911	-0.692051	-0.427382	0.197304	0.043217	0.808731	0.919489	0.207449
ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE 9 KD SUBUNIT PRECURSOR [Bos taurus]	97874_at	-0.073632	-0.024833	-1.252833	-0.812443	-0.374397	0.228398	-0.009569	0.204639	0.325966	0.17065
proteasome (prosome, macropain) subunit, beta type 5	101558_s_at	0.123749	0.082462	-0.114974	-0.106944	-0.12194	0.349507	0.445931	0.614592	0.983355	0.214369
ESTs	95707_at	-0.020517	0.088117	-0.546453	-0.39278	-0.320594	0.122097	0.203476	0.839593	0.764645	0.058394
adrenergic receptor, beta 2	93193_at	-1.064519	-0.216789	0.47569	-0.128186	0.293896	0.507309	0.377819	0.698666	0.490612	1.101583
hexokinase 2	94375_at	0.181305	0.122136	-0.583401	-0.480609	-0.28466	0.059766	0.099517	0.727122	0.698373	0.64174
ESTs, Highly similar to T17338 hypothetical protein DKFZp434O125.1 - human [H.sapiens]	96732_at	0.093802	0.782961	-0.205488	0.5513	-0.239396	0.574507	1.033997	0.905436	0.919203	0.812219
ESTs	95905_at	-0.53532	0.38738	-0.504969	0.501309	-0.552174	0.514265	0.591902	0.483466	0.615413	0.449929
ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE PDSW SUBUNIT [Bos taurus]	101525_at	0.074498	0.035168	-0.676922	-0.474797	-0.033193	0.241689	0.206448	0.552353	0.616765	0.261448
DNA segment, Chr X, Wayne State University 72, expressed	104201_at	-0.386538	0.024411	0.578914	-0.408948	-0.049137	0.222261	-0.023436	0.932851	1.252454	1.187707
ESTs, Highly similar to unnamed protein product [H.sapiens]	97356_at	-0.108277	-0.134283	-0.218044	-0.14217	-0.2852	0.174493	-0.012705	0.963433	0.592739	0.244695
ESTs	94430_at	-0.661094	-0.071407	0.176267	-0.271017	0.004963	0.844099	0.03964	0.50749	0.600303	0.184772
laminin, beta 3	92759_at	-0.844308	-0.794703	-1.026064	-0.578658	-0.481212	0.022684	0.255877	-0.482693	-0.501039	-0.076028
sialyltransferase 4C (beta-galactosidase alpha-2,3-sialytransferase)	95599_at	-0.240047	0.376114	0.226181	-0.621955	0.184963	0.367968	0.286034	1.177878	0.838189	0.597794
matrix metalloproteinase 11	100016_at	-1.058549	-0.389963	-0.847003	-0.300183	-0.205376	0.122002	-0.334566	-0.167077	0.306972	0.387771
myeloid leukemia factor 1	102061_at	0.072441	0.066475	-1.473741	-0.639887	-0.826099	-0.528515	-0.337399	1.497503	0.906074	0.446169
Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	101973_at	-0.019551	0.35638	-0.615176	-0.23536	-0.141203	0.132954	0.174509	0.627011	0.829206	0.677716
DNA segment, Chr 15, ERATO Doi 221, expressed	100948_at	0.048373	-0.110981	-0.823099	-0.522067	-0.275813	0.051276	0.157203	0.490941	0.254523	0.207042
ESTs, Highly similar to sarcosine dehydrogenase [R.norvegicus]	96763_at	-0.540883	-0.055556	-0.109343	-0.11433	0.202719	0.365624	0.069301	0.493612	0.567612	0.565875
outer dense fiber of sperm tails 1	101968_at	-0.648547	-0.216152	0.278893	-0.537827	0.267397	0.819865	0.288674	0.666074	0.051511	0.56863
glutathione S-transferase, mu 3	97681_f_at	0.113111	-0.134143	-0.522623	-0.314562	-0.088201	0.580283	0.278147	0.238143	0.32486	0.157848
ESTs	95937_at	-0.526229	-0.171026	0.168018	-0.137056	-0.063765	0.211423	0.251254	0.33609	0.449596	0.529642
ESTs, Highly similar to sodium-dependent multi-vitamin transporter [R.norvegicus]	104200_at	-0.540346	-0.739755	-0.457067	-0.413387	0.030244	0.007489	0.00533	0.35365	-0.095984	0.284736
ESTs, Moderately similar to AF126743_1 DNAJ domain-containing protein MCJ [H.sapiens]	97204_s_at	0.395396	0.178196	-0.43995	-0.475554	-0.290305	0.102313	0.24099	0.894108	0.87295	0.430125
ESTs, Moderately similar to ubiquitin/60S ribosomal fusion protein [M.musculus]	102841_at	0.177131	0.238495	0.232694	-0.00343	0.00465	0.632553	0.155686	0.685143	0.967928	0.715195
SH3-domain GRB2-like B1 (endophilin)	98945_at	0.030465	0.302247	-0.555207	-0.281028	-0.176472	0.171981	0.14765	0.860634	0.962841	0.269407
Stearoyl-coenzyme A desaturase 1	94057_g_at	0.303912	0.950794	-0.31627	1.041261	0.404316	0.409511	0.587308	1.619581	2.817202	1.689801
chromobox homolog 4 (Drosophila Pc class)	93697_at	0.360534	-0.005263	-0.028649	-0.30578	-0.182933	0.53399	0.301059	0.421546	0.751245	0.324248
adenylate kinase 3 alpha like	92492_at	-0.330142	0.049376	-0.821627	0.049423	0.094204	0.060317	0.227361	0.487739	0.739135	0.509605
DNA segment, Chr 16, ERATO Doi 36, expressed	103790_at	-0.233533	-0.447007	0.727108	-0.188015	0.180315	0.795472	0.512592	0.612853	0.830898	0.293319
histone H2a.2-615 (H2a-615), and histone H3.2-615 (H3-615) genes	93068_r_at	0.320665	-0.231647	-0.276499	-0.407592	0.101045	0.964413	0.320938	0.511717	0.57375	-0.014672
ESTs	103935_at	-0.223624	0.093666	-0.310826	-0.120414	0.035901	0.37098	0.025537	0.556259	0.506668	0.340899
peptidase 4	101042_f_at	-0.210646	0.117247	-0.408224	0.037927	-0.287277	0.211771	0.20856	0.56373	0.553607	0.120714
ESTs	104076_at	0.31351	0.221816	-0.689206	-0.513082	-0.442927	0.275976	0.400147	0.419036	0.710977	0.088078
myelin and lymphocyte protein; T-cell differentiation protein	99089_at	0.300032	-0.019883	0.054784	-0.117076	-0.641382	0.786547	0.40919	0.315729	0.249914	0.461207
interferon gamma inducing factor binding protein	92689_at	-0.76187	-0.257326	0.5288	-0.64457	-0.243401	0.107405	0.218551	0.378061	0.533959	0.418611
CBFA2T3 identified gene homolog (human)	102397_at	-0.254152	-0.739559	-0.56024	-0.503923	-0.321096	0.331183	0.306177	-0.011025	-0.028244	-0.429756
Stearoyl-coenzyme A desaturase 1	94056_at	0.55294	0.203639	-0.105981	-0.119576	0.170509	0.176501	0.281519	1.004728	1.949333	0.876711
Nsp-like 1 protein (Nspl1) gene; tRNA-Sec gene, complete sequence; and FosB protein (Fosb) gene	104607_at	-0.042628	-0.097752	-0.940553	-0.573274	-0.619393	-0.007426	-0.069467	0.065315	0.302033	0.085254
short stature homeobox 2	99042_s_at	-0.070764	0.050006	0.484228	-0.057103	0.068837	0.319309	0.234886	1.180783	0.600674	0.885051
suppressor of Ty 4 homolog (S. cerevisiae)	100587_f_at	0.227726	0.385978	-0.78568	-0.637303	-0.505942	0.428358	0.395765	0.264058	0.489686	0.142046
cytochrome c oxidase, subunit Vb	93119_at	0.145317	0.026424	-0.380616	-0.511927	-0.160763	0.16424	0.147824	0.505643	0.645275	0.154937
ESTs, Moderately similar to unnamed protein product [H.sapiens]	104767_f_at	0.207327	-0.140288	-0.118352	-0.022089	-0.401551	0.50768	0.35315	0.275846	0.41893	0.129299
myosin light chain, regulatory A	100403_at	0.98121	3.891829	-2.457717	0.584858	-2.102374	2.7936	1.633966	3.134263	3.631305	-0.636409
peroxisomal membrane protein 2, 22 kDa	104098_at	-0.060581	-0.118424	-0.699239	-0.726005	-0.349553	-0.029052	0.332567	0.132069	0.043588	0.067945
hemoglobin, beta adult major chain	101869_s_at	-0.228087	-0.290147	0.024163	-0.161093	0.139829	0.215491	-0.012456	0.602127	0.647139	0.363533
growth arrest specific 1	94813_at	-0.107812	-0.058521	-0.880582	0.156361	0.241797	0.526053	0.377371	0.673838	0.515702	0.048075
phosphoglycerate mutase muscle-specific subunit	92599_at	0.21076	-0.026581	-0.479796	-0.392076	-0.07431	0.107627	0.085324	0.579052	0.652336	0.289662
polynucleotide kinase 3'- phosphatase	97332_at	0.244662	0.096784	0.008889	-0.5695	-0.080076	0.515293	0.494525	0.252067	0.603579	0.246545
ESTs	104267_at	-0.208187	0.347125	0.145297	0.277737	-0.06196	0.304951	0.489228	0.867127	0.810709	0.37221
DNA segment, Chr 5, ERATO Doi 708, expressed	103884_at	-1.357964	-0.952733	-1.275922	-1.010515	-0.216471	-0.698939	-0.152647	-0.300556	-0.627729	-0.12543

peroxisome proliferator activated receptor alpha	102668_at	0.137021	-0.357493	-0.913808	-0.563959	-0.104907	-0.184894	0.310348	0.487798	0.313879	0.01316
ESTs, Weakly similar to unknown [S.cerevisiae]	96122_at	0.085884	0.158636	-1.152241	-1.205262	-0.575317	-0.339072	0.154952	0.452976	0.195967	0.173135
transgene insert site 737, insertional mutation, polycystic kidney disease	100404_at	-0.452418	-0.233127	0.389696	-0.053399	-0.074202	0.221964	0.209887	0.524925	0.380108	0.551934
major histocompatibility complex region	102343_at	0.718705	-0.301673	-0.021452	-0.275018	-0.137707	0.304013	0.41813	0.887077	0.791754	0.233413
ESTs, Highly similar to HYPOTHETICAL 13.6 KD PROTEIN IN NUP170-ILS1 INTERGENIC REGION [Saccharomyces	97447_at	0.18411	0.000451	-0.095156	-0.265408	-0.275184	0.246815	-0.226998	0.720479	0.889825	0.455494
putative TNF-resistance related protein	100717_at	-0.331223	-0.334007	0.647981	-0.198925	-0.146079	0.516533	0.360456	0.401853	0.405227	0.367421
Mus musculus DAZ-associated protein 1 (Dazap1) mRNA, complete cds	97372_at	-0.724978	-0.793283	0.650104	0.400943	-0.185995	0.172871	0.45214	0.694296	0.471686	0.603122
stearoyl-Coenzyme A desaturase 2	95758_at	-0.193501	-0.073342	0.448344	0.095219	0.288721	0.56702	0.375961	0.654558	0.74217	0.351873
eukaryotic translation initiation factor 1A	94745_f_at	-0.975185	0.321602	1.450434	0.214157	-0.274341	0.697612	0.115881	1.257798	1.176878	1.409663
interleukin 10 receptor, beta	99491_at	0.254044	0.283457	-0.981466	-0.380045	-0.285265	-0.00414	0.237568	0.565642	0.637048	0.305492
aquaporin 1	93330_at	-0.143584	0.163867	-1.328985	-1.008356	-0.241992	-0.117193	0.371719	0.189344	0.048427	0.015046
colony stimulating factor 1 (macrophage)	101450_at	0.253229	-0.266024	0.269777	-0.072709	-0.079614	0.727336	0.329277	0.130368	0.836214	0.313979
ESTs, Weakly similar to CG7979 gene product [D.melanogaster]	102423_at	0.38077	-0.255202	0.33688	-0.192932	0.421275	0.051581	-0.777399	2.597684	1.749457	1.993014
utrophin	92507_at	0.65342	-0.140988	-0.297915	-0.196032	-0.453173	0.103477	0.50098	0.237039	0.798373	0.515131
ESTs	104034_at	0.355576	-0.534956	0.03472	-0.101802	-0.268641	0.436455	0.12807	0.200994	0.453659	0.441107
Mus musculus clone BAC126c8 Rsp29-like protein (Rsp29)	95730_at	-0.068187	0.081403	-0.195974	-0.313257	0.263395	0.262665	0.362138	0.532562	0.701456	0.074153
ESTs, Moderately similar to AF121893_1 sequence-specific single-stranded-DNA-binding protein [R.norvegicus]	103504_at	0.198943	0.036829	0.015919	-0.033101	0.132953	0.222882	0.550234	0.774916	0.502932	0.255106
ESTs	100828_at	-0.196147	0.497839	0.641566	0.342429	-0.004691	1.224778	0.439224	1.202952	1.147402	0.066472
Myxovirus (influenza virus) resistance 2	102699_at	0.025491	-0.559342	0.082088	0.298275	0.071174	0.538807	0.198154	0.65975	0.425822	0.242219
ESTs, Moderately similar to BIOTIN CARBOXYLASE [Anabaena pcc7120]	95674_r_at	-0.010415	-0.066355	0.146305	0.267927	0.016207	0.643383	0.564907	0.251279	0.336198	0.366482
ESTs	104342_i_at	1.323621	0.047786	-0.854379	-0.320162	-0.447166	0.036025	0.75882	0.699708	1.143213	0.65893
zinc finger protein X-linked	101919_at	-0.227108	-0.242614	-1.122049	-0.219542	-0.522554	-0.124848	0.302266	0.103087	-0.162104	-0.066606
ESTs	98837_at	-0.788393	-0.380932	0.75415	0.342632	-0.183402	0.804461	1.11392	0.039778	0.24159	0.625558
ATP synthase, H transporting, mitochondrial F0 complex, subunit f, isoform 2	93114_at	0.174373	-0.237953	0.450015	-0.459083	-0.185505	0.776412	0.220945	0.446631	0.206845	0.391331
transducer of ErbB-2.1	99532_at	0.485808	0.371126	-0.675675	-0.366125	-0.076697	-0.004044	0.138391	0.901118	0.919523	0.648796
fractured callus expressed transcript 1	99123_s_at	0.280918	-0.016256	-0.157038	-0.143671	-0.044935	0.145271	0.220601	0.509286	0.498881	0.397796
vesicle-associated membrane protein 2	98926_at	-0.377819	-0.158984	-0.662848	-0.26504	-0.449824	0.212929	-0.444098	-0.053884	0.163767	0.270121
phospholipase A2, group V	101328_at	-1.968817	0.204163	0.14254	-0.861847	-0.907252	-0.043467	0.210394	-0.256964	-0.109673	0.287662
ESTs	97260_at	-0.226026	-0.546319	-1.13397	-0.401332	0.098959	0.13845	0.393249	-0.143875	-0.191072	0.114199
FK506 binding protein 4 (59 kDa)	92808_f_at	0.202558	0.221267	-1.203009	-0.856501	-0.650225	0.078149	0.037438	0.202838	0.267112	-0.066041
DNA segment, Chr 15, Wayne State University 97, expressed	97132_at	-0.187592	-0.215144	0.532223	0.107513	-0.199919	0.473838	0.469557	0.329419	0.378275	0.335855
nuclear receptor co-repressor 2	95129_at	0.324858	-0.243875	0.152691	0.186575	0.297545	0.950399	0.017789	0.510709	0.855454	0.499084
5-hydroxytryptamine (serotonin) receptor 5A	101152_at	-0.296176	0.397615	0.728033	-0.519789	0.141104	0.598241	0.539111	0.59168	0.465604	0.694754
olfactory receptor 71	97004_at	-0.244427	0.001639	0.528975	-0.345214	0.035122	0.59513	0.547981	0.319595	0.364598	0.227741
ESTs, Moderately similar to dolichol-phosphate-mannose synthase [H.sapiens]	101084_f_at	-0.056399	-0.773576	-0.357492	-0.552745	-0.13331	0.172785	0.179829	0.182428	-0.040851	-0.353171
ESTs	92281_at	-0.906549	-0.175941	-0.452081	-0.29221	-0.575075	-0.188726	0.301664	-0.203029	-0.294926	0.065709
CCCTC-binding factor	100148_at	-1.131281	-1.201982	-1.885453	0.238894	0.033929	-0.469697	-0.061041	0.061538	0.062653	-0.294539
ESTs	104160_at	0.331081	-0.241278	0.68841	-0.398872	0.337148	0.76977	0.60495	0.578143	0.638392	0.353424
ESTs	100965_at	-0.547697	-0.397736	0.705244	0.223137	0.038639	0.646412	0.355615	0.657053	0.24652	0.431248
DNA segment, Chr 7, Roswell Park 2 complex, expressed	96629_at	0.691051	0.161196	-0.080879	-0.129264	-0.086724	0.49728	0.46625	0.568915	0.632887	0.336654
ESTs, Highly similar to unnamed protein product [H.sapiens]	93992_at	0.248528	0.180062	-0.111824	0.002238	-0.071278	0.562261	0.208765	0.198564	0.758115	0.277558
glyceraldehyde-3-phosphate dehydrogenase	101214_f_at	0.144326	-0.031954	-0.360311	-0.115587	0.231729	0.289367	0.195231	0.34398	0.527781	0.247247
ryanodine receptor 3	101830_at	-0.295261	-0.2864	0.613657	-0.184294	0.1254	0.410192	0.211294	0.616997	0.156596	0.727579
ESTs, Highly similar to HYPOTHETICAL PROTEIN C22G7.01C IN CHROMOSOME I [Schizosaccharomyces pombe]	101591_at	-0.075718	0.146185	-0.094223	-0.11946	0.273555	0.162996	0.379892	0.266271	0.584177	0.453277
Mus musculus domesticus partial mRNA for oxystyrol-binding protein homologue 1 (Obph1 gene)	103311_at	0.236998	-0.088981	-0.09619	-0.10307	0.349837	0.278283	0.197913	0.619105	0.493614	0.439731
Mus musculus X chromosome: L1cam locus	96154_at	0.150049	-0.327523	0.142278	0.305172	0.150186	0.620426	0.244508	0.416094	0.53283	0.265528
ryanodine receptor 3	97126_at	0.795999	-0.330001	-0.086333	-0.820748	0.410402	0.188021	0.819069	0.642918	0.34231	0.626866
Mus musculus Bat-4 gene, complete cds	101416_f_at	0.258046	-0.10311	0.149362	-0.127094	0.007574	0.539158	0.54448	0.334963	0.353441	0.072058
seven in absentia 2	97906_at	-0.482676	0.063295	0.306616	-0.203303	0.160065	0.716618	0.548197	0.449125	0.402024	-0.163779
ESTs, Highly similar to MITOCHONDRIAL PROCESSING PROTEASE BETA SUBUNIT PRECURSOR [Rattus norvegic	94005_at	0.302348	0.437039	-0.847128	-0.044914	-0.275063	0.200517	0.275907	0.45917	0.521801	0.390115
pleiotropic regulator 1, PRL1 homolog (Arabidopsis)	101064_at	0.149941	0.178149	-0.147342	0.069592	-0.201411	0.197654	0.403912	0.579744	0.574162	0.026151
ESTs, Highly similar to Ror2 [M.musculus]	93724_at	-1.197939	-0.2409	1.13237	0.285272	-0.194356	0.378328	-0.295094	0.882049	1.050347	0.983729
ESTs	103927_at	0.206713	0.292622	0.043178	-0.074469	0.169783	0.435667	0.601538	0.357664	0.615645	0.207906
fatty acid synthase	98575_at	0.246513	0.653538	-0.008894	0.211301	-0.318951	0.612507	-0.181308	0.729606	1.382319	0.647077
proteasome (prosome, macropain) subunit, beta type 5, pseudogene	101741_at	-0.144253	-0.306213	0.419597	-0.0454	0.154782	0.236313	0.119584	0.546864	0.6687	0.286893
integral membrane protein 2 B	104033_at	-0.495946	-0.057692	-1.415459	-0.354648	-0.490695	-0.608994	0.101463	0.005787	-0.016839	-0.027747
ESTs, Moderately similar to Y110_HUMAN HYPOTHETICAL PROTEIN KIAA0110 [H.sapiens]	95565_at	0.267385	0.130226	-0.177323	-0.100433	0.059314	0.3752	0.458568	0.478442	0.293194	0.102019
glucose phosphate isomerase 1 complex	100574_f_at	0.240575	0.297388	-0.807631	-0.028278	0.093983	0.153931	-0.052842	0.871288	0.849984	0.248023
tubulin alpha 1	100342_i_at	-0.998138	-0.580662	1.043946	0.594664	0.323089	0.167772	-0.105599	1.631962	1.624276	0.465956
dynein, cytoplasmic, intermediate chain 1	103809_r_at	-0.237703	-0.123207	0.703034	0.414375	-0.017443	0.404354	0.651086	0.497461	0.570217	0.445407
angiopoietin 2	92210_at	-0.840159	0.266481	0.137559	0.056883	0.62967	0.073968	0.335872	0.49597	0.724311	0.993408
antigen identified by monoclonal antibodies 4F2	99133_at	0.279496	-0.025765	0.560269	-0.235022	-0.111364	0.377015	0.167161	0.342595	0.657086	0.719407
G-protein-coupled receptor 50	101763_at	-0.458375	-0.21683	0.761328	0.322622	0.056636	0.434561	0.368875	0.81421	0.369743	0.470868
clone BPS3.23 germline Ig variable region heavy chain precursor gene, partial cds	93927_f_at	-1.313652	-0.530486	2.110619	0.425808	-0.428433	1.835343	0.812172	0.871462	-0.499444	1.398423
glucose phosphate isomerase 1 complex	100573_f_at	-0.226027	0.489746	-0.949169	0.470626	-0.056413	0.453984	0.496012	0.758983	0.561408	-0.189035
Actin, gamma 2, smooth muscle, enteric	93102_f_at	-0.101096	0.048649	1.038172	0.399721	0.295699	0.910385	0.641388	0.707258	0.845138	0.446691
ESTs, Weakly similar to CG13922 gene product [D.melanogaster]	104567_at	-1.004751	-0.380613	0.224955	-0.647247	-0.342203	-0.086057	0.292828	-0.059826	-0.326499	0.04193
M.musculus mRNA for transferrin receptor	103958_g_at	-0.788028	-0.659128	1.420099	-0.256958	0.588281	0.179594	0.593265	0.928473	0.784515	0.724955
protein that interacts with C kinase 1	97684_at	-1.226564	-0.089037	0.093047	-1.10677	-1.066712	-0.464224	0.117138	-0.509801	-0.149316	-0.040062
eyes absent 1 homolog (Drosophila)	94706_s_at	-0.841508	-0.276614	1.013004	0.103642	0.146354	0.310579	0.38868	0.536317	0.611615	0.608998
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	97060_at	0.68321	-0.079689	-0.180755	0.008783	0.371084	0.258856	-0.065488	0.867833	0.884926	0.921793
M.musculus mRNA for transferrin receptor	103957_at	-1.346625	0.067496	0.912969	-0.203098	0.747244	-0.305312	0.053854	1.741897	1.337977	0.763937
ATP-binding cassette, sub-family G (WHITE), member 2	95023_at	0.105668	-0.078096	0.065329	0.24019	-0.031492	0.30885	0.108415	0.456863	0.492811	0.189602

ESTs	96864_at	0.439223	0.402404	-0.182565	-0.121564	-0.405931	0.162581	0.128988	0.574943	0.7082	0.366411
Ras-like GTP-binding protein rad	97319_at	0.822493	0.477628	0.582404	0.186688	0.035864	0.529122	0.716672	0.849754	0.978337	0.607456
mutS homolog 2 (E. coli)	100033_at	-0.920116	-0.708121	-0.377905	-0.866202	0.321973	-0.063042	0.197453	-0.364886	-0.294234	-0.004591
granzyme G	102876_at	-0.596218	-0.97455	-0.025746	-0.675015	-0.353072	-0.063108	-0.306859	-0.231761	-0.346015	-0.070214
insulin-like growth factor I receptor	102224_at	0.507825	0.049458	0.147273	0.154856	-0.099634	0.013501	0.467634	0.517663	1.045258	0.396009
ESTs	97265_at	-0.192132	-0.278882	-1.113801	-0.59564	-0.142592	-0.104381	-0.15959	-0.094143	-0.208592	-0.063948
glycophorin A	102770_at	-0.347396	0.134109	0.485689	0.275601	-0.032638	-0.166838	-0.191265	1.161247	0.910909	1.090701
ESTs	101665_at	-0.550504	-0.397307	0.855528	0.120337	-0.058308	0.322862	0.2429	0.42471	0.344652	0.554829
secretin	92756_r_at	-0.346155	-0.274964	0.359848	-0.059086	1.034361	0.599292	0.672147	0.578753	0.64254	0.227812
RAN binding protein 9	97812_at	0.60251	0.536175	-0.669528	0.079155	-0.415803	0.45734	0.269609	0.472329	0.552403	0.324241
ESTs, Highly similar to NIFU PROTEIN [Anabaena pcc7120]	95645_at	0.105169	0.105326	0.864887	-0.085885	0.004571	0.837065	0.704409	0.73816	-0.029069	0.585686
ribophorin II	94076_i_at	0.82423	-0.145272	-0.042568	0.273394	0.021059	1.14768	0.44753	0.156009	0.76929	0.269207
EST	101229_at	0.013785	-0.109197	0.465894	0.392815	0.026633	0.251154	-0.18687	1.028029	0.405697	1.408225
ubiquitin specific protease 23	95027_at	-0.055194	-0.689881	-0.940688	-0.401336	-0.138965	0.049472	-0.181719	-0.336596	0.249489	-0.349926
elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2	94393_r_at	-0.264929	-0.374174	0.86185	1.077583	-0.738562	0.171009	-0.241718	1.255945	0.819428	1.309427
karyopherin (importin) alpha 2	92790_at	0.250818	0.523936	-0.151953	0.064084	-0.176864	0.497613	0.252517	0.461964	0.58635	0.157519
ESTs, Highly similar to mediator [H.sapiens]	95616_at	0.546814	-0.019977	0.118446	-0.247043	-0.245403	0.491745	0.24121	0.242471	0.221543	0.42186
phospholipase A2, group V	94665_at	-0.285186	-0.368608	-0.396478	-1.042287	-0.615423	-0.505013	-0.165564	-0.322406	-0.250052	0.103042
ESTs, Highly similar to 2118318A promyelocyte leukemia Zn finger protein [M.musculus]	92202_g_at	-0.505942	0.185528	-1.196727	-0.260844	-0.725279	-0.104591	-0.320897	0.182144	0.215408	-0.579442
solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	102642_at	-0.219324	-0.128147	0.682089	0.331992	-0.126833	0.246213	0.351013	0.694279	0.433334	0.324164
copper chaperone for superoxide dismutase	103909_at	0.147038	-0.223338	-0.460695	-1.204849	-0.865884	-0.294081	0.015224	-0.140586	-0.432401	0.089907
cathepsin B	95608_at	0.427905	0.347734	-0.530242	0.275819	-0.113505	0.549262	0.310788	0.431174	0.620502	0.060737
mitochondrial carrier homolog 1 isoform b	95689_at	-0.456106	-0.201273	0.682001	0.424371	0.180021	0.309515	0.08943	0.783884	0.615169	0.522109
CD1d1 antigen	103422_at	-1.106616	-0.117224	-1.093292	0.154604	-0.533767	-0.486587	0.220642	0.248508	-0.367092	-0.34452
histocompatibility 2, M region locus 9	101341_at	-0.653283	-0.524998	1.217394	0.237272	0.393868	0.487339	-0.621582	1.024763	1.067153	1.333241
DNA segment, Chr 15, ERATO Doi 55, expressed	95861_at	-0.102393	-0.22924	1.276463	-0.0942	-0.196864	0.423317	0.323339	0.606111	0.397859	0.799037
Mus musculus eukaryotic translation elongation factor 1-delta mRNA, complete cds	99142_at	-0.585266	-0.517468	0.784365	0.130786	0.139302	0.338395	-0.08693	0.567676	0.471037	0.420079
ESTs, Moderately similar to KIAA0943 protein [H.sapiens]	94551_at	-0.318148	0.018471	0.316078	0.201429	0.368075	0.222108	0.260774	0.216987	0.475592	0.741585
peptidylprolyl isomerase B	94915_at	0.206986	0.137207	0.52677	0.35793	0.158573	0.431751	0.427431	0.797785	1.02217	0.046114
ganglioside-induced differentiation-associated-protein 10	94192_at	-0.787022	-0.42991	-1.299454	-0.344691	-0.224624	-0.763387	-0.219311	0.044004	-0.305902	-0.232241
ESTs, Moderately similar to A54691 octamer-binding protein NonO - mouse [M.musculus]	103393_at	-1.623901	-0.680204	-0.824596	-0.425244	-0.158924	-0.797304	-0.183127	-0.587904	-0.229342	-0.143938
odd Oz/ten-m homolog 4 (Drosophila)	97581_at	0.337076	-0.202205	0.516485	0.356087	0.059059	0.372163	0.046305	0.836255	0.271884	1.029197
farnesyl diphosphate farnesyl transferase 1	97518_at	-0.064616	-0.259777	-0.406621	-0.348414	-0.457751	0.222088	0.446269	-0.172478	-0.116399	-0.542774
ESTs, Moderately similar to unnamed protein product [H.sapiens]	96621_at	-0.042263	0.089917	-0.144613	0.192826	0.515978	0.305343	0.252129	0.528277	0.780193	0.042461
S100 calcium binding protein A3	101051_at	-0.165984	-0.179053	0.790396	-0.135426	0.130094	-0.00255	0.039754	0.54668	0.648744	0.773533
ESTs, Weakly similar to PROBABLE PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE FAB1 [Saccharomyces cer	92182_at	0.117626	-0.412833	-0.882706	-0.493829	-0.30298	-0.314145	-0.038124	-0.016654	-0.026688	-0.266875
haptoglobin	96092_at	0.0031	0.220257	0.684386	0.077933	-0.08006	0.256002	0.037723	0.456423	0.681078	0.823753
myocyte enhancer factor 2B	93417_at	-0.289987	-0.119525	0.527494	0.230941	0.166346	0.390012	0.293612	0.283198	0.145603	0.633687
connective tissue growth factor	93294_at	-0.044479	1.781996	1.878405	2.136207	1.424384	-0.368089	-0.202687	-1.989831	-1.777713	-2.196326
enabled homolog (Drosophila)	93864_s_at	1.423037	2.425833	2.990955	1.149261	1.632775	-0.346902	0.0165	-0.676596	-0.265445	-0.008183
B-cell translocation gene 2, anti-proliferative	101583_at	1.418129	1.332521	0.633509	0.753403	0.200547	-0.609097	-0.522826	-1.868078	-1.670861	-1.682387
nuclear receptor subfamily 4, group A, member 1	102371_at	0.640059	0.876154	0.29729	0.457674	0.431653	-0.600302	-0.825437	-1.328757	-1.285266	-1.118296
serine protease inhibitor 2-2	104374_at	0.899723	0.615667	1.343104	1.078329	0.834082	-0.281425	-0.202577	-0.552999	-0.72277	-0.57701
Myelocytomatosis oncogene	104712_at	1.577575	2.534677	1.138772	-0.209638	-0.293766	-1.06253	-1.71793	-1.288818	-0.671883	-1.808596
brain derived neurotrophic factor	102727_at	0.446273	0.906665	0.223145	0.242823	0.204441	-1.265285	-0.419086	-1.550686	-1.272251	-1.041794
ceruloplasmin	92851_at	0.575824	0.302653	-0.100169	0.426425	0.637221	-0.696925	-0.740481	-1.394221	-0.918781	-0.918578
integrin alpha 5 (fibronectin receptor alpha)	103039_at	0.515697	2.279611	3.220285	1.912429	-0.556933	0.56539	-1.656924	-1.004694	-0.912503	-1.456433
ESTs	95978_at	0.637703	0.801205	1.171061	1.104682	0.193823	-0.613852	0.01026	-1.008301	-1.569215	-0.621959
ESTs, Highly similar to serine protease [H.sapiens]	94238_at	2.34843	1.817072	0.974275	1.135736	0.807167	0.354835	-0.025668	-0.425348	-0.211427	-0.2464
a disintegrin and metalloproteinase domain 19 (meltrin beta)	103554_at	1.126538	0.263959	0.43866	1.12276	1.101566	-0.002606	-0.171453	-1.282697	-0.805158	-1.367586
Fibrinogen-like protein 2	97949_at	0.975569	1.484109	0.903138	1.142259	0.948865	-0.217875	-0.45116	0.258493	-0.006776	-0.091549
GRO1 oncogene	95349_g_at	0.502175	3.026377	2.615156	-0.137658	0.474437	-0.503885	-0.895555	-1.577828	-0.608656	-0.399455
ESTs, Moderately similar to URIDINE KINASE [Escherichia coli]	94367_at	0.763204	0.93516	2.267056	1.69587	0.471282	-0.004261	-0.215721	-0.296323	-0.277501	-0.228421
DNA segment, Chr 2, ERATO Doi 198, expressed	104639_i_at	0.504805	0.934593	1.407047	0.803608	0.576469	-0.430634	-0.017068	-0.4303	-0.692643	-0.242905
CD44 antigen	103005_s_at	0.646466	1.244165	2.783508	1.187047	0.386487	0.178506	0.082328	-1.847697	-0.706269	-0.301987
procollagen, type III, alpha 1	102990_at	3.276422	-0.71594	2.636518	1.019916	0.661023	0.24761	-0.831371	-1.314762	-0.138353	-1.629397
ESTs, Highly similar to G33_RAT GENE 33 POLYPEPTIDE [R.norvegicus]	93975_at	1.239925	0.771514	-0.33169	0.697538	-0.199134	-0.7046	-0.602684	-0.953952	-1.428724	-1.070462
natriuretic peptide precursor type B	104184_at	0.693059	1.668498	1.986334	1.095484	0.747987	0.346947	0.077078	-0.646241	-0.013869	-0.264797
plasminogen activator inhibitor, type I	94147_at	-0.371289	0.980606	2.187135	1.708013	0.835098	-0.220213	0.059802	-0.61818	-1.028148	-0.960082
histocompatibility 2, D region locus 1	97540_f_at	0.323642	0.101587	0.35669	0.714064	0.035385	-0.254096	-0.791767	-0.929943	-1.040528	-1.048976
ESTs	102936_at	0.393205	0.315821	0.767481	0.258828	0.307418	-0.672114	-0.393535	-1.11744	-0.99363	-0.367873
fibrinogen/angiopoietin-related protein	102114_f_at	1.017435	1.091726	-0.044427	0.920417	-0.375786	-1.696979	0.032723	-0.78695	-0.929495	-1.471748
Mus musculus mRNA for slow myosin heavy chain-beta, partial	98616_f_at	0.271896	-0.2777	0.689039	1.30535	0.843434	0.251473	-0.066327	-1.930316	-2.046316	-1.797255
interleukin 4 receptor, alpha	102021_at	1.301467	0.53187	1.526064	1.148166	0.264522	0.510931	-1.026274	-0.810766	-0.326661	-0.251214
purine-nucleoside phosphorylase	93290_at	0.376475	0.089334	0.249957	0.137007	0.127045	-0.778239	-0.434746	-1.062518	-0.972865	-0.838777
ESTs, Highly similar to G33_RAT GENE 33 POLYPEPTIDE [R.norvegicus]	93974_at	0.526634	0.677281	-0.05341	0.065337	0.370903	-0.67475	-0.426328	-0.735964	-1.024853	-1.059645
small inducible cytokine A2	102736_at	2.343038	3.634905	4.437081	1.088562	0.087433	0.409769	-0.667716	0.396726	1.195944	0.27264
secreted frizzled-related sequence protein 3	104672_at	0.790686	-0.33989	1.67533	1.971734	1.305057	0.23785	-0.574523	-0.27675	-0.312628	-0.522134
NPC derived proline rich protein 1	100472_at	0.6634	0.817798	0.442064	0.732315	0.758508	-0.07625	-0.108555	-0.731627	-0.367302	-0.192401
ESTs, Moderately similar to 1905361A AKR Qa protein [M.musculus]	93714_f_at	1.623767	-0.145171	-0.003673	0.70429	0.282607	-0.198651	-1.023174	-0.684848	-1.288861	-0.674475
ESTs	95936_at	-0.805263	-0.612278	1.712933	0.267052	0.285665	-0.981772	-0.387604	-1.533076	-1.563783	-2.194
insulin-like growth factor binding protein 3	95082_at	0.752805	1.410179	-0.862872	0.237746	0.62527	-0.492732	-0.78419	-1.172401	-1.209323	-0.734178
CD2-associated proten	103281_at	-0.508535	0.166347	-0.215796	1.897686	0.672505	-1.239678	-0.62595	-0.959937	-0.573033	-1.403625

lymphocyte antigen 57	100772_g_at	0.710735	1.179494	0.747661	1.26278	-0.50166	-0.054725	-0.846688	-0.44435	-0.320333	-1.042401
osteoblast specific factor 2 (fasciclin I-like)	92593_at	-0.194561	0.103874	3.14774	3.031569	2.496345	-0.1552	-0.45937	0.185706	0.362278	-0.02272
pleckstrin homology, Sec7 and coiled/coil domains 3	103434_at	0.525091	0.914889	0.250478	0.143158	2.004785	0.140093	-0.375733	-1.105517	-0.535884	-0.688431
follistatin-like	94833_at	0.479773	0.177143	1.845953	1.17469	1.135799	-0.116848	-0.527781	-0.274744	0.015007	0.027774
catechol-O-methyltransferase	98535_at	0.749591	-0.337036	-0.259713	0.433461	0.689908	-0.302562	-0.726902	-1.062032	-1.104422	-1.020944
solute carrier family 20, member 1	103065_at	1.177405	1.011167	0.771586	0.278213	0.178597	-0.187282	-0.110769	-0.614202	-0.523277	-0.298486
Mus musculus collagenous repeat-containing sequence of 26kDa protein (CORS26) mRNA, complete cds	103570_at	-0.231677	0.063209	1.896222	2.048282	0.711508	-0.121883	-0.34262	-0.560752	-0.513517	-0.486315
insulin receptor substrate 1	98824_at	1.417668	0.658361	0.831902	0.184959	2.954708	-1.133966	-0.465642	0.184139	0.068347	0.398155
Kruppel-like factor 4 (gut)	99622_at	0.198592	0.257738	-0.067635	0.143293	0.339493	-0.4862	-0.38044	-0.936203	-0.756475	-0.959613
Early growth response 1	98579_at	0.551939	1.633444	0.77457	0.240172	0.417116	0.114092	-0.422896	-0.474119	-0.395193	-0.347941
serine racemase	93488_at	0.187804	0.037067	0.483525	-0.00536	0.197497	-0.521914	-0.440078	-0.812542	-0.972114	-0.650085
fibrinogen/angiopoietin-related protein	96119_s_at	0.089476	0.369039	-0.11308	0.241713	-0.248051	-0.841392	-0.608794	-0.598921	-1.006845	-0.928733
SIK similar protein	92569_f_at	0.034484	0.46903	0.760041	0.331372	0.284066	-0.569187	-0.41025	-0.547555	-0.730154	-0.215144
zinc finger protein 36	92830_s_at	0.422397	0.021728	0.76266	0.408129	-0.129207	0.193067	-0.437821	-0.95842	-1.609696	-1.17099
DNA segment, Chr 15, ERATO Doi 621, expressed	98013_at	2.427299	1.544017	-0.079475	0.427717	0.686175	0.14566	0.198448	-0.415407	-0.719176	-0.50763
ESTs	98083_at	0.222878	1.142074	-0.146457	0.400893	-0.119596	-0.714063	-0.459327	-0.4834	-0.812718	-0.948612
acid phosphatase 1, soluble	93219_at	0.710928	-0.199878	0.295178	0.434782	-0.266358	-1.126935	0.0392	-0.903852	-1.421149	-0.83357
histocompatibility 2, L region	101886_f_at	0.173966	-0.085449	0.418325	0.43705	0.164246	-0.270418	-0.825632	-0.898297	-0.666309	-0.428304
heat shock protein, 86 kDa 1	95282_at	0.736183	1.29054	0.175655	0.434455	0.588474	-0.893606	-0.667188	-0.30577	0.300229	-0.216842
histocompatibility 2, K region	93120_f_at	0.213879	0.064853	0.161848	0.736366	0.194788	-0.038832	-0.737545	-0.708329	-0.637456	-0.821356
ESTs	96532_at	0.420121	-0.01192	-0.024507	0.114578	0.617263	-0.294206	-1.367422	-0.393637	-0.464205	-1.028188
histocompatibility 2, K region locus 2	97173_f_at	-0.990031	-1.199259	1.170179	0.900369	-0.001464	-0.661484	-1.323068	-1.783031	-1.614189	-1.011842
Mus musculus putative RNA helicase RCK mRNA, partial cds	93965_r_at	-0.388647	0.307963	0.509872	-0.334641	0.244889	-0.604957	-0.630245	-1.909886	-1.807722	-0.282829
DNA segment, Chr 5, ERATO Doi 189, expressed	103538_at	0.825456	1.110371	-0.317574	0.65594	0.001852	-0.489271	-0.067255	-0.589661	-0.586343	-1.113639
interferon activated gene 204	98465_f_at	-0.060637	0.285102	-0.249329	0.304224	0.263923	-0.898823	-0.543771	-0.834181	-0.650824	-0.631108
ESTs	96207_at	0.602558	0.147577	0.282465	0.153196	0.108512	-0.868062	-0.203732	-0.846096	-0.47582	-0.530432
glutathione peroxidase 3	101676_at	0.522328	0.048124	-0.027724	1.09492	0.55393	-0.006304	-0.819686	-0.935203	-0.437939	-0.332215
ESTs	92971_at	0.122626	-0.009444	0.041625	0.425236	-0.168396	-0.36808	-0.901889	-0.713856	-1.013353	-0.648564
fibrillin 1	101090_at	-0.416862	0.432223	1.681274	1.781112	0.882968	0.549394	-0.228386	-0.707837	-0.290198	-0.86097
CCAAT/enhancer binding protein (C/EBP), beta	92925_at	-0.040556	0.545521	-0.310201	0.28437	-0.23952	-0.557627	-1.155077	-0.615739	-0.76714	-0.995232
secreted phosphoprotein 1	97519_at	0.079727	0.011195	6.266377	2.525576	2.414031	0.009238	-0.64811	-0.170764	0.14055	1.908232
heat shock protein 40	96254_at	1.803552	1.672396	0.177733	-0.124581	0.024392	-0.421576	-0.432897	-0.579378	-0.333666	-0.342451
RAN GTPase activating protein 1	98603_s_at	0.743077	0.321181	0.231787	1.752149	1.423976	-0.249741	-0.904094	-1.041865	0.38882	0.610545
T-cell specific GTPase	102906_at	-0.634376	-0.327445	-0.383082	0.368448	-0.496175	-0.475886	-0.202025	-2.053788	-2.501192	-2.292985
CD53 antigen	94939_at	0.320359	1.64322	1.36486	0.992152	0.38688	-1.008136	-0.454416	0.130312	0.277266	0.52526
ESTs	93439_f_at	-0.356	0.249237	-0.037434	0.565416	-0.016933	-0.642733	-1.972401	-0.511731	-0.552742	-0.6794
four and a half LIM domains 1	97500_g_at	0.361903	0.89596	2.282789	1.377623	1.311755	0.136614	0.46512	0.293299	0.04591	0.405263
serum/glucocorticoid regulated kinase	97890_at	0.455552	0.528946	-0.457575	0.716644	-0.106056	-0.211261	-0.394499	-0.674787	-0.907588	-1.399471
ring finger protein 2	93164_at	0.561651	1.129994	0.136057	-1.147931	0.869865	-0.95417	0.066008	-1.235653	-1.068172	-0.951881
potassium voltage gated channel, shaker related subfamily, member 5	102295_at	-0.142355	0.226288	-0.412945	-0.099601	-0.377337	-0.663504	-0.972847	-0.928905	-1.18948	-0.950909
ESTs, Weakly similar to DYNA_RAT DYNACTIN, 150 KD ISOFORM [R.norvegicus]	97276_at	1.346355	0.520655	0.224705	0.208177	0.287909	-0.220253	-0.241935	-0.443939	-0.53883	-0.286605
ESTs, Weakly similar to HYPOTHETICAL 51.6 KD PROTEIN ZK353.8 IN CHROMOSOME III [Caenorhabditis elegans]	104311_at	0.323032	0.613009	0.055251	0.377452	0.167733	-0.656685	-0.146701	-0.89584	-0.496333	-0.306738
natriuretic peptide precursor type A	103593_at	0.290039	0.743007	0.894518	2.009901	1.423113	0.273546	0.203117	-0.045966	0.019481	0.236562
ESTs, Highly similar to U05334_1 rap7a [R.norvegicus]	93842_at	1.147571	0.054968	1.038009	0.823368	0.733905	0.275157	-0.158379	-0.211963	0.021414	-0.268768
WSB-1	98946_at	-0.027086	0.888895	0.340096	0.65305	-0.044894	-0.314103	-0.080682	-0.540358	-1.062938	-0.587125
chromobox homolog 1 (Drosophila HP1 beta)	96775_at	0.748023	0.801293	0.693699	0.208009	0.709479	-0.126119	-0.318159	0.136915	-0.964639	0.117168
ESTs, Weakly similar to female sterile homeotic-related protein Frg-1 [M.musculus]	97892_at	0.464128	0.357867	0.127522	0.505361	0.008125	-0.702174	-0.497331	-0.575186	-0.372312	-0.159105
multidrug-resistance protein (MDR1) gene, exons 1 and 2	93414_at	0.182641	1.429261	0.330129	0.442222	-0.518623	-0.55049	-0.22616	-0.775278	-0.529337	-0.846855
DNA segment, Chr 6, Wayne State University 176, expressed	95541_at	-0.466533	0.304992	1.053965	0.800286	1.048915	-0.411056	-0.259451	-0.346731	-0.163073	-0.636013
procollagen, type V, alpha 2	92567_at	0.113551	-0.099944	2.706678	2.940866	1.549529	0.394485	-0.426404	0.383278	0.809787	-0.30947
activating transcription factor 3	104155_f_at	1.053722	2.892277	0.874443	0.639912	0.161055	1.332704	1.013668	-1.149394	-1.225832	-1.148836
ESTs	97154_f_at	-0.298922	1.200819	0.181974	-0.019538	0.99347	-1.418091	-1.115308	-0.892258	-0.077253	0.309531
acyl-CoA thioesterase 1, cytosolic	103581_at	0.934362	0.352821	-0.443284	-0.762453	-0.857208	-0.133299	-0.047451	-2.073964	-2.258488	-2.499895
cathepsin S	98543_at	0.403588	0.200128	2.141695	1.168404	0.207606	-0.410754	-0.097475	0.108238	-0.072772	-0.289507
P lysozyme structural	101753_s_at	0.737929	0.634211	2.581448	0.987521	0.368265	-0.407042	-0.034241	-0.011068	0.062616	0.620003
fibulin 2	100928_at	0.126889	0.011596	1.294428	1.203166	0.894727	0.195468	0.008428	-0.52545	-0.065243	-0.516877
nidogen 2	93563_s_at	-0.016575	0.956402	0.315619	1.050273	0.456036	0.081491	-0.329353	-0.339241	-0.232688	-0.437428
nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha	101554_at	0.524071	0.042925	-0.269734	0.174735	-0.142489	-0.188354	-0.305915	-1.184254	-1.199728	-1.03878
procollagen, type I, alpha 1	94305_at	0.662495	-0.133044	2.169968	1.858587	1.530609	0.467567	-0.341869	0.214176	0.719356	-0.109667

Table 3: Genes With Common Expression Profiles

Table 3 contains the set of 136 genes identified to have common expression profiles in the exercise and banding hypertrophy models in the Statistical Investigator of Transcriptional Homology (SITH) analysis of the Log2-transformed signal ratios (SLR) computed for the transcripts in the exercise and banding hypertrophy models identified in Table 1. The table is organized such that the name of each gene is associated with its corresponding Affymetrix probe identification number and its for each measurement interval in both hypertrophy models.

Gene Name	Affymetrix Probe ID	Banding HW/BW (mg/g)					Exercise HW/BW (mg/g)				
		4.4	4.6	5.1	5.5	5.6	4.4	4.6	5.1	5.5	5.6
nuclear factor, interleukin 3, regulated	102955_at	0.611749	1.346668	0.684929	-0.402479	0.731082	0.784484	0.915171	0.834618	1.246376	0.446849

Ras-like GTP-binding protein rad	97319_at	0.822493	0.477628	0.582404	0.186688	0.035864	0.529122	0.716672	0.849754	0.978337	0.607456
ESTs, Highly similar to T17338 hypothetical protein DKFZp434O125.1 - human [H.sapiens]	96732_at	0.093802	0.782961	-0.205488	0.5513	-0.239396	0.574507	1.033997	0.905436	0.919203	0.812219
Actin, gamma 2, smooth muscle, enteric	93102_f_at	-0.101096	0.048649	1.038172	0.399721	0.295699	0.910385	0.641388	0.707258	0.845138	0.446691
hemoglobin alpha, pseudogene 3	101703_at	-0.476836	-0.039781	0.162977	-0.337403	0.291865	0.501029	0.285358	0.697138	1.180277	0.870824
ribosomal protein L29	95418_at	0.004752	0.926028	0.974628	0.512772	0.258695	0.609671	0.398621	0.67018	0.724894	0.678116
DNA segment, Chr 16, ERATO Doi 36, expressed	103790_at	-0.233533	-0.447007	0.727108	-0.188015	0.180315	0.795472	0.512592	0.612853	0.830898	0.293319
sialyltransferase 4C (beta-galactosidase alpha-2,3-sialytransferase)	95599_at	-0.240047	0.376114	0.226181	-0.621955	0.184963	0.367968	0.286034	1.177878	0.838189	0.597794
carbon catabolite repression 4 homolog (S. cerevisiae)	99535_at	-0.078362	0.366227	0.156727	-0.390537	-0.527448	0.264118	0.574426	0.748691	0.928506	0.556767
adrenergic receptor, beta 2	93193_at	-1.064519	-0.216789	0.47569	-0.128186	0.293896	0.507309	0.377819	0.698666	0.490612	1.101583
metallothionein 2	101561_at	1.283515	0.97877	1.111424	1.554173	1.24287	0.117861	0.567167	0.674328	1.228729	1.148309
metallothionein 1	93573_at	1.016799	0.30002	0.457689	0.371623	0.311366	0.571081	0.372389	0.648265	0.672944	0.345293
ESTs, Moderately similar to ubiquitin/60S ribosomal fusion protein [M.musculus]	102841_at	0.177131	0.238495	0.232694	-0.00343	0.00465	0.632553	0.155686	0.685143	0.967928	0.715195
stearoyl-Coenzyme A desaturase 2	95758_at	-0.193501	-0.073342	0.448344	0.095219	0.288721	0.56702	0.375961	0.654558	0.74217	0.351873
calmodulin 3	92631_f_at	0.231029	0.020312	-0.05858	-0.25244	-0.022185	0.636053	0.494501	0.784486	0.764194	0.255523
ESTs	95374_f_at	-0.458697	-0.038745	-0.033292	0.368918	0.096177	0.581045	0.650628	0.558107	0.64104	0.498318
procollagen C-proteinase enhancer protein	93349_at	0.404126	0.00671	0.709088	0.647922	0.765432	0.541174	0.159169	0.676661	0.926224	0.610821
ESTs	104267_at	-0.208187	0.347125	0.145297	0.277737	-0.06196	0.304951	0.489228	0.867127	0.810709	0.37221
ESTs, Highly similar to AF173682_1 system A transporter isoform 2 [R.norvegicus]	94433_at	0.319699	1.505071	0.141937	0.286635	0.119004	0.343218	0.397126	0.858493	1.292391	0.424033
polymeric immunoglobulin receptor	99926_at	-0.366794	-0.211988	0.383322	-0.004187	-0.188495	0.58776	0.325607	0.697186	0.57763	0.55644
prostaglandin I2 (prostacyclin) synthase	104538_at	0.015677	0.207459	0.751279	0.573554	0.961261	0.740019	-0.03487	0.67565	1.336286	0.53179
major histocompatibility complex region	102343_at	0.718705	-0.301673	-0.021452	-0.275018	-0.137707	0.304013	0.41813	0.887077	0.791754	0.233413
proteasome (prosome, macropain) subunit, beta type 5	101558_s_at	0.123749	0.082462	-0.114974	-0.106944	-0.12194	0.349507	0.445931	0.614592	0.983355	0.214369
secretin	92756_r_at	-0.346155	-0.274964	0.359848	-0.059086	1.034361	0.599292	0.672147	0.578753	0.64254	0.227812
chromobox homolog 4 (Drosophila Pc class)	93697_at	0.360534	-0.005263	-0.028649	-0.30578	-0.182933	0.53399	0.301059	0.421546	0.751245	0.324248
DNA segment, Chr 7, Roswell Park 2 complex, expressed	96629_at	0.691051	0.161196	-0.080879	-0.129264	-0.086724	0.49728	0.46625	0.568915	0.632887	0.336654
ESTs	96546_r_at	-0.12335	-0.25648	0.112743	0.107868	0.02647	0.550246	0.392602	0.503544	0.577413	0.318402
ESTs, Moderately similar to BILIVERDIN REDUCTASE A PRECURSOR [Rattus norvegicus]	104124_at	-0.716295	-0.607093	0.458849	-0.126674	-0.444165	0.383058	0.463505	0.795372	0.584603	0.49796
nuclear receptor co-repressor 2	95129_at	0.324858	-0.243875	0.152691	0.186575	0.297545	0.950399	0.017789	0.510709	0.855454	0.499084
protein phosphatase 2, regulatory subunit B (B56), gamma isoform	98993_at	0.610955	0.818874	-0.061075	0.439685	-0.24091	0.422696	0.732613	0.679433	0.670852	0.262922
transforming growth factor, beta 3	102751_at	0.467826	0.069792	0.989126	0.643304	0.578364	0.316121	0.420078	0.473775	0.658264	0.552751
peptidylprolyl isomerase B	94915_at	0.206986	0.137207	0.52677	0.35793	0.158573	0.431751	0.427431	0.797785	1.02217	0.046114
ESTs, Weakly similar to similar to tyrosyl-tRNA synthetase. [C.elegans]	101023_f_at	-0.31019	0.311545	-0.457779	-0.055173	-0.235905	0.554257	0.345661	0.491331	0.626045	0.23153
ESTs, Weakly similar to FORM_MOUSE FORMIN [M.musculus]	103424_at	-0.223367	0.347444	1.312015	0.968863	0.061095	1.046069	0.325315	0.789158	0.640524	0.069623
short stature homeobox 2	99042_s_at	-0.070764	0.050006	0.484228	-0.057103	0.068837	0.319309	0.234886	1.180783	0.600674	0.885051
pigment epithelium-derived factor	93574_at	0.164177	0.189517	0.020319	1.314065	1.335979	0.610782	-0.156958	1.139759	1.107598	0.615749
prohibitin	94855_at	-0.019928	0.089314	-0.049368	-0.396291	-0.347387	0.456094	0.3888	0.647932	0.78181	0.117076
ribophorin II	94076_i_at	0.82423	-0.145272	-0.042568	0.273394	0.021059	1.14768	0.44753	0.156009	0.76929	0.269207
antigen identified by monoclonal antibodies 4F2	99133_at	0.279496	-0.025765	0.560269	-0.235022	-0.111364	0.377015	0.167161	0.342595	0.657086	0.719407
dynein, cytoplasmic, intermediate chain 1	103809_r_at	-0.237703	-0.123207	0.703034	0.414375	-0.017443	0.404354	0.651086	0.497461	0.570217	0.445407
solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	100618_f_at	-0.21292	-0.144876	0.034182	0.035123	0.148333	0.278908	0.161891	0.919688	0.744185	0.664199
colony stimulating factor 1 (macrophage)	101450_at	0.253229	-0.266024	0.269777	-0.072709	-0.079614	0.727336	0.329277	0.130368	0.836214	0.313979
ESTs, Moderately similar to ELL2_HUMAN RNA POLYMERASE II ELONGATION FACTOR ELL2 [H.sapiens]	103891_i_at	0.574097	1.438238	0.084519	0.219799	-0.078985	-0.481097	0.607936	1.511261	1.37214	0.927131
lectin, galactose binding, soluble 1	99669_at	0.190113	0.09443	0.995931	0.58854	0.296481	0.542392	0.214705	0.844703	1.006153	-0.002183
insulin-like growth factor I receptor	102224_at	0.507825	0.049458	0.147273	0.154856	-0.099634	0.013501	0.467634	0.517663	1.045258	0.396009
Parathyroid hormone-like peptide	104262_at	0.423805	0.129687	1.191815	0.26289	0.306398	0.438992	0.198196	0.595567	0.534751	0.292143
epithelial membrane protein 1	97426_at	0.563736	0.956743	1.39164	1.199544	0.890644	0.147161	0.243843	0.870148	0.977058	0.366206
histone H2a.2-615 (H2a-615), and histone H3.2-615 (H3-615) genes	93068_r_at	0.320665	-0.231647	-0.276499	-0.407592	0.101045	0.964413	0.320938	0.511717	0.57375	-0.014672
CD14 antigen	98088_at	-0.14526	0.370904	0.99766	0.422279	0.136068	0.242628	0.321288	0.64387	0.448227	0.333788
DNA segment, Chr 14, University of California at Los Angeles 1	102356_at	-0.149765	-0.05661	-0.215418	-0.108664	0.02756	0.333144	0.120775	0.742628	0.770069	0.274661
mitochondrial carrier homolog 1 isoform b	95689_at	-0.456106	-0.201273	0.682001	0.424371	0.180021	0.309515	0.08943	0.783884	0.615169	0.522109
ESTs	104160_at	0.331081	-0.241278	0.68841	-0.398872	0.337148	0.76977	0.60495	0.578143	0.638392	0.353424
DNA segment, Chr 6, ERATO Doi 772, expressed	96875_r_at	-0.237215	0.805654	-0.128298	0.885872	-0.19202	0.298449	0.28392	0.614999	0.392606	0.993409
ESTs	97933_at	0.106147	0.33281	0.536642	0.289265	0.393686	0.649395	0.256878	0.528669	0.300434	0.456589
RAN binding protein 9	97812_at	0.60251	0.536175	-0.669528	0.079155	-0.415803	0.45734	0.269609	0.472329	0.552403	0.324241
Mus musculus X chromosome: L1cam locus	96154_at	0.150049	-0.327523	0.142278	0.305172	0.150186	0.620426	0.244508	0.416094	0.53283	0.265528
ESTs, Moderately similar to AF121893_1 sequence-specific single-stranded-DNA-binding protein [R.norvegicus]	103504_at	0.198943	0.036829	0.015919	-0.033101	0.132953	0.222882	0.550234	0.774916	0.502932	0.255106
ESTs, Weakly similar to BRAIN SPECIFIC POLYPEPTIDE PEP-19 [Rattus norvegicus; Mus musculus]	97297_at	0.312493	-0.158118	-0.572514	-0.440724	-0.082069	0.563057	0.331991	0.527407	0.404912	0.230898
deiodinase, iodothyronine, type II	103438_at	-0.723496	0.299577	0.859024	1.046199	1.228104	0.390629	-0.015553	0.743032	0.74922	0.441665
cysteine-rich protein 2	93550_at	0.621156	0.15514	1.320989	1.002607	0.21532	-0.271646	0.142708	1.414784	1.357556	0.401334
phosphofructokinase, platelet	97834_g_at	0.045333	0.555881	0.793003	1.260084	1.079061	0.062068	0.121925	0.864174	0.741286	0.383323
tubulin alpha 4	92635_at	-0.08508	-0.011793	0.052911	-0.692051	-0.427382	0.197304	0.043217	0.808731	0.919489	0.207449
adenylate kinase 3 alpha like	92492_at	-0.330142	0.049376	-0.821627	0.049423	0.094204	0.060317	0.227361	0.487739	0.739135	0.509605
glyceraldehyde-3-phosphate dehydrogenase	101214_f_at	0.144326	-0.031954	-0.360311	-0.115587	0.231729	0.289367	0.195231	0.34398	0.527781	0.247247
CD68 antigen	103016_s_at	0.269903	-0.153363	1.467172	0.684512	0.09452	0.301453	-0.037794	0.411495	0.723017	0.556151
glucose phosphate isomerase 1 complex	100573_f_at	-0.226027	0.489746	-0.949169	0.470626	-0.056413	0.453984	0.496012	0.758983	0.561408	-0.189035
heparin binding epidermal growth factor-like growth factor	92730_at	0.411571	2.029934	1.063759	0.255168	0.392311	0.517991	0.488085	0.262804	0.317117	0.186183
histocompatibility 2, M region locus 9	101341_at	-0.653283	-0.524998	1.217394	0.237272	0.393868	0.487339	-0.621582	1.024763	1.067153	1.333241
myocyte enhancer factor 2B	93417_at	-0.289987	-0.119525	0.527494	0.230941	0.166346	0.390012	0.293612	0.283198	0.145603	0.633687
phosphoglycerate mutase muscle-specific subunit	92599_at	0.21076	-0.026581	-0.479796	-0.392076	-0.07431	0.107627	0.085324	0.579052	0.652336	0.289662
plasminogen activator, tissue	93981_at	0.288956	-0.237521	0.261306	0.332937	0.386632	0.48737	0.39651	0.159131	0.357619	0.251902
ATP-binding cassette, sub-family G (WHITE), member 2	95023_at	0.105668	-0.078096	0.065329	0.24019	-0.031492	0.30885	0.108415	0.456863	0.492811	0.189602
ryanodine receptor 3	101830_at	-0.295261	-0.2864	0.613657	-0.184294	0.1254	0.410192	0.211294	0.616997	0.156596	0.727579
Rho-associated coiled-coil forming kinase 1	100980_at	0.148353	-0.422497	-0.088807	-0.013681	0.120769	-1.078349	-0.384768	-0.828837	-0.776092	-0.451214

ESTs	96526_at	-0.016545	-0.262264	-0.318742	0.159672	-0.624083	-1.204388	-0.349339	-0.44127	-0.680478	-0.883867
M.musculus TOP gene for topoisomerase I, exons 19-21	95694_at	0.238455	-0.242457	0.201052	-0.663408	-0.251143	-1.090468	-0.49191	-0.66966	-0.594655	-0.533001
ESTs	104193_at	-0.164407	-0.118138	-0.940656	0.243944	-0.316757	-1.085039	-0.307016	-0.504701	-0.747043	-0.39234
inositol trisphosphate receptor type 2 (Itpr2) gene, partial cds	101441_i_at	-0.184443	0.494752	-0.500835	-0.417068	-0.275811	-0.638091	-0.214002	-1.197606	-0.746942	-0.278425
GATA-binding protein 6	104698_at	0.241575	0.096598	-0.238541	-0.546438	-0.136336	-0.512397	-0.361178	-1.094349	-0.738466	-0.246391
calcium channel, voltage-dependent, alpha2/delta subunit 1	104510_at	0.069954	0.064987	-0.603	-0.620611	-0.09678	-0.869514	-0.01084	-1.226966	-0.858563	-0.530258
calpain 12	95093_at	-0.697655	-0.399471	0.445978	0.221293	0.346475	-1.19665	-0.648388	-0.813824	-0.611712	0.028853
cofilin 1, non-muscle	93667_at	0.59444	-0.660665	-1.049373	-0.32822	-0.056749	-0.399708	-0.292932	-0.827896	-0.8766	-0.238506
carnitine deficiency-associated gene expressed in ventricle 1	102215_at	0.096325	-0.306493	-1.122399	-0.909055	-0.56371	-0.797838	-0.29349	-0.457995	-0.707466	-0.225662
programmed cell death 4	103029_at	0.067019	-0.454271	-0.938966	0.043965	-0.294704	-1.182625	-0.635722	-0.187212	-0.276288	-0.783302
heart and neural crest derivatives expressed transcript 2	99914_at	0.422507	-0.089602	-0.417212	-0.591852	-0.208779	0.013896	-0.251532	-1.637194	-0.957589	-0.319136
myomesin 2	102041_at	-0.110574	-0.032352	-0.74487	0.026355	-0.135276	-0.292083	-0.155964	-0.907315	-0.92101	-0.450076
myosin X	100923_at	0.505186	-0.035504	-0.496283	-0.502974	0.00912	-0.287188	-0.25741	-0.84665	-0.721112	-0.367412
platelet derived growth factor, alpha	94932_at	0.277178	-0.611914	0.30974	0.044924	-0.042088	-0.01624	-0.464622	-1.043022	-0.726882	-0.232219
ATP-binding cassette, sub-family B (MDR/TAP), member 4	102910_at	0.045833	-0.458802	-1.085255	-0.279141	-0.045112	-0.745158	-0.088589	-0.362152	-0.864914	-0.309853
zinc finger protein 106	101456_at	-0.381288	-0.25765	0.166594	-0.054803	0.642665	-1.129859	-0.239167	-0.880565	-0.786918	0.090219
ESTs, Weakly similar to lysophospholipase I [M.musculus]	100880_at	-0.152734	-0.179543	0.164111	0.103996	-0.438802	-1.43246	-0.46253	-0.266749	-0.149246	-0.451437
ESTs, Weakly similar to junctional adhesion molecule [M.musculus]	98957_at	-0.347923	-1.096353	-0.063604	-0.021089	-0.080766	-0.714721	-0.719459	-0.560982	-0.337795	-0.290554
ESTs	103552_at	-0.117605	0.558119	-0.628791	-0.039456	0.015039	-1.258445	-0.366293	-0.267735	-0.64239	-0.073989
potassium channel, subfamily K, member 3	102020_at	0.045839	-0.035619	0.037176	-1.240051	-0.574148	-0.01678	-0.465258	-1.40284	-0.913172	-0.096245
ESTs, Highly similar to H<BETA>58 PROTEIN [Mus musculus]	96665_at	-0.211906	-0.115137	-0.515257	0.297083	-0.084548	-1.131073	-0.042612	-0.464752	-0.629377	-0.191904
FXYD domain-containing ion transport regulator 5	103394_at	2.319813	0.630208	1.266871	0.572288	0.542671	0.417786	0.130123	0.221048	0.574704	0.038341
ESTs, Highly similar to ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM [Homo sapiens]	104578_f_at	0.324987	0.524777	1.540381	1.011281	0.651005	0.283708	-0.034351	0.377251	0.738648	0.341089
ESTs, Highly similar to ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM [Homo sapiens]	104579_r_at	0.266193	0.396659	1.064664	0.588147	0.595583	0.766457	-0.415386	0.422228	0.623009	0.226235
cyclin-dependent kinase inhibitor 1A (P21)	94881_at	0.896864	1.197141	0.720501	0.686639	0.041632	0.68175	0.686842	-0.647415	0.07645	-0.62711
phosphofructokinase, platelet	97833_at	0.513542	0.127196	1.015957	0.823648	0.700993	0.462135	0.056214	0.162992	0.585607	0.315657
Mus musculus TNF intracellular domain-interacting protein mRNA, complete cds	95152_g_at	0.455091	0.32978	1.111826	0.727923	0.19864	0.49742	0.014732	0.19513	0.538648	0.1737
actin, alpha 1, skeletal muscle	100381_at	0.245005	0.450645	0.93033	0.911128	0.334738	0.422998	0.163627	0.688193	0.739672	-0.343721
cysteine rich protein 61	92777_at	0.796322	1.824274	0.859545	-0.003005	0.324082	0.683352	0.174506	0.107009	-0.375304	-0.107701
cathepsin Z	92633_at	0.477369	1.086035	0.154236	0.694196	0.330906	0.264133	-0.046904	0.371773	0.516492	-0.318787
dynein, cytoplasmic, light chain 1	96298_f_at	0.550596	-0.013757	1.135388	0.880408	0.810417	0.030851	-0.12078	0.557494	0.735175	0.129382
actin, gamma, cytoplasmic	96573_at	0.494114	0.504194	1.143136	0.432997	0.053542	0.180243	-0.337411	-0.118308	-0.128295	-0.592902
calcium binding protein A6 (calcyclin)	92770_at	0.474969	-0.072682	1.285171	0.967211	0.490838	0.543418	0.267586	0.278098	0.279284	-0.086075
cardiac morphogenesis	102213_at	0.834963	1.680522	0.726925	0.144607	-0.019137	0.792622	0.043138	0.076835	0.287985	0.078477
ESTs, Highly similar to TROPOMYOSIN 4, EMBRYONIC FIBROBLAST ISOFORM [Rattus norvegicus]	95542_at	0.324474	0.187186	0.833252	0.664631	0.303909	-0.261714	-0.20714	0.238612	0.557426	0.387586
calcium binding protein A11 (calgizzarin)	92539_at	0.221298	0.25752	1.616015	0.426204	0.229879	0.236432	-0.16765	0.431607	0.314159	-0.021378
collagen binding protein 1	94817_at	0.559572	0.117189	1.077142	0.314848	0.328858	0.372573	-0.424948	0.620443	0.905967	0.249186
procollagen, type IV, alpha 1	101093_at	0.316278	0.439054	0.630936	0.898303	0.122271	0.420172	-0.377638	-0.081647	0.245686	-0.472475
actinin alpha 2 associated LIM protein	101089_at	0.525031	0.653099	0.095821	0.503694	0.226588	0.300175	0.13199	0.362511	0.346268	0.528035
transforming growth factor, beta induced, 68 kDa	92877_at	0.127121	0.192596	1.256435	0.609513	0.379241	0.628109	-0.029583	0.269797	0.276881	-0.128648
Lamin A	98059_s_at	0.293237	-0.003353	1.063849	0.74308	0.372693	0.337976	-0.105274	0.164749	0.365985	0.137587
tubulin, beta 5	94788_f_at	0.268954	0.017928	1.472174	0.56238	0.212916	0.486959	-0.19581	0.346319	0.618233	-0.12996
ESTs	98346_at	-0.298955	1.041677	0.474802	0.485865	0.933109	0.788779	-0.284729	0.299086	-0.018654	0.172497
Intercellular adhesion molecule	96752_at	1.1134	1.335823	0.294069	0.154769	-0.117336	1.032653	-0.190495	-0.219524	0.086995	0.15879
procollagen, type IV, alpha 2	101039_at	-0.046107	0.110588	0.74361	0.801582	0.544584	0.56576	-0.294996	-0.162261	0.063329	0.061536
alpha actinin 4	96343_at	0.680848	0.592559	0.217558	0.574832	0.224138	0.302276	-0.184547	-0.206922	-0.088776	-0.204823
tubulin alpha 2	98759_f_at	0.212911	0.127285	1.219979	0.345907	0.1102	0.24649	-0.482547	0.901031	0.551637	0.280601
sodium channel, voltage-gated, type I, beta polypeptide	102808_at	0.25586	-0.081711	0.724866	0.77293	0.490301	0.088128	-0.364848	0.432925	0.841756	0.291954
procollagen, type XV	99637_at	0.391513	-0.162265	1.044238	1.102739	0.401082	0.403017	-0.254686	-0.35669	0.216715	-0.01153
immediate early response 3	94384_at	0.23705	-0.1763	1.167892	0.054257	0.447563	0.151535	0.287016	0.281759	0.46541	0.054902
rabaptin 5	101381_at	0.066447	1.218102	0.107432	0.110974	0.38247	-0.222123	0.106019	-0.526258	-0.641235	-0.254441
tubulin alpha 6	101543_f_at	0.374882	0.145942	0.79231	-0.033118	0.120353	0.281654	0.071464	0.754047	0.702142	-0.083208
actin related protein 2/3 complex, subunit 3 (21 kDa)	95434_at	0.543139	0.356395	-0.028976	0.277969	0.466749	0.089632	0.345631	0.043594	0.102171	-0.13301
procollagen, type VI, alpha 2	93517_at	0.386882	-0.289732	0.865564	1.222689	0.593479	0.267766	-0.579264	0.650253	0.373278	0.000871
calmodulin	96522_at	0.194291	-0.082504	0.762351	0.321272	0.3235	-0.344334	-0.458556	0.131698	0.2309	0.010419
GTP cyclohydrolase 1	102313_at	0.367012	1.663663	0.295522	-0.113518	0.234106	0.444737	-0.074793	0.234968	0.309656	-0.145866
procollagen, type VI, alpha 1	95493_at	0.125848	-0.219055	0.600584	1.077328	0.565205	0.402758	-0.310874	0.095112	0.393766	-0.122525
tubulin alpha 7	93924_f_at	0.132951	0.471513	0.740143	0.072511	-0.18001	0.616488	-0.537446	0.759258	1.042636	0.07834
growth arrest and DNA-damage-inducible, alpha	102292_at	-0.242245	-0.08768	-1.535559	-0.228088	-0.509692	-1.002098	-0.466973	-0.041719	-0.106981	0.099249
RAB9, member RAS oncogene family	95516_at	-0.103664	-0.134246	-0.534003	-0.431326	-0.318162	-0.662898	0.044825	-0.337076	-0.571363	-0.270508
FK506 binding protein 4 (59 kDa)	92808_f_at	0.202558	0.221267	-1.203009	-0.856501	-0.650225	0.078149	0.037438	0.202838	0.267112	-0.066041