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Comparison of Non-Human Primate and Human Whole Blood Tissue Gene Expression Profiles

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In conducting the research described in this report, the investigators complied with the regulations and standards of the Animal Welfare Act and adhered to the principles of the Guide for the Care and Use of Laboratory Animals (NRC 1996).

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14. ABSTRACT

Gene expression profiling is utilized in the development of medical countermeasures against chemical warfare agents (CWAs). Non-human primates (NHPs), specifically the rhesus macaque, the cynomologus macaque and the African green monkey, are vital models in the development of CWA prophylactics, therapeutics, and diagnostics. Gene expression profiling of NHPs is complicated by the fact that the genomes of these NHPs are not completely sequenced, and no oligonucleotide microarrays (genechips) are commercially available. We sought to determine whether gene expression profiling of NHP could be carried out using human genechips. Whole blood tissue RNA was isolated from each species of primate and used to generate genechip probes. Hybridization of the NHP samples to the human gene chips (Affymetrix Human U133 Plus 2.0 arrays) resulted in comparable numbers of transcripts detected when compared with human samples. Statistical analysis revealed intraspecies reproducibility of genechip quality control metrics; interspecies comparison between NHPs and humans showed little significant difference in the quality and reproducibility of data generated using human genechips. These results show that human genechips can be used for gene expression profiling of NHP samples and provide a foundation for the development of tools for the comparison of human and NHP gene expression profiles.

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ABSTRACT

Gene expression profiling is an important tool in toxicology and is utilized in the development of medical countermeasures against chemical warfare agents (CWAs). Non-human primates (NHPs), specifically the rhesus macaque (*Macaca mulatta*), the cynomologus macaque (*Macaca fascicularis*) and the African green monkey (*Cercopithecus aethiops*), are vital models in the development of CWA prophylactics, therapeutics, and diagnostics. However, gene expression profiling of NHPs is complicated by the fact that the genomes of these NHPs are not completely sequenced, and that there are no commercially available oligonucleotide microarrays (genechips). We therefore sought to determine whether gene expression profiling of NHP could be carried out using human genechips. Whole blood tissue RNA was isolated from each species of primate (n=4 for each NHP species; n=5 for humans) and used to generate genechip probes. Hybridization of the NHP samples to the human gene chips (Affymetrix Human U133 Plus 2.0 arrays) resulted in comparable numbers of transcripts detected when compared with human samples. Statistical analysis revealed intraspecies (i.e., within the same species) reproducibility of genechip quality control metrics; interspecies (i.e., cross-species) comparison between NHPs and humans showed little significant difference in the quality and reproducibility of data generated using human genechips. Gene expression profiles of each species were compared using principal component analysis (PCA) and hierarchical clustering to determine the similarity of the expression profiles within and across the species. The cynomologus group showed the least intraspecies variability, while the human group showed the greatest intraspecies variability. Intraspecies comparison of the gene expression profiles identified probesets that were reproducibly detected within each species. Each NHP species was found to be dissimilar from humans, with the cynomologus group being the most dissimilar compared with humans. Interspecies comparison of the gene expression profiles revealed probesets that were reproducibly detected in all species examined. These results show that human genechips can be used for gene expression profiling of NHP samples and provide a foundation for the development of tools for the comparison of human and NHP gene expression profiles.

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INTRODUCTION

Gene expression profiling using microarrays is an important tool in efforts to develop medical countermeasures against chemical warfare agents (CWAs) (Draghici et al., 2004). Gene expression profiling has been used to uncover mechanisms of toxicity of the vesicant sulfur mustard (Dillman et al, in press; Sabourin et al., submitted) and to characterize the effects of low-level exposure to the organophosphonate nerve agent VX (Blanton et al., 2004). Gene expression profiling is also an important tool in CWA drug development (Dillman et al., 2004).

A variety of models have been utilized in these gene expression profiling studies, including rats, mice, and cultured human cells. These studies have been facilitated by commercially available oligonucleotide microarrays that are based on the sequenced genomes of rats, mice, and humans. Non-human primates (NHPs), particularly the rhesus macaque (*Macaca mulatta*), the cynomologus macaque (*Macaca fascicularis*) and the African green monkey (*Cercopithecus aethiops,* AGM), are also important animal models used in efforts to develop CWA medical countermeasures. However, gene expression profiling of these species is problematic given that the genomes of these species have not been completely sequenced and there are no commercially available oligonucleotide microarrays (genechips). Given the high similarity between NHP and human genomes (e.g. 98.77% similarity between chimpanzee and human genomes, Fujiyama et al., 2002), it is reasonable to hypothesize that human genechips could be used for gene expression profiling of NHPs. Indeed, several studies have been published which have successfully utilized Affymetrix human genechips for gene expression profiling of NHPs (Wang et al., 2004; Uddin et al., 2004; Kayo et al., 2001; Enard et al., 2002; Chismar et al., 2002; Caceres et al., 2003; Vahey et al.,2003). These studies have used rhesus, chimpanzee, gorilla, or orangutan RNA, but to date no gene expression profiling studies are available that use AGM or cynomologus RNA. To develop methods for gene expression profiling of NHPs in support of efforts to develop CWA medical countermeasures, we compared the results of rhesus, cynomolous, AGM and human samples analyzed using human genechips. We measured the quality control metrics (e.g. fluorescent intensity, gene detection, background, noise) of human genechips probed with RNA from each of these species. Intraspecies (i.e. within a species) comparisons were made to verify data reproducibility and data quality. Interspecies (i.e. cross-species) comparisons were made to determine the performance of NHP samples relative to human samples on a human genechip. We used this data to assess the practicality of using human genechips for gene expression profiling of these NHP species. Furthermore, we evaluated the feasibility of utilizing gene expression profiling for interspecies comparison.

MATERIALS AND METHODS

Non-human primate and human test subjects.

In conducting the research described in this report, the investigators adhered to the Guide for the Care and Use of Laboratory Animals by the Institute of Laboratory Animal Resources, National Research Council, in accordance with the stipulations mandated for an AAALAC accredited facility. To conserve animals, we acquired blood samples from NHPs already in use with other research protocols. Female rhesus macaques (n=4) were of Indian origin and weighed 4-5.5 kg at the time of blood sampling. In a separate experiment, these animals were previously exposed to human butrylylcholinesterase (July 2003), huprezine A (December 2003) and physostigmine (October 2003). These animals were certified to be in good health at the time of the blood collection (June 17, 2004). Male cynomologus macaques (Covance, Denver, PA) were wild caught and of Vietnamese origin. In a separate experiment, these animals had been previously exposed to human butyrylcholinesterase and survived a $5.5xLD_{50}$ challenge of soman in December 2003. The animals were certified to be in good health and weighed 3-4 kg at the time of the blood collection (May 13, 2004). Both the rhesus and cynomologus macaques were housed at the Walter Reed Army Institute of Research (WRAIR, Silver Spring, MD) at the time of the blood collection. Blood from these test subjects was collected by WRAIR personnel and shipped at ambient temperature to USAMRICD on the day of the blood collection. Male African green monkeys (n=4) were wild caught from the Caribbean island of St. Kitts. These animals were naïve and certified in good health at the time of the blood collection. These animals were housed at USAMRICD and weighed 5.5-6.8 kg at the time of the blood collection.

Human blood samples (n=5) were collected in accordance with approved human use protocols at USAMRICD. The test subjects were all Caucasian males ranging in age from 23-39 years at the time of the blood collection. All human test subjects were in apparent good health at the time of the blood collection.

Collection of blood tissue.

Whole blood tissue from each donor was collected using a 5 cc syringe and immediately injected into a PAXgene™ Blood RNA Collection Tube (PreAnalytiX, Franklin Lakes, NJ). For NHP donors, whole blood tissue was withdrawn from the right or left saphenous vein. For human donors whole blood tissue was withdrawn from the median cubital vein. Approximately 1.0 mL of whole blood tissue was obtained from the rhesus macaques, and 2.5 mL of whole blood tissue was obtained from all other donors. All samples were incubated in the PAXgene™ Blood RNA tube for 24hrs prior to extraction.

Isolation of RNA from whole blood tissue.

RNA was extracted from whole blood tissue according to the PAXgene™ Blood RNA Kit Handbook (April, 2001), with minor modifications. Initial centrifugation time in step 1 of the handbook was increased from 10 minutes at 3000 x g to 15min at 3000 x g to obtain a sufficient pellet. After proteinase K treatment, the centrifugation time was increased from 3 minutes to 7 minutes to obtain a well-defined interface. The quality and amount of RNA was analyzed by UV spectrophotometry with a Nanodrop® ND-1000 UV-Vis Spectrophotometer (Nanodrop Technologies, Rockland, DE). All RNA was precipitated with 3M sodium acetate, glycogen and 100% ethanol and stored at -80° C.

Gene expression profiling.

Gene expression profiling was performed using Affymetrix Human Genome U133 2.0 Plus oligonucleotide microarrays, as described at http://www.affymetrix.com/support/technical/datasheets/human_datasheet.pdf (Affymetrix, Santa Clara, CA). Precipitated RNA was removed from the -80° C freezer, thawed on ice, and centrifuged for 15 minutes at 16,000 x g, 4° C. The supernatants were removed via pipette, and the pelleted RNA was washed with 75% ethanol and centrifuged for 10 minutes at 16,000 x g, 4° C. The supernatant was removed, and the pelleted RNA was washed a second time with 95% ethanol and centrifuged for 10 minutes at 16,000 x g, 4° C. The supernatant was removed, and the RNA pellets were allowed to air dry at room temperature for approximately 15 minutes. Samples were reconstituted in 60 µL of RNase-free water and analyzed by UV spectrophotometry and by microcapillary electrophoresis using an Agilent Bioanalyzer (Agilent, Palo Alto, CA).

Due to a limited supply of total RNA from the rhesus macaques and cynomologus macaques, two rounds of linear amplification were performed on all samples using the Bioarray™ RNA Amplification and Labeling System (Enzo Life Sciences, Farmingdale, NY). Briefly, 75-500ng of total RNA was used to generate first-strand cDNA. A T7-dt primer was used to prime reverse transcription and incorporate a T7 promoter sequence into the cDNA. RNA was eliminated by base hydrolysis followed by neutralization. A proprietary homopolymeric tail was added to the 3' end of the first-strand cDNA followed by chain termination. A site-specific primer complimentary to the homopolymeric tail was used to initiate second strand cDNA synthesis. After second strand synthesis the purified double-stranded cDNA was used to perform *in vitro* transcription resulting in approximately 100-fold increase of copy RNA (cRNA). The cRNA was purified using RNeasy columns (Qiagen, Valencia, CA) and the concentration was determined via UV spectrophotometry. A maximum of 2,000 ng of purified cRNA was utilized as the template in a second round of cDNA synthesis as described above. Purified double-stranded cDNA was utilized in an *in vitro* transcription labeling reaction using biotinylated UTP and CTP, resulting in a 100-fold increase of labeled target cRNA. The target cRNA generated from each sample was processed as per manufacturer's recommendation using an Affymetrix Genechip Instrument System (http://www.affymetrix.com/support/technical/manual/expression_manual.affx). Briefly, spiked controls were added to 15µg of fragmented cRNA before hybridizing at 45° C at 40 revolutions per minute for 40-45 hours using 10µg of cRNA (Sartor et al., 2004). Arrays were then washed and stained with streptavidin-phycoerythrin before being scanned on the Affymetrix Genechip® Scanner. After scanning, array images were visually inspected to confirm scanner alignment and the absence of significant bubbles or scratches on the chip surface.

Data Analysis.

Scanned output files from each array were obtained using Affymetrix Gene Chip Operating Software (GCOS v 1.2). Raw signal intensities were normalized using either the GCOS algorithm (Affymetrix) followed by addition of a constant (c=1) and log transformation ($\log_2$), or using the robust multi-array averaging (RMA) algorithm (Irizarry et al., 2003). The normalized data were imported as a comma separated values (.csv) file into Partek Pro 6.0 (Partek, St. Louis, MO). The imported data was analyzed by principal component analysis (PCA) to determine the significant sources of variability in the data. For hierarchical clustering, Euclidian parameters were specified to calculate interpoint distances and single linkage was specified to calculate the intercluster distances. Boolean analysis of the data was performed using Excel 2003 (Microsoft, Redmond, WA). Probesets that exhibited an intensity with an associated p-value $p<0.05$ for any given sample were called present. To generate the most stringent list of probesets for intra- and inter-species comparison, we only included probesets that were called present for each biological replicate within a given species (100% reproducibility). Once all comparisons were made the probeset list was tabulated for each respective group comparison. The probesets were imported into Onto-Express (Khatri et al., 2002) as a text file to classify the molecular function and biological processes represented by the probesets.

RESULTS

Intra- and interspecies comparison of quality control metrics for human genechips hybridized with NHP or human RNA probes.

RNA probes were synthesized from NHP or human RNA isolated from whole blood tissue as described and were hybridized to human genechips. A number of quality control metrics are reported when a genechip is scanned to determine a gene expression profile. These metrics include chip background, chip noise (also termed Raw Q), total fluorescent intensity, the number of genes detected (called "present") and the 3'/5' ratio of the housekeeping gene GAPDH (a measure of probe quality). These metrics are assessed to determine the validity of the data obtained from the scanned genechip. We compared these quality control metrics for each chip probed with a particular species to determine intraspecies reproducibility and signal intensity (Table 1). We found that results were consistent within each species based on a 95% confidence interval (Table 1). We also performed an interspecies comparison of quality control metrics between each NHP and humans. We found that the only significant difference was the percent marginal call (transcripts near the threshold of detection are called marginal) for the cynomologus group. No other significant differences were observed.

Analysis of gene expression profiles: Principal component analysis.

The gene expression profiles for NHP and human whole blood tissue were analyzed by principal component analysis (PCA; Figure 1). Each of our samples is defined by 54,000 probesets, which represent 38,500 well-characterized genes from the completely sequenced human genome (Affymetrix Data Sheet, 2004). These 54,000 probesets represent 54,000 response variables, giving us a 54,000-dimensional data set. PCA reduces the complexity of high-dimensional data and simplifies the task of identifying patterns and sources of variability in a large data set (Hotelling, 1933; Joffille, 1986). The samples (four or five biological replicates each hybridized to a separate genechip) are represented by the spheres in the three-dimensional plot (Figure 1). The distance between any pair of points is related to the similarity between the two samples in high-dimensional space (in this case, 54,000 variables and 54,000-dimensional space). Samples that are near each other in the plot are similar in a large number of variables (i.e., expression level of individual probe pairs). Conversely, samples that are far apart in the plot are different in a large number of variables.

Analysis of the whole blood tissue gene expression profiles by PCA revealed a distinct partition between the human samples and the NHP samples (Figure 1A-D). This is the case using two different data normalization algorithms (GCOS, Figure 1A, 1B; RMA Figure 1C, 1D), indicating that the partition in the data set is independent of data transformation methods. Based on the whole blood tissue gene expression profile, no single NHP species partitions closer to humans than the others. Ellipsoids which represent space two standard deviations from the mean of the sample set are all closely aligned for each NHP species (Figure 1B, 1D). Thus, our data suggest that each of the three NHP species tested is equally different from humans in an interspecies comparison of whole blood tissue gene expression profiles. Within each NHP species, the cynomologus group appears to have the least intraspecies variability. The rhesus, AGM, and human groups appear to have comparable intraspecies variability.

Analysis of gene expression profiles: Hierarchical clustering.

The gene expression profiles for NHP and human whole blood tissue were analyzed by hierarchical clustering (Figure 2). Hierarchical clustering is used to group similar objects into clusters. At the start of the analysis each sample is considered a cluster. The two most similar clusters are combined and continue to combine until all objects are in the same cluster (termed the root). Hierarchical clustering produces a tree (dendogram) that shows the hierarchy of the clusters. The distance between the two members of the cluster determines its height. Groups of samples that are similar will be combined with short clusters, whereas tall clusters will separate dissimilar groups. The width of the clusters has no mathematical value.

Analysis of the whole blood tissue gene expression profiles by hierarchical clustering confirmed many of the observations made by PCA. An intensity map of pairwise comparisons of interpoint distances revealed that the cynomologus group shows the least intraspecies variability (Figure 2A, center of intensity map). In contrast, the rhesus and AGM groups show more intraspecies variability than the cynomologus group (Figure 2A, bottom right corner of intensity map). Variability in the human group appears comparable to that of the rhesus and AGM groups. Interestingly, sample H1 shows the least similarity to the other human group members (Figure 2A, note red blocks in the top left corner of the intensity map). In interspecies comparisons, the greatest dissimilarity appears to be between the human group and the cynomologus group (Figure 2A, left center of the intensity map). A detailed view of the dendogram generated by the hierarchical clustering is shown in Figure 2B. The human samples and the NHP samples separate into two distinct clusters. The human group has the greatest intraspecies variability, and thus this cluster has the greatest height. The cynomologus group has the least intraspecies variability and thus this cluster has the smallest height. Interestingly, the cynomologus samples cluster away from the rhesus and AGM samples, while the AGM and rhesus samples are not discretely clustered into separate distinct AGM and rhesus clusters. One AGM sample is observed clustering away from the rest of the AGM and rhesus samples nearer to the human cluster.

Analysis of gene expression profiles: Boolean analysis.

The gene expression profiles for NHP and human whole blood tissue were examined using an intraspecies Boolean analysis (Boole, 1848). Probesets having a detection p-value of $p<0.05$ for all biological replicates within a given species (100% reproducibility) were included in the total number of probesets detected (called "present") for that species. These results are summarized in Table 2. The Boolean analysis identified 6,820 probesets detected in the cynomologus group; 2,643 probesets detected in the AGM group; 2,757 probesets detected in the rhesus group; and 2,303 probesets detected in the human group. The results of interspecies comparisons (2-way, 3-way, and 4-way comparisons) of the probesets reproducibly detected in each intraspecies comparison are summarized in Table 2 and in a Venn diagram in Figure 3. In a

4-way interspecies comparison, 1079 probesets were 100% reproducibly detected. These 1079 probesets represent 1009 unique genes.

Characterization of probe sets reproducibly detected in intra- and interspecies comparisons.

To identify the molecular functions and biological processes represented by the probesets reproducibly detected in each species and determine whether they are similar across the species, we mapped this group of probesets to the Gene Ontology^{TM} (The Gene Ontology Consortium, 2000). The Gene Ontology (GO) project is a collaborative effort to address the need for consistent descriptions of gene products in different databases. A controlled GO vocabulary is maintained in a curated database. GO provides three structured networks of defined terms to describe gene product attributes. These are biological process, molecular function, and cellular compartment. We used the web-based search engine Onto-Express to map our genes to the GO database (Khatri et al., 2002). Onto-Express translates lists of differentially regulated transcripts identified in high throughput gene expression experiments into functional profiles based on the GO. The statistical significance value is calculated, and results are displayed graphically as GO hierarchical trees. Table 3 summarizes the molecular functions represented by each group of probesets ($p<0.01$), and Table 4 summarizes the biological processes represented by each group of probesets. Although there is overlap among the species with regards to the molecular functions and biological processes represented by each group of probesets, the cynomologus group appears to be less similar to humans than either the AGM or rhesus groups.

To identify the molecular functions and biological processes represented by the probe pairs reproducibly detected in all species (100% reproducibility in both intra- and interspecies comparisons), we mapped these 1079 probesets (Table 5) to the Gene Ontology^{TM} (The Gene Ontology Consortium, 2000). Table 6 summarizes the molecular functions represented by this group of probesets ($p<0.01$), and Table 7 summarizes the biological processes represented by this group of probesets ($p<0.01$).

DISCUSSION

Non-human primates (NHPs) are an important animal model in the development of medical countermeasures against CWAs, particularly for determining safety and efficacy in lieu of human clinical trials. Our objective was to evaluate the suitability of using human genechips for gene expression profiling of NHPs. We compared the quality control metrics (e.g., fluorescent intensity, gene detection, background, noise) of human genechips probed with RNA from each NHP species and humans to assess the quality and intraspecies reproducibility of the fluorescent signal. Furthermore, we assessed of the feasibility of utilizing gene expression profiling for interspecies comparison.

Although previous work has been published using human genechips to study NHPs, particularly rhesus, chimpanzee, gorilla, and orangutan (Uddin et al., 2004; Kayo et al., 2001; Enard et al., 2002; Chismar et al., 2002; Caceres et al., 2003) an evaluation of the response of cynomologus macaque or AGM RNA on a human genechip is not available in the open literature. In this study we found that whole blood tissue RNA from each NHP tested generated reproducible data comparable to the data obtained using human RNA on a human genechip (Table 1). These results suggest that gene expression profiling of rhesus, cynomologus, or AGM can be performed reliably using human genechips. This is in agreement with previous studies that have examined the performance of rhesus RNA on human genechips (Chismar et al., 2002; Wang et al., 2004) and extends these observations to cynomologus and AGM RNA.

Since NHP RNA performed well on human genechips, we analyzed the actual gene expression profiles of the NHPs and humans. Analysis of the gene expression data by PCA revealed that each NHP whole blood tissue gene expression profile appears to be equally dissimilar to humans (Figure 1). These results are supported by the hierarchical clustering analysis, in which the human group clusters away from the NHPs (Figure 2). However, the intensity map representing interpoint distances between clusters suggests that the cynomologus group is more dissimilar than the rhesus or AGM compared to humans (Figure 2A). As observed in the PCA, the intensity map, and the cluster dendogram, the cynomologus group shows the least intraspecies variability while the human group shows the greatest intraspecies variability.

The low intraspecies variability of the cynomologus group may be a factor in the 2.5- to 3-fold greater number of probesets observed as reproducibly detected in this group compared with the other groups (Boolean analysis, Table 2). Since a probeset was counted if it was detected (called "present") in all replicates for a species, lower intraspecies variability would tend to result in a higher number of probesets counted. The tight clustering of the cynomologus group (observed by PCA and cluster analysis) may be due to any of a number of factors. These animals were wild caught and they may be genetically related in some way (e.g., siblings). Another factor that may result in the apparent lower intraspecies variability of the cynomologus group is the exposure history of these animals. In a previous unrelated experiment, these animals were exposed to human butrylylcholinesterase and survived a 5.5xLD_{50} challenge of soman. Although this occurred five months prior to our blood collection and the animals were certified to be in good health and fully recovered from the soman exposure, long-term alterations in the whole blood gene expression profile may have been induced. Furthermore, when we mapped the genes that are reproducibly detected within each species to the Gene Ontology, we discovered that the molecular functions and biological processes associated with these genes appear more similar among humans, AGM and rhesus but appear less similar in the cynomologus group compared with other groups (Tables 3 and 4). While this may be attributed to the greater number of probesets available for gene ontology mapping in the cynomologus group (>6K probesets compared with ~2-3K probesets in the other species) there are also biological processes that are significant in humans, AGM, and rhesus not detected in the cynomologus group, for example, antigen presentation of exogenous antigen (Human p=6.31x10-7; AGM p=1.49x10-4; rhesus p=4.32x10-7; cynomologus p>0.01 Table 4). These observations would require further research to determine their significance, including gene expression profiling of completely naïve cynomologus macaques. Furthermore, a greater number of subjects in each group representing variations across gender, age, and ethnicity would be needed to assess more accurately the intraspecies biological variability.

In our interspecies comparison of the probesets reproducibly detected across all replicates within a species, we identified a group of probesets that is reproducibly detected across all species examined in our study. This group of probesets maps to 1009 unique genes (Table 5). Although the significance of this group of probesets is not clear at the present time, it is interesting to speculate about potential uses for this group of probesets. Since genes in this group of probesets are reproducibly detected within and across the species studied, they may serve as controls useful in normalizing data collected from these different species using human genechips. Thus, these probesets, or more likely a subset of these probesets, have the potential to serve the purpose that "housekeeping" genes do in other types of experiments, such as Western blotting or PCR experiments. While it is becoming clear that there are likely no universal housekeeping genes, housekeeping genes can be useful if they have been validated in a particular system (Bustin, 2003). This would require additional research looking at detection of these probesets across an expanded population of test subjects, and examining how detection of these probesets may change after a chemical exposure. For now, this group of probesets provides a source of potentially valuable normalization control genes useful for the future development of tools for interspecies comparisons.

One issue that is critical to consider when interpreting our data is the difference in the genomes and the mechanisms of gene expression between humans and NHPs. Although the genomes of humans and chimpanzees have been shown to be highly similar (98.77% similarity, Fujiyama et al., 2002), and presumably this is true of other NHP species, there are obviously still differences that may affect the interspecies detection of certain genes. In addition, focusing on genome similarity neglects the fact that gene expression profiling is based on mRNA expression and not on DNA sequence. A single gene does not necessarily generate a single transcript. Splicing variants are very common in the human, and humans and NHPs may use different splicing strategies in some genes. Recently, several publications have begun to address these issues of interspecies variation in gene expression and genomic sequence as it relates to the issue of analyzing NHP gene expression profiles with human genechips. Chismar and colleagues (2002) used the U95Av2 human genechip and compared the expression patterns of humans with rhesus. They concluded that the percentage of detected genes (genes called "present") in the rhesus brain is lower than that of human brain, and that this is especially true for genes with lower signal intensity. Caceres and colleagues (2003) used the HG-U95Av2 human genechip to identify upregulated genes in the human cortex compared with those of the NHPs. Since sequence divergence could lead to an underestimation of expression levels in NHPs, they excluded 4572 probesets that exhibited different hybridization behavior between two sets of samples in order to reduce false positives. However, this analysis is solely based on probeset signal intensities and not on actual sequence data. Wang and colleagues (2004) employed a sequence analysis approach to assess the utility of human genechips for the study of NHP gene expression profiles. They identified probesets conserved between rhesus and human based on sequence analysis and identified these probesets as providing a more accurate reflection of gene expression profiles. They found that of the 54,675 probesets on the HG-U133 Plus 2.0 genechip (representing the entire human genome), that 3636 of these were interspecies conserved between humans and rhesus (6.6%). Pair-wise correlation coefficients of 20 samples (12 human and 8 rhesuses) were calculated for expressed probesets (0.65±0.044) and for the ISC probesets (0.80±0.026). These results suggest that the reproducibility of interspecies comparisons can be increased by using a subset of probesets that have been previously defined based on sequence analysis. This worked well for rhesus since there is a considerable amount of sequence information available in public databases (as of December 16, 2004, there were 56,063 entries in Genbank under the organism term "*Macaca mulatta*"). However, in the case of cynomologus macaques, the number drops to 3,717 Genbank entries under the organism term "*Macaca fascicularis,*" and is even lower for African green monkeys (3,059 Genbank entries under the organism term "*Cercopithecus aethiops*"). However, none of these compares to humans, for which there are 9,018,755 Genbank entries under the organism term "*Homo sapiens.*" Thus, there is still a considerable amount of work to be done in developing tools to compare the gene expression profiles of humans and NHPs.

The work described herein represents an initial starting point in the development of methods to analyze the gene expression profiles of NHPs and to make comparisons with human gene expression profiles. Larger sample sizes are obviously an important component of developing these tools. One way to address this would be to perform gene expression profiling of NHPs housed at USAMRICD and/or at WRAIR on an ongoing basis. Blood samples could be taken when NHPs first arrive, thereby increasing the sample size of naïve test subjects. In addition, as animals are used in a research context and are exposed to various chemical agents, blood samples could be collected, their gene expression profiles determined, and that data entered into a gene expression profile database. Over time, the database would grow to include not only baseline parameters of naïve animals, but also gene expression profiles of animals exposed or treated with various chemicals or countermeasures. A human baseline can also be developed by collecting blood samples from human volunteers at USAMRICD. Metadata (e.g. age, diet, gender, etc.) would be included in the database for all samples (both human and NHP). Over the course of time, this database would become a powerful tool by enabling statistical comparison of the gene expression profiles of naïve animals with exposed animals, identifying potential genomic biomarkers of exposure for future development of diagnostics tests, comparing the effects of various agents within a class of agents (e.g., subtle differences in the effects of the G-agents), comparing humans and NHPs, and developing a statistically robust dataset that could potentially be used in support of submissions for regulatory approval of CWA medical countermeasures.

In conclusion, we have shown that gene expression profiling of NHP samples using human genechips gives reliable, reproducible data. Comparison of humans with NHPs will become more robust as new tools are advanced to address this challenge. This preliminary dataset serves as the foundation for the genomic assessment of NHP responses to CWA exposure and medical countermeasures, and will enhance efforts to develop CWA medical countermeasures that are safe and effective in humans.

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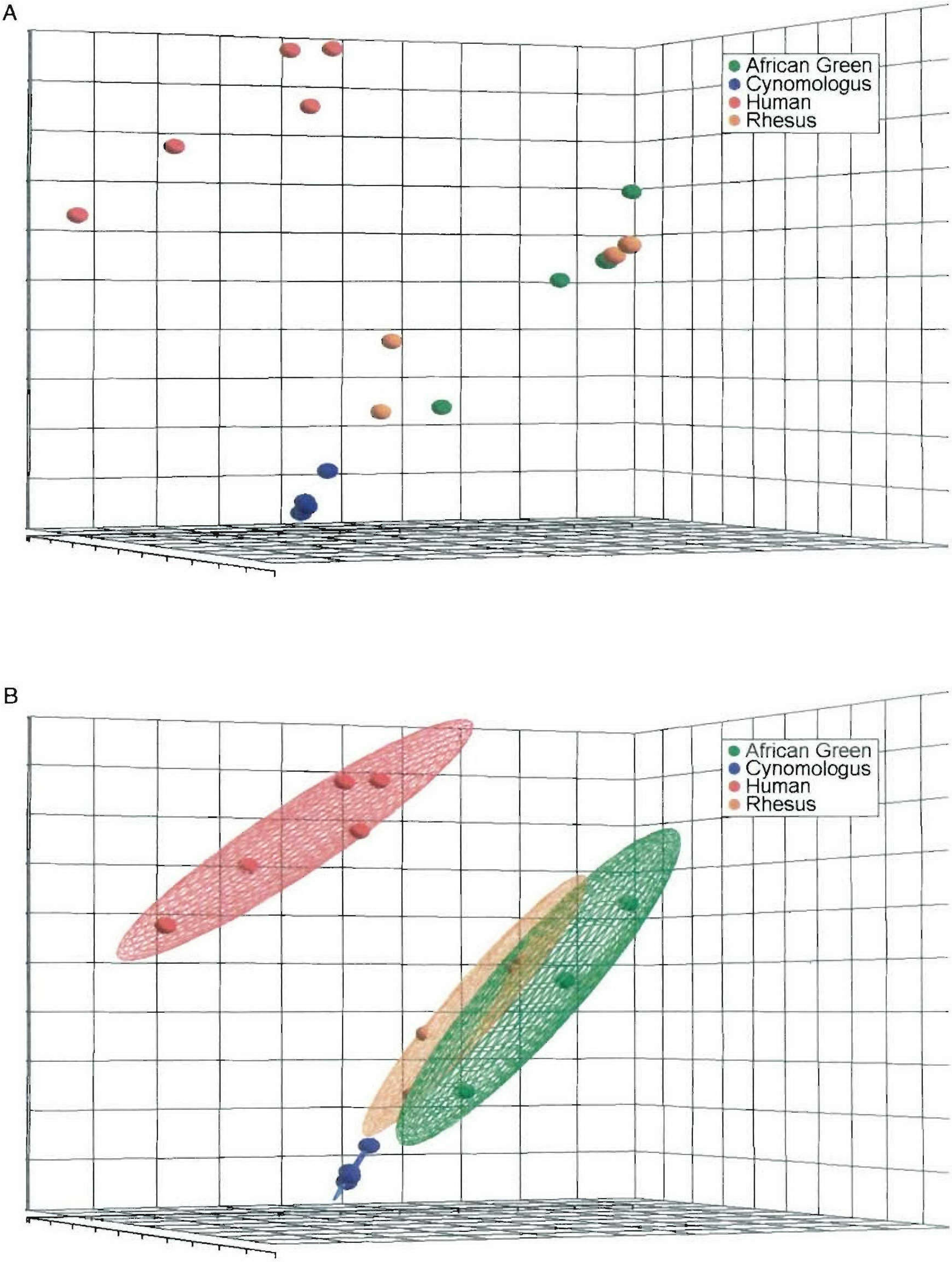
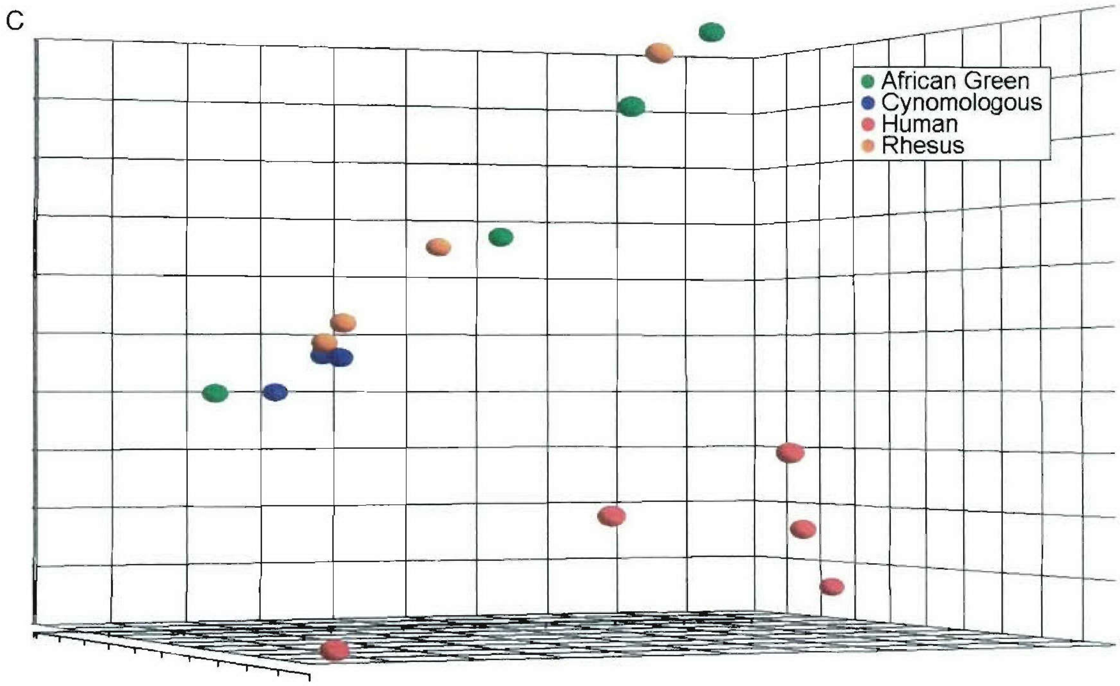
FIGURE LEGENDS

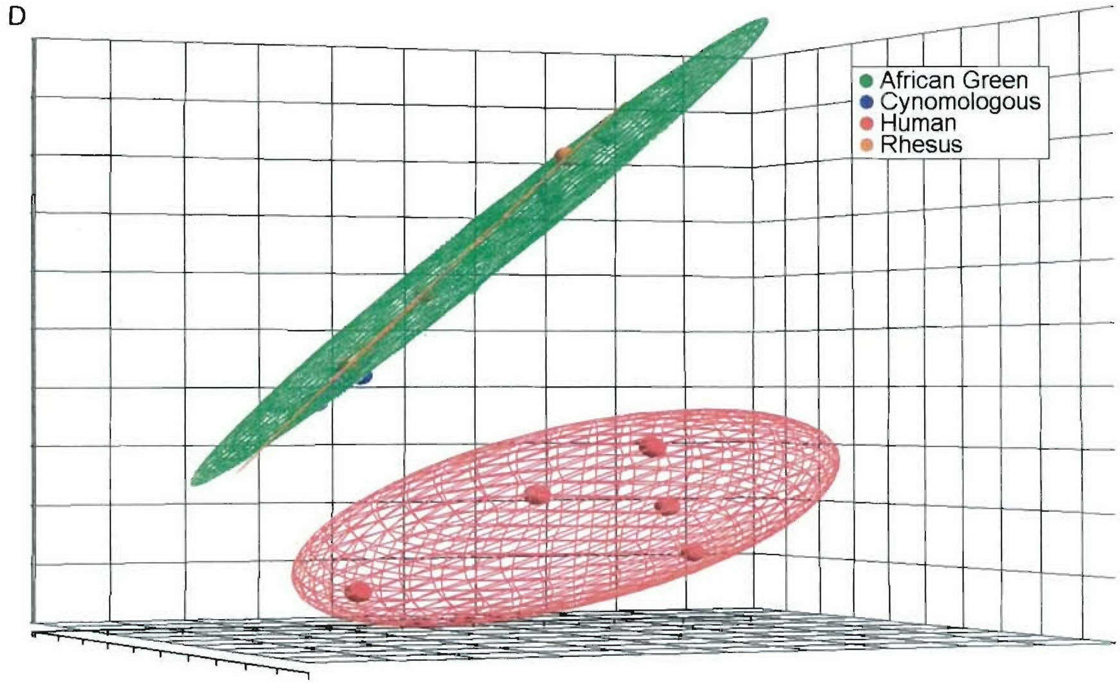
Figure 1. Principal component analysis of primate whole blood tissue gene expression profiles.
Gene expression levels for 54,000 probe pairs (representing 38,500 genes) were uploaded to Partek Pro 6.0 and analyzed by principal component analysis. The GeneChip Operating System (GCOS) normalization algorithm (A, B) and the RMA normalization algorithm (C, D) are shown for comparison. The ellipsoids (B, D) represent a two-standard deviation space from the mean of each sample set.

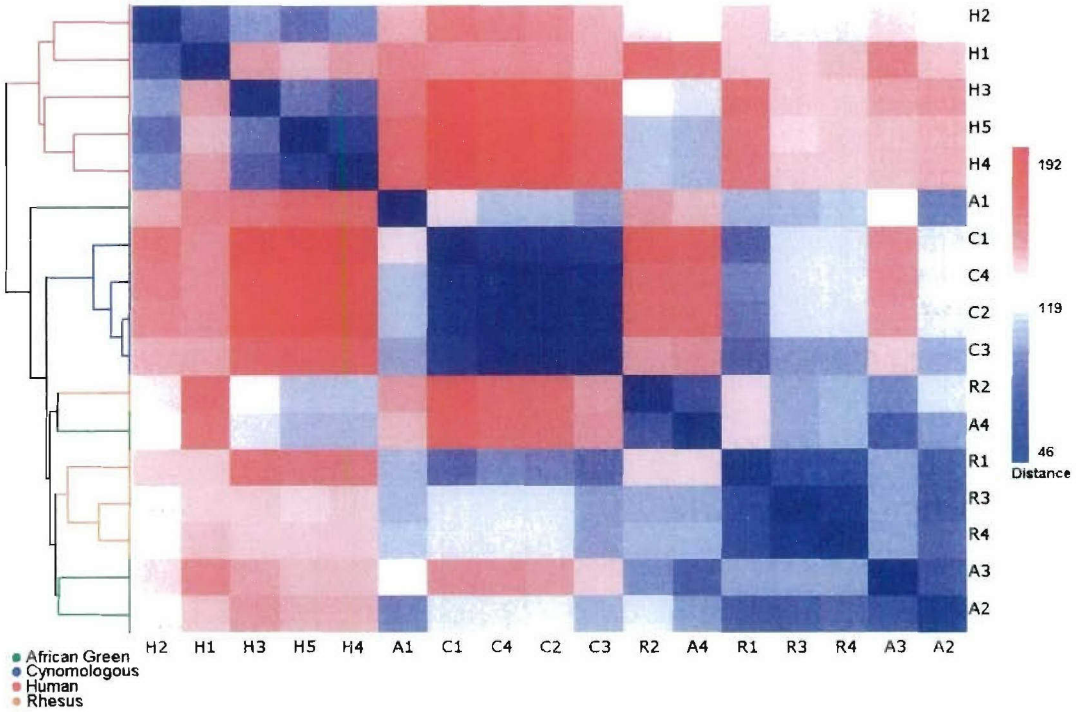
Figure 2. Hierarchical cluster analysis of primate whole blood tissue gene expression profiles.
The dataset was clustered based on sample gene expression profile as described. A) Pairwise comparisons of sample interpoint distances are displayed as an intensity map. The color intensity is related to the interpoint distance between samples and is indicated by the intensity scale to the right of the map. Similar samples are colored blue, while dissimilar samples are colored red in the intensity map. Each sample is indicated along the bottom and to the right of the map (H=human, C=cynomologus, R=rhesus, A=African green). A dendogram of the clusters is indicated on the left of the intensity map. B) The cluster dendogram in greater detail. The samples are indicated by color and by alphanumeric designation as described for the intensity plot.

Figure 3. Venn diagram summarizing the Boolean analysis of primate whole blood gene expression profiles.
Intra- and interspecies Boolean analyses were performed as described and probe pair sets representing the intersection of all inter- and intraspecies comparisons were identified.


A
African Green
Cynomologus
Human
Rhesus
B
African Green
Cynomologus
Human
Rhesus


C
African Green
Cynomologous
Human
Rhesus


D
African Green
Cynomologous
Human
Rhesus


H2
H1
H3
H5
H4
A1
C1
C4
C2
C3
R2
A4
R1
R3
R4
A3
A2
H2 H1 H3 H5 H4 A1 C1 C4 C2 C3 R2 A4 R1 R3 R4 A3 A2
192
119
46
Distance
● African Green
● Cynomologous
● Human
● Rhesus

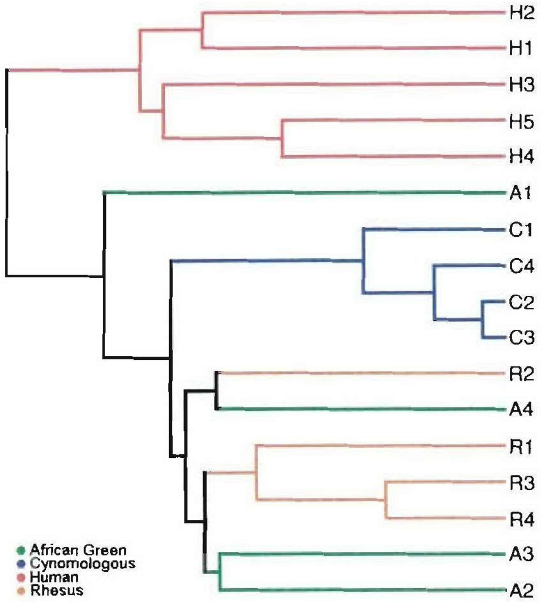
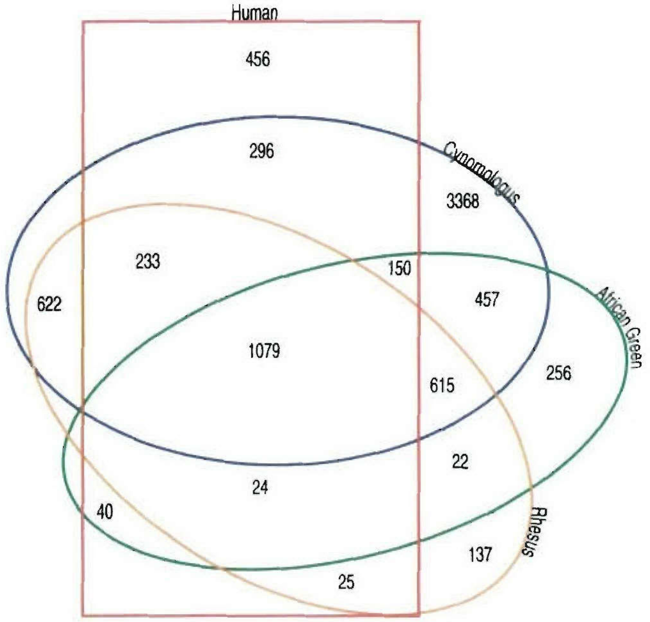

H2
H1
H3
H5
H4
A1
C1
C4
C2
C3
R2
A4
R1
R3
R4
A3
A2
● African Green
● Cynomologous
● Human
● Rhesus

FIGURE 3


Human
456
296
Cynomologus
3368
233
150
622
457
African Green
1079
615
256
22
24
40
Rhesus
137
25

		N	Mean	Std. Deviation	Std. Error	95% Confidence Interval for Mean		Min	Max
						Lower Bound	Upper Bound		
Background	African Green	4	46.36	6.51	3.26	35.99	56.72	38.89	54.7
	Cynamologous	4	49.81	4.84	2.42	42.10	57.52	43.62	55.3
	Rhesus	4	48.19	10.80	5.40	31.01	65.37	38.17	61.4
	Human	5	45.81	5.93	2.65	38.45	53.17	35.89	50.2
Noise (Raw Q)	African Green	4	2.54	0.59	0.30	1.60	3.49	1.81	3.1
	Cynomologus	4	3.17	0.51	0.25	2.36	3.98	2.50	3.7
	Rhesus	4	2.92	0.95	0.48	1.40	4.43	1.99	3.8
	Human	5	2.60	0.53	0.24	1.94	3.26	1.70	2.9
Total Fluor. Intensity	African Green	4	1.32E+07	7.33E+06	3.67E+06	1.56E+06	2.49E+07	2.3E+06	1.8E+0
	Cynomologus	4	1.82E+07	1.61E+06	8.050E+05	1.57E+07	2.08E+07	1.6E+07	2.0E+0
	Rhesus	4	9.76E+06	9.64E+06	4.82E+06	5.57E+06	2.51E+07	8.9E+05	1.8E+0
	Human	5	1.51E+07	1.02E+06	4.58E+05	1.38E+07	1.63E+07	1.4E+07	1.7E+0
%Present	African Green	4	0.1365	0.0334	0.0167	0.0833	0.1897	0.0920	0.166
	Cynomologus	4	0.2005	0.0226	0.0113	0.1645	0.2365	0.1810	0.233
	Rhesus	4	0.1405	0.0402	0.0201	0.0765	0.2045	0.0890	0.187
	Human	5	0.1402	0.0550	0.0246	0.0719	0.2085	0.0990	0.230
%Absent	African Green	4	0.8490	0.0347	0.0173	0.7938	0.9042	0.8180	0.895
	Cynomologus	4	0.7820	0.0236	0.0118	0.7444	0.8196	0.7480	0.802
	Rhesus	4	0.8450	0.0423	0.0212	0.7777	0.9123	0.7960	0.899
	Human	5	0.8460	0.0566	0.0253	0.7758	0.9162	0.7540	0.889
%Marginal	African Green	4	0.0148	0.0013	0.0006	0.0127	0.0168	0.0130	0.016
	Cynomologus	4	0.0175*	0.0010	0.0005	0.0159	0.0191	0.0170	0.019
	Rhesus	4	0.0145	0.0021	0.0010	0.0112	0.0178	0.0120	0.017
	Human	5	0.0140	0.0016	0.0007	0.0120	0.0160	0.0120	0.016
3'/5' Ratio GAPDH**	African Green	4	7.73	3.92	1.96	1.50	13.96	4.43	13.3
	Cynomologus	4	2.74	0.44	0.22	2.04	3.43	2.15	3.1
	Rhesus	4	3.49	1.85	0.92	0.55	6.42	2.45	6.2
	Human	5	4.62	2.59	1.16	1.40	7.84	1.41	7.2

* Significantly different than human, p<0.05.

** Non-normal distributions.

Table 1. Intra- and interspecies comparison of quality control metrics for human genechips hybridized with NHP or human probes.
Genechip quality control metrics were compared both intraspecies and interspecies. All data was tested for normality. All parameters had normal distributions except for total fluorescence intensity and the 3'/5' ratio of glyceraldehyde-3-phosphate dehydrogenase (GAPDH). Comparison of the three NHPs to humans for each parameter was made using a one-factor analysis of variance (ANOVA) for the normally distributed parameters and a Kruskal-Wallis test (non-parametric ANOVA) for total fluorescence intensity and the 3'/5' ratio of GAPDH. Species group was statistically significant, $p<0.05$ for the marginal (%) parameter. A Dunnett's test was used to compare the three NHPs to humans. Only the cynomologus group was found to be significantly different than the humans, $p<0.05$. No other significant differences were observed.

Comparison	Total # of probesets	N=
Human (H)	2303	5
Cynomologous macaque (CM)	6820	4
African green monkey(AG)	2643	4
Rhesus macaque (RM)	2757	4
CM and AG	2301	8
CM and RM	2549	8
AG and RM	1704	8
H and CM	1758	9
H and AG	1293	9
H and RM	1361	9
CM, AG, RM	1694	12
H, CM, AG	1229	13
H, CM, RM	1312	13
H, RM, AG	1103	13
H, RM, AG,CM	1079	17

Table 2. Boolean analysis of NHP and human whole blood tissue gene expression profiles.
An intraspecies Boolean analysis was performed to identify genechip probesets detected with 100% reproducibility. A series of 2-way, 3-way, and 4-way interspecies Boolean analyses were performed to identify genechip probesets detected with 100% reproducibility across the various species.

Table 3. Molecular functions represented by each species probe pair set. The top ranked biological processes are indicated in the shaded area, and those that are in common among the species are indicated in bolded text.

Index	Human	P-Value	AGM	P-Value	Cyno	P-Value	Rhesus	P-Value
1	**RNA binding**	1.28E-13	**RNA binding**	1.11E-16	**RNA binding**	3.79E-13	**RNA binding**	1.53E-13
2	**structural constituent of ribosome**	8.52E-14	**structural constituent of ribosome**	1.11E-16	**structural constituent of ribosome**	2.52E-13	**structural constituent of ribosome**	1.02E-13
3	**hydrogen-transporting ATP synthase activity, rotational mechanism**	8.31E-13	**hydrogen-transporting ATP synthase activity, rotational mechanism**	1.62E-12	DNA binding	1.89E-13	**hydrogen-transporting ATP synthase activity, rotational mechanism**	8.42E-13
4	**hydrogen-transporting ATPase activity, rotational mechanism**	2.25E-12	**cytochrome-c oxidase activity**	4.22E-12	ubiquitin-protein ligase activity	4.54E-13	**hydrogen-transporting ATPase activity, rotational mechanism**	2.57E-12
5	**oxidoreductase activity**	4.28E-11	**hydrogen-transporting ATPase activity, rotational mechanism**	4.94E-12	pre-mRNA splicing factor activity	3.53E-12	**oxidoreductase activity**	2.88E-11
6	**NADH dehydrogenase (ubiquinone) activity**	2.12E-10	**GTP binding**	1.94E-09	**translation initiation factor activity**	3.25E-11	pre-mRNA splicing factor activity	7.21E-11
7	**NADH dehydrogenase activity**	3.39E-10	**GTPase activity**	2.10E-09	ubiquitin conjugating enzyme activity	8.82E-11	**GTP binding**	7.65E-11
8	**MHC class I receptor activity**	7.59E-08	**rRNA binding**	1.04E-08	**GTP binding**	1.34E-10	**translation initiation factor activity**	1.13E-10
9	**MHC class II receptor activity**	1.04E-07	**single-stranded DNA binding**	4.35E-08	transferase activity	1.54E-10	**GTPase activity**	3.37E-10
10	**cytochrome-c oxidase activity**	1.36E-07	endopeptidase activity	5.80E-08	single-stranded DNA binding	3.40E-09	**NADH dehydrogenase (ubiquinone) activity**	4.44E-09
11	**rRNA binding**	5.48E-07	**translation initiation factor activity**	1.25E-07	**GTPase activity**	5.37E-09	**NADH dehydrogenase activity**	6.45E-09
12	**GTPase activity**	1.17E-05	**MHC class II receptor activity**	1.24957E-07	zinc ion binding	1.30E-08	**MHC class II receptor activity**	1.04E-07
13	**binding**	1.11E-05	**NADH dehydrogenase activity**	1.77E-07	**oxidoreductase activity**	1.34E-08	**MHC class I receptor activity**	
14	**ubiquinol-cytochrome-c reductase activity**	5.49E-05	**oxidoreductase activity**	1.85E-07	ATP binding	1.58E-08	**rRNA binding**	9.88E-08
15	signal transducer activity	6.51E-05	**NADH dehydrogenase (ubiquinone) activity**	4.35E-07	protein transporter activity	1.73E-08	**protein domain specific binding**	2.05E-07
16	**GTP binding**	9.58E-05	protein kinase C binding	5.33E-07	hydrolase activity	2.77E-08	**cytochrome-c oxidase activity**	
17	molecular_function unknown	9.58E-04	**MHC class I receptor activity**	5.97E-07	**NADH dehydrogenase (ubiquinone) activity**	2.52E-07	single-stranded DNA binding	3.58E-07
18	**protein domain specific binding**	0.001240137	transcription corepressor activity	6.61E-07	**hydrogen-transporting ATPase activity, rotational mechanism**	2.76E-07	protein transporter activity	1.01E-06
19	**translation initiation factor activity**	0.001335895	ubiquitin conjugating enzyme activity	8.97E-07	**NADH dehydrogenase activity**	5.78E-07	**ubiquinol-cytochrome-c reductase activity**	2.58E-06
20	double-stranded DNA binding	0.001446557	DNA binding	9.58E-07	**hydrogen-transporting ATP synthase activity, rotational mechanism**	9.19E-07	endopeptidase activity	4.28E-06
21	hematopoietin/interferon-class (D200-domain) cytokine receptor signal transducer activity	0.001520146	pre-mRNA splicing factor activity	1.63E-06	ubiquitin thiolesterase activity	1.01E-06	calcium-dependent phospholipid binding	1.55E-05

22	positive transcription elongation factor activity	0.001454052	ATP-dependent RNA helicase activity	1.67E-06	**cytochrome-c oxidase activity**	2.51E-06	DNA binding	8.70E-05
23	pre-mRNA splicing factor activity	0.002500888	translation elongation factor activity	6.00E-06	cysteine-type endopeptidase activity	5.87E-06	ubiquitin conjugating enzyme activity	1.38E-04
24	IgE binding	0.002422089	**ubiquinol-cytochrome-c reductase activity**	7.58E-06	chaperone activity	6.39E-06	nuclear localization sequence binding	1.73E-04
25	aspartate-tRNA ligase activity	0.002518972	ribosome binding	1.11E-05	nucleic acid binding	1.35E-05	phospholipase inhibitor activity	7.11E-04
26	chaperone activity	0.002764454	**protein domain specific binding**	1.64E-05	endopeptidase activity	2.51E-05	protein kinase C binding	7.87E-04
27	endopeptidase activity	0.003037016	positive transcription elongation factor activity	2.45E-05	protein serine/threonine kinase activity	2.95E-05	translation elongation factor activity	8.72E-04
28	superoxide dismutase activity	0.003779546	double-stranded RNA binding	2.79E-05	nuclear localization sequence binding	4.84E-05	double-stranded DNA binding	9.55E-04
29	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity	0.00531967	phospholipase inhibitor activity	4.44E-05	**protein domain specific binding**	9.01E-05	molecular_function unknown	0.001099747
30	interleukin-10 receptor activity	0.006531985	tRNA binding	9.05E-05	double-stranded RNA binding	1.54E-04	double-stranded RNA binding	0.001288252
31	monodehydroascorbate reductase (NADH) activity	0.006339867	oxygen transporter activity	1.07E-04	transcription coactivator activity	1.67E-04	actin filament binding	0.001389533
32	NAD+ kinase activity	0.006158728	RNA polymerase II transcription factor activity	1.09E-04	molecular_function unknown	3.05E-04	chaperone activity	0.001719332
33	ATP:ADP antiporter activity	0.006736109	molecular_function unknown	1.19E-04	ligase activity	3.31E-04	ATP-dependent RNA helicase activity	0.002503838
34	adenine phosphoribosyltransferase activity	0.006953403	monodehydroascorbate reductase (NADH) activity	1.22E-04	poly(A) binding	4.80E-04	diamine N-acetyltransferase activity	0.003474918
35	receptor signaling protein activity	0.008181251	cadmium ion binding	1.40E-04	**ubiquinol-cytochrome-c reductase activity**	8.49E-04	IgE binding	0.003733962
36	heat shock protein activity	0.008347023	proteasome activator activity	1.40E-04	**rRNA binding**	0.001501768	electron carrier activity	0.004626459
37	Rho GDP-dissociation inhibitor activity	0.008422553	ATPase stimulator activity	1.40E-04	chromatin binding	0.001494511	superoxide dismutase activity	0.004877425
38	structural constituent of cytoskeleton	0.008459726	hydrolase activity	1.40E-04	**MHC class I receptor activity**	0.001674147	poly-pyrimidine tract binding	0.00475497
39	prenylated protein tyrosine phosphatase activity	0.010406451	protein transporter activity	1.48E-04	transcription corepressor activity	0.00180975	hydrolase activity	0.007783135
40	hematopoietin/interferon-class (D200-domain) cytokine receptor activity	0.011051476	voltage-dependent ion-selective channel activity	2.25E-04	transcriptional repressor activity	0.001953484	oxygen transporter activity	0.007987954
41	single-stranded DNA binding	0.013957622	eukaryotic initiation factor 4E binding	2.34E-04	mRNA binding	0.004427766	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity	0.008007505
42	tRNA binding	0.014910737	biliverdin reductase activity	2.34E-04	rhodopsin-like receptor activity	0.005573604	peroxidase activity	0.00917697
43	U-plasminogen activator receptor activity	0.014100202	chaperone activity	2.34E-04	**MHC class II receptor activity**	0.00594393	cadmium ion binding	0.009043513
44	interleukin-7 receptor activity	0.015666892	cysteine-type endopeptidase activity	2.78E-04	protein binding	0.007346836	proteasome activator activity	0.009618186

45	tripeptidyl-peptidase I activity	0.015326307	thiol-disulfide exchange intermediate activity	4.09E-04	ATP-dependent helicase activity	0.008528088	ATP:ADP antiporter activity	0.009507767
46	kinase binding	0.014687711	interleukin-7 receptor activity	4.17E-04	isomerase activity	0.009427467	isomerase activity	0.009719051
47	voltage-dependent anion channel porin activity	0.013823728	recombinase activity	4.56E-04	double-stranded DNA binding	0.012998944	poly(A) binding	0.009939939
48	lysine-tRNA ligase activity	0.013557887	hypoxanthine phosphoribosyltransferase activity	4.56E-04	tRNA binding	0.014582858	tubulin binding	0.010443445
49	glyoxylate reductase (NADP) activity	0.015000215	voltage-dependent anion channel porin activity	4.56E-04	**binding**	0.018712292	dolichyl-diphosphooligosaccharide-protein glycotransferase activity	0.015257115
50	farnesyl-diphosphate farnesyltransferase activity	0.016022957	lysine-tRNA ligase activity	4.56E-04	RNA polymerase II transcription factor activity	0.019442597	**binding**	0.015444557
51	cathepsin S activity	0.014387962	aryl sulfotransferase activity	4.56E-04	protein-tyrosine kinase activity	0.01988462	positive transcription elongation factor activity	0.015135666
52	alpha-mannosidase activity	0.017524475	Hsp70/Hsc70 protein regulator activity	4.56E-04	DNA-directed RNA polymerase activity	0.021211222	3-alpha(17-beta)-hydroxysteroid dehydrogenase (NAD+) activity	0.019330006
53	L-lactate dehydrogenase activity	0.017855125	**binding**	4.56E-04	superoxide dismutase activity	0.020525471	cadherin binding	0.025908732
54	protein binding	0.019763377	IgE binding	5.75E-04	phospholipase inhibitor activity	0.020898661	N-acetylglucosamine-6-sulfatase activity	0.025848504
55	signal sequence binding	0.026183111	aspartate-tRNA ligase activity	6.86E-04	ATP-dependent RNA helicase activity	0.020385301	voltage-dependent anion channel porin activity	0.025386923
56	phospholipase inhibitor activity	0.025723758	L-lactate dehydrogenase activity	6.86E-04	epsilon DNA polymerase activity	0.020072393	lysine-tRNA ligase activity	0.024941539
57	benzodiazepine receptor binding	0.026550547	double-stranded DNA binding	6.86E-04	hormone activity	0.02093143	aryl sulfotransferase activity	0.023694462
58	diamine N-acetyltransferase activity	0.027450566	epsilon DNA polymerase activity	9.02E-04	intracellular transporter activity	0.025134255	UTP-glucose-1-phosphate uridylyltransferase activity	0.026823919
59	ceramidase activity	0.026993056	benzodiazepine receptor binding	0.001043661	calcium-dependent phospholipid binding	0.029998339	racemase and epimerase activity	0.024096063
60	hydrogen-exporting ATPase activity, phosphorylative mechanism	0.027923851	thioredoxin peroxidase activity	0.001043661	acyl-CoA binding	0.031331593	peptidylglycine monooxygenase activity	0.02632718
61	caspase activity	0.028929848	superoxide dismutase activity	0.001043661	MHC class I protein binding	0.031111071	structural constituent of cytoskeleton	0.023306028
62	poly(A) binding	0.022712537	signal sequence binding	0.001057036	exonuclease activity	0.036060773	receptor signaling protein activity	0.024511512
63	cathepsin B activity	0.032966408	ubiquitin thiolesterase activity	0.001057036	RNA helicase activity	0.03797489	tRNA binding	0.029552012
64	manganese superoxide dismutase activity	0.034448044	calcium-dependent phospholipid binding	0.001086004	protein phosphatase type 2A regulator activity	0.041144027	aspartate-tRNA ligase activity	0.032815511
65	glucocorticoid receptor activity	0.034065288	protein disulfide isomerase activity	0.001101799	electron transporter activity	0.045371607	L-lactate dehydrogenase activity	0.034426337
66	ornithine decarboxylase inhibitor activity	0.033324738	MHC class I protein binding	0.001218009	protein kinase C binding	0.046368761	transferase activity	0.033465329
67	aldehyde reductase activity	0.033690944	nuclear localization sequence binding	0.001265677	general RNA polymerase II transcription factor activity	0.045950705	peptidyl-prolyl cis-trans isomerase activity	0.03398018
68	MAP kinase phosphatase activity	0.052749518	poly(A) binding	0.001552894	aldehyde reductase activity	0.045811231	cofactor binding	0.034037866

69	KDEL sequence binding	0.051869733	manganese ion binding	0.001585526	receptor signaling protein activity	0.051608991	thioredoxin peroxidase activity	0.035632192
70	voltage-dependent ion-selective channel activity	0.050344153	transferase activity	0.001635712	aspartate-tRNA ligase activity	0.055752985	acyltransferase activity	0.046370992
71	protein channel activity	0.052939212	microtubule binding	0.001660474	glutathione disulfide oxidoreductase activity	0.055258106	ubiquitin-protein ligase activity	0.047043036
72	5S rRNA binding	0.052399016	peroxidase activity	0.001721862	phosphatidylcholine transporter activity	0.056772027	protein disulfide isomerase activity	0.038744964
73	cysteine-tRNA ligase activity	0.051351036	manganese superoxide dismutase activity	0.001721862	Hsp70/Hsc70 protein regulator activity	0.056004838	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	0.038711571
74	ribonucleoside-diphosphate reductase activity	0.05084261	ornithine decarboxylase inhibitor activity	0.001966646	voltage-dependent anion channel porin activity	0.054531026	MHC class I protein binding	0.039966172
75	MHC protein binding	0.053490662	prenylated protein tyrosine phosphatase activity	0.001966646	manganese ion binding	0.054847477	ATP-dependent DNA helicase activity	0.039574347
76	chemokine activity	0.051704012	polynucleotide adenylyltransferase activity	0.00298118	SH3/SH2 adaptor protein activity	0.057980167	RNA polymerase II transcription factor activity	0.041865228
77	profilin binding	0.053757487	protein channel activity	0.003279034	magnesium ion binding	0.08082752	ion channel activity	0.055099478
78	ferric iron binding	0.05819671	tubulin binding	0.003279034	steroid hormone receptor activity	0.088853507	alcohol dehydrogenase activity	0.055542498
79	protein kinase C binding	0.068639699	co-chaperone activity	0.003279034	glutamate-cysteine ligase activity	0.086803823	manganese superoxide dismutase activity	0.055912789
80	phosphatidylinositol-4,5-bisphosphate 3-kinase activity	0.058988256	catalase activity	0.003279034	co-chaperone activity	0.087862406	ornithine decarboxylase inhibitor activity	0.055520637
81	thiol-disulfide exchange intermediate activity	0.059431777	glutamate-ammonia ligase activity	0.003279034	succinate-CoA ligase (GDP-forming) activity	0.08476138	tRNA-intron endonuclease activity	0.05603
82	hydrolase activity	0.064181446	5S rRNA binding	0.003279034	polynucleotide adenylyltransferase activity	0.085770444	U6 snRNA binding	0.05707729
83	oxygen transporter activity	0.067718324	electron transporter activity	0.003279034	ethanolaminephosphotransferase activity	0.083775783	microtubule binding	0.056548796
84	casein kinase I activity	0.068216252	protein phosphatase inhibitor activity	0.003621083	voltage-dependent ion-selective channel activity	0.088947128	chemokine activity	0.055020451
85	ATP-dependent RNA helicase activity	0.080016796	profilin binding	0.003790891	ion channel activity	0.083257703	BRE binding	0.056103013
86	glutathione peroxidase activity	0.081701312	acyl-CoA binding	0.003953756	single-stranded RNA binding	0.082348814	translation repressor activity, nucleic acid binding	0.056666605
87	drug binding	0.082289091	ARF guanyl-nucleotide exchange factor activity	0.003953756	signal sequence binding	0.083284596	ligase activity	0.060954479
88	protein disulfide isomerase activity	0.08242098	structural constituent of cytoskeleton	0.003953756	poly-pyrimidine tract binding	0.081433827	prenylated protein tyrosine phosphatase activity	0.061489167
89	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	0.081840551	hematopoietin/interferon-class (D200-domain) cytokine receptor signal transducer activity	0.004220301	protein carrier activity	0.080334829	phosphatidylinositol transporter activity	0.075673743
90	ubiquitin conjugating enzyme activity	0.081331647	delta DNA polymerase activity	0.005024605	protein disulfide isomerase activity	0.081217629	acetylglucosaminyltransferase activity	0.080876796
91	antigen binding	0.085343399	calcium-dependent protein serine/threonine phosphatase activity	0.005024605	metal ion binding	0.089773584	voltage-dependent ion-selective channel activity	0.080197159

92	endoribonuclease activity	0.108889947	heat shock protein activity	0.005024605	peptidyl-prolyl cis-trans isomerase activity	0.09667712	polynucleotide adenylyltransferase activity	0.081568051
93	poly-pyrimidine tract binding	0.108144125	polypeptide N-acetylgalactosaminyltransferase activity	0.005086811	protein serine/threonine phosphatase activity	0.095310914	eukaryotic initiation factor 4E binding	0.084027419
94	interleukin-6 receptor activity	0.107408451	ubiquitin-protein ligase activity	0.005120962	ATP-dependent peptidase activity	0.100375192	Rho GDP-dissociation inhibitor activity	0.08333867
95	peptide antigen binding	0.106682718	chemokine activity	0.005500935	diamine N-acetyltransferase activity	0.118720991	protein channel activity	0.07943217
96	transcription corepressor activity	0.112702552	phosphatidylinositol binding	0.005596762	phosphoglycerate kinase activity	0.117545535	ethanolaminephosphotransferase activity	0.084727648
97	transmembrane receptor activity	0.0969089	peptidyl-prolyl cis-trans isomerase activity	0.005679646	benzodiazepine receptor binding	0.119920193	5S rRNA binding	0.081338542
98	ATPase activity, coupled	0.097612231	ATP-dependent DNA helicase activity	0.005977504	chymotrypsin activity	0.117459712	succinate-CoA ligase (GDP-forming) activity	0.081994498
99	protein transporter activity	0.103636031	casein kinase I activity	0.00626004	extracellular matrix structural constituent	0.117137658	acetyl-CoA C-acyltransferase activity	0.080692998
100	glutathione transferase activity	0.104691621	ligase activity	0.006498865	transmembrane receptor protein tyrosine kinase adaptor protein activity	0.119457472	electron transporter activity	0.08266112
101	translation elongation factor activity	0.107546634	glutathione peroxidase activity	0.006667466	heat shock protein activity	0.119261946	transcription coactivator activity	0.08005762
102	MAP kinase kinase activity	0.1132146	ribose-phosphate diphosphokinase activity	0.007238247	peroxidase activity	0.127368316	GTPase activator activity	0.080321909
103	chemokine receptor activity	0.112294453	clathrin binding	0.007238247	positive transcription elongation factor activity	0.131449464	profilin binding	0.083859109
104	oligopeptide transporter activity	0.112898187	isomerase activity	0.007238247	protein kinase C inhibitor activity	0.130232339	retinol dehydrogenase activity	0.086258873
105	ligase activity	0.114573188	protein heterodimerization activity	0.007734842	ATP:ADP antiporter activity	0.132183811	ARF guanyl-nucleotide exchange factor activity	0.095732846
106	protein phosphatase inhibitor activity	0.116088687	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	0.008041072	non-selenium glutathione peroxidase activity	0.125405154	helicase activity	0.094303998
107	hyaluronic acid binding	0.116240504	receptor signaling protein tyrosine kinase activity	0.008102439	interleukin-10 receptor activity	0.126486233	ATPase activity, coupled	0.095013051
108	calcium ion binding	0.115666472	RNA helicase activity	0.008102439	cadmium ion binding	0.12870529	asparagine-tRNA ligase activity	0.095374057
109	transporter activity	0.118170017	endoribonuclease activity	0.009945471	proteasome activator activity	0.131003599	phosphoprotein phosphatase activity	0.096049505
110			poly-pyrimidine tract binding	0.00994688	GDP-mannose 4,6-dehydratase activity	0.133385482	7S RNA binding	0.091767727
111			peptide antigen binding	0.00994688	plus-end-directed microtubule motor activity	0.134609202	phosphatidylinositol-4,5-bisphosphate 3-kinase activity	0.090181
112			protein-L-isoaspartate (D-aspartate) O-methyltransferase activity	0.00994688	asparagine-tRNA ligase activity	0.129844275	thiol-disulfide exchange intermediate activity	0.090972352
113				0.00994688	carbon-sulfur lyase activity	0.127586114	delta DNA polymerase activity	0.09315133
114					transcriptional activator activity	0.136270802	protein kinase C inhibitor activity	0.092048948
115					translation elongation factor activity	0.140127207	high-density lipoprotein binding	0.093712483

116	G-protein coupled receptor activity	0.151947786	cytoskeletal protein binding	0.091507483
117	thyroid hormone receptor binding	0.157486991	nucleic acid binding	0.092596858
118	actin filament binding	0.158309118	signal transducer activity	0.098108629
119	3'-5'-exoribonuclease activity	0.159606734	casein kinase I activity	0.103778602
120	protein phosphatase type 2C activity	0.159941309	glutathione peroxidase activity	0.117973978
121	electron carrier activity	0.169257296	alpha-mannosidase activity	0.118317102
122	Probe		transcriptional repressor activity	0.12641845
123	ribose-phosphate diphosphokinase activity	0.195094221	cysteine-type endopeptidase activity	0.127136736
124	t-SNARE activity	0.193570048		0.127724047
125	IgE binding	0.196642588		0.148003172
126	catalytic activity	0.198667798		
127	Probe			
128	manganese superoxide dismutase activity	0.19911516		
129	telomerase activity	0.200635123		
130	ornithine decarboxylase inhibitor activity	0.20217847		
131	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity	0.197618054		
132	transcription factor binding	0.196877614		
133	protein kinase activity	0.200063448		
134	cation channel activity	0.20568846		
135	voltage-gated potassium channel activity	0.205348863		
136	Ras guanyl-nucleotide exchange factor activity	0.207589506		
137	growth factor activity	0.213242078		
138	phosphatidylinositol transporter activity	0.215225089		
139	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	0.217172462		
140	monooxygenase activity	0.216649098		
141	trypsin activity	0.252074309		
142	FK506 binding	0.264086943		
143	signal transducer activity	0.26768353		
144	acyltransferase activity	0.269188396		
145	endoribonuclease activity	0.270849171		
146	rRNA methyltransferase activity	0.272679233		

147	rRNA (adenine-N6,N6-)-dimethyltransferase activity	0.274534194
148	protein tyrosine phosphatase activity	0.269215294
149	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	0.269212424
150	profilin binding	0.288926523
151	phosphoprotein phosphatase activity	0.288295807
152	phosphoric ester hydrolase activity	0.28051976
153	tRNA guanylyltransferase activity	0.265668714
154	UDP-galactose transporter activity	0.258078179
155	interleukin-7 receptor activity	0.28766676
156	N-acetylglucosamine-6-sulfatase activity	0.278788156
157	RAB GDP-dissociation inhibitor activity	0.285846084
158	recombinase activity	0.28404831
159	tripeptidyl-peptidase I activity	0.282273008
160	kynurenine 3-monooxygenase activity	0.259561387
161	cytidylate kinase activity	0.255162041
162	[RNA-polymerase]-subunit kinase activity	0.262579543
163	orotate phosphoribosyltransferase activity	0.277077799
164	kinase binding	0.270441205
165	geranyltranstransferase activity	0.272070369
166	ceramide cholinephosphotransferase activity	0.289510778
167	ADP-ribosylarginine hydrolase activity	0.291378589
168	orotidine-5'-phosphate decarboxylase activity	0.261061742
169	cathepsin S activity	0.268831436
170	phosphotransferase activity, phosphate group as acceptor	0.267240718
171	dUTP diphosphatase activity	0.264115095
172	mRNA (2'-O-methyladenosine-N6-)-methyltransferase activity	0.275388301
173	pre-mRNA cleavage factor	0.273719281

	activity	
174	DNA photolyase activity	0.256611826
175	importin-alpha export receptor activity	0.253728547
176	lysine-tRNA ligase activity	0.293270658
177	hydrolase activity, acting on glycosyl bonds	0.2679555
178	SH2 domain binding	0.203473159
179	dolichyl-diphosphooligosaccharide-protein glycotransferase activity	0.199370877
180	eukaryotic initiation factor 4E binding	0.200178047
181	biliverdin reductase activity	0.200991779
182	lipoate-protein ligase B activity	0.204313957
183	tubulin binding	0.205161733
184	satellite DNA binding	0.201812153
185	ribonucleoside-diphosphate reductase activity	0.202639252
186	peptidase activity	0.202188181
187	symporter activity	0.203321288
188	hyaluronic acid binding	0.210096839
189	RAN protein binding	0.212159846
190	kinase activity	0.21267561
191	specific RNA polymerase II transcription factor activity	0.218953358
192	calcium ion storage activity	0.242308752
193	nucleocytoplasmic transporter activity	0.24139304
194	phosphatidylinositol binding	0.247489377
195	protein dimerization activity	0.258100087

Table 4. Biological processes represented by each species probe pair set. The top ranked biological processes are indicated in the shaded areas, and those that are in common among the species are indicated in bolded text.

Index	Human	P-Value	AGM	P-Value	Cyno	P-Value	Rhesus	Corrected P-Value
1	**immune response**	8.52E-14	**protein biosynthesis**	1.47E-13	**protein biosynthesis**	3.79E-13	**protein biosynthesis**	1.53E-13
2	**protein biosynthesis**	1.28E-13	**immune response**	4.30E-10	ubiquitin-dependent protein catabolism	2.52E-13	**immune response**	6.12E-13
3	**ATP synthesis coupled proton transport**	9.01E-12	**ATP synthesis coupled proton transport**	9.28E-09	nuclear mRNA splicing, via spliceosome	3.79E-13	**ATP synthesis coupled proton transport**	1.12E-11

4	**antigen presentation, endogenous antigen**	2.65E-09	ubiquitin-dependent protein catabolism	1.53E-07	RNA splicing	3.18E-12	proton transport	2.36E-09
5	**antigen processing, endogenous antigen via MHC class I**	1.78E-08	protein transport	3.20E-07	mRNA processing	7.57E-12	nuclear mRNA splicing, via spliceosome	2.18E-09
6	proton transport	2.73E-08	translational elongation	3.04E-07	protein transport	1.09E-11	**antigen presentation, endogenous antigen**	3.18E-09
7	antigen presentation, exogenous antigen	6.31E-07	proton transport	1.93E-06	**immune response**	4.00E-10	regulation of translational initiation	8.19E-09
8	inflammatory response	8.04E-07	**antigen presentation, endogenous antigen**	9.04E-06	ubiquitin cycle	1.29E-09	RNA splicing	7.86E-09
9	**antigen processing, exogenous antigen via MHC class II**	7.24E-07	**antigen processing, endogenous antigen via MHC class I**	3.53E-05	protein ubiquitination	9.70E-09	**antigen processing, endogenous antigen via MHC class I**	2.47E-08
10	translational elongation	1.78E-06	regulation of translational initiation	1.56E-04	regulation of translational initiation	3.50E-08	translational elongation	4.60E-08
11	positive regulation of I-kappaB kinase/NF-kappaB cascade	3.04E-06	response to oxidative stress	1.55E-04	protein folding	1.65E-07	protein transport	8.62E-08
12	cellular defense response	6.40E-06	antigen presentation, exogenous antigen	1.49E-04	RNA processing	5.84E-07	antigen presentation, exogenous antigen	4.32E-07
13	nucleosome assembly	6.93E-06	regulation of translation	1.49E-04	**ATP synthesis coupled proton transport**	1.35E-06	mRNA processing	5.64E-07
14	chemotaxis	1.38E-05	microtubule polymerization	1.68E-04	regulation of translation	1.45E-06	**antigen processing, exogenous antigen via MHC class II**	5.50E-07
15	negative regulation of lymphocyte proliferation	1.45E-05	**antigen processing, exogenous antigen via MHC class II**	1.63E-04	regulation of transcription, DNA-dependent	1.49E-06	mitochondrial electron transport, NADH to ubiquinone	3.08E-06
16	antimicrobial humoral response (sensu Vertebrata)	1.47E-05	RNA splicing	6.48E-04	small GTPase mediated signal transduction	2.09E-06	ubiquitin-dependent protein catabolism	1.41E-05
17	cell surface receptor linked signal transduction	1.62E-05	cotranslational membrane targeting	6.50E-04	intracellular protein transport	2.60E-06	microtubule polymerization	3.44E-05
18	cell motility	1.53E-05	nuclear mRNA splicing, via spliceosome	7.32E-04	mitochondrial electron transport, NADH to ubiquinone	3.51E-06	cotranslational membrane targeting	6.84E-05
19	mitochondrial electron transport, NADH to ubiquinone	2.22E-05	electron transport	0.001145698	transcription	5.12E-06	nucleosome assembly	9.54E-05
20	regulation of apoptosis	3.57E-05	ubiquitin cycle	0.001186297	synaptic transmission	8.16E-06	protein folding	1.67E-04
21	RNA splicing	4.21E-05	RNA processing	0.001562438	protein-nucleus import, docking	9.60E-06	RNA processing	2.98E-04
22	dendrite morphogenesis	7.08E-05	energy pathways	0.00208299	regulation of transcription from Pol II promoter	9.78E-06	protein-nucleus import, docking	5.77E-04
23	anti-apoptosis	2.18E-04	nucleosome assembly	0.002297439	protein amino acid phosphorylation	1.02E-05	glycolysis	6.13E-04
24	protein transport	4.26E-04	dendrite morphogenesis	0.00294977	cotranslational membrane targeting	4.24E-05	mRNA splice site selection	0.001071317
25	energy pathways	5.42E-04	mitochondrial electron	0.003550205	apoptosis	4.27E-05	protein-nucleus import,	0.001150072

			transport, NADH to ubiquinone				translocation	
26	mitochondrial electron transport, ubiquinol to cytochrome c	5.93E-04	cellular defense response (sensu Vertebrata)	0.005116885	**antigen presentation, endogenous antigen**	4.84E-05	regulation of cell cycle	0.001143308
27	cell proliferation	6.63E-04	microtubule-based movement	0.006033093	nucleosome assembly	7.51E-05	transcription from Pol III promoter	0.001258488
28	regulation of actin filament polymerization	0.001192353	protein-nucleus import, translocation	0.006148958	proton transport	1.11E-04	mitochondrial electron transport, ubiquinol to cytochrome c	0.001561506
29	regulation of translational initiation	0.001457896	negative regulation of transcription from Pol II promoter	0.006538419	signal transduction	1.22E-04	small GTPase mediated signal transduction	0.001924091
30	intracellular signaling cascade	0.001580303	response to biotic stimulus	0.007717436	negative regulation of transcription	1.40E-04	response to oxidative stress	0.001923494
31	mRNA processing	0.00168203	cell surface receptor linked signal transduction	0.007598477	**antigen processing, endogenous antigen via MHC class I**	2.15E-04	regulation of translation	0.001901321
32	neutrophil chemotaxis	0.00163442	DNA unwinding	0.008709177	ion transport	5.79E-04	microtubule-based movement	0.002388466
33	protein folding	0.001657432	oxygen transport	0.008453025	dendrite morphogenesis	7.77E-04	cell motility	0.002386708
34	aspartyl-tRNA aminoacylation	0.001799266	mRNA processing	0.009843993	RAS protein signal transduction	7.63E-04	translational initiation	0.002666689
35	intracellular iron ion storage	0.001826791	neurotransmitter receptor biosynthesis	0.01029218	potassium ion transport	7.55E-04	regulation of actin filament polymerization	0.003113392
36	negative regulation of axon extension	0.001877535	negative regulation of proteolysis and peptidolysis	0.010014013	transcription from Pol II promoter	8.74E-04	response to biotic stimulus	0.008203845
37	negative regulation of anti-apoptosis	0.001778717			microtubule polymerization	9.41E-04	oxidative phosphorylation	0.007987954
38	superoxide metabolism	0.002458647			positive regulation of I-kappaB kinase/NF-kappaB cascade	0.001389008	oxygen transport	0.009647584
39	response to virus	0.002636446			protein-nucleus import, translocation	0.00210331	N-linked glycosylation via asparagine	0.009495689
40	response to biotic stimulus	0.002609686			response to oxidative stress	0.002748022	natural killer cell mediated cytolysis	0.012028445
41	oxidative phosphorylation	0.002673337			glycolysis	0.002815047	actin cytoskeleton organization and biogenesis	0.012990152
42	response to oxidative stress	0.002761128			antigen presentation, exogenous antigen	0.003080958	viral genome replication	0.014273034
43	response to pest/pathogen/parasite	0.003452017			NLS-bearing substrate-nucleus import	0.003058925		
44	microtubule polymerization	0.003409326			G-protein coupled receptor protein signaling pathway	0.003806245		
45	apoptotic nuclear changes	0.004685989			anti-apoptosis	0.00399148		
46	adenine salvage	0.004586287			**antigen processing, exogenous antigen via MHC class II**	0.003987654		

47	nuclear mRNA splicing, via spliceosome	0.005447671	regulation of cell cycle	0.003956367
48	hemocyte development	0.005578146	cell cycle	0.004384896
49	defense response to fungi	0.005691985	mRNA splice site selection	0.004856594
50	transcription from Pol III promoter	0.005585252	DNA replication	0.005533476
51	cation transport	0.005646594	translational elongation	0.00612315
52	rRNA transcription	0.006038812	negative regulation of lymphocyte proliferation	0.006190458
53	cell growth and/or maintenance	0.006764303	negative regulation of transcription from Pol II promoter	0.006210897
54	Golgi to secretory vesicle transport	0.007568328	response to stress	0.00719669
55	microtubule-based movement	0.00825348	cell proliferation	0.008965414
56	protein complex assembly	0.008146572	chromatin assembly/disassembly	0.009534971
57	cell homeostasis	0.0098879	polyamine biosynthesis	0.009674197
58	regulation of viral genome replication	0.009720309	cell surface receptor linked signal transduction	0.009895085
59	cellular morphogenesis	0.009982177	phosphate transport	0.01177921
60	G-protein signaling, adenylate cyclase activating pathway	0.00967738	chromosome organization and biogenesis (sensu Eukarya)	0.011819967
61	cotranslational membrane targeting	0.009836025	tricarboxylic acid cycle	0.01283557
62	monocyte differentiation	0.011015783	mitochondrial electron transport, ubiquinol to cytochrome c	0.013993397
63	regulation of peptidyl-tyrosine phosphorylation	0.011190637	intracellular signaling cascade	0.014098666
64	lysyl-tRNA aminoacylation	0.010522539	transcription from Pol III promoter	0.014568711
65	nascent polypeptide association	0.010681972		
66	clathrin cage assembly	0.01084631		
67	response to stress	0.010453268		
68	detection of pest/pathogen/parasite	0.013518881		
69	cellular defense response (sensu Vertebrata)	0.013714806		
70	ubiquitin-dependent protein catabolism	0.013531002		

Table 5. Group of probesets reproducibly detected in intra- and interspecies comparisons by Boolean analysis.

Probe Set ID	**Public ID**	**Gene Description**
218011_at	NM_024292	ubiquitin-like 5 (UBL5),
217882_at	NM_018447	30 kDa protein
AFFX-hum_alu_at	AFFX-hum_alu	Human ALU-Sq subfamily consensus sequence
244145_at	BG260337	602371458F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4479327 5'
44120_at	AI879381	aarF domain containing kinase 2
214274_s_at	AI860341	acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)
201051_at	BE560202	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A
221505_at	AW612574	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E
207988_s_at	NM_005731	actin related protein 2/3 complex, subunit 2, 34kDa
208679_s_at	AF279893	actin related protein 2/3 complex, subunit 2, 34kDa
213513_x_at	BG034239	actin related protein 2/3 complex, subunit 2, 34kDa
208736_at	AF004561	actin related protein 2/3 complex, subunit 3, 21kDa
200801_x_at	NM_001101	actin, beta
213867_x_at	AA809056	actin, beta
224594_x_at	AK025873	actin, beta
AFFX-HSAC07/X00351_3_at	Unknown	actin, beta
201550_x_at	NM_001614	actin, gamma 1
211970_x_at	BG026805	actin, gamma 1
211983_x_at	BE741683	actin, gamma 1
211995_x_at	AL567820	actin, gamma 1
212363_x_at	AU145192	actin, gamma 1
212988_x_at	AL515810	actin, gamma 1
213214_x_at	AW190090	actin, gamma 1
221607_x_at	BC001920	actin, gamma 1
224585_x_at	AA703939	actin, gamma 1
212857_x_at	BG231551	activated RNA polymerase II transcription cofactor 4
224586_x_at	BE784583	activated RNA polymerase II transcription cofactor 4
200058_s_at	BC001417	activating signal cointegrator 1 complex subunit 3-like 1 /// activating signal cointegrator 1 complex subunit 3-like 1
225917_at	AA766897	activating transcription factor 7 interacting protein
231825_x_at	AK025060	activating transcription factor 7 interacting protein
211047_x_at	BC006337	adaptor-related protein complex 2, sigma 1 subunit
201197_at	NM_001634	adenosylmethionine decarboxylase 1
200065_s_at	AF052179	ADP-ribosylation factor 1 /// ADP-ribosylation factor 1
200781_s_at	NM_001019	ADP-ribosylation factor-like 6 interacting protein /// ribosomal protein S15a
202207_at	BG435404	ADP-ribosylation factor-like 7

Probe Set ID	Public ID	Gene Description
225956_at	AL565238	adult retina protein
211986_at	BG287862	AHNAK nucleoprotein (desmoyokin)
201425_at	NM_000690	aldehyde dehydrogenase 2 family (mitochondrial)
204976_s_at	AK023637	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region, gene 1
216187_x_at	AF222691	Alu repeat (LNX1)
208248_x_at	NM_001642	amyloid beta (A4) precursor-like protein 2
223266_at	AB038950	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2
226861_at	BF223343	ankyrin repeat and SOCS box-containing 8
201590_x_at	NM_004039	annexin A2
210427_x_at	BC001388	annexin A2
213503_x_at	BE908217	annexin A2
225524_at	AU152178	anthrax toxin receptor 2
205434_s_at	AW451954	AP2 associated kinase 1
204174_at	NM_001629	arachidonate 5-lipoxygenase-activating protein
202655_at	NM_006010	arginine-rich, mutated in early stage tumors
200996_at	NM_005721	ARP3 actin-related protein 3 homolog (yeast)
213101_s_at	Z78330	ARP3 actin-related protein 3 homolog (yeast)
222047_s_at	AI523895	arsenate resistance protein ARS2
200027_at	NM_004539	asparaginyl-tRNA synthetase /// asparaginyl-tRNA synthetase
211755_s_at	BC005960	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1 /// ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1
207507_s_at	NM_001689	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3
207508_at	NM_001689	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3
207335_x_at	NM_007100	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e
209492_x_at	BC003679	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e
202961_s_at	NM_004889	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2
207573_x_at	NM_006476	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g
208746_x_at	AF070655	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g
210453_x_at	AL050277	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g
213738_s_at	AI587323	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle
201322_at	NM_001686	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide (ATP5B), nuclear gene encoding mitochondrial protein
217801_at	NM_006886	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit
208870_x_at	BC000931	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1
205711_x_at	NM_005174	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1 (ATP5C1), nuclear gene encoding mitochondrial protein, transcript variant 2
200818_at	NM_001697	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)
214594_x_at	BG252666	ATPase, Class I, type 8B, member 1

Probe Set ID	Public ID	Gene Description
208737_at	BC003564	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G isoform 1
36994_at	M62762	ATPase, H+ transporting, lysosomal 16kDa, V0 subunit c
208898_at	AF077614	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D
201172_x_at	NM_003945	ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e
200096_s_at	AI862255	ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e /// ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e
201443_s_at	AF248966	ATPase, H+ transporting, lysosomal accessory protein 2
208836_at	U51478	ATPase, Na+/K+ transporting, beta 3 polypeptide
200045_at	NM_001090	ATP-binding cassette, sub-family F (GCN20), member 1 /// ATP-binding cassette, sub-family F (GCN20), member 1
242578_x_at	AV699746	AV699746 GKC Homo sapiens cDNA clone GKCBYE11
226453_at	BF982002	AYP1 protein
203066_at	NM_014863	B cell RAG associated protein
216380_x_at	AC005011	BAC clone GS1-111G14 from 7
208517_x_at	NM_001207	basic transcription factor 3
211939_x_at	X74070	basic transcription factor 3
214800_x_at	R83000	basic transcription factor 3
219528_s_at	NM_022898	B-cell CLL/lymphoma 11B (zinc finger protein)
203140_at	NM_001706	B-cell CLL/lymphoma 6 (zinc finger protein 51)
200921_s_at	NM_001731	B-cell translocation gene 1, anti-proliferative (BTG1)
221479_s_at	AF060922	BCL2/adenovirus E1B 19kDa interacting protein 3-like
201084_s_at	NM_014739	BCL2-associated transcription factor 1
1555372_at	AF455755	BCL2-like 11 (apoptosis facilitator)
212320_at	BC001002	beta 5-tubulin
201891_s_at	NM_004048	beta-2-microglobulin
216231_s_at	AW188940	beta-2-microglobulin
202391_at	NM_006317	brain abundant, membrane attached signal protein 1
204820_s_at	NM_006994	butyrophilin, subfamily 3, member A3
221249_s_at	NM_030802	C/EBP-induced protein /// C/EBP-induced protein
201953_at	NM_006384	calcium and integrin binding 1 (calmyrin)
200653_s_at	M27319	calmodulin 1 (phosphorylase kinase, delta)
200655_s_at	NM_006888	calmodulin 1 (phosphorylase kinase, delta)
209563_x_at	BC000454	calmodulin 1 (phosphorylase kinase, delta)
207243_s_at	NM_001743	calmodulin 2 (phosphorylase kinase, delta)
200068_s_at	M94859	calnexin /// calnexin
208683_at	M23254	calpain 2, (m/II) large subunit
200625_s_at	NM_006367	CAP, adenylate cyclase-associated protein 1 (yeast)
213798_s_at	AA806142	CAP, adenylate cyclase-associated protein 1 (yeast)
208374_s_at	NM_006135	capping protein (actin filament) muscle Z-line, alpha 1

Probe Set ID	Public ID	Gene Description
37012_at	U03271	capping protein (actin filament) muscle Z-line, beta
201850_at	NM_001747	capping protein (actin filament), gelsolin-like
225231_at	AI828967	Cas-Br-M (murine) ecotropic retroviral transforming sequence
208865_at	BG534245	casein kinase 1, alpha 1
213860_x_at	AW268585	casein kinase 1, alpha 1
202573_at	AL530441	casein kinase 1, gamma 2
209970_x_at	M87507	caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase)
200839_s_at	NM_001908	cathepsin B
202295_s_at	NM_004390	cathepsin H
212501_at	AL564683	CCAAT/enhancer binding protein (C/EBP), beta
203973_s_at	NM_005195	CCAAT/enhancer binding protein (C/EBP), delta
213539_at	NM_000732	CD3D antigen, delta polypeptide (TiT3 complex)
212063_at	BE903880	CD44 antigen (homing function and Indian blood group system)
213857_s_at	BG230614	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)
203416_at	NM_000560	CD53 antigen
200663_at	NM_001780	CD63 antigen (melanoma 1 antigen)
201029_s_at	NM_002414	CD99 antigen
213151_s_at	AU157515	CDC10 cell division cycle 10 homolog (S. cerevisiae)
229120_s_at	BG150636	CDC42 small effector 1
209057_x_at	AB007892	CDC5 cell division cycle 5-like (S. pombe)
221844_x_at	AV756161	cDNA clone BMFBGA04 5'
217679_x_at	AI683552	cDNA clone IMAGE:2274675 3' similar to contains Alu repetitive element;, MRNA sequence
222279_at	AI669379	cDNA clone IMAGE:2280726 3' similar to SW:RL2B_HUMAN P29316 60S RIBOSOMAL PROTEIN L23A. ;, MRNA
227346_at	AI741188	cDNA clone IMAGE:2366204 3'
235084_x_at	AI809831	cDNA clone IMAGE:2386802 3' similar to contains Alu repetitive element
230208_at	BE552011	cDNA clone IMAGE:3196174
212044_s_at	BE737027	cDNA clone IMAGE:3641231
211927_x_at	BE963164	cDNA clone IMAGE:3865650
212790_x_at	BF942308	cDNA clone IMAGE:4119332 3' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A
225340_s_at	BG107845	cDNA clone IMAGE:4365933 5'
225494_at	BG478726	cDNA clone IMAGE:4643722 5', MRNA sequence
1558142_at	AL831862	CDNA clone IMAGE:6195280, partial cds
213567_at	BF431965	CDNA clone IMAGE:6503168, partial cds
210679_x_at	BC002629	cDNA clone MGC:3878
215978_x_at	AK021514	cDNA FLJ11452 fis, clone HEMBA1001435

Probe Set ID	Public ID	Gene Description
231812_x_at	AK023255	cDNA FLJ13193 fis, clone NT2RP3004348, moderately similar to R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein
233319_x_at	AK023907	cDNA FLJ13845 fis, clone THYRO1000815
1559467_at	BI520422	CDNA FLJ36734 fis, clone UTERU2012890
237475_x_at	AI151104	CDNA FLJ45442 fis, clone BRSSN2011843
233702_x_at	AK024599	CDNA: FLJ20946 fis, clone ADSE01819
216526_x_at	AK024836	cDNA: FLJ21183 fis, clone CAS11634, highly similar to HSHLACW07 Homo sapiens mRNA for human leukocyte antigen C alpha chain
233041_x_at	AK025009	CDNA: FLJ21356 fis, clone COL02831
34210_at	N90866	CDW52 antigen (CAMPATH-1 antigen)
232266_x_at	AK024379	cell division cycle 2-like 5 (cholinesterase-related cell division controller)
208728_s_at	BC003682	cell division cycle 42 (GTP binding protein, 25kDa)
219206_x_at	NM_016056	CGI-119 protein
201570_at	NM_015380	CGI-51 protein
200877_at	NM_006430	chaperonin containing TCP1, subunit 4 (delta)
200873_s_at	NM_006585	chaperonin containing TCP1, subunit 8 (theta)
1405_i_at	M21121	chemokine (C-C motif) ligand 5
205898_at	U20350	chemokine (C-X3-C motif) receptor 1
217028_at	AJ224869	chemokine (C-X-C motif) receptor 4
219161_s_at	NM_016951	chemokine-like factor
223451_s_at	AF096895	chemokine-like factor
208659_at	AF034607	chloride intracellular channel 1
204620_s_at	NM_004385	chondroitin sulfate proteoglycan 2 (versican)
221731_x_at	BF218922	chondroitin sulfate proteoglycan 2 (versican)
201518_at	NM_006807	chromobox homolog 1 (HP1 beta homolog Drosophila)
202808_at	AK000161	chromosome 10 open reading frame 26
218213_s_at	NM_014206	chromosome 11 open reading frame 10
228332_s_at	AA526939	chromosome 11 open reading frame 31
201216_at	NM_006817	chromosome 12 open reading frame 8
218422_s_at	NM_022118	chromosome 13 open reading frame 10
221434_s_at	NM_031210	chromosome 14 open reading frame 156 /// chromosome 14 open reading frame 156
217768_at	NM_016039	chromosome 14 open reading frame 166
210532_s_at	AF116639	chromosome 14 open reading frame 2
208837_at	BC000027	chromosome 15 open reading frame 22
221190_s_at	NM_013326	chromosome 18 open reading frame 8
55705_at	W07773	chromosome 19 open reading frame 22
218037_at	NM_024293	chromosome 2 open reading frame 17
221983_at	AL040896	chromosome 2 open reading frame 17

Probe Set ID	Public ID	Gene Description
221984_s_at	AL040896	chromosome 2 open reading frame 17
200070_at	BC001393	chromosome 2 open reading frame 24 /// chromosome 2 open reading frame 24
217883_at	NM_015702	chromosome 2 open reading frame 25
225498_at	AV713673	chromosome 20 open reading frame 178
206656_s_at	BC000353	chromosome 20 open reading frame 3
217737_x_at	NM_016407	chromosome 20 open reading frame 43
233842_x_at	AK000586	chromosome 20 open reading frame 43
224972_at	BF381837	chromosome 20 open reading frame 52
224575_at	BE868361	chromosome 3 open reading frame 10
206707_x_at	NM_015864	chromosome 6 open reading frame 32
209829_at	AB002384	chromosome 6 open reading frame 32
218233_s_at	NM_017601	chromosome 6 open reading frame 49
223516_s_at	AF216754	chromosome 6 open reading frame 49
208809_s_at	AL136632	chromosome 6 open reading frame 62
225849_s_at	BF975327	chromosome 6 open reading frame 83
1558426_x_at	BC016797	chromosome 7 open reading frame 19
226385_s_at	BG397444	chromosome 7 open reading frame 30
223396_at	AF260336	chromosome 7 open reading frame 35
200774_at	BE963765	chromosome 9 open reading frame 10
225602_at	H92988	chromosome 9 open reading frame 19
204923_at	AL023653	chromosome X open reading frame 9
203804_s_at	NM_006107	cisplatin resistance-associated overexpressed protein
200614_at	NM_004859	clathrin, heavy polypeptide (Hc)
211452_x_at	AF130054	clone FLB4816 PRO1252
224752_at	BG031051	Clone IMAGE:5285814, mRNA
216505_x_at	AL118502	clone RP11-371L19 on chromosome 20 Contains the C20orf54 gene, the C20orf55 gene, the RPS10L gene for ribosomal protein S10-like and five CpG islands
215452_x_at	AL031133	clone RP1-281H8 on chromosome 6q25.1-25.3
222229_x_at	AL121871	clone RP13-258O15 on chromosome X
216570_x_at	AL096829	clone RP4-595K12 on chromosome 1p31.2-31.3 Contains a pseudogene similar to 60S RPL29 (ribosomal protein L29 (cell surface heparin binding protein HIP)), a chromosome 1 specific mRNA (KIAA0499), a novel mRNA (KIAA0433), ESTs, STSs, GSSs and a CpG Island, complete sequence
216348_at	AL049693	clone RP4-753D5 on chromosome 6p12.1-12.3. Contains the 3' end of the TFAP2B gene for transcription factor AP-2 beta (activating enhancer-binding protein 2 beta), the gene for a novel protein similar to RPS17 (40S ribosomal protein S17), a pseudogene similar to part of nuclear transport receptor MTR10A, an FTH1 (ferritin, heavy polypeptide 1) pseudogene, ESTs, STSs and GSSs
217752_s_at	NM_018235	CNDP dipeptidase 2 (metallopeptidase M20 family)
221059_s_at	NM_021615	coactosin-like 1 (Dictyostelium)
224583_at	AL565621	coactosin-like 1 (Dictyostelium)

Probe Set ID	Public ID	Gene Description
203305_at	NM_000129	coagulation factor XIII, A1 polypeptide
200087_s_at	AK024976	coated vesicle membrane protein /// coated vesicle membrane protein
217720_at	NM_016139	coiled-coil-helix-coiled-coil-helix domain containing 2
225312_at	AV704551	COMM domain containing 6
201405_s_at	NM_006833	COP9 constitutive photomorphogenic homolog subunit 6 (Arabidopsis)
203445_s_at	NM_005730	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2
201220_x_at	NM_001329	C-terminal binding protein 2
209489_at	N25915	CUG triplet repeat, RNA binding protein 1
221743_at	AI472139	CUG triplet repeat, RNA binding protein 1
202157_s_at	U69546	CUG triplet repeat, RNA binding protein 2
201700_at	NM_001760	cyclin D3
208655_at	BG530368	cyclin I
208656_s_at	AF135162	cyclin I
205081_at	NM_001311	cysteine-rich protein 1 (intestinal)
202698_x_at	NM_001861	cytochrome c oxidase subunit IV isoform 1
200086_s_at	AA854966	cytochrome c oxidase subunit IV isoform 1 /// cytochrome c oxidase subunit IV isoform 1
202343_x_at	NM_001862	cytochrome c oxidase subunit Vb
213735_s_at	AI557312	cytochrome c oxidase subunit Vb
211025_x_at	BC006229	cytochrome c oxidase subunit Vb /// cytochrome c oxidase subunit Vb
200925_at	NM_004373	cytochrome c oxidase subunit VIa polypeptide 1
201597_at	NM_001865	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)
202110_at	NM_001866	cytochrome c oxidase subunit VIIb
217491_x_at	AF042165	cytochrome c oxidase subunit VIIc
229813_x_at	BF512907	DAZ associated protein 1
214334_x_at	N34846	DAZ associated protein 2
208718_at	Z97056	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17
200694_s_at	NM_020414	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24
201584_s_at	NM_005804	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39
200033_at	NM_004396	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 /// DEAD (Asp-Glu-Ala-Asp) box polypeptide 5
225549_at	BF129093	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6
202420_s_at	NM_001357	DEAH (Asp-Glu-Ala-His) box polypeptide 9
225434_at	AW245401	death effector domain containing 2
226875_at	AI742838	dedicator of cytokinesis 11
200046_at	NM_001344	defender against cell death 1 /// defender against cell death 1
208763_s_at	AL110191	delta sleep inducing peptide, immunoreactor
202231_at	NM_006360	dendritic cell protein
202810_at	NM_004147	developmentally regulated GTP binding protein 1
202428_x_at	NM_020548	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)

Probe Set ID	**Public ID**	**Gene Description**
226659_at	Z97832	differentially expressed in FDCP 6 homolog (mouse)
214198_s_at	AU150824	DiGeorge syndrome critical region gene 2
205370_x_at	NM_001918	dihydrolipoamide branched chain transacylase E2 (DBT)
200762_at	NM_001386	dihydropyrimidinase-like 2
233056_x_at	AK024674	discs, large (Drosophila) homolog-associated protein 4
219678_x_at	NM_022487	DNA cross-link repair 1C (PSO2 homolog, S. cerevisiae)
215963_x_at	Z98200	DNA sequence from clone RP1-111B22 on chromosome 6q16-21
208674_x_at	BC002594	dolichyl-diphosphooligosaccharide-protein glycosyltransferase
208891_at	BC003143	dual specificity phosphatase 6
213848_at	AI655015	dual specificity phosphatase 7
208956_x_at	U62891	dUTP pyrophosphatase
217918_at	NM_014183	dynein, cytoplasmic, light polypeptide 2A
209473_at	AV717590	ectonucleoside triphosphate diphosphohydrolase 1
202596_at	BC000436	endosulfine alpha
217497_at	AW613387	endothelial cell growth factor 1 (platelet-derived)
1555306_a_at	AF521189	endothelin converting enzyme 2
234969_s_at	AK024117	enhancer of polycomb homolog 1 (Drosophila)
32259_at	AB002386	enhancer of zeste homolog 1 (Drosophila)
201231_s_at	NM_001428	enolase 1, (alpha)
219672_at	NM_016633	erythroid associated factor
209009_at	BC001169	esterase D/formylglutathione hydrolase
215096_s_at	AU145746	esterase D/formylglutathione hydrolase
204892_x_at	NM_001402	eukaryotic translation elongation factor 1 alpha 1
206559_x_at	NM_001403	eukaryotic translation elongation factor 1 alpha 1
213477_x_at	AL515273	eukaryotic translation elongation factor 1 alpha 1
213614_x_at	BE786672	eukaryotic translation elongation factor 1 alpha 1
200705_s_at	NM_001959	eukaryotic translation elongation factor 1 beta 2
203113_s_at	NM_001960	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)
200689_x_at	NM_001404	eukaryotic translation elongation factor 1 gamma (EEF1G),
204102_s_at	NM_001961	eukaryotic translation elongation factor 2
208726_s_at	BC000461	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa
224936_at	BE252813	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa
212716_s_at	AW083133	eukaryotic translation initiation factor 3 subunit k
221494_x_at	AF085358	eukaryotic translation initiation factor 3 subunit k
201592_at	NM_003756	eukaryotic translation initiation factor 3, subunit 3 gamma, 40kDa
200023_s_at	NM_003754	eukaryotic translation initiation factor 3, subunit 5 epsilon, 47kDa /// eukaryotic translation initiation factor 3, subunit 5 epsilon, 47kDa
217719_at	NM_016091	eukaryotic translation initiation factor 3, subunit 6 interacting protein
200004_at	NM_001418	eukaryotic translation initiation factor 4 gamma, 2 /// eukaryotic translation initiation factor 4 gamma, 2

Probe Set ID	Public ID	Gene Description
201530_x_at	NM_001416	eukaryotic translation initiation factor 4A, isoform 1
211787_s_at	BC006210	eukaryotic translation initiation factor 4A, isoform 1 /// eukaryotic translation initiation factor 4A, isoform 1
200912_s_at	NM_001967	eukaryotic translation initiation factor 4A, isoform 2
211938_at	BF247371	eukaryotic translation initiation factor 4B
224645_at	BG106477	eukaryotic translation initiation factor 4E binding protein 2
202651_at	NM_014873	family with sequence similarity 34, member A
215600_x_at	AK022174	F-box and WD-40 domain protein 12
218941_at	NM_012164	F-box and WD-40 domain protein 2
224369_s_at	AF251055	F-box protein 38 /// F-box protein 38
1554423_a_at	AF233225	F-box protein 7
201178_at	NM_012179	F-box protein 7
212987_at	AL031178	F-box protein 9
1554899_s_at	BC020763	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide
204232_at	NM_004106	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide
200748_s_at	NM_002032	ferritin, heavy polypeptide 1
211628_x_at	J04755	ferritin, heavy polypeptide pseudogene 1 /// ferritin, heavy polypeptide pseudogene 1
212788_x_at	BG537190	ferritin, light polypeptide
213187_x_at	BG538564	ferritin, light polypeptide
227811_at	AK000004	FGD1 family, member 3
204834_at	NM_006682	fibrinogen-like 2
200019_s_at	NM_001997	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived); ribosomal protein S30 /// Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived); ribosomal protein S30
200709_at	NM_000801	FK506 binding protein 1A, 12kDa
211445_x_at	AF315951	FKSG17
212473_s_at	BE965029	flavoprotein oxidoreductase MICAL2
238701_x_at	BE176566	FLJ45803 protein
35254_at	AB007447	FLN29 gene product
201350_at	NM_004475	flotillin 2
224891_at	AV725666	forkhead box O3A
224837_at	AW080845	forkhead box P1
224838_at	AK026898	forkhead box P1
212829_at	BE878277	Full-length cDNA clone CS0DC028YI02 of Neuroblastoma Cot 25-normalized of Homo sapiens (human)
209899_s_at	AF217197	fuse-binding protein-interacting repressor
210105_s_at	M14333	FYN oncogene related to SRC, FGR, YES
205220_at	NM_006018	G protein-coupled receptor 109B
225558_at	R38084	G protein-coupled receptor kinase interactor 2
200645_at	NM_007278	GABA(A) receptor-associated protein

Probe Set ID	Public ID	Gene Description
211458_s_at	AF180519	GABA(A) receptor-associated protein like 1
209046_s_at	AB030710	GABA(A) receptor-associated protein-like 2
208949_s_at	BC001120	galectin-3 internal gene
200009_at	NM_001494	GDP dissociation inhibitor 2 /// GDP dissociation inhibitor 2
215091_s_at	BE542815	general transcription factor IIIA
204220_at	NM_004877	glia maturation factor, gamma
217807_s_at	NM_015710	glioma tumor suppressor candidate region gene 2
212334_at	BE880245	glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID)
215001_s_at	AL161952	glutamate-ammonia ligase (glutamine synthase)
217202_s_at	U08626	glutamate-ammonia ligase (glutamine synthase)
217846_at	NM_005051	glutaminyl-tRNA synthetase
200736_s_at	NM_000581	glutathione peroxidase 1
201106_at	NM_002085	glutathione peroxidase 4 (phospholipid hydroperoxidase)
AFFX-HUMGAPDH/M33197_3_at	Unknown	glyceraldehyde-3-phosphate dehydrogenase
AFFX-HUMGAPDH/M33197_5_at	Unknown	glyceraldehyde-3-phosphate dehydrogenase
207389_at	NM_000173	glycoprotein Ib (platelet), alpha polypeptide
200780_x_at	NM_000516	GNAS complex locus
200981_x_at	NM_016592	GNAS complex locus
211858_x_at	AF088184	GNAS complex locus
212273_x_at	AI591100	GNAS complex locus
50277_at	AW001443	golgi associated, gamma adaptin ear containing, ARF binding protein 1
210164_at	J03189	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)
200651_at	NM_006098	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1
204115_at	NM_004126	guanine nucleotide binding protein (G protein), gamma 11
207157_s_at	NM_005274	guanine nucleotide binding protein (G protein), gamma 5
213911_s_at	BF718636	H2A histone family, member Z
200853_at	NM_002106	H2A histone family, member Z (H2AFZ),
208755_x_at	BF312331	H3 histone, family 3A
211940_x_at	BE869922	H3 histone, family 3A
213828_x_at	AA477655	H3 histone, family 3A
200080_s_at	AI955655	H3 histone, family 3A /// H3 histone, family 3A
209069_s_at	BC001124	H3 histone, family 3B (H3.3B)
211997_x_at	NM_005324	H3 histone, family 3B (H3.3B)
211999_at	Z48950	H3 histone, family 3B (H3.3B)
211946_s_at	AL096857	HBxAg transactivated protein 2
218603_at	NM_016217	headcase homolog (Drosophila)
200807_s_at	NM_002156	heat shock 60kDa protein 1 (chaperonin)

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208687_x_at	AF352832	heat shock 70kDa protein 8
221891_x_at	AA704004	heat shock 70kDa protein 8
224187_x_at	AF217511	heat shock 70kDa protein 8
211969_at	BG420237	heat shock 90kDa protein 1, alpha
200064_at	AF275719	heat shock 90kDa protein 1, beta /// heat shock 90kDa protein 1, beta
200942_s_at	NM_001537	heat shock factor binding protein 1
202957_at	NM_005335	hematopoietic cell-specific Lyn substrate 1
217736_s_at	NM_014413	heme-regulated initiation factor 2-alpha kinase
204018_x_at	NM_000558	hemoglobin, alpha 2
209458_x_at	AF105974	hemoglobin, alpha 2
214414_x_at	T50399	hemoglobin, alpha 2
217414_x_at	V00489	hemoglobin, alpha 2
211699_x_at	AF349571	hemoglobin, alpha 2 /// hemoglobin, alpha 2
211745_x_at	BC005931	hemoglobin, alpha 2 /// hemoglobin, alpha 2
209116_x_at	M25079	hemoglobin, beta
211696_x_at	AF349114	hemoglobin, beta /// hemoglobin, beta
206834_at	NM_000519	hemoglobin, delta
204419_x_at	NM_000184	hemoglobin, gamma A
213515_x_at	AI133353	hemoglobin, gamma A
202300_at	NM_006402	hepatitis B virus x interacting protein
223042_s_at	BC000255	hepatitis C virus core-binding protein 6
214280_x_at	X79536	heterogeneous nuclear ribonucleoprotein A1
200016_x_at	NM_002136	heterogeneous nuclear ribonucleoprotein A1 /// heterogeneous nuclear ribonucleoprotein A1
213356_x_at	AL568186	heterogeneous nuclear ribonucleoprotein A1 /// hypothetical protein LOC144983
205292_s_at	NM_002137	heterogeneous nuclear ribonucleoprotein A2/B1
225932_s_at	AI375753	heterogeneous nuclear ribonucleoprotein A2/B1
211931_s_at	BG505670	heterogeneous nuclear ribonucleoprotein A3 /// heterogeneous nuclear ribonucleoprotein A3 pseudogene 1
211933_s_at	AA528233	heterogeneous nuclear ribonucleoprotein A3 /// heterogeneous nuclear ribonucleoprotein A3 pseudogene 1
212626_x_at	AA664258	heterogeneous nuclear ribonucleoprotein C (C1/C2)
214737_x_at	AV725195	heterogeneous nuclear ribonucleoprotein C (C1/C2)
200014_s_at	NM_004500	heterogeneous nuclear ribonucleoprotein C (C1/C2) /// heterogeneous nuclear ribonucleoprotein C (C1/C2)
212454_x_at	AI762552	heterogeneous nuclear ribonucleoprotein D-like
207127_s_at	NM_021644	heterogeneous nuclear ribonucleoprotein H3 (2H9)
200775_s_at	BC000355	heterogeneous nuclear ribonucleoprotein K
200072_s_at	AF061832	heterogeneous nuclear ribonucleoprotein M /// heterogeneous nuclear ribonucleoprotein M
208766_s_at	BC001449	heterogeneous nuclear ribonucleoprotein R

Probe Set ID	**Public ID**	**Gene Description**
200594_x_at	NM_004501	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)
208713_at	BF724216	heterogeneous nuclear ribonucleoprotein U-like 1
201944_at	NM_000521	hexosaminidase B (beta polypeptide)
200680_x_at	NM_002128	high-mobility group box 1
214938_x_at	AF283771	high-mobility group box 1
208668_x_at	BC003689	high-mobility group nucleosomal binding domain 2
200943_at	NM_004965	high-mobility group nucleosome binding domain 1
200944_s_at	NM_004965	high-mobility group nucleosome binding domain 1
1555961_a_at	AK054976	histidine triad nucleotide binding protein 1
200093_s_at	N32864	histidine triad nucleotide binding protein 1 /// histidine triad nucleotide binding protein 1
213318_s_at	BG028844	HLA-B associated transcript 3
200904_at	X56841	HLA-E gene
211528_x_at	M90685	HLA-G histocompatibility antigen, class I, G
211529_x_at	M90684	HLA-G histocompatibility antigen, class I, G
209058_at	AB002282	hMBF1alpha
208557_at	NM_024014	homeo box A6
226297_at	AV693403	homeodomain interacting protein kinase 3
213366_x_at	AV711183	Homo sapiens cDNA clone CuAAOG09 5'
228869_at	AI081246	Homo sapiens cDNA clone IMAGE:1670867
214394_x_at	AI613383	Homo sapiens cDNA clone IMAGE:2247110 3' similar to gb:Z21507 ELONGATION FACTOR 1-DELTA (HUMAN);,
210524_x_at	AF078844	hqp0376 protein
209481_at	AF226044	HSNFRK (HSNFRK)
218026_at	NM_014019	HSPC009 protein
223051_at	AF277178	HSPC182 protein
211623_s_at	M30448	Human casein kinase II beta subunit
210915_x_at	M15564	Human T-cell receptor rearranged beta-chain V-region
203040_s_at	NM_000190	hydroxymethylbilane synthase
225794_s_at	AV751709	hypothetical gene supported by AL449243
234981_x_at	BE537881	hypothetical protein BC001573
225404_at	R75637	hypothetical protein BC011880
201581_at	BF572868	hypothetical protein DJ971N18.2
208091_s_at	NM_030796	hypothetical protein DKFZp564K0822 /// hypothetical protein DKFZp564K0822
44563_at	AI858000	hypothetical protein FLJ10385
232215_x_at	AK000296	hypothetical protein FLJ11029
226062_x_at	AB037811	hypothetical protein FLJ11280
45526_g_at	AI246641	hypothetical protein FLJ14154
208246_x_at	NM_017618	hypothetical protein FLJ20006
207783_x_at	NM_017627	hypothetical protein FLJ20030

Probe Set ID	Public ID	Gene Description
218068_s_at	NM_024836	hypothetical protein FLJ22301
218454_at	NM_024829	hypothetical protein FLJ22662
220486_x_at	NM_017698	hypothetical protein FLJ22679
1552942_at	NM_153009	hypothetical protein FLJ30430
221791_s_at	BG167522	hypothetical protein HSPC016
223067_at	AF110775	hypothetical protein HSPC148
224826_at	AK001947	hypothetical protein KIAA1434
224835_at	AL109935	hypothetical protein KIAA1434
212697_at	AL515874	hypothetical protein LOC162427
201812_s_at	NM_019059	hypothetical protein LOC201725 /// translocase of outer mitochondrial membrane 7 homolog (yeast)
51774_s_at	AW014299	hypothetical protein LOC222070
58900_at	AW025284	hypothetical protein LOC222070
225117_at	AL137317	hypothetical protein LOC284058
1555847_a_at	BU617052	hypothetical protein LOC284454
224765_at	AA001203	hypothetical protein LOC339287
231770_x_at	AK022647	hypothetical protein LOC51057
225509_at	AI862477	hypothetical protein LOC56757
224512_s_at	BC006407	hypothetical protein MGC14151 /// hypothetical protein MGC14151
238430_x_at	AI923675	hypothetical protein MGC19764
228532_at	AW662189	hypothetical protein MGC24133
223003_at	AF061732	hypothetical protein MGC2803
221255_s_at	NM_031298	hypothetical protein MGC2963 /// hypothetical protein MGC2963
226876_at	AI961778	hypothetical protein MGC45871
225793_at	AW500180	hypothetical protein MGC46719
225799_at	BF209337	hypothetical protein MGC4677
224573_at	BE744389	hypothetical protein MGC49942
62212_at	W37846	hypothetical protein MGC955
219293_s_at	NM_013341	hypothetical protein PTD004
212725_s_at	N37081	hypothetical protein TI-227H
212221_x_at	AV703259	iduronate 2-sulfatase (Hunter syndrome)
202081_at	NM_004907	immediate early response 2
64064_at	AI435089	immune associated nucleotide 4 like 1 (mouse)
212827_at	X17115	immunoglobulin heavy constant mu
239748_x_at	H09533	infant brain 1NIB Homo sapiens cDNA clone IMAGE:46131 3' similar to contains Alu repetitive element
203006_at	NM_005539	inositol polyphosphate-5-phosphatase, 40kDa
201393_s_at	NM_000876	insulin-like growth factor 2 receptor
217731_s_at	NM_021999	integral membrane protein 2B
217732_s_at	AF092128	integral membrane protein 2B

Probe Set ID	Public ID	Gene Description
213475_s_at	AC002310	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)
211945_s_at	BG500301	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)
201601_x_at	NM_003641	interferon induced transmembrane protein 1 (9-27)
214022_s_at	AA749101	interferon induced transmembrane protein 1 (9-27)
201315_x_at	NM_006435	interferon induced transmembrane protein 2 (1-8D)
224569_s_at	AW242432	interferon regulatory factor 2 binding protein 2
204912_at	NM_001558	interleukin 10 receptor, alpha
201887_at	NM_001560	interleukin 13 receptor, alpha 1
226333_at	AV700030	interleukin 6 receptor
226218_at	BE217880	interleukin 7 receptor
217908_s_at	NM_018442	IQ motif and WD repeats 1
201648_at	AL039831	Janus kinase 1 (a protein tyrosine kinase)
41387_r_at	AB002344	jumonji domain containing 3
203297_s_at	BG029530	Jumonji, AT rich interactive domain 2
210434_x_at	AF151056	jumping translocation breakpoint
210927_x_at	BC004239	jumping translocation breakpoint
203752_s_at	NM_005354	jun D proto-oncogene
208974_x_at	BC003572	karyopherin (importin) beta 1
200700_s_at	NM_006854	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2
225225_at	BF791544	Keratin associated protein 4-7
224885_s_at	BE260771	keratinocyte associated protein 2
212846_at	AA811192	KIAA0179
215696_s_at	BC001404	KIAA0310
202860_at	NM_014856	KIAA0476
205788_s_at	NM_014827	KIAA0663 gene product
203906_at	AI652645	KIAA0763 gene product
225266_at	AA526904	KIAA0924 protein
200860_s_at	BC000779	KIAA1007 protein
209229_s_at	BC002799	KIAA1115
221952_x_at	AB037814	KIAA1393
226720_at	AI686303	KIAA1935 protein
224691_at	BE622897	kinase interacting with leukemia-associated gene (stathmin)
203943_at	NM_004798	kinesin family member 3B
225390_s_at	AL390127	Kruppel-like factor 13
219371_s_at	NM_016270	Kruppel-like factor 2 (lung)
200650_s_at	NM_005566	lactate dehydrogenase A
201030_x_at	NM_002300	lactate dehydrogenase B
213564_x_at	BE042354	lactate dehydrogenase B

Probe Set ID	Public ID	Gene Description
213801_x_at	AW304232	laminin receptor 1 (ribosomal protein SA, 67kDa)
57082_at	AA169780	LDL receptor adaptor protein
202595_s_at	AF161461	leptin receptor overlapping transcript-like 1
213975_s_at	AV711904	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1 /// lysozyme (renal amyloidosis)
218132_s_at	NM_024075	leukocyte receptor cluster (LRC) member 5
214574_x_at	NM_007161	leukocyte specific transcript 1
208771_s_at	J02959	leukotriene A4 hydrolase
224719_s_at	BG339653	likely ortholog of mouse gene rich cluster, C10 gene
212137_at	AV746402	likely ortholog of mouse la related protein
220990_s_at	NM_030938	likely ortholog of rat vacuole membrane protein 1 /// likely ortholog of rat vacuole membrane protein 1
200618_at	NM_006148	LIM and SH3 protein 1
212114_at	BE967207	LOC387869
201568_at	NM_014402	low molecular mass ubiquinone-binding protein (9.5kD)
211747_s_at	BC005938	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae) /// LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)
204891_s_at	NM_005356	lymphocyte-specific protein tyrosine kinase
207339_s_at	NM_002341	lymphotoxin beta (TNF superfamily, member 3)
201552_at	NM_005561	lysosomal-associated membrane protein 1
201553_s_at	NM_005561	lysosomal-associated membrane protein 1
200840_at	NM_005548	lysyl-tRNA synthetase
200079_s_at	AF285758	lysyl-tRNA synthetase /// lysyl-tRNA synthetase
226818_at	T64884	macrophage expressed gene 1
217871_s_at	NM_002415	macrophage migration inhibitory factor (glycosylation-inhibiting factor)
215313_x_at	AA573862	major histocompatibility complex, class I, A
209140_x_at	L42024	major histocompatibility complex, class I, B
214459_x_at	M12679	major histocompatibility complex, class I, C
211911_x_at	L07950	major histocompatibility complex, class I, C /// major histocompatibility complex, class I, C
200905_x_at	NM_005516	major histocompatibility complex, class I, E
217456_x_at	M31183	major histocompatibility complex, class I, E
221875_x_at	AW514210	major histocompatibility complex, class I, F
217478_s_at	X76775	major histocompatibility complex, class II, DM alpha
203932_at	NM_002118	major histocompatibility complex, class II, DM beta
211991_s_at	M27487	major histocompatibility complex, class II, DP alpha 1
201137_s_at	NM_002121	major histocompatibility complex, class II, DP beta 1
212671_s_at	BG397856	major histocompatibility complex, class II, DQ alpha 1
204670_x_at	NM_002125	major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 3 /// major histocompatibility complex, class II, DR beta 4
208306_x_at	NM_021983	major histocompatibility complex, class II, DR beta 3

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215193_x_at	AJ297586	major histocompatibility complex, class II, DR beta 3
217362_x_at	AF005487	major histocompatibility complex, class II, DR beta 6 (pseudogene)
201285_at	NM_013446	makorin, ring finger protein, 1
209845_at	AF117233	makorin, ring finger protein, 1
208082_x_at	NM_030757	makorin, ring finger protein, 4 /// makorin, ring finger protein, 4
209036_s_at	BC001917	malate dehydrogenase 2, NAD (mitochondrial)
204153_s_at	NM_002405	manic fringe homolog (Drosophila)
218205_s_at	NM_017572	MAP kinase interacting serine/threonine kinase 2
211678_s_at	AF090934	maternally expressed 3 /// zinc finger protein 313 /// maternally expressed 3 /// zinc finger protein 313
214363_s_at	AA129420	matrin 3
226275_at	AI188653	MAX dimerization protein 1
228846_at	AW071793	MAX dimerization protein 1
202364_at	NM_005962	MAX interactor 1
209332_s_at	BC003525	MAX protein, transcript variant 2
200768_s_at	BC001686	methionine adenosyltransferase II, alpha
217993_s_at	NM_013283	methionine adenosyltransferase II, beta
209312_x_at	U65585	MHC class II antigen (HLA-DRB1)
208634_s_at	AB029290	microtubule-actin crosslinking factor 1
212566_at	AL523310	microtubule-associated protein 4
221619_s_at	AF189289	mitochondrial carrier homolog 1 (C. elegans)
204387_x_at	NM_024026	mitochondrial ribosomal protein 63
213897_s_at	AI832239	mitochondrial ribosomal protein L23
203152_at	NM_003776	mitochondrial ribosomal protein L40
223086_x_at	AF151075	mitochondrial ribosomal protein L51
218106_s_at	NM_018141	mitochondrial ribosomal protein S10
224621_at	AA129773	mitogen-activated protein kinase 1
225927_at	AA541479	mitogen-activated protein kinase kinase kinase 1
203652_at	NM_002419	mitogen-activated protein kinase kinase kinase 11
41220_at	AB023208	MLL septin-like fusion
217982_s_at	NM_006791	mortality factor 4 like 1
201994_at	NM_012286	mortality factor 4 like 2
32209_at	AF052151	Mouse Mammary Turmor Virus Receptor homolog 1
213583_x_at	BE964125	MRNA expressed only in placental villi, clone SMAP83. /// Full-length cDNA clone CS0DF006YK07 of Fetal brain of Homo sapiens (human)
1559436_x_at	AL832061	MRNA; cDNA DKFZp313M2114 (from clone DKFZp313M2114)
1555832_s_at	BU683415	MRNA; cDNA DKFZp564C2063 (from clone DKFZp564C2063)
215628_x_at	AL049285	MRNA; cDNA DKFZp564M193 (from clone DKFZp564M193)
214902_x_at	AL080232	MRNA; cDNA DKFZp586A061 (from clone DKFZp586A061)
201254_x_at	NM_001010	MRNA; cDNA DKFZp586I041 (from clone DKFZp586I041)

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209134_s_at	BC000524	MRNA; cDNA DKFZp586I041 (from clone DKFZp586I041)
225893_at	AL589593	MRNA; cDNA DKFZp686D04119 (from clone DKFZp686D04119)
225176_at	AA156754	MSTP146 (MST146) mRNA, complete cds
1566887_x_at	AY094612	multiple myeloma susceptibility
217232_x_at	AF059180	mutant beta-globin (HBB) gene
226544_x_at	AV734582	muted homolog (mouse)
200797_s_at	AI275690	myeloid cell leukemia sequence 1 (BCL2-related)
204959_at	NM_002432	myeloid cell nuclear differentiation antigen
201924_at	NM_005935	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 2
228098_s_at	AW292746	myosin regulatory light chain interacting protein
201319_at	NM_006471	myosin regulatory light chain MRCL3
201318_s_at	NM_006471	myosin regulatory light chain MRCL3 /// myosin regulatory light chain MRLC2
221474_at	U26162	myosin regulatory light chain MRLC2
212082_s_at	BE734356	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle
224656_s_at	AL533334	myotrophin
226547_at	AI817830	MYST histone acetyltransferase (monocytic leukemia) 3
202298_at	NM_004541	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa
209224_s_at	BC003674	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa
217773_s_at	NM_002489	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa
202001_s_at	NM_002490	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa
206790_s_at	NM_004545	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7kDa
218320_s_at	NM_019056	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11, 17.3kDa
218200_s_at	NM_004546	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa
201227_s_at	NM_005004	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa
222992_s_at	AF261090	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa
202077_at	NM_005003	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa
201757_at	NM_004552	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase)
232169_x_at	AK002110	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)
200735_x_at	NM_005594	nascent-polypeptide-associated complex alpha polypeptide
208635_x_at	BF976260	nascent-polypeptide-associated complex alpha polypeptide
244197_x_at	AI859990	NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2436700 3' similar to contains Alu repetitive element
48612_at	AA225490	Nedd4 binding protein 1
234762_x_at	AK026655	neurolysin (metallopeptidase M3 family)
218455_at	NM_021100	NFS1 nitrogen fixation 1 (S. cerevisiae)
200701_at	NM_006432	Niemann-Pick disease, type C2
201268_at	NM_002512	non-metastatic cells 2, protein (NM23B) expressed in
200057_s_at	NM_007363	non-POU domain containing, octamer-binding /// non-POU domain containing, octamer-binding
210774_s_at	AL162047	nuclear receptor coactivator 4

Probe Set ID	Public ID	Gene Description
208628_s_at	BC002411	nuclease sensitive element binding protein 1
217962_at	NM_018648	nucleolar protein family A, member 3 (H/ACA small nucleolar RNPs)
200610_s_at	NM_005381	nucleolin
200063_s_at	BC002398	nucleophosmin (nucleolar phosphoprotein B23, numatrin) /// nucleophosmin (nucleolar phosphoprotein B23, numatrin)
213682_at	AL036344	nucleoporin 50kDa
204528_s_at	NM_004537	nucleosome assembly protein 1-like 1
208752_x_at	AI888672	nucleosome assembly protein 1-like 1
212967_x_at	AW148801	nucleosome assembly protein 1-like 1
213864_s_at	AI985751	nucleosome assembly protein 1-like 1
208093_s_at	NM_030808	nudE nuclear distribution gene E homolog like 1 (A. nidulans) /// nudE nuclear distribution gene E homolog like 1 (A. nidulans)
215952_s_at	AF090094	ornithine decarboxylase antizyme 1
200077_s_at	D87914	ornithine decarboxylase antizyme 1 /// ornithine decarboxylase antizyme 1
232644_x_at	AK024302	ovarian carcinoma immunoreactive antigen
222218_s_at	AJ400843	paired immunoglobin-like type 2 receptor alpha
200975_at	NM_000310	palmitoyl-protein thioesterase 1 (ceroid-lipofuscinosis, neuronal 1, infantile)
218809_at	NM_024960	pantothenate kinase 2 (Hallervorden-Spatz syndrome)
200006_at	NM_007262	Parkinson disease (autosomal recessive, early onset) 7 /// Parkinson disease (autosomal recessive, early onset) 7
201293_x_at	NM_021130	peptidylprolyl isomerase A (cyclophilin A)
211378_x_at	BC001224	peptidylprolyl isomerase A (cyclophilin A)
211978_x_at	AI708767	peptidylprolyl isomerase A (cyclophilin A)
212661_x_at	BE731738	peptidylprolyl isomerase A (cyclophilin A)
211765_x_at	BC005982	peptidylprolyl isomerase A (cyclophilin A) /// peptidylprolyl isomerase A (cyclophilin A)
208680_at	L19184	peroxiredoxin 1
1560587_s_at	AI718223	peroxiredoxin 5
222994_at	AF197952	peroxiredoxin 5
49878_at	AA523441	peroxisomal biogenesis factor 16
40446_at	AL021366	PHD finger protein 1
205570_at	NM_005028	phosphatidylinositol-4-phosphate 5-kinase, type II, alpha
206792_x_at	NM_000923	phosphodiesterase 4C, cAMP-specific (phosphodiesterase E1 dunce homolog, Drosophila)
200738_s_at	NM_000291	phosphoglycerate kinase 1
204613_at	NM_002661	phospholipase C, gamma 2 (phosphatidylinositol-specific)
200788_s_at	NM_003768	phosphoprotein enriched in astrocytes 15
224842_at	AK025794	PI-3-kinase-related kinase SMG-1
215179_x_at	AK023843	placental growth factor, vascular endothelial growth factor-related protein
219014_at	NM_016619	placenta-specific 8
206390_x_at	NM_002619	platelet factor 4 (chemokine (C-X-C motif) ligand 4)

Probe Set ID	Public ID	Gene Description
201410_at	AI983043	pleckstrin homology domain containing, family B (evectins) member 2
202880_s_at	NM_004762	pleckstrin homology, Sec7 and coiled-coil domains 1(cytohesin 1)
219183_s_at	NM_013385	pleckstrin homology, Sec7 and coiled-coil domains 4
213241_at	AF035307	plexin C1
222983_s_at	BC001716	poly(A) binding protein interacting protein 2
215157_x_at	AI734929	poly(A) binding protein, cytoplasmic 1
215823_x_at	U64661	poly(A) binding protein, cytoplasmic 1
208113_x_at	NM_030979	poly(A) binding protein, cytoplasmic 1 /// poly(A) binding protein, cytoplasmic 1
201544_x_at	BF675004	poly(A) binding protein, nuclear 1
212718_at	BF797555	poly(A) polymerase alpha
208620_at	U24223	poly(rC) binding protein 1
204031_s_at	NM_005016	poly(rC) binding protein 2
203366_at	NM_002693	polymerase (DNA directed), gamma
1555837_s_at	BE614461	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa
211730_s_at	BC005903	polymerase (RNA) II (DNA directed) polypeptide L, 7.6kDa /// polymerase (RNA) II (DNA directed) polypeptide L, 7.6kDa
211271_x_at	BC004383	polypyrimidine tract binding protein 1
227647_at	AI692703	potassium voltage-gated channel, Isk-related family, member 3
225373_at	BE271644	PP2135 protein
207132_x_at	NM_002624	prefoldin 5
220856_x_at	NM_014128	PRO0470 protein (PRO0470),
211345_x_at	AF119850	PRO1608
217746_s_at	NM_013374	programmed cell death 6 interacting protein
211178_s_at	AF038602	proline-serine-threonine phosphatase interacting protein 1
214146_s_at	R64130	pro-platelet basic protein (chemokine (C-X-C motif) ligand 7)
200871_s_at	NM_002778	prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)
200882_s_at	NM_002810	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4
211609_x_at	U51007	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4 /// proteasome (prosome, macropain) 26S subunit, non-ATPase, 4
201762_s_at	NM_002818	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)
201317_s_at	NM_002787	proteasome (prosome, macropain) subunit, alpha type, 2
200876_s_at	NM_002793	proteasome (prosome, macropain) subunit, beta type, 1
214288_s_at	W86293	proteasome (prosome, macropain) subunit, beta type, 1
200039_s_at	NM_002794	proteasome (prosome, macropain) subunit, beta type, 2 /// proteasome (prosome, macropain) subunit, beta type, 2
202244_at	NM_002796	proteasome (prosome, macropain) subunit, beta type, 4
208827_at	BC000835	proteasome (prosome, macropain) subunit, beta type, 6
204279_at	NM_002800	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2)
226091_s_at	BG435643	protein associated with MRG, 14 kDa

Probe Set ID	Public ID	Gene Description
209685_s_at	M13975	protein kinase C, beta 1
200603_at	AL050038	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)
1555248_a_at	AY082340	protein kinase, lysine deficient 3
201500_s_at	NM_021959	protein phosphatase 1, regulatory (inhibitor) subunit 11
203966_s_at	NM_021003	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform
208615_s_at	BF795101	protein tyrosine phosphatase type IVA, member 2
208616_s_at	U48297	protein tyrosine phosphatase type IVA, member 2
221840_at	AA775177	protein tyrosine phosphatase, receptor type, E
201859_at	NM_002727	proteoglycan 1, secretory granule
200773_x_at	NM_002823	prothymosin, alpha (gene sequence 28)
217780_at	NM_016145	PTD008 protein
216221_s_at	D87078	pumilio homolog 2 (Drosophila)
202121_s_at	NM_014453	putative breast adenocarcinoma marker (32kD)
223276_at	AF313413	putative small membrane protein NID67
211956_s_at	BF246436	putative translation initiation factor
212130_x_at	AL537707	putative translation initiation factor
212227_x_at	W67644	putative translation initiation factor
203020_at	NM_014857	RAB GTPase activating protein 1-like
200863_s_at	AI215102	RAB11A, member RAS oncogene family
209089_at	BC001267	RAB5A, member RAS oncogene family
211961_s_at	AK000826	RAB7, member RAS oncogene family
218699_at	BG338251	RAB7, member RAS oncogene family-like 1
213923_at	AW005535	RAP2B, member of RAS oncogene family
223322_at	BC004270	Ras association (RalGDS/AF-6) domain family 5
200059_s_at	BC001360	ras homolog gene family, member A /// ras homolog gene family, member A
203175_at	NM_001665	ras homolog gene family, member G (rho G)
208640_at	BG292367	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)
208641_s_at	BC004247	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)
213603_s_at	BE138888	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)
211974_x_at	AL513759	recombining binding protein suppressor of hairless (Drosophila)
202388_at	NM_002923	regulator of G-protein signalling 2, 24kDa
201600_at	NM_007273	repressor of estrogen receptor activity
202296_s_at	NM_007033	RER1 homolog (S. cerevisiae)
224564_s_at	BE544689	reticulon 3
211509_s_at	AB015639	reticulon 4
201288_at	NM_001175	Rho GDP dissociation inhibitor (GDI) beta
38149_at	D29642	Rho GTPase activating protein 25
225415_at	AA577672	rhysin 2

Probe Set ID	Public ID	Gene Description
217983_s_at	NM_003730	ribonuclease T2
217984_at	NM_003730	ribonuclease T2
206050_s_at	NM_002939	ribonuclease/angiogenin inhibitor
200725_x_at	NM_006013	ribosomal protein L10
229563_s_at	BG231561	ribosomal protein L10a
200036_s_at	NM_007104	ribosomal protein L10a /// ribosomal protein L10a
200010_at	NM_000975	ribosomal protein L11 /// ribosomal protein L11
200809_x_at	NM_000976	ribosomal protein L12
214271_x_at	AA281332	ribosomal protein L12
200088_x_at	AK026491	ribosomal protein L12 /// ribosomal protein L12
208929_x_at	BC004954	ribosomal protein L13
212191_x_at	AW574664	ribosomal protein L13
212734_x_at	AI186735	ribosomal protein L13
212933_x_at	AA961748	ribosomal protein L13
214351_x_at	AA789278	ribosomal protein L13
200715_x_at	BC000514	ribosomal protein L13a
210646_x_at	BC001675	ribosomal protein L13a
211942_x_at	BF979419	ribosomal protein L13a
200716_x_at	NM_012423	ribosomal protein L13a (RPL13A)
213588_x_at	AA838274	ribosomal protein L14
200074_s_at	U16738	ribosomal protein L14 /// ribosomal protein L14
221475_s_at	NM_002948	ribosomal protein L15
212270_x_at	BG168283	ribosomal protein L17
212537_x_at	BE733979	ribosomal protein L17
200038_s_at	NM_000985	ribosomal protein L17 /// ribosomal protein L17
200022_at	NM_000979	ribosomal protein L18 /// ribosomal protein L18
200869_at	NM_000980	ribosomal protein L18a (RPL18A)
200029_at	NM_000981	ribosomal protein L19 /// ribosomal protein L19
200012_x_at	NM_000982	ribosomal protein L21 /// ribosomal protein L21
208768_x_at	D17652	ribosomal protein L22
220960_x_at	NM_000983	ribosomal protein L22
221775_x_at	BG152979	ribosomal protein L22
200888_s_at	NM_000978	ribosomal protein L23
203012_x_at	NM_000984	ribosomal protein L23a
208825_x_at	U43701	ribosomal protein L23a
208834_x_at	BC001865	ribosomal protein L23a
213084_x_at	BF125158	ribosomal protein L23a
200013_at	NM_000986	ribosomal protein L24 (RPL24)

Probe Set ID	Public ID	Gene Description
200025_s_at	NM_000988	ribosomal protein L27 /// ribosomal protein L27
203034_s_at	NM_000990	ribosomal protein L27a
200003_s_at	NM_000991	ribosomal protein L28 /// ribosomal protein L28
200823_x_at	NM_000992	ribosomal protein L29
213969_x_at	BF683426	ribosomal protein L29
201217_x_at	NM_000967	ribosomal protein L3
212039_x_at	BG339228	ribosomal protein L3
211073_x_at	BC006483	ribosomal protein L3 /// ribosomal protein L3
211666_x_at	L22453	ribosomal protein L3 /// ribosomal protein L3
200062_s_at	L05095	ribosomal protein L30
200963_x_at	NM_000993	ribosomal protein L31 (RPL31)
200674_s_at	NM_000994	ribosomal protein L32
200026_at	NM_000995	ribosomal protein L34 /// ribosomal protein L34
200002_at	NM_007209	ribosomal protein L35 /// ribosomal protein L35
213687_s_at	BE968801	ribosomal protein L35a
225190_x_at	AW402660	ribosomal protein L35a
219762_s_at	NM_015414	ribosomal protein L36
201406_at	NM_021029	ribosomal protein L36a
207585_s_at	NM_001001	ribosomal protein L36a-like
200092_s_at	BF216701	ribosomal protein L37 /// ribosomal protein L37
201429_s_at	NM_000998	ribosomal protein L37a
202029_x_at	NM_000999	ribosomal protein L38
208695_s_at	BC001019	ribosomal protein L39
201154_x_at	NM_000968	ribosomal protein L4
200089_s_at	AI953886	ribosomal protein L4 /// ribosomal protein L4
211710_x_at	BC005817	ribosomal protein L4 /// ribosomal protein L4
201492_s_at	NM_021104	ribosomal protein L41
200937_s_at	NM_000969	ribosomal protein L5
213080_x_at	BF214492	ribosomal protein L5
200034_s_at	NM_000970	ribosomal protein L6 /// ribosomal protein L6
200717_x_at	NM_000971	ribosomal protein L7
212042_x_at	BG389744	ribosomal protein L7
217740_x_at	NM_000972	ribosomal protein L7a
224930_x_at	BE559788	ribosomal protein L7a
234512_x_at	AL136226	ribosomal protein L7a
234873_x_at	AJ224080	ribosomal protein L7a
200936_at	NM_000973	ribosomal protein L8
200032_s_at	NM_000661	ribosomal protein L9 /// ribosomal protein L9

Probe Set ID	Public ID	Gene Description
200817_x_at	NM_001014	ribosomal protein S10
211542_x_at	BC004334	ribosomal protein S10
200095_x_at	AA320764	ribosomal protein S10 /// ribosomal protein S10
200031_s_at	NM_001015	ribosomal protein S11 /// ribosomal protein S11
213377_x_at	AI799007	ribosomal protein S12
200018_at	NM_001017	ribosomal protein S13 /// ribosomal protein S13
208645_s_at	AF116710	ribosomal protein S14
200819_s_at	NM_001018	ribosomal protein S15
201258_at	NM_001020	ribosomal protein S16
213890_x_at	AI200589	ribosomal protein S16
226131_s_at	AA583817	ribosomal protein S16
201665_x_at	NM_001021	ribosomal protein S17
211487_x_at	BC004886	ribosomal protein S17
212578_x_at	BF026595	ribosomal protein S17
201049_s_at	NM_022551	ribosomal protein S18 (RPS18),
202649_x_at	NM_001022	ribosomal protein S19
213414_s_at	BE259729	ribosomal protein S19
203107_x_at	NM_002952	ribosomal protein S2
212433_x_at	AA630314	ribosomal protein S2
221798_x_at	AI183766	ribosomal protein S2
200949_x_at	NM_001023	ribosomal protein S20
214003_x_at	BF184532	ribosomal protein S20
200834_s_at	NM_001024	ribosomal protein S21
200926_at	NM_001025	ribosomal protein S23
200061_s_at	BC000523	ribosomal protein S24 /// ribosomal protein S24
200091_s_at	AA888388	ribosomal protein S25 /// ribosomal protein S25
217753_s_at	NM_001029	ribosomal protein S26
200741_s_at	NM_001030	ribosomal protein S27 (metallopanstimulin 1)
200017_at	NM_002954	ribosomal protein S27a /// ribosomal protein S27a
208904_s_at	BC000354	ribosomal protein S28
201094_at	NM_001032	ribosomal protein S29
208692_at	U14990	ribosomal protein S3
201257_x_at	NM_001006	ribosomal protein S3A
212391_x_at	AI925635	ribosomal protein S3A
200099_s_at	AL356115	ribosomal protein S3A /// ribosomal protein S3A
200933_x_at	NM_001007	ribosomal protein S4, X-linked
213347_x_at	AW132023	ribosomal protein S4, X-linked
200024_at	NM_001009	ribosomal protein S5 (RPS5)

Probe Set ID	Public ID	Gene Description
200081_s_at	BE741754	ribosomal protein S6 /// ribosomal protein S6
213941_x_at	AI970731	ribosomal protein S7
200082_s_at	AI805587	ribosomal protein S7 /// ribosomal protein S7
200858_s_at	NM_001012	ribosomal protein S8
214317_x_at	BE348997	ribosomal protein S9
217747_s_at	NM_001013	ribosomal protein S9
200909_s_at	NM_001004	ribosomal protein, large P2
201033_x_at	NM_001002	ribosomal protein, large, P0
208856_x_at	BC003655	ribosomal protein, large, P0
211972_x_at	AI953822	ribosomal protein, large, P0
214167_s_at	AA555113	ribosomal protein, large, P0
211720_x_at	BC005863	ribosomal protein, large, P0 /// ribosomal protein, large, P0
200763_s_at	NM_001003	ribosomal protein, large, P1
201845_s_at	AB029551	RING1 and YY1 binding protein
218117_at	NM_014248	ring-box 1
215127_s_at	AL517946	RNA binding motif, single stranded interacting protein 1
204197_s_at	NM_004350	runt-related transcription factor 3
200872_at	NM_002966	S100 calcium binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11))
208540_x_at	NM_021039	S100 calcium binding protein A11 pseudogene
203186_s_at	NM_002961	S100 calcium binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homolog)
217728_at	NM_014624	S100 calcium binding protein A6 (calcyclin)
202917_s_at	NM_002964	S100 calcium binding protein A8 (calgranulin A)
203535_at	NM_002965	S100 calcium binding protein A9 (calgranulin B)
222986_s_at	BC001463	scotin
203133_at	NM_006808	Sec61 beta subunit
203484_at	NM_014302	Sec61 gamma subunit
221931_s_at	AV701173	SEH1-like (S. cerevisiae)
204563_at	NM_000655	selectin L (lymphocyte adhesion molecule 1)
233168_s_at	BC001099	selenoprotein O
1555851_s_at	AW514401	selenoprotein W, 1
216342_x_at	AL121916	sequence from clone RP1-189G13 on chromosome 20. Contains an RPL7A (60S ribosomal protein L7A) (SURF3) pseudogene, an RPS4 (40S ribosomal protein S4) pseudogene, ESTs, STSs and GSSs
217256_x_at	Z98950	sequence from clone RP3-507I15 on chromosome Xq26.3-27.3
40420_at	AB015718	serine/threonine kinase 10
36019_at	L26260	serine/threonine kinase 19
208855_s_at	AF083420	serine/threonine kinase 24 (STE20 homolog, yeast)
200870_at	NM_007178	serine/threonine kinase receptor associated protein
200630_x_at	AV702810	SET translocation (myeloid leukemia-associated)
201312_s_at	NM_003022	SH3 domain binding glutamic acid-rich protein like

Probe Set ID	**Public ID**	**Gene Description**
201811_x_at	NM_004844	SH3-domain binding protein 5 (BTK-associated)
1554168_a_at	AF542051	SH3-domain kinase binding protein 1
223082_at	AF230904	SH3-domain kinase binding protein 1
214853_s_at	AI091079	SHC (Src homology 2 domain containing) transforming protein 1
56256_at	AA150165	SID1 transmembrane family, member 2
217927_at	NM_014041	signal peptidase 12kDa
201290_at	NM_014300	signal peptidase complex (18kD)
200652_at	NM_003145	signal sequence receptor, beta (translocon-associated protein beta)
201004_at	NM_006280	signal sequence receptor, delta (translocon-associated protein delta)
222411_s_at	AW087870	signal sequence receptor, gamma (translocon-associated protein gamma)
209969_s_at	BC002704	signal transducer and activator of transcription 1, 91kDa
217446_x_at	AL080160	Similar to cyclin-like F-box (3A784)
225522_at	AW628987	Similar to expressed sequence C79663
224867_at	BF244614	Similar to ribosomal protein S14
224637_at	BF211019	Similar to RIKEN cDNA 2310016E02
AFFX-HUMRGE/M10098_5_at	Unknown	Similar to rRNA intron-encoded homing endonuclease
202591_s_at	NM_003143	single-stranded DNA binding protein 1
212852_s_at	AL538601	Sjogren syndrome antigen A2 (60kDa, ribonucleoprotein autoantigen SS-A/Ro)
201575_at	NM_012245	SKI interacting protein
222401_s_at	AL550722	small membrane protein 1
203316_s_at	NM_003094	small nuclear ribonucleoprotein polypeptide E
205644_s_at	NM_003096	small nuclear ribonucleoprotein polypeptide G
208738_x_at	AK024823	SMT3 suppressor of mif two 3 homolog 2 (yeast)
208739_x_at	L76416	SMT3 suppressor of mif two 3 homolog 2 (yeast)
213881_x_at	AI971724	SMT3 suppressor of mif two 3 homolog 2 (yeast)
201522_x_at	NM_003097	SNRPN upstream reading frame /// small nuclear ribonucleoprotein polypeptide N
213344_s_at	H51429	Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:179551 3'
200657_at	NM_001152	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5),
200030_s_at	NM_002635	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3 /// solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3
204204_at	NM_001860	solute carrier family 31 (copper transporters), member 2
220796_x_at	NM_024881	solute carrier family 35, member E1
214143_x_at	AI560573	solute carrier family 36 (proton/amino acid symporter), member 2
219229_at	NM_013272	solute carrier organic anion transporter family, member 3A1
214988_s_at	X63071	SON DNA binding protein
226465_s_at	BF676840	SON DNA binding protein
208921_s_at	L12387	sorcin
212560_at	AV728268	sortilin-related receptor, L(DLR class) A repeats-containing
203509_at	NM_003105	sortilin-related receptor, L(DLR class) A repeats-containing (SORL1),

Probe Set ID	Public ID	Gene Description
204655_at	NM_002985	sortilin-related receptor, L(DLR class) A repeats-containing (SORL1),
53912_at	AI668643	sorting nexin 11
210648_x_at	AB047360	sorting nexin 3
221498_at	BF939727	sorting nexin family member 27
209762_x_at	AF280094	SP110 nuclear body protein
202524_s_at	NM_014767	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2
215383_x_at	AL137312	spastic paraplegia 21 (autosomal recessive, Mast syndrome)
202761_s_at	NM_015180	spectrin repeat containing, nuclear envelope 2
210592_s_at	M55580	spermidine/spermine N1-acetyltransferase
200711_s_at	NM_003197	S-phase kinase-associated protein 1A (p19A)
200718_s_at	AA927664	S-phase kinase-associated protein 1A (p19A)
226068_at	BF593625	spleen tyrosine kinase
216457_s_at	AK026080	splicing factor 3a, subunit 1, 120kDa
211784_s_at	BC006181	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor) /// splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)
200893_at	NM_004593	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)
214882_s_at	BG254869	splicing factor, arginine/serine-rich 2
201698_s_at	NM_003769	splicing factor, arginine/serine-rich 9
AFFX-M27830_5_at	AFFX-M27830_5	SRY (sex determining region Y)-box 18
AFFX-M27830_M_at	AFFX-M27830_M	SRY (sex determining region Y)-box 18
217713_x_at	AA126763	Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565149 3' similar to contains Alu repetitive element;contains element MER22 repetitive element ;, MRNA sequence
200971_s_at	NM_014445	stress-associated endoplasmic reticulum protein 1
215088_s_at	BG110532	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa
210580_x_at	L25275	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3
215223_s_at	W46388	superoxide dismutase 2, mitochondrial
207040_s_at	NM_003932	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)
201827_at	AF113019	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2
200958_s_at	NM_005625	syndecan binding protein (syntenin)
204466_s_at	BG260394	synuclein, alpha (non A4 component of amyloid precursor)
211546_x_at	L36674	synuclein, alpha (non A4 component of amyloid precursor)
211796_s_at	AF043179	T cell receptor beta chain
209813_x_at	M16768	T cell receptor gamma variable 9
211144_x_at	M30894	T cell receptor gamma variable 9
213193_x_at	AL559122	T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED Homo sapiens cDNA clone CS0DJ014YE01 5-PRIME
200055_at	NM_006284	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 30kDa /// TAF10 RNA

Probe Set ID	Public ID	Gene Description
		polymerase II, TATA box binding protein (TBP)-associated factor, 30kDa
201023_at	NM_005642	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55kDa
208829_at	AF029750	TAP binding protein (tapasin)
200020_at	NM_007375	TAR DNA binding protein /// TAR DNA binding protein
201999_s_at	NM_006519	t-complex-associated-testis-expressed 1-like 1
218020_s_at	NM_021943	testis expressed sequence 27
208944_at	D50683	TGF-betaIIR alpha
208864_s_at	AF313911	thioredoxin
208959_s_at	BC005374	thioredoxin domain containing 4 (endoplasmic reticulum)
201010_s_at	NM_006472	thioredoxin interacting protein
201588_at	NM_004786	thioredoxin-like 1
217733_s_at	NM_021103	thymosin, beta 10
216438_s_at	AL133228	thymosin, beta 4, X-linked /// thymosin-like 6
200792_at	NM_001469	thyroid autoantigen 70kDa (Ku antigen)
212208_at	AK023837	thyroid hormone receptor associated protein 2
207196_s_at	NM_006058	TNFAIP3 interacting protein 1
201463_s_at	NM_006755	transaldolase 1
224915_x_at	AV756131	transaldolase 1
226227_x_at	BF185165	transaldolase 1
226835_s_at	BG330520	transaldolase 1
200085_s_at	NM_007108	transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B) /// transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B)
205255_x_at	NM_003202	transcription factor 7 (T-cell specific, HMG-box)
208700_s_at	L12711	transketolase (Wernicke-Korsakoff syndrome)
201738_at	NM_005875	translation factor sui1 homolog
201398_s_at	BC000687	translocation associated membrane protein 1
223105_s_at	BC002496	transmembrane protein 14B /// transmembrane protein 14C
207657_x_at	NM_002270	transportin 1
221012_s_at	NM_030912	tripartite motif-containing 8 /// tripartite motif-containing 8
222976_s_at	BC000771	tropomyosin 3
221493_at	AL136629	TSPY-like 1
212242_at	AL565074	tubulin, alpha 1 (testis specific)
209118_s_at	AF141347	tubulin, alpha 3
201090_x_at	NM_006082	tubulin, alpha, ubiquitous
212639_x_at	AL581768	tubulin, alpha, ubiquitous
213646_x_at	BE300252	tubulin, alpha, ubiquitous
211058_x_at	BC006379	tubulin, alpha, ubiquitous /// tubulin, alpha, ubiquitous
211072_x_at	BC006481	tubulin, alpha, ubiquitous /// tubulin, alpha, ubiquitous
213726_x_at	AA515698	tubulin, beta, 2

Probe Set ID	Public ID	Gene Description
225912_at	AW341649	tumor protein p53 inducible nuclear protein 1
211943_x_at	AL565449	tumor protein, translationally-controlled 1
212284_x_at	BG498776	tumor protein, translationally-controlled 1
212869_x_at	AI721229	tumor protein, translationally-controlled 1
214327_x_at	AI888178	tumor protein, translationally-controlled 1
216520_s_at	AF072098	tumor protein, translationally-controlled 1
204122_at	NM_003332	TYRO protein tyrosine kinase binding protein
208743_s_at	BC001359	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide
217717_s_at	BF246499	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide
217718_s_at	NM_014052	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide
222985_at	AB024334	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide
213699_s_at	AA854017	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide
200639_s_at	NM_003406	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide
200640_at	NM_003406	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide
222990_at	AW204104	ubiquilin 1
205849_s_at	NM_006294	ubiquinol-cytochrome c reductase binding protein
218190_s_at	NM_013387	ubiquinol-cytochrome c reductase complex (7.2 kD)
202233_s_at	NM_006004	ubiquinol-cytochrome c reductase hinge protein (UQCRH),
221700_s_at	AF348700	ubiquitin A-52 residue ribosomal protein fusion product 1 /// ubiquitin A-52 residue ribosomal protein fusion product 1
200633_at	NM_018955	ubiquitin B
208980_s_at	M26880	ubiquitin C
211296_x_at	AB009010	ubiquitin C
211285_s_at	U84404	ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome)
226357_at	AW473649	ubiquitin specific protease 19
221654_s_at	AF077040	ubiquitin specific protease 3
207365_x_at	NM_014709	ubiquitin specific protease 34
201343_at	BE621259	ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast)
200668_s_at	BC003395	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)
212519_at	AL518159	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)
200682_s_at	BG531983	ubiquitin-conjugating enzyme E2L 3
201649_at	NM_004223	ubiquitin-conjugating enzyme E2L 6
218495_at	NM_004182	ubiquitously-expressed transcript
235327_x_at	BG111015	UBX domain containing 4
200627_at	BC003005	unactive progesterone receptor, 23 kD
212144_at	AL021707	unc-84 homolog B (C. elegans)
208998_at	U94592	uncoupling protein 2 (mitochondrial, proton carrier)
202646_s_at	AA167775	upstream of NRAS
203459_s_at	NM_022575	vacuolar protein sorting 16 (yeast)

Probe Set ID	Public ID	Gene Description
217837_s_at	NM_016079	vacuolar protein sorting 24 (yeast)
208780_x_at	AF154847	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa
224833_at	BE218980	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)
201426_s_at	AI922599	vimentin
200931_s_at	NM_014000	vinculin
212038_s_at	AL515918	voltage-dependent anion channel 1
211662_s_at	L08666	voltage-dependent anion channel 2 /// voltage-dependent anion channel 2
208845_at	BC002456	voltage-dependent anion channel 3
202625_at	AI356412	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog
224789_at	AL555107	WD repeat domain 40A
229630_s_at	AU147416	Wilms tumor 1 associated protein
38964_r_at	U12707	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)
202664_at	AW058622	Wiskott-Aldrich syndrome protein interacting protein
217742_s_at	NM_016628	WW domain containing adaptor with coiled-coil
222390_at	AL135461	WW domain containing adaptor with coiled-coil
208642_s_at	AA205834	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kDa)
221741_s_at	AL096828	YTH domain family 1
200047_s_at	NM_003403	YY1 transcription factor /// YY1 transcription factor
225629_s_at	AI669498	zinc finger and BTB domain containing 4
214715_x_at	AK024789	zinc finger protein 160
200829_x_at	NM_003457	zinc finger protein 207
212774_at	AJ223321	zinc finger protein 238
201368_at	U07802	zinc finger protein 36, C3H type-like 2
209944_at	BC000330	zinc finger protein 410
219981_x_at	NM_017961	zinc finger protein 587
208137_x_at	NM_030972	zinc finger protein 611 /// zinc finger protein 611
206158_s_at	NM_003418	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein)
221613_s_at	AL136598	zinc finger, A20 domain containing 3
202136_at	BE250417	zinc finger, MYND domain containing 11
228009_x_at	NM_014596	zinc ribbon domain containing, 1

Table 6. Molecular functions represented by the group of probesets reproducibly detected in intra- and interspecies comparisons.

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
GO:0046961	hydrogen-transporting ATPase activity, rotational mechanism	19	73	19	33	8.56E-15
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_006476	107476	ATP5L	10632		
	AF070655	107476	ATP5L	10632		
	AL050277	107476	ATP5L	10632		
	AI862255	440165	ATP6V0E	8992		
	NM_003945	440165	ATP6V0E	8992		
	AF077614	272630	ATP6V1D	51382		
	NM_001697	409140	ATP5O	539		
	M62762		ATP6V0C	527		
	NM_007100	85539	ATP5I	521		
	BC003679	85539	ATP5I	521		
	NM_001689	429	ATP5G3	518		
	NM_001689	429	ATP5G3	518		
	BC005960	81634	ATP5F1	515		
	NM_006886	177530	ATP5E	514		
	NM_005174	155433	ATP5C1	509		
	BC000931	155433	ATP5C1	509		
	AV711183		ATP5C1	509		
	NM_001686	406510	ATP5B	506		
	AI587323	298280	ATP5A1	498		
GO:0003735	structural constituent of ribosome	109	345	109	165	2.40E-14
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_000985	374588	RPL17	6139		
	BG168283	374588	RPL17	6139		
	BE733979	374588	RPL17	6139		
	NM_002948	381219	RPL15	6138		
	BC004954	410817	RPL13	6137		
	AW574664	410817	RPL13	6137		
	AI186735	410817	RPL13	6137		
	AA961748	410817	RPL13	6137		
	AA789278	410817	RPL13	6137		
	NM_000976	408054	RPL12	6136		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	AA281332	408054	RPL12	6136		
	NM_000975	388664	RPL11	6135		
	NM_006013	401929	RPL10	6134		
	NM_000661	412370	RPL9	6133		
	NM_000973	178551	RPL8	6132		
	NM_000971	421257	RPL7	6129		
	BG389744	421257	RPL7	6129		
	NM_000970	528668	RPL6	6128		
	BG435643	406590	PGR1	93621		
	NM_000969	469653	RPL5	6125		
	BF214492	469653	RPL5	6125		
	AI953886	186350	RPL4	6124		
	NM_000968	186350	RPL4	6124		
	BC005817	186350	RPL4	6124		
	NM_000967	119598	RPL3	6122		
	BC006483	119598	RPL3	6122		
	L22453	119598	RPL3	6122		
	BG339228	119598	RPL3	6122		
	NM_018141	380887	MRPS10	55173		
	U16738	446522	RPL14	9045		
	AA838274	446522	RPL14	9045		
	NM_015414	408018	RPL36	25873		
	AF348700	5308	UBA52	7311		
	AW304232	374553	LAMR1	3921		
	NM_024026	458367	MRP63	78988		
	NM_001997	387208	FAU	2197		
	AF151075	55847	MRPL51	51258		
	NM_003776	431307	MRPL40	64976		
	BC000514	449070	RPL13A	23521		
	NM_012423	449070	RPL13A	23521		
	BC001675	449070	RPL13A	23521		
	BF979419	449070	RPL13A	23521		
	BF942308	449070	RPL13A	23521		
	NM_007209	182825	RPL35	11224		
	NM_000978	406300	RPL23	9349		
	NM_007104	448396	RPL10A	4736		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	BG231561	448396	RPL10A	4736		
	NM_001032	539	RPS29	6235		
	BC000354	153177	RPS28	6234		
	NM_002954	311640	RPS27A	6233		
	NM_001030	337307	RPS27	6232		
	NM_001029	480569	RPS26	6231		
	AA888388	512676	RPS25	6230		
	BC000523	356794	RPS24	6229		
	NM_001024	372960	RPS21	6227		
	NM_001022	381184	RPS19	6223		
	BE259729	381184	RPS19	6223		
	NM_001021	433427	RPS17	6218		
	NM_001020	397609	RPS16	6217		
	AI200589	397609	RPS16	6217		
	AA583817	397609	RPS16	6217		
	NM_001019	370504	RPS15A	6210		
	NM_001018	406683	RPS15	6209		
	NM_001017	446588	RPS13	6207		
	AI799007	380956	RPS12	6206		
	AA320764	406620	RPS10	6204		
	NM_001014	406620	RPS10	6204		
	BE348997	139876	RPS9	6203		
	NM_001013	139876	RPS9	6203		
	BE741754	408073	RPS6	6194		
	NM_001010	408073	RPS6	6194		
	BC000524	408073	RPS6	6194		
	NM_001009	378103	RPS5	6193		
	NM_001007	446628	RPS4X	6191		
	AW132023	446628	RPS4X	6191		
	U14990	387576	RPS3	6188		
	NM_002952	498569	RPS2	6187		
	AA630314	498569	RPS2	6187		
	AI183766	498569	RPS2	6187		
	NM_001004	437594	RPLP2	6181		
	NM_001003	356502	RPLP1	6176		
	NM_001002		RPLP0	6175		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	BC003655	443796	RPLP0	6175		
	BC005863	443796	RPLP0	6175		
	AI953822	443796	RPLP0	6175		
	NM_021104	381172	RPL41	6171		
	NM_000999	380953	RPL38	6169		
	NM_001001	444749	RPL36AL	6166		
	BE968801	289093	RPL35A	6165		
	AW402660	289093	RPL35A	6165		
	NM_000995	250895	RPL34	6164		
	NM_000993	375921	RPL31	6160		
	NM_000992	430207	RPL29	6159		
	NM_000991	356371	RPL28	6158		
	NM_000990	356342	RPL27A	6157		
	BE737027	356342	RPL27A	6157		
	L05095	400295	RPL30	6156		
	NM_000988	405528	RPL27	6155		
	AI832239	3254	MRPL23	6150		
	NM_000984	419463	RPL23A	6147		
	U43701	419463	RPL23A	6147		
	BC001865		RPL23A	6147		
	BF125158	419463	RPL23A	6147		
	D17652	326249	RPL22	6146		
	NM_000983	326249	RPL22	6146		
	NM_000982	381123	RPL21	6144		
	NM_000981	381061	RPL19	6143		
	NM_000980	337766	RPL18A	6142		
	NM_000979	409634	RPL18	6141		
GO:0005198	structural molecule activity	14	475	14	230	1.92E-16
	Probe	UniGene cluster	Gene	LocusLink ID		
	AI922599	435800	VIM	7431		
	NM_014000	75350	VCL	7414		
	NM_004859	187416	CLTC	1213		
	NM_006082	446608	K-ALPHA-1	10376		
	BC006379	446608	K-ALPHA-1	10376		
	BC006481	446608	K-ALPHA-1	10376		
	BE300252	446608	K-ALPHA-1	10376		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	AL565074	75318	TUBA1	7277		
	AL523310	31095	MAP4	4134		
	AU157515	396503	CDC10	989		
	AA129420	223745	MATR3	9782		
	BC001002	356729	OK	203068		
	NM_015180	444069	SYNE2	23224		
	AF154847	165195	VAPA	9218		
GO:0015078	hydrogen ion transporter activity	1	22	1	9	1.75E-16
	Probe	UniGene cluster	Gene	LocusLink ID		
	BC003564	90336	ATP6V1G1	9550		
GO:0046933	hydrogen-transporting ATP synthase activity, rotational mechanism	19	69	19	32	3.99E-14
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_006476	107476	ATP5L	10632		
	AF070655	107476	ATP5L	10632		
	AL050277	107476	ATP5L	10632		
	AI862255	440165	ATP6V0E	8992		
	NM_003945	440165	ATP6V0E	8992		
	AF077614	272630	ATP6V1D	51382		
	NM_001697	409140	ATP5O	539		
	M62762		ATP6V0C	527		
	NM_007100	85539	ATP5I	521		
	BC003679	85539	ATP5I	521		
	NM_001689	429	ATP5G3	518		
	NM_001689	429	ATP5G3	518		
	BC005960	81634	ATP5F1	515		
	NM_006886	177530	ATP5E	514		
	NM_005174	155433	ATP5C1	509		
	BC000931	155433	ATP5C1	509		
	AV711183		ATP5C1	509		
	NM_001686	406510	ATP5B	506		
	AI587323	298280	ATP5A1	498		
GO:0003676	nucleic acid binding	28	1201	28	541	1.38E-16
	Probe	UniGene cluster	Gene	LocusLink ID		
	BC001417	246112	U5-200KD	23020		
	AA526904	190386	KIAA0924	22834		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	AK024789	271511	ZNF160	90338		
	AJ223321		ZNF238	10472		
	NM_022118	408487	C13orf10	64062		
	NM_005804	311609	DDX39	10212		
	AW080845	235860	FOXP1	27086		
	AK026898	235860	FOXP1	27086		
	NM_014827	17969	KIAA0663	9877		
	AF285758	3100	KARS	3735		
	NM_005548	3100	KARS	3735		
	NM_013446	7838	MKRN1	23608		
	AF117233	7838	MKRN1	23608		
	X63071	430541	SON	6651		
	BF676840	430541	SON	6651		
	NM_030972	446500	MGC5384	81856		
	NM_005195	381058	KIAA0146	23514		
	NM_022898	57987	BCL11B	64919		
	NM_001967	511904	EIF4A2	1974		
	NM_001416	129673	EIF4A1	1973		
	BC006210	129673	EIF4A1	1973		
	NM_001404	256184	EEF1G	1937		
	BF797555	201085	PAPOLA	10914		
	AB007447	5148	FLN29	10906		
	NM_024836	181406	FLJ22301	79894		
	NM_004539	427212	NARS	4677		
	NM_004541	74823	ZNF183	7737		
	NM_030757	458363	MKRN4	7682		
GO:0003723	RNA binding	114	864	114	332	5.99E-14
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_000985	374588	RPL17	6139		
	BG168283	374588	RPL17	6139		
	BE733979	374588	RPL17	6139		
	BC004954	410817	RPL13	6137		
	AW574664	410817	RPL13	6137		
	AI186735	410817	RPL13	6137		
	AA961748	410817	RPL13	6137		
	AA789278	410817	RPL13	6137		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	NM_000976	408054	RPL12	6136		
	AA281332	408054	RPL12	6136		
	NM_000661	412370	RPL9	6133		
	NM_000971	421257	RPL7	6129		
	BG389744	421257	RPL7	6129		
	NM_000970	528668	RPL6	6128		
	AI953886	186350	RPL4	6124		
	NM_000968	186350	RPL4	6124		
	BC005817	186350	RPL4	6124		
	NM_000967	119598	RPL3	6122		
	BC006483	119598	RPL3	6122		
	L22453	119598	RPL3	6122		
	BG339228	119598	RPL3	6122		
	U69546	211610	CUGBP2	10659		
	BE542815	445977	GTF3A	2971		
	U16738	446522	RPL14	9045		
	AA838274	446522	RPL14	9045		
	AL517946	241567	RBMS1	5937		
	BC000461	429180	EIF2S2	8894		
	BC001449	15265	HNRPR	10236		
	NM_003769	77608	SFRS9	8683		
	NM_003730	388130	RNASET2	8635		
	NM_003730	388130	RNASET2	8635		
	AI734929	387804	PABPC1	26986		
	AI762552	372673	HNRPDL	9987		
	NM_001997	387208	FAU	2197		
	BC005938	424908	LSM5	23658		
	AL538601	288178	SSA2	6738		
	AA129420	223745	MATR3	9782		
	BE622897		KIS	127933		
	U24223	2853	PCBP1	5093		
	NM_001418	183684	EIF4G2	1982		
	BF247371	93379	EIF4B	1975		
	NM_001967	511904	EIF4A2	1974		
	NM_030979	458280	PABPC3	5042		
	BF512907	439505	DAZAP1	26528		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	NM_007375	300624	TARDBP	23435		
	BF724216	155218	E1B-AP5	11100		
	NM_004593	30035	SFRS10	6434		
	BG254869	73965	SFRS2	6427		
	NM_020414	372267	DDX24	57062		
	NM_007363	355861	NONO	4841		
	BF797555	201085	PAPOLA	10914		
	AA167775	69855	D1S155E	7812		
	NM_004501	166463	HNRPU	3192		
	BF129093	271541	DDX6	1656		
	NM_004396	279806	DDX5	1655		
	NM_021644	156481	HNRPH3	3189		
	NM_004500	476302	HNRPC	3183		
	AA664258	476302	HNRPC	3183		
	AV725195	476302	HNRPC	3183		
	NM_002137	232400	HNRPA2B1	3181		
	AI375753	232400	HNRPA2B1	3181		
	NM_002136	356721	HNRPA1	3178		
	AL568186	356721	HNRPA1	3178		
	X79536	356721	HNRPA1	3178		
	BC000354	153177	RPS28	6234		
	NM_001030	337307	RPS27	6232		
	NM_001029	480569	RPS26	6231		
	AA888388	512676	RPS25	6230		
	BC000523	356794	RPS24	6229		
	NM_001024	372960	RPS21	6227		
	NM_005381	79110	NCL	4691		
	NM_001022	381184	RPS19	6223		
	BE259729	381184	RPS19	6223		
	NM_001021	433427	RPS17	6218		
	NM_001019	370504	RPS15A	6210		
	NM_001018	406683	RPS15	6209		
	AI799007	380956	RPS12	6206		
	AF061832	385766	HNRPM	4670		
	AA320764	406620	RPS10	6204		
	NM_001014	406620	RPS10	6204		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	BE348997	139876	RPS9	6203		
	NM_001013	139876	RPS9	6203		
	BE741754	408073	RPS6	6194		
	NM_001010	408073	RPS6	6194		
	BC000524	408073	RPS6	6194		
	NM_001009	378103	RPS5	6193		
	NM_001007	446628	RPS4X	6191		
	AW132023	446628	RPS4X	6191		
	U14990	387576	RPS3	6188		
	NM_002952	498569	RPS2	6187		
	AA630314	498569	RPS2	6187		
	AI183766	498569	RPS2	6187		
	NM_001004	437594	RPLP2	6181		
	NM_001003	356502	RPLP1	6176		
	NM_001002		RPLP0	6175		
	BC003655	443796	RPLP0	6175		
	BC005863	443796	RPLP0	6175		
	AI953822	443796	RPLP0	6175		
	NM_021104	381172	RPL41	6171		
	NM_000999	380953	RPL38	6169		
	NM_000995	250895	RPL34	6164		
	NM_000993	375921	RPL31	6160		
	NM_000992	430207	RPL29	6159		
	NM_000991	356371	RPL28	6158		
	NM_000990	356342	RPL27A	6157		
	BE737027	356342	RPL27A	6157		
	L05095	400295	RPL30	6156		
	AI832239	3254	MRPL23	6150		
	D17652	326249	RPL22	6146		
	NM_000983	326249	RPL22	6146		
	NM_000982	381123	RPL21	6144		
	NM_000981	381061	RPL19	6143		
	NM_000980	337766	RPL18A	6142		
	NM_000979	409634	RPL18	6141		
GO:0005488	binding	9	151	9	70	5.55E-16
	Probe	UniGene cluster	Gene	LocusLink ID		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	U94592	80658	UCP2	7351		
	BG537190	433670	FTL	2512		
	BG538564		FTL	2512		
	NM_002032	448738	FTH1	2495		
	AF189289	279939	MTCH1	23787		
	NM_002635	290404	SLC25A3	5250		
	NM_001642	279518	APLP2	334		
	NM_001152	79172	SLC25A5	292		
	NM_001629	100194	ALOX5AP	241		
GO:0015075	ion transporter activity	1	29	1	15	2.86E-15
	Probe	UniGene cluster	Gene	LocusLink ID		
	AV699746	242721	SLC22A3	6581		
GO:0030106	MHC class I receptor activity	12	46	12	13	6.48E-10
	Probe	UniGene cluster	Gene	LocusLink ID		
	M90685	512152	HLA-G	3135		
	M90684	512152	HLA-G	3135		
	AW514210	411958	HLA-F	3134		
	AI669379	411958	HLA-F	3134		
	X56841	381008	HLA-E	3133		
	NM_005516	381008	HLA-E	3133		
	M31183	381008	HLA-E	3133		
	M12679	274485	HLA-C	3107		
	AK024836	274485	HLA-C	3107		
	L42024	77961	HLA-B	3106		
	L07950	77961	HLA-B	3106		
	AA573862	181244	HLA-A	3105		
GO:0019843	rRNA binding	8	16	8	6	2.06E-09
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_000975	388664	RPL11	6135		
	NM_000973	178551	RPL8	6132		
	NM_000969	469653	RPL5	6125		
	BF214492	469653	RPL5	6125		
	NM_000984	419463	RPL23A	6147		
	U43701	419463	RPL23A	6147		
	BC001865		RPL23A	6147		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	BF125158	419463	RPL23A	6147		
GO:0008135	translation factor activity, nucleic acid binding	1	8	1	5	5.79E-10
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_001090	9573	ABCF1	23		
GO:0042623	ATPase activity, coupled	4	40	4	17	4.76E-09
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_006585	416211	CCT8	10694		
	AF352832	180414	HSPA8	3312		
	AA704004	180414	HSPA8	3312		
	AF217511	180414	HSPA8	3312		
GO:0016887	ATPase activity	1	51	1	23	2.25E-09
	Probe	UniGene cluster	Gene	LocusLink ID		
	BG252666	418426	ATP8B1	5205		
GO:0045012	MHC class II receptor activity	9	34	9	11	7.25E-08
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_002125	308026	HLA-DRB3	3125		
	NM_021983	308026	HLA-DRB3	3125		
	U65585	308026	HLA-DRB3	3125		
	AJ297586	308026	HLA-DRB3	3125		
	AF005487	308026	HLA-DRB3	3125		
	BG397856	387679	HLA-DQA1	3117		
	NM_002121	368409	HLA-DPB1	3115		
	M27487	914	HLA-DPA1	3113		
	NM_002118	1162	HLA-DMB	3109		
GO:0003954	NADH dehydrogenase activity	10	56	10	33	1.79E-07
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_019056	433328	P17.3	54539		
	AK002110	90443	NDUFS8	4728		
	NM_004552	409829	NDUFS5	4725		
	AF261090	15977	NDUFB9	4715		
	NM_005004	198273	NDUFB8	4714		
	NM_004546	27262	NDUFB2	4708		
	NM_004545	183435	NDUFB1	4707		
	NM_002490	274416	NDUFA6	4700		
	NM_002489	50098	NDUFA4	4697		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	BC003674	163867	NDUFA2	4695		
GO:0016820	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	1	73	1	28	2.82E-08
	Probe	UniGene cluster	Gene	LocusLink ID		
	AI587323	298280	ATP5A1	498		
GO:0004129	cytochrome-c oxidase activity	8	35	8	21	1.19E-06
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_001866	432170	COX7B	1349		
	NM_001865	70312	COX7A2	1347		
	NM_004373	180714	COX6A1	1337		
	NM_001862	1342	COX5B	1329		
	BC006229	1342	COX5B	1329		
	AI557312	1342	COX5B	1329		
	AA854966	433419	COX4I1	1327		
	NM_001861	433419	COX4I1	1327		
GO:0008137	NADH dehydrogenase (ubiquinone) activity	10	61	10	35	1.39E-06
	Probe	UniGene cluster	Gene	LocusLink ID		
	AK002110	90443	NDUFS8	4728		
	NM_004552	409829	NDUFS5	4725		
	AF261090	15977	NDUFB9	4715		
	NM_005004	198273	NDUFB8	4714		
	NM_004546	27262	NDUFB2	4708		
	NM_004545	183435	NDUFB1	4707		
	NM_005003	5556	NDUFAB1	4706		
	NM_002490	274416	NDUFA6	4700		
	NM_002489	50098	NDUFA4	4697		
	BC003674	163867	NDUFA2	4695		
GO:0003924	GTPase activity	23	344	23	141	4.34E-06
	Probe	UniGene cluster	Gene	LocusLink ID		
	BE138888	301175	RAC2	5880		
	BG292367	413812	RAC1	5879		
	BC004247	413812	RAC1	5879		
	BC001267	73957	RAB5A	5868		
	BG338251	115325	RAB7L1	8934		
	NM_000516	157307	GNAS	2778		
	NM_016592	157307	GNAS	2778		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	AF088184	157307	GNAS	2778		
	AI591100	157307	GNAS	2778		
	AA515698		TUBB2	10383		
	NM_006082	446608	K-ALPHA-1	10376		
	BC006379	446608	K-ALPHA-1	10376		
	BC006481	446608	K-ALPHA-1	10376		
	BE300252	446608	K-ALPHA-1	10376		
	AL565074	75318	TUBA1	7277		
	AI215102	75618	RAB11A	8766		
	BG435404	111554	ARL7	10123		
	BC001002	356729	OK	203068		
	BE252813	480368	EIF2S3	1968		
	NM_001665	75082	ARHG	391		
	AF052179	286221	ARF1	375		
	AK000826		RAB7	7879		
	NM_000992	430207	RPL29	6159		
GO:0003824	catalytic activity	2	325	2	144	4.78E-07
	Probe	UniGene cluster	Gene	LocusLink ID		
	AL137312	242458	ACP33	51324		
	NM_000923	437211	PDE4C	5143		
GO:0003743	translation initiation factor activity	13	126	13	52	7.93E-06
	Probe	UniGene cluster	Gene	LocusLink ID		
	AW083133	143773	eIF3k	27335		
	AF085358	143773	eIF3k	27335		
	BC000461	429180	EIF2S2	8894		
	NM_005875	315230	GC20	10289		
	BF246436	150580	SUI1	10209		
	AL537707	150580	SUI1	10209		
	W67644	150580	SUI1	10209		
	NM_003756	127149	EIF3S3	8667		
	NM_003754	381255	EIF3S5	8665		
	NM_001418	183684	EIF4G2	1982		
	BF247371	93379	EIF4B	1975		
	NM_001967	511904	EIF4A2	1974		
	BE252813	480368	EIF2S3	1968		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
GO:0016787	hydrolase activity	49	1755	49	811	1.21E-06
	Probe	UniGene cluster	Gene	LocusLink ID		
	BC001417	246112	U5-200KD	23020		
	NM_004390	114931	CTSH	1512		
	NM_001908	135226	CTSB	1508		
	J03189	1051	GZMB	3002		
	AI862255	440165	ATP6V0E	8992		
	NM_003945	440165	ATP6V0E	8992		
	BE880245	334534	GNS	2799		
	AA775177	437980	PTPRE	5791		
	NM_005804	311609	DDX39	10212		
	NM_003730	388130	RNASET2	8635		
	NM_003730	388130	RNASET2	8635		
	AV717590	444105	ENTPD1	953		
	NM_000310	3873	PPT1	5538		
	NM_005730	355816	CTDSP2	10106		
	NM_021003	130036	PPM1A	5494		
	M87507	2490	CASP1	834		
	M23254	350899	CAPN2	824		
	AF077040	251636	USP3	9960		
	NM_002661	512298	PLCG2	5336		
	AF077614	272630	ATP6V1D	51382		
	AK026655	22151	NLN	57486		
	BE537881		LOC134147	134147		
	BG252666	418426	ATP8B1	5205		
	BC001169	432491	ESD	2098		
	AU145746	432491	ESD	2098		
	NM_005539	408063	INPP5A	3632		
	NM_001697	409140	ATP5O	539		
	NM_000923	437211	PDE4C	5143		
	M62762		ATP6V0C	527		
	NM_006886	177530	ATP5E	514		
	NM_005174	155433	ATP5C1	509		
	BC000931	155433	ATP5C1	509		
	AV711183		ATP5C1	509		
	AF521189	129801	ECE2	9718		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	NM_001686	406510	ATP5B	506		
	AI587323	298280	ATP5A1	498		
	NM_001967	511904	EIF4A2	1974		
	NM_001416	129673	EIF4A1	1973		
	BC006210	129673	EIF4A1	1973		
	AV703259		IDS	3423		
	BC003564	90336	ATP6V1G1	9550		
	U62891	367676	DUT	1854		
	AI655015	3843	DUSP7	1849		
	BC003143	298654	DUSP6	1848		
	NM_001386	173381	DPYSL2	1808		
	NM_020414	372267	DDX24	57062		
	AW473649	255596	USP19	10869		
	AK054976	256697	HINT1	3094		
	N32864	256697	HINT1	3094		
GO:0005215	transporter activity	16	559	16	290	1.07E-05
	Probe	UniGene cluster	Gene	LocusLink ID		
	AI862255	440165	ATP6V0E	8992		
	NM_003945	440165	ATP6V0E	8992		
	U94592	80658	UCP2	7351		
	AI215102	75618	RAB11A	8766		
	NM_013272	113657	SLCO3A1	28232		
	NM_001697	409140	ATP5O	539		
	NM_001689	429	ATP5G3	518		
	NM_001689	429	ATP5G3	518		
	BC005960	81634	ATP5F1	515		
	NM_005174	155433	ATP5C1	509		
	BC000931	155433	ATP5C1	509		
	AV711183		ATP5C1	509		
	NM_001686	406510	ATP5B	506		
	AI587323	298280	ATP5A1	498		
	NM_000876	76473	IGF2R	3482		
	NM_001152	79172	SLC25A5	292		
GO:0005200	structural constituent of cytoskeleton	15	211	15	90	1.17E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	AI922599	435800	VIM	7431		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	AA515698		TUBB2	10383		
	NM_005731	83583	ARPC2	10109		
	AF279893	83583	ARPC2	10109		
	BG034239	83583	ARPC2	10109		
	AF004561	439511	ARPC3	10094		
	NM_001614	14376	ACTG1	71		
	BG026805	14376	ACTG1	71		
	BE741683	14376	ACTG1	71		
	AL567820	14376	ACTG1	71		
	AU145192	14376	ACTG1	71		
	AL515810	14376	ACTG1	71		
	AW190090	14376	ACTG1	71		
	BC001920	14376	ACTG1	71		
	AA703939	14376	ACTG1	71		
GO:0006330	single-stranded DNA binding	9	82	9	29	1.43E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	AL517946	241567	RBMS1	5937		
	AI762552	372673	HNRPDL	9987		
	NM_003143	923	SSBP1	6742		
	U24223	2853	PCBP1	5093		
	BC002411	74497	NSEP1	4904		
	BG231551	229641	PC4	10923		
	BE784583	229641	PC4	10923		
	NM_002128	434102	HMGB1	3146		
	AF283771	434102	HMGB1	3146		
GO:0003754	chaperone activity	16	247	16	109	1.92E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	BC003005	355693	TEBP	10728		
	NM_006585	416211	CCT8	10694		
	NM_006430	374334	CCT4	10575		
	AA515698		TUBB2	10383		
	NM_021130	356331	PPIA	5478		
	BC005982	356331	PPIA	5478		
	AI708767	356331	PPIA	5478		
	M94859	155560	CANX	821		
	AF029750	370937	TAPBP	6892		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	NM_004182	172791	UXT	8409		
	NM_016633	274309	ERAF	51327		
	NM_002624	288856	PFDN5	5204		
	BC001002	356729	OK	203068		
	BG420237	446579	HSPCA	3320		
	BC005374	154023	TXNDC4	23071		
	NM_002118	1162	HLA-DMB	3109		
GO:0008121	ubiquinol-cytochrome-c reductase activity	4	15	4	8	2.04E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_006004	285761	UQCRH	7388		
	NM_006294	131255	UQCRB	7381		
	NM_014402	146602	QP-C	27089		
	NM_013387	284292	HSPC051	29796		
GO:0005525	GTP binding	28	612	28	269	3.06E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	BE138888	301175	RAC2	5880		
	BG292367	413812	RAC1	5879		
	BC004247	413812	RAC1	5879		
	BC001267	73957	RAB5A	5868		
	BG338251	115325	RAB7L1	8934		
	NM_000516	157307	GNAS	2778		
	NM_016592	157307	GNAS	2778		
	AF088184	157307	GNAS	2778		
	AI591100	157307	GNAS	2778		
	AA515698		TUBB2	10383		
	NM_006082	446608	K-ALPHA-1	10376		
	BC006379	446608	K-ALPHA-1	10376		
	BC006481	446608	K-ALPHA-1	10376		
	BE300252	446608	K-ALPHA-1	10376		
	AL565074	75318	TUBA1	7277		
	AI215102	75618	RAB11A	8766		
	AU157515	396503	CDC10	989		
	BG435404	111554	ARL7	10123		
	NM_013341	348282	PTD004	29789		
	BC001002	356729	OK	203068		
	BE252813	480368	EIF2S3	1968		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	NM_001961	75309	EEF2	1938		
	NM_001665	75082	ARHG	391		
	AF052179	286221	ARF1	375		
	AK000826		RAB7	7879		
	NM_004147	115242	DRG1	4733		
	AI435089		IAN4L1	55340		
	AB023208	288094	MSF	10801		
GO:0004459	L-lactate dehydrogenase activity	3	8	3	5	3.03E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_002300	234489	LDHB	3945		
	BE042354		LDHB	3945		
	NM_005566	2795	LDHA	3939		
GO:0019863	IgE binding	3	8	3	5	2.92E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	BC001120	411701	LGALS3	3958		
	BC020763		FCER1G	2207		
	NM_004106	433300	FCER1G	2207		
GO:0004815	aspartate-tRNA ligase activity	3	8	3	5	3.07E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	AF285758	3100	KARS	3735		
	NM_005548	3100	KARS	3735		
	NM_004539	427212	NARS	4677		
GO:0016491	oxidoreductase activity	32	681	32	351	4.47E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_001329	171391	CTBP2	1488		
	NM_001866	432170	COX7B	1349		
	NM_001865	70312	COX7A2	1347		
	NM_002085	433951	GPX4	2879		
	NM_000581	76686	GPX1	2876		
	NM_004373	180714	COX6A1	1337		
	NM_001862	1342	COX5B	1329		
	BC006229	1342	COX5B	1329		
	AI557312	1342	COX5B	1329		
	AA854966	433419	COX4I1	1327		
	NM_001861	433419	COX4I1	1327		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	NM_006004	285761	UQCRH	7388		
	NM_006294	131255	UQCRB	7381		
	BC001917	405860	MDH2	4191		
	NM_014402	146602	QP-C	27089		
	NM_002300	234489	LDHB	3945		
	BE042354		LDHB	3945		
	NM_005566	2795	LDHA	3939		
	NM_019056	433328	P17.3	54539		
	NM_013387	284292	HSPC051	29796		
	W46388	384944	SOD2	6648		
	L19184	180909	PRDX1	5052		
	AW514401	433941	SEPW1	6415		
	NM_000690	331141	ALDH2	217		
	AK002110	90443	NDUFS8	4728		
	NM_004552	409829	NDUFS5	4725		
	NM_005004	198273	NDUFB8	4714		
	NM_004546	27262	NDUFB2	4708		
	NM_004545	183435	NDUFB1	4707		
	NM_005003	5556	NDUFAB1	4706		
	NM_002489	50098	NDUFA4	4697		
	BC003674	163867	NDUFA2	4695		
GO:0015482	voltage-dependent anion channel porin activity	2	3	2	3	3.96E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	L08666	355927	VDAC2	7417		
	AL515918	404814	VDAC1	7416		
GO:0004824	lysine-tRNA ligase activity	2	3	2	2	3.92E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	AF285758	3100	KARS	3735		
	NM_005548	3100	KARS	3735		
GO:0019904	protein domain specific binding	6	17	6	8	8.05E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_003406	386834	YWHAZ	7534		
	NM_003406	386834	YWHAZ	7534		
	AB024334	25001	YWHAG	7532		
	BC001359	279920	YWHAB	7529		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	BF246499	279920	YWHAB	7529		
	NM_014052		YWHAB	7529		
GO:0004859	phospholipase inhibitor activity	3	9	3	5	0.001702626
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_004039	462864	ANXA2	302		
	BC001388	462864	ANXA2	302		
	BE908217		ANXA2	302		
GO:0008073	ornithine decarboxylase inhibitor activity	2	5	2	2	0.001526963
	Probe	UniGene cluster	Gene	LocusLink ID		
	D87914	446427	OAZ1	4946		
	AF090094	334644	OAZ1	4946		
GO:0004215	cathepsin H activity	1	1	1	1	0.00181945
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_004390	114931	CTSH	1512		
GO:0000036	acyl carrier activity	1	1	1	1	0.001633207
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_005003	5556	NDUFAB1	4706		
GO:0004418	hydroxymethylbilane synthase activity	1	1	1	1	0.001525127
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_000190	82609	HMBS	3145		
GO:0004278	granzyme B activity	1	1	1	1	0.001646169
	Probe	UniGene cluster	Gene	LocusLink ID		
	J03189	1051	GZMB	3002		
GO:0045545	syndecan binding	1	1	1	1	0.001728477
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_005625	164067	SDCBP	6386		
GO:0047066	phospholipid-hydroperoxide glutathione peroxidase activity	1	1	1	1	0.001868624
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_002085	433951	GPX4	2879		
GO:0008428	ribonuclease inhibitor activity	1	1	1	1	0.00154789
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_002939	130958	RNH	6050		
GO:0015283	apoptogenic cytochrome c release channel activity	1	1	1	1	0.001620447
	Probe	UniGene cluster	Gene	LocusLink ID		
	AL515918	404814	VDAC1	7416		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
GO:0004801	transaldolase activity	1	1	1	1	0.00178808
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_006755	438678	TALDO1	6888		
GO:0004819	glutamine-tRNA ligase activity	1	1	1	1	0.001803628
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_005051	79322	QARS	5859		
GO:0050659	N-acetylgalactosamine 4-sulfate 6-O-sulfotransferase activity	1	1	1	1	0.00185194
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_014863		GALNAC4S-6ST	51363		
GO:0016309	1-phosphatidylinositol-5-phosphate 4-kinase activity	1	1	1	1	0.001757773
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_005028	108966	PIP5K2A	5305		
GO:0005080	protein kinase C binding	3	14	3	6	0.001530544
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_006098	5662	GNB2L1	10399		
	AK054976	256697	HINT1	3094		
	N32864	256697	HINT1	3094		
GO:0003746	translation elongation factor activity	5	41	5	18	0.00151984
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_001961	75309	EEF2	1938		
	NM_001404	256184	EEF1G	1937		
	NM_001960	334798	EEF1D	1936		
	AI613383	334798	EEF1D	1936		
	NM_001959	421608	EEF1B2	1933		
GO:0005489	electron transporter activity	11	391	11	175	2.99E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_001865	70312	COX7A2	1347		
	NM_002085	433951	GPX4	2879		
	AI718223	31731	PRDX5	25824		
	AF197952	31731	PRDX5	25824		
	AF313911	395309	TXN	7295		
	AK000161	10346	C10orf26	54838		
	BF572868	169358	DJ971N18.2	56255		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	NM_000690	331141	ALDH2	217		
	AV734582		TXNDC5	81567		
	NM_004786	114412	TXNL	9352		
	BC005374	154023	TXNDC4	23071		
GO:0005344	oxygen transporter activity	3	15	3	9	0.00190245
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_000519	36977	HBD	3045		
	M25079		HBB	3043		
	AF349114	155376	HBB	3043		
GO:0004681	casein kinase I activity	3	15	3	4	0.001943217
	Probe	UniGene cluster	Gene	LocusLink ID		
	AL530441	181390	CSNK1G2	1455		
	BG534245	519667	CSNK1A1	1452		
	AW268585	318381	CSNK1A1	1452		
GO:0008308	voltage-dependent ion-selective channel activity	2	6	2	5	0.001882844
	Probe	UniGene cluster	Gene	LocusLink ID		
	L08666	355927	VDAC2	7417		
	AL515918	404814	VDAC1	7416		
GO:0008097	5S rRNA binding	2	6	2	1	0.001895919
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_000969	469653	RPL5	6125		
	BF214492	469653	RPL5	6125		
GO:0000049	tRNA binding	4	29	4	13	0.002266386
	Probe	UniGene cluster	Gene	LocusLink ID		
	AF285758	3100	KARS	3735		
	NM_005548	3100	KARS	3735		
	BE968801	289093	RPL35A	6165		
	AW402660	289093	RPL35A	6165		
GO:0008159	positive transcription elongation factor activity	2	7	2	5	0.002774145
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_004965	356285	HMGN1	3150		
	NM_004965	356285	HMGN1	3150		
GO:0030508	thiol-disulfide exchange intermediate activity	2	7	2	4	0.002756247
	Probe	UniGene cluster	Gene	LocusLink ID		
	AF313911	395309	TXN	7295		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	NM_004786	114412	TXNL	9352		
GO:0015266	protein channel activity	1	6	1	1	0.001227639
	Probe	UniGene cluster	Gene	LocusLink ID		
	AI275690		MCL1	4170		
GO:0015288	porin activity	1	14	1	5	8.01E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	AL036344	362841	NUP50	10762		
GO:0008143	poly(A) binding	3	17	3	5	0.002719156
	Probe	UniGene cluster	Gene	LocusLink ID		
	AI734929	387804	PABPC1	26986		
	AI762552	372673	HNRPDL	9987		
	NM_030979	458280	PABPC3	5042		
GO:0008009	chemokine activity	6	66	6	46	0.002709567
	Probe	UniGene cluster	Gene	LocusLink ID		
	R64130	2164	PPBP	5473		
	NM_002619	81564	PF4	5196		
	NM_016951	15159	CKLF	51192		
	AF096895	15159	CKLF	51192		
	M21121	489044	CCL5	6352		
	NM_002985	489044	CCL5	6352		
GO:0005048	signal sequence binding	2	9	2	4	0.002268504
	Probe	UniGene cluster	Gene	LocusLink ID		
	AW087870	28707	SSR3	6747		
	NM_003145	74564	SSR2	6746		
GO:0042287	MHC protein binding	1	6	1	2	0.001546046
	Probe	UniGene cluster	Gene	LocusLink ID		
	M16768		TRGV9	6983		
GO:0003729	mRNA binding	1	37	1	10	7.27E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_007209	182825	RPL35	11224		
GO:0003690	double-stranded DNA binding	5	50	5	15	0.004410198
	Probe	UniGene cluster	Gene	LocusLink ID		
	AA205834	257082	XRCC5	7520		
	AL517946	241567	RBMS1	5937		
	NM_001469	169744	G22P1	2547		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	AI762552	372673	HNRPDL	9987		
	BC002411	74497	NSEP1	4904		
GO:0009032	thymidine phosphorylase activity	1	2	1	1	0.004242825
	Probe	UniGene cluster	Gene	LocusLink ID		
	AW613387	435067	ECGF1	1890		
GO:0005026	type II transforming growth factor beta receptor activity	1	2	1	1	0.004524117
	Probe	UniGene cluster	Gene	LocusLink ID		
	D50683		TGFBR2	7048		
GO:0046870	cadmium ion binding	1	2	1	1	0.004474673
	Probe	UniGene cluster	Gene	LocusLink ID		
	AF078844		MT1F	4494		
GO:0015320	phosphate carrier activity	1	2	1	1	0.004177883
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_002635	290404	SLC25A3	5250		
GO:0048270	methionine adenosyltransferase regulator activity	1	2	1	1	0.004199309
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_013283	54642	MAT2B	27430		
GO:0008574	plus-end-directed microtubule motor activity	1	2	1	1	0.004264923
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_004798	301206	KIF3B	9371		
GO:0005137	interleukin-5 receptor binding	1	2	1	2	0.004135683
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_005625	164067	SDCBP	6386		
GO:0008538	proteasome activator activity	1	2	1	2	0.004378958
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_002818	434081	PSME2	5721		
GO:0008831	dTDP-4-dehydrorhamnose reductase activity	1	2	1	1	0.003975074
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_013283	54642	MAT2B	27430		
GO:0050178	phenylpyruvate tautomerase activity	1	2	1	1	0.004094326
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_002415	407995	MIF	4282		
GO:0015207	adenine transporter activity	1	2	1	1	0.004426298
	Probe	UniGene cluster	Gene	LocusLink ID		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	NM_001152	79172	SLC25A5	292		
GO:0004816	asparagine-tRNA ligase activity	1	2	1	2	0.004033819
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_004539	427212	NARS	4677		
GO:0001517	N-acetylglucosamine 6-O-sulfotransferase activity	1	2	1	1	0.004626357
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_021615	157439	CHST6	4166		
GO:0004920	interleukin-10 receptor activity	1	2	1	2	0.004499259
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_001558	327	IL10RA	3587		
GO:0016209	antioxidant activity	2	11	2	6	0.004762009
	Probe	UniGene cluster	Gene	LocusLink ID		
	AI718223	31731	PRDX5	25824		
	AF197952	31731	PRDX5	25824		
GO:0008199	ferric iron binding	3	22	3	9	0.005203027
	Probe	UniGene cluster	Gene	LocusLink ID		
	BG537190	433670	FTL	2512		
	BG538564		FTL	2512		
	NM_002032	448738	FTH1	2495		
GO:0004602	glutathione peroxidase activity	2	8	2	6	0.007011748
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_002085	433951	GPX4	2879		
	NM_000581	76686	GPX1	2876		
GO:0042288	MHC class I protein binding	3	24	3	9	0.006951921
	Probe	UniGene cluster	Gene	LocusLink ID		
	AA515698		TUBB2	10383		
	AF029750	370937	TAPBP	6892		
	BC001002	356729	OK	203068		
GO:0042835	BRE binding	2	11	2	2	0.006918271
	Probe	UniGene cluster	Gene	LocusLink ID		
	N25915	321390	CUGBP1	10658		
	AI472139	321390	CUGBP1	10658		
GO:0000900	translation repressor activity, nucleic acid binding	2	11	2	2	0.006827638
	Probe	UniGene cluster	Gene	LocusLink ID		
	N25915	321390	CUGBP1	10658		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	AI472139	321390	CUGBP1	10658		
GO:0000166	nucleotide binding	3	251	3	116	0.001622988
	Probe	UniGene cluster	Gene	LocusLink ID		
	BC001417	246112	U5-200KD	23020		
	NM_001686	406510	ATP5B	506		
	NM_001090	9573	ABCF1	23		
GO:0003823	antigen binding	2	26	2	12	0.004038333
	Probe	UniGene cluster	Gene	LocusLink ID		
	BE217880	362807	IL7R	3575		
	X17115		IGHM	3507		
GO:0030492	hemoglobin binding	1	3	1	3	0.007483513
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_016633	274309	ERAF	51327		
GO:0004062	aryl sulfotransferase activity	1	3	1	2	0.007514436
	Probe	UniGene cluster	Gene	LocusLink ID		
	L25275	415067	SULT1A3	6818		
GO:0003895	gamma DNA-directed DNA polymerase activity	1	3	1	1	0.007075851
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_002693	290921	POLG	5428		
GO:0000150	recombinase activity	1	3	1	1	0.007640729
	Probe	UniGene cluster	Gene	LocusLink ID		
	AL513759	347340	RBPSUH	3516		
GO:0005055	laminin receptor activity	1	3	1	2	0.007244994
	Probe	UniGene cluster	Gene	LocusLink ID		
	AW304232	374553	LAMR1	3921		
GO:0004917	interleukin-7 receptor activity	1	3	1	2	0.007872267
	Probe	UniGene cluster	Gene	LocusLink ID		
	BE217880	362807	IL7R	3575		
GO:0016512	endothelin-converting enzyme 1 activity	1	3	1	2	0.007906494
	Probe	UniGene cluster	Gene	LocusLink ID		
	AF521189	129801	ECE2	9718		
GO:0004170	dUTP diphosphatase activity	1	3	1	1	0.007159424
	Probe	UniGene cluster	Gene	LocusLink ID		
	U62891	367676	DUT	1854		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
GO:0008449	N-acetylglucosamine-6-sulfatase activity	1	3	1	1	0.007838334
	Probe	UniGene cluster	Gene	LocusLink ID		
	BE880245	334534	GNS	2799		
GO:0050220	prostaglandin-E synthase activity	1	3	1	2	0.007545617
	Probe	UniGene cluster	Gene	LocusLink ID		
	BC003005	355693	TEBP	10728		
GO:0005093	RAB GDP-dissociation inhibitor activity	1	3	1	2	0.007738271
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_001494	56845	GDI2	2665		
GO:0004871	signal transducer activity	20	635	20	264	0.004156266
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_000985	374588	RPL17	6139		
	BG168283	374588	RPL17	6139		
	BE733979	374588	RPL17	6139		
	NM_002923	78944	RGS2	5997		
	NM_005274	436765	GNG5	2787		
	NM_000516	157307	GNAS	2778		
	NM_016592	157307	GNAS	2778		
	AF088184	157307	GNAS	2778		
	AI591100	157307	GNAS	2778		
	NM_021003	130036	PPM1A	5494		
	AI828967	41324	CBL	867		
	M87507	2490	CASP1	834		
	NM_002661	512298	PLCG2	5336		
	BC002704	21486	STAT1	6772		
	BC001463	414579	SCOTIN	51246		
	NM_001960	334798	EEF1D	1936		
	AI613383	334798	EEF1D	1936		
	NM_030796	4750	DKFZP564K0822	81552		
	NM_002965	112405	S100A9	6280		
	AF154847	165195	VAPA	9218		
GO:0004727	prenylated protein tyrosine phosphatase activity	2	12	2	3	0.007694094
	Probe	UniGene cluster	Gene	LocusLink ID		
	BF795101	82911	PTP4A2	8073		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	U48297	82911	PTP4A2	8073		
GO:0003774	motor activity	9	145	9	63	0.010508698
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_001614	14376	ACTG1	71		
	BG026805	14376	ACTG1	71		
	BE741683	14376	ACTG1	71		
	AL567820	14376	ACTG1	71		
	AU145192	14376	ACTG1	71		
	AL515810	14376	ACTG1	71		
	AW190090	14376	ACTG1	71		
	BC001920	14376	ACTG1	71		
	AA703939	14376	ACTG1	71		
GO:0003724	RNA helicase activity	2	17	2	8	0.006729576
	Probe	UniGene cluster	Gene	LocusLink ID		
	BF129093	271541	DDX6	1656		
	NM_004396	279806	DDX5	1655		
GO:0003773	heat shock protein activity	5	65	5	31	0.008488443
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_002156	79037	HSPD1	3329		
	AF275719	74335	HSPCB	3326		
	AF352832	180414	HSPA8	3312		
	AA704004	180414	HSPA8	3312		
	AF217511	180414	HSPA8	3312		
GO:0005086	ARF guanyl-nucleotide exchange factor activity	2	13	2	6	0.009283655
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_013385	7189	PSCD4	27128		
	NM_004762	1050	PSCD1	9267		
GO:0005554	molecular_function unknown	28	820	28	373	0.009487505
	Probe	UniGene cluster	Gene	LocusLink ID		
	AV713673	399981	C20orf178	128866		
	NM_006472	179526	TXNIP	10628		
	NM_015380	505824	CGI-51	25813		
	NM_014453	12107	BC-2	27243		
	BE544689		RTN3	10313		
	NM_016217	6679	HECA	51696		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	NM_017627		TPT1	7178		
	AL565449	374596	TPT1	7178		
	BG498776	374596	TPT1	7178		
	AI721229	374596	TPT1	7178		
	AI888178	374596	TPT1	7178		
	NM_016079	512608	NEDF	51652		
	NM_024292	386532	UBL5	59286		
	AI523895	111801	ARS2	51593		
	BC002496	30376	C6orf53	51522		
	AF110775	42743	HSPC148	51503		
	NM_015710	421907	GLTSCR2	29997		
	NM_021943	6120	TEX27	60685		
	NM_016145	108969	PTD008	51398		
	AK023637	433256	AMMECR1	9949		
	NM_012286	411358	MORF4L2	9643		
	NM_003197		SKP1A	6500		
	AA927664	171626	SKP1A	6500		
	AF116639	109052	C14orf2	9556		
	NM_007033	40500	RER1	11079		
	BG397444	87385	C7orf30	115416		
	NM_007161	436066	LST1	7940		
	NM_018648	14317	NOLA3	55505		
GO:0042605	peptide antigen binding	2	9	2	4	0.014485361
	Probe	UniGene cluster	Gene	LocusLink ID		
	M16768		TRGV9	6983		
	AF029750	370937	TAPBP	6892		
GO:0008553	hydrogen-exporting ATPase activity, phosphorylative mechanism	1	4	1	3	0.011275324
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_001686	406510	ATP5B	506		
GO:0004563	beta-N-acetylhexosaminidase activity	1	4	1	2	0.011645682
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_000521	69293	HEXB	3074		
GO:0004478	methionine adenosyltransferase activity	1	4	1	2	0.011478118
	Probe	UniGene cluster	Gene	LocusLink ID		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	BC001686	77502	MAT2A	4144		
GO:0004618	phosphoglycerate kinase activity	1	4	1	1	0.011003161
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_000291	78771	PGK1	5230		
GO:0004145	diamine N-acetyltransferase activity	1	4	1	1	0.011118177
	Probe	UniGene cluster	Gene	LocusLink ID		
	M55580	28491	SAT	6303		
GO:0004802	transketolase activity	1	4	1	2	0.010743828
	Probe	UniGene cluster	Gene	LocusLink ID		
	L12711	89643	TKT	7086		
GO:0046979	TAP2 binding	1	4	1	2	0.010780124
	Probe	UniGene cluster	Gene	LocusLink ID		
	AF029750	370937	TAPBP	6892		
GO:0030060	L-malate dehydrogenase activity	1	4	1	2	0.011436978
	Probe	UniGene cluster	Gene	LocusLink ID		
	BC001917	405860	MDH2	4191		
GO:0008474	palmitoyl-(protein) hydrolase activity	1	4	1	2	0.01096535
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_000310	3873	PPT1	5538		
GO:0030911	TPR domain binding	1	4	1	1	0.011315308
	Probe	UniGene cluster	Gene	LocusLink ID		
	AF275719	74335	HSPCB	3326		
GO:0004301	epoxide hydrolase activity	1	4	1	4	0.011079572
	Probe	UniGene cluster	Gene	LocusLink ID		
	J02959	81118	LTA4H	4048		
GO:0046978	TAP1 binding	1	4	1	2	0.011157052
	Probe	UniGene cluster	Gene	LocusLink ID		
	AF029750	370937	TAPBP	6892		
GO:0030156	benzodiazepine receptor binding	1	4	1	2	0.010816667
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_020548	78888	DBI	1622		
GO:0008248	pre-mRNA splicing factor activity	8	147	8	56	0.010858723
	Probe	UniGene cluster	Gene	LocusLink ID		
	N25915	321390	CUGBP1	10658		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	AI472139	321390	CUGBP1	10658		
	BC006407	333414	MGC14151	84316		
	NM_003769	77608	SFRS9	8683		
	BC005938	424908	LSM5	23658		
	NM_004593	30035	SFRS10	6434		
	BG254869	73965	SFRS2	6427		
	NM_007363	355861	NONO	4841		
GO:0005544	calcium-dependent phospholipid binding	3	32	3	17	0.014059314
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_004039	462864	ANXA2	302		
	BC001388	462864	ANXA2	302		
	BE908217		ANXA2	302		
GO:0003756	protein disulfide isomerase activity	2	16	2	8	0.014384282
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_006817	511762	C12orf8	10961		
	BC005374	154023	TXNDC4	23071		
GO:0008320	protein carrier activity	2	16	2	8	0.014477384
	Probe	UniGene cluster	Gene	LocusLink ID		
	BC000027	424551	P24B	23423		
	AK024976	75914	RNP24	10959		
GO:0008383	manganese superoxide dismutase activity	1	5	1	1	0.015622861
	Probe	UniGene cluster	Gene	LocusLink ID		
	W46388	384944	SOD2	6648		
GO:0000213	tRNA-intron endonuclease activity	1	5	1	3	0.015283234
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_024075	15580	LENG5	79042		
GO:0004213	cathepsin B activity	1	5	1	2	0.014958059
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_001908	135226	CTSB	1508		
GO:0004601	peroxidase activity	4	55	4	25	0.016517148
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_002085	433951	GPX4	2879		
	NM_000581	76686	GPX1	2876		
	L19184	180909	PRDX1	5052		
	AA167775	69855	D1S155E	7812		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
GO:0004840	ubiquitin conjugating enzyme activity	8	164	8	54	0.019203271
	Probe	UniGene cluster	Gene	LocusLink ID		
	U84404	180686	UBE3A	7337		
	BG531983	108104	UBE2L3	7332		
	AL518159	163546	UBE2E1	7324		
	BC003395	411826	UBE2D3	7323		
	BE621259	108332	UBE2D2	7322		
	AW014299	19196	LOC51619	51619		
	AW025284	19196	LOC51619	51619		
	NM_004223	425777	UBE2L6	9246		
GO:0042043	neurexin binding	1	6	1	3	0.019163984
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_005625	164067	SDCBP	6386		
GO:0050656	3'-phosphoadenosine 5'-phosphosulfate binding	1	6	1	4	0.019759475
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_014863		GALNAC4S -6ST	51363		
GO:0008190	eukaryotic initiation factor 4E binding	1	6	1	2	0.019985298
	Probe	UniGene cluster	Gene	LocusLink ID		
	BG106477	278712	EIF4EBP2	1979		
GO:0005094	Rho GDP-dissociation inhibitor activity	1	6	1	2	0.019322802
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_001175	292738	ARHGDIB	397		
GO:0004694	eukaryotic translation initiation factor 2alpha kinase activity	1	6	1	3	0.019216632
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_014413	434986	HRI	27102		
GO:0004652	polynucleotide adenylyltransferase activity	1	6	1	1	0.01992836
	Probe	UniGene cluster	Gene	LocusLink ID		
	BF797555	201085	PAPOLA	10914		
GO:0004594	pantothenate kinase activity	1	6	1	3	0.020216342
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_024960	203589	PANK2	80025		
GO:0004579	dolichyl-diphosphooligosaccharide-protein glycotransferase activity	1	6	1	3	0.020042562
	Probe	UniGene cluster	Gene	LocusLink ID		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	BC002594	301882	DDOST	1650		
GO:0003988	acetyl-CoA C-acyltransferase activity	1	6	1	3	0.020393161
	Probe	UniGene cluster	Gene	LocusLink ID		
	AI860341	166160	ACAA1	30		
GO:0004356	glutamate-ammonia ligase activity	1	6	1	3	0.019871745
	Probe	UniGene cluster	Gene	LocusLink ID		
	AL161952	442669	GLUL	2752		
GO:0005046	KDEL sequence binding	1	6	1	2	0.019484274
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_006854	446645	KDELR2	11014		
GO:0008026	ATP-dependent helicase activity	6	178	6	72	0.01127708
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_005804	311609	DDX39	10212		
	NM_001967	511904	EIF4A2	1974		
	NM_001416	129673	EIF4A1	1973		
	BC006210	129673	EIF4A1	1973		
	BF129093	271541	DDX6	1656		
	NM_004396	279806	DDX5	1655		
GO:0003720	telomerase activity	1	5	1	3	0.029368161
	Probe	UniGene cluster	Gene	LocusLink ID		
	BC003005	355693	TEBP	10728		
GO:0008077	Hsp70/Hsp90 organizing protein activity	1	7	1	3	0.024283751
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_003932	377199	ST13	6767		
GO:0005062	hematopoietin/interferon-class (D200-domain) cytokine receptor signal transducer activity	1	7	1	3	0.025195205
	Probe	UniGene cluster	Gene	LocusLink ID		
	BC002704	21486	STAT1	6772		
GO:0004157	dihydropyrimidinase activity	1	7	1	4	0.025127839
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_001386	173381	DPYSL2	1808		
GO:0004634	phosphopyruvate hydratase activity	1	7	1	4	0.024666172
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_001428	433455	ENO1	2023		
GO:0003891	delta DNA polymerase activity	1	7	1	4	0.024537367

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_002693	290921	POLG	5428		
GO:0017017	MAP kinase phosphatase activity	2	21	2	10	0.024121627
	Probe	UniGene cluster	Gene	LocusLink ID		
	AI655015	3843	DUSP7	1849		
	BC003143	298654	DUSP6	1848		
GO:0019212	phosphatase inhibitor activity	1	3	1	1	0.0398592
	Probe	UniGene cluster	Gene	LocusLink ID		
	AW612574	385913	ANP32E	81611		
GO:0005057	receptor signaling protein activity	6	100	6	39	0.032727531
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_003332	9963	TYROBP	7305		
	NM_003641	458414	IFITM1	8519		
	AA749101	458414	IFITM1	8519		
	BC020763		FCER1G	2207		
	NM_004106	433300	FCER1G	2207		
	AF052179	286221	ARF1	375		
GO:0004784	superoxide dismutase activity	2	9	2	3	0.051010541
	Probe	UniGene cluster	Gene	LocusLink ID		
	W46388	384944	SOD2	6648		
	AA811192	129621	KIAA0179	23076		

Table 7. Biological processes represented by the group of probesets reproducibly detected in intra- and interspecies comparisons.

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
GO:0006955	immune response	42	649	42	338	3.99E-15
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_006435	174195	IFITM2	10581		
	NM_002415	407995	MIF	4282		
	NM_002818	434081	PSME2	5721		
	NM_002800	381081	PSMB9	5698		
	NM_002341	376208	LTB	4050		
	NM_002032	448738	FTH1	2495		
	R64130	2164	PPBP	5473		
	NM_003641	458414	IFITM1	8519		
	AA749101	458414	IFITM1	8519		
	M30894	385086	TRG@	6965		
	NM_003202	169294	TCF7	6932		
	AF029750	370937	TAPBP	6892		
	BC020763		FCER1G	2207		
	NM_004106	433300	FCER1G	2207		
	NM_002619	81564	PF4	5196		
	BE218980		ETS1	2113		
	NM_004048	48516	B2M	567		
	AW188940	48516	B2M	567		
	BE217880	362807	IL7R	3575		
	AV700030	193400	IL6R	3570		
	X17115		IGHM	3507		
	NM_001175	292738	ARHGDIB	397		
	NM_007161	436066	LST1	7940		
	AW514210	411958	HLA-F	3134		
	AI669379	411958	HLA-F	3134		
	X56841	381008	HLA-E	3133		
	NM_005516	381008	HLA-E	3133		
	M31183	381008	HLA-E	3133		
	NM_002125	308026	HLA-DRB3	3125		
	NM_021983	308026	HLA-DRB3	3125		
	U65585	308026	HLA-DRB3	3125		
	AJ297586	308026	HLA-DRB3	3125		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	AF005487	308026	HLA-DRB3	3125		
	BG397856	387679	HLA-DQA1	3117		
	NM_002121	368409	HLA-DPB1	3115		
	M27487	914	HLA-DPA1	3113		
	NM_002118	1162	HLA-DMB	3109		
	M12679	274485	HLA-C	3107		
	AK024836	274485	HLA-C	3107		
	L42024	77961	HLA-B	3106		
	L07950	77961	HLA-B	3106		
	AA573862	181244	HLA-A	3105		
GO:0008152	metabolism	6	619	6	287	2.02E-16
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_021100	194692	NFS1	9054		
	BE880245	334534	GNS	2799		
	NM_014873		KIAA0205	9926		
	AW613387	435067	ECGF1	1890		
	AV703259		IDS	3423		
	NM_001918	139410	DBT	1629		
GO:0006412	protein biosynthesis	129	513	129	237	2.00E-14
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_000985	374588	RPL17	6139		
	BG168283	374588	RPL17	6139		
	BE733979	374588	RPL17	6139		
	NM_002948	381219	RPL15	6138		
	BC004954	410817	RPL13	6137		
	AW574664	410817	RPL13	6137		
	AI186735	410817	RPL13	6137		
	AA961748	410817	RPL13	6137		
	AA789278	410817	RPL13	6137		
	NM_000976	408054	RPL12	6136		
	AA281332	408054	RPL12	6136		
	NM_000975	388664	RPL11	6135		
	NM_006013	401929	RPL10	6134		
	NM_000661	412370	RPL9	6133		
	NM_000973	178551	RPL8	6132		
	NM_000971	421257	RPL7	6129		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	BG389744	421257	RPL7	6129		
	NM_000970	528668	RPL6	6128		
	NM_000969	469653	RPL5	6125		
	BF214492	469653	RPL5	6125		
	AI953886	186350	RPL4	6124		
	NM_000968	186350	RPL4	6124		
	BC005817	186350	RPL4	6124		
	NM_000967	119598	RPL3	6122		
	BC006483	119598	RPL3	6122		
	L22453	119598	RPL3	6122		
	BG339228	119598	RPL3	6122		
	NM_018141	380887	MRPS10	55173		
	U16738	446522	RPL14	9045		
	AA838274	446522	RPL14	9045		
	NM_015414	408018	RPL36	25873		
	NM_005051	79322	QARS	5859		
	AW083133	143773	eIF3k	27335		
	AF085358	143773	eIF3k	27335		
	BC000461	429180	EIF2S2	8894		
	AF348700	5308	UBA52	7311		
	BF246436	150580	SUI1	10209		
	AL537707	150580	SUI1	10209		
	W67644	150580	SUI1	10209		
	NM_003756	127149	EIF3S3	8667		
	NM_003754	381255	EIF3S5	8665		
	AW304232	374553	LAMR1	3921		
	NM_016091	119503	EIF3S6IP	51386		
	AF285758	3100	KARS	3735		
	NM_005548	3100	KARS	3735		
	NM_001997	387208	FAU	2197		
	BC000514	449070	RPL13A	23521		
	NM_012423	449070	RPL13A	23521		
	BC001675	449070	RPL13A	23521		
	BF979419	449070	RPL13A	23521		
	BF942308	449070	RPL13A	23521		
	NM_007209	182825	RPL35	11224		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	BF247371	93379	EIF4B	1975		
	NM_001967	511904	EIF4A2	1974		
	BE252813	480368	EIF2S3	1968		
	NM_001961	75309	EEF2	1938		
	NM_001404	256184	EEF1G	1937		
	NM_001960	334798	EEF1D	1936		
	AI613383	334798	EEF1D	1936		
	NM_001959	421608	EEF1B2	1933		
	NM_000978	406300	RPL23	9349		
	NM_007104	448396	RPL10A	4736		
	BG231561	448396	RPL10A	4736		
	NM_001032	539	RPS29	6235		
	BC000354	153177	RPS28	6234		
	NM_002954	311640	RPS27A	6233		
	NM_001030	337307	RPS27	6232		
	NM_001029	480569	RPS26	6231		
	AA888388	512676	RPS25	6230		
	BC000523	356794	RPS24	6229		
	NM_001024	372960	RPS21	6227		
	NM_001022	381184	RPS19	6223		
	BE259729	381184	RPS19	6223		
	NM_001021	433427	RPS17	6218		
	NM_001020	397609	RPS16	6217		
	AI200589	397609	RPS16	6217		
	AA583817	397609	RPS16	6217		
	NM_004539	427212	NARS	4677		
	NM_001019	370504	RPS15A	6210		
	NM_001018	406683	RPS15	6209		
	NM_001017	446588	RPS13	6207		
	AI799007	380956	RPS12	6206		
	AA320764	406620	RPS10	6204		
	NM_001014	406620	RPS10	6204		
	BE348997	139876	RPS9	6203		
	NM_001013	139876	RPS9	6203		
	NM_005594	32916	NACA	4666		
	BF976260	32916	NACA	4666		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	BE741754	408073	RPS6	6194		
	NM_001010	408073	RPS6	6194		
	BC000524	408073	RPS6	6194		
	NM_001009	378103	RPS5	6193		
	NM_001007	446628	RPS4X	6191		
	AW132023	446628	RPS4X	6191		
	U14990	387576	RPS3	6188		
	NM_002952	498569	RPS2	6187		
	AA630314	498569	RPS2	6187		
	AI183766	498569	RPS2	6187		
	NM_001004	437594	RPLP2	6181		
	NM_001003	356502	RPLP1	6176		
	NM_001002		RPLP0	6175		
	BC003655	443796	RPLP0	6175		
	BC005863	443796	RPLP0	6175		
	AI953822	443796	RPLP0	6175		
	NM_021104	381172	RPL41	6171		
	NM_000999	380953	RPL38	6169		
	NM_001001	444749	RPL36AL	6166		
	BE968801	289093	RPL35A	6165		
	AW402660	289093	RPL35A	6165		
	NM_000995	250895	RPL34	6164		
	NM_001090	9573	ABCF1	23		
	NM_000993	375921	RPL31	6160		
	NM_000992	430207	RPL29	6159		
	NM_000991	356371	RPL28	6158		
	NM_000990	356342	RPL27A	6157		
	BE737027	356342	RPL27A	6157		
	L05095	400295	RPL30	6156		
	NM_000988	405528	RPL27	6155		
	AI832239	3254	MRPL23	6150		
	NM_000984	419463	RPL23A	6147		
	U43701	419463	RPL23A	6147		
	BC001865		RPL23A	6147		
	BF125158	419463	RPL23A	6147		
	D17652	326249	RPL22	6146		

GO ID	**Function Name**	**Unique Input Total**	**Unique Reference Total**	**Unique UniGene Total**	**Unique Reference UniGene Total**	**Corrected P-Value**
	NM_000983	326249	RPL22	6146		
	NM_000982	381123	RPL21	6144		
	NM_000981	381061	RPL19	6143		
	NM_000980	337766	RPL18A	6142		
	NM_000979	409634	RPL18	6141		
GO:0009607	response to biotic stimulus	3	9	3	7	1.30E-15
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_006435	174195	IFITM2	10581		
	NM_003641	458414	IFITM1	8519		
	AA749101	458414	IFITM1	8519		
GO:0006754	ATP biosynthesis	1	5	1	4	3.77E-16
	Probe	UniGene cluster	Gene	LocusLink ID		
	BC003564	90336	ATP6V1G1	9550		
GO:0006119	oxidative phosphorylation	2	9	2	4	5.68E-16
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_006004	285761	UQCRH	7388		
	NM_006294	131255	UQCRB	7381		
GO:0015986	ATP synthesis coupled proton transport	19	77	19	35	1.89E-14
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_006476	107476	ATP5L	10632		
	AF070655	107476	ATP5L	10632		
	AL050277	107476	ATP5L	10632		
	AI862255	440165	ATP6V0E	8992		
	NM_003945	440165	ATP6V0E	8992		
	AF077614	272630	ATP6V1D	51382		
	NM_001697	409140	ATP5O	539		
	M62762		ATP6V0C	527		
	NM_007100	85539	ATP5I	521		
	BC003679	85539	ATP5I	521		
	NM_001689	429	ATP5G3	518		
	NM_001689	429	ATP5G3	518		
	BC005960	81634	ATP5F1	515		
	NM_006886	177530	ATP5E	514		
	NM_005174	155433	ATP5C1	509		
	BC000931	155433	ATP5C1	509		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	AV711183		ATP5C1	509		
	NM_001686	406510	ATP5B	506		
	AI587323	298280	ATP5A1	498		
GO:0009142	nucleoside triphosphate biosynthesis	1	3	1	3	2.53E-15
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_002512	433416	NME2	4831		
GO:0006952	defense response	1	130	1	74	9.14E-15
	Probe	UniGene cluster	Gene	LocusLink ID		
	U12707	2157	WAS	7454		
GO:0015992	proton transport	19	106	19	44	5.22E-11
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_006476	107476	ATP5L	10632		
	AF070655	107476	ATP5L	10632		
	AL050277	107476	ATP5L	10632		
	AI862255	440165	ATP6V0E	8992		
	NM_003945	440165	ATP6V0E	8992		
	U94592	80658	UCP2	7351		
	AF077614	272630	ATP6V1D	51382		
	NM_001697	409140	ATP5O	539		
	M62762		ATP6V0C	527		
	NM_001689	429	ATP5G3	518		
	NM_001689	429	ATP5G3	518		
	BC005960	81634	ATP5F1	515		
	NM_006886	177530	ATP5E	514		
	NM_005174	155433	ATP5C1	509		
	BC000931	155433	ATP5C1	509		
	AV711183		ATP5C1	509		
	NM_001686	406510	ATP5B	506		
	AI587323	298280	ATP5A1	498		
	BC003564	90336	ATP6V1G1	9550		
GO:0019885	antigen processing, endogenous antigen via MHC class I	13	47	13	11	7.10E-11
	Probe	UniGene cluster	Gene	LocusLink ID		
	AF029750	370937	TAPBP	6892		
	M90685	512152	HLA-G	3135		
	M90684	512152	HLA-G	3135		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	AW514210	411958	HLA-F	3134		
	AI669379	411958	HLA-F	3134		
	X56841	381008	HLA-E	3133		
	NM_005516	381008	HLA-E	3133		
	M31183	381008	HLA-E	3133		
	M12679	274485	HLA-C	3107		
	AK024836	274485	HLA-C	3107		
	L42024	77961	HLA-B	3106		
	L07950	77961	HLA-B	3106		
	AA573862	181244	HLA-A	3105		
GO:0019883	antigen presentation, endogenous antigen	12	35	12	7	2.14E-10
	Probe	UniGene cluster	Gene	LocusLink ID		
	M90685	512152	HLA-G	3135		
	M90684	512152	HLA-G	3135		
	AW514210	411958	HLA-F	3134		
	AI669379	411958	HLA-F	3134		
	X56841	381008	HLA-E	3133		
	NM_005516	381008	HLA-E	3133		
	M31183	381008	HLA-E	3133		
	M12679	274485	HLA-C	3107		
	AK024836	274485	HLA-C	3107		
	L42024	77961	HLA-B	3106		
	L07950	77961	HLA-B	3106		
	AA573862	181244	HLA-A	3105		
GO:0006414	translational elongation	11	43	11	19	5.22E-09
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_001961	75309	EEF2	1938		
	NM_001404	256184	EEF1G	1937		
	NM_001960	334798	EEF1D	1936		
	AI613383	334798	EEF1D	1936		
	NM_001959	421608	EEF1B2	1933		
	NM_001004	437594	RPLP2	6181		
	NM_001003	356502	RPLP1	6176		
	NM_001002		RPLP0	6175		
	BC003655	443796	RPLP0	6175		
	BC005863	443796	RPLP0	6175		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	AI953822	443796	RPLP0	6175		
GO:0019884	antigen presentation, exogenous antigen	9	32	9	10	4.43E-08
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_002125	308026	HLA-DRB3	3125		
	NM_021983	308026	HLA-DRB3	3125		
	U65585	308026	HLA-DRB3	3125		
	AJ297586	308026	HLA-DRB3	3125		
	AF005487	308026	HLA-DRB3	3125		
	BG397856	387679	HLA-DQA1	3117		
	NM_002121	368409	HLA-DPB1	3115		
	M27487	914	HLA-DPA1	3113		
	NM_002118	1162	HLA-DMB	3109		
GO:0019886	antigen processing, exogenous antigen via MHC class II	9	33	9	11	5.77E-08
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_002125	308026	HLA-DRB3	3125		
	NM_021983	308026	HLA-DRB3	3125		
	U65585	308026	HLA-DRB3	3125		
	AJ297586	308026	HLA-DRB3	3125		
	AF005487	308026	HLA-DRB3	3125		
	BG397856	387679	HLA-DQA1	3117		
	NM_002121	368409	HLA-DPB1	3115		
	M27487	914	HLA-DPA1	3113		
	NM_002118	1162	HLA-DMB	3109		
GO:0016070	RNA metabolism	1	7	1	3	2.17E-08
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_020414	372267	DDX24	57062		
GO:0008151	cell growth and/or maintenance	21	642	21	238	4.68E-08
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_005962	118630	MXI1	4601		
	NM_000516	157307	GNAS	2778		
	NM_016592	157307	GNAS	2778		
	AF088184	157307	GNAS	2778		
	AI591100	157307	GNAS	2778		
	NM_005935	114765	MLLT2	4299		
	AB002282	174050	EDF1	8721		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	BC000771	178468	TPM3	7170		
	M14333	390567	FYN	2534		
	BF246436	150580	SUI1	10209		
	AL537707	150580	SUI1	10209		
	W67644	150580	SUI1	10209		
	AI356412	80887	LYN	4067		
	AI828967	41324	CBL	867		
	NM_005356	1765	LCK	3932		
	NM_001706	155024	BCL6	604		
	BE218980		ETS1	2113		
	AL162047	422334	NCOA4	8031		
	AI817830	93231	MYST3	7994		
	AV702810	436687	SET	6418		
	BF129093	271541	DDX6	1656		
GO:0009613	response to pest/pathogen/parasite	4	31	4	23	1.32E-07
	Probe	UniGene cluster	Gene	LocusLink ID		
	AF038602	129758	PSTPIP1	9051		
	NM_001747	82422	CAPG	822		
	BC002704	21486	STAT1	6772		
	BC002411	74497	NSEP1	4904		
GO:0006446	regulation of translational initiation	9	62	9	27	6.56E-07
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_005875	315230	GC20	10289		
	BF246436	150580	SUI1	10209		
	AL537707	150580	SUI1	10209		
	W67644	150580	SUI1	10209		
	NM_003756	127149	EIF3S3	8667		
	NM_003754	381255	EIF3S5	8665		
	NM_001418	183684	EIF4G2	1982		
	BF247371	93379	EIF4B	1975		
	NM_001967	511904	EIF4A2	1974		
GO:0009117	nucleotide metabolism	1	37	1	22	7.26E-08
	Probe	UniGene cluster	Gene	LocusLink ID		
	U62891	367676	DUT	1854		
GO:0006334	nucleosome assembly	13	104	13	53	1.57E-06

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	Probe	UniGene cluster	Gene	LocusLink ID		
	BC001124	180877	H3F3B	3021		
	NM_005324	180877	H3F3B	3021		
	Z48950		H3F3B	3021		
	NM_002106	119192	H2AFZ	3015		
	BF718636	119192	H2AFZ	3015		
	H51429		H2AFX	3014		
	AL136629	458358	TSPYL	7259		
	AI817830	93231	MYST3	7994		
	AV702810	436687	SET	6418		
	NM_004537	419776	NAP1L1	4673		
	AI888672	419776	NAP1L1	4673		
	AW148801	419776	NAP1L1	4673		
	AI985751	419776	NAP1L1	4673		
GO:0006445	regulation of translation	8	90	8	30	3.97E-06
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_017572	512094	MKNK2	2872		
	AL517946	241567	RBMS1	5937		
	BF246436	150580	SUI1	10209		
	AL537707	150580	SUI1	10209		
	W67644	150580	SUI1	10209		
	AW304232	374553	LAMR1	3921		
	BC001716	396644	PAIP2	51247		
	BG106477	278712	EIF4EBP2	1979		
GO:0016310	phosphorylation	1	23	1	11	6.04E-07
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_005028	108966	PIP5K2A	5305		
GO:0006396	RNA processing	9	144	9	51	5.22E-06
	Probe	UniGene cluster	Gene	LocusLink ID		
	U69546	211610	CUGBP2	10659		
	AL517946	241567	RBMS1	5937		
	AI762552	372673	HNRPDL	9987		
	BF724216	155218	E1B-AP5	11100		
	AW245401	293225	DEDD2	162989		
	NM_004501	166463	HNRPU	3192		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	NM_002137	232400	HNRPA2B1	3181		
	AI375753	232400	HNRPA2B1	3181		
	NM_001019	370504	RPS15A	6210		
GO:0006413	translational initiation	4	55	4	21	3.11E-06
	Probe	UniGene cluster	Gene	LocusLink ID		
	BC000461	429180	EIF2S2	8894		
	BF246436	150580	SUI1	10209		
	AL537707	150580	SUI1	10209		
	W67644	150580	SUI1	10209		
GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolism	2	86	2	38	1.31E-06
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_001386	173381	DPYSL2	1808		
	NM_014596	57813	ZNRD1	30834		
GO:0046785	microtubule polymerization	7	40	7	20	3.40E-05
	Probe	UniGene cluster	Gene	LocusLink ID		
	AA515698		TUBB2	10383		
	NM_006082	446608	K-ALPHA-1	10376		
	BC006379	446608	K-ALPHA-1	10376		
	BC006481	446608	K-ALPHA-1	10376		
	BE300252	446608	K-ALPHA-1	10376		
	AL565074	75318	TUBA1	7277		
	BC001002	356729	OK	203068		
GO:0045069	regulation of viral genome replication	3	7	3	2	4.80E-05
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_021130	356331	PPIA	5478		
	BC005982	356331	PPIA	5478		
	AI708767	356331	PPIA	5478		
GO:0006950	response to stress	7	150	7	66	1.18E-05
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_017572	512094	MKNK2	2872		
	NM_014445	439874	SERP1	27230		
	NM_014413	434986	HRI	27102		
	BF246436	150580	SUI1	10209		
	AL537707	150580	SUI1	10209		

GO ID	**Function Name**	**Unique Input Total**	**Unique Reference Total**	**Unique UniGene Total**	**Unique Reference UniGene Total**	**Corrected P-Value**
	W67644	150580	SUI1	10209		
	AA129773	324473	MAPK1	5594		
GO:0006810	transport	21	990	21	477	5.13E-06
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_000519	36977	HBD	3045		
	M25079		HBB	3043		
	AF349114	155376	HBB	3043		
	NM_001860	24030	SLC31A2	1318		
	AJ223321		ZNF238	10472		
	U94592	80658	UCP2	7351		
	BC006337	119591	AP2S1	1175		
	NM_003768	194673	PEA15	8682		
	AF189289	279939	MTCH1	23787		
	NM_002635	290404	SLC25A3	5250		
	L12387	422340	SRI	6717		
	BC000436	511916	ENSA	2029		
	U51478	76941	ATP1B3	483		
	NM_000876	76473	IGF2R	3482		
	NM_001152	79172	SLC25A5	292		
	NM_024881	134074	SLC35E1	79939		
	NM_002136	356721	HNRPA1	3178		
	AL568186	356721	HNRPA1	3178		
	X79536	356721	HNRPA1	3178		
	NM_020548	78888	DBI	1622		
	NM_001090	9573	ABCF1	23		
GO:0006894	Golgi to secretory vesicle transport	4	12	4	1	8.55E-05
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_000516	157307	GNAS	2778		
	NM_016592	157307	GNAS	2778		
	AF088184	157307	GNAS	2778		
	AI591100	157307	GNAS	2778		
GO:0006417	regulation of protein biosynthesis	1	5	1	3	2.02E-05
	Probe	UniGene cluster	Gene	LocusLink ID		
	AL533334	21321	MTPN	136319		
GO:0006122	mitochondrial electron transport, ubiquinol to cytochrome c	3	6	3	3	1.21E-04

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_006004	285761	UQCRH	7388		
	NM_006294	131255	UQCRB	7381		
	NM_013387	284292	HSPC051	29796		
GO:0006091	energy pathways	13	183	13	86	1.20E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_004373	180714	COX6A1	1337		
	AA854966	433419	COX4I1	1327		
	NM_001861	433419	COX4I1	1327		
	NM_002635	290404	SLC25A3	5250		
	NM_001689	429	ATP5G3	518		
	NM_001689	429	ATP5G3	518		
	NM_005174	155433	ATP5C1	509		
	BC000931	155433	ATP5C1	509		
	AV711183		ATP5C1	509		
	NM_001686	406510	ATP5B	506		
	NM_004546	27262	NDUFB2	4708		
	BC003674	163867	NDUFA2	4695		
	AI860341	166160	ACAA1	30		
GO:0008154	actin polymerization and/or depolymerization	2	13	2	4	8.15E-05
	Probe	UniGene cluster	Gene	LocusLink ID		
	AW058622	401414	WASPIP	7456		
	U12707	2157	WAS	7454		
GO:0006422	aspartyl-tRNA aminoacylation	3	8	3	5	2.96E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	AF285758	3100	KARS	3735		
	NM_005548	3100	KARS	3735		
	NM_004539	427212	NARS	4677		
GO:0006511	ubiquitin-dependent protein catabolism	16	244	16	94	3.43E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	AF233225	5912	FBXO7	25793		
	NM_012179	5912	FBXO7	25793		
	U84404	180686	UBE3A	7337		
	BG531983	108104	UBE2L3	7332		
	AL518159	163546	UBE2E1	7324		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	BE621259	108332	UBE2D2	7322		
	NM_002800	381081	PSMB9	5698		
	BC000835	77060	PSMB6	5694		
	NM_002796	89545	PSMB4	5692		
	NM_002794	432607	PSMB2	5690		
	NM_002793	352768	PSMB1	5689		
	W86293	352768	PSMB1	5689		
	NM_002787	333786	PSMA2	5683		
	AF077040	251636	USP3	9960		
	NM_014709	507665	USP34	9736		
	AW473649	255596	USP19	10869		
GO:0030833	regulation of actin filament polymerization	4	12	4	4	4.43E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_005731	83583	ARPC2	10109		
	AF279893	83583	ARPC2	10109		
	BG034239	83583	ARPC2	10109		
	AF004561	439511	ARPC3	10094		
GO:0006333	chromatin assembly/disassembly	1	78	1	28	3.08E-05
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_006791	374503	MORF4L1	10933		
GO:0006954	inflammatory response	14	280	14	160	2.05E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	BG292367	413812	RAC1	5879		
	BC004247	413812	RAC1	5879		
	AI718223	31731	PRDX5	25824		
	AF197952	31731	PRDX5	25824		
	NM_002415	407995	MIF	4282		
	AL564683		CEBPB	1051		
	J02959	81118	LTA4H	4048		
	NM_001706	155024	BCL6	604		
	NM_001629	100194	ALOX5AP	241		
	M21121	489044	CCL5	6352		
	NM_002985	489044	CCL5	6352		
	NM_002965	112405	S100A9	6280		
	NM_002964	416073	S100A8	6279		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	NM_001090	9573	ABCF1	23		
GO:0006430	lysyl-tRNA aminoacylation	2	3	2	2	4.01E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	AF285758	3100	KARS	3735		
	NM_005548	3100	KARS	3735		
GO:0006444	nascent polypeptide association	2	3	2	1	4.05E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_005594	32916	NACA	4666		
	BF976260	32916	NACA	4666		
GO:0006457	protein folding	17	287	17	115	4.24E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_006585	416211	CCT8	10694		
	NM_006430	374334	CCT4	10575		
	NM_021130	356331	PPIA	5478		
	BC005982	356331	PPIA	5478		
	AI708767	356331	PPIA	5478		
	NM_000801	374638	FKBP1A	2280		
	NM_004182	172791	UXT	8409		
	NM_003932	377199	ST13	6767		
	NM_002624	288856	PFDN5	5204		
	NM_002156	79037	HSPD1	3329		
	AF275719	74335	HSPCB	3326		
	BG420237	446579	HSPCA	3320		
	AF352832	180414	HSPA8	3312		
	AA704004	180414	HSPA8	3312		
	AF217511	180414	HSPA8	3312		
	NM_006817	511762	C12orf8	10961		
	BC005374	154023	TXNDC4	23071		
GO:0019079	viral genome replication	2	31	2	14	7.11E-05
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_001329	171391	CTBP2	1488		
	NM_006402	367886	HBXIP	10542		
GO:0006120	mitochondrial electron transport, NADH to ubiquinone	5	32	5	18	5.74E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	AK002110	90443	NDUFS8	4728		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	NM_004552	409829	NDUFS5	4725		
	AF261090	15977	NDUFB9	4715		
	NM_005004	198273	NDUFB8	4714		
	NM_004546	27262	NDUFB2	4708		
GO:0007018	microtubule-based movement	8	92	8	38	5.50E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	AA515698		TUBB2	10383		
	NM_006082	446608	K-ALPHA-1	10376		
	BC006379	446608	K-ALPHA-1	10376		
	BC006481	446608	K-ALPHA-1	10376		
	BE300252	446608	K-ALPHA-1	10376		
	AL565074	75318	TUBA1	7277		
	NM_014183	100002	DNCL2A	83658		
	BC001002	356729	OK	203068		
GO:0007190	adenylate cyclase activation	6	49	6	17	7.45E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_006367	104125	CAP1	10487		
	AA806142	104125	CAP1	10487		
	NM_000516	157307	GNAS	2778		
	NM_016592	157307	GNAS	2778		
	AF088184	157307	GNAS	2778		
	AI591100	157307	GNAS	2778		
GO:0016071	mRNA metabolism	2	5	2	4	7.19E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	U24223	2853	PCBP1	5093		
	NM_030979	458280	PABPC3	5042		
GO:0006880	intracellular iron ion storage	2	4	2	2	8.41E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_002032	448738	FTH1	2495		
	L12387	422340	SRI	6717		
GO:0007189	G-protein signaling, adenylate cyclase activating pathway	4	13	4	2	0.00150912
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_000516	157307	GNAS	2778		
	NM_016592	157307	GNAS	2778		
	AF088184	157307	GNAS	2778		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	AI591100	157307	GNAS	2778		
GO:0006979	response to oxidative stress	8	80	8	34	0.001121373
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_002085	433951	GPX4	2879		
	NM_000581	76686	GPX1	2876		
	AI718223	31731	PRDX5	25824		
	AF197952	31731	PRDX5	25824		
	W46388	384944	SOD2	6648		
	M21121	489044	CCL5	6352		
	NM_002985	489044	CCL5	6352		
	AA167775	69855	D1S155E	7812		
GO:0030595	immune cell chemotaxis	1	6	1	4	3.41E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_002619	81564	PF4	5196		
GO:0030593	neutrophil chemotaxis	3	13	3	5	0.00152254
	Probe	UniGene cluster	Gene	LocusLink ID		
	BF593625	192182	SYK	6850		
	NM_016951	15159	CKLF	51192		
	AF096895	15159	CKLF	51192		
GO:0006968	cellular defense response	8	103	8	56	0.001182115
	Probe	UniGene cluster	Gene	LocusLink ID		
	U20350	78913	CX3CR1	1524		
	NM_002432	153837	MNDA	4332		
	NM_003332	9963	TYROBP	7305		
	BG500301		ITGB1	3688		
	M21121	489044	CCL5	6352		
	NM_002985	489044	CCL5	6352		
	M90685	512152	HLA-G	3135		
	M90684	512152	HLA-G	3135		
GO:0007010	cytoskeleton organization and biogenesis	1	131	1	52	1.96E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_021103	446574	TMSB10	9168		
GO:0045071	negative regulation of viral genome replication	1	1	1	1	0.001700141
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_006058	355141	TNIP1	10318		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
GO:0001522	pseudouridine synthesis	1	1	1	1	0.001583338
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_018648	14317	NOLA3	55505		
GO:0016075	rRNA catabolism	1	1	1	1	0.001743002
	Probe	UniGene cluster	Gene	LocusLink ID		
	AW245401	293225	DEDD2	162989		
GO:0006425	glutaminyl-tRNA aminoacylation	1	1	1	1	0.001571343
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_005051	79322	QARS	5859		
GO:0045059	positive thymic T-cell selection	1	1	1	1	0.001885611
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_000732	95327	CD3D	915		
GO:0045653	negative regulation of megakaryocyte differentiation	1	1	1	1	0.001595517
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_002619	81564	PF4	5196		
GO:0006397	mRNA processing	9	133	9	50	0.001316111
	Probe	UniGene cluster	Gene	LocusLink ID		
	N25915	321390	CUGBP1	10658		
	AI472139	321390	CUGBP1	10658		
	BC006407	333414	MGC14151	84316		
	BC001449	15265	HNRPR	10236		
	NM_007363	355861	NONO	4841		
	NM_021644	156481	HNRPH3	3189		
	NM_002136	356721	HNRPA1	3178		
	AL568186	356721	HNRPA1	3178		
	X79536	356721	HNRPA1	3178		
GO:0006596	polyamine biosynthesis	2	8	2	4	0.001255596
	Probe	UniGene cluster	Gene	LocusLink ID		
	D87914	446427	OAZ1	4946		
	AF090094	334644	OAZ1	4946		
GO:0009596	detection of pest/pathogen/parasite	3	8	3	3	0.002557128
	Probe	UniGene cluster	Gene	LocusLink ID		
	M90685	512152	HLA-G	3135		
	M90684	512152	HLA-G	3135		
	NM_002118	1162	HLA-DMB	3109		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
GO:0030036	actin cytoskeleton organization and biogenesis	5	98	5	43	5.02E-04
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_021103	446574	TMSB10	9168		
	U03271	333417	CAPZB	832		
	NM_006135	309415	CAPZA1	829		
	NM_001175	292738	ARHGDIB	397		
	NM_005625	164067	SDCBP	6386		
GO:0015031	protein transport	18	380	18	159	0.001758435
	Probe	UniGene cluster	Gene	LocusLink ID		
	BG292367	413812	RAC1	5879		
	BC004247	413812	RAC1	5879		
	BC001267	73957	RAB5A	5868		
	BG338251	115325	RAB7L1	8934		
	NM_001494	56845	GDI2	2665		
	AI215102	75618	RAB11A	8766		
	AB047360	12102	SNX3	8724		
	NM_019059		TOMM7	54543		
	NM_002270	405954	KPNB2	3842		
	BC003572	439683	KPNB1	3837		
	AI668643	15827	SNX11	29916		
	NM_007278	84359	GABARAP	11337		
	AV701173	301048	SEC13L	81929		
	AF052179	286221	ARF1	375		
	Z97056		KDELR3	11015		
	AK000826		RAB7	7879		
	NM_015180	444069	SYNE2	23224		
	AL036344	362841	NUP50	10762		
GO:0007585	respiratory gaseous exchange	5	43	5	18	0.001942545
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_001862	1342	COX5B	1329		
	BC006229	1342	COX5B	1329		
	AI557312	1342	COX5B	1329		
	AI718223	31731	PRDX5	25824		
	AF197952	31731	PRDX5	25824		
GO:0015671	oxygen transport	3	15	3	9	0.001915848

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_000519	36977	HBD	3045		
	M25079		HBB	3043		
	AF349114	155376	HBB	3043		
GO:0048246	macrophage chemotaxis	2	7	2	4	0.002721135
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_016951	15159	CKLF	51192		
	AF096895	15159	CKLF	51192		
GO:0048247	lymphocyte chemotaxis	2	7	2	3	0.002703913
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_016951	15159	CKLF	51192		
	AF096895	15159	CKLF	51192		
GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB cascade	11	185	11	75	0.002720104
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_000985	374588	RPL17	6139		
	BG168283	374588	RPL17	6139		
	BE733979	374588	RPL17	6139		
	NM_021003	130036	PPM1A	5494		
	M87507	2490	CASP1	834		
	NM_000801	374638	FKBP1A	2280		
	BC001463	414579	SCOTIN	51246		
	NM_001960	334798	EEF1D	1936		
	AI613383	334798	EEF1D	1936		
	NM_030796	4750	DKFZP564 K0822	81552		
	AF154847	165195	VAPA	9218		
GO:0045898	regulation of transcriptional preinitiation complex formation	2	8	2	4	0.003718539
	Probe	UniGene cluster	Gene	LocusLink ID		
	AA766897		ATF7IP	55729		
	AK025060	272210	ATF7IP	55729		
GO:0020027	hemoglobin metabolism	1	1	1	1	0.005068009
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_016633	274309	ERAF	51327		
GO:0008380	RNA splicing	8	167	8	55	0.002013903
	Probe	UniGene cluster	Gene	LocusLink ID		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	BC001417	246112	U5-200KD	23020		
	BC004383	172550	PTBP1	5725		
	NM_006107	130293	LUC7A	51747		
	BG254869	73965	SFRS2	6427		
	NM_007363	355861	NONO	4841		
	NM_004500	476302	HNRPC	3183		
	AA664258	476302	HNRPC	3183		
	AV725195	476302	HNRPC	3183		
GO:0045045	secretory pathway	3	12	3	5	0.007460959
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_016951	15159	CKLF	51192		
	AF096895	15159	CKLF	51192		
	BC005374	154023	TXNDC4	23071		
GO:0048146	positive regulation of fibroblast proliferation	1	2	1	1	0.00433262
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_014624	275243	S100A6	6277		
GO:0006556	S-adenosylmethionine biosynthesis	1	2	1	1	0.004600366
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_013283	54642	MAT2B	27430		
GO:0007097	nuclear migration	1	2	1	1	0.004287252
	Probe	UniGene cluster	Gene	LocusLink ID		
	AL021707		UNC84B	25777		
GO:0042730	fibrinolysis	1	2	1	2	0.004220954
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_000173	1472	GP1BA	2811		
GO:0006421	asparaginyl-tRNA aminoacylation	1	2	1	2	0.004450354
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_004539	427212	NARS	4677		
GO:0006610	ribosomal protein-nucleus import	1	2	1	1	0.00467923
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_000978	406300	RPL23	9349		
GO:0000002	mitochondrial genome maintenance	1	2	1	1	0.004014045
	Probe	UniGene cluster	Gene	LocusLink ID		
	AW613387	435067	ECGF1	1890		
GO:0046325	negative regulation of glucose import	1	2	1	1	0.004574666

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_003768	194673	PEA15	8682		
GO:0045226	extracellular polysaccharide biosynthesis	1	2	1	1	0.0041149
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_013283	54642	MAT2B	27430		
GO:0045947	negative regulation of translational initiation	1	6	1	2	0.002463051
	Probe	UniGene cluster	Gene	LocusLink ID		
	BG106477	278712	EIF4EBP2	1979		
GO:0007249	I-kappaB kinase/NF-kappaB cascade	1	16	1	9	0.001710245
	Probe	UniGene cluster	Gene	LocusLink ID		
	BC002704	21486	STAT1	6772		
GO:0042267	natural killer cell mediated cytolysis	2	10	2	4	0.00544291
	Probe	UniGene cluster	Gene	LocusLink ID		
	AA515698		TUBB2	10383		
	BC001002	356729	OK	203068		
GO:0006118	electron transport	22	612	22	285	0.004401978
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_001866	432170	COX7B	1349		
	NM_001865	70312	COX7A2	1347		
	NM_004373	180714	COX6A1	1337		
	NM_001862	1342	COX5B	1329		
	BC006229	1342	COX5B	1329		
	AI557312	1342	COX5B	1329		
	AA854966	433419	COX4I1	1327		
	NM_001861	433419	COX4I1	1327		
	NM_006004	285761	UQCRH	7388		
	NM_006294	131255	UQCRB	7381		
	AF313911	395309	TXN	7295		
	AK000161	10346	C10orf26	54838		
	BF572868	169358	DJ971N18.2	56255		
	NM_014402	146602	QP-C	27089		
	NM_013387	284292	HSPC051	29796		
	AV734582		TXNDC5	81567		
	NM_004786	114412	TXNL	9352		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	AK002110	90443	NDUFS8	4728		
	AF261090	15977	NDUFB9	4715		
	NM_005004	198273	NDUFB8	4714		
	NM_002490	274416	NDUFA6	4700		
	BC005374	154023	TXNDC4	23071		
GO:0006612	protein-membrane targeting	1	7	1	3	0.004123081
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_005625	164067	SDCBP	6386		
GO:0007516	hemocyte development	2	11	2	6	0.006949018
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_001022	381184	RPS19	6223		
	BE259729	381184	RPS19	6223		
GO:0019725	cell homeostasis	2	7	2	2	0.010899694
	Probe	UniGene cluster	Gene	LocusLink ID		
	AI275690		MCL1	4170		
	AW245401	293225	DEDD2	162989		
GO:0006325	establishment and/or maintenance of chromatin architecture	1	33	1	13	0.002067519
	Probe	UniGene cluster	Gene	LocusLink ID		
	BC003689	181163	HMGN2	3151		
GO:0046986	negative regulation of hemoglobin biosynthesis	1	3	1	1	0.007804694
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_014413	434986	HRI	27102		
GO:0006266	DNA ligation	1	3	1	2	0.007048425
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_001469	169744	G22P1	2547		
GO:0006597	spermine biosynthesis	1	3	1	1	0.007216244
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_001634	159118	AMD1	262		
GO:0010002	cardioblast differentiation	1	3	1	2	0.00777134
	Probe	UniGene cluster	Gene	LocusLink ID		
	AF521189	129801	ECE2	9718		
GO:0050823	peptide antigen stabilization	1	3	1	1	0.007705481
	Probe	UniGene cluster	Gene	LocusLink ID		
	AF029750	370937	TAPBP	6892		
GO:0046080	dUTP metabolism	1	3	1	1	0.00739225

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	Probe	UniGene cluster	Gene	LocusLink ID		
	U62891	367676	DUT	1854		
GO:0045993	negative regulation of translational initiation by iron	1	3	1	1	0.00760876
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_014413	434986	HRI	27102		
GO:0048227	plasma membrane to endosome transport	1	3	1	1	0.007187722
	Probe	UniGene cluster	Gene	LocusLink ID		
	AI215102	75618	RAB11A	8766		
GO:0048268	clathrin cage assembly	1	3	1	1	0.007362322
	Probe	UniGene cluster	Gene	LocusLink ID		
	BC006337	119591	AP2S1	1175		
GO:0006303	double-strand break repair via nonhomologous end-joining	2	12	2	4	0.007664614
	Probe	UniGene cluster	Gene	LocusLink ID		
	AA205834	257082	XRCC5	7520		
	NM_001469	169744	G22P1	2547		
GO:0006260	DNA replication	9	181	9	75	0.007055992
	Probe	UniGene cluster	Gene	LocusLink ID		
	AL517946	241567	RBMS1	5937		
	NM_003143	923	SSBP1	6742		
	AW613387	435067	ECGF1	1890		
	U62891	367676	DUT	1854		
	AV702810	436687	SET	6418		
	NM_004537	419776	NAP1L1	4673		
	AI888672	419776	NAP1L1	4673		
	AW148801	419776	NAP1L1	4673		
	AI985751	419776	NAP1L1	4673		
GO:0006935	chemotaxis	8	177	8	99	0.005728882
	Probe	UniGene cluster	Gene	LocusLink ID		
	U20350	78913	CX3CR1	1524		
	AA129773	324473	MAPK1	5594		
	R64130	2164	PPBP	5473		
	NM_016951	15159	CKLF	51192		
	AF096895	15159	CKLF	51192		
	AW613387	435067	ECGF1	1890		
	M21121	489044	CCL5	6352		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	NM_002985	489044	CCL5	6352		
GO:0006812	cation transport	1	323	1	148	0.00549913
	Probe	UniGene cluster	Gene	LocusLink ID		
	BG252666	418426	ATP8B1	5205		
GO:0019835	cytolysis	1	14	1	12	0.004318099
	Probe	UniGene cluster	Gene	LocusLink ID		
	J03189	1051	GZMB	3002		
GO:0000060	protein-nucleus import, translocation	2	20	2	5	0.006407126
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_002270	405954	KPNB2	3842		
	BC003572	439683	KPNB1	3837		
GO:0009306	protein secretion	5	54	5	20	0.011289406
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_000516	157307	GNAS	2778		
	NM_016592	157307	GNAS	2778		
	AF088184	157307	GNAS	2778		
	AI591100	157307	GNAS	2778		
	M94859	155560	CANX	821		
GO:0006890	retrograde transport, Golgi to ER	2	13	2	6	0.009352936
	Probe	UniGene cluster	Gene	LocusLink ID		
	AF029750	370937	TAPBP	6892		
	NM_007033	40500	RER1	11079		
GO:0006401	RNA catabolism	3	30	3	11	0.00862849
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_002939	130958	RNH	6050		
	NM_003730	388130	RNASET2	8635		
	NM_003730	388130	RNASET2	8635		
GO:0009966	regulation of signal transduction	1	18	1	11	0.004337645
	Probe	UniGene cluster	Gene	LocusLink ID		
	AF189289	279939	MTCH1	23787		
GO:0006323	DNA packaging	1	20	1	11	0.004068342
	Probe	UniGene cluster	Gene	LocusLink ID		
	AI817830	93231	MYST3	7994		
GO:0006879	iron ion homeostasis	2	43	2	12	0.004584021
	Probe	UniGene cluster	Gene	LocusLink ID		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	BG537190	433670	FTL	2512		
	BG538564		FTL	2512		
GO:0030517	negative regulation of axon extension	1	4	1	1	0.011396131
	Probe	UniGene cluster	Gene	LocusLink ID		
	AB015639	436349	RTN4	57142		
GO:0006930	substrate-bound cell migration, cell extension	1	4	1	4	0.011519555
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_005625	164067	SDCBP	6386		
GO:0045429	positive regulation of nitric oxide biosynthesis	1	4	1	1	0.010890501
	Probe	UniGene cluster	Gene	LocusLink ID		
	AF275719	74335	HSPCB	3326		
GO:0018105	peptidyl-serine phosphorylation	1	4	1	1	0.011603334
	Probe	UniGene cluster	Gene	LocusLink ID		
	BE622897		KIS	127933		
GO:0019987	negative regulation of anti-apoptosis	1	4	1	1	0.010636389
	Probe	UniGene cluster	Gene	LocusLink ID		
	AB015639	436349	RTN4	57142		
GO:0006376	mRNA splice site selection	3	26	3	7	0.013116792
	Probe	UniGene cluster	Gene	LocusLink ID		
	N25915	321390	CUGBP1	10658		
	AI472139	321390	CUGBP1	10658		
	NM_003769	77608	SFRS9	8683		
GO:0008584	male gonad development	2	15	2	12	0.012262454
	Probe	UniGene cluster	Gene	LocusLink ID		
	AL162047	422334	NCOA4	8031		
	AA167775	69855	D1S155E	7812		
GO:0006268	DNA unwinding	2	15	2	7	0.012302791
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_002128	434102	HMGB1	3146		
	AF283771	434102	HMGB1	3146		
GO:0009060	aerobic respiration	2	16	2	8	0.014430683
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_006004	285761	UQCRH	7388		
	NM_006294	131255	UQCRB	7381		
GO:0016246	RNA interference	2	11	2	2	0.019620665

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	Probe	UniGene cluster	Gene	LocusLink ID		
	N25915	321390	CUGBP1	10658		
	AI472139	321390	CUGBP1	10658		
GO:0007262	STAT protein nuclear translocation	1	5	1	3	0.015426963
	Probe	UniGene cluster	Gene	LocusLink ID		
	BC002704	21486	STAT1	6772		
GO:0000303	response to superoxide	1	5	1	1	0.015573422
	Probe	UniGene cluster	Gene	LocusLink ID		
	W46388	384944	SOD2	6648		
GO:0046685	response to arsenate	1	5	1	2	0.01509571
	Probe	UniGene cluster	Gene	LocusLink ID		
	AI523895	111801	ARS2	51593		
GO:0018279	N-linked glycosylation via asparagine	1	5	1	2	0.015049545
	Probe	UniGene cluster	Gene	LocusLink ID		
	BC002594	301882	DDOST	1650		
GO:0001315	age-dependent response to reactive oxygen species	1	5	1	1	0.015235917
	Probe	UniGene cluster	Gene	LocusLink ID		
	W46388	384944	SOD2	6648		
GO:0030150	mitochondrial matrix protein import	1	5	1	2	0.014822896
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_002156	79037	HSPD1	3329		
GO:0006613	cotranslational membrane targeting	2	13	2	6	0.01980687
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_003145	74564	SSR2	6746		
	BC000687	4147	TRAM1	23471		
GO:0007001	chromosome organization and biogenesis (sensu Eukarya)	6	116	6	58	0.013577495
	Probe	UniGene cluster	Gene	LocusLink ID		
	BC001124	180877	H3F3B	3021		
	NM_005324	180877	H3F3B	3021		
	Z48950		H3F3B	3021		
	NM_002106	119192	H2AFZ	3015		
	BF718636	119192	H2AFZ	3015		
	H51429		H2AFX	3014		
GO:0030097	hemopoiesis	2	49	2	17	0.008708902
	Probe	UniGene cluster	Gene	LocusLink ID		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	AK024789	271511	ZNF160	90338		
	NM_016633	274309	ERAF	51327		
GO:0019735	antimicrobial humoral response (sensu Vertebrata)	8	155	8	79	0.019382698
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_001311	70327	CRIP1	1396		
	NM_003403	388927	YY1	7528		
	NM_000560	443057	CD53	963		
	AV717590	444105	ENTPD1	953		
	NM_021130	356331	PPIA	5478		
	BC005982	356331	PPIA	5478		
	AI708767	356331	PPIA	5478		
	BE217880	362807	IL7R	3575		
GO:0006096	glycolysis	5	80	5	39	0.0180812
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_002300	234489	LDHB	3945		
	BE042354		LDHB	3945		
	NM_005566	2795	LDHA	3939		
	NM_000291	78771	PGK1	5230		
	NM_001428	433455	ENO1	2023		
GO:0019370	leukotriene biosynthesis	2	18	2	12	0.018251413
	Probe	UniGene cluster	Gene	LocusLink ID		
	J02959	81118	LTA4H	4048		
	NM_001629	100194	ALOX5AP	241		
GO:0000018	regulation of DNA recombination	2	11	2	5	0.027256515
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_014863		GALNAC4S-6ST	51363		
	BE217880	362807	IL7R	3575		
GO:0009605	response to external stimulus	1	14	1	7	0.011452982
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_014413	434986	HRI	27102		
GO:0016481	negative regulation of transcription	4	84	4	30	0.012250866
	Probe	UniGene cluster	Gene	LocusLink ID		
	AF130054	512387	LRRFIP1	9208		
	NM_007273	444499	REA	11331		

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	U64661		RNF12	51132		
	AW245401	293225	DEDD2	162989		
GO:0009303	rRNA transcription	1	6	1	2	0.02045279
	Probe	UniGene cluster	Gene	LocusLink ID		
	BE542815	445977	GTF3A	2971		
GO:0006388	tRNA splicing	1	6	1	4	0.019430151
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_024075	15580	LENG5	79042		
GO:0009399	nitrogen fixation	1	6	1	3	0.019815451
	Probe	UniGene cluster	Gene	LocusLink ID		
	AL161952	442669	GLUL	2752		
GO:0045577	regulation of B-cell differentiation	1	1	1	1	0.052592889
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_014863		GALNAC4S-6ST	51363		
GO:0008295	spermidine biosynthesis	1	6	1	3	0.020333879
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_001634	159118	AMD1	262		
GO:0030323	respiratory tube development	1	2	1	1	0.036815022
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_016217	6679	HECA	51696		
GO:0007612	learning	1	6	1	2	0.019269571
	Probe	UniGene cluster	Gene	LocusLink ID		
	M14333	390567	FYN	2534		
GO:0006302	double-strand break repair	1	21	1	8	0.010649617
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_006384	135471	CIB1	10519		
GO:0007281	germ cell development	2	20	2	6	0.022163696
	Probe	UniGene cluster	Gene	LocusLink ID		
	N25915	321390	CUGBP1	10658		
	AI472139	321390	CUGBP1	10658		
GO:0030503	regulation of cell redox homeostasis	1	7	1	3	0.024158899
	Probe	UniGene cluster	Gene	LocusLink ID		
	BC005374	154023	TXNDC4	23071		
GO:0016486	peptide hormone processing	1	7	1	3	0.024346662

GO ID	Function Name	Unique Input Total	Unique Reference Total	Unique UniGene Total	Unique Reference UniGene Total	Corrected P-Value
	Probe	UniGene cluster	Gene	LocusLink ID		
	AF521189	129801	ECE2	9718		
GO:0015937	coenzyme A biosynthesis	1	7	1	4	0.024927882
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_024960	203589	PANK2	80025		
GO:0050672	negative regulation of lymphocyte proliferation	1	5	1	1	0.029276672
	Probe	UniGene cluster	Gene	LocusLink ID		
	NM_007161	436066	LST1	7940		
GO:0001508	regulation of action potential	1	7	1	3	0.024601601
	Probe	UniGene cluster	Gene	LocusLink ID		
	L12387	422340	SRI	6717		
GO:0015721	bile acid transport	1	4	1	2	0.033444169
	Probe	UniGene cluster	Gene	LocusLink ID		
	BG252666	418426	ATP8B1	5205		
GO:0008632	apoptotic program	2	26	2	9	0.024021339
	Probe	UniGene cluster	Gene	LocusLink ID		
	AL515918	404814	VDAC1	7416		
	AI275690		MCL1	4170		
GO:0006378	mRNA polyadenylation	2	22	2	7	0.027058891
	Probe	UniGene cluster	Gene	LocusLink ID		
	AI734929	387804	PABPC1	26986		
	BF797555	201085	PAPOLA	10914		