

A COMPARATIVE ANALYSIS OF GENE EXPRESSION AMONG CASTES OF THE
TERMITE *RETICULITERMES FLAVIPES* USING EXPRESSED SEQUENCE TAGS (ESTS)
AND A MICROARRAY

by

MATTHEW MICHAEL STELLER

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Approved by:

Major Professor
Srini Kambhampati

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Abstract

Termites (Isoptera) are separated into morphologically and behaviorally specialized castes of sterile workers and soldiers, and the reproductive alates. Previous research on eusocial insects has indicated that caste differentiation has a genetic basis. Although much has been studied about the genetic basis of caste differentiation and behavior in the honey bee, *Apis mellifera*, termites remain comparatively understudied. Therefore, my objective was to compare the gene expression patterns of different castes of the termite *Reticulitermes flavipes* based on EST analyses and a microarray.

Soldier, worker, and alate caste and two larval life stage cDNA libraries were constructed, and ~15,000 randomly chosen clones were sequenced to compile an EST database. Putative gene functions were assigned based on a BLASTX Swissprot search. Categorical expression patterns for each library were compared using the *in silico* methods of BLAST2GO and r-statistics. I chose 2,240 unique-ESTs based on their putative function and sequence quality, which I used to fabricate a Combimatrix microarray. I used the microarray to compare expression levels between workers and soldiers from Kansas and Florida populations.

Seventy to ninety percent of the sequences from the ESTs of each caste and life stages had no significant similarity to those in existing databases. All libraries contained sequences with putative reproductive functions, which was unexpected in the non-reproductive soldier and worker castes. Sequences of interest that showed a putative bias among castes include a viral protein in soldiers and a possible chemosensory protein in alates, which may be involved in termite reproductive functionality or communication. The microarray showed increased

expression in the soldier caste of a sequence that matched tropomyosin and an increased expression level of a sequence that matched a PDZ-domain containing protein in some worker samples.

This study leads to several candidate genes of potential caste specific function, which can be further tested using functional analysis and between the different castes and life stages of *R. flavipes*. These genes include the sequences similar to *pebIII* and *RGS-GAIP*. I have also expanded upon the available sequences for this termite and utilized the r-statistic *in silico* method for the first time to putatively compare gene expression in the different castes of a eusocial insect. The *in silico* analysis allowed us to identify several genes which may show biased expression patterns in the different cDNA libraries and which may reveal caste-specific expression controlling important functions after further analysis. These candidates include: an alate-biased gene, which had a predicted function of neurotransmitter secretion and cholesterol absorption as well as a late larval-biased gene which was predicted to be involved in protein biosynthesis and ligase activity.

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CHAPTER 1 - Analysis of Caste-Specific Gene Expression Patterns

INTRODUCTION

Examining the genetic basis underlying social development and behavior has been termed sociogenomics (1). Sociogenomics is predicated on two observations: “social life has a biological basis and thereby is influenced by genes and evolution” and “molecular functions of many genes are conserved across species” (1). Therefore, it is possible to examine social organisms such as termites, honey bees, ants, and social wasps in an ecological and molecular context to better understand the genetic basis, function, and origins of social behavior.

Termites (Isoptera) are a large group of diverse eusocial insects. Although eusociality is believed to have evolved only once in Isoptera, the ~2600 species show enormous diversity in life history, behavior, colony composition, morphology, physiology, ecology, and biogeography (2,3). *Reticulitermes* (Rhinotermitidae) species are found throughout much of the contiguous United States, with introduced populations in Europe, South America, and the Bahamas (4). *Reticulitermes flavipes* (Kollar) is the most common species in the United States. *R. flavipes* colonies, like other eusocial insects, consist of morphologically and behaviorally specialized castes. All individuals emerge from eggs as larvae, beyond which the development is somewhat flexible in that larvae may develop into nymphs and subsequently into dispersing alates, or into the sterile workers or soldiers (2). Workers maintain the termite nest, build tunnels, and take care of the brood, whereas soldiers are thought to defend the colony and possibly communicate general colony fitness. Workers and nymphs of this species may eventually develop into supplementary reproductives under the appropriate conditions (2,3).

Historically subterranean termites have been difficult to study, mainly due to the complicating factor of their cryptic living conditions and amorphous nest structure (2,5). However, the advent of genomic and bioinformatic methods has provided new opportunities to study these organisms. A macroarray study of *R. flavipes* (6) demonstrated the differences in gene expression differences among the different castes. Genes that exhibited differential expression between workers and soldiers included salivary cellulases, endoglucanases, tubulins, and troponins (6).

Some general trends found in other sociogenomic studies of additional species of termites include higher expression of the mitochondrial cytochrome oxidase-III subunit in workers and nymphs of *R. santonesis* (7); increased cytochrome P450 levels after methoprene application in soldier and presoldier fat body in *Hodotermopsis sjostedti* and *Nasutitermes takasagoensis* (8,9); and a gene found to be specifically expressed in *H. japonica* soldier mandibles termed SOL1 thought to be involved in soldier specific behavior (10).

In the well-studied eusocial honey bee, *A. mellifera*, there is a trend for behaviorally associated genes showing a C+G bias within promoter regions when compared to *Drosophila melanogaster* and also show more *cis* regulatory elements (11) as well as high levels of expression of ribosomal and hexameric storage proteins in queen and worker cDNA libraries (12). An EST analysis found that workers showed a bias for putative cell differentiation and hydrolase activity, while queens exhibited an upregulation of genes involved in metabolism and oxidoreductase activity (13).

Given that there has been no large-scale effort to identify expressed genes in termites my first objective was to characterize *R. flavipes* genes by analyzing an EST database of ~15,000 clones from three cDNA libraries constructed from workers, soldiers, and alates as well as two

cDNA libraries constructed from early and late termite larval stages. My second objective was to use a microarray based on a subset of the EST library to quantify gene expression differences between soldiers and workers, and validate these differences using quantitative real-time polymerase chain reaction (q-PCR).

MATERIALS AND METHODS

Termites

For the construction of the cDNA libraries *R. flavipes* workers, soldiers, alates, and larval stages were collected from a single colony on the campus of the University of Florida, Gainesville. The larvae were divided into early (putatively stages 1-2) and late (putatively stages 3-4) stages based on size. Several hundred individuals of each caste/stage totaling about 2 gm of wet weight were obtained and stored at -80°C until used. Termites from the same colony as those used for cDNA library construction were also used for the microarray analysis; in addition, I also collected *R. flavipes* workers and soldiers from a colony near Pillsbury Crossing (near Manhattan, Kansas).

cDNA Libraries

mRNA isolation, cDNA synthesis and library construction was undertaken by AGCT Corp. (Cranston, RI). The cDNA was cloned into pBluescript II SK+ vector after digestion with *EcoRV* and *NotI*. Libraries were plated on LB medium with 50mg/litre ampicillin and grown at 37°C overnight. Several hundred colonies were randomly sampled from the plates for further processing and sequencing. Colonies were placed in 150µl liquid LB+ampicillin medium, grown overnight at 37°C, and stored at -80°C after adding 20µl of sterile glycerol. The colonies were then shipped on dry ice to the University of California-Riverside sequencing facility for sequencing using the T3 primer for 5'-ends of the clones.

Sequence Analyses

Using Sequencher (v4.7, Gene Codes Corp, Ann Arbor, MI), I removed the vector sequence and trimmed ends using program defaults. Sequences shorter than 150 bp were discarded from further analysis after trimming. ESTs were organized into contiguous sequences using the default parameters in EGassembler (<http://egassembler.hgc.jp/>), highly repetitive sequences were masked using the *Drosophila* RepBase library in EGassembler.

New gene discovery rate for each library was estimated by dividing the number of contiguous sequences by the total number of singleton sequences. Minimum average sequence insert sizes of cDNA clones were estimated by dividing the total number of basepairs sequenced by the number of ESTs in each library the maximum length is limited by the length of sequence. Thus, the actual length of insert is likely underestimated. Both singletons and contigs were assigned putative functions using a batch BLASTX reference search from the non-redundant protein database using BlastStation (v2.61, TMSoftware, Arcadia, CA), with an e-value $\leq 1e^{-10}$. Genes assigned putative housekeeping roles were identified using a list derived from Eisenberg et al. (15). Gene ontology (GO) comparisons were performed using BLAST2GO annotations (16). All EST sequences were submitted to the EST database, dbEST, at <http://ncbi.nlm.nih.gov/dbEST/>.

In silico transcript abundance

Relative transcript abundance in the ESTs derived from each caste-specific cDNA library was analyzed using r-statistics (17). The analysis is based on the entropy of partitioning genes among multiple cDNA libraries into contiguous sequences, and includes a quantitative measure of the degree of confidence in the results termed the r-value (17). I analyzed 20 sequences with the highest r-value composed of 10 contigs that returned a BLASTX hit with an e-value $\leq 1e^{-10}$

and 10 that had no BLAST hit or a hit with an e-value $\geq 1e^{-10}$. I identified contiguous sequences by investigating the frequency of R among the contigs and chose the cutoff for genes of higher interest looking at where the slope of the line was not close to 1, similarly to the method used in Stekel et al., 2000 (Fig 1.6). Putative protein functional analysis of the latter group was performed using the protein function predictor (<http://dragon.bio.purdue.edu/pfp>), which pools sequences with similar structural motifs and assigns GO terms, to obtain an initial indication of gene function. I further validated the r-value measure of significant difference using a chi-squared analysis.

Microarray Construction and Gene Selection

For the microarray fabrication, I chose genes whose putative function was either coding for various enzymes or transcription factors. Of the 2,240 genes chosen for the microarray, 11 genes (cytochrome c oxidase subunit 1; actin-5C; cytochrome b; cytochrome c oxidase subunit 2; nucleotide-binding protein 2; 40S ribosomal protein S23; 60S ribosomal protein L10; NADH dehydrogenase 1 alpha subcomplex subunit 4; 40S ribosomal protein S14; cuticle protein 16.5, isoform B; histone H3.2) were utilized as potential positive controls, and evaluated after hybridization for constant expression patterns between arrays. Of the remaining genes 697 had an e-value $\leq 1.0e^{-10}$, 87 had e-values falling between $1.0e^{-5}$ and $1.0e^{-9}$, 846 had an e-value $< 1.0e^{-5}$, and 599 returned no BLAST hits and were chosen as they were expected to be termite specific sequences, because they were not found in other organisms, with potential to influence caste-specific traits. Oligonucleotide probes (35-mers; one oligonucleotide per gene) and CustomArray 4x2K microarrays were designed and constructed for the 2,240 genes of interest by Combimatrix, Corp (Mukilteo, WA).

Total RNA isolation, Labeled-cDNA synthesis, and Microarray Hybridization

I isolated total RNA from 10 whole body preparations of workers and soldiers using a modified TRIZOL reagent protocol, adding an RNA precipitation solution (0.8M disodium citrate and 1.2M sodium chloride) for better extraction efficiency during the precipitation phase of the protocol. cDNA synthesis, amplification, purification, and labeling was performed using the Amino Allyl MessageAmpTM II aRNA Amplification Kit (Ambion, Inc. Austin, TX) and coupled to Cy3 dye for both castes tested. Labeled aRNA was hybridized to each array by first fragmenting the RNA using an RNA fragmentation solution (1M Tris Acetate pH 8.1 (2ml), KOAc (0.49g), MgOAc (0.32g), and water to 10ml). I took 1.2 μ l of the fragmentation solution and added 2 μ g of labeled RNA, and added water to a total volume of 6 μ l. I incubated the solution at 95°C for 20 minutes and placed it on ice. Slides were prepared for hybridization using pre-hybridization solution (2X Hybridization Solution (75 μ l), Nuclease Free Water (51 μ l), 50X Denhardt's solution (15 μ l), denatured salmon sperm (1.5 μ l), and 1% SDS (7.5 μ l)), and placed into a hybridization oven at 65°C for 10 minutes on gentle rotation. I then added 30 μ l of hybridization solution (2X Hybridization Solution (15 μ l); DI formamide (7.5 μ l); fragmented RNA (6 μ l); denatured salmon sperm (0.3 μ l); 1% SDS (1.2 μ l); nuclease free water to 30 μ l) to each array. The array was incubated at 45°C in a hybridization oven on gentle rotation overnight. Arrays were washed using progressively lower concentrations (6X, 3X, 0.5X) of SSPET solution (20X SSPE, 10% Tween-20, and Nuclease-free water) and finished by washing with a PBST solution (10X PBS (2ml); 10% Tween-20 (100 μ l); Nuclease-free Water (7.9ml)) until slides were imaged. I included 4 biological replicates each of the worker and soldier caste for a total of 8 hybridizations.

Microarray Imaging

Imaging was performed using an Axon GenePix 4000B Scanner at 500 PMT at the Kansas State University Integrated Genomics Facility; the image was acquired using GenePix (v6.1, Molecular Devices, Union City, CA). Digitized values for each spot were normalized and analyzed using GeneSpring (v10.0, Agilent Technologies, Santa Clara, CA). Slides were first normalized to the 50th percentile and then normalized to three internal positive controls (Contig456, MMS083_C01, and MMS159_D11). Analysis was performed on 3 biological replicates of workers and 4 biological replicates of soldiers, one of the microarrays had a high amount of background noise when visualized and was unusable for my calculations and discarded. Comparisons of fluorescence between worker and soldier microarrays were performed using a Student's t-test and p-values obtained for the various resultant fold-changes.

Quantitative PCR for Validation of Microarray Results

Results were verified using qPCR on 10 genes that had the highest up- or down regulation with ≥ 2 -fold change. Primers were successfully designed for 9 of the 10 genes (Table 1.1) using Beacon Designer (v7.5, Premier Biosoft International, Palo Alto, CA). Individual primer efficiency was quantified using a total of three dilutions (0.2X, 0.04X, 0.008X) of worker cDNA for each primer using three technical replicates; primer efficiency was determined using the iCycler software (v3.1.7050, Biorad Inc., Hercules, CA). Worker and soldier template expression levels were standardized using the housekeeping gene β -actin, which was previously shown to be the least variable reference gene for *R. flavipes* (30). The PCR program used in the analysis included 95°C for 5 minutes, 40 cycles of 95°C for 15 seconds, 55°C for 30 seconds, and 70°C for 30 seconds, after which time the data were collected. Efficiency was calculated and used in the qPCR analysis of worker/soldier expression ratios as described (21). qPCR for each

gene included 3 technical replicates using both worker and soldier total RNA from microarray experiments.

RESULTS

General Library Analysis

I sequenced 4031 worker, 3836 alate, 3548 soldier, 2111 early larval stage, and 1733 late larval stage cDNA clones from each library for a total of 15,259 clones. Each cDNA library had a minimum average insert size ranging from 570 to 1086 bp, gene discovery rate ranged from 47% to 60% and is generally expected to decrease with increased sequencing (Table 1.2). Each EST library had a high proportion of sequences with no known BLASTX hit, of the remaining sequences the worker and late larval libraries had the highest proportion of ribosomal sequences and both larval libraries exhibited the highest level of sequence redundancy after the BLASTX analysis (Table 1.2). Each library contained between 5% and 16% of sequences that had a significant e-value and were used in the GO analysis.

Sequence Analysis

Analysis of the sequences using level two cellular component GO putative terms showed similar proportions across castes with cell part, cell, and organelle being the most frequent term assigned to sequences (Fig 1.1A-E). The GO analysis of level two molecular function terms showed, in general, that the binding term was the largest proportion in each library followed by catalytic activity, except for the late larval library where the pattern was reversed (Fig 1.2A-E). The final GO category I investigated was that of biological process. The proportion of level two terms showed an abundance of those associated with cellular and metabolic processes (Fig 1.3A-E). Interestingly, I also discovered a portion of sequences that were putatively associated with reproductive functionality, even in sterile castes. The alates showed the highest number and

variety of sequences assigned with a reproductive term, but soldiers also exhibited a large number of genes putatively associated with reproductive functions (Fig 1.4).

Due to the small number of BLASTX hits, I was unable to obtain many GO terms in proportion to the number of total EST sequences to use in the GO analysis. Therefore, I chose a less stringent significance threshold than normally utilized with p-values ≤ 0.15 ; no differences were found with a smaller p-value threshold for significant GO abundance between libraries.

In Silico Analysis- Significant BLAST Hits

As previously mentioned, the r-statistic analyses were split into two separate groups of sequences, those that returned a significant BLASTX hit, and those that did not. For the first group, (Table 1.3) the soldier library showed a bias of sequences that putatively matched a protein from the cricket paralysis virus. Two separate contigs with an abundance of soldier and alate transcripts showed different sequence identity to the same ejaculatory bulb-specific protein in *Drosophila melanogaster* [Flybase:CG11390]. Three other contigs showed a bias within the alate library that matched closely with cytochrome c oxidase (*Blatella germanica*), cellulase b (*Cellulomonas fimi*), and ATP synthase subunit a (*Drosophila simulans*). A number of contigs also showed overrepresentation from the early and late larval stage libraries and included cytochrome b (*Drosophila sechellia*), tropomyosin (*Dermatophagoides farinae*), troponin c (*Tachypleus tridentatus*), cytochrome oxidase subunit 3 (*Drosophila melanogaster*), and 60s ribosomal protein l31 (*Spodoptera frugiperda*).

In Silico Analysis- Protein Prediction

The second in silico analysis of the EST libraries (Table 1.4) was analyzed using the protein function predictor. Proteins associated with anti-bacterial humoral response and

translational elongation were two protein functions predicted from contigs with a transcript bias in the soldier cDNA library (Table 1.4). Putative functions of neurotransmitter secretion, cholesterol absorption, cell adhesion, and hydrolase activity were predicted for contigs with a transcript bias in the alate cDNA library. Predicted protein functions of protein synthesis, ligase activity, regulation of transcription, metabolism, stress response, cell adhesion, and spermatogenesis were discovered in contigs with a transcript bias of the late larval stage cDNA library.

Microarrays Combined

I analyzed the microarray results together and separately based on location of sampling of termites to detect potential differences in gene expression between Kansas and Florida samples, while evaluating gene expression patterns conserved across populations. I found one gene expressed at 42-fold greater (p-value <0.05) in the worker caste, this gene returned no BLASTX hit with an e-value <1.0E⁻¹⁰. Among the remainder, I found 141 genes that showed >2-fold higher in soldiers as compared to workers (Table 1.5) and 411 with >2-fold higher in workers versus soldiers (Table 1.6). Due to the small number of significant expression differences (p-value <0.05) between castes in my combined location analysis, I examined fold-change differences in the microarrays. I set aside the top and bottom 5 fold-change genes as possible genes of interest to validate using qPCR. The top fold-change sequences in worker expression had no known function and did not match any proteins in the BLASTX database (Table 1.6). Those genes that exhibited lower expression in workers relative to soldiers matched tropomyosin (99% amino acid identity), RGS-GAIP (68% amino acid identity), probable exocyst complex component 4 (57% amino acid identity), and troponin C isoform 1 (81% amino acid identity). The fifth sequence had no matches in the BLASTX query (Table 1.7).

Microarrays of Florida Samples

My second analysis of the data was of only the Florida microarrays as I had insufficient replicates of successful arrays from Kansas for accurate analysis. I found 20 significant ($P < 0.05$) genes with expression differences (Table 1.8) 11 of which were overexpressed in workers and 9 that were overexpressed in soldiers. Expression differences between these two castes ranged between 1.0 and 1.4 fold.

Quantitative PCR for Validation of Microarray Results

Expression patterns were variable across biological replicates for all genes of the combined microarray dataset except for troponin C, which was consistently overexpressed in soldiers across all samples (Table 1.9). Although the putative RGS-GAIP exhibited variable expression patterns in several biological replicates of the qPCR validation, its expression was greatly increased in two of the worker samples as compared to soldiers (12- and 4-fold expression difference).

DISCUSSION

General Library Analysis

The gene discovery rate of sequences for each library ranged from 47% to 60%, which is indicative of a good rate of unique genes found for each caste; however, it does indicate a need for more sequencing from each library. The high level of unknown genes in this analysis indicates a high probability of unique sequences from *R. flavipes* specifically which are not currently available is most likely due to the reduced number of related sequences in public databases.

About 12% of the sequences in the worker and late larval libraries were associated with ribosomal function; however a previous study on termites (20) found lower levels of rRNA gene expression in workers; an exception to this general trend was an 18-S-rRNA-like sequence. My results may be somewhat biased as I was not specifically testing expression levels and focused on transcript abundance of these sequences in workers.

In the GO analysis I found that a large proportion of genes in all the libraries were associated with reproductive function. This may reflect the possibility that the workers have the ability to express sequences that can be co-opted under certain conditions to allow them to reproduce, such as in the absence of a primary reproductive; however, it is also possible that these genes have other functions and are not restricted to reproductive function. Most of the other terms involved binding or translation/transcription control, which I took into account while choosing sequences for construction of the microarray. The fact that most of the GO term representation patterns were repeated among libraries is understandable as I hypothesize that each termite shares the same genetic code, but regulation of post-transcriptional expression most

likely causes much of caste-specific differences. More rigorous testing of this hypothesis is needed before I can draw any general conclusions from these patterns.

This general trend of expression may not be maintained across all populations of termites as it was shown between Kansas and Florida populations in this study. I also did not control for sample selection, choosing termites randomly without concern for sex, age, or environmental conditions, which also could have obscured some caste-specific expression patterns. In addition, the implications of expression differences based on ESTs alone are tentative and may not be reflective of an actual expression difference.

In Silico Analysis

The most bias from the first grouping of sequences used for the *in silico* analysis was composed mostly of soldier singletons which matched a viral protein; this raises the possibility of viral contamination in the soldier library, or soldiers could have a protein similar to the sequence of the viral protein that is expressed at a higher level than in the other castes.

Two contigs that showed transcript over-representation in soldier and alate libraries matched a protein that was similar to an ejaculatory bulb-specific protein in *D. melanogaster* *pebIII*. This protein was implicated in odorant binding due to its expression in glands that produce pheromones in male flies and its sequence similarity to a odorant binding protein in *Mamestra brassica* that has been implicated in sexual attraction and repulsion (22); however, recent research has also reported this protein from fly heads (23), the female reproductive tract (24), and in response to viral challenge (25). This sequence was also found to match a chemosensory protein in *A. mellifera* (AmelCSP3); however, the expression pattern of this protein after a Northern blot analysis seemed to indicate a function in cuticle maturation based on its timing of expression (26). The termite sequence showed a sequence identity to the *D.*

melanogaster sequence [REFSEQ:NP_524966.1] of 55% (e-value: $2.00e^{-28}$) and the *A. mellifera* sequence showed a 52% identity to the *R. flavipes* sequence I recovered (e-value: $2.00e^{-26}$). It is unknown what role these proteins play in termites, but they are about 97% similar to each other, with a larger proportion of the transcripts being of alate origin, implicating that alates have a higher number of transcripts produced than the soldiers. One intriguing possibility is that the alates produce this as a method of reproductive suppression of other castes, or it is possibly involved in termite communication.

Three other genes showed a significant transcript bias in the alate library. The first gene was most similar to the mitochondrial cytochrome c oxidase subunit. Higher levels of cytochrome c oxidase expression were previously discovered in dealate ants and hypothesized to be involved with programmed cell death of wing cells (27). The second gene matched the cellulase b gene in the bacteria *Cellulomonas firmi*; the prevalence of this in alates may simply reflect higher levels of symbiont load in alates relative to other castes as the gene is of bacterial origin. One reason why this pattern may be seen is that alates need extra stores of symbionts to establish the bacteria in workers and soldiers in a nascent colony, to assist in cellulose degradation (3). The final gene matched an ATP synthase subunit a gene that could be an indicator of higher initial energetic needs of colony founders.

The remaining genes analyzed showed biases primarily in the early larval stage libraries. Most of the genes that matched are involved with general energy production and muscle contraction (28). These could indicate a higher need for energetic reserves and muscle contraction as larvae perform general colony tasks rather than specialized tasks such as those by older workers and soldiers.

My other grouping of r-statistic analysis was of genes that showed a library bias of singleton composition that did not have a significant BLAST hit, but which was submitted for a putative function prediction based on the protein translation.

My results suggested that soldiers have a high level of expression of genes putatively involved in immune function, whereas in other eusocial insects, the pattern of increased immune investment was seen in the reproductive caste (29). It is important to consider that this sequence was on the lower end of my r-value acceptance levels, and thereby its representation was not as biased for one caste or the other as those with higher r-values. These predicted functions may also indicate that soldiers invest more in antibacterial responses because termites in general are exposed to bacteria and other microbes in the soil and wood. This abundance may also indicate that the soldiers used in cDNA library construction may have been recently challenged by a microbial infection.

The two transcripts with an alate bias included proteins putatively involved in neurotransmitter secretion, cholesterol absorption, cell adhesion, and hydrolase activity. These may indicate a higher level of investment by the alates in brain and cell-cell communication that may be helpful in colony establishment and mate recognition. Many of the transcripts from late larval stage library have a putative function involved with energetic needs and metabolism. I also found a gene predicted to be involved with spermatogenesis in the late larval library, but as workers can eventually develop into reproductive individuals (2), it is possible that late larval stages express some proteins with putative reproductive functions in case there is an opportunity to become secondary reproductives (2). A general pattern in my analysis was the existence of genes putatively associated with reproduction that were discovered even within sterile caste libraries. This is unexpected but it is possible that these genes are regulated post-transcriptionally

or they exist in sterile castes because sterile castes can differentiate into supplementary reproductives under certain conditions (2). Further analysis of these larval individuals is needed to assess reproductive capabilities and eventual caste determination.

Previous studies have implicated two hexamerins (*Hex-I* and *Hex-II*) in soldier-worker differentiation in *R. flavipes* (19,30). I recovered both hexamerin I and II in worker, alate, and early larval stage libraries and hexamerin-I in the soldier library; however they did not exhibit differential expression in the *in silico* analyses, most likely because I was not examining the transitional form between soldiers and workers, as was done in the previous studies.

Microarrays of Combined Samples

The higher expression levels of tropomyosin seen in soldier populations is most likely due to the larger size of individuals of that caste when compared to workers and the presence of strong musculature associated with mandible function. The other pattern of interest seen in the analysis was the higher expression level of the RGS-GAIP sequence, which contains a single PDZ domain, in some of the worker comparisons, which is similar to kermit in *D. melanogaster* [REFSEQ:NM_143771.2]. PDZ domains are well conserved across kingdoms being found in many diverse taxa. The PDZ domain-containing proteins are found in many neuronal junctions, have been implicated in proper function of tight junctions, and the construction and maintenance of molecular and neuronal signaling complexes (31-34). They have been found to accomplish this by bringing signaling components in closer proximity to one another allowing for more efficient signaling, and can act on polarized epithelial cells for proper orientation to avoid tumorous cell growth (31). The *D. melanogaster kermit*, was shown to affect planar polarity of pupal wing development (35). *Kermit* was originally isolated from *Xenopus laevis* and was found to be expressed throughout its development. It was found to interact most strongly with frizzled-

3, and when *kermit* functionality was blocked it inhibited neural crest induction, while over-expression of the specific frizzled sequence lead to an overwhelming translocation of marked *kermit* to the membrane, with very little in the cytoplasm (36). The suspected homologue of *kermit* in humans is GIPC1 [GenBank:AF089816] and has been found to be highly expressed in breast cancer cells (37). In addition, GIPC1 was also found to bind myosin VI (38) and possibly interact with another protein (APPL) through interactions with other GIPC1 monomers (39) forming a complex, which is proposed to shuttle clatherin-coated vesicles and be involved with TrkA signaling (40). These findings all seem to suggest a possible role for this protein in cellular growth and polarity in insects and a possible signalling role in humans. In termites its role could be similar, by some undiscovered trigger workers will develop into soldiers producing the characteristic of enlarged head capsules and body size. It is tempting to interpret the lower level of expression of this protein in some soldier samples as some mechanism for maintaining or creating the new body plan of soldiers during the worker-soldier transition. However, this cDNA sequence needs to be fully sequenced and qPCR experiments on samples of workers that I know are currently transitioning to the soldier caste are needed. The implications of fully characterizing this gene and understanding its functionality would help us to understand how termites can undergo such a radical change and to better realize the genetic underpinnings behind controlled cell division and expansion.

The remaining sequences from the qPCR validation did not show an expression difference of greater than 2-fold and were not consistent between samples. The variable expression patterns found in the qPCR of the combined locale array set can be explained by differing expression produced by exposure to different environmental conditions, as well as differences produced by my random sampling design pooling 10 individuals from the same

sample which were most likely composed of different sexes and ages, which was done in order to extract sufficient cDNA for the microarray hybridization.

Microarray Analysis of Florida Samples

Although I found several significant expression differences, the fold-change between workers and soldiers was low (Table 1.9). Further expression analysis of these 20 sequences is needed using qPCR methods to confirm the validity of these patterns seen in the worker and soldier comparisons. By separating my analysis by location I decreased the amount of biological replicates being compared and this may have introduced some bias in the analysis and indicates that additional Florida replicates are needed. I was unable to effectively analyze the Kansas microarrays due to the small number of successful array replicates, but an increased number of microarrays with specific focus on each location will yield better results.

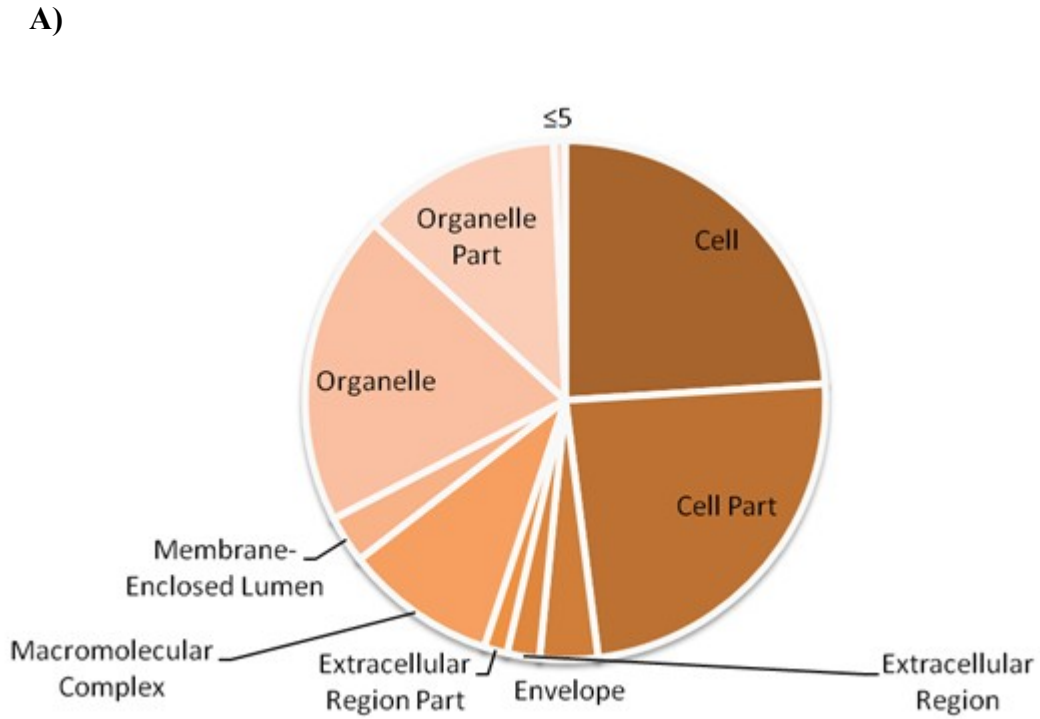
CONCLUSION

In conclusion, I presented the EST analysis of 15,351 randomly chosen cDNA fragments from 5 different cDNA libraries. As indicated, relative to the honey bees, little is known about the genetics of caste differentiation and behavior in the termites. Therefore, the EST database reported here is likely to be a valuable resource for future studies on the sociogenomics of termites in general and *R. flavipes* in particular. In addition, the in silico analysis revealed several patterns that could be the subject of future functional genomics studies. For example, the caste-biased transcript abundance of several genes indicates that these proteins may be playing specialized roles in each of the castes or developmental stages. The presence of proteins putatively involved in reproduction in sterile castes is intriguing. It is possible that these proteins

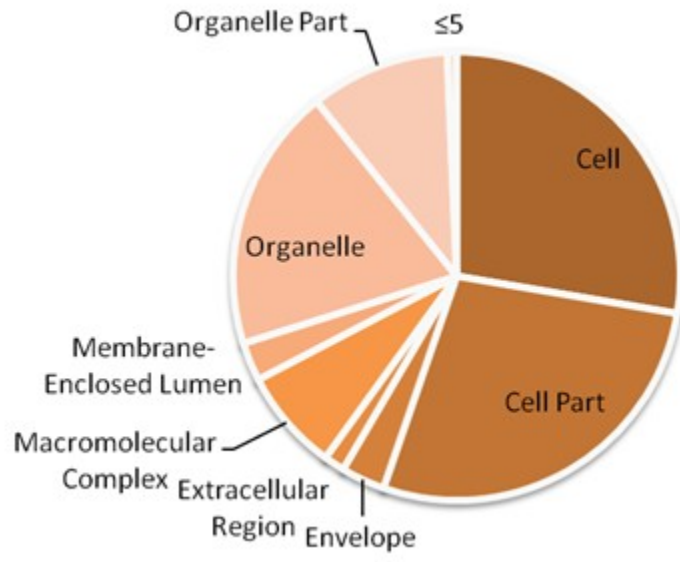
play multiple roles or they may be subject to post-transcriptional or post-translational modifications.

Figures and Tables

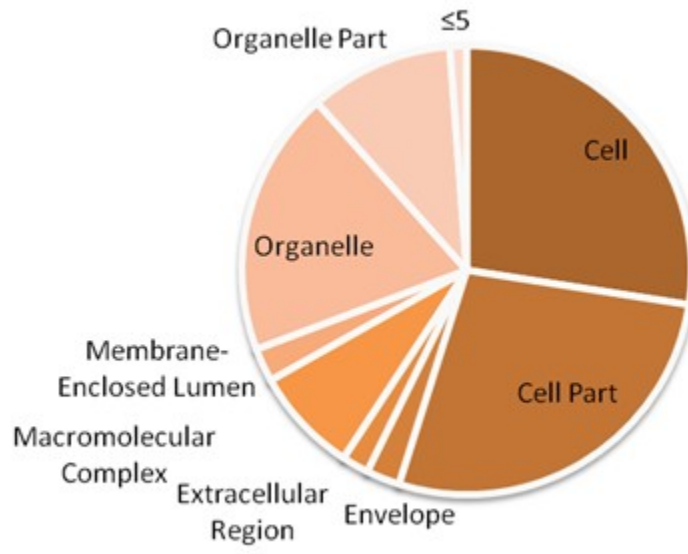
Figure 1.1 Proportions of GO cellular component terms (level two) in each EST library sequences annotated by Blast2GO A) Soldiers; B) Alates; C) Workers; D) Early Larval; E) Late Larval



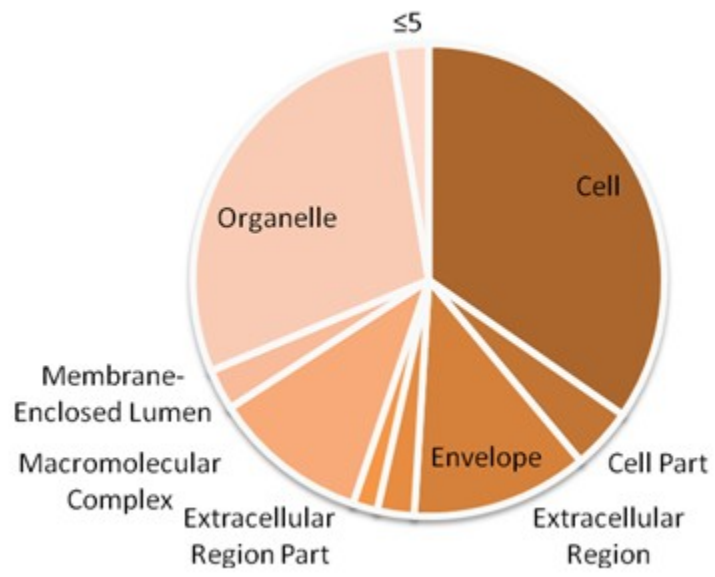
B)



C)



D)



E)

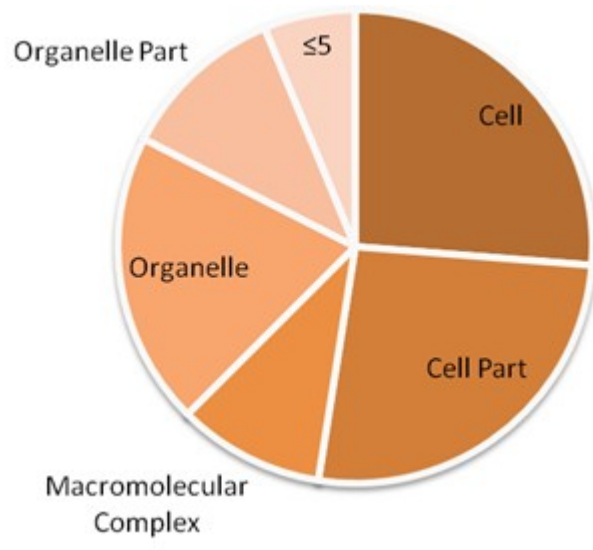
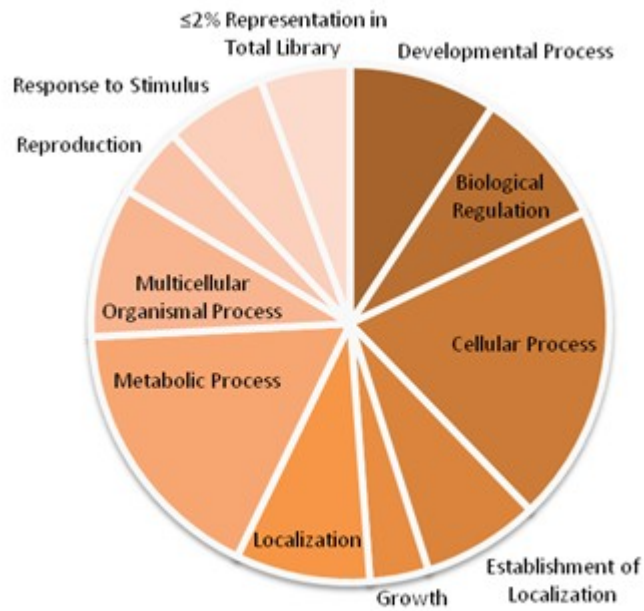
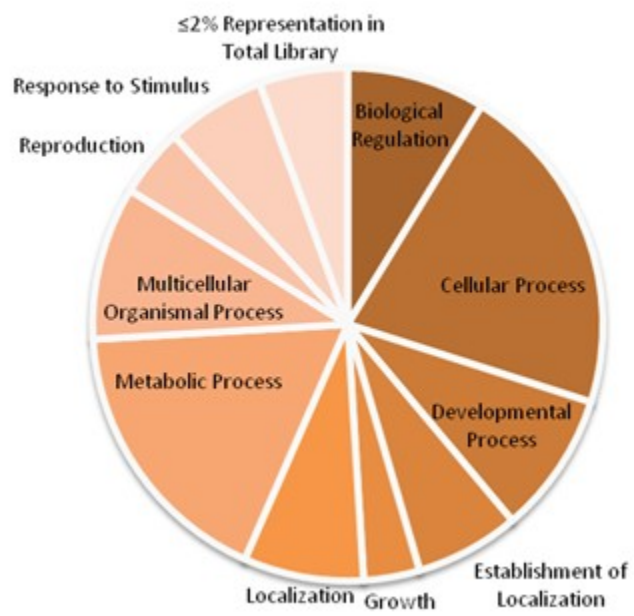


Figure 1.2 Proportions of GO biological process terms (level two) of each EST library annotated by Blast2GO A) Soldiers; B) Alates; C) Workers; D) Early Larval; E) Late Larval

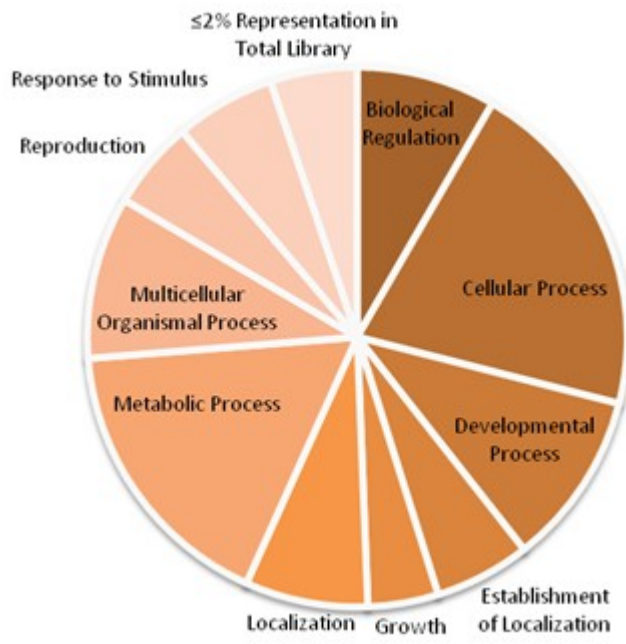
A)



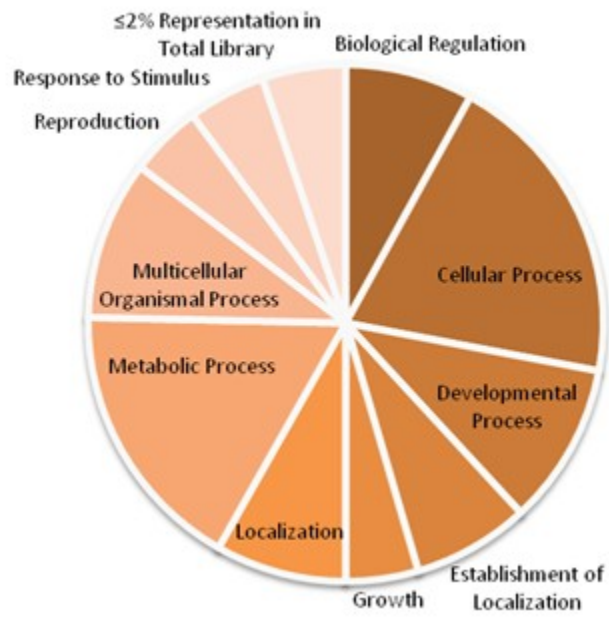
B)



C)



D)



E)

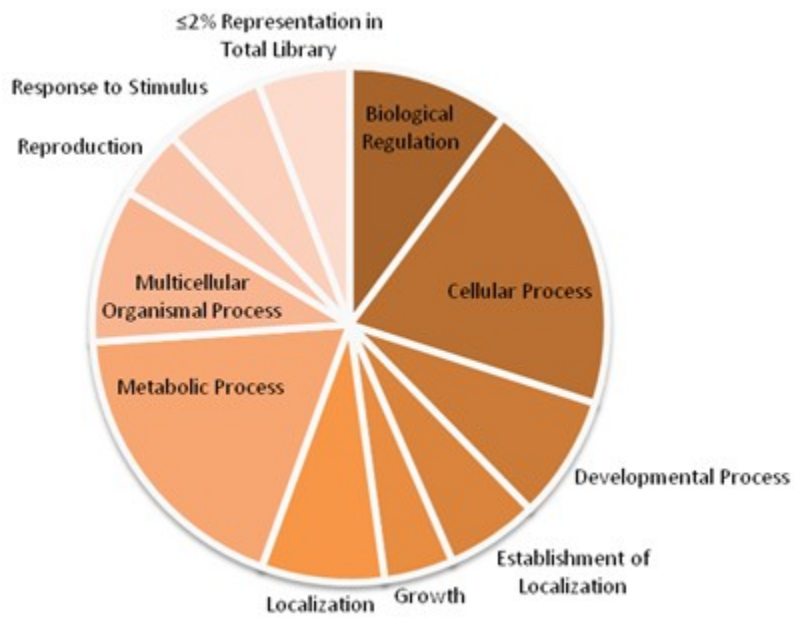
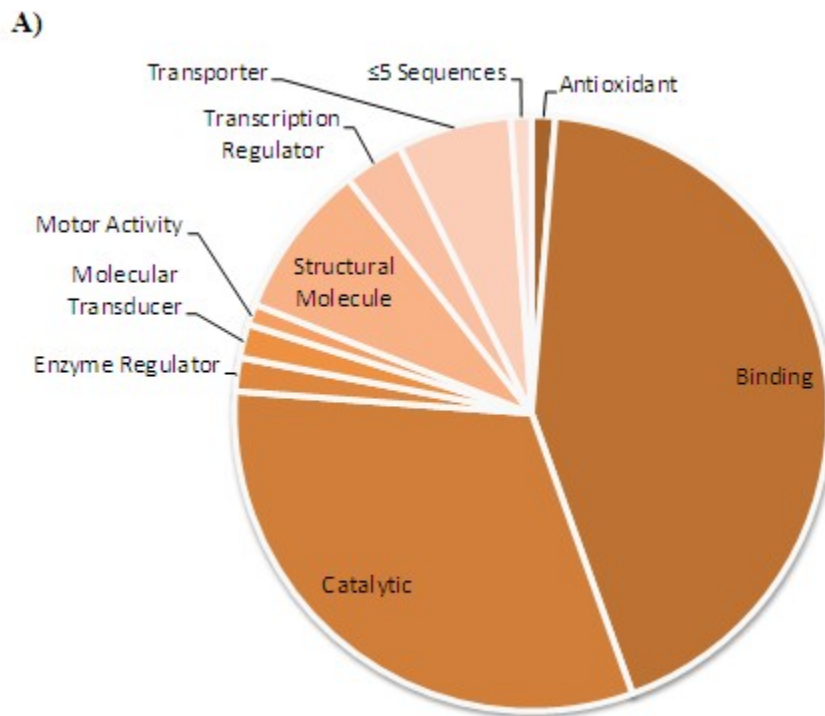
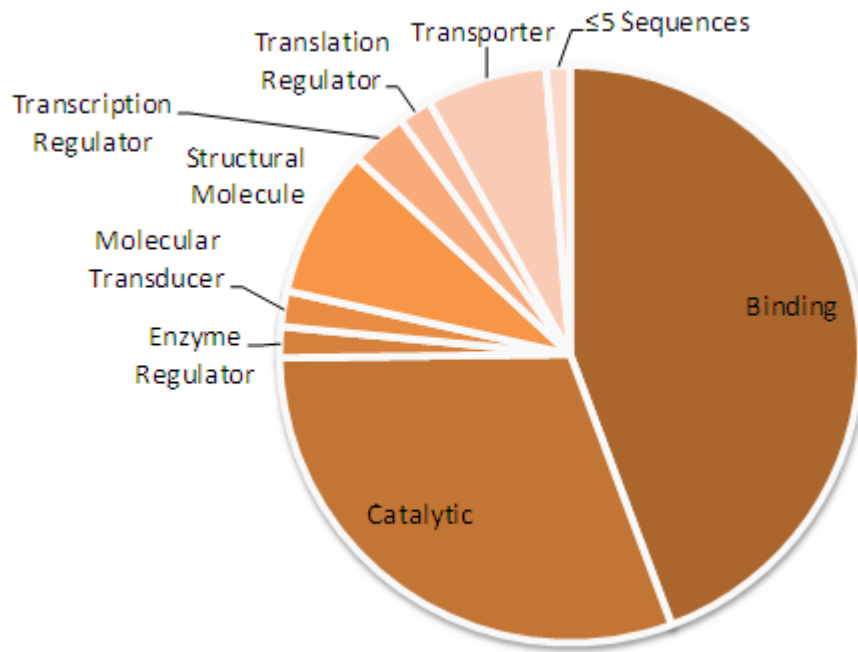


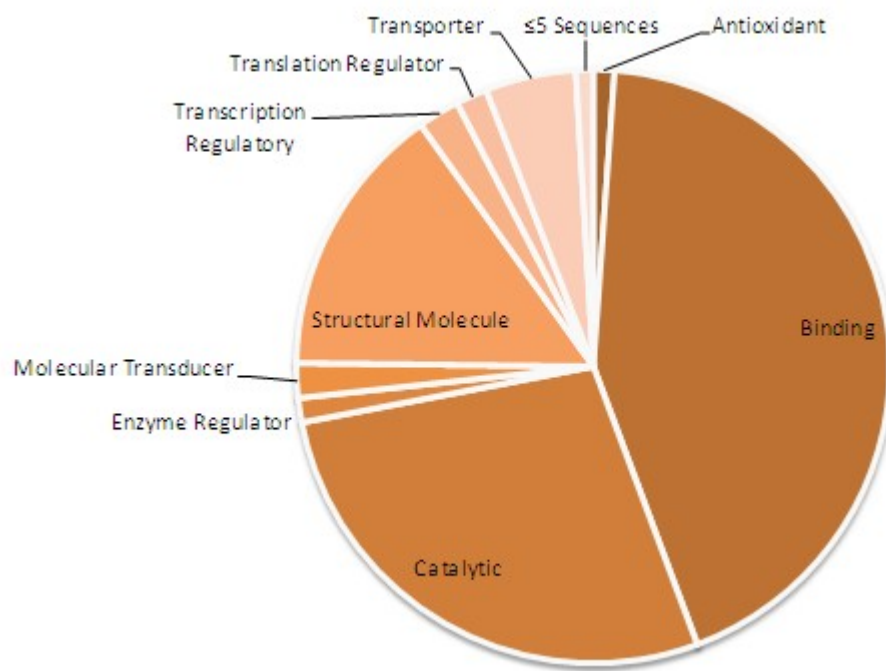
Figure 1.3 Proportional analysis of GO molecular function terms (level two) of each individual EST library annotated by Blast2GO A) Soldiers; B) Alates; C) Workers; D) Early Larval; E) Late Larval



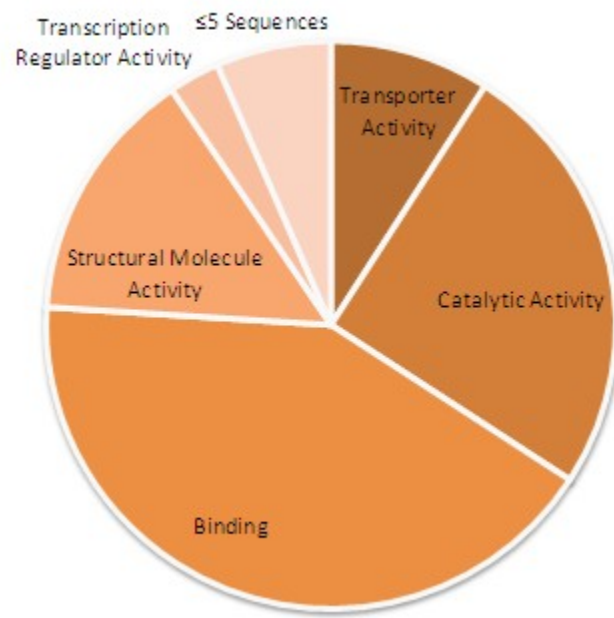
B)



C)



D)



E)

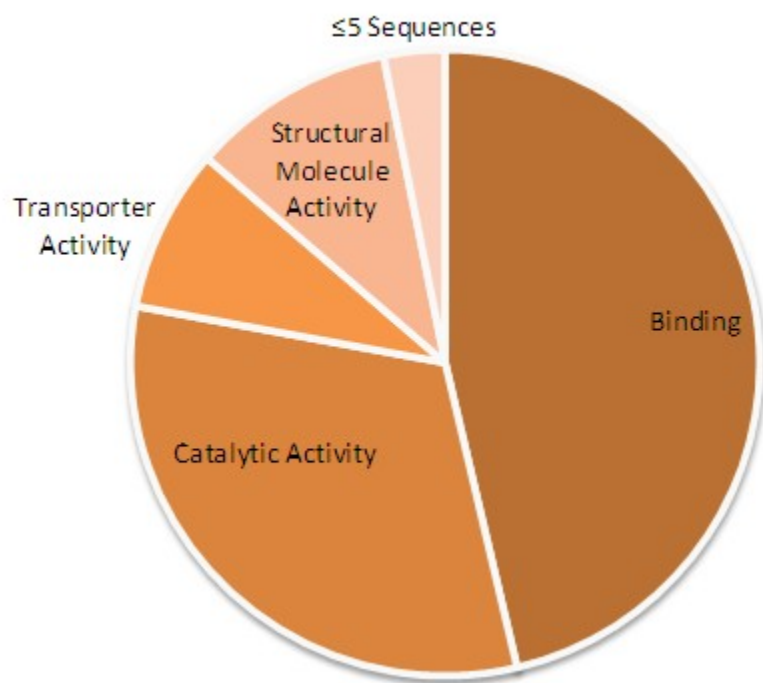


Figure 1.4 Frequency of putatively reproductive GO terms in each EST library as a fraction to total number of unigenes.

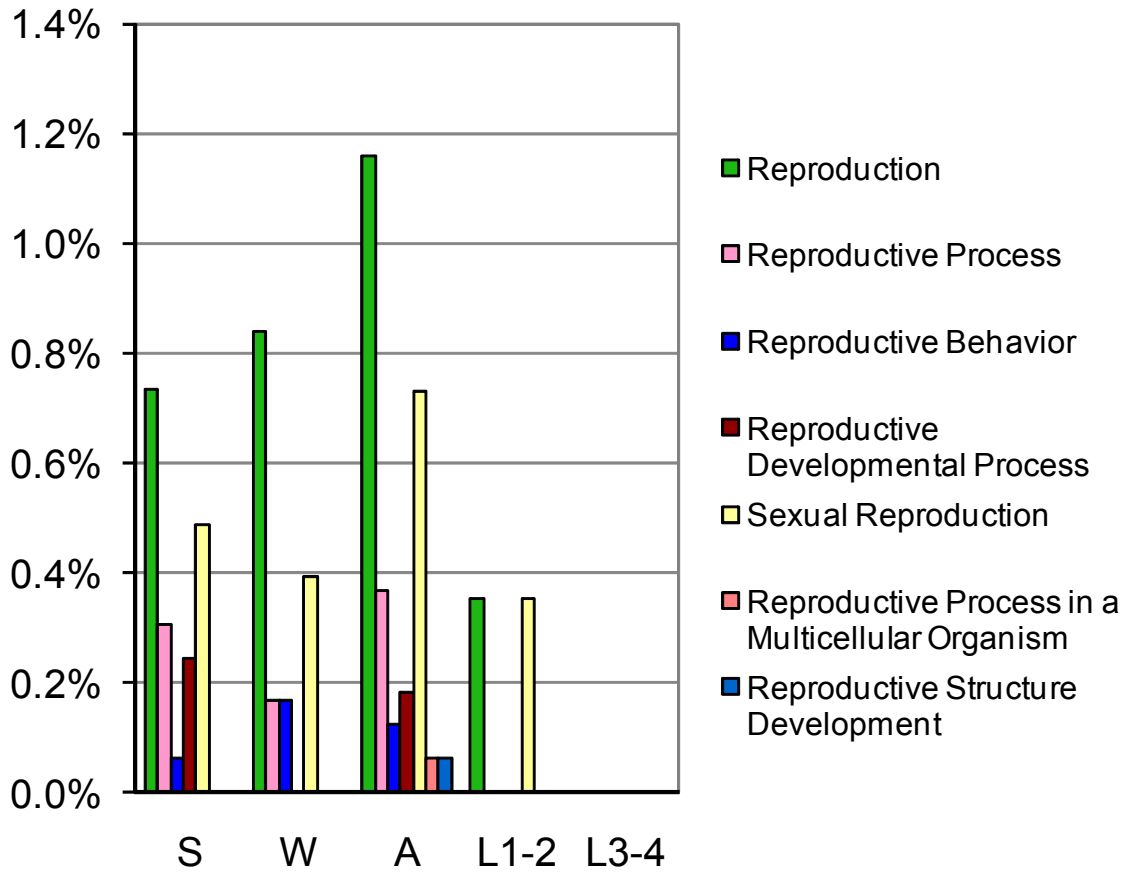


Figure 1.5 Measure of statistical significance, resultant significant r-values were validated using a chi-squared analysis. R-statistic measure of relative entropy and significance was done as in Stekel et al. 2000.

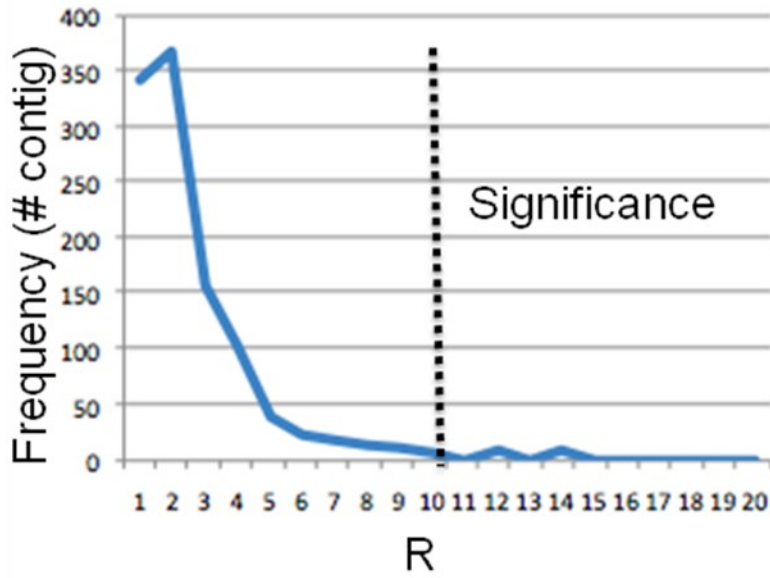


Figure 1.6 R-statistic comparison of contig composition and alate singleton bias of contig545 of predicted neurotransmitter secretion or cholesterol absorption functioning.



Figure 1.7 R-statistic comparison of contig composition and late larval singleton bias of contig366 of predicted protein biosynthesis or ligase activity functionality.

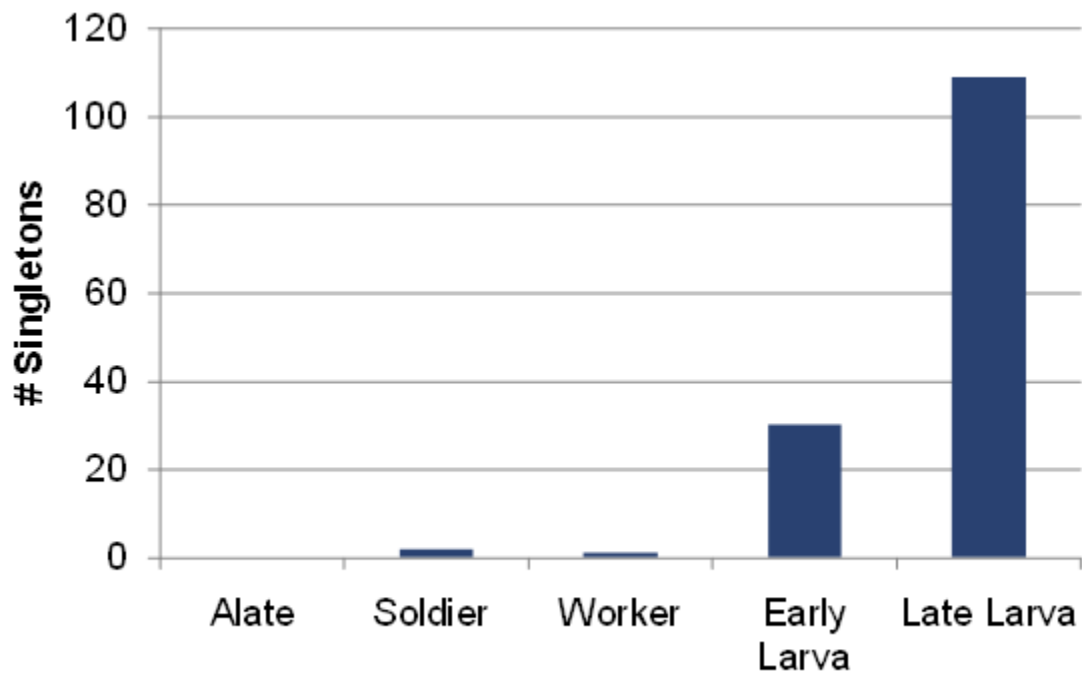


Figure 1.8 R-statistic comparison of contig composition and soldier singleton bias of contig3 of BLASTX putative viral protein.



Figure 1.9 R-statistic comparison of contig composition and soldier singleton bias of contig794 of BLASTX putative ejaculatory bulb protein.

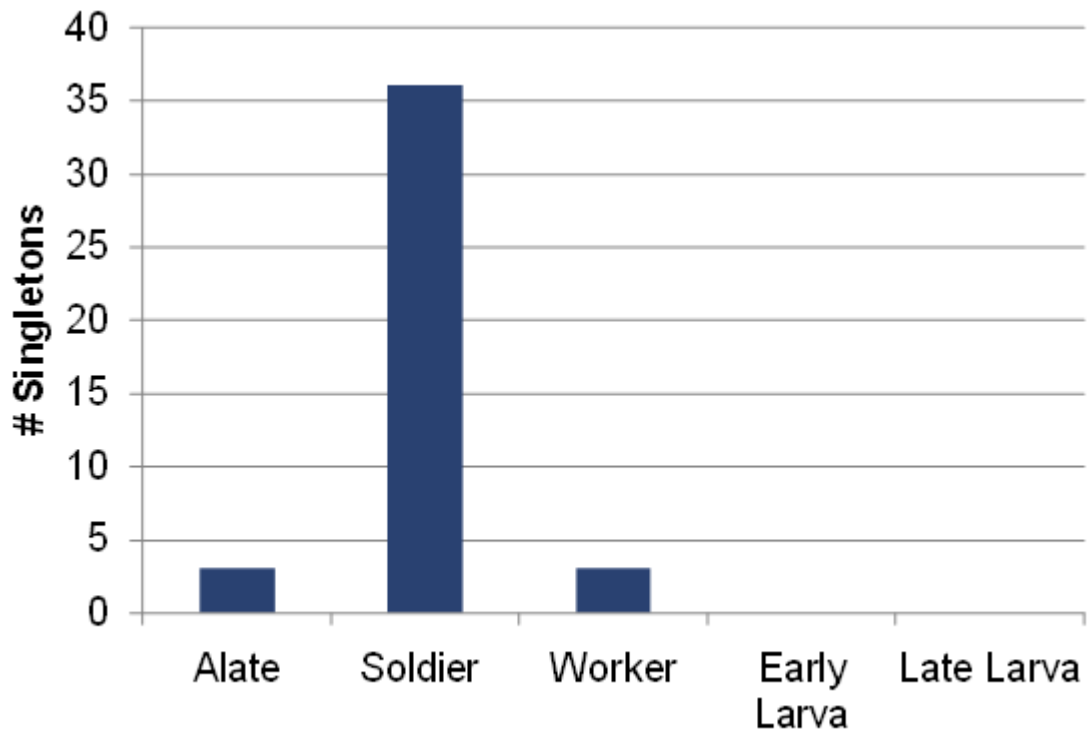


Figure 1.10 R-statistic comparison of contig composition and alate singleton bias of contig827 of BLASTX putative ejaculatory bulb protein.

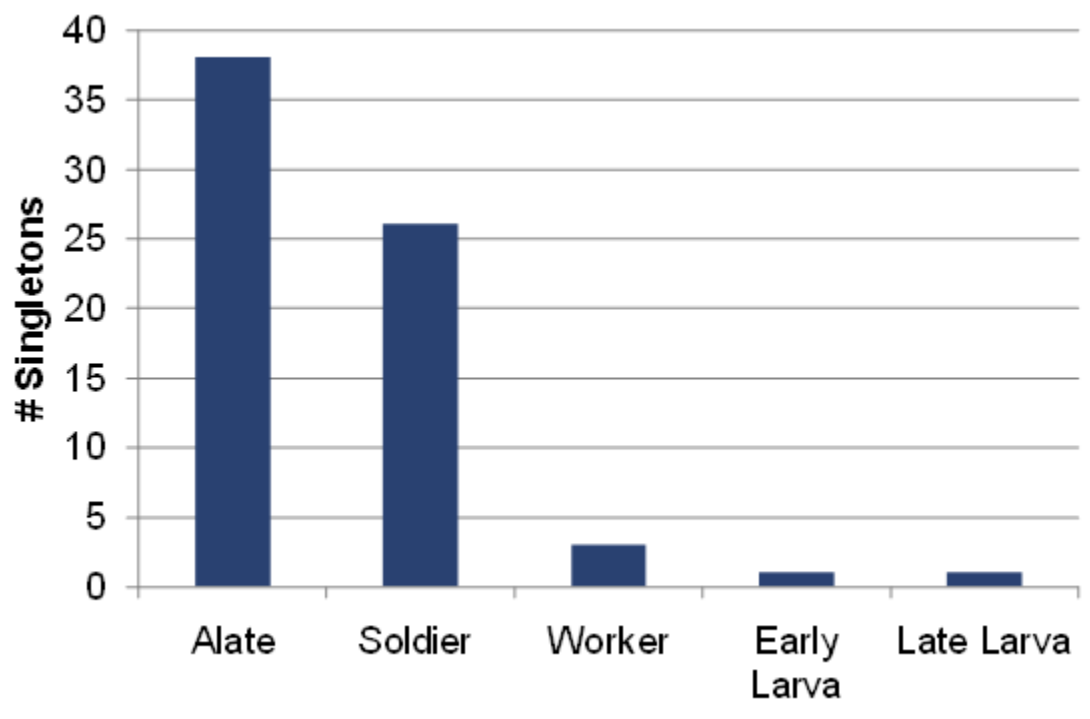


Figure 1.11 Frequency of fold-change distribution of worker expression compared to soldiers. Top five fold change sequences were analyzed with qPCR from top 5% of total sequences arranged by fold-change (>3.1-fold).

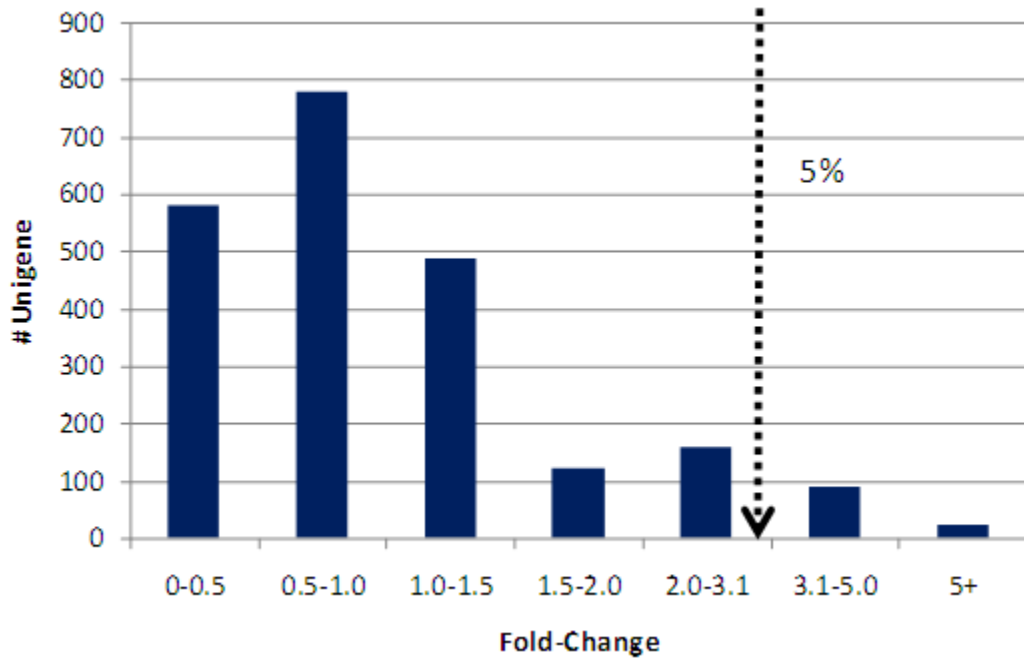


Figure 1.12 Frequency of fold-change distribution of soldier expression compared to soldiers. Top five fold change sequences were analyzed with qPCR from top 5% of total sequences arranged by fold-change (>6.6-fold).

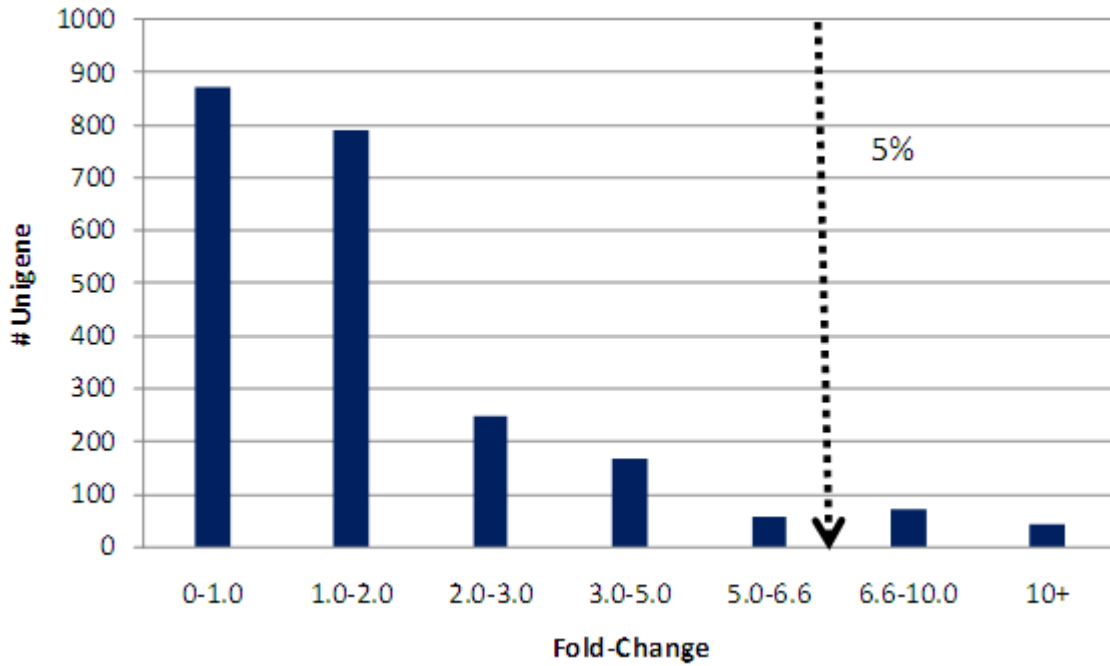


Table 1.1 Primers designed for qPCR of nine highly expressed genes from the microarray analysis.

Systematic Name	Forward Primer	Reverse Primer
Contig[0330]	TGATGTATGGGTCTTGTTTCAGTTG	AGCACCTTCAAGAAGCATGATG
MMS206_H0 2	GCAGAGCACTTCCTATCCATTATC	ACTTGATGAAACGGCTGATGTC
MMS220_B04	TGTGAAACCAAATTCTTCCAGTTC	ATAGAGCAGGCTACCGATGAG
Contig[0358]	GGAAGGTAATGGCTACATCAC	ATTGTTCTGTCACTCATTCTCC
MMS170_B03	ACATGGTGTACATTCCAGAAGG	CCCAAACAGTAATAAGCCCACAAG
Contig[2197]	ACTTGTTGGGAAATGCGTTAAGC	CATGTCAGTTGTCCTTCAGGTAAC
Contig[0515]	GCAGACGCAGCACAGACTAC	CAGCAAGTAGAGTAGGTGGATCAG
MMS108_H0 2	AGTCATTGTCACTGGAGGTCTTG	GCTGGCAATCACACTGTAACTC
MMS230_H1 2	ACAGGAGGCACTGGTAGGAG	GGTGTTCATCCCATTCTACTCTTTG

Table 1.2 cDNA library analysis including total number of clones sequenced, amount of <150bp sequences in each library, which were discarded from further analysis, minimum average insert size, gene discovery rate, and number of unigenes obtained from each library.

	Worker	Alate	Soldier	Early Larva	Late Larva
Total sequenced	4031	3836	3548	2111	1733
Total <150 bp	1069	330	705	99	113
Min Mean Insert Size (bp) ¹	570	1086	638	681	416
Gene Discovery Rate ²	60%	47%	58%	56%	51%
Unigenes	1787	1639	1637	1136	792

¹: Min Mean Insert Size calculated by total number of basepairs (after sequence trimming, vector removal, and discard of sequences less than 150bp) divided by the number of clones sequenced

²: Gene Discovery Rate calculated by number of contigs divided by total number of clones sequenced

Table 1.3 *In silico* analysis of transcript bias in contigs formed from all sequences in each library, the ten highest r-values were analyzed using BLASTX (e-value \leq 1E⁻¹⁰). P-value is in reference to significance of caste bias of singletons in contigs formed using a chi-squared test on singleton representation in each contig.

Library Bias	Contig #	Length (bp)	R ¹	p-value ²	Sequence Name	e-value	Identity (%)
Soldier	3	2647	106	5.24E-50	Viral Protein	1.00E-170	44
Soldier	794	1435	42	4.51E-25	Ejaculatory Bulb-specific Protein 3	1.00E-25	67
Alate	827	1036	31	1.42E-10	Ejaculatory Bulb-specific Protein 3	1.00E-29	73
Alate	148	981	66	6.63E-21	ATP Synthase Subunit A	1.00E-27	68
Alate	168	1724	26	1.03E-10	Cytochrome C Oxidase Subunit 1	1.00E-180	86
Alate	352	1550	22	1.58E-11	Endoglucanase B Precursor (Cellulase B)	1.00E-109	59
Early Larva	472	954	92	3.61E-48	Cytochrome Oxidase Subunit 3	1.00E-86	76
Early Larva	479	1740	74	2.82E-35	Cytochrome B	1.00E-134	77
Early Larva	507	735	40	3.24E-20	Tropomyosin	1.00E-18	89
Early Larva	821	1349	18	7.46E-05	Troponin C	1.00E-38	70
Late Larva	412	975	80	3.10E-22	Ribosomal Protein L31	1.00E-51	83

¹: R-statistics were based on equations in Stekel et al. 2000 and compared relative abundance of each libraries prevalence in contiguous sequences from all available sequences

²: P-values were calculated to establish appropriate significance thresholds to confirm individual library abundance.

Table 1.4 *In silico* analysis and predicted protein function of 10 contigs with the highest r-value with no putative role assigned by a BLASTX search. P-value is in reference to significance of caste bias of singletons in contigs formed using a chi-squared test on singleton representation in each contig.

Library Bias	Contig	Length (bp)	R ¹	p-value ²	Predicted Protein Function ³
Soldier	910	1255	15	6.92E-11	Antibacterial humoral response; Translation elongation
Alate	545	1346	382	6.39E-128	Neurotransmitter secretion; Cholesterol absorption
Alate	142	1745	76	1.54E-25	Cell adhesion; Hydrolase activity
Late Larva	366	478	97	5.45E-70	Protein biosynthesis; Ligase activity
Late Larva	598	903	49	2.00E-19	Regulation of transcription; Metabolism
Late Larva	516	393	39	2.04E-16	Stress Response
Late Larva	533	474	31	7.12E-13	Cell adhesion
Late Larva	582	1133	26	9.43E-09	Spermatogenesis; Cell-cell adhesion
Late Larva	560	197	24	3.89E-09	Ribosomal protein-nucleus import
Late Larva	596	747	14	1.27E-07	Amino acid metabolism

¹: R-statistics were based on equations in Stekel et al. 2000 and compared relative abundance of each libraries prevalence in contiguous sequences from all available sequences

²: P-values were calculated to establish appropriate significance thresholds to confirm individual library abundance

³: Putative protein functions were predicted using: dragon.bio.purdue.edu/pfp/

Table 1.5 Microarray results of 5% of the total sequences applied that were expressed at a 3.1-fold or greater level in soldiers relative to workers as estimated by the microarray analysis. All genes had a non-significant p-value (>0.05). N.H. refers to sequences with no BLASTX sequence match.

Systematic Name	Fold-Change	Accession	Definition	e-value	ID (%)
Contig[0330]	46.95	Q8T6L5	Tropomyosin.	6.00E-137	99
Contig[0358]	26.81	Q9VNH6	Probable exocyst complex component 4 (Exocyst complex component Sec8).	1.00E-34	57
MMS170_B03	16.90	Q498D9	PDZ domain-containing protein GIPC2.	5.20E-14	41
MMS206_H02	15.17	P47947	Troponin C, isoform 1.	1.70E-59	81
MMS220_B04	12.91	N.M.	N.M.	N.M.	N.M.
Contig[0147]	9.84	P41822	Ferritin subunit precursor (EC 1.16.3.1) (Ferritin heavy chain-like protein) (AeFer(H)).	7.40E-11	62
Contig[0232]	8.91	P48610	Arginine kinase (EC 2.7.3.3) (AK).	5.00E-95	90
Contig[0454]	8.88	N.M.	N.M.	N.M.	N.M.
Contig[0460]	8.12	Q9VG95	Glutathione S-transferase D5 (EC 2.5.1.18) (DmGST24).	1.20E-51	51
Contig[0618]	7.46	Q7RX84	Pre-mRNA-splicing factor cwc-22.	0.00055	34
Contig[0672]	7.46	Q9S7L2	Transcription factor MYB98 (Myb-related protein 98) (AtMYB98).	3.60E-17	34
Contig[1424]	6.54	P05227	Histidine-rich protein precursor (Clone PFHRP-II).	1.90E-21	30
Contig[2440]	6.33	Q9VRL3	Probable prefoldin subunit 4.	1.80E-32	49
MMS010_C03	6.29	P81160	Ductus ejaculatorius peptide 99B precursor.	2.4	47
MMS086_A05	6.10	N.M.	N.M.	N.M.	N.M.
MMS087_H01	5.88	P47948	Troponin C, isoform 2.	4.50E-61	81
MMS110_F12	5.72	Q96KD8	Lung squamous cell carcinoma-related protein 1.	0.0041	48
MMS146_F04	5.61	N.M.	N.M.	N.M.	N.M.
MMS147_B02	5.15	Q6BSK5	Autophagy-related protein 17.	7.5	38
MMS155_G08	5.14	P82174	Lysozyme (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase).	1.30E-21	47
MMS190_D06	5.10	N.M.	N.M.	N.M.	N.M.
MMS206_F02	5.02	N.M.	N.M.	N.M.	N.M.
MMS278_D11	4.94	Q27319	Gelsolin, cytoplasmic (Actin-depolymerizing factor) (ADF).	5.60E-29	50

Systematic Name	Fold-Change	Accession	Definition	e-value	ID (%)
Contig[0479]	4.88	P80958	Cobrotoxin-b precursor (CBT-b) (Short neurotoxin) (NT3) (Atratoxin-b) (Cobrotoxin III) (CBT-III) (Cobrotoxin IV) (CBT IV).	0.21	34
Contig[0702]	4.75	P35502	Esterase FE4 precursor (EC 3.1.1.1) (Carboxylic-ester hydrolase).	1.20E-65	47
Contig[1713]	4.73	Q99KK7	Dipeptidyl-peptidase 3 (EC 3.4.14.4) (Dipeptidyl-peptidase III) (DPP III) (Dipeptidyl aminopeptidase III) (Dipeptidyl arylamidase III).	1.10E-24	36
Contig[2359]	4.71	P25407	STI1-like protein (Fragment).	0.55	23
Contig[2498]	4.69	N.M.	N.M.	N.M.	N.M.
MMS008_A07	4.65	P53777	Muscle LIM protein 1.	1.40E-39	83
MMS008_B09	4.64	Q96PY6	Serine/threonine-protein kinase Nek1 (EC 2.7.11.1) (NimA-related protein kinase 1) (Renal carcinoma antigen NY-REN-55).	2.10E-37	31
MMS063_H05	4.47	N.M.	N.M.	N.M.	N.M.
MMS108_G03	4.45	P16630	Endoglucanase S precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase S) (Cellulase S).	3.2	42
MMS114_D07	4.43	Q93092	Transaldolase (EC 2.2.1.2).	#####	72
MMS116_E03	4.43	Q7SA23	Exoglucanase 1 precursor (EC 3.2.1.91) (Exocellobiohydrolase 1) (1,4- beta-cellobiohydrolase 1).	1.60E-73	56
MMS139_E05	4.35	Q99954	Submaxillary gland androgen-regulated protein 3 homolog A precursor (Proline-rich protein 5) (Proline-rich protein PBI).	2.00E-11	37
MMS144_B04	4.35	Q943E7	16.9 kDa class I heat shock protein 3.	6.40E-14	41
MMS164_B01	4.30	P35134	Ubiquitin-conjugating enzyme E2-17 kDa 11 (EC 6.3.2.19) (Ubiquitin-protein ligase 11) (Ubiquitin carrier protein 11).	7.90E-55	70
MMS166_C12	4.20	Q0HLD7	Chaperone protein torD.	2.3	28
MMS170_A10	4.20	O14164	Probable eukaryotic translation initiation factor 3 subunit C (eIF3 p93).	0.76	20
MMS204_E06	4.12	Q9NXR7	Protein BRE (Brain and reproductive organ-expressed protein) (BRCA1/BRCA2-containing complex subunit 45).	6.00E-50	40

Systematic Name	Fold-Change	Accession	Definition	e-value	ID (%)
MMS219_C06	4.07	N.M.	N.M.	N.M.	N.M.
MMS219_G01	4.04	Q9ZJZ9	Cytochrome c-553 precursor (Cytochrome c553).	1.7	30
MMS233_B11	3.93	Q07372	Ubiquitin-like protein 1.	5.6	33
Contig[0334]	3.90	N.M.	N.M.	N.M.	N.M.
Contig[0594]	3.86	N.M.	N.M.	N.M.	N.M.
Contig[0603]	3.85	N.M.	N.M.	N.M.	N.M.
Contig[0782]	3.82	Q9BUJ2	Heterogeneous nuclear ribonucleoprotein U-like protein 1 (Adenovirus early region 1B-associated protein 5) (E1B-55 kDa-associated protein 5) (E1B-AP5).	0.00031	34
Contig[1473]	3.81	N.M.	N.M.	N.M.	N.M.
Contig[1711]	3.80	O15143	Actin-related protein 2/3 complex subunit 1B (Arp2/3 complex 41 kDa subunit) (p41-ARC).	1.20E-33	33
Contig[1732]	3.79	P15147	Insect toxin 2 precursor (AaH IT2) (AaHIT2) (AaIT2).	3.4	36
Contig[1740]	3.77	Q8CGA2	TBC1 domain family member 14.	4.40E-86	57
Contig[2063]	3.76	N.M.	N.M.	N.M.	N.M.
Contig[2112]	3.70	Q02EU8	Sec-independent protein translocase protein tatB homolog.	0.00038	47
Contig[2454]	3.67	N.M.	N.M.	N.M.	N.M.
Contig[2594]	3.63	N.M.	N.M.	N.M.	N.M.
MMS007_D12	3.59	O61064	Tectonin-2 (Tectonin II).	2.00E-26	33
MMS008_G04	3.58	Q4ZYC0	UPF0243 zinc-binding protein Psyr_0794.	9.6	44
MMS009_C05	3.57	Q92044	Metallothionein A (MT A).	1.1	37
MMS009_G07	3.57	P18379	Uncharacterized 5.3 kDa protein.	7.1	28
MMS010_B02	3.56	Q2TAL5	Smoothelin-like protein 2.	1.60E-24	58
MMS010_B09	3.55	N.M.	N.M.	N.M.	N.M.
MMS063_H10	3.54	O70584	Homeobox protein Nkx-2.8 (Homeobox protein NK-2 homolog H) (Homeobox protein Nkx-2.9).	5.9	40
MMS083_C02	3.54	N.M.	N.M.	N.M.	N.M.
MMS087_F08	3.53	Q3SYC2	2-acylglycerol O-acyltransferase 2 (EC 2.3.1.22) (Monoacylglycerol O-acyltransferase 2) (Acyl CoA:monoacylglycerol acyltransferase 2) (MGAT2) (hMGAT2) (Diacylglycerol acyltransferase 2-like protein 5) (Diacylglycerol O-acyltransferase candidate 5) (hDC5).	2.40E-71	52

Systematic Name	Fold-Change	Accession	Definition	e-value	ID (%)
MMS088_F10	3.53	P48613	Protein tipE (Temperature-induced paralytic E).	6.40E-23	45
MMS090_C02	3.53	N.M.	N.M.	N.M.	N.M.
MMS090_G07	3.52	P35630	NADP-dependent alcohol dehydrogenase (EC 1.1.1.2).	7.50E-59	51
MMS091_C09	3.48	Q8TGN5	Uncharacterized protein YIL105W-A.	7.3	50
MMS091_D05	3.48	P13825	Aspartic acid-rich protein precursor.	0.13	66
MMS093_B12	3.47	N.M.	N.M.	N.M.	N.M.
MMS101_G09	3.47	Q5U581	Myotubularin-related protein 10-A.	8.50E-24	50
MMS105_E09	3.47	N.M.	N.M.	N.M.	N.M.
MMS106_G10	3.47	Q9VYF8	Ubiquinone biosynthesis methyltransferase COQ5, mitochondrial precursor (EC 2.1.1.-).	3.10E-92	68
MMS110_C01	3.46	Q9UQ35	Serine/arginine repetitive matrix protein 2 (Serine/arginine-rich splicing factor-related nuclear matrix protein of 300 kDa) (Ser/Arg- related nuclear matrix protein) (SR-related nuclear matrix protein of 300 kDa) (Splicing coactivator subunit SRm300) (300 kDa nuclear matrix antigen).	2.7	24
MMS112_C04	3.44	P48375	12 kDa FK506-binding protein (EC 5.2.1.8) (FKBP) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (Macrolide-binding protein).	5.10E-44	76
MMS114_A02	3.44	P50497	Merozoite surface antigen 2 precursor (MSA-2).	1	33
MMS116_C01	3.40	Q17RH7	Putative protein TPRXL.	3.50E-20	40
MMS116_E05	3.40	N.M.	N.M.	N.M.	N.M.
MMS117_B05	3.38	N.M.	N.M.	N.M.	N.M.
MMS118_A09	3.38	N.M.	N.M.	N.M.	N.M.
MMS119_E06	3.38	Q9MUM7	Uncharacterized 8.0 kDa protein in ndhF-psbD intergenic region.	3.7	48
MMS121_F08	3.37	N.M.	N.M.	N.M.	N.M.
MMS123_A02	3.36	Q3E7B5	Uncharacterized protein YMR230W-A.	0.19	30
MMS136_G08	3.35	N.M.	N.M.	N.M.	N.M.
MMS139_D10	3.33	Q9TU34	Inositol 1,4,5-trisphosphate receptor type 1 (Type 1 inositol 1,4,5-trisphosphate receptor) (Type 1 InsP3 receptor) (IP3 receptor isoform 1) (InsP3R1).	0.17	27

Systematic Name	Fold-Change	Accession	Definition	e-value	ID (%)
MMS139_H10	3.32	P36027	Cell wall integrity sensor MID2 precursor (Mating pheromone-induced death protein 2) (Serine-rich multicopy suppressor protein 1) (Protein kinase A interference protein 1).	7.4	22
MMS141_C02	3.30	N.M.	N.M.	N.M.	N.M.
MMS142_B09	3.29	P24868	G2/mitotic-specific cyclin-1.	0.0049	29
MMS143_C01	3.29	P04733	Metallothionein-1F (MT-1F) (Metallothionein-IF) (MT-IF).	0.21	58
MMS143_D07	3.28	O28466	Uncharacterized protein AF 1809.	4.6	44
MMS144_D04	3.26	Q9CJM5	Uncharacterized protein PM1972 precursor.	7.6	43
MMS146_A10	3.24	N.M.	N.M.	N.M.	N.M.
MMS146_E08	3.24	O18391	Probable serine hydrolase (EC 3.1.-.-) (Kraken protein).	2.30E-32	32
MMS146_F01	3.23	Q63073	Protein BTG1 (Anti-proliferative factor).	6.40E-30	60
MMS147_B06	3.21	Q5HP88	Probable ATP-dependent helicase dinG homolog (EC 3.6.1.-).	3.9	30
MMS152_H05	3.20	N.M.	N.M.	N.M.	N.M.
MMS165_A02	3.20	N.M.	N.M.	N.M.	N.M.
MMS171_E07	3.20	Q917S8	Multifunctional protein ADE2 (Protein adenosine-5) [Includes: Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6) (SAICAR synthetase); Phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21) (AIR carboxylase) (AIRC)].	1.30E-88	64
MMS173_D02	3.18	P04371	Cytochrome c oxidase subunit 1 (EC 1.9.3.1) (Cytochrome c oxidase polypeptide I).	0.037	33
MMS174_A09	3.17	N.M.	N.M.	N.M.	N.M.
MMS176_A10	3.17	Q5F433	PRA1 family protein 3 (ADP-ribosylation factor-like protein 6-interacting protein 5) (ARL-6-interacting protein 5) (Aip-5).	3.70E-34	47
MMS176_G05	3.16	N.M.	N.M.	N.M.	N.M.
MMS177_E11	3.16	Q5F359	Trafficking protein particle complex subunit 5.	5.00E-62	64
MMS179_H08	3.16	Q3MHV9	Serine incorporator 1 (Tumor differentially expressed protein 2).	2.70E-47	47
MMS190_C04	3.15	Q1HPK6	Translation elongation factor 2 (EF-2).	4.90E-66	90
MMS198_G11	3.15	N.M.	N.M.	N.M.	N.M.

Systematic Name	Fold-Change	Accession	Definition	e-value	ID (%)
MMS199_H03	3.14	Q5ECE3	Lopap precursor (EC 3.4.21.-) (Prothrombin activator) (Lipocalin-1/4).	0.01	25
MMS200_B10	3.14	Q09MJ5	Photosystem II reaction center protein K precursor (PSII-K).	1.1	32
MMS204_H07	3.13	Q92HI5	Uncharacterized protein RC0786.	4.4	28
MMS232_A08	3.12	Q9Y673	Dolichyl-phosphate beta- glucosyltransferase (EC 2.4.1.117)	2.60E-56	66

Table 1.6 Microarray results of 5% of the total sequences applied that were expressed at a 6.6-fold or greater level in worlkers relative to soldiers as estimated by the microarray analysis. All genes had a non-significant p-value (>0.05). N.H. refers to sequences with no BLASTX sequence match.

Systematic Name	Fold-Change	Accession	Definition	e-value	ID (%)
Contig[2197]	42.4	Q9ZE67	Uncharacterized protein RP080.	0.76	38
Contig[2263]	38.1	N.H.	N.H.	N/A	N/A
Contig[0515]	37.6	N.H.	N.H.	N/A	N/A
MMS108_H02	35.9	N.H.	N.H.	N/A	N/A
MMS230_H12	29.4	N.H.	N.H.	N/A	N/A
MMS093_C06	28.1	N.H.	N.H.	N/A	N/A
MMS230_D02	27.7	N.H.	N.H.	N/A	N/A
Contig[2611]	26.5	N.H.	N.H.	N/A	N/A
MMS172_A03	25.0	O18405	Surfeit locus protein 4 homolog.	4.60E-43	86
MMS146_F09	23.8	Q9HBH5	Retinol dehydrogenase 14 (EC 1.1.1.-) (Alcohol dehydrogenase PAN2).	1.70E-59	50
MMS108_A06	23.8	Q5BJJ5	Haloacid dehalogenase-like hydrolase domain-containing protein 2.	1.00E-68	61
MMS145_D08	23.3	N.H.	N.H.	N/A	N/A
Contig[2295]	21.7	N.H.	N.H.	N/A	N/A
MMS136_G05	20.6	Q7TSH4	Centrosomal protein of 110 kDa (Cep110).	2.4	31
MMS090_B10	20.4	N.H.	N.H.	N/A	N/A
Contig[0708]	20.4	P68620	Protein A54.	0.33	30
Contig[2279]	20.2	Q62635	Mucin-2 precursor (Intestinal mucin-2) (Fragment).	0.0057	51
MMS174_B05	20.0	N.H.	N.H.	N/A	N/A
Contig[0674]	19.4	N.H.	N.H.	N/A	N/A
MMS008_G08	17.1	N.H.	N.H.	N/A	N/A
Contig[0592]	16.3	Q292F0	Eukaryotic translation initiation factor 3 subunit M (eIF3m) (Transport and Golgi organization protein 7) (Tango-7).	5.20E-136	68
MMS094_E01	16.2	P54319	Phospholipase A-2-activating protein (PLAP).	2.00E-33	45
MMS234_F03	16.0	N.H.	N.H.	N/A	N/A
MMS064_E01	14.5	N.H.	N.H.	N/A	N/A
MMS094_C11	14.3	P50429	Arylsulfatase B precursor (EC 3.1.6.12) (ASB) (N-acetylgalactosamine- 4-sulfatase) (G4S).	0.00014	30
MMS115_B07	14.3	Q9UHE5	Probable N-acetyltransferase 8 (EC 2.3.1.-) (Camello-like protein 1).	0.04	28

Systematic Name	Fold-Change	Accession	Definition	e-value	ID (%)
Contig[0716]	13.7	Q5ZLM8	Protein FAM133.	0.21	70
MMS177_E10	13.5	Q01644	Male-specific sperm protein Mst84Dc.	3.8	44
MMS219_H09	13.5	Q9GLD9	UDP-glucuronosyltransferase 2B33 precursor (EC 2.4.1.17) (UDPGT).	4.80E-32	49
MMS094_D01	13.4	N.H.	N.H.	N/A	N/A
Contig[1534]	13.3	Q501J6	Probable ATP-dependent RNA helicase DDX17 (EC 3.6.1.-) (DEAD box protein 17).	4.30E-17	71
Contig[0278]	13.3	N.H.	N.H.	N/A	N/A
Contig[2614]	12.9	P0A4L2	Thioredoxin-1 (Trx-1) (Thioredoxin-M).	0.21	42
MMS140_A07	12.9	Q1RMU5	RNA-binding protein 5 (RNA-binding motif protein 5) (Tumor suppressor LUCA15).	8.50E-19	52
Contig[0225]	12.8	N.H.	N.H.	N/A	N/A
MMS172_G01	12.7	N.H.	N.H.	N/A	N/A
MMS169_A12	12.5	Q96I36	Uncharacterized protein C12orf62.	4.2	55
MMS116_D11	12.1	P42574	Caspase-3 precursor (EC 3.4.22.56) (CASP-3) (Apopain) (Cysteine protease CPP32) (Yama protein) (CPP-32) (SREBP cleavage activity 1) (SCA-1) [Contains: Caspase-3 subunit p17; Caspase-3 subunit p12]	2.60E-17	55
Contig[0337]	12.0	Q00871	Chymotrypsin BI precursor (EC 3.4.21.1).	8.80E-45	40
MMS170_A08	11.9	N.H.	N.H.	N/A	N/A
MMS219_B11	11.7	P32292	Indole-3-acetic acid-induced protein ARG2.	0.21	27
Contig[0536]	11.7	Q6L6Q6	Lysozyme precursor (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase).	6.00E-11	33
MMS236_A06	11.6	P81305	Uncharacterized protein MJ0226.2.	0.0018	32
Contig[1728]	11.5	O97557	Tuftelin (Fragment).	0.0014	26
MMS229_D06	11.2	P34103	Protein kinase 4 (EC 2.7.11.1) (Fragment).	2.5	26
Contig[0501]	11.1	N.H.	N.H.	N/A	N/A
MMS207_H10	11.0	N.H.	N.H.	N/A	N/A
MMS179_E01	11.0	N.H.	N.H.	N/A	N/A
Contig[1631]	11.0	P34121	Coactosin (Cytoskeletal protein p17) (Cyclic AMP-regulated protein p16).	1.40E-18	37

Systematic Name	Fold-Change	Accession	Definition	e-value	ID (%)
MMS198_D07	10.8	P50532	Structural maintenance of chromosomes protein 4 (Chromosome-associated protein C) (Chromosome assembly protein XCAP-C).	0.00027	25
Contig[0690]	10.7	N.H.	N.H.	N/A	N/A
Contig[0556]	10.6	P39989	Putative uncharacterized protein YEL028W precursor.	3.8	24
MMS164_B12	10.6	N.H.	N.H.	N/A	N/A
MMS229_C07	10.5	N.H.	N.H.	N/A	N/A
MMS204_G12	10.5	Q7ZZP9	Metallothionein (MT).	2.5	46
MMS115_A06	10.4	N.H.	N.H.	N/A	N/A
MMS164_G04	10.4	P08897	Collagenase precursor (EC 3.4.21.-) (Hypodermin C) (HC).	0.017	53
MMS091_B07	10.3	N.H.	N.H.	N/A	N/A
MMS176_A05	10.3	N.H.	N.H.	N/A	N/A
Contig[0090]	10.2	N.H.	N.H.	N/A	N/A
MMS199_H06	10.2	P32189	Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase) (Glycerokinase) (GK).	7.40E-91	59
MMS089_C07	9.8	Q9DBF7	Coiled-coil domain-containing protein 49.	0.85	43
MMS063_F12	9.8	Q8N1V2	WD repeat-containing protein 16 (WD40-repeat protein up-regulated in HCC).	2.90E-39	39
Contig[1983]	9.7	P20547	Uncharacterized 11.2 kDa protein.	7.9	50
MMS117_G11	9.5	Q57643	Uncharacterized protein MJ0184.	5.5	21
MMS201_E10	9.5	N.H.	N.H.	N/A	N/A
MMS234_C09	9.5	N.H.	N.H.	N/A	N/A
Contig[0160]	9.4	Q9N2W7	Probable NADH dehydrogenase [ubiquinone]	1.10E-32	48
Contig[0486]	9.4	N.H.	N.H.	N/A	N/A
MMS088_A11	9.3	P54654	Adenylyl cyclase-associated protein (CAP).	6.20E-24	28
MMS199_A10	9.3	Q6DFS6	Charged multivesicular body protein 2a (Chromatin-modifying protein 2a) (CHMP2a).	1.30E-79	79
MMS142_A02	9.3	Q94517	Histone deacetylase Rpd3 (HD) (dRPD3).	1.90E-85	77
MMS220_H01	9.2	Q5UQT2	Uncharacterized protein R335.	3.90E-08	29
MMS103_C04	9.0	Q6C141	Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23) (dUTPase) (dUTP pyrophosphatase).	1.20E-19	59

Systematic Name	Fold-Change	Accession	Definition	E-value	ID (%)
MMS143_G12	9.0	Q9Y826	Meiotic expression up-regulated protein 31.	2.6	33
MMS092_A08	8.9	N.H.	N.H.	N/A	N/A
MMS090_G03	8.9	P32392	Actin-related protein 3 (Actin-like protein 3) (Actin-like protein 66B).	1.20E-99	87
Contig[0739]	8.8	P00771	Brachyurin (EC 3.4.21.32) (Collagenolytic protease).	8.80E-43	45
Contig[0758]	8.8	N.H.	N.H.	N/A	N/A
MMS245_H05	8.7	N.H.	N.H.	N/A	N/A
Contig[0063]	8.7	Q9GJW7	Gamma-aminobutyric acid receptor-associated protein (GABA(A) receptor-associated protein).	1.10E-55	93
MMS114_E12	8.6	N.H.	N.H.	N/A	N/A
Contig[2450]	8.6	N.H.	N.H.	N/A	N/A
MMS114_H02	8.5	N.H.	N.H.	N/A	N/A
MMS065_D04	8.4	N.H.	N.H.	N/A	N/A
Contig[0285]	8.3	P32583	Suppressor protein SRP40.	8.30E-09	29
Contig[1736]	8.3	N.H.	N.H.	N/A	N/A
MMS218_C02	8.2	N.H.	N.H.	N/A	N/A
MMS138_B04	8.1	P98092	Hemocytin precursor (Humoral lectin).	1.20E-31	36
Contig[0286]	8.1	P60984	Glia maturation factor beta (GMF-beta).	2.70E-38	51
MMS260_A12	7.9	N.H.	N.H.	N/A	N/A
MMS121_D04	7.8	P16607	Putative uncharacterized 9.3 kDa protein.	9.4	35
MMS205_E06	7.8	N.H.	N.H.	N/A	N/A
MMS190_E11	7.7	Q9RMW7	Uncharacterized protein pXO2-67/BXB0090/GBAA_pXO2_0090.	1.3	30
MMS174_E06	7.7	P37703	Glycine-rich protein DC9.1.	1.60E-05	36
Contig[2096]	7.7	P15811	Uncharacterized protein ycf49 (ORF10)	4.1	38
MMS108_A07	7.7	Q0U3A4	Histone-lysine N-methyltransferase SET9 (EC 2.1.1.43) (SET domain protein 9).	0.3	23
MMS222_D04	7.4	N.H.	N.H.	N/A	N/A
MMS112_G02	7.4	N.H.	N.H.	N/A	N/A
MMS143_H05	7.3	N.H.	N.H.	N/A	N/A
MMS173_E02	7.3	N.H.	N.H.	N/A	N/A
MMS065_C04	7.2	Q9VE00	Probable cytochrome P450 12a4, mitochondrial precursor (EC 1.14.-.-) (CYPXIIA4).	4.10E-23	51

Systematic Name	Fold-Change	Accession	Definition	E-value	ID (%)
MMS166_G07	7.2	Q6PFS5	ER lumen protein retaining receptor 3 (KDEL receptor 3) (KDEL endoplasmic reticulum protein retention receptor 3).	3.1	39
Contig[0750]	7.1	N.H.	N.H.	N/A	N/A
Contig[1999]	6.9	N.H.	N.H.	N/A	N/A
MMS204_H03	6.9	Q10690	Uncharacterized protein Rv2082.	0.00013	29
MMS233_D06	6.9	N.H.	N.H.	N/A	N/A
MMS148_C05	6.9	Q9CQE8	Protein C14orf166 homolog.	1.60E-17	64
MMS176_H04	6.7	N.H.	N.H.	N/A	N/A
Contig[0480]	6.7	P04814	Trypsin alpha precursor (EC 3.4.21.4).	4.00E-60	50
MMS145_A04	6.7	Q6VEQ5	Protein FAM39B (CXYorf1-like protein on chromosome 2).	0.14	52
MMS126_D11	6.6	P34067	Proteasome subunit beta type-4 precursor (EC 3.4.25.1) (Proteasome beta chain) (Macropain beta chain) (Multicatalytic endopeptidase complex beta chain) (Proteasome chain 3) (RN3).	1.60E-24	36
MMS278_D04	6.6	N.H.	N.H.	N/A	N/A
Contig[0610]	6.6	Q94550	Metallothionein (MT).	1.7	41

Table 1.7 Microarray results of the highest expressed genes in workers compared to soldiers in the combined Florida and Kansas location analysis.

Systematic Name	p-value	Fold-Difference ¹	Definition	e-value	Identity (%)
Contig[2197]	0.0485	42	Uncharacterized protein RP080	0.76	38
Contig[0515]	0.0572	38	Unknown	N/A	N/A
MMS108_H02	0.0578	36	Unknown	N/A	N/A
MMS230_H12	0.0642	29	Unknown	N/A	N/A

¹: Fold-change was calculated from normalized fluorescence data of workers divided soldiers.

Table 1.8 Microarray results of the highest expressed genes in soldiers compared to workers in the combined Florida and Kansas location analysis.

Systematic Name	p-value	Fold-Difference	Definition	e-value	Identity(%)
Contig[0330]	0.109	47	Tropomyosin	6.00E-137	99
MMS206_H02	0.158	27	Probable exocyst complex component 4	1.00E-34	57
MMS220_B04	0.159	17	Predicted: Similar to RGS-GAIP interacting protein GIPC	8.00E-30	68
Contig[0358]	0.0543	15	Troponin C, isoform 1	1.70E-59	81
MMS170_B03	0.227	13	Unknown	N/A	N/A

¹: Fold-Difference was calculated from normalized fluorescence data of soldiers divided by wor

Table 1.9 Microarray analysis of Florida termite populations with a p-value<0.05. Non-significant BLASTX hits denoted as NS

Name	Absolute Fold Change	Expression Up	Accession	Organism	BLAST Sequence Match	E-value	ID (%)
Contig[1722]	1.23	W	NS	NS	NS	NS	NS
Contig[2279]	1.37	W	Q62635	<i>Rattus norvegicus</i>	Mucin-2 precursor	0.006	51
MMS120 D09	1.24	W	P31809	<i>Mus musculus</i>	Carcinoembryonic antigen-related cell adhesion molecule 1	0.08	36
MMS123 G04	1.22	W	EEB11603.1	<i>Pediculus humanus</i>	synaptotagmin-15, putative	9.00E-25	50
MMS133 D04	1.17	W	NS	NS	NS	NS	NS
MMS135 E10	1.18	W	XP_001606006.1	<i>Nasonia vitripennis</i>	Predicted: similar to EG:8D8.7	1.00E-69	70
MMS141 H04	1.26	W	NS	NS	NS	NS	NS
MMS165 E12	1.34	W	XP_001317269.1	<i>Trichamonas vaginalis</i>	hypothetical protein	1.00E-05	44
MMS201 H03	1.17	W	Q4P7C7	<i>Ustilago maydis</i>	UPF0390 protein UM03986	2.00E-06	34
MMS221 E12	1.16	W	P15690	<i>Bos Taurus</i>	NADH-ubiquinone oxidoreductase 75 kDa subunit	2.50E-22	62
MMS233 G08	1.19	W	NS	NS	NS	NS	NS
Contig[0274]	1.31	S	AAW28819.1	<i>Periplenta Americana</i>	Parcxpwnx01	1.00E-16	44
Contig[2070]	1.18	S	NS	NS	NS	NS	NS
Contig[2472]	1.37	S	ACL26692.1	<i>Nilparvata lugens</i>	farnesoic acid O-methyltransferase	1.00E-38	68

Name	Absolute Fold Change	Expression Up	Accession	Organism	BLAST Sequence Match	E-value	ID (%)
MMS134_F02	1.18	S	Q868Z9	<i>D. melanogaster</i>	Papilin precursor	1.70E-31	44
MMS144_F03	1.32	S	EEB11032.1	<i>P. humanus</i>	conserved hypothetical protein	1.00E-24	54
MMS173_E03	1.15	S	XP_001580858.1	<i>T. vaginalis</i>	hypothetical protein	1.00E-36	55
MMS173_H08	1.15	S	NS	NS	NS	NS	NS
MMS206_C06	1.27	S	NS	NS	NS	NS	NS
MMS220_E02	1.19	S	NS	NS	NS	NS	NS

Table 1.10 Quantitative PCR validation of top 5 worker and top 5 soldier expression of combined location dataset. Data is in relation of worker expression patterns compared to those of soldiers of four independent qPCR replicates.

Systematic Name	Average Ratio	Standard Deviation
Contig[0358] (Troponin C, isoform 1)	0.18	0.108
Contig[0330] (Tropomyosin)	0.66	0.195
Contig[0515]	0.95	0.516
MMS206_H02 (Probable exocyst complex component 4)	0.97	0.646
MMS170_B03	1.02	0.572
MMS230_H12	1.02	0.723
MMS108_H02	1.11	0.735
Contig[2197] (uncharacterized protein RP080)	1.16	0.861
MMS220_B04 (Predicted: Similar to RGS-GAIP interacting protein GIPC)	4.57	5.221

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Appendix -A Total BLAST Results

Total Microarray BLAST

Figure A.13 Complete table of all sequences used for microarray construction BLASTX results.

Query Desc	Accession	Definition	Length	E Value	ID (%)
Contig[0006]	P54193	Pheromone-binding protein-related protein 3 precursor (PBPRP-3) (Odorant-binding protein OS-F).	154	2.70E-12	30
Contig[0008]	P50269	ATP synthase a chain (EC 3.6.3.14) (ATPase protein 6).	224	9.80E-66	64
Contig[0012]	P26305	Hemolymph lipopolysaccharide-binding protein precursor (LPS-binding protein) (LPS-BP).	256	1.80E-18	41
Contig[0013]	Q26365	ADP,ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT) (Stress sensitive B protein).	312	2.10E-134	84
Contig[0016]	Q2NКУ6	Dpy-30-like protein.	99	6.50E-14	54
Contig[0020]	Q8VC97	Beta-ureidopropionase (EC 3.5.1.6) (Beta-alanine synthase) (N- carbamoyl-beta-alanine amidohydrolase).	393	1.40E-75	70
Contig[0023]	Q8TA86	Retinitis pigmentosa 9 protein (Pim-1-associated protein) (PAP-1).	221	0.13	58
Contig[0027]	Q91YU8	Suppressor of SWI4 1 homolog (Ssf-1) (Peter Pan homolog).	470	1.40E-42	47
Contig[0029]	Q5TM23	Leukocyte-specific transcript 1 protein.	93	0.61	66
Contig[0031]	P53245	Uncharacterized protein YGR069W.	111	0.036	68
Contig[0039]	Q2KII4	Transcription elongation factor B polypeptide 1 (RNA polymerase II transcription factor SIII subunit C) (SIII p15) (Elongin-C) (EloC) (Elongin 15 kDa subunit).	112	1.10E-52	95
Contig[0042]	P09849	Lactase-phlorizin hydrolase precursor (Lactase-glycosylceramidase) [Includes: Lactase (EC 3.2.1.108);	1926	1.50E-29	51

		Phlorizin hydrolase (EC 3.2.1.62)].			
Contig[0059]	P26221	Endoglucanase E-4 precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase E-4) (Cellulase E-4) (Cellulase E4).	880	7.60E-107	47
Contig[0063]	Q9GJW7	Gamma-aminobutyric acid receptor-associated protein (GABA(A) receptor-associated protein).	117	9.00E-56	93
Contig[0115]	Q80X19	Collagen alpha-1(XIV) chain precursor.	1797	1.20E-08	26
Contig[0117]	P06281	Renin-1 precursor (EC 3.4.23.15) (Angiotensinogenase) (Kidney renin).	402	3.90E-06	34
Contig[0141]	P30238	Non-structural protein 3a precursor (ns3a) (Accessory protein 3a).	57	6.1	30
Contig[0144]	P05659	Myosin-2 heavy chain, non muscle (Myosin II heavy chain, non muscle).	1509	0.0021	34
Contig[0147]	P82174	Lysozyme (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase).	121	1.00E-21	47
Contig[0149]	P29310	14-3-3-like protein (Leonardo protein) (14-3-3 protein zeta).	248	4.00E-117	91
Contig[0156]	P62756	Inter-alpha-trypsin inhibitor (ITI) (GIK-14) (Inhibitory fragment of ITI) (Fragment).	123	7.40E-13	53
Contig[0160]	Q9N2W7	Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 (EC 1.6.5.3) (EC 1.6.99.3) (NADH-ubiquinone oxidoreductase 17.0 kDa subunit).	146	8.90E-33	48
Contig[0161]	Q75VN3	Translationally-controlled tumor protein homolog (TCTP) (BmTCTP).	172	2.40E-71	77
Contig[0166]	Q9I7U4	Titin (D-Titin) (Kettin).	18074	4.60E-46	43
Contig[0205]	Q06684	Thrombin inhibitor rhodniin.	103	0.00023	55
Contig[0207]	Q02446	Transcription factor Sp4 (SPR-1).	784	0.23	26
Contig[0231]	P54516	Uncharacterized protein yqhR.	178	3.8	32
Contig[0232]	P48610	Arginine kinase (EC 2.7.3.3) (AK).	356	4.00E-95	90
Contig[0236]	A0AUQ6	Lin-52 homolog.	112	9.30E-22	53
Contig[0240]	Q9ZT17	Classical arabinogalactan protein 3 precursor.	139	0.19	47
Contig[0242]	Q8TFG9	Uncharacterized serine/threonine-rich protein PB15E9.01c precursor.	943	1.20E-09	25
Contig[0244]	P60372	Keratin-associated protein 10-4 (Keratin-associated protein 10.4) (High sulfur keratin-associated protein 10.4) (Keratin-associated protein 18-4) (Keratin-associated protein 18.4).	401	0.39	30

Contig[0248]	Q9U505	ATP synthase lipid-binding protein, mitochondrial precursor (EC 3.6.3.14) (ATPase protein 9) (ATPase subunit C).	131	1.10E-43	73
Contig[0250]	P41973	Superoxide dismutase [Cu-Zn] (EC 1.15.1.1).	153	6.70E-60	73
Contig[0274]	P34549	Uncharacterized protein R10E11.5.	444	0.0069	21
Contig[0276]	P75130	Uncharacterized protein MG447 homolog.	549	1	28
Contig[0277]	O60658	High affinity cAMP-specific and IBMX-insensitive 3',5'-cyclic phosphodiesterase 8A (EC 3.1.4.17).	829	8.50E-67	48
Contig[0279]	Q8K9N4	UPF0135 protein BUsg_291.	247	0.35	27
Contig[0284]	Q86QH9	Sperm-specific H1/protamine-like protein type 1 precursor [Contains: Sperm-specific protein OE1 (Sperm-specific linker histone H1-like protein OE1); Sperm-specific protein OE3 (Protamine-like OS3)].	202	0.52	100
Contig[0285]	P32583	Suppressor protein SRP40.	406	6.60E-09	29
Contig[0286]	P60984	Glia maturation factor beta (GMF-beta).	142	2.20E-38	51
Contig[0289]	Q8MIT7	Eotaxin precursor (Small-inducible cytokine A11) (CCL11).	97	1.5	33
Contig[0292]	P67837	Sperm protamine-P1.	58	0.013	47
Contig[0294]	Q8I9B4	Metallothionein-4 (MT-4) (Metallothionein D).	44	7.4	59
Contig[0295]	Q6UWN8	Serine protease inhibitor Kazal-type 6 precursor.	80	0.37	28
Contig[0296]	P35550	rRNA 2'-O-methyltransferase fibrillar (EC 2.1.1.-) (Nucleolar protein 1).	327	3.20E-21	65
Contig[0319]	Q17040	Protein G12 precursor (ANG12).	211	3.60E-34	35
Contig[0330]	Q8T6L5	Tropomyosin.	284	4.70E-137	99
Contig[0332]	Q9BTX7	CRAL-TRIO domain-containing protein C20orf121.	342	1.10E-10	24
Contig[0336]	P31402	Vacuolar ATP synthase subunit E (EC 3.6.3.14) (V-ATPase subunit E) (Vacuolar proton pump subunit E) (V-ATPase 26 kDa subunit).	226	6.70E-83	74
Contig[0337]	Q00871	Chymotrypsin BI precursor (EC 3.4.21.1).	271	7.00E-45	40
Contig[0339]	Q02427	RNA-binding protein 1.	144	1.00E-38	71
Contig[0344]	Q94518	Nascent polypeptide-associated complex subunit alpha (NAC-alpha) (Alpha-NAC).	217	9.60E-68	67
Contig[0350]	Q2RJF9	Protein hfq.	84	2.3	38

Contig[0358]	P47947	Troponin C, isoform 1.	154	1.40E-59	81
Contig[0363]	Q5VWG9	Transcription initiation factor TFIID subunit 3 (TBP-associated factor 3) (Transcription initiation factor TFIID 140 kDa subunit) (140 kDa TATA box-binding protein-associated factor) (TAF140) (TAFII140).	929	1.90E-10	61
Contig[0364]	P95509	UPF0231 protein in hemN 3' region (orf1).	125	1	27
Contig[0369]	Q2KI95	Four and a half LIM domains protein 2 (FHL-2).	279	1.70E-100	58
Contig[0370]	P52826	Carnitine O-acetyltransferase precursor (EC 2.3.1.7) (Carnitine acetylase) (CAT) (Carnitine acetyltransferase) (CrAT).	627	5.80E-52	44
Contig[0371]	Q4L9P0	Serine-rich adhesin for platelets precursor.	3608	5.90E-09	23
Contig[0372]	Q17127	Hexamerin precursor.	733	1.70E-54	75
Contig[0373]	P82620	Uncharacterized protein SCRL1 precursor.	92	1.4	34
Contig[0374]	P21138	Serine-rich 25 kDa antigen protein (SHEHP) (SREHP).	233	2.40E-07	29
Contig[0378]	P46150	Moesin/ezrin/radixin homolog 1 (Ezrin-moesin-radixin 1) (Protein D17) (Protein moesin) (dMoesin).	578	5.70E-128	80
Contig[0379]	Q61335	B-cell receptor-associated protein 31 (BCR-associated protein Bap31) (p28 Bap31).	245	4.20E-42	42
Contig[0381]	P23380	Vacuolar ATP synthase 16 kDa proteolipid subunit (EC 3.6.3.14) (Ductin) (VHA16K).	159	6.30E-71	94
Contig[0403]	P12026	Acyl-CoA-binding protein (ACBP) (Diazepam-binding inhibitor) (DBI) (Endozepine) (EP) [Contains: DBI(32-86)].	87	3.80E-22	61
Contig[0407]	P81695	Cadmium-metallothionein (MT) (Fragment).	75	6.3	55
Contig[0409]	O97477	Inositol-3-phosphate synthase (EC 5.5.1.4) (Myo-inositol-1-phosphate synthase) (MI-1-P synthase) (IPS).	565	1.00E-128	72
Contig[0410]	P35779	Venom allergen 3 (Venom allergen III) (Allergen Sol r 3) (Sol r III).	211	1.70E-45	47
Contig[0411]	P25069	Calmodulin-2/3/5 (CaM-2/3/5).	149	8.90E-08	24
Contig[0424]	P06603	Tubulin alpha-1 chain.	450	2.10E-244	98
Contig[0430]	P02993	Elongation factor 1-alpha (EF-1-alpha).	462	2.60E-192	79
Contig[0432]	Q53VB8	Ferritin light chain (Ferritin L subunit).	175	8.20E-12	27
Contig[0435]	Q0VCU1	Iron-responsive element-binding protein 1 (IRE-BP 1) (Iron regulatory protein 1) (IRP1) (Ferritin repressor protein)	889	1.10E-32	65

		(Aconitate hydratase) (EC 4.2.1.3) (Citrate hydro-lyase) (Aconitase).			
Contig[0440]	P53820	Putative uncharacterized protein YNL338W.	52	2.1	54
Contig[0454]	Q9VG95	Glutathione S-transferase D5 (EC 2.5.1.18) (DmGST24).	216	9.60E-52	51
Contig[0457]	O52179	Sulfur globule protein CV2 precursor.	124	0.00013	56
Contig[0458]	Q9BQE4	Selenoprotein S (VCP-interacting membrane protein).	189	6.00E-15	31
Contig[0460]	P81160	Ductus ejaculatorius peptide 99B precursor.	54	1.9	47
Contig[0462]	P62593	Beta-lactamase TEM precursor (EC 3.5.2.6) (TEM-1) (TEM-2) (TEM-3) (TEM-4) (TEM-5) (TEM-6) (TEM-8/CAZ-2) (TEM-16/CAZ-7) (TEM-24/CAZ-6) (IRT-4) (Penicillinase).	286	1.80E-66	81
Contig[0464]	Q9NZ56	Formin-2.	1865	0.0057	45
Contig[0473]	Q2TGJ1	Palmitoyltransferase ZDHHC18 (EC 2.3.1.-) (Zinc finger DHHC domain- containing protein 18) (DHHC-18).	386	2	23
Contig[0479]	P53777	Muscle LIM protein 1.	92	1.20E-39	83
Contig[0480]	P04814	Trypsin alpha precursor (EC 3.4.21.4).	256	3.20E-60	50
Contig[0481]	Q97VE1	UPF0248 protein SSO2687.	81	9	38
Contig[0485]	Q5RAV9	Guanine deaminase (EC 3.5.4.3) (Guanase) (Guanine aminase) (Guanine aminohydrolase) (GAH).	454	3.00E-73	54
Contig[0491]	Q10475	Eukaryotic translation initiation factor 4 gamma (eIF-4-gamma) (eIF- 4G).	1403	2.20E-12	47
Contig[0493]	P35554	Flightin (Muscle protein 27).	182	9.30E-22	38
Contig[0497]	Q9YJU5	Genome polyprotein B (RNA1 polyprotein) [Contains: Protease cofactor (32 kDa protein); Putative helicase (EC 3.6.1.-) (NTP-binding protein) (NTB) (Membrane-binding protein) (58 kDa protein); Viral genome-linked protein (VPg); Picornain 3C-like protease (EC 3.4.22.-) (3C-like protease) (24 kDa protein); RNA-directed RNA polymerase (EC 2.7.7.48) (87 kDa protein)].	1850	3.40E-07	26
Contig[0499]	Q9VQ66	Neuropeptide-like 4 precursor (YSY peptide).	64	0.057	37
Contig[0506]	Q9C102	Putative glutamate synthase [NADPH] (EC 1.4.1.13) (NADPH-GOGAT).	2111	2.30E-67	54
Contig[0509]	P80966	Phospholipase A2, acidic 1 precursor (EC 3.1.1.4)	151	1.9	40

		(Phosphatidylethanolamine 2-acylhydrolase) (APLA2-1) (OHV A-PLA2) (OHV-APLA2).			
Contig[0511]	P09789	Glycine-rich cell wall structural protein 1 precursor.	384	3.00E-24	42
Contig[0512]	P60467	Protein transport protein Sec61 subunit beta.	96	1.30E-31	75
Contig[0515]	P57538	Uncharacterized transporter BU466.	390	8.1	25
Contig[0516]	O60613	15 kDa selenoprotein precursor.	162	1.50E-23	55
Contig[0518]	P51734	Uncharacterized 20.8 kDa protein in lys 3'region (ORF30).	174	8.6	39
Contig[0519]	Q2PQM7	Chitinase-like protein Idgf4 precursor (Imaginal disk growth factor protein 4).	444	3.40E-85	50
Contig[0528]	Q96QK8	Uncharacterized protein C4orf34.	99	1.50E-19	52
Contig[0531]	P97347	Repetin.	1130	0.0056	33
Contig[0532]	P06460	Probable protein E5A.	91	1.4	24
Contig[0533]	Q9UNL2	Translocon-associated protein subunit gamma (TRAP-gamma) (Signal sequence receptor subunit gamma) (SSR-gamma).	185	8.20E-62	68
Contig[0536]	Q6L6Q6	Lysozyme precursor (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase).	137	4.80E-11	33
Contig[0545]	Q9VZ23	GTP-binding nuclear protein Ran.	216	1.40E-107	90
Contig[0547]	O76217	Peritrophin-1 precursor (Peritrophin A) (Peritrophic matrix protein 1) (AgAper-1).	153	1.20E-12	31
Contig[0548]	P13696	Phosphatidylethanolamine-binding protein 1 (PEBP-1) (HCNPpp) (Basic cytosolic 21 kDa protein) [Contains: Hippocampal cholinergic neurostimulating peptide (HCNP)].	187	4.50E-54	61
Contig[0556]	P39989	Putative uncharacterized protein YEL028W precursor.	153	3	24
Contig[0559]	O60356	Nuclear protein 1 (Protein p8) (Candidate of metastasis 1).	82	9.50E-07	42
Contig[0561]	Q99MQ3	Serine/threonine-protein kinase PINK1, mitochondrial precursor (EC 2.7.11.1) (PTEN-induced putative kinase protein 1) (BRPK).	580	1.20E-46	51
Contig[0572]	P02640	Villin-1.	826	4.40E-08	54
Contig[0574]	P60256	Alpha-neurotoxin Bom alpha-6b.	66	0.094	43
Contig[0579]	P58910	Kurtoxin (Ktx).	63	5.2	28

Contig[0586]	P50438	Uncharacterized protein F12A10.7 precursor.	113	6.00E-05	74
Contig[0592]	Q94261	Probable COP9 signalosome complex subunit 7 (Signalosome subunit 7).	390	7.30E-30	26
Contig[0594]	Q9BUJ2	Heterogeneous nuclear ribonucleoprotein U-like protein 1 (Adenovirus early region 1B-associated protein 5) (E1B-55 kDa-associated protein 5) (E1B-AP5).	856	0.00025	34
Contig[0602]	P89079	E4-ORF1 (EC 3.6.1.23) (Probable dUTPase E4 ORF1) (Early E4 14.0 kDa protein) (9ORF1).	125	6.9	36
Contig[0603]	O61064	Tectonin-2 (Tectonin II).	353	1.60E-26	33
Contig[0610]	Q94550	Metallothionein (MT).	73	1.4	41
Contig[0611]	Q7RTY7	Ovochymase-1 precursor (EC 3.4.21.-).	1134	4.10E-11	32
Contig[0613]	Q8N339	Metallothionein-1M (MT-1M) (Metallothionein-1M) (MT-1M).	61	3.2	33
Contig[0618]	P41822	Ferritin subunit precursor (EC 1.16.3.1) (Ferritin heavy chain-like protein) (AeFer(H)).	209	5.90E-11	62
Contig[0619]	P04836	Carboxypeptidase E (EC 3.4.17.10) (CPE) (Carboxypeptidase H) (CPH) (Enkephalin convertase) (Prohormone-processing carboxypeptidase).	434	1.70E-25	48
Contig[0623]	Q9XZ71	Troponin T (TnT).	384	8.30E-172	87
Contig[0625]	Q12797	Aspartyl/asparaginyl beta-hydroxylase (EC 1.14.11.16) (Aspartate beta- hydroxylase) (ASP beta-hydroxylase) (Peptide-aspartate beta- dioxygenase).	758	2.10E-63	47
Contig[0626]	A2ZJC9	Putative glycine-rich cell wall structural protein 1 precursor.	165	0.062	57
Contig[0627]	Q97FK1	Nuclease sbcCD subunit C.	1163	0.0097	27
Contig[0628]	Q9W1C9	Ejaculatory bulb-specific protein 3 precursor (Ejaculatory bulb- specific protein III) (PEB-meIII).	126	6.30E-32	53
Contig[0631]	P29341	Polyadenylate-binding protein 1 (Poly(A)-binding protein 1) (PABP 1).	636	7.00E-41	59
Contig[0633]	Q9UBI1	COMM domain-containing protein 3 (Protein Bup) (Protein PIL).	195	3.90E-20	35
Contig[0637]	O77237	Protein pellino.	424	3.90E-20	67
Contig[0643]	P83360	Cuticle protein 7 isoform b (LpCP7b).	59	6.7	30
Contig[0649]	P32323	A-agglutinin anchorage subunit precursor (A-agglutinin cell	725	1.00E-06	34

		wall attachment subunit).			
Contig[0651]	P25679	Weak toxin CM-9a.	64	1.8	37
Contig[0652]	P35501	Esterase E4 precursor (EC 3.1.1.1) (Carboxylic-ester hydrolase).	552	3.20E-12	26
Contig[0653]	Q4U3L0	Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH).	333	1.20E-142	83
Contig[0654]	P47179	Cell wall protein DAN4 precursor.	1161	1.10E-18	45
Contig[0657]	P20962	Parathymosin.	102	0.28	61
Contig[0660]	Q7Z1B8	Protein transport protein SEC61 subunit gamma.	68	3.10E-30	97
Contig[0666]	Q7T6T0	Envelope small membrane protein (E protein) (sM protein).	82	0.53	35
Contig[0668]	Q9U8M0	Vitellogenin-1 precursor (Vg-1).	1896	2.50E-77	40
Contig[0672]	P05227	Histidine-rich protein precursor (Clone PFHRP-II).	332	1.50E-21	30
Contig[0676]	Q97K14	ATP phosphoribosyltransferase regulatory subunit.	407	5	28
Contig[0677]	Q25641	Allergen Cr-PI precursor (Allergen Per a 3).	685	3.00E-74	74
Contig[0679]	P39561	Uncharacterized protein YAR061W/YHR212W-A.	67	2.6	40
Contig[0680]	P11860	Sperm-specific protein Phi-3 (PL-IV).	45	1.2	55
Contig[0684]	O42395	Cellular nucleic acid-binding protein (CNBP) (Zinc finger protein 9).	172	1.00E-16	42
Contig[0685]	O70556	Small proline-rich protein 2E.	76	8.3	50
Contig[0689]	P62147	Calmodulin-1 (CaM 1).	149	1.60E-74	100
Contig[0694]	P21525	Transcription factor kayak (Fos-related antigen) (dFra) (AP-1).	722	4.70E-11	48
Contig[0697]	P41509	Fatty acid-binding protein, muscle (M-FABP).	134	1.90E-30	56
Contig[0698]	Q9VHT4	Probable GDP-fucose transporter.	337	4.90E-48	65
Contig[0702]	Q7SA23	Exoglucanase 1 precursor (EC 3.2.1.91) (Exocellobiohydrolase 1) (1,4- beta-cellobiohydrolase 1).	521	1.30E-73	56
Contig[0703]	Q9QXT0	MIR-interacting saposin-like protein precursor (Transmembrane protein 4) (Putative secreted protein ZSIG9).	182	1.10E-29	42
Contig[0707]	P37167	Actophorin.	138	7.40E-29	48
Contig[0708]	P68620	Protein A54.	90	0.26	30
Contig[0712]	O24463	Dof zinc finger protein PBF (Prolamin box-binding factor).	328	0.55	65

Contig[0714]	O62809	Orexin receptor type 2 (Ox2r) (Hypocretin receptor type 2) (Fragment).	77	5.3	34
Contig[0716]	Q5ZLM8	Protein FAM133.	250	0.17	70
Contig[0719]	Q8N1F7	Nuclear pore complex protein Nup93 (Nucleoporin Nup93) (93 kDa nucleoporin).	819	0.0011	63
Contig[0720]	O51318	Glutamyl-tRNA(Gln) amidotransferase subunit C (EC 6.3.5.-) (Glu-ADT subunit C).	91	0.042	34
Contig[0723]	P22700	Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type (EC 3.6.3.8) (Calcium pump).	1020	3.60E-109	81
Contig[0726]	P83311	Bowman-Birk type proteinase inhibitor (TBPI-B).	80	0.23	52
Contig[0727]	P40945	ADP-ribosylation factor 2 (dARF II).	180	9.30E-22	90
Contig[0739]	P00771	Brachyurin (EC 3.4.21.32) (Collagenolytic protease).	226	7.00E-43	45
Contig[0741]	Q74CA8	Exodeoxyribonuclease 7 small subunit (EC 3.1.11.6) (Exodeoxyribonuclease VII small subunit) (Exonuclease VII small subunit).	76	4.1	32
Contig[0744]	P26199	Profilin-1 (Profilin I).	126	2.60E-17	35
Contig[0753]	Q96D42	Hepatitis A virus cellular receptor 1 precursor (HAVcr-1) (T cell immunoglobulin and mucin domain-containing protein 1) (TIMD-1) (T cell membrane protein 1) (TIM-1) (TIM).	359	2.2	40
Contig[0759]	Q9NY64	Solute carrier family 2, facilitated glucose transporter member 8 (Glucose transporter type 8) (GLUT-8) (Glucose transporter type X1).	477	1.30E-48	36
Contig[0762]	P44836	Probable hemoglobin and hemoglobin-haptoglobin-binding protein 3 precursor.	1084	3.50E-07	44
Contig[0765]	Q70PU1	Peptidoglycan-recognition protein-SC2 precursor (EC 3.5.1.28).	184	2.00E-37	48
Contig[0767]	O96049	Defensin precursor.	79	3.10E-15	52
Contig[0768]	Q9V8Y9	General odorant-binding protein 56h precursor.	134	0.0016	28
Contig[0770]	P28086	Small hydrophobic protein.	57	1.6	44
Contig[0774]	P14318	Muscle-specific protein 20.	184	3.30E-65	72
Contig[0776]	Q9W141	Putative ATP synthase f chain, mitochondrial (EC 3.6.3.14).	107	7.30E-45	73
Contig[0779]	P02840	Salivary glue protein Sgs-3 precursor.	307	0.0014	43

Contig[0781]	Q751F9	Elongin-C.	100	3.60E-05	34
Contig[0783]	Q9UNQ2	Probable dimethyladenosine transferase (EC 2.1.1.-) (S-adenosylmethionine-6-N',N'-adenosyl(rRNA) dimethyltransferase) (18S rRNA dimethylase) (DIM1 dimethyladenosine transferase 1-like).	313	2.50E-110	82
Contig[0786]	P82321	Termicin.	36	2.60E-08	66
Contig[0790]	Q0GY41	Potassium channel toxin beta-KTx precursor (Hge-beta-KTx).	79	0.013	52
Contig[0796]	P33506	ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).	53	0.28	42
Contig[0798]	Q06852	Cell surface glycoprotein 1 precursor (Outer layer protein B) (S-layer protein 1).	2313	0.039	30
Contig[1313]	P15145	Aminopeptidase N (EC 3.4.11.2) (pAPN) (Alanyl aminopeptidase) (Microsomal aminopeptidase) (Aminopeptidase M) (gp130) (CD13 antigen).	963	1.90E-26	28
Contig[1354]	P45376	Aldose reductase (EC 1.1.1.21) (AR) (Aldehyde reductase).	316	2.40E-58	55
Contig[1362]	O64818	Uncharacterized protein At2g23090.	78	5.90E-11	47
Contig[1364]	P31478	Vacuolar ATP synthase subunit F (EC 3.6.3.14) (V-ATPase subunit F) (Vacuolar proton pump subunit F) (V-ATPase 14 kDa subunit).	124	1.40E-23	48
Contig[1366]	P30740	Leukocyte elastase inhibitor (LEI) (Serpin B1) (Monocyte/neutrophil elastase inhibitor) (M/NEI) (EI).	379	2.00E-26	55
Contig[1370]	P52907	F-actin capping protein subunit alpha-1 (CapZ alpha-1).	286	3.10E-30	30
Contig[1393]	Q6DCP1	FAD-dependent oxidoreductase domain-containing protein 1.	499	2.20E-34	61
Contig[1422]	Q9P0U1	Probable mitochondrial import receptor subunit TOM7 homolog (Translocase of outer membrane 7 kDa subunit homolog).	55	8.40E-12	50
Contig[1423]	Q9UHA4	Mitogen-activated protein kinase kinase 1-interacting protein 1 (MEK-binding partner 1) (Mp1).	124	2.70E-15	33
Contig[1424]	P47948	Troponin C, isoform 2.	155	3.50E-61	81
Contig[1427]	Q8VCS0	N-acetylmuramoyl-L-alanine amidase precursor (EC 3.5.1.28) (Peptidoglycan recognition protein long) (PGRP-	530	1.70E-36	50

		L) (Peptidoglycan recognition protein 2) (TagL).			
Contig[1434]	P05661	Myosin heavy chain, muscle.	1962	2.30E-69	91
Contig[1443]	O75533	Splicing factor 3B subunit 1 (Spliceosome-associated protein 155) (SAP 155) (SF3b155) (Pre-mRNA-splicing factor SF3b 155 kDa subunit).	1304	3.50E-18	76
Contig[1473]	O49996	14-3-3-like protein D.	249	1.00E-31	43
Contig[1474]	Q13131	5'-AMP-activated protein kinase catalytic subunit alpha-1 (EC 2.7.11.1) (AMPK alpha-1 chain).	550	2.80E-52	43
Contig[1476]	Q9CPU0	Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D- lactoylglutathione methylglyoxal lyase).	184	2.60E-63	65
Contig[1484]	Q20655	14-3-3-like protein 2.	248	3.50E-45	42
Contig[1494]	Q9N1F5	Glutathione transferase omega-1 (EC 2.5.1.18) (GSTO 1-1) (Glutathione- dependent dehydroascorbate reductase).	241	4.30E-43	43
Contig[1503]	P40320	S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine adenosyltransferase) (AdoMet synthetase).	408	9.90E-148	79
Contig[1509]	P21914	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial precursor (EC 1.3.5.1) (IP).	297	1.10E-114	80
Contig[1533]	P24067	Luminal-binding protein 2 precursor (BiP2) (Heat shock protein 70 homolog 2) (B70) (B-70).	663	1.20E-106	62
Contig[1534]	Q501J6	Probable ATP-dependent RNA helicase DDX17 (EC 3.6.1.-) (DEAD box protein 17).	650	3.30E-17	71
Contig[1538]	Q9NJH0	Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma).	431	8.60E-81	76
Contig[1541]	P55115	Zinc metalloproteinase nas-15 precursor (EC 3.4.24.21) (Nematode astacin 15).	571	2.00E-32	57
Contig[1546]	P08841	Tubulin beta-3 chain (Beta-3 tubulin).	454	1.10E-107	94
Contig[1548]	Q7XMK8	DEAD-box ATP-dependent RNA helicase 6 (EC 3.6.1.-).	498	5.10E-60	54
Contig[1583]	Q3ZBV9	Dehydrogenase/reductase SDR family member 11 precursor (EC 1.-.-.-).	255	3.50E-61	53
Contig[1594]	P22907	Porphobilinogen deaminase (EC 2.5.1.61) (Hydroxymethylbilane synthase) (HMBS) (Pre-uroporphyrinogen synthase) (PBG-D).	361	6.20E-39	45

Contig[1597]	Q9M3T9	Defender against cell death 1 (DAD-1).	115	1.70E-13	35
Contig[1600]	Q8NFH4	Nucleoporin Nup37 (p37).	326	4.90E-14	43
Contig[1605]	Q5ZME2	Malate dehydrogenase, cytoplasmic (EC 1.1.1.37) (Cytosolic malate dehydrogenase).	334	1.80E-101	68
Contig[1606]	Q9GZR5	Elongation of very long chain fatty acids protein 4.	314	3.30E-24	51
Contig[1607]	P36188	Troponin I (Tn I) (Protein wings apart-A) (Protein heldup).	269	4.00E-83	79
Contig[1615]	Q8SX83	Protein split ends.	5560	1.90E-71	75
Contig[1629]	P07103	Endoglucanase Z precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase Z) (Cellulase Z) (EGZ).	426	1.20E-49	40
Contig[1630]	P54680	Fimbrin.	610	2.50E-74	50
Contig[1631]	P34121	Coactosin (Cytoskeletal p17 protein) (Cyclic AMP-regulated protein p16).	146	1.10E-18	37
Contig[1633]	Q9W092	Probable chitinase 2 precursor (EC 3.2.1.14).	484	9.10E-61	42
Contig[1638]	Q9VSA3	Probable medium-chain specific acyl-CoA dehydrogenase, mitochondrial precursor (EC 1.3.99.3) (MCAD).	419	8.30E-140	79
Contig[1639]	Q02960	Macrophage migration inhibitory factor (MIF) (Phenylpyruvate tautomerase) (EC 5.3.2.1).	115	1.20E-21	43
Contig[1646]	Q27268	ATP-dependent RNA helicase WM6 (EC 3.6.1.-) (DEAD box protein UAP56) (HEL/UAP56).	424	1.00E-36	89
Contig[1649]	O15258	Protein RER1.	196	2.10E-47	72
Contig[1656]	Q9V3P0	Peroxiredoxin 1 (EC 1.11.1.15) (Thioredoxin peroxidase) (Cytosolic thioredoxin peroxidase) (DmTPx-1) (DPx-4783).	194	2.70E-77	75
Contig[1658]	Q9C5W6	14-3-3-like protein GF14 iota (General regulatory factor 12).	268	1.50E-51	42
Contig[1662]	P81225	Cuticle protein 21 (LM-ACP 21).	169	2.10E-43	72
Contig[1663]	Q64617	Protein kinase C eta type (EC 2.7.11.13) (nPKC-eta) (PKC-L).	683	2.60E-10	42
Contig[1667]	P18172	Glucose dehydrogenase [acceptor] precursor (EC 1.1.99.10) [Contains: Glucose dehydrogenase [acceptor] short protein].	625	7.20E-34	48
Contig[1671]	Q17005	Lysozyme c-1 precursor (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase).	140	2.10E-29	46
Contig[1672]	Q99PV0	Pre-mRNA-processing-splicing factor 8 (Splicing factor Prp8).	2335	4.70E-134	89

Contig[1675]	Q8MJY8	15-hydroxyprostaglandin dehydrogenase [NAD+] (EC 1.1.1.141) (PGDH) (Prostaglandin dehydrogenase 1).	266	4.80E-32	43
Contig[1678]	Q2KJE4	Electron transfer flavoprotein subunit alpha, mitochondrial precursor (Alpha-ETF).	333	4.50E-109	61
Contig[1681]	O33600	DNA double-strand break repair rad50 ATPase.	886	3.00E-06	27
Contig[1684]	P53880	Putative uncharacterized protein YNL179C.	145	0.87	38
Contig[1688]	Q8K2A8	Dolichyl-P-Man:Man(5)GlcNAc(2)-PP-dolichyl mannosyltransferase (Dol-P-Man-dependent alpha(1-3)-mannosyltransferase) (Not56-like protein)	438	1.7	37
Contig[1695]	Q6GUG4	P2Y purinoceptor 13 (P2Y13).	336	6.5	29
Contig[1697]	O22263	Probable protein disulfide-isomerase A6 precursor (EC 5.3.4.1) (P5).	361	4.80E-42	40
Contig[1709]	P30883	Tubulin beta-4 chain.	445	1.90E-216	93
Contig[1710]	Q9Y6X3	Uncharacterized protein KIAA0892 precursor	613	3.6	38
Contig[1711]	Q0AUH7	Elongation factor G 2 (EF-G 2)	694	1.6	53
Contig[1713]	P36265	Transcription antitermination protein nusG	205	1.7	41
Contig[1715]	Q9H2K2	Tankyrase-2 (EC 2.4.2.30) (TANK2) (Tankyrase II) (TNKS-2) (TRF1- interacting ankyrin-related ADP-ribose polymerase 2) (Tankyrase-like protein) (Tankyrase-related protein).	1166	5.40E-19	36
Contig[1716]	P42660	Vitellogenic carboxypeptidase precursor (EC 3.4.16.-).	471	1.90E-20	44
Contig[1718]	Q03385	Ral guanine nucleotide dissociation stimulator (RalGEF) (RalGDS)	852	0.82	36
Contig[1719]	Q6CF41	FK506-binding protein 1 (EC 5.2.1.8) (FKBP) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rapamycin-binding protein).	108	6.40E-21	49
Contig[1720]	Q8STA9	UPF0329 protein ECU05_1680/ECU11_0050.	612	9.60E-11	44
Contig[1722]	Q645U4	Taste receptor type 2 member 4 (T2R4)	299	7.9	24
Contig[1726]	P49023	Paxillin.	591	1.40E-78	59
Contig[1726]	P41877	Chromatin remodelling complex ATPase chain isw-1 (Nucleosome remodeling factor subunit isw-1)	1009	7	36
Contig[1727]	Q3IYI5	DNA mismatch repair protein mutS	875	0.075	37
Contig[1728]	O15439	Multidrug resistance-associated protein 4 (ATP-binding)	1325	3.20E-09	66

		cassette sub- family C member 4) (MRP/cMOAT-related ABC transporter) (Multi-specific organic anion transporter-B) (MOAT-B).			
Contig[1728]	Q51UJ9	Autophagy-related protein 11	1337	0.034	31
Contig[1730]	P20241	Neuroglian precursor.	1302	1.90E-49	34
Contig[1731]	Q9H8Y1	Uncharacterized protein C14orf115	702	0.22	36
Contig[1732]	P07882	Bile salt-activated lipase precursor (BAL) (Bile salt-stimulated lipase) (BSSL) (Carboxyl ester lipase) (Sterol esterase) (Cholesterol esterase) (Pancreatic lysophospholipase)	612	7.00E-06	25
Contig[1733]	Q88893	RNA1 polyprotein (P1) [Contains: P1A protein (1A) (Protease cofactor); Putative ATP-dependent helicase (NTP-binding protein) (NTB) (1B) (Membrane-binding protein); Viral genome-linked protein (1C-VPg); Picornain 3C-like protease (3C-like protease) (1D-PRO); RNA-directed RNA polymerase (1E-POL)]	2304	3.4	36
Contig[1734]	Q9Z1D8	Zinc finger protein with KRAB and SCAN domains 5 (Zinc finger protein 95) (Zfp-95)	819	7	42
Contig[1736]	P46640	Homeobox protein knotted-1-like 2 (KNAT2) (ATK1)	310	0.11	27
Contig[1737]	P10762	Apolipoprotein-3b precursor (Apolipoprotein-IIIb) (ApoLp-IIIb).	179	1.00E-05	28
Contig[1741]	P04733	Metallothionein-1F (MT-1F) (Metallothionein-IF) (MT-IF).	61	0.17	58
Contig[1758]	P41951	Glutamine/asparagine-rich protein pqn-25 (Prion-like-(Q/N-rich) domain-bearing protein 25).	672	3.70E-07	31
Contig[1895]	Q870V7	Protein PNS1	554	1.1	35
Contig[1915]	Q23868	Prestalk-specific protein tagC precursor	1743	2.4	32
Contig[1919]	Q01027	Hypothetical gene 41 protein	161	5.6	44
Contig[1924]	P53849	Zinc finger protein GIS2	153	2.3	30
Contig[1927]	Q8BI22	Uncharacterized protein C14orf145 homolog	524	0.55	22
Contig[1931]	O60312	Probable phospholipid-transporting ATPase VA (ATPVA) (Aminophospholipid translocase VA)	1499	2.8	35
Contig[1932]	O51762	Uncharacterized protein BB_0822.	31	8.2	53
Contig[1933]	O62709	Endothelin B receptor precursor (ET-B) (Endothelin	443	1.5	26

		receptor Non-selective type)			
Contig[1936]	Q0VDE8	Adipogenin.	80	7.5	60
Contig[1937]	O14718	Visual pigment-like receptor peropsin	337	6.4	31
Contig[1940]	Q944R7	Probable protein arginine N-methyltransferase 7	724	6.8	32
Contig[1945]	P82107	Bdellastasin (Bdellin A).	59	5.6	40
Contig[1946]	Q2KIL5	Protein disulfide-isomerase A5 precursor	521	0.08	31
Contig[1947]	P08155	Krueppel homologous protein 1	845	2.9	34
Contig[1949]	Q68XA0	Ubiquinol-cytochrome c reductase iron-sulfur subunit (Rieske iron-sulfur protein) (RISP)	177	4	42
Contig[1956]	Q3THG9	Alanyl-tRNA synthetase domain-containing protein 1	412	3.1	34
Contig[1958]	Q8MSS1	Protein lava lamp	2779	0.006	31
Contig[1959]	P41809	Hansenula MRAKII killer toxin-resistant protein 1 precursor	1802	1.8	37
Contig[1960]	Q9ES73	Melanoma-associated antigen D1 (MAGE-D1 antigen) (Neurotrophin receptor-interacting MAGE homolog) (Sertoli cell necdin-related gene protein 1) (SNERG-1)	775	0.017	53
Contig[1961]	P15306	Thrombomodulin precursor (TM) (Fetomodulin) (CD141 antigen)	577	1.7	24
Contig[1962]	Q5KLN2	Transcription factor FET5 (Factor of eukaryotic transcription 5)	287	6.2	37
Contig[1963]	Q5UNX5	Uncharacterized protein L725	224	9.7	34
Contig[1967]	Q5X9M0	Probable dipeptidase B	499	8.6	66
Contig[1972]	Q62901	Arginine-glutamic acid dipeptide repeats protein (Atrophin-1-related protein).	1559	0.2	42
Contig[1978]	Q9UVG6	Putative serine/threonine-protein kinase VPS15 (Vacuolar protein sorting-associated protein 15)	1340	9.6	37
Contig[1979]	Q9SZ44	F-box/LRR-repeat protein At4g27050	453	4.9	45
Contig[1980]	O35923	Breast cancer type 2 susceptibility protein homolog (Fanconi anemia group D1 protein homolog)	3343	3.9	37
Contig[1982]	P54739	Serine/threonine protein kinase pkaA	543	3.00E-09	29
Contig[1983]	P20547	Uncharacterized 11.2 kDa protein.	91	6.3	50
Contig[1984]	Q9HGQ3	Uncharacterized transporter C17D4.03c	732	0.14	37
Contig[1986]	O95487	Protein transport protein Sec24B (SEC24-related protein B)	1268	0.89	25

Contig[1987]	P23225	Ferredoxin-dependent glutamate synthase, chloroplast precursor (Fd-GOGAT)	1616	0.21	29
Contig[1988]	Q8K9M6	Zinc import ATP-binding protein znuC (EC 3.6.3.-).	238	7.2	44
Contig[1989]	O32101	Bacteriophage SPP1 adsorption protein yueB (Bacteriophage SPP1 receptor protein yueB)	1076	0.94	28
Contig[1991]	Q7REH6	Glutathione S-transferase (EC 2.5.1.18).	209	0.17	39
Contig[1992]	Q09666_1	[Segment 1 of 2] Neuroblast differentiation-associated protein AHNAK (Desmoyokin)	1683	0.004	21
Contig[1995]	Q96KM6	Zinc finger protein 512B.	892	4.50E-06	30
Contig[1996]	P54479	Zinc-specific metallo-regulatory protein	145	3.1	33
Contig[1998]	Q49409	Uncharacterized protein MG277	970	2.5	27
Contig[2000]	Q09638	Probable G-protein coupled receptor T27D1.3	356	3.1	30
Contig[2002]	Q5DID0	Uromodulin-like 1 precursor (Olfactorin)	1318	3	37
Contig[2004]	O29249	Uncharacterized protein AF_1013	136	7.5	31
Contig[2025]	P38628	Phosphoacetylglucosamine mutase (PAGM) (Acetylglucosamine phosphomutase) (N-acetylglucosamine-phosphate mutase)	557	6.1	24
Contig[2048]	Q38861	DNA repair helicase XPB1 (XPB homolog 1) (ERCC3 homolog 1) (RAD25 homolog 1) (AtXPB1) (Protein araXPB)	767	1.4	35
Contig[2051]	Q9P6S0	Uncharacterized threonine-rich protein C1742.01 precursor	1563	7.00E-08	33
Contig[2054]	Q09684	Nuclear fusion protein tht1	577	4.6	30
Contig[2055]	Q04688	DNA-binding protein D-ELG	464	2.4	35
Contig[2057]	Q19269	Zinc metalloproteinase nas-14 precursor (Nematode astacin 14)	503	2.00E-06	35
Contig[2058]	P12954	ATP-dependent DNA helicase SRS2	1174	0.7	23
Contig[2060]	P11799	Myosin light chain kinase, smooth muscle (MLCK) (Telokin)	1906	6.00E-05	45
Contig[2061]	Q9D5U9	MICAL C-terminal-like protein	520	3.1	46
Contig[2064]	Q9NZR2	Low-density lipoprotein receptor-related protein 1B precursor (Low-density lipoprotein receptor-related protein-deleted in tumor) (LRP-DIT)	4599	0.36	28
Contig[2067]	Q5UPL6	Putative BTB/POZ domain and WD-repeat protein R154	468	3.5	26

Contig[2070]	P09344	Hemagglutinin precursor [Contains: Hemagglutinin HA1 chain; Hemagglutinin HA2 chain]	563	8.5	32
Contig[2072]	Q3V0Q7	Transmembrane protease, serine 12 precursor	336	2.7	39
Contig[2077]	Q93A44	Amino acid racemase (Vancomycin E-type resistance protein vanT)	702	6.6	22
Contig[2090]	P41849	Uncharacterized glycine receptor-like protein T20B12.9	476	7.1	50
Contig[2096]	P15811	Uncharacterized protein ycf49 (ORF102).	102	3.2	38
Contig[2110]	P22100	Trp operon leader peptide.	41	1.6	66
Contig[2112]	Q7K480	BIN3 domain-containing protein bin3 (Bicoid-interacting protein 3)	1367	9.1	48
Contig[2114]	P39016	Suppressor protein MPT5 (Protein HTR1)	859	2.5	23
Contig[2115]	P09290	Gene 39 membrane protein	240	1.7	31
Contig[2117]	O60813	PRAME family member 11	436	3.4	34
Contig[2118]	Q7MLY4	Error-prone DNA polymerase	1024	1.9	34
Contig[2119]	A2RRS8	Centrosomal protein of 78 kDa (Protein Cep78)	727	4.8	36
Contig[2121]	P23487	Protein midgut expression 1.	83	0.053	46
Contig[2122]	P09342	Acetolactate synthase 1, chloroplast precursor (Acetolactate synthase I) (Acetohydroxy-acid synthase I) (ALS I)	667	1.7	40
Contig[2123]	Q01157	Glycine-rich cell wall structural protein (Clone W10-1) (Fragment).	43	6.3	46
Contig[2145]	Q09574	Hypothetical 31.5 kDa protein K02A2.4 in chromosome II	276	1.8	46
Contig[2151]	P47436	Phenylalanyl-tRNA synthetase alpha chain (Phenylalanine--tRNA ligase alpha chain) (PheRS)	341	8.9	32
Contig[2162]	P76616	Uncharacterized protein ygaQ	750	7.1	37
Contig[2166]	P07589	Fibronectin (FN)	2265	2.6	55
Contig[2182]	O31555	Uncharacterized lipoprotein yfjD precursor	185	1.6	45
Contig[2184]	P50493	Duffy receptor beta form precursor (Erythrocyte-binding protein)	1153	1.4	34
Contig[2186]	O96651	DNA topoisomerase 3-beta (DNA topoisomerase III beta)	875	5.6	34
Contig[2188]	P17053	G surface protein, allelic form 168 precursor.	2704	5.00E-09	26
Contig[2191]	Q93YQ7	Endoglucanase 24 precursor (Endo-1,4-beta glucanase 24)	497	2.6	28
Contig[2192]	Q12452	3-keto-steroid reductase	347	1.7	34

Contig[2197]	Q9ZE67	Uncharacterized protein RP080	50	3.4	38
Contig[2211]	O50248	DNA repair and recombination protein radB	216	1.6	36
Contig[2213]	Q89AY6	Protein pmbA homolog	448	0.2	22
Contig[2214]	Q9X0D2	ATP phosphoribosyltransferase (ATP-PRTase) (ATP-PRT)	208	2.7	27
Contig[2225]	Q60976	Jerky protein	557	3.00E-06	34
Contig[2230]	P29754	Type-1A angiotensin II receptor (AT1) (AT1A)	359	5.9	27
Contig[2237]	O57030	Probable DNA-directed RNA polymerase beta chain (Late expression factor 8)	909	5.8	27
Contig[2238]	Q96688	Early E3 22.1 kDa glycoprotein	194	3	31
Contig[2246]	Q5VZM2	Ras-related GTP-binding protein B (Rag B) (RagB)	374	0.004	95
Contig[2247]	Q6FK87	Histone transcription regulator 3 homolog	1615	2.4	26
Contig[2250]	Q8W104	F-box/LRR-repeat protein 17	593	0.18	27
Contig[2257]	Q9MTH5	Putative membrane protein ycf1	2434	0.53	31
Contig[2260]	Q70EL1	Inactive ubiquitin carboxyl-terminal hydrolase 54 (Inactive ubiquitin-specific peptidase 54)	891	4.8	23
Contig[2263]	Q91WW4	Mas-related G-protein coupled receptor member A2	305	0.86	22
Contig[2264]	Q6F598	Reverse gyrase [Includes: Helicase ; Topoisomerase] [Contains: Pko r-Gyr intein]	1711	6.6	30
Contig[2265]	P36133	Putative uncharacterized protein YKR040C.	167	2.60E-05	47
Contig[2267]	Q44906	Flagellar biosynthetic protein fliQ.	87	1.8	25
Contig[2279]	Q62635	Mucin-2 precursor (Intestinal mucin-2) (Fragment).	1513	0.0045	51
Contig[2281]	Q86VI3	Ras GTPase-activating-like protein IQGAP3	1631	4.4	22
Contig[2282]	Q9IKD1	Spike glycoprotein precursor (S glycoprotein) (Peplomer protein) (E2) [Contains: Spike protein S1 (90B); Spike protein S2 (90A)]	1360	4.1	40
Contig[2283]	Q44775	Cell division protein ftsW	364	5.4	35
Contig[2284]	Q8WY91	THAP domain-containing protein 4	577	3.2	33
Contig[2293]	O76879	Circadian clock-controlled protein precursor	260	6.00E-10	23
Contig[2298]	Q9H386	Uncharacterized protein C21orf116.	69	0.084	35
Contig[2302]	O60412	Olfactory receptor 7C2 (Olfactory receptor 19-18) (OR19-18)	319	5	33
Contig[2306]	Q898C7	Chaperone clpB	865	4.9	30

Contig[2307]	O83052	Uncharacterized protein TP_0007	216	7.3	38
Contig[2310]	Q06077	Abrin-b precursor [Contains: Abrin-b A chain (rRNA N-glycosidase); Linker peptide; Abrin-b B chain]	527	0.001	29
Contig[2320]	Q4J9A0	CCA-adding enzyme (tRNA nucleotidyltransferase) (tRNA adenyl-yl-/cytidyl-yl- transferase) (tRNA CCA-pyrophosphorylase) (tRNA-NT)	416	3	27
Contig[2324]	Q867Z4	Longitudinals lacking protein, isoforms F/I/K/T.	970	0.55	34
Contig[2325]	Q8K9S5	Uncharacterized protein BUsg_231 precursor	799	9.6	29
Contig[2326]	Q6Y657	Ribonucleoside-diphosphate reductase small chain B (Ribonucleotide reductase small subunit B) (Ribonucleoside-diphosphate reductase R2B subunit)	333	10	41
Contig[2327]	Q03153	Uncharacterized protein YMR098C	612	0.7	28
Contig[2336]	Q95LH1	Probable G-protein coupled receptor 1	355	3.3	21
Contig[2338]	Q9GK79	Urokinase plasminogen activator surface receptor precursor (uPAR) (U-PAR) (CD87 antigen)	335	3.8	31
Contig[2339]	P17991	C-hordein (Clone PC HOR1-3) (Fragment).	72	8.2	34
Contig[2340]	P49291	Lazarillo protein precursor	214	4.00E-07	23
Contig[2343]	Q9ZAA7	Glutaconyl-CoA decarboxylase subunit gamma (EC 4.1.1.70) (Biotin carrier).	145	0.004	54
Contig[2347]	Q6K117	Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase) (HisRS).	445	0.43	37
Contig[2357]	Q8VGG7	Olfactory receptor 181 (Olfactory receptor 184-4)	317	0.27	30
Contig[2359]	P58727	Toll-like receptor 4 precursor (CD284 antigen)	833	5.7	42
Contig[2360]	Q7T6Y1	Putative serine/threonine-protein kinase R436	276	3.1	34
Contig[2363]	O75445	Usherin precursor (Usher syndrome type-2A protein) (Usher syndrome type IIa protein)	5202	0.62	31
Contig[2366]	Q24048	Sodium/potassium-transporting ATPase subunit beta-2 (Sodium/potassium-dependent ATPase beta-2 subunit) (Protein nervana 2)	323	2.00E-05	47
Contig[2373]	P51914	Gap junction Cx41 protein (Connexin-41)	352	0.41	45
Contig[2378]	P83212	Sperm protamine P2.	58	0.00072	45
Contig[2380]	Q8NH02	Olfactory receptor 2T29	315	7.5	28
Contig[2384]	Q6FJJ0	Presequence translocated-associated motor subunit PAM17,	186	0.2	47

		mitochondrial precursor.			
Contig[2389]	P25050	Saimiri transformation-associated protein (stpC) (Collagen-like protein).	105	0.076	55
Contig[2393]	P03596	Movement protein (MP) (Protein 3A)	300	1.7	30
Contig[2402]	P38834	Putative uncharacterized protein YHR130C.	111	0.52	33
Contig[2403]	A3LRW2	ATP-dependent RNA helicase DBP3 (EC 3.6.1.-).	526	7.50E-07	68
Contig[2409]	O60157	Leucine carboxyl methyltransferase 2 (tRNA wybutosine-synthesizing protein 4)	681	1.4	37
Contig[2420]	Q12460	Protein SIK1 (Nucleolar protein NOP56) (Suppressor of I kappa b protein 1).	504	0.0097	65
Contig[2421]	P17469	Major DNA-binding protein (Infected cell protein 8) (ICP 8 protein)	1196	5.4	33
Contig[2423]	Q969W8	Zinc finger protein 566	418	7	46
Contig[2424]	Q92968	Peroxisomal membrane protein PEX13 (Peroxin-13)	403	5.00E-04	59
Contig[2432]	Q9JHY7	Baculoviral IAP repeat-containing protein 5 (Apoptosis inhibitor survivin)	142	8.9	40
Contig[2439]	Q9BGL9	Uncharacterized protein C6orf15 homolog precursor (Protein STG) (rmSTG)	314	0.47	36
Contig[2440]	Q2YDN4	Coiled-coil domain-containing protein 105	500	8	31
Contig[2445]	P26514	Endo-1,4-beta-xylanase A precursor (Xylanase A) (1,4-beta-D-xylan xylanohydrolase A)	477	3.00E-08	29
Contig[2449]	Q07647	Solute carrier family 2, facilitated glucose transporter member 3 (Glucose transporter type 3, brain) (GLUT-3)	493	2.4	50
Contig[2451]	P50487	Putative purine permease CPE0397	452	2	36
Contig[2461]	Q0VGE8	Zinc finger protein 816A	652	0.06	43
Contig[2464]	Q13606	Olfactory receptor 5I1 (Olfactory receptor OR11-159) (Olfactory receptor-like protein OLF1).	314	0.65	33
Contig[2471]	P35459	Lymphocyte antigen 6D precursor (Ly-6D) (Thymocyte B-cell antigen) (ThB)	127	8.00E-04	27
Contig[2472]	Q66S17	Natterin-3 precursor (EC 3.4.-.-).	364	0.0066	33
Contig[2477]	O13854	Serine/threonine-rich protein adg2 precursor (Meiotically up-regulated gene 46 protein)	670	0.11	23
Contig[2482]	P19086	Guanine nucleotide-binding protein G(z) subunit alpha	355	3.7	51

		(G(x) alpha chain) (Gz-alpha)			
Contig[2491]	P41044	Calbindin-32	310	1.00E-05	59
Contig[2495]	Q3T0C8	PDZ and LIM domain protein 2	348	6.00E-06	36
Contig[2496]	O67248	Uncharacterized protein aq_1188	155	3.8	37
Contig[2498]	O14164	Probable eukaryotic translation initiation factor 3 subunit 8 (eIF3 p93)	918	0.029	21
Contig[2500]	P83213	Sperm protamine P3.	54	5.3	50
Contig[2512]	Q7NST5	HPr kinase/phosphorylase (HPrK/P) (HPr(Ser) kinase/phosphorylase)	318	9	29
Contig[2523]	O62589	Serine protease gd precursor (Protein gastrulation defective)	528	0.42	28
Contig[2524]	Q02892	Nucleolar GTP-binding protein 1	647	9.3	39
Contig[2529]	Q03751	Cysteine string protein.	249	0.45	58
Contig[2532]	Q8K4N2	Sperm-associated antigen 11 precursor.	71	2	57
Contig[2537]	Q8MTI2	Putative surface protein bspA-like (TvBspA-like-625)	625	7.00E-06	23
Contig[2546]	Q8K3I8	Beta-defensin 19 precursor (Defensin, beta 19) (BD-19) (mBD-19) (Testis-specific beta-defensin-like protein).	83	8.8	28
Contig[2548]	P14586	Histidine-rich protein.	82	0.0054	56
Contig[2555]	Q9W4E2	Protein neurobeachin (Protein rugose) (A-kinase anchor protein 550) (AKAP 550) (dAKAP550)	3584	3.6	46
Contig[2558]	Q8TE57	ADAMTS-16 precursor (A disintegrin and metalloproteinase with thrombospondin motifs 16) (ADAM-TS 16) (ADAM-TS16)	1224	0.28	28
Contig[2561]	Q7Z2C4	Glycine-rich selenoprotein (G-rich selenoprotein) (dSelG).	110	0.0088	40
Contig[2562]	Q02722	Protein Q300.	77	0.071	58
Contig[2567]	P44125	Uncharacterized protein HI1192 precursor.	47	8	37
Contig[2570]	Q62940	E3 ubiquitin-protein ligase NEDD4	887	0.001	35
Contig[2572]	O31087	Tyrosine recombinase xerC	303	1.7	35
Contig[2573]	Q9PLI5	Uncharacterized protein TC_0114	122	0.36	44
Contig[2574]	P14349	Gag polyprotein (Pr71Gag) [Contains: Gag protein (p68Gag); p3 (p3Gag)]	648	3.2	28
Contig[2576]	P12297	Protein suppressor of white apricot	963	0.65	34
Contig[2579]	O51880	UPF0070 protein BUsg_583.	194	0.39	32

Contig[2581]	P48532	Pleiotrophic factor-beta-1 precursor (PTF-beta-1)	161	0.005	37
Contig[2583]	Q923M0	Protein phosphatase 1 regulatory subunit 16A (Myosin phosphatase targeting subunit 3).	524	2.60E-07	42
Contig[2586]	P17146	Early glycoprotein GP48 precursor	152	7.8	44
Contig[2589]	P41823	Synaptotagmin-1 (Synaptotagmin I) (p65).	428	3.60E-05	26
Contig[2594]	Q7VRQ7	Uracil-DNA glycosylase (UDG)	221	0.62	23
Contig[2596]	P35662	Cylicin-1 (Cylicin I) (Multiple-band polypeptide I).	667	0.014	29
Contig[2597]	P06333	T-cell receptor beta chain ANA 11	319	6.1	30
Contig[2598]	Q5E9J2	Uncharacterized protein C2orf24 homolog	411	8	33
Contig[2608]	O17450	Peritrophin-48 precursor	379	9.00E-04	21
Contig[2611]	Q9JLZ8	Single Ig IL-1-related receptor (Single Ig IL-1R-related molecule) (Single immunoglobulin domain-containing IL1R-related protein) (Toll/interleukin-1 receptor 8) (TIR8)	409	6.3	31
Contig[2612]	P21260	Uncharacterized proline-rich protein (Fragment).	141	0.00016	48
Contig[2614]	P0A4L1	Thioredoxin 1 (TRX-1) (Thioredoxin M)	107	1.8	42
Contig[2616]	P34036	Dynein heavy chain, cytosolic (DYHC)	4725	2.5	34
Contig[2617]	P27473	Interferon-induced protein 44 (Antigen p44) (Non-A non-B hepatitis-associated microtubular aggregates protein)	444	0.077	38
Contig[2618]	Q5F836	Nicotinate phosphoribosyltransferase (NAPRTase)	402	8.3	30
Contig[2619]	P00202	Ferredoxin	59	0.001	38
Contig[2620]	Q6XQH0	Galactose 3-O-sulfotransferase 2 (Gal3ST-2) (Galbeta1-3GalNAc 3	394	2.1	40
MMS006_E05_039 8-24- 2006MMS006-T3	Q9BX10	GTP-binding protein 2	602	2.5	42
MMS006_G08_052 8-24- 2006MMS006-T3	Q9HLE6	Probable 3-phosphoshikimate 1-carboxyvinyltransferase (5-enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS)	410	4	31
MMS007_A10_080 9-5- 2006MMS007 T3	P42915	Uncharacterized outer membrane usher protein yraJ precursor	838	5.9	27
MMS007_A11_095 9-5-	Q8K424	Transient receptor potential cation channel subfamily V member 3 (TrpV3)	791	0.91	30

2006MMS007 T3					
MMS007_B02_014 9-5- 2006MMS007 T3	Q9H1A4	Anaphase-promoting complex subunit 1 (APC1) (Cyclosome subunit 1) (Protein Tsg24) (Mitotic checkpoint regulator)	1944	3.6	26
MMS007_B04_030 9-5- 2006MMS007 T3	P19543	Pyruvate-flavodoxin oxidoreductase (EC 1.2.7.-).	1173	2.10E-06	44
MMS007_B10_078 9-5- 2006MMS007 T3	Q4KMG9	Uncharacterized protein C12orf59 precursor	183	1.9	27
MMS007_C09_075 9-5- 2006MMS007 T3	Q5ZID5	Ubiquitin carboxyl-terminal hydrolase 28 (Ubiquitin thioesterase 28) (Ubiquitin-specific-processing protease 28) (Deubiquitinating enzyme 28)	1047	6.4	34
MMS007_D12_090 9-5- 2006MMS007 T3	Q5HP88	Probable ATP-dependent helicase dinG homolog	902	0.15	30
MMS007_E08_056 9-5- 2006MMS007_T3	Q10254	Alpha-1,2 glucosyltransferase ALG10 (Alpha-2- glucosyltransferase ALG10) (Dolichyl-phosphoglucose- dependent glucosyltransferase ALG10) (Asparagine-linked glycosylation protein 10)	445	0.74	28
MMS007_E11_087 9-5- 2006MMS007 T3	Q9VM95	Protein AATF-like	488	0.014	35
MMS007_F02_006 9-5- 2006MMS007 T3	Q80Y24	Prickle-like protein 2.	845	1.30E-17	42
MMS007_F05_037 9-5- 2006MMS007 T3	P83183	Cysteine-rich protamine.	84	2.2	38
MMS007_F06_038 9-5- 2006MMS007 T3	Q09614	Protein patched homolog 1.	1405	4.50E-60	45
MMS007_F09_069	Q6MD10	Lipoprotein-releasing system ATP-binding protein lolD	228	6	50

9-5- 2006MMS007 T3					
MMS007_F12_086 9-5- 2006MMS007 T3	P08432	Ornithine decarboxylase (ODC)	466	1.8	24
MMS007_G03_019 9-5- 2006MMS007 T3	Q9C098	Serine/threonine-protein kinase DCLK3 (Doublecortin-like and CAM kinase-like 3) (Doublecortin-like kinase 3)	648	3.1	29
MMS007_G05_035 9-5- 2006MMS007 T3	O95377	Gap junction beta-5 protein (Connexin-31.1) (Cx31.1)	273	3.4	36
MMS007_H12_082 9-5- 2006MMS007 T3	Q8IWB4	Uncharacterized protein C9orf36	1272	4.1	24
MMS008_A01_015 9-5- 2006MMS008 T3	Q96GP6	Scavenger receptor class F member 2 precursor (Scavenger receptor expressed by endothelial cells 2 protein) (SREC-II) (SRECRP-1)	866	0.28	42
MMS008_A06_048 9-5- 2006MMS008 T3	Q5QJF4	UPF0401 protein yubL	79	9	37
MMS008_A09_079 9-5- 2006MMS008 T3	Q9Q9G3	Hemagglutinin-esterase precursor (HE protein) (E3 glycoprotein)	416	3.3	31
MMS008_B04_030 9-5- 2006MMS008 T3	P16811	Uncharacterized protein IRL13 (TRL13)	147	2.4	37
MMS008_B09_077 9-5- 2006MMS008 T3	P35363	5-hydroxytryptamine 2A receptor (5-HT-2A) (Serotonin receptor 2A) (5-HT-2)	471	9	31
MMS008_B12_094 9-5- 2006MMS008 T3	Q5F3V0	SET and MYND domain-containing protein 4	742	8.5	33
MMS008_C05_043	Q6H3X3	Retinoic acid early transcript 1G protein precursor	334	7	39

9-5- 2006MMS008 T3					
MMS008_D03_025 9-5- 2006MMS008 T3	P46896	Solute carrier family 2, facilitated glucose transporter member 1 (Glucose transporter type 1) (GLUT-1) (GT1).	490	5.50E-17	50
MMS008_D04_026 9-5- 2006MMS008 T3	Q9V3H8	NTF2-related export protein (p15).	133	5.80E-36	50
MMS008_D12_090 9-5- 2006MMS008 T3	Q6C216	GPI mannosyltransferase 2 (GPI mannosyltransferase II) (GPI-MT-II) (Glycosylphosphatidylinositol-anchor biosynthesis protein 18)	357	8.9	40
MMS008_E02_008 9-5- 2006MMS008 T3	P57386	Deoxyribodipyrimidine photo-lyase (DNA photolyase) (Photoreactivating enzyme)	483	6.9	24
MMS008_E07_055 9-5- 2006MMS008 T3	Q19952	Probable U6 snRNA-associated Sm-like protein LSm4.	123	3.90E-37	68
MMS008_F08_054 9-5- 2006MMS008 T3	P07221	Calsequestrin-1 precursor (Calsequestrin, skeletal muscle isoform) (Aspartactin) (Laminin-binding protein)	395	5.00E-09	30
MMS008_G04_020 9-5- 2006MMS008 T3	O60934	Nibrin (Nijmegen breakage syndrome protein 1) (Cell cycle regulatory protein p95)	754	0.9	27
MMS008_G08_052 9-5- 2006MMS008 T3	P53349	Mitogen-activated protein kinase kinase kinase 1 (MAPK/ERK kinase kinase 1) (MEK kinase 1) (MEKK 1)	1493	3.6	40
MMS008_H02_002 9-5- 2006MMS008 T3	P74839	Propionate catabolism operon regulatory protein	541	0.98	35
MMS008_H04_018 9-5- 2006MMS008 T3	Q02158	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (PLC) (Phosphoinositide phospholipase C)	801	1.4	36
MMS008_H08_050	P83993	Cuticle protein 16.5, isoform B (LM-16.5B) (LM-ACP)	175	2.40E-07	46

9-5- 2006MMS008 T3		16.5B).			
MMS009_A02_016 9-5- 2006MMS009 T3	Q42093	Multidrug resistance-associated protein 2 (Glutathione S-conjugate-transporting ATPase 2) (ATP-energized glutathione S-conjugate pump 2)	1623	4.2	32
MMS009_A03_031 9-5- 2006MMS009 T3	Q6J163	Auxin-induced protein 5NG4	410	2.9	48
MMS009_A04_032 9-5- 2006MMS009 T3	Q3C258	Acrorhagin-1 precursor (Acrorhagin I).	70	2.1	39
MMS009_A05_047 9-5- 2006MMS009 T3	P52698	HTH-type transcriptional regulator phcA (Virulence genes transcriptional regulator phcA)	347	5.7	37
MMS009_A07_063 9-5- 2006MMS009 T3	Q737Z5	UPF0078 membrane protein BCE_2500	182	0.87	25
MMS009_A10_080 9-5- 2006MMS009 T3	Q17Y01	tRNA (guanine-N(7)-)-methyltransferase (tRNA(m7G46)-methyltransferase)	398	2.9	42
MMS009_B04_030 9-5- 2006MMS009 T3	Q66FF2	HTH-type transcriptional activator rhaS (L-rhamnose operon regulatory protein rhaS)	273	1.4	39
MMS009_B08_062 9-5- 2006MMS009 T3	Q57486	Uncharacterized transporter HI0608	461	3.2	33
MMS009_B09_077 9-5- 2006MMS009 T3	Q56032	Probable lipoprotein envF precursor	262	2.7	41
MMS009_B12_094 9-5- 2006MMS009 T3	P47152	Uncharacterized protein YJR115W	169	0.89	52
MMS009_C05_043	Q9D6I7	Protein FAM69A	428	1.9	26

9-5- 2006MMS009 T3					
MMS009_C11_091 9-5- 2006MMS009 T3	Q9BYQ4	Keratin-associated protein 9-2 (Keratin-associated protein 9.2) (Ultrahigh sulfur keratin-associated protein 9.2)	174	0.047	42
MMS009_D09_073 9-5- 2006MMS009 T3	Q9VKM6	Vacuolar protein sorting-associated protein 72 homolog (Protein YL-1).	351	7.90E-58	54
MMS009_E07_055 9-5- 2006MMS009 T3	P06682	Complement component C9	574	0.68	30
MMS009_E08_056 9-5- 2006MMS009 T3	P64700	Uncharacterized protein Mb0489c	348	6.8	34
MMS009_G07_051 9-5- 2006MMS009 T3	Q9WVI9	C-jun-amino-terminal kinase-interacting protein 1 (JNK-interacting protein 1) (JIP-1) (JNK MAP kinase scaffold protein 1) (Islet-brain-1) (IB-1) (Mitogen-activated protein kinase 8-interacting protein 1)	707	3.4	22
MMS009_H06_034 9-5- 2006MMS009 T3	Q8WWY8	Lipase member H precursor (Membrane-associated phosphatidic acid-selective phospholipase A1-alpha) (mPA-PLA1 alpha) (LPD lipase-related protein) (Phospholipase A1 member B)	451	1.00E-06	30
MMS009_H08_050 9-5- 2006MMS009 T3	Q10669	Protein sur-2	1587	0.092	33
MMS009_H12_082 9-5- 2006MMS009 T3	O43044	Nucleoporin nup120 (Nuclear pore protein nup120)	1136	3.7	35
MMS010_A05_047 9-7- 2006MMS010 T3	Q9LQT8	DELLA protein GAI (Gibberellic acid-insensitive mutant protein) (Restoration of growth on ammonia protein 2)	533	7	41
MMS010_B02_014 9-7-	Q9JMD2	Scm-like with four MBT domains protein 1	863	4.9	35

2006MMS010 T3					
MMS010_B03_029 9-7- 2006MMS010 T3	Q9NZW4	Dentin sialophosphoprotein precursor [Contains: Dentin phosphoprotein (Dentin phosphophoryn) (DPP); Dentin sialoprotein (DSP)]	1253	3.00E-04	24
MMS010_B07_061 9-7- 2006MMS010 T3	Q6B4Z3	Ubiquitously transcribed Y chromosome tetratricopeptide repeat protein (Ubiquitously transcribed TPR protein on the Y chromosome)	1079	1	41
MMS010_B09_077 9-7- 2006MMS010 T3	P18379	Uncharacterized 5.3 kDa protein.	44	5.7	28
MMS010_C03_027 9-7- 2006MMS010 T3	Q9NRP7	Serine/threonine-protein kinase 36 (Fused homolog)	1315	4.8	45
MMS010_D01_009 9-7- 2006MMS010 T3	P83348	Trypsin (EC 3.4.21.4) (Fragment).	21	7.9	60
MMS010_D03_025 9-7- 2006MMS010 T3	Q8NGN8	Olfactory receptor 4A4 (Olfactory receptor OR11-107)	299	1.2	28
MMS010_E01_007 9-7- 2006MMS010 T3	P80513	ARMET protein precursor (Arginine-rich protein).	179	6.20E-39	50
MMS010_E11_087 9-7- 2006MMS010 T3	Q4L4V4	UPF0349 protein SH2012.	81	6.1	28
MMS010_F01_005 9-7- 2006MMS010 T3	O13961	Nuclear envelope protein ndc1 (Cell untimely torn protein 11)	601	4.5	36
MMS010_F02_006 9-7- 2006MMS010 T3	O74815	Serine/threonine-protein kinase ppk27	413	1.1	25
MMS010_F09_069 9-7-	P17657	Cuticle collagen dpy-13 (Protein dumpy-13).	302	3.50E-29	73

2006MMS010 T3					
MMS010_G05_035 9-7- 2006MMS010 T3	Q6IV82	Tafazzin	292	2.00E-06	53
MMS010_H01_001 9-7- 2006MMS010 T3	Q92540	Protein SMG7 (SMG-7 homolog) (EST1-like protein C)	1137	0.89	40
MMS061_A04_032 11-6- 2006MMS061_T3	A1S6Z5	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase (Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase)	245	3	34
MMS061_B05_045 11-6- 2006MMS061 T3	O01377	Proliferating cell nuclear antigen (PCNA) (Cyclin).	260	1.70E-45	82
MMS061_B06_046 11-6- 2006MMS061 T3	P39864	Nitrate reductase [NADPH] (NR)	902	8.8	25
MMS061_B11_093 11-6- 2006MMS061 T3	Q9Z2X3	26S proteasome non-ATPase regulatory subunit 10 (26S proteasome regulatory subunit p28) (Gankyrin).	231	1.50E-14	33
MMS061_C02_012 11-6- 2006MMS061 T3	Q92F40	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase 1 (4-diphosphocytidyl-2C-methyl-D-erythritol synthase 1) (MEP cytidyltransferase 1) (MCT 1)	232	6.6	52
MMS061_C03_027 11-6- 2006MMS061 T3	Q5NGK7	Uncharacterized transporter FTT0829c	571	6.5	43
MMS061_C05_043 11-6- 2006MMS061 T3	P49859	Portal protein (GP3)	424	0.49	32
MMS061_C06_044 11-6- 2006MMS061 T3	O42933	Dolichyl-phosphate-mannose--protein mannosyltransferase 4	778	3.6	36
MMS061_C08_060	P12357	Photosystem I reaction center subunit V, chloroplast	167	8.6	45

11-6-2006MMS061_T3		precursor (PSI-G) (Photosystem I 9 kDa protein)			
MMS061_C09_075 11-6-2006MMS061_T3	Q503I8	Peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase (PNGase) (Peptide:N-glycanase) (N-glycanase 1)	644	2.00E-07	34
MMS061_D11_089 11-6-2006MMS061_T3	A3R4N4	Large T antigen (LT) (LT-AG)	641	6.9	26
MMS061_E03_023 11-6-2006MMS061_T3	Q6P3D7	Transcription factor Spi-C (Pu.1-related factor) (Prf)	242	3.6	38
MMS061_E07_055 11-6-2006MMS061_T3	Q7L775	EPM2A-interacting protein 1 (Laforin-interacting protein).	607	9.60E-30	27
MMS061_E08_056 11-6-2006MMS061_T3	Q922Y2	Tripartite motif-containing protein 59 (RING finger protein 1)	403	3.6	45
MMS061_F12_086 11-6-2006MMS061_T3	Q3MHX1	COMM domain-containing protein 7.	200	2.80E-11	36
MMS061_G10_068 11-6-2006MMS061_T3	Q8SQ34	Tumor necrosis factor receptor superfamily member 5 precursor (CD40L receptor) (B-cell surface antigen CD40)	278	0.17	25
MMS061_G12_084 11-6-2006MMS061_T3	P36417	G-box-binding factor (GBF).	708	1.20E-23	37
MMS061_H11_081 11-6-2006MMS061_T3	Q8R100	Protein FAM26E	309	4.2	32
MMS061_H12_082 11-6-2006MMS061_T3	Q6DF57	Coiled-coil domain-containing protein 75	261	2.00E-05	67
MMS063_B05_045	P54191	Pheromone-binding protein-related protein 1 precursor	148	3.00E-07	27

10-25-2006MMS063-T3		(PBPRP-1)			
MMS063_B12_094 10-25-2006MMS063-T3	Q8MXS1	Ras-related protein Rab-18	203	2.1	30
MMS063_D03_025 10-25-2006MMS063-T3	Q5URA8	Uncharacterized protein L876	413	3.6	34
MMS063_D08_058 10-25-2006MMS063-T3	Q9R160	ADAM 24 precursor (A disintegrin and metalloproteinase domain 24) (Testase 1)	761	1.6	39
MMS063_E09_071 10-25-2006MMS063-T3	O78441	Preprotein translocase subunit secA	877	1.8	25
MMS063_E10_072 10-25-2006MMS063-T3	P57540	Protoheme IX farnesyltransferase (Heme O synthase)	285	4.9	26
MMS063_E12_088 10-25-2006MMS063-T3	Q05469	Hormone-sensitive lipase (HSL)	1076	2.2	31
MMS063_F10_070 10-25-2006MMS063-T3	Q9BYJ1	Epidermis-type lipoxygenase 3 (e-LOX-3)	711	4.4	41
MMS063_F12_086 10-25-2006MMS063-T3	Q8N1V2	WD repeat protein 16 (WD40-repeat protein up-regulated in HCC).	620	2.30E-39	39
MMS063_G02_004 10-25-2006MMS063-T3	P62261	14-3-3 protein epsilon (14-3-3E).	255	2.30E-32	81
MMS063_G09_067 10-25-2006MMS063-T3	Q9XIR1	F-box/Kelch-repeat protein At1g64840	383	7.8	30
MMS063_G11_083	Q5WJE6	Chaperone protein htpG (Heat shock protein htpG) (High	625	9.2	36

10-25-2006MMS063-T3		temperature protein G)			
MMS063_H05_033 10-25-2006MMS063-T3	Q27319	Gelsolin, cytoplasmic (Actin-depolymerizing factor) (ADF).	754	4.40E-29	50
MMS063_H06_034 10-25-2006MMS063-T3	Q4WDD7	E3 ubiquitin-protein ligase bre1	725	0.012	22
MMS063_H08_050 10-25-2006MMS063-T3	P46280	Elongation factor Tu, chloroplast precursor (EF-Tu)	479	5.3	30
MMS063_H10_066 10-25-2006MMS063-T3	Q57661	Uncharacterized protein MJ0208	246	4.6	38
MMS064_A03_031 10-25-2006MMS064-T3	Q5HBJ6	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (CMK) (4-(cytidine-5	281	1.4	34
MMS064_C01_011 10-25-2006MMS064-T3	Q9P7M8	Nucleoporin nup184 (Nuclear pore protein nup184)	1564	2.6	34
MMS064_C02_012 10-25-2006MMS064-T3	Q24K15	Angiopoietin-4 precursor (ANG-4)	498	7	32
MMS064_C10_076 10-25-2006MMS064-T3	P17003	Hemagglutinin-esterase-fusion glycoprotein precursor (HEF) [Contains: Hemagglutinin-esterase-fusion glycoprotein chain 1 (HEF1); Hemagglutinin-esterase-fusion glycoprotein chain 2 (HEF2)]	641	1.8	36
MMS064_D03_025 10-25-2006MMS064-T3	P83669	Defensin-A	43	0.033	50
MMS064_D09_073 10-25-2006MMS064-T3	Q9W0T5	Transient receptor potential channel pyrexia.	956	1.80E-18	35

MMS064_D11_089 10-25- 2006MMS064-T3	Q5SSH7	Zinc finger ZZ-type and EF-hand domain-containing protein 1	2924	9.1	37
MMS064_E01_007 10-25- 2006MMS064-T3	O88799	Zonadhesin precursor	5376	6.5	44
MMS064_E02_008 10-25- 2006MMS064-T3	O95222	Olfactory receptor 6A2 (Olfactory receptor OR11-83) (Olfactory receptor 11-55) (OR11-55) (hP2 olfactory receptor)	327	2.7	41
MMS064_E10_072 10-25- 2006MMS064-T3	Q9BZV1	UBX domain-containing protein 1	441	0.034	41
MMS064_H03_017 10-25- 2006MMS064-T3	Q9VX91	E3 ubiquitin-protein ligase UBR1 (N-recognin) (Ubiquitin-protein ligase E3-alpha)	1824	7.5	32
MMS065_A02_016 10-25- 2006MMS065-T3	P34220	Uncharacterized deoxyribonuclease YBL055C	418	8.2	36
MMS065_A08_064 10-25- 2006MMS065-T3	Q15842	ATP-sensitive inward rectifier potassium channel 8 (Potassium channel, inwardly rectifying subfamily J member 8) (Inwardly rectifier K(+) channel Kir6.1) (uKATP-1)	424	2.1	32
MMS065_B06_046 10-25- 2006MMS065-T3	Q99N05	Membrane-spanning 4-domains subfamily A member 4D	225	3.1	54
MMS065_B11_093 10-25- 2006MMS065-T3	Q90660	Inhibitor of apoptosis protein (IAP) (Inhibitor of T-cell apoptosis protein)	611	1.00E-07	53
MMS065_C04_028 10-25- 2006MMS065-T3	Q9VE00	Probable cytochrome P450 12a4, mitochondrial precursor (EC 1.14.-.-) (CYPXIIA4).	536	3.20E-23	51
MMS065_D04_026 10-25-	O25170	Uncharacterized mscS family protein HP_0415	623	0.87	31

2006MMS065-T3					
MMS065_D11_089 10-25- 2006MMS065-T3	P75384	Uncharacterized protein MG280 homolog	287	7	43
MMS065_E01_007 10-25- 2006MMS065-T3	Q5SSI6	U3 small nucleolar RNA-associated protein 18 homolog (WD repeat protein 50).	552	4.60E-28	50
MMS065_E02_008 10-25- 2006MMS065-T3	Q8VIM5	Myocardin (SRF cofactor protein) (Basic SAP coiled-coil transcription activator 2)	935	9.1	38
MMS065_F02_006 10-25- 2006MMS065-T3	Q61038	Psychosine receptor (G-protein coupled receptor 65) (T cell death-associated protein 8)	337	0.29	33
MMS065_H04_018 10-25- 2006MMS065-T3	Q03468	DNA excision repair protein ERCC-6 (ATP-dependent helicase ERCC6) (Cockayne syndrome protein CSB)	1493	0.003	40
MMS065_H11_081 10-25- 2006MMS065-T3	P29702	Protein farnesyltransferase/geranylgeranyltransferase type I alpha subunit (CAAX farnesyltransferase alpha subunit) (Ras proteins prenyltransferase alpha) (FTase-alpha) (Type I protein geranyl-geranyltransferase alpha subunit) (GGTase-I-alpha)	375	7.00E-06	30
MMS086_A12_096 10-9- 2006MMS086 T3	Q2M2S8	Alkylated repair protein alkB homolog 7 precursor.	221	2.10E-38	58
MMS086_C02_012 10-9- 2006MMS086 T3	Q2KI69	Kv channel-interacting protein 4 (KChIP4)	250	3.00E-04	41
MMS086_C08_060 10-9- 2006MMS086 T3	A5DVM3	ATP-dependent RNA helicase eIF4A (Eukaryotic initiation factor 4A) (eIF-4A) (Translation initiation factor 1)	397	2	34
MMS086_C12_092 10-9- 2006MMS086 T3	Q26630	33 kDa inner dynein arm light chain, axonemal (p33).	260	1.20E-49	44

MMS086_D03_025 10-9- 2006MMS086 T3	O13944	Oxysterol-binding protein homolog C23H4.01c	945	4.2	27
MMS086_D05_041 10-9- 2006MMS086 T3	P04929	Histidine-rich glycoprotein precursor.	351	8.20E-14	45
MMS086_D12_090 10-9- 2006MMS086 T3	P15903	Gene 12 protein.	49	0.49	75
MMS086_G01_003 10-9- 2006MMS086 T3	Q9VEB3	Brix domain-containing protein 1 homolog.	320	4.70E-50	56
MMS086_G05_035 10-9- 2006MMS086 T3	P43142	Adrenomedullin receptor (AM-R) (G10D) (NOW)	395	2.5	29
MMS086_H01_001 10-9- 2006MMS086 T3	Q5R6F1	Mesoderm development candidate 2.	234	8.10E-46	44
MMS086_H07_049 10-9- 2006MMS086 T3	Q5UQA5	Uncharacterized protein L544	387	5.5	25
MMS086_H08_050 10-9- 2006MMS086 T3	Q811X6	Lambda-crystallin homolog.	319	6.60E-83	56
MMS087_A02_016 10-9- 2006MMS087 T3	Q6NJD6	Elongation factor G (EF-G)	704	1.8	28
MMS087_A08_064 10-9- 2006MMS087 T3	Q9WTP7	GTP:AMP phosphotransferase mitochondrial (Adenylate kinase 3) (AK3) (Adenylate kinase 3 alpha-like 1)	227	1.00E-09	56
MMS087_B01_013 10-9- 2006MMS087 T3	Q8L796	Phosphatidylinositol-4-phosphate 5-kinase 2 (EC 2.7.1.68) (AtPIP5K2) (1-phosphatidylinositol-4-phosphate kinase 2) (PtdIns(4)P-5-kinase 2) (Diphosphoinositide kinase 2).	754	1.00E-17	36

MMS087_B07_061 10-9- 2006MMS087 T3	O81155	Cysteine synthase, chloroplast/chromoplast precursor (EC 2.5.1.47) (O- acetylserine sulphydrylase) (O-acetylserine (Thiol)-lyase) (CSase B) (CS-B) (OAS-TL B).	386	1.10E-80	59
MMS087_C01_011 10-9- 2006MMS087 T3	Q8UW59	Protein DJ-1 (Parkinson disease protein 7 homolog).	189	9.20E-22	40
MMS087_C10_076 10-9- 2006MMS087 T3	Q5ZL57	Coatomer subunit delta (Delta-coat protein) (Delta-COP) (Archain).	510	6.80E-65	65
MMS087_F04_022 10-9- 2006MMS087 T3	Q9FDL5	Phosphoribosylamine--glycine ligase (GARS) (Glycinamide ribonucleotide synthetase) (Phosphoribosylglycinamide synthetase)	417	4.2	37
MMS087_F08_054 10-9- 2006MMS087 T3	Q60285	Uncharacterized ATP-binding protein MJECL26	343	0.41	31
MMS087_F11_085 10-9- 2006MMS087 T3	Q5T200	Zinc finger CCCH domain-containing protein 13.	1668	1.80E-07	39
MMS087_G08_052 10-9- 2006MMS087 T3	Q06974	Flagellin (Phase 1-C flagellin)	508	6.4	34
MMS087_H01_001 10-9- 2006MMS087 T3	Q9S7L2	Transcription factor MYB98 (Myb-related protein 98) (AtMYB98).	427	2.80E-17	34
MMS088_A03_031 10-10- 2006MMS088 T3	P53202	Cullin-3 (Cullin-B)	744	4.3	32
MMS088_A11_095 10-10- 2006MMS088 T3	P54654	Adenylyl cyclase-associated protein (CAP).	464	4.80E-24	28
MMS088_B08_062 10-10- 2006MMS088 T3	Q9VWH4	Probable isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial precursor (EC 1.1.1.41) (Isocitric dehydrogenase) (NAD(+)-specific ICDH).	377	6.10E-48	88

MMS088_C06_044 10-10- 2006MMS088 T3	P97283	DNA polymerase delta catalytic subunit	1103	2.8	25
MMS088_D07_057 10-10- 2006MMS088 T3	Q8CJ11	G-protein coupled receptor 64 precursor (Epididymis-specific protein 6) (Re6 receptor).	1013	1.20E-15	28
MMS088_D08_058 10-10- 2006MMS088 T3	Q49WB0	Coenzyme A disulfide reductase (EC 1.8.1.14) (CoA-disulfide reductase) (CoADR).	440	1.10E-09	42
MMS088_D11_089 10-10- 2006MMS088_T3	Q8NCW6	Polypeptide N-acetylgalactosaminyltransferase 11 (EC 2.4.1.41) (Protein-UDP acetylgalactosaminyltransferase 11) (UDP- GalNAc:polypeptide N-acetylgalactosaminyltransferase 11) (Polypeptide GalNAc transferase 11) (GalNAc-T11) (pp-GaNTase 11).	608	3.10E-40	49
MMS088_E07_055 10-10- 2006MMS088 T3	Q58036	Uncharacterized protein MJ0619	506	3.4	33
MMS088_F04_022 10-10- 2006MMS088 T3	P08441	Growth factor precursor (Secreted epidermal growth factor-like).	80	7.5	39
MMS089_A05_047 10-10- 2006MMS089 T3	P08962	CD63 antigen (Melanoma-associated antigen ME491) (Ocular melanoma- associated antigen) (OMA81H) (Granulophysin) (Tetraspanin-30) (Tspan- 30).	238	4.40E-38	37
MMS089_B11_093 10-10- 2006MMS089 T3	P15605	Hypothetical 18.8 kDa protein (ORF4).	156	6.80E-10	38
MMS089_B12_094 10-10- 2006MMS089_T3	Q492K0	Imidazole glycerol phosphate synthase subunit hisH (IGP synthase glutamine amidotransferase subunit) (IGP synthase subunit hisH) (ImGP synthase subunit hisH) (IGPS subunit hisH)	196	4.3	26
MMS089_C04_028 10-10- 2006MMS089 T3	Q8UWA5	Carbonic anhydrase 2 (EC 4.2.1.1) (Carbonic anhydrase II) (Carbonate dehydratase II) (CA-II).	260	1.50E-08	52

MMS089_C07_059 10-10- 2006MMS089 T3	P49150	Salivary plasminogen activator gamma precursor (DSPA gamma)	394	5.4	28
MMS089_D04_026 10-10- 2006MMS089 T3	Q09323	Beta-N-acetyl-D-glucosaminide beta-1,4-N-acetylglucosaminyl-transferase (UDP-GlcNAc:GlcNAc beta-R beta-1,4-N-acetylglucosaminyl-transferase) (Beta-1,4-GlcNAcT)	490	2.9	32
MMS089_D06_042 10-10- 2006MMS089 T3	Q9C8Z4	Uncharacterized protein At3g06530	1830	6.4	36
MMS089_E07_055 10-10- 2006MMS089 T3	Q641G3	Cell division cycle and apoptosis regulator protein 1	1157	2.4	25
MMS089_E08_056 10-10- 2006MMS089 T3	Q6ZU67	Coiled-coil domain-containing protein 4	530	0.38	41
MMS089_E09_071 10-10- 2006MMS089 T3	Q8LCS8	Membrane-anchored ubiquitin-fold protein 2 (Membrane-anchored ub-fold protein 2) (AtMUB2) (NTGP5)	124	2.5	39
MMS089_E10_072 10-10- 2006MMS089 T3	Q5RBM6	Beta-ureidopropionase (Beta-alanine synthase) (N-carbamoyl-beta-alanine amidohydrolase)	384	2.6	30
MMS089_F01_005 10-10- 2006MMS089 T3	Q96DR5	Short palate, lung and nasal epithelium carcinoma-associated protein 2 precursor (Parotid secretory protein) (PSP)	249	1.4	45
MMS089_F02_006 10-10- 2006MMS089 T3	Q19459	Golgi apparatus protein 1 homolog precursor	1149	0.19	34
MMS089_F03_021 10-10- 2006MMS089 T3	Q39613	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin) (Cyclosporin A-binding protein).	172	6.10E-64	75
MMS089_F05_037 10-10-	P03667	Gene IV protein (GPIV)	437	1.3	26

2006MMS089 T3					
MMS089_F08_054 10-10- 2006MMS089 T3	Q5R789	Zinc finger CCHC domain-containing protein 8	704	0.031	23
MMS089_G05_035 10-10- 2006MMS089 T3	Q9N1Q4	Large neutral amino acids transporter small subunit 2 (L-type amino acid transporter 2) (4F2lc-5).	535	3.50E-27	60
MMS089_G07_051 10-10- 2006MMS089 T3	Q03602	Patched-related protein 9	844	0.52	36
MMS089_H06_034 10-10- 2006MMS089 T3	Q9YW29	Early transcription factor 82 kDa subunit (VETF large subunit)	760	3	37
MMS089_H09_065 10-10- 2006MMS089 T3	Q9SRM0	Probable RING-H2 finger protein ATL3D	158	8	46
MMS089_H11_081 10-10- 2006MMS089 T3	Q8CHU3	Epsin-2 (EPS-15-interacting protein 2) (Intersectin-EH-binding protein 2) (Ibp2).	595	4.20E-21	29
MMS090_A01_015 10-25- 2006MMS090-T3	Q08473	RNA-binding protein squid (Heterogeneous nuclear ribonucleoprotein 40) (HNRNP 40).	344	4.10E-81	71
MMS090_A09_079 10-25- 2006MMS090-T3	Q9W568	Protein halfway precursor (Protein singed wings).	611	8.00E-29	60
MMS090_A11_095 10-25- 2006MMS090-T3	Q96R19	Trace amine-associated receptor 9 (Trace amine receptor 3) (TaR-3)	348	2.4	25
MMS090_A12_096 10-25- 2006MMS090-T3	P57546	Trigger factor (TF)	442	0.55	27
MMS090_B01_013 10-25-	Q04597	Uncharacterized protein YDR114C.	100	1.5	64

2006MMS090-T3					
MMS090_B02_014 10-25- 2006MMS090-T3	Q5UNY1	Putative BTB/POZ domain and WD-repeat protein R731	518	7.1	32
MMS090_B07_061 10-25- 2006MMS090-T3	P17036	Zinc finger protein 38 (Zinc finger protein KOX25) (Zinc finger protein HF.12) (Zinc finger protein 3) (HZF3.1).	446	1.50E-41	50
MMS090_B09_077 10-25- 2006MMS090-T3	P26506	Nitrogenase iron-molybdenum cofactor biosynthesis protein nifE	547	4.4	32
MMS090_B12_094 10-25- 2006MMS090-T3	Q7N3Q5	UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase (UDP-(beta-L-threo-pentapyranosyl-4	381	9.7	26
MMS090_C01_011 10-25- 2006MMS090-T3	Q5UQR4	Uncharacterized protein R327	1588	6.3	29
MMS090_C02_012 10-25- 2006MMS090-T3	Q9UKN5	PR domain zinc finger protein 4 (PR domain-containing protein 4)	801	2.1	37
MMS090_C12_092 10-25- 2006MMS090-T3	Q9BVK2	Probable dolichyl pyrophosphate Glc1Man9GlcNAc2 alpha-1,3- glucosyltransferase (EC 2.4.1.-) (Dolichyl-P-Glc:Glc1Man9GlcNAc2-PP- dolichyl glucosyltransferase) (Asparagine-linked glycosylation protein 8 homolog).	526	1.30E-75	57
MMS090_D01_009 10-25- 2006MMS090-T3	Q9W422	Josephin-like protein.	221	2.70E-45	53
MMS090_D08_058 10-25- 2006MMS090-T3	Q6ZPR5	Sphingomyelin phosphodiesterase 4 (Neutral sphingomyelinase 3) (Neutral sphingomyelinase III) (nSMase3) (nSMase-3)	823	0.038	24
MMS090_E03_023 10-25- 2006MMS090-T3	Q6YHK3	CD109 antigen precursor (p180) (150 KDa TGF-beta-1-binding protein) (r150) (Platelet-specific Gov antigen)	1445	3.7	37
MMS090_E05_039	P16620	Tyrosine-protein phosphatase 69D precursor (Protein-	1462	0.87	33

10-25- 2006MMS090-T3		tyrosine-phosphate phosphohydrolase) (DPTP)			
MMS090_E06_040 10-25- 2006MMS090-T3	P27571	X inactive-specific transcript protein	298	1.2	43
MMS090_F01_005 10-25- 2006MMS090-T3	Q4J8X1	Valyl-tRNA synthetase (Valine--tRNA ligase) (ValRS)	831	3.7	26
MMS090_F08_054 10-25- 2006MMS090-T3	P40927	NADP-dependent malic enzyme (EC 1.1.1.40) (NADP- ME).	557	1.20E-72	56
MMS090_F09_069 10-25- 2006MMS090-T3	P82987	ADAMTS-like protein 3 precursor (ADAMTSL-3) (Punctin-2)	1691	7.1	54
MMS090_G01_003 10-25- 2006MMS090-T3	Q9DFG8	Makorin-2	414	7.9	55
MMS090_G03_019 10-25- 2006MMS090-T3	P32392	Actin-like protein 3 (Actin-related protein 3) (Actin-like protein 66B) (Actin-2).	418	9.30E-100	87
MMS090_G08_052 10-25- 2006MMS090-T3	Q80TB8	Probable oxidoreductase KIAA1576	417	1.00E-05	34
MMS090_H06_034 10-25- 2006MMS090-T3	Q920A7	AFG3-like protein 1 (EC 3.4.24.-).	663	2.10E-19	73
MMS090_H09_065 10-25- 2006MMS090-T3	Q86T82	Ubiquitin carboxyl-terminal hydrolase 37 (EC 3.1.2.15) (Ubiquitin thioesterase 37) (Ubiquitin-specific-processing protease 37) (Deubiquitinating enzyme 37).	979	6.20E-14	32
MMS091_A01_015 10-25- 2006MMS091-T3	P50464	LIM domain-containing protein unc-97 (Uncoordinated protein 97) (PINCH homolog)	348	7.9	31
MMS091_B05_045	Q9ZPB7	Aldehyde dehydrogenase family 7 member A1 (Antiquitin-	508	3.6	53

10-25-2006MMS091-T3		1) (Matured fruit 60 kDa protein) (MF-60)			
MMS091_B07_061 10-25-2006MMS091-T3	P97433	Rho-guanine nucleotide exchange factor (Rho-interacting protein 2) (RhoGEF) (RIP2)	1693	2.5	29
MMS091_B11_093 10-25-2006MMS091-T3	P35037	Trypsin-3 precursor (EC 3.4.21.4).	275	1.50E-50	38
MMS091_C08_060 10-25-2006MMS091-T3	P21994	Gap junction beta-2 protein (Connexin-26) (Cx26)	226	6.3	35
MMS091_C09_075 10-25-2006MMS091-T3	Q3MHV9	Serine incorporator 1 (Tumor differentially expressed protein 2).	453	2.10E-47	47
MMS091_D04_026 10-25-2006MMS091-T3	Q22067	Probable aspartate aminotransferase, cytoplasmic (Transaminase A) (Glutamate oxaloacetate transaminase 1)	408	7.6	42
MMS091_D05_041 10-25-2006MMS091-T3	P58798	Probable actin-related protein 2/3 complex subunit 4 (ARP2/3 complex 20 kDa subunit) (p20-ARC)	169	2.9	36
MMS091_D06_042 10-25-2006MMS091-T3	P04137	Uncharacterized protein in transposable element ISH50	294	6.3	35
MMS091_D07_057 10-25-2006MMS091-T3	Q10126	Uncharacterized protein F52C9.6.	279	7.90E-16	27
MMS091_D08_058 10-25-2006MMS091-T3	P18407	Allantoicase	354	8.7	38
MMS091_D09_073 10-25-2006MMS091-T3	Q6DFN1	Uncharacterized protein C3orf60 homolog	183	5.00E-06	54
MMS091_D10_074	Q80XI3	Eukaryotic translation initiation factor 4 gamma 3 (eIF-4-	1579	2.00E-25	48

10-25- 2006MMS091-T3		gamma 3) (eIF-4G 3) (eIF4G 3) (eIF-4-gamma II) (eIF4GII).			
MMS091_F03_021 10-25- 2006MMS091-T3	Q95050	Probable cation-transporting ATPase 9	1133	1.7	23
MMS091_F05_037 10-25- 2006MMS091-T3	Q9NRG9	Aladin (Adracalin).	546	7.90E-12	37
MMS091_F07_053 10-25- 2006MMS091-T3	Q14508	WAP four-disulfide core domain protein 2 precursor (Major epididymis- specific protein E4) (Epididymal secretory protein E4) (Putative protease inhibitor WAP5).	124	1.20E-15	36
MMS091_F09_069 10-25- 2006MMS091-T3	Q5UPX8	Uncharacterized protein L234	288	7.6	38
MMS091_F11_085 10-25- 2006MMS091-T3	Q5N0F0	5'-nucleotidase surE (Nucleoside 5'-monophosphate phosphohydrolase)	258	2.5	36
MMS091_G01_003 10-25- 2006MMS091-T3	P48935	Succinate dehydrogenase cytochrome b560 subunit (Succinate dehydrogenase, subunit III)	132	4.3	31
MMS091_G09_067 10-25- 2006MMS091-T3	Q9U5L1	Signal recognition particle receptor subunit alpha homolog (SR-alpha) (Docking protein alpha) (DP-alpha) (GTP-binding protein).	614	8.40E-115	81
MMS092_A01_015 10-26- 2006MMS092-T3	P34520	Uncharacterized protein K11H3.4	717	8.5	23
MMS092_A06_048 10-26- 2006MMS092-T3	Q9P2X0	Dolichol-phosphate mannosyltransferase subunit 3 (Dolichol-phosphate mannose synthase subunit 3) (Dolichyl-phosphate beta-D- mannosyltransferase subunit 3) (Mannose-P-dolichol synthase subunit 3) (MPD synthase subunit 3) (DPM synthase complex subunit 3) (Prostin-1).	92	3.00E-16	45
MMS092_A08_064 10-26-	Q2NNR5	Cysteinyl leukotriene receptor 1 (CysLTR1) (Cysteinyl leukotriene D4 receptor) (LTD4 receptor)	340	5	45

2006MMS092-T3					
MMS092_C03_027 10-26- 2006MMS092-T3	Q8TAG9	Exocyst complex component 6 (Exocyst complex component Sec15A) (Sec15- like 1).	804	1.90E-60	56
MMS092_C09_075 10-26- 2006MMS092-T3	Q6PNC0	DmX-like protein 1 (X-like 1 protein)	3013	1.9	21
MMS092_D03_025 10-26- 2006MMS092-T3	P13213	SPARC precursor (Secreted protein acidic and rich in cysteine) (Osteonectin) (ON) (Basement-membrane protein 40) (BM-40)	303	6.1	25
MMS092_E01_007 10-26- 2006MMS092-T3	Q5EA59	Abhydrolase domain-containing protein 4 (EC 3.1.1.-) (Lyso-N- acylphosphatidylethanolamine lipase) (Alpha/beta-hydrolase 4).	342	6.50E-60	53
MMS092_E07_055 10-26- 2006MMS092-T3	Q8YM13	Protein ycf12.	40	7.2	32
MMS092_E09_071 10-26- 2006MMS092-T3	P07092	Glia-derived nexin precursor (GDN) (Protease nexin I) (PN-1).	397	2.10E-13	29
MMS092_F01_005 10-26- 2006MMS092-T3	Q96RD3	Olfactory receptor 52E6	313	1.7	32
MMS092_F07_053 10-26- 2006MMS092-T3	Q687Y7	Interleukin-17A precursor (IL-17A) (IL-17)	153	5	30
MMS092_F12_086 10-26- 2006MMS092-T3	Q8R1F6	Uncharacterized protein C17orf28 homolog	788	2.7	43
MMS093_A04_032 10-26- 2006MMS093-T3	O73700	Voltage-dependent L-type calcium channel subunit alpha-1D (Voltage-gated calcium channel subunit alpha Cav1.3) (CHCACHA1D)	2190	2.6	43
MMS093_B02_014 10-26-	Q25532	Vacuolar ATP synthase subunit G (EC 3.6.3.14) (V-ATPase subunit G) (Vacuolar proton pump subunit G) (V-ATPase	117	2.60E-40	77

2006MMS093-T3		13 kDa subunit).			
MMS093_B03_029 10-26- 2006MMS093-T3	P81917	Odorant receptor 43a	376	9.1	35
MMS093_B07_061 10-26- 2006MMS093-T3	P36776	Lon protease homolog, mitochondrial precursor (EC 3.4.21.-) (Lon protease-like protein) (LONP) (Mitochondrial ATP-dependent protease Lon) (LONHs) (Serine protease 15).	959	8.30E-100	75
MMS093_B10_078 10-26- 2006MMS093-T3	P15305	Dynein heavy chain (DYHC) (Fragment).	515	1.70E-13	21
MMS093_B12_094 10-26- 2006MMS093-T3	P10392	Protein nifQ	167	4.1	50
MMS093_C02_012 10-26- 2006MMS093-T3	Q07895	FAS1 domain-containing protein YLR001C precursor	862	2.7	22
MMS093_C03_027 10-26- 2006MMS093-T3	Q8NBX0	Probable saccharopine dehydrogenase (EC 1.5.1.9).	429	7.80E-23	40
MMS093_C06_044 10-26- 2006MMS093-T3	Q88920	RNA-directed RNA polymerase (180 kDa protein) [Contains: Methyltransferase/RNA helicase (MT/HEL) (125 kDa protein)]	1601	1.4	24
MMS093_D11_089 10-26- 2006MMS093-T3	Q63198	Contactin-1 precursor (Neural cell surface protein F3)	1021	0.52	29
MMS093_E02_008 10-26- 2006MMS093-T3	Q63661	Mucin-4 precursor (Pancreatic adenocarcinoma mucin) (Testis mucin) (Ascites sialoglycoprotein) (ASGP) (Sialomucin complex) (Pre-sialomucin complex) (pSMC) [Contains: Mucin-4 alpha chain (Ascites sialoglycoprotein 1) (ASGP-1); Mucin-4 beta chain (Ascites sialoglycoprotein 2) (ASGP-2)]	2344	2.2	36
MMS093_E05_039	Q5ZIU8	Katanin p80 WD40-containing subunit B1 (Katanin p80	657	0.87	26

10-26-2006MMS093-T3		subunit B1) (p80 katanin)			
MMS093_E06_040 10-26-2006MMS093-T3	P79351	Brain ribonuclease (BRB)	151	2.2	58
MMS093_E07_055 10-26-2006MMS093-T3	Q15398	Disks large-associated protein DLG7 (Discs large homolog 7) (Hepatoma up-regulated protein) (HURP)	846	4	29
MMS093_E12_088 10-26-2006MMS093-T3	Q74ZX0	Protein CSF1	2887	0.41	36
MMS093_F03_021 10-26-2006MMS093-T3	Q5ZI57	Trafficking protein particle complex subunit 3	180	2.00E-07	66
MMS093_G05_035 10-26-2006MMS093-T3	Q0IHA2	UPF0405 protein TMEM103	265	0.004	31
MMS093_G07_051 10-26-2006MMS093-T3	Q8KA15	Primosomal protein N	720	7.5	22
MMS093_G12_084 10-26-2006MMS093-T3	P07041	Histone H3	136	0.27	31
MMS093_H01_001 10-26-2006MMS093-T3	Q3ZBK6	U6 snRNA-associated Sm-like protein LSm4.	139	7.40E-52	76
MMS093_H05_033 10-26-2006MMS093-T3	Q14934	Nuclear factor of activated T-cells, cytoplasmic 4 (NF-ATc4) (NFATc4) (T cell transcription factor NFAT3) (NF-AT3)	902	0.81	40
MMS093_H08_050 10-26-2006MMS093-T3	Q9CZV5	STAGA complex 65 subunit gamma (STAF65gamma) (SPTF-associated factor 65 gamma) (Suppressor of Ty 7-like).	412	1.40E-34	37
MMS093_H10_066	Q87XL0	Glycerol kinase (ATP:glycerol 3-phosphotransferase)	501	0.54	28

10-26-2006MMS093-T3		(Glycerokinase) (GK)			
MMS094_A02_016 10-26-2006MMS094-T3	Q8K449	ATP-binding cassette sub-family A member 9	1623	4.2	36
MMS094_A05_047 10-26-2006MMS094-T3	O32450	4-alpha-glucanotransferase (Amylomaltase) (Disproportionating enzyme) (D-enzyme)	653	5.8	43
MMS094_A06_048 10-26-2006MMS094-T3	O75880	SCO1 protein homolog, mitochondrial precursor.	301	1.70E-38	49
MMS094_B01_013 10-26-2006MMS094-T3	Q64424	Pancreatic lipase-related protein 2 precursor (EC 3.1.1.3) (PL-RP2).	470	5.20E-35	41
MMS094_B10_078 10-26-2006MMS094-T3	P01474	Cytotoxin-2 (Cytotoxin V-II-2/V-II-3).	61	0.26	36
MMS094_C06_044 10-26-2006MMS094-T3	Q9VGX3	Protein anoxia up-regulated	619	2.00E-06	31
MMS094_C07_059 10-26-2006MMS094-T3	Q9QYI4	DnaJ homolog subfamily B member 12 (mDJ10).	376	3.80E-16	44
MMS094_C11_091 10-26-2006MMS094-T3	Q5FVB0	Arylsulfatase J precursor (ASJ)	599	7.00E-04	24
MMS094_C12_092 10-26-2006MMS094-T3	P13607	Sodium/potassium-transporting ATPase subunit alpha (EC 3.6.3.9) (Sodium pump subunit alpha) (Na ⁺ /K ⁺) ATPase alpha subunit).	1041	3.70E-144	95
MMS094_D05_041 10-26-2006MMS094-T3	Q9JI66	Electrogenic sodium bicarbonate cotransporter 1 (Sodium bicarbonate cotransporter) (Na ⁺ /HCO ₃ ⁻) cotransporter) (Solute carrier family 4 member 4) (NBC-like protein)	1079	1.4	33
MMS094_E01_007	P54319	Phospholipase A-2-activating protein (PLAP).	795	1.50E-33	45

10-26-2006MMS094-T3					
MMS094_E03_023 10-26-2006MMS094-T3	P40301	Proteasome subunit alpha type 2 (EC 3.4.25.1) (Proteasome 25 kDa subunit) (PROS-Dm25).	234	5.40E-104	83
MMS094_E11_087 10-26-2006MMS094-T3	Q8NEB9	Phosphatidylinositol 3-kinase catalytic subunit type 3 (EC 2.7.1.137) (PtdIns-3-kinase type 3) (PI3-kinase type 3) (PI3K type 3) (Phosphoinositide-3-kinase class 3) (Phosphatidylinositol 3-kinase p100 subunit).	887	2.60E-77	56
MMS094_E12_088 10-26-2006MMS094-T3	O95848	Uridine diphosphate glucose pyrophosphatase (EC 3.6.1.45) (UDPG pyrophosphatase) (UGPPase) (Nucleoside diphosphate-linked moiety X motif 14) (Nudix motif 14).	222	9.70E-27	46
MMS094_F08_054 10-26-2006MMS094-T3	Q646E3	Taste receptor type 2 member 49 (T2R49)	309	2.7	30
MMS094_H01_001 10-26-2006MMS094-T3	Q641F8	tRNA wybutosine-synthesizing protein 3 homolog (EC 2.1.1.-).	251	1.60E-27	43
MMS094_H02_002 10-26-2006MMS094-T3	Q60303	Uncharacterized protein MJ ECS04	135	0.002	29
MMS094_H11_081 10-26-2006MMS094-T3	Q6P698	Plastin-2 (L-plastin) (Lymphocyte cytosolic plastin 1).	624	4.40E-35	46
MMS105_A03_031 11-1-2006MMS105 T3	Q1D2K0	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase (UDP-3-O-acyl-GlcNAc deacetylase)	314	0.25	32
MMS105_B01_013 11-1-2006MMS105 T3	Q8ZIF7	S-adenosyl-L-methionine-dependent methyltransferase mraW	320	4	28
MMS105_B03_029 11-1-2006MMS105 T3	O50580	D-tagatose 3-epimerase	290	5	46

MMS105_B12_094 11-1- 2006MMS105 T3	Q7NAQ4	Triosephosphate isomerase (TIM) (Triose-phosphate isomerase)	252	7	36
MMS105_C06_044 11-1- 2006MMS105 T3	P84157	Matrix-remodeling-associated protein 7 (Transmembrane anchor protein 1).	204	0.0019	34
MMS105_E09_071 11-1- 2006MMS105 T3	Q1HPK6	Translation elongation factor 2 (EF-2).	844	3.80E-66	90
MMS105_F12_086 11-1- 2006MMS105 T3	Q96JI7	Spatacsin (Spastic paraplegia 11 protein) (Colorectal carcinoma-associated protein)	2443	1	24
MMS105_G04_020 11-1- 2006MMS105 T3	Q08696	Axoneme-associated protein mst101(2).	1391	5.90E-05	30
MMS105_G11_083 11-1- 2006MMS105 T3	Q9HFS2	DNA-binding protein creA (Carbon catabolite repressor)	430	0.22	36
MMS105_G12_084 11-1- 2006MMS105 T3	Q9ULJ7	Ankyrin repeat domain-containing protein 50	1375	1.00E-06	31
MMS105_H03_017 11-1- 2006MMS105 T3	Q09788	Uncharacterized serine-rich protein C13G6.10c precursor.	530	2.80E-36	38
MMS105_H05_033 11-1- 2006MMS105 T3	P19003	Cytotoxin homolog S3C2.	63	4	43
MMS105_H10_066 11-1- 2006MMS105 T3	Q9VAQ7	Pre-mRNA-splicing factor SLU7.	574	2.20E-22	44
MMS105_H11_081 11-1- 2006MMS105 T3	P18084	Integrin beta-5 precursor	799	3	35

MMS106_A05_047 11-2- 2006MMS106 T3	P61549	HERV-H_19p13.11 provirus ancestral Env polyprotein precursor (Envelope polyprotein) (Env protein RGH1) (Env protein RTLHV-H) [Includes: Surface protein (SU)]	369	3.8	31
MMS106_A06_048 11-2- 2006MMS106 T3	P20126	RNA replicase polyprotein	1839	6.9	44
MMS106_B01_013 11-2- 2006MMS106 T3	Q6GQN4	Protein FAM32A-like	109	0.034	73
MMS106_B02_014 11-2- 2006MMS106 T3	P34124	26S protease regulatory subunit 8 (TAT-binding protein homolog 10) (Fragment).	389	2.40E-92	79
MMS106_B03_029 11-2- 2006MMS106 T3	O48686	Paired amphipathic helix protein Sin3 (Transcriptional corepressor Sin3) (Histone deacetylase complex subunit Sin3) (AtSin3)	1353	9	42
MMS106_B07_061 11-2- 2006MMS106 T3	Q05164	Haze protective factor 1 precursor	967	2.9	30
MMS106_C05_043 11-2- 2006MMS106 T3	P20654	Serine/threonine-protein phosphatase PP1 (EC 3.1.3.16).	323	7.70E-41	38
MMS106_C10_076 11-2- 2006MMS106 T3	Q9D2G2	Dihydrolipoyllysine-residue succinyltransferase component of 2- oxoglutarate dehydrogenase complex, mitochondrial precursor (EC 2.3.1.61) (Dihydrolipoamide succinyltransferase component of 2- oxoglutarate dehydrogenase complex) (E2) (E2K).	454	1.30E-54	81
MMS106_C11_091 11-2- 2006MMS106 T3	P24639	Annexin A7 (Annexin-7) (Annexin VII) (Synexin).	462	2.30E-19	57
MMS106_D06_042 11-2- 2006MMS106 T3	Q29627	Pituitary adenylate cyclase-activating polypeptide type I receptor precursor (PACAP type I receptor) (PACAP-R-1)	513	1.4	30
MMS106_D11_089	P78611	Chitin synthase D (Chitin-UDP acetyl-glucosaminyl	1184	3.1	31

11-2- 2006MMS106 T3		transferase D) (Class-V chitin synthase D)			
MMS106_E02_008 11-2- 2006MMS106 T3	Q9LKW9	Sodium/hydrogen exchanger 7 (Na ⁺ /H ⁺ exchanger 7) (NHE-7) (Protein SALT OVERLY SENSITIVE 1)	1146	0.26	43
MMS106_E12_088 11-2- 2006MMS106 T3	Q6ZPV2	Putative DNA helicase INO80 complex homolog 1 (EC 3.6.1.-).	1559	1.90E-11	36
MMS106_F09_069 11-2- 2006MMS106 T3	P01473	Cytotoxin-3 (Venom component 3.20).	61	3.6	52
MMS106_F11_085 11-2- 2006MMS106 T3	P39960	GTPase-activating protein BEM2/IPL2 (Bud emergence protein 2)	2167	2.4	32
MMS106_G04_020 11-2- 2006MMS106 T3	Q57R15	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (EC 5.4.2.1) (Phosphoglyceromutase) (PGAM) (BPG-dependent PGAM) (dPGM).	250	2.40E-76	61
MMS106_H05_033 11-2- 2006MMS106 T3	Q07832	Serine/threonine-protein kinase PLK1 (Polo-like kinase 1) (PLK-1) (Serine/threonine-protein kinase 13) (STPK13)	603	0.18	27
MMS106_H11_081 11-2- 2006MMS106 T3	Q1RMX6	Coiled-coil domain-containing protein C1orf110 homolog	296	0.82	26
MMS107_A04_032 11-2- 2006MMS107 T3	Q746Y3	Phosphoenolpyruvate carboxykinase [GTP] (EC 4.1.1.32) (PEP carboxykinase) (Phosphoenolpyruvate carboxylase) (PEPCK).	618	6.90E-77	61
MMS107_A08_064 11-2- 2006MMS107 T3	Q8CIY2	Dual oxidase 1 precursor (EC 1.6.3.1) (EC 1.11.1.-).	1551	2.00E-38	56
MMS107_A11_095 11-2- 2006MMS107 T3	P12024	Chaoptin precursor (Photoreceptor cell-specific membrane protein)	1315	0.44	38
MMS107_B04_030	P28875	Zinc finger protein 1	388	7.1	50

11-2- 2006MMS107 T3					
MMS107_B09_077 11-2- 2006MMS107 T3	Q58791	Uncharacterized protein MJ1396	2894	4.00E-04	32
MMS107_C05_043 11-2- 2006MMS107 T3	O43681	Arsenical pump-driving ATPase (EC 3.6.3.16) (Arsenite-translocating ATPase) (Arsenical resistance ATPase) (Arsenite-transporting ATPase) (ARSA) (ASNA-I).	348	1.60E-47	33
MMS107_C11_091 11-2- 2006MMS107 T3	P35951	Low-density lipoprotein receptor precursor (LDL receptor)	864	9.8	27
MMS107_D10_074 11-2- 2006MMS107 T3	Q07963	E3 ubiquitin-protein ligase UBR2 (Ubiquitin-protein ligase E3 component N-recognin-1 homolog)	1872	3.1	35
MMS107_E03_023 11-2- 2006MMS107 T3	P31547	D-methionine transport system permease protein metI	217	5.1	33
MMS107_E05_039 11-2- 2006MMS107 T3	P47090	Uncharacterized endoplasmic reticulum membrane protein YJR015W	510	4.4	48
MMS107_E12_088 11-2- 2006MMS107 T3	Q6D7U0	Probable hydrogenase nickel incorporation protein hypA	117	0.55	35
MMS107_F11_085 11-2- 2006MMS107 T3	Q58196	Uncharacterized protein MJ0786	186	5.9	35
MMS107_G02_004 11-2- 2006MMS107 T3	Q5HZ36	GATA transcription factor 24	398	7.7	36
MMS107_G09_067 11-2- 2006MMS107 T3	Q9BXM7	Serine/threonine-protein kinase PINK1, mitochondrial precursor (PTEN-induced putative kinase protein 1) (BRPK)	581	3.00E-06	27
MMS107_G12_084	P29172	Microtubule-associated protein tau (Neurofibrillary tangle	448	4.30E-31	38

11-2- 2006MMS107 T3		protein) (Paired helical filament-tau) (PHF-tau).			
MMS107_H12_082 11-2- 2006MMS107 T3	P12337	Liver carboxylesterase 1 precursor (Acyl coenzyme A:cholesterol acyltransferase)	565	2.5	29
MMS108_A06_048 11-2- 2006MMS108 T3	Q5BJJ5	Haloacid dehalogenase-like hydrolase domain-containing protein 2.	262	8.10E-69	61
MMS108_A07_063 11-2- 2006MMS108 T3	Q9C0H9	p130Cas-associated protein (p140Cap) (SNAP-25-interacting protein) (SNIP)	1055	0.21	23
MMS108_A08_064 11-2- 2006MMS108 T3	O70421	Frizzled-1 precursor (Fz-1) (mFz1)	642	1.9	42
MMS108_A10_080 11-2- 2006MMS108 T3	P29349	Tyrosine-protein phosphatase corkscrew	845	9	46
MMS108_D08_058 11-2- 2006MMS108 T3	Q9D6Z1	Nucleolar protein 5A (Nucleolar protein Nop56).	580	1.20E-115	77
MMS108_E01_007 11-2- 2006MMS108 T3	Q7RVM2	ADP-ribosylation factor.	185	5.00E-53	58
MMS108_E02_008 11-2- 2006MMS108 T3	Q0CIC7	Mitogen-activated protein kinase mpkC (MAP kinase C)	370	0.046	31
MMS108_E07_055 11-2- 2006MMS108 T3	Q5RBA5	Sequestosome-1 (Ubiquitin-binding protein p62)	440	7.1	26
MMS108_E09_071 11-2- 2006MMS108 T3	P09309	Transcriptional repressor IE61 (Immediate-early protein 61) (IE61)	467	7.5	38
MMS108_F01_005	O00622	Protein CYR61 precursor (Cysteine-rich, angiogenic	381	9.00E-06	36

11-2- 2006MMS108 T3		inducer, 61) (Insulin-like growth factor-binding protein 10) (Protein GIG1)			
MMS108_F08_054 11-2- 2006MMS108 T3	Q99296	Uncharacterized protein YLR149C	730	2.4	34
MMS108_G03_019 11-2- 2006MMS108 T3	P35134	Ubiquitin-conjugating enzyme E2-17 kDa 11 (EC 6.3.2.19) (Ubiquitin- protein ligase 11) (Ubiquitin carrier protein 11).	148	6.20E-55	70
MMS108_H02_002 11-2- 2006MMS108 T3	Q821S0	Phospho-N-acetylmuramoyl-pentapeptide-transferase (UDP-MurNAc-pentapeptide phosphotransferase)	348	8.1	28
MMS108_H11_081 11-2- 2006MMS108 T3	Q9W6S8	Survival motor neuron protein 1.	281	2.10E-12	48
MMS109_A03_031 11-2- 2006MMS109 T3	P82147	Protein lethal(2)essential for life (Protein Efl21).	187	1.10E-43	54
MMS109_A12_096 11-2- 2006MMS109 T3	P24369	Peptidyl-prolyl cis-trans isomerase B precursor (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin B) (S-cyclophilin) (SCYLP) (CYP-S1).	208	3.80E-55	62
MMS109_B09_077 11-2- 2006MMS109 T3	Q6FEV2	tRNA pseudouridine synthase A (tRNA-uridine isomerase I) (tRNA pseudouridylate synthase I)	271	5.3	34
MMS109_C10_076 11-2- 2006MMS109 T3	Q7VMW3	DNA replication and repair protein recF	360	3.7	27
MMS109_E08_056 11-2- 2006MMS109 T3	P87228	Putative D-3-phosphoglycerate dehydrogenase (3-PGDH)	466	0.35	25
MMS109_F03_021 11-2- 2006MMS109 T3	Q95QW4	Cation diffusion facilitator family protein 1	561	2	26
MMS109_F04_022	Q8MY6	Putative polypeptide N-acetylgalactosaminyltransferase 13	558	1.00E-04	26

11-2- 2006MMS109_T3		(Protein-UDP acetylgalactosaminyltransferase 13) (UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 13) (pp-GaNTase 13)			
MMS109_F08_054 11-2- 2006MMS109_T3	Q9WVK7	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial precursor (EC 1.1.1.35) (Short chain 3-hydroxyacyl-CoA dehydrogenase) (HCDH) (Medium and short chain L-3-hydroxyacyl-coenzyme A dehydrogenase).	314	2.00E-24	48
MMS109_G02_004 11-2- 2006MMS109_T3	Q0DJA0	Coatomer subunit delta-1 (Delta-coat protein 1) (Delta-COP 1)	524	8.2	35
MMS109_H03_017 11-2- 2006MMS109_T3	O59852	Invertase precursor (Beta-fructofuranosidase) (Saccharase)	581	0.49	25
MMS109_H06_034 11-2- 2006MMS109_T3	Q02722	Protein Q300	77	0.16	32
MMS109_H10_066 11-2- 2006MMS109_T3	Q8K9L1	Putative flagella synthesis protein flgN	138	3.1	26
MMS110_A03_031 11-3- 2006MMS110_T3	P28785	Low affinity tryptophan permease	417	0.21	34
MMS110_A07_063 11-3- 2006MMS110_T3	P44543	Sialic acid TRAP transporter permease protein siaT (N-acetylneuraminic acid permease) (Neu5Ac permease) (N-acetylneuraminic acid transporter)	616	5.1	35
MMS110_A08_064 11-3- 2006MMS110_T3	Q5ZMJ9	Serine/arginine repetitive matrix protein 1.	888	1.20E-07	75
MMS110_A09_079 11-3- 2006MMS110_T3	Q9D753	Exosome complex exonuclease RRP43 (EC 3.1.13.-) (Ribosomal RNA- processing protein 43) (Exosome component 8).	276	3.90E-30	47
MMS110_B04_030 11-3-	Q13617	Cullin-2 (CUL-2)	745	6.1	25

2006MMS110 T3					
MMS110_C01_011 11-3- 2006MMS110 T3	O60488	Long-chain-fatty-acid--CoA ligase 4 (Long-chain acyl-CoA synthetase 4) (LACS 4)	711	0.2	35
MMS110_D02_010 11-3- 2006MMS110 T3	P63171	Dynein light chain Tctex-type 1 (T-complex testis-specific protein 1 homolog).	113	2.00E-42	82
MMS110_D03_025 11-3- 2006MMS110 T3	Q5UQH0	Putative sell-like repeat-containing protein R815	540	0.065	23
MMS110_D11_089 11-3- 2006MMS110 T3	Q5E9T9	UPF0027 protein C22orf28 homolog.	505	1.80E-78	64
MMS110_E08_056 11-3- 2006MMS110 T3	Q5M948	Protein JOSD3.	285	1.5	39
MMS110_E12_088 11-3- 2006MMS110 T3	Q5ZKX6	NEDD8-conjugating enzyme UBE2F (EC 6.3.2.-) (Ubiquitin-conjugating enzyme E2 F) (NEDD8 protein ligase UBE2F) (NEDD8 carrier protein UBE2F).	185	5.40E-43	75
MMS110_F01_005 11-3- 2006MMS110 T3	Q8N6M3	Uncharacterized protein C20orf142 precursor	262	8.7	37
MMS110_F12_086 11-3- 2006MMS110 T3	P47161	Vacuolar protein sorting-associated protein 70	811	1.2	25
MMS110_H01_001 11-3- 2006MMS110 T3	O67813	Flagellar biosynthetic protein flhB	350	6.8	26
MMS110_H06_034 11-3- 2006MMS110 T3	P47520	Probable guanosine-3	720	2.3	32
MMS110_H09_065 11-3-	Q8CIN4	Serine/threonine-protein kinase PAK 2 (p21-activated kinase 2) (PAK-2) (Gamma-PAK)	524	8.00E-07	39

2006MMS110 T3					
MMS111_A10_080 11-6- 2006MMS111 T3	P28246	Bicyclomycin resistance protein (Sulfonamide resistance protein)	396	8.4	36
MMS111_B03_029 11-6- 2006MMS111 T3	Q8NGT9	Olfactory receptor 2A42 (Olfactory receptor OR7-19) (Olfactory receptor OR7-16)	310	3.4	43
MMS111_B06_046 11-6- 2006MMS111 T3	Q05808	Vitellogenin precursor [Contains: YP47; YP160]	1790	3.8	31
MMS111_B08_062 11-6- 2006MMS111 T3	P36362	Endochitinase precursor	554	0.14	32
MMS111_B10_078 11-6- 2006MMS111 T3	P45699	Putative endoglucanase type K precursor (Endo-1,4-beta-glucanase) (Cellulase)	376	0.56	46
MMS111_C03_027 11-6- 2006MMS111 T3	Q13118	Krueppel-like factor 10 (Transforming growth factor-beta-inducible early growth response protein 1) (TGFB-inducible early growth response protein 1) (TIEG-1) (EGR-alpha).	480	4.00E-26	57
MMS111_C07_059 11-6- 2006MMS111 T3	P40747	Uncharacterized oxidoreductase yuxG (ORF2)	689	5.3	33
MMS111_C09_075 11-6- 2006MMS111 T3	Q7TPN3	GPI mannosyltransferase 2 (GPI mannosyltransferase II) (GPI-MT-II) (Phosphatidylinositol-glycan biosynthesis class V protein) (PIG-V)	493	0.012	27
MMS111_E01_007 11-6- 2006MMS111 T3	Q8K451	Probable G-protein coupled receptor 156 (GABAB-related G-protein coupled receptor)	792	4.3	26
MMS111_E09_071 11-6- 2006MMS111 T3	P38295	Medium-chain fatty acid ethyl ester synthase/esterase 2 (Alcohol O-acetyltransferase) (Ethanol hexanoyl transferase 1)	451	1.4	33
MMS111_F09_069 11-6-	P90648	Myosin heavy chain kinase B (MHCK B)	732	4.7	32

2006MMS111 T3					
MMS111_F11_085 11-6- 2006MMS111 T3	Q1KKS3	Dual 3	903	2.5	37
MMS111_G04_020 11-6- 2006MMS111_T3	Q5TKR9	Histone acetyltransferase MYST3 (MYST protein 3) (MOZ, YBF2/SAS3, SAS2 and TIP60 protein 3) (Monocytic leukemia zinc finger protein) (Monocytic leukemia zinc finger homolog)	1998	0.44	27
MMS111_H02_002 11-6- 2006MMS111 T3	Q6CAD2	Serine/threonine-protein kinase TEL1 (DNA-damage checkpoint kinase TEL1) (Telomere length regulation protein 1) (ATM homolog)	2282	2	34
MMS111_H07_049 11-6- 2006MMS111_T3	Q93KF3	Peptide methionine sulfoxide reductase msrA/msrB [Includes: Peptide methionine sulfoxide reductase msrA (Protein-methionine-S-oxide reductase) (Peptide-methionine (S)-S-oxide reductase) (Peptide Met(O) reductase); Peptide methionine sulfoxide reductase msrB (Peptide-methionine (R)-S-oxide reductase)]	337	0.36	28
MMS111_H10_066 11-6- 2006MMS111 T3	P28514	Arylphorin subunit C223 precursor	759	8.7	33
MMS111_H12_082 11-6- 2006MMS111 T3	Q8M9Y1	tRNA(Ile)-lysidine synthase (tRNA(Ile)-lysidine synthetase) (tRNA(Ile)-2-lysyl-cytidine synthase)	341	1.8	33
MMS112_A02_016 11-6- 2006MMS112 T3	P27125	L-rhamnose-proton symporter (L-rhamnose-H(+)) transport protein)	344	8.4	37
MMS112_A05_047 11-6- 2006MMS112 T3	Q9VLT5	Protein purity of essence (Protein pushover) (Protein Calossin) (Interaction calmodulin and colossal molecular mass protein)	5322	0.57	28
MMS112_A09_079 11-6- 2006MMS112 T3	Q9Z4I3	Major outer membrane protein mspA precursor (Major sheath protein)	575	2.2	31
MMS112 A10 080	Q57934	Uncharacterized polyferredoxin-like protein MJ0514	250	8.00E-07	46

11-6-2006MMS112 T3					
MMS112_B01_013 11-6-2006MMS112 T3	P03586	RNA-directed RNA polymerase (183 kDa protein) [Contains: Methyltransferase/RNA helicase (MT/HEL) (126 kDa protein)]	1616	2.1	26
MMS112_B12_094 11-6-2006MMS112 T3	Q7Z5W3	BIN3 domain-containing protein 2 (BCDIN3 domain-containing protein)	292	1.8	38
MMS112_C04_028 11-6-2006MMS112 T3	Q3E7B5	Uncharacterized protein YMR230W-A	62	0.8	30
MMS112_C08_060 11-6-2006MMS112 T3	Q9RMV5	Uncharacterized protein pXO2-80/BXB0110/GBAA_pXO2_0110	328	2.2	21
MMS112_D03_025 11-6-2006MMS112 T3	Q25197	Putative insulin-like peptide receptor precursor	1477	0.87	29
MMS112_D08_058 11-6-2006MMS112 T3	Q91Z22	Porimin precursor (Transmembrane protein 123)	195	2.4	33
MMS112_D09_073 11-6-2006MMS112 T3	Q9QAS1	Non-structural protein of 4.9 kDa (ns4.9) (4.9 kDa accessory protein).	44	4.3	52
MMS112_E10_072 11-6-2006MMS112 T3	Q9FKF6	Cyclin-U4-3 (CycU4;3) (Cyclin P4.2) (CycP4;2)	219	4.6	66
MMS112_E12_088 11-6-2006MMS112 T3	P84843	Vasotab precursor.	76	4.30E-08	38
MMS112_G01_003 11-6-2006MMS112 T3	P35133	Ubiquitin-conjugating enzyme E2-17 kDa 10/12 (EC 6.3.2.19) (Ubiquitin- protein ligase 10/12) (Ubiquitin carrier protein 10/12).	148	4.10E-35	47
MMS112_G07_051	Q969H9	Disrupted in renal carcinoma protein 1 (Disrupted in renal	104	0.97	31

11-6-2006MMS112 T3		cancer protein).			
MMS113_A11_095 11-6-2006MMS113 T3	Q4V8A8	Zinc finger protein 90 (Zfp-90)	633	8.2	35
MMS113_A12_096 11-6-2006MMS113 T3	P33750	Protein SOF1 (U3 small nucleolar RNA-associated protein SOF1) (U3 snoRNA-associated protein SOF1).	489	5.60E-27	48
MMS113_B02_014 11-6-2006MMS113 T3	O75462	Cytokine receptor-like factor 1 precursor (Cytokine-like factor 1) (CLF-1) (ZcytoR5)	422	1.1	35
MMS113_E06_040 11-6-2006MMS113 T3	P42203	Interleukin-13 precursor (IL-13) (T-cell activation protein P600)	131	4.3	23
MMS113_E12_088 11-6-2006MMS113 T3	Q9GZS0	Dynein intermediate chain 2, axonemal (Axonemal dynein intermediate chain 2)	605	2.00E-05	47
MMS113_F08_054 11-6-2006MMS113 T3	O82291	Probable plastid-lipid-associated protein 3, chloroplast precursor (AtPap3) (Fibrillin-3)	376	1.7	34
MMS113_G05_035 11-6-2006MMS113 T3	Q5UQW7	Putative endonuclease L386	473	1.3	26
MMS113_H09_065 11-6-2006MMS113 T3	P54357	Myosin-2 essential light chain (Myosin II essential light chain) (Nonmuscle myosin essential light chain).	147	4.90E-62	84
MMS114_A02_016 11-6-2006MMS114 T3	P24868	G2/mitotic-specific cyclin-1	471	0.24	29
MMS114_A10_080 11-6-2006MMS114 T3	O02414	Dynein light chain LC6, flagellar outer arm.	89	1.80E-32	86
MMS114_C02_012	P06422	Regulatory protein E2.	498	0.005	45

11-6- 2006MMS114 T3					
MMS114_C07_059 11-6- 2006MMS114 T3	P19749	DNA-directed RNA polymerase 35 kDa polypeptide	126	1.3	34
MMS114_C12_092 11-6- 2006MMS114 T3	Q28009	RNA-binding protein FUS (Pigpen protein).	513	3.50E-22	55
MMS114_D07_057 11-6- 2006MMS114 T3	Q9NXR7	Protein BRE (Brain and reproductive organ-expressed protein) (BRCA1/BRCA2-containing complex subunit 45).	415	4.70E-50	40
MMS114_D08_058 11-6- 2006MMS114 T3	O15736	Protein tipD	612	5.00E-09	23
MMS114_D12_090 11-6- 2006MMS114 T3	Q2YV67	Sensory transduction protein lytR	246	4.1	31
MMS114_E01_007 11-6- 2006MMS114 T3	A0JMA8	LisH domain-containing protein ARMC9	808	3.6	26
MMS114_E07_055 11-6- 2006MMS114 T3	O29710	Uncharacterized protein AF_0540 precursor	228	0.003	26
MMS114_E11_087 11-6- 2006MMS114 T3	Q17QE5	Calcium and integrin-binding protein 1 (Calmyrin).	191	2.00E-24	35
MMS114_F03_021 11-6- 2006MMS114 T3	Q42456	Aspartic proteinase oryzasin-1 precursor (EC 3.4.23.-).	509	4.40E-55	47
MMS114_F05_037 11-6- 2006MMS114 T3	Q12361	G protein-coupled receptor GPR1	961	0.33	32
MMS114_F06_038	Q5R4L1	Serine/threonine-protein kinase PLK2 (Polo-like kinase 1)	685	6.4	36

11-6- 2006MMS114 T3		(PLK-2)			
MMS114_F11_085 11-6- 2006MMS114 T3	Q3ST04	UPF0161 protein Nwi_1326	117	1.3	40
MMS114_G11_083 11-6- 2006MMS114 T3	Q59037	Chromosome partition protein smc homolog	1169	0.067	25
MMS114_H02_002 11-6- 2006MMS114 T3	Q92793	CREB-binding protein	2442	2.7	44
MMS114_H07_049 11-6- 2006MMS114 T3	P18844	Neuroendocrine protein 7B2 (Secretogranin V) [Contains: N-terminal peptide; C-terminal peptide] (Fragment).	161	4.40E-13	38
MMS115_A01_015 11-18- 2006MMS115 T3	Q6FS63	Spindle assembly checkpoint component MAD1 (Mitotic arrest deficient protein 1)	657	0.027	30
MMS115_A02_016 11-18- 2006MMS115 T3	Q2QMX9	Calcium-transporting ATPase 1, plasma membrane-type (EC 3.6.3.8) (Ca(2+)-ATPase isoform 1) (Plastid envelope ATPase 1).	1020	1.10E-37	44
MMS115_A05_047 11-18- 2006MMS115 T3	Q8RCX1	Pyrophosphate-energized proton pump (Pyrophosphate-energized inorganic pyrophosphatase) (H(+)-PPase) (Membrane-bound proton-translocating pyrophosphatase)	711	5.4	46
MMS115_A06_048 11-18- 2006MMS115 T3	Q8VE88	Protein FAM114A2	497	1.5	33
MMS115_A07_063 11-18- 2006MMS115 T3	Q9ZC99	Uncharacterized protein RP867	231	4.3	35
MMS115_B01_013 11-18- 2006MMS115 T3	P52960	Peroxisome proliferation transcriptional regulator (Oleate-activated transcription factor 2)	996	0.51	30
MMS115_B02_014	Q502C1	28S ribosomal protein S24, mitochondrial precursor	163	6	46

11-18-2006MMS115 T3		(S24mt) (MRP-S24)			
MMS115_B05_045 11-18-2006MMS115 T3	P07308	Acyl-CoA desaturase 1 (EC 1.14.19.1) (Stearoyl-CoA desaturase 1) (Fatty acid desaturase 1) (Delta(9)-desaturase 1).	358	6.50E-28	41
MMS115_B07_061 11-18-2006MMS115 T3	Q9UHE5	Probable N-acetyltransferase 8 (Camello-like protein 1)	227	0.003	28
MMS115_B08_062 11-18-2006MMS115 T3	Q96N68	Uncharacterized protein C18orf15	181	0.74	57
MMS115_C12_092 11-18-2006MMS115 T3	P52740	Zinc finger protein 132	589	5.3	52
MMS115_D04_026 11-18-2006MMS115 T3	P40208	Glucose-induced degradation protein 8 (Dosage-dependent cell cycle regulator 1)	455	4.8	28
MMS115_D08_058 11-18-2006MMS115 T3	Q5E9K3	Pyridoxine-5'-phosphate oxidase (EC 1.4.3.5) (Pyridoxamine-phosphate oxidase).	261	2.20E-27	60
MMS115_D10_074 11-18-2006MMS115 T3	P53338	Maltose fermentation regulatory protein MAL13	473	0.73	32
MMS115_F01_005 11-18-2006MMS115 T3	Q6NYV8	Lysocardiolipin acyltransferase	388	0.41	41
MMS115_F08_054 11-18-2006MMS115 T3	P61702	Alanyl-tRNA synthetase (Alanine--tRNA ligase) (AlaRS)	882	0.029	27
MMS115_G10_068 11-18-2006MMS115 T3	P97826	Steroidogenic acute regulatory protein, mitochondrial precursor (StAR) (StARD1)	284	2.5	31
MMS115_H05_033	Q5UIP0	Telomere-associated protein RIF1 (Rap1-interacting factor	2472	7.4	36

11-18- 2006MMS115 T3		1 homolog)			
MMS115_H06_034 11-18- 2006MMS115 T3	O18304	Uncharacterized protein ZK849.5	411	0.42	30
MMS115_H10_066 11-18- 2006MMS115 T3	Q10076	Zinc finger protein C3H1.11	582	0.26	34
MMS115_H11_081 11-18- 2006MMS115 T3	Q92161	Cyclin-A1 (Cyclin-A)	391	1.2	36
MMS116_A01_015 11-6- 2006MMS116 T3	P76134	Uncharacterized protein ydeM	385	9	52
MMS116_A04_032 11-6- 2006MMS116 T3	Q8VEX6	Olfactory receptor 187 (Olfactory receptor 183-8)	308	8.4	21
MMS116_B01_013 11-6- 2006MMS116_T3	P80147	4-aminobutyrate aminotransferase, mitochondrial precursor (EC 2.6.1.19) ((S)-3-amino-2-methylpropionate transaminase) (EC 2.6.1.22) (Gamma-amino-N-butyrate transaminase) (GABA transaminase) (GABA aminotransferase) (GABA-AT) (GABA-T) (L-AIBAT).	500	9.30E-68	52
MMS116_B06_046 11-6- 2006MMS116 T3	Q07622	Activator of C kinase protein 1	623	9.1	45
MMS116_B09_077 11-6- 2006MMS116 T3	P45243	Protease 4 (Protease IV) (Endopeptidase IV) (Signal peptide peptidase)	615	5	37
MMS116_B11_093 11-6- 2006MMS116 T3	Q5PRC0	Cholesterol 25-hydroxylase-like protein A	251	0.16	31
MMS116_C01_011 11-6-	Q6DHK8	Sodium/bile acid cotransporter 7 (Na(+)/bile acid cotransporter 7) (Solute carrier family 10 member 7)	336	5.5	32

2006MMS116 T3					
MMS116_C04_028 11-6- 2006MMS116 T3	P09181	Lysis protein for colicin N precursor	52	5.3	40
MMS116_C10_076 11-6- 2006MMS116 T3	Q2EEX5	Uncharacterized membrane protein ycf78 (ycf1)	1168	8.4	32
MMS116_C11_091 11-6- 2006MMS116 T3	Q69ZU6	Thrombospondin type-1 domain-containing protein 7A precursor	1645	4.6	34
MMS116_D07_057 11-6- 2006MMS116 T3	Q4AEG9	Phospholipid hydroperoxide glutathione peroxidase, mitochondrial precursor (EC 1.11.1.12) (PHGPx) (Glutathione peroxidase 4) (GPx-4).	197	4.70E-41	57
MMS116_D11_089 11-6- 2006MMS116 T3	P42574	Caspase-3 precursor (EC 3.4.22.56) (CASP-3) (Apopain) (Cysteine protease CPP32) (Yama protein) (CPP-32) (SREBP cleavage activity 1) (SCA-1) [Contains: Caspase-3 p17 subunit; Caspase-3 p12 subunit].	277	2.00E-17	55
MMS116_E03_023 11-6- 2006MMS116 T3	P25407	Hypothetical protein in calmodulin 5	252	0.042	22
MMS116_E05_039 11-6- 2006MMS116 T3	Q8R5A3	Amyloid beta A4 precursor protein-binding family B member 1-interacting protein (APBB1-interacting protein 1) (Proline-rich EVH1 ligand 1) (PREL-1) (Proline-rich protein 48)	670	4.4	30
MMS116_E07_055 11-6- 2006MMS116 T3	P56603	Secretory carrier-associated membrane protein 1 (Secretory carrier membrane protein 1) (SCAMP 37)	338	1.2	29
MMS116_E10_072 11-6- 2006MMS116 T3	Q4R3W4	Putative adenylate kinase-like protein C9orf98 homolog	479	1.1	28
MMS116_F01_005 11-6- 2006MMS116 T3	P09081	Homeotic protein bicoid (PRD-4)	494	3.2	48

MMS116_F12_086 11-6- 2006MMS116_T3	O15266	Short stature homeobox protein (Short stature homeobox-containing protein) (Pseudoautosomal homeobox-containing osteogenic protein)	292	3.5	36
MMS116_G10_068 11-6- 2006MMS116_T3	A1C3U1	Protein cft1 (Cleavage factor two protein 1)	1401	4.2	42
MMS116_G11_083 11-6- 2006MMS116_T3	Q2M329	Coiled-coil domain-containing protein 96	555	0.22	26
MMS116_H01_001 11-6- 2006MMS116_T3	Q12788	WD repeat protein SAZD (Transducin beta-like 3 protein)	519	4.8	48
MMS116_H02_002 11-6- 2006MMS116_T3	P96463	Alpha-L-arabinofuranosidase precursor (Arabinosidase)	475	1.00E-09	31
MMS116_H08_050 11-6- 2006MMS116_T3	Q14137	Ribosome biogenesis protein BOP1 (Block of proliferation 1 protein)	746	9.00E-08	75
MMS116_H11_081 11-6- 2006MMS116_T3	P47171	Histone transcription regulator 3	1648	1.8	31
MMS117_A05_047 11-6- 2006MMS117_T3	Q31BS3	Bifunctional protein glmU [Includes: UDP-N-acetylglucosamine pyrophosphorylase (N-acetylglucosamine-1-phosphate uridyltransferase); Glucosamine-1-phosphate N-acetyltransferase]	449	3.2	29
MMS117_A10_080 11-6- 2006MMS117_T3	Q5NTB3	Coagulation factor XI precursor (Plasma thromboplastin antecedent) (PTA) (FXI) [Contains: Coagulation factor XIa heavy chain; Coagulation factor XIa light chain]	625	5.5	24
MMS117_B10_078 11-6- 2006MMS117_T3	P56597	Nucleoside diphosphate kinase homolog 5 (NDK-H 5) (NDP kinase homolog 5) (nm23-H5) (Testis-specific nm23 homolog) (Inhibitor of p53-induced apoptosis-beta) (IPIA-beta).	212	3.70E-34	44
MMS117_C04_028	Q3V1M1	Immunoglobulin superfamily member 10 precursor	2594	0.083	30

11-6- 2006MMS117 T3					
MMS117_C07_059 11-6- 2006MMS117_T3	P28175	Limulus clotting factor C precursor (EC 3.4.21.84) (FC) [Contains: Limulus clotting factor C heavy chain; Limulus clotting factor C light chain; Limulus clotting factor C chain A; Limulus clotting factor C chain B].	1019	9.40E-32	35
MMS117_C09_075 11-6- 2006MMS117_T3	O14829	Serine/threonine-protein phosphatase with EF-hands 1 (PPEF-1) (Protein phosphatase with EF calcium-binding domain) (PPEF) (Serine/threonine-protein phosphatase 7) (PP7)	653	2.7	56
MMS117_C10_076 11-6- 2006MMS117 T3	P08045	Zinc finger protein Xfin	1350	4.1	33
MMS117_D04_026 11-6- 2006MMS117 T3	O51879	tRNA uridine 5-carboxymethylaminomethyl modification enzyme gidA (Glucose-inhibited division protein A)	631	2.4	46
MMS117_D07_057 11-6- 2006MMS117 T3	P39985	DNA polymerase V (POL V)	1022	0.33	33
MMS117_D09_073 11-6- 2006MMS117 T3	Q1IWC9	Malate dehydrogenase (EC 1.1.1.37).	334	4.80E-71	55
MMS117_E01_007 11-6- 2006MMS117 T3	Q01033	Hypothetical gene 48 protein	797	8	30
MMS117_E02_008 11-6- 2006MMS117 T3	Q924T7	RING finger protein 31.	1066	3.20E-30	32
MMS117_E05_039 11-6- 2006MMS117 T3	P40026	DNA repair protein KRE29 (Killer toxin-resistance protein 29)	464	9	50
MMS117_E06_040 11-6-	Q61999	Outer dense fiber protein	247	3	32

2006MMS117 T3					
MMS117_E07_055 11-6- 2006MMS117 T3	Q7ZXT3	Enhancer of mRNA-decapping protein 4	1391	0.62	45
MMS117_E12_088 11-6- 2006MMS117 T3	Q5XI70	Polycomb group RING finger protein 6 (RING finger protein 134)	351	2.00E-05	36
MMS117_F08_054 11-6- 2006MMS117 T3	P97868	Retinoblastoma-binding protein 6 (p53-associated cellular protein of testis) (Proliferation potential-related protein) (Protein P2P-R)	1790	9.2	37
MMS117_F09_069 11-6- 2006MMS117 T3	Q5UP38	Putative FNIP repeat-containing protein L162	521	4.7	28
MMS117_G07_051 11-6- 2006MMS117 T3	Q7TUG9	Glutathione synthetase (Glutathione synthase) (GSH synthetase) (GSH-S) (GSHase)	307	0.012	30
MMS117_G09_067 11-6- 2006MMS117_T3	P60412	Keratin-associated protein 10-11 (Keratin-associated protein 10.11) (High sulfur keratin-associated protein 10.11) (Keratin-associated protein 18-11) (Keratin-associated protein 18.11)	298	1.00E-06	28
MMS117_G10_068 11-6- 2006MMS117 T3	Q67ET4	Taste receptor type 2 member 125 (T2r125) (Taste receptor type 2 member 16) (T2R16)	310	6	26
MMS117_G11_083 11-6- 2006MMS117 T3	Q9N0Y3	Interferon-induced GTP-binding protein Mx1	657	0.89	36
MMS117_H12_082 11-6- 2006MMS117 T3	Q91987	BDNF/NT-3 growth factors receptor precursor (Neurotrophic tyrosine kinase receptor type 2) (TrkB tyrosine kinase) (Trk-B)	818	6.2	31
MMS118_A06_048 11-17- 2006MMS118 T3	Q5RES8	Zinc finger protein 334	678	4	26
MMS118_A09_079	P35630	NADP-dependent alcohol dehydrogenase (EC 1.1.1.2).	360	5.80E-59	51

11-17-2006MMS118 T3					
MMS118_A11_095 11-17-2006MMS118 T3	Q9CPU4	Microsomal glutathione S-transferase 3 (EC 2.5.1.18) (Microsomal GST- 3) (Microsomal GST-III).	153	2.90E-32	55
MMS118_B02_014 11-17-2006MMS118 T3	Q96L34	MAP/microtubule affinity-regulating kinase 4 (EC 2.7.11.1) (MAP/microtubule affinity-regulating kinase-like 1).	752	9.20E-29	33
MMS118_B05_045 11-17-2006MMS118 T3	Q9CN94	1,4-alpha-glucan-branching enzyme (Glycogen-branching enzyme) (BE) (1,4-alpha-D-glucan:1,4-alpha-D-glucan 6- glucosyl-transferase)	730	0.61	38
MMS118_B07_061 11-17-2006MMS118 T3	Q0V7P8	FBD-associated F-box protein At5g27750	459	6.8	22
MMS118_D04_026 11-17-2006MMS118 T3	Q9BTX7	Uncharacterized protein C20orf121.	342	1.40E-23	27
MMS118_D10_074 11-17-2006MMS118 T3	P34672	Uncharacterized protein ZK688.2	632	4	42
MMS118_D11_089 11-17-2006MMS118 T3	Q9U943	Apolipoporphins precursor [Contains: Apolipoporphin-2 (Apolipoporphin II) (apoLp-2); Apolipoporphin-1 (Apolipoporphin I) (apoLp-1)].	3380	1.70E-69	46
MMS118_E10_072 11-17-2006MMS118 T3	P45699	Putative endoglucanase type K precursor (EC 3.2.1.4) (Endo-1,4-beta- glucanase) (Cellulase).	376	4.40E-61	52
MMS118_E12_088 11-17-2006MMS118 T3	Q6AYL4	RIB43A-like with coiled-coils protein 1.	378	1.80E-19	32
MMS118_F01_005 11-17-2006MMS118 T3	Q02930	cAMP response element-binding protein 5 (CRE-BPa)	508	0.003	38
MMS118_F03_021	Q7KKH3	Protein SDA1 homolog (Mystery protein 45A).	712	1.50E-22	60

11-17- 2006MMS118 T3					
MMS118_F05_037 11-17- 2006MMS118 T3	O08707	Chemokine-binding protein 2 (Chemokine-binding protein D6) (C-C chemokine receptor D6)	378	2	32
MMS118_F06_038 11-17- 2006MMS118 T3	O74526	Probable serine/threonine-protein kinase C70.05c	781	4.5	36
MMS118_F10_070 11-17- 2006MMS118 T3	Q9CQ48	NudC domain-containing protein 2	157	1.00E-05	52
MMS118_G06_036 11-17- 2006MMS118 T3	P83912	Zinc metalloproteinase jerdonitin precursor [Contains: Disintegrin jerdonitin]	484	4.7	30
MMS118_G08_052 11-17- 2006MMS118 T3	Q10231	Lanosterol synthase (Oxidosqualene--lanosterol cyclase) (2,3-epoxysqualene--lanosterol cyclase) (OSC)	721	4.1	36
MMS118_G10_068 11-17- 2006MMS118 T3	Q9U1H0	Putative transcription factor capicua (Protein fettucine)	1403	2.00E-04	37
MMS119_A08_064 11-17- 2006MMS119 T3	Q9QX29	Short transient receptor potential channel 5 (TrpC5) (Transient receptor protein 5) (Mtrp5) (Trp-related protein 5) (Capacitative calcium entry channel 2) (CCE2)	975	7.6	27
MMS119_B07_061 11-17- 2006MMS119 T3	Q89AB3	Exodeoxyribonuclease V beta chain	1180	7.1	35
MMS119_C02_012 11-17- 2006MMS119 T3	P49579	Acetylcholine receptor subunit beta precursor	489	3.2	35
MMS119_C03_027 11-17- 2006MMS119 T3	P53861	Elongin-A	379	6.4	40
MMS119_C10_076	P32449	Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-	370	6.2	40

11-17-2006MMS119_T3		inhibited (Phospho-2-keto-3-deoxyheptonate aldolase) (DAHP synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase)			
MMS119_C11_091 11-17-2006MMS119_T3	Q5T124	UBX domain-containing protein 5 (Socius) (Colorectal tumor-associated antigen COA-1)	520	5.2	47
MMS119_D06_042 11-17-2006MMS119_T3	Q96T91	Glycoprotein hormone alpha-2 precursor (Thyrostimulin subunit alpha)	129	2.00E-07	33
MMS119_D09_073 11-17-2006MMS119_T3	Q6ZMT4	JmjC domain-containing histone demethylation protein 1D	941	1.4	37
MMS119_E05_039 11-17-2006MMS119_T3	Q09302	Uncharacterized protein F07F6.1	428	1.9	31
MMS119_E06_040 11-17-2006MMS119_T3	Q5F433	PRA1 family protein 3 (ADP-ribosylation-like factor 6-interacting protein 5).	188	2.90E-34	47
MMS119_E09_071 11-17-2006MMS119_T3	Q8BKC5	Importin beta-3 (Karyopherin beta-3) (Ran-binding protein 5) (RanBP5).	1097	2.20E-35	46
MMS119_F09_069 11-17-2006MMS119_T3	Q9XZS3	Coiled-coil domain-containing protein 72 homolog.	64	1.20E-21	76
MMS119_G02_004 11-17-2006MMS119_T3	Q9H6U6	Breast carcinoma amplified sequence 3 (GAOB1) (Maab1 protein)	928	3.9	34
MMS119_H07_049 11-17-2006MMS119_T3	Q20496	Probable rho GDP-dissociation inhibitor (Rho GDI).	191	3.10E-12	28
MMS119_H10_066 11-17-2006MMS119_T3	P41177	Monensin polyketide synthase putative ketoacyl reductase (ORF5)	261	0.01	60

MMS120_B07_061 11-17- 2006MMS120_T3	P21231	Genome polyprotein [Contains: P1 proteinase (N-terminal protein); Helper component proteinase (HC-pro); Protein P3; 6 kDa protein 1 (6K1); Cytoplasmic inclusion protein (CI); 6 kDa protein 2 (6K2); Viral genome-linked protein (VPg); Nuclear inclusion protein A (NI-a) (NIa) (NIa-pro) (49 kDa proteinase) (49 kDa-Pro); Nuclear inclusion protein B (NI-b) (NIb) (RNA-directed RNA polymerase); Coat protein (CP)]	3066	0.95	24
MMS120_C03_027 11-17- 2006MMS120_T3	P56851	Epididymal secretory protein E3 beta precursor (HE3 beta)	147	4.7	32
MMS120_C04_028 11-17- 2006MMS120_T3	P34400	Abnormal cell migration protein 10	779	4.6	32
MMS120_D09_073 11-17- 2006MMS120_T3	Q89AD7	Endonuclease-1 (Endonuclease I) (Endo I)	245	3	27
MMS120_F03_021 11-17- 2006MMS120_T3	Q9VCF0	Uncharacterized protein CG5902.	243	1.00E-10	33
MMS120_F06_038 11-17- 2006MMS120_T3	Q24498	Ryanodine receptor 44F.	5127	1.10E-34	73
MMS120_F07_053 11-17- 2006MMS120_T3	Q8VDC1	FYVE and coiled-coil domain-containing protein 1	1437	5.1	29
MMS120_F11_085 11-17- 2006MMS120_T3	O35547	Long-chain-fatty-acid--CoA ligase 4 (EC 6.2.1.3) (Long-chain acyl-CoA synthetase 4) (LACS 4).	670	8.70E-44	48
MMS120_G07_051 11-17- 2006MMS120_T3	Q7ZY86	Transmembrane protein 168	700	3.4	34
MMS120_G09_067	P17297	Biphenyl-2,3-diol 1,2-dioxygenase (23OHBP oxygenase)	293	1.4	38

11-17- 2006MMS120 T3		(2,3-dihydroxybiphenyl dioxygenase) (DHBD)			
MMS120_H02_002 11-17- 2006MMS120 T3	P53539	Protein fosB (G0/G1 switch regulatory protein 3).	338	3.80E-23	39
MMS120_H05_033 11-17- 2006MMS120 T3	Q8BFR6	AN1-type zinc finger protein 1.	268	1.20E-24	33
MMS120_H11_081 11-17- 2006MMS120 T3	Q9BUT9	Uncharacterized protein C16orf14	160	0.05	32
MMS121_A04_032 11-17- 2006MMS121 T3	P43509	Cathepsin B-like cysteine proteinase 5 precursor (EC 3.4.22.-) (Cysteine protease-related 5).	344	4.90E-52	60
MMS121_A09_079 11-17- 2006MMS121 T3	Q13501	Sequestosome-1 (Phosphotyrosine-independent ligand for the Lck SH2 domain of 62 kDa) (Ubiquitin-binding protein p62) (EBI3-associated protein of 60 kDa) (p60) (EBIAP)	440	7.00E-07	50
MMS121_B05_045 11-17- 2006MMS121 T3	Q9NSG0	Rho GTPase-activating protein 8	718	4.6	31
MMS121_B07_061 11-17- 2006MMS121 T3	Q93353	Probable isocitrate dehydrogenase [NAD] subunit beta, mitochondrial precursor (Isocitric dehydrogenase) (NAD(+)-specific ICDH)	379	4.00E-05	45
MMS121_B09_077 11-17- 2006MMS121 T3	Q9Y262	Eukaryotic translation initiation factor 3 subunit 6-interacting protein.	564	2.00E-100	69
MMS121_B11_093 11-17- 2006MMS121 T3	Q889E3	Lipoprotein signal peptidase (Prolipoprotein signal peptidase) (Signal peptidase II) (SPase II)	173	3.9	25
MMS121_D04_026 11-17- 2006MMS121 T3	P16607	Putative uncharacterized 9.3 kDa protein.	75	7.5	35
MMS121_D05_041	Q75E32	Serine/threonine-protein phosphatase 4 regulatory subunit 3	687	3.2	31

11-17- 2006MMS121 T3		(PP4R3)			
MMS121_D06_042 11-17- 2006MMS121 T3	P14561	L-lactate dehydrogenase P (L-LDH P)	318	4.5	44
MMS121_E03_023 11-17- 2006MMS121 T3	P08122	Collagen alpha-2(IV) chain precursor (Canstatin)	1707	0.35	28
MMS121_E05_039 11-17- 2006MMS121 T3	P23497	Nuclear autoantigen Sp-100 (Speckled 100 kDa) (Nuclear dot-associated Sp100 protein) (Lysp100b)	879	0.085	36
MMS121_F01_005 11-17- 2006MMS121 T3	P50389	S-methyl-5-thioadenosine phosphorylase (5	236	1.00E-08	25
MMS121_F02_006 11-17- 2006MMS121 T3	Q9NY74	Ewing	926	3.2	57
MMS121_F08_054 11-17- 2006MMS121 T3	Q8BGZ4	Cell division cycle protein 23 homolog (Anaphase-promoting complex subunit 8) (APC8) (Cyclosome subunit 8)	597	2.3	24
MMS121_F11_085 11-17- 2006MMS121 T3	Q9HDY9	Cell agglutination protein mam3 precursor	1082	4.8	29
MMS121_G06_036 11-17- 2006MMS121 T3	Q9JII6	Alcohol dehydrogenase [NADP+] (EC 1.1.1.2) (Aldehyde reductase) (Aldo- keto reductase family 1 member A1).	325	1.90E-53	46
MMS121_H02_002 11-17- 2006MMS121 T3	Q3HNM7	Protein inscuteable homolog (Minsc)	579	2.00E-06	36
MMS121_H04_018 11-17- 2006MMS121 T3	P15381	Voltage-dependent L-type calcium channel subunit alpha-1C (Voltage-gated calcium channel subunit alpha Cav1.2) (Calcium channel, L type, alpha-1 polypeptide, isoform 1, cardiac muscle) (Smooth muscle calcium channel blocker	2171	1.8	23

		receptor) (CACB-receptor)			
MMS121_H05_033 11-17- 2006MMS121 T3	Q57852	Uncharacterized protein MJ0650 precursor	692	0.031	42
MMS121_H08_050 11-17- 2006MMS121 T3	O75437	Zinc finger protein 254 (Bone marrow zinc finger 5) (BMZF-5) (Hematopoietic cell-derived zinc finger protein 1) (HD-ZNF1) (Zinc finger protein 539) (Zinc finger protein 91-like)	659	2.6	27
MMS132_A01_015 11-27- 2006MMS132 T3	P63988	DNA polymerase IV 2 (Pol IV 2)	346	8.8	39
MMS132_A02_016 11-27- 2006MMS132 T3	P18431	Protein kinase shaggy (EC 2.7.11.1) (Protein zeste-white 3).	1067	7.10E-86	71
MMS132_A03_031 11-27- 2006MMS132 T3	O94855	Protein transport protein Sec24D (SEC24-related protein D)	1032	0.17	54
MMS132_A12_096 11-27- 2006MMS132 T3	Q9VP04	ORM1-like protein (dORMDL).	154	2.50E-51	61
MMS132_B01_013 11-27- 2006MMS132 T3	Q61UC4	Raf homolog serine/threonine-protein kinase (Abnormal cell lineage protein 45)	811	0.91	30
MMS132_C03_027 11-27- 2006MMS132 T3	Q66KY3	Protein CutA homolog precursor.	151	2.70E-14	65
MMS132_E12_088 11-27- 2006MMS132 T3	Q9NTG7	NAD-dependent deacetylase sirtuin-3, mitochondrial precursor (EC 3.5.1.-) (SIR2-like protein 3) (hSIRT3).	399	8.80E-29	67
MMS132_F04_022 11-27- 2006MMS132 T3	P15202	Peroxisomal catalase A	515	4.3	50
MMS132_G04_020	Q05049	Integumentary mucin C.1 (FIM-C.1) (Fragment).	662	1.60E-32	57

11-27- 2006MMS132 T3					
MMS132_G07_051 11-27- 2006MMS132 T3	P36146	Protein LAS1	502	6.9	40
MMS132_H01_001 11-27- 2006MMS132 T3	Q6FTY5	GPI mannosyltransferase 3 (GPI mannosyltransferase III) (GPI-MT-III) (Glycosylphosphatidylinositol-anchor biosynthesis protein 10)	612	3.3	38
MMS133_A03_031 11-6- 2006MMS114 T3	P34361	Uncharacterized protein C48B4.7	159	3.8	41
MMS133_B01_013 11-6- 2006MMS114 T3	O13735	Actin-interacting protein 3 homolog	1385	3.5	45
MMS133_B02_014 11-6- 2006MMS114 T3	Q9QWS8	Potassium voltage-gated channel subfamily H member 8 (Voltage-gated potassium channel subunit Kv12.1) (Ether-a-go-go-like potassium channel 3) (ELK channel 3)	1102	0.12	37
MMS133_B08_062 11-6- 2006MMS114 T3	P45478	Palmitoyl-protein thioesterase 1 precursor (PPT-1) (Palmitoyl-protein hydrolase 1)	306	0.15	31
MMS133_C02_012 11-6- 2006MMS114 T3	Q70CQ2	Ubiquitin carboxyl-terminal hydrolase 34 (EC 3.1.2.15) (Ubiquitin thioesterase 34) (Ubiquitin-specific-processing protease 34) (Deubiquitinating enzyme 34).	3395	3.20E-13	41
MMS133_C03_027 11-6- 2006MMS114 T3	Q0VC03	Major facilitator superfamily domain-containing protein 5	450	1.00E-05	24
MMS133_D04_026 11-6- 2006MMS114 T3	P15151	Poliovirus receptor precursor (Nectin-like protein 5) (Nect-5) (CD155 antigen)	417	3	28
MMS133_D05_041 11-6- 2006MMS114 T3	Q66KB9	Biogenesis of lysosome-related organelles complex-1 subunit 2.	147	1.20E-33	53
MMS133_E01_007	Q9USP7	Uncharacterized protein C902.06	397	1.3	36

11-6-2006MMS114 T3					
MMS133_E05_039 11-6-2006MMS114 T3	Q6ZQK0	Condensin-II complex subunit D3 (Non-SMC condensin II complex subunit D3)	1506	4.1	37
MMS133_F06_038 11-6-2006MMS114 T3	P76352	Uncharacterized transporter yeeO	547	2.4	33
MMS133_F09_069 11-6-2006MMS114 T3	Q4ZJM9	Complement C1q-like protein 4 precursor (C1q and tumor necrosis factor-related protein 11) (C1qTNF11)	238	0.004	27
MMS133_G04_020 11-6-2006MMS114 T3	Q9BYQ8	Keratin-associated protein 4-9 (Keratin-associated protein 4.9) (Ultrahigh sulfur keratin-associated protein 4.9)	191	0.98	38
MMS133_G05_035 11-6-2006MMS114 T3	Q95JJ0	Protein kinase-like protein SgK196 (Sugen kinase 196).	350	1.90E-53	42
MMS133_G09_067 11-6-2006MMS114 T3	Q6AZD1	Transmembrane protein 179	232	0.011	23
MMS133_G10_068 11-6-2006MMS114 T3	P36645	Protein transport protein hofB	461	2.8	40
MMS134_A05_047 12-4-2006MMS134	O45700	UPF0375 protein R05A10.4 precursor	112	4	33
MMS134_A06_048 12-4-2006MMS134	Q13472	DNA topoisomerase 3-alpha (DNA topoisomerase III alpha)	1001	8.5	44
MMS134_B01_013 12-4-2006MMS134	Q9VZI3	Unc-112-related protein (Fermitin-1).	708	2.30E-78	53
MMS134_B10_078 12-4-2006MMS134	P04843	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit precursor (EC 2.4.1.119) (Ribophorin I) (RPN-I).	607	1.80E-37	43
MMS134_B12_094	P16810	Uncharacterized protein IRL12 (TRL12)	416	2.5	30

12-4-2006MMS134					
MMS134_C10_076 12-4-2006MMS134	P46094	Chemokine XC receptor 1 (XC chemokine receptor 1) (Lymphotactin receptor) (G-protein coupled receptor 5)	333	0.77	34
MMS134_C11_091 12-4-2006MMS134	O70244	Cubilin precursor (Intrinsic factor-cobalamin receptor) (Intrinsic factor-vitamin B12 receptor) (Glycoprotein 280) (gp280) (460 kDa receptor)	3623	0.062	37
MMS134_D05_041 12-4-2006MMS134	Q9I993	Beta,beta-carotene 15,15'-monooxygenase (EC 1.14.99.36) (Beta-carotene dioxygenase 1).	526	5.90E-43	36
MMS134_E11_087 12-4-2006MMS134	Q7ZW46	UDP-xylose and UDP-N-acetylglucosamine transporter (Solute carrier family 35 member B4)	331	1.9	31
MMS134_F02_006 12-4-2006MMS134	Q868Z9	Papilin precursor.	2898	1.30E-31	44
MMS134_F09_069 12-4-2006MMS134	Q9LNV3	Sugar transport protein 2 (Hexose transporter 2)	522	4.3	25
MMS134_F11_085 12-4-2006MMS134	O07684	Beta-galactosidase large subunit (Lactase)	628	2.7	34
MMS134_F12_086 12-4-2006MMS134	P52556	Flavin reductase (EC 1.5.1.30) (FR) (NADPH-dependent diaphorase) (NADPH-flavin reductase) (FLR) (Biliverdin reductase B) (EC 1.3.1.24) (BVR-B) (Biliverdin-IX beta-reductase) (Green heme-binding protein) (GHBP).	206	1.70E-38	51
MMS134_G05_035 12-4-2006MMS134	Q9VCE6	Probable N6-adenosine-methyltransferase MT-A70-like protein	608	3.5	57
MMS134_G07_051 12-4-2006MMS134	Q22431	Probable protein ariadne-2 (Ari-2)	482	0.52	50
MMS134_G10_068 12-4-2006MMS134	Q922M3	BTB/POZ domain-containing protein KCTD10.	315	3.20E-19	62
MMS134_H03_017 12-4-2006MMS134	Q9U539	Organic cation transporter 1 (CeOCT1).	576	2.10E-20	31
MMS135_A06_048 12-5-2006MMS135	P06811	Laccase precursor (Benzenediol:oxygen oxidoreductase) (Urishiol oxidase) (Diphenol oxidase)	619	0.11	36
MMS135_A09_079 12-5-2006MMS135	Q62523	Zyxin	564	3	37
MMS135_A10_080	Q65TP0	HTH-type transcriptional repressor purR (Purine nucleotide	334	7.9	55

12-5-2006MMS135		synthesis repressor) (Pur regulon repressor)			
MMS135_A11_095 12-5-2006MMS135	P31825	Uncharacterized protein yfiC	245	0.22	38
MMS135_A12_096 12-5-2006MMS135	Q5TGI0	Uncharacterized protein C6orf168.	409	4.00E-12	25
MMS135_B04_030 12-5-2006MMS135	Q9V727	Polycomb protein Asx (Additional sex combs).	1669	1.60E-15	30
MMS135_B05_045 12-5-2006MMS135	Q8X529	Uncharacterized protein yghZ	346	6	40
MMS135_B06_046 12-5-2006MMS135	P0C0R6	Bifunctional polymyxin resistance protein arnA [Includes: UDP-4-amino-4-deoxy-L-arabinose formyltransferase (UDP-L-Ara4N formyltransferase) (ArnAFT); UDP-glucuronic acid oxidase, UDP-4-keto-hexauronic acid decarboxylating (UDP-GlcUA decarboxylase) (UDP-glucuronic acid dehydrogenase) (ArnADH)]	660	3.1	30
MMS135_B12_094 12-5-2006MMS135	Q22021	Putative ATP synthase f chain, mitochondrial	153	3.2	25
MMS135_C05_043 12-5-2006MMS135	P52462	Probable DNA packaging protein (Terminase)	663	3.7	35
MMS135_C07_059 12-5-2006MMS135	O83446	Type III pantothenate kinase (Pantothenic acid kinase) (PanK-III)	273	1.3	31
MMS135_C08_060 12-5-2006MMS135	Q13796	Protein Shroom2 (Apical-like protein) (Protein APXL)	1616	1.8	33
MMS135_C12_092 12-5-2006MMS135	P17152	Transmembrane protein 11 (Protein PM1).	192	1.80E-41	54
MMS135_D04_026 12-5-2006MMS135	Q0IHF1	Transmembrane protein 39A-A	488	6.8	21
MMS135_D08_058 12-5-2006MMS135	Q9K4U6	15,16-dihydrobiliverdin:ferredoxin oxidoreductase	241	9.2	38
MMS135_E06_040 12-5-2006MMS135	Q7N6I1	Putative histidine biosynthesis bifunctional protein hisCD [Includes: Histidinol dehydrogenase (HDH); Histidinol-phosphate aminotransferase (Imidazole acetol-phosphate transaminase)]	807	1.5	38

MMS135_E09_071 12-5-2006MMS135	P24388	Corticotropin-releasing factor-binding protein precursor (CRF-binding protein) (CRF-BP) (Corticotropin-releasing hormone-binding protein) (CRH-BP)	322	1.5	38
MMS135_E10_072 12-5-2006MMS135	Q3ZBH3	CD151 antigen.	253	2.50E-19	26
MMS135_F12_086 12-5-2006MMS135	Q60294	UPF0252 protein MJECL39	351	7.7	28
MMS135_G01_003 12-5-2006MMS135	P80489	Coenzyme F420 hydrogenase subunit alpha (8-hydroxy-5-deazaflavin-reducing hydrogenase subunit alpha) (FRH)	456	1.2	41
MMS135_G04_020 12-5-2006MMS135	P29551	Elongation factor 3 (EF-3)	1042	3.1	29
MMS135_G07_051 12-5-2006MMS135	Q969H6	Ribonuclease P/MRP protein subunit POP5 (EC 3.1.26.5) (hPop5).	163	3.90E-13	31
MMS135_G11_083 12-5-2006MMS135	Q08180	Irregular chiasm C-roughest protein precursor (Protein IRREC)	764	1.5	26
MMS135_G12_084 12-5-2006MMS135	Q2KIY5	LAMA-like protein 2 precursor.	589	1.90E-76	55
MMS135_H04_018 12-5-2006MMS135	P08399	Per-hexamer repeat protein 5.	672	1.80E-39	52
MMS135_H08_050 12-5-2006MMS135	P36079	Hypothetical 23.7 kDa protein in MDH1-VMA5 intergenic region	204	0.35	30
MMS135_H12_082 12-5-2006MMS135	Q93YR3	FAM10 family protein At4g22670.	441	2.30E-32	45
MMS136_B05_045 11-30- 2006MMS136 T3	Q0DHL2	Laccase-12/13 precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase 12/13) (Urishiol oxidase 12/13) (Diphenol oxidase 12/13).	574	3.30E-19	34
MMS136_B11_093 11-30- 2006MMS136 T3	O77645	Nuclear transition protein 2 (TP-2) (TP2)	129	6	31
MMS136_C04_028 11-30- 2006MMS136 T3	Q8VZ96	Derlin-2.1 (AtDerlin2-1)	244	5.2	33
MMS136_C06_044	Q5UQU8	Uncharacterized protein L357	496	2.4	30

11-30-2006MMS136 T3					
MMS136_D06_042 11-30-2006MMS136_T3	Q8WYB5	Histone acetyltransferase MYST4 (MYST protein 4) (MOZ, YBF2/SAS3, SAS2 and TIP60 protein 4) (Histone acetyltransferase MOZ2) (Monocytic leukemia zinc finger protein-related factor) (Histone acetyltransferase MORF)	2073	2.2	29
MMS136_D10_074 11-30-2006MMS136 T3	P17157	Cyclin-dependent protein kinase PHO85 (Serine/threonine-protein kinase PHO85) (Negative regulator of the PHO system)	305	2.1	34
MMS136_D12_090 11-30-2006MMS136 T3	Q9LUC4	F-box/LRR-repeat protein At3g14710	442	9.5	35
MMS136_E07_055 11-30-2006MMS136 T3	Q38VP0	Undecaprenyl-diphosphatase (Undecaprenyl pyrophosphate phosphatase) (Bacitracin resistance protein)	275	7.1	38
MMS136_E10_072 11-30-2006MMS136 T3	Q8BVI4	Dihydropteridine reductase (HDHPR) (Quinoid dihydropteridine reductase)	241	1.6	43
MMS136_F04_022 11-30-2006MMS136 T3	Q9Z2G8	Nucleosome assembly protein 1-like 1 (NAP-1-related protein)	390	2.3	43
MMS136_F09_069 11-30-2006MMS136 T3	Q5JPI3	Uncharacterized protein C3orf38.	329	2.70E-08	32
MMS136_G05_035 11-30-2006MMS136 T3	Q7TSH4	Centrosomal protein of 110 kDa (Cep110 protein)	1004	0.003	31
MMS136_G07_051 11-30-2006MMS136 T3	Q07093	Head-specific guanylate cyclase (EC 4.6.1.2) (Gycalpa99B).	676	6.30E-62	64
MMS136_G08_052 11-30-2006MMS136 T3	P82013	Voltage-dependent anion-selective channel protein 2 (VDAC-2) (Outer mitochondrial membrane protein porin 2).	282	2.70E-94	66

MMS136_G11_083 11-30- 2006MMS136_T3	P55824	Probable ubiquitin carboxyl-terminal hydrolase FAF (Ubiquitin thioesterase FAF) (Ubiquitin-specific-processing protease FAF) (Deubiquitinating enzyme FAF) (Protein fat facets)	2778	0.58	27
MMS136_H03_017 11-30- 2006MMS136_T3	Q8NFT8	Delta and Notch-like epidermal growth factor-related receptor precursor	737	3.7	25
MMS136_H08_050 11-30- 2006MMS136_T3	Q96NU7	Probable imidazolonepropionase (Amidohydrolase domain-containing protein 1)	426	0.67	24
MMS137_A01_015 12-20- 2006MMS137_T3	O13332	Aureobasidin A resistance protein homolog	471	7.1	38
MMS137_B01_013 12-20- 2006MMS137_T3	Q8BWP8	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase (EC 2.4.1.149) (Poly-N-acetyllactosamine extension enzyme) (I-beta-1,3-N-acetylglucosaminyltransferase) (iGnT) (UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1).	415	1.10E-55	49
MMS137_C05_043 12-20- 2006MMS137_T3	P47050	Cullin-8	842	9.6	43
MMS137_D04_026 12-20- 2006MMS137_T3	P11899	Colicin-D immunity protein (Microcin-D immunity protein).	87	4.4	46
MMS137_D10_074 12-20- 2006MMS137_T3	Q14012	Calcium/calmodulin-dependent protein kinase type 1 (CaM kinase I) (CaM-KI) (CaM kinase I alpha) (CaMKI-alpha)	370	2.3	36
MMS137_D11_089 12-20- 2006MMS137_T3	O46640	Amine sulfotransferase (Sulfotransferase 3A1) (AST-RB1)	301	1.1	44
MMS137_E02_008 12-20-	Q4ICM0	Nuclear distribution protein PAC1 (nudF homolog)	464	6.8	33

2006MMS137 T3					
MMS137_E07_055 12-20- 2006MMS137 T3	Q67VS5	Potassium transporter 10 (OsHAK10)	843	3.9	26
MMS137_G02_004 12-20- 2006MMS137 T3	Q12840	Kinesin heavy chain isoform 5A (Neuronal kinesin heavy chain) (NKHC) (Kinesin heavy chain neuron-specific 1)	1032	0.075	31
MMS137_G05_035 12-20- 2006MMS137 T3	P53920	Uncharacterized protein YNL123W	997	2.1	30
MMS137_H06_034 12-20- 2006MMS137 T3	P61228	Uncharacterized protein C02F5.13.	210	1.20E-14	36
MMS137_H07_049 12-20- 2006MMS137_T3	Q0Q476	Replicase polyprotein 1ab (pp1ab) (ORF1ab polyprotein) [Includes: Replicase polyprotein 1a (pp1a) (ORF1A)] [Contains: Non-structural protein 1 (nsp1) (Leader protein); Non-structural protein 2 (nsp2) (p65 homolog); Non-structural protein 3 (nsp3) (Papain-like proteinase) (PL-PRO) (PL2-PRO); Non-structural protein 4 (nsp4); 3C-like proteinase (3CL-PRO) (3CLp) (nsp5); Non-structural protein 6 (nsp6); Non-structural protein 7 (nsp7); Non-structural protein 8 (nsp8); Non-structural protein 9 (nsp9); Non-structural protein 10 (nsp10) (Growth factor-like peptide) (GFL); RNA-directed RNA polymerase (RdRp) (Pol) (nsp12); Helicase (Hel) (nsp13); Exoribonuclease (ExoN) (nsp14); Uridylate-specific endoribonuclease (NendoU) (nsp15); Putative 2	7079	1.5	27
MMS137_H10_066 12-20- 2006MMS137 T3	O76002	Olfactory receptor 2J2 (Olfactory receptor OR6-19) (Olfactory receptor 6-8) (OR6-8) (Hs6M1-6)	312	5.8	29
MMS138_A03_031 12-20- 2006MMS138 T3	Q8NI51	Transcriptional repressor CTCFL (CCCTC-binding factor) (Brother of the regulator of imprinted sites) (Zinc finger protein CTCF-T) (CTCF paralog)	663	6.00E-09	26

MMS138_B02_014 12-20- 2006MMS138 T3	Q03426	Mevalonate kinase (EC 2.7.1.36) (MK).	396	2.40E-37	39
MMS138_B04_030 12-20- 2006MMS138 T3	P98092	Hemocytin precursor (Humoral lectin).	3133	9.70E-32	36
MMS138_B06_046 12-20- 2006MMS138 T3	O13067	Condensin complex subunit 2 (Non-SMC condensin I complex subunit H) (Chromosome-associated protein H) (Chromosome assembly protein xCAP-H) (Barren homolog).	699	1.00E-21	32
MMS138_B08_062 12-20- 2006MMS138 T3	Q67W65	Transcription initiation factor TFIID subunit 1 (TAFII250)	1810	0.67	29
MMS138_B12_094 12-20- 2006MMS138 T3	P16070	CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I) (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor) (Heparan sulfate proteoglycan) (Epican) (CDw44)	742	7.4	43
MMS138_C04_028 12-20- 2006MMS138 T3	Q19970	C-type lectin domain-containing protein F32E10.3 precursor	876	0.001	32
MMS138_C08_060 12-20- 2006MMS138 T3	P40004	UDP-N-acetylglucosamine transporter YEA4	342	0.43	30
MMS138_C10_076 12-20- 2006MMS138 T3	P53697	Protein MNN9	368	8.3	48
MMS138_C12_092 12-20- 2006MMS138 T3	O35565	Fibroblast growth factor 10 precursor (FGF-10) (Keratinocyte growth factor 2)	209	4.1	50
MMS138_D06_042 12-20- 2006MMS138 T3	Q24214	Calcineurin subunit B isoform 2 (Protein phosphatase 2B regulatory subunit).	170	6.60E-83	94

MMS138_E06_040 12-20- 2006MMS138 T3	Q5EAR6	Coiled-coil domain-containing protein 115.	206	1.60E-15	32
MMS138_E08_056 12-20- 2006MMS138 T3	Q08677	Hemolysin 4 precursor	578	2.1	36
MMS138_F01_005 12-20- 2006MMS138 T3	Q93212	Suppressor of lurcher protein 1 precursor.	594	4.30E-29	39
MMS138_F06_038 12-20- 2006MMS138 T3	Q61324	Aryl hydrocarbon receptor nuclear translocator 2 (ARNT protein 2)	712	5.2	33
MMS138_F10_070 12-20- 2006MMS138 T3	P15309	Prostatic acid phosphatase precursor (EC 3.1.3.2).	386	2.00E-42	36
MMS138_G02_004 12-20- 2006MMS138 T3	Q6FXQ5	GPI mannosyltransferase 1 (GPI mannosyltransferase I) (GPI-MT-I) (Glycosylphosphatidylinositol-anchor biosynthesis protein 14)	431	1.5	30
MMS138_G04_020 12-20- 2006MMS138 T3	Q9STT5	Probable ABC2 homolog 6	935	0.19	32
MMS138_G05_035 12-20- 2006MMS138 T3	O43497	Voltage-dependent T-type calcium channel subunit alpha-1G (Voltage-gated calcium channel subunit alpha Cav3.1) (Cav3.1c) (NBR13)	2377	8.1	43
MMS138_G06_036 12-20- 2006MMS138 T3	O62619	Pyruvate kinase (EC 2.7.1.40) (PK).	533	6.30E-78	64
MMS138_H01_001 12-20- 2006MMS138 T3	Q6AY19	Uncharacterized aarF domain-containing protein kinase 4 (EC 2.7.-.-).	528	1.80E-34	70
MMS138_H03_017 12-20- 2006MMS138 T3	Q9K8A9	UvrABC system protein C (Protein uvrC) (Excinuclease ABC subunit C)	591	1.2	34

MMS138_H04_018 12-20- 2006MMS138 T3	Q5ZK69	Proteasomal ATPase-associated factor 1 (WD repeat protein 71).	392	9.00E-63	45
MMS138_H05_033 12-20- 2006MMS138 T3	Q6KEQ9	Protocadherin-11 X-linked precursor (Protocadherin-11) (Protocadherin on the X chromosome)	1117	2.6	35
MMS139_A06_048 1-5- 2006MMS137 T3	Q8BV42	Zinc finger protein 786.	777	4.80E-08	51
MMS139_A09_079 1-5- 2006MMS137 T3	Q5E950	H/ACA ribonucleoprotein complex subunit 2 (Nucleolar protein family A member 2)	153	1	22
MMS139_B09_077 1-5- 2006MMS137 T3	Q9W3C2	Uncharacterized protein CG1785.	478	1.60E-16	35
MMS139_B12_094 1-5- 2006MMS137 T3	Q9LRB7	E3 ubiquitin-protein ligase EL5	325	3.6	39
MMS139_C08_060 1-5- 2006MMS137 T3	P46572	Serpentine receptor class gamma-3 (Protein srg-3)	332	7.8	28
MMS139_D03_025 1-5- 2006MMS137 T3	Q66KH2	Endoplasmic reticulum-Golgi intermediate compartment protein 3	389	4.00E-07	43
MMS139_D04_026 1-5- 2006MMS137 T3	P20268	Homeobox protein ceh-6	380	1.7	26
MMS139_D05_041 1-5- 2006MMS137 T3	Q68XK6	N utilization substance protein B homolog (Protein nusB)	154	1.5	30
MMS139_D06_042 1-5- 2006MMS137 T3	P51871	Cytochrome P450 4F6 (CYPIVF6)	537	9.00E-08	35

MMS139_D08_058 1-5- 2006MMS137 T3	O61703	Phosphate carrier protein, mitochondrial precursor (Phosphate transport protein) (PTP).	349	4.60E-43	77
MMS139_D09_073 1-5- 2006MMS137 T3	Q9EQS3	C-Myc-binding protein (Associate of Myc 1) (AMY-1)	103	1.00E-05	42
MMS139_D10_074 1-5- 2006MMS137 T3	P53355	Death-associated protein kinase 1 (DAP kinase 1)	1432	0.29	38
MMS139_D11_089 1-5- 2006MMS137 T3	Q9W5D4	Protein O-mannosyl-transferase 2 (EC 2.4.1.109) (Dolichyl- phosphate- mannose--protein mannosyltransferase 2) (dPOMT2).	765	4.10E-37	61
MMS139_E05_039 1-5- 2006MMS137 T3	P35502	Esterase FE4 precursor (EC 3.1.1.1) (Carboxylic-ester hydrolase).	564	9.70E-66	47
MMS139_E09_071 1-5- 2006MMS137 T3	Q8N7X0	Uncharacterized protein C6orf103	754	3.9	29
MMS139_F08_054 1-5- 2006MMS137 T3	Q7ZVW9	UPF0430 protein A.	269	4.10E-19	44
MMS139_F11_085 1-5- 2006MMS137 T3	Q5RF70	Zinc finger protein 501	271	0.057	58
MMS139_G02_004 1-5- 2006MMS137 T3	Q5UPY0	Kinesin-like protein L294	2959	4.9	39
MMS139_G10_068 1-5- 2006MMS137 T3	Q04712	RNA polymerase I-specific transcription initiation factor RRN11	507	0.75	24
MMS139_G11_083 1-5- 2006MMS137 T3	P60163	Toxin Cg2.	68	5.3	45

MMS139_H09_065 1-5- 2006MMS137 T3	Q6NW34	Uncharacterized protein C3orf17	567	2.1	36
MMS139_H10_066 1-5- 2006MMS137 T3	Q9CJM5	Uncharacterized protein PM1972 precursor.	71	6.1	43
MMS139_H12_082 1-5- 2006MMS137 T3	P08941	Proto-oncogene tyrosine-protein kinase ROS precursor (c-ros-1)	2311	4	38
MMS140_A07_063 1-5- 2006MMS140 T3	Q1RMU5	RNA-binding protein 5 (RNA-binding motif protein 5) (Tumor suppressor LUCA15).	815	6.60E-19	52
MMS140_A10_080 1-5- 2006MMS140 T3	Q12432	Chromatin modification-related protein EAF3 (ESA1-associated factor 3)	401	0.58	33
MMS140_A11_095 1-5- 2006MMS140 T3	P38150	Uncharacterized deaminase YBR284W	797	3.9	26
MMS140_A12_096 1-5- 2006MMS140 T3	O73590	Zinc finger homeobox protein 4 (Zinc finger homeodomain protein 4) (ZFH-4) (Zinc finger/apterous-related homeobox protein)	3573	1.4	40
MMS140_B04_030 1-5- 2006MMS140 T3	Q18164	Probable dihydropyrimidine dehydrogenase [NADP+] (DPD) (DHPDHase) (Dihydrouracil dehydrogenase) (Dihydrothymine dehydrogenase)	1059	3.9	46
MMS140_B08_062 1-5- 2006MMS140 T3	P23098	Dynein beta chain, ciliary	4466	5.5	29
MMS140_B12_094 1-5- 2006MMS140 T3	Q9VYX7	Peptidoglycan-recognition protein-SA precursor (Protein semmelweis)	203	4.00E-06	33
MMS140_C01_011 1-5- 2006MMS140 T3	Q5NVG2	Dehydrogenase/reductase SDR family member 8 precursor (EC 1.1.1.-) (17-beta-hydroxysteroid dehydrogenase 11) (17-beta-HSD 11) (17-beta- HSD XI) (17betaHSDXI)	300	3.70E-48	40

		(17bHSD11) (17betaHSD11).			
MMS140_C02_012 1-5- 2006MMS140 T3	P36085	Protein STB6	766	7	31
MMS140_C04_028 1-5- 2006MMS140 T3	P32313	Red-sensitive opsin (Red cone photoreceptor pigment)	357	3.5	28
MMS140_C10_076 1-5- 2006MMS140 T3	P53709	DNA repair protein RAD14 (Fragment).	121	0.00016	52
MMS140_D04_026 1-5- 2006MMS140 T3	Q9SEE5	Galactokinase (Galactose kinase)	496	0.81	43
MMS140_D07_057 1-5- 2006MMS140 T3	Q4KMI4	Receptor expression-enhancing protein 2.	268	2.40E-52	66
MMS140_D08_058 1-5- 2006MMS140 T3	Q3TZ65	Uncharacterized protein C19orf19 homolog	277	0.039	40
MMS140_E03_023 1-5- 2006MMS140 T3	P16154	Toxin A	2710	5.7	29
MMS140_E10_072 1-5- 2006MMS140 T3	O08901	Mitotic checkpoint serine/threonine-protein kinase BUB1 (MBUB1) (BUB1A)	1058	0.044	32
MMS140_F10_070 1-5- 2006MMS140 T3	Q12465	Bud site selection protein RAX2 precursor (Revert to axial protein 2)	1220	1.3	29
MMS140_F12_086 1-5- 2006MMS140 T3	Q9LU43	Putative F-box protein At3g21170	395	4.9	37
MMS140_G01_003 1-5-	Q8N766	Uncharacterized protein KIAA0090 precursor.	993	4.50E-34	55

2006MMS140 T3					
MMS140_G07_051 1-5- 2006MMS140 T3	Q20025	Profilin-2	131	0.008	25
MMS140_H10_066 1-5- 2006MMS140 T3	Q02772	Protein PET191, mitochondrial precursor	108	3.00E-05	35
MMS140_H11_081 1-5- 2006MMS140 T3	Q90693	Protein patched homolog 1 (PTC1) (PTC)	1442	6	29
MMS141_A06_048 1-5- 2006MMS141 T3	P62869	Transcription elongation factor B polypeptide 2 (RNA polymerase II transcription factor SIII subunit B) (SIII p18) (Elongin B) (EloB) (Elongin 18 kDa subunit).	118	1.70E-29	59
MMS141_B10_078 1-5- 2006MMS141_T3	Q99590	SFRS2-interacting protein (Splicing factor, arginine/serine-rich 2-interacting protein) (SC35-interacting protein 1) (CTD-associated SR protein 11) (Splicing regulatory protein 129) (SRrp129) (Renal carcinoma antigen NY-REN-40)	1148	8	28
MMS141_C01_011 1-5- 2006MMS141_T3	Q68798	Genome polyprotein [Contains: Core protein p21 (Capsid protein C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTPase/helicase NS3 (Hepacivirin) (NS3P) (p70); Non-structural protein 4A (NS4A) (p8); Non-structural protein 4B (NS4B) (p27); Non-structural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]	3022	6.3	36
MMS141_C02_012 1-5- 2006MMS141 T3	Q8CGA2	TBC1 domain family member 14.	679	3.40E-86	57
MMS141_C12_092 1-5- 2006MMS141 T3	Q801F7	Protein Wnt-10b precursor	427	3.3	43
MMS141_D04_026	Q9QZZ4	Myosin-XV (Unconventional myosin-15)	3511	5.2	36

1-5- 2006MMS141 T3					
MMS141_F03_021 1-5- 2006MMS141 T3	Q9UPA5	Protein bassoon (Zinc finger protein 231)	3926	3.6	48
MMS141_F06_038 1-5- 2006MMS141 T3	Q9R158	ADAM 26A precursor (A disintegrin and metalloproteinase domain 26A) (Testase-3)	697	3.8	33
MMS141_G02_004 1-5- 2006MMS141 T3	Q9U9P7	Cytoplasmic phosphatidylinositol transfer protein 1 (Retinal degeneration B homolog beta) (RdgBbeta).	273	3.40E-14	59
MMS141_G03_019 1-5- 2006MMS141 T3	Q13889	TFIIH basal transcription factor complex p34 subunit (Basic transcription factor 2 34 kDa subunit) (BTF2-p34) (General transcription factor IIH polypeptide 3).	308	7.00E-67	49
MMS141_G04_020 1-5- 2006MMS141 T3	Q8IUH3	Developmentally-regulated RNA-binding protein 1 (RB-1).	476	9.00E-51	47
MMS141_G05_035 1-5- 2006MMS141 T3	Q3B6H8	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B (Asp/Glu-ADT subunit B)	475	4.3	36
MMS141_G08_052 1-5- 2006MMS141 T3	Q39079	Chaperone protein dnaJ 13 (AtJ13) (AtDjB13)	538	1.8	39
MMS141_H04_018 1-5- 2006MMS141 T3	O14964	Hepatocyte growth factor-regulated tyrosine kinase substrate (Protein pp110) (Hrs)	777	9.9	31
MMS142_A02_016 12-19- 2006MMS142 T3	Q94517	Histone deacetylase Rpd3 (HD) (dRPD3).	521	1.50E-85	77
MMS142_A06_048 12-19- 2006MMS142 T3	P12807	Peroxisomal copper amine oxidase (Methylamine oxidase)	692	2.3	37
MMS142_B07_061	Q9LZG0	Adenosine kinase 2 (AK 2) (Adenosine 5	345	6.4	35

12-19-2006MMS142 T3					
MMS142_B09_077 12-19-2006MMS142 T3	O15143	Actin-related protein 2/3 complex subunit 1B (ARP2/3 complex 41 kDa subunit) (p41-ARC).	372	9.70E-34	33
MMS142_C05_043 12-19-2006MMS142 T3	Q9SCM4	Zinc finger AN1 and C2H2 domain-containing stress-associated protein 13 (AtSAP13)	249	8.5	47
MMS142_C10_076 12-19-2006MMS142 T3	Q3SZE2	Prefoldin subunit 1.	122	6.80E-26	53
MMS142_D10_074 12-19-2006MMS142 T3	P31647	Sodium- and chloride-dependent GABA transporter 3	627	8.5	41
MMS142_E03_023 12-19-2006MMS142 T3	P05142	Proline-rich protein MP-2 precursor.	261	6.10E-16	43
MMS142_E04_024 12-19-2006MMS142 T3	O49397	Two-component response regulator ARR10 (Receiver-like protein 4)	552	4.7	26
MMS142_E06_040 12-19-2006MMS142 T3	P04045	Alpha-1,4 glucan phosphorylase L-1 isozyme, chloroplast precursor (Starch phosphorylase L-1)	966	6.4	30
MMS142_E07_055 12-19-2006MMS142 T3	Q9J507	Putative ankyrin repeat protein FPV228	525	4.00E-07	30
MMS142_E07_055 12-19-2006MMS142 T3	Q4UKJ3	Putative ankyrin repeat protein RF_1087.	124	5.90E-07	32
MMS142_E09_071 12-19-2006MMS142 T3	Q9XZK2	Omega-type conotoxin SO3 precursor (SO-3).	71	3.8	34
MMS142_E10_072	Q90ZE2	NocA-like zinc finger protein 1 (NocA-related zinc finger	589	1.9	26

12-19- 2006MMS142 T3		protein 1)			
MMS142_F07_053 12-19- 2006MMS142 T3	P08144	Alpha-amylase A precursor (1,4-alpha-D-glucan glucanohydrolase)	494	2.00E-08	62
MMS142_G09_067 12-19- 2006MMS142 T3	Q8CXS1	UPF0176 protein LA_3128	367	2	37
MMS142_G10_068 12-19- 2006MMS142 T3	Q7A154	UPF0348 protein MW1008	379	5.4	28
MMS142_G11_083 12-19- 2006MMS142 T3	Q03567	Uncharacterized transporter C38C10.2.	493	6.40E-13	35
MMS142_H04_018 12-19- 2006MMS142 T3	Q58679	Uncharacterized protein MJ1283	220	0.17	31
MMS143_A07_063 1-8- 2006MMS143 T3	Q9VWH8	Transmembrane protein 167 homolog precursor.	74	4.60E-11	43
MMS143_C01_011 1-8- 2006MMS143 T3	O18391	Probable serine hydrolase (EC 3.1.-.) (Kraken protein).	331	1.80E-32	32
MMS143_C03_027 1-8- 2006MMS143 T3	Q3SZJ4	NADP-dependent leukotriene B4 12- hydroxydehydrogenase (EC 1.3.1.74) (15-oxoprostaglandin 13-reductase) (EC 1.3.1.48).	329	4.00E-60	52
MMS143_C05_043 1-8- 2006MMS143 T3	Q2HY54	Violacin-A precursor (Violacin 1)	106	2.5	37
MMS143_C08_060 1-8- 2006MMS143 T3	Q8N8A2	Ankyrin repeat domain-containing protein 44.	944	1.90E-28	40
MMS143_D01_009	Q5I0J5	MIT domain-containing protein 1.	249	7.70E-41	53

1-8- 2006MMS143 T3					
MMS143_E09_071 1-8- 2006MMS143 T3	P12348	Period circadian protein	1241	1.6	24
MMS143_E10_072 1-8- 2006MMS143 T3	P51660	Peroxisomal multifunctional enzyme type 2 (MFE-2) (D-bifunctional protein) (DBP) (17-beta-hydroxysteroid dehydrogenase 4) (17-beta-HSD 4) (D-3-hydroxyacyl-CoA dehydratase) (EC 4.2.1.107) (3-alpha,7- alpha,12-alpha-trihydroxy-5-beta-cholest-24-enoyl-CoA hydratase) (3-hydroxyacyl-CoA dehydrogenase) (EC 1.1.1.35).	735	3.00E-55	40
MMS143_F01_005 1-8- 2006MMS143 T3	Q8ML92	Protein aveugle.	106	8.30E-28	58
MMS143_F09_069 1-8- 2006MMS143 T3	Q8C5P5	5'-nucleotidase domain-containing protein 1 (5'-nucleotidase cytosolic II-like protein 1)	467	4.00E-07	32
MMS143_F10_070 1-8- 2006MMS143 T3	P03425	Hemagglutinin-neuraminidase (HN protein)	576	2.9	26
MMS143_G03_019 1-8- 2006MMS143 T3	P58985	Putative gustatory receptor 59d	390	3.3	23
MMS143_G08_052 1-8- 2006MMS143 T3	Q9V5P6	H/ACA ribonucleoprotein complex subunit 3 (Nucleolar protein family A member 3) (snoRNP protein dNop10).	64	5.20E-19	68
MMS143_G12_084 1-8- 2006MMS143 T3	Q9Y826	Meiotic expression up-regulated protein 31	185	0.5	40
MMS143_H02_002 1-8- 2006MMS143 T3	Q7NEZ5	UDP-N-acetylmuramoylalanine--D-glutamate ligase (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) (D-glutamic acid-adding enzyme)	441	7.2	35
MMS143_H04_018	Q9BYR3	Keratin-associated protein 4-4 (Keratin-associated protein	166	0.015	34

1-8- 2006MMS143_T3		4.4) (Ultrahigh sulfur keratin-associated protein 4.4) (Keratin-associated protein 4-13) (Keratin-associated protein 4.13) (Ultrahigh sulfur keratin-associated protein 4.13).			
MMS143_H05_033 1-8- 2006MMS143 T3	Q06821	Uncharacterized protein YPR084W	456	3.8	42
MMS143_H06_034 1-8- 2006MMS143 T3	O14002	Peroxide stress-activated histidine kinase mak2 (Mcs4-associated kinase 2) (His-Asp phosphorelay kinase phk1)	2310	0.27	25
MMS143_H06_034 1-8- 2006MMS143 T3	Q9ZM10	Polyphosphate kinase (EC 2.7.4.1) (Polyphosphoric acid kinase) (ATP- polyphosphate phosphotransferase).	675	6.5	33
MMS143_H09_065 1-8- 2006MMS143 T3	Q9XZK8	Omega-type conotoxin TxO1 precursor.	76	1.3	36
MMS144_A01_015 1-8- 2006MMS144 T3	Q97Z99	UPF0100 protein SSO1031	402	0.2	27
MMS144_A03_031 1-8- 2006MMS144 T3	P51734	Uncharacterized 20.8 kDa protein in lys 3	174	0.95	36
MMS144_A08_064 1-8- 2006MMS144 T3	Q60V75	Vacuolar protein sorting-associated protein 16 homolog	858	5.4	45
MMS144_B04_030 1-8- 2006MMS144 T3	Q99954	Submaxillary gland androgen-regulated protein 3 homolog A precursor (Proline-rich protein 5) (Proline-rich protein PBI).	134	1.60E-11	37
MMS144_B06_046 1-8- 2006MMS144 T3	P12844	Myosin-3 (Myosin heavy chain A) (MHC A).	1969	3.90E-05	26
MMS144_C05_043 1-8-	P24156	Protein l(2)37Cc.	276	6.90E-111	84

2006MMS144 T3					
MMS144_C09_075 1-8- 2006MMS144 T3	Q64693	POU domain class 2-associating factor 1 (B-cell-specific coactivator OBF-1) (OCT-binding factor 1) (BOB-1) (BOB1) (OCA-B)	256	0.87	27
MMS144_C12_092 1-8- 2006MMS144 T3	P27091	Protein 60A precursor (Protein glass bottom boat)	455	0.022	32
MMS144_D04_026 1-8- 2006MMS144 T3	Q5F359	Trafficking protein particle complex subunit 5.	188	3.90E-62	64
MMS144_D07_057 1-8- 2006MMS144 T3	Q491Z0	Dihydroxy-acid dehydratase (DAD)	616	1.6	21
MMS144_D09_073 1-8- 2006MMS144 T3	Q5R890	Multiple inositol polyphosphate phosphatase 1 precursor (EC 3.1.3.62) (Inositol (1,3,4,5)-tetrakisphosphate 3-phosphatase) (Ins(1,3,4,5)P(4) 3-phosphatase).	487	1.40E-27	32
MMS144_D10_074 1-8- 2006MMS144 T3	Q24297	Small nuclear ribonucleoprotein F (snRNP-F) (Sm protein F) (Sm-F) (SmF) (Membrane-associated protein Deb-B).	88	2.80E-36	81
MMS144_E12_088 1-8- 2006MMS144 T3	O35598	ADAM 10 precursor (A disintegrin and metalloproteinase domain 10) (Mammalian disintegrin-metalloprotease) (Kuzbanian protein homolog) (CD156c antigen)	749	0.87	46
MMS144_F02_006 1-8- 2006MMS144 T3	P41252	Isoleucyl-tRNA synthetase, cytoplasmic (Isoleucine--tRNA ligase) (IleRS) (IRS)	1266	1.5	35
MMS144_F03_021 1-8- 2006MMS144 T3	Q96GD3	Polycomb protein SCM1 (Sex comb on midleg homolog 1)	660	4.3	33
MMS144_F03_021 1-8- 2006MMS144 T3	Q5R9Q8	Uncharacterized protein C6orf89 homolog.	347	6.9	28
MMS144_F09_069 1-8-	Q5R691	Aspartate aminotransferase, cytoplasmic (EC 2.6.1.1) (Transaminase A) (Glutamate oxaloacetate transaminase 1).	413	7.60E-66	47

2006MMS144 T3					
MMS144_G05_035 1-8- 2006MMS144 T3	Q6DJ35	Uncharacterized protein C19orf12 homolog.	141	4.80E-18	31
MMS144_G05_035 1-8- 2006MMS144 T3	Q1MLB6	Bifunctional protein fold [Includes: Methylenetetrahydrofolate dehydrogenase ; Methenyltetrahydrofolate cyclohydrolase]	299	9.3	33
MMS144_H06_034 1-8- 2006MMS144 T3	Q91XM9	Disks large homolog 2 (Postsynaptic density protein PSD-93) (Channel-associated protein of synapse-110) (Chapsyn-110)	852	6.5	30
MMS144_H09_065 1-8- 2006MMS144 T3	P52339	Major DNA-binding protein (MDBP)	1131	2	42
MMS145_A04_032 1-8- 2006MMS145 T3	Q6VEQ5	Protein FAM39B (CXYorf1-like protein on chromosome 2)	264	0.035	50
MMS145_A05_047 1-8- 2006MMS145 T3	Q8MQI6	Transcription elongation factor 1 homolog.	82	2.10E-38	89
MMS145_A07_063 1-8- 2006MMS145 T3	Q95221	Inositol hexakisphosphate kinase 2 (EC 2.7.4.21) (InsP6 kinase 2) (P(i)-uptake stimulator) (PiUS).	425	1.80E-34	63
MMS145_A08_064 1-8- 2006MMS145 T3	Q9BYR4	Keratin-associated protein 4-3 (Keratin-associated protein 4.3) (Ultrahigh sulfur keratin-associated protein 4.3) (Fragment).	98	0.082	33
MMS145_A08_064 1-8- 2006MMS145 T3	Q9BYQ9	Keratin-associated protein 4-8 (Keratin-associated protein 4.8) (Ultrahigh sulfur keratin-associated protein 4.8)	114	0.14	27
MMS145_A09_079 1-8- 2006MMS145 T3	Q8WTQ7	G protein-coupled receptor kinase 7 precursor (G protein-coupled receptor kinase GRK7)	553	1.2	45
MMS145_B06_046 1-8-	P48591	Ribonucleoside-diphosphate reductase large subunit (EC 1.17.4.1) (Ribonucleoside-diphosphate reductase M1	812	5.30E-10	55

2006MMS145 T3		subunit) (Ribonucleotide reductase large chain).			
MMS145_B08_062 1-8- 2006MMS145 T3	Q9Z270	Vesicle-associated membrane protein-associated protein A (VAMP- associated protein A) (VAMP-A) (VAP-A) (33 kDa Vamp-associated protein) (VAP-33).	249	3.00E-55	46
MMS145_C07_059 1-8- 2006MMS145 T3	Q8XVK0	UPF0243 zinc-binding protein RSc2830.	71	6.2	38
MMS145_C09_075 1-8- 2006MMS145 T3	P38241	Pre-mRNA-splicing factor SLT11 (Synthetic lethality with U2 protein 11) (Extracellular mutant protein 2)	364	2.7	33
MMS145_C09_075 1-8- 2006MMS145 T3	Q60791	Fibrosin-1 (Fragment).	71	5.9	63
MMS145_D04_026 1-8- 2006MMS145 T3	O46651	CD166 antigen (Activated leukocyte-cell adhesion molecule) (ALCAM) (SB-10 antigen) (Fragment).	521	5.2	38
MMS145_D04_026 1-8- 2006MMS145 T3	P17453	Bactericidal permeability-increasing protein precursor (BPI)	482	5.4	39
MMS145_D05_041 1-8- 2006MMS145 T3	P53307	Uncharacterized protein YGR219W.	113	9.7	32
MMS145_D06_042 1-8- 2006MMS145 T3	Q9PQW0	Uncharacterized protein UU183	291	0.54	35
MMS145_D08_058 1-8- 2006MMS145 T3	Q9Y2L9	Leucine-rich repeat and calponin homology domain-containing protein 1 (Calponin homology domain-containing protein 1) (Neuronal protein 81) (NP81)	728	2.5	56
MMS145_D10_074 1-8- 2006MMS145 T3	Q13231	Chitotriosidase-1 precursor (Chitinase-1)	466	0.096	50
MMS145_E03_023 1-8-	Q9YW06	Nucleoside triphosphatase II (NTPase II) (Nucleoside triphosphate phosphohydrolase II) (NPH II)	717	4.7	27

2006MMS145 T3					
MMS145_E03_023 1-8- 2006MMS145 T3	P04734	Metallothionein-A (MTA).	64	9.8	29
MMS145_E04_024 1-8- 2006MMS145 T3	Q864U8	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5 (Beta3Gn-T5) (BGnT-5) (Beta1,3-N-Acetylglucosaminyltransferase-5)	377	1.2	31
MMS145_F05_037 1-8- 2006MMS145 T3	P08352	Uncharacterized protein E8.	52	9.2	50
MMS145_F09_069 1-8- 2006MMS145 T3	Q8P9R0	Dihydroorotate dehydrogenase (Dihydroorotate oxidase) (DHodehase) (DHODase) (DHOD)	351	0.97	27
MMS145_G03_019 1-8- 2006MMS145 T3	Q99NF1	Beta,beta-carotene 9	532	6.00E-05	51
MMS145_G03_019 1-8- 2006MMS145 T3	Q99NF1	Beta,beta-carotene 9',10'-dioxygenase (EC 1.14.99.-) (Beta-carotene dioxygenase 2) (B-diox-II).	532	0.0063	51
MMS145_G05_035 1-8- 2006MMS145 T3	Q3V0B4	Coiled-coil domain-containing protein 108	1847	0.25	31
MMS145_G06_036 1-8- 2006MMS145 T3	Q8INK6	Peptidoglycan-recognition protein-LB precursor (EC 3.5.1.28).	232	1.20E-42	49
MMS145_G09_067 1-8- 2006MMS145 T3	P73836	Uncharacterized protein ssr3402 precursor.	96	4.1	31
MMS145_G12_084 1-8- 2006MMS145 T3	Q96PY6	Serine/threonine-protein kinase Nek1 (NimA-related protein kinase 1) (Renal carcinoma antigen NY-REN-55)	1258	1.8	30
MMS145_H07_049 1-8-	Q9Y720	Orotidine 5	263	3.1	57

2006MMS145 T3					
MMS145_H10_066 1-8- 2006MMS145 T3	P81918	Odorant receptor 43b	403	2.1	26
MMS145_H12_082 1-8- 2006MMS145 T3	Q5UPV4	Uncharacterized acetyltransferase L280	204	2.7	29
MMS145_H12_082 1-8- 2006MMS145 T3	Q91124	Cardiotoxin-8 precursor (Cardiotoxin VIII).	81	10	22
MMS146_A06_048 1-11- 2006MMS146 T3	P23733	Serine/threonine-protein phosphatase PP1(4.8)	346	0.58	40
MMS146_A07_063 1-11- 2006MMS146 T3	Q8C3Y4	Kinetochores-associated protein 1	2207	7.7	30
MMS146_A10_080 1-11- 2006MMS146 T3	Q9VSF4	Probable deoxyhypusine synthase (EC 2.5.1.46) (DHS).	368	3.00E-78	66
MMS146_B03_029 1-11- 2006MMS146 T3	Q5ALR8	Antagonist of mitotic exit network protein 1	658	6.7	29
MMS146_B05_045 1-11- 2006MMS146 T3	O00841	Putative transcriptional regulator cudA	791	1.1	29
MMS146_B05_045 1-11- 2006MMS146 T3	P14592	24 kDa antigen (Fragment).	37	4.1	48
MMS146_B09_077 1-11- 2006MMS146 T3	Q3ZC08	Annexin A9 (Annexin-9)	345	7.8	30
MMS146_B10_078 1-11-	Q92466	DNA damage-binding protein 2 (Damage-specific DNA-binding protein 2) (DDB p48 subunit) (DDBb) (UV-	427	0.23	53

2006MMS146 T3		damaged DNA-binding protein 2) (UV-DDB 2).			
MMS146_C04_028 1-11- 2006MMS146 T3	Q8BLQ9	Cell adhesion molecule 2 precursor (Immunoglobulin superfamily member 4D) (Nectin-like protein 3)	435	2.00E-05	27
MMS146_C11_091 1-11- 2006MMS146 T3	P14346	Helicase/primase complex protein (Probable DNA replication gene 56 protein)	835	0.006	31
MMS146_D05_041 1-11- 2006MMS146 T3	Q7UID0	Thymidylate synthase (TS) (TSase)	264	6.2	42
MMS146_D08_058 1-11- 2006MMS146 T3	Q9V535	RNA-binding protein 8A (Protein tsunagi).	165	7.80E-64	75
MMS146_D11_089 1-11- 2006MMS146 T3	P26779	Proactivator polypeptide precursor [Contains: Saposin-A (Protein A); Saposin-B (Sphingolipid activator protein 1) (SAP-1) (Cerebroside sulfate activator) (CSAct) (Dispersin) (Sulfatide/GM1 activator); Saposin-C (Co-beta-glucosidase) (A1 activator) (Glucosylceramidase activator) (Sphingolipid activator protein 2) (SAP-2); Saposin-D (Protein C) (Component C)].	525	2.10E-20	37
MMS146_D12_090 1-11- 2006MMS146 T3	P82755	Putative low-molecular-weight cysteine-rich protein LCR40 precursor.	74	7	36
MMS146_E01_007 1-11- 2006MMS146 T3	Q9BYQ3	Keratin-associated protein 9-3 (Keratin-associated protein 9.3) (Ultrahigh sulfur keratin-associated protein 9.3).	159	1.5	30
MMS146_E01_007 1-11- 2006MMS146 T3	P61677	UDP-N-acetylmuramate--L-alanine ligase (UDP-N-acetylmuramoyl-L-alanine synthetase)	477	1.6	26
MMS146_E03_023 1-11- 2006MMS146 T3	Q9VR94	General odorant-binding protein 19a precursor.	159	3.00E-16	29
MMS146_E08_056	P33438	Glutactin precursor	1026	2.4	36

1-11-2006MMS146 T3					
MMS146_E08_056 1-11-2006MMS146 T3	Q9MUM7	Uncharacterized 8.0 kDa protein in ndhF-psbD intergenic region.	70	2.9	48
MMS146_E11_087 1-11-2006MMS146 T3	P79303	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) (UDP- glucose pyrophosphorylase) (UDPGP) (UGPase).	508	3.30E-20	41
MMS146_F03_021 1-11-2006MMS146 T3	Q15392	24-dehydrocholesterol reductase precursor (EC 1.3.1.-) (3-beta- hydroxysterol delta-24-reductase) (Seladin-1) (Diminuto/dwarf1 homolog).	516	1.80E-87	61
MMS146_F04_022 1-11-2006MMS146 T3	Q96KD8	Lung squamous cell carcinoma-related protein 1.	94	0.0033	48
MMS146_F04_022 1-11-2006MMS146 T3	Q4V8A3	Dual specificity tyrosine-phosphorylation-regulated kinase 3	586	2.5	30
MMS146_F09_069 1-11-2006MMS146 T3	Q9HBH5	Retinol dehydrogenase 14 (EC 1.1.1.-) (Alcohol dehydrogenase PAN2).	336	1.30E-59	50
MMS146_G03_019 1-11-2006MMS146 T3	P04474	Acidic proline-rich protein PRP33 precursor (Proline-rich proteoglycan 1).	206	0.00015	42
MMS146_G03_019 1-11-2006MMS146 T3	Q86VE3	Spermidine/spermine N(1)-acetyltransferase-like protein 1	508	0.54	37
MMS146_G08_052 1-11-2006MMS146 T3	P62286	Abnormal spindle-like microcephaly-associated protein homolog	3452	2.2	39
MMS146_G09_067 1-11-2006MMS146 T3	Q89AY7	Uncharacterized protein bbp_081	717	9.2	24
MMS146_G10_068	Q9V BV3	Protein takeout precursor.	249	2.10E-31	36

1-11- 2006MMS146 T3					
MMS146_H04_018 1-11- 2006MMS146 T3	Q6AYQ6	Uncharacterized protein C2orf25 homolog, mitochondrial precursor.	296	3.30E-28	36
MMS147_A05_047 1-11- 2006MMS147 T3	O02437	Protein yellow precursor	568	1.00E-05	29
MMS147_B02_014 1-11- 2006MMS147 T3	Q6BSK5	Autophagy-related protein 17	487	0.29	38
MMS147_B04_030 1-11- 2006MMS147 T3	Q96D59	RING finger protein 183	192	2.7	32
MMS147_B06_046 1-11- 2006MMS147 T3	Q8XP15	Mannonate dehydratase (D-mannonate hydrolase)	350	2.6	52
MMS147_B08_062 1-11- 2006MMS147 T3	Q6CWE8	FK506-binding protein 3 (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase)	418	4.1	34
MMS147_C02_012 1-11- 2006MMS147 T3	Q3SX64	Uncharacterized protein C19orf19.	289	0.22	28
MMS147_C02_012 1-11- 2006MMS147 T3	Q3SX64	Uncharacterized protein C19orf19	289	0.31	26
MMS147_C12_092 1-11- 2006MMS147 T3	P29829	Guanine nucleotide-binding protein subunit beta 2.	346	3.00E-19	54
MMS147_D11_089 1-11- 2006MMS147 T3	Q85X26	Photosystem I reaction center subunit VIII (PSI-I).	56	8.4	46
MMS147_E06_040	Q2L969	Metaxin-2.	267	7.40E-75	56

1-11-2006MMS147 T3					
MMS147_E09_071 1-11-2006MMS147 T3	P26003	Non-structural protein NS-S.	467	2.9	25
MMS147_E10_072 1-11-2006MMS147 T3	Q9UDR5	Alpha-aminoadipic semialdehyde synthase, mitochondrial precursor (LKR/SDH) [Includes: Lysine ketoglutarate reductase (EC 1.5.1.8) (LOR) (LKR); Saccharopine dehydrogenase (EC 1.5.1.9) (SDH)].	926	8.10E-31	42
MMS147_F07_053 1-11-2006MMS147 T3	Q9NBW1	Frizzled-4 precursor (dFz4)	705	4.5	37
MMS147_F08_054 1-11-2006MMS147 T3	P31721	Complement C1q subcomponent subunit B precursor	253	0.013	28
MMS147_F08_054 1-11-2006MMS147 T3	Q5RAW7	Spindlin-3 (Spindlin-like protein 3) (SPIN-3).	77	0.37	33
MMS147_F09_069 1-11-2006MMS147 T3	Q15397	Pumilio domain-containing protein KIAA0020 (HBV X-transactivated gene 5 protein) (Minor histocompatibility antigen HA-8) (HLA-HA8)	648	6.4	29
MMS147_F10_070 1-11-2006MMS147 T3	A4H230	Beta-defensin 120 precursor (Defensin, beta 120).	88	7.4	35
MMS147_G12_084 1-11-2006MMS147 T3	P10379	Protein unzipped precursor (Protein zipper).	488	4.90E-30	36
MMS147_H08_050 1-11-2006MMS147 T3	Q3YSZ0	CTP synthase (UTP--ammonia ligase) (CTP synthetase)	538	1.6	31
MMS147_H09_065 1-11-2006MMS147 T3	Q8TAX7	Mucin-7 precursor (MUC-7) (Salivary mucin-7) (Apo-MG2).	377	1.50E-12	31

MMS163_A04_032 4-10-2007- MMS163 T3	P20108	Thioredoxin-dependent peroxide reductase, mitochondrial precursor (EC 1.11.1.15) (Perioredoxin-3) (PRX III) (Antioxidant protein 1) (AOP-1) (Protein MER5).	257	1.20E-67	70
MMS163_A05_047 4-10-2007- MMS163 T3	P40472	Protein SIM1 precursor.	475	0.2	31
MMS163_A09_079 4-10-2007- MMS163 T3	Q9HDT9	Uncharacterized protein PB2B2.18	175	5.2	24
MMS163_B01_013 4-10-2007- MMS163 T3	Q9TUP7	Orexin receptor type 2 (Ox2r) (Hypocretin receptor type 2)	444	1.8	31
MMS163_B02_014 4-10-2007- MMS163 T3	P11673	Uncharacterized 8.5 kDa protein (ORF B72).	72	1	29
MMS163_B02_014 4-10-2007- MMS163 T3	Q3T8J9	GON-4-like protein (GON-4 homolog)	2241	4.4	41
MMS163_B08_062 4-10-2007- MMS163 T3	Q9UHT9	Protein PRO1768.	52	6	48
MMS163_B08_062 4-10-2007- MMS163 T3	P23090	Gag polyprotein (Core polyprotein) [Contains: Matrix protein p15 (MA); RNA-binding phosphoprotein p12; Capsid protein p30 (CA); Nucleocapsid protein p10 (NC)]	529	7.9	39
MMS163_C05_043 4-10-2007- MMS163 T3	Q3TJ91	Lethal(2) giant larvae protein homolog 2 (Lethal giant larvae-like protein 2)	1027	4.2	38
MMS163_C06_044 4-10-2007- MMS163 T3	Q7RY78	Probable tRNA-splicing endonuclease subunit sen-15 (tRNA-intron endonuclease sen-15)	223	9	40
MMS163_C07_059 4-10-2007- MMS163 T3	P21997	Sulfated surface glycoprotein 185 precursor (SSG 185).	485	1.30E-19	54

MMS163_C10_076 4-10-2007- MMS163 T3	Q9WTU3	Sodium channel protein type 8 subunit alpha (Sodium channel protein type VIII subunit alpha) (Voltage-gated sodium channel subunit alpha Nav1.6)	1978	1.7	30
MMS163_D02_010 4-10-2007- MMS163 T3	Q9R0I7	YLP motif-containing protein 1 (Nuclear protein ZAP3).	1386	0.24	37
MMS163_D02_010 4-10-2007- MMS163 T3	Q64MG4	Leucyl-tRNA synthetase (Leucine--tRNA ligase) (LeuRS)	943	0.29	27
MMS163_D06_042 4-10-2007- MMS163 T3	P19246	Neurofilament heavy polypeptide (NF-H) (Neurofilament triplet H protein) (200 kDa neurofilament protein).	1090	2.30E-06	26
MMS163_D06_042 4-10-2007- MMS163 T3	O94913	Pre-mRNA cleavage complex 2 protein Pcf11 (Pre-mRNA cleavage complex II protein Pcf11)	1654	0.029	25
MMS163_E01_007 4-10-2007- MMS163 T3	Q86XX4	Extracellular matrix protein FRAS1 precursor	4007	2.5	47
MMS163_E01_007 4-10-2007- MMS163 T3	Q27Q53	Toxin 4 precursor (LiTx4) (Fragment).	81	4.4	37
MMS163_E04_024 4-10-2007- MMS163 T3	Q9DAE3	Late cornified envelope-like proline-rich protein 1.	120	0.00067	37
MMS163_E04_024 4-10-2007- MMS163 T3	Q8CG47	Structural maintenance of chromosomes protein 4 (Chromosome-associated polypeptide C) (XCAP-C homolog)	1286	5.5	32
MMS163_E07_055 4-10-2007- MMS163 T3	Q3ANY2	Arginyl-tRNA synthetase (Arginine--tRNA ligase) (ArgRS)	552	6.2	40
MMS163_F07_053 4-10-2007- MMS163 T3	Q9M0F2	Putative low-molecular-weight cysteine-rich protein LCR26.	65	0.26	38

MMS163_F07_053 4-10-2007- MMS163 T3	Q7YS88	Receptor activity-modifying protein 3 precursor	151	1.8	39
MMS163_G04_020 4-10-2007- MMS163 T3	Q8C010	Probable G-protein coupled receptor 61	449	1.4	52
MMS163_G05_035 4-10-2007- MMS163 T3	Q5M9I6	Multiple myeloma tumor-associated protein 2 homolog.	260	7.70E-06	62
MMS163_H03_017 4-10-2007- MMS163 T3	P53501	Actin-57B	376	3.00E-06	62
MMS163_H05_033 4-10-2007- MMS163 T3	Q12480	Probable electron transfer flavoprotein subunit alpha, mitochondrial precursor (Alpha-ETF)	344	4.9	33
MMS163_H06_034 4-10-2007- MMS163 T3	Q8BQZ4	Protein KIAA1219.	1484	1.00E-07	44
MMS163_H08_050 4-10-2007- MMS163 T3	Q1DR06	Histone-lysine N-methyltransferase, H3 lysine-4 specific (COMPASS component SET1) (SET domain-containing protein 1)	1271	8	26
MMS163_H12_082 4-10-2007- MMS163_T3	Q57T35	1-deoxy-D-xylulose 5-phosphate reductoisomerase (DXP reductoisomerase) (1-deoxyxylulose-5-phosphate reductoisomerase) (2-C-methyl-D-erythritol 4-phosphate synthase)	398	8.2	44
MMS164_A02_016 4-10- 2007 MMS164 T3	P06017	Variant surface glycoprotein ANTAT 1.8 precursor (VSG) (Fragment).	115	0.055	26
MMS164_A02_016 4-10- 2007 MMS164 T3	P06014	Variant surface glycoprotein ILTAT 1.3 precursor (VSG)	503	0.12	29
MMS164_A03_031 4-10-	Q9C0A0	Contactin-associated protein-like 4 precursor (Cell recognition molecule Caspr4)	1308	1.5	35

2007 MMS164 T3					
MMS164_A05_047 4-10- 2007 MMS164 T3	Q6DRL5	Myb-binding protein 1A-like protein.	1269	6.60E-07	43
MMS164_B01_013 4-10- 2007 MMS164 T3	Q74N29	DNA polymerase II large subunit (Pol II)	1243	1.3	26
MMS164_C02_012 4-10- 2007 MMS164 T3	Q8BTI8	Serine/arginine repetitive matrix protein 2.	2703	0.0048	42
MMS164_D05_041 4-10- 2007 MMS164 T3	Q3YS31	Glutamyl-tRNA synthetase 1 (Glutamate--tRNA ligase 1) (GluRS 1)	469	3.1	29
MMS164_D05_041 4-10- 2007 MMS164 T3	Q3LHN2	Keratin-associated protein 19-2.	52	3.9	37
MMS164_D06_042 4-10- 2007 MMS164 T3	Q9VL00	Ubiquitin thioesterase otubain-like (EC 3.1.2.-) (Ubiquitin-specific- processing protease otubain-like) (Deubiquitinating enzyme otubain- like).	262	4.60E-43	59
MMS164_D10_074 4-10- 2007 MMS164 T3	Q9BYP8	Keratin-associated protein 17-1 (Keratin-associated protein 16.1).	105	0.044	43
MMS164_D10_074 4-10- 2007 MMS164 T3	O61735	Circadian locomoter output cycles protein kaput (dCLOCK) (dPAS1)	1027	0.21	39
MMS164_D12_090 4-10- 2007 MMS164 T3	Q60368	Uncharacterized ferredoxin MJ0061.	80	4.4	31
MMS164_D12_090 4-10- 2007_MMS164_T3	P03315	Structural polyprotein (p130) [Contains: Capsid protein (Coat protein) (C); p62 (E3/E2); E3 protein (Spike glycoprotein E3); E2 envelope glycoprotein (Spike glycoprotein E2); 6K protein; E1 envelope glycoprotein (Spike glycoprotein E1)]	1253	7.1	30

MMS164_E05_039 4-10- 2007 MMS164 T3	P18379	Uncharacterized 5.3 kDa protein.	44	2.1	38
MMS164_E06_040 4-10- 2007 MMS164 T3	Q6Z4U2	CRS2-associated factor 1, mitochondrial precursor	428	1.4	41
MMS164_F06_038 4-10- 2007 MMS164 T3	P01507	Cecropin-A precursor (Cecropin-C).	64	0.06	45
MMS164_F06_038 4-10- 2007 MMS164 T3	Q8CGB6	Tensin-like C1 domain-containing phosphatase (C1 domain-containing phosphatase and tensin homolog) (C1-TEN) (Tensin-2)	1400	4.2	33
MMS164_F10_070 4-10- 2007 MMS164 T3	Q6K1Z1	Putative cyclin-F1-1 (CycF1;1)	369	2.8	40
MMS164_G02_004 4-10- 2007 MMS164 T3	P84969	Defensin Tk-AMP-D6.1.	46	0.5	66
MMS164_G02_004 4-10- 2007 MMS164 T3	Q6R748	Syntaxin-binding protein 1 (Unc-18 homolog) (Unc-18A) (Unc-18-1) (N-Sec1)	594	2.4	38
MMS164_G04_020 4-10- 2007 MMS164 T3	P08897	Collagenase precursor (Hypodermin C) (HC)	260	0.007	53
MMS164_G04_020 4-10- 2007 MMS164 T3	P08897	Collagenase precursor (EC 3.4.21.-) (Hypodermin C) (HC).	260	0.013	53
MMS164_G06_036 4-10- 2007 MMS164 T3	Q95WC9	Neurotoxin 9 precursor (CsE9).	84	7.3	32
MMS164_G08_052 4-10- 2007 MMS164 T3	Q9W2B2	Putative gustatory receptor 58c	412	5.8	40

MMS164_G08_052 4-10- 2007 MMS164 T3	O76534	Probable molt-inhibiting hormone precursor (MEE-MIH).	105	7.8	29
MMS164_G11_083 4-10- 2007 MMS164 T3	Q5T6V5	Uncharacterized protein C9orf64.	341	2.80E-59	47
MMS164_H01_001 4-10- 2007 MMS164 T3	Q8D2B6	UPF0350 protein WIGBR4380.	84	1.1	29
MMS164_H01_001 4-10- 2007 MMS164 T3	P71345	Branched-chain amino acid transport system carrier protein (Branched-chain amino acid uptake carrier)	436	5.3	44
MMS164_H03_017 4-10- 2007 MMS164 T3	Q0G9Q1	Protein ycf2	2091	1.5	26
MMS164_H07_049 4-10- 2007 MMS164 T3	Q9JLV6	Bifunctional polynucleotide phosphatase/kinase (Polynucleotide kinase-3)	522	0.85	28
MMS165_A02_016 4-10- 2007 MMS165 T3	P51450	Nuclear receptor ROR-gamma (Retinoid-related orphan receptor-gamma) (Nuclear receptor RZR-gamma) (Thymus orphan receptor) (TOR)	516	5.5	40
MMS165_A03_031 4-10- 2007 MMS165 T3	P18294	Creatine kinase, flagellar	1174	6.6	38
MMS165_A04_032 4-10- 2007 MMS165 T3	Q6P7W5	tRNA-splicing endonuclease subunit Sen2 (EC 3.1.27.9) (tRNA-intron endonuclease Sen2).	460	0.85	37
MMS165_C04_028 4-10- 2007 MMS165 T3	Q6BSE2	Origin recognition complex subunit 1	810	3	36
MMS165_C11_091 4-10- 2007 MMS165 T3	Q6L8H1	Keratin-associated protein 5-4 (Keratin-associated protein 5.4) (Ultrahigh sulfur keratin-associated protein 5.4).	288	2.00E-07	33

MMS165_C11_091 4-10- 2007 MMS165 T3	Q99ME6	X/potassium-transporting ATPase subunit beta-m (X,K-ATPase beta-m subunit)	356	3.2	27
MMS165_D08_058 4-10- 2007 MMS165 T3	Q8BN78	Transcriptional regulator Kaiso (Zinc finger and BTB domain-containing protein 33).	671	0.0065	26
MMS165_E04_024 4-10- 2007 MMS165 T3	P46501	Serpentine receptor class beta-10 (Protein srb-10)	185	1.9	38
MMS165_E05_039 4-10- 2007 MMS165 T3	O75820	Zinc finger protein 189.	626	2.80E-13	50
MMS165_E12_088 4-10- 2007 MMS165 T3	Q5UQF0	Putative ankyrin repeat protein L484	1908	0.006	30
MMS165_E12_088 4-10- 2007 MMS165 T3	Q6WJF5	Neurotoxin BmKBTx precursor.	80	2.4	41
MMS165_F04_022 4-10- 2007 MMS165 T3	Q9NVV5	Androgen-induced protein 1 (AIG-1)	245	2.4	57
MMS165_F04_022 4-10- 2007 MMS165 T3	Q753W8	DASH complex subunit HSK3 (Outer kinetochore protein HSK3).	68	9.6	29
MMS165_G09_067 4-10- 2007 MMS165 T3	P45410	[Citrate [pro-3S]-lyase] ligase (Citrate lyase synthetase) (Acetate:SH-citrate lyase ligase)	342	4.00E-06	39
MMS166_A01_015 4-10- 2007 MMS166 T3	Q03792	Calpain-like protease 1 (Cysteine protease RIM13) (Calpain-7) (Regulator of IME2 protein 13)	727	5	43
MMS166_A02_016 4-10- 2007 MMS166 T3	Q613L4	Histone deacetylase 4	892	9.5	40

MMS166_A04_032 4-10- 2007 MMS166 T3	P15224	Neurotoxin Os1 (Os-1).	66	3	33
MMS166_A04_032 4-10- 2007 MMS166 T3	Q5YSW2	Dihydrodipicolinate reductase (DHPR)	248	4.1	36
MMS166_A06_048 4-10- 2007 MMS166 T3	P34537	E3 ubiquitin-protein ligase bre-1 (RING finger protein rfp-1) (Bt toxin-resistant protein 1)	837	1.6	31
MMS166_A06_048 4-10- 2007 MMS166 T3	Q8N9X5	Transmembrane protein 75.	138	2.9	33
MMS166_B12_094 4-10- 2007 MMS166 T3	Q92JF7	Putative surface cell antigen sca2 precursor	1795	0.37	50
MMS166_C07_059 4-10- 2007 MMS166 T3	Q9DBT5	AMP deaminase 2 (EC 3.5.4.6) (AMP deaminase isoform L).	798	5.00E-51	81
MMS166_C12_092 4-10- 2007 MMS166 T3	Q99KK7	Dipeptidyl-peptidase 3 (EC 3.4.14.4) (Dipeptidyl-peptidase III) (DPP III) (Dipeptidyl aminopeptidase III) (Dipeptidyl arylamidase III).	738	8.60E-25	36
MMS166_D09_073 4-10- 2007 MMS166 T3	Q3LI61	Keratin-associated protein 20-2.	65	0.17	43
MMS166_D09_073 4-10- 2007 MMS166 T3	P11982	Tyrosine 3-monooxygenase (Tyrosine 3-hydroxylase) (TH)	491	0.94	30
MMS166_D11_089 4-10- 2007 MMS166 T3	Q8IQC1	Uncharacterized FAM18-like protein CG5021	223	4.00E-06	47
MMS166_E03_023 4-10- 2007 MMS166 T3	P36030	UPF0320 protein YKL225W.	115	4.1	35

MMS166_E12_088 4-10- 2007 MMS166 T3	Q9SZG1	Glycosyltransferase 6 (AtGT6)	432	4.1	31
MMS166_F01_005 4-10- 2007 MMS166 T3	Q9PW35	Acutolysin-A precursor (HI)	413	6.3	33
MMS166_F04_022 4-10- 2007 MMS166 T3	P18761	Carbonic anhydrase 6 precursor (Carbonic anhydrase VI) (Carbonate dehydratase VI) (CA-VI) (Secreted carbonic anhydrase) (Salivary carbonic anhydrase)	317	1.9	37
MMS166_F05_037 4-10- 2007 MMS166 T3	Q06666	Octapeptide-repeat protein T2.	185	2.40E-07	34
MMS166_F11_085 4-10- 2007 MMS166 T3	Q9H081	Protein MIS12 homolog.	205	4.10E-11	32
MMS166_F12_086 4-10- 2007 MMS166 T3	Q24439	ATP synthase O subunit, mitochondrial precursor (EC 3.6.3.14) (Oligomycin sensitivity conferral protein) (OSCP).	209	2.20E-50	58
MMS166_G02_004 4-10- 2007 MMS166 T3	Q9UST4	Eukaryotic translation initiation factor 5A-2 (eIF-5A-2).	157	3.40E-38	50
MMS166_G05_035 4-10- 2007 MMS166 T3	Q5M9Q1	UPF0396 protein C6orf194.	402	0.00031	66
MMS166_G07_051 4-10- 2007 MMS166 T3	Q6PFS5	ER lumen protein retaining receptor 3 (KDEL receptor 3) (KDEL endoplasmic reticulum protein retention receptor 3).	215	2.5	39
MMS166_H02_002 4-10- 2007 MMS166 T3	O92404	Late expression factor 11.	112	1.6	32
MMS166_H05_033 4-10- 2007 MMS166 T3	P36514	UDP-glucuronosyltransferase 2C1 (EC 2.4.1.17) (UDPGT) (Fragment).	502	3.70E-30	40

MMS166_H06_034 4-10- 2007 MMS166 T3	Q9V8R9	Protein 4.1 homolog (Protein coracle).	1698	1.50E-91	69
MMS166_H09_065 4-10- 2007 MMS166 T3	P40021	Uncharacterized protein YER033C	1076	0.048	24
MMS166_H09_065 4-10- 2007 MMS166 T3	Q3E790	Serine palmitoyltransferase-regulating protein TSC3 (Temperature- sensitive CSG2-mutant suppressor protein 3).	80	2.9	36
MMS166_H10_066 4-10- 2007 MMS166 T3	Q09572	Serpentine receptor class delta-55 (Protein srd-55)	334	3.4	28
MMS167_B02_014 4-16- 2007 MMS167 T3	Q23280	Hypothetical protein ZC395.10 in chromosome III.	175	6.80E-10	39
MMS167_C03_027 4-16- 2007 MMS167 T3	O66960	Uncharacterized protein aq_758	165	4	50
MMS167_C08_060 4-16- 2007 MMS167 T3	Q8K996	Cytochrome o ubiquinol oxidase protein cyoD.	108	5	40
MMS167_C12_092 4-16- 2007 MMS167 T3	P53161	Hypothetical 13.4 kDa protein in HSF1-AFT1 intergenic region	119	0.52	48
MMS167_D05_041 4-16- 2007 MMS167 T3	Q810K9	Glycosyltransferase 8 domain-containing protein 4	444	1.1	35
MMS167_E01_007 4-16- 2007 MMS167 T3	P59943	Potassium channel toxin alpha-KTx 1.12 precursor (Charybdotoxin b) (ChTx-b).	59	5.5	45
MMS167_E02_008 4-16- 2007 MMS167 T3	P25404	Antimicrobial peptide 2 precursor (AMP2) (MJ-AMP2).	63	0.26	63

MMS167_E02_008 4-16- 2007 MMS167 T3	Q8NGZ6	Olfactory receptor 6F1 (Olfactory receptor OR1-38)	308	3.8	31
MMS167_E10_072 4-16- 2007 MMS167 T3	P32634	Negative regulator of sporulation PMD1	1753	5.4	57
MMS167_E12_088 4-16- 2007 MMS167 T3	Q3T030	26S protease regulatory subunit 6B (Proteasome 26S subunit ATPase 4).	418	1.10E-110	85
MMS167_F04_022 4-16- 2007 MMS167 T3	P04060	Ribonuclease pancreatic (RNase 1) (RNase A)	128	3.7	29
MMS167_F05_037 4-16- 2007 MMS167 T3	Q01414	Transcriptional regulator ERG homolog (Fragment).	173	0.08	41
MMS167_H08_050 4-16- 2007 MMS167 T3	P40618	High mobility group protein B3 (High mobility group protein 4) (HMG-4) (High mobility group protein 2a) (HMG-2a).	202	9.10E-07	35
MMS167_H08_050 4-16- 2007 MMS167 T3	Q03435	Non-histone protein 10 (High mobility group protein 2)	203	0.16	27
MMS169_A01_015 5-31- 2007 MMS169 T3	Q9VP48	Ras-related protein Rab-26	388	1.8	38
MMS169_A05_047 5-31- 2007 MMS169 T3	P60371	Keratin-associated protein 10-6 (Keratin-associated protein 10.6) (High sulfur keratin-associated protein 10.6) (Keratin-associated protein 18-6) (Keratin-associated protein 18.6)	365	0.79	40
MMS169_A05_047 5-31- 2007 MMS169 T3	Q39458	Metallothionein-like protein 1 (MT-1).	75	9.2	43
MMS169_A08_064 5-31- 2007 MMS169 T3	P38748	RING finger protein YHL010C.	585	5.40E-07	39

MMS169_A10_080 5-31- 2007 MMS169 T3	Q8SY72	UPF0443 protein CG33169.	58	1.10E-09	48
MMS169_A12_096 5-31- 2007 MMS169 T3	Q12632	Chitin synthase 1 (Chitin-UDP acetyl-glucosaminyl transferase 1) (Class-II chitin synthase 1)	852	3.1	32
MMS169_A12_096 5-31- 2007 MMS169 T3	Q96I36	Uncharacterized protein C12orf62.	57	3.3	55
MMS169_B06_046 5-31- 2007 MMS169 T3	Q96P26	Cytosolic 5	610	0.022	43
MMS169_B06_046 5-31- 2007_MMS169_T3	P14151	L-selectin precursor (Lymph node homing receptor) (Leukocyte adhesion molecule 1) (LAM-1) (Leukocyte surface antigen Leu-8) (TQ1) (gp90-MEL) (Leukocyte-endothelial cell adhesion molecule 1) (LECAM1) (CD62L antigen).	372	1.2	30
MMS169_B10_078 5-31- 2007 MMS169 T3	P61506	Lasiotoxin-2 (LpTX2).	49	1.1	75
MMS169_B11_093 5-31- 2007 MMS169 T3	Q10219	Very hypothetical protein C4H3.12c in chromosome I	101	0.48	31
MMS169_B11_093 5-31- 2007 MMS169 T3	Q10219	Uncharacterized protein C4H3.12c.	101	3.6	31
MMS169_C08_060 5-31- 2007 MMS169 T3	P26896	Interleukin-2 receptor subunit beta precursor (IL-2 receptor) (P70-75) (High affinity IL-2 receptor subunit beta) (CD122 antigen)	537	0.96	28
MMS169_C11_091 5-31- 2007 MMS169 T3	Q90ZM2	Protein transport protein Sec61 subunit alpha isoform A.	476	1.80E-50	54
MMS169_D05_041	Q6INU3	PDZ and LIM domain protein 7.	421	5.30E-21	55

5-31- 2007 MMS169 T3					
MMS169_D06_042 5-31- 2007 MMS169 T3	Q92963	GTP-binding protein Rit1 (Ras-like protein expressed in many tissues) (Ras-like without CAAX protein 1)	219	2.00E-06	33
MMS169_D08_058 5-31- 2007 MMS169 T3	Q8BHE1	Gem-associated protein 8 (Protein FAM51A1).	238	5.70E-06	29
MMS169_E06_040 5-31- 2007 MMS169 T3	Q02752	Acidic phosphoprotein precursor (50 kDa antigen).	441	4.70E-10	65
MMS169_E10_072 5-31- 2007 MMS169 T3	Q9BTE1	Dynaactin subunit 5 (Dynaactin subunit p25).	182	1.00E-70	72
MMS169_G01_003 5-31- 2007 MMS169 T3	P97535	Phospholipase A1 member A precursor (EC 3.1.1.-) (Phosphatidylserine- specific phospholipase A1) (PS-PLA1).	456	1.40E-30	39
MMS169_G03_019 5-31- 2007 MMS169 T3	Q5UPJ3	Uncharacterized protein L116	563	2.1	30
MMS169_G08_052 5-31- 2007 MMS169 T3	Q05319	Serine proteinase stubble (EC 3.4.21.-) (Protein stubble-stubbloid) [Contains: Serine proteinase stubble non-catalytic chain; Serine proteinase stubble catalytic chain].	787	6.00E-36	34
MMS169_H05_033 5-31- 2007 MMS169 T3	Q21180	Zinc metalloproteinase nas-16 precursor (EC 3.4.24.21) (Nematode astacin 16).	451	4.1	34
MMS169_H07_049 5-31- 2007 MMS169 T3	Q66JS6	Eukaryotic translation initiation factor 3 subunit 1 (eIF-3 alpha).	263	4.90E-23	41
MMS169_H10_066 5-31- 2007 MMS169 T3	Q0P5D0	Peptidyl-prolyl cis-trans isomerase H (EC 5.2.1.8) (PPIase H) (Rotamase H).	177	1.30E-47	83
MMS169_H12_082	A4III8	Tetratricopeptide repeat protein 26 (TPR repeat protein 26).	554	2.10E-86	76

5-31- 2007 MMS169 T3					
MMS170_A01_015 5-31- 2007 MMS170 T3	Q50L43	Cytosolic phospholipase A2 delta (EC 3.1.1.4) (cPLA2-delta) (Phospholipase A2 group IVD).	825	2.50E-13	33
MMS170_A07_063 5-31- 2007 MMS170 T3	Q66PG1	Glycosyltransferase-like protein LARGE2 (EC 2.4.-.-) (Glycosyltransferase-like 1B).	750	1.70E-84	77
MMS170_A08_064 5-31- 2007 MMS170 T3	Q6BEA0	Plexin-A4 precursor	1903	0.93	29
MMS170_A08_064 5-31- 2007 MMS170 T3	Q68PG8	Neurotoxin Cex7 precursor (Fragment).	69	8	31
MMS170_A10_080 5-31- 2007 MMS170 T3	P16630	Endoglucanase S precursor (Endo-1,4-beta-glucanase S) (Cellulase S)	264	2.4	39
MMS170_B02_014 5-31- 2007 MMS170 T3	Q59MJ2	Probable transporter MCH1.	436	1.4	35
MMS170_B03_029 5-31- 2007 MMS170 T3	Q9SKD6	Cyclic nucleotide-gated ion channel 11 (Cyclic nucleotide- and calmodulin-regulated ion channel 11)	621	7.8	31
MMS170_B04_030 5-31- 2007 MMS170 T3	Q8CIZ7	Dihydrolipoyl dehydrogenase, mitochondrial precursor (EC 1.8.1.4) (Dihydrolipoamide dehydrogenase).	509	4.70E-41	80
MMS170_B12_094 5-31- 2007 MMS170 T3	Q5ZJ24	LisH domain-containing protein C16orf63 homolog.	175	2.20E-13	35
MMS170_C04_028 5-31- 2007 MMS170 T3	O82374	Putative F-box/Kelch-repeat protein At2g29820	388	4.3	27
MMS170_D12_090	O73691	Early growth response protein 1 (EGR-1) (Zinc finger	194	9.2	36

5-31-2007 MMS170 T3		protein ZENK)			
MMS170_E03_023 5-31-2007 MMS170 T3	P13816	Glutamic acid-rich protein precursor.	678	1.10E-10	86
MMS170_E07_055 5-31-2007 MMS170 T3	Q9CHE0	Methionyl-tRNA synthetase (Methionine--tRNA ligase) (MetRS)	662	0.54	34
MMS170_E08_056 5-31-2007 MMS170 T3	P52446	Probable ganciclovir kinase	563	1	33
MMS170_F02_006 5-31-2007 MMS170 T3	P49459	Ubiquitin-conjugating enzyme E2 A (EC 6.3.2.19) (Ubiquitin-protein ligase A) (Ubiquitin carrier protein A) (HR6A) (hHR6A).	152	6.80E-13	34
MMS170_F04_022 5-31-2007 MMS170 T3	P15988	Collagen alpha-2(VI) chain precursor	1022	5.3	37
MMS170_F06_038 5-31-2007 MMS170 T3	P40442	Putative uncharacterized protein YIL169C precursor.	995	7.20E-07	21
MMS170_F06_038 5-31-2007 MMS170 T3	P20782	Acetylcholine receptor subunit epsilon precursor	493	6.5	34
MMS170_F09_069 5-31-2007 MMS170 T3	Q8IRG6	FACT complex subunit spt16 (Facilitates chromatin transcription complex subunit SPT16) (dSPT16).	1083	3.10E-22	63
MMS170_F12_086 5-31-2007 MMS170 T3	O10350	Uncharacterized 6.7 kDa protein (ORF111).	56	1.1	56
MMS170_F12_086 5-31-2007 MMS170 T3	P09462	Alpha-lactalbumin precursor (Lactose synthase B protein)	142	8.9	44
MMS170_G07_051	P32633	Putative uncharacterized protein YEL033W.	139	0.077	33

5-31- 2007 MMS170 T3					
MMS170_G09_067 5-31- 2007 MMS170 T3	Q9JVQ2	Na(+)-translocating NADH-quinone reductase subunit E (Na(+)-translocating NQR subunit E) (Na(+)-NQR subunit E) (NQR complex subunit E) (NQR-1 subunit E)	197	5.8	32
MMS170_G10_068 5-31- 2007 MMS170 T3	Q99279	Receptor-type adenylate cyclase GRESAG 4.1 (ATP pyrophosphate-lyase) (Adenylyl cyclase)	1242	9	45
MMS170_H02_002 5-31- 2007 MMS170 T3	Q9VW71	Putative fat-like cadherin-related tumor suppressor homolog precursor	4705	2.9	46
MMS170_H05_033 5-31- 2007 MMS170 T3	P04326	Protein Tat (Transactivating regulatory protein).	86	2.6	41
MMS170_H05_033 5-31- 2007 MMS170 T3	P13405	Retinoblastoma-associated protein (PP105) (RB)	921	4.2	25
MMS171_A03_031 5-31- 2007 MMS171 T3	P38830	Meiosis-specific transcription factor NDT80	627	7	61
MMS171_A05_047 5-31- 2007 MMS171 T3	Q9HUA5	Glucans biosynthesis protein G precursor	525	2.3	36
MMS171_A08_064 5-31- 2007_MMS171_T3	P35603	AP-2 complex subunit mu (Clathrin coat assembly protein AP50) (Clathrin coat-associated protein AP50) (Plasma membrane adaptor AP-2 50 kDa protein) (Clathrin assembly protein complex 2 medium chain) (Protein dumpy-23).	441	1.10E-08	100
MMS171_B10_078 5-31- 2007 MMS171 T3	Q06SI7	Photosystem II reaction center protein N (PSII-N).	44	0.76	41
MMS171_B10_078 5-31-	P04491	E1B protein, large T-antigen	482	1.5	45

2007 MMS171 T3					
MMS171_C07_059 5-31- 2007 MMS171 T3	P15215	Laminin subunit gamma-1 precursor (Laminin B2 chain)	1639	1.00E-05	42
MMS171_D02_010 5-31- 2007 MMS171 T3	Q5WDU0	UPF0349 protein ABC2936.	78	9	38
MMS171_D04_026 5-31- 2007 MMS171 T3	Q3E7Z4	Uncharacterized protein YIL046W-A	54	0.81	35
MMS171_D07_057 5-31- 2007 MMS171 T3	Q8VXX5	Monocopper oxidase-like protein SKS1 precursor	589	5.5	33
MMS171_D09_073 5-31- 2007 MMS171 T3	Q9EP71	Ankyrin repeat and coiled-coil structure-containing protein (Retinoic acid-induced protein 14) (Novel retinal pigment epithelial cell protein) (p125)	979	0.21	50
MMS171_D09_073 5-31- 2007 MMS171 T3	Q8Q0U0	Putative ankyrin repeat protein MM_0045.	360	3	35
MMS171_D11_089 5-31- 2007 MMS171 T3	Q8VBW9	Olfactory receptor 63 (Olfactory receptor 267-1) (Odorant receptor M4)	316	5.5	30
MMS171_E07_055 5-31- 2007 MMS171 T3	Q52TG9	Maturase K (Intron maturase)	517	4.1	27
MMS171_F01_005 5-31- 2007 MMS171 T3	Q03406	DNA replication complex GINS protein SLD5.	294	6.30E-11	29
MMS171_F02_006 5-31- 2007 MMS171 T3	Q9J5G9	Putative ankyrin repeat protein FPV034	415	0.36	40
MMS171_F09_069 5-31-	Q57630	UPF0204 protein MJ0166	255	1.5	41

2007 MMS171 T3					
MMS171_F09_069 5-31- 2007 MMS171 T3	O20118	Uncharacterized 16.5 kDa protein in psaC-atpA intergenic region (ORF138).	138	2	47
MMS171_G01_003 5-31- 2007 MMS171 T3	P20910	Mycolysin precursor (Neutral metalloproteinase) (NPR) (Pronase)	550	0.31	38
MMS171_G06_036 5-31- 2007 MMS171 T3	Q9GZU8	NEFA-interacting nuclear protein NIP30.	254	1.60E-33	41
MMS171_G08_052 5-31- 2007 MMS171 T3	P60924	Uncharacterized protein KIAA0141 homolog.	509	0.04	29
MMS171_G09_067 5-31- 2007 MMS171 T3	Q9UKX7	Nucleoporin 50 kDa (Nuclear pore-associated protein 60 kDa-like)	468	7	42
MMS171_G10_068 5-31- 2007 MMS171 T3	Q06688	SRR1-like protein	274	3.2	43
MMS171_G11_083 5-31- 2007 MMS171 T3	Q4G2S9	Bladder cancer-associated protein.	87	2.6	28
MMS171_H03_017 5-31- 2007 MMS171 T3	P11609	T-cell surface glycoprotein CD1d1 precursor (CD1.1 antigen)	336	4.5	40
MMS171_H04_018 5-31- 2007 MMS171 T3	Q17802	Cytokinesis protein cej-1 precursor (Cell junction protein 1)	584	0.015	32
MMS171_H09_065 5-31- 2007 MMS171 T3	Q5TA76	Late cornified envelope protein 3A (Late envelope protein 13).	89	6.1	31
MMS171_H09_065 5-31-	P50359	Uncharacterized protein y4hO	115	8.5	34

2007 MMS171 T3					
MMS172_A03_031 5-31- 2007 MMS172 T3	O18405	Surfeit locus protein 4 homolog.	270	3.60E-43	86
MMS172_A04_032 5-31- 2007 MMS172 T3	P54142	Serpentine receptor class beta-7 (Protein srb-7)	348	1.9	40
MMS172_A07_063 5-31- 2007 MMS172 T3	Q14162	Endothelial cells scavenger receptor precursor (Acetyl LDL receptor) (Scavenger receptor class F member 1)	830	6.4	32
MMS172_B01_013 5-31- 2007 MMS172 T3	P35359	Rhodopsin	354	7.7	55
MMS172_B09_077 5-31- 2007 MMS172 T3	Q5E964	26S proteasome non-ATPase regulatory subunit 13 (26S proteasome regulatory subunit S11) (26S proteasome regulatory subunit p40.5)	376	6.3	41
MMS172_B12_094 5-31- 2007 MMS172 T3	P19385	Lysozyme (Endolysin) (Muramidase) (CP-7 lysin)	342	0.3	38
MMS172_C02_012 5-31- 2007 MMS172 T3	P69930	Peptide toxin Am-2 precursor (Peptide toxin Am II).	80	4.6	35
MMS172_C06_044 5-31- 2007 MMS172 T3	Q06578	Pyocin-S1 immunity protein.	87	1.3	28
MMS172_C06_044 5-31- 2007 MMS172 T3	Q8BWW4	La-related protein 4 (La ribonucleoprotein domain family member 4)	719	3.4	25
MMS172_C07_059 5-31- 2007 MMS172 T3	O89039	C-X-C chemokine receptor type 7 (CXC-R7) (CXCR-7) (G-protein coupled receptor RDC1 homolog) (RDC-1) (Chemokine orphan receptor 1)	362	2.5	29
MMS172_C08_060 5-31-	Q9Y115	UNC93-like protein.	538	2.10E-26	54

2007 MMS172 T3					
MMS172_D11_089 5-31- 2007 MMS172 T3	Q7MYE5	UDP-N-acetylenolpyruvoylglucosamine reductase (UDP-N-acetylmuramate dehydrogenase)	341	5.9	35
MMS172_E01_007 5-31- 2007 MMS172 T3	Q6DHB5	Lipoma HMGIC fusion partner-like 3 protein	216	1.1	57
MMS172_E01_007 5-31- 2007 MMS172 T3	Q9TVX3	Potassium channel toxin alpha-KTx 5.3 precursor (Neurotoxin BmP05) (Potassium ion channel blocker P05).	61	2.4	25
MMS172_E07_055 5-31- 2007 MMS172 T3	O23039	Zinc transporter 5 precursor (ZRT/IRT-like protein 5).	360	1.7	45
MMS172_F01_005 5-31- 2007 MMS172 T3	Q24JY7	Protein FAM14A precursor (Protein ISG12(b)).	133	3.80E-16	51
MMS172_F09_069 5-31- 2007 MMS172 T3	Q08495	Dematin (Erythrocyte membrane protein band 4.9).	405	0.4	42
MMS172_F10_070 5-31- 2007 MMS172 T3	P11441	Ubiquitin-like protein 4A (Ubiquitin-like protein GDX)	157	2.00E-04	37
MMS172_F11_085 5-31- 2007 MMS172 T3	P01415	Weak toxin CM-2.	61	6.1	36
MMS172_G01_003 5-31- 2007 MMS172 T3	Q68XP0	Succinate dehydrogenase hydrophobic membrane anchor subunit	125	3.7	37
MMS172_G02_004 5-31- 2007 MMS172 T3	Q08695	Axoneme-associated protein mst101(1).	344	1.70E-05	43
MMS172_H03_017 5-31-	P21422	DNA-directed RNA polymerase beta	575	9	34

2007 MMS172_T3					
MMS172_H04_018 5-31- 2007_MMS172_T3	Q5HU62	UDP-N-acetylglucosamine--N-acetylmuramyl- (pentapeptide) pyrophosphoryl-undecaprenol N- acetylglucosamine transferase (Undecaprenyl-PP-MurNAc- pentapeptide-UDPGlcNAc GlcNAc transferase)	342	0.3	38
MMS172_H04_018 5-31- 2007_MMS172_T3	Q6XLL9	Potassium channel toxin alpha-KTx 6.6 precursor (OcKTx1).	61	0.55	50
MMS172_H06_034 5-31- 2007_MMS172_T3	P81127	Gamma-soluble NSF attachment protein (SNAP-gamma) (N-ethylmaleimide- sensitive factor attachment protein, gamma).	312	1.20E-28	31
MMS172_H09_065 5-31- 2007_MMS172_T3	Q931R3	6-phosphogluconate dehydrogenase, decarboxylating	468	7.6	46
MMS172_H12_082 5-31- 2007_MMS172_T3	Q9CR27	Coiled-coil domain-containing protein 53.	194	2.50E-33	44
MMS173_A07_063 6-6- 2007_MMS173_T3	Q9N281	Collagen alpha-1(XVII) chain (Bullous pemphigoid antigen 2) (180 kDa bullous pemphigoid antigen 2)	709	6.7	41
MMS173_B07_061 6-6- 2007_MMS173_T3	Q8WX94	NACHT, LRR and PYD domains-containing protein 7 (PYRIN-containing APAF1-like protein 3) (Nucleotide- binding oligomerization domain protein 12)	980	0.28	34
MMS173_B11_093 6-6- 2007_MMS173_T3	Q4WNH8	Histone-lysine N-methyltransferase, H3 lysine-4 specific (EC 2.1.1.43) (COMPASS component set1) (SET domain- containing protein 1).	1241	0.09	31
MMS173_C06_044 6-6- 2007_MMS173_T3	P54360	Protein four-jointed [Contains: Protein four-jointed, secreted isoform]	583	0.51	28
MMS173_C09_075 6-6- 2007_MMS173_T3	P82627	Uncharacterized protein SCRL8 precursor.	89	1.1	34
MMS173_C09_075	P82627	Uncharacterized protein SCRL8 precursor	89	4.1	34

6-6- 2007 MMS173 T3					
MMS173_D02_010 6-6- 2007 MMS173 T3	P13825	Aspartic acid-rich protein precursor.	253	0.1	66
MMS173_D09_073 6-6- 2007 MMS173 T3	Q08C53	Uncharacterized protein C14orf45 homolog	520	3.4	31
MMS173_D11_089 6-6- 2007 MMS173 T3	P83332	Thaumatococcus-like protein 1 precursor (PpAZ44)	246	2.4	36
MMS173_E02_008 6-6- 2007 MMS173 T3	O34841	Uncharacterized protein yoeB precursor	181	1.6	33
MMS173_E03_023 6-6- 2007 MMS173 T3	Q80W93	Hydrocephalus-inducing protein (Protein Hy-3).	5099	1.10E-10	31
MMS173_E08_056 6-6- 2007 MMS173 T3	Q9VLJ6	Angiotensin-converting enzyme-related protein precursor (EC 3.4.15.1).	630	4.60E-36	52
MMS173_E11_087 6-6- 2007 MMS173 T3	Q9PDM3	Carboxylesterase bioH (Biotin synthesis protein bioH)	255	6.1	33
MMS173_F03_021 6-6- 2007 MMS173 T3	Q5RFE9	Leucine-rich repeat-containing protein 40	602	2	25
MMS173_F04_022 6-6- 2007 MMS173 T3	Q03569	G-protein regulator 2	525	9	26
MMS173_F05_037 6-6- 2007 MMS173 T3	Q57M54	Undecaprenyl phosphate-alpha-4-amino-4-deoxy-L-arabinose arabinosyl transferase (EC 2.-.-.-) (Undecaprenyl phosphate-alpha-L-Ara4N transferase) (4-amino-4-deoxy-L-arabinose lipid A transferase).	547	1.4	27

MMS173_F05_037 6-6- 2007 MMS173 T3	Q96MU5	Uncharacterized protein C17orf77 precursor	206	8	34
MMS173_F10_070 6-6- 2007 MMS173 T3	Q9BYR0	Keratin-associated protein 4-7 (Keratin-associated protein 4.7) (Ultrahigh sulfur keratin-associated protein 4.7).	210	7.30E-29	39
MMS173_F12_086 6-6- 2007 MMS173 T3	Q09765	NEDD8-activating enzyme E1 catalytic subunit (EC 6.3.2.-) (Ubiquitin- activating enzyme E1 3).	444	1.00E-65	58
MMS173_G01_003 6-6- 2007 MMS173 T3	Q9ZQX4	Probable vacuolar ATP synthase subunit F (EC 3.6.3.14) (V-ATPase subunit F) (Vacuolar proton pump subunit F) (V-ATPase 14 kDa subunit).	128	3.00E-23	52
MMS173_H05_033 6-6- 2007 MMS173 T3	P84843	Vasotab precursor	76	7.00E-07	31
MMS173_H08_050 6-6- 2007 MMS173 T3	Q80VR2	RNA polymerase II elongation factor ELL3.	395	0.5	30
MMS173_H08_050 6-6- 2007 MMS173 T3	Q9N9W8	Proteasome subunit beta type 3	207	1.2	31
MMS173_H11_081 6-6- 2007 MMS173 T3	Q8VHF0	MAP/microtubule affinity-regulating kinase 3 (EC 2.7.11.1).	797	8.50E-33	36
MMS174_A01_015 6-6- 2007 MMS174 T3	P49858	Protein cornichon	144	9.00E-05	28
MMS174_A02_016 6-6- 2007 MMS174 T3	P48043	Vasopressin V1a receptor (V1aR) (Vascular/hepatic-type arginine vasopressin receptor) (Antidiuretic hormone receptor 1a) (AVPR V1a)	418	5.2	25
MMS174_A05_047 6-6- 2007 MMS174 T3	Q9NR33	DNA polymerase epsilon subunit 4 (EC 2.7.7.7) (DNA polymerase II subunit 4) (DNA polymerase epsilon subunit p12).	117	2.80E-20	55

MMS174_A06_048 6-6- 2007 MMS174 T3	Q9M571	Phosphoethanolamine N-methyltransferase	494	7	42
MMS174_A07_063 6-6- 2007 MMS174 T3	P13021	F-actin capping protein subunit beta (CAP32).	272	2.80E-43	42
MMS174_A11_095 6-6- 2007 MMS174 T3	Q86VD1	MORC family CW-type zinc finger protein 1	984	7	25
MMS174_A12_096 6-6- 2007 MMS174 T3	Q5E6A2	Aspartyl-tRNA synthetase (Aspartate--tRNA ligase) (AspRS)	591	5.3	50
MMS174_B05_045 6-6- 2007 MMS174 T3	P38739	Cell wall integrity and stress response component 4 precursor	605	8.4	39
MMS174_B06_046 6-6- 2007 MMS174 T3	P18834	Cuticle collagen 14	345	0.058	92
MMS174_B06_046 6-6- 2007 MMS174 T3	P18834	Cuticle collagen 14.	345	1	92
MMS174_B12_094 6-6- 2007 MMS174 T3	Q9VDW3	Dystrophin, isoform B.	1669	2.90E-11	55
MMS174_C08_060 6-6- 2007 MMS174 T3	Q70KH2	Glucosylceramidase precursor (EC 3.2.1.45) (Beta- glucocerebrosidase) (Acid beta-glucosidase) (D-glucosyl-N- acylsphingosine glucohydrolase).	536	3.80E-48	38
MMS174_D11_089 6-6- 2007 MMS174 T3	Q9GV72	Toxin 1 precursor (CrTX-A / CrTX-B)	450	1.6	26
MMS174_E01_007 6-6- 2007 MMS174 T3	Q9GRJ1	Calmodulin (CaM).	149	5.60E-70	93

MMS174_E06_040 6-6- 2007 MMS174 T3	P37703	Glycine-rich protein DC9.1.	144	1.30E-05	36
MMS174_E06_040 6-6- 2007 MMS174 T3	Q58559	Replication factor A (RP-A) (RF-A) (Replication factor-A protein 1) (Single-stranded DNA-binding protein) (mjaSSB)	645	0.005	29
MMS174_F07_053 6-6- 2007_MMS174_T3	Q5VT25	Serine/threonine-protein kinase MRCK alpha (EC 2.7.11.1) (CDC42-binding protein kinase alpha) (Myotonic dystrophy kinase-related CDC42-binding kinase alpha) (Myotonic dystrophy protein kinase-like alpha) (MRCK alpha) (DMPK-like alpha).	1732	0.00057	31
MMS174_H04_018 6-6- 2007 MMS174 T3	Q5U2T8	CBF1-interacting corepressor.	451	0.19	41
MMS174_H04_018 6-6- 2007 MMS174 T3	Q00174	Laminin subunit alpha precursor (Laminin A chain)	3712	3.1	32
MMS174_H05_033 6-6- 2007 MMS174 T3	P29082	Sulfur oxygenase reductase	309	1.3	26
MMS174_H06_034 6-6- 2007 MMS174 T3	P17205	Serine proteases 1/2 precursor (Protein Jonah 99Cii/99Ciii)	265	6.00E-07	59
MMS176_A04_032 6-6- 2007 MMS176 T3	P19816	Lipopolysaccharide 1,3-galactosyltransferase (Lipopolysaccharide 3-alpha-galactosyltransferase)	337	2.2	45
MMS176_A04_032 6-6- 2007 MMS176 T3	P41663	Uncharacterized 6.8 kDa protein in HE65-PK2 intergenic region.	56	2.5	33
MMS176_A05_047 6-6- 2007 MMS176 T3	Q28943	Dihydropyrimidine dehydrogenase [NADP+] precursor (DPD) (DHPDHase) (Dihydrouracil dehydrogenase) (Dihydrothymine dehydrogenase)	1025	1.4	44
MMS176_A07_063	Q8NDZ0	Uncharacterized protein CXorf20	799	7.4	27

6-6- 2007 MMS176 T3					
MMS176_A09_079 6-6- 2007 MMS176 T3	P09956	Regulatory protein zeste	575	0.96	35
MMS176_A09_079 6-6- 2007 MMS176 T3	Q12358	Alpha-ketoglutarate-dependent sulfonate dioxygenase (EC 1.14.11.-).	412	7.1	27
MMS176_A10_080 6-6- 2007_MMS176_T3	Q3SYC2	2-acylglycerol O-acyltransferase 2 (EC 2.3.1.22) (Monoacylglycerol O- acyltransferase 2) (Acyl CoA:monoacylglycerol acyltransferase 2) (MGAT2) (hMGAT2) (Diacylglycerol acyltransferase 2-like protein 5) (Diacylglycerol O-acyltransferase candidate 5) (hDC5).	334	1.80E-71	52
MMS176_B06_046 6-6- 2007 MMS176 T3	Q9HBM0	Vezatin	779	4.2	43
MMS176_C06_044 6-6- 2007 MMS176 T3	P87362	Bleomycin hydrolase (EC 3.4.22.40) (BLM hydrolase) (BMH) (BH) (Aminopeptidase H).	455	4.30E-40	54
MMS176_C10_076 6-6- 2007 MMS176 T3	Q45743	Pesticidal crystal protein cry2Ac (Insecticidal delta-endotoxin CryIIA(c)) (Crystalline entomocidal protoxin) (70 kDa crystal protein)	622	7.4	26
MMS176_D07_057 6-6- 2007 MMS176 T3	P52340	Large tegument protein	2077	2.7	31
MMS176_D08_058 6-6- 2007 MMS176 T3	Q9EZK4	HTH-type transcriptional regulator sarU (Staphylococcal accessory regulator U)	247	2.9	33
MMS176_D10_074 6-6- 2007 MMS176 T3	Q9XWH8	BTB/POZ domain-containing protein Y57A10B.3 precursor	316	9.6	56
MMS176_D11_089 6-6-	Q32PF3	PEST proteolytic signal-containing nuclear protein (PEST-containing nuclear protein) (PCNP).	178	3.30E-24	45

2007 MMS176 T3					
MMS176_E01_007 6-6- 2007 MMS176 T3	Q04503	Prespore protein DP87 precursor	555	0.67	52
MMS176_E02_008 6-6- 2007 MMS176 T3	Q98TX1	Thioredoxin (Trx).	105	3.00E-23	54
MMS176_F01_005 6-6- 2007 MMS176 T3	Q06839	PX domain-containing protein YPR097W	1073	3.4	33
MMS176_F12_086 6-6- 2007 MMS176 T3	P46562	Putative aldehyde dehydrogenase family 7 member A1 homolog (EC 1.2.1.3) (ALH-9).	531	0.015	94
MMS176_G04_020 6-6- 2007 MMS176 T3	P32221	Uncharacterized protein C12.	75	4.5	32
MMS176_G05_035 6-6- 2007 MMS176 T3	Q09MJ5	Photosystem II reaction center protein K precursor (PSII-K).	61	0.89	32
MMS176_G11_083 6-6- 2007 MMS176 T3	O46680	TGF-beta receptor type-1 precursor (TGF-beta receptor type I) (TGFR-1) (TGF-beta type I receptor) (Transforming growth factor-beta receptor type I) (TbetaR-I)	499	8.8	55
MMS176_H04_018 6-6- 2007 MMS176 T3	Q08732	Serine/threonine-protein kinase HRK1 (Hygromycin resistance kinase 1)	759	5.9	32
MMS176_H06_034 6-6- 2007 MMS176 T3	O04096	F-box protein At1g10890.	592	9.00E-06	36
MMS177_A04_032 MMS177	Q5M8Y1	Probable signal peptidase complex subunit 2 (EC 3.4.-.-) (Microsomal signal peptidase 25 kDa subunit) (SPase 25 kDa subunit).	201	6.60E-35	46
MMS177_A07_063 MMS177	Q5HNY6	DNA primase (EC 2.7.7.-).	598	1.7	22

MMS177_A08_064 MMS177	Q9D099	Alkaline phytoceramidase (aPHC) (Alkaline ceramidase)	267	4.7	40
MMS177_A09_079 MMS177	P23148	Acyl transferase (ACT) (Myristoyl-ACP-specific thioesterase) (C14ACP-TE)	307	3.6	28
MMS177_B06_046 MMS177	Q9LTV2	Putative FBD-associated F-box protein At3g12840	179	3.9	34
MMS177_B10_078 MMS177	Q61790	Lymphocyte activation gene 3 protein precursor (LAG-3) (CD223 antigen)	521	7.4	30
MMS177_B12_094 MMS177	P10724	Alanine racemase	388	7.4	48
MMS177_C02_012 MMS177	Q5UQU3	Uncharacterized protein R349	964	9	28
MMS177_C03_027 MMS177	Q5UNY6	Putative BTB/POZ domain-containing protein R738	497	0.88	41
MMS177_C07_059 MMS177	Q9VL18	Probable elongation factor 1-delta (EF-1-delta)	256	1.00E-08	76
MMS177_C09_075 MMS177	P05790	Fibroin heavy chain precursor (Fib-H) (H-fibroin).	5263	8.60E-11	66
MMS177_D01_009 MMS177	Q9ZB80	Uncharacterized protein MG149.1.	137	0.41	29
MMS177_D03_025 MMS177	Q9H344	Olfactory receptor 51I2 (Olfactory receptor OR11-38) (Odorant receptor HOR5'beta12).	312	9.4	37
MMS177_E09_071 MMS177	Q9R0K7	Plasma membrane calcium-transporting ATPase 2 (PMCA2) (Plasma membrane calcium pump isoform 2) (Plasma membrane calcium ATPase isoform 2)	1198	6.6	48
MMS177_E10_072 MMS177	Q9MBA1	Chlorophyllide a oxygenase, chloroplast precursor (Chlorophyll a oxygenase) (Chlorophyll b synthase) (AtCAO)	536	0.88	36
MMS177_E10_072 MMS177	Q01644	Male-specific sperm protein Mst84Dc.	55	3	44
MMS177_F07_053 MMS177	Q6DFB8	Tetratricopeptide repeat protein 37 (TPR repeat protein 37)	1564	0.13	35
MMS177_G05_035	Q9R1C6	Diacylglycerol kinase epsilon (EC 2.7.1.107) (Diglyceride	564	4.40E-28	41

MMS177		kinase epsilon) (DGK-epsilon) (DAG kinase epsilon).			
MMS177_G08_052 MMS177	Q25434	Adhesive plaque matrix protein precursor (Foot protein 1) (MCFP1)	872	0.44	22
MMS177_G08_052 MMS177	Q7TPS0	Ribosomal protein S6 kinase alpha-6 (EC 2.7.11.1) (S6K-alpha 6).	764	6.4	30
MMS177_G09_067 MMS177	P08175	Male-specific sperm protein Mst87F.	56	0.56	46
MMS177_G09_067 MMS177	P15619	Serendipity locus protein H-1 (Protein wings-down) (Protein pourquoi-pas)	869	4.2	56
MMS177_H05_033 MMS177	O15078	Centrosomal protein Cep290 (Nephrocystin-6) (Tumor antigen se2-2)	2479	1.5	30
MMS177_H05_033 MMS177	Q8YY05	Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI).	528	2.3	26
MMS178_A01_015 MMS	Q10008	Uncharacterized protein T19C3.2	269	0.27	41
MMS178_A04_032 MMS	Q57594	Type I restriction enzyme MjaXIP specificity protein (S protein) (S.MjaXIP)	425	0.73	34
MMS178_A04_032 MMS	Q03643	Merozoite surface antigen 2 precursor (MSA-2).	280	8	43
MMS178_B07_061 MMS	Q4WP03	Chromatin modification-related protein vid21	1467	1.8	34
MMS178_B09_077 MMS	Q76VG7	Uncharacterized 8.8 kDa protein in frd-Gp32 intergenic region.	75	4.4	38
MMS178_B09_077 MMS	Q5UQ08	Putative ankyrin repeat protein R787	437	5.6	28
MMS178_B12_094 MMS	P21415	Envelope glycoprotein precursor (Env polyprotein) [Contains: Surface protein (Glycoprotein 70) (gp70); Transmembrane protein (Envelope protein p15E); R-peptide (p2E)]	685	0.76	30
MMS178_C03_027 MMS	O14127	Uncharacterized protein C3C7.01c	611	4.1	28
MMS178_C06_044	P53706	ATP-dependent permease HST6 (STE6 homolog)	1323	3.7	38

MMS					
MMS178_D02_010 MMS	P15786	Metallothionein-1 (MT-1) (Metallothionein-I) (MT-I).	63	0.95	60
MMS178_D02_010 MMS	Q05733	Histidine decarboxylase (HDC)	847	2.7	51
MMS178_D03_025 MMS	P24915	Hypothetical gene 12 protein	169	4.3	34
MMS178_D03_025 MMS	P55943	Metallothionein-II, hippocampal (MT-2).	61	9.4	35
MMS178_D08_058 MMS	P84080	ADP-ribosylation factor 1.	181	2.40E-62	71
MMS178_D11_089 MMS	Q63016	Large neutral amino acids transporter small subunit 1 (L-type amino acid transporter 1) (4F2 light chain) (4F2 LC) (4F2LC) (Integral membrane protein E16) (TA1 protein).	512	8.10E-11	33
MMS178_D12_090 MMS	P59995	Potassium voltage-gated channel subfamily D member 2 (Voltage-gated potassium channel subunit Kv4.2)	630	2	26
MMS178_D12_090 MMS	P0C1Z9	Tachystatin-B2.	42	5.9	50
MMS178_E02_008 MMS	Q02031	Protein hunchback (Fragment).	50	6.6	33
MMS178_E03_023 MMS	P38825	TPR repeat-containing protein YHR117W	639	4.3	30
MMS178_E04_024 MMS	P77581	Succinylornithine transaminase (Succinylornithine aminotransferase) (Carbon starvation protein C)	406	5.9	38
MMS178_E05_039 MMS	P52423	Phosphoribosylglycinamide formyltransferase, chloroplast precursor (GART) (GAR transformylase) (5)	312	9	36
MMS178_E07_055 MMS	P14198	AAC-rich mRNA clone pLK330 protein (Fragment).	317	0.0021	78
MMS178_E07_055 MMS	Q9ZPY7	Importin-alpha re-exporter (Cellular apoptosis susceptibility protein homolog)	972	0.81	48
MMS178_E09_071 MMS	Q823A7	5'-nucleotidase surE 2 (Nucleoside 5'-monophosphate phosphohydrolase 2)	283	0.049	29
MMS178_E09_071	Q823A7	5'-nucleotidase surE 2 (EC 3.1.3.5) (Nucleoside	283	0.1	29

MMS		5'-monophosphate phosphohydrolase 2).			
MMS178_F05_037 MMS	Q3SPE0	Ribonuclease HII (RNase HII)	258	9.8	52
MMS178_F07_053 MMS	P23918	Uncharacterized deoxyribonuclease in metS 3' region (EC 3.1.21.-) (Fragment).	49	0.2	34
MMS178_F07_053 MMS	Q81LU1	UPF0085 protein BA_4520/GBAA4520/BAS4196	270	9	47
MMS178_F08_054 MMS	Q9SMP0	Nuclear transcription factor Y subunit C-1 (AtNF-YC-1) (Transcriptional activator HAP5A)	234	7.3	46
MMS178_F09_069 MMS	Q8EPA3	NADPH-dependent 7-cyano-7-deazaguanine reductase (NADPH-dependent nitrile oxidoreductase)	165	2	26
MMS178_G04_020 MMS	Q8VIG3	Radial spoke head 1 homolog (Testis-specific gene A2 protein) (Male meiotic metaphase chromosome-associated acidic protein) (Meichroacidin).	301	2.70E-08	44
MMS178_G04_020 MMS	Q9M1K2	Putative phosphatidylinositol-4-phosphate 5-kinase 4 (AtPIP5K4) (1-phosphatidylinositol-4-phosphate kinase 4) (PtdIns(4)P-5-kinase 4) (Diphosphoinositide kinase 4)	779	0.02	40
MMS178_G05_035 MMS	P20432	Glutathione S-transferase 1-1 (EC 2.5.1.18) (GST class-theta).	209	7.00E-69	64
MMS178_G08_052 MMS	P19455	25 kDa ookinete surface antigen precursor (Prs25)	217	7	32
MMS178_H11_081 MMS	P59469	Putative LOB domain-containing protein 34.	141	1.1	29
MMS178_H11_081 MMS	P30957	Ryanodine receptor 2 (Cardiac muscle-type ryanodine receptor) (RyR2) (RYR-2) (Cardiac muscle ryanodine receptor-calcium release channel)	4969	1.2	26
MMS179_A06_048 MMS	P19301	Uncharacterized 7.3 kDa protein.	63	7.6	27
MMS179_A09_079 MMS	Q09213	Serpentine receptor class epsilon-1 (Protein sre-1)	355	0.42	32
MMS179_A10_080 MMS	Q6GN15	Cyclin-L1.	496	0.16	31
MMS179_A10_080	P21561	Hypothetical 50.6 kDa protein in the 5	437	0.22	30

MMS					
MMS179_A12_096 MMS	P59093	Uncharacterized protein C21orf99.	68	5.8	32
MMS179_A12_096 MMS	Q5VWM5	PRAME family member 9/15	478	9.1	29
MMS179_B03_029 MMS	P25782	Digestive cysteine proteinase 2 precursor (EC 3.4.22.-).	323	7.10E-38	46
MMS179_C02_012 MMS	Q69ZX6	MORC family CW-type zinc finger protein 2A (Zinc finger CW-type coiled-coil domain protein 1).	1030	0.044	27
MMS179_C02_012 MMS	Q6GX35	Translocated actin-recruiting phosphoprotein (Tarp protein)	1005	5.3	40
MMS179_C06_044 MMS	Q8WUI4	Histone deacetylase 7a (HD7a)	952	1.4	32
MMS179_C09_075 MMS	P02585	Troponin C, skeletal muscle	160	1.00E-06	23
MMS179_C10_076 MMS	Q9DA08	Coiled-coil domain-containing protein 101.	293	1.70E-45	66
MMS179_D12_090 MMS	P06273	DNA-directed RNA polymerase subunit beta' (EC 2.7.7.6) (PEP) (Plastid- encoded RNA polymerase subunit beta'); (RNA polymerase subunit beta').	684	4.7	50
MMS179_D12_090 MMS	P39542	Uncharacterized transporter YJL193W	402	5.4	31
MMS179_E10_072 MMS	Q82WS3	Phosphoenolpyruvate carboxylase (PEPCase) (PEPC)	933	9.6	27
MMS179_E11_087 MMS	Q9VQZ6	Putative elongator complex protein 3 (EC 2.3.1.48).	552	4.80E-14	81
MMS179_E12_088 MMS	P39012	GPI transamidase component GAA1	614	5.3	25
MMS179_F01_005 MMS	Q99IB8	Genome polyprotein [Contains: Core protein p21 (Capsid protein C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTPase/helicase NS3 (Hepacivirin) (NS3P) (p70); Non-structural	3033	6.7	32

		protein 4A (NS4A) (p8); Non-structural protein 4B (NS4B) (p27); Non-structural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]			
MMS179_F03_021 MMS	P31370	POU domain protein 1 (DjPOU1)	559	0.4	54
MMS179_H01_001 MMS	Q7V2R0	UPF0161 protein PMM0411.	78	4.6	40
MMS179_H01_001 MMS	Q5M2R5	Elongation factor P (EF-P)	186	9.2	33
MMS179_H08_050 MMS	Q9HUB4	Sec-independent protein translocase protein tatB homolog.	141	0.0003	47
MMS179_H08_050 MMS	Q62415	Apoptosis-stimulating of p53 protein 1 (Protein phosphatase 1 regulatory subunit 13B)	1087	3.9	36
MMS179_H10_066 MMS	Q7VRI8	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (Methionine synthase, vitamin-B12 independent isozyme) (Cobalamin-independent methionine synthase)	769	0.47	22
MMS180_A01_015 MMS	P36607	DNA repair protein rad5	1133	0.16	20
MMS180_A01_015 MMS	Q3E811	Uncharacterized protein YLR162W-A.	62	1.3	41
MMS180_A03_031 MMS	Q9VTE2	Protein suppressor of underreplication	962	1.2	29
MMS180_A03_031 MMS	P24642	Protamine-2 (P2).	40	4.1	63
MMS180_A11_095 MMS	P09568	Lymphocyte antigen 6C precursor (Ly-6C)	131	0.022	27
MMS180_A12_096 MMS	P56562	Endocuticle structural glycoprotein SgAbd-5.	82	1.30E-22	63
MMS180_B03_029 MMS	Q8WWF8	Calcyphosin-like protein.	198	6.60E-35	39
MMS180_C04_028 MMS	Q5TGZ0	UPF0327 protein C1orf151.	78	2.60E-17	56

MMS180_C07_059 MMS	Q9SJK6	Protein ROS1 (Repressor of silencing 1) (DEMETER-like protein 1)	1393	9.2	37
MMS180_D01_009 MMS	P20393	Orphan nuclear receptor NR1D1 (V-erbA-related protein EAR-1) (Rev-erbA-alpha)	614	0.36	33
MMS180_D03_025 MMS	O02626	MAP kinase-activating death domain protein (Regulator of presynaptic activity aex-3) (Aboc, expulsion defective protein 3)	1409	1.4	30
MMS180_D07_057 MMS	Q9QZ09	Putative homeodomain transcription factor 1	761	7.4	35
MMS180_D11_089 MMS	P11004	Photosystem II 44 kDa reaction center protein (P6 protein) (CP43)	461	0.002	34
MMS180_D11_089 MMS	P11022	Membrane protein P8A7.	138	0.0028	38
MMS180_E04_024 MMS	Q66J97	E3 ubiquitin-protein ligase arkadia-C (RING finger protein 111-C)	967	3	28
MMS180_E07_055 MMS	Q57287	Uncharacterized glycosyltransferase HI1578	323	7.2	28
MMS180_F05_037 MMS	Q56TU0	Type-4 ice-structuring protein precursor (Antifreeze protein type IV).	125	0.61	19
MMS180_F05_037 MMS	Q96NX5	Calcium/calmodulin-dependent protein kinase type 1G (CaM kinase IG) (CaM kinase I gamma) (CaMKI gamma) (CaMKI-gamma) (CaM-KI gamma) (CaMKIG) (CaMK-like CREB kinase III) (CLICK III)	476	2.5	29
MMS180_F10_070 MMS	P32217	Uncharacterized protein C18.	67	1.5	27
MMS180_F10_070 MMS	Q5ZJZ6	Nuclear cap-binding protein subunit 1	793	3.8	34
MMS180_F12_086 MMS	P32616	Uncharacterized protein YEL045C.	141	0.01	32
MMS180_F12_086 MMS	O50286	Dihydrolipoyl dehydrogenase (E3 component of 2-oxoglutarate dehydrogenase complex) (Dihydrolipoamide dehydrogenase)	475	4.9	35
MMS180_G09_067	Q9P1W3	Transmembrane protein 63C	806	5.2	26

MMS					
MMS180_H10_066 MMS	Q9LU89	Serine/threonine protein phosphatase 2A 59 kDa regulatory subunit B	510	0.54	26
MMS190_A04_032 6-6- 2007 MMS190 T3	O01159	Probable splicing factor, arginine/serine-rich 7 (p54).	452	6.60E-09	33
MMS190_A06_048 6-6- 2007 MMS190 T3	P77280	Uncharacterized zinc-type alcohol dehydrogenase-like protein ydjJ.	347	3.20E-37	39
MMS190_B06_046 6-6- 2007 MMS190 T3	Q03211	Pistil-specific extensin-like protein precursor (PELP).	426	0.00053	59
MMS190_C05_043 6-6- 2007 MMS190 T3	P29362	Latent membrane protein 1 (LMP-1) (Protein p63).	404	0.53	32
MMS190_C07_059 6-6- 2007 MMS190 T3	P60409	Keratin-associated protein 10-7 (Keratin-associated protein 10.7) (High sulfur keratin-associated protein 10.7) (Keratin-associated protein 18-7) (Keratin-associated protein 18.7).	375	0.002	32
MMS190_C08_060 6-6- 2007 MMS190 T3	P98164	Low-density lipoprotein receptor-related protein 2 precursor (Megalin) (Glycoprotein 330) (gp330).	4655	7.50E-39	40
MMS190_C09_075 6-6- 2007 MMS190 T3	Q9VNE2	Protein extra bases (eIF5C domain-containing protein) (Eukaryotic translation initiation factor 5C domain-containing protein) (Decp).	422	1.10E-100	67
MMS190_D01_009 6-6- 2007 MMS190 T3	O20118	Uncharacterized 16.5 kDa protein in psaC-atpA intergenic region (ORF138).	138	0.17	40
MMS190_D06_042 6-6- 2007 MMS190 T3	Q7RX84	Pre-mRNA-splicing factor cwc-22.	1010	0.00044	34
MMS190_D10_074 6-6- 2007 MMS190 T3	Q8BYN5	FSD1-like protein (FSD1 N-terminal-like protein) (Coiled-coil domain-containing protein 10).	131	2.6	30

MMS190_D11_089 6-6- 2007 MMS190 T3	P80017	Globin D, coelomic.	159	1.60E-17	36
MMS190_E03_023 6-6- 2007_MMS190_T3	Q9YHT4	5-aminolevulinate synthase, erythroid-specific, mitochondrial precursor (EC 2.3.1.37) (5-aminolevulinic acid synthase) (Delta- aminolevulinate synthase) (Delta-ALA synthetase) (ALAS-E).	583	4.10E-29	73
MMS190_E11_087 6-6- 2007 MMS190 T3	Q9RMW7	Uncharacterized protein pXO2-67/BXB0090/GBAA_pXO2_0090.	58	1	30
MMS190_G09_067 6-6- 2007 MMS190 T3	Q89707	Major core protein precursor (Protein VII) (pVII).	72	0.91	48
MMS190_H06_034 6-6- 2007 MMS190 T3	Q04398	Stationary phase protein 3.	127	0.027	33
MMS198_A10_080 4-16- 2007 MMS199 T3	Q941L0	Cellulose synthase A catalytic subunit 3 [UDP-forming] (AtCesA-3) (Constitutive expression of VSP1 protein 1) (Isoxaben-resistant protein 1) (Ath-B)	1065	1.5	29
MMS198_B02_014 4-16- 2007 MMS199 T3	Q493S3	Isoleucyl-tRNA synthetase (Isoleucine--tRNA ligase) (IleRS)	942	5.1	41
MMS198_B05_045 4-16- 2007 MMS199 T3	Q8NBN7	Retinol dehydrogenase 13 (EC 1.1.1.-).	331	7.70E-42	47
MMS198_C01_011 4-16- 2007 MMS199 T3	P84014	Neurotoxin PRTx23C2.	55	4.1	61
MMS198_C01_011 4-16- 2007 MMS199 T3	Q84TX2	SCAR-like protein 1	2097	6	31
MMS198_C03_027 4-16-	Q95Y12	Probable histone-lysine N-methyltransferase Y41D4B.12	244	6.3	32

2007 MMS199 T3					
MMS198_C09_075 4-16- 2007 MMS199 T3	P34878	Modification methylase ScrFIB (Cytosine-specific methyltransferase ScrFIB) (M.ScrFIB) (M.ScrFI-B)	360	7	55
MMS198_C10_076 4-16- 2007 MMS199 T3	Q21389	Glycosyltransferase-like protein LARGE	631	0.001	26
MMS198_C10_076 4-16- 2007 MMS199 T3	P19817	Lipopolysaccharide 1,2-glycosyltransferase (EC 2.4.1.58).	336	0.0027	24
MMS198_D06_042 4-16- 2007 MMS199 T3	P37509	Uncharacterized protein yyaO.	79	1.2	41
MMS198_D06_042 4-16- 2007 MMS199 T3	Q19749	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial precursor (E2) (Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex)	507	3.9	26
MMS198_D07_057 4-16- 2007 MMS199 T3	P50532	Structural maintenance of chromosomes protein 4 (Chromosome-associated protein C) (Chromosome assembly protein XCAP-C).	1290	0.00021	25
MMS198_D07_057 4-16- 2007 MMS199 T3	P50532	Structural maintenance of chromosomes protein 4 (Chromosome-associated protein C) (Chromosome assembly protein XCAP-C)	1290	0.002	22
MMS198_E02_008 4-16- 2007 MMS199 T3	Q1M5X4	Ribose import ATP-binding protein rbsA 2	512	2.2	39
MMS198_E09_071 4-16- 2007 MMS199 T3	Q9U620	Copper-specific metallothionein-2 (CuMT-II).	64	7.20E-08	45
MMS198_F06_038 4-16- 2007 MMS199 T3	Q2M3X8	Phosphatase and actin regulator 1	580	1.2	34
MMS198_F11_085	P04278	Sex hormone-binding globulin precursor (SHBG) (Sex	402	3.3	35

4-16- 2007_MMS199_T3		steroid-binding protein) (SBP) (Testis-specific androgen-binding protein) (ABP) (Testosterone-estrogen-binding globulin) (Testosterone-estradiol-binding globulin) (TeBG)			
MMS198_G02_004 4-16- 2007 MMS199 T3	O14026	Histone-lysine N-methyltransferase, H3 lysine-36 specific (SET domain-containing protein 2)	798	1.1	29
MMS198_G09_067 4-16- 2007 MMS199 T3	P41479	Uncharacterized 24.1 kDa protein in LEF4-P33 intergenic region.	224	1.40E-09	43
MMS198_G11_083 4-16- 2007 MMS199 T3	Q6DD32	RING finger protein 121	327	4.6	42
MMS198_H02_002 4-16- 2007 MMS199 T3	Q31125	Zinc transporter SLC39A7 (Solute carrier family 39 member 7) (Histidine-rich membrane protein Ke4)	476	4.8	80
MMS198_H12_082 4-16- 2007 MMS199 T3	Q57899	Uncharacterized protein MJ0457	410	2.9	35
MMS199_A02_016 4-16- 2007 MMS198 T3	Q93075	TatD DNase domain-containing deoxyribonuclease 2 (EC 3.1.21.-).	761	4.30E-37	35
MMS199_A05_047 4-16- 2007 MMS198 T3	P87179	Cell wall integrity and stress response component 1 precursor.	374	0.022	29
MMS199_A05_047 4-16- 2007 MMS198 T3	P59510	ADAMTS-20 precursor (A disintegrin and metalloproteinase with thrombospondin motifs 20) (ADAM-TS 20) (ADAM-TS20)	1911	2.7	32
MMS199_A07_063 4-16- 2007 MMS198 T3	O94556	Anaphase-promoting complex subunit 8 (20S cyclosome/APC complex protein apc8) (Cell untimely torn protein 23)	565	5.2	32
MMS199_A09_079 4-16- 2007 MMS198 T3	P84180	Putative gustatory receptor 22b	386	3.2	30

MMS199_A10_080 4-16- 2007 MMS198 T3	Q6DFS6	Charged multivesicular body protein 2a (Chromatin-modifying protein 2a) (CHMP2a).	220	9.90E-80	79
MMS199_A11_095 4-16- 2007 MMS198 T3	Q8MUF6	Paramyosin (Allergen Blo t 11)	875	0.06	24
MMS199_A11_095 4-16- 2007 MMS198 T3	P59617	Argininosuccinate lyase (EC 4.3.2.1) (Arginosuccinase) (ASAL).	467	0.14	31
MMS199_A12_096 4-16- 2007 MMS198 T3	Q60610	T-lymphoma invasion and metastasis-inducing protein 1 (TIAM-1 protein)	1591	8.8	33
MMS199_B03_029 4-16- 2007 MMS198 T3	P37370	Verprolin	817	2.8	43
MMS199_B05_045 4-16- 2007 MMS198 T3	Q5M8I4	Protein TSSC1	387	0.094	33
MMS199_B05_045 4-16- 2007 MMS198 T3	Q5T0W9	Protein FAM83B.	1011	2	25
MMS199_B06_046 4-16- 2007 MMS198 T3	Q95327	Beta-mannosidase precursor (EC 3.2.1.25) (Lysosomal beta A mannosidase) (Mannanase) (Mannase).	879	2.80E-19	33
MMS199_B08_062 4-16- 2007 MMS198 T3	Q8EKT5	UPF0161 protein SO_0005.	84	5.1	27
MMS199_B08_062 4-16- 2007 MMS198 T3	P44277	Uncharacterized protein HI1625	165	6.8	32
MMS199_B10_078 4-16- 2007 MMS198 T3	Q39214	Disease resistance protein RPM1 (Resistance to Pseudomonas syringae protein 3)	926	2.1	51

MMS199_B10_078 4-16- 2007 MMS198 T3	P20530	Uncharacterized 8.8 kDa protein.	72	3.9	33
MMS199_C04_028 4-16- 2007 MMS198 T3	Q67ES5	Taste receptor type 2 member 124 (T2R124) (Taste receptor type 2 member 25) (T2R25)	309	0.28	25
MMS199_C04_028 4-16- 2007 MMS198 T3	O73943	Homing endonuclease I-ApeII (EC 3.1.-.-) (rRNA intron-encoded homing endonuclease 2).	167	2.5	39
MMS199_E02_008 4-16- 2007 MMS198 T3	Q24560	Tubulin beta-1 chain (Beta-1 tubulin).	447	7.10E-141	83
MMS199_E04_024 4-16- 2007 MMS198 T3	Q2T9N3	UPF0351 protein C9orf32 homolog	223	2	33
MMS199_E06_040 4-16- 2007 MMS198 T3	Q4AAV9	ATP synthase subunit alpha (ATPase subunit alpha) (ATP synthase F1 sector subunit alpha)	507	4.1	41
MMS199_E09_071 4-16- 2007 MMS198 T3	P48814	Alcohol dehydrogenase 1 (EC 1.1.1.1).	257	1.80E-16	38
MMS199_E10_072 4-16- 2007 MMS198 T3	Q9GL30	LAMA-like protein 1 precursor	545	3.9	31
MMS199_F01_005 4-16- 2007 MMS198 T3	Q9R1Q2	Cyclin-L1 (Cyclin-L) (Cyclin Ania-6a).	527	7.70E-57	53
MMS199_F04_022 4-16- 2007 MMS198 T3	Q3ZBU2	Zinc finger CDGSH domain-containing protein 1.	106	1.30E-22	69
MMS199_G02_004 4-16- 2007 MMS198 T3	O45228	Probable proline oxidase, mitochondrial precursor (Proline dehydrogenase)	616	1.9	25

MMS199_G02_004 4-16- 2007 MMS198 T3	P47427	Uncharacterized protein MG181.	420	5.4	47
MMS199_G08_052 4-16- 2007 MMS198 T3	Q3ZCB2	Placenta-specific gene 8 protein.	116	0.0023	26
MMS199_G09_067 4-16- 2007 MMS198 T3	A2CG63	AT-rich interactive domain-containing protein 4B (ARID domain- containing protein 4B) (Histone deacetylase complex subunit SAP180) (180 kDa Sin3-associated polypeptide) (Sin3-associated polypeptide p180).	1314	4.40E-50	50
MMS199_H01_001 4-16- 2007 MMS198 T3	Q6P635	COP9 signalosome complex subunit 5 (EC 3.4.-.-) (Signalosome subunit 5).	334	2.80E-130	80
MMS199_H03_017 4-16- 2007 MMS198 T3	Q5U581	Myotubularin-related protein 10-A.	765	6.70E-24	50
MMS199_H06_034 4-16- 2007 MMS198 T3	P32189	Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase) (Glycerokinase) (GK).	524	5.80E-91	59
MMS199_H09_065 4-16- 2007 MMS198 T3	Q4GZT3	Polycystin-2 (Polycystic kidney disease 2 protein homolog)	970	8.5	40
MMS199_H11_081 4-16- 2007 MMS198 T3	P19075	Tetraspanin-8 (Tspan-8) (Transmembrane 4 superfamily member 3) (Tumor-associated antigen CO-029)	237	5.8	40
MMS200_A02_016 4-16- 2007 MMS200 T3	O13913	Uncharacterized protein C23C11.07.	110	5.3	31
MMS200_A08_064 4-16- 2007 MMS200 T3	P78811	Probable UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) (UDP-glucose pyrophosphorylase) (UDPGP) (UGPase).	506	9.20E-45	39
MMS200_B08_062 4-16-	Q9PT92	Catalase (EC 1.11.1.6).	526	1.80E-101	75

2007 MMS200 T3					
MMS200_B10_078 4-16- 2007 MMS200 T3	Q5ECE3	Lopap precursor (EC 3.4.21.-) (Prothrombin activator) (Lipocalin-1/4).	201	0.0081	25
MMS200_B10_078 4-16- 2007 MMS200 T3	Q46036	Outer membrane lipoprotein blc precursor	177	0.42	30
MMS200_C02_012 4-16- 2007 MMS200 T3	P01001	Acrosin inhibitors IIA and IIB (BUSI-II).	57	4.6	37
MMS200_C02_012 4-16- 2007 MMS200 T3	Q07928	Protein GAT3	141	7.6	43
MMS200_C08_060 4-16- 2007 MMS200 T3	P14095	Growth-regulated alpha protein precursor (CXCL1) (Cytokine-induced neutrophil chemoattractant) (CINC-1) (Platelet-derived growth factor- inducible protein KC).	96	2.3	41
MMS200_C09_075 4-16- 2007 MMS200 T3	Q9JM76	Actin-related protein 2/3 complex subunit 3 (ARP2/3 complex 21 kDa subunit) (p21-ARC).	178	2.00E-17	40
MMS200_D03_025 4-16- 2007_MMS200_T3	P97756	Calcium/calmodulin-dependent protein kinase kinase 1 (EC 2.7.11.17) (Calcium/calmodulin-dependent protein kinase kinase alpha) (CaM-kinase kinase alpha) (CaM-KK alpha) (CaMKK alpha) (alpha CaMKK) (CaMKK 1) (CaM-kinase IV kinase).	505	3.90E-28	40
MMS200_D05_041 4-16- 2007 MMS200 T3	Q4A0V8	Uro-adherence factor A precursor.	2316	0.33	25
MMS200_D07_057 4-16- 2007 MMS200 T3	Q15612	Olfactory receptor 1Q1 (Olfactory receptor OR9-25) (Olfactory receptor TPCR106) (Olfactory receptor 9-A) (OR9-A) (OST226)	314	1.1	23
MMS200_D08_058 4-16- 2007 MMS200 T3	P82174	Lysozyme (1,4-beta-N-acetylmuramidase)	121	0.13	46

MMS200_E04_024 4-16- 2007 MMS200 T3	P04170	Rubredoxin 1 (Rd-1).	45	3.5	44
MMS200_E12_088 4-16- 2007 MMS200 T3	P34280	Uncharacterized GTP-binding protein C02F5.3	366	2.5	34
MMS200_G04_020 4-16- 2007 MMS200 T3	Q9NDM2	Gustatory receptor trehalose 1 (Trehalose receptor 1)	392	6.8	28
MMS200_H03_017 4-16- 2007 MMS200 T3	Q62193	Replication protein A 32 kDa subunit (RP-A) (RF-A) (Replication factor-A protein 2) (p32).	270	1.00E-29	33
MMS200_H09_065 4-16- 2007 MMS200 T3	Q4WP12	Peptidyl-prolyl cis-trans isomerase B precursor (EC 5.2.1.8) (PPIase B) (Rotamase B).	209	4.40E-54	64
MMS201_A02_016 4-24- 2007 MMS201 T3	P43461	Uncharacterized HTH-type transcriptional regulator in cgkA 5	166	6.9	40
MMS201_A03_031 4-24- 2007 MMS201 T3	Q62622	Eukaryotic translation initiation factor 4E-binding protein 1 (4E-BP1) (eIF4E-binding protein 1) (Phosphorylated heat- and acid-stable protein regulated by insulin 1) (PHAS-I).	117	4.80E-08	39
MMS201_A04_032 4-24- 2007 MMS201 T3	Q9Y587	AP-4 complex subunit sigma-1 (Adapter-related protein complex 4 sigma- 1 subunit) (Sigma subunit of AP-4) (AP- 4 adapter complex sigma subunit).	144	2.30E-20	32
MMS201_B02_014 4-24- 2007 MMS201 T3	P42286	Protein three rows	1379	9	61
MMS201_B08_062 4-24- 2007 MMS201 T3	P22472	Major 114 kDa structural protein (Core protein P3)	1019	2.4	32
MMS201_B12_094 4-24- 2007 MMS201 T3	P17276	Protein henna [Includes: Phenylalanine-4-hydroxylase (EC 1.14.16.1) (PAH) (Phe-4-monooxygenase); Tryptophan 5- monooxygenase (EC 1.14.16.4) (TRH) (Tryptophan 5-	452	6.60E-10	64

		hydroxylase)].			
MMS201_C02_012 4-24- 2007 MMS201 T3	Q95LF0	Interleukin-13 receptor alpha-2 chain precursor (CD213a2 antigen)	386	0.5	23
MMS201_C03_027 4-24- 2007 MMS201 T3	Q8I8V0	Transcriptional adapter 2B (dADA2b).	555	0.00046	46
MMS201_C12_092 4-24- 2007 MMS201 T3	Q9BW72	HIG1 domain family member 2A.	106	2.00E-17	54
MMS201_D02_010 4-24- 2007 MMS201 T3	P68501	Metallothionein B (MT-B).	60	0.24	50
MMS201_D02_010 4-24- 2007 MMS201 T3	Q80W03	TOX high mobility group box family member 3 (Trinucleotide repeat-containing protein 9)	575	2.8	33
MMS201_D03_025 4-24- 2007 MMS201 T3	Q9LN59	Putative wall-associated receptor kinase-like 11 precursor	788	9.7	37
MMS201_D06_042 4-24- 2007 MMS201 T3	P97430	Antileukoproteinase precursor (ALP) (Secretory leukocyte protease inhibitor)	131	0.025	31
MMS201_D06_042 4-24- 2007 MMS201 T3	A4K2S3	WAP four-disulfide core domain protein 5 precursor.	123	0.03	45
MMS201_D10_074 4-24- 2007 MMS201 T3	O01509	Serpentine receptor class beta-15 (Protein srb-15)	336	5.9	40
MMS201_E02_008 4-24- 2007 MMS201 T3	Q6GL92	Protein BCCIP homolog.	310	2.00E-25	40
MMS201_E04_024 4-24-	Q95SX7	Probable RNA-directed DNA polymerase from transposon BS (EC 2.7.7.49) (Reverse transcriptase).	906	3.20E-29	38

2007 MMS201 T3 MMS201_E08_056 4-24-	Q5RDY4	Long-chain fatty acid transport protein 4 (Fatty acid transport protein 4) (FATP-4) (Solute carrier family 27 member 4)	643	6.3	32
2007 MMS201 T3 MMS201_E11_087 4-24-	O24035	Pantoate--beta-alanine ligase precursor (Pantothenate synthetase) (Pantoate-activating enzyme)	308	2.9	33
2007 MMS201 T3 MMS201_F05_037 4-24-	Q9UVU5	Peroxisomal biogenesis factor 6 (Peroxin-6)	1135	2.4	32
2007 MMS201 T3 MMS201_F07_053 4-24-	P15879	Mono-ADP-ribosyltransferase C3 precursor (Exoenzyme C3)	251	4	48
2007 MMS201 T3 MMS201_F07_053 4-24-	O51077	Uncharacterized protein BB_0048.	56	6.3	41
2007 MMS201 T3 MMS201_F08_054 4-24-	P50462	Cysteine and glycine-rich protein 3 (Cysteine-rich protein 3) (CRP3) (LIM domain protein, cardiac) (Muscle LIM protein).	194	3.70E-18	44
2007 MMS201 T3 MMS201_H01_001 4-24-	Q5KI47	Protein GRC3	744	1	34
2007 MMS201 T3 MMS201_H03_017 4-24-	Q4P7C7	UPF0390 protein UM03986.	94	1.60E-06	34
2007 MMS201 T3 MMS201_H03_017 4-24-	Q24JV4	UPF0390 protein zgc136864	98	1.4	40
2007 MMS201 T3 MMS201_H04_018 4-24-	O93279	Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer disease amyloid A4 A4 protein homolog) [Contains: Beta-amyloid protein (Beta-APP) (A-beta)]	737	5	43
2007 MMS201 T3 MMS201_H07_049 4-24-	Q09702	Negative regulator of differentiation 1 (Multicopy suppressor of sporulation protein msa2).	529	4.80E-11	37

2007 MMS201 T3					
MMS201_H08_050 4-24- 2007 MMS201 T3	O15229	Kynurenine 3-monooxygenase (Kynurenine 3-hydroxylase)	486	2.8	30
MMS201_H11_081 4-24- 2007 MMS201 T3	Q6NS52	Diacylglycerol kinase beta (Diglyceride kinase beta) (DGK-beta) (DAG kinase beta)	802	8.4	33
MMS202_C07_059 4-24- 2007 MMS202 T3	Q6ZW76	Ankyrin repeat and SAM domain-containing protein 3.	656	2.70E-19	39
MMS204_B05_045 4-25- 2007 MMS204 T3	O46107	Lipase 1 precursor (EC 3.1.1.-) (DmLip1).	439	6.40E-08	37
MMS204_B06_046 4-25- 2007 MMS204 T3	P68604	Protein I2.	73	8.6	37
MMS204_B10_078 4-25- 2007 MMS204 T3	P79769	Translin.	229	9.10E-38	71
MMS204_B11_093 4-25- 2007 MMS204 T3	P20039	HLA class II histocompatibility antigen, DRB1-11 beta chain precursor (MHC class I antigen DRB1*11) (DR-5) (DR5) (DRw11)	266	5	32
MMS204_B12_094 4-25- 2007 MMS204 T3	Q8VIB2	Death domain-associated protein 6 (Daxx).	731	2.60E-09	29
MMS204_C04_028 4-25- 2007 MMS204 T3	Q02942	Transferrin precursor.	726	3.90E-124	77
MMS204_C07_059 4-25- 2007 MMS204 T3	Q9UID3	Uncharacterized protein C11orf2 (Another new gene 2 protein).	782	1.40E-72	64
MMS204_D03_025 4-25-	Q6ZN16	Mitogen-activated protein kinase kinase kinase 15 (MAPK/ERK kinase kinase 15) (MEK kinase 15) (MEKK 15)	1313	1.9	31

2007 MMS204 T3					
MMS204_D03_025 4-25- 2007 MMS204 T3	Q8K353	UPF0467 protein C5orf32 homolog.	104	2	31
MMS204_D08_058 4-25- 2007 MMS204 T3	Q5X1N2	Ferrous iron transport protein B	751	2	39
MMS204_D11_089 4-25- 2007 MMS204 T3	Q8C129	Leucyl-cystinyl aminopeptidase (Cystinyl aminopeptidase) (Oxytocinase) (OTase)	1025	2.7	30
MMS204_D11_089 4-25- 2007 MMS204 T3	Q3MIV0	Keratin-associated protein 22-1.	48	7.7	52
MMS204_E03_023 4-25- 2007 MMS204 T3	O95007	Olfactory receptor 6B1 (Olfactory receptor 7-3) (OR7-3)	311	4.7	45
MMS204_E05_039 4-25- 2007 MMS204 T3	Q8TDN2	Potassium voltage-gated channel subfamily V member 2 (Voltage-gated potassium channel subunit Kv8.2)	545	8.7	40
MMS204_E06_040 4-25- 2007 MMS204 T3	Q93092	Transaldolase (EC 2.2.1.2).	337	7.30E-109	72
MMS204_E11_087 4-25- 2007 MMS204 T3	Q8ZYP9	DNA-directed RNA polymerase subunit N (EC 2.7.7.6).	66	0.15	60
MMS204_E11_087 4-25- 2007 MMS204 T3	P53791	Sodium/glucose cotransporter 1 (Na ⁽⁺⁾ /glucose cotransporter 1) (High affinity sodium-glucose cotransporter)	664	1.4	26
MMS204_F01_005 4-25- 2007 MMS204 T3	P35604	Coatomer subunit zeta-1 (Zeta-1 coat protein) (Zeta-1 COP).	177	3.40E-47	66
MMS204_G01_003 4-25-	P43413	Ferrochelatase (Protoheme ferro-lyase) (Heme synthetase)	322	2.7	27

2007 MMS204 T3					
MMS204_G01_003 4-25- 2007 MMS204 T3	O80995	Probable cysteine-rich antifungal protein At2g26010 precursor (AFP).	80	2.8	40
MMS204_G07_051 4-25- 2007 MMS204 T3	Q95JC3	Liver-expressed antimicrobial peptide 2 precursor (LEAP-2).	77	1.5	50
MMS204_H01_001 4-25- 2007 MMS204 T3	Q8IZQ1	WD repeat and FYVE domain-containing protein 3 (Autophagy-linked FYVE protein) (Alfy)	3526	0.5	38
MMS204_H02_002 4-25- 2007 MMS204 T3	Q2KJH9	4-trimethylaminobutyraldehyde dehydrogenase (TMABADH) (Aldehyde dehydrogenase 9A1)	494	5	25
MMS204_H03_017 4-25- 2007 MMS204 T3	Q10690	Uncharacterized protein Rv2082.	721	0.0001	29
MMS204_H03_017 4-25- 2007 MMS204 T3	P62575	Sialidase A precursor (Neuraminidase A)	1035	5	23
MMS204_H05_033 4-25- 2007 MMS204 T3	Q5K8D3	Serine/threonine-protein kinase ATG1 (Autophagy-related protein 1)	988	6.2	32
MMS205_A08_064 4-25- 2007 MMS205 T3	O70143	SHC-transforming protein 3 (SH2 domain protein C3) (Src homology 2 domain-containing-transforming protein C3) (Neuronal Shc) (N-Shc)	594	6	35
MMS205_A10_080 4-25- 2007 MMS205 T3	Q9BW60	Elongation of very long chain fatty acids protein 1.	279	3.40E-10	38
MMS205_A12_096 4-25- 2007 MMS205 T3	O74870	Meiotically up-regulated gene 73 protein	306	3.8	24
MMS205_B08_062 4-25-	O60671	Cell cycle checkpoint protein RAD1 (EC 3.1.11.2) (DNA repair exonuclease rad1 homolog) (Rad1-like DNA damage	282	8.10E-30	46

2007 MMS205 T3		checkpoint protein) (hRAD1).			
MMS205_B11_093 4-25- 2007 MMS205 T3	Q8MY85	Fibroblast growth factor receptor 2 precursor (FGFR-2) (DjFgfr2) (DjPTK1)	887	4.5	20
MMS205_C03_027 4-25- 2007 MMS205 T3	P15515	Histatin-1 precursor (Histidine-rich protein 1) (Post-PB protein) (PPB) [Contains: Histatin-2].	57	0.33	57
MMS205_C03_027 4-25- 2007 MMS205 T3	P07988	Pulmonary surfactant-associated protein B precursor (SP-B) (6 kDa protein) (Pulmonary surfactant-associated proteolipid SPL(Phe)) (18 kDa pulmonary-surfactant protein)	381	3.7	27
MMS205_C04_028 4-25- 2007 MMS205 T3	Q60309	Uncharacterized protein MJEC510	286	1.3	29
MMS205_C08_060 4-25- 2007 MMS205 T3	O43262	Leukemia-associated protein 2 (Deleted in lymphocytic leukemia 2).	84	4.9	30
MMS205_D05_041 4-25- 2007 MMS205 T3	Q3KPU8	RING finger protein 166	241	1.4	39
MMS205_D05_041 4-25- 2007 MMS205 T3	P59092	Uncharacterized protein C21orf94.	62	5.3	37
MMS205_D12_090 4-25- 2007 MMS205 T3	P41700	Hypothetical 55.4 kDa protein in IE0-IE1 intergenic region	477	0.3	37
MMS205_E03_023 4-25- 2007 MMS205 T3	P24911	Probable processing and transport protein	679	6.1	50
MMS205_E04_024 4-25- 2007 MMS205 T3	Q8BDG6	Protein E7	124	1.1	62
MMS205_E06_040	Q89E33	UPF0283 membrane protein blr7254	343	1.6	42

4-25- 2007 MMS205 T3					
MMS205_E09_071 4-25- 2007 MMS205 T3	P48375	12 kDa FK506-binding protein (EC 5.2.1.8) (FKBP) (Peptidyl-prolyl cis- trans isomerase) (PPIase) (Rotamase) (Macrolide-binding protein).	108	4.00E-44	76
MMS205_E10_072 4-25- 2007 MMS205 T3	P40764	Homeobox protein DLX-2 (Homeobox protein TES-1)	332	0.85	36
MMS205_F02_006 4-25- 2007 MMS205 T3	P36011	Cell pattern formation-associated protein stuA	622	0.082	35
MMS205_F05_037 4-25- 2007 MMS205 T3	Q8K368	Fanconi anemia group I protein homolog (Protein FANCI)	1330	6.8	25
MMS205_F06_038 4-25- 2007 MMS205 T3	Q3E820	Uncharacterized protein YBR196C-A.	49	1.1	33
MMS205_F09_069 4-25- 2007 MMS205 T3	O83968	Uncharacterized protein TP_1003	345	8.1	29
MMS205_F11_085 4-25- 2007 MMS205 T3	Q9M7D0	Terpinolene synthase, chloroplast precursor (Aggteo)	630	2.5	39
MMS205_H05_033 4-25- 2007 MMS205 T3	Q1T765	Centromere protein N (CENP-N)	344	5.9	32
MMS205_H06_034 4-25- 2007 MMS205 T3	Q80UM7	Mannosyl-oligosaccharide glucosidase (EC 3.2.1.106) (Glycoprotein- processing glucosidase I) (Glucosidase 1).	834	7.10E-28	37
MMS205_H10_066 4-25- 2007 MMS205 T3	Q8WXI7	Mucin-16 (Ovarian carcinoma antigen CA125) (Ovarian cancer related tumor marker CA125) (CA-125)	22152	0.008	24
MMS205_H10_066	P39806	Homeotic protein spalt-major.	1402	0.061	24

4-25- 2007 MMS205 T3					
MMS205_H11_081 4-25- 2007 MMS205 T3	Q9NKV0	Myeloid leukemia factor (Myelodysplasia-myeloid leukemia factor) (dMLF)	376	1.1	32
MMS206_A07_063 4-25- 2007 MMS206 T3	Q9ZMB8	Sec-independent protein translocase protein tatA/E homolog.	79	9.7	37
MMS206_A10_080 4-25- 2007 MMS206 T3	Q8CFQ3	Intron-binding protein aquarius.	1481	6.10E-40	57
MMS206_A11_095 4-25- 2007 MMS206 T3	Q7K0S9	Zinc finger protein GLIS2 homolog (Protein sugarbabe).	384	1.20E-56	51
MMS206_D07_057 4-25- 2007 MMS206 T3	Q24K03	THUMP domain-containing protein 1.	357	2.00E-42	38
MMS206_E07_055 4-25- 2007 MMS206 T3	P58604	Toxin CSTX-9.	68	3.1	34
MMS206_H02_002 4-25- 2007 MMS206 T3	Q9VNH6	Probable exocyst complex component 4 (Exocyst complex component Sec8).	985	8.30E-35	57
MMS206_H05_033 4-25- 2007 MMS206 T3	Q58922	UPF0132 membrane protein MJ1527.	140	6	35
MMS207_A06_048 5-14- 2007 MMS207 T3	O54798	Bombesin receptor subtype-3 (BRS-3).	399	3.80E-25	30
MMS207_A07_063 5-14- 2007 MMS207 T3	Q5UQE2	Uncharacterized protein R474.	413	2.6	21
MMS207_B02_014	Q9VCI3	Lipid storage droplets surface-binding protein 1.	431	2.60E-41	45

5-14- 2007 MMS207 T3					
MMS207_D03_025 5-14- 2007 MMS207 T3	O64255	Gene 63 protein (Gp63).	78	5.3	33
MMS207_D11_089 5-14- 2007_MMS207_T3	P63283	SUMO-conjugating enzyme UBC9 (EC 6.3.2.-) (SUMO-protein ligase) (Ubiquitin-conjugating enzyme E2 I) (Ubiquitin-protein ligase I) (Ubiquitin carrier protein I) (Ubiquitin carrier protein 9).	158	2.20E-75	85
MMS207_E01_007 5-14- 2007 MMS207 T3	P82798	Transcriptional regulator ATRX (EC 3.6.1.-) (ATP-dependent helicase ATRX) (X-linked nuclear protein) (Fragment).	497	2.50E-23	41
MMS207_E05_039 5-14- 2007 MMS207 T3	Q6GPQ6	Endothelial differentiation-related factor 1 homolog (EDF-1).	147	1.00E-47	65
MMS207_F09_069 5-14- 2007 MMS207 T3	Q7TQM5	Keratinocyte proline-rich protein.	699	0.0021	33
MMS207_G03_019 5-14- 2007 MMS207 T3	Q7ZU92	Poly(A)-specific ribonuclease PARN (EC 3.1.13.4) (Polyadenylate- specific ribonuclease).	660	0.00028	35
MMS207_G05_035 5-14- 2007 MMS207 T3	Q8X7U9	Putative protein hokG.	50	7.1	31
MMS207_G08_052 5-14- 2007 MMS207 T3	Q07372	Ubiquitin-like protein 1.	70	4.4	33
MMS208_A11_095 5-14- 2007 MMS208 T3	O28049	Uncharacterized protein AF_2234.	67	3.6	31
MMS208_D01_009 5-14- 2007 MMS208 T3	P18489	Synaptobrevin.	152	3.70E-34	77

MMS208_F03_021 5-14- 2007 MMS208 T3	Q9TU34	Inositol 1,4,5-trisphosphate receptor type 1 (Type 1 inositol 1,4,5- trisphosphate receptor) (Type 1 InsP3 receptor) (IP3 receptor isoform 1) (InsP3R1).	2709	0.14	27
MMS208_F10_070 5-14- 2007 MMS208 T3	Q58526	Uncharacterized GTP-binding protein MJ1126.	402	2.40E-15	36
MMS208_G05_035 5-14- 2007 MMS208 T3	P29522	Elongation factor 1-beta'.	222	8.10E-71	67
MMS208_G08_052 5-14- 2007 MMS208 T3	P84843	Vasotab precursor.	76	7.90E-07	40
MMS208_H12_082 5-14- 2007 MMS208 T3	O74460	Uncharacterized protein C16C4.16c.	161	0.00039	35
MMS218_A05_047 5-14- 2007 MMS218 T3	Q28915	Glycophorin-E precursor.	78	7.2	30
MMS218_B07_061 5-14- 2007 MMS218 T3	Q9VWV8	Nitric oxide synthase-interacting protein-like.	307	2.80E-84	58
MMS218_B08_062 5-14- 2007 MMS218 T3	Q27377	Putative odorant-binding protein A10 precursor (Antennal protein 10) (OS-D protein).	155	1.30E-05	26
MMS218_D01_009 5-14- 2007 MMS218 T3	Q9Z812	Tyrosyl-tRNA synthetase (EC 6.1.1.1) (Tyrosine--tRNA ligase) (TyrRS).	412	6.6	28
MMS218_D06_042 5-14- 2007 MMS218 T3	Q03973	High mobility group protein 1 (High spontaneous mutagenesis protein 2).	246	0.0048	82
MMS218_E04_024 5-14- 2007 MMS218 T3	Q9U5Y0	Protein anon-73B1.	87	1.10E-05	40

MMS218_E08_056 5-14- 2007 MMS218 T3	Q3U0K8	2-oxoglutarate and iron-dependent oxygenase domain-containing protein 1 (EC 1.14.11.-).	545	4.70E-17	45
MMS218_F04_022 5-14- 2007 MMS218 T3	P41996	Cytokinesis protein B0280.5 precursor.	524	3.00E-08	32
MMS218_F07_053 5-14- 2007 MMS218 T3	P14198	AAC-rich mRNA clone pLK330 protein (Fragment).	317	0.00021	90
MMS218_F08_054 5-14- 2007 MMS218 T3	Q58437	Uncharacterized transporter MJ1031.	308	3.4	23
MMS218_G01_003 5-14- 2007 MMS218 T3	Q26474	Lachesin precursor.	349	5.70E-22	36
MMS218_H01_001 5-14- 2007 MMS218 T3	Q70XC3	Allatotropin precursor (Spofr-AT) (AT).	182	3.80E-12	43
MMS218_H09_065 5-14- 2007 MMS218 T3	Q8BYI6	Acyltransferase-like 1-A (EC 2.3.1.-).	544	1.50E-11	29
MMS219_A01_015 5-15- 2007 MMS219 T3	Q63073	Protein BTG1 (Anti-proliferative factor).	171	5.10E-30	60
MMS219_B10_078 5-15- 2007 MMS219 T3	P83097	Putative tyrosine-protein kinase Wsck precursor (EC 2.7.10.1).	791	3.30E-09	28
MMS219_B11_093 5-15- 2007 MMS219 T3	P32292	Indole-3-acetic acid-induced protein ARG2.	99	0.17	27
MMS219_C01_011 5-15- 2007 MMS219 T3	P47377	Uncharacterized protein MG131.	74	8.9	45

MMS219_C03_027 5-15- 2007 MMS219 T3	P38042	Anaphase-promoting complex subunit CDC27 (Cell division control protein 27) (Anaphase-promoting complex subunit 3).	758	0.00055	47
MMS219_C06_044 5-15- 2007 MMS219 T3	P80958	Cobrotoxin-b precursor (CBT-b) (Short neurotoxin) (NT3) (Atratoxin-b) (Cobrotoxin III) (CBT-III) (Cobrotoxin IV) (CBT IV).	82	0.17	34
MMS219_C12_092 5-15- 2007 MMS219 T3	Q9U4L6	Probable mitochondrial import receptor subunit TOM40 homolog (Translocase of outer membrane 40 kDa subunit homolog) (Male sterile protein 15).	344	7.20E-69	56
MMS219_E02_008 5-15- 2007 MMS219 T3	Q9SVA3	F-box/Kelch-repeat protein At4g39550.	392	0.07	66
MMS219_E09_071 5-15- 2007 MMS219 T3	P0C1W3	Alpha-S-conotoxin RVIIIA.	47	9	50
MMS219_E10_072 5-15- 2007 MMS219 T3	P35416	Paramyosin, short form (Miniparamyosin).	640	2.20E-57	75
MMS219_E12_088 5-15- 2007 MMS219 T3	Q94522	Succinyl-CoA ligase [GDP-forming] subunit alpha, mitochondrial precursor (EC 6.2.1.4) (Succinyl-CoA synthetase subunit alpha) (SCS- alpha).	328	9.60E-88	73
MMS219_F01_005 5-15- 2007 MMS219 T3	P55012	Solute carrier family 12 member 2 (Bumetanide-sensitive sodium- (potassium)-chloride cotransporter 1) (Basolateral Na-K-Cl symporter).	1205	1.50E-06	54
MMS219_F03_021 5-15- 2007 MMS219 T3	Q09770	Probable phosphoacetylglucosamine mutase 2 (EC 5.4.2.3) (PAGM) (Acetylglucosamine phosphomutase) (N-acetylglucosamine-phosphate mutase).	542	0.31	62
MMS219_F04_022 5-15- 2007 MMS219 T3	Q32PC9	ADP-ribosylation factor-like protein 2-binding protein (ARF-like 2- binding protein) (Binder of ARF2 protein 1).	163	8.00E-16	58
MMS219_F05_037 5-15- 2007 MMS219 T3	Q92044	Metallothionein A (MT A).	60	0.55	55

MMS219_F09_069 5-15- 2007 MMS219 T3	O75897	Sulfotransferase 1C2 (EC 2.8.2.-) (SULT1C) (SULT1C#2).	302	1.10E-38	35
MMS219_G01_003 5-15- 2007 MMS219 T3	Q96PY6	Serine/threonine-protein kinase Nek1 (EC 2.7.11.1) (NimA-related protein kinase 1) (Renal carcinoma antigen NY-REN-55).	1258	1.70E-37	31
MMS219_G04_020 5-15- 2007 MMS219 T3	P73528	Photosystem II reaction center protein Z (PSII-Z).	62	8.4	30
MMS219_G05_035 5-15- 2007 MMS219 T3	P51658	Estradiol 17-beta-dehydrogenase 2 (EC 1.1.1.62) (17-beta-HSD 2) (17- beta-hydroxysteroid dehydrogenase 2).	381	4.10E-44	46
MMS219_G10_068 5-15- 2007 MMS219 T3	Q5K2N9	Keratin, type I cytoskeletal 18 (Cytokeratin-18) (CK-18) (Keratin-18) (K18).	438	4.2	33
MMS219_H09_065 5-15- 2007 MMS219 T3	Q9GLD9	UDP-glucuronosyltransferase 2B33 precursor (EC 2.4.1.17) (UDPGT).	529	3.80E-32	49
MMS219_H11_081 5-15- 2007 MMS219 T3	P56679	Seed trypsin/chymotrypsin inhibitor IVB (PSTI-IVB) [Contains: Seed trypsin/chymotrypsin inhibitor II (PSTI II)].	72	3	33
MMS220_A04_032 7-25-07	Q86YQ8	Copine-8 (Copine VIII).	564	1.50E-62	62
MMS220_A07_063 7-25-07	P51772	Tail protein X (GpX).	67	3.5	70
MMS220_B04_030 7-25-07	Q498D9	PDZ domain-containing protein GIPC2.	314	4.10E-14	41
MMS220_B10_078 7-25-07	O18894	Chloride channel protein 3 (ClC-3).	760	2.40E-114	68
MMS220_C06_044 7-25-07	Q8IWL3	Co-chaperone protein HscB, mitochondrial precursor (Hsc20) (DnaJ homolog subfamily C member 20).	235	6.00E-25	42
MMS220_D12_090 7-25-07	O07680	Uncharacterized protein HP_1070 (ORFX).	84	1.7	24

MMS220_E12_088 7-25-07	P15690	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-75kD) (CI-75kD).	727	2.00E-22	62
MMS220_F06_038 7-25-07	Q9U6M0	Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial precursor.	409	1.30E-70	64
MMS220_F07_053 7-25-07	O28466	Uncharacterized protein AF_1809.	88	3.7	44
MMS220_F11_085 7-25-07	P26371	Keratin-associated protein 5-9 (Keratin-associated protein 5.9) (Ultrahigh sulfur keratin-associated protein 5.9) (Keratin, cuticle, ultrahigh sulfur 1) (Keratin, ultra high-sulfur matrix protein A) (UHS keratin A) (UHS KerA).	169	3.7	30
MMS220_G06_036 7-25-07	P30878	Melibiose carrier protein (Thiomethylgalactoside permease II) (Melibiose permease) (Na ⁺ (Li ⁺)/melibiose symporter) (Melibiose transporter).	476	5.8	39
MMS220_H01_001 7-25-07	Q5UQT2	Uncharacterized protein R335.	306	3.10E-08	29
MMS220_H02_002 7-25-07	Q9VHS2	Probable cytochrome c oxidase polypeptide VIIa, mitochondrial precursor (EC 1.9.3.1) (Cytochrome c oxidase subunit VIIa).	89	3.00E-09	49
MMS220_H04_018 7-25-07	Q9BZL3	Putative small membrane protein NID67 (NGF-induced differentiation clone 67 protein).	60	5.5	38
MMS220_H05_033 7-25-07	P32334	Protein MSB2 (Multicopy suppressor of bud emergence 2).	1306	3.90E-11	38
MMS220_H12_082 7-25-07	Q1LZC5	Ankyrin repeat domain-containing protein 54.	299	0.00029	30
MMS221_A07_063 7-25-07	Q27597	NADPH--cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).	679	1.10E-124	69
MMS221_B01_013 7-25-07	Q04521	Putative uncharacterized protein YML084W precursor.	102	0.25	35
MMS221_B03_029 7-25-07	Q8NGS0	Olfactory receptor 1N1 (Olfactory receptor 1-26) (OR1-26) (Olfactory receptor 1N3) (Olfactory receptor OR9-22).	311	9.8	31
MMS221_B04_030 7-25-07	Q58063	Uncharacterized protein MJ0647.	71	0.11	77

MMS221_B07_061 7-25-07	P24833	Probable protein E5.	72	2.1	60
MMS221_B12_094 7-25-07	Q9W3C2	Uncharacterized protein CG1785.	478	5.60E-47	43
MMS221_D02_010 7-25-07	P04554	Protamine-2 (Sperm protamine-P2) (Sperm histone P2) [Contains: Basic nuclear protein HPI1; Basic nuclear protein HPI2; Basic nuclear protein HPS1; Basic nuclear protein HPS2; Sperm histone HP4 (Sperm protamine P4); Sperm histone HP2 (Sperm protamine P2) (P2'); Sperm histone HP3 (Sperm protamine P3) (P2'')].	102	0.21	30
MMS221_D03_025 7-25-07	Q00963	Spectrin beta chain.	2291	1.70E-16	39
MMS221_E02_008 7-25-07	Q5R655	Pentatricopeptide repeat protein 1.	698	0.015	30
MMS221_E11_087 7-25-07	Q95029	Cathepsin L precursor (EC 3.4.22.15) (Cysteine proteinase 1) [Contains: Cathepsin L heavy chain; Cathepsin L light chain].	371	2.20E-91	73
MMS221_E12_088 7-25-07	P11414	DNA-directed RNA polymerase II subunit RPB1 (EC 2.7.7.6) (RNA polymerase II subunit B1) (DNA-directed RNA polymerase II subunit A) (DNA-directed RNA polymerase III largest subunit) (Fragment).	467	0.45	35
MMS221_F05_037 7-25-07	Q8BMF3	NADP-dependent malic enzyme, mitochondrial precursor (EC 1.1.1.40) (NADP-ME) (Malic enzyme 3).	604	5.00E-55	47
MMS221_F09_069 7-25-07	P10161	Basic salivary proline-rich protein 4 allele M (Salivary proline-rich protein Po) (Parotid o protein) [Contains: Peptide P-D] (Fragment).	238	6.10E-06	30
MMS221_F11_085 7-25-07	P0C251	I-superfamily conotoxin Bt11.1 precursor.	73	9.6	45
MMS221_G02_004 7-25-07	P51909	Apolipoprotein D precursor (Apo-D) (ApoD).	189	9.30E-22	32
MMS221_G12_084 7-25-07	Q3ZBS9	Neuronatin.	81	6.7	28

MMS221_H02_002 7-25-07	P26461	Sperm-associated acrosin inhibitor precursor (AI).	97	1.9	31
MMS221_H04_018 7-25-07	Q3E7Y7	Uncharacterized protein YOR293C-A.	49	2.1	37
MMS222_A05_047 7-25-07	Q9GMA3	Visual system homeobox 1 (Transcription factor VSX1) (Retinal inner nuclear layer homeobox protein) (Homeodomain protein RINX).	365	1.1	45
MMS222_A07_063 7-25-07	P26372	Keratin, ultra high-sulfur matrix protein (UHS keratin).	182	1.40E-08	35
MMS222_B02_014 7-25-07	Q50774	Tetrahydromethanopterin S-methyltransferase subunit G (EC 2.1.1.86) (N5-methyltetrahydromethanopterin-- coenzyme M methyltransferase subunit G).	86	2.1	38
MMS222_B07_061 7-25-07	Q8TF74	WAS/WASL-interacting protein family member 2 (WIP- related protein) (WASP-interacting protein-related protein) (WIP- and CR16-homologous protein).	440	1.30E-25	36
MMS222_C01_011 7-25-07	Q6P4J8	Smu-1 suppressor of mec-8 and unc-52 protein homolog.	513	8.10E-71	86
MMS222_C07_059 7-25-07	P09638	Homeobox protein Hox-B2 (S6) (Fragment).	60	6.5	31
MMS222_C10_076 7-25-07	Q13316	Dentin matrix acidic phosphoprotein 1 precursor (Dentin matrix protein 1) (DMP-1).	513	0.095	22
MMS222_D02_010 7-25-07	Q3LAC4	DEP domain-containing protein 2 (Phosphatidylinositol 3,4,5- trisphosphate-dependent Rac exchanger 2) (PtdIns(3,4,5)-dependent Rac exchanger 2) (P-Rex2).	1598	6.50E-12	25
MMS222_D08_058 7-25-07	Q30KL4	Beta-defensin 113 precursor (Defensin, beta 113).	82	6.3	25
MMS222_D11_089 7-25-07	Q02053	Ubiquitin-activating enzyme E1 X (Ubiquitin-activating enzyme E1).	1058	1.00E-35	67
MMS222_E03_023 7-25-07	Q9Z0N2	Eukaryotic translation initiation factor 2 subunit 3, Y-linked (Eukaryotic translation initiation factor 2 subunit gamma, Y-linked) (eIF-2-gamma Y).	472	1.90E-88	92
MMS222_F04_022 7-25-07	Q2GWZ4	Cytosolic Fe-S cluster assembling factor CFD1.	303	1.30E-12	61

MMS222_F09_069 7-25-07	P43752	Anaerobic ribonucleoside-triphosphate reductase (EC 1.17.4.2).	707	5.20E-19	27
MMS222_G05_035 7-25-07	P08621	U1 small nuclear ribonucleoprotein 70 kDa (U1 snRNP 70 kDa) (snRNP70) (U1-70K).	437	2.20E-21	45
MMS222_H03_017 7-25-07	P32761	DNA endonuclease I-CeuI (EC 3.1.-.-) (23S rRNA intron 1 protein).	218	2.6	22
MMS229_A06_048 7-17-07	Q8NCQ3	Putative uncharacterized protein C11orf64.	95	0.96	50
MMS229_A08_064 7-17-07	Q7VQJ7	3-isopropylmalate dehydrogenase (EC 1.1.1.85) (Beta-IPM dehydrogenase) (IMDH) (3-IPM-DH).	364	6.3	39
MMS229_B05_045 7-17-07	Q5K0C0	Conotoxin-3 precursor.	81	7.7	26
MMS229_B10_078 7-17-07	Q58702	Uncharacterized protein MJ1306.	83	7.9	35
MMS229_C03_027 7-17-07	Q7ZXF5	Fatty acyl-CoA reductase 1 (EC 1.2.1.-) (Male sterility domain- containing protein 2).	515	4.20E-23	28
MMS229_C04_028 7-17-07	P10482	Beta-glucosidase A (EC 3.2.1.21) (Gentiobiase) (Cellobiase) (Beta-D- glucoside glucohydrolase) (Amygdalase).	455	7.30E-54	48
MMS229_D06_042 7-17-07	P93746	EC protein homolog 1.	84	2.5	35
MMS229_D08_058 7-17-07	Q4L7H2	UPF0374 protein SH1094.	180	4.2	35
MMS229_E02_008 7-17-07	P83474	Uncharacterized protein CG31818.	202	0.0023	37
MMS229_E03_023 7-17-07	Q8R2I3	Beta-defensin 35 precursor (Defensin, beta 35) (BD-35) (mBD-35).	63	0.073	31
MMS229_E07_055 7-17-07	P34774	Uncharacterized 7.2 kDa protein in rps2-rps9 intergenic region (ORF57).	57	7.7	31
MMS229_F04_022 7-17-07	Q3E7Z4	Uncharacterized protein YIL046W-A.	54	6.4	41
MMS229_F09_069 7-17-07	Q9BYQ6	Keratin-associated protein 4-14 (Keratin-associated protein 4.14) (Ultrahigh sulfur keratin-associated protein 4.14).	195	0.11	27

MMS229_G05_035 7-17-07	Q9VYF8	Ubiquinone biosynthesis methyltransferase COQ5, mitochondrial precursor (EC 2.1.1.-).	301	2.50E-92	68
MMS230_A04_032 6-27- 2007 MMS230 T3	P49756	Probable RNA-binding protein 25 (RNA-binding motif protein 25) (RNA- binding region-containing protein 7) (Protein S164).	784	0.0038	82
MMS230_B10_078 6-27- 2007 MMS230 T3	P42678	Protein translation factor SUI1 homolog.	110	5.70E-54	97
MMS230_C09_075 6-27- 2007 MMS230 T3	Q58003	Uncharacterized protein MJ0583.	57	0.69	44
MMS230_D03_025 6-27- 2007 MMS230 T3	P36099	Putative uncharacterized protein YKL030W.	201	1.2	66
MMS230_D10_074 6-27- 2007 MMS230 T3	Q0IIS3	Abhydrolase domain-containing protein 7.	367	3.70E-43	38
MMS230_F07_053 6-27- 2007 MMS230 T3	P15974	Putative per-hexamer repeat protein 4.	95	0.087	31
MMS230_F09_069 6-27- 2007 MMS230 T3	Q4V8T0	Inositol oxygenase (EC 1.13.99.1) (Myo-inositol oxygenase).	278	2.20E-91	60
MMS230_F10_070 6-27- 2007 MMS230 T3	P60487	Pyridoxal phosphate phosphatase (EC 3.1.3.74) (PLP phosphatase).	292	0.27	35
MMS230_F11_085 6-27- 2007 MMS230 T3	Q9Y2C2	Uronyl 2-sulfotransferase (EC 2.8.2.-).	406	2.3	54
MMS230_H04_018 6-27- 2007 MMS230 T3	P70052	Orphan nuclear receptor NR2E1 (Nuclear receptor TLX) (Tailless homolog) (Tll) (xTLL).	386	0.033	54
MMS231_A06_048	Q8TQ79	Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-	429	4.50E-54	47

6-27- 2007MMS231 T3		phospho-D- glycerate hydro-lyase).			
MMS231_A08_064 6-27- 2007MMS231 T3	P82764	Low-molecular-weight cysteine-rich protein LCR49 precursor.	80	3.2	38
MMS231_A09_079 6-27- 2007MMS231 T3	Q01603	Peroxidase precursor (EC 1.11.1.7) (DmPO) (Chorion peroxidase).	690	2.10E-41	43
MMS231_A11_095 6-27- 2007MMS231 T3	O55654	Early E3B 10.4 kDa protein precursor.	91	9.7	32
MMS231_B02_014 6-27- 2007MMS231 T3	Q03276	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R1 (Retrovirus-related Pol polyprotein from type I retrotransposable element R1) [Includes: Reverse transcriptase (EC 2.7.7.49); Endonuclease] (Fragment).	245	6.90E-06	30
MMS231_B09_077 6-27- 2007MMS231 T3	P30397	Ribosomal operon-associated A protein (RoA).	516	3.1	30
MMS231_B12_094 6-27- 2007MMS231 T3	P56667	Homeobox protein knotted-1-like 10 (Fragment).	88	3.3	41
MMS231_C04_028 6-27- 2007MMS231 T3	Q8TGT1	Uncharacterized protein YLR406C-A precursor.	49	8.9	37
MMS231_D04_026 6-27- 2007MMS231 T3	Q922J3	CAP-Gly domain-containing linker protein 1 (Restin).	1391	2.10E-40	45
MMS231_D07_057 6-27- 2007MMS231 T3	P15648	Protein 2C.	98	3.3	40
MMS231_D08_058 6-27-	Q9BXU8	Ferritin heavy polypeptide-like 17.	183	1.20E-09	27

2007MMS231 T3					
MMS231_D11_089 6-27- 2007MMS231 T3	Q69ZN6	N-acetylglucosamine-1-phosphotransferase subunits alpha/beta precursor (EC 2.7.8.17) (GlcNAc-1-phosphotransferase alpha/beta subunits) (UDP- N-acetylglucosamine-1-phosphotransferase alpha/beta subunits) (Stealth protein GNPTAB) [Contains: N-acetylglucosamine-1-phosphotransferase subunit alpha; N-acetylglucosamine-1-phosphotransferase subunit beta].	1235	1.10E-07	50
MMS231_E02_008 6-27- 2007MMS231 T3	Q9ES87	Prostasin precursor (EC 3.4.21.-) (Serine protease 8) [Contains: Prostasin light chain; Prostasin heavy chain].	342	6.8	33
MMS231_E04_024 6-27- 2007MMS231 T3	Q2KJG3	Asparaginyl-tRNA synthetase, cytoplasmic (EC 6.1.1.22) (Asparagine-- tRNA ligase) (AsnRS).	548	1.10E-89	54
MMS231_F01_005 6-27- 2007MMS231 T3	Q9UKB1	F-box/WD repeat protein 11 (F-box/WD repeat protein 1B) (F-box and WD repeats protein beta-TrCP2).	542	1.00E-38	79
MMS231_F05_037 6-27- 2007MMS231 T3	P37709	Trichohyalin.	1407	1.30E-09	29
MMS231_G03_019 6-27- 2007MMS231 T3	Q3E816	Uncharacterized protein YGR121W-A.	71	5.6	37
MMS231_H06_034 6-27- 2007MMS231 T3	Q91955	Myotrophin (Protein V-1) (Granule cell differentiation protein).	118	2.30E-27	53
MMS231_H09_065 6-27- 2007MMS231 T3	Q15911	Alpha-fetoprotein enhancer-binding protein (AT motif-binding factor) (AT-binding transcription factor 1).	3703	1.50E-12	85
MMS232_A08_064 6-27- 2007MMS232 T3	Q92HI5	Uncharacterized protein RC0786.	83	3.5	28
MMS232_A11_095	Q80Y14	Glutaredoxin-related protein 5.	152	1.30E-40	70

6-27- 2007MMS232 T3					
MMS232_B02_014 6-27- 2007MMS232 T3	Q21376	Putative extracellular sulfatase Sulf-1 homolog precursor (EC 3.1.6.-) (CeSulf-1).	709	0.44	55
MMS232_C01_011 6-27- 2007MMS232 T3	P0A0V7	Histidine-rich metal-binding polypeptide.	60	0.2	34
MMS232_C11_091 6-27- 2007MMS232 T3	Q5MGH0	Serine protease inhibitor 3/4 precursor (Serp-3/4) (Fragment).	383	2.10E-33	31
MMS232_E07_055 6-27- 2007MMS232 T3	P11203	11 kDa protein in segment S11.	92	8.2	30
MMS232_F04_022 6-27- 2007MMS232 T3	P12613	T-complex protein 1 subunit alpha (TCP-1-alpha) (CCT-alpha).	557	9.00E-27	75
MMS232_F05_037 6-27- 2007MMS232 T3	O43261	Leukemia-associated protein 1 (Deleted in lymphocytic leukemia 1).	78	3.7	48
MMS232_H03_017 6-27- 2007MMS232 T3	Q8IUR7	Armadillo repeat-containing protein 8.	673	1.20E-85	67
MMS232_H04_018 6-27- 2007MMS232 T3	Q9BYT1	Uncharacterized MFS-type transporter C20orf59.	436	0.013	40
MMS232_H10_066 6-27- 2007MMS232 T3	P20075	Embryonic protein DC-8.	555	0.0034	29
MMS232_H12_082 6-27- 2007MMS232 T3	Q3T0B6	Complement component 1 Q subcomponent-binding protein, mitochondrial precursor.	278	7.00E-28	33
MMS233_A05_047	Q502M5	Enhancer of mRNA-decapping protein 3 (YjeF domain-	507	9.70E-25	51

6-27- 2007MMS233 T3		containing protein 1) (LSM16 protein homolog).			
MMS233_B02_014 6-27- 2007MMS233 T3	Q0DJC7	Zinc finger AN1 domain-containing stress-associated protein 15 (OsSAP15).	174	0.99	48
MMS233_B04_030 6-27- 2007MMS233 T3	Q96MW7	Tigger transposable element-derived protein 1.	591	2.7	25
MMS233_C01_011 6-27- 2007MMS233 T3	Q9BXY4	R-spondin-3 precursor (Roof plate-specific spondin-3) (hRspo3) (Thrombospondin type-1 domain-containing protein 2) (Protein with TSP type-1 repeat) (hPWTSR).	272	4.10E-06	43
MMS233_C02_012 6-27- 2007MMS233 T3	P34088	V(D)J recombination-activating protein 1 (RAG-1).	1042	8.8	27
MMS233_C09_075 6-27- 2007MMS233 T3	Q6RZF9	Intermediate transcription factor 3 large subunit (VITF-3 45 kDa subunit).	382	2.1	27
MMS233_C11_091 6-27- 2007MMS233 T3	Q7SYL3	E3 ubiquitin-protein ligase Siah2 (EC 6.3.2.-) (Seven in absentia homolog 2-like) (Siah-2).	331	8.60E-67	91
MMS233_D01_009 6-27- 2007MMS233 T3	Q4V8C4	WD repeat domain 5B.	328	2.30E-09	25
MMS233_E09_071 6-27- 2007MMS233 T3	P51571	Translocon-associated protein subunit delta precursor (TRAP-delta) (Signal sequence receptor subunit delta) (SSR-delta).	173	6.10E-34	43
MMS233_E12_088 6-27- 2007MMS233 T3	Q3T132	Mitogen-activated protein-binding protein-interacting protein.	125	2.70E-47	75
MMS233_F05_037 6-27- 2007MMS233 T3	P25228	Ras-related protein Rab-3.	220	1.50E-96	95
MMS233_F11_085	P22792	Carboxypeptidase N subunit 2 precursor (Carboxypeptidase	545	1.80E-19	31

6-27- 2007MMS233_T3		N polypeptide 2) (Carboxypeptidase N 83 kDa chain) (Carboxypeptidase N regulatory subunit) (Carboxypeptidase N large subunit).			
MMS233_H01_001 6-27- 2007MMS233_T3	Q86BE9	Gamma-secretase subunit pen-2 (Presenilin enhancer protein 2).	101	2.40E-30	60
MMS233_H09_065 6-27- 2007MMS233_T3	P47813	Eukaryotic translation initiation factor 1A, X-chromosomal (eIF-1A X isoform) (eIF-4C).	144	2.70E-56	77
MMS234_A05_047 7-2-07	Q8T6B9	Poly U-binding-splicing factor half pint (68 kDa poly U- binding- splicing factor) (Protein half pint) (PUF60 homolog).	637	9.90E-50	72
MMS234_B10_078 7-2-07	P52366	Putative membrane protein U46.	86	5.1	26
MMS234_C10_076 7-2-07	Q6L8G9	Keratin-associated protein 5-6 (Keratin-associated protein 5.6) (Ultrahigh sulfur keratin-associated protein 5.6).	129	1.4	37
MMS234_D08_058 7-2-07	Q5UNW5	Uncharacterized protein R703.	135	5.2	55
MMS234_G01_003 7-2-07	Q64016	Defensin-related cryptdin 17 precursor (CRYP17) (Fragment).	82	2.1	40
MMS234_G02_004 7-2-07	Q8INK9	Methionine-R-sulfoxide reductase (EC 1.8.4.-) (Selenoprotein R).	208	1.60E-40	54
MMS234_G03_019 7-2-07	P26352	Thymosin beta-12.	43	1.40E-06	63
MMS235_E12_088 7-2-07	Q5UQU9	Uncharacterized protein L356.	621	0.019	21
MMS235_F02_006 7-2-07	Q5WGC5	UPF0403 protein ABC2045.	145	7.2	34
MMS235_F03_021 7-2-07	P37044	Progonadoliberin-2 precursor (Progonadoliberin II) [Contains: Gonadoliberin-2 (Gonadoliberin II) (Luteinizing hormone-releasing hormone II) (LH-RH II) (Gonadotropin- releasing hormone II) (GnRH-II) (Luliberin II); GnRH- associated peptide 2-1 (GnRH-associated peptide II-1);	85	2.9	62

		GnRH-associated peptide 2-2 (GnRH-associated peptide II-2)].			
MMS235_F06_038 7-2-07	Q9MUN7	Chloroplast envelope membrane protein.	236	3.9	50
MMS235_G02_004 7-2-07	Q24238	Alkaline phosphatase 4 precursor (EC 3.1.3.1).	596	3.70E-36	51
MMS235_H04_018 7-2-07	Q7SYR1	Probable O-sialoglycoprotein endopeptidase (EC 3.4.24.57).	335	2.50E-60	77
MMS235_H08_050 7-2-07	O31422	Uncharacterized protein ybcO.	55	6.9	32
MMS235_H11_081 7-2-07	Q8N4C7	Syntaxin-19.	294	7	30
MMS236_A06_048 7-6-07	P81305	Uncharacterized protein MJ0226.2.	122	0.0014	32
MMS236_A12_096 7-6-07	P40490	Putative uncharacterized protein YIL100W.	117	3.9	45
MMS236_B10_078 7-6-07	Q6FT26	Protein DSE2 precursor (Daughter-specific expression protein 2).	294	0.8	35
MMS236_D06_042 7-6-07	P56708	Mu-O-conotoxin MrVIA.	31	8.3	52
MMS236_D09_073 7-6-07	A4H255	Beta-defensin 128 precursor (Defensin, beta 128).	93	6.2	31
MMS236_E09_071 7-6-07	Q9UQ35	Serine/arginine repetitive matrix protein 2 (Serine/arginine-rich splicing factor-related nuclear matrix protein of 300 kDa) (Ser/Arg- related nuclear matrix protein) (SR-related nuclear matrix protein of 300 kDa) (Splicing coactivator subunit SRm300) (300 kDa nuclear matrix antigen).	2752	2.1	24
MMS236_F01_005 7-6-07	Q8AVR4	Programmed cell death protein 10.	212	9.50E-29	59
MMS236_F04_022 7-6-07	Q03601	RING finger protein nhl-1.	974	1.1	45
MMS236_F07_053 7-6-07	Q5ZKN2	Membrane-associated progesterone receptor component 1.	192	9.4	47

MMS236_F11_085 7-6-07	O70584	Homeobox protein Nkx-2.8 (Homeobox protein NK-2 homolog H) (Homeobox protein Nkx-2.9).	235	4.7	40
MMS236_G02_004 7-6-07	P19191	Uncharacterized 9.4 kDa protein (ORF6).	82	3.3	31
MMS245_A02_016 7-16-07	Q9ZDP8	Uncharacterized protein RP279.	55	8.4	35
MMS245_B10_078 7-16-07	O58584	UPF0076 protein PH0854.	126	1.30E-15	37
MMS245_C09_075 7-16-07	Q9P2C4	Transmembrane protein 181.	612	2.00E-07	23
MMS245_D11_089 7-16-07	O24575	S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC) (SamDC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain].	400	0.71	32
MMS245_E01_007 7-16-07	Q58119	Uncharacterized transporter MJ0709.	450	0.01	20
MMS245_E06_040 7-16-07	P27824	Calnexin precursor (Major histocompatibility complex class I antigen- binding protein p88) (p90) (IP90).	592	4.50E-74	48
MMS245_F08_054 7-16-07	A4H236	Beta-defensin 123 precursor (Defensin, beta 123).	67	2.5	38
MMS245_G01_003 7-16-07	Q96GM5	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1 (SWI/SNF complex 60 kDa subunit) (60 kDa BRG-1/Brm-associated factor subunit A) (BRG1-associated factor 60A).	476	5.80E-90	67
MMS245_G04_020 7-16-07	Q9USI5	Heat shock protein sti1 homolog.	591	5.60E-22	38
MMS245_G09_067 7-16-07	P35811	Endo-1,4-beta-xylanase C precursor (EC 3.2.1.8) (Xylanase C) (1,4- beta-D-xylan xylanohydrolase C).	608	0.27	66
MMS246_A09_079 7-16-07	P13216	Adrenodoxin, mitochondrial precursor (Adrenal ferredoxin) (Fragment).	143	3.50E-31	52
MMS246_A11_095 7-16-07	Q601U7	tRNA pseudouridine synthase B (EC 5.4.99.-) (tRNA pseudouridine 55 synthase) (Psi55 synthase) (tRNA-uridine isomerase) (tRNA pseudouridylylate synthase).	327	0.7	70

MMS246_B09_077 7-16-07	Q8JFV8	Synaptic vesicle membrane protein VAT-1 homolog (EC 1.-.-.-).	484	0.6	41
MMS246_C04_028 7-16-07	P50841	Uncharacterized protein yptA precursor.	63	4.9	29
MMS246_D04_026 7-16-07	Q6GXJ1	Gallinacin-4 precursor (Gal-4) (Beta-defensin 4) (Gallinacin-7) (Gal- 7).	63	8.9	35
MMS246_D07_057 7-16-07	Q5RK23	Abhydrolase domain-containing protein 1 (EC 3.1.1.-).	412	5.60E-20	26
MMS246_F04_022 7-16-07	P37928	Fimbriae W protein.	198	8.8	35
MMS246_F07_053 7-16-07	Q9D6J1	LAG1 longevity assurance homolog 4 (Translocating chain-associating membrane protein homolog 1) (TRAM homolog 1).	393	5.8	42
MMS246_G10_068 7-16-07	P30826	NADH-ubiquinone oxidoreductase subunit 8 (EC 1.6.5.3) (Maxicircle iron-sulfur protein 1).	145	0.024	55
MMS246_H01_001 7-16-07	Q9Y6C7	Loss of heterozygosity 3 chromosomal region 2 gene A protein.	94	0.56	37
MMS246_H05_033 7-16-07	P84000	Non-toxic venom protein PRTx22C5 (Fragment).	34	1.8	62
MMS246_H09_065 7-16-07	Q319G0	UPF0078 membrane protein PMT9312_1425.	197	0.39	42
MMS246_H10_066 7-16-07	P14195	AAC-rich mRNA clone AAC1 protein (Fragment).	183	0.14	23
MMS247_A01_015 8-2-07	Q9VRL2	Probable Golgi SNAP receptor complex member 2.	216	6.80E-51	49
MMS247_A06_048 8-2-07	Q32L78	Trafficking protein particle complex subunit 6B.	158	2.00E-35	46
MMS247_B10_078 8-2-07	P97762	Retinitis pigmentosa 9 protein homolog (Pim-1-associated protein) (PAP-1).	213	0.13	70
MMS247_C03_027 8-2-07	Q03575	Transthyretin-like protein C40H1.5 precursor.	139	1.2	38
MMS247_C10_076 8-2-07	O54873	Multisynthetase complex auxiliary component p43 [Contains: Endothelial monocyte-activating polypeptide 2	359	2.20E-52	63

		(EMAP-II) (Small inducible cytokine subfamily E member 1)].			
MMS247_D05_041 8-2-07	Q9FFP8	Putative low-molecular-weight cysteine-rich protein LCR74 precursor.	73	2.5	33
MMS247_E04_024 8-2-07	Q1KVV1	Photosystem I iron-sulfur center (Photosystem I subunit VII) (9 kDa polypeptide) (PSI-C) (PsaC).	81	3.1	28
MMS247_E10_072 8-2-07	Q5EB97	Zinc finger CCHC domain-containing protein 10.	173	0.32	29
MMS247_F03_021 8-2-07	P18715	Gastrula zinc finger protein XICGF26.1 (Fragment).	337	7.60E-27	52
MMS247_F12_086 8-2-07	Q58983	Uncharacterized protein MJ1588.	112	5.3	66
MMS247_H07_049 8-2-07	Q9BY11	Protein kinase C and casein kinase substrate in neurons protein 1.	444	1.70E-36	53
MMS247_H11_081 8-2-07	P69495	I-superfamily conotoxin-1 precursor.	64	3.7	34
MMS247_H12_082 8-2-07	Q38WY3	UPF0346 protein LSA0996.	74	4.1	30
MMS248_B04_030 8-2-07	Q6B8Q5	Uncharacterized protein ycf92.	245	2.2	38
MMS248_B10_078 8-2-07	P38834	Putative uncharacterized protein YHR130C.	111	7	43
MMS248_B11_093 8-2-07	P43316	Endoglucanase-5 (EC 3.2.1.4) (Endoglucanase V) (Endo-1,4-beta- glucanase V) (Cellulase V) (EG V).	213	2.30E-66	61
MMS248_C05_043 8-2-07	P13837	G surface protein, allelic form 156 precursor.	2715	0.045	26
MMS248_D04_026 8-2-07	Q9UAC8	Neurotoxin BmK AS-1 precursor (Toxin BmP09).	85	5.2	45
MMS248_D08_058 8-2-07	O60154	Uncharacterized protein C19C7.05.	150	0.14	32
MMS248_D12_090 8-2-07	P28086	Small hydrophobic protein.	57	1.8	59
MMS248_E05_039	Q8K4J6	MKL/myocardin-like protein 1 (Myocardin-related	964	8.00E-07	33

8-2-07		transcription factor A) (MRTF-A) (Megakaryoblastic leukemia 1 protein homolog) (Basic SAP coiled-coil transcription activator).			
MMS248_E10_072 8-2-07	O96614	Sericin-1 (Silk gum protein 1) (Fragment).	115	1.90E-05	39
MMS248_F03_021 8-2-07	P34780	Uncharacterized 13.3 kDa protein in rpl23-rpl2 intergenic region (ORF105).	105	0.47	40
MMS248_G06_036 8-2-07	Q2KIW6	26S protease regulatory subunit S10B (Proteasome 26S subunit ATPase 6).	389	2.70E-102	61
MMS248_G08_052 8-2-07	Q9Y3T9	Nucleolar complex protein 2 homolog (Protein NOC2 homolog) (NOC2- like).	749	2.00E-07	24
MMS248_G09_067 8-2-07	Q58132	Uncharacterized ferredoxin MJ0722.	77	3.30E-08	33
MMS248_G11_083 8-2-07	P67415	Uridine kinase (EC 2.7.1.48) (Uridine monophosphokinase) (Cytidine monophosphokinase).	208	5.4	43
MMS248_H10_066 8-2-07	O94410	Meiotically up-regulated gene 163 protein.	186	9.4	27
MMS248_H12_082 8-2-07	Q569B7	RWD domain-containing protein 4.	188	1.40E-36	43
MMS260_A06_048 7-19-07	P05687	Chorion class high-cysteine HCA protein 12 precursor (HC-A.12).	124	6.60E-05	56
MMS260_B06_046 7-19-07	Q68PG5	Neurotoxin Cex10.	67	2.7	34
MMS260_B11_093 7-19-07	P89116	Caspase-1 precursor (EC 3.4.22.-) [Contains: Caspase-1 subunit p19/18; Caspase-1 subunit p12].	299	1.20E-21	39
MMS260_C05_043 7-19-07	P41688	T-cell surface glycoprotein CD8 alpha chain precursor (CD8a antigen).	239	8.6	56
MMS260_D05_041 7-19-07	Q9QY94	Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase) (GS).	373	1.50E-101	72
MMS260_D10_074 7-19-07	Q27367	Protein croquemort (d-CD36).	457	1.80E-25	36
MMS260_D12_090 7-19-07	P83943	Beta-defensin 1 precursor (BD-1) (Defensin, beta 1) (cBD-1).	67	4.3	54

MMS260_G08_052 7-19-07	Q5J5Z9	Beta-defensin 122 precursor (Defensin, beta 122).	69	6.1	31
MMS260_G09_067 7-19-07	Q27287	Metallothionein-B (MTB).	65	0.56	40
MMS260_G12_084 7-19-07	Q5FWF5	N-acetyltransferase ESCO1 (EC 2.3.1.-) (Establishment of cohesion 1 homolog 1) (ECO1 homolog 1) (ESO1 homolog 1) (Establishment factor- like protein 1) (EFO1p) (hEFO1) (CTF7 homolog 1).	840	6.80E-08	58
MMS260_H08_050 7-19-07	Q696W0	Striated muscle preferentially expressed protein kinase (EC 2.7.11.1).	2995	2.30E-31	32
MMS260_H12_082 7-19-07	O70247	Sodium-dependent multivitamin transporter (Na(+)-dependent multivitamin transporter).	634	0.23	30
MMS276_A03_031 7-25-07	P10435	Uncharacterized immunity region protein 12.	87	0.75	40
MMS276_D02_010 7-25-07	Q5ZPR3	CD276 antigen precursor (Costimulatory molecule) (B7 homolog 3) (B7- H3) (4Ig-B7-H3).	534	0.23	22
MMS276_D05_041 7-25-07	P59945	Probable GTPase engC (EC 3.6.1.-).	274	7.7	41
MMS276_D08_058 7-25-07	O08784	Treacle protein (Treacher Collins syndrome protein homolog).	1320	0.00023	24
MMS276_E01_007 7-25-07	Q9DCL8	Protein phosphatase inhibitor 2 (IPP-2).	206	0.68	42
MMS276_E11_087 7-25-07	O31479	Uncharacterized protein yczF precursor.	73	1.1	28
MMS276_F06_038 7-25-07	Q8BUH8	Sentrin-specific protease 7 (EC 3.4.22.-) (Sentrin/SUMO-specific protease SENP7) (SUMO-1-specific protease 2).	1037	2.2	48
MMS276_G12_084 7-25-07	P23435	Cerebellin-1 precursor (Precerebellin) [Contains: Cerebellin (CER); [des-Ser1]-cerebellin].	193	2.8	28
MMS276_H09_065 7-25-07	Q8DL15	Coproporphyrinogen 3 oxidase, aerobic (EC 1.3.3.3) (Coproporphyrinogen III oxidase, aerobic) (Coproporphyrinogenase) (Coprogen oxidase).	338	1.8	22
MMS278_B02_014 8-2-07	Q28GF5	Transmembrane protein 18.	136	0.25	39

MMS278_B07_061 8-2-07	P07733	Gastrula-specific protein 17.	147	0.03	31
MMS278_B09_077 8-2-07	Q68DN1	Uncharacterized protein C2orf16.	1984	0.022	27
MMS278_C01_011 8-2-07	Q9VH39	UPF0240 protein CG11722.	203	1.80E-18	34
MMS278_C06_044 8-2-07	P08640	Mucin-like protein 1 precursor.	1367	8.70E-19	36
MMS278_D06_042 8-2-07	Q61077	Fibroblast growth factor-inducible protein 14 (FIN14).	61	3.9	37
MMS278_D09_073 8-2-07	P41884	Uncharacterized protein F37A4.6.	389	6.7	46
MMS278_D11_089 8-2-07	Q5P9E0	Chaperone protein dnaJ.	379	0.00017	36
MMS278_F01_005 8-2-07	Q9NP73	Probable glycosyltransferase GLT28D1 (EC 2.4.-.-) (Glycosyltransferase 28 domain-containing protein 1).	165	1.00E-40	53
MMS278_G12_084 8-2-07	P64462	Uncharacterized protein yneC.	96	6.00E-05	29
MMS278_H01_001 8-2-07	P54681	Protein rtoA (Ratio-A).	400	1.70E-14	34
MMS278_H02_002 8-2-07	Q32618	Uncharacterized 6.4 kDa protein in atpA-psbA intergenic region (ORF50).	50	0.037	31
MMS278_H04_018 8-2-07	Q5REX0	Uncharacterized protein C6orf162 homolog.	97	1.20E-12	44
MMS278_H11_081 8-2-07	P33391	Protein DVU_0533 (HMC operon ORF 4).	47	6.1	48