GENE AND MIR EXPRESSION IN THE YELLOW FEVER MOSQUITO *AEDES AEGYPTI*

A Dissertation

by

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ABSTRACT

When animals are exposed to new conditions they need to tune the expression of hundreds of genes in specific tissues and at a specific time requires the interplay of multiple processes. Females are required to locate suitable oviposition sites after acquiring a blood meal. Mosquitoes possess a variety of genes responsible for chemosensation, with four families standing out: Olfaction Receptors (ORs), Ionotropic Receptors (IRs), Odorant Binding Proteins (OBPs), and Gustatory Receptors (GRs). To investigate the genes that may be involved in host seeking behavior, mRNA was sequenced from samples of *A. aegypti* male and female tissues using RNA-seq analysis. Simultaneously, small RNA was isolated and sequenced. MicroRNAs (miRs) can regulate genes post-transcriptionally and are thought to be important for olfaction gene regulation in the antenna of mosquitoes. *Or46* and *Or99* are expressed only in unfed females, while *Or49* is only expressed post blood meal. A total of 14 IRs, 6 ORs and 6 OBPs are up regulated post feeding, while 8 IRs, 4 ORs and 11 OBPs are down regulated post feeding. A total of 16 new miRs were discovered in the antenna of females. miR-34, miR-79, miR-929, and miR-965 are uniquely expressed in the female antenna; while miR-92b is uniquely expressed in male antenna, while miR-279 is up regulated in the antenna of both males and females. The expression of the miR-275, which is associated with blood meal digestion, increases 3h after blood feeding in the head and thorax and miR-305 displays a similar expression pattern. This is the first study to find miRs that are uniquely expressed in the antenna of mosquitoes. Although there are differences in the expression of olfaction genes in the antenna of 12h old females and

4-day-old females, no changes are observed after blood feeding and similar observations were noted for miRs. Changes may occur only in a specific subset of sensory neurons in the antenna of females and for this reason could not be detected. Olfaction transcripts with long 3’UTR may compete for miRs binding and gene regulation in the antenna of mosquitoes without dramatic changes at the transcript level.

DEDICATION

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NOMENCLATURE

miR	microRNA
mRNA	messenger RNA
GR	Gustatory receptor
IR	Ionotropic receptor
OR	Odorant receptor
OBP	Odorant binding protein
RNA-Seq	RNA sequencing
RPKMs	Reads per kilobase per million of mapped reads
Ant	Antenna
HT	Head plus thorax

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CHAPTER I

INTRODUCTION AND LITERATURE REVIEW

All living organisms must adapt their biological functions to environmental changes and conditions of stress; genes are expressed in response or anticipation of these conditions. Tuning expression of hundreds of genes at a specific time and in specific tissues requires the interplay of multiple processes. The transcription initiation depends on both *cis*-regulatory and *trans*-acting factors that regulate the recruitment of the transcriptional machinery to the promoter regions of specific genes. Also, a second turning mechanism involves *trans*-acting factors acting on the messenger RNA (mRNA) to stall the translation of the protein, if the protein encoded by a gene is no longer necessary. There are several cellular processes influencing mRNA levels besides the factors that regulate transcription, elongation and termination. For example, 3’ end cleavage, polyadenylation, mRNA modifications, translation and mRNA decay (Beckwith and Yanovsky 2014), all influencing mRNA levels. The gene expression profiles of individual organisms; or in a pool of several organisms of the same age, encountering the same environmental conditions and stresses are complex phenotypic measurements that can be used to predict their behavior and to evaluate their phenotypic plasticity. Gene expression profiles can be used to develop techniques for behavioral manipulation and to test hypotheses focused on the adaptation of organisms to certain conditions (Rittschof and Robinson 2014). For example, certain species of mosquitoes are known to be attracted to bite humans and it is thought that this trait is genetically controlled. The evolution of preference for human odor is linked to an increased expression of an odorant receptor (*AaegOr4*) in the yellow fever mosquito *A. aegypti* (McBride et al. 2014), the receptor recognizes compounds found in high levels in the odor of humans. Complex traits such as mosquito attraction to humans presumably involves hundreds of genes, in which the levels of expression are required to be tuned to display a specific behavior according to the insect's age, sex, tissue and physiological status and also to external conditions. Changes in the environment or fluctuations in the utilization of nutritionally different diets (i.e. mosquitoes feeding on nectar and human blood) are stressful and unpredictable events that organism will encounter during their life cycle. To cope with the fluctuating conditions, organisms not only have to stop the transcription of several genes that are no longer needed for the new conditions, but also stop the translation of mRNA that is already in the cytosol. More than four decades ago it was hypothesized that intergenic genomic regions have an important role in gene regulatory patterns (Britten and Davidson 1969; Britten and Davidson 1971; Romero et al. 2012), we now know that these regions encode genes that are not translated to proteins. Furthermore, some of these newly discovered genes were found to be encoded within introns of known protein coding genes and instead of protein coding, these genes encode a form of single functional stranded RNA, which is typically between 20 to 25 nucleotides long. These molecules, named microRNAs (miRs), regulate the expression of other genes by either inhibition of translation or degradation of mRNAs transcripts (Jacquier 2009). In one of the largest studies of gene expression evolution in mammals (Brawand et al. 2011) it was found that adaptation possibly happens by regulatory changes, rather than changes in the coding region of the genes which are expressed in a tissue specific manner. Most biological processes however are dynamic, and most studies take a “snapshot” of what happens at specific time points in different organisms throughout their lifetime. Most studies focus on mRNA or miRs levels in either cross species or tissue specificity comparisons. To elucidate the dynamical role of miRs in the regulation of gene expression, I examined mRNA and miRNA expression in different mosquitoes tissues in a time-series manner both from males and females, in order to characterize the function of specific genes, the relationship among these genes (mRNA:miR), and their coordinated regulation that ultimately result in ecological and biological implications. The main focus of my study is on the antenna, the main olfactory organ of mosquitoes and chemosensory gene families. Below I will describe briefly the sensory system, chemosensation system, the olfaction system, the antenna and the antennal lobe, the medical and economic importance of aboviruses, miRs and gene expression studies in mosquitoes.

1.1 The insect sensory systems

Insects rely on their sensory systems to locate and evaluate food, shelter, potential mates; and to avoid predators and other dangers they may encounter. The outputs of these sensory systems are ultimately processed by the nervous system and all the information gathered is used to produce a simple representation of its complex habitat. Based on this representation, decisions are made and a specific behavior is displayed. Although variation in vision, hearing, touch and proprioception systems are all important senses in insects, chemosensation (olfaction and gustatory systems) plays a major role in their behavior, adaptation and even speciation. Observation of the variation in antennal shapes found across different insect families show how diverse and specialized insects are. Chemosensation can be a primitive sense found even in prokaryotic organisms, but higher eukaryotes rely on complex olfactory system that relies on completely different receptor families in worms, insects and vertebrates (Bargmann 2006). Arguably, this variation violates evolutionary conservation but should be interpreted as an adaptation to the fluctuating environmental odor profiles that animals are exposed to. Furthermore, one group of organism is especially adapted to "see the world" through smells. They are the insects, the most diverse and numerous organisms on Earth.

Considerable diversity is found within insect olfactory systems as well, with greatly varying numbers of receptors found in various groups. This diversity could be due to different factors. Flowering plant expansion could have led to the expansion of olfactory receptors in pollinators, insect herbivores and their predators and parasitoids. For example, sympatric species rely on their olfactory system to localize their host and mates, and to avoid overlap with closely related species feeding and living in comparable habitats (Smadja and Butlin 2009). Secondly, when living organisms progressed from an aquatic habitat to a terrestrial habitat they encountered new odors. This happened around 400 million years ago in nematodes, insect's ancestors and vertebrates (Bargmann 2006). In vertebrates, adaptation to terrestrial environment correlates with an expansion of olfaction gene repertoire (Glusman et al. 2000). Today about 3% of insects are aquatic (Crespo 2011), a secondary adaptation to the aquatic environment that occured appeared around 150 million years ago. Insects that spend at least a developmental stage in the water (such as mosquitoes and black flies) rely on chemosensation as their primary sensory modality (Hildebrand and Shepherd 1997) since the visual and auditory systems are stable due to the immutable nature of light and sound (Bargmann 2006) the insect olfactory system is thought to be a primary source of adaptation or speciation.

In parallel to our immune system, the insect olfaction system is exposed daily to a variance of signals produced by other organisms. Variation in the insect olfaction gene repertoire is essential for adaptation in a dynamic environment. Over evolutionary time genetic variation is constantly altered and tested by natural selection. Alternative receptor genes or coding strategies that are used consequently cause the original gene to be discarded (Bargmann 2006). In the post genomic era of current times, new insights about gene regulation and function, as well as new techniques to study neural networks can help us to understand the complexity of insect olfaction systems and could produce strategies to precisely manipulate insect behavior, specially for those species that are vector of important human diseases in the future.

The evolution of barriers to gene flow involving olfaction genes and chemical signals is characteristic of chemosensory speciation. Studies on this topic tend to focus on the sexual isolation of pheromone divergence, but other chemically based characteristics of behavior can also play a role in speciation. Prezygotic barriers can result from adaptive divergence of chemosensory traits in response to a variety of factors including hosts, pollinators and conspecifics (Smadja and Butlin 2009). The genetic basis of chemosensory speciation is unknown, but recent genomic approaches (Dicke and Takken 2006; McBride 2007; McBride et al. 2014), especially those using next-generation sequencing (Ozsolak and Milos 2011; Severson and Behura 2012), offer unique opportunities to uncover the genetic basis of complex chemosensory traits and to understand its divergence among taxa of insect.

1.2 Insect chemosensation

The gustatory and olfaction system are highly complex systems in terms of gene expression patterns and neural network integration, and although gustatory receptors may play an important role in host, mate and food recognition it occurs at a short range after other olfaction cues have primarily functioned for these tasks.

The first odorant receptor was discovered over 20 years ago using molecular biology techniques (Buck and Axel 1991). Gene families involved in odor detection are very large and highly diverse and new receptor genes are frequently identified by new genome or transcriptome projects (Bargmann 2006), making this a highly interesting area of research.

1.3 Olfaction receptors in insects

The fruit fly, *Drosophila melanogaster*, has 62 odorant receptors (ORs) encoded by 60 genes, and 68 gustatory receptors (GRs) encoded by another 60 genes (Vosshall et al. 1999). The vector of malaria, *Anopheles gambiae*, has a slight higher number of chemosensory genes: 85 odorant receptors (ORs) and 76 gustatory receptors (GRs). Analysis of chemosensory genes in the yellow fever mosquito, *Aedes aegypti*, revealed a potentially large number of GRs, totaling 114 potential proteins encoded by 79 genes (Kent et al. 2008) as well as 23 putative pseudogenic GRs. Analysis of alternative splicing suggested that the GRs family expanded with the divergence of *A. gambiae* and *A. aegypti* (culicine-anopheline split), which occurred about 150 million years ago (Kent et al. 2008). Bioinformatic analyses has also identified 131 odorant receptor genes in *A. aegypti* , which show a high degree of divergence from *A. gambiae* (Bohbot et al. 2007b).

Ionotorpic receptors are a group of chemosensory receptors that have recently been found to function as olfaction receptors in insect as well (Benton et al. 2009). These new chemosensory genes are related to the ionotropic glutamate receptors (iGluRs), which are a conserved family of inhibitory ligand-gated ion channels present in both eukaryotes and prokaryotes. iGluRs regulate cation flow across the plasma membrane in response to binding of extracellular glutamate and related ligands. The proteins encoded by these genes are known for their role in the communication of the central nervous system (Croset et al. 2010). A variant of the iGluR subfamily, the Ionotropic Receptors (IRs), were proposed to detect volatile chemicals in olfactory cilia of *D. melanogaster* (Benton et al. 2009; Croset et al. 2010; Abuin et al. 2011). IRs act in combinations with up to three subunits, comprising individual odor-specific receptors and one or two broadly expressed co-receptors (Abuin et al. 2011). IRs are expressed in a combinatorial mode in sensory neurons that respond to many different odors but express either insect ORs or GRs (Croset et al. 2010). In *D. melanogaster* the IRs gene repertoire is similar to ORs and they have some similarities: a) they are specifically expressed in a small number of chemosensory neurons and regulated by small upstream regulatory regions; b) neurons that express IRs show similar characteristics to those expressing ORs, where the neurons converge to a single glomerulus in the antennal lobe (Benton et al. 2009). There are also differences between IRs and ORs of *D. melanogaster*: a) chemosensory neurons may only express one OR and OR83b in a single separated cluster which innervate specific olfactory sensilla, while IRs-expressing neurons can have up to three different IRs, besides the broadly expressed IR8a and IR25a genes; b) there is also a overlap between the molecular composition of different IRs and the combination of neurons that innervate a specific sensillum (Benton et al. 2009; Abuin et al. 2011).

A total of 63 IRs and 62 ORs have been identified in *D. melanogaster* and the question of which group arose first during the fly evolution is interesting. Expression analysis of IRs in *Aplysia molluscus*, whose last common ancestor with *D. melanogaster* existed 550–850 million years ago, revealed that IRs genes are expressed in sensory, nervous and reproductive tissues. However, the mollusk IR25a orthologue is expressed mainly in the olfactory organs. IR25a is thought to be the most ancestral IR gene (Croset et al. 2010). Besides IR25a, IR8a other IRs show high sequence and expression pattern conservation in insects. In contrast, the sequence and expression patterns of ORs in insects are extremely divergent. It is speculated that ORs genes only evolved in terrestrial insects (Benton et al. 2006b). The most conserved OR is OR83b, which singularly shows orthology among several insect odors. ORs are thought to have originated from GRs, but the exact origins are unknown. It has also been found that some ORs confined to nematodes and water fleas may not be involved in chemosensation (Penalva-Arana et al. 2009; Croset et al. 2010). It is therefore suggested that IRs may have been the first olfaction receptor family.

Studies aimed at characterizing IR ligands are limited but show that carboxylic acids, water and ammonia are among the stimuli detected by these neurons (Croset et al. 2010). It is hypothesized that ORs might be involved in more species-specific odor detection. Since IRs only recently have been discovered and characterized, consequently limited information is known about them in insects other than *D. melanogaster*. Although several insect genomes are currently available, most of IRs have not yet been annotated and efforts to annotate these genes are needed.

Since most odorants are air-borne hydrophobic molecules, they require assistance in the transportation to the ORs through an aqueous medium, the sensillum lymph, which is a hydrophilic barrier formed for these molecules to reach the ORs. Odorant binding proteins (OBPs) are one class of olfactory proteins identified to facilitate the transportation of odorants and pheromones to ORs (Vogt and Riddiford 1981; Vogt et al. 1985; Zhou 2010). Putative OBPs have been identified in several insect orders, particularly in Lepidoptera, Coleoptera, Hymenoptera, and Diptera. OBPs have three characteristic features: a) they have six highly conserved cysteines with a specific position between them; b) there are always three amino acids between the second and the third cysteine; c) there are eight amino acids between the fifth and sixth cysteine (Zhou 2010). OBPs are diverse and fast evolving gene family through gene duplication (Zhou et al. 2008), however, in butterflies and moths the OBPs subclass is named GOBPs and PBPs (Vogt et al. 2015). The Lepidoptera OBPs are considerably divergent when compared to those from other insect orders (Zhou 2010). There is an expansion of OBPs in mosquitoes. For example, in *D. melanogaster* there are 61 genes encoding OBPs (Hekmat-Scafe et al. 2002), while *A. gambiae* has 72 OBPs genes (Biessmann et al. 2002; Vogt et al. 2002), and *A. aegypti* has 66 OBPs genes (Zhou et al. 2008). OBPs are generally divergent between species from different genera can even vary within the same species.

Insect pheromones and other odorant molecules bind reversibly to OBPs. Pheromones are a blend of chemicals which are intrinsically important in communication within species to induce specific behaviors, in isolation, the individual components of the pheromone mixture would induce different behaviors than those produced when a component is part of a compound (Zhou 2010). It is not known whether OBPs can selectively bind and discriminate between the thousands of air-born chemicals that they are exposed to. There is evidence for selective binding, but OBPs ability to discriminate odors still remains obscure.

It is still questionable how insects are able to instantly react when they are exposed to specific odors or mixture of odors. Hundreds of genes are expressed throughout thousands of neurons, each being interconnected in the antennal lobe. With this evidence, there are an abundance of genes where selection acts and sexual isolation arises resulting from changes in host or food preference, as well as mating success.

1.4 Antenna of flies and mosquitoes

Fruit flies track food using volatile metabolites of live plants, whereas mosquitoes find their host by tracking volatiles of live animals. Flesh flies can find their host by tracking volatiles from live animals or bacterial decomposition. Insects and flowering plants (Angiosperms) are the largest group of multicellular organisms and it’s thought that have diverged between 167-199 million years ago (Bell et al. 2010). Insects adapted to pollinate these plants, and plants have also developed strategies to avoid herbivores by using chemical and mechanical strategies. For example, plants developed trichomes, deterrent allelochemicals, as well as semiochemicals to attract natural enemies of herbivores or make them less palatable to insects. This has resulted in a need for a large set of specific insect receptors, expecially with the increase of angiosperm diversity. Antenna morphology has evidently become greatly adapted to the life cycle behavior of insects to their adapted environments. The antennal morphology is very variable, throughout both insect orders and within species, but a common characteristic is that the olfactory sensilla have the same function in all insects, which is to encapsulate and protect dendrites of the olfactory sensory neurons (OSNs) (Hansson and Stensmyr 2011). It is not known if the shape of the antenna has evolved as a result of the necessity to detect odors, or to enhance adaptation to a specific environment. Each species is adapted to its habitat, and the antennae are specialized to serve efficiently as possible in each species related to the tasks to which it conducts. The antennal flagellum also bears a large number of long hairs, especially in males where it is said to be plumose, and it propose to serve as a sound-receiving structure. For example, male *A. aegypti* detect sound induced vibrations in the frequency around 380 Hz, while in females the best frequency is approximately 230 Hz (Gopfert et al. 1999). These frequencies correspond to the opposite sex flight sounds.

Dipterans insects serve as a model organism for studies concerning the olfactory sensory system, particularly fruit flies and mosquitoes. The sophisticated genetics and molecular tools available to *D. melanogaster* have elucidated several mechanisms of chemosensation in insects and other taxa. Mosquitoes have also been widely studied due their health and economic impacts on humans through the ability to vector a wide variety of diseases

1.5 Origin of new olfaction receptor genes

For a species to detect a new odor in their environment it may be necessary to develop a new OR gene (Ramdya and Benton 2010). Many OR genes are found in tandem arrays in insect genomes, which potentially could be the result of unequal crossing over (Sanchez-Gracia et al. 2009), a hallmark of gene duplication. In *Drosophila* ORs that are physically neighbors in the genome are also phylogenetic related, but have diverged independently after gene duplication (Sanchez-Gracia et al. 2009). The process of gene duplication might involve a positive feedback loop, in which duplicated genes have higher chance for additional allelic mis-pairings. There are also

ORs positioned outside of these tandem arrays, and phylogenetic closely related genes can also be found in distant sites across insect genomes, even on different chromosomes (Robertson et al. 2003). The mechanism of intra- or trans-chromosomal translocation of OR genes is not known, but potentially could involve or be a product of chromosomal rearrangements, which is hypothesized to be the case in *A. gambiae,* where there is chromosomal translocation in two molecular forms of the species (Fox et al. 2002).

OBPs may undergo similar duplication processes of ORs, but there is less information known about them. The mechanism through which the recently discovered IRs originated in *Drosophila* is not known (Benton et al. 2006a; Benton et al. 2009), molecularly unrelated and under the control of different developmental programs and located in different sensory structures, with different morphologies (Benton et al. 2009).

1.6 Olfaction receptors and chemosensation isolation

Two types of pre-mating reproductive isolation phenomenon can be observed in several groups of insects: mate choice and host choice. The first one leads to behavioral isolation, whereas the second can lead to habitat and pollinator isolation (Smadja and Butlin 2009). Behavioral isolation is well documented in *Drosophila* species. Habitat isolation in phytophagous insects by host shift has been reported in several studies (Berlocher and Feder 2002). Plant volatiles are important for host recognition and habitat isolation has been reported in pea aphids, *Acyrthosiphon pisum* and the apple maggot fly, *Rhagoletis pomonella*.

One of the best-studied examples of the evolution of the ORs and GRs during host specialization is found within endemic populations of *D. sechellia* in the Seychelles archipelago in the Indian Ocean (McBride 2007). *D. sechellia* is losing ORs and GRs almost 10 times faster than its sibling species *D. melanogaster*. The reason for this loss is that *D. sechellia* feeds only on the fruit of *Morinda citrifolia*, whereas *D. melanogaster* is a more generalist feeder. It is proposed that a change in GRs and ORs loci reflect a positive selection to its host association.

Although there is a bias towards *D. melanogaster* and *Bombix moris* in regards to chemosensory speciation, it has been documented (Smadja and Butlin 2009) in a total of 16 species of moth, 14 drosophilids, and other species and orders including sulphur butterflies, apple maggot flies, bees, leaf beetles, bark beetles, pea aphids, aphids, meadow grasshoppers and walking sticks. It is not just confined to insects as chemosensory speciation has also been found in seven mammal species, seven squamates species, eleven fish species, one annelid species and six plant species.

1.7 The antennal lobe

The antennal lobe is the primary olfactory center of the insect brain and adaptations can be mirrored through its organization. The antennal lobe contains approximately 50 to 200 glomeruli, which are usually spheroid structures housing interneurons and the dendrites of projection neurons that transmit the processed information to higher brain areas (Getz and Lutz 1999; Schlief and Wilson 2007). Sexual dimorphism of the antennal lobe is reported in several moth species, where an enlargement is found in species that have increased sensitive towards sex pheromones (Hansson and Stensmyr 2011). Enlargement of the antennal lobe is also reported in *Drosophila* (Kondoh et al. 2003) and a comparison of the central brain anatomy of 37 Drosophilidae species from the Hawaiian archipelago, revealed an extreme sexual dimorphism within the antennal lobe with two out of the 51 identifiable glomeruli were markedly enlarged in males. A phylogenetic study showed that the sexual dimorphism of these glomeruli arose 0.4 to 1.9 million years ago in two species of the Hawaiian drosophilids.

Besides sexual dimorphism of pheromone attraction in the antennal lobe, there are also studies showing that food and oviposition site odors might also be under environmental selection pressures (Dekker et al. 2006; Kuebler et al. 2010). *D. sechellia* is more attracted to methyl hexanoate, a chemical produce by its host, the morinda fruit, than its sibling species, *D. melanogaster*. Comparisons between these two species showed a 3x overrepresentation of neurons to detect methyl hexanoate and also 2.9x increase in the corresponding glomerulus in the antennal lobe of *D. sechellia* (Dekker et al. 2006).

Leaf-cutting ants show sex size dimorphism, but size differences are also found in the worker caste (Kuebler et al. 2010). Workers have three extremely enlarged glomeruli out of 242 found in their antennal lobe. Calcium imaging studies showed that a protein used to detect the trail pheromone was represented in regions of these big glomeruli. It is suggested that alterations in the ant antennal lobe leads to differences in the odor information processing that results in behavioral changes of the ant workers.

The antennal lobe is an important component of the olfactory system. Differences in the size of the antennal lobe glomeruli have been documented in moths, flies, ants, cockroaches, wasps, bees, and grasshoppers (Hansson and Stensmyr 2011). An interesting insight may come from studies on the different effects of odors on the behavior of insects and how the sensory system, receptors, and neuronal arrangement change in response to different odors. For example, *D. melanogaster* have a longer life span if the larval stage is subjected to a dietary restriction but exposure to nutrient-derived odorants can modulate life span and partially mimic the life-extending effects of dietary restriction (Libert et al. 2007), indicating that olfaction influences adult physiology and aging in *Drosophila*. Epigenetic influence of food odors and pheromones continues throughout the life of social organisms (Kohl 2012).

1.8 Mosquito olfaction

A study looking at the changes in gene expression in the antenna of females after blood feeding (Rinker et al. 2013a) revealed that several genes, not related to chemosensation, are significantly enhanced or down-regulated after blood feeding. However, the chemosensory genes show subtle changes. Not all olfaction genes were detected in the antenna of *A. gambiae* in this study. The missing genes may be expressed in other olfaction organs (maxillary palpi or labellum). OBPs were the most expressed olfaction genes with a peak of expression at 36h after blood feeding. Nine OBPs were only detected after 36h of blood feeding. However, 24h after feeding the expression levels of 50 OBPs were decreased. The chemosensory genes involved in CO_2 detection and gustation, GRs, were the least enriched genes in the antenna of females. The composition of odorant sensory neurons in the antenna of the malaria mosquito was suggested to explain the subtle changes in the expression of chemosensory genes. The antennal sensilla may temporarily change its response to odors after blood feeding. The authors suggest that a transient change in the expression of these genes in sub-populations of neurons in the antenna might be responsible for the sensitivity to different odors. Therefore, it is not possible to detect such changes when the antenna of several dozens of mosquitoes is pooled together to obtain enough RNA for sequencing.

The differences in the chemosensory gene expression between males and females were also studied before (Pitts et al. 2011). *A. gambiae* females have an enhanced expression of the olfaction genes in their antenna. In males the expression levels of chemosensory genes as remarkably low compared to the females. However, the expression of chemosensory genes in the maxillary palpi was very similar between males and females. It suggests that males and female antennae have similar perception of the same stimuli, but the sensitivity and the priority of the odors to be detected are different.

The maxillary palpi of *A. aegypti* detect stimuli at close range with the host and vibrate when the female is blood feeding. There are several chemosensory genes expressed in the maxillary palpi of *A. aegypti* (Bohbot et al. 2014). However, only 3 ORs are expressed in this tissue. There are GRs expressed in the maxillary palpi with suggested novel thermosensation functions. Similar to what is observed to the with malaria mosquito, there are a few IRs, GRs and ORs transcripts detected in *A. aegypti* maxillary palpi. However, there is an overrepresentation of OBPs. It is suggested that it happens because of the nature of the tissue of maxillary palpi. A high number of OBP is needed to transport odors through the aqueous lumen of this tissue.

It will be interesting to study the expression of chemosensory genes in single sensory neurons as the females display different behaviors throughout the gonotrophic cycles. Another option would be divide the antenna in different sectors depending on the population of sensory neurons. Ultimately, via different genetic manipulation techniques (for example, GAL4:UAS), we could isolate the expression of these genes in sub-populations of sensory neurons. Until then, the power studies where the antenna of hundreds of individuals are pooled in one sample is not enough to single out which transcripts of chemosensory genes are being enhanced or down-regulated after blood feeding.

1.9 The yellow fever mosquito *A. aegypti*

The yellow fever mosquito, *A. aegypti,* is the main vector of dengue and yellow fever virus, which are pathogens affecting humans. The vector is prevalent in tropical and subtropical regions around the world. Dengue fever is a re-emerging disease, contributing millions of cases worldwide with most cases occurring in Asia and South America. Each year, approximately 50 million human cases of dengue are reported and approximately 22,000 people succumb to Dengue Hemorrhagic Fever. Because *A. aegypti* preferentially locates human hosts, it readily transmits Dengue virus from infected people to uninfected people (Mondet et al. 1996; Robertson et al. 1996;

Thonnon et al. 1998a; Thonnon et al. 1998b; Zeller 1998; Digoutte 1999; Mondet 2001; Lourenco-De-Oliveira et al. 2004; Tomori 2004; Halstead 2006; Ellis et al. 2007; Vezzani and Carbajo 2008). *A. aegypti*, can additionally spread other arbovirusses including Chikungunya. The mosquito vector is closely associated with humans, and its preferential breeding sites are containers with stagnant water (flower vases, buckets, discarded tires), which are difficult to control.

Various genes regulate the host seeking behavior of *A. aegypti*, including multiple Olfaction Receptors (ORs) and Olfaction Binding Proteins (OBPs) (Focks et al. 1993; Klowden and Briegel 1994; Canyon et al. 1999; Harrington et al. 2001; Sanders et al. 2003; Franz and Sanchez-Vargas 2006; Bartholomay et al. 2007). Electroantennogram studies of the antenna of *A. aegypti* females show that odorant receptor neurons down-regulate their sensitivity to lactic acid after blood feeding. (Davis 1984). Lactic acid is a key host attractant for mosquitoes, it has also been suggested that there is a direct relationship between the down-regulation of sensitivity to lactic acid and suppression of host seeking behavior (Bowen 1991). Electrophysiological recordings show that neurons sensitivity to indole and phenolic compounds increases 24 and 72 hours after blood feeding (Siju et al. 2010). Furthermore, sensitivity to undecanone, acetic acid and propionic acid is increased 72 hours after blood feeding. This data suggests that these neurons may be also involved in the identification of oviposition sites, but there is no change in the response spectrum of the odorant receptor neurons towards lactic acid. It could be that the odorant receptor neurons for acid lactic are housed in other types of sensilla than those studied.

Mosquitoes can identify predator-release hydrocarbons allowing them to avoid oviposition sites with high risk of predation (Silberbush et al. 2010). The ovipostion site selection is critical for mosquito survival and population dynamics, having important concerns to mosquito control. For example, *A. aegypti* lay its eggs most of the time in man-made oviposition sites. The final decision about where to lay eggs is a result of the interaction of a complex array of chemical and physical factors (Bentley and Day 1989). Similar to the host seeking behavior, ovipostion site seeking behavior is crucial to mosquito survival and had not been extensively studied as a potential point to break its life cycle.

The likely polygenic nature of host seeking behavior appears to make it an elusive target for transgenic approaches to vector control, because the replacement or suppressing of a single or very few olfaction genes is unlikely to affect major changes in host-seeking behavior (Coates et al. 1998; Coates and Jasinskiene 1998; Franz and Sanchez-Vargas 2006).

1.10 miRs and their potential in insect transgenesis

MiRs are a class of small (~22 nucleotides), non-coding RNAs which typically bind to the 3' untranslated regions (UTR) of their target mRNA, preventing its translation into protein (Lai 2003; Wilkie et al. 2003; Bartel 2004; Baskerville and Bartel 2005; Yang et al. 2005; Kim and Nam 2006; Wang and Li 2009). MiRs appear to be involved in the regulation of all aspects of eukaryotic biology. It is now estimated that as many of 30-50% of human genes are controlled by miRs (Inui et al. 2010). An interesting, and potentially very useful feature of miRs appears to be that a single or very few miRs can control the expression of many protein-coding genes underlying a phenotypic trait (Yang et al., 2005). For example, in human cell lines injection of miR-124 and miR-1 lead to changes in the expression profile of up to 100 genes associated with brain or muscle cells, respectively (Mattick and Makunin 2005). In *Drosophila melanogaster*, the silencing of one miR has been associated with the development of CO_2 olfactory neurons in the maxillary palps. Additionally, in the malaria mosquito *A. gambiae* the expression levels of only four miRs changed after infection with *Plasmodium* spp. (Xue et al. 2008). The far reaching effects of single miRs opens up the possibility of using these molecules to affect complex traits and the development of miR-based gene therapy for cancers and other disease.

Much recent work on the development of transgenic mosquitoes has focused on identifying single protein-coding genes that might be introduced into mosquito populations to prevent the development of pathogens. Besides the difficulties in identifying single proteins with absolute effect, adaptive evolution of the pathogen in response to the proteins targeting them is possible. Until recently, the lack of an available drive mechanism for disease vectors led some to question such an approach (Franz et al. 2006). However, the development of new biotechnological tools that can be used as genetic drive mechanisms has made considerable progress and could possibly be used to the near future to genetically manipulate field populations of mosquitoes. For example, the homing endonuclease-based gene drive system using of *A. gambiae* (Windbichler et al. 2011).

1.11 miRs may regulate the expression of olfaction receptors

The host specialization between hybrids of *D. sechellia* and *D. simulans* is a result of loss-of-function mutations instead of gain of new ORs genes (Jones 2005; Stensmyr 2009; Croset et al. 2010). IRs have been lost at an accelerated rate in *D. sechellia* and this is understood as a genetic adaptation of the olfaction system to a specific host, in this case, the morinda fruit, *Morinda citrifolia*. It creates a higher level of complexity to sophisticated olfaction system. In a mutant screen of *D. melanogaster*, it was found that some flies had a population of CO_2 neurons in their maxillary palp (Cayirlioglu et al. 2008). Fruit flies do not have CO_2 detecting neurons in the maxillary palp, but possess them in the antenna. CO_2 elicits a repulsive behavior in fruit flies indicating a crowded environment. In contrast, mosquitoes have CO_2 in their maxillary palp using it to detect CO_2 from potential hosts. The presence of these CO_2 sensing neurons in the maxillary palp of mutant fruit flies created in the laboratory is a reminiscent of the CO_2 sensing neurons in the maxillary palps of mosquitoes (Cayirlioglu et al. 2008; Jones 2008). Fruit flies with CO_2 sensing neurons housed in the maxillary palp are a laboratory generated fossil, representing an intermediate form in the evolution of Diptera; the split between Nematocera (mosquitoes) and Brachycera (flies). These sensing neurons expressing two CO_2 receptors form connections characteristic of CO_2 sensing neurons, while also show wiring and receptor characteristics of olfaction receptor neurons in the maxillary palp. These hybrid neurons were activated following the disruption of a microRNA (miR) locus. Disruption of the miR-279 locus leads to an up-regulation of the transcription factor Nerfin-1, which is expressed in neuronal precursors. Interestingly similar hybrid sensory system is observed in the recent host plant switch of the apple maggot fly and the hawthorn maggot fly (both from the *Rhagoletis* genus), which results in sympatric speciation. The exact cause of this speciation event is hard to determine, but it potentially be that changes in the olfactory system are responsible for different feeding behaviors (Linn et al. 2003). The F1 hybrids of these two species show novel electrophysiological olfactory response profiles, which is different from both parental species (Olsson et al. 2006). This novel electrophysiological profile could be due to co-expression of odorant receptors of each parental species combined, similarly to those found in the mutant screen of *D. melanogaster*. It is an unprecedented mechanism by which insects may evolve, and the loss of olfaction receptors reported in *D. sechellia*, for example, could be a result of selection pressures on the hybrids. Importantly, IRs were discovered after the discovery of these hybrid olfaction receptor neurons in *Drosophila*. Multiple IRs can be expressed in one olfactory neuron, whereas ORs are usually uniquely expressed in olfaction neurons. Therefore, the location of IRs in different sensing neurons may have implications in the evolution of host association.

1.12 Transcriptome studies of olfaction organs of *A. aegypti*

Next-generation sequencing technology (NGS) has been an accessible technology for more than 10 years (van Dijk et al. 2014), and is used for a variety of functions. Descriptive studies using the NGS have been performed on several species of insects. Usually gene sets representing the unique functional categories that are overrepresented in a tissue or life stage are described (Kim et al. 2014). To go beyond these types of studies, several factors influencing the mRNA levels in the cytoplasm should be examined. For example, studies should be dedicated to looking at post-transcriptional regulatory mechanisms performed by miRs, alternative splicing, 3' end processing, polyadenylation, RNA methylation, mRNA nuclear export, polyadenylation dynamics, and translation (Beckwith and Yanovsky 2014). There are several studies on the transcriptome of *A. aegypti* (Feitosa et al. 2006; Champagne and Brown 2007; Erickson et al. 2008; Thangamani and Wikel 2009; Venancio et al. 2009; Bonizzoni et al. 2010; Choi et al. 2010; David et al. 2010; Colpitts et al. 2011; Martins et al. 2011; Poelchau et al. 2011; Zou et al. 2011; Bonizzoni et al. 2012a; Bonizzoni et al. 2012b; Choi et al. 2012; Akbari et al. 2013; David et al. 2013; Poelchau et al. 2013; Juneja et al. 2015) but only a few have tissue specific data. There are however some RNAseq studies on the olfaction organs of mosquitoes (the antenna and maxillary palp). In one study, several mRNA samples from different strains were sequenced. It was found that *Or4* is potentially involved in the adaptation of *A. aegypti* feeding on human hosts (McBride et al. 2014). *Or4* was has a higher expression level in "domestic" strains of *A. aegypti*, which prefer to feed on humans, when compared to "forest" strains, which prefer to bite non-human hosts. *Or4* was also found to recognize a compound present at high levels in the human odor. Another study sequenced mRNA from the maxillary palp of host seeking females of *A. aegypti* (Bohbot et al. 2014) and in these study genes involved in thermosensation and mechanosensation were discovered, however, in both studies the RNA samples came from mature females and it remains unknown if there are changes in the olfaction receptors during maturation of the females, and if there are changes between males and females. There increasing studies on the expression of olfaction genes in the malaria mosquito antennae and maxillary palpi (Pitts et al. 2011; Rinker et al. 2013a; Rinker et al. 2013b; Hodges et al. 2014; Pitts et al. 2014).

MiRs play an important role in the interaction of pathogens and *A. aegypti* (Hussain et al. 2013; Zhang et al. 2013; Campbell et al. 2014; Zhang et al. 2014). For example, *aa-miR-375* enhances Dengue virus serotype 2 in cell lines (Hussain et al. 2013), while *Wolbachia* uses a host miR to regulate transcripts of a methyltransferase inhibiting Dengue virus replication (Zhang et al. 2013). Currently, there are only two publications concerning identification of miRs in *A. aegypti* (Li et al. 2009; Skalsky et al. 2010). A total of 124 mature miRs have been identified in *A. aegypti* which suggests that we know just a fraction of the total number of miRs present in this species. For example, in *Drosophila melanogaster* 466 matures miRs have been identified. There are no studies on miR expression levels in the olfaction organs, age and sex specific data are available.

In this study my goal was to perform a transcriptome study of the main olfaction organ of *A. aegypti*, the antenna, at different time points involving not only protein coding genes but also miRs. After the identification of the miRs expressed in the antennae, as well new miRs, and those with potential impact to disrupt the life cycle of mosquitoes, a synthetic miR was used to knock down the expression of the target miR.

CHAPTER II

GENE EXPRESSION CHANGES AFTER BEHAVIORAL SWITCHES IN THE YELLOW FEVER MOSQUITO *AEDES AEGYPTI*

2.1 Introduction

The yellow fever mosquito, *Aedes aegypti*, is prevalent in tropical and subtropical regions around the world and is both an economic pest and a threat to public health to being the main vector of Chikungunya, yellow fever and dengue fever arboviruses and with a consequent preference for human blood. Each year, approximately 50 million cases of dengue are reported in humans and approximately 22,000 people succumb to dengue hemorrhagic fever. *A. aegypti* preference to human hosts results in the ability to transmit Dengue virus from infected hosts to uninfected hosts (Mondet et al. 1996; Robertson et al. 1996; Thonnon et al. 1998a; Thonnon et al. 1998b; Zeller 1998; Digoutte 1999; Mondet 2001; Lourenco-De-Oliveira et al. 2004; Tomori 2004; Halstead 2006; Ellis et al. 2007; Vezzani and Carbajo 2008). *A. aegypti* maintain close association with human habitats, and have a preference to oviposit in man-made habitats which readily collect rainfall such as, flower vases, buckets, discarded tires, etc. making them an extremely difficult vector to control based upon its life cycle. It is clearly an important organism to study due to its close association with humans and its consequent impacts on medical and economic well-being. The adaptation to feed on humans results from a complex and unique combination of morphological, behavioral, physiological and genetic traits of the mosquito sensory system, which includes vision, thermosensation and chemosensation (Bohbot et al. 2014).

Since light and temperature are not considerably variable between potential hosts, but because chemical cues do show variation, it is widely believed that the chemosensory system plays a primary role in the adaptation of mosquitoes, which feed almost exclusively on humans. The major sensory systems of mosquitoes are located in the head region, which includes the proboscis, antenna, eyes, Johnston's organs and maxillary palpi. Most of the sensory neurons which house the genes which detect odors are present in the antenna of *A. aegypti* (Mciver 1972; Mciver and Hutchins.Sa 1972; Rossignol and Mciver 1977; Mciver 1978; Mciver and Siemicki 1979; Mciver and Siemicki 1981).

2.1.1 The antenna of A. aegypti

In both sexes of the mosquito the antenna is comprised of 15 segments. The first two segments are called the scape and pedicel (or torus) respectively. The scape is a narrow ring that attaches the antenna to the head and the pedicel contains a mass of neurons innervating the Johnston's organ (Steward and Atwood 1963), which is the main auditory organ of mosquitoes. The last 13 segments of the antennae form the flagellum. Muscles are only found in the first three segments of the antenna and are attached to the base of the third segment, or the first segment of the flagellum. There are approximately 1,000 sensilla on each antenna of the *A. aegypti* and they are classified in five morphological types: bristles (sensilla chaetica), grooved pegs (sensilla basiconica), pegs in pits (sensilla coelonica), pegs in long tubes (sensilla ampullaceal) and hairs (sensilla trichodea) (Mciver 1978). Sensilla trichodea are the most numerous on the antenna of the female (from 523 to 752) (Steward and Atwood 1963) and house sensory neurons expressing olfaction genes. There are two nerves and a single blood vessel that runs through the flagellum in both males and females of the species.

The male antenna is shorter and has more bristles than the female antenna. The first segment of the female antenna is about 2 mm long (Figure 1.1), with the pedicel being only 0.16 mm long. There are 514 neurons innervating the different types of sensilla in the male antenna, only 91 of these are believed to house olfaction receptors (Mciver and Siemicki 1979; Mciver and Siemicki 1981), while seven neurons are believed to be involved in mechanoreception and two in thermoreception. Although the females have four times more neurons in the antenna than males, the ratio of those responding to various stimuli is similar in both sexes, for example, each nerve in the flagellum of the female antenna has 2,058 neurons of which only 93 innervate olfaction sensilla, five mechanoreceptors, and two thermoreceptors (Mciver 1978; Mciver and Siemicki 1979; Mciver and Siemicki 1981). In addition to the differences in the antennae between both sexes, males have longer maxillary palpi as well (Figure 2.1). The maxillary palpi may potentially express transcripts of not only known olfaction genes, but also involved in mechanosensation and thermosensation (Bohbot et al. 2014).

2.1.2 Behavioral states of A. aegypti

Although the number of olfactory neurons is similar in both sexes, only the females utilize and feed on blood. After emergence from the pupal stage females feed on nectar and for the first days do not seek a host for a blood meal. They become highly attracted to humans at 5 days old. In comparison, males feed only on nectar throughout their life cycle, while females feed firstly on nectar then rely on a blood meal in order to produce eggs but may need to feed on nectar between the gonotrophic cycles (Andersson and Jaenson 1987; Foster 1995; Gary and Foster 2004) andfeed on extra floral nectar throughout adult life (Martinez-Ibarra et al. 1997). There are several factors influencing the host seeking behavior of mosquitoes, such as larval diet and competition, temperature, size of blood meal and egg maturation in the ovaries.

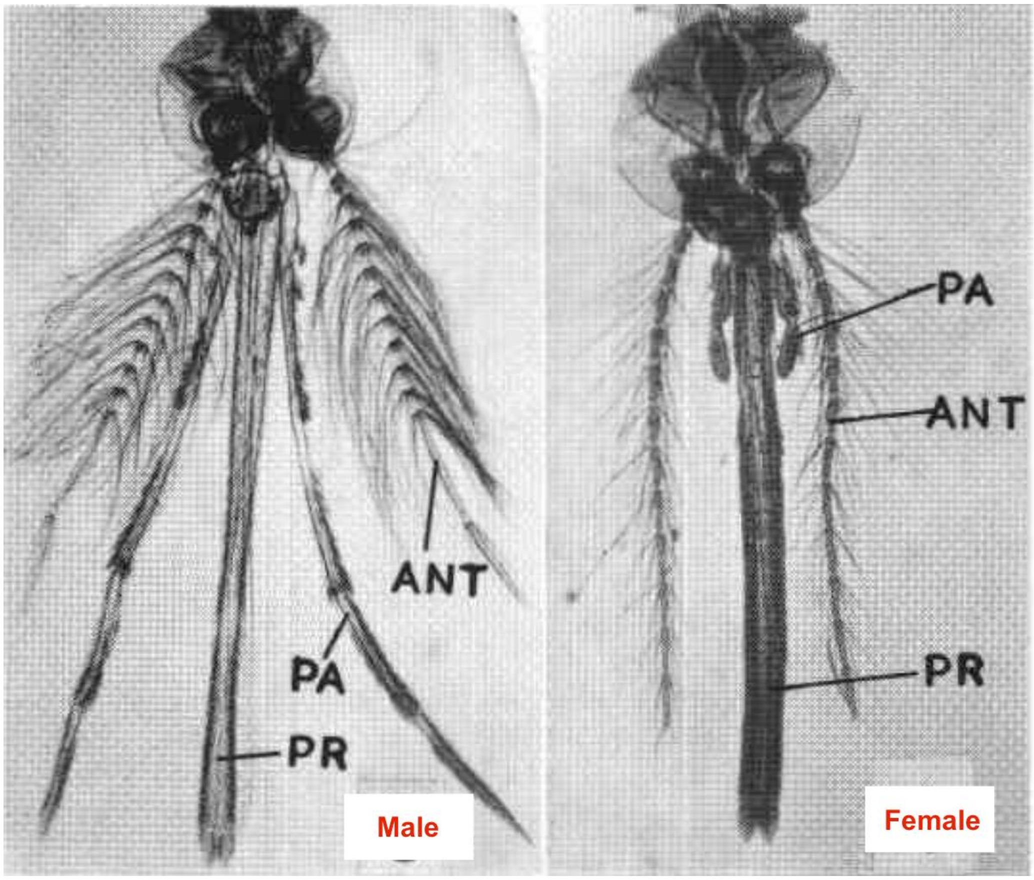

Figure 2.1 Male and female antenna of *A. aegypti* (Steward and Atwood 1963). Ant: antennae; PA: maxillary palp; PR: proboscis. Male antenna is shorter than female antenna while the maxillary palpi are longer.

There are several points where host seeking is suppressed, which, if understood at a mechanistic level, could provide a means of controlling this pest. There is a period of at least two days after adult emergence where the host seeking behavior is suppressed. Females will readily respond to host odor when they reach 5 days old (Figure 2.2). Once the blood meal is acquired, the host seeking behavior is suppressed once again (Klowden 1994). *A. aegypti* is an active diurnal feeder and its behavior is influenced by an endogenous circadian clock (Taylor and Jones 1969). The abdominal distention after a blood meal inhibits the host seeking behavior when blood volume is above a given threshold (Klowden and Lea 1978). The development of eggs after feeding will also suppress the host seeking behavior if it is below a threshold (Figure 2.3)

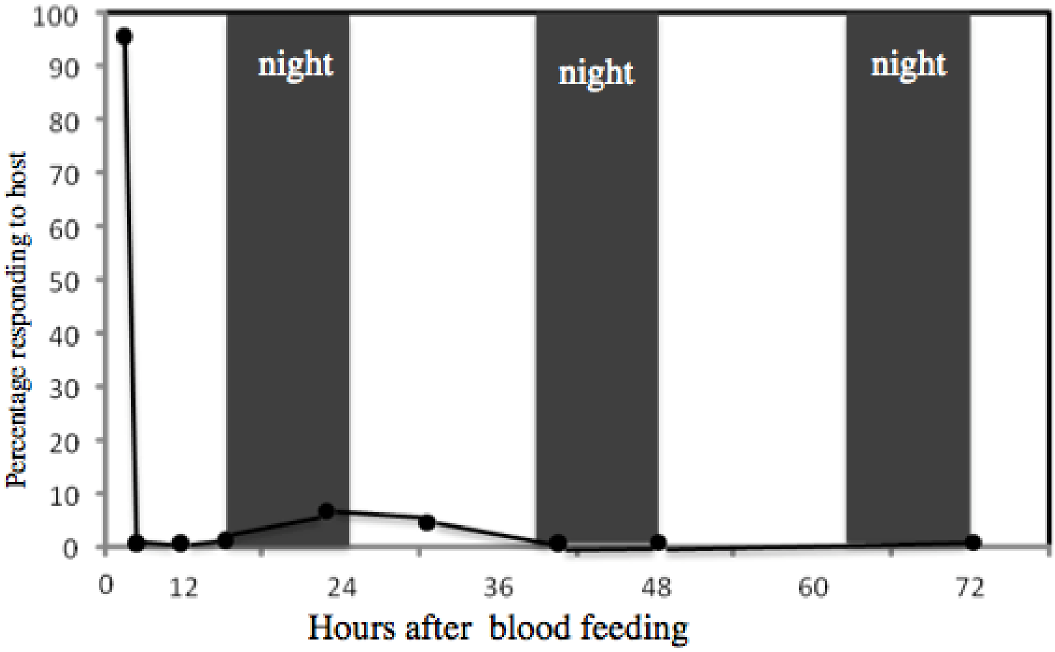

Figure 2.2 *Aedes aegypti* response to humans. Adapted (Klowden 1994). More than 95% of five days old females take the opportunity to feed on humans. After feeding they do not respond to the host and remain stationary, typically on the side of the cages where colonies are kept. However, in some cases females may not take a full blood meal and will take the opportunity to feed again. They do not seek a blood meal from humans again until they lay eggs.

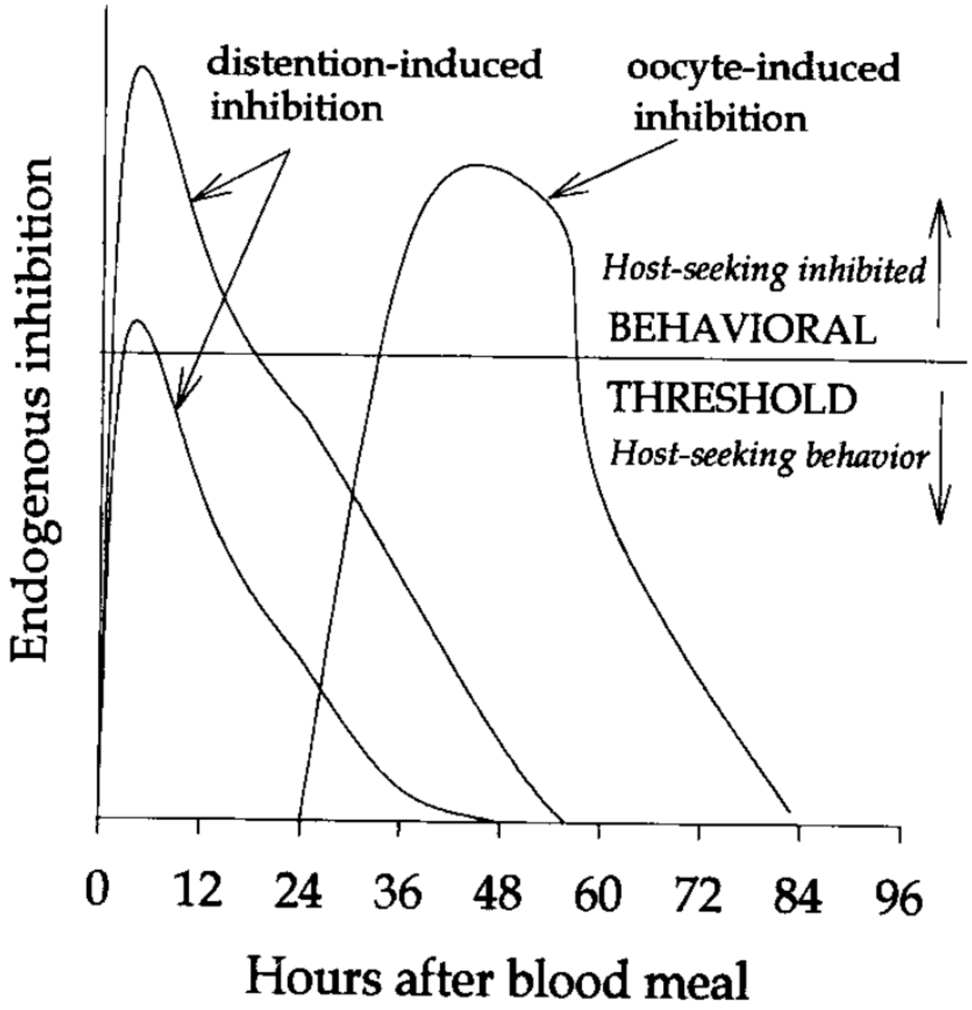

Figure 2.3 The behavioral threshold of *A. aegypti* during host seeking (Klowden 1994). Abdominal distention and oocyte development act as checkpoints, which determine the necessity to find a host to obtain a blood meal.

After digesting and process the blood meal, females perform oviposition site seeking behavior if three conditions are met: 1) mating has occurred; 2) there is endogenous information about the presence of eggs; 3) and possibly there is exogenous information about a suitable oviposition site (Klowden 1990). Females are able to retain their eggs if no oviposition sites are available. In laboratory colonies, cups containing water with a piece of filter paper can be used as oviposition sites. On the third day after blood feeding females will start laying eggs under laboratory conditions, even though they might respond to odors associated of oviposition sites earlier (Figure 2.4). The pre-oviposition behavior is displayed only by gravid females, which have eggs in their ovaries and respond to odors from oviposition sites at 72h (Figure 2.4).

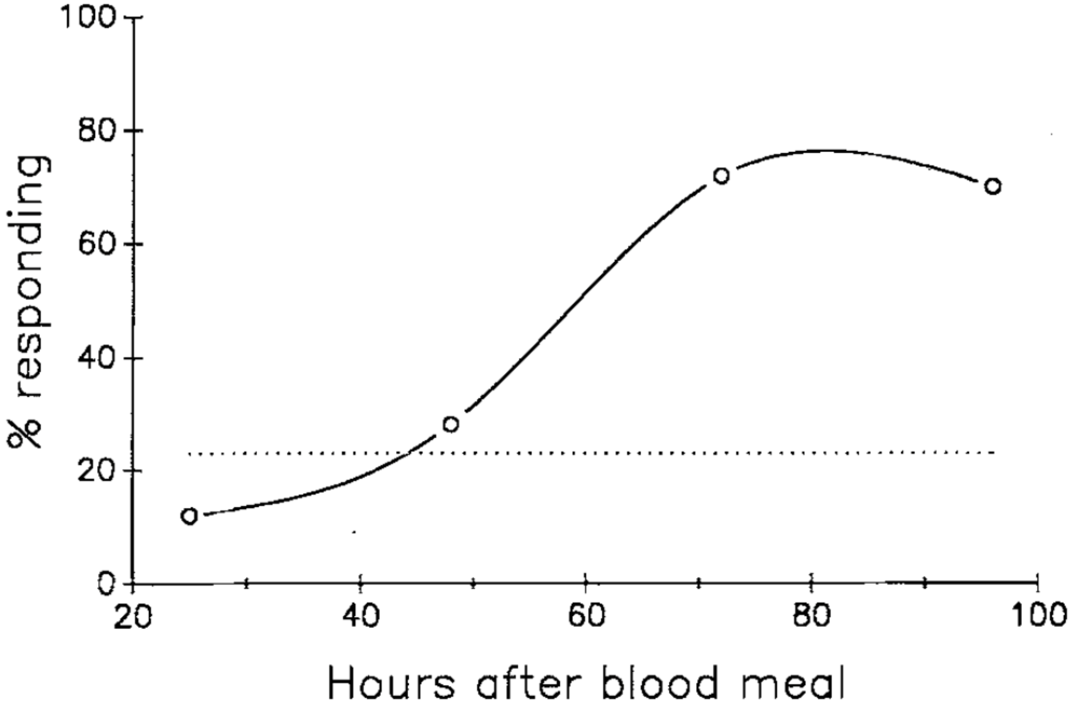

Figure 2.4 The pre-ovipostion behavior of gravid females of *A. aegypti* (Klowden 1990). The dotted line represents the behavior of females that did not blood feed or had their ovaries surgically removed.

Although males and females maintain a similar ratio of odor sensing neurons in their antennae (91 for males and 93 for females), the expression patterns of ORs appear to be different between the sexes. Qualitative data obtained from real time PCR reveals 8 odorant receptors found exclusively in female antenna (Figure 2.5), in addition 3 ORs specific to the maxillary palpi and proboscis (Bohbot et al. 2007b). In a recent study, it was found that the maxillary palp of *A. aegypti* also has transcripts involved in mechanosensation and thermosensation. *Orco, Or8* and *Or49* are highly expressed in the maxillary palp of females. Besides these ORs, *Or6* and *Or99* may also functional in the maxillary palp, but their expression levels are considerably low (Bohbot et al. 2014).

In *A. gambiae* olfaction genes are highly expressed in the female antenna, although male and females may share a similar range of odor coding ability (Pitts et al. 2011). The opposite occurs with genes involved in the hearing, which are highly expressed in the male antenna. Therefore the modality of the sensory systems in the antenna of male and female is different. Males have specialized for hearing female wing beats, which is crucial for mating success. Female, have specialized in olfaction to find hosts and therefore be able to acquire enough protein for egg development and to locate oviposition sites.

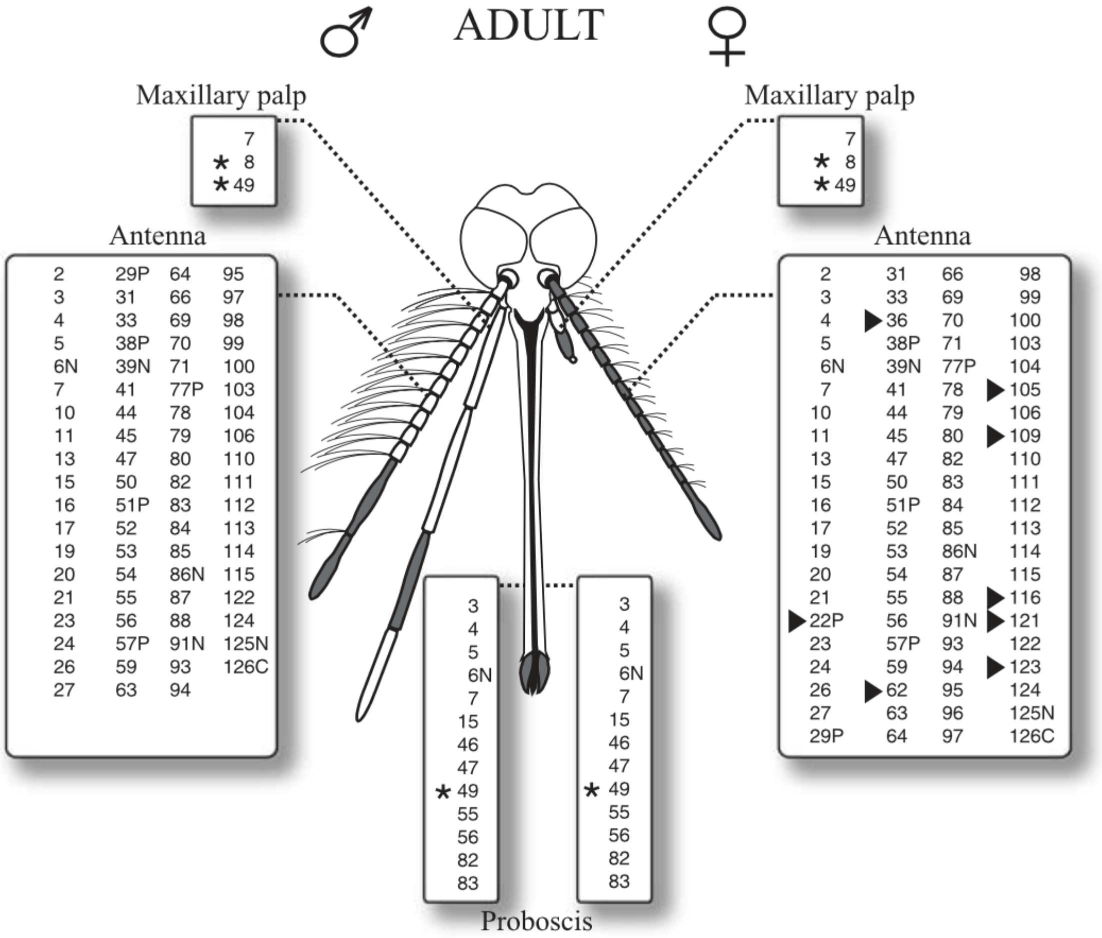

Figure 2.5 Topography of the odorant receptors expression in the olfaction organs of *A. aegypti* adults (Bohbot et al. 2007b). Female specific ORs are indicated by an arrow head. Asterisks indicate ORs not expressed in the antenna.

In this study I categorize adult mosquito behavior in 4 phases: 1) non-host seeking individuals - females and males (recently emerged) that are seeking nectar food sources (which can be up to 2 days for females). Females will not take a blood meal humans or respond to CO_2 or humans' odors during this time; 2) host-seeking females - after 4 days females are actively seeking humans; 3) non-host seeking females – which are blood fed, with enough blood to distend their abdomen, signaling the suppression of host seeking behavior; 4) oviposition site seeking females - females which have developing eggs in their ovaries (gravid females) (Figure 2.6). If a female has not found a host to feed on it will not switch to this phase. In addition and do not look for oviposition sites if they have not mated, as the male accessory gland substance transferred during mating also influences the onset of the oviposition site seeking (Klowden 1994).

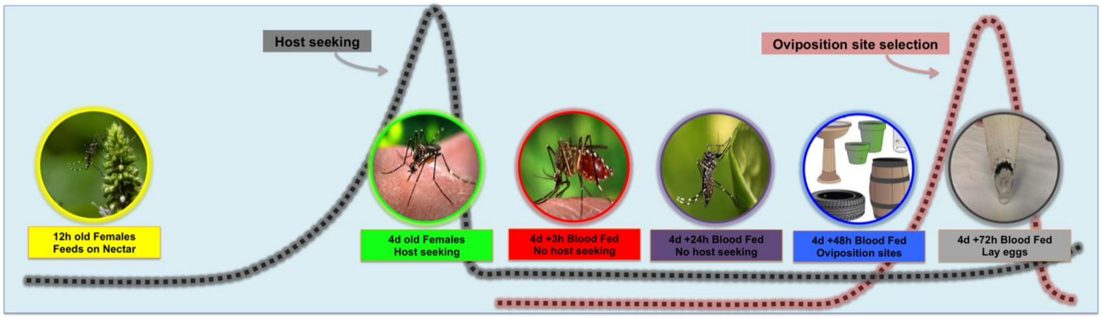

Figure 2.6 The behavioral states of the yellow fever mosquito females under laboratory conditions. The yellow circle indicates females that have emerged from the pupal stage, feeding on nectar and not seeking hosts; the green circle indicates females after 4 days, actively seeking hosts; the red circle indicates females which have blood fed and are not searching for a host; the purple circle indicates females feeding on a nectar/sugar solution anticipating the search for oviposition sites; the blue circle indicates females looking for oviposition sites; the gray circle indicates females starting to lay eggs dependent on if they find a suitable oviposition site (in the case of laboratory conditions, the sites are egg cups). The gray dotted line represents the host seeking behavior of females while the red dotted line represents the oviposition site seeking behavior.

It is unknown how olfaction transcripts levels change in the antenna of females as they switch from a behavioral state to the next. To elucidate the changes in olfaction gene expression in the antenna of *A. aegypti* during behavioral switches, I isolated mRNA from females of different ages (listed in Figure 2. 6), non-gravid and gravid females, and four-days-old males with another sample of the head plus thorax simultaneously. Both mRNA and small RNA (miRs) were used to prepare sequencing libraries. In this chapter I will present the work with mRNA and in the next chapter I will focus on the miRs profiling, identification and discovery.

The main hypothesis is that changes on the transcript levels of olfaction genes would be observed if narrow tuning of the receptors occurs. Alternatively, if broad receptor tuning occurs, no changes in olfaction gene expression would be observed after blood feeding. However, a mixed system may be present where the majority of the receptors detect multiple odors (broad tuning) and a few receptors are specifically tuned to host odors. In this case, I expect not to observe changes in the expression levels of olfaction genes after blood feeding.

2.2 Materials and methods

2.2.1 Mosquito reading

Mosquito larvae (Liverpool strain) were reared at standard conditions (25^{o}C, 75% RH) in plastic containers (4L) (Figure 2.7) and fed with fish food. I allowed eggs to hatch for only 6h as this facilitates most of the larvae pupating in parallel. Larvae were fed daily. For each experimental replicate, approximately 25,000 mosquitoes were reared in 200 plastic containers. Pupae were transferred to 25 ml cups and placed inside cages (25cm high x 10cm wide) (Figure 2.7) (150 to 200 females per cage). Cups containing the pupae were removed 24h after the first adults emerged. Adults were fed with a 5% sucrose sugar solution.

Figure 2.7 Plastic containers used to rear larvae (left) and paper cages used to keep the adult mosquitoes (right).

2.2.2 Blood feeding

I blood fed mosquitoes with an artificial blood feeding system that I independently developed. Initially, mice were used but the high number of mosquitoes, in conjunction with the need to synchronize feeding, required artificial membrane feeding. The system consisted of a water bath heated to 37°C and a small water pump to circulate the warm water into blood feeding units (units consisted of cell culture flasks (40mL). I replaced the lid of each flask with a rubber stopper containing two holes connected by tubing to the water pump. Several blood feeding units could be attached to one another to allow feeding of 50 mosquito cages. All mosquitoes were fed at the same time when carrying out an experiment (see details in the experimental design section). I used a parafilm membrane stretched over one side of the flasks to create a small chamber for containing 2 ml of defibrillated rabbit blood (Hemostat, CA) in each blood feeding unit and allowed mosquitoes to feed for 20 min.

2.2.3 Experimental design

My first experimental samples consisted of 3 biological replicates of female antenna only. All females came from a single batch of larvae. Blood feeding of the females occurred in the morning using total approximately 700 mosquitoes for each biological replicate. 50 cages were blood fed at 8AM, whereas10 cages were not blood fed. All mosquitoes were starved for 12h before feeding. Immediately after feeding, cotton balls were restored to the cages, soaked in 5% sucrose, and places on the top of each cage. This component of the study consisted of the following samples: four-day-old unfed females (host seeking), 3h and 24h post-bloodmeal females (not host seeking) and 48h and 72h post-bloodmeal females (oviposition site seeking).

In addition to the samples described above, antennae were collected (see below) of 12h old females (nectar seeking) and four-day-old males (2 replicates for each). Simultaneously, I collected head plus thorax (without wings, legs and olfactory organs) for two biological replicates for all samples described in Figure 2.8.

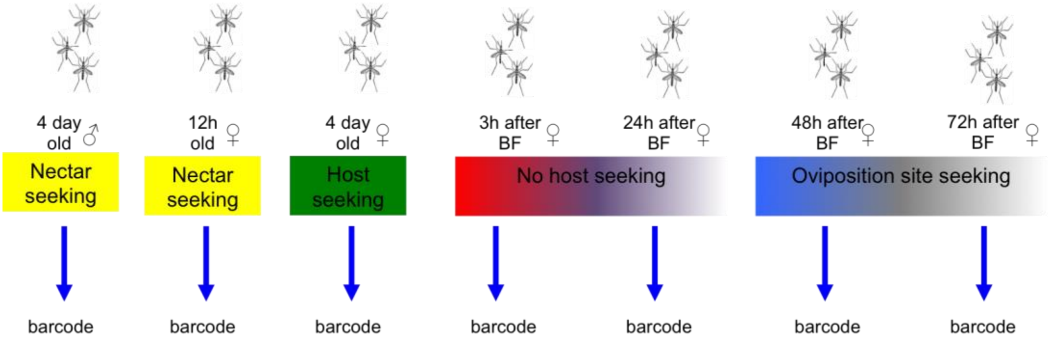

Figure 2.8 Treatments for the mRNA profiling experiment. Each RNA sample was submitted to a sequencing facility with unique barcodes used during RNA-seq library preparation.

2.2.4 Antenna dissections

Mosquitoes were knocked down at -20°C for 30 seconds and transferred to Petri dishes and kept them at -20°C until dissection. Each dish containing mosquitoes was transferred to ice right before dissection. Subsequently, approximately 30 individuals were placed on a dry ice block. After mosquitoes were frozen, antenna were collected using a system that I created independently, by inserting a pipette tip into a Qiagen PCR purification kit (Qiagen) spin column connected to a vacuum pump (approximately 15 psi). The antennae are brittle when frozen, and can easily be extracted by sucking them into the spin column. After antennae from approx. 150 females were collected, the spin column was transferred to a 2mL tube containing RNAlater (Ambion). For each biological replicate the antennae from approximately 700 females were collected. Tubes with antennae were stored at 4°C overnight. The tissue was removed from RNAlater the following morning and samples put into a single empty 2 mL tube. These tubes were stored in -80^{o}C until RNA extraction. Head and thorax samples were processed were dissected manually, but processed for storage in the same way.

2.2.5 RNA isolation

Samples were removed from -80^{o}C freezer (one each time) and homogenized in QIAzol (Qiagen) using a tissue tearer for 20 seconds. Total RNA was extracted using the miRNeasy kit (Qiagen) protocol, which retains RNA molecules larger than 17 nucleotides. Total RNA was eluted in 50µL of RNAse free water and the RNA quality was assessed using a bioanalyzer (Agilent), Qubit (Invitrogen), and Nanodrop (Thermo Scientific). Samples showing any signs of RNA degradation or salt/phenol contamination were discarded. Samples presenting a yield higher than 1µg of total RNA and no signs of degradation or contamination were used in subsequent analyses. In addition, the sequencing facility also performed quality control in all samples prior library construction.

2.2.6 Dissection validation experiments

Two validation experiments were performed to verify the robustness of our novel antennal dissection method. First, co-workers examined the mosquitoes from which antennae were collected using the vacuum system under a stereoscopic microscope. Observations included looking for missing maxillary palp or proboscis, which are the appendages could potentially have been removed along with the antennae. The maxillary palpi of females are small and difficult to see with naked eye. For this validation experiment, antennae were collected from 200 females in the course of 1hr and each female was examined immediately following dissection. Every single mosquito that had its antennae sucked by the vaccum system was checked under a stereoscopic microscope. Only samples with intact maxillary palpi and proboscis were used for RNA extraction. If one mosquito had one maxillary palp missing or proboscis was damage the entire antennal sample was discarded.

In the second experiment the effect of CO_2 exposure on the female antennal gene expression was examined. This validation experiment consisted of the following treatments: 12h and 4 days old unfed females on dry ice (400 per replicate) and sucked their antennae using the method previously described, while a co-worker validated every insect for missing maxillary palpi or damaged proboscis. Next antennae were dissected manually from 12h and 4 day-old unfed females (400 females per replicate) under a stereoscopic microscope in a room next to a block of dry ice that produces CO_2. All antennae were subsequently processed as outline above.

2.2.7 mRNA sequencing

RNA samples were submitted to the Buffalo Genomics and Bioinformatics Core of the State University of New York at Buffalo and Texas A&M AgriLife Genomics and Bioinformatics Service at College Station (Table 2.1). Library preparation was carried out using TruSeq RNA Sample Preparation Kit v2. Five libraries were multiplexed and sequenced in a single lane of Illumina Hiseq2000 for samples submitted to SUNY, eight libraries were sequenced in a single lane on a Hiseq2500 (50 cycles, single end reads) for the validation experiment samples submitted to Texas A&M.

Table 2.1 Samples submitted to different sequencing facilities and their sequencing platforms. Ant: antennae; HT: head plus thorax.

Sample	Tissue	Sequencer	Sequencing facility
12h old female	Ant and HT	HiSeq2500	Texas A&M
4d old males	Ant and HT	HiSeq2500	Texas A&M
4d, +3h, +24h , +48h, +72h BF	Ant	HiSeq2000	State University NY
4d, +3h, +24h , +48h, +72h	HT	HiSeq2500	Texas A&M
12h and 4d old CO_2 experiment	Ant	HiSeq2500	Texas A&M

2.2.8 Genomic analyses

The NGS QC toolkit (Patel and Jain 2012) was used to remove adapter sequences, to trim reads with low quality, and to filter reads based on their length and Phred quality scores (each raw reads base has a Phred quality score from 0 to 40). The cutoff was set for 50% of the read having Phred > 30. Reads shorter than 40bps were also discarded.

The reference genome (AaegL3.23.fa) and annotation files (AaegL3.23.gtf) were downloaded from the Esembl Metazoa database (http://metazoa.ensembl.org/info/website/ftp/index.html). STAR v2.4.1.a (Dobin et al. 2013) were used to map the reads to the reference genome. A bash script allowing all mapping analysis to be queued and run via Linux command line was used to avoiding human mistakes.

Subsequently, HTSeq (version 0.6.1p1) (Anders et al. 2015) was used to count the number of mapped reads for each annotated gene. The ollowing bash script was used to queue and run the analyses via command line in Linux.

All the statistical analyses were performed in R using DESeq2 (Love et al. 2014). The goal was to test the null hypothesis that the logarithmic fold changes between the treatment and control for a specific gene is zero, which means that the gene is not affected by the treatment. I used clustering analysis with the variant transformed data to detect any replicate showing skewed data. A generalized linear model was used to block the effect of tissue or sex, and pairwise comparison to look for differential expression between the samples.

Subsequent to DESeq2 analyses I exported the results and used bash scripts to filter the genes that were up- or down-regulated. The filtering was based on $p < 0.05$ for adjusted values representing the false discovery rate, RPKMs > 1 in at least one of the compared samples, and at least a two fold changes difference between the samples).

gProfiler (Reimand et al. 2011) was used to perform gene ontology analyses on genes whose expression varied significantly between samples. I primarily focused on overrepresented genes according to their molecular function or biological process. I used the following settings with gProfiler for all gene ontologies: p value < 0.05, functional category size = 3, size of query/tested = 5, Benjamini-Hochberg *FDR* correction.

DEXSeq (Anders et al. 2012) was used to test for differential exon usage among selected experimental conditions. The relative exon usage is defined as the number of transcripts from the gene that contains the exon divided by the number of all transcripts from the gene. For each exon and sample, DEXSeq counts how many reads are mapped to a particular exon and how many reads are mapped to any exons of the same gene. It considers the ratio of exons and how these ratios change across the treatments. This indicates changes in the rate that this exon is spliced into transcripts. However, differential exons usage is a broader term than alternative splicing since it also accounts for transcription of each exon and polyadenylation sites (Anders et al. 2012). Similarly to DESeq2 (Love et al. 2014), DEXSeq uses generalized linear models and controls for false discoveries by taking biological variation into account.

All the analyses were performed by first preparing the reference genome (AaegL3.23.gff) using the Python script from DEXSeq. Next, I used the SAM alignment generated by STAR and a second Python script from DEXSeq to count how many reads were mapped to each exon. Finally, the statistical analysis was performed in R following the DEXSeq protocol. In this analyses I focused on differential exon usage between male and female antennae, between 12h old females (nectar seeking) and four-day-old females (host seeking), and finally between the four-day-old females (host seeking) and 72h post-bloodmeal females (oviposition site seeking). Because of the computational requirements for these analyses, only olfaction genes were included. Results were filtered using bash scripts requiring that the exons fold changes between the pairwise comparisons were at least 2 fold and that the normalized counts in one of the samples were higher than 1.

After mapping the reads to the reference genome I notice several potential new transcripts or genes throughout the genome. The fragmented nature of the genome assembly of *A. aegypti*, combined with the fact that it has over 5,000 more annotated genes than the genome of *Anopheles gambiae*, more annotated olfaction genes, and that a high number of reads mapping to intergenic or intronic regions, indicates the presence of several unknown transcripts. Therefore, I used the output of STAR (aligned reads in BAM sorted format) and Cufflinks (Trapnell et al. 2010) to assemble the alignments into a parsimonious set of transcripts. Besides using my own data, I included data from a recent *A. aegypti* transcriptome study of domestic (anthropophilic) and forest (zoophilic) strains (McBride et al. 2014). Cufflinks generates an annotation file for each sample with the transcripts and compares it to the reference annotation file, generating a new annotation file with previously unannotated transcripts. Expression levels of these new genes were then compared as described above.

In this analyses I focused on the transcripts with the following class codes generated by Cufflinks: class code 'j' - potential new isoform (at least one splice junction is shared with the reference transcript); class code 'u' - unknown gene (intergenic transcript); and class code class code 'I' – the transfag fails entirely within an reference intron (it could be mirtrons). However, after statistical analyses I used bash scripts to filter the transcripts mentioned above that have RPKMs > 1 in at least one sample of the pairwise comparison, changed at least 4-fold, and had *p* adjusted value < 0.01 (false discovery rate). I used these stringent filtering parameters to make sure the transcripts were expressed at a considerable level and to reduce false positives.

Finally, I hypothesized that genes with an unknown biological function but with similar expression patterns to known olfaction genes could have a related molecular function or biological process. For example, a gene that has same expression pattern as a known odorant receptor and its gene ontology/protein domains indicate a potential olfactory function could potentially be an unknown olfaction gene that might not have been identified through homology search previously due to a high level of divergence. To examine this, I used STEM (short time-series expression miner) (Ernst et al. 2005; Ernst and Bar-Joseph 2006), which is a time series analysis algorithm to locate expression patterns across experimental conditions. STEM supports Gene Ontology (GO) and enrichment analyses for gene-sets that have the same temporal expression pattern. This allowed the identification of significant temporal expression patterns for olfaction genes.

2.3 Results

2.3.1 Gene expression changes in the antenna of females after blood feeding

A considerable number of transcripts significantly change their expression in the antenna of females after they acquire a blood meal. However, olfaction gene transcripts levels remain steady with a few exceptions. Gene expression changes occur fast, and within 3h after blood feeding a total of 68 genes are differentially expressed (false discovery rate < 0.05, RPKMs > 1 in one sample of the pairwise comparison, and more than 2 fold changes) (Table 2.2). Of these, 47 genes are up regulated, whereas the expression of 21 genes is reduced. Among the up-regulated genes with known function, a few stand out. Two vitellogenin precursors are enriched almost 3 fold within 3h of blood feeding (Table A1). Furthermore, a Toll-like receptor (2 fold) and a putative juvenile hormone-inducible protein (3 fold) are also enriched post-feeding. The highest number of significant changes occur within 24h of blood feeding, when a total of 101 genes are differentially expressed.

Among the olfaction genes, only *Obp18* and *Obp22* stand out as significantly enhanced after blood feeding. These OBPs are expressed at relatively low levels compared to other genes in the same family. For example, *Obp22* has higher expression than *Obp18*, and its transcript levels vary from 23.04 RPKMs at 3h to 129.34 RPKMs at 24h after blood feeding (5.35 fold increase) (Table A1). Among the genes with higher enrichment, 4 cathepsin b genes stand out with up to 140 fold increase (Table A1).

At 48h post blood feeding there is an inversion in expression pattern, with a higher number of genes now being down regulated (89 genes) versus up regulated (8 genes). *Obp18*, *Obp22* and *Obp21* transcript levels are reduced significantly (Table 2.2). The vitellogenin precursor and cathepsin b genes are among the genes with a large reduction in their transcript levels (up to 35 fold reduction) (Table A3). The changes in the transcript levels of the 8 genes enriched at 48h post blood feeding are relatively small (less than 3.48 fold) compared to those that are depleted. Finally, at 72h the transcript level of 6 genes is reduced and no enrichment of any transcript is observed (Table 2.1 and Table A4).

These results show considerable changes in the transcript levels of several genes in the female antenna after blood feeding, although only 2 OBPs are enriched at 24h post blood feeding. These results indicate that olfaction genes expression does not directly correlate with host seeking suppression after blood feeding or the start of oviposition site seeking.

Table 2.2 Global gene expression changes in the antenna of females after blood feeding. Olfaction genes that are differentially expressed shown in brackets.

Sample	Number of genes down regulated	Number of genes up regulated
4d host seeking versus +3h	21	47
+3h versus +24h	40	61 (*Obp18*, *Obp22*)
+24h versus +48h	89 (*Obp18*, *Obp21*, *Obp22*)	8
+48h versus +72h	6	0

2.3.2 Gene expression changes in the HT of females after blood feeding

A higher number of transcripts are differentially expressed in the HT of females after blood feeding. The changes in expression follow the pattern found in the antenna of females, with most changes occurring between 3h and 24h after blood feeding. However, 470 transcripts are enriched rapidly after feeding (Table 2.3). Among these transcripts, vitellogenin-A1 precursor and other genes involved in lipid metabolism stand out with fold up to 242 fold changes (Table A5). Within the 171 genes that are down regulated rapidly after blood feeding, the allantoinase enzyme transcript is the most depleted (118 fold) with its transcript levels below 1 RPKM 3h after blood feeding (Table A5). This protein converts uric acid to urea (Scaraffia et al. 2008).

Two members of the olfaction gene families show significant changes in their expression in the HT 3h after blood feeding, *Ir75k.2* and *Obp26* (Table 2.3), however it is known that IRs and OBPs can have have functions not necessarily related to olfaction. Interestingly, the transcript levels *Ir75k.2* is reduced at 24h after feeding, whereas *Obp26* transcripts levels remain constant until 72h. Other OBPs also display significant changes in their transcript levels after blood feeding. OBPs may act not only as solubilizers and carriers of the lipophilic odorants in the sensillum lymph of the antenna, for example they may clean the perireceptor space from unwanted and toxic compounds (Steinbrecht 1998).

A total of 1,150 genes show significant changes at 24h post blood feeding in the HT (Table 2.3, Table A6). The majority of these genes have functions related to proteolysis, lipid transport or metabolism, sugar transport, and other catalytic or enzymatic activity. Four cathepsin genes, which are involved in vitellogenesis and yolk protein synthase and degradation, display the highest increase in their transcript levels (approximately 200 fold).

At 48h post blood feeding some genes involved in vitellogenesis still display enhanced transcript levels. For example, cathepsin gene AAEL007590 is up regulated (928 fold) (Table A7). On the other hand the cathepsin gene AAEL007599 is down regulated (33 fold). This implies they play different roles in vitellogenesis.

Finally, between 48h and 72h the number of differentially expressed genes decreases to 382 (Table 2.3). The cathepsin and vitellogenin transcripts are depleted and the overall changes in the other genes are considerably smaller than between previous time points (-11 fold to +31 fold) (Table A8).

The comparison between 4 days old unfed and 72h blood fed females reveals a small number of significant changes (Table A9). A total of 157 genes are up regulated, including the vitellogenin and cathepsin genes. Although these transcripts levels are higher at 72h than in unfed females; their expression is reduced compared to 48h after blood feeding. The overall changes between unfed and 72h blood fed females are relative small. For example, most of the genes being down regulated display less than 4 fold changes, and genes involved in vitellogenesis are enriched the most.

Table 2.3 Global gene expression changes in the HT of females after blood feeding. Olfaction genes that are differentially expressed are shown in brackets.

Sample	Number of genes down regulated	Number of genes up regulated
4d host seeking versus +3h	171	470 (*Ir75k.2*, *Obp26*)
+3h versus +24h	675 (*Ir75k.2*)	475 (*Obp21*, *Obp22*)
+24h versus +48h	387 (*Obp19*, *Obp22*)	248
+48h versus +72h	160 (*Obp22*)	222 (*Obp19*)

2.3.3 Gene expression changes in the antenna 12h and 4 day old females

Contrary to what is detected after females switch from the host seeking to oviposition site seeking when few changes in olfaction gene expression are observed, drastic changes occur in the expression of both olfaction genes as well as other genes as females switch from exclusively nectar/sugar feeding to host seeking. A total of 1,304 genes display significant changes in the antenna as females start host seeking, with the majority (985) being down regulated (Table 2.4 and Table A10). Genes with the highest changes (40 to 442 fold changes – down regulated) code for proteins with chitinase activity, structural constituent of the cuticle or chitin binding (data not shown).

Table 2.4 Global gene expression changes in the antenna of 12h vs. 4 days old females.

Sample	Number of genes down regulated	Number of genes up regulated
Antenna	985	319
HT	1,149	1,082

A small number of olfaction genes are down regulated in the antenna of the females as they start looking for hosts: *Obp5, Irf, Obp9, Obp22*, *Obp24* (Table 2.5). Conversely, the number of olfaction genes up regulated is large (Table 2.5). Out of the 33 olfaction genes enriched when the female start looking for host, 23 are ORs, 2 are GRs, 6 are OBPS and one is an IR.

Finally, 286 other genes are up regulated as the female start looking for hosts. Among these genes, several cytochrome P450 and heat shock protein genes stand out. These genes are involved in detoxification and response to stress as mosquitoes avoid overheating after blood feeding (Lahondere and Lazzari 2012).

Table 2.5 Olfaction genes down regulated in 4 day old females as they start looking for hosts.

Gene ID	Gene Name	12h (RPKMs)	4 day Unfed (RPKMs)	Fold	*p* adj.
AAEL002596	*Obp9*	7.77	0.75	-7.26	0.0001
AAEL005772	*Obp22*	118.39	28.22	-4.21	0.0000
AAEL000139	*Obp5*	13.76	3.58	-3.84	0.0000
AAEL006108	*Obp24*	36.36	12.89	-2.98	0.0000
AAEL002506	*Irf*	21.25	9.59	-2.34	0.0004

Table 2.6 Olfaction genes up regulated as females start looking for hosts. 12h females do not host seek, whereas 4 days old actively look for hosts.

Gene ID	Gene Name	12h (RPKMs)	4 day Unfed (RPKMs)	Fold	*p* adj.
AAEL002617	*Obp12*	162.09	3477.87	19.56	0.0000
AAEL002591	*Obp13*	50.90	860.04	15.00	0.0000
AAEL017505	*Or103*	13.41	72.26	4.87	0.0000
AAEL013420	*Or79*	4.67	23.09	4.41	0.0000
AAEL016981	*Or36*	2.94	12.25	3.52	0.0008
AAEL010428	*Or26*	5.13	19.58	3.49	0.0000
AAEL017123	*Or113*	27.26	101.98	3.43	0.0000
AAEL017000	*Or97*	1.73	6.68	3.34	0.0025
AAEL017065	*Or92*	1.20	4.28	3.14	0.0002
AAEL011499	*Obp47*	599.90	1972.10	3.00	0.0000
AAEL017143	*Or102*	0.76	2.49	2.81	0.0241
AAEL010418	*Or27*	6.64	20.56	2.81	0.0000
AAEL017537	*Or123*	3.70	11.62	2.80	0.0021
AAEL017296	*Or93*	1.19	3.85	2.75	0.0359
AAEL013423	*Or78*	4.00	11.25	2.56	0.0000
AAEL007940	*Gr77*	1.57	4.37	2.52	0.0048
AAEL000162	*Gr34*	0.75	2.13	2.44	0.0346
AAEL017043	*Or84*	142.26	367.38	2.38	0.0000
AAEL013893	*Or125*	6.07	15.67	2.37	0.0000
AAEL017201	*Or94*	9.96	24.90	2.30	0.0000
AAEL017009	*Or119*	2.16	5.47	2.28	0.0155
AAEL014197	*Or88*	25.57	61.91	2.23	0.0000
AAEL011583	*Or11*	22.81	56.10	2.23	0.0016
AAEL017149	*Or91*	8.82	21.32	2.23	0.0000
AAEL000047	*Ir41i*	3.28	7.86	2.18	0.0027
AAEL012377	*Obp55*	15371.44	35491.55	2.13	0.0000
AAEL011895	*Or48*	1.11	2.59	2.07	0.0375
AAEL017129	*Or72*	7.16	16.12	2.07	0.0024
AAEL017219	*Or114*	7.12	16.00	2.06	0.0094
AAEL008368	*Or13*	3.69	8.21	2.04	0.0007
AAEL015313	*Obp59*	222.55	492.02	2.02	0.0012
AAEL000073	*Obp4*	2152.58	4715.27	2.02	0.0000
AAEL016966	*Or104*	17.18	37.56	2.01	0.0027

2.3.4 Gene expression changes in the HT of 12h and 4 day old females

A total of 2,531 genes significant change their expression in the HT between 12h and 4 days old females (Table 2.3). Among the 1,449 transcripts that are reduced are several genes involved in cuticle formation, sclerotization and other structural functions.

Genes involved in the cuticle structure display the highest reduction in mRNA levels (Table 2.7). For example, AAEL004292 and AAEL009577 are not expressed at all when the females are looking for hosts, with a reduction of -3,930.88 and -2,544.73 fold respectively (Table 2.7).

Table 2.7 Top 20 genes with the highest reduction in their transcripts in the HT in four day old females.

Gene ID	Description	12h (RPKMs)	4 day Unfed (RPKMs)	Fold	*p* ajust.
AAEL004292	hypothetical protein	1,333.80	0.44	-3,930.88	0.0000
AAEL009577	hypothetical protein	213.19	0.07	-2,544.73	0.0000
AAEL001704	hypothetical protein	139.33	0.16	-899.40	0.0000
AAEL003049	pupal cuticle protein 78E	167.03	0.30	-771.55	0.0000
AAEL003888	ubiquitin	27,790.44	85.04	-487.66	0.0000
AAEL017987		192.97	0.76	-364.25	0.0000
AAEL001951	actin	15,509.75	79.61	-292.21	0.0000
AAEL017402		476.20	2.51	-270.84	0.0000
AAEL001319	hypothetical protein	200.21	1.05	-270.59	0.0000
AAEL010886	carbonic anhydrase II	7.45	0.02	-243.67	0.0000
AAEL002654	hypothetical protein	5.99	0.02	-242.01	0.0000
AAEL013722	partner of burs, putative	6.60	0.01	-239.44	0.0000
AAEL009193	glucose dehydrogenase	11.40	0.05	-217.04	0.0000
AAEL012573	serine protease, putative	8.17	0.01	-216.86	0.0000
AAEL013511	hypothetical protein	147.09	1.13	-185.50	0.0000
AAEL001677	hypothetical protein	148.87	1.19	-135.20	0.0000
AAEL002099	cuticle protein, putative	19.73	0.10	-130.10	0.0000
AAEL000259	superoxide dismutase	503.04	5.83	-127.91	0.0000
AAEL012575	serine protease, putative	19.89	0.14	-123.36	0.0000
AAEL004994	hypothetical protein	59.45	0.67	-122.84	0.0000

The genes enriched in the HT of 4 days old female (1,082 genes) display relative small changes in their transcript levels (Table 2.8), and most of the genes with the highest change in expression have low expression or are not expressed in 12h old female HT. Most of the genes showing up-regulation in host seeking females code for enzymes or structural proteins. Among these genes, several cytochrome P450 genes stand similar to what is observed in the antenna of females.

Table 2.8 Top 20 genes with the highest enrichment in the HT in 4 day old females

Gene ID	Description	12h (RPKMs)	4 day Unfed (RPKMs)	Fold	*p* ajust.
AAEL002675	arginase	0.14	91.61	352.61	0.0000
AAEL009669	hypothetical protein	0.01	13.91	282.24	0.0000
AAEL006138	hypothetical protein	0.01	4.95	126.12	0.0000
AAEL003881	ubiquitin	0.95	163.71	105.44	0.0000
AAEL014128	hypothetical protein	0.22	49.50	97.01	0.0000
AAEL009875	alanine aminotransferase	0.28	29.63	66.43	0.0000
AAEL002696	hypothetical protein	0.09	8.98	56.51	0.0000
AAEL011926	brachyury	0.00	1.18	55.13	0.0000
AAEL010183	hypothetical protein	9.34	790.17	54.67	0.0000
AAEL003457	hypothetical protein	0.33	27.11	49.35	0.0000
AAEL013990	hexamerin 2 beta	0.13	9.36	43.92	0.0000
AAEL007653	allantoinase	0.96	65.12	43.62	0.0000
AAEL006909	hypothetical protein	0.00	2.94	43.21	0.0000
AAEL002046	cytochrome P450	0.13	18.06	43.00	0.0000
AAEL004701	argininosuccinate synthase	0.04	3.93	42.22	0.0000
AAEL001414	hypothetical protein	4.88	311.96	41.08	0.0000
AAEL014830	cytochrome P450	0.32	21.68	40.57	0.0000
AAEL009018	cytochrome P450	0.41	25.07	38.15	0.0000
AAEL010161	hypothetical protein	12.46	630.08	32.88	0.0000
AAEL007818	trypsin	1.37	67.31	30.61	0.0000

The olfaction genes expressed in the HT are not likely to be involved in the detection of volatiles of host, nectar or oviposition sites. Fifteen olfaction genes show significant changes in their transcript levels as females start looking for hosts, and most of them are expressed at considerable low levels. *Obp18* and *Obp19* stand out as the genes with the highest expression levels that are enriched in 4 days old females (Table 2.9). Among the depleted genes *Obp35* and *Obp22* stand out as the most expressed in 12h old females HT. Overall these results indicate that only a limited number of genes from olfaction gene families are expressed in the HT of females, and all are expressed at low levels.

Table 2.9 Olfaction genes differentially expressed between the HT of 12h and 4 days old females.

Gene ID	Gene Name	12h (RPKMs)	4 day Unfed (RPKMs)	Fold	*p* adj.
		Up regulated			
AAEL012377	*Obp55*	0.15	2.06	6.79	0.0001
AAEL004343	*Obp19*	1.69	16.98	6.20	0.0000
AAEL012141	*Or43*	0.14	1.70	6.01	0.0003
AAEL004342	*Obp18*	10.55	83.07	5.11	0.0000
AAEL006176	*Obp27*	0.37	2.85	4.48	0.0003
AAEL010666	*Obp42*	0.63	4.63	4.38	0.0001
AAEL015567	*Obp63*	0.52	3.50	3.97	0.0005
AAEL000051	*Obp3*	0.28	2.09	3.68	0.0361
AAEL002617	*Obp12*	0.89	5.05	3.44	0.0012
AAEL007940	*Gr77*	0.61	2.65	2.78	0.0002
		Down regulated			
AAEL002606	*Obp35*	708.93	37.40	-22.82	0.0000
AAEL002596	*Obp9*	3.35	0.39	-10.40	0.0000
AAEL002591	*Obp13*	6.77	0.10	-5.14	0.0382
AAEL000071	*Obp2*	1.96	0.53	-4.47	0.0040
AAEL005772	*Obp22*	583.84	263.37	-3.36	0.0000

2.3.5 Sex biased gene expression in the antenna

A comparison of gene expression in the antennae of 4 day old males vs females, showed a 1,607 genes with sex-biased expression (Table A11). The majority of these genes (1,001) have higher expression in the antenna of males vs. females (606).

The magnitude of the difference in the transcript levels is also different between males and females. While the majority of the genes display significant, but small differences in their expression (between 2 and 10 fold), a total of 156 genes have expression values 10 fold higher in male antenna (from 10 to 285 fold). In females, only 29 genes have expression values higher than 10 fold (from 10 to 22 fold) (Table A11).

A considerably higher number of genes are almost exclusive in males, with a total of 387 genes with strikingly low expression levels in the antenna of females (< 1 RKMs) while having a noticeable higher expression in males (> 2 fold and RPKMs > 1) (Table A12). In contrast, a total of 118 genes are exclusive to female antenna (RPKMs < 1 in male antenna) (Table A13).

Olfaction appears to differ between the sexes considerably. A total of 102 olfaction genes have significant changes between male and female antenna. Not unexpectedly, the majority of these genes have higher transcript levels in the female antenna, particularly the odorant receptors (Table 2.10).

In the female antenna *Obp25* and *Obp55* have considerably higher expression when compared to males. Their expression values in males are approximately 4,800 RPKMs while in females their expression is approximately 36,000, representing a 7.5 fold difference (Table 2.10). Conversely, *Obp35* is male biased. Its expression level in males is 43,654 RPKMs while in females it is only 3,758, representing a 10.85 fold decrease. Other OBPs show similar differences in expression although at lower expression levels or with smaller fold changes. These results indicate that male and females use different OBPs, which bind hydrophilic volatiles and bring them to the ORs in the antenna.

As expected, ORs and IRs are expressed at considerably lower level than most OBPs in the antenna of both sexes. The OR co-receptor, *Or7*, is enriched by 3.84 fold in the female antenna. However, only one IR co-receptor, *Ir25a*, is enhanced in the female antenna (2.55 fold). The transcript level of the other IR co-receptor, *Ir76b*, is similar in male and female antennal tissues. Fifteen ORs have more than 10 fold enrichment in the female antenna, whereas in males there is no enrichment for any ORs.

Three IRs are enriched in the male antenna while 20 IRs are enriched in the female antenna (Table 2.10). Only two GRs were detected in the antenna. *Gr2* is a CO_2 receptor and is expressed at high levels in the palps. Although it is enhanced in the female antenna by 4.79 fold (Table 2.10) it is doubtful that it has a functional role there. The other CO_2 receptor genes are not detected in the antenna of either sex, suggesting that the presence of *Gr2* is not due to contamination of our antennae samples with palp tissue. Along with the absence of enrichment for any OR in the male antenna, our results indicate that several IRs and OBPs in the antenna of males may underlie the detection of different ecologically relevant volatiles.

Finally, the transcripts of a cgmp-dependent protein kinase gene are enriched in male antenna by 6.54 fold (Table 2.10). The orthologs of this gene are associated with foraging behavior in other insect species. Interestingly, 3h and 24h after blood feeding the expression levels of other cgmp-dependent protein kinase gene are enhanced in the HT of females (Table A5), when they are no longer looking for hosts. However, the expression level of AAEL007826, one of the cgmp-dependent protein kinase genes, is reduced from 48h to 72h post blood feeding in the HT. These results suggest that this gene might be involved in mosquito foraging behavior.

Table 2.10 Olfaction genes with significant changes in the antenna of males and females.

Gene ID	Gene Name	Male	Female	Fold	*p* adj.
Enriched in Females					
AAEL016981	*Or36*	0.53	12.23	19.46	0.0000
AAEL017065	*Or92*	0.21	4.28	18.55	0.0000
AAEL017316	*Or107*	0.16	3.53	17.63	0.0000
AAEL017014	*Or105*	1.82	33.69	17.44	0.0000
AAEL017537	*Or123*	0.64	11.63	16.64	0.0000
AAEL017377	*Or117*	0.64	11.72	16.22	0.0000
AAEL017043	*Or84*	24.49	367.48	14.65	0.0000
AAEL017505	*Or103*	4.77	72.29	14.46	0.0000
AAEL017000	*Or97*	0.42	6.69	14.15	0.0000
AAEL017201	*Or94*	1.72	24.91	13.98	0.0000
AAEL017219	*Or114*	1.22	16.01	12.28	0.0000
AAEL017123	*Or113*	9.04	102.03	11.00	0.0000
AAEL011796	*Or62*	1.80	19.09	10.51	0.0000
AAEL013507	*Or52*	1.25	14.07	10.43	0.0000
AAEL014197	*Or88*	6.06	61.91	10.07	0.0000
AAEL017178	*Or111*	5.80	52.94	8.85	0.0000
AAEL017361	*Or115*	1.59	14.53	8.46	0.0000
AAEL016966	*Or104*	4.41	37.58	8.37	0.0000
AAEL017129	*Or72*	1.84	16.13	7.99	0.0000
AAEL011409	*Or100*	8.31	68.82	7.97	0.0000
AAEL012377	*Obp55*	4,416.69	35,491.10	7.92	0.0000
AAEL006176	*Obp27*	5,291.54	39,345.98	7.20	0.0000
AAEL017296	*Or93*	0.44	3.85	7.16	0.0000
AAEL017050	*Or101*	0.60	4.84	7.04	0.0000
AAEL017463	*Or98*	0.56	3.74	6.41	0.0000
AAEL017347	*Or87*	12.04	77.99	6.24	0.0000
AAEL017104	*Or121*	1.94	12.64	6.18	0.0000
AAEL017149	*Or91*	3.64	21.32	5.77	0.0000
AAEL014085	*Ir75k.2*	2.28	13.26	5.73	0.0000
AAEL017495	*Or95*	0.96	5.38	5.44	0.0000
AAEL011583	*Or11*	9.78	56.07	5.43	0.0000
AAEL004218	*Or85*	6.37	34.75	5.41	0.0000
AAEL017370	*Or126*	2.06	12.74	5.34	0.0000
AAEL013563	*Or122*	0.76	4.27	5.31	0.0000
AAEL013893	*Or125*	3.06	15.68	5.06	0.0000
AAEL017143	*Or102*	0.46	2.49	5.02	0.0000
AAEL001617	*Or124*	0.27	1.61	4.97	0.0017
AAEL017009	*Or119*	1.08	5.47	4.93	0.0000
AAEL014270	*Ir40a*	0.48	2.48	4.80	0.0000
AAEL002167	*Gr2*	2.73	13.65	4.79	0.0000
AAEL008368	*Or13*	2.00	8.21	3.91	0.0000
AAEL000066	*Ir41k*	9.09	36.03	3.91	0.0000
AAEL001342	*Or59*	6.12	24.51	3.86	0.0000
AAEL005776	*Or7*	604.69	2,323.57	3.84	0.0000
AAEL002617	*Obp12*	869.08	3,478.15	3.80	0.0001
AAEL000039	*Ir41o*	0.51	1.96	3.67	0.0006
AAEL011499	*Obp47*	515.39	1,971.01	3.66	0.0000

Table 2.10 Continued

Gene ID	Gene Name	Male	Female	Fold	*p* adj.
AAEL015479	*Ir75k.4*	1.63	5.88	3.60	0.0000
AAEL002922	*Ir8a*	13.09	47.25	3.58	0.0000
AAEL011895	*Or48*	0.71	2.59	3.52	0.0000
AAEL017427	*Or96*	2.27	8.15	3.43	0.0005
AAEL010775	*Ir75e.3*	4.71	16.30	3.42	0.0000
AAEL013366	*Ir21a*	0.73	2.54	3.39	0.0000
AAEL006345	*Or39*	1.13	3.77	3.25	0.0004
AAEL009982	*Or12*	3.63	12.31	3.23	0.0009
AAEL002591	*Obp13*	267.32	860.32	3.18	0.0000
AAEL000071	*Obp2*	151.92	491.70	3.09	0.0016
AAEL013423	*Or78*	3.68	11.25	3.07	0.0000
AAEL015566	*Obp62*	442.54	1,268.24	2.86	0.0000
AAEL013153	*Ir31a*	4.24	12.10	2.86	0.0000
AAEL000089	*Ir41n*	22.41	63.15	2.82	0.0000
AAEL000011	*Ir41e*	1.10	3.07	2.76	0.0000
AAEL006454	*Obp1*	2,500.59	6,951.88	2.74	0.0001
AAEL000007	*Ir41a.1*	6.82	18.68	2.71	0.0000
AAEL004343	*Obp19*	2.04	5.94	2.70	0.0228
AAEL000051	*Obp3*	2,322.94	6,299.41	2.65	0.0021
AAEL008442	*Or14*	11.71	31.07	2.64	0.0000
AAEL010662	*Obp43*	1,256.80	3,335.18	2.64	0.0000
AAEL015567	*Obp63*	1,446.10	3,769.70	2.60	0.0000
AAEL010409	*Or30*	2.35	6.13	2.57	0.0001
AAEL017105	*Or106*	2.29	5.98	2.57	0.0012
AAEL009813	*Ir25a*	89.20	228.53	2.55	0.0000
AAEL001510	*Or23*	5.41	13.49	2.47	0.0000
AAEL018198	*Ir75e.2*	6.22	14.76	2.35	0.0017
AAEL013198	*Ir75i*	4.31	10.10	2.32	0.0013
AAEL008448	*Or15*	6.60	15.23	2.29	0.0006
AAEL014087	*Ir75k.3*	5.40	12.20	2.27	0.0000
AAEL006003	*Or10*	10.25	23.55	2.26	0.0030
AAEL010666	*Obp42*	2,568.24	5,816.78	2.25	0.0008
AAEL000095	*Ir41d.3*	12.66	28.23	2.25	0.0000
AAEL010428	*Or26*	8.78	19.58	2.24	0.0000
AAEL014086	*Ir75o*	4.05	9.31	2.24	0.0111
AAEL000047	*Ir41i*	3.43	7.85	2.24	0.0168
AAEL011843	*Or5*	2.10	4.76	2.20	0.0197
AAEL014089	*Ir75k.1*	6.08	13.09	2.14	0.0022
AAEL000628	*Or63*	10.46	22.14	2.12	0.0018
AAEL013420	*Or79*	11.00	23.11	2.10	0.0046
AAEL005999	*Or2*	6.88	14.40	2.10	0.0004
AAEL000048	*Gr4*	2.83	5.94	2.10	0.0246
AAEL010418	*Or27*	9.86	20.57	2.09	0.0050
AAEL015313	*Obp59*	239.29	491.79	2.06	0.0009
	Enriched in Males				
AAEL005770	*Obp21*	14.84	0.50	-22.47	0.0000
AAEL002606	*Obp35*	43,654.92	3,758.14	-10.85	0.0000
AAEL006109	*Obp23*	7.27	0.67	-9.19	0.0000

Table 2.10 Continued

Gene ID	Gene Name	Male	Female	Fold	*p* adj.
AAEL002518	*Irg*	5.31	0.64	-7.01	0.0000
AAEL006106	*Obp26*	22.45	2.89	-6.63	0.0000
AAEL007826	*Forage*	199.41	29.67	-6.54	0.0000
AAEL005772	*Obp22*	153.87	28.24	-4.96	0.0000
AAEL002506	*Irf*	38.95	9.59	-3.89	0.0000
AAEL002587	*Obp11*	809.73	225.52	-3.48	0.0000
AAEL018149	*Irc*	8.96	2.57	-3.25	0.0000
AAEL007603	*Obp10*	1,218.87	403.83	-2.95	0.0000

2.3.6 Sex biased gene expression in the HT

A smaller number of genes are differentially expressed in the HT than in the antenna of males and females. While 1,607 genes display significant changes in the antenna between both sexes, only 1,172 have significant changes in the HT (Table A14). Contrary to what is observed in the antenna, the majority of the genes in the HT are enriched in in females (713 genes) rather than in males (459). In female genes with enrichment higher than 10 fold (56 genes) are involved in the glycine, serine and threonine metabolism among others. In males only 19 genes are enriched more than 10 fold and these are implicated in microtubule motor activity, for example *actin*, and chloride channel activity.

At total of 232 genes are enriched in males HT and have expression levels (below the 1 RPKM) in female HT. Most of these genes have also very low expression levels in males. However, 10 genes have expression levels (higher than 10 RPKMs) in males and can therefore be considered to be expressed exclusively in males (Table 2.11). Similarly, 100 genes enriched in female HT have expression levels below 1 RPKMs in males. Among these genes, only 8 have expression levels above 10 RPKMs in female HT (Table 2.11).

These analyses have identified genes that are mainly expressed in one sex, genes that are enhanced in one sex, and finally a lower number of differentially expressed genes in the HT compared to antenna. It was unexpected since the HT samples include the brain and salivary glands and the gonads.

Table 2.11 Genes with biased expression in male and female HT.

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
		Female biased				
AAEL007394		hypothetical protein	0.27	42.20	16.30	0.0000
AAEL007872		hypothetical protein	0.74	34.66	13.44	0.0000
AAEL009992		hypothetical protein	0.88	26.63	6.99	0.0004
AAEL000733		hydroxysteroid dehydrogenase	0.60	22.57	41.09	0.0000
AAEL006351		hypothetical protein	0.83	22.05	5.16	0.0041
AAEL003585		hypothetical protein	0.27	17.22	24.41	0.0000
AAEL003584		hypothetical protein	0.23	10.69	49.30	0.0000
		Male biased				
AAEL004292		hypothetical protein	56.17	0.44	-6.37	0.0010
AAEL009451		actin	34.34	0.30	-77.46	0.0000
AAEL008304		hypothetical protein	21.02	0.51	-18.98	0.0000
AAEL006824		cytochrome P450	14.15	0.90	-11.21	0.0000
AAEL008855		dynein heavy chain	12.04	0.89	-10.56	0.0000
AAEL000627	CECA	antibacterial peptide	11.33	0.81	-5.41	0.0008
AAEL013043		NADH dehydrogenase	11.25	0.06	-26.78	0.0000
AAEL009577		hypothetical protein	10.29	0.08	-4.88	0.0057
AAEL017987			10.20	0.76	-5.01	0.0022

Six OBPs show significant differences between the HT of 4 days old males and females (Table 2.11). The expression levels of these genes are low compared to those expressed in the antenna (Table 2.9). For example, *Obp55* is also enriched in the female antenna, but its expression levels are approximately 5,300 RPKMs in male antenna and

39,350 RPKMs in female antenna (7.2 fold difference) while in the HT it changes from 1 RPKM in males to 2 RPKMs in females. On the other hand, *Obp18* expression in the antenna is low (about 5 RPKMs in both male and female, data not shown) when compared to HT (41.73 RPMKs in male and 83.01 RPKMs in females) (Table 2.11).

The OBPs enriched in the male HT have low expression levels in the antenna of males and females. *Obp9* expression in the antenna is approximately 1 RPKMs in both sexes and no significant differences are observed. However, in the HT it is enriched in males by 4.11 fold, although also at low expression level (Table 2.11). Finally, *Obp21* is not detected in the female antenna (0.5 RPKMs) but enriched in both male antenna (22.47 fold) (Table 2.11) and male HT (2.92 fold) (Table 2.11). It therefore appears that some OBPs are specifically enriched in one sex or tissue.

Table 2.12 Olfaction genes with significant changes in the HT of 4 days old males and females.

Gene ID	Gene Name	Male	Female	Fold	p adj.
	High in Females				
AAEL002617	*Obp12*	1.98	5.05	2.90	0.0004
AAEL004342	*Obp18*	41.73	83.01	2.43	0.0000
AAEL006176	*Obp27*	0.92	2.86	3.24	0.0017
AAEL012377	*Obp55*	1.01	2.06	2.25	0.0418
	High in Males				
AAEL002596	*Obp9*	2.71	0.39	-4.11	0.0009
AAEL005770	*Obp21*	21.87	5.89	-2.92	0.0000

2.3.7 Multi-factor generalized linear model

A total of 22 genes have significant enhanced expression in the antenna of host seeking females when a multi-factor generalized linear model is used to take into consideration all the factors in the experiment (sex, age and preference) (Figure 2.9). These genes have higher expression in the antenna of females when compared to males, when compared to the HT, and when compared to the antenna of 12h old females (Table A15, Figure 2.10). Interestingly, 17 of these genes are ORs, one is *Obp27* and 4 have unknown functions. One of the genes with unknown function (AAEL018095) is a likely new OR. A protein BLAST search revealed that it has high similarity with ORs from mosquitoes. For two of the other 3 genes with unknown functions, the BLAST did shown some potential function in related species. For example, AAEL014811 probably belongs to the protein family THEM6 since it has several hits for proteins of this family in other insect species. However, AAEL016412 is annotated as a non-coding RNA and is very short (73bp). No significant hits are found for AAEL010242 in other insect species. Nonetheless, it is a secreted protein.

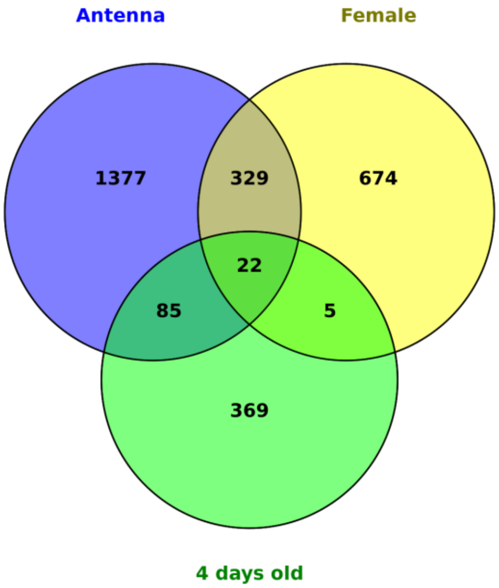

Figure 2.9 Venn diagram of genes enriched in the antenna of host seeking females. A full multi-factor GLM was used to take in consideration the effect of sex, age and preference before performing the contrast between each treatment. To goal was to find genes up-regulated when females look for hosts which also had higher expression in females than in males and enriched in the antenna. Blue: 1,813 genes enriched in the antenna; Yellow: 1,020 genes enriched in females; Green: 481 genes enriched in host seeking females.

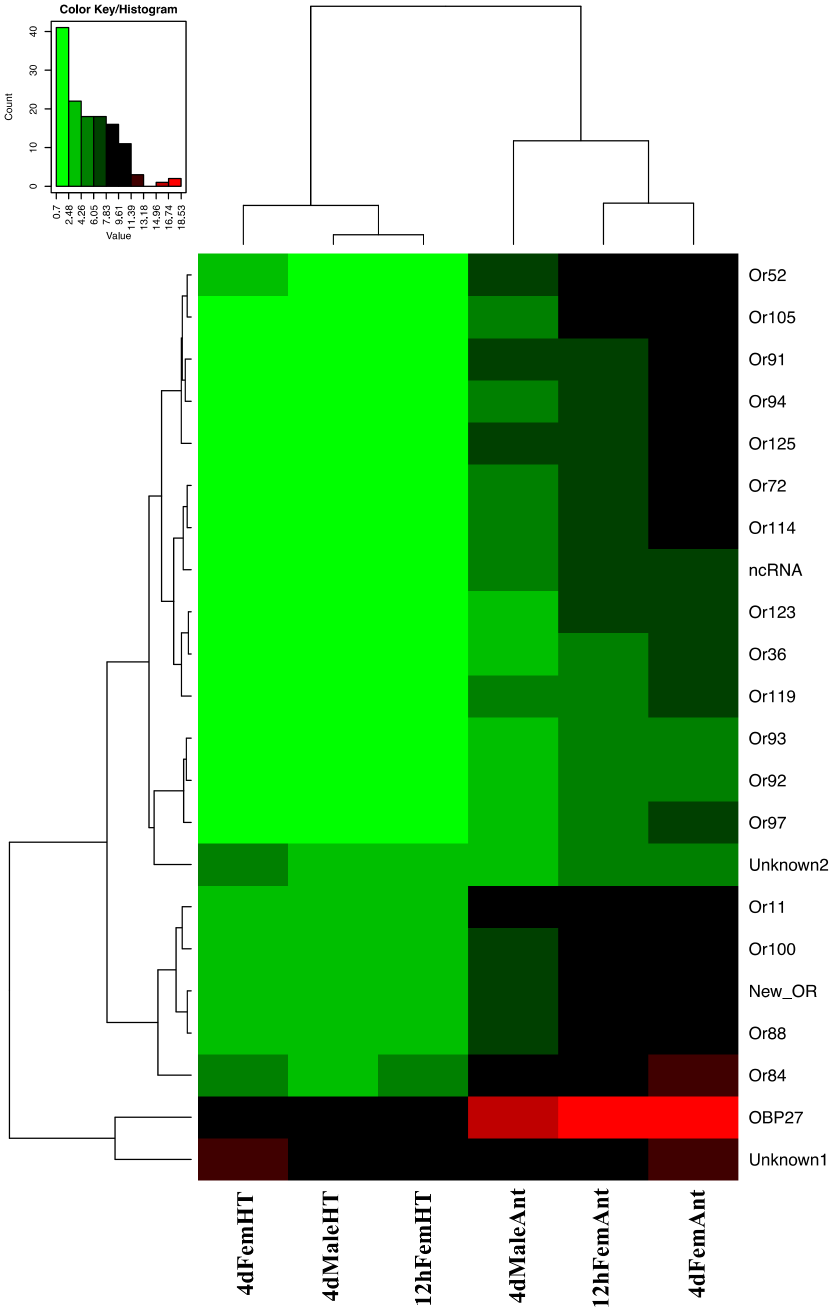

Figure 2.10 Genes enriched in the antenna of host seeking females. A multi-factor GLM to take into consideration the effect of sex, age and preference of mosquitoes. Green indicates low expression levels; black indicates intermediate expression levels; red indicates high expression levels.

A total of 85 genes are enriched in the antenna of mosquitoes when they reach 4 days old (Figure 2.9), however, the majority of these genes are not differentially expressed between males and females. Among these, 12 olfaction genes stand out as being enriched in the antenna of both 4 days old males and females (Figure 2.11). These olfaction genes are therefore not differentially expressed between males and females, but increase their expression as the females start looking for hosts and have enhanced expression levels in the antenna in comparison to the HT.

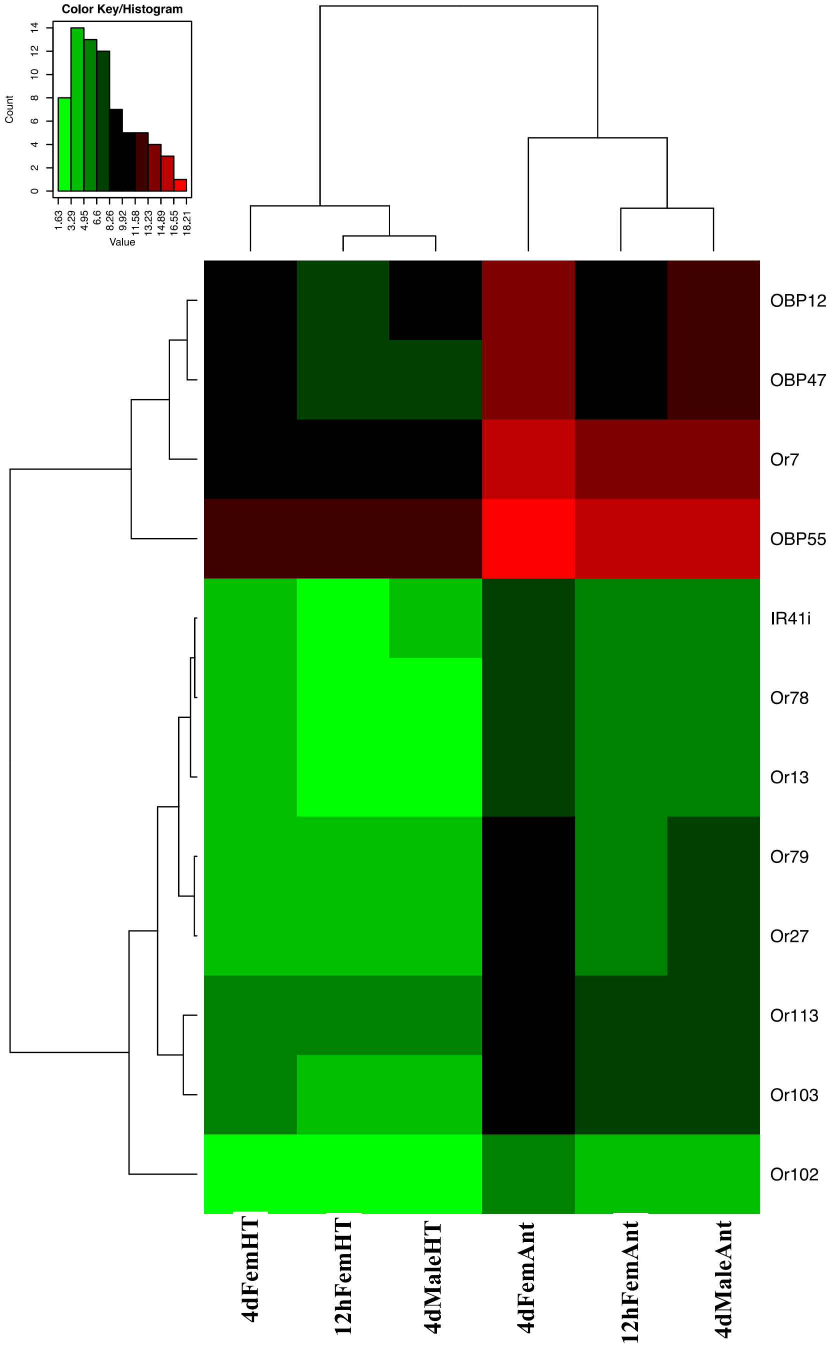

Figure 2.11 Genes enriched in the antenna of both male and females based on a multi-factor GLM. The effect of sex, age and preference of mosquitoes were taken into consideration. Green indicates low expression levels; black indicates intermediate expression levels; red indicates high expression levels.

Among the 85 genes enriched in the antenna of both sexes and when females are host seeking, 8 cytochrome P450, 4 head shock protein and 4 proteases genes stand out. These genes transcripts levels are significant higher in the antenna and enriched in the host seeking females.

Gene ontology analyses of this group of 85 genes revealed an enrichment of genes with molecular functions other than those related to olfaction (Figure 2.12). Most notably, the iron ion, heme and tetrapyrrole binding genes are enriched in the antenna of both male and females, even though males do not blood feed. These genes are potentially involved in the digestion of the blood meal.

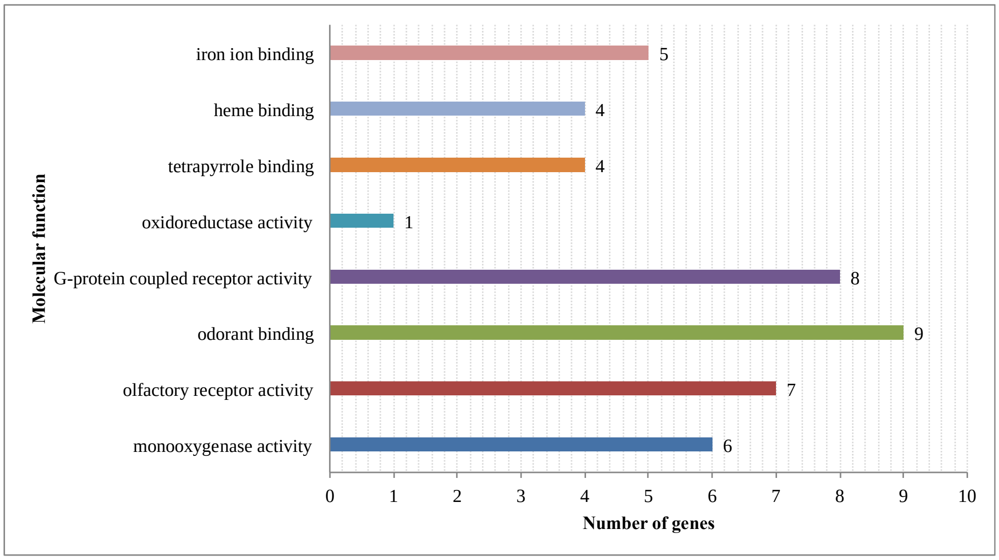

Figure 2.12 Gene ontology analyses of the 85 genes enriched in the antennae of males and females compared to HT and nectar seeking females.

Only 4 genes are enriched in the HT of females when they are host seeking when a multi-factor GLM is used in the analysis (AAEL003585, AAEL007394, AAEL009459 and AAEL017467) (Figure 2.13). These genes are not enriched in the antenna of either male or female and their expression levels are considerably lower in nectar seeking females. The function of these genes is unknown. Although pairwise comparisons revealed a greater number of genes with significant changes between nectar and host seeking females in the HT vs the antennae, the multi-factor GLM shows that a higher number of genes (22 genes) are enriched in the antennae of host seeking females (Figure 2.9) than in the HT of *A. aegypti*.

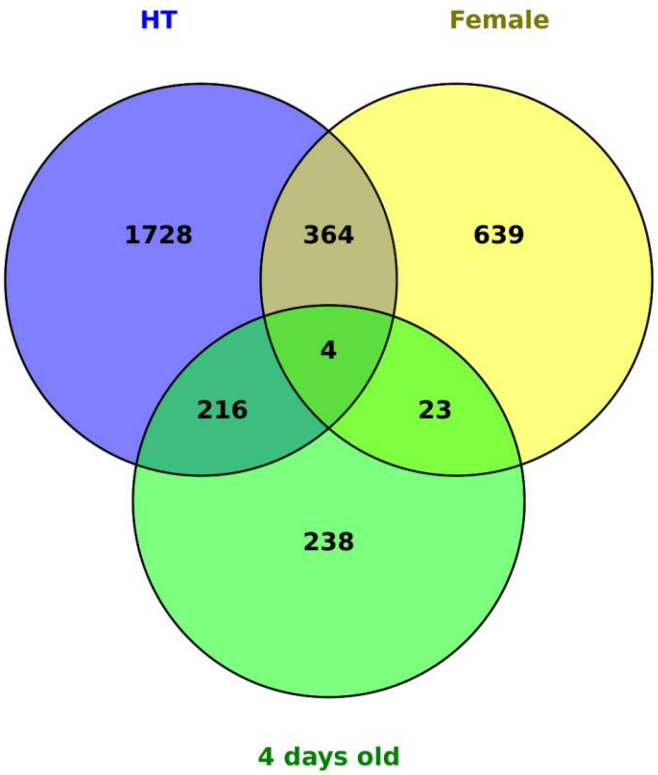

Figure 2.13 Venn diagram with genes enriched in the HT of host seeking females. A full multi-factor GLM was used to take in consideration the effect of sex, age and preference before performing the contrast between each treatment. Blue: 2,312 genes enriched in the HT of both sexes; Yellow: 1,030 genes enriched in females independent of the tissue; Green: 481 genes enriched in host seeking females. Intersection of the 3 circles represents genes that are enriched in the HT of host seeking females.

Another group of genes of interest is those enriched in the antennae of males. The multi-factor GLM analysis revealed a greater number of genes enriched in the male antenna (39 genes) than in females (22 genes) (Figure 2.14).

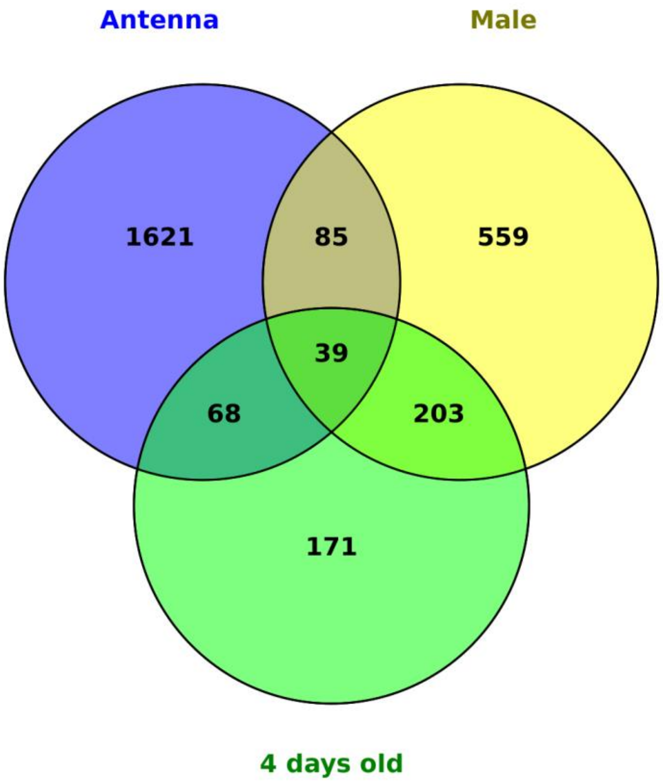

Figure 2.14 Venn diagram with genes enriched in the antenna of 4 days old males. A full multi-factor GLM was used to take in consideration the effect of sex, age and preference before performing the contrast between each treatment. Blue: 1,813 genes enriched in the antenna of both sexes; Yellow: 886 genes enriched in males independent of the tissue; Green: 481 genes enriched at 4 days old (when females are host seeking). Intersection of the 3 circles represents genes that are enriched in the antenna of 4 days old males.

Out of the 39 genes enriched in the antenna of 4 days old males (Figure 2.14), *Or79* stands out as the only olfaction gene. However, the pairwise comparison of the antennal data shows that the transcripts levels of *Or79* are 2 fold higher in females, and only 7 OBPs and 3 IRs are enriched in male antennae. These genes do not display significant changes when the other factors are taken into consideration, mainly because they are also expressed in the HT. This indicates that *Or79*, although it has higher expression in the female antenna, it has considerable expression in the male antennae and pairwise comparisons did not reveal it potential role in males' antenna.

Gene ontology analysis of these 39 genes did not reveal enrichment for any molecular function. However, a few genes do stand out: 3 cytochrome P450 genes (AAEL007816, AAEL0122772 and AAEL014411); 2 heat shock protein genes (AAEL017978 and AAEL013350); and 3 serine protease genes (AAEL003632, AAEL004524 and AAEL007993). Other genes of these gene families are also enriched in the female antennae when they are 4 days old, perhaps suggesting divergence in the detoxification pathways in the antenna of male and females.

Finally, the last group of genes of interest is those that are enriched in the HT of males, but were not detected in female tissues. A total of 138 genes are enriched in the male HT (Figure 2.15) in contrast to only 4 in the HT of females. *Obp18* is the only olfaction related gene to stand out. Gene ontology analyses revealed overrepresentation of genes in 4 molecular function categories (Figure 2.15). Overall, these results indicate great differences in the transcripts identity and levels in both sexes.

Figure 2.15 Venn diagram with genes enriched in the HT of 4 days old males (148 genes in the center). A full multi-factor GLM was used to take in consideration the effect of sex, age and preference before performing the contrast between each treatment. Blue: 2,312 genes enriched in the HT of both sexes; Yellow: 886 genes enriched in males independent of the tissue; Green: 481 genes enriched at 4 days old (when females are host seeking). Intersection of the 3 circles represents genes that are enriched in the HT of 4 days old males.

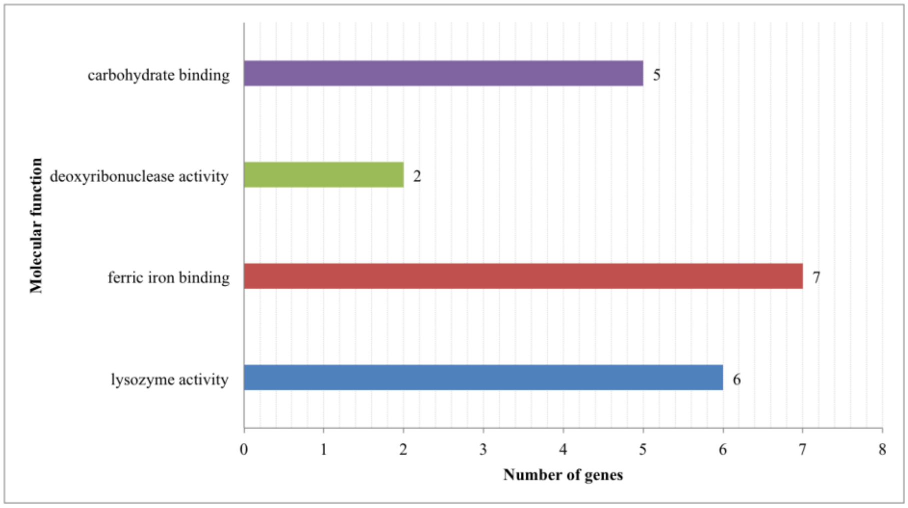

Figure 2.16 Gene ontology analyses of the 138 genes enriched in the HT of 4 days males. Genes from 4 different molecular functions are overrepresented.

2.4 Discussion

Mosquitoes detect odors from the surrounding environment to find food, host, mates and oviposition sites, and to avoid predators and pathogens. Therefore, olfaction is critically important for survival and it is linked to fitness (Cande et al. 2013). The olfaction system has evolved and diversified to fit the various ecological lifestyles of insects. For example, *A. aegypti* may use up to 110 ORs genes to detect an unknown number of volatiles from host, mates, oviposition sites and flowers (Sparks et al. 2015). It has been suggested the insect olfactory system may contain narrowly and broadly tuned ORs, suggesting a hybrid system with dedicated channels and the combinatorial coding model observed in mammals (Andersson et al. 2015). Although, it is not clear which model is predominant in mosquitoes, especially in the case of ORs potentially displaying narrow tuning due to the lack of key ligands which were missed during the screening or the concentration used was too high, it may have remarkable implications in the transcript levels detected by RNAseq experiments and expectations of differential expression as mosquitoes display drastic changes in behavior. For example, the expression levels of broadly tuned receptors may not change after blood feeding since the ORs may be used to detect a variety of volatiles in different ecological contexts. To make this scenario more complex, it was recently discovered that OSNs may express up to four different ORs transcripts besides the co-receptor *Orco*, and even polycistronic mRNA transcripts from two ORs found from gene cluster in the genome of *Anopheles gambiae* (Schultze et al. 2015) is reported. It is not known if the same pattern is observed in *A. aegypti*. However, since there was an expansion in the ORs repertoire of *A. aegypti* (Bohbot et al. 2007a) and several OR genes are found in clusters throughout *A. aegypti* genome, it is possible that these patterns occur in this mosquito as well.

The olfaction genes transcript levels remain quite stable in the antenna of *A. aegypti* after blood feeding, although a few *Obps* show subtle changes in expression before the onset of oviposition. Similar observation was made for *A. gambiae,* where there are no significant changes in the transcript levels of ORs, OBPs and IRs in the antenna of female after blood feeding (Rinker et al. 2013a). Although it could be due to the experimental design and lack of statistical power, other genes display significant changes soon after blood feeding and do have similarly low expression levels, indicating that our analyses has the power to detect fluctuations in transcript levels olfaction receptor genes.

A total of 93 OR expressing neurons are found in the antenna of *A. aegypti* female (Mciver 1972; Mciver and Hutchins.Sa 1972; Mciver 1978; Klowden 1994), which are housed in different types of sensilla, out of around 2,000 neurons in all 13 antennal segments. In my experiments the antenna of approximately 700 females or males were dissected and total RNA was extracted. Since there are two antennae per animal, the total number of OSNs is about 130,200. Surprisingly even when pooling all these samples, changes in the transcript levels of several olfaction genes are detected in the antenna of 12h old and 4 days old females (Table 2.5), even small changes (2 fold) can be observed. Therefore, the power of our experiment was adequate to detect even subtle changes in low expressed genes.

My hypothesis was that due to the specific tuning of olfaction genes, their transcript levels would change after the female has blood fed and switched its behavior from host seeking to oviposition site seeking at 48h post feeding. Additionally, olfaction gene expression might change from their emergence to the moment they start actively searching for human around day 4. For example, the transcript levels of *Or4*, which was recently found to be important to detect a compound present at high levels in human odor (McBride et al. 2014), might change after blood feeding since females would not blood feed if she acquired a full blood meal. However, no changes are observed in the transcript levels of this gene after blood feeding, between males and females, or even between 12h old females and 4 days old females. Differential expression of this gene was observed between a domestic and a forest strain, which were anthropophilic and zoophilic, respectively (McBride et al. 2014). It is believed that *Or4* may be important for the specialization of *A. aegypti* to feed on humans.

Why does the expression of such important gene not change between 12h old and 4 days old females, between males and females, or after blood feeding? It would be reasonable to assume that because this OR is used to detect a specific human odor (sulcatone), its transcript levels would fluctuate as the female's requirement for detecting humans change. However, the results found here, showing constant expression levels, indicate the opposite. Perhaps this is partially explained by the fact that outside the laboratory setup where the day biting *A. aegypti* females do not often have a change to acquire a full blood meal in a single feeding and therefore may have to feed several times before the host seeking behavior is suppressed. In such a situation it may be beneficial to maintain a constant transcript level, as females have to be able to find hosts even after acquiring a small blood meal. In the laboratory conditions used in my experiments, females had a change to acquire a full blood meal and therefore host seeking was suppressed right away. It may be possible that a gene regulation mechanism exists where a constant expression of such ORs is guaranteed. Another possibility is that ORs involved in human host preference are broadly tuned and can detect different volatiles, which were not used in the screening tests that have been carried out so far.

The olfaction gene expression data available so far from both malaria and dengue mosquitoes indicate no significant changes in the olfaction gene expression when females switch from host seeking to oviposition site seeking. Although, the current knowledge about olfaction receptor tuning is limited, it suggests that broad tuning may be more common than previously thought. Another possibility is the even if dedicated channels exist to detect specific volatiles from different ecological context, there are no changes in the transcript levels of olfaction genes, but rather what might change is how the information is processed in the antennal lobe. This might allow more flexibility in the mosquito behavior and the cost of maintaining a constant expression of the generally lowly expressed receptor genes may be small.

The unexpected presence of polycistronic mRNA of clustered ORs in the antenna of *A. gambiae* females indicate how little we know about the expression of olfaction genes in sensory neurons (Schultze et al. 2015). Clustered OR gene organization also occurs in *A. aegypti* (Bohbot et al. 2007a) and it is not known if the same mechanism of gene expression occurs in this species. Similar observations were made in a gustatory receptor gene cluster for the fruit fly, *Drosophila melanogaster* (Slone et al. 2007). The sugar receptors of the fly, DmGR64a and GR64f are co-expressed in sensory neurons and RT-PCR experiments indicate that a total of six GRs genes are transcribed in a polycistronic mRNA molecule. Furthermore, two types of polycistronic mRNA molecules were observed from *A. gambiae* OR cluster 1b in different OSNs (Schultze et al. 2015). A sub-population of neurons has polycistronic mRNA molecules compromised of four ORs where other sub-population the mRNA is comprised of six ORs. Ultimately, this observation indicates that these ORs may be broadly tuned since they are expression pattern is very similar. Otherwise they may be used to detect a similar range of odors. This is observed in mice where the bitter sensing neurons express multiple T2R receptors types (Chandrashekar et al. 2000). As a result the taste cells detect a wide range of compounds without being limited to a specific ligand. Finally, the presence of polycistronic mRNA molecules in sensing neurons suggest that these genes have same expression levels and no significant changes should be observed in RNAseq experiments. It also suggests that these antennal neurons with multiple receptors act as “general” sensors of volatiles in the first phases of host seeking or oviposition site seeking. Narrowly tuned ORs may be important discriminating the most suitable hosts. Nonetheless, if they exist in *A. aegypti* their transcript levels do not change after blood feeding, or in the case of *Or4* not even between 12h females which do not host seek and 4 days old host seeking females.

The dengue fever mosquito, *A. aegypti*, exhibits sexually dimorphic behavior that might contribute to the transmission of dengue and other arboviruses. Unfortunately, knowledge about gene expression, neuronal structure, and the developmental genetic basis is very limited, especially in the adult stage. Recently, a studied using custom microarrays examined global gene expression in the head of 24h old pupae (Tomchaney et al. 2014), a time point which is critical for nervous system development including the antennal lobe. Similar to what is observed between male and female adult tissues in our study, a total of 2,527 transcripts were differentially expressed between both sexes. Some of the changes in gene expression at the adult stage may be a consequence of or resemble the effects of transcription factors action during the nervous system development during the pupal stage. For example, male and female *doublesex* (*dsx*) splice variants were identified in *A. aegypti* (Salvemini et al. 2011) and they display dimorphic expression patterns in the antennal love and mushroom body (Tomchaney et al. 2014). Furthermore, *dsx* is more widely expressed in the brain of *A. aegypti* pupa than in *D. melanogaster* pupae, indicating it may have a prominent role in the regulation of sex specific neuronal development in *A. aegypti*. A total of 732 *dsx* binding sites were found in the genome of *A. aegypti* (Tomchaney et al. 2014) and are associated with genes whose predicted function is associated with neuronal development or neuronal processes, and especially sensory system. Moreover, a total of 48 binding sites are associated with genes that are differentially expressed between males and females, which is an indication that this transcription factor might influence the development of sensory system in males and females differentially.

The differences in gene expression in the antenna of males and females are remarkable (1,607 differentially expressed genes, Table A11). Not surprisingly the majority of genes have higher transcripts levels in the male antenna supporting the hypothesis that *dsx* is a regulator of sexually dimorphic gene expression in the *A. aegypti* nervous system (Tomchaney et al. 2014). Furthermore, 387 genes are exclusively expressed in male antenna (Table A12), while only 118 are exclusive to the female antenna (Table A13). However, out of 102 olfaction genes displaying significant changes in their transcript levels between male and female antenna, 107 are female biased. All ORs have higher expression in the antenna of females (Table 2.10). This is particularly interesting since the number of OR sensing neurons are quite similar between males and females in *A. aegypti* (Klowden 1990; Klowden 1994). Taken together these results indicate that *dsx* may have a limited effect on the olfaction system at the transcription level of genes involved in host seeking behavior, even though there may be differences in the neuronal wiring between males and females.

The number of transcripts differentially expressed between sexes in the antenna is higher than in the HT, where the brain with the antennal lobe and the salivary glands are located. While in the antenna 1,607 genes have significant differences between males and females, only 1,172 are differentially expressed in the HT. Besides, the number of genes with higher expression in the HT of females is higher than in males, 713 vs. 56, respectively. This is the opposite of what is observed in the antenna. The total number of neurons in the antenna of females is 3x higher than in males, and therefore one might expect higher transcripts levels for genes primarily expressed in neurons. In the HT the trend is inverted and females have the more genes with higher transcript levels. Our data indicates different expression patterns for hundreds of genes in the antenna and HT.

The antenna of *A. aegypti* males house olfactory sensilla only in the two terminal segments while they are present in all segments in the female antenna (Duman-Scheel and Syed 2015). Besides, the most common type of sensilla in the antenna that house ORs, the trichodea sensilla, is four times more abundant in the female antenna. The sensilla that house IRs, the grooved pegs sensilla, are two times more abundant in females. There is a clear correlation between the number of sensilla and the expression level of olfaction genes in females. However, the global gene expression shows an opposite picture, with most genes having a higher expression in males rather than in females. During the development in the pupa head, 180 transcripts are up-regulated in males and 201 up-regulated in females (Tomchaney et al. 2014). Therefore, a similar pattern is observed in our HT samples, but this pattern is inverted in the antenna. This is the first report about such expression pattern inversion and it is unknown why it is present.

The differences in mapping success observed between the antennal samples and the HT could be due to two factors. First, it could be due to the number of individuals used to obtain the RNA used to prepare the sequencing libraries. On average the antennal samples came from 700 individuals, while the HT samples came from 10 individuals. Therefore, one could expect that the reads obtained from a pool with more individuals could have a higher probability to match the reference genome. The reference genome sequence comes from DNA of newly hatched larvae of strain LVP^{ib12} that was derived after 12 consecutive generations of single pairing breeding of the LVP^{sbm} substrain (Nene et al. 2007). Second, the higher mapping rate observed with the antennal samples could be due the nature of the genes that are expressed in the HT (includes brain and salivary glands) or the presence of a higher number of ribosomal RNA. It could be that the genes expressed in the HT have more isoforms that have not been annotated, or come from regions that are not present in the current version of the genome, since it has almost 5,000 supercontigs. Interestingly, the higher intergenic mapping observed in the antenna did not result in a higher number of new genes discovered with the assisted assembly.

Mosquitoes, flies, nematodes, rodents, and humans are able to detect CO_2 in in their environment (Taylor and Cummins 2011). Two gustatory receptors are used by *Drosophila melanogaster* to detect CO_2: *Gr63a* and *Gr21a* (Jones et al. 2007). The long-term exposure to CO_2 results in changes in transcription rate of several genes, such as stress hormone genes that can ultimately change the expression of several hundred genes (Taylor and Cummins 2011). Interestingly, even a short time exposure seems to affect the expression of a couple olfaction genes in *A. aegypti.* The mosquitoes I used in my experiments were exposed to CO_2 concentrations up to 1,500 ppm, which is 3x higher than what they experience in nature. The effects of short term CO_2 exposure are stronger in young females, and impact the expression of one *A. aegypti* CO_2 receptor (*Gr1,* not *Gr2* or *Gr3*). For example, the expression levels of 21 olfaction genes increase in the antenna of 12h old females exposed less than 15 min to 1,500 ppm of CO_2 (Table A16). At the same time a gustatory receptor, *Gr20,* is up regulated and the expression of the CO2 receptors is not altered. However, in 4 days old females the effect on *Gr20* is not present and the CO_2 receptor, *Gr1,* is down regulated (-2.25 fold). The total number differentially expressed genes in the antenna of 4 days old female is decrease when compared to the 12h old females. Even though the expression of some olfaction genes was different between the samples exposed to CO_2 and those that were not, the global gene expression did not change the general interpretation of results.

Contamination of the antennae sample was also ruled out since the global gene expression did not change between the samples where mosquitoes were check for missing body parts and those from the time series experiments. Only 4 olfaction genes show significant changes between these samples.

Thousands of genes change expression between 12h and 4 day 4, when females switch from nectar seeking to host-seeking behavior. On the other hand, only a few hundred genes are differentially expressed after a blood meal, when females switch to oviposition site seeking. This could indicate that the changes in behavior are neurological and not tied to gene expression itself. Where the transcript levels of olfaction genes may not change but the sensitivity of the receptors or how the information is processed in the antennal lobe or higher brain areas is altered. Similar results have been observed in the malaria mosquito, *Anopheles gambiae* (Pitts et al. 2011; Rinker et al. 2013a; Rinker et al. 2013b; Hodges et al. 2014; Pitts et al. 2014). Electrophysiological recordings of sensory neurons housed in the sensilla trichodea of *A. aegypti* show no changes in response to blood feeding (Siju et al. 2010). Not surprisingly, there is a biased expression of olfaction genes in the antenna of both males and females. Gene ontology of the genes that are exclusively enhanced in the antenna of females revealed an overrepresentation of genes with molecular function related to olfaction. However, in males there are fewer genes with olfaction related molecular function. However, there are olfaction genes with similar expression patterns in the antenna both males and females (Figure 2.8 and Figure 2.13). Finally, gene ontology of the genes revealed that genes with oxireductase activity are overrepresented in the males' antenna. Oxidoreductase enzymes can play important roles in both aerobic and anaerobic metabolism, but it is not clear why there are so many transcripts of genes with these functions in the male antenna.

The expression of olfaction genes in the antenna of females is higher than in males (Table 2.10). All the ORs are more expressed in the female antenna (except those with no differential expression). Interestingly, the number of sensory neurons believed to house OR genes is very similar in males and females (91 in males and 93 in females) (Klowden 1994). Besides, only 3 ORs are expressed in the maxillary palpi (Bohbot et al. 2014), no odorant receptor is expressed the tarsi of *A. aegypti*, and 10 ORs are expressed in the proboscis (Sparks et al. 2014). However, not only ORs have higher expression levels in the antenna of females, but also several other genes including IRs, OBPs, and GRs. As expected, the co-receptor *Or7* has higher expression in the female antennae. It could be that the female antenna house more olfaction sensing neurons than previously reported. Females have approximately 1,550 more neurons in their antenna than males. Electrophysiological recordings of *A. gambaie* antenna revealed that females responded to volatiles contained in larval breeding site water at considerably lower threshold than males (Blackwell and Johnson 2000). Therefore, the differences in gene expression profiles are most likely functionally relevant and are an indication of male and female chemosensory abilities. However, ultimately, the OR expression patterns between males and females support the speculation that male and female share a similar range of odor coding (Pitts et al. 2011). Similar to what is observed in the antenna of *A. gambiae* the expression levels of ORs in females are considerably higher, indicating an enhancement for odor sensitivity. By contrast, the antenna of *A. gambiae* males is enriched with transcripts associated with hearing (Rinker et al. 2013a; Rinker et al. 2013b). Male mosquitoes are more specialized in audition since they need to find females based on their wing beat frequencies. Females seem to be more specialized to detect odors from hosts.

The time series analyses and the assisted assembly revealed new genes with a potential role in olfaction. What is different from previous identification work is that I did not use homology search, but instead the expression levels. All the genes that have been indicated as potential olfaction genes have similar expression patters of the known olfaction genes. Probably they were not identified before because of high sequence divergence. *A. aegypti* has more olfaction genes than any other mosquito and *D. melanogaster*.

There are no reports about differential exon usage of olfaction genes in mosquitoes. Even the OR co-receptor, *Or7,* was found to have specific isoforms for males and females. It will be interesting to verify these results with molecular techniques, for example immunohistochemistry. There are also olfaction genes with specific isoforms that are expressed in nectar-seeking or host-seeking. Therefore, gene expression studies should also take in consideration the different isoforms of the olfaction genes. Depending on which exons are differentially expressed for a particular gene, the RPKMs values can be very different. For example, the RPKMs values or the normalized number of reads that map to a gene will be lower if two exons are not expressed in a specific tissue.

Although the gene expression differences between the antenna of 12h old and 4 days old females cannot be linked to the initiation of host-seeking at 4 days, my data did show that most olfaction genes increase their expression considerably as the female seek hosts. There no other reports about gene expression in young adult mosquitoes. Since *A. aegypti* females supposedly look for nectar for their entire life cycle (Martinez-Ibarra et al. 1997) and 12h old females already sugar feed in laboratory conditions, these changes in olfaction gene expression may be essential for females to successfully find hosts.

Finally, not unexpectedly, the expression profiles of the four families of olfaction genes in the HT and antenna of *A. aegypti* are quite different from its proboscis, legs (Sparks et al. 2014) and maxillary palps (Bohbot et al. 2014). This indicates a high degree of tissue specialization in mosquitoes, where maxillary palp has not only chemosensory abilities, but also thermo and mechanosensory abilities. Most of GR transcripts are expressed in the maxillary palp and proboscis. Not all IRs transcripts are enriched in the antenna however. Some IRs are enriched in legs, proboscis, maxillary palp or even the HT. This indicates that IRs may be involved in detection of not only exogenous signals, but also in changes in *A. aegypti* physiology.

The steady levels of olfaction genes transcripts in the antenna of *A. aegypti* and *A. gambiae* (Rinker et al. 2013a; Rinker et al. 2013b) indicate that the hypothesis tested was not true. No significant changes in the olfaction gene expression occur when females switch from host to oviposition site seeking. It suggests that broadly tuning may be more common than previously thought. Another possibility is that even if dedicated channels to detect specific volatiles from different ecological context exist, changes in the transcript levels of olfaction genes may be subtle or at a level other than mRNA.

CHAPTER III

MIR EXPRESSION IN *AEDES AEGYPTI* ACCOMPANYING BEHAVIORAL CHANGES

3.1 Introduction

In the previous chapter, I investigated hypotheses regarding the tuning of olfactory gene expression. However, there are other levels of regulation of a gene beyond mRNA. Transcriptional initiation depends on both *cis*-regulatory and *trans*-acting factors that regulate the recruitment of the transcriptional machinery to the promoter regions of specific genes. In addition, a second mechanism that regulates RNA levels in the cytoplasm involves *trans*-acting factors acting on the messenger RNA (mRNA) to stall the translation of the protein, if the protein encoded by a gene is no longer necessary. For example, 3’ end cleavage can result in mRNA decay (Beckwith and Yanovsky 2014). Therefore, while mRNA effects were not observed, it remains possible that variation in olfaction occurs at other levels of gene expression control.

Due to these multiple levels of control, gene expression profiles of insects are complex phenotypic measurements; however they can be used to predict behavior (Loohuis et al. 2012; McBride et al. 2014) and to evaluate their phenotypic plasticity (Loya et al. 2009). Gene expression profiles can be used to develop techniques for behavioral manipulation and to test hypotheses focused on the adaptation of organisms to certain conditions (Rittschof and Robinson 2014). For example, some mosquito species are known to primarily blood feed on humans and it is hypothesized that this trait is genetically and transcriptionally controlled. The evolution of preference for human odor has recently been linked to an increased expression of an odorant receptor (*AaegOr4*) in the yellow fever mosquito *A. aegypti* (McBride et al. 2014). This receptor recognizes compounds found in high levels in the odor of humans. Complex traits such as mosquito attraction to humans presumably involves numerous genes whose expression levels need to be tuned according to the insect's age, sex, tissue and physiological status, as well as external conditions. Changes in the environment or diets (i.e. mosquitoes feeding on nectar and human blood) are stressful and not always predictable events that organisms will encounter during their life cycle. To cope with the fluctuating conditions, organisms not only have to stop the transcription of genes that are no longer suitable for the new conditions, but also stop the translation of mRNA that is already in the cytosol.

More than four decades ago it was hypothesized that intergenic genomic regions have an important role in gene regulatory patterns (Britten and Davidson 1969; Britten and Davidson 1971; Romero et al. 2012). We now know that these regions encode genes that are not translated into proteins. Furthermore, newly discovered genes that do not code for proteins can be encoded within introns of known protein coding genes. These genes can encode a form of functional single stranded RNA, which is typically between 20 to 25 nucleotides long. It is thought that these molecules, named microRNAs (miRs), regulate the expression of other genes by either inhibiting translation or by degrading mRNAs transcripts (Jacquier 2009). As an indication of the importance of gene regulation, one of the largest studies of gene expression evolution in mammals

(Brawand et al. 2011) found that adaptation frequently involves intrinsic regulatory changes, rather than changes in the coding region of the genes.

MiRs are a class of small (~22 nucleotides), non-coding RNAs that typically bind to the 3' untranslated regions (UTR) of their target mRNA, preventing its translation into protein (Lai 2003; Wilkie et al. 2003; Bartel 2004; Baskerville and Bartel 2005; Yang et al. 2005; Kim and Nam 2006; Wang and Li 2009). Mature miRs are the product of a complex biogenesis process (Carrington and Ambros 2003; Liu et al. 2008; Krol et al. 2010; Berezikov 2011; Campo-Paysaa et al. 2011; Griffiths-Jones et al. 2011). One or more mature miRs can be encoded in primary miR transcripts (pri-miR), and are transcribed by RNA Polymerase II (Poli II). They are capped and polyadenylated as any other transcript processed by Poli II. Some miRs in *Drosophila* were found to be within the introns of protein coding genes, and are called mirtrons (Chung et al. 2011). In the nucleus, the pre-miR are cleaved into stem-loop structures of approximately 70 nucleotides in length by an enzyme called Drosha. Drosha is an RNA III endo-nuclease found in a protein complex called Microprocessor complex (Lee et al. 2003). The hairpin structures, known as miR precursors, are exported from nucleus to the cytoplasm by enzymes called karyopherin exportin 5 (Kohler and Hurt 2007). Mature miRs can be imported to the nucleus by importin 8, where they can regulate their own transcription or other genes' transcription (Wei et al. 2014). The miR precursors are then cleaved by a second RNA III endonuclease called Dicer. Pri miR precursors are cleaved into mature RNA duplexes of 21 to 25 nucleotides with 3' overhangs (Gregory et al. 2004). After Dicer cleavage, the mature single strand of a miR is incorporated in the RNA-induced silencing complex (RISC). Argonaute proteins that are the core proteins of RISC recognizing the miRs' 3' overhangs of the now single stranded miRs. A very few number of miRs have both strands loaded into the RISC, most of the time only one strand is loaded (the guide or star strand) and the other strand is degraded (the passenger strand). If both strands are loaded into the RISC, they will normally have different targets (Okamura et al. 2008). miRs appear to be involved in the regulation of all aspects of eukaryotic biology. It is now estimated that as many of 30-50% of human genes are controlled by miRs (Inui et al. 2010). An interesting, and potentially useful feature of miRs appears to be that a single or very few miRs can control the expression of many protein-coding genes underlying a phonotypical trait (Yang et al., 2005). For example, in human cell lines injection of miR-124 and miR-1 led to changes in the expression profile of up to 100 genes associated with brain and muscle cells, respectively (Mattick and Makunin 2005). In *Drosophila melanogaster*, the silencing of a single miR has been associated with the development of CO_2 olfactory neurons in the maxillary palpi (Cayirlioglu et al. 2008). Additionally, in the malaria mosquito *A. gambiae* the expression levels of only four miRs changed after infection with *Plasmodium* spp. (Xue et al. 2008), while several hundreds of protein coding transcripts are differentially expressed. Therefore, miRs could be important targets for vector control efforts targeting the interaction of the pathogens and their hosts. The far reaching effects of single miRs opens up the possibility of using these molecules to affect complex traits and the development of miR-based gene therapy for cancers and other disease. Not much is known about the role of miRs in *A. aegypti*. Aae-miR-275 is necessary for blood meal digestion (Bryant et al. 2010), while over 20 miRs are differentially expressed after infection of mosquitoes or cell lines with Dengue virus (Campbell et al. 2014). *Wolbachia* bacteria also uses miRs to interfere with the mosquito physiology and possibly its behavior, suppressing Dengue virus replication (Zhang et al. 2013). It still unknown if miRs can regulate genes thought to be important in mosquito attraction to humans.

To elucidate the dynamical role of miRs in the regulation of gene expression in the antenna of *A. aegypti*, I analyzed miRs expression in several tissues in a time-series manner both from male and female mosquitoes. I characterized miRs expression and identified new miRs. I hypothesized that miRs are more important than mRNA in regulating olfactory responses in host and oviposition site-seeking mosquitoes.

3.2 Material and methods

The experimental design, mosquito rearing, tissue collection, RNA extractions and quality control of sequencing data were performed as described in chapter 2, with the exception that small RNAs from the head and thorax of 12h old females were not included in this study. Three biological replicates were used for antennal samples, except for males and 12h old females, which had 2 biological replicates. Two biological replicates were used for head and thorax samples. Small RNA libraries were constructed using TruSeq Small RNA sample prep (Illumina) from the antenna of host-seeking females and post-blood feeding (4 days old unfed females, +3h, +24h, +48h, and +72h post blood feeding) at the DNA Sequencing and Genomics Facility of University of

Utah. The remaining samples (head and thorax samples, antenna of 12h old females and 4 days old males) were prepped and sequenced at Texas A&M AgriLife Genomics and Bioinformatics Service at College Station. Each sample was barcoded and 5 samples were sequenced per lane on a HiSeq 2000 (Illumina) for 50 cycles generating approximately 30 to 40 million reads (1.5 to 2 billion bases).

The available miRs from miRBase (release 20) (Griffiths-Jones et al. 2006; Enright and Griffiths-Jones 2008) were used to annotate the known *A. aegypti* miRs and quantify the expression.

Expression values of known *A. aegypti* miRs were calculated using the CLC Workbench software (CLC Genomics workbench-Qiagen, Aarhus, Denmark). Sequences were trimmed and adapters removed prior to analyses. After trimming by sequence quality (Phred score > 30) samples were filtered by size (>17bp). Differential expression analyses of known miRs were performed using DESeq (Love et al. 2014). Only reads that perfectly match the mature region of known miRs were included in the statistical analyses. Trimmed reads with a high quality score and mapped to other regions of the genome (between 18 to 25 nucleotides) could be potential new miRs, and were later used for miR discovery.

3.2.1 Sample clustering

The first step in my statistical analyses was to verify all sample clusters using the miRs expression levels obtained from CLC genomics workbench (perfect matches at the mature miR region). I entered the read count data in R and used DESeq2 to calculate normalized read counts taking into account the libraries' size. The variant stabilizing data generated by DESeq2 was used to calculate the correlation factors between all the samples using the Pearson correlation function available in R.

Another way to assess the overall similarity between the samples is to calculate the Euclidean distance between the samples. To avoid that genes with high variance dominate the clustering, the rlog data was used for clustering.

I used Venn diagrams or a generalized linear model (GLM) to obtain miRs that are "uniquely" expressed in the antenna or HT of males or females. The idea is to block the effect of tissue or sex. For example, which miRs are enriched in the female antenna (comparison between male and female antennal samples) but also enhanced in the antenna (comparison between female tissues – antenna vesus HT). miRs that are differentially expressed in a tissue comparison between males and females, but also enhanced in one tissue are designated as "uniquely expressed". Using a Venn diagram is a straightforward method, but the similar result can be obtained using a complex GLM model.

3.3 Results

3.3.1 Quality control

A total of 706,153,392 reads were generated for this experiment. After adapter removal and trimming by quality score was performed, 636,911,077 reads were kept

(92.29%) with an average length of 26.4bp (Table A17 and Table A18). Only a small number of reads were discarded after quality control (Table A19).

3.3.2 Annotation of known miRs

All the 121 miRs known miRs of *A. aegypti* were detected in our samples. The overall percentage of unannotated reads is higher in HT samples, but also in 12hAnt samples (Table A19). I also observed differences in the annotation success of reads generated in different sequencing facilities. For example, samples sequenced at the University of Utah sequencing facility have lower percentage of unannotated reads (Table A19) and considerably higher number of reads that perfectly match known *A. aegypti* miRs (5' mature, usually the guide strand).

3.2.3 Clustering of samples using known miRs expression levels

The clustering analyses revealed a striking pattern among the samples showing that the antennal expression of miRs is different from HT (Figure 3.1 and Figure 3.2). Samples from the antenna and HT form two different clusters. PCA analyses also produced similar results (Figure 3.3). While the samples from HT of females form a tight cluster (see top right cluster on Figure 3.3), the antennal samples did not cluster as well, displaying more biological variance within the treatments. The samples from the antenna of 12h old females and males fall between the HT samples and remaining samples, while the samples from male HT are different from all the other samples

(Figure 3.3). Finally, the effect of normalization by library size can be visualized comparing Figures 3.1 and Figure 3.2.

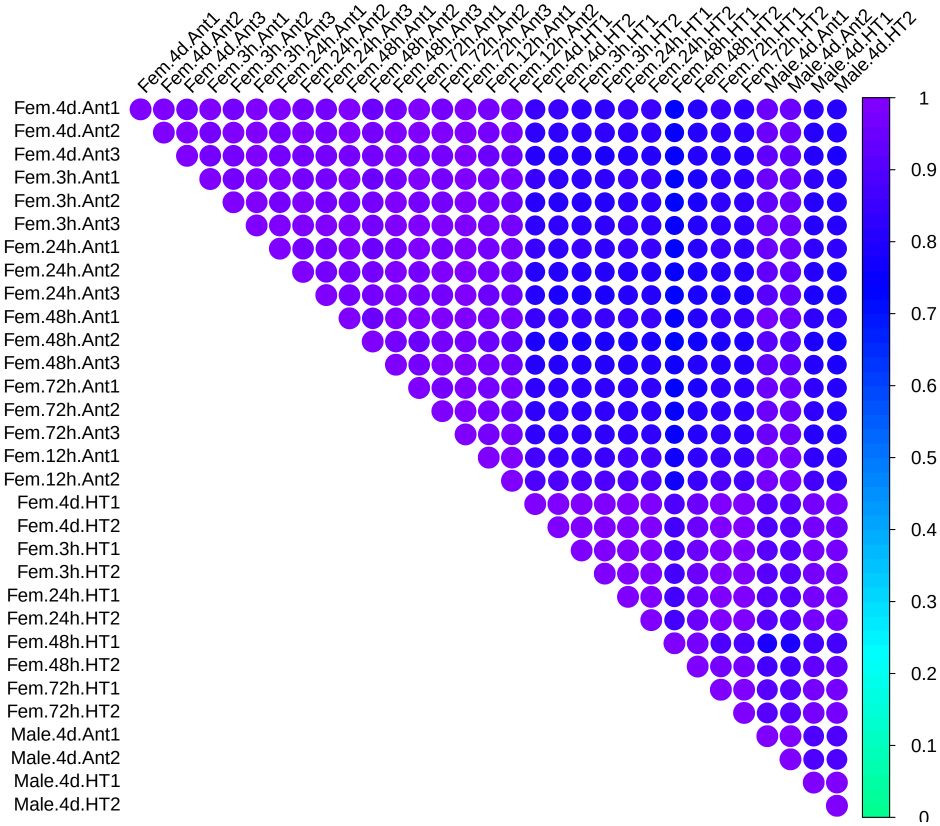

Figure 3.1 Pearson correlations of the miR samples. The variant stabilizing data from DESeq2 of the read counts from DESeq2 was used to calculate the correlation among all the samples. The read count for all 121 known miRs was used to calculate the correlations.

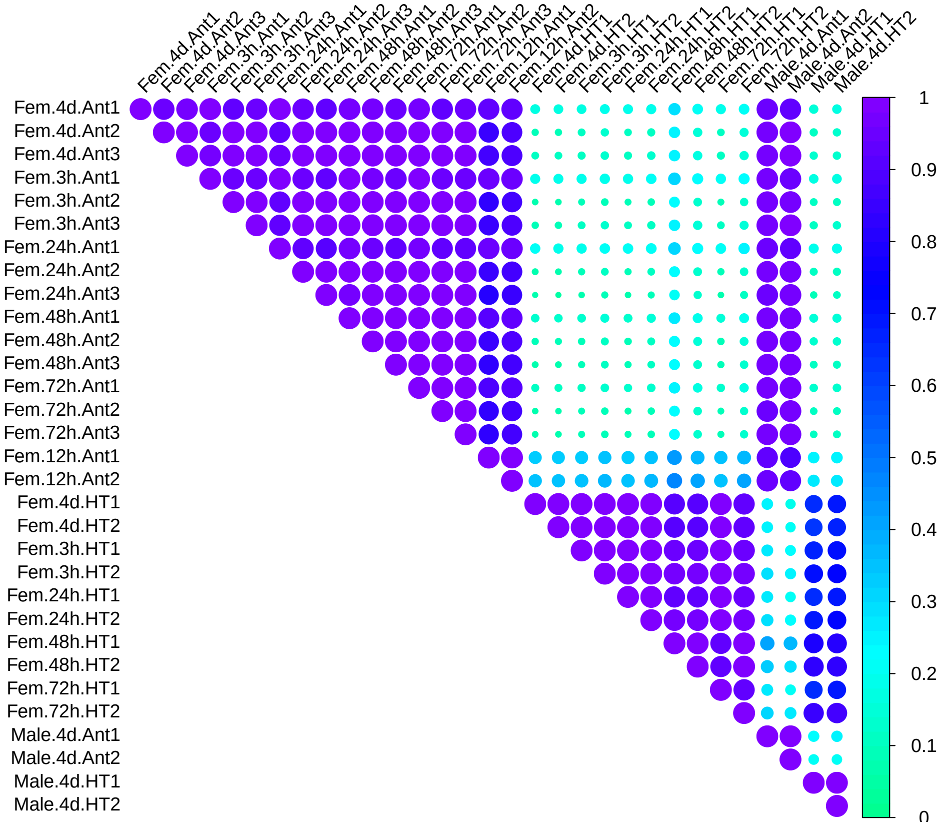

Figure 3.2 Pearson correlation of normalized reads counts (values multiplied by the size factor of each library) of miR expressed in the antenna and head and thorax of *A. aegypti*.

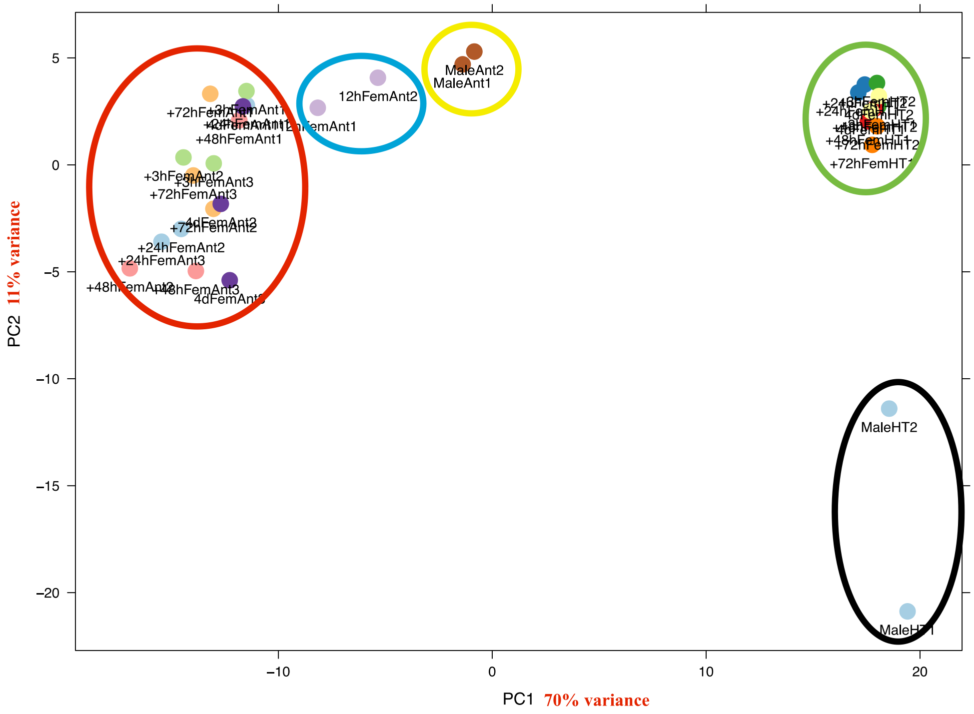

Figure 3.3 Principal component analyses plots using the variant stabilizing data. Red circle: unfed and blood-fed female antenna; blue: 12h old female antenna; yellow: male antenna; green: female head and thorax samples; black: male head and thorax samples.

3.2.4 Hierarchical clustering of the samples

When I calculated the Euclidean distance between the samples with the R function *dist*, I obtained a similar result to the Pearson correlation and PCA analyses (Figure 3.4). It indicates the unique expression pattern of miRs expressed in the antenna of either males or females compared to the HT samples. Again, the male antenna and the 12hAnt samples are different from the remaining antennal samples. Overall, there was little differences in the expression of miRs in the antenna of *A. aegypti* before and after blood feeding.

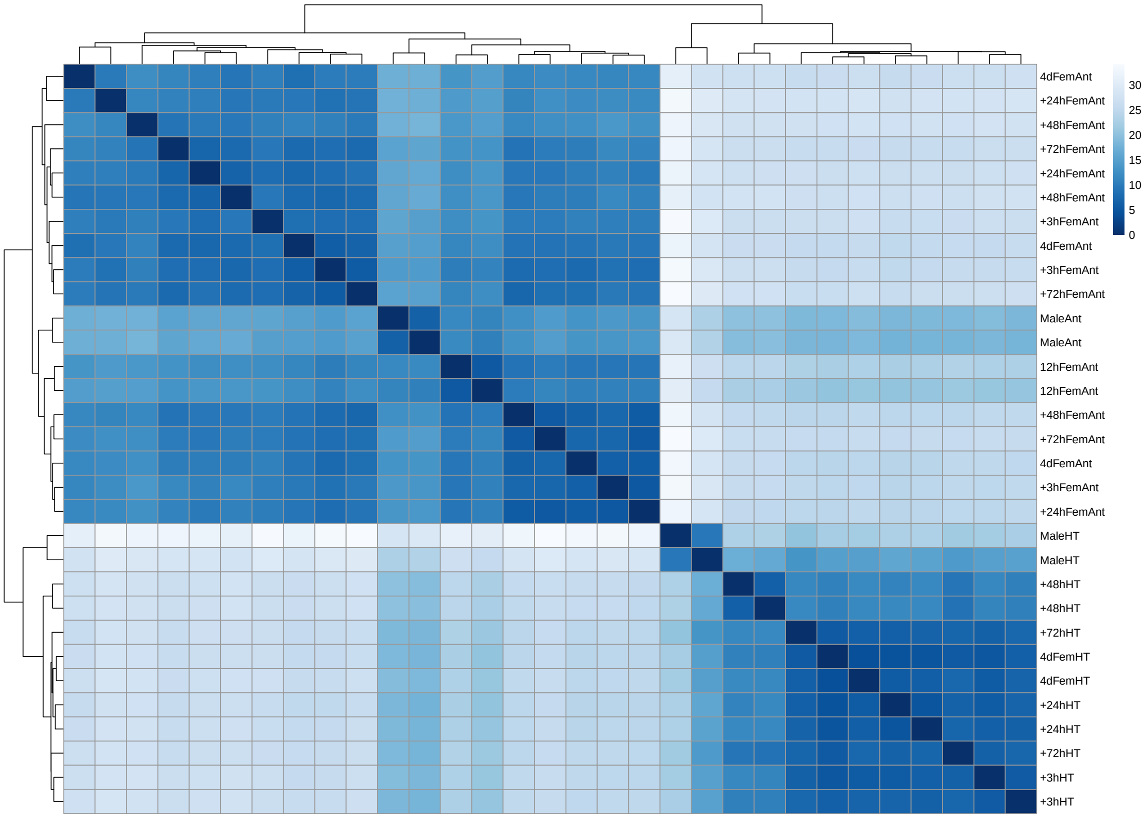

Figure 3.4 Heatmap built with the Euclidean distance between the samples from antenna and head and thorax of *A. aegypti*. rlog-transformed data was used.

Finally, the clustering of samples based on the 20 most variable miRs using the rlog-transformed data revealed two main clusters of samples (Figure 3.5). Although there are differences between the antennal samples, the variation within the biological replicates is quite high. On Figure 3.5 the colors represent how much the replicate deviates from the average expression across all the replicates. It indicates again that the miRs expressed in the antenna have a unique expression pattern.

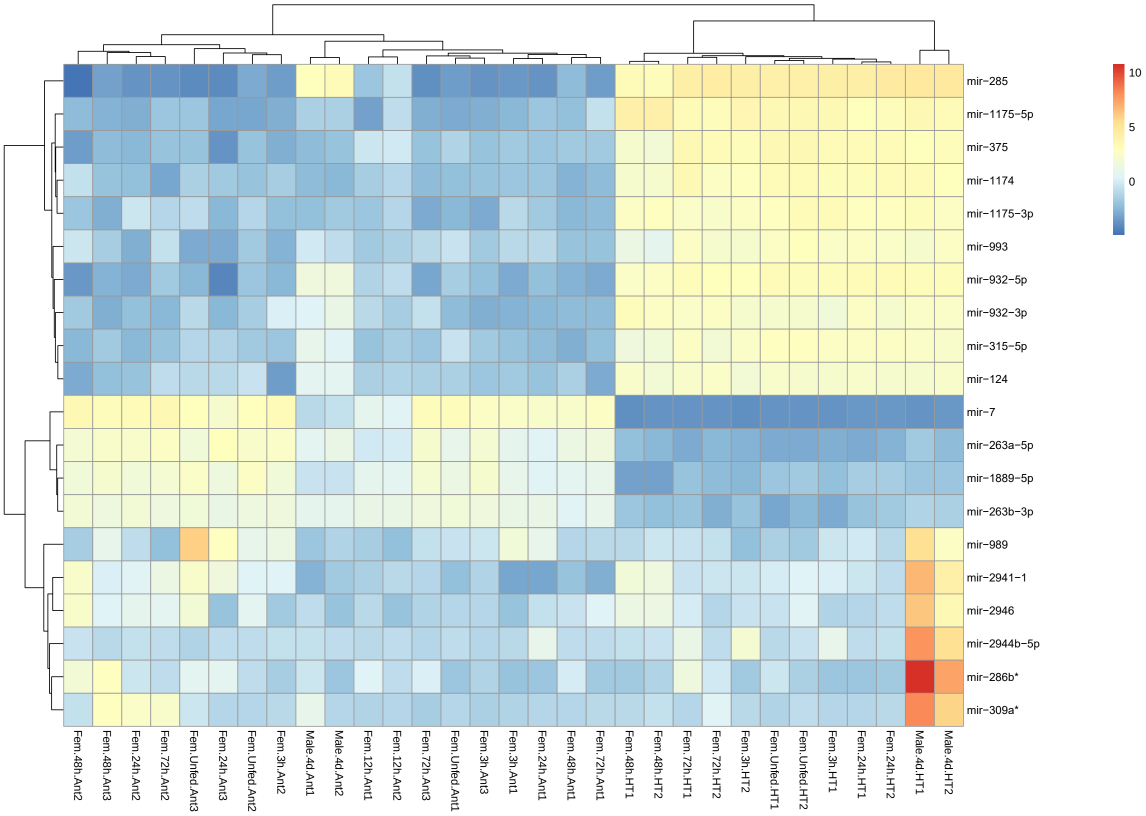

Figure 3.5 Top 20 most variable miRs across all samples. rlog-transformed counts were used to calculate the average expression for each miR across all samples. The colors represent the deviation from the average for each miR in a particular sample.

3.2.5 miRs with sex biased expression

A total of 22 miRs have enhanced expression in the antenna of males when compared to the female antennal samples. 15 miRs have enhanced expression in the female antenna (Table 3.1 and Table A19) when compared to males. The most significantly enhanced miR in the antenna of females is miR-7 (23.21 fold increase in females), while in males miR-285 is most significantly enhanced with a 341.34 fold change (Table 3.4).

Table 3.1 miRs with biased expression in the antennal samples of males and females of *A. aegypti*.

miR	Female (reads)	Male (reads)	Fold change	*p* adj. value
mir-12-5p	24,415.99	6,191.13	-3.88	0.0000
mir-13-3p	2,834.94	1,343.14	-2.09	0.0006
mir-14	180,239.38	88,948.96	-2.01	0.0003
mir-1889-5p	24,870.66	2,663.14	-8.54	0.0000
mir-193	197.43	73.25	-2.59	0.0040
mir-252-5p	15,865.92	7,450.33	-2.09	0.0125
mir-2765	62.69	14.83	-3.84	0.0008
mir-281-3p	703.69	168.70	-4.11	0.0000
mir-2940-5p	7,065.30	2,358.77	-2.96	0.0000
mir-2941-1	34.22	1.11	-8.86	0.0106
mir-34-5p	41,087.56	18,921.17	-2.15	0.0003
mir-7	193,969.35	8,074.83	-23.12	0.0000
mir-79-3p	44.15	11.75	-3.39	0.0119
mir-929*	107.95	40.06	-2.63	0.0049
mir-965	83.86	22.95	-3.40	0.0041
mir-1	1,026.53	2,201.32	2.12	0.0011
mir-10	18,032.18	53,498.62	2.85	0.0031
mir-124	16.09	65.23	3.79	0.0005
mir-133	256.45	823.28	3.06	0.0031
mir-137*	121.40	354.23	2.85	0.0000
mir-184	18,534.32	38,023.82	2.03	0.0007
mir-1891*	10,977.79	24,918.66	2.22	0.0074
mir-190	298.96	739.92	2.42	0.0020
mir-275-3p	5,546.29	13,382.17	2.39	0.0000
mir-275-5p	197.39	920.06	4.23	0.0014
mir-285	36.13	16,577.22	341.34	0.0000
mir-305-3p	215.70	1,023.87	4.60	0.0000
mir-308-5p	47.92	138.90	2.74	0.0289
mir-315-5p	178.21	823.27	4.29	0.0003
mir-316	52.50	331.74	6.04	0.0000
mir-8-3p	18,674.51	43,643.74	2.31	0.0001
mir-8-5p	1,073.64	5,095.56	4.63	0.0000
mir-927	69.33	169.74	2.41	0.0003
mir-92b-3p	1,975.29	5,945.06	2.95	0.0000
mir-932-3p	1.10	13.14	6.27	0.0181
mir-932-5p	13.08	324.58	23.11	0.0000
mir-957	1,684.98	6,201.48	3.55	0.0000

MiR-285 is highly expressed in male antenna and in females its expression decreases 4.65 fold when they switch from nectar-seeking to host-seeking behavior. Therefore, this miR is highly expressed when mosquitoes are nectar seeking. A total of 16 miRs are down regulated when females begin host seeking, while other 13 miRs are up regulated (Figure 3.6). These 13 miRs maybe be involved in the regulation of genes related to host seeking. Their targets were predicted and are presented in the following chapter.

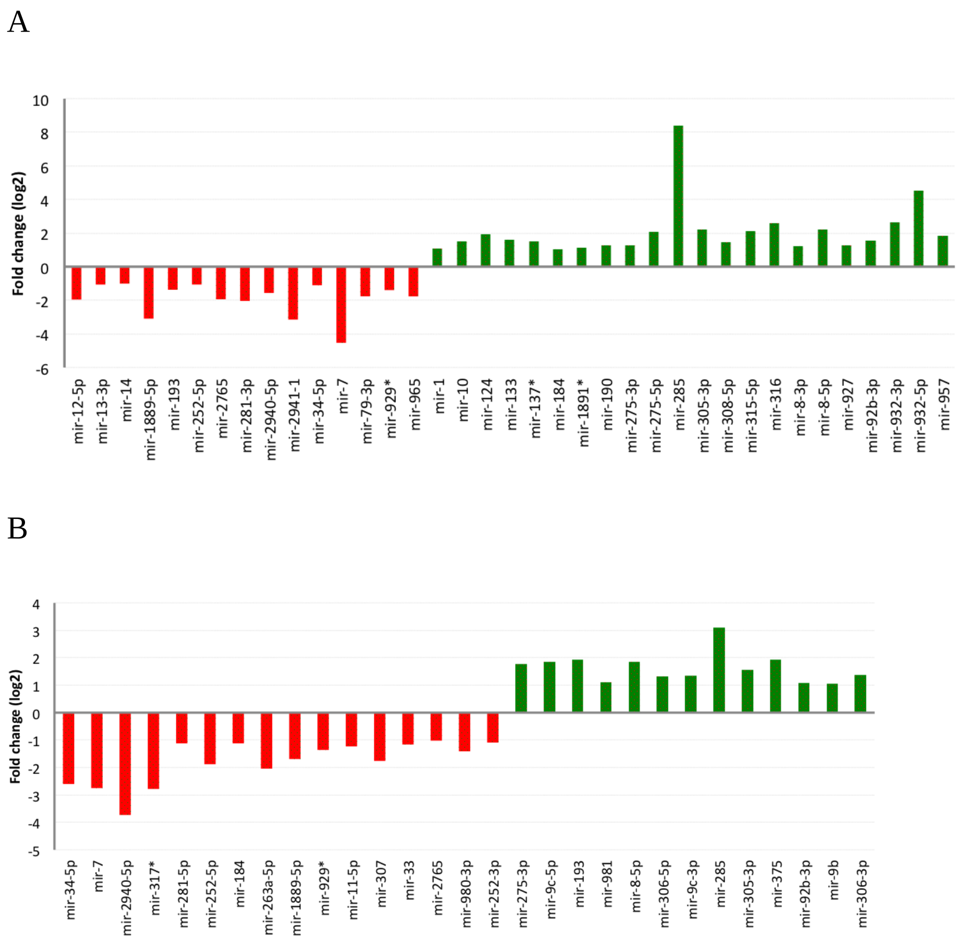

Figure 3.6 miRs with differential expression in *A. aegypti*. A: sex differences (red: enhanced in females; green; enhanced in males). B: behavioral switches (green: enhanced in nectar seeking; red: enhance in host seeking).

3.2.6 Tissue specific miRs

Males have 26 miRs that are up regulated in the antenna and 30 that are up regulated in the HT (Figure 3.7) (Table A21). miR-286b* is predominately expressed in the HT and is almost absent in the antenna (0.58 counts in the antenna and 5,823.75 counts in the HT – 315.84 fold), followed by miR-2944b-5p (164.74 fold) and mir-2941-

1 (161.95 fold), and miR-1891* with 49.82 fold up regulation in the antenna (16,788.14 counts in antenna versus 332.28 counts in the head and thorax).

Females have 29 miRs with enhanced expression in the antenna and the changes in the expression levels are considerably higher when compared male tissues (Figure 3.8). For example, miR-7 expression in the antenna is 528.00 fold higher than the HT (196,155.44 read counts in the antenna versus 365.92 read counts in the head and thorax). MiR-263a has the highest expression of all known miRs, it is 76.58 fold up regulated in the antenna (1,589,485.30 read counts in the antenna versus 19,895.10 read counts in the head and thorax (Table A22).

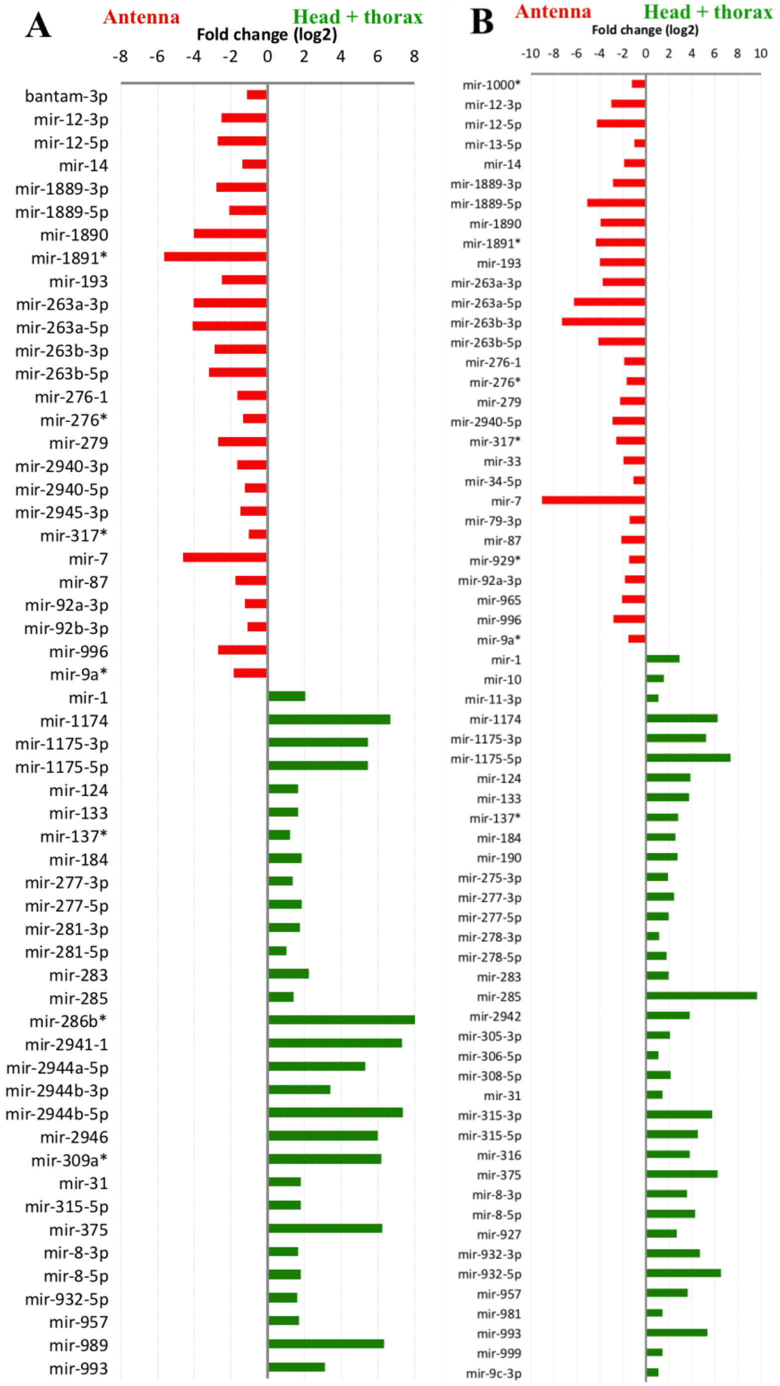

Figure 3.7 miRs differential expression between the antenna and head plus thorax of males (A) and females (B). Red: miRs with higher expression in the antenna; Green: miRs with higher expression in the head plus thorax.

The Venn diagram analysis revealed 4 miRs with enhanced expression in the antenna of females compared to both male antenna and HT samples: miR-34-5p, miR-79-3p, miR-929*, and miR-965 (Figure 3.8). In males only miR-92b-3p is uniquely expressed in the antenna. However, the changes in expression of these miRs are relative small compared to other previously mentioned (less than 10 fold) (Figure 3.8).

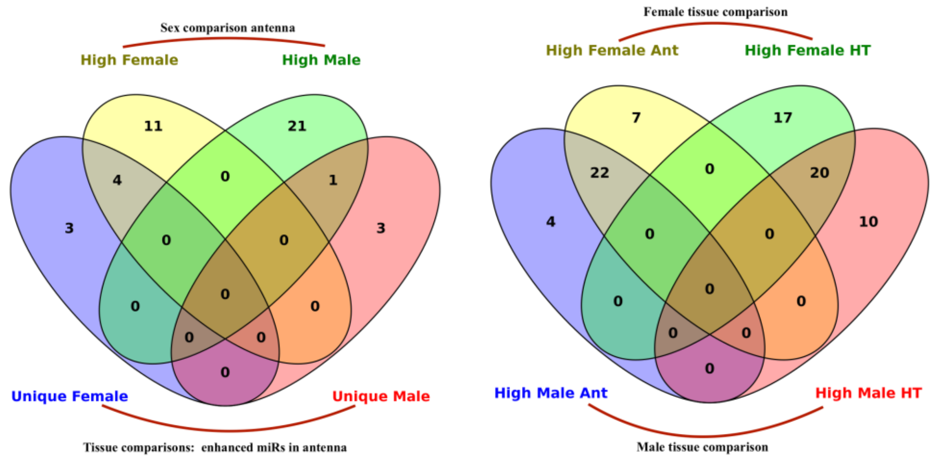

Figure 3.8 miRs uniquely expressed in the antenna of males or females. Left: tissue comparisons. Right: unique female = 7 miRs from yellow circle of the Venn diagram at left (miRs higher in the female antenna); Unique male: 4 miRs from blue circle (miRs with enhanced expression in male antenna).

3.2.7 miR with enhanced expression after blood feeding

No changes are observed in the miR levels in the female antenna after blood feeding, therefore all I will discuss only the changes in the expression in the HT samples. Three hours after blood feeding significant changes in miR expression is observed in the

HT samples. miR-275-5p and miR-305-3p are enhanced in the HT samples 3h after blood feeding, 5.6 and 2.69 fold respectively (Figure 3.9) (Table A23).

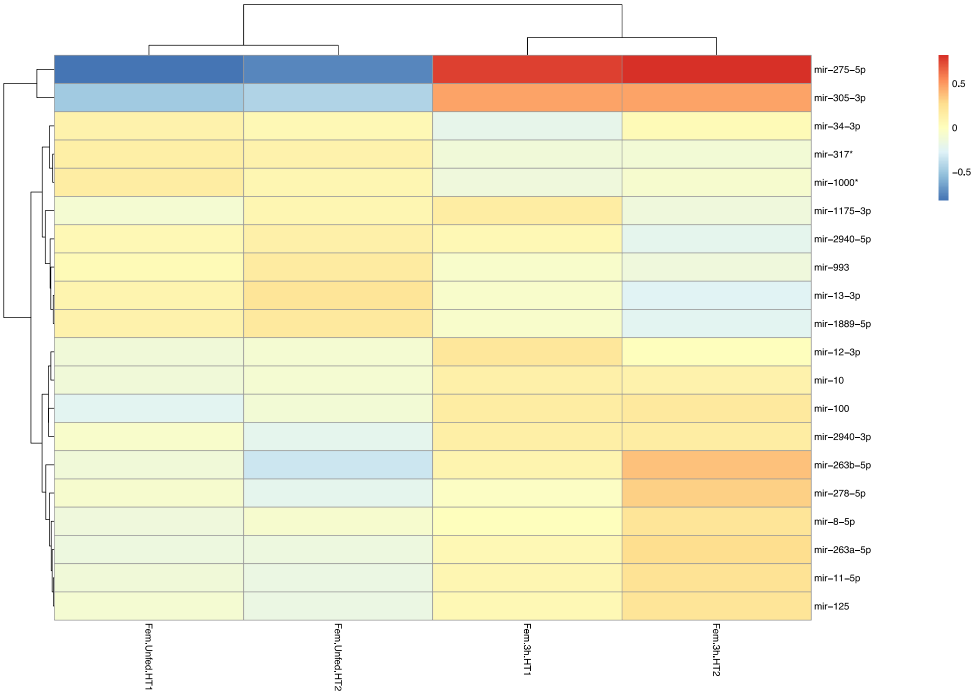

Figure 3.9 Clustering of head plus thorax samples' replicates. The variant stabilizing data from DESeq2 was used to construct the heatmap.

At 24h after blood feeding the expression levels of miR-275-5p and miR-305-3p in the HT are still increasing (compared to levels observed in the HT of unfed females), while miR-263b-5p expression decrease by 2.16 fold.

The highest change in miR expression in the HT is seen at the onset of the oviposition site seeking behavior (at 48h after blood feeding) (Figure 3.10a). A total of 44 miRs are differentially expressed compared to the unfed females. 22 miRs are down regulated and other 22 miRs are up regulated (Figure 3.10b). In the HT the expression of miR-275-5p and miR-305-3p decrease at 48h post blood feeding, along with another 20 miRs, while the expression of miR-263b-5p still increases.

No differences in miR expression are observed between the unfed females and those that begin egg laying at 72h post blood feeding. However, comparisons between samples from 48h and 72h blood fed females reveal changes in the expression of miRs in the HT but not in the antenna. The changes in expression are relatively small compared to those previously reported (highest is 4 fold). A total of 14 and 16 miRs are down and up-regulated, respectively. MiR-275-5p, miR-305-3p, and miR-263b-5p expression does not change after 48h post blood feeding.

3.2.8 Clustering of miRs enhanced in the antenna of A. aegypti

Clustering and statistical analyses revealed few miRs that are enhanced in the antenna of *A. aegypti* compared to HT. Antennal samples do not show any clear clustering pattern among the replicates post blood feeding, but the antennal samples from 12h old females, unfed females and male cluster in 3 groups (Figure 3.11) (Table A20).

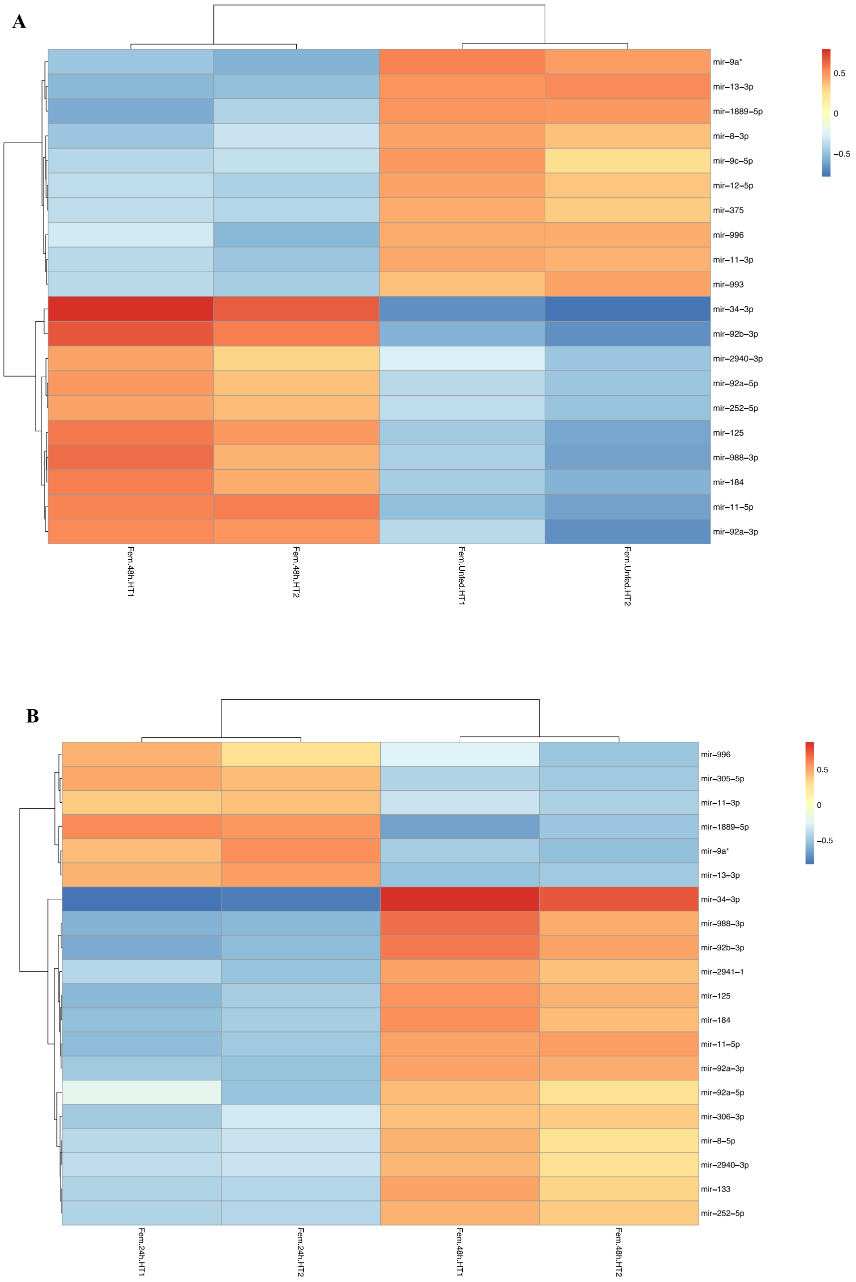

Figure 3.10 Heatmap of miRs differentially expressed in the head and thorax of females. A. Unfed females and +48h blood fed females; B. +24h and +48h blood fed females.

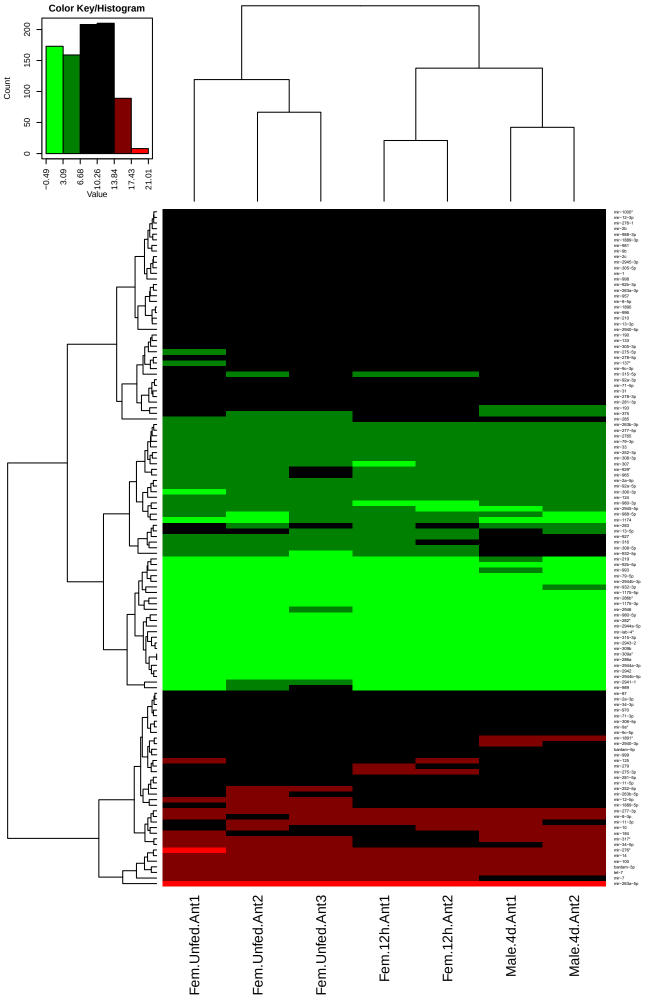

Figure 3.11 Clustering of antennal samples of 12h, unfed females and 4 days old males.

MiR-263a-5p is the most expressed miR in the antenna of *A. aegypti* (bottom line on Figure 3.11). Although present in the HT samples, its expression is 76.58 fold less in females and 16.9 fold less in males (Table A21 and A22). A total of four miRs are upregulated in the antenna of males compared to females: miR-927, miR-316, miR-308-

5p, and miR-932-5p (Figure 3.12). The miRs miR-10, miR-277, miR-184, miR-100 are consistently highly expressed across all HT samples, including the male samples (Figure 3.12), but not in antenna. In the male HT 7 miRs stand out with higher expression: miR-2944b, miR-2946, miR-989, miR-2941-1, miR286b, miR-2944b-5p, and miR-309a. Finally, clustering of the samples (Figure 3.13) reveals that miR-263a is highly expressed in the antennal tissues (Figure 3.14), and that miR-8-3p is highly expressed in the HT (Figure 3.15).

The miR-279 is enhanced in the antenna of females (4.75 fold higher than in the thorax and head samples) and males (6.48 fold). Although there are no changes in its expression from 12h old to 4 days old unfed females, it down regulates in the HT 48h after blood feeding when the females start searching for oviposition sites, whereas its expression returns to the initial level 72 hours after blood feeding.

Although miR expression in the antenna remains steady after blood feeding, several miRs are up or down regulated as females start looking for hosts. However, after blood feeding several miRs show significant changes in their expression levels in HT after blood feeding. Overall, these results indicates that miRs expression in the antenna is quite different from HT, and also that the expression profiles of males and females is distinctive.

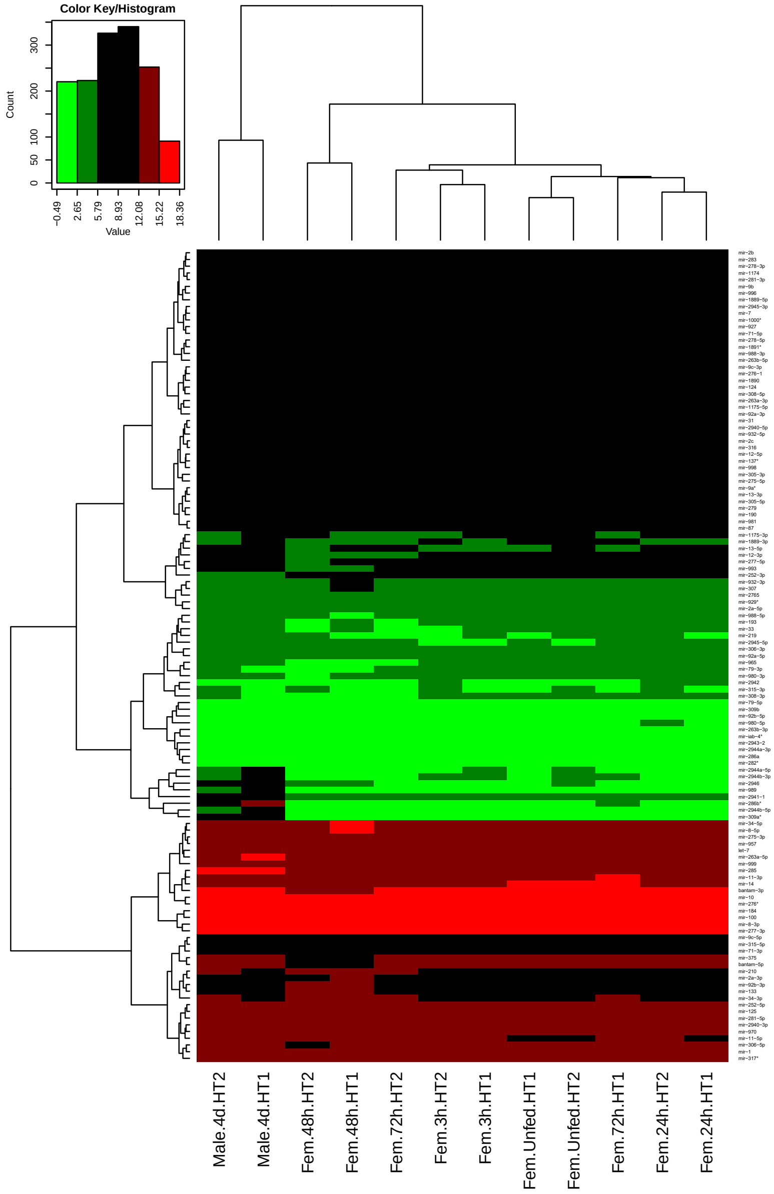

Figure 3.12 Heatmap with all known miRs of *A. aegypti*. Light green indicates low expression levels, red indicates high expression. The expression level of most miRs do not change afer blood feeding.

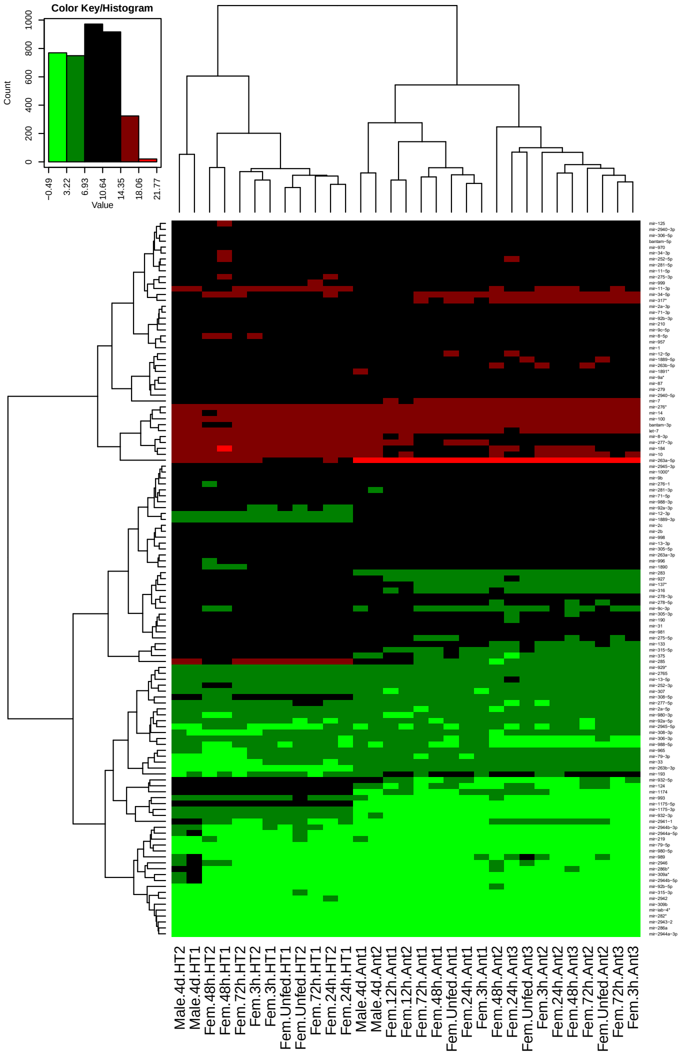

Figure 3.13 Heatmap of miR expression of *A. aegypti* antennal and head plus thorax samples.

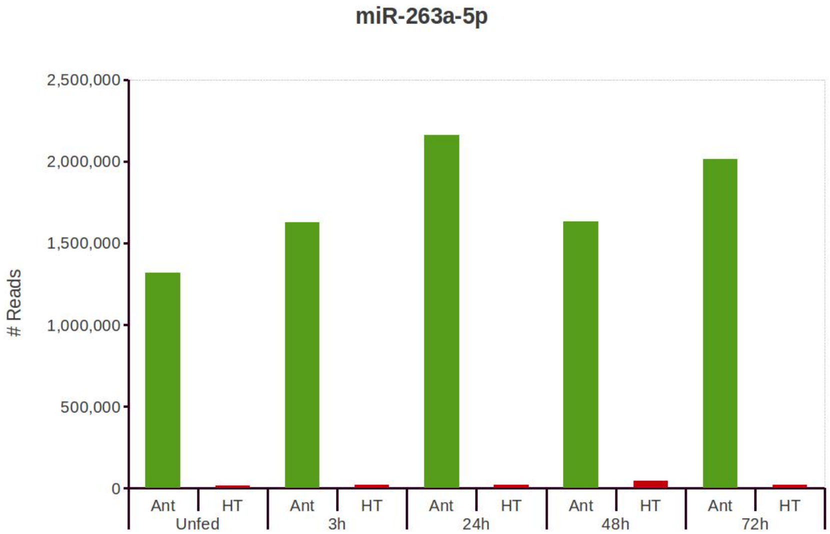

Figure 3.14 Expression of miR-263a in *A. aegypti*. Normalized counts were obtained from DESeq2.

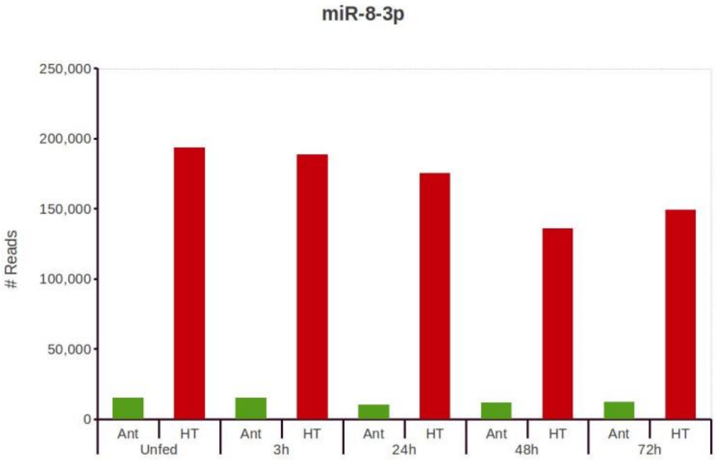

Figure 3.15 Expression of miR-8-3p in *A. aegypti*. Normalized counts were obtained from DESeq2.

3.4 Discussion

miRs are an important category of non-coding RNA that regulate biological processes and can even interfere with the response of mosquitoes to Dengue virus and *Plasmodium* infections (Campbell et al. 2014; Jain et al. 2014). However, it is not known if miRs can regulate gene expression of olfaction genes or other important genes involved in mosquito behavior concerning the searching for nectar, hosts or suitable oviposition sites. This is the first study to look at expression of miRs in the antenna of mosquitoes, their main olfactory organ.

The most striking discovery is the high expression of miR-263a in the antenna of *A. aegypti*. Its mature miR sequence is identical to that of *D. melanogaster* and *A. gambiae*. During fly development, this miR along with miR-263b protects the mechanosensory bristles from apoptosis by down-regulation of the pro-apoptotic gene, *head involution defective* (*hid*) (Hilgers et al. 2010). The effects are mainly seen in the eye of the flies, but also reduce the number of bristles in the head and thorax. Due to the high expression in the antenna of *A. aegypti*, we speculate that it may have other functions rather than protection of sensory neurons or other cell types from apoptosis during the antenna development. Importantly, its expression in the antenna of 12h old female is present the same levels found in 4-day-old females. Since the adult antenna is formed during pupal development, it may play a crucial role in the process only during that stage. Target prediction for this miR is presented in the next chapter.

MiR-7 is highly expressed in the antenna of *A. aegypti* females (528 fold higher than head plus thorax), but less so in males. In *Drosophila* over expression of miR-7 blocks the follicle cells from switching from the endocycle to gene amplification phase, and is also implicated in cell differentiation events, for example in the formation of mature eggs (Huang et al. 2013). The high expression in the antenna of mosquitos is puzzling since miR-7 might be involved with the regulation of cell cycle (G1 to S phase) and cell mass and it is reported to control the wing development in flies (Aparicio et al. 2015). Similar to miR-263a, which is the most highly expressed miR in the antenna of *A.* aegypti, the known function of miR-7 are related to development but little is known of the function on the adult organism.

Surprisingly, similar to the observation in olfaction genes, no significant changes are observed in the expression of miRs in the antenna of *A. aegypti* after blood feeding. Significant changes are observed in the HT after blood feeding, where within 3h of blood feeding the expression of miR-275 and miR-305 are up regulated. MiR-275 is essential for blood meal digestion (Bryant et al. 2010). While the function of miR-305 is currently unknown in mosquitoes. According to its expression profile it may be also involved in blood meal digestion since it clusters well with miR-275. In *D. melanogaster* miR-305 is associated with memory formation and retention (Busto et al. 2015). It could also be associated with memory formation in mosquitoes. For example, during my experiments I observed that mosquitoes being blood feed for the second time respond quickly to the membrane feeder and blood feed faster.

Comparisons between antenna and HT revealed striking changes in the expression of some miRs, with fold differences higher than any protein-coding gene. For example, miR-7 display a 52 fold up regulation compared to HT in the 4-day-old female.

There are also significant changes between males and females, and significant changes with age, 12h old and 4 day old females.

The high expression of miR-8 in the HT when compared to the antenna (Figure 3.15) may indicate its role in mosquito attraction to humans but at the higher areas of the brain or at the antennal lobe. In *D. melanogaster* miR-8 was previously reported to cause neurodegeneration and make flies unable to climb (Karres et al. 2007). MiR-8 is reported to have diverse roles in fruit flies, including neuronal cell survival, control of neuroblast proliferation, neuromuscular junction formation, innate immunity, metabolism, and organismal growth (Chen et al. 2014). Its function might be conserved in mosquitoes and may be important as a potential target to develop transgenic mosquitoes as a potential target to disrupt mosquito biology and also study the function of this miR.

An interesting question is the role of miR-279 in olfaction gene regulation in mosquitoes. If miR-279 is knocked down during embryogenesis in *D. melanogaster* leads to the formation of CO_2 sensing neurons in the maxillary palpi. In *D. melanogaster* it acts to down-regulate the transcription factor, *nerfin-1*(Cayirlioglu et al. 2008). *Nerfin-1* is expressed in neuronal precursors and nascent neurons in the embryonic central nervous system of the fly. While in *Drosophila* the CO_2 detection occurs mainly through the antenna, in mosquitoes it is located in the maxillary palps. I did not collect relative data from maxillary palpi of *A. aegypti*, but miR-279 expression is up regulated in the antenna of both sexes of mosquito when compared to HT samples, with the expression decreasing when females begin seeking oviposition sites (48h), and rapidly increasing during egg laying behavior (72h). It is difficult to speculate regarding the function of miR-279 in the mosquito antenna without first knowing the expression profiles in the maxillary palpi. However, we could hypothesize that its decrease in expression at 2 days after blood feeding in the HT could indicate that suppression of genes involved in oviposition site seeking. These probably are not olfaction genes and may be expressed in the antennal lobes or higher brain regions where the information about the suitability of the potential oviposition site is processed. The adult antenna and maxillary palp are formed during the pupal stage, when they originate from the eye-antennal disc, which are a small epithelial tissue that is preserved during development to give rise to specific adults tissues (Barish and Volkan 2015). Therefore, the expression of miR-279 in the adult tissue indicates that it might have other important functions in mosquitoes.

The high number of differentially expressed miRs at 48h after blood feeding in the HT samples was also reported in *Anopheles stephensi* body (Jain et al. 2014), although surprisingly no significant changes in miR expression occur in the antenna of mosquitoes after blood feeding. This could be due to the nature of the olfaction system, where the expression of genes might change in single sensory neurons but not in all neurons in the antenna of mosquitoes, for example, if the expression of a miR only changes in 5 out of the 91 olfactory neurons found in the antenna of females, it likely would not be detected in my analyses.

miRs play an important role in *D. melanogaster* larvae presynaptic control of synapse structure and function of the neuromuscular junctions (Nesler et al. 2013). miR-8 down-regulation results in significant decreases in synapse size during development of the larval neuromuscular junctions (Loya et al. 2009) and the abundance of postsynaptic glutamate receptors (GluRs) in *Drosophila* neuromuscular junctions are also controlled by miRs (Karr et al. 2009). MiRs control the abundance of the subunits of the glutamate receptors in the fly neuromuscular junctions, knockout of miR-284 in *Drosophila* results in changes in the synaptic GluR subunit composition and causes accumulation of nonsynaptic subunit proteins. MiR-285, from the same family of miR-284, shows 341.34 fold higher expression in male antenna. Since *A. aegypti* males have less neurons in their antenna than females (females have approximately 2,000 while males have 500), the higher expression of this miR could indicate a necessity to optimize the function of the present neurons.

It is unclear if males of *A. aegypti* are also attracted to a host because of the higher chance to find a female mate. In wind tunnel experiments only a few males enter the collection chambers with human odors (personal observation), most males remain flying around the entrance. In the field it is reported that males stay in the vicinity of hosts to intercept females coming to feed (Jaenson 1985). Even though miR-285 is more expressed in the male antenna, the expression in female antennae decreases 4.65 fold when females switch from nectar seeking to host seeking.

The mapping of reads to mature miR was biased for the 5’mature sequences (Table 12), which supports the current knowledge of miR biogenesis, where the guide strand is retained and the passenger strand is degraded. There are exceptions to this, like miR-8-3p, where the guide strand is not at the 5’ end. During the miR biosynthesis, the double strand precursor is detected and loaded onto the RISC complex, one strand being removed by an Argonaute protein (usually Arganaute-2) and the remaining strand is loaded onto a second RISC. The passenger strand is lost and miRISC complex will act by binding to the 3’UTR of mRNA molecules and these molecules are degraded (Berezikov 2011).

Functional assays are needed to elucidate the function of these miRs that are uniquely expressed in the antenna of *A. aegypti*. However, tissue-specific methods, for example microRNA sponge (Loya et al. 2009) developed for *Drosophila*, need to be developed for mosquitoes. The use of techniques to detect genome wide alternative polyadenylation sites are essential to understanding the role of miRs in host seeking behavior of mosquitoes. Only fractions of the 3’UTRs in protein coding genes have been annotated in the *A. aegypti* genome. Finally, experiments to determine the location of miRs being expressed are necessary. For example, in human brains, miRs regulating ion channel/transport genes are expressed in the axons of neurons housing their targets (Wehrspaun et al. 2014). These targets also have long 3’UTRs similar to the observation in some olfaction genes.

The lack of differential expression in olfaction genes in the known miRs in the antenna of females after blood feeding may be caused by two different reasons. First, olfaction genes and miRs that regulate genes post-transcriptionally may change their expression levels in a small subset of sensory neurons in the antenna. Female antennae have approximately 2,000 neurons, with only 93 being sensory neurons that house olfaction genes. If the expression of olfaction genes or miRs changes in only a small population of sensory neurons it may not be detected. Secondly, olfaction gene transcripts may compete for binding sites of shared miR regulators and modulate the abundance of each other, a mechanism named miR-mediated cross talk (Tan and Marques 2014). Recently, it was found that some coding and non-coding transcripts regulate expression in this way, for example, *PTEN* and several non-coding RNAs (Karreth et al. 2011a; Karreth et al. 2011b; Tay et al. 2011). Olfaction genes may indeed be regulated by miRs located in axons of sensory neurons in the female antennae, but the expression levels of miRs or olfaction genes do not need to change for the translation of olfaction transcripts to be stalled or the mRNA targeted for degradation. Olfaction genes with long 3'UTR may have multiple polyadenylation sites and therefore multiple isoforms with different biding sites for miRs. These isoforms may compete for miRs that are stably expressed in the antenna after blood feeding and normal gene expression studies have not been able to detect these changes.

Following up studies will be needed to elucidate the biological function of the miRs expressed in the antenna of *A. aegypti*. Although studies from *D. melanogaster* give us insights on their potential function in mosquitoes, these functions may not be conserved.

CHAPTER IV

MIR TARGET DISCOVERY, MIR DISCOVERY AND FUNCTIONAL ASSAY

4.1 Introduction

The yellow fever mosquito, *Aedes aegypti*, displays considerable behavioral changes from its emergence until it starts looking for hosts. After blood feeding there is a new switch in behavior accompanied by physiological changes (Klowden 1990; Klowden 1994). Females stop host-seeking after acquiring a full blood meal and within 48 hours they switch to oviposition site seeking behavior (Klowden and Lea 1978). Potentially, these changes could be correlated with the expression of olfaction genes that play a crucial role in mosquito host and oviposition site seeking behavior. Over three hundred olfaction related genes have been identified in *A. aegypti*. Many olfaction genes, some of which may be involved in host seeking behavior, are up-regulated when *Aedes aegypti* females switch from nectar-seeking to host-seeking (see chapter 2) (Martinez-Ibarra et al. 1997), although few changes were observed after females took a blood meal and cease host-seeking.

Among several factors known to regulate gene expression, microRNAs (miRs) have been found to be the most important regulatory molecules. miRs can bind to the 3'UTR of their mRNA of targets stalling translation or degrade it via the RNA interference (Carrington and Ambros 2003). The role of miRs in insect biology has been demonstrated in fruit flies. During the *Drosophila* life cycle several miRs are differentially expressed and found to be involved in important cellular processes such as apoptosis, cell division, and differentiation (Casci 2012; Nesler et al. 2013; Aparicio et al. 2015). Previous studies have also demonstrated that miRs play an important role in mosquito physiology and vector competence. For example, miR-275 is essential for blood meal digestion in *A. aegypti* (Bryant et al. 2010) and infection of mosquitoes by dengue virus or *Plasmodium* spp. results in changes in the expression of over 20 miRs (Campbell et al. 2014; Jain et al. 2014). Currently, nothing is known about the expression of miRs in the olfaction organs of mosquitoes, nor about any differences between the expression profiles of miRs in males and females of *A. aegypti*. Considering the roles of miRs in blood meal digestion, reproduction, and response to infection, an exploration of their possible role in regulating olfaction gene expression could be important as this aspect of the mosquito's biology is directly tied to its ability to transmit disease. No studies have been performed to see if miRs can regulate the expression of olfaction genes in any blood-feeding insect. However, target prediction for was performed for miRs whose expression increases with Dengue virus or *Plasmodium* infection. None of these miRs were predicted to regulate olfaction genes. Finally, new miRs being expressed in the antenna may regulate olfaction genes.

MiR-263a and miR-263b protect the mechanosensory bristles of *Drosophila* from apoptosis by down-regulating the pro-apoptotic gene *head involution defective* (*hid*) during eye development (Hilgers et al. 2010). It is the most expressed miR in the antenna of *A. aegypti* and has the exact same mature sequence in *Anopheles gambiae, D. melanogaster* and *A. aegypti*. Therefore one could expect that it also has conserved targets across the species. Its knockout effects in flies are mainly seen in the eye of the flies, but there are also a reduced number of bristles in the head and thorax. Therefore it could be protecting neurons in the antenna of *A. aegypti* from cell death. Most important, its expression in 12h old female antenna is already at high levels compared to other miRs.

In chapter 3, I examined the expression patterns of known miRs in various tissues, in different sexes and behavioral states of *A. aegypti*. Here, I expand on those results by identifying new, previously unknown *A. aegypti* miRs and by identifying potential targets of antennal miRs with a focus on olfaction genes. 16 new miRs were discovered and five olfaction genes were identified that are potential targets of miRs with high expression in *A. aegypti* antenna. Finally, I made an attempt to knock down the expression of miR-263a with a microRNA sponge (antagomir).

4.2 Material and methods

4.2.1 miRs used for target prediction

Target prediction was done for all known miRs using the 3'UTR of olfaction genes, but the following miRs have more biological relevance according to their expression pattern: miR-285 has 341-fold increased expression in male compared female antenna, and down-regulated expression in the female antenna during host-seeking behavior; mir-263b is 318-fold enriched in the male head and thorax compared to antenna); mir-1891 has 50 fold expression in male antennae versus head and thorax; mir-

7 has 528 fold expression in female antennae compared to head and thorax; mir-263a has very high expression across all antennal samples compared very low expression in the head and thorax; miR-34-5p, miR-79-3p, miR-929, and miR-965 are uniquely expressed in the female antenna (high expression when compared to female head and thorax or male antenna - see chapter 3); miR-92b-3p is the only miR uniquely expressed in male antenna; and finally miR-279 is enhanced in antenna of both male and female and has been related to the development of sensory neurons in *Drosophila*. Although its expression does not change from 12h old to 4 days old unfed females, it's down regulated in the head and thorax 48h after blood feeding when the females start looking for oviposition sites. However, its expression returns to initial levels 72 hours after blood feeding.

4.2.2 miR target prediction

The miR target prediction was performed using miRanda (Enright et al. 2004) for all 340 olfaction genes. The 3'UTR of olfaction genes was downloaded from the European Bioinformatics Institute (EBI) via Biomart. For transcripts without an annotated 3'UTR (228 out of 340), a 200bp sequence downstream of the stop codon was used as 3'UTR covering its average average length. miRanda was used with the following parameters: energy <= 20kcal/mol, score > 140, scale = 2, gap-opening penalty = 8, and gap-extend penalty = 8. These are stringent setting compared to the defaults settings of the algorithm which has a high false positive rate for miR target prediction. The miR sequences used were obtained from miRBase version 21. The results from miRanda were filtered using custom bash scripts to obtain the prediction statistics from the output file and sorted by the overall score. A high score means high complementarity and low energy required for the interaction of the miR and the target.

4.2.3 miR discovery

Discovery of new miRs was performed using miRDeep* (An et al. 2013). This algorithm predicts the secondary pre-miRNA structure of each new miR and records the read locations. miRDeep* does not require training with any data similar to other algorithms. Other methods work similar to a homology search, where you cannot identify new genes if they are too divergent. miRDeep* incorporates the miR predicting tools of miRDeep2 (Friedlander et al. 2012) but does not require species specific data training. miRDeep* considers the highest expressed read at the potential miR locus to be the mature miRNA. One side of the read is extended by 22 bp (where the miR might start), and the other side of the read is extended by 15 bp (loop region). The mature RNA* or guide sequence has the same number of nucleotides as the mature miRNA. The computation effort is considerable since every read that maps to a genomic region has to be analyzed following this procedure. The input reads that I used were obtained from CLC genomics workbench after miR analyses. The software generates two sets of reads, one that matches the known annotated miRs, and another set that contains potential new miRs. The unannotated reads were exported in fasta format. Ideally all reads can be used for miR discovery, but due to great computational requirement, reads from each replicate were run separately and the results pooled at the end. For example, reads that did not map any known miRs (539,537,383 reads) took over a month of computing time on our fastest computer. This problem is aggravated by the lack of a physical map of the *A. aegypti* genome and the high number of transposons and repetitive sequences since miR sequences are short and can potentially map to these regions. Until today, only two studies have identified miRs in *A. aegypti* (Li et al. 2009; Skalsky et al. 2010). However, in these studies a homology based search strategy was used to identify miRs. Therefore, our approach using miRDeep* has the potential to reveal a great number of new miRs.

An important setting is the number of reads that have to map to a location for it to be considered a novel miR. Due to both the reduced computation time and the possibility of false positives; I used the threshold of five reads. Therefore, if five reads mapped to a potential site where a hairpin loop could form with low energy requirements, a locus was considered a new miR.

4.2.4 MiR-263a inhibition

Because miR-263a is expressed at such high levels in the antennae of *Aedes aegypti*, in contrast to the head and thorax, and because it plays an important role during eye development in *Drosophila,* we speculated that it may play an important role during antennal development in mosquitoes. Therefore, I injected synthetic miRs into last instar larvae, pupae and 12h old females with the purpose of examining the ability of injected mosquitoes to detect human odor.

An antagomir against mir-263a was obtained from Qiagen. Its sequence was complementary to the guide strand (mature region). The control antagomir termed missense was 5′ mC* mG* mC mU mU mU mC mG mU mG mG mU mU mC mU mG mG mU mA mC* mC* mU* mU* mA 3′. “*” is a PS backbone instead of the usual PO backbone. “m” is an OCH_3 group on the 2′ end of the base instead of the usual OH group. A 3′ cholesterol group was added to each RNA oligo for potency reasons. Similar modifications were used for the miR-263a inhibitor. The antogomir and control were injected into mosquitoes at a dose of at least 300ng in a volume of 0.5 μL (water and 1% red food die). Mosquitoes were anesthetized with CO_2 12h after eclosion and injected into the thorax. Late larvae and early pupae were injected directly on wet Kimwipes resting over glass slides. Needles were prepared in a micropipette puller (P-97, Sutter Instruments). Needles were then connected to the Transjector (Eppendorf), which controls the injection time (1 to 2s) and pressure (100 – 200 psi), and the backpressure (10 to 30 psi). Microinjections were performed using a microscope with a moving stage (Leica) at x 4 to 20x magnification and micromanipulator.

4.3 Results

4.3.1 miR target prediction

A total of 43,075 potential combinations of all miRs and 340 olfaction genes transcripts were obtained. The results were ranked by the overall score and the energy required for the pairing of miR:mRNA. Two olfaction genes (*Or16* and *Irc*) are the best potential targets of several miRs (low energy requirement and highest score). Next, *Or52, Or42, Ird, Obp11, Or11, Ir7v.3, Or49* and *Ir104.3* (Table 4.1) have the highest scores. Interestingly, Bantam and mir-7 can potentially regulate all the olfaction genes mentioned previously. Among the miRs that could target olfaction genes, miR-7 stands out since it is enhanced in the female antenna.

As mentioned previously a couple of miRs have expression profile suggesting they could regulate the expression of genes only expressed in certain tissue, antenna, sex or behavioral state (top 10 miRs). Surprisingly, these 10 miRs are in the 1.17% miRs within the highest score and lowest required energy for interaction with their potential targets (miRs requiring less than -20 kcal/mol: 506 miR/targets out of 43,074 possible interactions). The top 5 targets for these miRs are: *Or52, Or2, Ir25a, Or16,* and *Ir7v.2* (Table 4.2, Table A25). *Or16* is the best potential target for all the 10 miRs. The higher scores and low energy requirements for these olfaction genes indicate that regulation of these genes is very important in *A. aegypti*.

Table 4.1 Top 10 olfaction genes with the highest potential to be regulated by miRs in *A. aegypti*. The top 5 miRs with highest score and lowest energy are shown for each gene.

miR	Gene	Gene Name	Transcript	Total Score	Total Energy	Max Score	Max Energy	miR (bp)	3'UTR(bp)	Positions
aae-miR-79-5p	AAEL013507	*Or52*	AAEL013507-RA	444	-55.99	152	-25.49	23	1608	190 738 657
aae-miR-277-3p	AAEL013507	*Or52*	AAEL013507-RA	306	-19.39	157	-11.47	22	1608	1451 447
aae-miR-33	AAEL013507	*Or52*	AAEL013507-RA	293	-26.22	152	-13.61	21	1608	1447 1506
aae-miR-190	AAEL013507	*Or52*	AAEL013507-RA	143	-13.11	143	-13.11	24	1608	1585
aae-miR-12-5p	AAEL013507	*Or52*	AAEL013507-RA	143	-16.18	143	-16.18	23	1608	1560
aae-miR-283	AAEL005999	*Or2*	AAEL005999-RA	319	-47.47	174	-27.27	24	1012	747 537
aae-miR-306-3p	AAEL005999	*Or2*	AAEL005999-RA	150	-18.42	150	-18.42	22	1012	841
aae-miR-281-5p	AAEL005999	*Or2*	AAEL005999-RA	149	-13.39	149	-13.39	19	1012	848
aae-miR-2944b-3p	AAEL005999	*Or2*	AAEL005999-RA	141	-13.82	141	-13.82	22	1012	868
aae-miR-2940-3p	AAEL005999	*Or2*	AAEL005999-RA	140	-13.28	140	-13.28	22	1012	896
aae-miR-1889-3p	AAEL009813	*IR25a*	AAEL009813-RA	426	-43.17	145	-14.39	22	721	12 611 563
aae-miR-315-5p	AAEL009813	*IR25a*	AAEL009813-RA	316	-35.65	168	-21.31	22	721	404 125
aae-miR-2a-5p	AAEL009813	*IR25a*	AAEL009813-RA	159	-19.76	159	-19.76	21	721	603
aae-miR-8-5p	AAEL009813	*IR25a*	AAEL009813-RA	155	-10.31	155	-10.31	22	721	655
aae-miR-932-5p	AAEL009813	*IR25a*	AAEL009813-RA	140	-19.54	140	-19.54	22	721	511
aae-miR-277-3p	AAEL007110	*Or16*	AAEL007110-RA	430	-35.78	147	-13.79	22	1776	853 1556 1335
aae-miR-9c-3p	AAEL007110	*Or16*	AAEL007110-RA	302	-34.38	157	-20.72	22	1776	1462 706
aae-bantam-3p	AAEL007110	*Or16*	AAEL007110-RA	292	-30.75	147	-16.12	22	1776	1073 718
aae-miR-308-5p	AAEL007110	*Or16*	AAEL007110-RA	290	-29.87	148	-16.71	22	1776	125 1397
aae-miR-1890	AAEL007110	*Or16*	AAEL007110-RA	286	-34.54	145	-21.3	22	1776	1526 1593
aae-miR-79-3p	AAEL018101	*IR7v.3*	AAEL018101-RA	308	-23.38	156	-12.67	22	1110	780 341
aae-miR-190	AAEL018101	*IR7v.3*	AAEL018101-RA	300	-31.16	156	-20.59	24	1110	895 650
aae-miR-2940-5p	AAEL018101	*IR7v.3*	AAEL018101-RA	159	-17.31	159	-17.31	23	1110	1007
aae-miR-980-5p	AAEL018101	*IR7v.3*	AAEL018101-RA	146	-19.01	146	-19.01	24	1110	860
aae-miR-315-3p	AAEL018101	*IR7v.3*	AAEL018101-RA	146	-14.17	146	-14.17	22	1110	840
aae-miR-999	AAEL006360	*IR76b*	AAEL006360-RA	299	-22.98	154	-12.44	22	471	46 139
aae-miR-133	AAEL006360	*IR76b*	AAEL006360-RA	296	-38.03	156	-21.19	22	471	398 340
aae-miR-1890	AAEL006360	*IR76b*	AAEL006360-RA	163	-27.12	163	-27.12	22	471	255
aae-miR-277-3p	AAEL006360	*IR76b*	AAEL006360-RA	143	-16.52	143	-16.52	22	471	260
aae-miR-190	AAEL006360	*IR76b*	AAEL006360-RA	141	-15.91	141	-15.91	24	471	431
aae-miR-2944b-5p	AAEL000011	*IR41e*	AAEL000011-RA	302	-26.15	156	-13.97	23	515	468 29

Table 4.1 Continued

miR	Gene	Gene Name	Transcript	Total Score	Total Energy	Max Score	Max Energy	miR (bp)	3'UTR(bp)	Positions
aae-miR-2944a-5p	AAEL000011	*IR41e*	AAEL000011-RA	293	-35.46	149	-21.13	24	515	467 28
aae-miR-92b-3p	AAEL000011	*IR41e*	AAEL000011-RA	156	-22.21	156	-22.21	22	515	334
aae-miR-92a-3p	AAEL000011	*IR41e*	AAEL000011-RA	155	-21.88	155	-21.88	21	515	335
aae-miR-137	AAEL000011	*IR41e*	AAEL000011-RA	143	-14.45	143	-14.45	22	515	451
aae-miR-315-5p	AAEL018149	*IRc*	AAEL018149-RA	575	-36.94	150	-14.69	22	1769	1569 816 839 876
aae-miR-71-3p	AAEL018149	*IRc*	AAEL018149-RA	292	-32.99	148	-23.23	22	1769	198 376
aae-let-7	AAEL018149	*IRc*	AAEL018149-RA	291	-34.08	151	-20.37	21	1769	517 1032
aae-miR-309b-5p	AAEL018149	*IRc*	AAEL018149-RA	285	-42.12	145	-23.07	23	1769	42 1405
aae-miR-281-3p	AAEL018149	*IRc*	AAEL018149-RA	152	-18.8	152	-18.8	22	1769	1691
aae-miR-263a-3p	AAEL017285	*Or130*	AAEL017285-RA	292	-38.91	150	-22.1	22	200	45 30
aae-miR-1	AAEL017285	*Or130*	AAEL017285-RA	140	-13.02	140	-13.02	22	200	22
aae-miR-1	AAEL002587	*OBP11*	AAEL002587-RA	312	-29.21	172	-16.69	22	1220	1047 841
aae-miR-305-5p	AAEL002587	*OBP11*	AAEL002587-RA	291	-44.23	149	-24.55	24	1220	218 766
aae-miR-92a-3p	AAEL002587	*OBP11*	AAEL002587-RA	158	-21.73	158	-21.73	21	1220	770
aae-miR-31	AAEL002587	*OBP11*	AAEL002587-RA	145	-20.14	145	-20.14	23	1220	782
aae-miR-1174	AAEL002587	*OBP11*	AAEL002587-RA	145	-11.36	145	-11.36	21	1220	1016

Table 4.2 Targets of miRs with specific expression profiles in *A. aegypti*. The top 5 targets with the highest score and the lowest energy are shown for each miR.

miR	Gene	Gene Name	Transcript	Total Score	Total Energy	Max Score	Max Energy	miR (bp)	3'UTR (bp)	Positions
aae-miR-285	AAEL001617	*Or124*	AAEL001617-RA	303	-34.17	160	-18.37	22	200	122 145
aae-miR-285	AAEL013507	*Or52*	AAEL013507-RA	150	-15.47	150	-15.47	22	1608	1146
aae-miR-285	AAEL013893	*Or125*	AAEL013893-RA	148	-17.1	148	-17.1	22	960	160
aae-miR-285	AAEL001221	*Or69*	AAEL001221-RA	144	-15.63	144	-15.63	22	200	97
aae-miR-285	AAEL009696	*IR75d*	AAEL009696-RA	141	-14.86	141	-14.86	22	200	84
aae-miR-263a-5p	AAEL011571	*Gr14*	AAEL011571-RA	163	-22.66	163	-22.66	23	200	79
aae-miR-263a-5p	AAEL001617	*Or124*	AAEL001617-RA	152	-13.91	152	-13.91	23	200	123
aae-miR-263a-5p	AAEL013893	*Or125*	AAEL013893-RA	148	-13.52	148	-13.52	23	960	136
aae-miR-263a-5p	AAEL000018	*IR41j*	AAEL000018-RA	147	-17.87	147	-17.87	23	200	16
aae-miR-263a-5p	AAEL007826	*Forage2*	AAEL007826-RA	143	-13.58	143	-13.58	23	841	451
aae-miR-1891	AAEL002596	*OBP9*	AAEL002596-RA	158	-21.74	158	-21.74	22	93	9
aae-miR-1891	AAEL003341	*IR7q.2*	AAEL003341-RA	151	-16.52	151	-16.52	22	200	21
aae-miR-1891	AAEL002605	*OBP14*	AAEL002605-RA	148	-13.44	148	-13.44	22	200	159
aae-miR-1891	AAEL015554	*OBP61*	AAEL015554-RA	148	-13.44	148	-13.44	22	200	159
aae-miR-1891	AAEL011127	*IR104.3*	AAEL011127-RA	145	-17.93	145	-17.93	22	1024	195
aae-miR-34-5p	AAEL005999	*Or2*	AAEL005999-RA	162	-24.54	162	-24.54	22	1012	769
aae-miR-34-5p	AAEL013507	*Or52*	AAEL013507-RA	149	-23.66	149	-23.66	22	1608	732
aae-miR-34-5p	AAEL017305	*Or81*	AAEL017305-RA	147	-23.98	147	-23.98	22	200	158
aae-miR-34-5p	AAEL014430	*OBP58*	AAEL014430-RA	147	-22.11	147	-22.11	22	200	110
aae-miR-34-5p	AAEL011804	*IR107.1*	AAEL011804-RA	146	-16.41	146	-16.41	22	200	63
aae-miR-79-3p	AAEL018101	*IR7v.3*	AAEL018101-RA	308	-23.38	156	-12.67	22	1110	780 341
aae-miR-79-3p	AAEL017347	*Or87*	AAEL017347-RA	297	-22.25	152	-11.84	22	200	48 1
aae-miR-79-3p	AAEL005770	*OBP21*	AAEL005770-RA	155	-9.52	155	-9.52	22	565	401
aae-miR-79-3p	AAEL010718	*OBP44*	AAEL010718-RA	155	-17.76	155	-17.76	22	200	149
aae-miR-79-3p	AAEL017505	*Or103*	AAEL017505-RA	155	-11.22	155	-11.22	22	200	62
aae-miR-929	AAEL007826	*Forage2*	AAEL007826-RA	175	-21.53	175	-21.53	21	841	695
aae-miR-929	AAEL017394	*Gr66*	AAEL017394-RA	149	-13	149	-13	21	200	120
aae-miR-929	AAEL008013	*OBP38*	AAEL008013-RA	145	-14.47	145	-14.47	21	643	280
aae-miR-929	AAEL011174	*Gr11*	AAEL011174-RA	145	-22.92	145	-22.92	21	200	153
aae-miR-929	AAEL006360	*IR76b*	AAEL006360-RA	145	-14.72	145	-14.72	21	471	139
aae-miR-965	AAEL018097	*IR115*	AAEL018097-RA	165	-21.77	165	-21.77	22	200	87

Table 4.2 Continued

miR	Gene	Gene Name	Transcript	Total Score	Total Energy	Max Score	Max Energy	miR (bp)	3'UTR (bp)	Positions
aae-miR-965	AAEL005875	*IR75l*	AAEL005875-RA	158	-10.96	158	-10.96	22	331	288
aae-miR-965	AAEL007786	*IR120*	AAEL007786-RA	155	-14.7	155	-14.7	22	239	121
aae-miR-965	AAEL008332	*IR100c.1*	AAEL008332-RA	151	-17.15	151	-17.15	22	200	155
aae-miR-965	AAEL017182	*Gr43*	AAEL017182-RA	148	-9.5	148	-9.5	22	200	105
aae-miR-92b-3p	AAEL005754	*Forage1*	AAEL005754-RA	159	-23.68	159	-23.68	22	200	5
aae-miR-92b-3p	AAEL002587	*OBP11*	AAEL002587-RA	158	-22.46	158	-22.46	22	1220	769
aae-miR-92b-3p	AAEL000011	*IR41e*	AAEL000011-RA	156	-22.21	156	-22.21	22	515	334
aae-miR-92b-3p	AAEL015227	*IR7h.2*	AAEL015227-RA	155	-14.02	155	-14.02	22	200	94
aae-miR-92b-3p	AAEL001303	*Or49*	AAEL001303-RA	152	-15.75	152	-15.75	22	1039	349
aae-miR-279	AAEL008442	*Or14*	AAEL008442-RA	169	-19.77	169	-19.77	22	200	1
aae-miR-279	AAEL017246	*Or86*	AAEL017246-RA	153	-13.38	153	-13.38	22	200	14
aae-miR-279	AAEL017305	*Or81*	AAEL017305-RA	151	-11.55	151	-11.55	22	200	145
aae-miR-279	AAEL017534	*Or56*	AAEL017534-RA	147	-15.24	147	-15.24	22	200	28
aae-miR-279	AAEL013214	*Forage3*	AAEL013214-RA	142	-15.87	142	-15.87	22	259	53

4.3.2 miR discovery

A total of 16 new miRs were discovered in the antenna of host-seeking females (Table 4.3). Twelve novel miRs have reads mapping only to the guide sequence regions, in other words, to only one end of the hairpin structure (Figure 4.1). This indicates that the “passenger strand” was not detected. It was possibly that it was already degraded when total RNA was isolated. The remaining four novel miRs have reads mapping to both ends of the hairpin structure. The hairpin loop structures of all new miRs are similar to the known miRs (Figure 4.1).

4.3.3 Target prediction for novel miRs

The 3’UTRs of the olfaction genes were used for target prediction with the novel miRs sequences. The same parameters used for target prediction of known miRs were used in miRanda. The top five targets of all novel miRs are *Or103, Or49*, *IRc*, *Or47*, and *IR75k.3*. These are the same targets found for the known miRs with unique expression patters, for example highly expressed in the antenna of host-seeking females (Table 4.4 and Table A26). It indicates that the long 3’UTRs of these olfaction genes have multiple binding sites for several miRs.

4.3.4 miR-263a genome wide targets

Since miR-263a is mainly expressed in the antenna of *A. aegypti* and protects sensory cells from apoptosis during *Drosophila* eye development (Hilgers et al. 2010), I checked for all possible targets of this miR in the *A. aegypti* genome. Our target prediction suggests it may also be able to regulate the expression of olfaction genes in *A. aegypti* (*Gr14, Or124, Or125, Ir41j* and *Forage2*). However, it could also interact with other genes not related to olfaction. Taking advantage of its 100% sequence identity with the *A. gambiae* miR-263a (exact the same sequence), I obtained its targets from the European Bioinformatics Institute (MicroCosm Targets). The targets of aga-miR-263a in *A. aegypti* genome were also predicted using miRanda. The top 20 potential targets of aga-miR-263a are shown on Table 4.5. Unfortunately the majority of the potential targets do not have any functional annotation in the *A. aegypti* genome. The *D. melanogaster* orthologs of the targets genes were obtained from Biomart for all genes (Table 4.6). Surprisingly, two IRs (*Ir100e.1* and *Ir100e.2*) and a glutamate receptor were predicted as potential targets. However, their transcript levels do not change after blood feeding. The remaining targets have a variety of functions, such as sugar transport, DNA binding, transcription factor, ligase, positive regulation of Notch signaling pathway, etc. However, some to the targets with the highest scores do not have any known function and a BLAST search did not generate any hits with known functions in other species (data not shown).

Table 4.3 Novel miRs expressed in the antenna of host-seeking females of *A. aegypti*. miRs with positive scores have reads mapping to the both ends of the hairpin loop structure (guide and passenger strands). miRs with negative scores have reads mapping only to one end of the hairpin loop structure (guide strand).

Name	Score	Reads	Loci	Sequence
Novel-miR1	828.09	44	supercont1.371-280438~280508	GCCGGUUCGGGCAAUGGG
Novel-miR2	405.96	37	supercont1.836-102185~102255	GCCGGUUCGGGCAAUGGG
Novel-miR3	112.68	160	supercont1.39-1286383~1286461	GAAUGAGCGAAAGGGAAUCCGG
Novel-miR4	0.41	13	supercont1.241+1025592~1025662	ACAAUUCCGGAGCCUGUU
Novel-miR5	-1.04	83	supercont1.112-1359802~1359882	CGGCUAGCUCAGUCGGUAGAGCA
Novel-miR6	-2.09	63	supercont1.183-227028~227104	GCAAGCGCGGGUAAACGGCGG
Novel-miR7	-2.53	212	supercont1.562+528318~528398	GGGAAGAGCUCAGCACGUAGGGG
Novel-miR8	-2.67	29	supercont1.50+1768498~1768576	GGGUCGGGUUACGGACUGAUUU
Novel-miR9	-2.73	32	supercont1.342-249434~249514	GUCGGGAUUAUGGAUUGAAAUGG
Novel-miR10	-3.54	27	supercont1.607+494439~494515	GGGCUUGGAAACACUAGCGGG
Novel-miR11	-4.11	8	supercont1.478+517744~517822	ACGGCGGGAUUUGUAGACAGGG
Novel-miR12	-4.24	203	supercont1.472+424409~424487	GCCGGUUCGGGCAAUGGGCGCC
Novel-miR13	-4.3	83	supercont1.1244-96672~96744	GACUGAAUAUACCGAGAAA
Novel-miR14	-5.28	82	supercont1.281-1192150~1192220	GGCCCGUAGAGCGGCGCA
Novel-miR15	-5.36	143	supercont1.478+538060~538134	GACCGAUAGCUCUUCCGGAA
Novel-miR16	-5.7	83	supercont1.32-472366~472446	CGGCUAGCUCAGUCGGUAGAGCA

Table 4.4 Targets of novel miRs expressed in the antenna of host seeking females of *A. aegypti*.

miR	Gene ID	Gene Name	Transcript	Total Score	Total Energy	Max Score	Max Energy	miR (bp)	3'UTR (bp)	Positions
Novel-miR1	AAEL014270	*IR40a*	AAEL014270-RA	146	-18.94	146	-18.94	18	200	180
Novel-miR1	AAEL018084	*IR107.2*	AAEL018084-RA	146	-18.94	146	-18.94	18	200	181
Novel-miR1	AAEL007110	*Or16*	AAEL007110-RA	140	-16.57	140	-16.57	18	1776	333
Novel-miR2	AAEL014270	*IR40a*	AAEL014270-RA	146	-18.94	146	-18.94	18	200	180
Novel-miR2	AAEL018084	*IR107.2*	AAEL018084-RA	146	-18.94	146	-18.94	18	200	181
Novel-miR2	AAEL007110	*Or16*	AAEL007110-RA	140	-16.57	140	-16.57	18	1776	333
Novel-miR3	AAEL017565	*Gr63*	AAEL017565-RA	152	-17.52	152	-17.52	22	200	5
Novel-miR3	AAEL018090	*IR110*	AAEL018090-RA	150	-22.81	150	-22.81	22	280	86
Novel-miR3	AAEL000012	*Gr6*	AAEL000012-RA	150	-18.73	150	-18.73	22	200	42
Novel-miR3	AAEL014690	*IR7n.2*	AAEL014690-RA	143	-14.24	143	-14.24	22	200	100
Novel-miR3	AAEL005772	*OBP22*	AAEL005772-RA	142	-10.2	142	-10.2	22	130	91
Novel-miR3	AAEL009599	*OBP41*	AAEL009599-RA	141	-13.41	141	-13.41	22	80	53
Novel-miR3	AAEL017347	*Or87*	AAEL017347-RA	141	-14.24	141	-14.24	22	200	16
Novel-miR3	AAEL017065	*Or92*	AAEL017065-RA	140	-13.2	140	-13.2	22	200	76
Novel-miR4	AAEL003341	*IR7q.2*	AAEL003341-RA	284	-23.44	142	-11.98	18	200	119 170
Novel-miR4	AAEL018149	*IRc*	AAEL018149-RA	159	-19.11	159	-19.11	18	1769	71
Novel-miR4	AAEL017271	*Or127*	AAEL017271-RA	148	-11.42	148	-11.42	18	200	74
Novel-miR4	AAEL008090	*IRa*	AAEL008090-RA	145	-15.78	145	-15.78	18	1016	32
Novel-miR4	AAEL013695	*IRh*	AAEL013695-RA	145	-15.78	145	-15.78	18	995	32
Novel-miR4	AAEL001303	*Or49*	AAEL001303-RA	144	-12.58	144	-12.58	18	1039	806
Novel-miR4	AAEL018100	*IR7v.2*	AAEL018100-RA	144	-11.3	144	-11.3	18	200	130
Novel-miR4	AAEL007110	*Or16*	AAEL007110-RA	142	-13.59	142	-13.59	18	1776	1102
Novel-miR4	AAEL011490	*OBP50*	AAEL011490-RA	142	-10.39	142	-10.39	18	200	1
Novel-miR4	AAEL002587	*OBP11*	AAEL002587-RA	141	-12.89	141	-12.89	18	1220	39
Novel-miR4	AAEL007786	*IR120*	AAEL007786-RA	140	-14.01	140	-14.01	18	239	168
Novel-miR5	AAEL000035	*OBP57*	AAEL000035-RA	144	-23.49	144	-23.49	23	200	88
Novel-miR5	AAEL010275	*Gr29*	AAEL010275-RA	141	-18.23	141	-18.23	23	200	87
Novel-miR6	AAEL006108	*OBP24*	AAEL006108-RA	151	-14.28	151	-14.28	21	158	14
Novel-miR6	AAEL006103	*OBP25*	AAEL006103-RB	151	-14.28	151	-14.28	21	155	14
Novel-miR6	AAEL006103	*OBP25*	AAEL006103-RA	151	-14.28	151	-14.28	21	155	14
Novel-miR6	AAEL003340	*IR7k.1*	AAEL003340-RA	147	-21.98	147	-21.98	21	200	69
Novel-miR6	AAEL018104	*IR108*	AAEL018104-RA	143	-21.04	143	-21.04	21	144	122

Table 4.4 Continued

miR	Gene ID	Gene Name	Transcript	Total Score	Total Energy	Max Score	Max Energy	miR (bp)	3'UTR (bp)	Positions
Novel-miR7	AAEL005770	*OBP21*	AAEL005770-RA	155	-25.88	155	-25.88	23	565	258
Novel-miR7	AAEL005999	*Or2*	AAEL005999-RA	153	-17.82	153	-17.82	23	1012	12
Novel-miR7	AAEL008332	*IR100c.1*	AAEL008332-RA	152	-17.97	152	-17.97	23	200	86
Novel-miR7	AAEL013200	*Gr59*	AAEL013200-RA	150	-19.2	150	-19.2	23	200	138
Novel-miR7	AAEL017063	*Gr32*	AAEL017063-RA	147	-20.14	147	-20.14	23	200	101
Novel-miR7	AAEL000616	*Or42*	AAEL000616-RA	146	-20.86	146	-20.86	23	1395	670
Novel-miR7	AAEL011127	*IR104.3*	AAEL011127-RA	140	-16.03	140	-16.03	23	1024	607
Novel-miR8	AAEL018149	*IRc*	AAEL018149-RA	148	-29.56	148	-29.56	22	1769	15
Novel-miR8	AAEL001303	*Or49*	AAEL001303-RA	147	-28.79	147	-28.79	22	1039	935
Novel-miR8	AAEL011499	*OBP47*	AAEL011499-RA	143	-25.81	143	-25.81	22	200	111
Novel-miR8	AAEL008090	*IRa*	AAEL008090-RA	142	-18.21	142	-18.21	22	1016	158
Novel-miR8	AAEL013695	*IRh*	AAEL013695-RA	142	-18.21	142	-18.21	22	995	158
Novel-miR8	AAEL010714	*OBP45*	AAEL010714-RA	141	-22.06	141	-22.06	22	200	136
Novel-miR9	AAEL017505	*Or103*	AAEL017505-RA	314	-42.48	163	-21.52	23	200	140 37
Novel-miR9	AAEL006396	*OBP31*	AAEL006396-RA	167	-24.13	167	-24.13	23	200	117
Novel-miR9	AAEL010277	*Gr28*	AAEL010277-RA	149	-16.48	149	-16.48	23	200	122
Novel-miR9	AAEL015556	*Gr27*	AAEL015556-RA	149	-15.61	149	-15.61	23	200	179
Novel-miR9	AAEL000012	*Gr6*	AAEL000012-RA	147	-14.28	147	-14.28	23	200	32
Novel-miR9	AAEL011690	*IR87a.2*	AAEL011690-RA	146	-20.82	146	-20.82	23	649	309
Novel-miR9	AAEL009696	*IR75d*	AAEL009696-RA	141	-18.56	141	-18.56	23	200	163
Novel-miR9	AAEL010058	*Gr3*	AAEL010058-RA	140	-13.32	140	-13.32	23	200	1
Novel-miR10	AAEL014086	*IR75o*	AAEL014086-RA	148	-20.34	148	-20.34	21	200	90
Novel-miR10	AAEL000011	*IR41e*	AAEL000011-RA	142	-19.5	142	-19.5	21	515	22
Novel-miR11	AAEL014087	*IR75k.3*	AAEL014087-RA	151	-26.83	151	-26.83	22	200	87
Novel-miR11	AAEL006393	*OBP28*	AAEL006393-RA	140	-20.79	140	-20.79	22	200	32
Novel-miR12	AAEL014270	*IR40a*	AAEL014270-RA	146	-19.55	146	-19.55	22	200	176
Novel-miR12	AAEL018084	*IR107.2*	AAEL018084-RA	146	-19.55	146	-19.55	22	200	177
Novel-miR12	AAEL007110	*Or16*	AAEL007110-RA	143	-21.13	143	-21.13	22	1776	328
Novel-miR12	AAEL017277	*Or61*	AAEL017277-RA	142	-26.07	142	-26.07	22	200	129
Novel-miR12	AAEL018149	*IRc*	AAEL018149-RA	141	-23.34	141	-23.34	22	1769	174
Novel-miR13	AAEL011895	*Or48*	AAEL011895-RA	153	-11.45	153	-11.45	19	612	476
Novel-miR13	AAEL002605	*OBP14*	AAEL002605-RA	150	-12.39	150	-12.39	19	200	106

Table 4.4 Continued

miR	Gene ID	Gene Name	Transcript	Total Score	Total Energy	Max Score	Max Energy	miR (bp)	3'UTR (bp)	Positions
Novel-miR13	AAEL015554	*OBP61*	AAEL015554-RA	150	-12.39	150	-12.39	19	200	106
Novel-miR13	AAEL002380	*Gr1*	AAEL002380-RA	147	-8.42	147	-8.42	19	200	66
Novel-miR13	AAEL000628	*Or63*	AAEL000628-RA	147	-7.9	147	-7.9	19	200	171
Novel-miR13	AAEL018105	*IR112*	AAEL018105-RA	145	-12.65	145	-12.65	19	373	144
Novel-miR13	AAEL018072	*IR118.2*	AAEL018072-RA	145	-15.25	145	-15.25	19	200	36
Novel-miR13	AAEL018073	*IR118.1*	AAEL018073-RA	145	-15.25	145	-15.25	19	200	36
Novel-miR13	AAEL017236	*Or99*	AAEL017236-RA	143	-18.11	143	-18.11	19	200	100
Novel-miR13	AAEL000011	*IR41e*	AAEL000011-RA	140	-7.68	140	-7.68	19	515	463
Novel-miR13	AAEL017040	*Gr62*	AAEL017040-RA	140	-7.85	140	-7.85	19	200	145
Novel-miR15	AAEL013893	*Or125*	AAEL013893-RA	151	-21.56	151	-21.56	20	960	73
Novel-miR15	AAEL002538	*IRe*	AAEL002538-RA	142	-11.31	142	-11.31	20	200	74
Novel-miR15	AAEL003340	*IR7k.1*	AAEL003340-RA	141	-11.39	141	-11.39	20	200	181
Novel-miR15	AAEL017569	*Gr44*	AAEL017569-RA	140	-14.7	140	-14.7	20	200	33
Novel-miR16	AAEL000035	*OBP57*	AAEL000035-RA	144	-23.49	144	-23.49	23	200	88
Novel-miR16	AAEL010275	*Gr29*	AAEL010275-RA	141	-18.23	141	-18.23	23	200	87

Table 4.5 Targets of aga-miR-263 in the *A. aegypti* genome. Targets were predicted using miRanda with the 3'UTR or 200bp flanking region after the stop codon of all transcripts of *A. aegypti*.

Transcript ID	Location	Start	End	Strand	Score	*p* value
AAEL005464-RA	supercont1.158	1976691	1976713	-	19.82	0.0024
AAEL010944-RA	supercont1.524	742155	742178	+	19.48	0.0032
AAEL001641-RA	supercont1.38	1724938	1724959	-	19.14	0.0044
AAEL001868-RA	supercont1.44	107450	107473	+	18.98	0.0052
AAEL014016-RA	supercont1.984	343681	343704	-	18.80	0.0019
AAEL013405-RA	supercont1.838	275249	275272	+	18.80	0.0061
AAEL007541-RA	supercont1.262	1540065	1540091	-	18.69	0.0068
AAEL015647-RA	supercont1.4210	3688	3711	+	18.65	0.0070
AAEL015079-RA	supercont1.1462	49528	49551	+	18.65	0.0070
AAEL014912-RA	supercont1.1334	47367	47390	+	18.65	0.0070
AAEL009873-RA	supercont1.435	944655	944678	+	18.65	0.0070
AAEL004053-RA	supercont1.106	699071	699093	+	18.58	0.0075
AAEL013135-RA	supercont1.795	211585	211608	+	18.54	0.0078
AAEL000988-RA	supercont1.20	3006446	3006469	-	18.54	0.0078
AAEL003804-RA	supercont1.97	160330	160354	-	18.50	0.0081
AAEL013388-RA	supercont1.834	245576	245599	+	18.38	0.0091
AAEL009400-RC	supercont1.394	166888	166914	+	18.35	0.0093
AAEL007398-RA	supercont1.253	860669	860692	-	18.35	0.0001
AAEL003003-RA	supercont1.74	904107	904130	+	18.32	0.0095
AAEL012288-RA	supercont1.675	10268	10291	-	18.32	0.0095

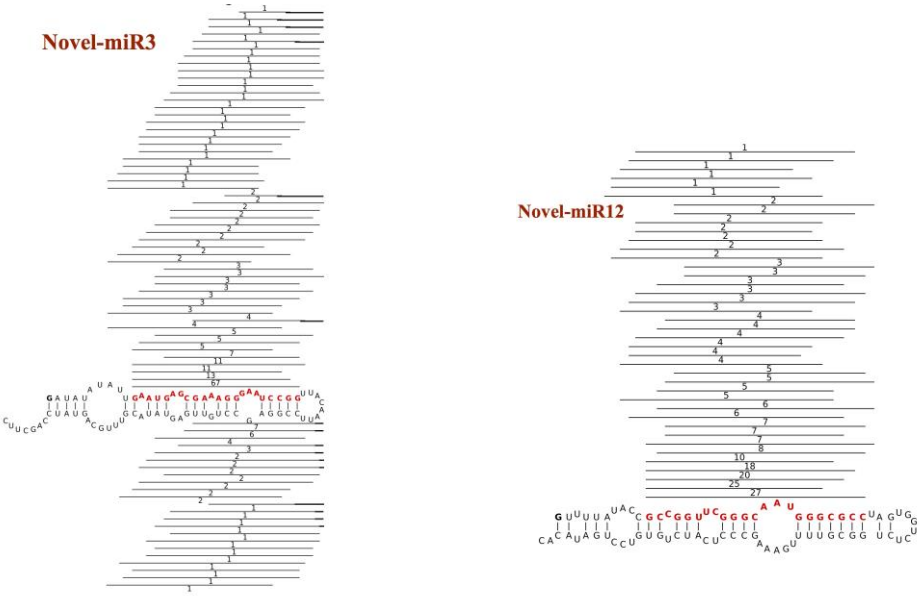

Figure 4.1 Hairpin loop structure of novel miRs and how the reads map to different miRs. Sequence in red font is the mature miR. Left: Novel-miR3 – reads mapping to the guide and passenger strands; Right: Novel-miR12 – reads mapping to only one end of the guide strands.

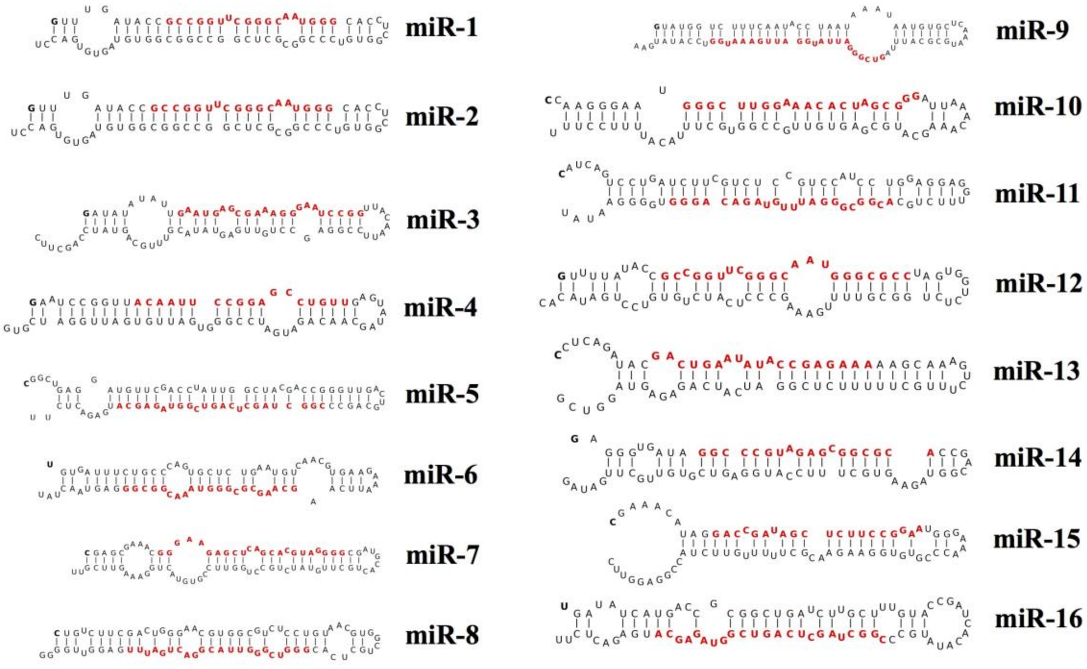

Figure 4.2 Novel miRs discovered and expressed in the antenna of *A. aegypti*. Red font represents the mature sequences.

Table 4.6 Targets of aga-miR-263a in the *A. aegypti* genome. MiR-263a has the same mature sequence in *Drosophila*, *Aedes* and *Anopheles*.

Gene stable ID	Transcript stable ID	Gene description	*Drosophila melanogaster* Ortholog	Name	Prediction	Homology type	% identity
AAEL000988	AAEL000988-RA	conserved hypothetical protein	FBgn0033225	CG1550	tubulin-tyrosine ligase activity	ortholog_one2one	54
AAEL001641	AAEL001641-RA	deoxyribonuclease I, putative					
AAEL001868	AAEL001868-RA	conserved hypothetical protein					
AAEL003003	AAEL003003-RA	glutamate-gated chloride channel	FBgn0024963	GluCl	extracellular-glutamate-gated chloride channel activity	ortholog_one2one	80
AAEL003804	AAEL003804-RA	conserved hypothetical protein					
AAEL004053	AAEL004053-RA	conserved hypothetical protein	FBgn0030943	CG6540	nucleocytoplasmic transporter activity	ortholog_one2one	36
AAEL005464	AAEL005464-RA	conserved hypothetical protein	FBgn0027585	CG8740		ortholog_one2one	30
AAEL007398	AAEL007398-RA	hypothetical protein					
AAEL007541	AAEL007541-RA	DNA polymerase delta small subunit	FBgn0027903	CG12018	DNA binding	ortholog_one2many	49
AAEL009400	AAEL009400-RC	ccr4-associated factor	FBgn0036239	Pop2	poly(A)-specific ribonuclease activity	ortholog_one2one	54
AAEL009873	AAEL009873-RA	conserved hypothetical protein					
AAEL010944	AAEL010944-RA	conserved hypothetical protein					
AAEL012288	AAEL012288-RA	sugar transporter	FBgn0029932	CG4607	substrate-specific transmembrane transporter activity	ortholog_many2many	35
AAEL012288	AAEL012288-RA	sugar transporter	FBgn0034045	CG8249	glucose transmembrane transporter activity	ortholog_many2many	38
AAEL013135	AAEL013135-RA	chromodomain helicase DNA binding protein	FBgn0262519	Mi-2	nucleosome-dependent ATPase activity	ortholog_many2many	88
AAEL013135	AAEL013135-RA	chromodomain helicase DNA binding protein	FBgn0023395	Chd3	DNA binding	ortholog_many2many	74
AAEL013388	AAEL013388-RA	conserved hypothetical protein					
AAEL013405	AAEL013405-RA	nk homeobox protein	FBgn0002941	slou	sequence-specific DNA binding	ortholog_one2one	64

Table 4.6 Continued

Gene stable ID	Transcript stable ID	Gene description	*Drosophila melanogaster* Ortholog	Name	Prediction	Homology type	% identity
AAEL014016	AAEL014016-RA	breast cancer metastasis-suppressor	FBgn0030434	Brms1	positive regulation of Notch signaling pathway	ortholog_one2one	60
AAEL014912	AAEL014912-RA	RrnaAD	FBgn0037778	mtTFB2	mitochondrial transcription factor B2	ortholog_one2many	32
AAEL015079	AAEL015079-RA	IR100e.1	FBgn0039879	Ir100a	ligand-gated ion channel activity	ortholog_many2many	25
AAEL015079	AAEL015079-RA	IR100e.1	FBgn0083979	Ir10a	ligand-gated ion channel activity	ortholog_many2many	22
AAEL015647	AAEL015647-RA	IR100e.2	FBgn0039879	Ir100a	ligand-gated ion channel activity	ortholog_many2many	24
AAEL015647	AAEL015647-RA	IR100e.2	FBgn0083979	Ir10a	ligand-gated ion channel activity	ortholog_many2many	23

4.3.5 Injection of antagomir in larvae, pupae and 12h old adult females

Initially I injected 6h old pupae with mir-263a antagomir solution (300ng). However, less than 5% of the pupae survived to become adults, which resulted in a low number of insects to perform behavioral experiments. Next, I injected 12h old females with both antagomir and scrambled miR. Although most of the adults survived, no phenotype was observed (mortality or morphological changes in antennae). Finally, the injection of antagomir in late instar larvae also caused high mortality, not only right after the injection but also during the metamorphosis (Figure 4.3). No phenotype was observed in the adults that emerged (deformed or missing body parts, longer pupation period, differences in size, or anything different from the wild type), and the numbers of adults obtained was not enough to run choice experiments in the wind tunnel.

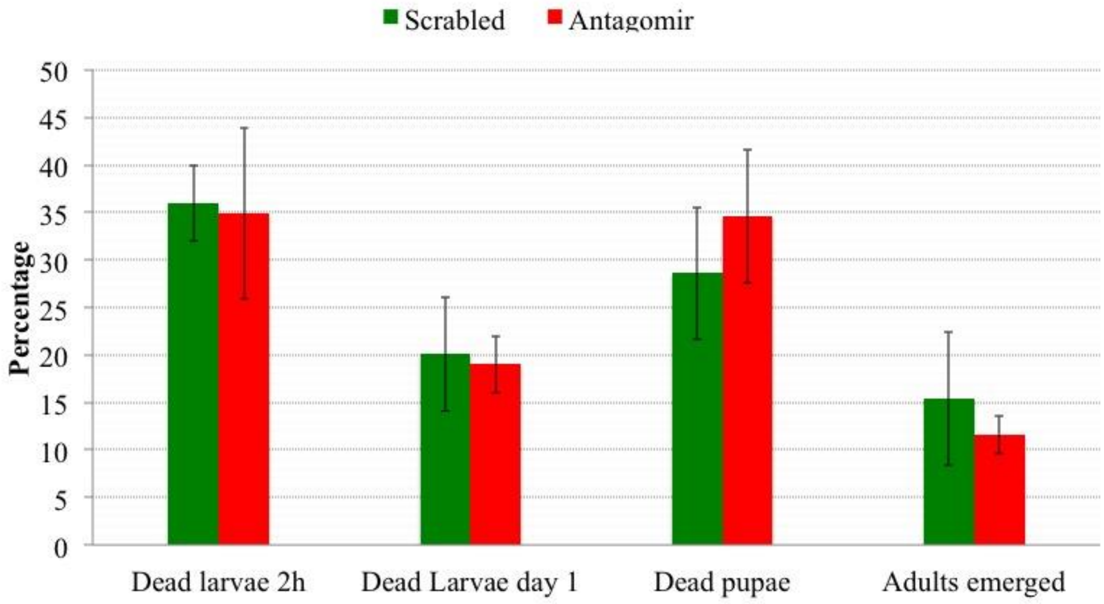

Figure 4.3 Percentage of emerged adults and mortality of larvae/pupae after injection of antagomir and scrabled miR in late last instar larvae. Average of three replicates (approximately 100 larvae injected for each replicate).

4.3.6 Olfaction genes with long 3'UTR are targeted by multiple miRs

I notice that the olfaction genes potentially regulated by known miRs (top 10 with the highest score) or all new miRs had long 3'UTR. Indeed, olfaction genes with long 3'UTR are predicted to be good targets of several miRs with an overall high score (Table A24). However, not all olfaction genes have long 3'UTR and more than 50% of them do not have an annotated 3'UTR. The number of polyadenylation sites (PAS) in these olfaction genes is very high (Table A24). For example, *Or16* has 21 predicted PAS and *IRd* has 41. These results indicated an incredible high number of isoforms that could be expressed in the antenna of mosquitoes. However, traditional gene expression analysis cannot detect any of them since they only look or the number of reads mapped to the exonic regions.

4.4 Discussion

Target prediction revealed that known or new miRs roughly target the can potentially target the olfaction genes (Table A25 and A26). Interestingly, the miRs with a unique expression profile (expressed in antenna or in host-seeking females) were among the top 1.17% of miRs that are predicted to regulate olfaction genes in the antenna of *A. aegypti*. It suggests that their expression profiles might be a good indication of their specific biological role in the antenna of mosquitoes. Another important observation is the long 3'UTR that olfaction genes have. Unfortunately the majority of the olfaction genes have an unknown 3'UTR length. The main implication of a gene that has a long 3'UTR is that the number of miRs that it can interact with will be greater than a gene with a shorter UTR. miRs play an important role in the evolution of 3'UTRs and the establishment of tissue identity (Chen et al. 2012). Genes with longer 3'UTRs can have more polyadenylation sites and therefore produce transcripts with different miR binding sites. Having a longer 3'UTR can also be advantageous since the translation of mRNA to protein can be modified by competition among the transcripts for miR interactions. For example, rapid response to environmental stress, changes in diet, fine-tuning of protein amount needed, coordinate the regulation of protein families, and tissue specific control of transcript levels (Mazumder et al. 2003) may be regulated by the different isoforms generated by having multiple polyadenylation sites in the

3’UTRThe overall length of the 3’UTR has increased over the evolutionary time alongside with the morphological complexity of the organisms (Mazumder et al. 2003; Li and Su 2006; Wehrspaun et al. 2014), suggesting it is important for gene regulation.

It is important to note that *A. aegypti* has more annotated olfaction genes than any other mosquito species and *D. melanogaster*. The expansion of the olfactory gene repertory has been associated with the adaptation to feed on humans and breed on human made habitats (Melo et al. 2004; Bohbot and Vogt 2005; Nene et al. 2007; Zhou et al. 2008). It will be interesting to compare the 3’UTRs of olfaction genes between anthropophilic and zoophilic mosquitoes. It will also important to compare the 3’UTR of olfaction genes expressed in multiple tissues, such as the antenna, maxillary palpi, and proboscis. It is not known if the isoform varying on the 3’UTR are differentially expressed as the mosquitoes switch between different behavioral states. For example, typical gene expression analyses looks for the number of reads mapping to exonic regions, but does not examine different isoforms which are different only by the length of their 3’UTR.

In mammals the lengthening of 3’UTR have been associated with increase coordination in the expression of ion channel/transport in the brain via miRs (Wehrspaun et al. 2014). 3’UTR can modulate the relative transcriptional abundance of protein coding genes via miR mediated cross talk. In humans, genes expressed in the brain have long alternative 3’UTR with multiple polyadenylation sites. Ion channel/transporter genes are enriched in human brain and exhibit an increased transcriptional coordination via the competition of binding sites for miRs. For example, different transcripts can be generated with long or short 3'UTRs. Those with long 3'UTRs usually have multiple miR binding sites and can be regulated by several miRs. Therefore, typical RNAseq experiments for mRNA would not detect these different transcripts and no change in the expression can be noticed.

Ionotropic and odorant receptors are enriched in the female antenna and their regulation may be achieved by competition of miRs to bind to their different 3'UTRs. For instance, different isoforms of genes can be expressed in the antenna of males and females or nectar-seeking and host-seeking females. These isoforms may have different binding sites for miRs. Consequently, even though the expression level of olfaction genes may not change after blood feeding, the isoforms being expressed can be regulated by different miRs. Moreover, in humans several brain-expressed miRs are found within the axonal compartments (Loohuis et al. 2012) and are able to actively regulate the local mRNA translation. The overlapped localization with ion channel/transporter transcripts indicates the presence of a regulatory feedback loop. Given that multiple miRs appear to target the same olfaction genes, it is possible that such mechanism of co-localization of miRs and mRNA transcripts in olfaction neurons may be present in the antennae of mosquitoes, providing dynamic and robust changes in the abundance of olfactory receptors transcripts. Therefore miRs may function in the sensory neurons of the antenna as molecular switches, regulating the olfaction gene expression as a mosquito age or change its behavior due to blood feeding or egg laying. miRs may be responsible for fine-tuning and robustness of olfaction gene expression in the antenna. By tweaking the transcript levels in the antenna, miRs act to reinforce robust olfactory gene expression responses post-transcriptionally. These functions may be important only when mosquitoes are under stressful conditions.

The lack of phenotypes after the injection of high amounts of miR-263a antagomir in larva, pupa, and 12h old females may be due to different reasons. First, this is the most expressed miR in the antenna of mosquitoes and the antagomir may not have reached the antennal tissue at a concentration high enough to act as an effective sponge for the endogenous miRs. Second, the expression of miR-263a may increase to overcome the levels of the exogenous inhibitor. Third, only miR-275 was successfully knocked down with antagormirs in *A. aegypti* (Bryant et al. 2010), and it is mainly expressed in the midgut, a tissue that the inhibitor molecules can reach more easily. Finally, mosquito larvae are very sensitive to injections and only 10% of the injected larvae will become adults. Therefore, transgenic miR sponges (Loya et al. 2009) may be more suitable for knocking out the expression of miRs in the antenna of mosquitoes in the future. Another possibility is to use the CRISPR-Cas9 system (Kistler et al. 2015) to conditionally knock down the expression of miRs in specific tissues of *A. aegypti* only during the pupal or adults stages.

The relevance of this work was to find novel miRs and olfaction genes that may be targeted by miRs expressed in the antenna of *A. aegypti*. Additionally, our data suggest that mosquitoes may use a more complex gene regulation strategy in the antenna. Several olfaction genes (*Or52*, *Or42, Ird*, *Obp11*, *Or11*, *Ir7v.3, Or49* and *Ir104.3*) have multiple binding sites for several miRs and long 3’UTRs. Therefore, olfaction genes may have several polyadenylation sites in their 3’UTR and multiple isoforms.

CHAPTER V

CONCLUSION

The chemosensory system of the mosquito is diverse and displays differences within the olfaction organs with contrasting transcript levels of the olfaction genes. In this study the olfaction transcript profile was evaluated in the head and thorax (HT), and antenna of *Aedes aegypti*. Not surprisingly, the expression profile found in the antenna is quite different from contrast to from maxillary palp, proboscis, and legs reported in other studies (Bohbot et al. 2014; Sparks et al. 2014). It indicates each sensory organ performs different roles in *A. aegypti* regarding the detection of chemical cues.

Males and females have different levels of olfaction transcripts in their antenna, which reflects the modulation of chemosensation in mosquitoes. In the female antenna the expression level of most odorant receptors is higher than in males. In males, only a few odorant binding proteins and ionotropic receptors are enhanced in the antenna. It validates the hypothesis that females rely on the olfactory system to find hosts, whereas males rely more on the auditory system to find mates (Rinker et al. 2013a) but also uses olfaction cues to find hosts where females may be present. Further work need to address the fact that the expression of other non-olfaction genes in the male antenna is higher than in the female antenna, which has more sensory neurons.

The females of *A. aegypti f*eed on nectar throughout their lives and I found several olfaction transcripts whose expression increases as females start looking for host and not only nectar sources. It is unclear whether the 12h old females feed on nectar in nature, but in a laboratory setting they begin sugar feeding almost immediately after emerging from the pupa stage. Therefore, olfaction genes that are upregulated when females begin host-seeking behavior at 4 days old may be important in order to locate a human host. For example, the transcripts levels of *Or4* are higher in the antenna of anthropophilic strains of *A. aegypti* and this has been associated mosquito sensitivity to chemicals overrepresented in human odor (McBride et al. 2014). However, *Or4* expression does not increase significantly in the female antenna between 12h and 4 days.

The miR expression profile changes are similar to the olfaction gene expression changes with no miRs changing expression after blood feeding in the antenna of *A. aegypti*. Changes are observed in the HT 3h after feeding (especially miR-275 and miR-305). The expression profile of male and female antenna is considerably different: for example, miR-7 is enhanced in females (23 fold) and miR-285 is enhanced in males (341 fold). The role of these miRs in the antenna of *A. aegypti* remains unknown but in *Drosophila melanogaster* miR-7 is associated with regulation of cell cycle (Aparicio et al. 2015) and memory formation (Busto et al. 2015). Target prediction revealed that a few olfaction genes are regulated by several miRs (*Or52, Or42, Ird, Obp11, Or11, Ir7v.3, Or49* and *Ir104.3*). These olfaction genes have longer 3'UTR and several predicted polyadenylation sites. Potentially, miRs compete with each other to bind these 3'UTRs, and olfaction transcripts may auto regulate the expression of one another via competitive binding. This miR-mediated cross talk may be associated with the lack of differential expression of olfaction genes and miRs after blood feeding. In other organisms (including humans) up to 85% of the genes have alternative polyadenylation resulting in an increased number of isoforms (Tan and Marques 2014; Wehrspaun et al.

2014). These isoforms, along with their miRs regulators, are differentially expressed depending on the tissue type. For example, in the human brain miRs are found in the axons of neurons and can regulate the expression of ion channel/transporter genes. My data suggests a similar mechanism might occur in the sensory neurons present in the antenna of *A. aegypti* and changes in the expression of both miRs and olfaction transcripts would not be detectable in such a case since different isoforms may be present and interacting with different miRs.

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APPENDIX

Table A1 Comparison between genes differentially expressed in the antenna of unfed females and 3h after blood feeding (RPKMs).

IDs	Gene name	Gene description	Unfed	+3h	Fold	*p* adj.
		Up regulated				
AAEL006126		conserved hypothetical protein	0.25	10.03	9.32	0.0000
AAEL006581		juvenile hormone-inducible protein, putative	10.51	125.84	9.06	0.0000
AAEL006138		hypothetical protein	0.62	30.8	7.57	0.0000
AAEL010434		Vitellogenin-A1 Precursor	0.68	37.09	7.52	0.0000
AAEL006563		Vitellogenic carboxypeptidase Precursor	0.37	11.23	7.26	0.0000
AAEL003443		threonine dehydrogenase	7.35	78.43	5.62	0.0000
AAEL000797		dimethylaniline monooxygenase	6.88	52.89	4.92	0.0000
AAEL001888		hypothetical protein	47.6	316.65	4.76	0.0000
AAEL000057	TOLL5B	Toll-like receptor	2.77	15.5	4.26	0.0000
AAEL006319		hypothetical protein	1.98	13.66	3.92	0.0000
AAEL001100		phosphoserine phosphatase	29.2	190.21	3.81	0.0000
AAEL010442		4-hydroxyphenylpyruvate dioxygenase	1.88	13.43	3.53	0.0000
AAEL012318		2-amino-3-ketobutyrate coenzyme a ligas	4.56	23.04	3.43	0.0000
AAEL014600		4-hydroxyphenylpyruvate dioxygenase	32.41	173.81	3.41	0.0000
AAEL000006		phosphoenolpyruvate carboxykinase	2.06	9.04	3.25	0.0000
AAEL010276		aminomethyltransferase	0.61	5.68	3.14	0.0002
AAEL003581		amidophosphoribosyltransferase	3.5	13.55	2.89	0.0000
AAEL010640		phosphoribosylamine-glycine ligase	1.9	8.06	2.89	0.0000
AAEL007555		acyl-coa dehydrogenase	20.55	67.07	2.62	0.0000
AAEL002269		purine nucleoside phosphorylase	13.92	49.19	2.62	0.0001
AAEL005384		phosphoribosylformylglycinamidine synthase	3.24	12.56	2.62	0.0007
AAEL009875		alanine aminotransferase	1.64	8.81	2.60	0.0049
AAEL008450		conserved hypothetical protein	9.58	30.59	2.53	0.0000
AAEL014599		hypothetical protein	5.71	31.05	2.53	0.0075
AAEL001134		methylmalonate-semialdehyde dehydrogenase	41.06	117.25	2.45	0.0000
AAEL001158		fructose-1,6-bisphosphatase	7.97	23.63	2.45	0.0000
AAEL004220		hypothetical protein	41.68	125.31	2.41	0.0001
AAEL002683		aldehyde oxidase	3.01	8.8	2.39	0.0001
AAEL006542		retinoid-inducible serine carboxypeptidas	0.68	3.58	2.36	0.0209
AAEL000897		conserved hypothetical protein	31.4	82.85	2.25	0.0001
AAEL003606		purine biosynthesis protein 6, pur6	12.49	35.89	2.25	0.0032
AAEL013637		homogentisate 1,2-dioxygenase	50.83	153.65	2.20	0.0136
AAEL010248		fibrillarin	1.28	3.94	2.20	0.0173
AAEL005988	LYSC6	C-Type Lysozyme	3.4	9.21	2.19	0.0021
AAEL011729		Molybdenum cofactor sulfurase 3	10.53	26.57	2.17	0.0000
AAEL001663		hypothetical protein	3.71	10.83	2.17	0.0141
AAEL004870	CYP18A1	cytochrome P450	2.39	6.7	2.16	0.0051
AAEL014811		conserved hypothetical protein	4.12	11.47	2.16	0.0056
AAEL006442		conserved hypothetical protein	0.78	2.61	2.16	0.0351
AAEL012825		bifunctional purine biosynthesis protein	7.24	19.23	2.14	0.0049
AAEL014381		Molybdenum cofactor sulfurase 1	43.36	111.96	2.13	0.0029
AAEL008028		monocarboxylate transporter	8.47	19.43	2.11	0.0000
AAEL009766		lipoamide acyltransferase	7.42	20.52	2.11	0.0150
AAEL000845		protein-tyrosine phosphatase	3.3	7.91	2.10	0.0000
AAEL005132		hypothetical protein	2.84	6.88	2.08	0.0019
AAEL012578		phosphoserine aminotransferase	9.71	24.82	2.08	0.0055

Table A1 Continued

IDs	Gene name	Gene description	Unfed	+3h	Fold	*p* adj.
AAEL007887		ornithine decarboxylase	58.42	135.38	2.07	0.0000
		Down regulated				
AAEL010764		aldehyde dehydrogenase	103.96	11.36	-6.50	0.0000
AAEL008785		hypothetical protein	1,391.29	438.39	-3.10	0.0000
AAEL001680		hypothetical protein	36.23	8.69	-3.48	0.0000
AAEL007197		amino acid transporter	44.52	17.85	-2.43	0.0000
AAEL000609		conserved hypothetical protein	57.67	22.17	-2.46	0.0000
AAEL013432		serine protease, putative	23.77	8.64	-2.57	0.0000
AAEL006609		zinc finger protein	128.40	56.67	-2.19	0.0000
AAEL017974	HSP70Ab	heat shock protein HSP70	4.15	1.3	-2.66	0.0000
AAEL012772	CYP325G3	cytochrome P450	44.18	17.22	-2.33	0.0001
AAEL000519		hypothetical protein	312.21	136.29	-2.16	0.0001
AAEL008701		myoinositol oxygenase	12.48	3.72	-2.64	0.0003
AAEL001675	CLIPA10	Clip-Domain Serine Protease	8.58	3.94	-2.04	0.0006
AAEL013427		serine protease, putative	11.99	3.81	-2.48	0.0008
AAEL002655		matrix metalloproteinase	9.07	3.16	-2.36	0.0018
AAEL001435	SPZ2	spaetzle-like cytokine	5.59	1.28	-2.51	0.0069
AAEL008885		hypothetical protein	1.61	0.58	-2.23	0.0110
AAEL005330		atrial natriuretic peptide receptor	6.26	2.06	-2.23	0.0175
AAEL001818		conserved hypothetical protein	8.49	2.41	-2.27	0.0248
AAEL003041		conserved hypothetical protein	8.44	3.48	-2.04	0.0267
AAEL003816		hypothetical protein	7.91	1.63	-2.30	0.0298
AAEL013345		alphaA-crystallin, putative	4.27	1.47	-2.14	0.0390

Table A2 Comparison between genes differentially expressed in the antenna of 3h female and 24h after blood feeding (RPKMs).

Gene ID	Gene Name	Wiki Description	3h	24h	Fold	*p* adj.
		Up regulated				
AAEL007599		cathepsin b	1.00	262.10	140.14	0.0000
AAEL012216		cathepsin b	0.58	113.78	119.80	0.0000
AAEL007585		cathepsin b	0.27	55.09	100.53	0.0000
AAEL015312		cathepsin b	1.07	183.93	97.87	0.0000
AAEL006563		serine carboxypeptidase	10.86	525.72	31.45	0.0000
AAEL002482		hypothetical protein	0.10	5.31	14.85	0.0000
AAEL006138		hypothetical protein	27.78	663.10	14.19	0.0000
AAEL006126		hypothetical protein	9.68	175.31	11.32	0.0000
AAEL010434		hypothetical protein	35.79	703.83	10.32	0.0000
AAEL001307		SEC14, putative	2.12	34.15	7.86	0.0000
AAEL002413		sphingomyelin phosphodiesterase	0.06	1.15	7.13	0.0000
AAEL017451			1.87	12.61	5.51	0.0000
AAEL005772	OBP22	Odorant-binding protein 99c, putative	23.04	129.34	5.35	0.0000
AAEL006568		serine protease	1.24	11.44	4.97	0.0000
AAEL006446		trehalose-6-phosphate synthase	1.18	7.58	4.61	0.0000
AAEL004027		glucose dehydrogenase	28.26	127.28	4.46	0.0000
AAEL006542		serine carboxypeptidase	3.47	20.33	4.34	0.0000
AAEL001219		hypothetical protein	7.55	37.26	4.32	0.0000
AAEL007686		hypothetical protein	0.45	2.17	4.04	0.0000
AAEL002049		circadian protein clock/arnt/bmal/pas	8.69	48.79	3.98	0.0001
AAEL006834		glutamate semialdehyde dehydrogenase	4.11	21.56	3.97	0.0000
AAEL008752		hypothetical protein	4.49	20.64	3.95	0.0000

Table A2 Continued

Gene ID	Gene Name	Wiki Description	3h	24h	Fold	*p* adj.
AAEL009116		hypothetical protein	14.27	58.59	3.93	0.0000
AAEL012855		hypothetical protein	0.78	3.51	3.74	0.0000
AAEL007878		ornithine decarboxylase	0.20	1.26	3.62	0.0062
AAEL013027		hypothetical protein	0.00	3.35	3.55	0.0148
AAEL009948		aldehyde dehydrogenase	1.10	3.99	3.39	0.0000
AAEL011191		protein phosphatase 1 binding protein	2.65	9.58	3.38	0.0000
AAEL005842		hypothetical protein	0.12	1.01	3.38	0.0228
AAEL006824		cytochrome P450	0.28	2.30	3.33	0.0298
AAEL008885		hypothetical protein	0.56	2.15	3.27	0.0001
AAEL015606		hypothetical protein	0.12	1.09	3.22	0.0445
AAEL008345	CYP4G35	cytochrome P450	0.23	1.75	3.21	0.0411
AAEL000642		alpha-amylase	1.18	4.16	3.17	0.0000
AAEL006122		hypothetical protein	2.92	9.53	3.10	0.0000
AAEL009114		hypothetical protein	3.42	12.44	3.09	0.0002
AAEL005850	HR4	orphan nuclear receptor nr6a1	0.28	1.01	3.01	0.0020
AAEL011763	PPO3	prophenoloxidase	0.34	1.53	3.01	0.0219
AAEL004728		homocysteine methyltransferase	4.65	14.20	3.00	0.0000
AAEL001293		hypothetical protein	1.50	5.90	2.98	0.0125
AAEL009115		hypothetical protein	160.85	523.58	2.98	0.0000
AAEL010028		sarcosine dehydrogenase	1.23	4.57	2.97	0.0066
AAEL009955		hypothetical protein	13.38	52.17	2.96	0.0120
AAEL002665		matrix metalloproteinase	0.28	1.14	2.90	0.0437
AAEL011423		sugar transporter	1.29	4.31	2.69	0.0201
AAEL013156		hypothetical protein	0.34	1.20	2.68	0.0416
AAEL014551		triacylglycerol lipase, pancreatic	1.00	2.95	2.60	0.0092
AAEL001402	LRIM10B	hypothetical protein	7.88	23.60	2.59	0.0130
AAEL000105		beta-alanine synthase, putative	1.86	5.53	2.57	0.0219
AAEL008701		myoinositol oxygenase	3.02	8.07	2.46	0.0088
AAEL010853		AMP dependent ligase	2.61	6.75	2.45	0.0003
AAEL013492	PPO5	prophenoloxidase	2.58	6.40	2.39	0.0004
AAEL008485		hypothetical protein	5.64	14.42	2.38	0.0085
AAEL003593		hypothetical protein	38.70	99.82	2.32	0.0306
AAEL012764		hypothetical protein	10.72	24.39	2.28	0.0000
AAEL004342	OBP18	hypothetical protein	7.25	17.67	2.27	0.0156
AAEL009588		expressed protein (HR3)	4.64	10.89	2.27	0.0004
AAEL007064	GNBPB6	gram-negative bacteria binding protein	6.13	14.38	2.26	0.0007
AAEL009291		serine carboxypeptidase	6.12	14.21	2.21	0.0072
AAEL008785		hypothetical protein	425.14	900.24	2.14	0.0000
		Down regulated				
AAEL003443		threonine dehydrogenase	76.47	4.68	-10.80	0.0000
AAEL000797		dimethylaniline monooxygenase	51.43	6.90	-6.16	0.0000
AAEL011451		hypothetical protein	7.03	1.23	-4.43	0.0000
AAEL009577		hypothetical protein	19.71	2.98	-4.30	0.0000
AAEL008855		dynein heavy chain	2.64	0.50	-3.64	0.0005
AAEL013339		alphaA-crystallin, putative	2.08	0.32	-3.60	0.0057
AAEL003894	GNBPB5	gram-negative bacteria binding protein	1.89	0.13	-3.26	0.0417
AAEL006498	GPROP1	rhodopsin	20.43	4.37	-3.19	0.0065
AAEL014823		hypothetical protein	12.65	3.58	-3.07	0.0000
AAEL000057	TOLL5B	toll	15.06	4.38	-2.96	0.0000
AAEL018011			14.00	4.38	-2.83	0.0000
AAEL005720		hypothetical protein	3.41	0.96	-2.81	0.0057
AAEL010276		aminomethyltransferase	5.49	1.48	-2.80	0.0139
AAEL002305		hypothetical protein	2.79	0.70	-2.76	0.0418
AAEL014231		hypothetical protein	7.69	2.23	-2.75	0.0071

Table A2 Continued

Gene ID	Gene Name	Wiki Description	3h	24h	Fold	*p* adj.
AAEL009875		alanine aminotransferase	5.87	1.75	-2.74	0.0028
AAEL013535		phosrestin ii (arrestin a) (arrestin 1)	3.39	0.98	-2.73	0.0122
AAEL008141	PER		763.79	238.54	-2.66	0.0046
AAEL011771		hypothetical protein	4.42	1.30	-2.63	0.0262
AAEL014600		4-hydroxyphenylpyruvate dioxygenase	169.38	57.15	-2.60	0.0003
AAEL016996			33.33	11.67	-2.56	0.0001
AAEL012318		coenzyme a ligase	22.46	7.80	-2.50	0.0029
AAEL009881		dynein heavy chain	13.26	4.58	-2.44	0.0127
AAEL014238		aromatic amino acid decarboxylase	30.43	11.85	-2.38	0.0000
AAEL003352		ribosomal protein l7ae	43.37	16.76	-2.34	0.0004
AAEL008828		carbonic anhydrase	2.76	1.03	-2.33	0.0085
AAEL000845			5.69	2.29	-2.31	0.0000
AAEL003476		calpain-c	6.47	2.47	-2.31	0.0062
AAEL010737		aromatic amino acid decarboxylase	66.47	27.01	-2.31	0.0000
AAEL012131		cationic amino acid transporter	9.26	3.61	-2.29	0.0047
AAEL008450		hypothetical protein	27.93	11.14	-2.26	0.0020
AAEL009258		hypothetical protein	4.52	1.71	-2.25	0.0411
AAEL007511		serine protease	1.90	0.73	-2.25	0.0419
AAEL010640		phosphoribosylamine-glycine ligase	6.66	2.58	-2.24	0.0266
AAEL003581		amidophosphoribosyltransferase	13.13	5.24	-2.23	0.0057
AAEL010248		fibrillarin	3.62	1.41	-2.20	0.0470
AAEL011584		chaperonin-60kD, ch60	39.65	16.55	-2.17	0.0050
AAEL001498		hypothetical protein	1.91	0.77	-2.15	0.0490
AAEL011967		DNA photolyase	59.76	26.40	-2.11	0.0001
AAEL007802		multicopper oxidase	93.69	42.54	-2.09	0.0000

Table A3 Comparison between genes differentially expressed in the antenna of 24h female and 48h after blood feeding (RPKMs).

IDs	Gene name	Gene description	24h	48h	Fold	*p* adj.
		Up regulated				
AAEL007590		cathepsin b	0.07	1.24	3.39	0.0006
AAEL010485		sugar transporter	1.52	5.71	3.11	0.0000
AAEL001289		permease, putative	0.87	3.39	2.87	0.0002
AAEL010822		sulphate transporter	13.68	37.27	2.64	0.0000
AAEL010764		aldehyde dehydrogenase	21.38	73.54	2.57	0.0030
AAEL001498		hypothetical protein	2.14	6.05	2.30	0.0088
AAEL001675	CLIPA10	Clip-Domain Serine Protease	3.81	8.85	2.16	0.0000
AAEL014615	CYP9J23	cytochrome P450	3,162.63	7,397.47	2.15	0.0001
		Down regulated				
AAEL006563		Vitellogenic carboxypeptidase Precursor	539.79	13.29	-35.07	0.0000
AAEL006138		hypothetical protein	730.48	9.77	-34.09	0.0000
AAEL001307		SEC14, putative	35.07	0.60	-33.22	0.0000
AAEL006126		conserved hypothetical protein	180.34	2.58	-32.85	0.0000
AAEL010434		Vitellogenin-A1 Precursor	724.12	12.37	-27.73	0.0000
AAEL015312		cathepsin b	188.65	8.65	-16.28	0.0000
AAEL007599		cathepsin b	269.01	10.36	-14.56	0.0000
AAEL012216		cathepsin b	116.74	6.18	-13.85	0.0000
AAEL006581		juvenile hormone-inducible protein, putative	141.80	8.18	-12.49	0.0000

Table A3 Continued

IDs	Gene name	Gene description	24h	48h	Fold	*p* adj.
AAEL007585		cathepsin b	56.52	3.98	-11.61	0.0000
AAEL006542		retinoid-inducible serine carboxypeptidase	20.92	0.83	-11.34	0.0000
AAEL007686		conserved hypothetical protein	2.23	0.03	-10.89	0.0000
AAEL002482		hypothetical protein	6.43	0.25	-8.76	0.0000
AAEL010028		sarcosine dehydrogenase	4.70	0.47	-7.42	0.0000
AAEL014551		triacylglycerol lipase, pancreatic	4.33	0.31	-7.23	0.0000
AAEL010442		4-hydroxyphenylpyruvate dioxygenase	6.77	0.59	-6.47	0.0000
AAEL009955		conserved hypothetical protein	53.71	5.36	-5.63	0.0000
AAEL001888		hypothetical protein	314.87	47.83	-5.39	0.0000
AAEL007226		nidogen	2.96	0.26	-5.18	0.0000
AAEL001100		phosphoserine phosphatase	134.22	19.66	-4.91	0.0000
AAEL011756		aldehyde dehydrogenase	4.16	0.53	-4.89	0.0000
AAEL014600		4-hydroxyphenylpyruvate dioxygenase	58.66	10.39	-4.71	0.0000
AAEL006319		hypothetical protein	7.88	1.46	-4.29	0.0000
AAEL013637		homogentisate 1,2-dioxygenase	126.64	25.66	-3.98	0.0000
AAEL012855		hypothetical protein	3.61	0.65	-3.96	0.0000
AAEL014599		hypothetical protein	11.84	1.83	-3.81	0.0000
AAEL001293		conserved hypothetical protein	6.07	1.25	-3.78	0.0000
AAEL005957		phospholipase b, plb1	6.25	1.32	-3.77	0.0000
AAEL005772	OBP22	odorant binding protein OBP22	132.69	32.32	-3.60	0.0000
AAEL000213		d-amino acid oxidase	7.95	1.54	-3.51	0.0000
AAEL013156		hypothetical protein	1.41	0.24	-3.45	0.0001
AAEL013492	PPO5	prophenoloxidase	6.58	1.65	-3.42	0.0000
AAEL004870	CYP18A1	cytochrome P450	5.53	1.29	-3.35	0.0000
AAEL001402	LRIM10B	leucine-rich immune protein	24.28	4.83	-3.28	0.0001
AAEL002413		sphingomyelin phosphodiesterase	1.18	0.19	-3.19	0.0006
AAEL012318		2-amino-3-ketobutyrate coenzyme a ligase	8.00	2.02	-3.18	0.0000
AAEL004220		hypothetical protein	92.42	21.93	-3.14	0.0000
AAEL011962		conserved hypothetical protein	7.77	1.93	-3.05	0.0000
AAEL000797		dimethylaniline monooxygenase	7.09	1.85	-3.04	0.0000
AAEL004342	OBP18	odorant binding protein OBP18	18.14	5.33	-3.04	0.0000
AAEL004969		conserved hypothetical protein	1.86	0.33	-2.99	0.0023
AAEL008485		conserved hypothetical protein	14.82	4.39	-2.96	0.0000
AAEL009588		expressed protein	11.21	2.94	-2.95	0.0001
AAEL007795	CYP4D37	cytochrome P450	48.22	11.56	-2.91	0.0005
AAEL003443		threonine dehydrogenase	4.80	1.33	-2.89	0.0001
AAEL008384		ATP-binding cassette	5.59	1.74	-2.89	0.0000
AAEL002683		aldehyde oxidase	6.17	2.02	-2.89	0.0000
AAEL009116		hypothetical protein	60.13	18.10	-2.76	0.0000
AAEL000080		phosphoenolpyruvate carboxykinase	37.61	11.60	-2.70	0.0001
AAEL017330			4.41	1.12	-2.69	0.0028
AAEL005770	OBP21	odorant binding protein OBP21	2.26	0.61	-2.64	0.0033
AAEL001414	LRIM9	leucine-rich immune protein	45.54	9.58	-2.61	0.0194
AAEL009115		hypothetical protein	538.16	181.98	-2.58	0.0000
AAEL008620		D7 protein, putative	11.73	3.67	-2.57	0.0009
AAEL001401	LRIM10A	leucine-rich immune protein	22.32	6.51	-2.52	0.0073
AAEL000897		conserved hypothetical protein	47.49	17.73	-2.50	0.0000
AAEL005800	CLIPE11	Clip-Domain Serine Protease	9.21	3.40	-2.50	0.0000
AAEL009875		alanine aminotransferase	2.62	0.70	-2.46	0.0259
AAEL002181		cuticle protein, putative	244.81	94.11	-2.43	0.0000

Table A3 Continued

IDs	Gene name	Gene description	24h	48h	Fold	*p* adj.
AAEL017484	CTLGA4	C-Type Lectin	9.56	2.46	-2.41	0.0487
AAEL002185		cuticle protein, putative	227.25	76.22	-2.41	0.0039
AAEL017029			36.91	14.07	-2.40	0.0000
AAEL005336		d-3-phosphoglycerate dehydrogenase	34.19	13.19	-2.40	0.0000
AAEL014366		conserved hypothetical protein	5.55	2.11	-2.39	0.0000
AAEL000774		conserved hypothetical protein	2.80	0.82	-2.39	0.0400
AAEL006752		Misexpression suppressor of ras, putative	41.52	16.28	-2.37	0.0000
AAEL005807		conserved hypothetical protein	6.21	2.03	-2.37	0.0145
AAEL001134		semialdehyde dehydrogenase	71.28	26.86	-2.34	0.0004
AAEL001683		conserved hypothetical protein	3.52	1.05	-2.33	0.0308
AAEL012764		conserved hypothetical protein	38.96	16.29	-2.33	0.0000
AAEL010529		conserved hypothetical protein	4.44	1.54	-2.30	0.0150
AAEL007909		branched-chain amino acid aminotransferase	7.28	2.60	-2.30	0.0118
AAEL008494		mitochondrial carrier protein ymc	11.78	4.39	-2.29	0.0052
AAEL009114		conserved hypothetical protein	12.77	4.58	-2.28	0.0103
AAEL005416		oxidase/peroxidase	20.29	8.45	-2.28	0.0000
AAEL007216		elongase, putative	29.66	12.35	-2.25	0.0000
AAEL012578		phosphoserine aminotransferase	15.44	6.24	-2.24	0.0002
AAEL008963		tyrosine aminotransferase	334.02	127.39	-2.21	0.0122
AAEL013857		conserved hypothetical protein	55.92	24.83	-2.16	0.0000
AAEL004728		homocysteine methyltransferase	14.58	6.29	-2.16	0.0000
AAEL004399	GPRFSH	GPCR Glycoprotein Hormone Family	2.92	1.26	-2.15	0.0010
AAEL004027		glucose dehydrogenase	130.82	58.13	-2.13	0.0000
AAEL011973		fumarylacetoacetate hydrolase	47.45	21.07	-2.12	0.0001
AAEL013904		3-hydroxyisobutyrate dehydrogenase	12.94	5.35	-2.11	0.0115
AAEL007887		ornithine decarboxylase	96.56	43.02	-2.10	0.0002
AAEL001793		conserved hypothetical protein	9.53	4.43	-2.08	0.0000
AAEL010049		hypothetical protein	28.52	13.60	-2.04	0.0000
AAEL002815		conserved hypothetical protein	49.10	21.81	-2.00	0.0265

Table A4 Comparison between genes differentially expressed in the antenna of 48h female and 72h after blood feeding.

Gene ID	Gene Name	Wiki Description	48h (RPKMs)	72h (RPKMs)	Fold	*p* adj.
AAEL006138		hypothetical protein	8.84	0.44	-9.23	0.0000
AAEL006563		serine carboxypeptidase	12.91	1.09	-8.86	0.0000
AAEL010434		hypothetical protein	12.00	0.71	-7.91	0.0000
AAEL006126		hypothetical protein	2.50	0.20	-7.15	0.0000
AAEL007590		cathepsin b	1.20	0.02	-4.14	0.0117
AAEL006568		serine protease	11.79	2.47	-3.39	0.0035

Table A5. Genes differentially expressed in the HT of 4 days unfed females and 3h after blood feeding.

IDs	Gene name	Gene description	4 days	3h	Fold	*p* adj
		Up regulated				
AAEL010435		conserved hypothetical protein	0.60	271.70	242.63	0.0000
AAEL013577		conserved hypothetical protein	0.14	65.92	183.99	0.0000
AAEL013584		conserved hypothetical protein	1.02	261.03	173.77	0.0000
AAEL010434		Vitellogenin-A1 Precursor	6.41	1,046.22	135.66	0.0000
AAEL013127		conserved hypothetical protein	0.04	39.88	94.63	0.0000
AAEL013118		conserved hypothetical protein	0.32	57.64	86.60	0.0000
AAEL010429		conserved hypothetical protein	0.67	61.76	57.82	0.0000
AAEL006138		hypothetical protein	5.42	390.75	47.35	0.0000
AAEL000080		phosphoenolpyruvate carboxykinase	9.55	462.37	45.48	0.0000
AAEL000006		phosphoenolpyruvate carboxykinase	7.53	330.65	39.71	0.0000
AAEL006563		Vitellogenic carboxypeptidase Precursor	3.17	191.55	39.54	0.0000
AAEL000025		phosphoenolpyruvate carboxykinase	0.32	16.94	37.63	0.0000
AAEL006126		conserved hypothetical protein	2.31	118.12	34.48	0.0000
AAEL010431		conserved hypothetical protein	0.04	8.95	24.45	0.0000
AAEL001100		phosphoserine phosphatase	22.21	525.60	21.70	0.0000
AAEL017465			0.09	16.13	20.16	0.0000
AAEL002269		purine nucleoside phosphorylase	53.77	1,305.41	18.91	0.0000
AAEL003606		purine biosynthesis protein 6, pur6	46.81	973.35	17.69	0.0000
AAEL007905		hypothetical protein	13.68	260.39	17.38	0.0000
AAEL013352		lethal	0.17	7.78	16.94	0.0000
AAEL007909		branched-chain amino acid aminotransferase	7.72	137.29	16.39	0.0000
AAEL010640		phosphoribosylamine-glycine ligase	10.19	188.29	15.78	0.0000
AAEL005384		phosphoribosylformylglycinamidine synthase	13.08	248.65	15.32	0.0000
AAEL000213		d-amino acid oxidase	8.09	127.25	14.54	0.0000
AAEL014206		sugar transporter	1.94	30.95	13.87	0.0000
AAEL014871		methylenetetrahydrofolate dehydrogenase	3.84	57.75	13.38	0.0000
AAEL007432		serine collagenase 1 precursor, putative	33.63	506.91	13.31	0.0000
AAEL012825		bifunctional purine biosynthesis protein	23.77	332.15	13.06	0.0000
AAEL000797		dimethylaniline monooxygenase	1.34	20.06	12.64	0.0000
AAEL001806		conserved hypothetical protein	3.36	50.50	12.46	0.0000
AAEL001674		serine-type enodpeptidase,	0.10	7.04	12.27	0.0000
AAEL012287		sugar transporter	0.71	10.64	12.09	0.0000
AAEL014734		hypothetical protein	7.23	91.91	11.98	0.0000
AAEL015312		cathepsin b	0.67	14.19	11.93	0.0000
AAEL002467		conserved hypothetical protein	1.36	22.57	11.86	0.0000
AAEL001793		conserved hypothetical protein	2.88	40.24	11.75	0.0000
AAEL008468		cysteine synthase	4.27	53.79	11.59	0.0000
AAEL003443		threonine dehydrogenase	4.46	65.01	11.56	0.0000
AAEL010751		methylenetetrahydrofolate dehydrogenase	6.57	87.96	11.56	0.0000
AAEL003581		amidophosphoribosyltransferase	23.96	331.66	11.16	0.0000
AAEL010280		conserved hypothetical protein	2.45	29.23	10.70	0.0000
AAEL011756		aldehyde dehydrogenase	22.42	258.21	10.53	0.0000
AAEL012216		cathepsin b	0.62	8.67	10.20	0.0000
AAEL007555		acyl-coa dehydrogenase	43.21	468.09	9.99	0.0000
AAEL005429		2-oxoglutarate dehydrogenase	3.35	34.51	9.66	0.0000
AAEL002510		serine hydroxymethyltransferase	59.80	610.17	9.58	0.0000
AAEL008096		mitochondrial ornithine transporter	1.80	19.19	9.40	0.0000
AAEL000621	CECN	cecropin anti-microbial peptide	6.88	79.45	9.28	0.0000
AAEL004870	CYP18A1	cytochrome P450	0.50	7.34	9.26	0.0000
AAEL013363		ubiquitously transcribed sex	2.12	20.34	8.78	0.0000

Table A5 Continued

IDs	Gene name	Gene description	4 days	3h	Fold	*p* adj
AAEL014412	CYP304B2	cytochrome P450	17.05	146.37	8.19	0.0000
AAEL013644		ubiquitously transcribed sex	1.80	15.80	8.11	0.0000
AAEL007585		cathepsin b	0.34	5.28	7.99	0.0000
AAEL007599		cathepsin b	1.08	14.45	7.98	0.0000
AAEL007795	CYP4D37	cytochrome P450	0.22	3.05	7.90	0.0000
AAEL006581		juvenile hormone-inducible protein, putative	7.22	61.50	7.64	0.0000
AAEL006085		methylenetetrahydrofolate dehydrogenase	33.04	264.45	7.52	0.0000
AAEL014426		glycine dehydrogenase	4.03	34.80	7.45	0.0000
AAEL007878		ornithine decarboxylase	0.71	6.40	7.41	0.0000
AAEL001887		glutamine synthetase 1, 2	64.20	508.16	7.28	0.0000
AAEL001690		serine-type enodpeptidase,	0.80	7.28	7.15	0.0000
AAEL016968			2.40	18.08	7.02	0.0000
AAEL017333			1.14	10.15	7.00	0.0000
AAEL002063		cationic amino acid transporter	2.02	17.42	6.68	0.0000
AAEL014381		Molybdenum cofactor sulfurase 1	2.50	18.65	6.66	0.0000
AAEL013349		lethal	0.33	6.29	6.66	0.0000
AAEL000625	CECF	cecropin anti-microbial peptide	1.93	21.04	6.58	0.0000
AAEL000566		conserved hypothetical protein	2.42	20.48	6.55	0.0000
AAEL009766		lipoamide acyltransferase	14.58	102.44	6.55	0.0000
AAEL010442		4-hydroxyphenylpyruvate dioxygenase	1.17	9.75	6.54	0.0000
AAEL011729		Molybdenum cofactor sulfurase 3	0.76	5.68	6.48	0.0000
AAEL008222		lipase	3.62	26.59	6.46	0.0000
AAEL017402			2.56	19.88	6.23	0.0000
AAEL012041		sulphate transporter	2.12	15.92	6.21	0.0000
AAEL013350		heat shock protein 26kD, putative	0.93	9.63	6.07	0.0000
AAEL007250		conserved hypothetical protein	2.45	17.74	6.02	0.0000
AAEL013884		synaptic vesicle protein	6.52	43.76	5.98	0.0000
AAEL014754		conserved hypothetical protein	1.46	10.47	5.97	0.0000
AAEL009853		trypsin, putative	0.57	5.16	5.85	0.0000
AAEL006012		factor for adipocyte differentiation	0.75	5.30	5.82	0.0000
AAEL010630		xanthine dehydrogenase	1.26	8.38	5.81	0.0000
AAEL013642		acyl-CoA dehydrogenase	6.38	41.13	5.80	0.0000
AAEL002937		hypothetical protein	2.58	18.20	5.80	0.0000
AAEL000611	CECE	cecropin anti-microbial peptide	5.19	41.28	5.62	0.0000
AAEL005762		leucine-rich transmembrane proteins	1.89	11.58	5.59	0.0000
AAEL009166		conserved hypothetical protein	0.02	1.76	5.56	0.0000
AAEL001888		hypothetical protein	23.44	137.79	5.55	0.0000
AAEL000598	CECD	cecropin anti-microbial peptide	0.67	10.28	5.53	0.0000
AAEL002683		aldehyde oxidase	10.11	60.22	5.50	0.0000
AAEL006542		retinoid-inducible serine carboxypeptidase	10.56	62.81	5.43	0.0000
AAEL000627	CECA	cecropin anti-microbial peptide	0.83	18.29	5.39	0.0000
AAEL017349			106.18	605.48	5.38	0.0000
AAEL002815		conserved hypothetical protein	42.06	232.54	5.29	0.0000
AAEL014797		acyl-coa dehydrogenase	6.19	35.76	5.25	0.0000
AAEL000402		conserved hypothetical protein	0.51	3.55	5.16	0.0000
AAEL006466		chondroitin synthase	7.19	39.56	5.09	0.0000
AAEL011338		conserved hypothetical protein	9.16	51.64	5.05	0.0000
AAEL014365		chromaffin granule amine transporter, putative	4.22	23.52	5.03	0.0000
AAEL001134		methylmalonate-semialdehyde dehydrogenase	106.08	558.20	4.98	0.0000
AAEL005336		d-3-phosphoglycerate dehydrogenase	45.16	252.37	4.98	0.0000
AAEL013351		lethal	0.12	1.93	4.90	0.0000
AAEL013857		conserved hypothetical protein	47.19	264.68	4.87	0.0000

Table A5 Continued

IDs	Gene name	Gene description	4 days	3h	Fold	*p* adj
AAEL013145		conserved hypothetical protein	1.31	8.79	4.87	0.0000
AAEL000774		conserved hypothetical protein	25.03	131.89	4.87	0.0000
AAEL007802		multicopper oxidase	2.34	12.13	4.84	0.0000
AAEL001158		fructose-1,6-bisphosphatase	23.70	122.65	4.81	0.0000
AAEL017139			2.29	12.60	4.80	0.0000
AAEL009875		alanine aminotransferase	43.62	239.73	4.79	0.0000
AAEL003125		acyl-coa dehydrogenase	25.37	129.36	4.77	0.0000
AAEL000471		monocarboxylate transporter	5.31	29.05	4.77	0.0000
AAEL010204		dihydropyrimidine dehydrogenase	7.09	36.01	4.75	0.0000
AAEL013630		mitochondrial ornithine transporter	0.10	1.53	4.75	0.0000
AAEL001707		epsilon-trimethyllysine 2-oxoglutarate dioxyg.	5.01	24.89	4.71	0.0000
AAEL011811		DNA replication licensing factor MCM3	0.71	4.05	4.71	0.0000
AAEL017974	HSP70Ab	heat shock protein HSP70	0.16	1.81	4.66	0.0000
AAEL015515	CECG	cecropin anti-microbial peptide	3.66	26.97	4.62	0.0000
AAEL012578		phosphoserine aminotransferase	51.57	247.00	4.60	0.0000
AAEL005822		conserved hypothetical protein	12.60	60.98	4.60	0.0000
AAEL007544		serine/threonine-protein kinase chk2	0.69	3.72	4.60	0.0000
AAEL008028		monocarboxylate transporter	38.37	181.80	4.49	0.0000
AAEL007799		regulator of chromosome condensation	18.19	85.83	4.49	0.0000
AAEL017973	HSP70Aa	heat shock protein HSP70	0.10	1.56	4.48	0.0000
AAEL010276		aminomethyltransferase	33.93	173.23	4.48	0.0000
AAEL012265		transcription initiation factor RRN3	4.56	21.91	4.47	0.0000
AAEL013364		hypothetical protein	34.97	164.86	4.44	0.0000
AAEL009362		cationic amino acid transporter	3.66	17.44	4.43	0.0000
AAEL004292		hypothetical protein	0.45	2.88	4.42	0.0000
AAEL000640		alanine-glyoxylate aminotransferase	7.26	33.51	4.41	0.0000
AAEL012443		sugar transporter	0.34	2.37	4.38	0.0000
AAEL006562		acid phosphatase	4.64	21.46	4.30	0.0000
AAEL011470		cis,cis-muconate transport protein MucK	10.55	47.79	4.27	0.0000
AAEL011137		succinyl-coa:3-ketoacid-coenzyme a transferase	52.70	230.71	4.22	0.0000
AAEL014599		hypothetical protein	3.13	15.09	4.18	0.0000
AAEL014600		4-hydroxyphenylpyruvate dioxygenase	16.77	74.78	4.16	0.0000
AAEL002731	SRPN14	Serine Protease Inhibitor	7.67	34.31	4.12	0.0000
AAEL012932		conserved hypothetical protein	25.43	108.75	4.10	0.0000
AAEL010265		hypothetical protein	2.50	12.20	4.10	0.0000
AAEL002810		DNA replication licensing factor MCM5	0.58	2.83	4.08	0.0000
AAEL003857	DEFD	defensin anti-microbial peptide	15.23	77.26	4.01	0.0000
AAEL007993	CLIPB27	Clip-Domain Serine Protease family B.	0.99	4.79	3.90	0.0000
AAEL017134			23.43	97.97	3.88	0.0000
AAEL002963		conserved hypothetical protein	74.54	300.38	3.88	0.0000
AAEL013320		translocon-associated protein, delta subunit	53.81	223.12	3.86	0.0000
AAEL001052		heat shock protein, putative	85.39	347.47	3.84	0.0000
AAEL017388			85.51	353.24	3.84	0.0000
AAEL005833		cytosolic purine 5-nucleotidase	28.77	114.23	3.82	0.0000
AAEL000834		dimethylaniline monooxygenase	34.89	146.44	3.82	0.0000
AAEL012546		DNA replication licensing factor MCM6	1.06	4.95	3.82	0.0000
AAEL017098			36.70	144.39	3.77	0.0000
AAEL012187		lethal	7.50	29.44	3.74	0.0000
AAEL003255		hypothetical protein	1.23	5.28	3.71	0.0000
AAEL007401		roundabout, putative	0.37	1.62	3.70	0.0000
AAEL012827		endoplasmin	75.03	287.71	3.67	0.0000
AAEL011584		chaperonin-60kD, ch60	31.85	123.92	3.66	0.0000

Table A5 Continued

IDs	Gene name	Gene description	4 days	3h	Fold	*p* adj
AAEL012183		mfs transporter	1.13	5.08	3.64	0.0000
AAEL003841	DEFA	defensin anti-microbial peptide	12.86	52.67	3.63	0.0000
AAEL010032		translocon-associated protein	61.27	236.50	3.61	0.0000
AAEL013276		acid phosphatase	1.98	8.61	3.61	0.0000
AAEL001866		hypothetical protein	103.99	404.74	3.60	0.0000
AAEL003084		dolichyl-phosphate beta-D-mannosyltransferase	3.28	13.07	3.59	0.0000
AAEL017373			19.94	86.18	3.55	0.0000
AAEL012974		glycine cleavage system h protein	34.23	130.46	3.54	0.0000
AAEL007686		conserved hypothetical protein	1.32	5.43	3.53	0.0000
AAEL013141		mfs transporter	1.53	6.81	3.52	0.0000
AAEL009479		amino acid transporter	3.24	12.50	3.51	0.0000
AAEL014361		amidase	5.38	20.70	3.50	0.0000
AAEL011998		hypothetical protein	5.25	19.84	3.44	0.0000
AAEL011901		1-acyl-sn-glycerol-3-phosphate acyltransferase	17.66	64.49	3.44	0.0000
AAEL013637		homogentisate 1,2-dioxygenase	31.87	114.15	3.42	0.0000
AAEL010248		fibrillarin	4.62	16.84	3.40	0.0000
AAEL001857		conserved hypothetical protein	17.66	62.77	3.39	0.0000
AAEL012133		conserved hypothetical protein	1.53	8.28	3.38	0.0000
AAEL001328		hypothetical protein	10.17	39.53	3.37	0.0000
AAEL004969		conserved hypothetical protein	10.45	39.02	3.36	0.0000
AAEL014199		dihydropyrimidine dehydrogenase	2.80	10.05	3.36	0.0000
AAEL006836		dihydropteridine reductase	50.76	183.38	3.36	0.0000
AAEL005220		60S ribosomal protein L30	4.25	16.41	3.35	0.0000
AAEL007007		DNA replication licensing factor MCM2	1.28	4.70	3.35	0.0000
AAEL014299		conserved hypothetical protein	1.33	5.08	3.32	0.0000
AAEL009883		26S protease	12.75	45.71	3.32	0.0000
AAEL012224		zinc finger protein	1.10	4.08	3.32	0.0000
AAEL009596		sterol o-acyltransferase	2.59	10.75	3.32	0.0000
AAEL004523		preprotein translocase secy subunit	72.81	254.97	3.32	0.0000
AAEL003832	DEFC	defensin anti-microbial peptide	21.52	77.96	3.30	0.0000
AAEL003524		monocarboxylate transporter	17.71	61.57	3.30	0.0000
AAEL004461		lamin, putative	20.40	70.71	3.29	0.0000
AAEL008724		conserved hypothetical protein	0.43	1.88	3.28	0.0000
AAEL003664		lupus la ribonucleoprotein	15.54	53.99	3.28	0.0000
AAEL015606		hypothetical protein	0.36	2.16	3.28	0.0000
AAEL004452		fast myosin heavy chain HCIII, putative	8.73	30.09	3.26	0.0000
AAEL013142		conserved hypothetical protein	1.63	5.69	3.23	0.0000
AAEL014551		triacylglycerol lipase, pancreatic	18.36	64.28	3.23	0.0000
AAEL001626		zinc/iron transporter	14.86	49.98	3.22	0.0000
AAEL011773		calreticulin	35.65	121.09	3.22	0.0000
AAEL009765		choline/ethanolamine kinase	13.65	46.71	3.18	0.0000
AAEL009347		hypothetical protein	2.06	7.32	3.18	0.0000
AAEL002242		conserved hypothetical protein	3.04	11.20	3.18	0.0000
AAEL007397	E75	Ecdysone-induced Nuclear receptor	6.69	22.25	3.17	0.0000
AAEL010109		conserved hypothetical protein	9.07	30.49	3.17	0.0000
AAEL009842	GALE12	galectin	9.91	34.43	3.16	0.0000
AAEL010716		preprotein translocase secy subunit	41.76	140.47	3.16	0.0000
AAEL002741	SCRB6	Class B Scavenger Receptor	1.73	5.95	3.14	0.0000
AAEL017133			21.09	69.27	3.13	0.0000
AAEL001423		acid phosphatase-1	18.58	61.99	3.13	0.0000
AAEL002795		rfx transcription factor	0.35	1.41	3.13	0.0000
AAEL006634		acetyl-coa acetyltransferase, mitochondrial	40.14	132.12	3.12	0.0000

Table A5 Continued

IDs	Gene name	Gene description	4 days	3h	Fold	*p* adj
AAEL017975	HSP70Ba	heat shock protein HSP70	1.72	6.02	3.12	0.0000
AAEL013013		hypothetical protein	17.70	60.53	3.10	0.0000
AAEL010379		ATP-binding cassette transporter	17.13	55.64	3.08	0.0000
AAEL009935		conserved hypothetical protein	0.52	2.21	3.07	0.0000
AAEL004178		ribose-phosphate pyrophosphokinase 1,	183.32	595.75	3.07	0.0000
AAEL004335		secreted ferritin G subunit precursor, putative	2.94	10.71	3.05	0.0000
AAEL010028		sarcosine dehydrogenase	11.38	36.96	3.05	0.0000
AAEL000057	TOLL5B	Toll-like receptor	0.53	1.92	3.05	0.0000
AAEL017843			8.36	35.38	3.04	0.0000
AAEL001869		gmp synthase	40.78	132.14	3.04	0.0000
AAEL008668	CLIPB22	Clip-Domain Serine Protease family B.	3.87	12.86	3.02	0.0000
AAEL004043		conserved hypothetical protein	11.12	35.28	3.02	0.0000
AAEL010808		conserved hypothetical protein	0.24	1.12	3.00	0.0000
AAEL001005		calreticulin	56.55	177.56	2.99	0.0000
AAEL002898		conserved hypothetical protein	6.97	23.10	2.98	0.0000
AAEL013346		lethal	0.40	1.97	2.96	0.0000
AAEL009669		conserved hypothetical protein	14.25	45.64	2.95	0.0000
AAEL013989		protein translocation complex beta subunit	86.90	275.16	2.94	0.0000
AAEL001331		mannose-1-phosphate guanyltransferase	11.67	37.54	2.94	0.0000
AAEL004116		hypothetical protein	33.30	102.50	2.94	0.0000
AAEL012545		proliferating cell nuclear antigen	3.20	11.06	2.92	0.0000
AAEL011520		sucrose transport protein	1.66	5.40	2.92	0.0000
AAEL004229	GSTT4	glutathione transferase	40.41	122.80	2.92	0.0000
AAEL006887		mRNA turnover protein 4 mrt4	13.37	41.39	2.91	0.0000
AAEL004592		tyrosine-protein kinase src64b	1.74	5.54	2.91	0.0000
AAEL008728		DEAD box ATP-dependent RNA helicase	3.50	10.74	2.91	0.0000
AAEL009349		conserved hypothetical protein	0.87	3.10	2.90	0.0000
AAEL014840		short-chain dehydrogenase	2.68	11.15	2.89	0.0000
AAEL002757		hypothetical protein	1.03	3.49	2.89	0.0000
AAEL013345		alphaA-crystallin, putative	0.13	2.80	2.89	0.0002
AAEL000364		glycine cleavage system h protein	24.23	83.15	2.89	0.0000
AAEL005298		hypothetical protein	4.36	17.31	2.88	0.0000
AAEL010086		DNA replication licensing factor MCM4	0.39	1.42	2.88	0.0000
AAEL001478		bile acid beta-glucosidase, putative	5.62	16.68	2.84	0.0000
AAEL012100		conserved hypothetical protein	11.19	33.56	2.83	0.0000
AAEL001246		Thymidylate kinase, putative	0.93	3.43	2.82	0.0000
AAEL010906		conserved hypothetical protein	6.82	20.41	2.82	0.0000
AAEL014843		heat shock protein	30.43	88.64	2.81	0.0000
AAEL013075		conserved hypothetical protein	15.71	46.57	2.81	0.0000
AAEL012318		2-amino-3-ketobutyrate coenzyme a ligase	4.22	12.50	2.80	0.0000
AAEL004112	TPX2	Thioredoxin Peroxidase.	165.28	475.54	2.77	0.0000
AAEL001708		hypothetical protein	9.06	26.47	2.77	0.0000
AAEL007441		translocon-associated protein, gamma subunit	73.42	218.96	2.74	0.0000
AAEL012538	LRIM6	leucine-rich immune protein	7.99	24.46	2.74	0.0000
AAEL000551		hypothetical protein	64.97	187.87	2.74	0.0000
AAEL006870		sorting nexin	9.08	26.00	2.73	0.0000
AAEL013904		3-hydroxyisobutyrate dehydrogenase	17.89	50.83	2.73	0.0000
AAEL009925		amidase	5.13	15.41	2.71	0.0000
AAEL002255		conserved hypothetical protein	4.33	13.09	2.71	0.0000
AAEL002709		spliceosomal protein sap	14.96	42.46	2.71	0.0000
AAEL009636		conserved hypothetical protein	9.62	27.59	2.71	0.0000
AAEL001293		conserved hypothetical protein	7.81	22.99	2.69	0.0000

Table A5 Continued

IDs	Gene name	Gene description	4 days	3h	Fold	*p* adj
AAEL005289		ornithine aminotransferase	13.85	38.99	2.69	0.0000
AAEL003723	LYSC11	C-Type Lysozyme	17.13	51.14	2.69	0.0000
AAEL004482		conserved hypothetical protein	7.81	22.33	2.68	0.0000
AAEL010222		transcription factor GATA-4	2.90	8.35	2.68	0.0000
AAEL004247		Sialin, Sodium/sialic acid cotransporter, putative	5.76	16.24	2.66	0.0000
AAEL014321		glucosylceramidase	0.34	1.33	2.66	0.0001
AAEL002701		mannosyltransferase	26.59	73.54	2.64	0.0000
AAEL003303		conserved hypothetical protein	11.94	34.27	2.64	0.0000
AAEL001412		conserved hypothetical protein	20.32	56.33	2.63	0.0000
AAEL010035		WD-repeat protein	5.12	14.17	2.62	0.0000
AAEL000641		protein disulfide isomerase	224.81	625.68	2.62	0.0000
AAEL011158		disulfide oxidoreductase	4.75	13.05	2.61	0.0000
AAEL009829		ARL3, putative	14.51	39.75	2.60	0.0000
AAEL000674		RNA m5u methyltransferase	4.03	11.16	2.60	0.0000
AAEL007113		selenophosphate synthase	90.74	247.30	2.60	0.0000
AAEL012185		ribosome biogenesis regulatory protein	15.14	41.10	2.58	0.0000
AAEL001400		DNA-directed RNA polymerases III 12.5 kDa	15.92	43.61	2.57	0.0000
AAEL001392		hypothetical protein	1.15	4.21	2.57	0.0002
AAEL003646		conserved hypothetical protein	27.11	72.70	2.57	0.0000
AAEL015445		cysteine dioxygenase	0.81	2.45	2.57	0.0000
AAEL003993		cyclohex-1-ene-1-carboxyl-CoA hydratase	74.61	205.24	2.57	0.0000
AAEL016961			0.87	2.86	2.56	0.0000
AAEL014030		conserved hypothetical protein	0.80	2.30	2.55	0.0000
AAEL002686		testisin precursor, putative	13.68	38.90	2.54	0.0000
AAEL007226		nidogen	2.61	7.15	2.54	0.0000
AAEL003514		centromere/microtubule binding protein cbf5	19.75	54.15	2.54	0.0000
AAEL002483		conserved hypothetical protein	6.82	18.11	2.53	0.0000
AAEL007286		arginine-rich protein, putative	43.91	121.17	2.53	0.0000
AAEL014314		DNA primase	0.41	1.34	2.53	0.0000
AAEL005163		conserved hypothetical protein	10.82	29.45	2.52	0.0000
AAEL006549		conserved hypothetical protein	4.78	12.70	2.52	0.0000
AAEL009273		inosine-5-monophosphate dehydrogenase	22.58	60.97	2.52	0.0000
AAEL014298		ORF-A short, putative	3.88	10.49	2.52	0.0000
AAEL007270		hypothetical protein	2.57	6.81	2.51	0.0000
AAEL017367			1.75	4.91	2.51	0.0000
AAEL001767		conserved hypothetical protein	7.64	20.91	2.51	0.0000
AAEL013314		calicylin binding protein	11.17	29.33	2.51	0.0000
AAEL001641		deoxyribonuclease I, putative	85.48	227.71	2.50	0.0000
AAEL012123		conserved hypothetical protein	1.68	4.91	2.49	0.0000
AAEL005969		phospholipase b, plb1	1.13	3.21	2.49	0.0000
AAEL014449		ribose-phosphate pyrophosphokinase 1,	1.42	5.36	2.49	0.0007
AAEL000765		hexamerin 2 beta	1.11	3.04	2.49	0.0000
AAEL007416		cysteine dioxygenase	5.28	14.97	2.49	0.0000
AAEL002108		nucleolar essential protein 1	10.37	27.07	2.48	0.0000
AAEL006617		conserved hypothetical protein	24.57	69.31	2.48	0.0000
AAEL006883		conserved hypothetical protein	22.42	58.10	2.48	0.0000
AAEL003508		serine-pyruvate aminotransferase	16.53	45.55	2.47	0.0000
AAEL006196		hemomucin	31.31	80.08	2.46	0.0000
AAEL008220		conserved hypothetical protein	14.23	36.75	2.46	0.0000
AAEL011519		sucrose transport protein	2.79	8.39	2.45	0.0000
AAEL002194		uricase	33.64	86.46	2.44	0.0000
AAEL001917		ribosome biogenesis protein brix	0.70	2.06	2.44	0.0000

Table A5 Continued

IDs	Gene name	Gene description	4 days	3h	Fold	*p* adj
AAEL002861		conserved hypothetical protein	18.95	48.92	2.43	0.0000
AAEL015049		60S ribosomal protein L35	1.19	3.34	2.43	0.0000
AAEL003949		conserved hypothetical protein	7.43	18.82	2.43	0.0000
AAEL015199		WD-repeat protein	0.83	2.26	2.41	0.0000
AAEL011581		conserved hypothetical protein	3.26	8.65	2.41	0.0000
AAEL017154			1.50	5.18	2.40	0.0008
AAEL013940		chromatin assembly factor i P60 subunit	0.57	1.56	2.40	0.0000
AAEL017638			1.65	5.54	2.40	0.0006
AAEL009044		amine oxidase	0.86	2.40	2.39	0.0000
AAEL000786		hypothetical protein	41.09	111.57	2.39	0.0000
AAEL008292	GPRDIH1	GPCR Diuretic Insect Hormone/Kinin/CRF	4.77	12.45	2.39	0.0000
AAEL008054		conserved hypothetical protein	44.50	112.97	2.39	0.0000
AAEL006327		sulfotransferase	2.03	5.35	2.39	0.0000
AAEL007887		ornithine decarboxylase	1.08	2.86	2.37	0.0000
AAEL012864		conserved hypothetical protein	3.61	9.45	2.36	0.0000
AAEL004616		actin	17.99	44.59	2.36	0.0000
AAEL012629		deoxyuridine 5'-triphosphate nucleotidohydrol.	1.14	3.40	2.36	0.0002
AAEL004017		DNA polymerase v	9.45	23.48	2.36	0.0000
AAEL015441		spliceosomal protein sap	13.30	33.43	2.36	0.0000
AAEL012511		conserved hypothetical protein	32.09	79.94	2.36	0.0000
AAEL000859		hypothetical protein	5.38	13.38	2.35	0.0000
AAEL010118		kelch repeat protein	8.77	21.93	2.35	0.0000
AAEL003469		NHP2 protein, putative	21.67	54.28	2.35	0.0000
AAEL002482		hypothetical protein	1.80	4.93	2.35	0.0000
AAEL015446		conserved hypothetical protein	0.97	3.45	2.35	0.0018
AAEL015306		hypothetical protein	7.50	20.97	2.35	0.0000
AAEL011599		ADP-ribosylation factor, putative	3.19	8.17	2.35	0.0000
AAEL017029			58.59	149.83	2.35	0.0000
AAEL010529		conserved hypothetical protein	8.41	21.91	2.34	0.0000
AAEL004455		conserved hypothetical protein	17.67	43.73	2.34	0.0000
AAEL012842		trypsin, putative	2.01	6.19	2.34	0.0005
AAEL011704		heat shock protein	16.09	40.97	2.34	0.0000
AAEL010596		n-acetylgalactosaminyltransferase	15.99	38.92	2.34	0.0000
AAEL002231		cuticle protein, putative	31.86	79.29	2.33	0.0000
AAEL000293		ebna2 binding protein P100	43.17	105.42	2.33	0.0000
AAEL012519		actin binding protein, putative	0.39	1.13	2.33	0.0001
AAEL016996			8.70	22.00	2.33	0.0000
AAEL000999		DNA replication licensing factor MCM7	2.09	5.32	2.33	0.0000
AAEL002603		triacylglycerol lipase, putative	0.35	1.22	2.33	0.0021
AAEL008635		ABC transporter	17.88	43.02	2.31	0.0000
AAEL002966		conserved hypothetical protein	0.44	1.41	2.31	0.0013
AAEL008424		sodium/chloride dependent aa transporter	0.74	2.01	2.30	0.0000
AAEL010904		rothmund-thomson syndrome DNA helicase	0.78	1.95	2.30	0.0000
AAEL013944		hypothetical protein	3.57	9.00	2.30	0.0000
AAEL000313		conserved hypothetical protein	1.06	2.75	2.30	0.0000
AAEL005106		conserved hypothetical protein	42.33	101.76	2.30	0.0000
AAEL008450		conserved hypothetical protein	7.83	19.29	2.29	0.0000
AAEL001506		U3 small nucleolar ribonucleoprotein proteir	6.43	15.41	2.28	0.0000
AAEL001432		protein disulfide isomerase	96.36	232.23	2.28	0.0000
AAEL009909		cln3/battenin	3.47	8.60	2.28	0.0000
AAEL007578		shk1 kinase-binding protein	2.51	6.17	2.28	0.0000
AAEL014085	IR75k.2	ionotropic glutamate receptor-invertebrate	0.39	1.35	2.28	0.0031
AAEL014823		conserved hypothetical protein	1.24	3.43	2.27	0.0001

Table A5 Continued

IDs	Gene name	Gene description	4 days	3h	Fold	*p* adj
AAEL012851		WD-repeat protein	17.03	40.47	2.27	0.0000
AAEL004063		WD-repeat protein	10.92	25.91	2.26	0.0000
AAEL008572		RNA-binding protein, putative	5.85	14.21	2.25	0.0000
AAEL007880		ornithine decarboxylase	201.67	469.49	2.25	0.0000
AAEL001054	GSTD4	glutathione transferase	2.94	7.31	2.24	0.0000
AAEL001193		regulator of g protein signaling	1.21	3.57	2.24	0.0014
AAEL009250		conserved hypothetical protein	8.68	20.62	2.23	0.0000
AAEL004686		RuvB-like helicase 1	5.75	13.50	2.23	0.0000
AAEL002457		conserved hypothetical protein	17.20	39.95	2.23	0.0000
AAEL013685		WD-repeat protein	4.31	10.49	2.22	0.0000
AAEL017224			2.40	6.39	2.22	0.0002
AAEL006701		conserved hypothetical protein	3.81	9.08	2.22	0.0000
AAEL011212		nuclear transcription factor, x-box binding 1	1.31	3.22	2.22	0.0000
AAEL007697		conserved hypothetical protein	7.30	17.20	2.21	0.0000
AAEL017987			0.77	2.02	2.20	0.0001
AAEL017059			24.75	57.87	2.20	0.0000
AAEL008470		hypothetical protein	20.75	48.41	2.20	0.0000
AAEL008576		conserved hypothetical protein	0.87	2.14	2.19	0.0000
AAEL011899		beta-1,3-N-acetylglucosaminyltransferase	3.54	8.36	2.19	0.0000
AAEL008247		DNA polymerase alpha catalytic subunit	0.79	2.08	2.19	0.0002
AAEL005335		conserved hypothetical protein	1.16	2.90	2.19	0.0000
AAEL005474		hypothetical protein	91.31	216.28	2.19	0.0000
AAEL012655		sugar transporter	43.70	98.99	2.19	0.0000
AAEL005471		Sec61 protein complex gamma subunit, putative	146.32	334.67	2.18	0.0000
AAEL008849		selenophosphate synthase	34.48	78.02	2.18	0.0000
AAEL008366		pyruvate dehydrogenase	13.90	31.93	2.18	0.0000
AAEL010521		ribophorin ii	18.79	42.97	2.18	0.0000
AAEL011989		signal peptide peptidase	33.86	77.18	2.18	0.0000
AAEL011138		hypothetical protein	0.59	1.80	2.17	0.0038
AAEL009519		hypothetical protein	22.03	50.09	2.17	0.0000
AAEL013214	FORAGE3	cgmp-dependent protein kinase	4.11	9.35	2.16	0.0000
AAEL011536		phosphoglucomutase	5.08	11.49	2.16	0.0000
AAEL005296		conserved hypothetical protein	0.76	2.06	2.16	0.0011
AAEL013183		inositol triphosphate 3-kinase c	19.66	45.20	2.16	0.0000
AAEL009508		zinc finger protein	0.70	1.79	2.16	0.0002
AAEL007961		hypothetical protein	3.01	6.96	2.16	0.0000
AAEL005281		hypothetical protein	1.23	2.87	2.15	0.0000
AAEL013949		hypothetical protein	1.15	2.98	2.15	0.0004
AAEL000897		conserved hypothetical protein	11.78	26.53	2.15	0.0000
AAEL003742		glucosylceramidase	0.58	1.49	2.15	0.0004
AAEL012282		prohibitin	5.99	13.79	2.15	0.0000
AAEL010582	GSTD11	glutathione transferase	9.92	22.48	2.14	0.0000
AAEL006226		sam/hd domain protein	11.64	25.95	2.14	0.0000
AAEL010827		programmed cell death protein 11	5.74	12.84	2.14	0.0000
AAEL008942		conserved hypothetical protein	16.52	37.01	2.14	0.0000
AAEL012876		conserved hypothetical protein	2.75	6.46	2.14	0.0000
AAEL007271		basic helix-loop-helix zip transcription factor	1.45	3.63	2.13	0.0002
AAEL010398		hypothetical protein	9.59	23.16	2.12	0.0000
AAEL012447		elastase, putative	13.80	30.69	2.12	0.0000
AAEL017982	HSP70Cb'	heat shock protein HSP70	0.47	1.32	2.12	0.0043
AAEL011701		conserved hypothetical protein	9.87	21.82	2.12	0.0000
AAEL011538		conserved hypothetical protein	1.69	3.89	2.12	0.0000

Table A5 Continued

IDs	Gene name	Gene description	4 days	3h	Fold	*p* adj
AAEL017978	HSP70Cb	heat shock protein HSP70	1.38	3.21	2.11	0.0000
AAEL000659		exosome complex exonuclease rrp43	4.40	9.93	2.11	0.0000
AAEL006211		conserved hypothetical protein	0.87	2.15	2.11	0.0003
AAEL006063		U3 small nucleolar ribonucleoprotein protein i	8.40	18.48	2.10	0.0000
AAEL013114		DNA-J, putative	13.74	30.24	2.10	0.0000
AAEL010290		short-chain dehydrogenase	10.83	23.76	2.10	0.0000
AAEL002888		williams-beuren syndrome critical region protein	7.02	15.45	2.10	0.0000
AAEL001169		Ribosome biogenesis protein BOP1 homolog	9.88	21.79	2.09	0.0000
AAEL010855		cdc6	0.39	1.07	2.09	0.0044
AAEL007136		sugar transporter	17.65	39.01	2.09	0.0000
AAEL010937		conserved hypothetical protein	3.21	7.19	2.09	0.0000
AAEL001195		juvenile hormone-inducible protein, putative	0.67	1.88	2.09	0.0057
AAEL002048		histidyl-tRNA synthetase	13.44	29.18	2.08	0.0000
AAEL011827		conserved hypothetical protein	10.64	23.09	2.08	0.0000
AAEL005125		conserved hypothetical protein	21.67	49.34	2.08	0.0000
AAEL008404	CLIPA16	Clip-Domain Serine Protease family A.	0.29	1.01	2.08	0.0158
AAEL008656		UDP-galactose transporter	28.42	62.54	2.08	0.0000
AAEL004918		brat protein	0.73	1.69	2.08	0.0000
AAEL008716		conserved hypothetical protein	5.15	11.23	2.07	0.0000
AAEL010644		ribonucleoside-diphosphate reductase	2.94	6.51	2.07	0.0000
AAEL015655	CYP302A1	cytochrome P450	0.64	1.59	2.07	0.0008
AAEL002959		brain chitinase and chia	2.20	5.71	2.07	0.0028
AAEL003285		translocation associated membrane protein	56.76	123.17	2.07	0.0000
AAEL011224		hypothetical protein	17.34	38.08	2.07	0.0000
AAEL015143		glycine rich RNA binding protein, putative	10.31	22.23	2.06	0.0000
AAEL009490		carbamoyl-phosphate synthase large chain	2.25	4.88	2.06	0.0000
AAEL003246		deoxyribose-phosphate aldolase	6.19	13.75	2.06	0.0000
AAEL005327		hypothetical protein	2.73	6.10	2.06	0.0000
AAEL010476		sil1	3.32	7.30	2.06	0.0000
AAEL004722		GABA-A receptor interacting factor-1, putative	15.80	33.67	2.05	0.0000
AAEL003070		conserved hypothetical protein	3.02	6.60	2.05	0.0000
AAEL004263		small nuclear ribonucleoprotein sm d1	2.36	5.63	2.05	0.0006
AAEL008832		forkhead box protein	21.50	45.51	2.04	0.0000
AAEL012725		conserved hypothetical protein	0.46	1.04	2.04	0.0000
AAEL002174		protein glycosyltransferase	33.11	70.53	2.04	0.0000
AAEL003975		WD-repeat protein	4.09	8.96	2.04	0.0000
AAEL002010		conserved hypothetical protein	6.03	13.19	2.03	0.0000
AAEL004228		oligosaccharyl transferase	11.65	24.91	2.03	0.0000
AAEL008330		hexaprenyldihydroxybenzoate methyltransferase	13.73	30.24	2.03	0.0000
AAEL017421			40.45	85.64	2.03	0.0000
AAEL000759		gamma-glutamylcysteine synthetase, putative	28.35	59.47	2.03	0.0000
AAEL004698		DNA primase large subunit	0.72	1.73	2.02	0.0015
AAEL006310		conserved hypothetical protein	0.73	1.98	2.02	0.0095
AAEL003313		alkaline phosphatase	1.55	3.38	2.02	0.0000
AAEL017508			31.08	66.09	2.02	0.0000
AAEL000300		WD-repeat protein	8.23	17.49	2.02	0.0000
AAEL008494		mitochondrial carrier protein ymc	105.09	226.43	2.02	0.0000
AAEL017286			36.50	76.83	2.02	0.0000

Table A5 Continued

IDs	Gene name	Gene description	4 days	3h	Fold	*p* adj
AAEL008370	SCRB17	Class B Scavenger Receptor	23.84	50.05	2.01	0.0000
AAEL015572		ribophorin ii	4.61	9.90	2.01	0.0000
AAEL003352		ribosomal protein l7ae	90.26	191.17	2.01	0.0000
AAEL013952		prohibitin	7.38	15.58	2.01	0.0000
AAEL006106	OBP26	odorant binding protein OBP26	0.48	2.70	2.00	0.0253
AAEL009149		kinectin, putative	0.98	2.19	2.00	0.0001
AAEL014252		sulfite reductase	0.80	1.81	2.00	0.0002
		Down regulated				
AAEL007653		allantoinase	66.66	0.40	-118.57	0.0000
AAEL010764		aldehyde dehydrogenase	67.61	0.66	-64.37	0.0000
AAEL005120		zinc finger protein	7.06	0.38	-12.72	0.0000
AAEL011319		hypothetical protein	65.41	3.64	-12.17	0.0000
AAEL001087		synaptic vesicle protein	23.54	2.23	-8.65	0.0000
AAEL006446		trehalose-6-phosphate synthase	50.34	6.26	-7.48	0.0000
AAEL010656	LRIM12	leucine-rich immune protein	22.16	2.59	-7.30	0.0000
AAEL011130		alcohol dehydrogenase	3.29	0.25	-6.74	0.0000
AAEL000546			12.32	2.12	-5.25	0.0000
AAEL013555	CYP4J13	cytochrome P450	64.27	12.60	-5.01	0.0000
AAEL007680		hypothetical protein	53.68	11.67	-4.63	0.0000
AAEL007103	LRIM15	leucine-rich immune protein	9.44	1.89	-4.53	0.0000
AAEL014830		cytochrome P450	22.22	4.29	-4.52	0.0000
AAEL017136	CYP325V1	cytochrome P450	8.13	1.69	-4.50	0.0000
AAEL005731		forkhead box protein	13.05	2.16	-4.48	0.0000
AAEL012956		elastase, putative	8.37	1.77	-4.43	0.0000
AAEL005741		forkhead protein/ forkhead protein domain	37.69	8.39	-4.16	0.0000
AAEL006323		hypothetical protein	12.77	2.55	-3.94	0.0000
AAEL006805	CYP9J2	cytochrome P450	31.29	8.46	-3.72	0.0000
AAEL002665		matrix metalloproteinase	12.23	3.28	-3.61	0.0000
AAEL013554	CYP4J14	cytochrome P450	8.56	2.36	-3.45	0.0000
AAEL000678		alpha-amylase	1.46	0.31	-3.43	0.0000
AAEL010688		MRAS2, putative	6.38	1.85	-3.24	0.0000
AAEL004407		allergen, putative	4.71	1.39	-3.20	0.0000
AAEL014005		clip-domain serine protease, putative	2.34	0.55	-3.20	0.0000
AAEL006585		predicted protein	2.06	0.40	-3.14	0.0000
AAEL004277		conserved hypothetical protein	4.16	1.25	-3.11	0.0000
AAEL002378			8.52	2.48	-3.09	0.0000
AAEL013001		conserved hypothetical protein	11.71	3.50	-3.09	0.0000
AAEL014664		AMP dependent coa ligase	5.58	1.65	-3.07	0.0000
AAEL011764	PPO10	prophenoloxidase	2.94	0.88	-3.07	0.0000
AAEL001863		zinc carboxypeptidase	520.08	167.23	-3.02	0.0000
AAEL002669		AMP dependent ligase	5.46	1.70	-3.01	0.0000
AAEL001367		type IV inositol 5-phosphatase	41.34	14.10	-2.99	0.0000
AAEL010384		aldehyde oxidase	12.58	3.97	-2.99	0.0000
AAEL002658		AMP dependent ligase	8.87	3.00	-2.95	0.0000
AAEL002668		AMP dependent ligase	4.76	1.55	-2.95	0.0000
AAEL008785		hypothetical protein	731.79	254.16	-2.95	0.0000
AAEL008157		conserved hypothetical protein	5.84	1.93	-2.93	0.0000
AAEL000086	CLIPB32	Clip-Domain Serine Protease family B.	1.50	0.36	-2.90	0.0000
AAEL006576		clip-domain serine protease, putative	35.57	11.02	-2.90	0.0000
AAEL014045		allantoicase	11.10	3.74	-2.88	0.0000
AAEL013515		pupal cuticle protein, putative	40.54	13.54	-2.88	0.0000
AAEL006811	CYP9J8	cytochrome P450	8.19	2.83	-2.86	0.0000
AAEL013355		hypothetical protein	11.57	3.96	-2.85	0.0000
AAEL010946	CYP314A1	cytochrome P450	3.31	1.09	-2.84	0.0000

Table A5 Continued

IDs	Gene name	Gene description	4 days	3h	Fold	*p* adj
AAEL014004		clip-domain serine protease, putative	3.81	0.99	-2.83	0.0000
AAEL004786		conserved hypothetical protein	13.25	4.69	-2.83	0.0000
AAEL014663		AMP dependent coa ligase	3.69	1.16	-2.81	0.0000
AAEL000820		dimethylaniline monooxygenase	4.85	1.67	-2.80	0.0000
AAEL006568		serine protease	35.70	12.89	-2.80	0.0000
AAEL013112	PGRPLE	Peptidoglycan Recognition Protein	1.46	0.43	-2.79	0.0000
AAEL013432		serine protease, putative	17.64	6.37	-2.78	0.0000
AAEL011676		AMP dependent coa ligase	3.03	1.05	-2.72	0.0000
AAEL009127	CYP6M11	cytochrome P450	7.81	2.78	-2.70	0.0000
AAEL010206		xylulose kinase	11.11	4.02	-2.67	0.0000
AAEL011766		conserved hypothetical protein	2.02	0.70	-2.67	0.0000
AAEL006609		zinc finger protein	73.21	28.07	-2.67	0.0000
AAEL008632		ABC transporter	15.20	5.77	-2.66	0.0000
AAEL003128		conserved hypothetical protein	44.35	16.87	-2.65	0.0000
AAEL001818		conserved hypothetical protein	61.59	23.86	-2.64	0.0000
AAEL013821		xylulose kinase	8.76	3.13	-2.64	0.0000
AAEL009487		hypothetical protein	266.09	104.46	-2.61	0.0000
AAEL014553		triacylglycerol lipase, pancreatic	5.17	1.51	-2.61	0.0001
AAEL004301		conserved hypothetical protein	2.41	0.54	-2.61	0.0007
AAEL014956		internalin A, putative	1.99	0.67	-2.60	0.0000
AAEL000044		ornithine decarboxylase	13.36	5.12	-2.60	0.0000
AAEL000101		AMP dependent coa ligase	4.81	1.80	-2.59	0.0000
AAEL011129		alcohol dehydrogenase	27.64	10.58	-2.58	0.0000
AAEL003884		conserved hypothetical protein	10.88	3.89	-2.58	0.0000
AAEL001864		translation initiation factor 4E binding protein	178.33	69.67	-2.56	0.0000
AAEL009131	CYP6Z8	cytochrome P450	89.49	34.31	-2.54	0.0000
AAEL001289		permease, putative	18.75	7.48	-2.53	0.0000
AAEL013975		transcription factor IIIA, putative	1.69	0.56	-2.52	0.0000
AAEL017022			192.85	78.26	-2.52	0.0000
AAEL017523	TOLL4	Toll-like receptor	2.01	0.73	-2.51	0.0000
AAEL004097		enhancer of split protein, putative	15.37	6.19	-2.51	0.0000
AAEL003877		ubiquitin	316.02	130.06	-2.49	0.0000
AAEL017245			307.64	127.45	-2.46	0.0000
AAEL009899		conserved hypothetical protein	129.62	52.85	-2.44	0.0000
AAEL014893	CYP6BB2	cytochrome P450	135.14	55.45	-2.42	0.0000
AAEL015093		triacylglycerol lipase, pancreatic	1.04	0.24	-2.42	0.0027
AAEL010479		sugar transporter	412.81	177.10	-2.39	0.0000
AAEL006487		sodium/solute symporter	18.15	7.74	-2.38	0.0000
AAEL012953		conserved hypothetical protein	2.99	1.17	-2.37	0.0000
AAEL013703		trypsin	112.84	48.52	-2.37	0.0000
AAEL009513		adenylate cyclase	12.68	5.39	-2.37	0.0000
AAEL011139		conserved hypothetical protein	3.21	1.29	-2.37	0.0000
AAEL009507		glucose-6-phosphate 1-dehydrogenase	20.07	8.60	-2.36	0.0000
AAEL008782		serine-type enodpeptidase,	3.29	1.21	-2.35	0.0001
AAEL010171	PGRPLB	peptidoglycan recognition protein	141.14	61.36	-2.35	0.0000
AAEL003881		ubiquitin, putative	167.56	73.16	-2.34	0.0000
AAEL013629		trypsin-alpha, putative	11.74	5.04	-2.34	0.0000
AAEL010485		sugar transporter	8.17	3.50	-2.34	0.0000
AAEL001646	Kir3	inward-rectifying potassium channel	1.45	0.47	-2.34	0.0013
AAEL010634		hypothetical protein	77.45	31.77	-2.34	0.0000
AAEL014579		trypsin, putative	1.23	0.34	-2.34	0.0029
AAEL014955		tartan protein, putative	1.42	0.54	-2.34	0.0000
AAEL007818		Trypsin 3A1 Precursor	68.99	25.48	-2.32	0.0002

Table A5 Continued

IDs	Gene name	Gene description	4 days	3h	Fold	*p* adj
AAEL010337		CRAL/TRIO domain-containing protein	24.25	10.38	-2.32	0.0000
AAEL012711	CLIPC12	Clip-Domain Serine Protease family C.	5.21	2.18	-2.31	0.0000
AAEL000581		conserved hypothetical protein	13.81	6.02	-2.31	0.0000
AAEL005790		malic enzyme	211.32	92.84	-2.31	0.0000
AAEL002696		hypothetical protein	9.20	3.95	-2.30	0.0000
AAEL001002		sodium/solute symporter	38.74	16.78	-2.30	0.0000
AAEL003090		malate synthase	2.53	0.96	-2.30	0.0001
AAEL007748	SCRB10	Class B Scavenger Receptor	6.60	2.84	-2.30	0.0000
AAEL009856		sodium/dicarboxylate cotransporter, putative	17.81	7.76	-2.30	0.0000
AAEL011852		hypothetical protein	9.52	3.83	-2.28	0.0000
AAEL013427		serine protease, putative	7.22	3.08	-2.28	0.0000
AAEL007260		conserved hypothetical protein	3.30	1.39	-2.27	0.0000
AAEL007784		conserved hypothetical protein	9.34	3.98	-2.25	0.0000
AAEL013484		hypothetical protein	88.60	40.11	-2.23	0.0000
AAEL011368		sugar transporter	14.42	6.54	-2.23	0.0000
AAEL013486		hypothetical protein	295.82	134.80	-2.23	0.0000
AAEL009199		1,3- galactosyltransferase	1.41	0.53	-2.23	0.0007
AAEL000992		hypothetical protein	48.73	22.31	-2.22	0.0000
AAEL014614		cytochrome P450	9.74	4.37	-2.22	0.0000
AAEL012360		hypothetical protein	5.14	2.22	-2.21	0.0000
AAEL012698		ATP-binding	7.35	3.39	-2.21	0.0000
AAEL001532		FAD NAD binding oxidoreductases	22.71	10.36	-2.21	0.0000
AAEL006484	GPROP3	long wavelength sensitive opsin	3.69	1.47	-2.18	0.0006
AAEL014608		cytochrome P450	2.23	0.94	-2.18	0.0001
AAEL008928	Kir2A	inward-rectifying potassium channel	54.53	25.57	-2.16	0.0000
AAEL006586		serine protease	8.44	3.47	-2.16	0.0003
AAEL005376		predicted protein	1.70	0.76	-2.16	0.0000
AAEL001771		toll	1.12	0.41	-2.15	0.0037
AAEL014609	CYP9J26	cytochrome P450	115.34	55.04	-2.15	0.0000
AAEL010478		sugar transporter	17.68	8.29	-2.15	0.0000
AAEL010151	CYP6N16	cytochrome P450	10.61	4.99	-2.14	0.0000
AAEL003345		argininosuccinate lyase	227.90	104.40	-2.14	0.0000
AAEL002950		conserved hypothetical protein	97.26	46.86	-2.13	0.0000
AAEL008767		serine protease	5.11	2.32	-2.12	0.0000
AAEL003954		juvenile hormone-inducible protein, putative	15.72	7.45	-2.12	0.0000
AAEL011325		gonadotropin-releasing hormone receptor	22.05	10.43	-2.12	0.0000
AAEL011371		conserved hypothetical protein	47.25	22.88	-2.11	0.0000
AAEL013775		conserved hypothetical protein	143.54	68.99	-2.10	0.0000
AAEL003978		hypothetical protein	7.14	3.40	-2.09	0.0000
AAEL008193		hypothetical protein	1.06	0.23	-2.08	0.0182
AAEL012255	LRIM13	leucine-rich immune protein	30.02	14.26	-2.08	0.0000
AAEL000609		conserved hypothetical protein	3.38	1.37	-2.08	0.0033
AAEL012409		pantothenate kinase	79.41	39.01	-2.07	0.0000
AAEL010099		4-nitrophenylphosphatase	8.30	4.00	-2.07	0.0000
AAEL003441		conserved hypothetical protein	7.62	3.72	-2.07	0.0000
AAEL009045		amine oxidase	1.60	0.66	-2.06	0.0032
AAEL014891		cytochrome P450	23.98	11.84	-2.06	0.0000
AAEL014411	CYP304B3	cytochrome P450	8.65	4.15	-2.06	0.0000
AAEL011191		protein phosphatase 1 binding protein	59.85	29.62	-2.06	0.0000
AAEL002385	CCEAE3B	Carboxy/choline esterase Alpha Esterase	12.10	5.76	-2.06	0.0000
AAEL005386		collagen alpha chain, anopheles	2.07	1.01	-2.06	0.0000
AAEL015315		malate synthase	1.68	0.65	-2.05	0.0074
AAEL008190		bhlh factor math6	18.81	8.68	-2.05	0.0001
AAEL013987		conserved hypothetical protein	118.97	59.47	-2.05	0.0000

Table A5 Continued

IDs	Gene name	Gene description	4 days	3h	Fold	*p* adj
AAEL014611		cytochrome P450	1.91	0.86	-2.05	0.0004
AAEL014141	SRPN5	Serine Protease Inhibitor	6.33	3.07	-2.04	0.0000
AAEL001566		bone morphogenetic protein	2.76	1.32	-2.04	0.0000
AAEL007055		lipase	72.63	35.82	-2.04	0.0000
AAEL013707		trypsin	2.92	1.24	-2.04	0.0030
AAEL009682		serine collagenase 1 precursor, putative	3.40	1.50	-2.04	0.0011
AAEL008285		pupal cuticle protein, putative	25.16	12.56	-2.03	0.0000
AAEL014353		conserved hypothetical protein	14.18	6.43	-2.03	0.0005
AAEL000519		hypothetical protein	7.93	3.18	-2.03	0.0076
AAEL008007		conserved hypothetical protein	23.77	11.40	-2.02	0.0000
AAEL002734		conserved hypothetical protein	2.62	1.12	-2.02	0.0036
AAEL003900		hypothetical protein	3.05	1.32	-2.02	0.0025
AAEL009771		hypothetical protein	14.67	7.01	-2.02	0.0000
AAEL006793	CYP9J9	cytochrome P450	11.94	5.91	-2.02	0.0000
AAEL000311		conserved hypothetical protein	42.14	20.21	-2.01	0.0000
AAEL006537		hypothetical protein	38.53	19.46	-2.00	0.0000
AAEL012536		hypothetical protein	14.85	7.52	-2.00	0.0000
AAEL010154	CYP4AR2	cytochrome P450	2.16	0.89	-2.00	0.0086

Table A6. Genes differentially expressed in the HT of 3h and 24h blood fed females.

Gene ID	Gene Name	Wiki Description	3h	24h	Fold	*p* adj
		Up regulated				
AAEL007599		cathepsin b	14.12	3,678.57	287.12	0.0000
AAEL012216		cathepsin b	8.47	1,488.61	201.76	0.0000
AAEL015312		cathepsin b	13.86	2,401.72	197.23	0.0000
AAEL007585		cathepsin b	5.16	821.16	178.32	0.0000
AAEL001307		SEC14, putative	3.49	283.78	91.25	0.0000
AAEL010656	LRIM12	hypothetical protein	2.53	89.94	40.88	0.0000
AAEL006563		serine carboxypeptidase	187.14	6,349.57	38.38	0.0000
AAEL006138		hypothetical protein	356.58	10,063.66	31.71	0.0000
AAEL006126		hypothetical protein	115.40	2,485.65	24.66	0.0000
AAEL001690		serine-type enodpeptidase, putative	7.11	152.01	23.58	0.0000
AAEL000678		alpha-amylase	0.30	5.76	19.39	0.0000
AAEL002482		hypothetical protein	4.09	59.83	16.45	0.0000
AAEL010946	CYP314A1	cytochrome P450	1.07	15.55	16.26	0.0000
AAEL013757		hexamerin 2 beta	0.56	7.82	15.61	0.0000
AAEL008781		serine-type enodpeptidase, putative	1.04	15.41	15.14	0.0000
AAEL001087		synaptic vesicle protein	1.54	29.72	15.02	0.0000
AAEL015606		hypothetical protein	2.11	25.56	13.72	0.0000
AAEL009588		expressed protein (HR3)	2.62	29.14	13.19	0.0000
AAEL004728		5-methyltetrahydrofolate:homocysteine methyltransferase	15.81	138.44	10.35	0.0000
AAEL013001		hypothetical protein	3.43	28.42	10.02	0.0000
AAEL006542		serine carboxypeptidase	61.38	526.75	10.01	0.0000
AAEL013294		hypothetical protein	0.50	4.46	9.98	0.0000
AAEL010434		hypothetical protein	1,022.26	8,402.07	9.71	0.0000
AAEL014537		maltose phosphorylase	0.11	1.31	9.34	0.0000
AAEL004277		hypothetical protein	0.70	5.58	9.19	0.0000
AAEL017451			20.13	154.55	9.16	0.0000
AAEL001703		serine-type enodpeptidase, putative	2.21	25.16	8.62	0.0000

Table A6 Continued

Gene ID	Gene Name	Wiki Description	3h	24h	Fold	*p* adj
AAEL013492	PPO5	prophenoloxidase	13.05	92.63	8.57	0.0000
AAEL007686		hypothetical protein	5.31	37.77	8.54	0.0000
AAEL009945		hypothetical protein	1.05	7.48	7.95	0.0000
AAEL008931	Kir2B	inwardly rectifying k+ channel, putative	0.12	1.02	7.88	0.0000
AAEL000298		sodium/shloride dependent aa transporter	0.45	3.33	7.47	0.0000
AAEL012555		maltose phosphorylase	0.85	5.20	7.33	0.0000
AAEL009636		hypothetical protein	24.08	144.43	7.17	0.0000
AAEL017484	CTLGA4		4.78	29.21	7.06	0.0000
AAEL015357		hypothetical protein	0.31	2.18	6.92	0.0000
AAEL006156		hypothetical protein	12.40	64.99	6.43	0.0000
AAEL012737		hypothetical protein	0.30	1.79	6.21	0.0000
AAEL002413		sphingomyelin phosphodiesterase	1.34	7.31	6.10	0.0000
AAEL015631		asparagine synthetase	1.30	6.90	6.08	0.0000
AAEL002699	SRPN7	serine protease inhibitor, serpin	0.17	1.18	6.04	0.0000
AAEL000828		vitellogenin, putative	1.09	5.85	5.98	0.0000
AAEL005186		tmc3 protein	0.29	1.63	5.94	0.0000
AAEL005621	GPROP4	rhodopsin	0.12	1.03	5.93	0.0000
AAEL010137		ketoreductase, putative	3.51	17.30	5.85	0.0000
AAEL013417		fibrinogen and fibronectin	1.13	5.82	5.77	0.0000
AAEL010634		hypothetical protein	15.88	74.72	5.67	0.0000
AAEL001674		serine-type enodpeptidase, putative	6.88	39.90	5.62	0.0000
AAEL009045		amine oxidase	0.54	2.62	5.54	0.0000
AAEL009194		hypothetical protein	1.21	5.80	5.52	0.0000
AAEL012693		tripartite motif protein	3.31	15.52	5.49	0.0000
AAEL000101		AMP dependent coa ligase	1.58	7.28	5.47	0.0000
AAEL003150		alpha-n-acetylglucosaminidase	2.10	9.59	5.47	0.0000
AAEL014541		maltose phosphorylase	1.42	6.49	5.34	0.0000
AAEL011126		alcohol dehydrogenase	1.42	6.25	5.33	0.0000
AAEL005763		lysosomal alpha-mannosidase	22.12	95.67	5.32	0.0000
AAEL005772	OBP22	Odorant-binding protein 99c, putative	286.65	1,237.43	5.28	0.0000
AAEL008663		aldo-keto reductase	2.60	11.48	5.24	0.0000
AAEL010938		l-asparaginase	0.74	3.44	5.24	0.0000
AAEL013112	PGRPLE	peptidoglycan recognition protein-lc isoform	0.42	1.97	5.21	0.0000
AAEL014455		hypothetical protein	1.39	6.12	5.18	0.0000
AAEL010337		CRAL/TRIO domain-containing protein	10.14	42.10	5.08	0.0000
AAEL001864		Eukaryotic translation initiation factor 4E	46.90	194.45	5.06	0.0000
AAEL005731		forkhead box protein (AaegFOXL)	2.11	10.27	5.05	0.0000
AAEL005800	CLIPE11	serine protease, putative	3.09	13.11	4.95	0.0000
AAEL001225		glycoside hydrolases	0.31	1.45	4.93	0.0000
AAEL002830		hypothetical protein	1.11	4.73	4.90	0.0000
AAEL014664		AMP dependent coa ligase	1.61	6.59	4.87	0.0000
AAEL009948		aldehyde dehydrogenase	3.88	15.76	4.84	0.0000
AAEL012856		hypothetical protein	26.88	108.78	4.84	0.0000
AAEL012764		hypothetical protein	32.94	131.47	4.80	0.0000
AAEL006446		trehalose-6-phosphate synthase	6.12	23.84	4.59	0.0000
AAEL007557		asparagine synthetase	1.74	6.97	4.56	0.0000
AAEL000340		cytochrome P450	1.22	4.66	4.50	0.0000
AAEL006876		igf2 mRNA binding protein, putative	0.29	1.16	4.44	0.0000
AAEL001059	GSTD3	GSTD1-6 protein, putative	0.74	3.03	4.36	0.0000
AAEL007315		hypothetical protein	8.01	28.80	4.36	0.0000
AAEL006877		prophenoloxidase	0.48	1.78	4.33	0.0000
AAEL001293		hypothetical protein	22.46	79.63	4.32	0.0000
AAEL008629		abc transporter	7.83	27.60	4.32	0.0000

Table A6 Continued

Gene ID	Gene Name	Wiki Description	3h	24h	Fold	*p* adj
AAEL017147			0.97	3.45	4.27	0.0000
AAEL003883		hypothetical protein	3.00	10.43	4.27	0.0000
AAEL013987		hypothetical protein	44.98	155.50	4.24	0.0000
AAEL009938		hypothetical protein	0.63	2.45	4.12	0.0000
AAEL003593		hypothetical protein	29.05	96.11	4.07	0.0000
AAEL010154	CYP4AR2	cytochrome P450	0.87	3.19	4.07	0.0000
AAEL008609		zinc carboxypeptidase	0.83	2.96	4.00	0.0000
AAEL011763	PPO3	prophenoloxidase	3.93	12.80	3.97	0.0000
AAEL005741		forkhead protein/ forkhead protein domain	8.20	26.89	3.94	0.0000
AAEL004665		hypothetical protein	2.64	8.80	3.91	0.0000
AAEL004369		alpha-glucosidase	242.24	778.79	3.91	0.0000
AAEL004672		hypothetical protein	0.78	2.74	3.90	0.0000
AAEL003651		hypothetical protein	4.15	13.10	3.88	0.0000
AAEL011676		AMP dependent coa ligase	1.04	3.33	3.85	0.0000
AAEL011446	CTL17	galactose-specific C-type lectin, putative	7.39	24.06	3.85	0.0000
AAEL013501	PPO4	prophenoloxidase	0.56	1.82	3.82	0.0000
AAEL015654	CYP6AG8	cytochrome P450	0.36	1.26	3.80	0.0000
AAEL006274		glucose transporter (sugar transporter	13.71	42.31	3.75	0.0000
AAEL011520		sucrose transport protein	5.28	16.58	3.75	0.0000
AAEL003884		hypothetical protein	3.80	12.20	3.74	0.0000
AAEL013784		hypothetical protein	10.40	31.89	3.73	0.0000
AAEL007653		allantoinase	0.39	1.37	3.72	0.0000
AAEL005770	OBP21	Odorant-binding protein 99c, putative	9.40	28.81	3.72	0.0000
AAEL001532		fad nad binding oxidoreductases	10.12	30.42	3.69	0.0000
AAEL015424		adult cuticle protein, putative	0.28	1.20	3.68	0.0012
AAEL011371		hypothetical protein	22.36	66.49	3.67	0.0000
AAEL003066		brain chitinase and chia	1.99	11.36	3.66	0.0059
AAEL008157		hypothetical protein	1.88	5.71	3.64	0.0000
AAEL015438		mannose-6-phosphate isomerase	19.78	57.70	3.60	0.0000
AAEL003899		sugar transporter	9.47	27.99	3.60	0.0000
AAEL004817		hypothetical protein	0.29	1.04	3.59	0.0001
AAEL002404		receptor protein tyrosine kinase	35.96	108.22	3.59	0.0000
AAEL014663		AMP dependent coa ligase	1.13	3.48	3.56	0.0000
AAEL017458			3.67	10.59	3.52	0.0000
AAEL012417		hypothetical protein	6.99	20.25	3.51	0.0000
AAEL003626		sodium/shloride dependent aa transporter	6.29	18.16	3.51	0.0000
AAEL007305		hypothetical protein	1.43	4.27	3.50	0.0000
AAEL005807		hypothetical protein	2.11	6.73	3.50	0.0000
AAEL009038		prolylcarboxypeptidase, putative	10.27	29.69	3.50	0.0000
AAEL013170		phosphatidylcholine-sterol acyltransferase	9.38	26.82	3.49	0.0000
AAEL014014		ornithine cyclodeaminase	0.67	2.00	3.48	0.0000
AAEL008889	CYP6AL1	cytochrome P450	2.78	8.09	3.48	0.0000
AAEL003294		fibrinogen and fibronectin	5.50	15.66	3.48	0.0000
AAEL017121			63.17	177.82	3.48	0.0000
AAEL003900		hypothetical protein	1.29	3.93	3.45	0.0000
AAEL012144	CYP303A1	cytochrome P450	0.38	1.26	3.42	0.0002
AAEL013655		hypothetical protein	0.66	2.11	3.37	0.0002
AAEL014386		clip-domain serine protease, putative	2.99	8.25	3.35	0.0000
AAEL011325		gonadotropin-releasing hormone receptor	8.03	22.01	3.34	0.0000
AAEL006798	CYP9J10	cytochrome P450	1.34	3.78	3.32	0.0000
AAEL010479		sugar transporter	173.06	469.66	3.32	0.0000
AAEL006805	CYP9J2	cytochrome P450	8.26	22.52	3.30	0.0000
AAEL013245	CLIPB28		1.34	3.89	3.28	0.0000
AAEL006168	CLIPB42	serine carboxypeptidase, putative	11.10	29.89	3.28	0.0000

Table A6 Continued

Gene ID	Gene Name	Wiki Description	3h	24h	Fold	*p* adj
AAEL006353		sulfotransferase (sult)	3.06	8.33	3.26	0.0000
AAEL012855		hypothetical protein	18.96	51.69	3.26	0.0000
AAEL002668		AMP dependent ligase	1.31	3.55	3.24	0.0000
AAEL008471		hypothetical protein	3.01	8.03	3.24	0.0000
AAEL001586		glucosyl/glucuronosyl transferases	9.71	25.79	3.24	0.0000
AAEL013775		hypothetical protein	66.35	190.29	3.23	0.0000
AAEL011800		hypothetical protein	0.48	1.32	3.22	0.0000
AAEL000660		peptide methionine sulfoxide reductase	7.30	19.50	3.22	0.0000
AAEL007792		hypothetical protein	3.08	8.19	3.22	0.0000
AAEL009131	CYP6Z8	cytochrome P450	33.52	87.87	3.21	0.0000
AAEL002492		hypothetical protein	1.93	5.24	3.20	0.0000
AAEL001863		zinc carboxypeptidase	163.42	426.30	3.20	0.0000
AAEL006467		alcohol dehydrogenase	0.35	1.05	3.20	0.0001
AAEL000021		hypothetical protein	0.45	1.30	3.19	0.0000
AAEL014956		internalin A, putative	0.66	1.81	3.18	0.0000
AAEL001392		hypothetical protein	4.11	26.46	3.18	0.0244
AAEL004884		hemomucin	3.15	8.26	3.17	0.0000
AAEL014893	CYP6BB2	cytochrome P450	54.19	139.49	3.16	0.0000
AAEL008620		D7 protein, putative	17.78	45.94	3.16	0.0000
AAEL016976			18.17	46.89	3.16	0.0000
AAEL015627	LRIM29	hypothetical protein	4.62	12.46	3.15	0.0000
AAEL008632		abc transporter	4.42	11.37	3.14	0.0000
AAEL006543		hypothetical protein	21.24	54.05	3.14	0.0000
AAEL006811	CYP9J8	cytochrome P450	2.76	7.17	3.13	0.0000
AAEL006609		zinc finger protein	17.10	43.23	3.12	0.0000
AAEL008097		trypsin-eta, putative	15.52	39.60	3.12	0.0000
AAEL004090			8.16	20.64	3.12	0.0000
AAEL012771	LRIM30	hypothetical protein	2.94	7.77	3.12	0.0000
AAEL000670		methionine sulfoxide reductase	219.80	560.72	3.12	0.0000
AAEL014955		tartan protein, putative	0.53	1.41	3.11	0.0000
AAEL003049		pupal cuticle protein 78E, putative	0.38	1.01	3.11	0.0000
AAEL005687		protein serine/threonine kinase, putative	4.98	12.74	3.09	0.0000
AAEL012955		phosphatidylethanolamine-binding protein	8.30	20.84	3.08	0.0000
AAEL003041		hypothetical protein	0.69	1.81	3.07	0.0000
AAEL009760		Niemann-Pick Type C-2, putative	278.22	694.07	3.06	0.0000
AAEL004230		hypothetical protein	21.28	52.67	3.06	0.0000
AAEL005043		ATP-dependent bile acid permease	2.27	5.70	3.05	0.0000
AAEL017299			0.44	1.22	3.05	0.0001
AAEL015051		glycoside hydrolases	0.92	2.39	3.05	0.0000
AAEL013525		Timp-3, putative	32.77	81.05	3.05	0.0000
AAEL010529		hypothetical protein	17.06	42.33	3.04	0.0000
AAEL010480		serine-pyruvate aminotransferase	1.63	4.14	3.03	0.0000
AAEL003903		475 (	14.89	36.55	3.01	0.0000
AAEL004786		hypothetical protein	4.58	11.41	3.01	0.0000
AAEL008751		glucosyl/glucuronosyl transferases	0.74	1.90	3.00	0.0000
AAEL002726		D7 protein, putative	3.04	7.62	2.99	0.0000
AAEL010125	LRIM17	mitotic protein phosphatase 1 regulator, putative	20.73	50.90	2.99	0.0000
AAEL017498	CASPS21		0.71	1.83	2.98	0.0000
AAEL011962		hypothetical protein	9.38	22.64	2.97	0.0000
AAEL001548		glucosyl/glucuronosyl transferases	21.15	51.66	2.97	0.0000
AAEL014045		allantoicase	3.65	8.93	2.97	0.0000
AAEL000904		carboxylesterase	2.15	5.30	2.96	0.0000
AAEL009132	CYP6Y3	cytochrome P450	3.40	8.34	2.95	0.0000

Table A6 Continued

Gene ID	Gene Name	Wiki Description	3h	24h	Fold	*p* adj
AAEL008478		hypothetical protein	28.10	67.73	2.95	0.0000
AAEL006834		glutamate semialdehyde dehydrogenase	124.39	299.34	2.92	0.0000
AAEL013171	HPX2	oxidase/peroxidase	12.38	29.61	2.92	0.0000
AAEL014141	SRPN5	serine protease inhibitor, serpin	3.00	7.29	2.92	0.0000
AAEL001513		wd-repeat protein	0.67	1.63	2.92	0.0000
AAEL007969		serine protease	1.86	4.45	2.91	0.0000
AAEL009543		hypothetical protein	4.30	10.68	2.90	0.0000
AAEL009126	CYP6N6	cytochrome P450	2.63	7.93	2.89	0.0085
AAEL014817		serine-pyruvate aminotransferase	1.65	3.95	2.89	0.0000
AAEL005948		hypothetical protein	13.38	31.52	2.88	0.0000
AAEL000915		hypothetical protein	1.32	3.85	2.88	0.0058
AAEL003715		hypothetical protein	1.52	3.77	2.88	0.0000
AAEL012929		CRAL/TRIO domain-containing protein	19.61	45.89	2.87	0.0000
AAEL006381		sphingomyelin phosphodiesterase	1.11	2.70	2.86	0.0000
AAEL000874	ARK	hypothetical protein	2.97	6.98	2.86	0.0000
AAEL011368		sugar transporter	6.39	15.03	2.86	0.0000
AAEL007179		hypothetical protein	20.78	48.24	2.85	0.0000
AAEL010936		gamma glutamyl transpeptidases	2.59	6.23	2.85	0.0000
AAEL007807	CYP4D38	cytochrome P450	4.91	11.51	2.85	0.0000
AAEL018172		breast carcinoma amplified sequence	2.95	6.84	2.85	0.0000
AAEL013717		sphingomyelin phosphodiesterase	26.71	62.29	2.85	0.0000
AAEL001646	Kir3	inward rectifier potassium channel, putative	0.44	1.13	2.84	0.0003
AAEL006338		sulfotransferase (sult)	1.91	4.56	2.84	0.0000
AAEL001492		cgmp-dependent 3,5-cyclic phosphodiesterase	8.12	18.89	2.83	0.0000
AAEL014662		AMP dependent coa ligase	0.57	1.47	2.83	0.0004
AAEL007878		ornithine decarboxylase	4.05	9.57	2.83	0.0000
AAEL007817		hypothetical protein	0.79	1.85	2.83	0.0000
AAEL007226		nidogen	6.43	14.76	2.81	0.0000
AAEL017248			26.99	61.54	2.81	0.0000
AAEL000651		alpha-amylase	22.94	53.15	2.81	0.0000
AAEL006449		ser/thr protein kinase-lyk4	9.49	21.77	2.81	0.0000
AAEL002833		cathepsin l	108.18	247.39	2.81	0.0000
AAEL012536		hypothetical protein	7.35	16.77	2.80	0.0000
AAEL001788		hypothetical protein	1.16	2.74	2.80	0.0000
AAEL006797			0.91	2.14	2.80	0.0000
AAEL013851		hypothetical protein	1.58	3.92	2.80	0.0001
AAEL009127	CYP6M11	cytochrome P450	2.72	6.24	2.80	0.0000
AAEL011764	PPO10	prophenoloxidase	0.86	2.02	2.79	0.0000
AAEL003402		sphingomyelin phosphodiesterase	2.90	6.57	2.78	0.0000
AAEL011597		hypothetical protein	12.64	28.67	2.78	0.0000
AAEL012415		hypothetical protein	3.20	8.05	2.77	0.0005
AAEL005739		hypothetical protein	4.99	11.27	2.77	0.0000
AAEL003974		hypothetical protein	2.69	6.14	2.77	0.0000
AAEL008050		hypothetical protein	5.51	12.77	2.77	0.0000
AAEL011980		hypothetical protein	2.09	4.97	2.75	0.0000
AAEL002307		leucine-rich transmembrane protein	1.41	3.24	2.75	0.0000
AAEL002612		hypothetical protein	0.67	1.71	2.74	0.0031
AAEL014166		hypothetical protein	3.95	8.88	2.72	0.0000
AAEL009208			5.34	11.76	2.71	0.0000
AAEL009955		hypothetical protein	265.95	594.39	2.71	0.0000
AAEL007748	SCRB10	cd36 antigen	2.78	6.21	2.70	0.0000
AAEL013498	PPO1	prophenoloxidase	1.50	3.36	2.70	0.0000
AAEL002665		matrix metalloproteinase	3.21	7.14	2.69	0.0000

Table A6 Continued

Gene ID	Gene Name	Wiki Description	3h	24h	Fold	*p* adj
AAEL015603		ceramide kinase	3.89	8.58	2.69	0.0000
AAEL009291		serine carboxypeptidase	40.13	86.96	2.66	0.0000
AAEL014609	CYP9J26	cytochrome P450	53.78	116.70	2.66	0.0000
AAEL007370		hypothetical protein	5.45	11.87	2.65	0.0000
AAEL008283		hypothetical protein	1.39	3.03	2.64	0.0000
AAEL010804		calcium/calmodulin-dependent protein kinase	1.83	4.00	2.64	0.0000
AAEL006793	CYP9J9	cytochrome P450	5.78	12.47	2.64	0.0000
AAEL012039		zinc finger protein	1.14	2.47	2.63	0.0000
AAEL013857		hypothetical protein	258.63	554.74	2.63	0.0000
AAEL008446		hypothetical protein	0.68	1.63	2.62	0.0022
AAEL005342			31.03	65.39	2.60	0.0000
AAEL003339		hypothetical protein	0.81	1.85	2.60	0.0007
AAEL018241		hypothetical protein	0.78	1.64	2.59	0.0000
AAEL008007		hypothetical protein	5.55	11.75	2.59	0.0000
AAEL011515		hypothetical protein	1.48	3.50	2.59	0.0021
AAEL008105		glutamate cysteine ligase	18.92	39.74	2.58	0.0000
AAEL003951		hypothetical protein	4.76	9.96	2.56	0.0000
AAEL005178		juvenile hormone esterase	7.32	15.75	2.56	0.0000
AAEL014275		molybdopterin cofactor sulfurase (mosc)	34.52	71.65	2.54	0.0000
AAEL011905		myosin i	26.01	53.72	2.54	0.0000
AAEL009124	CYP6N12	cytochrome P450	3.32	6.84	2.53	0.0000
AAEL006397		serine protease inhibitor	2.00	4.13	2.52	0.0000
AAEL003619		sodium/shloride dependent aa transporter	16.51	36.64	2.51	0.0016
AAEL018354		oxysterol-binding protein 1, putative	36.89	74.77	2.51	0.0000
AAEL014439		Juvenile hormone-inducible protein, putative	1.65	3.50	2.51	0.0000
AAEL009214		diazepam binding inhibitor, putative	153.95	313.41	2.50	0.0000
AAEL008785		hypothetical protein	248.37	503.36	2.50	0.0000
AAEL005787		serine protease, putative	2.37	4.90	2.50	0.0000
AAEL013211		hypothetical protein	4.57	9.49	2.50	0.0000
AAEL010338		hypothetical protein	11.64	23.49	2.49	0.0000
AAEL000278		poly(p)/atp nad kinase	18.00	36.47	2.49	0.0000
AAEL011133		hypothetical protein	15.94	32.09	2.49	0.0000
AAEL006188		hypothetical protein	2.05	4.20	2.48	0.0000
AAEL013774		hypothetical protein	15.10	31.29	2.48	0.0000
AAEL011553		trypsin	10.88	22.14	2.48	0.0000
AAEL003699		hypothetical protein	2.30	4.70	2.47	0.0000
AAEL014852		hypothetical protein	8.91	17.85	2.47	0.0000
AAEL001960		cytochrome P450	12.50	25.28	2.46	0.0000
AAEL014614		cytochrome P450	3.51	7.10	2.46	0.0000
AAEL013258		hypothetical protein	0.98	1.98	2.46	0.0000
AAEL014842		multiple inositol polyphosphate phosphatase	0.62	1.30	2.45	0.0002
AAEL003261		hypothetical protein	2.02	4.07	2.45	0.0000
AAEL010836		ribitol kinase	0.56	1.18	2.45	0.0002
AAEL002903		phosphatidylinositol 3-kinase	2.87	5.77	2.45	0.0000
AAEL003816		hypothetical protein	117.36	236.52	2.45	0.0000
AAEL009121	CYP6N9	cytochrome P450	0.51	1.10	2.45	0.0015
AAEL001840		zinc carboxypeptidase	11.60	23.27	2.45	0.0000
AAEL000745		hypothetical protein	21.16	42.35	2.44	0.0000
AAEL009074	IAP1	inhibitor of apoptosis 1, diap1	126.37	248.37	2.43	0.0000
AAEL012526		hypothetical protein	0.81	1.86	2.43	0.0134
AAEL002680		AMP dependent ligase	2.09	4.25	2.43	0.0000

Table A6 Continued

Gene ID	Gene Name	Wiki Description	3h	24h	Fold	*p* adj
AAEL003027		hypothetical protein	3.16	6.32	2.43	0.0000
AAEL001107		hypothetical protein	181.84	358.53	2.43	0.0000
AAEL001288		cytochrome P450	0.71	1.48	2.42	0.0009
AAEL003728		hypothetical protein	1.99	3.90	2.41	0.0000
AAEL018041			0.67	1.36	2.41	0.0002
AAEL014553		triacylglycerol lipase, pancreatic	1.08	2.30	2.40	0.0026
AAEL007432		serine collagenase 1 precursor, putative	495.30	982.24	2.40	0.0000
AAEL018150		hypothetical protein	16.82	32.82	2.40	0.0000
AAEL001098		clip-domain serine protease, putative	28.55	56.15	2.40	0.0000
AAEL014762		zinc transporter	78.04	150.76	2.39	0.0000
AAEL006622		multidrug resistance-associated protein	3.24	6.27	2.39	0.0000
AAEL010766		inositol triphosphate 3-kinase c	4.01	7.86	2.39	0.0000
AAEL007055		lipase	34.99	68.65	2.39	0.0000
AAEL000223		alpha-glucosidase	6.92	13.87	2.39	0.0000
AAEL007291		replication factor A, 14kD-subunit, putative	7.13	13.90	2.38	0.0000
AAEL012940		hypothetical protein	7.01	13.69	2.37	0.0000
AAEL015304		hypothetical protein	2.27	4.56	2.37	0.0000
AAEL006848		hypothetical protein	5.40	10.42	2.37	0.0000
AAEL014936		sarcosine dehydrogenase	1.72	3.38	2.37	0.0000
AAEL003098		glucosyl/glucuronosyl transferases	0.64	1.29	2.37	0.0001
AAEL009899		hypothetical protein	51.64	100.03	2.37	0.0000
AAEL001519		hypothetical protein	1.73	3.38	2.37	0.0000
AAEL007006	CLIPA17	serine protease	3.42	6.61	2.36	0.0000
AAEL000581		hypothetical protein	5.88	11.23	2.36	0.0000
AAEL003667		hypothetical protein	2.26	4.48	2.36	0.0000
AAEL010490		hypothetical protein	1.36	2.83	2.36	0.0029
AAEL007947	GSTE3	glutathione-s-transferase theta, gst	11.24	21.67	2.35	0.0000
AAEL001878		lipase	1.80	3.47	2.35	0.0000
AAEL006344		sulfotransferase (sult)	5.72	11.12	2.35	0.0000
AAEL008646		fibrinogen and fibronectin	10.56	20.33	2.35	0.0000
AAEL005199		hypothetical protein	11.04	21.82	2.35	0.0000
AAEL005439		mical	0.93	1.77	2.35	0.0000
AAEL010555		sterol regulatory element-binding protein	28.33	53.83	2.34	0.0000
AAEL017256			38.43	72.81	2.33	0.0000
AAEL002283		hypothetical protein	90.21	172.43	2.33	0.0000
AAEL008151		hypothetical protein	2.39	4.57	2.33	0.0000
AAEL002607		hypothetical protein	1.84	3.52	2.33	0.0000
AAEL010688		MRAS2, putative	1.81	3.49	2.33	0.0000
AAEL001844		zinc carboxypeptidase	8.08	15.42	2.33	0.0000
AAEL012763	LRIM24	hypothetical protein	8.37	15.91	2.32	0.0000
AAEL008701		myoinositol oxygenase	32.11	61.01	2.32	0.0000
AAEL005694		hypothetical protein	1.01	2.08	2.32	0.0089
AAEL011007		fibrinogen and fibronectin	1.23	2.52	2.32	0.0038
AAEL006823		AMP dependent ligase	9.57	18.09	2.31	0.0000
AAEL009682		serine collagenase 1 precursor, putative	1.47	2.86	2.31	0.0001
AAEL008286		hypothetical protein	0.93	1.84	2.31	0.0003
AAEL003877		ubiquitin	127.10	237.21	2.31	0.0000
AAEL015483		hypothetical protein	5.68	10.79	2.31	0.0000
AAEL003777		hypothetical protein	3.45	6.54	2.31	0.0000
AAEL008635		abc transporter	45.46	85.61	2.30	0.0000
AAEL006361	SCRC2	hypothetical protein	0.80	1.59	2.30	0.0023
AAEL007057		serine carboxypeptidase	2.37	4.56	2.30	0.0000
AAEL000956		hypothetical protein	10.60	19.80	2.30	0.0000
AAEL003102		glucosyl/glucuronosyl transferases	0.52	1.04	2.28	0.0034

Table A6 Continued

Gene ID	Gene Name	Wiki Description	3h	24h	Fold	*p* adj
AAEL014196		hypothetical protein	0.55	1.06	2.28	0.0005
AAEL006936		hypothetical protein	2.47	4.71	2.28	0.0000
AAEL011950		hypothetical protein	0.98	1.86	2.28	0.0001
AAEL015600		hypothetical protein	2.08	4.27	2.28	0.0157
AAEL006389		cathepsin l	23.07	42.84	2.28	0.0000
AAEL016964			62.42	115.24	2.28	0.0000
AAEL001833		Juvenile hormone-inducible protein, putative	3.49	6.67	2.27	0.0001
AAEL001998		hypothetical protein	36.81	68.25	2.27	0.0000
AAEL012711	CLIPC12	trypsin, putative	1.22	2.32	2.27	0.0000
AAEL009904		hypothetical protein	164.43	301.15	2.27	0.0000
AAEL009219		hypothetical protein	122.74	226.84	2.27	0.0000
AAEL001683		hypothetical protein	1.40	2.71	2.26	0.0012
AAEL013975		transcription factor IIIA, putative	0.55	1.09	2.26	0.0040
AAEL009637		cathepsin b	163.83	299.85	2.26	0.0000
AAEL009680		chymotrypsin, putative	358.23	657.80	2.25	0.0000
AAEL001607		galactose-1-phosphate uridylyltransferase	16.54	30.53	2.25	0.0000
AAEL011191		protein phosphatase 1 binding protein	28.95	53.06	2.25	0.0000
AAEL001610		hypothetical protein	1.35	2.50	2.23	0.0000
AAEL011420		hypothetical protein	3.06	5.58	2.23	0.0000
AAEL014199		dihydropyrimidine dehydrogenase	9.82	17.80	2.23	0.0000
AAEL015404	LYSC7B	lysozyme P, putative	36.73	66.22	2.23	0.0000
AAEL008720		hypothetical protein	0.64	1.33	2.22	0.0463
AAEL018140		hypothetical protein	58.50	105.63	2.22	0.0000
AAEL004999		hypothetical protein	18.32	32.84	2.22	0.0000
AAEL006487		sodium/solute symporter	7.56	13.64	2.22	0.0000
AAEL008395		hypothetical protein	7.00	12.59	2.21	0.0000
AAEL015161		hypothetical protein	4.59	8.24	2.21	0.0000
AAEL001446		testis-specific protein pbs13 (t-complex 11	11.41	20.49	2.21	0.0000
AAEL013833		ATP-binding cassette transporter	0.82	1.54	2.21	0.0008
AAEL017549	GPRNNA14		1.28	2.54	2.20	0.0200
AAEL011008		lipase	0.79	1.50	2.20	0.0041
AAEL014608		cytochrome P450	0.92	1.69	2.19	0.0002
AAEL009171		hypothetical protein	16.33	28.98	2.19	0.0000
AAEL005091		hypothetical protein	0.84	1.56	2.19	0.0006
AAEL006334		sulfotransferase (sult)	1.31	2.46	2.19	0.0021
AAEL010478		sugar transporter	8.10	14.52	2.18	0.0000
AAEL014272		molybdopterin cofactor sulfurase (mosc)	12.27	21.82	2.18	0.0000
AAEL007826		cgmp-dependent protein kinase	37.39	66.00	2.18	0.0000
AAEL010163		hypothetical protein	61.37	108.32	2.18	0.0000
AAEL003541	GALE1	galectin	14.32	25.33	2.18	0.0000
AAEL010314		f-box/lrr protein, putative	13.64	24.10	2.18	0.0000
AAEL004871		hypothetical protein	6.92	12.24	2.18	0.0000
AAEL002385	CCEAE3B		4.62	8.27	2.18	0.0000
AAEL010076		hypothetical protein	5.69	10.00	2.17	0.0000
AAEL010171	PGRPLB	peptidoglycan recognition protein sb2	59.96	106.49	2.17	0.0000
AAEL001312	CYP9M6	cytochrome P450	13.23	23.21	2.16	0.0000
AAEL001077	CLIPB45	hypothetical protein	14.85	26.03	2.16	0.0000
AAEL006433		hypothetical protein	9.65	16.86	2.16	0.0000
AAEL007948	GSTE7	glutathione-s-transferase theta, gst	2.44	4.53	2.16	0.0026
AAEL010866		serine protease	7.96	13.99	2.16	0.0000
AAEL008259		hypothetical protein	9.09	15.96	2.15	0.0000
AAEL012956		elastase, putative	1.53	2.79	2.15	0.0016
AAEL010442		4-hydroxyphenylpyruvate dioxygenase	9.52	16.64	2.15	0.0000

Table A6 Continued

Gene ID	Gene Name	Wiki Description	3h	24h	Fold	*p* adj
AAEL006815	CYP9J16	cytochrome P450	5.34	9.43	2.15	0.0000
AAEL007260		hypothetical protein	1.34	2.35	2.15	0.0000
AAEL003848		hypothetical protein	13.19	23.53	2.14	0.0001
AAEL009600	ECR	ecdysone receptor	0.76	1.39	2.14	0.0027
AAEL004941	CYP6AK1	cytochrome P450	8.45	14.83	2.14	0.0000
AAEL006649		tnf receptor associated factor	1.20	2.10	2.14	0.0000
AAEL014607		cytochrome P450	13.36	23.15	2.14	0.0000
AAEL011319		hypothetical protein	1.60	2.92	2.14	0.0015
AAEL014616	CYP9J27	cytochrome P450	4.46	7.83	2.14	0.0000
AAEL009130	CYP6Z7		7.08	12.27	2.13	0.0000
AAEL002816		hypothetical protein	25.18	43.57	2.13	0.0000
AAEL005955	CASPS17	hypothetical protein	1.34	2.48	2.13	0.0090
AAEL009935		hypothetical protein	1.63	2.92	2.13	0.0003
AAEL011548		hypothetical protein	3.03	5.26	2.13	0.0000
AAEL012341		lysosomal acid lipase, putative	23.20	40.06	2.12	0.0000
AAEL010223		phosphatidylserine decarboxylase	18.95	32.72	2.12	0.0000
AAEL015124		hypothetical protein	0.66	1.17	2.12	0.0006
AAEL000258		hypothetical protein	115.04	197.82	2.12	0.0000
AAEL007508		oviductin	0.87	1.64	2.12	0.0275
AAEL016991			1.65	3.03	2.12	0.0107
AAEL005536		tetraspanin 29fb	5.96	10.37	2.11	0.0000
AAEL012130		ordml, arthropod	12.29	21.13	2.11	0.0000
AAEL005071		GTP binding protein	63.61	108.48	2.11	0.0000
AAEL003448	GPRNNA13	hypothetical protein	0.87	1.63	2.11	0.0159
AAEL011892		receptor for activated C kinase, putative	8.48	14.54	2.11	0.0000
AAEL005000		hypothetical protein	3.99	6.92	2.11	0.0000
AAEL000234	SCRB7	antigen CD36, putative	20.42	34.99	2.11	0.0000
AAEL009246		glycoside hydrolases	2.63	4.53	2.10	0.0000
AAEL009128	CYP6M6	cytochrome P450	6.19	10.60	2.10	0.0000
AAEL007996		centaurin alpha	3.48	6.01	2.10	0.0000
AAEL004022		carboxylesterase	5.01	8.60	2.10	0.0000
AAEL005200		juvenile hormone esterase	9.23	15.84	2.10	0.0000
AAEL000669		hypothetical protein	80.50	136.17	2.10	0.0000
AAEL000206		ninjurin A, putative	19.89	34.06	2.09	0.0000
AAEL012518		hypothetical protein	40.34	68.61	2.09	0.0000
AAEL010151	CYP6N16	cytochrome P450	4.87	8.36	2.09	0.0000
AAEL004513		neurotransmitter gated ion channel	25.66	43.34	2.09	0.0000
AAEL000227	SCRB8	epithelial membrane protein	12.76	21.65	2.08	0.0000
AAEL013637		homogentisate 1,2-dioxygenase	83.36	140.07	2.08	0.0000
AAEL007216		elongase, putative	3.63	6.17	2.08	0.0000
AAEL005102		hypothetical protein	12.80	21.77	2.08	0.0000
AAEL001815		hypothetical protein	8.19	13.76	2.07	0.0000
AAEL002522		adenosine deaminase acting on RNA (adar)-2	3.36	5.69	2.07	0.0000
AAEL000287		hypothetical protein	1.65	2.77	2.07	0.0000
AAEL010100	LYSC7A	lysozyme P, putative	103.44	173.57	2.06	0.0000
AAEL006568		serine protease	12.59	21.27	2.06	0.0000
AAEL014864		hypothetical protein	1.80	3.09	2.06	0.0002
AAEL001308		CRAL/TRIO domain-containing protein	22.07	37.01	2.06	0.0000
AAEL009100		mitochondrial oxodicarboxylate carrier	3.54	5.96	2.06	0.0000
AAEL004995		caspase-activated nuclease, putative	7.99	13.38	2.06	0.0000
AAEL008606		hypothetical protein	1.05	1.90	2.06	0.0216
AAEL001892		hypothetical protein	8.09	13.63	2.06	0.0000
AAEL004009		glucose dehydrogenase	0.96	1.66	2.05	0.0052

Table A6 Continued

Gene ID	Gene Name	Wiki Description	3h	24h	Fold	*p* adj
AAEL013554	CYP4J14	cytochrome P450	2.31	3.96	2.05	0.0010
AAEL001316		hypothetical protein	36.22	59.99	2.05	0.0000
AAEL003890		cytochrome P450	0.64	1.11	2.05	0.0088
AAEL008610		myosin vii	7.09	11.78	2.05	0.0000
AAEL009117	CYP6M5	cytochrome P450	1.60	2.73	2.04	0.0004
AAEL014665		AMP dependent coa ligase	1.51	2.52	2.04	0.0000
AAEL009487		hypothetical protein	102.07	167.86	2.04	0.0000
AAEL001818		hypothetical protein	18.81	30.89	2.03	0.0000
AAEL008376		hypothetical protein	1.46	2.43	2.03	0.0000
AAEL000667		alpha-amylase	367.71	605.37	2.03	0.0000
AAEL013163		hypothetical protein	27.28	44.65	2.02	0.0000
AAEL006260		serine protease, putative	2.46	4.11	2.02	0.0001
AAEL006482		sugar transporter	1.30	2.16	2.02	0.0001
AAEL011979		calmodulin	20.02	32.86	2.02	0.0000
AAEL001614		hypothetical protein	3.67	6.07	2.02	0.0000
AAEL007816	CYP4D23	cytochrome P450	9.44	15.48	2.02	0.0000
AAEL001341		hypothetical protein	45.98	75.12	2.01	0.0000
AAEL000746		nadp-specific isocitrate dehydrogenase	39.27	64.00	2.01	0.0000
AAEL013290		hypothetical protein	47.43	77.17	2.01	0.0000
AAEL003720		leucine-rich transmembrane protein	2.22	3.73	2.01	0.0009
AAEL014658		caspase-1	1.97	3.29	2.01	0.0005
AAEL009085		rho/rac/cdc gtpase-activating protein	21.17	34.39	2.01	0.0000
AAEL012616		nadp transhydrogenase	33.26	53.96	2.01	0.0000
AAEL009513		adenylate cyclase	4.52	7.52	2.00	0.0003
		Down regulated				
AAEL002731	SRPN14	serine protease inhibitor, serpin	33.53	1.35	-18.43	0.0000
AAEL011811		DNA replication licensing factor MCM3	3.96	0.17	-15.57	0.0000
AAEL010248		fibrillarin	16.25	0.93	-13.03	0.0000
AAEL010640		phosphoribosylamine-glycine ligase	155.63	9.10	-12.98	0.0000
AAEL002194		uricase	84.49	4.91	-12.92	0.0000
AAEL010435		hypothetical protein	265.51	17.81	-11.70	0.0000
AAEL003352		ribosomal protein l7ae	186.81	12.24	-11.61	0.0000
AAEL013584		hypothetical protein	244.72	16.52	-11.43	0.0000
AAEL003514		centromere/microtubule binding protein cbf5	52.92	3.91	-10.47	0.0000
AAEL006674	CLIPB29	clip-domain serine protease, putative	136.42	10.17	-10.30	0.0000
AAEL002686		testisin precursor, putative	17.68	1.28	-10.22	0.0000
AAEL000733		hydroxysteroid dehydrogenase	18.04	1.40	-9.76	0.0000
AAEL010035			7.39	0.55	-9.69	0.0000
AAEL002810		DNA replication licensing factor MCM5	2.47	0.18	-9.64	0.0000
AAEL011584		chaperonin-60kD, ch60	121.09	9.89	-9.55	0.0000
AAEL000311		hypothetical protein	17.49	1.40	-9.28	0.0000
AAEL012851		wd-repeat protein	39.54	3.40	-9.16	0.0000
AAEL007799		regulator of chromosome condensation	86.19	7.33	-9.05	0.0000
AAEL002063		cationic amino acid transporter	17.03	1.47	-8.89	0.0000
AAEL013075		hypothetical protein	45.51	4.02	-8.82	0.0000
AAEL006617		hypothetical protein	67.73	6.12	-8.49	0.0000
AAEL011599		ADP-ribosylation factor, putative	4.73	0.41	-8.22	0.0000
AAEL012100		hypothetical protein	32.79	3.16	-8.06	0.0000
AAEL013013		hypothetical protein	59.15	5.42	-7.87	0.0000
AAEL004455		hypothetical protein	39.09	3.92	-7.80	0.0000
AAEL008220		hypothetical protein	35.91	3.61	-7.78	0.0000
AAEL003303		hypothetical protein	33.49	3.33	-7.65	0.0000
AAEL005220		60S ribosomal protein L30	16.03	1.57	-7.64	0.0000

Table A6 Continued

Gene ID	Gene Name	Wiki Description	3h	24h	Fold	*p* adj
AAEL014381		hypothetical protein	18.22	1.82	-7.64	0.0000
AAEL012932		hypothetical protein	106.27	11.21	-7.48	0.0000
AAEL001917		ribosome biogenesis protein brix	2.01	0.15	-7.47	0.0000
AAEL000530		hypothetical protein	5.78	0.57	-7.46	0.0000
AAEL013685		wd-repeat protein	10.25	1.02	-7.40	0.0000
AAEL013276		acid phosphatase	8.41	0.84	-7.26	0.0000
AAEL006887		mrna turnover protein 4 mrt4	40.44	4.33	-7.20	0.0000
AAEL012265		transcription initiation factor RRN3	21.41	2.28	-7.16	0.0000
AAEL008468		cysteine synthase	52.56	5.84	-6.94	0.0000
AAEL008728		DEAD box ATP-dependent RNA helicase	10.49	1.18	-6.89	0.0000
AAEL011729		hypothetical protein	5.55	0.62	-6.78	0.0000
AAEL010086		DNA replication licensing factor MCM4	1.31	0.13	-6.74	0.0000
AAEL006562		acid phosphatase	16.99	1.97	-6.67	0.0000
AAEL003664		lupus la ribonucleoprotein	58.32	6.89	-6.62	0.0000
AAEL017974	HSP70Ab		1.77	0.15	-6.61	0.0000
AAEL001866		hypothetical protein	395.50	47.94	-6.53	0.0000
AAEL004017		DNA polymerase v	22.32	2.73	-6.44	0.0000
AAEL000797		dimethylaniline monooxygenase	19.60	2.38	-6.43	0.0000
AAEL007697		hypothetical protein	16.81	1.97	-6.43	0.0000
AAEL001052		heat shock protein, putative	339.54	41.70	-6.42	0.0000
AAEL005384		phosphoribosylformylglycinamidine synthase	242.95	29.47	-6.40	0.0000
AAEL004063		wd-repeat protein	25.32	3.07	-6.39	0.0000
AAEL012185		ribosome biogenesis regulatory protein	36.40	4.45	-6.38	0.0000
AAEL012443		sugar transporter	2.32	0.26	-6.27	0.0000
AAEL017333			9.91	1.23	-6.19	0.0000
AAEL015441		spliceosomal protein sap	32.67	4.26	-6.03	0.0000
AAEL002709		spliceosomal protein sap	41.49	5.48	-6.02	0.0000
AAEL012546		DNA replication licensing factor MCM6	4.46	0.56	-6.01	0.0000
AAEL005482	CTL18	hypothetical protein	126.34	16.16	-5.98	0.0000
AAEL009596		sterol o-acyltransferase	8.82	1.14	-5.91	0.0000
AAEL013142		hypothetical protein	5.14	0.66	-5.90	0.0000
AAEL007270		hypothetical protein	6.30	0.82	-5.88	0.0000
AAEL001037		ribosomal RNA methyltransferase	26.68	3.59	-5.82	0.0000
AAEL005163		hypothetical protein	28.78	3.80	-5.81	0.0000
AAEL005822		hypothetical protein	41.99	5.73	-5.78	0.0000
AAEL013352		lethal(2)essential for life protein, l2efl	7.60	0.18	-5.64	0.0005
AAEL007555		acyl-coa dehydrogenase	457.40	64.47	-5.64	0.0000
AAEL006466		chondroitin synthase	32.24	4.59	-5.59	0.0000
AAEL016968			17.66	2.50	-5.57	0.0000
AAEL001869		gmp synthase	129.12	18.57	-5.51	0.0000
AAEL008572		RNA-binding protein, putative	13.88	1.97	-5.49	0.0000
AAEL009853		Trypsin, putative	5.04	0.67	-5.47	0.0000
AAEL003944		hypothetical protein	33.01	4.70	-5.45	0.0000
AAEL001423		acid phosphatase-1	55.87	8.03	-5.44	0.0000
AAEL005298		hypothetical protein	16.91	1.95	-5.42	0.0000
AAEL003568			1.14	0.13	-5.33	0.0000
AAEL006549		hypothetical protein	12.41	1.83	-5.31	0.0000
AAEL014300		hypothetical protein	7.74	0.99	-5.30	0.0000
AAEL003100		hypothetical protein	52.07	7.59	-5.30	0.0000
AAEL003975		wd-repeat protein	8.76	1.29	-5.27	0.0000
AAEL008222		lipase	25.99	1.24	-5.19	0.0009
AAEL003469		NHP2 protein, putative	53.04	8.12	-5.19	0.0000
AAEL003949		hypothetical protein	17.40	2.62	-5.17	0.0000

Table A6 Continued

Gene ID	Gene Name	Wiki Description	3h	24h	Fold	*p* adj
AAEL008886		hypothetical protein	33.11	4.97	-5.17	0.0000
AAEL009883		26S protease (S4) regulatory subunit, putative	44.67	6.83	-5.17	0.0000
AAEL008942		hypothetical protein	36.17	5.53	-5.14	0.0000
AAEL003606		purine biosynthesis protein 6, pur6	747.88	115.14	-5.12	0.0000
AAEL002963		hypothetical protein	168.48	26.37	-5.08	0.0000
AAEL008668	CLIPB22	MASP-2 protein, putative	12.57	1.89	-5.08	0.0000
AAEL000748		hypothetical protein	55.82	8.44	-5.05	0.0000
AAEL012827		endoplasmin	281.14	44.17	-5.04	0.0000
AAEL009669		hypothetical protein	44.60	6.90	-5.02	0.0000
AAEL011282		ribosomal RNA small subunit b	17.92	2.84	-5.00	0.0000
AAEL009766		lipoamide acyltransferase	100.10	16.12	-4.94	0.0000
AAEL009273		inosine-5-monophosphate dehydrogenase	52.21	8.41	-4.90	0.0000
AAEL009309		lipid depleted protein	23.60	3.80	-4.89	0.0000
AAEL013350		heat shock protein 26kD, putative	9.41	1.24	-4.87	0.0000
AAEL011624		granzyme A precursor, putative	14.14	2.21	-4.87	0.0000
AAEL000674		RNA m5u methyltransferase	10.91	1.74	-4.86	0.0000
AAEL000471		monocarboxylate transporter	23.59	3.85	-4.85	0.0000
AAEL010118		kelch repeat protein	21.43	3.50	-4.83	0.0000
AAEL010970		hypothetical protein	13.48	2.12	-4.82	0.0000
AAEL002242		hypothetical protein	8.96	1.42	-4.81	0.0000
AAEL017188			1.47	0.23	-4.80	0.0000
AAEL018061			141.02	23.43	-4.77	0.0000
AAEL009912		hypothetical protein	22.82	3.79	-4.74	0.0000
AAEL015440		hypothetical protein	66.12	11.00	-4.72	0.0000
AAEL007007		DNA replication licensing factor MCM2	4.50	0.74	-4.71	0.0000
AAEL007102		Trypsin, putative	7.58	1.28	-4.68	0.0000
AAEL018191		hypothetical protein	11.95	1.83	-4.66	0.0000
AAEL006347		apyrase, putative	424.67	70.42	-4.64	0.0000
AAEL017113			53.03	9.02	-4.63	0.0000
AAEL012629		deoxyuridine 5'-triphosphate nucleotidohydrolase	3.32	0.47	-4.60	0.0000
AAEL003125		acyl-coa dehydrogenase	92.97	16.09	-4.59	0.0000
AAEL014840		short-chain dehydrogenase	9.10	1.49	-4.57	0.0000
AAEL004526		hypothetical protein	9.01	1.53	-4.57	0.0000
AAEL013345		alphaA-crystallin, putative	2.74	0.35	-4.55	0.0000
AAEL001506		U3 small nucleolar ribonucleoprotein protein	12.00	2.09	-4.51	0.0000
AAEL017421			83.69	14.68	-4.50	0.0000
AAEL017402			19.43	3.25	-4.47	0.0000
AAEL008124		RNA methyltransferase, putative	10.27	1.70	-4.46	0.0000
AAEL004482		hypothetical protein	21.82	3.87	-4.41	0.0000
AAEL003581		amidophosphoribosyltransferase	324.09	58.15	-4.39	0.0000
AAEL007802		multicopper oxidase	11.86	2.13	-4.36	0.0000
AAEL014734		saccharopine dehydrogenase	89.81	16.32	-4.35	0.0000
AAEL001169		ribosome biogenesis protein bop1	21.29	3.89	-4.28	0.0000
AAEL012825		bifunctional purine biosynthesis protein	324.57	60.62	-4.24	0.0000
AAEL001080		RNA 3' terminal phosphate cyclase	12.00	2.23	-4.24	0.0000
AAEL004686		TATA-binding protein, putative	10.90	2.00	-4.23	0.0000
AAEL012876		hypothetical protein	6.32	1.16	-4.19	0.0000
AAEL006012		factor for adipocyte differentiation	5.18	0.94	-4.17	0.0000
AAEL001289		permease, putative	7.30	1.37	-4.17	0.0000
AAEL002108		nucleolar essential protein 1 (nep1)	26.46	5.06	-4.13	0.0000

Table A6 Continued

Gene ID	Gene Name	Wiki Description	3h	24h	Fold	*p* adj
AAEL001400		DNA-directed RNA polymerases III 12.5 kDa	42.61	7.93	-4.12	0.0000
AAEL000300		wd-repeat protein	5.87	1.10	-4.12	0.0000
AAEL005429		2-oxoglutarate dehydrogenase	28.67	5.56	-4.09	0.0000
AAEL003255		hypothetical protein	5.16	0.93	-4.06	0.0000
AAEL002022		protein serine/threonine kinase, putative	5.82	1.05	-4.05	0.0000
AAEL011470		cis,cis-muconate transport protein MucK	46.69	9.15	-4.05	0.0000
AAEL012119		hypothetical protein	3.20	0.51	-4.04	0.0000
AAEL003768		hypothetical protein	16.62	3.27	-4.02	0.0000
AAEL014265		hypothetical protein	1.01	0.16	-4.01	0.0000
AAEL017973	HSP70Aa		1.53	0.26	-4.00	0.0000
AAEL014843		heat shock protein	86.62	17.22	-4.00	0.0000
AAEL010906		hypothetical protein	16.74	3.28	-4.00	0.0000
AAEL008096		mitochondrial ornithine transporter	18.75	3.72	-3.98	0.0000
AAEL014051		nop14	11.71	2.34	-3.96	0.0000
AAEL006063		U3 small nucleolar ribonucleoprotein protein	18.06	3.58	-3.93	0.0000
AAEL010228		hypothetical protein	695.25	137.03	-3.91	0.0000
AAEL000774		hypothetical protein	128.88	25.66	-3.91	0.0000
AAEL009765		choline/ethanolamine kinase	45.64	9.28	-3.90	0.0000
AAEL007194		Pupal cuticle protein, putative	7.59	1.36	-3.88	0.0000
AAEL011357		maintenance of killer 16 (mak16) protein	31.91	6.48	-3.88	0.0000
AAEL001887		glutamine synthetase 1, 2	496.57	100.88	-3.88	0.0000
AAEL012255	LRIM13	hypothetical protein	13.94	2.87	-3.84	0.0000
AAEL017010			14.93	3.06	-3.82	0.0000
AAEL010827		programmed cell death protein 11	12.30	2.54	-3.82	0.0000
AAEL017286			75.07	15.75	-3.80	0.0000
AAEL009490		carbamoyl-phosphate synthase large chain	4.77	0.98	-3.79	0.0000
AAEL011762		hypothetical protein	18.61	3.90	-3.78	0.0000
AAEL010949		hypothetical protein	33.08	6.85	-3.76	0.0000
AAEL009285		DEAD box ATP-dependent RNA helicase	29.95	6.33	-3.74	0.0000
AAEL012545		proliferating cell nuclear antigen	10.80	2.16	-3.74	0.0000
AAEL018243		polypeptide of 976 aa, putative	12.64	2.68	-3.73	0.0000
AAEL003070		hypothetical protein	6.45	1.36	-3.71	0.0000
AAEL008876		deoxyribonuclease I, putative	2.00	0.37	-3.70	0.0000
AAEL000436		hypothetical protein	26.67	5.72	-3.70	0.0000
AAEL001412		hypothetical protein	55.04	11.74	-3.68	0.0000
AAEL004818		hypothetical protein	20.87	4.53	-3.67	0.0000
AAEL010235		hypothetical protein	1146.53	244.47	-3.65	0.0000
AAEL005281		hypothetical protein	2.66	0.56	-3.65	0.0000
AAEL017437			86.02	18.89	-3.63	0.0000
AAEL017373			37.72	8.12	-3.63	0.0000
AAEL014361		amidase	20.23	4.41	-3.62	0.0000
AAEL008716		hypothetical protein	10.98	2.40	-3.61	0.0000
AAEL010071		spermidine synthase	22.18	4.79	-3.60	0.0000
AAEL012974		glycine cleavage system h protein	75.13	16.49	-3.59	0.0000
AAEL018176		hypothetical protein	4.88	1.06	-3.59	0.0000
AAEL011581		hypothetical protein	8.46	1.76	-3.56	0.0000
AAEL006586		serine protease	2.08	0.41	-3.55	0.0000
AAEL007231	LRIM28	hypothetical protein	3.56	0.72	-3.55	0.0000
AAEL003443		threonine dehydrogenase	63.52	14.24	-3.55	0.0000
AAEL002322		hypothetical protein	7.51	1.66	-3.54	0.0000
AAEL000708		hiv-1 rev binding protein	13.84	3.03	-3.54	0.0000
AAEL011704		heat shock protein	40.03	8.92	-3.54	0.0000

Table A6 Continued

Gene ID	Gene Name	Wiki Description	3h	24h	Fold	*p* adj
AAEL002888		williams-beuren syndrome critical region	15.09	3.40	-3.52	0.0000
AAEL002555		sodium/solute symporter	29.49	6.62	-3.52	0.0000
AAEL008330		hexaprenyldihydroxybenzoate methyltransferase	25.05	5.67	-3.52	0.0000
AAEL006085		methylenetetrahydrofolate dehydrogenase	228.12	51.05	-3.51	0.0000
AAEL007578		shk1 kinase-binding protein	5.73	1.28	-3.50	0.0000
AAEL004116		hypothetical protein	100.16	22.52	-3.49	0.0000
AAEL003293		GTP-binding protein	28.33	6.44	-3.49	0.0000
AAEL015541		hypothetical protein	13.64	3.02	-3.49	0.0000
AAEL001238		bap28	6.13	1.38	-3.49	0.0000
AAEL005672		adenosine deaminase	98.78	22.08	-3.48	0.0000
AAEL002683		aldehyde oxidase	52.14	11.93	-3.47	0.0000
AAEL000659		exosome complex exonuclease rrp43	8.99	2.01	-3.46	0.0000
AAEL009925		amidase	10.65	2.41	-3.46	0.0000
AAEL009475		carbamoyl-phosphate synthase large chain	11.52	2.61	-3.46	0.0000
AAEL012233		hypothetical protein	19.79	4.55	-3.46	0.0000
AAEL008724		hypothetical protein	1.50	0.31	-3.45	0.0000
AAEL010349		tRNA (guanine-N2-)-methyltransferase	7.84	1.79	-3.44	0.0000
AAEL010317		DEAD box ATP-dependent RNA helicase	9.64	2.22	-3.41	0.0000
AAEL015455		hypothetical protein	1.66	0.36	-3.41	0.0000
AAEL009542		hypothetical protein	7.05	1.57	-3.40	0.0000
AAEL010630		xanthine dehydrogenase	8.19	1.91	-3.39	0.0000
AAEL009080		importin 7, putative	77.28	18.13	-3.39	0.0000
AAEL003654		hypothetical protein	13.43	3.10	-3.39	0.0000
AAEL002696		hypothetical protein	3.86	0.86	-3.38	0.0000
AAEL017898	RNaseP_nuc		3.93	0.79	-3.38	0.0004
AAEL012962		DEAD box ATP-dependent RNA helicase	4.62	1.06	-3.37	0.0000
AAEL006836		dihydropteridine reductase	179.20	42.47	-3.36	0.0000
AAEL004997		U3 small nucleolar ribonucleoprotein protein	20.71	4.86	-3.36	0.0000
AAEL008463		DEAD box ATP-dependent RNA helicase	4.14	0.96	-3.35	0.0000
AAEL013990		hexamerin 2 beta	16.07	3.75	-3.35	0.0000
AAEL013134		DNA-directed RNA polymerase I largest subunit	8.28	1.96	-3.34	0.0000
AAEL004292		hypothetical protein	2.81	0.60	-3.34	0.0000
AAEL007289		NBP2b protein, putative	19.94	4.71	-3.34	0.0000
AAEL013351		lethal(2)essential for life protein, l2efl	1.89	0.37	-3.33	0.0005
AAEL014085	IR75k.2	ionotropic glutamate receptor-invertebrate	1.32	0.20	-3.33	0.0117
AAEL000732		hypothetical protein	123.54	29.02	-3.31	0.0000
AAEL011756		aldehyde dehydrogenase	252.31	60.46	-3.30	0.0000
AAEL011827		hypothetical protein	18.02	4.35	-3.29	0.0000
AAEL000364		glycine cleavage system h protein	81.26	19.14	-3.28	0.0000
AAEL009308		wd-repeat protein	11.10	2.67	-3.28	0.0000
AAEL012187		lethal(3)malignant brain tumor	24.84	6.05	-3.28	0.0000
AAEL000726		fibrinogen and fibronectin	159.29	38.66	-3.27	0.0000
AAEL000988		hypothetical protein	12.38	3.01	-3.26	0.0000
AAEL005041		wd-repeat protein	20.56	4.94	-3.26	0.0000
AAEL011538		hypothetical protein	3.80	0.87	-3.26	0.0000
AAEL003584		hypothetical protein	12.90	3.11	-3.26	0.0000
AAEL010336		zinc phosphodiesterase	8.55	2.08	-3.25	0.0000
AAEL010613		hypothetical protein	5.09	1.23	-3.25	0.0000
AAEL014506			7.20	1.76	-3.25	0.0000
AAEL006485		inosine-uridine preferring nucleoside hydrolase	237.85	57.47	-3.24	0.0000

Table A6 Continued

Gene ID	Gene Name	Wiki Description	3h	24h	Fold	*p* adj
AAEL000749		hypothetical protein	116.36	28.49	-3.24	0.0000
AAEL013902			6.25	1.47	-3.24	0.0000
AAEL000046		hypothetical protein	6.19	1.42	-3.23	0.0000
AAEL010808		hypothetical protein	1.09	0.21	-3.23	0.0034
AAEL007872		hypothetical protein	40.43	9.67	-3.23	0.0000
AAEL014234		hypothetical protein	20.25	4.92	-3.22	0.0000
AAEL012359		nucleoside-diphosphate kinase NBR-A, putative	722.57	178.99	-3.22	0.0000
AAEL016996			21.50	5.11	-3.21	0.0000
AAEL000563	CTLMA15	galactose-specific C-type lectin, putative	5.75	1.37	-3.20	0.0000
AAEL002269		purine nucleoside phosphorylase	1275.62	316.09	-3.19	0.0000
AAEL014820		hypothetical protein	12.71	3.03	-3.19	0.0000
AAEL001134		methylmalonate-semialdehyde dehydrogenase	545.46	136.72	-3.19	0.0000
AAEL009044		amine oxidase	1.93	0.47	-3.19	0.0000
AAEL000556	CTL25	galactose-specific C-type lectin, putative	275.18	68.05	-3.19	0.0000
AAEL013642		acyl-coa dehydrogenase	19.80	4.92	-3.17	0.0000
AAEL007568		DNA-directed RNA polymerase	16.73	4.16	-3.17	0.0000
AAEL004112	TPX2	peroxiredoxins, prx-1, prx-2, prx-3	464.70	116.38	-3.16	0.0000
AAEL001246		Thymidylate kinase, putative	3.35	0.76	-3.16	0.0000
AAEL001318		CRAL/TRIO domain-containing protein	1.49	0.32	-3.16	0.0003
AAEL011460		hypothetical protein	23.23	5.82	-3.16	0.0000
AAEL009084		slender lobes, putative	8.95	2.24	-3.16	0.0000
AAEL006227		hypothetical protein	9.54	2.39	-3.15	0.0000
AAEL011338		hypothetical protein	50.47	12.75	-3.14	0.0000
AAEL015446		hypothetical protein	3.37	0.67	-3.14	0.0035
AAEL004592		tyrosine-protein kinase src64b	5.42	1.33	-3.13	0.0000
AAEL011309		orotidine-5'-phosphate decarboxylase, putative	54.41	13.87	-3.13	0.0000
AAEL007573		hypothetical protein	5.84	1.44	-3.12	0.0000
AAEL013688		hypothetical protein	1.84	0.43	-3.12	0.0000
AAEL011693		mitotic control protein dis3	7.68	1.96	-3.11	0.0000
AAEL009023		hypothetical protein	9.47	2.39	-3.11	0.0000
AAEL012721		hypothetical protein	6.77	1.66	-3.10	0.0000
AAEL010698		importin beta-4	51.40	13.21	-3.10	0.0000
AAEL007420	SRPN25	antithrombin, putative	53.57	13.61	-3.09	0.0000
AAEL013463		nucleolar protein 10	7.87	2.02	-3.08	0.0000
AAEL009842	GALE12	keratinocyte lectin, putative	33.64	8.38	-3.08	0.0000
AAEL001626		zinc/iron transporter	48.84	12.59	-3.08	0.0000
AAEL011114		serine/threonine-protein kinase rio2	17.62	4.52	-3.08	0.0000
AAEL014426		glycine dehydrogenase	26.66	6.68	-3.07	0.0000
AAEL008469		hypothetical protein	34.19	8.77	-3.06	0.0000
AAEL004368		nucleolar RNA-associated protein	5.32	1.38	-3.06	0.0000
AAEL012282		prohibitin	12.08	3.11	-3.05	0.0000
AAEL003601		hypothetical protein	109.75	28.21	-3.05	0.0000
AAEL006662		hypothetical protein	9.67	2.40	-3.05	0.0000
AAEL002937		hypothetical protein	17.79	4.58	-3.04	0.0000
AAEL008147		PAF acetylhydrolase 45 kDa subunit, putative	1.68	0.39	-3.04	0.0009
AAEL009519		hypothetical protein	48.95	12.74	-3.04	0.0000
AAEL008852		hypothetical protein	24.49	6.39	-3.04	0.0000
AAEL013314		calicylin binding protein	28.66	7.51	-3.04	0.0000
AAEL011651		l-caldesmon, putative	13.75	3.61	-3.03	0.0000
AAEL004328		origin recognition complex subunit	3.24	0.83	-3.03	0.0000

Table A6 Continued

Gene ID	Gene Name	Wiki Description	3h	24h	Fold	*p* adj
AAEL010988		cationic amino acid transporter	2.31	0.56	-3.03	0.0000
AAEL003057		allergen, putative	51.89	13.59	-3.00	0.0000
AAEL012133		hypothetical protein	8.09	2.10	-2.99	0.0000
AAEL011144		triacylglycerol lipase, pancreatic	4.03	0.98	-2.99	0.0000
AAEL002843		hypothetical protein	8.50	2.24	-2.99	0.0000
AAEL007655		hypothetical protein	9.55	2.49	-2.99	0.0000
AAEL003839		hypothetical protein	7.75	2.06	-2.99	0.0000
AAEL010139		serine protease, putative	163.41	31.16	-2.98	0.0148
AAEL013884		synaptic vesicle protein	40.00	10.70	-2.98	0.0000
AAEL002510		serine hydroxymethyltransferase	596.24	159.64	-2.98	0.0000
AAEL000173		chromatin assembly factor-I p150 subunit	20.57	5.48	-2.98	0.0000
AAEL003123		deoxyribonuclease I, putative	272.83	71.40	-2.97	0.0000
AAEL010161		hypothetical protein	553.10	146.49	-2.97	0.0000
AAEL008393		phosphatidylserine synthase	26.03	6.97	-2.97	0.0000
AAEL003182	SRPN26	SERPIN1 protein precursor, putative	226.70	59.46	-2.96	0.0000
AAEL006377	LRIM31	hypothetical protein	56.76	15.11	-2.96	0.0000
AAEL017975	HSP70Ba		5.88	1.56	-2.95	0.0000
AAEL009662		hypothetical protein	5.55	1.48	-2.95	0.0000
AAEL010276		aminomethyltransferase	169.27	45.14	-2.95	0.0000
AAEL005762		leucine-rich transmembrane proteins	9.53	2.58	-2.94	0.0000
AAEL009479		amino acid transporter	12.22	3.28	-2.94	0.0000
AAEL018287			1.64	0.43	-2.93	0.0000
AAEL003053		allergen, putative	508.13	135.36	-2.93	0.0000
AAEL011708		heat shock protein	14.04	3.83	-2.92	0.0000
AAEL011701		hypothetical protein	16.50	4.50	-2.92	0.0000
AAEL006211			2.12	0.56	-2.91	0.0000
AAEL007544		serine/threonine-protein kinase chk2 (cds1)	3.63	0.95	-2.91	0.0000
AAEL006031		hypothetical protein	14.15	3.86	-2.91	0.0000
AAEL013952		prohibitin	15.23	4.12	-2.90	0.0000
AAEL003313		alkaline phosphatase	3.30	0.86	-2.90	0.0000
AAEL013363		ubiquitously transcribed sex (x/y)	19.88	5.48	-2.89	0.0000
AAEL013968		hypothetical protein	19.23	5.21	-2.89	0.0000
AAEL015086		hypothetical protein	6.21	1.61	-2.88	0.0000
AAEL008706		smooth muscle caldesmon, putative	8.45	2.32	-2.87	0.0000
AAEL000422		U3 small nucleolar RNA-associated protein	6.55	1.77	-2.87	0.0000
AAEL011943		hairy protein	1.48	0.35	-2.86	0.0023
AAEL014314		DNA primase	1.31	0.33	-2.86	0.0007
AAEL006634		acetyl-coa acetyltransferase, mitochondrial	129.11	35.79	-2.85	0.0000
AAEL003585		hypothetical protein	20.69	5.59	-2.85	0.0000
AAEL006280		juvenile hormone acid methyltransferase, putative	7.47	2.04	-2.84	0.0000
AAEL001641		deoxyribonuclease I, putative	149.67	41.72	-2.84	0.0000
AAEL007414		hypothetical protein	6.14	1.67	-2.83	0.0000
AAEL003555		ribosome biogenesis protein	8.65	2.43	-2.83	0.0000
AAEL012131		cationic amino acid transporter	4.08	1.13	-2.82	0.0000
AAEL010716		preprotein translocase secy subunit (sec61)	137.26	38.67	-2.82	0.0000
AAEL007692		hypothetical protein	1.54	0.39	-2.81	0.0001
AAEL009993		hypothetical protein	38.21	10.70	-2.81	0.0000
AAEL002249		hypothetical protein	6.91	1.93	-2.81	0.0000
AAEL006039		dehydrodolichyl diphosphate synthase	21.05	5.96	-2.81	0.0000
AAEL011960		hypothetical protein	16.15	4.54	-2.81	0.0000
AAEL012227		hypothetical protein	88.23	24.94	-2.81	0.0000
AAEL008443		hypothetical protein	4.81	1.32	-2.81	0.0000
AAEL010594		hypothetical protein	1.66	0.41	-2.80	0.0024

Table A6 Continued

Gene ID	Gene Name	Wiki Description	3h	24h	Fold	*p* adj
AAEL011535		wd-repeat protein	4.25	1.18	-2.80	0.0000
AAEL006610		hypothetical protein	12.85	3.67	-2.80	0.0000
AAEL006417		D7 protein, putative	611.16	171.72	-2.79	0.0000
AAEL005125		hypothetical protein	19.43	5.48	-2.78	0.0000
AAEL013940		chromatin assembly factor i P60 subunit	1.43	0.40	-2.78	0.0000
AAEL009992		hypothetical protein	26.59	7.43	-2.78	0.0000
AAEL014502		hypothetical protein	1.20	0.33	-2.78	0.0000
AAEL014526		sideroflexin 1,2,3	138.37	39.67	-2.77	0.0000
AAEL013400		DEAD box ATP-dependent RNA helicase	4.62	1.31	-2.77	0.0000
AAEL014206		sugar transporter	30.25	8.72	-2.77	0.0000
AAEL018289		hypothetical protein	1.37	0.37	-2.76	0.0000
AAEL003084		dolichyl-phosphate beta-D-mannosyltransferase	12.77	3.65	-2.76	0.0000
AAEL011224		hypothetical protein	28.73	8.05	-2.76	0.0000
AAEL011884		hypothetical protein	25.69	7.41	-2.75	0.0000
AAEL016961			2.80	0.71	-2.75	0.0038
AAEL013707		trypsin	1.21	0.29	-2.75	0.0116
AAEL002784		zinc finger protein	27.53	8.00	-2.74	0.0000
AAEL009647		hypothetical protein	16.64	4.75	-2.74	0.0000
AAEL000999		DNA replication licensing factor MCM7	5.20	1.50	-2.74	0.0000
AAEL002985		mitchondrial carnitine/acylcarnitine carrier	3.32	0.92	-2.73	0.0000
AAEL008370	SCRB17		48.92	14.29	-2.73	0.0000
AAEL004142			9.99	2.91	-2.73	0.0000
AAEL014908		hypothetical protein	9.38	2.69	-2.73	0.0000
AAEL010109		hypothetical protein	20.91	6.08	-2.72	0.0000
AAEL008564		low-density lipoprotein receptor (ldl)	34.05	9.85	-2.72	0.0000
AAEL006424		D7 protein, putative	949.14	257.01	-2.72	0.0002
AAEL006131		hypothetical protein	17.75	5.05	-2.72	0.0000
AAEL010008		crotonobetainyl-CoA-hydratase, putative	36.68	10.65	-2.72	0.0000
AAEL005106		hypothetical protein	99.12	29.06	-2.72	0.0000
AAEL004345		cysteinyl-tRNA synthetase	17.30	5.04	-2.71	0.0000
AAEL011877		protein arginine n-methyltransferase	3.90	1.11	-2.71	0.0000
AAEL003600		hypothetical protein	602.36	173.83	-2.71	0.0000
AAEL006469		hypothetical protein	10.28	3.01	-2.71	0.0000
AAEL013725		hypothetical protein	2.10	0.59	-2.70	0.0000
AAEL008832		forkhead box protein (AaegFOXN1)	44.47	13.19	-2.67	0.0000
AAEL015306		hypothetical protein	20.50	5.79	-2.66	0.0000
AAEL009067		helicase	10.35	3.09	-2.66	0.0000
AAEL006697		hypothetical protein	9.16	2.69	-2.65	0.0000
AAEL002704	SRPN23	serine protease inhibitor (serpin-4), putative	412.82	121.63	-2.65	0.0000
AAEL004364		hypothetical protein	11.33	3.39	-2.65	0.0000
AAEL009382		hypothetical protein	6.02	1.78	-2.65	0.0000
AAEL010770		hypothetical protein	2.83	0.83	-2.65	0.0000
AAEL015199		wd-repeat protein	2.21	0.63	-2.64	0.0001
AAEL017134			95.74	28.56	-2.64	0.0000
AAEL000059	CLIPB19	proacrosin, putative	11.85	3.44	-2.64	0.0000
AAEL005567		nucleosome assembly protein	114.08	34.57	-2.63	0.0000
AAEL007656		receptor for activated C kinase, putative	11.80	3.55	-2.63	0.0000
AAEL006136		serine protease, putative	38.85	11.69	-2.63	0.0000
AAEL008247		DNA polymerase alpha catalytic subunit	2.03	0.61	-2.62	0.0000
AAEL003107		hypothetical protein	71.11	20.94	-2.62	0.0000
AAEL008865		oligoribonuclease, mitochondrial	11.41	3.38	-2.62	0.0000
AAEL002808		diphthine synthase	13.91	4.18	-2.62	0.0000
AAEL005635		nucleoporin	17.45	5.24	-2.61	0.0000

Table A6 Continued

Gene ID	Gene Name	Wiki Description	3h	24h	Fold	*p* adj
AAEL002741	SCRB6	neither inactivation nor afterpotential D	5.82	1.74	-2.61	0.0000
AAEL009634		steroid dehydrogenase	89.49	27.32	-2.61	0.0000
AAEL014238		aromatic amino acid decarboxylase	9.83	2.98	-2.61	0.0000
AAEL009944		hypothetical protein	9.21	2.78	-2.60	0.0000
AAEL011773		calreticulin	118.32	36.08	-2.60	0.0000
AAEL012260		wd-repeat protein	9.98	3.05	-2.60	0.0000
AAEL009149		kinectin, putative	2.14	0.61	-2.60	0.0000
AAEL011137		succinyl-coa:3-ketoacid-coenzyme a transferase	225.45	69.05	-2.59	0.0000
AAEL010128	LRIM4	hypothetical protein	3.34	0.94	-2.59	0.0020
AAEL005628		hypothetical protein	44.23	13.59	-2.58	0.0000
AAEL006496		steroid dehydrogenase	1.60	0.47	-2.58	0.0001
AAEL012731		adenylate kinase 1, putative	81.71	25.28	-2.58	0.0000
AAEL012973		uracil phosphoribosyltransferase	11.78	3.62	-2.58	0.0000
AAEL004178		ribose-phosphate pyrophosphokinase 1	524.90	162.84	-2.58	0.0000
AAEL006909		hypothetical protein	1.28	0.31	-2.58	0.0366
AAEL007150		ATP-dependent RNA helicase	6.21	1.91	-2.57	0.0000
AAEL011158		disulfide oxidoreductase	12.75	3.93	-2.57	0.0000
AAEL005932		hypothetical protein	1.41	0.41	-2.57	0.0006
AAEL007237		hypothetical protein	3.59	1.09	-2.56	0.0000
AAEL007684		tektin, putative	6.62	2.04	-2.56	0.0000
AAEL011505		integral membrane pore glycoprotein gp210	3.38	1.05	-2.55	0.0000
AAEL011996		hypothetical protein	4.51	1.28	-2.55	0.0004
AAEL012312		proliferation-associated 2g4 (pa2g4/ebp1)	86.46	27.03	-2.54	0.0000
AAEL010904		rothmund-thomson syndrome DNA helicase	1.57	0.48	-2.54	0.0000
AAEL000793		venom allergen	1084.46	336.23	-2.54	0.0000
AAEL012147		hypothetical protein	4.33	1.36	-2.54	0.0000
AAEL013305		thymidylate synthase	6.12	1.90	-2.54	0.0000
AAEL017419			145.35	45.68	-2.54	0.0000
AAEL001656		sodium-dependent phosphate transporter	15.26	4.79	-2.54	0.0000
AAEL014159		PAF acetylhydrolase 45 kDa subunit, putative	3.97	1.22	-2.53	0.0000
AAEL007818		trypsin	24.89	7.62	-2.53	0.0000
AAEL001195		Juvenile hormone-inducible protein, putative	1.84	0.53	-2.53	0.0005
AAEL006972		hepatocellular carcinoma-associated antigen	2.60	0.80	-2.52	0.0000
AAEL006033		dihydroorotate dehydrogenase	14.25	4.45	-2.52	0.0000
AAEL010062		hypothetical protein	20.11	6.32	-2.51	0.0000
AAEL015081		tRNA-methyltransferase	2.23	0.66	-2.51	0.0007
AAEL010222		transcription factor GATA	8.16	2.59	-2.50	0.0000
AAEL009287		ran	173.37	55.42	-2.49	0.0000
AAEL010290		short-chain dehydrogenase	12.88	4.11	-2.49	0.0000
AAEL010500	GSTX2	glutathione-s-transferase theta, gst	7.79	2.45	-2.48	0.0000
AAEL001128		AMP dependent coa ligase	45.13	14.43	-2.48	0.0000
AAEL014363		hypothetical protein	1.28	0.34	-2.48	0.0288
AAEL008766		hypothetical protein	42.41	13.19	-2.48	0.0000
AAEL006333		salivary apyrase, putative	99.04	31.38	-2.48	0.0000
AAEL009156		trna (guanine-n(7)-)-methyltransferase	16.04	5.08	-2.47	0.0000
AAEL010077		xpa-binding protein 1 (mbdin)	6.02	1.91	-2.47	0.0000
AAEL012123		hypothetical protein	4.80	1.50	-2.46	0.0000
AAEL007250		hypothetical protein	17.34	5.56	-2.46	0.0000
AAEL011692			1.03	0.33	-2.46	0.0000
AAEL009571		elongase, putative	14.41	4.58	-2.46	0.0000
AAEL010063		chaperonin	66.02	21.48	-2.46	0.0000

Table A6 Continued

Gene ID	Gene Name	Wiki Description	3h	24h	Fold	*p* adj
AAEL007858		ran gtpase-activating protein	6.51	2.11	-2.45	0.0000
AAEL017223			18.96	6.13	-2.45	0.0000
AAEL003661		translation initiation factor	67.97	22.03	-2.45	0.0000
AAEL008431		a kinase anchor protein	16.44	5.35	-2.45	0.0000
AAEL011696		hypothetical protein	3.82	1.19	-2.44	0.0000
AAEL003071		tRNA pseudouridine synthase D	38.32	12.46	-2.44	0.0000
AAEL000001		bystin	27.84	9.13	-2.44	0.0000
AAEL005833		cytosolic purine 5-nucleotidase	75.00	24.40	-2.44	0.0000
AAEL004899		hypothetical protein	98.50	31.74	-2.44	0.0000
AAEL009356		hypothetical protein	11.53	3.74	-2.44	0.0000
AAEL006819		hypothetical protein	10.00	3.16	-2.43	0.0000
AAEL008028		monocarboxylate transporter	177.65	58.59	-2.43	0.0000
AAEL006637		hypothetical protein	10.45	3.41	-2.42	0.0000
AAEL001328		hypothetical protein	38.63	12.65	-2.42	0.0000
AAEL007431		hypothetical protein	69.19	22.55	-2.42	0.0000
AAEL017368			50.67	16.72	-2.42	0.0000
AAEL004075		RNA binding motif protein	3.71	1.20	-2.42	0.0000
AAEL011857		serine/threonine-protein kinase rio1	11.39	3.71	-2.42	0.0000
AAEL004920		hypothetical protein	39.19	12.97	-2.42	0.0000
AAEL004558		hypothetical protein	8.36	2.73	-2.41	0.0000
AAEL013457		RNA polymerase small Zn-binding subunit	19.00	5.82	-2.41	0.0015
AAEL008743		Tetratricopeptide repeat protein, putative	6.35	2.01	-2.41	0.0000
AAEL004014		glucose dehydrogenase	4.83	1.59	-2.41	0.0000
AAEL004947		elongase, putative	3.51	1.11	-2.41	0.0000
AAEL004043		hypothetical protein	34.47	11.41	-2.40	0.0000
AAEL001005		calreticulin	136.60	45.26	-2.39	0.0000
AAEL012864		hypothetical protein	9.23	3.03	-2.39	0.0000
AAEL010644		ribonucleoside-diphosphate reductase	6.36	2.12	-2.38	0.0000
AAEL010710		gamma-aminobutyric-acid receptor	1.39	0.40	-2.38	0.0210
AAEL002457		hypothetical protein	39.04	13.02	-2.38	0.0000
AAEL004698		DNA primase large subunit	1.69	0.55	-2.37	0.0002
AAEL016998			1.16	0.37	-2.37	0.0003
AAEL010982	GPRMTH1_1		4.33	1.44	-2.37	0.0000
AAEL010296		carboxylase:pyruvate/acetyl-coa/propionyl-coa	13.03	4.39	-2.36	0.0000
AAEL004434		transketolase	105.74	35.74	-2.36	0.0000
AAEL011378			3.57	1.13	-2.36	0.0016
AAEL015143		glycine rich RNA binding protein, putative	21.73	7.25	-2.36	0.0000
AAEL012874		rrp4	3.08	1.00	-2.36	0.0000
AAEL006423		hypothetical protein	646.84	216.08	-2.36	0.0000
AAEL017059			56.55	19.03	-2.36	0.0000
AAEL001964		protein serine/threonine kinase, putative	815.15	275.95	-2.35	0.0000
AAEL001016		zinc finger protein	15.20	5.14	-2.35	0.0000
AAEL017508			43.25	14.67	-2.35	0.0000
AAEL009320		chaperonin	60.77	20.60	-2.35	0.0000
AAEL010362		hypothetical protein	6.00	2.03	-2.35	0.0000
AAEL005579		developmentally regulated GTP	25.65	8.71	-2.35	0.0000
AAEL010341		TATA-binding protein, putative	12.95	4.39	-2.34	0.0000
AAEL000677		DNA-directed RNA polymerase subunit rpb8	20.97	7.08	-2.34	0.0000
AAEL000551		hypothetical protein	183.59	61.91	-2.34	0.0000
AAEL000794		eukaryotic translation initiation factor	81.41	27.69	-2.33	0.0000
AAEL012235		IR75k.2	40.07	13.73	-2.33	0.0000
AAEL000115		hypothetical protein	7.44	2.53	-2.32	0.0000

Table A6 Continued

Gene ID	Gene Name	Wiki Description	3h	24h	Fold	*p* adj
AAEL009852		hypothetical protein	124.40	42.73	-2.32	0.0000
AAEL010242		hypothetical protein	436.79	147.63	-2.32	0.0000
AAEL010366		glucosyl/glucuronosyl transferases	55.60	19.06	-2.32	0.0000
AAEL004263		small nuclear ribonucleoprotein sm d1	5.50	1.82	-2.32	0.0008
AAEL010621		hypothetical protein	2.19	0.72	-2.32	0.0005
AAEL013577		hypothetical protein	64.42	22.19	-2.32	0.0000
AAEL002232		hypothetical protein	12.41	4.21	-2.31	0.0000
AAEL002898		hypothetical protein	22.57	7.59	-2.31	0.0000
AAEL017263			64.89	22.45	-2.31	0.0000
AAEL007356		hypothetical protein	15.67	5.32	-2.30	0.0000
AAEL013532		hypothetical protein	54.23	18.79	-2.30	0.0000
AAEL013114		DNA-J, putative	26.62	9.13	-2.30	0.0000
AAEL009345		prohibitin	83.98	29.33	-2.29	0.0000
AAEL000004		glycosyltransferase	18.80	6.55	-2.29	0.0000
AAEL006971		hypothetical protein	7.43	2.52	-2.29	0.0000
AAEL008882		hypothetical protein	11.34	3.96	-2.29	0.0000
AAEL011245		deoxyhypusine synthase	5.15	1.75	-2.28	0.0000
AAEL010075		oxidoreductase	10.05	3.48	-2.28	0.0000
AAEL006408		hypothetical protein	248.53	85.91	-2.28	0.0000
AAEL009603		hypothetical protein	6.73	2.32	-2.28	0.0000
AAEL002701		mannosyltransferase	71.86	25.20	-2.28	0.0000
AAEL004896		hypothetical protein	9.73	3.41	-2.28	0.0000
AAEL012725		hypothetical protein	1.01	0.35	-2.27	0.0001
AAEL009579		NBP2b protein, putative	10.34	3.56	-2.27	0.0000
AAEL008767		serine protease	2.27	0.70	-2.27	0.0380
AAEL011768		hypothetical protein	1.00	0.33	-2.27	0.0038
AAEL001900		lactosylceramide 4-alpha-galactosyltransferase	3.06	1.05	-2.27	0.0000
AAEL014845		heat shock protein	23.79	8.31	-2.27	0.0000
AAEL003625	CLIPB8	clip-domain serine protease, putative	72.79	25.56	-2.27	0.0000
AAEL003993		cyclohex-1-ene-1-carboxyl-CoA hydratase	134.83	47.40	-2.27	0.0000
AAEL000668		hypothetical protein	22.56	7.85	-2.26	0.0000
AAEL018277		hypothetical protein	4.42	1.55	-2.26	0.0000
AAEL002991		hypothetical protein	9.97	3.30	-2.25	0.0055
AAEL010249		hypothetical protein	1.44	0.47	-2.25	0.0113
AAEL010885		hypothetical protein	11.54	4.07	-2.25	0.0000
AAEL017467			5.03	1.71	-2.25	0.0004
AAEL010737		aromatic amino acid decarboxylase	18.60	6.54	-2.24	0.0000
AAEL001478			15.52	5.52	-2.24	0.0000
AAEL011536		phosphoglucomutase	11.23	3.99	-2.24	0.0000
AAEL013967		Methylmalonyl-CoA carboxyltransferase	43.82	15.63	-2.24	0.0000
AAEL010379		ATPe-binding cassette transporter	54.37	19.41	-2.24	0.0000
AAEL011087		DNA-directed RNA polymerase II	28.67	10.25	-2.23	0.0000
AAEL018323		fast myosin heavy chain HCIII, putative	76.90	27.51	-2.23	0.0000
AAEL005480		hairy protein	2.00	0.71	-2.23	0.0000
AAEL001216		DEAD box ATP-dependent RNA helicase	135.78	48.68	-2.23	0.0000
AAEL002354	HPX5	oxidase/peroxidase	1.67	0.57	-2.22	0.0003
AAEL007650		chaperonin	40.74	14.63	-2.22	0.0000
AAEL004464			7.09	2.52	-2.22	0.0000
AAEL005515		heterogeneous nuclear ribonucleoprotein	266.75	96.09	-2.22	0.0000
AAEL003086		hypothetical protein	59.07	21.23	-2.22	0.0000
AAEL014503		hypothetical protein	3.25	1.15	-2.21	0.0000
AAEL013249		eukaryotic translation initiation factor 4	31.62	11.45	-2.21	0.0000
AAEL002785		DNA polymerase epsilon subunit b	1.35	0.43	-2.21	0.0182

Table A6 Continued

Gene ID	Gene Name	Wiki Description	3h	24h	Fold	*p* adj
AAEL017275			52.67	19.08	-2.20	0.0000
AAEL014068		hypothetical protein	1.54	0.53	-2.20	0.0005
AAEL005474		hypothetical protein	211.34	76.56	-2.20	0.0000
AAEL015305		sulfotransferase (sult)	6.34	2.23	-2.19	0.0003
AAEL009508		zinc finger protein	1.33	0.47	-2.19	0.0001
AAEL015236		signal recognition particle, 9kD-subunit, putative	10.86	3.76	-2.19	0.0033
AAEL003908		nuclear pore complex protein nup107	7.00	2.53	-2.19	0.0000
AAEL012843		tubulin gamma chain	2.06	0.72	-2.18	0.0001
AAEL009264		hypothetical protein	1.55	0.56	-2.18	0.0002
AAEL003766		hypothetical protein	6.08	2.22	-2.18	0.0000
AAEL014950	SPZ3B	hypothetical protein	3.64	1.23	-2.18	0.0069
AAEL000952		hypothetical protein	7.80	2.86	-2.18	0.0000
AAEL008576		hypothetical protein	2.09	0.73	-2.17	0.0006
AAEL003179		protein arginine n-methyltransferase 1	40.77	14.99	-2.17	0.0000
AAEL013491		short-chain dehydrogenase	28.95	10.64	-2.17	0.0000
AAEL005821		alanyl aminopeptidase	2.83	1.02	-2.17	0.0002
AAEL012171		RNA recognition motif protein split ends	24.39	8.95	-2.17	0.0000
AAEL002781		galactokinase	29.24	10.68	-2.17	0.0000
AAEL001102		adenosine kinase	130.13	48.00	-2.17	0.0000
AAEL001305		hypothetical protein	10.40	3.72	-2.16	0.0002
AAEL012154		2,3-cyclic-nucleotide 2-phosphodiesterase	58.20	21.50	-2.16	0.0000
AAEL013033		serine protease, putative	31.64	11.51	-2.16	0.0000
AAEL011899		acetylglucosaminyltransferase	8.17	2.96	-2.16	0.0000
AAEL005463		calbindin-32	9.13	3.25	-2.16	0.0003
AAEL007674		hypothetical protein	3.66	1.32	-2.16	0.0000
AAEL002483		hypothetical protein	17.69	6.54	-2.16	0.0000
AAEL003332		hypothetical protein	8.78	3.19	-2.16	0.0000
AAEL012567		synaptic vesicle protein	1.39	0.49	-2.15	0.0123
AAEL007784		hypothetical protein	3.88	1.43	-2.15	0.0001
AAEL011738		hypothetical protein	3.94	1.46	-2.15	0.0000
AAEL000229		hypothetical protein	300.37	111.55	-2.15	0.0000
AAEL003742		glucosylceramidase	1.46	0.52	-2.15	0.0118
AAEL008073		hypothetical protein	212.86	79.32	-2.15	0.0000
AAEL001997		hypothetical protein	18.22	6.78	-2.14	0.0000
AAEL012205		hypothetical protein	4.33	1.60	-2.14	0.0000
AAEL002675		arginase	49.48	18.47	-2.14	0.0000
AAEL011820		hypothetical protein	14.07	5.19	-2.14	0.0000
AAEL006297		venom allergen	5.70	2.07	-2.14	0.0000
AAEL004877		hypothetical protein	5.26	1.96	-2.13	0.0000
AAEL017133			67.69	25.33	-2.13	0.0000
AAEL004136		hypothetical protein	1.38	0.51	-2.13	0.0006
AAEL010617		DNA-directed RNA polymerase II	2.60	0.95	-2.13	0.0000
AAEL006502		hypothetical protein	7.83	2.89	-2.13	0.0000
AAEL011632		fk506 binding protein	12.02	4.46	-2.13	0.0000
AAEL015609		small calcium-binding mitochondrial carrier	15.82	5.85	-2.13	0.0000
AAEL012266	CYP4C38	cytochrome P450	22.33	8.35	-2.13	0.0000
AAEL007077		integrin beta 1 binding protein (melusin)	22.50	8.45	-2.13	0.0000
AAEL011882		trypsin-zeta, putative	2.89	1.05	-2.12	0.0031
AAEL005851		exosome complex exonuclease rrp42	7.57	2.81	-2.12	0.0000
AAEL006009		hypothetical protein	11.63	4.31	-2.12	0.0000
AAEL015119		cuticle protein, putative	5.29	1.95	-2.12	0.0000
AAEL014250		insect replication protein a	8.66	3.23	-2.12	0.0000
AAEL009884			5.10	1.92	-2.12	0.0000

Table A6 Continued

Gene ID	Gene Name	Wiki Description	3h	24h	Fold	*p* adj
AAEL007501		nikI, nikkomycin biosynthesis protein P6, putative	9.01	3.37	-2.12	0.0000
AAEL013644		ubiquitously transcribed sex (x/y)	14.71	5.53	-2.11	0.0000
AAEL009520	LRIM2	hypothetical protein	15.38	5.74	-2.11	0.0000
AAEL013989		protein translocation complex beta subunit,	268.86	100.64	-2.11	0.0000
AAEL001861		nuclear pore complex protein nup154	5.36	2.02	-2.11	0.0000
AAEL001122		n-acetylgalactosaminyltransferase	4.88	1.81	-2.11	0.0005
AAEL008830		hypothetical protein	5.37	1.97	-2.11	0.0030
AAEL012726		hypothetical protein	7.00	2.56	-2.11	0.0015
AAEL017443			1.03	0.37	-2.11	0.0064
AAEL006133		cofactor A, putative	26.16	9.74	-2.11	0.0000
AAEL012990		mrg-binding protein	7.69	2.87	-2.10	0.0000
AAEL012746		chaperonin	56.18	21.31	-2.10	0.0000
AAEL011682		nuclear pore complex protein nup93]	9.33	3.53	-2.10	0.0000
AAEL001089		hypothetical protein		16.07	-2.10	0.0000
AAEL008619		hypothetical protein	495.56	187.80	-2.10	0.0000
AAEL017417			312.64	118.48	-2.10	0.0000
AAEL001724	GPRNNB3	hypothetical protein	4.13	1.54	-2.09	0.0002
AAEL010993		queuine tRNA-ribosyltransferase	1.29	0.46	-2.09	0.0060
AAEL008546		hypothetical protein	177.87	66.70	-2.09	0.0000
AAEL013143		hypothetical protein	35.00	13.42	-2.09	0.0000
AAEL000147		single-stranded DNA binding protein, putative	19.28	7.39	-2.08	0.0000
AAEL010183		hypothetical protein	594.98	225.02	-2.08	0.0000
AAEL010288		carboxylase:pyruvate/acetyl-coa/propionyl-coa	4.37	1.67	-2.08	0.0000
AAEL010003		splicesome protein, putative	8.64	3.25	-2.08	0.0000
AAEL012762	CYP325N2	cytochrome P450	6.11	2.33	-2.08	0.0000
AAEL006155		hypothetical protein	16.27	6.27	-2.07	0.0000
AAEL003655		hypothetical protein	9.88	3.80	-2.07	0.0000
AAEL000402		hypothetical protein	3.47	1.28	-2.07	0.0007
AAEL002720	SRPN20	serine protease inhibitors, serpins	77.52	29.77	-2.07	0.0000
AAEL001158		fructose-1,6-bisphosphatase	93.75	35.87	-2.06	0.0000
AAEL006026		leucine rich protein, putative	10.87	4.18	-2.06	0.0000
AAEL003648		hypothetical protein	2.77	1.00	-2.06	0.0075
AAEL003646		hypothetical protein	50.46	19.55	-2.06	0.0000
AAEL018213		hypothetical protein	6.73	2.61	-2.06	0.0000
AAEL011610	CTLGA8	galactose-specific C-type lectin, putative	8.08	2.82	-2.06	0.0382
AAEL006406		hypothetical protein	513.96	196.19	-2.06	0.0000
AAEL012767	LRIM5	hypothetical protein	9.78	3.80	-2.06	0.0000
AAEL006788		replication factor C, 37-kDa subunit, putative	6.14	2.36	-2.05	0.0000
AAEL014818		sil1	2.16	0.77	-2.05	0.0157
AAEL009392		chromosome protein 5/exportin	12.81	4.98	-2.05	0.0000
AAEL000313		hypothetical protein	1.23	0.46	-2.05	0.0025
AAEL014040		hypothetical protein	4.82	1.85	-2.05	0.0000
AAEL014650		mannose-binding protein-associated serine	6.78	2.57	-2.05	0.0019
AAEL005988	LYSC6	hypothetical protein	3.41	1.30	-2.05	0.0009
AAEL013904		3-hydroxyisobutyrate dehydrogenase	311.90	121.79	-2.05	0.0000
AAEL001085		hypothetical protein	59.85	23.25	-2.04	0.0000
AAEL003246		deoxyribose-phosphate aldolase	13.43	5.22	-2.04	0.0000
AAEL015336		hypothetical protein	1.30	0.48	-2.04	0.0121
AAEL001625		hypothetical protein	91.58	35.58	-2.04	0.0000
AAEL012251		low-density lipoprotein receptor (ldl)	76.07	29.84	-2.04	0.0000

Table A6 Continued

Gene ID	Gene Name	Wiki Description	3h	24h	Fold	*p* adj
AAEL007286		arginine-rich protein, putative	59.35	23.07	-2.04	0.0000
AAEL014037		PAF acetylhydrolase 45 kDa subunit, putative	17.67	6.92	-2.03	0.0000
AAEL014797		acyl-coa dehydrogenase	34.94	13.70	-2.03	0.0000
AAEL010855		cdc6	1.05	0.38	-2.03	0.0212
AAEL010333		hypothetical protein	11.50	4.47	-2.03	0.0000
AAEL017982	HSP70Cb'		1.29	0.48	-2.03	0.0118
AAEL017987			1.98	0.74	-2.03	0.0038
AAEL014494		methionine-tRNA synthetase	6.69	2.61	-2.03	0.0000
AAEL007050		sugar transporter	21.08	8.29	-2.03	0.0000
AAEL001708		hypothetical protein	25.86	10.12	-2.03	0.0000
AAEL002042		deoxyribonuclease I, putative	1.27	0.46	-2.03	0.0305
AAEL012287		sugar transporter	8.13	3.19	-2.02	0.0000
AAEL003291		hypothetical protein	4.06	1.57	-2.02	0.0000
AAEL011863		abc transporter	8.84	3.49	-2.02	0.0000
AAEL007372	GPRGBB1	gaba-b receptor	1.25	0.47	-2.02	0.0035
AAEL006351		hypothetical protein	26.91	10.47	-2.02	0.0000
AAEL004708		2-phosphodiesterase	4.87	1.90	-2.02	0.0000
AAEL011052		hypothetical protein	2.07	0.79	-2.02	0.0048
AAEL017309			7.08	2.74	-2.02	0.0001
AAEL009914		small nuclear ribonucleoprotein sm d2	2.49	0.96	-2.01	0.0062
AAEL004589		small calcium-binding mitochondrial carrie	125.70	49.81	-2.01	0.0000
AAEL013424		hypothetical protein	13.43	5.10	-2.01	0.0013
AAEL002339		hypothetical protein	5.18	2.04	-2.01	0.0000
AAEL011465		hypothetical protein	2.52	0.99	-2.01	0.0003
AAEL011771		hypothetical protein	6.91	2.73	-2.01	0.0000
AAEL002048		histidyl-tRNA synthetase	28.51	11.33	-2.01	0.0000
AAEL017224			6.25	2.44	-2.00	0.0005

Table A7. Genes differentially expressed in the HT of 24h and 48h blood fed females.

IDs	Gene name	Gene description	24h	48h	Fold	*p* adj.
		Up regulated				
AAEL007590		cathepsin b	0.16	532.63	926.76	0.0000
AAEL006586		serine protease	0.69	141.21	101.30	0.0000
AAEL001289		permease, putative	1.40	93.84	45.32	0.0000
AAEL015432		trypsin, putative	0.03	10.91	37.13	0.0000
AAEL010764		aldehyde dehydrogenase	0.50	32.73	30.67	0.0000
AAEL014005		clip-domain serine protease, putative	0.47	21.82	21.91	0.0000
AAEL006576		clip-domain serine protease, putative	8.79	286.27	21.19	0.0000
AAEL006568		serine protease	21.71	744.10	20.56	0.0000
AAEL000311		conserved hypothetical protein	1.61	51.53	18.68	0.0000
AAEL006323		hypothetical protein	2.28	62.76	16.98	0.0000
AAEL006674	CLIPB29	Clip-Domain Serine Protease family B.	10.37	249.73	15.88	0.0000
AAEL007102		trypsin, putative	1.56	34.04	15.21	0.0000
AAEL010684		conserved hypothetical protein	10.05	225.26	15.19	0.0000
AAEL011130		alcohol dehydrogenase	2.42	62.73	14.88	0.0000
AAEL007103	LRIM15	leucine-rich immune protein	1.98	44.44	14.05	0.0000
AAEL002576		sodium/solute symporter	2.94	53.82	12.70	0.0000
AAEL011624		granzyme A precursor, putative	3.55	65.24	12.06	0.0000
AAEL010075		oxidoreductase	6.45	103.72	10.95	0.0000

Table A7 Continued

IDs	Gene name	Gene description	24h	48h	Fold	*p* adj.
AAEL003568		threonine dehydratase/deaminase	0.16	4.33	10.32	0.0000
AAEL001128		AMP dependent coa ligase	14.71	197.93	9.65	0.0000
AAEL011319		hypothetical protein	6.56	92.06	9.30	0.0000
AAEL000629		adenylate kinase 3,	6.32	72.98	8.25	0.0000
AAEL000546			3.21	39.85	8.04	0.0000
AAEL012721		conserved hypothetical protein	1.69	21.64	7.91	0.0000
AAEL006446		trehalose-6-phosphate synthase	24.32	319.25	7.80	0.0000
AAEL006585		predicted protein	0.40	7.45	7.79	0.0000
AAEL002291		conserved hypothetical protein	0.42	6.11	7.70	0.0000
AAEL012255	LRIM13	leucine-rich immune protein	2.92	32.25	7.70	0.0000
AAEL014004		clip-domain serine protease, putative	1.10	13.32	7.52	0.0000
AAEL008473		cysteine-rich venom protein, putative	32.00	408.48	7.40	0.0000
AAEL014300		hypothetical protein	1.01	14.67	7.36	0.0000
AAEL007653		allantoinase	1.39	17.34	7.25	0.0000
AAEL010697		3-ketoacyl-coa thiolase, mitochondrial	52.61	499.80	7.14	0.0000
AAEL011126		alcohol dehydrogenase	19.87	194.52	7.11	0.0000
AAEL010937		conserved hypothetical protein	2.98	27.92	6.68	0.0000
AAEL002696		hypothetical protein	0.87	9.18	6.60	0.0000
AAEL012251		low-density lipoprotein receptor	30.44	273.66	6.59	0.0000
AAEL000744		troponin C	50.74	439.56	6.36	0.0000
AAEL011863		ABC transporter	3.56	30.04	6.10	0.0000
AAEL005790		malic enzyme	76.25	617.52	6.03	0.0000
AAEL005997		allergen, putative	92.55	754.67	6.02	0.0000
AAEL000530			0.94	9.05	5.89	0.0000
AAEL005434		conserved hypothetical protein	2.81	23.79	5.87	0.0000
AAEL002731	SRPN14	Serine Protease Inhibitor	1.38	12.63	5.85	0.0000
AAEL012614		NADP-specific isocitrate dehydrogenase	43.14	330.80	5.69	0.0000
AAEL014246		glucosyl/glucuronosyl transferases	27.08	204.32	5.66	0.0000
AAEL012430		AMP dependent ligase	0.52	4.64	5.60	0.0000
AAEL002658		AMP dependent ligase	4.29	34.02	5.54	0.0000
AAEL008365		conserved hypothetical protein	19.32	139.61	5.38	0.0000
AAEL001882		conserved hypothetical protein	2.00	15.53	5.21	0.0000
AAEL005032		conserved hypothetical protein	53.39	364.51	5.11	0.0000
AAEL007269		hypothetical protein	5.17	36.51	5.07	0.0000
AAEL011884		hypothetical protein	7.56	52.88	5.02	0.0000
AAEL017188			0.43	3.40	4.88	0.0000
AAEL012253		hypothetical protein	3.51	28.07	4.80	0.0000
AAEL012726		conserved hypothetical protein	2.61	21.14	4.79	0.0000
AAEL000668		conserved hypothetical protein	8.50	64.95	4.77	0.0000
AAEL000563	CTLMA15	C-Type Lectin	1.88	14.86	4.58	0.0000
AAEL011129		alcohol dehydrogenase	16.01	98.99	4.48	0.0000
AAEL012357		conserved hypothetical protein	35.52	244.07	4.47	0.0000
AAEL006662		hypothetical protein	2.85	19.53	4.39	0.0000
AAEL002242		conserved hypothetical protein	1.78	11.71	4.28	0.0000
AAEL006377	LRIM31	leucine-rich immune protein	15.42	94.94	4.27	0.0000
AAEL014045		allantoicase	9.11	51.60	4.17	0.0000
AAEL008144		AMP dependent ligase	18.29	101.27	4.14	0.0000
AAEL004278		conserved hypothetical protein	23.71	133.45	4.14	0.0000
AAEL003731		nuclear body associated kinase, putative	13.74	82.94	4.10	0.0000
AAEL003467		conserved hypothetical protein	38.19	220.40	4.10	0.0000
AAEL001194		fatty acid synthase	43.58	236.70	4.08	0.0000
AAEL009691		carboxylase:pyruvate/acetyl-coa/propionyl-coa	55.20	299.59	4.08	0.0000
AAEL005120		zinc finger protein	1.12	7.00	4.03	0.0000

Table A7 Continued

IDs	Gene name	Gene description	24h	48h	Fold	*p* adj.
AAEL007784		conserved hypothetical protein	1.45	8.44	3.96	0.0000
AAEL004088		aldo-keto reductase	59.83	312.96	3.95	0.0000
AAEL009558		serine protease, putative	0.75	6.00	3.92	0.0000
AAEL013305		dihydrofolate reductase-thymidylate synthase	2.39	13.49	3.90	0.0000
AAEL017399			0.23	1.86	3.90	0.0000
AAEL002781		galactokinase	10.89	60.89	3.90	0.0000
AAEL012722		conserved hypothetical protein	0.89	5.69	3.88	0.0000
AAEL002669		AMP dependent ligase	2.27	12.10	3.78	0.0000
AAEL000658		conserved hypothetical protein	1.10	8.63	3.77	0.0000
AAEL012956		elastase, putative	3.20	19.93	3.76	0.0000
AAEL003029		hypothetical protein	8.65	48.34	3.74	0.0000
AAEL008370	SCRB17	Class B Scavenger Receptor	14.58	73.16	3.69	0.0000
AAEL005026		ATP-dependent bile acid permease	0.29	1.64	3.68	0.0000
AAEL012710		conserved hypothetical protein	6.90	34.84	3.68	0.0000
AAEL003643		AMP dependent ligase	4.71	24.18	3.66	0.0000
AAEL013027		conserved hypothetical protein	0.54	8.08	3.60	0.0000
AAEL007255		conserved hypothetical protein	2.83	15.52	3.55	0.0000
AAEL013262		conserved hypothetical protein	8.47	50.38	3.55	0.0000
AAEL001813		sodium/solute symporter	1.57	7.90	3.54	0.0000
AAEL000111		nitrilase, putative	74.84	363.85	3.49	0.0000
AAEL002720	SRPN20	Serine Protease Inhibitor	30.37	148.81	3.46	0.0000
AAEL010366		glucosyl/glucuronosyl transferases	19.44	91.93	3.46	0.0000
AAEL006364		conserved hypothetical protein	6.86	32.09	3.42	0.0000
AAEL000044		ornithine decarboxylase	3.90	20.95	3.41	0.0000
AAEL002796		l-asparaginase i	3.85	17.83	3.33	0.0000
AAEL006920	LRIM20	leucine-rich immune protein	4.21	19.75	3.27	0.0000
AAEL010062		conserved hypothetical protein	6.45	28.78	3.27	0.0000
AAEL002950		conserved hypothetical protein	28.72	128.03	3.26	0.0000
AAEL011460		conserved hypothetical protein	5.94	26.26	3.25	0.0000
AAEL002568		conserved hypothetical protein	4.58	21.13	3.22	0.0000
AAEL001204		sterol o-acyltransferase	20.26	85.24	3.17	0.0000
AAEL015609		small calcium-binding mitochondrial carrier	5.97	26.31	3.16	0.0000
AAEL009359		conserved hypothetical protein	3.67	16.31	3.14	0.0000
AAEL009774		hypothetical protein	0.58	2.74	3.14	0.0000
AAEL008751		glucosyl/glucuronosyl transferases	1.69	8.59	3.13	0.0000
AAEL014452		acyl-coa dehydrogenase	77.74	325.84	3.11	0.0000
AAEL009198		conserved hypothetical protein	8.73	36.54	3.10	0.0000
AAEL007542		glutamate decarboxylase	54.55	223.75	3.08	0.0000
AAEL003347		CRAL/TRIO domain-containing protein	29.09	122.69	3.07	0.0000
AAEL000816		carbonic anhydrase	9.54	39.44	3.05	0.0000
AAEL001367		type IV inositol 5-phosphatase	7.80	31.76	3.04	0.0000
AAEL013984		conserved hypothetical protein	13.90	58.44	3.01	0.0000
AAEL005482	CTL18	C-Type Lectin	16.49	72.13	2.98	0.0000
AAEL004739		acyl-coa dehydrogenase	144.48	575.11	2.95	0.0000
AAEL002416		short-chain dehydrogenase	26.49	105.26	2.95	0.0000
AAEL000086	CLIPB32	Clip-Domain Serine Protease family B.	0.56	2.87	2.93	0.0000
AAEL003194		xaa-pro aminopeptidase	13.07	50.63	2.92	0.0000
AAEL008767		serine protease	0.71	4.81	2.91	0.0006
AAEL017536	GRRP	holotricin glycine rich repeat protein	416.05	1693.83	2.90	0.0000
AAEL010602		starch branching enzyme ii	10.06	39.82	2.89	0.0000
AAEL007680		hypothetical protein	9.71	38.29	2.89	0.0000
AAEL012266	CYP4C38	cytochrome P450	8.51	33.24	2.87	0.0000
AAEL011408	CTL21	C-Type Lectin	15.90	61.71	2.85	0.0000
AAEL003209		lachesin	4.29	16.42	2.84	0.0000

Table A7 Continued

IDs	Gene name	Gene description	24h	48h	Fold	*p* adj.
AAEL014454		hypothetical protein	4.73	21.24	2.83	0.0000
AAEL017835			0.78	8.54	2.82	0.0015
AAEL007231	LRIM28	leucine-rich immune protein	0.74	3.39	2.82	0.0000
AAEL002046	CYP6CB1	cytochrome P450	9.57	36.02	2.81	0.0000
AAEL015524		3-hydroxyacyl-coa dehyrogenase	15.42	57.63	2.80	0.0000
AAEL002985		mitchondrial carnitine	1.51	6.33	2.78	0.0000
AAEL001031		conserved hypothetical protein	12.32	46.65	2.78	0.0000
AAEL009856		sodium/dicarboxylate cotransporter, putative	5.85	22.49	2.78	0.0000
AAEL001724	GPRNNB3	GPCR Orphan/Putative Class B Family	1.57	6.24	2.77	0.0000
AAEL002615		leucine-rich transmembrane protein	5.06	19.61	2.77	0.0000
AAEL007046		mitochondrial brown fat uncoupling protein	1.42	5.75	2.76	0.0000
AAEL003079		glucosyl/glucuronosyl transferases	2.89	11.45	2.75	0.0000
AAEL000316		hypothetical protein	18.44	71.30	2.74	0.0000
AAEL006890		conserved hypothetical protein	37.61	142.59	2.74	0.0000
AAEL011183		conserved hypothetical protein	6.28	23.27	2.72	0.0000
AAEL004361		alpha-glucosidase	4.37	15.88	2.70	0.0000
AAEL007748	SCRB10	Class B Scavenger Receptor	6.33	23.29	2.69	0.0000
AAEL009596		sterol o-acyltransferase	1.38	5.35	2.69	0.0000
AAEL000471		monocarboxylate transporter	4.70	16.69	2.66	0.0000
AAEL013515		pupal cuticle protein, putative	8.31	32.71	2.65	0.0000
AAEL009018		cytochrome P450	11.97	43.42	2.63	0.0000
AAEL012967		ced-6	5.29	18.92	2.63	0.0000
AAEL009542		hypothetical protein	1.60	6.16	2.62	0.0000
AAEL009630		cgmp-specific 3,5-cyclic phosphodiesterase	0.58	2.34	2.61	0.0000
AAEL012208		hypothetical protein	6.74	24.38	2.60	0.0000
AAEL006486		hypothetical protein	5.18	18.49	2.57	0.0000
AAEL002062	BETAFTZF1	Betha Ftz transcription factor isoform A	0.25	1.10	2.56	0.0004
AAEL014950	SPZ3B	spaetzle-like cytokine	1.26	5.48	2.56	0.0004
AAEL010932		RNAse h	13.86	48.30	2.55	0.0000
AAEL000650		conserved hypothetical protein	9.81	36.77	2.54	0.0000
AAEL012423		conserved hypothetical protein	62.56	213.97	2.52	0.0000
AAEL002296		trifunctional enzyme beta subunit	114.74	383.73	2.52	0.0000
AAEL012439		enoyl-CoA hydratase	20.17	67.49	2.51	0.0000
AAEL011857		serine/threonine-protein kinase rio1	3.78	13.07	2.51	0.0000
AAEL010481		sugar transporter	33.15	120.97	2.51	0.0000
AAEL008393		phosphatidylserine synthase	8.58	28.80	2.51	0.0000
AAEL005221		internalin A, putative	77.79	258.52	2.50	0.0000
AAEL002022		protein serine/threonine kinase, putative	1.07	4.22	2.49	0.0001
AAEL008632		ABC transporter	14.68	49.30	2.48	0.0000
AAEL007194		pupal cuticle protein, putative	1.38	6.20	2.47	0.0016
AAEL012037		sulphate transporter	1.74	5.98	2.47	0.0000
AAEL006307		acetyl-coa carboxylase	20.23	66.34	2.46	0.0000
AAEL012970		hypothetical protein	7.53	26.22	2.46	0.0000
AAEL001325		conserved hypothetical protein	25.64	84.55	2.45	0.0000
AAEL000519		hypothetical protein	2.13	7.81	2.45	0.0000
AAEL001485		conserved hypothetical protein	10.10	35.22	2.44	0.0000
AAEL003345		argininosuccinate lyase	173.49	630.51	2.43	0.0000
AAEL010868		sugar transporter	0.53	2.08	2.42	0.0006
AAEL001305		conserved hypothetical protein	3.80	13.69	2.41	0.0000
AAEL008006		3-hydroxyacyl-coa dehyrogenase	81.04	272.81	2.41	0.0000
AAEL007892		xaa-pro aminopeptidase	1.69	5.64	2.39	0.0000
AAEL001020		anterior fat body protein	27.50	88.23	2.39	0.0000
AAEL004450		cytochrome b5, putative	32.47	104.08	2.38	0.0000

Table A7 Continued

IDs	Gene name	Gene description	24h	48h	Fold	*p* adj.
AAEL003641		sodium/chloride dependent amino acid transporter	3.98	12.81	2.37	0.0000
AAEL007976		conserved hypothetical protein	0.53	1.91	2.36	0.0003
AAEL002672		matrix metalloproteinase	2.11	6.96	2.36	0.0000
AAEL014820		conserved hypothetical protein	3.09	10.84	2.36	0.0000
AAEL010146		3-hydroxyacyl-coa dehyrogenase	2.93	9.42	2.35	0.0000
AAEL002043	CYP305A5	cytochrome P450	1.59	5.31	2.34	0.0000
AAEL002610		serine protease	58.69	189.77	2.33	0.0000
AAEL016967			11.52	35.96	2.32	0.0000
AAEL009507		glucose-6-phosphate 1-dehydrogenase	11.92	36.77	2.32	0.0000
AAEL003497		farnesyl-pyrophosphate synthetase	48.44	148.88	2.31	0.0000
AAEL006248		p37NB protein, putative	5.30	16.84	2.31	0.0000
AAEL008222		lipase	1.27	18.70	2.30	0.0088
AAEL015370			0.59	2.02	2.30	0.0003
AAEL014553		triacylglycerol lipase, pancreatic	3.18	12.30	2.29	0.0037
AAEL014753		mitochondrial solute carrier protein, putative	69.16	209.80	2.29	0.0000
AAEL001047		adenylate cyclase	32.50	98.88	2.27	0.0000
AAEL002670		AMP dependent ligase	0.57	2.12	2.27	0.0022
AAEL007033		pyrroline-5-carboxylate reductase	20.62	64.49	2.27	0.0000
AAEL001835		sodium/solute symporter	1.85	6.08	2.27	0.0000
AAEL002857		conserved hypothetical protein	5.19	16.08	2.26	0.0000
AAEL012853		hypothetical protein	14.86	45.37	2.24	0.0000
AAEL003253	CLIPB13B	Clip-Domain Serine Protease family B.	1.00	3.61	2.22	0.0034
AAEL017309			2.79	8.75	2.22	0.0000
AAEL010893		carbonic anhydrase	2.58	8.01	2.21	0.0000
AAEL000902		sugar transporter	55.83	167.10	2.21	0.0000
AAEL003279		clip-domain serine protease, putative	8.52	25.88	2.20	0.0000
AAEL012562		circadian locomoter output cycles kaput protein	0.51	1.71	2.20	0.0013
AAEL000567		Facilitated trehalose transporter Tret1	65.88	190.85	2.19	0.0000
AAEL008936		hypothetical protein	9.39	27.77	2.19	0.0000
AAEL001490		acylphosphatase, putative	313.09	945.66	2.18	0.0000
AAEL011852		hypothetical protein	4.34	13.16	2.16	0.0000
AAEL000165		conserved hypothetical protein	14.89	43.37	2.16	0.0000
AAEL014248		hypothetical protein	8.43	23.90	2.15	0.0000
AAEL014852		hypothetical protein	18.21	52.73	2.14	0.0000
AAEL007526		flavoprotein-ubiquinone oxidoreductase	29.88	84.79	2.14	0.0000
AAEL008285		pupal cuticle protein, putative	5.72	16.85	2.14	0.0000
AAEL010094		cyclin b	1.18	3.81	2.13	0.0018
AAEL004860		acireductone dioxygenase	26.65	75.27	2.13	0.0000
AAEL017132	LYSC4	C-Type Lysozyme	54.82	162.16	2.13	0.0000
AAEL006605		juvenile hormone-inducible protein, putative	2.47	7.27	2.12	0.0000
AAEL005378		set domain protein	0.48	1.81	2.10	0.0206
AAEL000412		conserved hypothetical protein	8.11	22.74	2.10	0.0000
AAEL013877		Glucosamine-6-phosphate isomerase	11.14	31.24	2.09	0.0000
AAEL003483		conserved hypothetical protein	32.78	94.14	2.09	0.0000
AAEL008532			5.98	16.78	2.09	0.0000
AAEL013486		hypothetical protein	93.43	260.44	2.08	0.0000
AAEL006526		neurotransmitter gated ion channel	29.75	82.45	2.08	0.0000
AAEL012567		synaptic vesicle protein	0.50	1.63	2.08	0.0104
AAEL001818		conserved hypothetical protein	40.00	110.56	2.08	0.0000
AAEL008246		phospholipase c epsilon	1.47	4.76	2.07	0.0064
AAEL002283		hypothetical protein	175.92	501.11	2.07	0.0000
AAEL011720		hypothetical protein	4.42	12.97	2.06	0.0001

Table A7 Continued

IDs	Gene name	Gene description	24h	48h	Fold	*p* adj.
AAEL000395	USP	Ultra spiracleisoform A nuclear receptor	14.94	40.66	2.05	0.0000
AAEL003627		sodium/chloride dependent amino acid transporter	1.27	3.62	2.05	0.0000
AAEL010527		endo beta n-acetylglucosaminidase	1.43	4.02	2.05	0.0000
AAEL011323	HNF4	Hepatocyte nuclear factor 4 receptor	36.90	99.90	2.04	0.0000
AAEL013355		hypothetical protein	4.97	13.86	2.04	0.0000
AAEL003482		hypothetical protein	10.16	28.52	2.03	0.0000
AAEL010474		conserved hypothetical protein	6.86	19.08	2.03	0.0000
AAEL003819		conserved hypothetical protein	25.53	69.22	2.03	0.0000
AAEL003243	CLIPB13A	Clip-Domain Serine Protease family B.	13.89	39.73	2.02	0.0002
AAEL014909		conserved hypothetical protein	0.76	2.33	2.02	0.0069
AAEL000059	CLIPB19	Clip-Domain Serine Protease	3.51	10.52	2.02	0.0033
AAEL004547		conserved hypothetical protein	71.65	206.06	2.02	0.0005
AAEL012821		ced-6	4.56	12.48	2.01	0.0000
AAEL003457		conserved hypothetical protein	29.67	81.98	2.01	0.0000
AAEL005093	CLIPB46	Clip-Domain Serine Protease family B.	10.90	31.79	2.00	0.0016
AAEL012534		hypothetical protein	9.98	27.92	2.00	0.0000
AAEL003123		deoxyribonuclease I, putative	72.84	205.28	2.00	0.0002
AAEL011686		starch branching enzyme ii	12.50	34.97	2.00	0.0001
		Down regulated				
AAEL013577		conserved hypothetical protein	22.63	0.29	-41.34	0.0000
AAEL001307		SEC14, putative	289.45	7.59	-39.17	0.0000
AAEL001690		serine-type enodpeptidase,	155.07	2.77	-36.94	0.0000
AAEL007599		cathepsin b	3751.47	125.12	-33.13	0.0000
AAEL007686		conserved hypothetical protein	38.53	1.01	-32.21	0.0000
AAEL006542		retinoid-inducible serine carboxypeptidase	537.32	16.73	-28.35	0.0000
AAEL013118		conserved hypothetical protein	62.45	1.70	-25.09	0.0000
AAEL013127		conserved hypothetical protein	29.75	0.67	-23.28	0.0000
AAEL010429		conserved hypothetical protein	21.18	0.73	-20.17	0.0000
AAEL009588		expressed protein	29.72	1.54	-19.13	0.0000
AAEL006126		conserved hypothetical protein	2534.78	140.51	-18.27	0.0000
AAEL017451			204.99	12.78	-16.74	0.0000
AAEL001806		conserved hypothetical protein	46.38	3.15	-15.97	0.0000
AAEL010435		conserved hypothetical protein	18.16	0.86	-15.06	0.0000
AAEL004870	CYP18A1	cytochrome P450	11.72	0.59	-14.92	0.0000
AAEL001793		conserved hypothetical protein	34.38	2.17	-14.84	0.0000
AAEL013584		conserved hypothetical protein	17.55	0.88	-14.01	0.0000
AAEL006581		juvenile hormone-inducible protein, putative	88.90	7.02	-13.66	0.0000
AAEL010946	CYP314A1	cytochrome P450	15.86	0.89	-13.39	0.0000
AAEL013757		hexamerin 2 beta	7.97	0.43	-13.35	0.0000
AAEL005200			21.01	1.54	-13.12	0.0000
AAEL007226		nidogen	16.21	1.34	-13.12	0.0000
AAEL010280		conserved hypothetical protein	21.79	1.53	-12.44	0.0000
AAEL013492	PPO5	prophenoloxidase	94.49	6.16	-11.42	0.0000
AAEL013857		conserved hypothetical protein	565.90	54.71	-11.24	0.0000
AAEL009945		conserved hypothetical protein	7.63	0.44	-10.78	0.0000
AAEL011520		sucrose transport protein	16.92	1.40	-10.48	0.0000
AAEL009636		conserved hypothetical protein	167.96	18.17	-10.29	0.0000
AAEL006156		hypothetical protein	66.29	9.16	-8.97	0.0000
AAEL002404		receptor protein tyrosine kinase	129.69	12.98	-8.96	0.0000
AAEL012737		conserved hypothetical protein	1.83	0.02	-8.82	0.0000
AAEL012855		hypothetical protein	52.73	4.35	-8.67	0.0000
AAEL015312		cathepsin b	2449.69	349.89	-8.58	0.0000
AAEL000006		phosphoenolpyruvate carboxykinase	296.10	36.61	-8.52	0.0000

Table A7 Continued

IDs	Gene name	Gene description	24h	48h	Fold	*p* adj.
AAEL007397	E75	Ecdysone-induced protein Nuclear receptor	34.22	5.11	-8.31	0.0000
AAEL007878		ornithine decarboxylase	14.83	1.38	-8.24	0.0000
AAEL007585		cathepsin b	837.61	124.10	-8.21	0.0000
AAEL001888		hypothetical protein	119.06	17.92	-8.17	0.0000
AAEL002815		conserved hypothetical protein	247.85	33.79	-8.17	0.0000
AAEL012216		cathepsin b	1518.33	223.72	-8.14	0.0000
AAEL013501	PPO4	prophenoloxidase	1.86	0.13	-8.03	0.0000
AAEL000670		methionine sulfoxide reductase	571.78	82.09	-8.01	0.0000
AAEL005800	CLIPE11	Clip-Domain Serine Protease family E. Protease	13.37	1.49	-7.75	0.0000
AAEL004969		conserved hypothetical protein	24.89	3.38	-7.58	0.0000
AAEL014412	CYP304B2	cytochrome P450	157.34	21.28	-7.51	0.0000
AAEL009045		amine oxidase	3.18	0.33	-7.29	0.0000
AAEL000080		phosphoenolpyruvate carboxykinase	335.12	54.43	-7.19	0.0000
AAEL009166		conserved hypothetical protein	2.94	0.06	-7.17	0.0000
AAEL011763	PPO3	prophenoloxidase	13.06	1.99	-7.16	0.0000
AAEL009955		conserved hypothetical protein	606.27	83.94	-7.07	0.0000
AAEL006563		Vitellogenic carboxypeptidase Precursor	6476.46	1114.62	-6.74	0.0000
AAEL005336		d-3-phosphoglycerate dehydrogenase	160.88	29.10	-6.68	0.0000
AAEL006877		prophenoloxidase	1.82	0.19	-6.66	0.0000
AAEL015357		conserved hypothetical protein	2.22	0.10	-6.65	0.0000
AAEL002482		hypothetical protein	71.83	11.23	-6.62	0.0000
AAEL013294		Tetratricopeptide repeat protein 30 homolog	4.55	0.68	-6.42	0.0000
AAEL008471		hypothetical protein	8.19	1.44	-6.39	0.0000
AAEL002467		conserved hypothetical protein	20.56	2.12	-6.32	0.0000
AAEL012856		hypothetical protein	154.34	28.64	-6.02	0.0000
AAEL000025		phosphoenolpyruvate carboxykinase	8.84	1.54	-5.95	0.0000
AAEL005807		conserved hypothetical protein	6.87	0.27	-5.93	0.0000
AAEL015606		hypothetical protein	26.08	4.75	-5.91	0.0000
AAEL009935		conserved hypothetical protein	3.95	0.48	-5.59	0.0000
AAEL001100		phosphoserine phosphatase	369.95	80.34	-5.57	0.0000
AAEL007795	CYP4D37	cytochrome P450	3.61	0.62	-5.54	0.0000
AAEL008620		D7 protein, putative	132.64	27.61	-5.49	0.0000
AAEL005770	OBP21	odorant binding protein OBP21	29.39	6.14	-5.45	0.0000
AAEL010938		l-asparaginase	3.51	0.55	-5.34	0.0000
AAEL008663		aldo-keto reductase	11.72	2.53	-5.08	0.0000
AAEL002830		conserved hypothetical protein	4.83	0.89	-5.01	0.0000
AAEL009938		conserved hypothetical protein	2.50	0.19	-4.98	0.0000
AAEL010276		aminomethyltransferase	46.05	10.32	-4.94	0.0000
AAEL005429		2-oxoglutarate dehydrogenase	6.64	1.59	-4.89	0.0000
AAEL003294		fibrinogen and fibronectin	15.97	3.96	-4.83	0.0000
AAEL009875		alanine aminotransferase	180.09	45.83	-4.79	0.0000
AAEL002937		hypothetical protein	4.68	0.99	-4.78	0.0000
AAEL014734		hypothetical protein	16.64	4.15	-4.64	0.0000
AAEL012693		tripartite motif protein	15.83	3.72	-4.60	0.0000
AAEL003581		amidophosphoribosyltransferase	59.30	14.72	-4.60	0.0000
AAEL005763		lysosomal alpha-mannosidase	97.60	27.30	-4.56	0.0000
AAEL012041		sulphate transporter	10.28	2.76	-4.56	0.0000
AAEL014426		glycine dehydrogenase	8.75	1.91	-4.51	0.0000
AAEL013717		sphingomyelin phosphodiesterase	63.55	16.61	-4.50	0.0000
AAEL012538	LRIM6	leucine-rich immune protein	14.00	3.23	-4.49	0.0000
AAEL001707		2-oxoglutarate dioxygenase	12.74	3.20	-4.45	0.0000
AAEL002390		zinc finger protein	6.30	1.67	-4.44	0.0000
AAEL004342	OBP18	odorant binding protein OBP18	201.90	50.66	-4.40	0.0000

Table A7 Continued

IDs	Gene name	Gene description	24h	48h	Fold	*p* adj.
AAEL013498	PPO1	prophenoloxidase	3.43	0.82	-4.40	0.0000
AAEL010442		4-hydroxyphenylpyruvate dioxygenase	16.98	4.70	-4.39	0.0000
AAEL010204		dihydropyrimidine dehydrogenase	26.93	7.54	-4.38	0.0000
AAEL007315		symbol, putative	29.38	8.02	-4.38	0.0000
AAEL014199		dihydropyrimidine dehydrogenase	18.16	5.15	-4.28	0.0000
AAEL012555		maltose phosphorylase	5.72	1.49	-4.27	0.0000
AAEL011756		aldehyde dehydrogenase	61.68	17.33	-4.27	0.0000
AAEL001059	GSTD3	glutathione transferase	3.09	0.47	-4.19	0.0000
AAEL014541		maltose phosphorylase	6.62	1.71	-4.17	0.0000
AAEL001674		serine-type enodpeptidase,	40.70	0.94	-4.16	0.0000
AAEL011515		hypothetical protein	3.57	0.37	-4.08	0.0000
AAEL004343	OBP19	odorant binding protein OBP19	30.02	8.20	-4.05	0.0000
AAEL014797		acyl-coa dehydrogenase	13.98	4.29	-4.02	0.0000
AAEL003899		sugar transporter	28.56	8.70	-3.98	0.0000
AAEL017121			181.37	58.99	-3.95	0.0000
AAEL007555		acyl-coa dehydrogenase	65.76	21.23	-3.94	0.0000
AAEL011901		1-acyl-sn-glycerol-3-phosphate acyltransferase	47.41	14.76	-3.92	0.0000
AAEL009527		conserved hypothetical protein	11.09	3.20	-3.86	0.0000
AAEL014600		4-hydroxyphenylpyruvate dioxygenase	98.90	31.61	-3.86	0.0000
AAEL013364		hypothetical protein	82.29	26.92	-3.82	0.0000
AAEL013245	CLIPB28	Clip-Domain Serine Protease family B.	3.97	0.78	-3.80	0.0000
AAEL017388			158.39	51.27	-3.80	0.0000
AAEL003443		threonine dehydrogenase	14.53	4.69	-3.79	0.0000
AAEL008635		ABC transporter	82.64	25.90	-3.79	0.0000
AAEL013637		homogentisate 1,2-dioxygenase	190.73	63.26	-3.75	0.0000
AAEL003651		conserved hypothetical protein	13.36	4.53	-3.73	0.0000
AAEL009766		lipoamide acyltransferase	16.44	5.33	-3.71	0.0000
AAEL014014		ornithine cyclodeaminase	2.78	0.69	-3.70	0.0000
AAEL012825		bifunctional purine biosynthesis protein	61.82	21.25	-3.67	0.0000
AAEL009214		diazepam binding inhibitor, putative	319.71	107.36	-3.65	0.0000
AAEL012287		sugar transporter	4.18	1.32	-3.65	0.0000
AAEL005792	CLIPE8	Clip-Domain Serine Protease family E. Protease	8.40	1.75	-3.64	0.0000
AAEL006381		sphingomyelin phosphodiesterase	2.76	0.73	-3.63	0.0000
AAEL013490		conserved hypothetical protein	74.37	25.84	-3.62	0.0000
AAEL014664		AMP dependent coa ligase	6.72	2.18	-3.61	0.0000
AAEL005384		phosphoribosylformylglycinamidine synthase putative	30.07	9.34	-3.61	0.0000
AAEL005188		acetylgalactosaminidase	1.32	0.19	-3.59	0.0000
AAEL008889	CYP6AL1	cytochrome P450	8.25	2.64	-3.58	0.0000
AAEL004313		fk506-binding protein	125.54	41.60	-3.57	0.0000
AAEL015631		asparagine synthetase	7.04	2.15	-3.56	0.0000
AAEL007557		asparagine synthetase	7.10	2.14	-3.54	0.0000
AAEL002964		brain chitinase and chia	26.44	9.36	-3.53	0.0000
AAEL006085		methylenetetrahydrofolate dehydrogenase	58.67	20.06	-3.53	0.0000
AAEL005416		oxidase/peroxidase	1167.31	402.08	-3.51	0.0000
AAEL010032		translocon-associated protein	116.42	41.72	-3.47	0.0000
AAEL007432		serine collagenase 1 precursor, putative	1001.81	43.04	-3.46	0.0001
AAEL001511		conserved hypothetical protein	89.50	31.30	-3.44	0.0000
AAEL000824		hypothetical protein	31.55	11.93	-3.39	0.0000
AAEL013644		ubiquitously transcribed sex	5.98	2.16	-3.38	0.0000
AAEL003626		sodium/chloride dependent amino acid transporter	23.87	8.60	-3.38	0.0000

Table A7 Continued

IDs	Gene name	Gene description	24h	48h	Fold	*p* adj.
AAEL004941	CYP6AK1	cytochrome P450	15.13	5.23	-3.33	0.0000
AAEL013642		acyl-CoA dehydrogenase	10.18	3.71	-3.32	0.0000
AAEL002413		sphingomyelin phosphodiesterase	7.46	2.18	-3.29	0.0000
AAEL013904		3-hydroxyisobutyrate dehydrogenase	23.20	8.91	-3.27	0.0000
AAEL014110		sulfite reductase	3.62	1.23	-3.26	0.0000
AAEL006280		juvenile hormone acid methyltransferase, putative	2.08	0.55	-3.25	0.0000
AAEL001134		methylmalonate-semialdehyde dehydrogenase	139.44	55.28	-3.24	0.0000
AAEL000223		alpha-glucosidase	14.15	4.46	-3.23	0.0000
AAEL001708		hypothetical protein	10.33	3.57	-3.23	0.0000
AAEL002185		cuticle protein, putative	419.66	158.32	-3.21	0.0000
AAEL010936		gamma glutamyl transpeptidases	6.35	2.16	-3.21	0.0000
AAEL012417		conserved hypothetical protein	20.66	7.92	-3.19	0.0000
AAEL004523		preprotein translocase secy subunit	115.88	44.58	-3.19	0.0000
AAEL005762		leucine-rich transmembrane proteins	3.27	1.23	-3.15	0.0000
AAEL008629		ABC transporter	28.15	11.32	-3.14	0.0000
AAEL014599		hypothetical protein	20.86	8.08	-3.13	0.0000
AAEL011676		AMP dependent coa ligase	3.22	1.22	-3.13	0.0000
AAEL000364		glycine cleavage system h protein	19.53	6.39	-3.11	0.0000
AAEL000741		ecdysone-induced protein 74EF	11.82	4.72	-3.10	0.0000
AAEL001414	LRIM9	leucine-rich immune protein	548.62	212.75	-3.09	0.0000
AAEL006543		conserved hypothetical protein	55.13	23.02	-3.07	0.0000
AAEL002959		brain chitinase and chia	5.27	1.99	-3.07	0.0000
AAEL014206		sugar transporter	8.89	3.51	-3.06	0.0000
AAEL007179		conserved hypothetical protein	49.19	20.25	-3.04	0.0000
AAEL012144	CYP303A1	cytochrome P450	1.29	0.34	-3.04	0.0001
AAEL000897		conserved hypothetical protein	21.50	8.91	-3.04	0.0000
AAEL006168	CLIPB42	Clip-Domain Serine Protease family B.	30.49	12.38	-3.01	0.0000
AAEL003618		sodium/chloride dependent aa transporter	5.61	2.21	-3.01	0.0000
AAEL013884		synaptic vesicle protein	11.67	4.92	-3.01	0.0000
AAEL011463		cytochrome P450	1.41	0.46	-3.01	0.0000
AAEL003285		translocation associated membrane protein	113.18	47.26	-3.00	0.0000
AAEL006823		AMP dependent ligase	19.94	8.15	-2.99	0.0000
AAEL007441		translocon-associated protein, gamma subunit	126.33	52.55	-2.98	0.0000
AAEL003606		purine biosynthesis protein 6, pur6	149.33	61.06	-2.97	0.0000
AAEL004672		conserved hypothetical protein	5.53	1.67	-2.96	0.0001
AAEL008097		trypsin-eta, putative	40.39	17.03	-2.95	0.0000
AAEL000859		hypothetical protein	11.57	4.83	-2.95	0.0000
AAEL013320		translocon-associated protein, delta subunit	95.98	40.95	-2.94	0.0000
AAEL006334		sulfotransferase	2.51	0.83	-2.92	0.0000
AAEL014936		sarcosine dehydrogenase	3.45	1.35	-2.92	0.0000
AAEL005199		hypothetical protein	22.25	8.23	-2.91	0.0000
AAEL003655		conserved hypothetical protein	3.87	1.61	-2.90	0.0000
AAEL004220		hypothetical protein	133.78	58.84	-2.90	0.0000
AAEL013612		conserved hypothetical protein	212.04	93.98	-2.89	0.0000
AAEL004884		hemomucin	8.43	3.53	-2.89	0.0000
AAEL009792	LRIM25	leucine-rich immune protein	8.26	3.40	-2.89	0.0000
AAEL013944		hypothetical protein	7.53	2.98	-2.89	0.0000
AAEL007905		hypothetical protein	158.23	68.62	-2.88	0.0000
AAEL003890		cytochrome P450	1.13	0.34	-2.88	0.0002
AAEL012783		protease m1 zinc metalloprotease	19.77	8.41	-2.87	0.0000
AAEL007909		branched-chain amino acid aminotransferase	69.37	30.23	-2.86	0.0000
AAEL002269		purine nucleoside phosphorylase	322.45	138.00	-2.86	0.0000
AAEL004728		homocysteine methyltransferase	141.23	58.29	-2.85	0.0000

Table A7 Continued

IDs	Gene name	Gene description	24h	48h	Fold	*p* adj.
AAEL006752		Misexpression suppressor of ras, putative	24.45	11.00	-2.85	0.0000
AAEL009904		conserved hypothetical protein	307.15	136.96	-2.84	0.0000
AAEL005178			16.06	5.97	-2.83	0.0000
AAEL000786		hypothetical protein	62.97	27.06	-2.83	0.0000
AAEL000834		dimethylaniline monooxygenase	191.15	84.23	-2.83	0.0000
AAEL001512		hypothetical protein	13.26	4.59	-2.83	0.0000
AAEL004230		hypothetical protein	53.72	24.40	-2.83	0.0000
AAEL005852		oxysterol-binding protein 1,	95.26	43.47	-2.82	0.0000
AAEL006883		conserved hypothetical protein	57.68	26.00	-2.82	0.0000
AAEL008310		hypothetical protein	179.79	79.70	-2.81	0.0000
AAEL005335		conserved hypothetical protein	1.53	0.54	-2.81	0.0000
AAEL008283		conserved hypothetical protein	6.26	2.57	-2.80	0.0000
AAEL000820		dimethylaniline monooxygenase	5.75	2.23	-2.80	0.0000
AAEL003150		alpha-n-acetylglucosaminidase	9.78	4.25	-2.80	0.0000
AAEL001857		conserved hypothetical protein	56.51	25.70	-2.80	0.0000
AAEL000556	CTL25	C-Type Lectin	69.40	27.71	-2.80	0.0000
AAEL014537		maltose phosphorylase	1.33	0.41	-2.79	0.0003
AAEL002255		conserved hypothetical protein	8.98	3.79	-2.77	0.0000
AAEL007887		ornithine decarboxylase	3.01	0.80	-2.76	0.0009
AAEL012183		mfs transporter	2.57	0.99	-2.76	0.0000
AAEL001767		conserved hypothetical protein	19.05	8.51	-2.75	0.0000
AAEL008781		serine-type enodpeptidase,	19.50	7.26	-2.74	0.0000
AAEL000641		protein disulfide isomerase	289.70	132.11	-2.74	0.0000
AAEL010398		hypothetical protein	22.44	9.15	-2.73	0.0000
AAEL010265		hypothetical protein	4.95	1.87	-2.73	0.0000
AAEL013363		ubiquitously transcribed sex	5.59	2.59	-2.72	0.0000
AAEL004335		secreted ferritin G subunit precursor, putative	12.47	5.44	-2.72	0.0000
AAEL003903		acid phosphatase-1	37.28	17.30	-2.72	0.0000
AAEL011764	PPO10	prophenoloxidase	2.06	0.84	-2.71	0.0000
AAEL012505		hypothetical protein	1.94	0.87	-2.70	0.0000
AAEL000298		sodium/chloride dependent aa transporter	3.39	1.18	-2.70	0.0003
AAEL001703		serine-type enodpeptidase,	25.66	9.36	-2.69	0.0002
AAEL001293		conserved hypothetical protein	81.23	37.95	-2.67	0.0000
AAEL000229		Prosialokinin Precursor	152.04	69.61	-2.67	0.0000
AAEL010028		sarcosine dehydrogenase	34.85	15.29	-2.67	0.0000
AAEL014252		sulfite reductase	1.99	0.83	-2.66	0.0000
AAEL007955	GSTE8	glutathione transferase	8.83	3.38	-2.65	0.0001
AAEL017154			7.05	2.40	-2.64	0.0005
AAEL012764		conserved hypothetical protein	209.75	96.17	-2.64	0.0000
AAEL005702		conserved hypothetical protein	7.09	2.13	-2.64	0.0014
AAEL015049		60S ribosomal protein L35	1.94	0.60	-2.63	0.0012
AAEL017098			92.44	44.94	-2.62	0.0000
AAEL000726		fibrinogen and fibronectin	39.43	18.14	-2.59	0.0000
AAEL013223		hypothetical protein	8.25	3.34	-2.59	0.0001
AAEL005327		hypothetical protein	4.21	1.80	-2.58	0.0000
AAEL003057		allergen, putative	13.86	6.26	-2.58	0.0000
AAEL013945		conserved hypothetical protein	12.61	5.95	-2.56	0.0000
AAEL007420	SRPN25	Serine Protease Inhibitor	13.88	6.01	-2.56	0.0000
AAEL012684		conserved hypothetical protein	234.83	116.06	-2.54	0.0000
AAEL015483		hypothetical protein	11.01	5.19	-2.54	0.0000
AAEL004451		organic cation transporter	33.18	16.70	-2.53	0.0000
AAEL007057		retinoid-inducible serine carboxypeptidase	4.65	1.99	-2.52	0.0001
AAEL013989		protein translocation complex beta subunit	102.67	50.08	-2.52	0.0000
AAEL001402	LRIM10B	leucine-rich immune protein	175.48	84.46	-2.52	0.0000

Table A7 Continued

IDs	Gene name	Gene description	24h	48h	Fold	*p* adj.
AAEL013946		conserved hypothetical protein	6.44	2.34	-2.51	0.0012
AAEL014663		AMP dependent coa ligase	3.55	1.57	-2.51	0.0000
AAEL008478		conserved hypothetical protein	69.09	34.52	-2.50	0.0000
AAEL001432		protein disulfide isomerase	144.61	73.69	-2.50	0.0000
AAEL004665		conserved hypothetical protein	8.97	4.21	-2.48	0.0000
AAEL002130		ecdysone inducible protein L2, putative	82.84	42.03	-2.47	0.0000
AAEL007374		yellow protein precursor, putative	112.31	57.03	-2.47	0.0000
AAEL008646		fibrinogen and fibronectin	18.92	9.12	-2.47	0.0000
AAEL000402		conserved hypothetical protein	1.31	0.48	-2.46	0.0018
AAEL005179		hypothetical protein	100.55	51.64	-2.46	0.0000
AAEL017268			22.99	11.61	-2.46	0.0000
AAEL003715		hypothetical protein	3.85	1.50	-2.45	0.0013
AAEL007271		basic helix-loop-helix zip transcription factor	3.47	1.73	-2.44	0.0000
AAEL012318		2-amino-3-ketobutyrate coenzyme a ligase	8.32	4.23	-2.44	0.0000
AAEL015655	CYP302A1	cytochrome P450	1.99	0.86	-2.43	0.0004
AAEL012054		quiescin-sulphydryl oxidase4, putative	89.99	46.21	-2.42	0.0000
AAEL011008		lipase	1.53	0.61	-2.41	0.0014
AAEL003066		brain chitinase and chia	11.58	1.63	-2.41	0.0094
AAEL003699		conserved hypothetical protein	4.79	2.35	-2.40	0.0000
AAEL012415		hypothetical protein	8.21	3.11	-2.40	0.0029
AAEL007993	CLIPB27	Clip-Domain Serine Protease family B.	3.92	1.36	-2.40	0.0051
AAEL000745		hypothetical protein	43.20	22.47	-2.39	0.0000
AAEL006617		conserved hypothetical protein	6.24	3.08	-2.39	0.0000
AAEL003098		glucosyl/glucuronosyl transferases	1.31	0.59	-2.39	0.0003
AAEL001766		leucine-rich transmembrane proteins	25.39	13.68	-2.38	0.0000
AAEL010630		xanthine dehydrogenase	1.94	1.00	-2.38	0.0000
AAEL011633		fibrinogen and fibronectin	1.48	0.60	-2.37	0.0029
AAEL011338		conserved hypothetical protein	13.00	6.87	-2.36	0.0000
AAEL006138		hypothetical protein	10990.58	537.71	-2.36	0.0097
AAEL000618		wingless protein, putative	2.47	1.18	-2.35	0.0002
AAEL006577		aspartyl-tRNA synthetase	46.20	24.81	-2.35	0.0000
AAEL006351		conserved hypothetical protein	13.09	6.20	-2.34	0.0003
AAEL012447		elastase, putative	20.52	10.78	-2.33	0.0000
AAEL010434		Vitellogenin-A1 Precursor	8569.64	867.94	-2.33	0.0123
AAEL006701		conserved hypothetical protein	8.33	4.39	-2.33	0.0000
AAEL014365		chromaffin granule amine transporter, putative	30.21	15.84	-2.32	0.0000
AAEL000749		conserved hypothetical protein	29.06	15.46	-2.32	0.0000
AAEL010782		carboxypeptidase	29.22	13.34	-2.32	0.0011
AAEL007136		sugar transporter	30.52	16.39	-2.32	0.0000
AAEL010776		carboxypeptidase	2.94	1.27	-2.32	0.0025
AAEL009909		cln3/battenin	10.95	6.02	-2.32	0.0000
AAEL000101		AMP dependent coa ligase	8.34	4.38	-2.31	0.0000
AAEL010223		phosphatidylserine decarboxylase	46.04	25.02	-2.31	0.0000
AAEL001829		beta nu integrin subunit	1.70	0.79	-2.31	0.0007
AAEL000124		conserved hypothetical protein	7.28	2.70	-2.31	0.0076
AAEL000340		cytochrome P450	5.19	2.62	-2.31	0.0000
AAEL010943		conserved hypothetical protein	13.27	7.31	-2.31	0.0000
AAEL008367		fk506-binding protein	34.68	19.19	-2.29	0.0000
AAEL017484	CTLGA4	C-Type Lectin	29.80	15.47	-2.29	0.0000
AAEL008598		conserved hypothetical protein	1.83	0.94	-2.28	0.0000
AAEL010396		secreted ferritin G subunit precursor, putative	4.64	1.42	-2.28	0.0142
AAEL017444			37.18	14.52	-2.28	0.0080

Table A7 Continued

IDs	Gene name	Gene description	24h	48h	Fold	*p* adj.
AAEL004743		multidrug resistance protein 2	10.65	5.85	-2.27	0.0000
AAEL001225		glycoside hydrolases	1.48	0.65	-2.27	0.0038
AAEL009474	PGRPS1	Peptidoglycan Recognition Protein	11.99	5.40	-2.26	0.0035
AAEL014754		conserved hypothetical protein	6.87	3.69	-2.26	0.0000
AAEL007967		conserved hypothetical protein	18.58	10.64	-2.25	0.0000
AAEL001158		fructose-1,6-bisphosphatase	46.77	25.00	-2.25	0.0000
AAEL000797		dimethylaniline monooxygenase	2.43	1.27	-2.25	0.0000
AAEL015654	CYP6AG8	cytochrome P450	1.28	0.58	-2.25	0.0042
AAEL001420	LRIM8	leucine-rich immune protein	327.06	173.98	-2.25	0.0000
AAEL002804		oligosaccharyl transferase	46.29	26.28	-2.24	0.0000
AAEL005772	OBP22	odorant binding protein OBP22	1262.40	715.63	-2.24	0.0000
AAEL015051		glycoside hydrolases	2.44	1.25	-2.23	0.0003
AAEL004995		caspase-activated nuclease, putative	17.94	10.18	-2.23	0.0000
AAEL008963		tyrosine aminotransferase	323.27	185.78	-2.23	0.0000
AAEL014658		caspase-1	3.36	1.73	-2.23	0.0002
AAEL009543		conserved hypothetical protein	10.89	5.46	-2.23	0.0007
AAEL011962		conserved hypothetical protein	23.09	13.37	-2.22	0.0000
AAEL008468		cysteine synthase	5.96	3.30	-2.22	0.0000
AAEL008878		diacylglycerol o-acyltransferase	4.31	2.40	-2.20	0.0000
AAEL008307		conserved hypothetical protein	7.14	3.97	-2.20	0.0000
AAEL005296		conserved hypothetical protein	1.05	0.46	-2.19	0.0084
AAEL012128		cationic amino acid transporter	44.49	25.73	-2.19	0.0000
AAEL010685		conserved hypothetical protein	7.93	4.44	-2.19	0.0000
AAEL007401		roundabout, putative	1.04	0.47	-2.19	0.0069
AAEL012395		ATP-binding cassette transporter	4.49	2.58	-2.19	0.0000
AAEL014298		ORF-A short, putative	5.62	3.05	-2.19	0.0001
AAEL001627		udp-n-acteylglucosamine pyrophosphorylase	10.23	5.83	-2.18	0.0000
AAEL001107		hypothetical protein	365.74	214.60	-2.17	0.0000
AAEL011519		sucrose transport protein	4.04	2.16	-2.17	0.0004
AAEL003229		hypothetical protein	31.34	18.61	-2.17	0.0000
AAEL002261		GTP cyclohydrolase i	68.81	40.81	-2.17	0.0000
AAEL003049		pupal cuticle protein 78E, putative	2.79	1.50	-2.17	0.0001
AAEL017018			47.43	28.06	-2.16	0.0000
AAEL001401	LRIM10A	leucine-rich immune protein	208.96	120.39	-2.16	0.0000
AAEL000551		hypothetical protein	63.15	36.01	-2.16	0.0000
AAEL012444		organic cation transporter	14.32	8.44	-2.16	0.0000
AAEL014551		triacylglycerol lipase, pancreatic	59.33	34.02	-2.16	0.0000
AAEL002010		conserved hypothetical protein	17.55	10.27	-2.15	0.0000
AAEL006274		glucose transporter	43.16	25.12	-2.14	0.0000
AAEL005008		aquaporin	64.80	38.77	-2.14	0.0000
AAEL011137		succinyl-coa:3-ketoacid-coenzyme a transferase	70.41	42.20	-2.13	0.0000
AAEL008479		hypothetical protein	10.60	6.07	-2.13	0.0000
AAEL002174		dolichyl-diphosphooligosaccharide protein glycosyltransferase	44.13	26.37	-2.13	0.0000
AAEL008395		hypothetical protein	12.84	7.57	-2.13	0.0000
AAEL007816	CYP4D23	cytochrome P450	15.79	9.32	-2.13	0.0000
AAEL000774		conserved hypothetical protein	26.18	14.87	-2.12	0.0001
AAEL002183		oligosaccharyl transferase, subunit, putative	106.11	64.46	-2.12	0.0000
AAEL016964			117.53	71.08	-2.12	0.0000
AAEL002412		monocarboxylate transporter	16.58	10.00	-2.11	0.0000
AAEL005749		lysosomal alpha-mannosidase	33.26	19.80	-2.11	0.0000
AAEL002683		aldehyde oxidase	13.66	8.04	-2.11	0.0000
AAEL005457		conserved hypothetical protein	83.95	51.29	-2.11	0.0000

Table A7 Continued

IDs	Gene name	Gene description	24h	48h	Fold	*p* adj.
AAEL009985		conserved hypothetical protein	400.16	239.29	-2.11	0.0000
AAEL008096		mitochondrial ornithine transporter	3.80	2.21	-2.11	0.0000
AAEL002816		conserved hypothetical protein	44.43	26.69	-2.10	0.0000
AAEL000610		hypothetical protein	7.00	3.79	-2.09	0.0017
AAEL005647		serine collagenase 1 precursor, putative	4.40	2.36	-2.09	0.0025
AAEL011802		allergen, putative	3.28	1.81	-2.09	0.0010
AAEL003005		hypothetical protein	19.80	12.23	-2.08	0.0000
AAEL004613		phenylalanyl-tRNA synthetase beta chain	45.72	28.30	-2.08	0.0000
AAEL015445		cysteine dioxygenase	2.51	1.39	-2.08	0.0008
AAEL009426		conserved hypothetical protein	19.88	12.13	-2.07	0.0000
AAEL012506		conserved hypothetical protein	1.35	0.63	-2.07	0.0188
AAEL009669		conserved hypothetical protein	7.04	3.78	-2.07	0.0051
AAEL006562		acid phosphatase	2.51	1.37	-2.06	0.0029
AAEL007872		hypothetical protein	9.86	5.78	-2.06	0.0002
AAEL005705		glucosaminephosphotransferase	24.71	14.86	-2.06	0.0000
AAEL002988		conserved hypothetical protein	72.55	44.51	-2.06	0.0000
AAEL008606		conserved hypothetical protein	1.94	0.89	-2.05	0.0220
AAEL007802		multicopper oxidase	2.18	1.31	-2.05	0.0000
AAEL000533	CTL16	C-Type Lectin	205.77	128.35	-2.05	0.0000
AAEL005900		UPF0443 protein AAEL005900	24.05	14.87	-2.04	0.0000
AAEL008279		conserved hypothetical protein	2.22	1.19	-2.04	0.0060
AAEL014279		glycosyltransferase	3.42	1.98	-2.04	0.0012
AAEL014455		hypothetical protein	7.64	4.58	-2.04	0.0002
AAEL012974		glycine cleavage system h protein	28.68	17.29	-2.04	0.0001
AAEL008450		conserved hypothetical protein	8.60	5.13	-2.03	0.0001
AAEL010490		hypothetical protein	2.89	1.43	-2.03	0.0173
AAEL008656		UDP-galactose transporter	38.55	24.07	-2.03	0.0000
AAEL010555		sterol regulatory element-binding protein	67.56	42.60	-2.03	0.0000
AAEL005268		hypothetical protein	4.71	2.78	-2.03	0.0004
AAEL014418		conserved hypothetical protein	1.87	0.93	-2.02	0.0210
AAEL013065		thiamin pyrophosphokinase	38.97	24.86	-2.02	0.0000
AAEL008259		conserved hypothetical protein	40.52	25.17	-2.02	0.0000
AAEL006362		mitochondrial solute carrier	38.99	24.68	-2.02	0.0000
AAEL017500			2.07	1.00	-2.01	0.0267
AAEL000021		conserved hypothetical protein	1.35	0.69	-2.01	0.0188
AAEL001392		hypothetical protein	27.00	2.49	-2.01	0.0426
AAEL009479		amino acid transporter	3.35	2.05	-2.01	0.0000
AAEL011989		signal peptide peptidase	44.59	28.25	-2.01	0.0000
AAEL004879		conserved hypothetical protein	33.98	21.34	-2.01	0.0000

Table A8. Genes differentially expressed in the HT of 48h and 72h blood fed females.

Gene ID	Gene Name	Wiki Description	48h	72h	Fold	*p* adj.
		Up regulated				
AAEL013584		hypothetical protein	0.82	43.56	31.46	0.0000
AAEL010435		hypothetical protein	0.84	46.61	31.22	0.0000
AAEL013338		lethal(2)essential for life protein, l2efl	0.62	21.05	18.79	0.0000
AAEL013577		hypothetical protein	0.28	10.13	18.56	0.0000
AAEL014561		hypothetical protein	0.00	8.55	14.40	0.0000
AAEL010097		hypothetical protein	0.40	7.51	13.40	0.0000
AAEL006280		juvenile hormone acid methyltransferase, putative	0.54	10.18	11.97	0.0000
AAEL007097		4-nitrophenylphosphatase	0.75	14.68	8.05	0.0000
AAEL000442		hypothetical protein	0.12	2.81	7.55	0.0000
AAEL006617		hypothetical protein	3.01	24.15	6.91	0.0000
AAEL015289		hypothetical protein	0.08	1.85	6.85	0.0000
AAEL011811		DNA replication licensing factor MCM3	0.08	1.32	6.45	0.0000
AAEL017022			21.12	149.74	6.39	0.0000
AAEL010128	LRIM4	hypothetical protein	1.05	8.30	6.14	0.0000
AAEL007555		acyl-coa dehydrogenase	20.72	124.32	5.47	0.0000
AAEL013127		hypothetical protein	0.66	6.38	5.38	0.0000
AAEL010280		hypothetical protein	1.49	9.43	5.35	0.0000
AAEL010640		phosphoribosylamine-glycine ligase	7.46	44.05	5.34	0.0000
AAEL003581		amidophosphoribosyltransferase	14.36	85.44	5.30	0.0000
AAEL004390	HPX8B	hypothetical protein	0.27	7.93	5.23	0.0001
AAEL014734		saccharopine dehydrogenase	4.05	22.78	4.98	0.0000
AAEL010276		aminomethyltransferase	10.07	53.07	4.72	0.0000
AAEL005429		2-oxoglutarate dehydrogenase	1.39	7.45	4.67	0.0000
AAEL005384		phosphoribosylformylglycinamidine synthase	9.12	58.11	4.65	0.0000
AAEL014426		glycine dehydrogenase	1.41	7.29	4.55	0.0000
AAEL009766		lipoamide acyltransferase	5.21	26.23	4.44	0.0000
AAEL000364		glycine cleavage system h protein	6.24	32.74	4.41	0.0000
AAEL000733		hydroxysteroid dehydrogenase	2.06	10.53	4.39	0.0000
AAEL013118		hypothetical protein	1.66	9.67	4.37	0.0000
AAEL003404		hypothetical protein	0.19	1.44	4.33	0.0001
AAEL003606		purine biosynthesis protein 6, pur6	46.85	221.63	4.26	0.0000
AAEL003352		ribosomal protein l7ae	20.95	98.24	4.24	0.0000
AAEL002652		hypothetical protein	0.22	1.35	4.00	0.0000
AAEL005940			0.14	1.16	3.97	0.0006
AAEL012825		bifunctional purine biosynthesis protein	20.74	88.58	3.91	0.0000
AAEL006562		acid phosphatase	1.06	4.80	3.62	0.0000
AAEL010248		fibrillarin	1.64	7.04	3.61	0.0000
AAEL000748		hypothetical protein	6.23	24.81	3.57	0.0000
AAEL006085		methylenetetrahydrofolate dehydrogenase	17.33	63.00	3.35	0.0000
AAEL003057		allergen, putative	6.11	23.78	3.34	0.0000
AAEL011756		aldehyde dehydrogenase	16.91	60.90	3.28	0.0000
AAEL003100		hypothetical protein	6.88	24.92	3.26	0.0000
AAEL007653		allantoinase	16.92	60.60	3.25	0.0000
AAEL008468		cysteine synthase	3.22	11.75	3.23	0.0000
AAEL007872		hypothetical protein	5.64	20.61	3.21	0.0000
AAEL010265		hypothetical protein	1.83	7.01	3.19	0.0000
AAEL002937		hypothetical protein	0.97	4.20	3.16	0.0006
AAEL001793		hypothetical protein	2.12	7.74	3.13	0.0000
AAEL005336		d-3-phosphoglycerate dehydrogenase	17.21	57.86	3.09	0.0000

Table A8 Continued

Gene ID	Gene Name	Wiki Description	48h	72h	Fold	*p* adj.
AAEL003726		hypothetical protein	0.82	3.04	3.07	0.0000
AAEL013642		acyl-coa dehydrogenase	1.78	6.03	2.98	0.0000
AAEL000765		hexamerin 2 beta	1.10	4.05	2.96	0.0002
AAEL002390		zinc finger protein	1.63	5.45	2.94	0.0000
AAEL000749		hypothetical protein	15.08	49.16	2.93	0.0000
AAEL011599		ADP-ribosylation factor, putative	0.39	1.66	2.92	0.0051
AAEL000774		hypothetical protein	14.51	46.43	2.92	0.0000
AAEL006887		mrna turnover protein 4 mrt4	6.98	22.66	2.91	0.0000
AAEL012851		wd-repeat protein	6.64	21.15	2.89	0.0000
AAEL005200		juvenile hormone esterase	1.26	4.35	2.87	0.0000
AAEL005327		hypothetical protein	1.27	4.30	2.84	0.0000
AAEL003313		alkaline phosphatase	0.57	2.13	2.80	0.0026
AAEL002810		DNA replication licensing factor MCM5	0.25	1.07	2.76	0.0122
AAEL001806		hypothetical protein	3.08	9.86	2.76	0.0000
AAEL008220		hypothetical protein	6.91	20.94	2.75	0.0000
AAEL005762		leucine-rich transmembrane proteins	0.93	3.00	2.75	0.0000
AAEL010139		serine protease, putative	21.94	66.29	2.74	0.0000
AAEL003514		centromere/microtubule binding protein cbf5	8.29	24.83	2.74	0.0000
AAEL013013		hypothetical protein	8.23	27.01	2.74	0.0001
AAEL002194		uricase	12.83	37.67	2.69	0.0000
AAEL001707		epsilon-trimethyllysine 2-oxoglutarate dioxygenase	3.12	9.25	2.68	0.0000
AAEL003664		lupus la ribonucleoprotein	10.58	30.87	2.67	0.0000
AAEL013703		trypsin	35.59	103.67	2.66	0.0000
AAEL003443		threonine dehydrogenase	4.58	13.72	2.66	0.0000
AAEL000229		hypothetical protein	50.59	147.63	2.64	0.0000
AAEL014526		sideroflexin 1,2,3	30.89	88.43	2.63	0.0000
AAEL010970		hypothetical protein	3.02	9.26	2.62	0.0001
AAEL008728		DEAD box ATP-dependent RNA helicase	2.03	6.01	2.62	0.0000
AAEL005220		60S ribosomal protein L30	1.87	6.30	2.62	0.0043
AAEL000797		dimethylaniline monooxygenase	1.24	4.03	2.62	0.0014
AAEL004455		hypothetical protein	7.35	21.14	2.61	0.0000
AAEL012185		ribosome biogenesis regulatory protein	6.88	19.78	2.60	0.0000
AAEL003584		hypothetical protein	2.08	6.05	2.60	0.0000
AAEL007989		hypothetical protein	1.08	3.16	2.59	0.0000
AAEL002269		purine nucleoside phosphorylase	134.67	378.98	2.59	0.0000
AAEL001134		methylmalonate-semialdehyde dehydrogenase	53.94	151.44	2.58	0.0000
AAEL008572		RNA-binding protein, putative	3.02	8.74	2.58	0.0000
AAEL000726		fibrinogen and fibronectin	17.70	61.38	2.58	0.0106
AAEL001887		glutamine synthetase	68.19	189.79	2.58	0.0000
AAEL009214		diazepam binding inhibitor, putative	104.77	292.89	2.57	0.0000
AAEL017018			27.38	75.74	2.55	0.0000
AAEL011610	CTLGA8	galactose-specific C-type lectin, putative	2.01	6.77	2.55	0.0101
AAEL015440		hypothetical protein	16.64	47.13	2.55	0.0000
AAEL012974		glycine cleavage system h protein	9.93	27.87	2.54	0.0000
AAEL005480		hairy protein	0.50	1.50	2.54	0.0007
AAEL009669		hypothetical protein	3.69	14.06	2.52	0.0360
AAEL003255		hypothetical protein	0.82	2.73	2.51	0.0134
AAEL003655		hypothetical protein	1.57	4.44	2.50	0.0000
AAEL002686		testisin precursor, putative	3.45	9.59	2.50	0.0000
AAEL007799		regulator of chromosome condensation	12.52	33.85	2.48	0.0000
AAEL008882		hypothetical protein	4.48	12.06	2.48	0.0000

Table A8 Continued

Gene ID	Gene Name	Wiki Description	48h	72h	Fold	*p* adj.
AAEL012265		transcription initiation factor RRN3	3.63	9.97	2.48	0.0000
AAEL005163		hypothetical protein	6.61	18.44	2.47	0.0000
AAEL009912		hypothetical protein	5.62	15.15	2.46	0.0000
AAEL012783		protease m1 zinc metalloprotease	8.18	21.78	2.45	0.0000
AAEL004466	LRIM23	hypothetical protein	1.29	4.13	2.45	0.0143
AAEL004343	OBP19	hypothetical protein	8.00	22.74	2.44	0.0005
AAEL010289		beta nu integrin subunit	0.38	1.27	2.44	0.0218
AAEL005604		trypsin-epsilon, putative	2.10	6.03	2.44	0.0009
AAEL009993		hypothetical protein	7.43	19.69	2.43	0.0000
AAEL011538		hypothetical protein	0.93	2.86	2.43	0.0100
AAEL017388			50.03	131.13	2.42	0.0000
AAEL004063		wd-repeat protein	6.10	16.27	2.41	0.0000
AAEL000551		hypothetical protein	35.13	91.49	2.40	0.0000
AAEL003235		hypothetical protein	17.57	46.66	2.39	0.0000
AAEL013532		hypothetical protein	12.31	32.41	2.39	0.0000
AAEL007802		multicopper oxidase	1.27	3.49	2.39	0.0002
AAEL009382		hypothetical protein	1.97	5.34	2.38	0.0001
AAEL008942		hypothetical protein	10.35	26.80	2.36	0.0000
AAEL003601		hypothetical protein	19.50	49.78	2.35	0.0000
AAEL007697		hypothetical protein	4.18	11.31	2.35	0.0007
AAEL003469		NHP2 protein, putative	11.40	29.16	2.34	0.0000
AAEL008124		RN methyltransferase	2.71	7.34	2.34	0.0006
AAEL003182	SRPN26	SERPIN1 protein precursor, putative	44.90	113.62	2.34	0.0000
AAEL017113			12.65	32.49	2.34	0.0000
AAEL017139			1.75	5.15	2.34	0.0154
AAEL004017		DNA polymerase v	4.92	12.50	2.33	0.0000
AAEL008310		hypothetical protein	77.75	198.17	2.33	0.0000
AAEL010228		hypothetical protein	146.12	367.35	2.33	0.0000
AAEL014234		hypothetical protein	8.08	20.83	2.33	0.0000
AAEL012100		hypothetical protein	6.15	15.79	2.32	0.0000
AAEL004667		hypothetical protein	5.20	13.62	2.32	0.0000
AAEL004031		hypothetical protein	0.50	1.52	2.31	0.0355
AAEL004997		U3 small nucleolar ribonucleoprotein protein imp4	6.35	16.21	2.31	0.0000
AAEL005008		aquaporin	37.83	94.25	2.31	0.0000
AAEL001656		sodium-dependent phosphate transporter	3.15	8.04	2.31	0.0000
AAEL001037		ribosomal RNA methyltransferase	7.54	18.81	2.30	0.0000
AAEL011693		mitotic control protein dis3	2.40	6.10	2.29	0.0000
AAEL011144		triacylglycerol lipase, pancreatic	0.95	2.63	2.29	0.0084
AAEL006417		D7 protein, putative	118.02	290.72	2.28	0.0000
AAEL009992		hypothetical protein	5.12	12.76	2.28	0.0000
AAEL002022		protein serine/threonine kinase, putative	4.12	10.97	2.27	0.0031
AAEL007302		hypothetical protein	0.78	2.12	2.27	0.0062
AAEL006483		hypothetical protein	68.59	170.32	2.27	0.0000
AAEL013075		hypothetical protein	8.81	22.22	2.27	0.0000
AAEL002683		aldehyde oxidase	6.92	17.14	2.27	0.0000
AAEL006581		Juvenile hormone-inducible protein, putative	6.85	16.97	2.26	0.0000
AAEL006347		apyrase, putative	76.05	185.92	2.25	0.0000
AAEL000786		hypothetical protein	26.40	64.55	2.25	0.0000
AAEL014937		hypothetical protein	15.51	39.08	2.24	0.0001
AAEL002709		spliceosomal protein sap	9.06	21.94	2.24	0.0000
AAEL003949		hypothetical protein	3.96	9.73	2.24	0.0000
AAEL001708		hypothetical protein	3.48	8.93	2.24	0.0015

Table A8 Continued

Gene ID	Gene Name	Wiki Description	48h	72h	Fold	*p* adj.
AAEL002963		hypothetical protein	22.25	53.47	2.23	0.0000
AAEL017421			20.15	48.35	2.22	0.0000
AAEL010827		programmed cell death protein 11	3.59	8.67	2.22	0.0000
AAEL008789		apolipophorin-III, putative	104.92	280.98	2.22	0.0142
AAEL010716		preprotein translocase secy subunit (sec61)	24.86	59.32	2.21	0.0000
AAEL012546		DNA replication licensing factor MCM6	0.86	2.22	2.21	0.0050
AAEL009309		lipid depleted protein	6.53	15.67	2.18	0.0000
AAEL013904		3-hydroxyisobutyrate dehydrogenase	43.14	102.06	2.18	0.0000
AAEL006549		hypothetical protein	3.11	7.54	2.18	0.0001
AAEL003303		hypothetical protein	6.99	16.94	2.18	0.0001
AAEL016968			2.37	5.75	2.18	0.0001
AAEL010485		sugar transporter	2.92	7.31	2.18	0.0016
AAEL003589		transcription factor, putative	52.70	123.74	2.17	0.0000
AAEL000674		RNA m5u methyltransferase	3.11	7.55	2.17	0.0001
AAEL003691		hypothetical protein	0.81	2.13	2.17	0.0193
AAEL018061			23.44	54.64	2.17	0.0000
AAEL010118		kelch repeat protein	5.81	13.83	2.17	0.0000
AAEL009662		hypothetical protein	2.32	5.44	2.15	0.0000
AAEL005672		adenosine deaminase	23.32	53.92	2.14	0.0000
AAEL008879		kynurenine 3-monooxygenase	2.42	5.85	2.14	0.0007
AAEL009084		slender lobes, putative	3.14	7.35	2.13	0.0000
AAEL004523		preprotein translocase secy subunit (sec61)	43.49	99.86	2.13	0.0000
AAEL006351		hypothetical protein	4.93	11.81	2.13	0.0003
AAEL010035			1.49	3.81	2.13	0.0239
AAEL011470		cis,cis-muconate transport protein MucK, putative	6.76	15.68	2.12	0.0000
AAEL011224		hypothetical protein	10.89	26.33	2.12	0.0035
AAEL009273		inosine-5-monophosphate dehydrogenase	10.82	24.74	2.11	0.0000
AAEL012932		hypothetical protein	18.60	42.28	2.10	0.0000
AAEL011282		ribosomal RNA small subunit methyltransferase	5.09	11.66	2.10	0.0000
AAEL011338		hypothetical protein	6.70	15.40	2.10	0.0000
AAEL002800		DNA polymerase epsilon, catalytic subunit	1.16	2.69	2.09	0.0001
AAEL013989		protein translocation complex beta subunit, putative	48.86	110.13	2.09	0.0000
AAEL006424		D7 protein, putative	181.71	411.50	2.09	0.0000
AAEL002815		hypothetical protein	32.97	74.59	2.09	0.0000
AAEL004135		sterol desaturase	1.33	3.38	2.08	0.0466
AAEL006227		hypothetical protein	3.70	8.47	2.08	0.0000
AAEL003944		hypothetical protein	9.84	22.48	2.08	0.0000
AAEL005416		oxidase/peroxidase	338.52	760.61	2.07	0.0000
AAEL009571		elongase, putative	4.58	11.49	2.07	0.0313
AAEL012359		nucleoside-diphosphate kinase NBR-A, putative	213.07	476.81	2.07	0.0000
AAEL002404		receptor protein tyrosine kinase	12.09	29.92	2.07	0.0307
AAEL008469		hypothetical protein	10.52	24.75	2.07	0.0042
AAEL004157		hypothetical protein	14.32	33.89	2.07	0.0051
AAEL012538	LRIM6	hypothetical protein	3.15	7.45	2.06	0.0095
AAEL015441		spliceosomal protein sap	7.40	16.57	2.06	0.0000
AAEL008096		mitochondrial ornithine transporter	2.16	5.09	2.06	0.0055
AAEL004526		hypothetical protein	2.62	5.99	2.05	0.0003

Table A8 Continued

Gene ID	Gene Name	Wiki Description	48h	72h	Fold	*p* adj.
AAEL013884		synaptic vesicle protein	4.50	10.09	2.05	0.0000
AAEL015136		Niemann-Pick Type C-2, putative	8.65	19.78	2.05	0.0012
AAEL014381		hypothetical protein	2.30	5.27	2.05	0.0010
AAEL010949		hypothetical protein	9.81	22.01	2.05	0.0000
AAEL007626	GNBPA1	hypothetical protein	3.42	7.81	2.04	0.0013
AAEL004464			2.90	6.53	2.04	0.0000
AAEL010242		hypothetical protein	109.00	239.83	2.04	0.0000
AAEL003768		hypothetical protein	4.64	10.23	2.04	0.0000
AAEL000300		wd-repeat protein	1.70	3.86	2.04	0.0010
AAEL010235		hypothetical protein	304.27	665.96	2.03	0.0000
AAEL000732		hypothetical protein	26.94	58.94	2.03	0.0000
AAEL004220		hypothetical protein	57.41	125.30	2.02	0.0000
AAEL002322		hypothetical protein	2.49	5.62	2.02	0.0007
AAEL014250		insect replication protein a	3.53	8.05	2.02	0.0035
AAEL001054	GSTD4	glutathione-s-transferase theta, gst	4.83	11.15	2.02	0.0112
AAEL006406		hypothetical protein	162.67	353.85	2.01	0.0000
AAEL006610		hypothetical protein	5.28	11.55	2.01	0.0000
AAEL004482		hypothetical protein	6.19	13.81	2.01	0.0006
AAEL009479		amino acid transporter	2.00	4.61	2.01	0.0094
AAEL008330		hexaprenyldihydroxybenzoate methyltransferase	5.18	11.35	2.01	0.0000
AAEL014051		nop14	4.09	8.96	2.01	0.0000
AAEL017010			4.85	10.55	2.00	0.0000
AAEL014506			2.96	6.39	2.00	0.0000
		Down regulated				
AAEL007585		cathepsin b	121.08	7.96	-11.22	0.0000
AAEL015312		cathepsin b	341.38	20.62	-10.45	0.0000
AAEL011130		alcohol dehydrogenase	12.47	1.05	-10.45	0.0000
AAEL012216		cathepsin b	218.28	13.67	-9.77	0.0000
AAEL006563		serine carboxypeptidase	1,087.50	74.93	-8.74	0.0000
AAEL007599		cathepsin b	122.08	14.67	-8.38	0.0000
AAEL011126		alcohol dehydrogenase	60.42	8.05	-7.67	0.0000
AAEL006568		serine protease	726.10	97.87	-7.57	0.0000
AAEL010684		hypothetical protein	106.23	16.02	-6.86	0.0000
AAEL014852		hypothetical protein	51.46	8.02	-6.41	0.0000
AAEL018102			2,852.55	468.67	-6.26	0.0000
AAEL008473		cysteine-rich venom protein, putative	398.60	71.23	-5.74	0.0000
AAEL006586		serine protease	84.78	15.32	-5.71	0.0000
AAEL002291		hypothetical protein	5.75	0.84	-5.70	0.0000
AAEL014005		clip-domain serine protease, putative	21.29	3.62	-5.60	0.0000
AAEL007103	LRIM15	p37NB protein, putative	43.37	8.59	-5.18	0.0000
AAEL004728		homocysteine methyltransferase	56.89	11.02	-5.16	0.0000
AAEL006323		hypothetical protein	61.04	12.24	-5.13	0.0000
AAEL010937		hypothetical protein	27.24	5.46	-5.03	0.0000
AAEL007590		cathepsin b	519.71	14.34	-4.81	0.0003
AAEL002576		sodium/solute symporter	41.90	8.95	-4.79	0.0000
AAEL008365		hypothetical protein	136.22	29.65	-4.77	0.0000
AAEL006576		clip-domain serine protease, putative	279.30	64.84	-4.48	0.0000
AAEL002670		AMP dependent ligase	1.93	0.31	-4.39	0.0000
AAEL001703		serine-type enodpeptidase, putative	9.13	1.99	-4.20	0.0000
AAEL015432		Trypsin, putative	10.65	2.42	-4.15	0.0000
AAEL006364		hypothetical protein	31.31	8.20	-3.88	0.0000
AAEL010434		hypothetical protein	846.86	228.28	-3.80	0.0000
AAEL006446		trehalose-6-phosphate synthase	311.53	85.82	-3.77	0.0000

Table A8 Continued

Gene ID	Gene Name	Wiki Description	48h	72h	Fold	*p* adj.
AAEL017835	18S_rRNA		6.77	0.47	-3.67	0.0043
AAEL002482		hypothetical protein	9.31	2.42	-3.60	0.0000
AAEL012430		AMP dependent ligase	4.53	1.18	-3.56	0.0000
AAEL008286		hypothetical protein	2.66	0.65	-3.46	0.0001
AAEL000828		vitellogenin, putative	6.93	1.95	-3.43	0.0000
AAEL011129		alcohol dehydrogenase	96.59	29.60	-3.40	0.0000
AAEL006486		hypothetical protein	18.04	5.42	-3.36	0.0000
AAEL012251		low-density lipoprotein receptor (ldl)	267.03	84.11	-3.32	0.0000
AAEL006138		hypothetical protein	489.90	107.80	-3.22	0.0029
AAEL011597		hypothetical protein	48.82	15.83	-3.20	0.0000
AAEL013556	CYP4J15	cytochrome P450	2.04	0.50	-3.18	0.0015
AAEL012970		hypothetical protein	25.58	8.02	-3.13	0.0000
AAEL009194		hypothetical protein	7.63	2.38	-3.12	0.0000
AAEL015606		hypothetical protein	4.63	1.29	-3.11	0.0003
AAEL007413		sulfotransferase (sult)	2.89	0.74	-3.08	0.0020
AAEL010932		rnase h (70)	47.13	15.86	-3.06	0.0000
AAEL003345		argininosuccinate lyase	615.22	211.26	-3.04	0.0000
AAEL014553		triacylglycerol lipase, pancreatic	8.69	2.92	-3.03	0.0000
AAEL003402		sphingomyelin phosphodiesterase	16.46	5.67	-3.00	0.0000
AAEL005997		allergen, putative	667.49	235.13	-2.98	0.0000
AAEL006126		hypothetical protein	137.08	35.50	-2.96	0.0048
AAEL011863		abc transporter	29.31	10.29	-2.95	0.0000
AAEL002283		hypothetical protein	488.96	174.00	-2.93	0.0000
AAEL008632		abc transporter	36.93	13.35	-2.89	0.0000
AAEL003347		CRAL/TRIO domain-containing protein	119.73	43.27	-2.88	0.0000
AAEL015093		triacylglycerol lipase, pancreatic	2.41	0.71	-2.87	0.0023
AAEL010697		3-ketoacyl-coa thiolase	487.68	179.05	-2.86	0.0000
AAEL000660		peptide methionine sulfoxide reductase, putative	17.82	6.31	-2.85	0.0000
AAEL013262		hypothetical protein	49.16	17.44	-2.83	0.0000
AAEL003497		farnesyl-pyrophosphate synthetase	145.27	54.07	-2.82	0.0000
AAEL013001		hypothetical protein	32.42	12.06	-2.78	0.0000
AAEL008006		3-hydroxyacyl-coa dehyrogenase	266.20	100.45	-2.77	0.0000
AAEL012253		hypothetical protein	27.39	9.97	-2.72	0.0000
AAEL001513		wd-repeat protein	2.62	0.95	-2.72	0.0000
AAEL013877		glucosamine-6-phosphate isomerase	30.48	11.70	-2.71	0.0000
AAEL014246		glucosyl/glucuronosyl transferases	107.32	41.70	-2.70	0.0000
AAEL000546		carboxylesterase	38.89	15.02	-2.69	0.0000
AAEL001289		permease, putative	91.57	36.15	-2.66	0.0000
AAEL012929		CRAL/TRIO domain-containing protein	63.38	25.06	-2.64	0.0000
AAEL004088		aldo-keto reductase	305.36	122.89	-2.61	0.0000
AAEL008781		serine-type enodpeptidase, putative	5.71	2.02	-2.60	0.0013
AAEL003898		hypothetical protein	85.96	34.73	-2.59	0.0000
AAEL000105		beta-alanine synthase, putative	133.20	53.77	-2.58	0.0000
AAEL002672			5.73	2.25	-2.57	0.0000
AAEL012967		ced-6	18.46	7.55	-2.51	0.0000
AAEL013417		fibrinogen and fibronectin	3.99	1.49	-2.49	0.0025
AAEL014045		allantoicase	50.35	21.17	-2.48	0.0000
AAEL011323	HNF4	hepatocyte nuclear factor 4-alpha (hnf-4-alpha)	97.48	41.36	-2.47	0.0000
AAEL013355		hypothetical protein	13.52	5.55	-2.47	0.0000
AAEL002658		AMP dependent ligase	33.19	14.07	-2.46	0.0000
AAEL002294			1.67	0.64	-2.46	0.0022
AAEL003029		hypothetical protein	47.17	19.58	-2.45	0.0000

Table A8 Continued

Gene ID	Gene Name	Wiki Description	48h	72h	Fold	*p* adj.
AAEL012518		hypothetical protein	97.12	41.53	-2.45	0.0000
AAEL009558		serine protease, putative	4.38	1.70	-2.44	0.0015
AAEL008370	SCRB17		71.38	30.52	-2.44	0.0000
AAEL000227	SCRB8	epithelial membrane protein	51.35	22.15	-2.42	0.0000
AAEL002612		hypothetical protein	4.41	1.37	-2.42	0.0479
AAEL002781		galactokinase	59.42	25.75	-2.42	0.0000
AAEL002568		hypothetical protein	20.62	8.67	-2.41	0.0000
AAEL002669		AMP dependent ligase	11.80	5.05	-2.41	0.0000
AAEL015370			1.97	0.71	-2.41	0.0175
AAEL005289		ornithine aminotransferase	45.13	19.74	-2.39	0.0000
AAEL000703		glycogen phosphorylase	516.81	228.86	-2.38	0.0000
AAEL012853		hypothetical protein	44.27	19.40	-2.37	0.0000
AAEL005772	OBP22	Odorant-binding protein 99c, putative	698.33	308.02	-2.37	0.0000
AAEL014004		clip-domain serine protease, putative	13.00	5.66	-2.34	0.0000
AAEL002659		hypothetical protein	15.76	5.81	-2.33	0.0316
AAEL005787		serine protease, putative	8.35	3.52	-2.32	0.0006
AAEL006995		sodium/solute symporter	1.56	0.61	-2.31	0.0211
AAEL000166		hypothetical protein	5.38	2.13	-2.30	0.0167
AAEL015438		mannose-6-phosphate isomerase	38.68	17.58	-2.29	0.0000
AAEL011789		citrate synthase	55.62	25.32	-2.29	0.0000
AAEL001492		cgmp-dependent 3,5-cyclic phosphodiesterase	22.30	10.15	-2.29	0.0000
AAEL014864		hypothetical protein	5.12	2.22	-2.29	0.0004
AAEL008222		lipase	18.24	8.19	-2.27	0.0000
AAEL005053		hypothetical protein	7.82	3.51	-2.26	0.0000
AAEL011908		histone H1, putative	6.28	2.68	-2.26	0.0038
AAEL010075		oxidoreductase	55.04	25.53	-2.26	0.0000
AAEL000271		gamma-glutamyl hydrolase, putative	49.31	22.93	-2.26	0.0000
AAEL007102		Trypsin, putative	26.61	12.33	-2.26	0.0000
AAEL010656	LRIM12	hypothetical protein	69.24	32.19	-2.24	0.0000
AAEL008751		glucosyl/glucuronosyl transferases	9.70	4.50	-2.24	0.0000
AAEL009637		cathepsin b	364.92	171.19	-2.24	0.0000
AAEL011608	PGRPLD	peptidoglycan recognition protein-1, putative	53.85	25.10	-2.22	0.0000
AAEL010076		hypothetical protein	19.44	9.16	-2.22	0.0000
AAEL010602		starch branching enzyme ii	38.85	18.42	-2.21	0.0000
AAEL012763	LRIM24	hypothetical protein	35.36	16.69	-2.21	0.0000
AAEL007826		cgmp-dependent protein kinase	139.37	66.23	-2.21	0.0000
AAEL001953		hypothetical protein	152.20	73.48	-2.18	0.0000
AAEL000258		hypothetical protein	177.67	85.70	-2.18	0.0000
AAEL012555		maltose phosphorylase	1.25	0.54	-2.18	0.0167
AAEL009291		serine carboxypeptidase	105.02	50.81	-2.17	0.0000
AAEL005221		internalin A, putative	132.18	64.27	-2.16	0.0000
AAEL003731		nuclear body associated kinase, putative	80.93	39.33	-2.16	0.0000
AAEL009682		serine collagenase 1 precursor, putative	5.05	2.22	-2.16	0.0161
AAEL001863		zinc carboxypeptidase	532.97	260.27	-2.15	0.0000
AAEL012302		hypothetical protein	5.63	2.59	-2.15	0.0023
AAEL001325		hypothetical protein	48.69	23.92	-2.14	0.0000
AAEL010931		hypothetical protein	27.10	13.26	-2.14	0.0000
AAEL012037		sulfate transporter	4.92	2.34	-2.14	0.0002
AAEL011112		alcohol dehydrogenase	187.08	92.03	-2.14	0.0000
AAEL012764		hypothetical protein	60.00	29.46	-2.13	0.0000
AAEL006876		igf2 mRNA binding protein, putative	3.12	1.45	-2.13	0.0030
AAEL010337		CRAL/TRIO domain-containing protein	59.27	29.20	-2.13	0.0000

Table A8 Continued

Gene ID	Gene Name	Wiki Description	48h	72h	Fold	*p* adj.
AAEL001864		Eukaryotic translation initiation factor 4E	340.78	168.46	-2.12	0.0000
AAEL012956		elastase, putative	17.06	8.37	-2.12	0.0000
AAEL007789		alkyldihydroxyacetonephosphate synthase	1.54	0.66	-2.12	0.0498
AAEL003593		hypothetical protein	162.16	80.27	-2.12	0.0000
AAEL013239		bone morphogenetic protein	11.88	5.87	-2.11	0.0000
AAEL014141	SRPN5	serine protease inhibitor, serpin	18.92	9.31	-2.11	0.0000
AAEL003781		zinc carboxypeptidase	3.15	1.43	-2.10	0.0220
AAEL004062		hypothetical protein	5.27	2.45	-2.10	0.0088
AAEL009872		alanine aminotransferase	243.62	122.92	-2.09	0.0000
AAEL006667		phosphatidyltransferase	18.76	9.40	-2.09	0.0000
AAEL003209		amalgam protein, putative	16.02	8.00	-2.09	0.0000
AAEL012614		nadp-specific isocitrate dehydrogenase	322.75	162.79	-2.09	0.0000
AAEL014913		pyruvate kinase	61.27	30.91	-2.08	0.0000
AAEL000395	USP	retinoid x receptor (rxr)	39.68	20.04	-2.08	0.0000
AAEL006240		purple acid phosphatase, putative	41.99	21.31	-2.07	0.0000
AAEL007390		UDP-glucose 4-epimerase	82.34	41.88	-2.06	0.0000
AAEL001204		sterol o-acyltransferase	44.36	22.85	-2.04	0.0000
AAEL000642		alpha-amylase	19.77	10.17	-2.03	0.0000
AAEL002726		D7 protein, putative	9.39	4.70	-2.02	0.0012
AAEL000213		d-amino acid oxidase	70.14	36.05	-2.02	0.0000
AAEL006834		glutamate semialdehyde dehydrogenase	750.14	392.05	-2.02	0.0000
AAEL001047		adenylate cyclase	96.48	50.40	-2.02	0.0000
AAEL000973		hypothetical protein	34.99	18.14	-2.01	0.0000
AAEL002524	CTL24	hypothetical protein	29.94	15.23	-2.01	0.0004
AAEL000471		monocarboxylate transporter	13.20	6.88	-2.01	0.0000
AAEL014820		hypothetical protein	10.58	5.37	-2.01	0.0004
AAEL000111		nitrilase, putative	355.02	186.63	-2.01	0.0000

Table A9 Genes differentially expressed in the HT of 4 days unfed and 72h blood fed females.

IDs	Gene name	Gene description	4 days	72h	Fold	*p* adj.
		Up regulated				
AAEL007097		4-nitrophenylphosphatase	0.03	20.24	54.28	0.0000
AAEL013338		lethal	0.03	21.60	36.07	0.0000
AAEL010435		conserved hypothetical protein	0.60	47.82	32.84	0.0000
AAEL010097		conserved hypothetical protein	0.07	7.71	32.76	0.0000
AAEL013584		conserved hypothetical protein	1.02	46.59	25.95	0.0000
AAEL013577		conserved hypothetical protein	0.14	10.40	21.86	0.0000
AAEL010434		Vitellogenin-A1 Precursor	6.41	234.20	20.65	0.0000
AAEL006563		Vitellogenic carboxypeptidase Precursor	3.17	76.86	10.01	0.0000
AAEL015312		cathepsin b	0.67	21.15	8.90	0.0000
AAEL013118		conserved hypothetical protein	0.32	9.92	8.28	0.0000
AAEL010429		conserved hypothetical protein	0.67	9.93	8.01	0.0000
AAEL000080		phosphoenolpyruvate carboxykinase	9.55	99.50	7.99	0.0000
AAEL007585		cathepsin b	0.34	8.17	7.88	0.0000
AAEL006126		conserved hypothetical protein	2.31	36.42	7.86	0.0000
AAEL000006		phosphoenolpyruvate carboxykinase	7.53	72.01	7.74	0.0000
AAEL012216		cathepsin b	0.62	14.02	7.62	0.0000
AAEL004388	HPX8A	heme peroxidase	0.02	1.33	7.61	0.0000
AAEL013127		conserved hypothetical protein	0.04	6.55	7.47	0.0000
AAEL001666		conserved hypothetical protein	0.02	1.01	6.96	0.0000
AAEL007599		cathepsin b	1.09	15.05	6.93	0.0000
AAEL000025		phosphoenolpyruvate carboxykinase	0.32	3.86	6.92	0.0000
AAEL000744		troponin C	54.73	518.55	6.88	0.0000
AAEL000776		conserved hypothetical protein	0.04	1.52	6.04	0.0000
AAEL002652		hypothetical protein	0.12	1.54	5.91	0.0000
AAEL007905		hypothetical protein	13.67	102.68	5.88	0.0000
AAEL004386	HPX8C	heme peroxidase	0.00	1.91	5.86	0.0000
AAEL003404		hypothetical protein	0.09	1.48	5.61	0.0000
AAEL002269		purine nucleoside phosphorylase	53.69	388.88	5.36	0.0000
AAEL004912		hypothetical protein	0.00	10.65	5.35	0.0000
AAEL014561		conserved hypothetical protein	0.00	10.49	5.02	0.0000
AAEL007909		branched-chain amino acid aminotransferase	7.71	46.09	4.95	0.0000
AAEL000442		conserved hypothetical protein	0.15	2.89	4.89	0.0000
AAEL003606		purine biosynthesis protein 6, pur6	46.77	289.26	4.83	0.0000
AAEL006138		hypothetical protein	5.42	118.40	4.55	0.0000
AAEL000923		conserved hypothetical protein	0.01	1.09	4.42	0.0000
AAEL003731		nuclear body associated kinase, putative	6.57	40.36	4.39	0.0000
AAEL017350			0.07	3.32	4.30	0.0000
AAEL000335		lamin	0.10	1.10	4.19	0.0000
AAEL015289		hypothetical protein	0.00	1.88	4.19	0.0000
AAEL010640		phosphoribosylamine-glycine ligase	10.18	53.42	4.17	0.0000
AAEL004466	LRIM23	leucine-rich immune protein	0.58	4.24	4.09	0.0000
AAEL001100		phosphoserine phosphatase	22.22	112.10	4.07	0.0000
AAEL006830		yellow protein precursor	0.09	1.04	3.91	0.0000
AAEL009962		hypothetical protein	0.00	1.13	3.85	0.0000
AAEL001128		AMP dependent coa ligase	42.46	201.65	3.75	0.0000
AAEL000213		d-amino acid oxidase	8.09	36.99	3.75	0.0000
AAEL014871		methylenetetrahydrofolate dehydrogenase	3.84	18.14	3.67	0.0000
AAEL005384		phosphoribosylformylglycinamidine synthase	13.07	59.65	3.54	0.0000
AAEL010751		methylenetetrahydrofolate dehydrogenase	6.56	29.57	3.46	0.0000

Table A9 Continued

IDs	Gene name	Gene description	4 days	72h	Fold	*p* adj.
AAEL010692		OCP-II protein, putative	0.00	1.13	3.40	0.0000
AAEL011183		conserved hypothetical protein	6.93	30.34	3.37	0.0000
AAEL008751		glucosyl/glucuronosyl transferases	0.94	4.39	3.34	0.0000
AAEL003726		conserved hypothetical protein	0.72	3.12	3.33	0.0000
AAEL013352		lethal	0.17	2.04	3.30	0.0000
AAEL003843		hypothetical protein	2.55	15.58	3.25	0.0000
AAEL002576		sodium/solute symporter	2.78	11.63	3.22	0.0000
AAEL010280		conserved hypothetical protein	2.45	9.68	3.17	0.0000
AAEL012825		bifunctional purine biosynthesis protein	23.76	90.89	3.13	0.0000
AAEL001293		conserved hypothetical protein	7.81	30.80	3.11	0.0000
AAEL010094		cyclin b	1.08	4.24	3.05	0.0000
AAEL005331		hypothetical protein	60.26	219.22	3.01	0.0000
AAEL017465			0.09	3.80	2.94	0.0000
AAEL001054	GSTD4	glutathione transferase	2.94	11.44	2.92	0.0000
AAEL005434		conserved hypothetical protein	8.65	38.45	2.91	0.0000
AAEL002510		serine hydroxymethyltransferase	59.78	205.96	2.88	0.0000
AAEL004904		hypothetical protein	0.00	1.00	2.87	0.0000
AAEL000765		hexamerin 2 beta	1.11	4.15	2.86	0.0000
AAEL003581		amidophosphoribosyltransferase	23.93	87.67	2.85	0.0000
AAEL006876		igf2 mRNA binding protein, putative	0.28	1.49	2.81	0.0000
AAEL012287		sugar transporter	0.71	2.95	2.80	0.0000
AAEL002626		odorant-binding protein 56e, putative	0.06	1.99	2.79	0.0001
AAEL012710		conserved hypothetical protein	8.71	29.30	2.78	0.0000
AAEL010529		conserved hypothetical protein	8.40	32.57	2.77	0.0000
AAEL012423		conserved hypothetical protein	51.94	180.14	2.74	0.0000
AAEL014734		hypothetical protein	7.23	23.38	2.74	0.0000
AAEL006920	LRIM20	leucine-rich immune protein	3.36	11.36	2.74	0.0000
AAEL000566		conserved hypothetical protein	2.41	9.68	2.69	0.0000
AAEL014206		sugar transporter	1.94	6.95	2.66	0.0000
AAEL000629		adenylate kinase 3,	13.48	51.26	2.60	0.0000
AAEL002596	OBP9	odorant binding protein OBP9	0.40	2.40	2.57	0.0003
AAEL013350		heat shock protein 26kD, putative	0.93	3.83	2.56	0.0000
AAEL001194		fatty acid synthase	93.85	301.44	2.55	0.0000
AAEL013349		lethal	0.33	2.03	2.55	0.0004
AAEL007046		mitochondrial brown fat uncoupling protein	1.66	5.86	2.52	0.0000
AAEL001887		glutamine synthetase 1, 2	64.16	194.75	2.52	0.0000
AAEL014363		hypothetical protein	0.83	3.79	2.52	0.0002
AAEL005790		malic enzyme	211.20	643.94	2.50	0.0000
AAEL014937		hypothetical protein	12.67	40.11	2.49	0.0000
AAEL007555		acyl-coa dehydrogenase	43.18	127.57	2.49	0.0000
AAEL011126		alcohol dehydrogenase	8.72	25.95	2.48	0.0000
AAEL003740		conserved hypothetical protein	0.72	2.30	2.46	0.0000
AAEL001690		serine-type enodpeptidase,	0.80	2.78	2.44	0.0000
AAEL007951	GSTE2	glutathione transferase	16.90	50.00	2.44	0.0000
AAEL013351		lethal	0.12	1.32	2.42	0.0012
AAEL007584		conserved hypothetical protein	0.06	1.19	2.41	0.0009
AAEL015432		trypsin, putative	0.68	2.48	2.41	0.0001
AAEL000678		alpha-amylase	1.47	4.78	2.41	0.0000
AAEL003457		conserved hypothetical protein	27.74	85.50	2.41	0.0000
AAEL001674		serine-type enodpeptidase,	0.10	1.27	2.40	0.0012
AAEL003099		glucosyl/glucuronosyl transferases	7.68	22.40	2.38	0.0000
AAEL001806		conserved hypothetical protein	3.36	10.11	2.38	0.0000
AAEL005940		hypothetical protein	0.03	1.18	2.37	0.0008

Table A9 Continued

IDs	Gene name	Gene description	4 days	72h	Fold	*p* adj.
AAEL010431		conserved hypothetical protein	0.04	1.20	2.37	0.0010
AAEL014412	CYP304B2	cytochrome P450	17.05	47.65	2.36	0.0000
AAEL006568		serine protease	35.70	100.42	2.34	0.0000
AAEL010684		conserved hypothetical protein	12.10	33.93	2.33	0.0000
AAEL011756		aldehyde dehydrogenase	22.41	62.49	2.32	0.0000
AAEL003443		threonine dehydrogenase	4.47	14.08	2.32	0.0000
AAEL009124	CYP6N12	cytochrome P450	5.23	15.67	2.31	0.0000
AAEL008096		mitochondrial ornithine transporter	1.80	5.22	2.31	0.0000
AAEL010265		hypothetical protein	2.51	7.19	2.31	0.0000
AAEL007878		ornithine decarboxylase	0.71	2.20	2.30	0.0000
AAEL006586		serine protease	8.42	25.59	2.30	0.0000
AAEL004090		conserved hypothetical protein	8.05	22.35	2.29	0.0000
AAEL007432		serine collagenase 1 precursor, putative	33.64	94.24	2.29	0.0000
AAEL003029		hypothetical protein	6.11	20.10	2.28	0.0001
AAEL008532			3.00	8.86	2.27	0.0000
AAEL008468		cysteine synthase	4.27	12.06	2.26	0.0000
AAEL007033		pyrroline-5-carboxylate reductase	14.78	43.77	2.26	0.0000
AAEL005429		2-oxoglutarate dehydrogenase	3.35	8.88	2.23	0.0000
AAEL000797		dimethylaniline monooxygenase	1.34	4.13	2.23	0.0001
AAEL007250		conserved hypothetical protein	2.45	6.92	2.22	0.0000
AAEL010697		3-ketoacyl-coa thiolase, mitochondrial	70.19	183.73	2.22	0.0000
AAEL003079		glucosyl/glucuronosyl transferases	5.61	16.90	2.21	0.0001
AAEL017179			1.03	3.05	2.20	0.0000
AAEL006820		lipid storage droplets surface binding protein 2	67.28	182.66	2.19	0.0000
AAEL008292	GPRDIH1	GPCR Diuretic Insect Hormone/Kinin/CRF Family	4.77	12.77	2.17	0.0000
AAEL012928		hypothetical protein	0.05	2.85	2.17	0.0025
AAEL000735		acyl-CoA oxidase	3.08	8.43	2.17	0.0000
AAEL007993	CLIPB27	Clip-Domain Serine Protease family B.	0.99	2.97	2.17	0.0002
AAEL001793		conserved hypothetical protein	2.87	7.94	2.16	0.0000
AAEL013851		conserved hypothetical protein	1.05	4.50	2.16	0.0053
AAEL003927		hypothetical protein	0.90	4.07	2.15	0.0064
AAEL000834		dimethylaniline monooxygenase	34.86	90.72	2.14	0.0000
AAEL002467		conserved hypothetical protein	1.36	4.04	2.11	0.0007
AAEL011948		conserved hypothetical protein	0.60	2.62	2.10	0.0086
AAEL003716		ribonuclease UK114, putative	57.51	157.21	2.10	0.0000
AAEL003641		sodium/chloride dependent amino acid transporter	3.32	8.84	2.10	0.0000
AAEL005203		conserved hypothetical protein	3.04	7.73	2.09	0.0000
AAEL004592		tyrosine-protein kinase src64b	1.74	4.41	2.08	0.0000
AAEL006106	OBP26	odorant binding protein OBP26	0.48	3.83	2.07	0.0102
AAEL000298		sodium/chloride dependent amino acid transporter	0.57	1.67	2.06	0.0014
AAEL004870	CYP18A1	cytochrome P450	0.49	1.61	2.06	0.0047
AAEL013363		ubiquitously transcribed sex	2.12	5.32	2.06	0.0000
AAEL016968			2.40	5.90	2.05	0.0000
AAEL014754		conserved hypothetical protein	1.47	4.07	2.05	0.0005
AAEL012443		sugar transporter	0.34	1.22	2.05	0.0094
AAEL007817		hypothetical protein	0.52	1.44	2.05	0.0004
AAEL014454		hypothetical protein	4.35	12.11	2.05	0.0006
AAEL013644		ubiquitously transcribed sex	1.80	4.43	2.05	0.0000
AAEL004976		conserved hypothetical protein	1.08	3.34	2.04	0.0038
AAEL007976		conserved hypothetical protein	0.66	1.71	2.04	0.0000

Table A9 Continued

IDs	Gene name	Gene description	4 days	72h	Fold	*p* adj.
AAEL015606		hypothetical protein	0.36	1.32	2.02	0.0119
AAEL002473		hypothetical protein	0.03	1.04	2.02	0.0071
AAEL013346		lethal	0.41	1.51	2.01	0.0134
AAEL005327		hypothetical protein	2.73	6.81	2.00	0.0000
AAEL006581		juvenile hormone-inducible protein, putative	7.21	17.41	2.00	0.0000
		Down regulated				
AAEL007818		Trypsin 3A1 Precursor	68.88	14.03	-4.22	0.0000
AAEL014820		conserved hypothetical protein	16.20	5.51	-3.21	0.0000
AAEL006484	GPROP3	long wavelength sensitive opsin	3.70	0.96	-3.16	0.0000
AAEL001625		conserved hypothetical protein	103.14	39.18	-2.96	0.0000
AAEL003873		glycerol-3-phosphate dehydrogenase	960.77	372.13	-2.94	0.0000
AAEL011926		brachyury	1.20	0.36	-2.88	0.0000
AAEL013283		serine-type enodpeptidase,	5.49	1.48	-2.85	0.0000
AAEL010884		ADP,ATP carrier protein	7647.85	3025.37	-2.74	0.0000
AAEL002675		arginase	93.76	37.63	-2.60	0.0000
AAEL006485		inosine-uridine preferring nucleoside hydrolase	410.14	183.71	-2.53	0.0000
AAEL001593		glycerol-3-phosphate dehydrogenase	471.54	212.18	-2.50	0.0000
AAEL001252		rap1 GTPase-gdp dissociation stimulator	89.66	41.20	-2.46	0.0000
AAEL003881		ubiquitin, putative	167.57	77.79	-2.45	0.0000
AAEL000711		hypothetical protein	183.68	85.30	-2.41	0.0000
AAEL011741	GSTS1	glutathione transferase	962.92	450.31	-2.41	0.0000
AAEL000733		hydroxysteroid dehydrogenase	23.44	10.97	-2.40	0.0000
AAEL011676		AMP dependent coa ligase	3.03	1.33	-2.40	0.0000
AAEL009992		conserved hypothetical protein	27.25	13.10	-2.39	0.0000
AAEL011764	PPO10	prophenoloxidase	2.94	0.97	-2.37	0.0006
AAEL006424		37 kDa salivary gland allergen Aed a 2 Precursor	908.42	444.77	-2.35	0.0000
AAEL011184		mitochondrial phosphate carrier protein	3699.08	1771.59	-2.35	0.0000
AAEL013880		MSF1 protein, putative	576.82	278.41	-2.34	0.0000
AAEL008018	CYP4C51	cytochrome P450	2.64	1.18	-2.33	0.0000
AAEL017558			785.47	386.81	-2.31	0.0000
AAEL003601		conserved hypothetical protein	103.48	51.08	-2.30	0.0000
AAEL003107		conserved hypothetical protein	69.72	34.12	-2.30	0.0000
AAEL000748		conserved hypothetical protein	50.97	25.46	-2.30	0.0000
AAEL014108		aquaporin, putative	8.29	3.84	-2.30	0.0000
AAEL014830		cytochrome P450	22.19	10.21	-2.27	0.0000
AAEL007680		hypothetical protein	53.67	26.99	-2.27	0.0000
AAEL017397			1.78	0.49	-2.26	0.0028
AAEL006347		Apyrase Precursor	375.67	190.77	-2.26	0.0000
AAEL013498	PPO1	prophenoloxidase	2.04	0.89	-2.25	0.0000
AAEL005672		adenosine deaminase	151.71	77.28	-2.25	0.0000
AAEL013555	CYP4J13	cytochrome P450	64.23	31.88	-2.25	0.0000
AAEL006372		sulphate transporter	8.53	4.17	-2.24	0.0000
AAEL007281		stretchin-mlck	144.40	74.28	-2.22	0.0000
AAEL002185		cuticle protein, putative	689.80	337.87	-2.22	0.0000
AAEL002827		ATP synthase beta subunit	2710.04	1403.62	-2.19	0.0000
AAEL001953		conserved hypothetical protein	153.34	79.87	-2.19	0.0000
AAEL011763	PPO3	prophenoloxidase	6.76	3.25	-2.18	0.0000
AAEL004899		hypothetical protein	101.53	53.27	-2.18	0.0000
AAEL001082		conserved hypothetical protein	3629.95	1923.53	-2.18	0.0000
AAEL010242		conserved hypothetical protein	469.27	246.10	-2.17	0.0000
AAEL002688		glucosyl/glucuronosyl transferases	49.21	25.52	-2.17	0.0000

Table A9 Continued

IDs	Gene name	Gene description	4 days	72h	Fold	*p* adj.
AAEL009045		amine oxidase	1.60	0.72	-2.17	0.0001
AAEL003182	SRPN26	Serine Protease Inhibitor	219.56	116.59	-2.16	0.0000
AAEL000726		fibrinogen and fibronectin	125.04	62.97	-2.16	0.0000
AAEL000556	CTL25	C-Type Lectin	185.96	90.41	-2.16	0.0000
AAEL002776		conserved hypothetical protein	1115.21	596.21	-2.15	0.0000
AAEL001863		zinc carboxypeptidase	519.48	267.06	-2.14	0.0000
AAEL006333		salivary apyrase, putative	91.21	49.11	-2.14	0.0000
AAEL009993		conserved hypothetical protein	37.39	20.21	-2.13	0.0000
AAEL003600		conserved hypothetical protein	623.77	337.16	-2.13	0.0000
AAEL010611		conserved hypothetical protein	46.91	24.62	-2.13	0.0000
AAEL003585		conserved hypothetical protein	17.63	9.24	-2.13	0.0000
AAEL001091		malic enzyme	513.58	274.45	-2.12	0.0000
AAEL003655		conserved hypothetical protein	8.82	4.55	-2.11	0.0000
AAEL016984			3402.67	1834.85	-2.11	0.0000
AAEL011915		F-box/lrr protein fragment	1.69	0.75	-2.11	0.0009
AAEL014673		NADH:ubiquinone dehydrogenase, putative	192.34	101.53	-2.11	0.0000
AAEL015249		sulphate transporter	58.48	31.56	-2.10	0.0000
AAEL006417		D7 protein, putative	547.49	298.32	-2.10	0.0000
AAEL012715		conserved hypothetical protein	38.54	20.07	-2.10	0.0000
AAEL006351		conserved hypothetical protein	27.66	14.85	-2.09	0.0000
AAEL002555		sodium/solute symporter	40.69	22.28	-2.09	0.0000
AAEL007684		tektin, putative	9.93	4.69	-2.09	0.0003
AAEL003100		conserved hypothetical protein	46.70	25.57	-2.09	0.0000
AAEL010688		MRAS2, putative	6.38	3.33	-2.09	0.0000
AAEL007235		mitochondrial uncoupling protein	114.55	62.66	-2.08	0.0000
AAEL007420	SRPN25	Serine Protease Inhibitor	38.94	19.86	-2.08	0.0000
AAEL008066		trkB protein, putative	134.64	74.31	-2.08	0.0000
AAEL013355		hypothetical protein	11.56	5.69	-2.07	0.0001
AAEL004097		enhancer of split protein, putative	15.37	8.41	-2.07	0.0000
AAEL000732		conserved hypothetical protein	108.49	60.48	-2.07	0.0000
AAEL004249		conserved hypothetical protein	1534.97	856.36	-2.06	0.0000
AAEL010004		conserved hypothetical protein	198.01	110.85	-2.06	0.0000
AAEL009112		conserved hypothetical protein	55.90	29.34	-2.05	0.0000
AAEL001429		amino acid transporter	341.80	189.95	-2.04	0.0000
AAEL014255		aquaporin, putative	38.43	21.02	-2.04	0.0000
AAEL008490		NADH dehydrogenase, putative	676.69	378.48	-2.03	0.0000
AAEL000749		conserved hypothetical protein	93.16	50.44	-2.03	0.0000
AAEL013438		LIM domain-binding protein 3, putative	106.49	59.29	-2.03	0.0000
AAEL006000		conserved hypothetical protein	463.38	258.47	-2.02	0.0000
AAEL002704	SRPN23	Serine Protease Inhibitor	375.45	213.54	-2.02	0.0000
AAEL013612		conserved hypothetical protein	207.33	117.08	-2.02	0.0000
AAEL010764		aldehyde dehydrogenase	67.53	36.77	-2.02	0.0000
AAEL009904		conserved hypothetical protein	170.91	94.82	-2.02	0.0000
AAEL011871		cytochrome C1	1960.50	1107.19	-2.02	0.0000
AAEL010180		conserved hypothetical protein	1303.84	744.33	-2.01	0.0000
AAEL003584		hypothetical protein	85.05	48.05	-2.01	0.0000
AAEL010228		conserved hypothetical protein	656.49	376.95	-2.01	0.0000
AAEL012740		ATPase subunit, putative	1976.67	1123.56	-2.01	0.0000
AAEL004065		conserved hypothetical protein	94.75	53.98	-2.00	0.0000

Table A10 Genes differentially expressed in the antenna of 12h and 4 days old females.

Gene ID	Gene Name	Wiki Description	12h	4 days	Fold	*p* adj.
		Up regulated				
AAEL001849			0.12	23.68	69.10	0.0000
AAEL012198		adp,atp carrier protein	0.04	11.88	61.90	0.0000
AAEL008946			0.08	9.50	28.97	0.0000
AAEL005687		protein serine/threonine kinase, putative	57.32	1,550.45	24.26	0.0000
AAEL002617	OBP12	Odorant-binding protein 56e, putative	162.09	3,477.87	19.56	0.0000
AAEL005330			0.22	5.52	18.06	0.0000
AAEL003269		hypothetical protein	16.45	297.92	16.07	0.0000
AAEL002591	OBP13	Odorant-binding protein 56e, putative	50.90	860.04	15.00	0.0000
AAEL017974	HSP70Ab		0.21	4.01	14.42	0.0000
AAEL001774		hypothetical protein	0.16	9.54	13.17	0.0001
AAEL012772	CYP325G3	cytochrome P450	2.58	42.68	12.36	0.0000
AAEL001414	LRIM9	hypothetical protein	0.64	10.90	11.78	0.0000
AAEL007145		hypothetical protein	0.04	1.41	11.61	0.0002
AAEL000252		hypothetical protein	4.67	58.93	11.12	0.0000
AAEL002655		matrix metalloproteinase	0.44	5.65	10.78	0.0000
AAEL013345		alphaA-crystallin, putative	0.24	4.11	10.52	0.0000
AAEL008876		deoxyribonuclease I, putative	0.15	2.40	9.84	0.0000
AAEL000351		hypothetical protein	0.12	2.32	9.71	0.0002
AAEL002675		arginase	0.20	2.63	9.56	0.0000
AAEL001420	LRIM8	hypothetical protein	0.95	19.41	9.51	0.0004
AAEL005711		protein serine/threonine kinase, putative	8.50	92.09	9.18	0.0000
AAEL017981	HSP70Ca'		0.07	1.59	9.15	0.0006
AAEL013351		lethal(2)essential for life protein, l2efl	0.10	1.99	8.93	0.0005
AAEL017366			0.22	2.73	8.50	0.0000
AAEL009563		hypothetical protein	2.74	26.75	8.31	0.0000
AAEL005691		protein serine/threonine kinase, putative	1.33	14.14	8.12	0.0000
AAEL017977	HSP70Ca		0.21	2.37	7.97	0.0000
AAEL008889	CYP6AL1	cytochrome P450	1.13	12.23	7.96	0.0000
AAEL011036		hypothetical protein	0.11	1.68	7.94	0.0008
AAEL001151		n-acetylgalactosaminyltransferase	1.66	14.19	7.63	0.0000
AAEL007147		hypothetical protein	1.97	17.70	7.62	0.0000
AAEL011423		sugar transporter	0.26	2.68	7.52	0.0000
AAEL001087		synaptic vesicle protein	0.53	4.76	7.26	0.0000
AAEL001402	LRIM10B	hypothetical protein	0.45	4.73	7.15	0.0001
AAEL005562		receptor for activated protein kinase c (rack1)	0.20	2.92	7.14	0.0037
AAEL003284		hypothetical protein	5.41	46.69	7.07	0.0000
AAEL017976	HSP70Bb		0.16	1.51	7.01	0.0001
AAEL014411	CYP304B3	cytochrome P450	192.42	1,481.31	6.91	0.0000
AAEL015639		transferrin	1.13	9.50	6.83	0.0000
AAEL017452			2.61	20.40	6.75	0.0000
AAEL010910		retina aberrant in pattern, putative	0.12	1.06	6.73	0.0000
AAEL003632	CLIPB39	clip-domain serine protease, putative	0.59	4.83	6.36	0.0000
AAEL008963		tyrosine aminotransferase	32.86	236.28	6.35	0.0000
AAEL008355		hypothetical protein	0.06	4.46	6.35	0.0251
AAEL008828		carbonic anhydrase	0.20	1.59	6.14	0.0000
AAEL015458		transferrin	6.25	41.79	5.95	0.0000
AAEL003345		argininosuccinate lyase	1.42	11.13	5.92	0.0001
AAEL004524	CLIPC5B	proacrosin, putative	11.84	75.59	5.82	0.0000
AAEL003622		delta(9)-desaturase, putative	4.94	31.85	5.77	0.0000

Table A10 Continued

Gene ID	Gene Name	Wiki Description	12h	4 days	Fold	*p* adj.
AAEL008785		hypothetical protein	214.28	1,343.45	5.71	0.0000
AAEL003200		hypothetical protein	0.09	1.54	5.67	0.0254
AAEL010139		serine protease, putative	1.05	7.61	5.63	0.0001
AAEL013961		hypothetical protein	0.86	7.80	5.30	0.0084
AAEL009568		hypothetical protein	3.82	24.55	5.19	0.0000
AAEL017145			0.80	4.98	5.15	0.0000
AAEL001401	LRIM10A	hypothetical protein	0.55	3.97	5.10	0.0025
AAEL013350		heat shock protein 26kD, putative	1.74	10.21	4.97	0.0000
AAEL017505	Or103		13.41	72.26	4.87	0.0000
AAEL010242		hypothetical protein	105.02	561.01	4.84	0.0000
AAEL009875		alanine aminotransferase	0.14	1.09	4.84	0.0108
AAEL010485		sugar transporter	0.94	5.45	4.76	0.0000
AAEL017973	HSP70Aa		0.33	2.13	4.70	0.0048
AAEL017325	CLIPB36		0.74	4.76	4.65	0.0032
AAEL009359		hypothetical protein	0.11	1.05	4.61	0.0385
AAEL017980	HSP70Ab'		0.34	1.91	4.56	0.0003
AAEL001320	CYP9M4	cytochrome P450	1.31	6.99	4.48	0.0000
AAEL003614	CLIPB40	clip-domain serine protease, putative	0.40	2.70	4.47	0.0192
AAEL013420	Or79	olfactory receptor, putative	4.67	23.09	4.41	0.0000
AAEL003299		hypothetical protein	0.72	4.17	4.35	0.0028
AAEL012086	LRIM1	hypothetical protein	1.88	9.49	4.31	0.0000
AAEL007969		serine protease	1.14	5.55	4.28	0.0000
AAEL007714		hypothetical protein	0.15	1.13	4.27	0.0442
AAEL001098		clip-domain serine protease, putative	22.51	105.11	4.24	0.0000
AAEL002301		serine protease	0.66	3.35	4.22	0.0000
AAEL017018			29.86	137.92	4.20	0.0000
AAEL004719		hypothetical protein	4.38	20.08	4.18	0.0000
AAEL007489		synaptic vesicle protein	0.56	2.72	4.17	0.0001
AAEL008527			4.51	21.19	4.16	0.0000
AAEL007993	CLIPB27	lumbrokinase-1T4 precursor, putative	1.32	6.32	4.11	0.0000
AAEL002524	CTL24	hypothetical protein	0.80	4.82	4.09	0.0204
AAEL002368		hypothetical protein	5.77	27.81	4.08	0.0002
AAEL006164		hypothetical protein	3.80	17.79	4.08	0.0000
AAEL000786		hypothetical protein	0.53	3.35	4.07	0.0364
AAEL001306		hypothetical protein	989.38	4,413.60	4.06	0.0000
AAEL001680		hypothetical protein	7.73	35.01	4.04	0.0000
AAEL000668		hypothetical protein	0.31	1.91	4.01	0.0370
AAEL004863		hypothetical protein	9.70	42.94	4.00	0.0000
AAEL003593		hypothetical protein	15.41	68.22	4.00	0.0000
AAEL013427		serine protease, putative	2.57	11.58	3.99	0.0000
AAEL009487		hypothetical protein	15.20	65.59	3.91	0.0000
AAEL013149			0.91	4.04	3.82	0.0001
AAEL011408	CTL21	galactose-specific C-type lectin, putative	0.52	3.02	3.81	0.0491
AAEL017023			0.37	1.77	3.75	0.0055
AAEL001671		hypothetical protein	1.25	5.13	3.73	0.0000
AAEL014078			0.64	2.71	3.73	0.0000
AAEL003697	SRPN17	serine protease inhibitor, serpin	35.90	145.73	3.71	0.0000
AAEL001287		hypothetical protein	62.66	254.78	3.71	0.0000
AAEL009127	CYP6M11	cytochrome P450	14.92	62.19	3.70	0.0000
AAEL006434		serine protease, putative	1.98	8.23	3.69	0.0000
AAEL003318		oligopeptide transporter	0.23	1.14	3.67	0.0182
AAEL013349		lethal(2)essential for life protein, l2efl	0.60	2.86	3.66	0.0231
AAEL010386		glucosyl/glucuronosyl transferases	5.90	23.52	3.65	0.0000

Table A10 Continued

Gene ID	Gene Name	Wiki Description	12h	4 days	Fold	*p* adj.
AAEL007808	CYP4D39	cytochrome P450	29.51	116.78	3.64	0.0000
AAEL005702		hypothetical protein	1.48	6.22	3.64	0.0001
AAEL002348		paired box protein pax-6	4.81	19.77	3.62	0.0000
AAEL009474	PGRPS1	peptidoglycan recognition protein-lc isoform	0.98	4.40	3.61	0.0046
AAEL006798	CYP9J10	cytochrome P450	0.27	1.28	3.54	0.0247
AAEL016981	Or36		2.94	12.25	3.52	0.0008
AAEL010428	Or26		5.13	19.58	3.49	0.0000
AAEL003934		hypothetical protein	125.07	479.99	3.46	0.0000
AAEL013432		serine protease, putative	6.10	22.94	3.45	0.0000
AAEL017123	Or113		27.26	101.98	3.43	0.0000
AAEL009197		hypothetical protein	0.90	3.77	3.43	0.0105
AAEL015181		hypothetical protein	0.37	1.71	3.41	0.0339
AAEL017982	HSP70Cb'		0.61	2.39	3.37	0.0023
AAEL000037	CLIPB35	serine protease	0.98	3.98	3.37	0.0028
AAEL000566		hypothetical protein	1.01	3.94	3.35	0.0003
AAEL017975	HSP70Ba		4.37	16.23	3.34	0.0000
AAEL017000	Or97		1.73	6.68	3.34	0.0025
AAEL013492	PPO5	prophenoloxidase	0.37	1.48	3.33	0.0144
AAEL013323		hypothetical protein	2.31	8.49	3.30	0.0000
AAEL012687		Juvenile hormone-inducible protein, putative	1.48	5.39	3.28	0.0000
AAEL001675	CLIPA10		2.29	8.29	3.26	0.0000
AAEL005289		ornithine aminotransferase	2.85	10.38	3.26	0.0000
AAEL003625	CLIPB8	clip-domain serine protease, putative	2.46	9.37	3.26	0.0005
AAEL009856		sodium/dicarboxylate cotransporter, putative	2.00	7.17	3.24	0.0000
AAEL008799		hypothetical protein	0.97	3.74	3.22	0.0167
AAEL009852		hypothetical protein	2.10	7.99	3.15	0.0044
AAEL017065	Or92		1.20	4.28	3.14	0.0002
AAEL000024		dopachrome-conversion enzyme (DCE)	3.48	12.43	3.12	0.0004
AAEL003816		hypothetical protein	1.89	7.62	3.12	0.0446
AAEL002969		brain chitinase and chia	10.38	35.45	3.11	0.0000
AAEL005672		adenosine deaminase	1.04	3.58	3.10	0.0000
AAEL004999		hypothetical protein	81.61	275.05	3.09	0.0000
AAEL008668	CLIPB22	MASP-2 protein, putative	2.92	10.29	3.09	0.0011
AAEL001794		macroglobulin/complement	0.48	1.71	3.09	0.0045
AAEL004390	HPX8B	hypothetical protein	0.53	1.89	3.07	0.0067
AAEL008701		myoinositol oxygenase	2.62	9.03	3.03	0.0007
AAEL001722		hypothetical protein	4.76	15.80	3.03	0.0000
AAEL014765		hypothetical protein	0.38	1.44	3.03	0.0240
AAEL011499	OBP47	Odorant-binding protein 58c, putative	599.90	1,972.10	3.00	0.0000
AAEL006260		serine protease, putative	0.78	2.89	2.99	0.0181
AAEL004027		glucose dehydrogenase	6.21	20.80	2.99	0.0001
AAEL012694		Juvenile hormone-inducible protein, putative	12.83	42.09	2.98	0.0000
AAEL004518	CLIPC5A	serine protease snake, putative	7.94	26.20	2.95	0.0000
AAEL017513			21.17	67.59	2.94	0.0000
AAEL005992		adam (a disintegrin and metalloprotease	2.10	6.78	2.94	0.0000
AAEL002553		hypothetical protein	0.88	2.97	2.91	0.0114
AAEL009859		nucleolar GTP-binding protein	87.00	274.87	2.91	0.0000
AAEL003724		hypothetical protein	3.32	10.55	2.89	0.0000

Table A10 Continued

Gene ID	Gene Name	Wiki Description	12h	4 days	Fold	*p* adj.
AAEL001697		adenylate cyclase, putative	1.22	3.93	2.88	0.0002
AAEL007444		hypothetical protein	50.73	160.28	2.88	0.0000
AAEL000019		hypothetical protein	32.82	108.82	2.87	0.0050
AAEL002629		serine protease	18.76	58.83	2.87	0.0000
AAEL017978	HSP70Cb		2.34	7.42	2.85	0.0002
AAEL008106		hypothetical protein	11.53	36.34	2.83	0.0000
AAEL014615	CYP9J23	cytochrome P450	2,185.42	6,698.66	2.82	0.0000
AAEL017143	Or102		0.76	2.49	2.81	0.0241
AAEL005349		hypothetical protein	4.52	14.10	2.81	0.0002
AAEL010418	Or27	hypothetical protein	6.64	20.56	2.81	0.0000
AAEL017537	Or123		3.70	11.62	2.80	0.0021
AAEL003294		fibrinogen and fibronectin	2.45	7.95	2.79	0.0260
AAEL008479		hypothetical protein	25.46	77.62	2.79	0.0000
AAEL004120		Niemann-Pick Type C-2, putative	5.92	18.11	2.79	0.0000
AAEL005763		lysosomal alpha-mannosidase	11.08	33.59	2.78	0.0000
AAEL012054		Quiescin-sulfhydryl oxidase4, putativ	36.88	111.47	2.78	0.0000
AAEL007855		hypothetical protein	1.11	3.60	2.78	0.0085
AAEL004736			18.46	55.96	2.77	0.0000
AAEL006024		Vanin-like protein 2 precursor, putative	0.54	1.87	2.76	0.0411
AAEL003316		hypothetical protein	64.51	193.06	2.75	0.0000
AAEL017296	Or93		1.19	3.85	2.75	0.0359
AAEL001435	SPZ2	Sptzle 2 (Spz2)	1.71	5.41	2.75	0.0146
AAEL007457		insect origin recognition complex subunit	1.06	3.30	2.74	0.0024
AAEL003951		hypothetical protein	0.98	3.11	2.74	0.0208
AAEL006811	CYP9J8	cytochrome P450	4.41	13.34	2.72	0.0002
AAEL009567		apolipoprotein D, putative	6.67	19.84	2.71	0.0001
AAEL001107		hypothetical protein	95.71	289.73	2.71	0.0002
AAEL006805	CYP9J2	cytochrome P450	16.05	47.49	2.70	0.0000
AAEL004713		hypothetical protein	0.84	2.69	2.70	0.0142
AAEL005706		triacylglycerol lipase	27.40	81.29	2.70	0.0000
AAEL011139		hypothetical protein	2.86	8.46	2.69	0.0000
AAEL013326		hypothetical protein	21.73	63.55	2.68	0.0000
AAEL014244		glucosyl/glucuronosyl transferases	0.71	2.16	2.67	0.0181
AAEL013699		hypothetical protein	70.59	206.39	2.67	0.0000
AAEL010996		hypothetical protein	6.56	19.16	2.64	0.0000
AAEL010381		glucosyl/glucuronosyl transferases	3.17	9.10	2.63	0.0000
AAEL001960		cytochrome P450	10.91	31.31	2.63	0.0000
AAEL014614		cytochrome P450	0.88	2.73	2.63	0.0217
AAEL009774			2.03	5.85	2.60	0.0012
AAEL012085		hypothetical protein	1.97	6.09	2.60	0.0313
AAEL009121	CYP6N9	cytochrome P450	0.55	1.69	2.58	0.0440
AAEL004301		hypothetical protein	13,751.21	38,502.79	2.58	0.0000
AAEL004220		hypothetical protein	14.32	40.22	2.58	0.0000
AAEL015404	LYSC7B	lysozyme P, putative	4.13	12.20	2.56	0.0057
AAEL011810		hypothetical protein	24.81	70.83	2.56	0.0008
AAEL013295		hypothetical protein	0.97	2.81	2.56	0.0212
AAEL013423	Or78	hypothetical protein	4.00	11.25	2.56	0.0000
AAEL009477		hypothetical protein	25.58	71.63	2.54	0.0000
AAEL001998		hypothetical protein	1.18	3.35	2.54	0.0024
AAEL005027		acidic ribosomal protein P1, putative	57.90	160.53	2.54	0.0000
AAEL007940	Gr77		1.57	4.37	2.52	0.0048
AAEL005480		hairy protein	1.12	3.16	2.52	0.0077

Table A10 Continued

Gene ID	Gene Name	Wiki Description	12h	4 days	Fold	*p* adj.
AAEL009955		hypothetical protein	1.96	5.73	2.51	0.0442
AAEL018095			21.07	57.62	2.51	0.0000
AAEL014451		hypothetical protein	1.35	3.74	2.51	0.0019
AAEL004909		hypothetical protein	0.69	1.93	2.50	0.0125
AAEL016412			67.87	183.91	2.47	0.0000
AAEL009181		hypothetical protein	13.13	38.05	2.47	0.0463
AAEL013422		Odorant receptor 42a, putative	1.05	2.98	2.46	0.0204
AAEL006749		hypothetical protein	2.83	7.77	2.46	0.0013
AAEL002046	CYP6CB1	cytochrome P450	53.41	142.70	2.45	0.0000
AAEL007283		acetyl-coa synthetase	1.83	5.09	2.45	0.0047
AAEL010513		class b basic helix-loop-helix protein	29.13	79.87	2.45	0.0047
AAEL012689			0.97	2.76	2.45	0.0301
AAEL000162	Gr34		0.75	2.13	2.44	0.0346
AAEL014137	CLIPB25	serine protease	217.95	583.35	2.43	0.0001
AAEL002610		serine protease	1.69	4.76	2.43	0.0379
AAEL001084	CLIPB21	hypothetical protein	3.40	9.09	2.42	0.0000
AAEL002880		hypothetical protein	8.53	22.47	2.40	0.0000
AAEL010930		l-asparaginase	0.83	2.28	2.39	0.0345
AAEL008232		sugar transporter	17.20	44.60	2.38	0.0000
AAEL017043	Or84		142.26	367.38	2.38	0.0000
AAEL010255		hypothetical protein	2.13	5.65	2.38	0.0256
AAEL005058		hypothetical protein	10.63	27.47	2.37	0.0000
AAEL008125		hypothetical protein	35.63	92.84	2.37	0.0001
AAEL003967		calpain, putative	0.67	1.80	2.37	0.0373
AAEL009479		amino acid transporter	27.74	71.49	2.37	0.0000
AAEL013893	Or125	hypothetical protein	6.07	15.67	2.37	0.0000
AAEL014580		gamma glutamyl transpeptidases	13.70	35.19	2.37	0.0000
AAEL006329		hypothetical protein	1.19	3.13	2.35	0.0017
AAEL007815	CYP4D24	cytochrome P450	192.25	487.66	2.34	0.0000
AAEL015663		cytochrome P450	1.14	3.04	2.32	0.0233
AAEL007880		ornithine decarboxylase	41.13	103.53	2.32	0.0000
AAEL011371		hypothetical protein	81.31	206.43	2.32	0.0001
AAEL007007		DNA replication licensing factor MCM2	0.69	1.85	2.31	0.0232
AAEL017201	Or94		9.96	24.90	2.30	0.0000
AAEL003899		sugar transporter	13.55	33.77	2.30	0.0000
AAEL017009	Or119		2.16	5.47	2.28	0.0155
AAEL017381			9.29	22.90	2.27	0.0000
AAEL013356		hypothetical protein	8.94	22.05	2.27	0.0000
AAEL013242			0.46	1.15	2.26	0.0037
AAEL017383			149.64	370.23	2.26	0.0001
AAEL009895		neprilysin	46.96	115.95	2.26	0.0000
AAEL011803		prohibitin, putative	12.82	31.68	2.25	0.0000
AAEL010390		glucosyl/glucuronosyl transferases	1.75	4.40	2.25	0.0045
AAEL011255		GTP-binding protein-invertebrate	16.44	40.16	2.25	0.0000
AAEL017354			76.51	189.27	2.24	0.0017
AAEL015475			21.93	53.67	2.24	0.0000
AAEL007624	REL2	hypothetical protein	12.62	30.71	2.24	0.0000
AAEL010867		serine protease	1.72	4.34	2.24	0.0404
AAEL017119			6,688.90	16,290.52	2.24	0.0000
AAEL014197	Or88	hypothetical protein	25.57	61.91	2.23	0.0000
AAEL011583	Or11	Odorant receptor 56a, putative	22.81	56.10	2.23	0.0016
AAEL003261		hypothetical protein	3.11	7.52	2.23	0.0000
AAEL017149	Or91		8.82	21.32	2.23	0.0000

Table A10 Continued

Gene ID	Gene Name	Wiki Description	12h	4 days	Fold	*p* adj.
AAEL010935		gamma glutamyl transpeptidases	77.48	186.20	2.21	0.0000
AAEL012303		hypothetical protein	1.62	4.10	2.21	0.0205
AAEL001641		deoxyribonuclease I, putative	14.14	34.14	2.20	0.0005
AAEL004059		cystathionine beta-lyase	89.45	214.54	2.20	0.0000
AAEL010656	LRIM12	hypothetical protein	1.53	3.70	2.20	0.0020
AAEL003071		tRNA pseudouridine synthase D	8.98	21.50	2.20	0.0000
AAEL011520		sucrose transport protein	1.56	3.85	2.19	0.0077
AAEL005673	SRPN2	serine protease inhibitor, serpin	6.65	16.12	2.19	0.0002
AAEL012430		AMP dependent ligase	1.71	4.16	2.19	0.0280
AAEL006752		Misexpression suppressor of ras, putative	8.90	21.13	2.18	0.0000
AAEL000047	IR41i	hypothetical protein	3.28	7.86	2.18	0.0027
AAEL009032		hypothetical protein	62.50	150.49	2.17	0.0099
AAEL009101		eukaryotic translation initiation factor 3f, eif3f	122.61	286.80	2.16	0.0000
AAEL012782		hypothetical protein	0.88	2.12	2.16	0.0073
AAEL006627		serine-type enodpeptidase, putative	12.27	29.40	2.16	0.0241
AAEL001077	CLIPB45	hypothetical protein	42.30	99.52	2.16	0.0000
AAEL009130	CYP6Z7		215.66	505.20	2.15	0.0000
AAEL003619		sodium/shloride dependent aa transporter	34.86	81.39	2.15	0.0000
AAEL018176		hypothetical protein	0.71	1.75	2.15	0.0346
AAEL015483		hypothetical protein	25.15	58.99	2.15	0.0000
AAEL004383		hypothetical protein	17.81	41.48	2.14	0.0000
AAEL012377	OBP55	Odorant-binding protein 56a, putative	15,371.44	35,491.55	2.13	0.0000
AAEL002639		ribosomal protein L36, putative	105.03	244.34	2.13	0.0005
AAEL008710		hypothetical protein	31.91	74.16	2.12	0.0042
AAEL012142		timeout/timeless-2	2.94	6.88	2.11	0.0029
AAEL013857		hypothetical protein	12.97	29.63	2.11	0.0001
AAEL010100	LYSC7A	lysozyme P, putative	13.78	32.06	2.11	0.0153
AAEL002080		septin interacting protein, putative	1.89	4.33	2.11	0.0094
AAEL007135		peroxiredoxin 5, prdx5	667.20	1,518.25	2.10	0.0000
AAEL002567		hypothetical protein	4.32	10.08	2.09	0.0203
AAEL013403		hypothetical protein	4.58	10.83	2.09	0.0302
AAEL006820		lipid storage droplets surface binding protein	41.54	94.08	2.08	0.0000
AAEL013163		hypothetical protein	6.19	14.11	2.08	0.0003
AAEL000148		hypothetical protein	3.73	8.47	2.08	0.0031
AAEL011895	Or48	hypothetical protein	1.11	2.59	2.07	0.0375
AAEL004278		hypothetical protein	49.52	111.64	2.07	0.0000
AAEL009233		zinc metalloprotease	12.06	27.04	2.07	0.0000
AAEL003626		sodium/shloride dependent aa transporter	16.00	36.30	2.07	0.0055
AAEL017129	Or72		7.16	16.12	2.07	0.0024
AAEL003676		myosin I, putative	20.45	45.87	2.07	0.0000
AAEL000260		hypothetical protein	2.26	5.13	2.06	0.0010
AAEL010492		hypothetical protein	2.86	6.59	2.06	0.0284
AAEL008096		mitochondrial ornithine transporter	1.05	2.45	2.06	0.0486
AAEL017219	Or114		7.12	16.00	2.06	0.0094
AAEL000859		hypothetical protein	4.52	10.04	2.06	0.0001
AAEL002190		hypothetical protein	13.46	29.96	2.05	0.0000
AAEL006479		hypothetical protein	5.00	11.15	2.05	0.0107
AAEL002182		t-diRNAhydrouridine synthase	10.48	23.35	2.04	0.0001
AAEL008368	Or13	olfactory receptor, putative	3.69	8.21	2.04	0.0007

Table A10 Continued

Gene ID	Gene Name	Wiki Description	12h	4 days	Fold	*p* adj.
AAEL008384		ATP-binding cassette sub-family A member	1.07	2.38	2.04	0.0015
AAEL013801		sulfate transporter	20.03	44.66	2.03	0.0030
AAEL002590		serine protease, putative	9.07	20.40	2.03	0.0240
AAEL013904		3-hydroxyisobutyrate dehydrogenase	16.59	37.24	2.03	0.0292
AAEL008427		smad nuclear interacting protein	7.08	15.75	2.02	0.0003
AAEL005744		DEAD box ATP-dependent RNA helicase	11.70	25.98	2.02	0.0005
AAEL015313	OBP59	hypothetical protein	222.55	492.02	2.02	0.0012
AAEL005481		alpha-glucosidase	92.06	201.58	2.02	0.0000
AAEL000073	OBP4	Odorant-binding protein 56e, putative	2,152.58	4,715.27	2.02	0.0000
AAEL010663		cleavage and polyadenylation specif. factor	12.31	26.99	2.02	0.0007
AAEL010977		ATP-dependent transporter	199.97	437.84	2.02	0.0000
AAEL003872		translationally controlled tumor protein	254.62	555.47	2.02	0.0000
AAEL012292		4-nitrophenylphosphatase	47.40	103.99	2.02	0.0001
AAEL016966	Or104		17.18	37.56	2.01	0.0027
AAEL008330		fmethyltransferase	1.12	2.47	2.01	0.0288
		Down regulated				
AAEL000878		cuticle protein, putative	285.68	0.47	-422.51	0.0000
AAEL004762		pupal cuticle protein, putative	345.02	1.17	-202.96	0.0000
AAEL001319		hypothetical protein	4,314.86	20.73	-200.79	0.0000
AAEL013829		cuticle protein, putative	422.31	2.15	-197.85	0.0000
AAEL009790		cuticle protein, putative	49.38	0.06	-185.71	0.0000
AAEL017500			4,902.46	24.19	-169.84	0.0000
AAEL012575		serine protease, putative	202.36	0.80	-163.23	0.0000
AAEL015163		cuticle protein, putative	244.09	1.46	-149.78	0.0000
AAEL011768		hypothetical protein	11.23	0.02	-143.87	0.0000
AAEL012573		serine protease, putative	88.09	0.56	-134.65	0.0000
AAEL005622		hypothetical protein	209.92	1.79	-112.95	0.0000
AAEL000098		hypothetical protein	12.15	0.05	-98.18	0.0000
AAEL014418		hypothetical protein	26.02	0.09	-90.72	0.0000
AAEL011504		pupal cuticle protein, putative	154.86	1.34	-90.32	0.0000
AAEL015119		cuticle protein, putative	755.50	7.68	-85.33	0.0000
AAEL009203		glucose dehydrogenase	20.47	0.04	-75.76	0.0000
AAEL014369		hypothetical protein	686.20	4.60	-74.85	0.0000
AAEL003041		hypothetical protein	425.05	5.35	-71.80	0.0000
AAEL004897		brain chitinase and chia	117.55	1.59	-63.91	0.0000
AAEL007483		hypothetical protein	29.29	0.44	-62.06	0.0000
AAEL015534		hypothetical protein	62.81	1.00	-57.75	0.0000
AAEL009580		hypothetical protein	41.96	0.72	-52.75	0.0000
AAEL000909		histone H1, putative	138.17	0.88	-51.27	0.0000
AAEL013303		hypothetical protein	130.60	2.37	-49.42	0.0000
AAEL001683		hypothetical protein	733.07	6.27	-49.26	0.0000
AAEL000879		cuticle protein, putative	233.99	0.98	-47.98	0.0000
AAEL005964		actin	152.76	3.15	-42.65	0.0000
AAEL011449		hypothetical protein	102.62	2.12	-41.09	0.0000
AAEL005917		hypothetical protein	58.40	1.24	-40.10	0.0000
AAEL013367			114.98	2.92	-39.73	0.0000
AAEL001437		hypothetical protein	33.18	0.75	-39.29	0.0000
AAEL004002		glucose dehydrogenase	9.92	0.26	-38.66	0.0000
AAEL010886		carbonic anhydrase II, putative	17.13	0.06	-38.12	0.0000
AAEL001837		lipase	12.99	0.20	-37.98	0.0000

Table A10 Continued

Gene ID	Gene Name	Wiki Description	12h	4 days	Fold	*p* adj.
AAEL001677		hypothetical protein	737.90	4.53	-36.88	0.0000
AAEL012467		brain chitinase and chia	23.35	0.57	-36.83	0.0000
AAEL012370		brain chitinase and chia	50.14	1.37	-35.77	0.0000
AAEL009219		hypothetical protein	3.26	0.04	-35.00	0.0000
AAEL003218		hypothetical protein	4.12	0.00	-34.98	0.0000
AAEL012090		hypothetical protein	18.40	0.53	-33.21	0.0000
AAEL010894		carbonic anhydrase II, putative	8.54	0.15	-32.83	0.0000
AAEL005906		serine protease	41.14	1.29	-32.78	0.0000
AAEL014879			5.08	0.04	-31.45	0.0000
AAEL009251		hypothetical protein	174.91	5.85	-31.12	0.0000
AAEL009577		hypothetical protein	1,218.16	10.42	-29.86	0.0000
AAEL003256		hypothetical protein	5.29	0.00	-29.57	0.0000
AAEL012423		hypothetical protein	7.01	0.00	-29.31	0.0000
AAEL013222		hypothetical protein	81.59	2.76	-28.78	0.0000
AAEL003027		hypothetical protein	328.72	11.83	-28.43	0.0000
AAEL017293			1,185.20	43.07	-27.87	0.0000
AAEL009796		cuticle protein, putative	33.99	1.06	-27.71	0.0000
AAEL018332			63.52	2.47	-26.83	0.0000
AAEL014366		hypothetical protein	43.58	1.54	-26.53	0.0000
AAEL010788		metalloprotease	3.86	0.04	-25.01	0.0000
AAEL004903			1.36	0.00	-23.78	0.0000
AAEL009794		cuticle protein, putative	6.75	0.08	-23.61	0.0000
AAEL000890		hypothetical protein	5.62	0.09	-23.58	0.0000
AAEL003419		hypothetical protein	354.88	14.02	-23.57	0.0000
AAEL000392		alpha-amylase	32.00	1.09	-23.55	0.0000
AAEL009791		cuticle protein, putative	4.71	0.05	-23.35	0.0000
AAEL008965		adult cuticle protein, putative	5.03	0.08	-22.38	0.0000
AAEL002911		lysosomal acid lipase, putative	11.60	0.33	-22.25	0.0000
AAEL008735		hypothetical protein	17.41	0.73	-22.15	0.0000
AAEL012399		hypothetical protein	6.78	0.00	-21.87	0.0000
AAEL003425		hypothetical protein	1,107.63	52.27	-21.66	0.0000
AAEL011041		hypothetical protein	2.49	0.00	-20.98	0.0000
AAEL002015		protein serine/threonine kinase, putative	7.88	0.09	-20.94	0.0000
AAEL008294		pupal cuticle protein 78E, putative	7.96	0.13	-20.83	0.0000
AAEL002212		cuticle protein, putative	6.62	0.08	-20.65	0.0000
AAEL003576		hypothetical protein	153.64	1.13	-20.58	0.0000
AAEL011068		hypothetical protein	9,426.96	457.82	-20.55	0.0000
AAEL005961		actin	5,356.91	246.81	-19.87	0.0000
AAEL003241		hypothetical protein	2.39	0.00	-19.86	0.0000
AAEL002780		hypothetical protein	22.57	1.19	-19.56	0.0000
AAEL007514		oviductin	2.57	0.06	-19.30	0.0000
AAEL001936		hypothetical protein	6.31	0.23	-19.29	0.0000
AAEL002191		cuticle protein, putative	4.86	0.00	-19.01	0.0000
AAEL009802		cuticle protein, putative	3.77	0.03	-18.40	0.0000
AAEL007780		hypothetical protein	4.17	0.06	-18.27	0.0000
AAEL005306		hypothetical protein	1.47	0.02	-18.25	0.0000
AAEL017139			14.85	0.67	-18.22	0.0000
AAEL000946		hypothetical protein	6.06	0.22	-18.13	0.0000
AAEL014456		hypothetical protein	124.12	6.96	-17.80	0.0000
AAEL008747		hypothetical protein	7.00	0.20	-17.60	0.0000
AAEL006334		sulfotransferase (sult)	30.33	1.56	-17.51	0.0000
AAEL015354		oxidase/peroxidase	3.93	0.21	-17.50	0.0000
AAEL013380		adult cuticle protein, putative	2.78	0.09	-16.98	0.0000

Table A10 Continued

Gene ID	Gene Name	Wiki Description	12h	4 days	Fold	*p* adj.
AAEL001330		zinc metalloproteinase	1.72	0.00	-16.88	0.0001
AAEL009510		glucosamine aminotransferase	339.58	20.24	-16.78	0.0000
AAEL011586		hypothetical protein	48.84	2.95	-16.75	0.0000
AAEL008421		cadherin	5.81	0.31	-16.50	0.0000
AAEL002024		protein serine/threonine kinase, putative	21.48	0.85	-16.47	0.0000
AAEL003049		pupal cuticle protein 78E, putative	843.13	5.56	-16.41	0.0002
AAEL001993		protein serine/threonine kinase, putative	7.49	0.11	-16.17	0.0000
AAEL004264		hypothetical protein	126.95	7.19	-16.12	0.0000
AAEL005960		hypothetical protein	3.62	0.11	-16.11	0.0000
AAEL012794		hypothetical protein	40.97	2.65	-15.95	0.0000
AAEL013766		hypothetical protein	1,174.26	9.92	-15.94	0.0002
AAEL002111		cuticle protein, putative	3.77	0.04	-15.50	0.0000
AAEL014823		hypothetical protein	76.27	5.02	-15.45	0.0000
AAEL004780		pupal cuticle protein, putative	11.01	0.55	-15.40	0.0000
AAEL011771		hypothetical protein	56.08	3.54	-15.29	0.0000
AAEL013156		hypothetical protein	2.77	0.12	-15.19	0.0000
AAEL014667		brain chitinase and chia	18.96	1.14	-15.14	0.0000
AAEL009853		Trypsin, putative	2.87	0.06	-15.05	0.0000
AAEL011440		hypothetical protein	43.17	2.89	-14.93	0.0000
AAEL018266		autoimmune regulator	7.21	0.49	-14.65	0.0000
AAEL002558		myomesin	7.79	0.47	-14.63	0.0000
AAEL002189		hypothetical protein	6.95	0.18	-14.61	0.0000
AAEL017553	CCEAE2B		3.60	0.16	-14.51	0.0000
AAEL012728		hypothetical protein	7.11	0.22	-14.47	0.0000
AAEL002759		tropomyosin invertebrate	1,199.86	75.59	-14.47	0.0000
AAEL001987		protein serine/threonine kinase, putative	115.33	7.63	-14.35	0.0000
AAEL003221		pupal cuticle protein 78E, putative	1.93	0.05	-14.24	0.0000
AAEL008987		hypothetical protein	2.18	0.00	-14.22	0.0003
AAEL012769	CYP325M2	hypothetical protein	1.90	0.06	-14.08	0.0000
AAEL001970		hypothetical protein	1.71	0.00	-14.05	0.0003
AAEL002246		cuticle protein, putative	5.61	0.15	-13.99	0.0000
AAEL002718		chitin synthase	70.12	5.09	-13.97	0.0000
AAEL008285		Pupal cuticle protein, putative	759.60	54.72	-13.86	0.0000
AAEL011043		hypothetical protein	3.83	0.05	-13.82	0.0001
AAEL006888			72.35	5.45	-13.79	0.0000
AAEL009193		glucose dehydrogenase	4.60	0.30	-13.68	0.0000
AAEL004036		glucose dehydrogenase	1.35	0.07	-13.67	0.0000
AAEL005988	LYSC6	hypothetical protein	43.03	3.28	-13.49	0.0000
AAEL011486		hypothetical protein	16.04	1.13	-13.45	0.0000
AAEL011699		hypothetical protein	6.30	0.46	-13.43	0.0000
AAEL005251		hypothetical protein	29.73	1.84	-13.37	0.0000
AAEL005969		phospholipase b, plb1	111.35	0.57	-13.11	0.0009
AAEL011177		hypothetical protein	6.46	0.46	-13.01	0.0000
AAEL006339		peptidylglycine interactor protein-1	33.12	2.54	-12.99	0.0000
AAEL014445		hypothetical protein	46.51	3.56	-12.99	0.0000
AAEL012464			38.96	2.93	-12.85	0.0000
AAEL003112		hypothetical protein	37.13	1.57	-12.83	0.0000
AAEL012174		metalloproteinase, putative	2.68	0.08	-12.57	0.0000
AAEL002693		venom allergen	11.41	0.00	-12.40	0.0013
AAEL008726		hypothetical protein	8.36	0.59	-12.07	0.0000
AAEL014802		hypothetical protein	7.36	0.49	-12.06	0.0000

Table A10 Continued

Gene ID	Gene Name	Wiki Description	12h	4 days	Fold	*p* adj.
AAEL001999		protein serine/threonine kinase, putative	11.03	0.62	-12.04	0.0000
AAEL008885		hypothetical protein	19.12	1.55	-11.97	0.0000
AAEL005733			2,454.59	201.89	-11.90	0.0000
AAEL002354	HPX5	oxidase/peroxidase	33.56	2.86	-11.82	0.0000
AAEL010392		hypothetical protein	7.93	0.58	-11.70	0.0000
AAEL009683		hypothetical protein	1.91	0.04	-11.69	0.0004
AAEL009467		hypothetical protein	23.23	1.97	-11.65	0.0000
AAEL002417		troponin t, invertebrate	2,789.90	227.24	-11.51	0.0000
AAEL010657		hypothetical protein	2.94	0.00	-11.51	0.0013
AAEL001627		UDP-n-acteylglucosamine pyrophosphorylase	82.07	7.27	-11.43	0.0000
AAEL004782		pupal cuticle protein, putative	1.75	0.00	-11.31	0.0014
AAEL004360		hypothetical protein	4.61	0.37	-11.30	0.0000
AAEL008546		hypothetical protein	62.51	5.48	-11.22	0.0000
AAEL012082		NF-180, putative	81.67	4.71	-11.13	0.0000
AAEL014978		adult cuticle protein, putative	29.76	2.37	-11.10	0.0000
AAEL006250		insulin receptor tyrosine kinase substrate	3.31	0.23	-11.01	0.0000
AAEL004765		pupal cuticle protein, putative	5.15	0.19	-10.90	0.0002
AAEL008844		calcium-binding protein, putative	7,400.81	662.07	-10.71	0.0000
AAEL004951		hypothetical protein	421.45	41.75	-10.70	0.0000
AAEL004806		hypothetical protein	7.45	0.64	-10.65	0.0000
AAEL002761		tropomyosin invertebrate	811.66	76.95	-10.64	0.0000
AAEL009336			6.10	0.52	-10.62	0.0000
AAEL006014	HPX1	oxidase/peroxidase	6.87	0.54	-10.61	0.0000
AAEL011620		hypothetical protein	24.69	2.39	-10.59	0.0000
AAEL017335	GPRGHP2		3.26	0.15	-10.56	0.0001
AAEL015591		cytochrome P450	1.25	0.03	-10.52	0.0012
AAEL008831		hypothetical protein	13.53	1.33	-10.41	0.0000
AAEL005586		transient receptor potential channel 4, putative	2.08	0.09	-10.40	0.0002
AAEL008764		cuticle protein, putative	120.36	12.21	-10.35	0.0000
AAEL011458		hypothetical protein	18.02	1.59	-10.31	0.0000
AAEL001050		hypothetical protein	2.64	0.21	-10.29	0.0000
AAEL007415		multicopper oxidase	36.14	3.51	-10.29	0.0000
AAEL002022		protein serine/threonine kinase, putative	68.60	5.98	-10.26	0.0000
AAEL011422		hypothetical protein	3.36	0.20	-10.25	0.0000
AAEL002070			17.03	1.61	-10.25	0.0000
AAEL002572		myosin regulatory light chain 2 (mlc-2)	4,360.53	323.02	-10.16	0.0000
AAEL010850		troponin i	936.70	87.63	-10.11	0.0000
AAEL010975		paramyosin, long form	551.23	53.09	-10.11	0.0000
AAEL014073		hypothetical protein	9.96	0.97	-10.07	0.0000
AAEL004680		nuclear lamin L1 alpha, putative	24.63	2.29	-10.06	0.0000
AAEL012342		lysosomal acid lipase, putative	6.23	0.61	-9.99	0.0000
AAEL011268		phosphatidylethanolamine-binding protein	1.86	0.03	-9.98	0.0018
AAEL018115		hypothetical protein	19.29	1.94	-9.93	0.0000
AAEL009385		hypothetical protein	30.41	3.19	-9.90	0.0000
AAEL018343		myosin light chain kinase	30.44	3.22	-9.86	0.0000
AAEL001745		candidate tumor suppressor protein	14.02	0.26	-9.82	0.0035
AAEL008762		hypothetical protein	109.52	11.60	-9.79	0.0000

Table A10 Continued

Gene ID	Gene Name	Wiki Description	12h	4 days	Fold	*p* adj.
AAEL001704		hypothetical protein	930.60	3.27	-9.78	0.0043
AAEL014255		aquaporin, putative	18.15	1.92	-9.77	0.0000
AAEL006572		troponin C	948.57	94.81	-9.77	0.0000
AAEL008988		adult cuticle protein, putative	21.24	1.86	-9.76	0.0000
AAEL012114		troponin C	99.56	10.17	-9.76	0.0000
AAEL005325		dopachrome-conversion enzyme (DCE)	4.27	0.34	-9.63	0.0000
AAEL001953		hypothetical protein	3.68	0.27	-9.60	0.0000
AAEL018202		hypothetical protein	130.16	13.45	-9.57	0.0000
AAEL007486	CCEAE20	alpha-esterase	4.47	0.36	-9.55	0.0000
AAEL010174		hypothetical protein	2.58	0.06	-9.53	0.0025
AAEL009784		cuticle protein, putative	2.66	0.17	-9.45	0.0003
AAEL018135		steroid dehydrogenase	1.37	0.10	-9.43	0.0000
AAEL010161		hypothetical protein	5.39	0.29	-9.40	0.0005
AAEL006933		hypothetical protein	6.35	0.53	-9.40	0.0000
AAEL001082		hypothetical protein	1,060.19	42.54	-9.38	0.0024
AAEL002239		hypothetical protein	10.30	0.55	-9.35	0.0006
AAEL003104		tripartite motif protein trim2,3	93.48	10.28	-9.34	0.0000
AAEL003961		short-chain dehydrogenase	15.21	1.58	-9.31	0.0000
AAEL002565		titin	100.65	10.81	-9.31	0.0000
AAEL002099		cuticle protein, putative	139.00	14.72	-9.21	0.0000
AAEL010160		hypothetical protein	5.07	0.42	-9.16	0.0001
AAEL001728		hypothetical protein	2.28	0.11	-9.13	0.0007
AAEL017177			44.37	4.96	-8.91	0.0000
AAEL012792		hypothetical protein	9.49	0.95	-8.91	0.0000
AAEL008752		hypothetical protein	71.34	8.10	-8.90	0.0000
AAEL016994			5,115.05	370.08	-8.74	0.0005
AAEL006245		insulin receptor tyrosine kinase substrate	20.80	2.39	-8.70	0.0000
AAEL003259		pupal cuticle protein 78E, putative	469.67	51.54	-8.67	0.0000
AAEL008513		hypothetical protein	55.73	6.71	-8.66	0.0000
AAEL014332		hypothetical protein	13.38	1.50	-8.66	0.0000
AAEL001995		protein serine/threonine kinase, putative	7.92	0.51	-8.63	0.0004
AAEL009002		hypothetical protein	3.27	0.26	-8.60	0.0000
AAEL014001		yellow protein precursor, putative	3.03	0.30	-8.54	0.0000
AAEL010147		hypothetical protein	21.17	2.51	-8.54	0.0000
AAEL009837		hypothetical protein	1.79	0.09	-8.45	0.0018
AAEL018228		monocarboxylate transporter	1.23	0.12	-8.43	0.0000
AAEL002241		cuticle protein, putative	7.76	0.45	-8.42	0.0016
AAEL003977		elongase, putative	14.04	1.40	-8.42	0.0000
AAEL013324		high affinity nuclear JH binding protein	1.41	0.14	-8.37	0.0001
AAEL018091			5,011.94	651.44	-8.20	0.0000
AAEL002035		protein serine/threonine kinase, putative	3.63	0.18	-8.17	0.0058
AAEL012217		protease m1 zinc metalloprotease	16.13	2.08	-8.15	0.0000
AAEL003038		hypothetical protein	33.71	4.13	-8.14	0.0000
AAEL005386		collagen alpha chain, anopheles	3.13	0.39	-8.12	0.0000
AAEL000445		hypothetical protein	1,531.83	200.00	-8.10	0.0000
AAEL009585		hypothetical protein	589.71	77.81	-8.04	0.0000
AAEL013209		hypothetical protein	6.67	0.56	-8.03	0.0000
AAEL007500		hypothetical protein	15.98	1.91	-8.00	0.0000
AAEL011923		f-box/lrr protein, putative	1.02	0.04	-7.99	0.0067

Table A10 Continued

Gene ID	Gene Name	Wiki Description	12h	4 days	Fold	*p* adj.
AAEL004776		pupal cuticle protein, putative	2.51	0.08	-7.94	0.0052
AAEL008847		wingless	5.65	0.67	-7.92	0.0000
AAEL009204		glucose dehydrogenase	42.30	5.29	-7.91	0.0000
AAEL001059	GSTD3	GSTD1-6 protein, putative	21.25	2.49	-7.90	0.0000
AAEL004279		hypothetical protein	20.23	2.78	-7.70	0.0000
AAEL005781		hypothetical protein	115.88	15.45	-7.69	0.0000
AAEL006154		hypothetical protein	23.31	3.12	-7.67	0.0000
AAEL009077		alkaline phosphatase	9.88	1.18	-7.67	0.0000
AAEL012207		myosin light chain 1, putative	2,768.22	272.67	-7.65	0.0002
AAEL003408		leucine-rich transmembrane protein	2.31	0.28	-7.65	0.0000
AAEL014108		aquaporin, putative	4.66	0.58	-7.65	0.0000
AAEL007216		elongase, putative	128.66	17.33	-7.61	0.0000
AAEL009009		hypothetical protein	4.80	0.22	-7.58	0.0069
AAEL001928		actin	573.38	75.55	-7.56	0.0000
AAEL007632		myosin light chain kinase	1.40	0.09	-7.41	0.0024
AAEL003790		hypothetical protein	12.13	1.36	-7.41	0.0012
AAEL009849		hypothetical protein	2.68	0.33	-7.39	0.0000
AAEL002997	CLIPD3	serine protease	2.22	0.19	-7.38	0.0002
AAEL002231		cuticle protein, putative	4.51	0.32	-7.36	0.0026
AAEL002596	OBP9	Odorant-binding protein 56e, putative	7.77	0.75	-7.26	0.0001
AAEL011291		protease m1 zinc metalloprotease	21.18	3.03	-7.26	0.0000
AAEL017987			10.86	1.32	-7.25	0.0001
AAEL001347		hypothetical protein	1.60	0.13	-7.25	0.0004
AAEL003476		calpain-c	28.68	4.07	-7.24	0.0000
AAEL002004		protein serine/threonine kinase, putative	5.81	0.46	-7.23	0.0017
AAEL003262		leucine-rich transmembrane protein	8.78	1.27	-7.22	0.0000
AAEL007676		hypothetical protein	2.60	0.15	-7.21	0.0048
AAEL000683		hypothetical protein	7.61	1.09	-7.09	0.0000
AAEL001068		myosin light chain 2V, putative	83.19	12.18	-7.08	0.0000
AAEL003295		hypothetical protein	8.90	0.48	-7.08	0.0118
AAEL007542		glutamate decarboxylase	164.55	24.24	-7.06	0.0000
AAEL003442		hypothetical protein	1.33	0.07	-7.06	0.0096
AAEL006827	CYP12F8	cytochrome P450	6.47	0.76	-7.04	0.0000
AAEL007942		fibrinogen and fibronectin	3.83	0.27	-7.00	0.0062
AAEL006675			4.07	0.60	-6.98	0.0000
AAEL014202		wd-repeat protein	2.03	0.22	-6.97	0.0000
AAEL011890		hypothetical protein	1,138.35	168.70	-6.91	0.0000
AAEL004042		hypothetical protein	201.53	30.24	-6.91	0.0000
AAEL005179		hypothetical protein	78.36	8.13	-6.87	0.0013
AAEL004564		hypothetical protein	2.78	0.34	-6.85	0.0000
AAEL000711		hypothetical protein	9.33	1.17	-6.75	0.0000
AAEL007226		nidogen	3.23	0.43	-6.68	0.0000
AAEL013566		hypothetical protein	28.65	4.03	-6.65	0.0000
AAEL000153		hypothetical protein	60.96	9.67	-6.64	0.0000
AAEL003753		fibrinogen and fibronectin	44.43	6.78	-6.64	0.0000
AAEL002029		protein serine/threonine kinase, putative	2.97	0.21	-6.64	0.0060
AAEL003727		ninjurin a	2.34	0.32	-6.64	0.0000
AAEL007104		voltage-gated potassium channel	5.25	0.71	-6.60	0.0000
AAEL012699		hypothetical protein	1.14	0.16	-6.55	0.0000
AAEL004133		echinoid	25.46	4.04	-6.52	0.0000
AAEL011779		hypothetical protein	4.95	0.79	-6.49	0.0000

Table A10 Continued

Gene ID	Gene Name	Wiki Description	12h	4 days	Fold	*p* adj.
AAEL009947		homeotic antennapedia protein, putative	1.96	0.29	-6.48	0.0000
AAEL011809		glucose dehydrogenase	2.24	0.30	-6.47	0.0000
AAEL003596		hypothetical protein	2.18	0.14	-6.43	0.0151
AAEL005416		oxidase/peroxidase	36.02	5.77	-6.37	0.0000
AAEL017417			80.20	12.47	-6.36	0.0000
AAEL005667		LIM domain-binding protein, putative	44.32	7.34	-6.36	0.0000
AAEL004335		secreted ferritin G subunit precursor, putative	8.24	1.32	-6.35	0.0000
AAEL002824		hypothetical protein	5.13	0.84	-6.33	0.0000
AAEL006442		hypothetical protein	10.24	1.69	-6.28	0.0000
AAEL002071	CYP305A6	cytochrome P450	14.04	2.11	-6.27	0.0000
AAEL006872		calponin/transgelin	186.59	30.19	-6.15	0.0000
AAEL001920		hypothetical protein	29.41	4.99	-6.15	0.0000
AAEL007997		hypothetical protein	43.10	7.44	-6.09	0.0000
AAEL011727		hypothetical protein	5.48	0.89	-6.07	0.0000
AAEL018136		hypothetical protein	28.88	5.01	-6.05	0.0000
AAEL011867		hypothetical protein	5.86	0.97	-6.03	0.0000
AAEL005404		hypothetical protein	9.78	1.03	-6.01	0.0023
AAEL000717		protocadherin	1.22	0.13	-5.99	0.0032
AAEL005387		wd-repeat protein	1.30	0.15	-5.94	0.0032
AAEL010064		hypothetical protein	1.34	0.17	-5.88	0.0005
AAEL002474		hypothetical protein	15.42	2.71	-5.83	0.0000
AAEL013304		hypothetical protein	51.05	9.19	-5.80	0.0000
AAEL001232		tubulointerstitial nephritis antigen	358.20	64.40	-5.79	0.0000
AAEL010793		f-box/leucine rich repeat protein	11.20	2.01	-5.79	0.0000
AAEL007776		hypothetical protein	18.10	0.33	-5.77	0.0386
AAEL005703		short-chain dehydrogenase	6.43	1.16	-5.76	0.0000
AAEL005316		hypothetical protein	14.68	2.53	-5.76	0.0000
AAEL017025			16.98	2.80	-5.75	0.0001
AAEL000419		hypothetical protein	140.09	25.75	-5.75	0.0000
AAEL013559		uncoordinated protein	48.76	8.66	-5.74	0.0000
AAEL002263		hypothetical protein	2.64	0.23	-5.70	0.0150
AAEL005989		hypothetical protein	1.67	0.21	-5.66	0.0047
AAEL006797			4.72	0.81	-5.64	0.0002
AAEL006927		hypothetical protein	29.55	5.50	-5.62	0.0000
AAEL003331			43.69	8.16	-5.60	0.0000
AAEL009663		hypothetical protein	5.07	0.89	-5.60	0.0000
AAEL001553		hypothetical protein	125.21	23.72	-5.59	0.0000
AAEL001673		actin	324.06	46.91	-5.56	0.0023
AAEL000797		dimethylaniline monooxygenase	36.43	6.65	-5.55	0.0000
AAEL002342		hypothetical protein	6.92	1.17	-5.54	0.0000
AAEL011166		cadherin	1.64	0.25	-5.54	0.0001
AAEL000398		sidestep protein	1.33	0.19	-5.46	0.0006
AAEL004447		hypothetical protein	4.01	0.34	-5.46	0.0202
AAEL003272		pupal cuticle protein 78E, putative	2.47	0.17	-5.43	0.0359
AAEL007154		phosphatidylethanolamine-binding protein	3.28	0.24	-5.43	0.0352
AAEL000259	CUSOD4	superoxide dismutase	16.79	2.53	-5.42	0.0026
AAEL018011			37.98	7.37	-5.41	0.0000
AAEL012789		hypothetical protein	5.82	1.05	-5.41	0.0004
AAEL002807		hypothetical protein	168.90	31.72	-5.37	0.0000
AAEL013325		hypothetical protein	42.31	7.81	-5.36	0.0000
AAEL010183		hypothetical protein	4.23	0.31	-5.36	0.0389

Table A10 Continued

Gene ID	Gene Name	Wiki Description	12h	4 days	Fold	*p* adj.
AAEL000263		hypothetical protein	2.38	0.42	-5.36	0.0000
AAEL006259	GPROP2	rhodopsin	869.73	59.84	-5.36	0.0439
AAEL002017		protein serine/threonine kinase, putative	2.96	0.28	-5.34	0.0206
AAEL018338		hypothetical protein	20.14	3.87	-5.34	0.0000
AAEL009632		short-chain dehydrogenase	6.80	1.28	-5.32	0.0000
AAEL017652	18S_rRNA		1.18	0.12	-5.32	0.0209
AAEL011153		hypothetical protein	14.56	2.01	-5.30	0.0013
AAEL010884		adp,atp carrier protein	747.03	100.05	-5.29	0.0115
AAEL002292		glucose transport protein, putative	8.14	1.50	-5.25	0.0000
AAEL001766		leucine-rich transmembrane protein, putative	10.32	1.88	-5.23	0.0000
AAEL014832			6.40	1.25	-5.21	0.0000
AAEL013117		hypothetical protein	1.57	0.10	-5.20	0.0393
AAEL001184		hypothetical protein	42.49	8.47	-5.20	0.0000
AAEL004249		hypothetical protein	725.01	73.31	-5.17	0.0365
AAEL000580		hypothetical protein	2.05	0.38	-5.17	0.0000
AAEL013806		hypothetical protein	46.34	9.07	-5.14	0.0000
AAEL014231		hypothetical protein	25.18	4.97	-5.13	0.0000
AAEL002181		cuticle protein, putative	1,325.00	275.64	-5.12	0.0000
AAEL002438			14.24	2.94	-5.12	0.0000
AAEL005117		hypothetical protein	36.53	7.08	-5.09	0.0000
AAEL012150		hypothetical protein	1.63	0.17	-5.09	0.0223
AAEL006702		fibrinogen and fibronectin	1.23	0.09	-5.09	0.0464
AAEL010190		hypothetical protein	1.14	0.21	-5.09	0.0001
AAEL017563			228.43	24.50	-5.04	0.0386
AAEL004994		hypothetical protein	3.16	0.29	-5.02	0.0436
AAEL004209		opioid-binding protein/cell adhes. molecule	8.39	1.65	-5.02	0.0000
AAEL006561		hypothetical protein	1.17	0.22	-5.00	0.0034
AAEL002776		hypothetical protein	164.15	33.16	-4.99	0.0000
AAEL009600	ECR	ecdysone receptor	5.07	0.93	-4.98	0.0000
AAEL018306			25.29	5.15	-4.97	0.0000
AAEL017389			1.86	0.23	-4.95	0.0156
AAEL012101		tubulin alpha chain	26.96	5.82	-4.93	0.0000
AAEL004824		hypothetical protein	19.88	4.12	-4.90	0.0000
AAEL012301		hypothetical protein	3.66	0.73	-4.90	0.0000
AAEL012134		pur-alpha	4.72	0.84	-4.87	0.0002
AAEL012614		nadp-specific isocitrate dehydrogenas	95.11	19.92	-4.87	0.0000
AAEL009352		hypothetical protein	3.61	0.68	-4.86	0.0000
AAEL008069			49.43	10.43	-4.86	0.0000
AAEL000640		alanine-glyoxylate aminotransferase	11.64	2.36	-4.85	0.0000
AAEL005338		novex-3 (titin isoform)	5.19	1.06	-4.82	0.0000
AAEL011022		cysteine-rich protein, putative	91.67	19.36	-4.81	0.0000
AAEL008654		hypothetical protein	1.77	0.29	-4.78	0.0028
AAEL012309		hypothetical protein	1.48	0.28	-4.77	0.0035
AAEL002171		ubiquitin specific proteinase	25.91	5.68	-4.76	0.0000
AAEL005376		hypothetical protein	2.84	0.59	-4.76	0.0000
AAEL001290		hypothetical protein	130.03	26.74	-4.76	0.0000
AAEL008082		hypothetical protein	5.69	0.56	-4.74	0.0427
AAEL008299	CTL11	galactose-specific C-type lectin, putative	4.09	0.73	-4.72	0.0140
AAEL010211		hypothetical protein	1.51	0.19	-4.72	0.0211
AAEL017576			49.51	11.21	-4.71	0.0000

Table A10 Continued

Gene ID	Gene Name	Wiki Description	12h	4 days	Fold	*p* adj.
AAEL013853	CTLGA2	hypothetical protein	30.17	6.65	-4.70	0.0000
AAEL000578		hypothetical protein	4.10	0.86	-4.70	0.0000
AAEL013438		LIM domain-binding protein 3, putative	25.07	5.73	-4.69	0.0000
AAEL011905		myosin i	13.63	3.05	-4.69	0.0000
AAEL011508		hypothetical protein	31.27	6.79	-4.68	0.0000
AAEL003029		hypothetical protein	13.76	2.59	-4.68	0.0022
AAEL012400		hydroxybutyrate dehydrogenase	25.05	5.52	-4.68	0.0000
AAEL011035		hypothetical protein	3.08	0.34	-4.68	0.0391
AAEL008441		hypothetical protein	14.31	2.36	-4.67	0.0233
AAEL014743		hypothetical protein	1.54	0.20	-4.65	0.0274
AAEL004269		hippocalcin	12.54	2.56	-4.64	0.0000
AAEL002040		protein serine/threonine kinase, putative	12.24	2.30	-4.63	0.0006
AAEL005378		set domain protein	3.67	0.72	-4.63	0.0004
AAEL002826		hypothetical protein	2.14	0.36	-4.62	0.0052
AAEL004446		hypothetical protein	3.72	0.52	-4.60	0.0340
AAEL003078		hypothetical protein	75.24	16.92	-4.58	0.0000
AAEL007306		alpha-actinin	433.80	99.45	-4.57	0.0000
AAEL001981		protein serine/threonine kinase, putative	11.46	1.71	-4.55	0.0298
AAEL013477		hypothetical protein	1.23	0.14	-4.52	0.0478
AAEL009468		hypothetical protein	5.92	1.21	-4.51	0.0017
AAEL001477		laminin alpha-1, 2 chain	2.65	0.59	-4.50	0.0000
AAEL012431		AMP dependent ligase	29.44	6.66	-4.48	0.0000
AAEL009801		cuticle protein, putative	1.83	0.28	-4.48	0.0242
AAEL002799		hypothetical protein	25.77	5.73	-4.48	0.0000
AAEL014274		hypothetical protein	501.56	118.43	-4.47	0.0000
AAEL009300		hypothetical protein	11.03	2.28	-4.46	0.0002
AAEL010785		hypothetical protein	15.15	3.45	-4.44	0.0000
AAEL007932		hypothetical protein	1.19	0.23	-4.43	0.0075
AAEL009751		hypothetical protein	12.47	2.92	-4.41	0.0000
AAEL013881		voltage-dependent calcium channel	1.88	0.40	-4.41	0.0001
AAEL004631		actin	600.14	133.29	-4.39	0.0001
AAEL012513		calcium-binding protein E63-1	19.10	4.51	-4.38	0.0000
AAEL007287		hypothetical protein	9.72	2.14	-4.38	0.0000
AAEL018153		rab6-interacting protein 2/elks/erc/cas	1.40	0.31	-4.36	0.0000
AAEL003965		calpain, putative	19.32	4.63	-4.36	0.0000
AAEL014893	CYP6BB2	cytochrome P450	5.46	0.97	-4.36	0.0290
AAEL017146			452.80	107.73	-4.33	0.0000
AAEL002305		hypothetical protein	7.23	1.62	-4.32	0.0008
AAEL018353		hypothetical protein	4.36	1.06	-4.32	0.0000
AAEL008303		calponin/transgelin	104.28	24.55	-4.31	0.0000
AAEL013788		sodium/calcium exchanger	30.67	7.44	-4.30	0.0000
AAEL001054	GSTD4	glutathione-s-transferase theta, gst	19.97	4.15	-4.30	0.0015
AAEL014200		hypothetical protein	1.35	0.21	-4.28	0.0223
AAEL005323		kinesin motor protein, putative	14.10	3.41	-4.27	0.0000
AAEL013564		hypothetical protein	16.48	3.89	-4.26	0.0000
AAEL002436		hypothetical protein	115.20	27.80	-4.26	0.0000
AAEL005440		hypothetical protein	1.37	0.24	-4.24	0.0125
AAEL014370		hypothetical protein	1.15	0.18	-4.23	0.0408
AAEL003252		hypothetical protein	5.64	1.38	-4.22	0.0000
AAEL014559			29.80	6.97	-4.22	0.0001
AAEL005772	OBP22	Odorant-binding protein 99c, putative	118.39	28.22	-4.21	0.0000

Table A10 Continued

Gene ID	Gene Name	Wiki Description	12h	4 days	Fold	*p* adj.
AAEL001868			1.33	0.29	-4.21	0.0002
AAEL001988		protein serine/threonine kinase, putative	21.54	5.31	-4.20	0.0000
AAEL006293		hypothetical protein	9.17	2.32	-4.20	0.0000
AAEL008092		hypothetical protein	31.14	7.74	-4.20	0.0000
AAEL003082		kinectin, putative	10.44	2.29	-4.19	0.0019
AAEL003443		threonine dehydrogenase	29.06	7.10	-4.17	0.0000
AAEL005959		phospholipase b, plb1	32.65	8.12	-4.16	0.0000
AAEL001857		hypothetical protein	4.79	1.19	-4.15	0.0000
AAEL000242		voltage-gated potassium channel	1.54	0.27	-4.15	0.0178
AAEL015095		hypothetical protein	3.34	0.60	-4.14	0.0151
AAEL007407		hypothetical protein	16.59	4.16	-4.14	0.0000
AAEL006583			1.43	0.33	-4.11	0.0007
AAEL002971		sarcalumenin	145.16	36.38	-4.11	0.0000
AAEL013886	GPRFZ9	frizzled-realted	6.75	1.39	-4.10	0.0025
AAEL015577		hypothetical protein	63.67	15.24	-4.10	0.0000
AAEL017397			2.20	0.42	-4.09	0.0297
AAEL011800		hypothetical protein	2.81	0.62	-4.08	0.0013
AAEL012480		sodium/calcium exchanger	43.15	11.13	-4.08	0.0000
AAEL001158		fructose-1,6-bisphosphatase	23.93	6.02	-4.07	0.0000
AAEL009466		protein kinase c	25.47	5.96	-4.06	0.0016
AAEL009583		filamin, putative	26.47	6.82	-4.05	0.0000
AAEL003837		ryanodine receptor 3, brain	47.09	12.27	-4.05	0.0000
AAEL009461		histone H1, putative	5.43	1.27	-4.02	0.0007
AAEL005317		titin (connectin)	104.80	26.85	-4.01	0.0000
AAEL011045		pupal cuticle protein, putative	70.82	18.53	-4.00	0.0000
AAEL001233	CLIPE9	hypothetical protein	48.87	12.42	-4.00	0.0000
AAEL017308			12.20	2.72	-3.99	0.0015
AAEL015525		hypothetical protein	1.93	0.35	-3.98	0.0218
AAEL000818		hypothetical protein	2.94	0.76	-3.98	0.0004
AAEL001026		hypothetical protein	17.02	3.82	-3.98	0.0031
AAEL008632		abc transporter	5.27	1.21	-3.94	0.0024
AAEL002754		nephrin	6.50	1.52	-3.94	0.0013
AAEL018222		allergen, putative	2,154.94	584.94	-3.92	0.0000
AAEL012909		hypothetical protein	1.63	0.37	-3.90	0.0070
AAEL005908		rolling pebbles	13.70	3.72	-3.90	0.0000
AAEL014693		hypothetical protein	1.96	0.40	-3.89	0.0161
AAEL009244		serine-type enodpeptidase, putative	7.52	1.64	-3.88	0.0218
AAEL008617		hypothetical protein	1.92	0.39	-3.88	0.0218
AAEL013596		phosphatidylinositol 3-kinase	6.82	1.55	-3.88	0.0074
AAEL000596		myosin	1.27	0.30	-3.87	0.0049
AAEL010597		hypothetical protein	4.61	1.18	-3.85	0.0105
AAEL010481		sugar transporter	19.35	4.86	-3.84	0.0006
AAEL000139	OBP5	hypothetical protein	13.76	3.58	-3.84	0.0000
AAEL006830		yellow protein precursor	223.53	60.70	-3.82	0.0000
AAEL013884		synaptic vesicle protein	1.13	0.26	-3.80	0.0249
AAEL003047		netrin	3.71	0.94	-3.78	0.0009
AAEL006481		hypothetical protein	4.98	1.21	-3.77	0.0018
AAEL004632		hypothetical protein	7.53	1.69	-3.75	0.0138
AAEL001245		heterogeneous nuclear ribonucleoprotein	3.99	0.79	-3.75	0.0295
AAEL001262		hypothetical protein	2.35	0.47	-3.75	0.0295
AAEL010988		cationic amino acid transporter	7.37	1.99	-3.73	0.0002
AAEL002093		hypothetical protein	4.29	1.05	-3.73	0.0036

Table A10 Continued

Gene ID	Gene Name	Wiki Description	12h	4 days	Fold	*p* adj.
AAEL017468			2,745.18	780.25	-3.72	0.0000
AAEL017098			1,169.04	334.51	-3.70	0.0000
AAEL009863		sodium/dicarboxylate cotransporter, putative	614.84	173.44	-3.70	0.0000
AAEL003527		hypothetical protein	14.53	4.05	-3.69	0.0000
AAEL008970		hypothetical protein	3.29	0.82	-3.69	0.0029
AAEL009258		hypothetical protein	10.74	3.06	-3.68	0.0000
AAEL008314		cadherin, putative	7.54	1.93	-3.68	0.0003
AAEL018236		crossveinless	4.89	1.33	-3.67	0.0000
AAEL012518		hypothetical protein	25.63	7.05	-3.65	0.0000
AAEL006705		hypothetical protein	8.25	2.37	-3.65	0.0002
AAEL018033		hypothetical protein	1.99	0.56	-3.64	0.0033
AAEL014453		hypothetical protein	2.50	0.62	-3.64	0.0250
AAEL008695		netrin receptor unc5	2.72	0.57	-3.63	0.0367
AAEL001946		four and a half lim domains	210.63	60.76	-3.60	0.0000
AAEL012910		hypothetical protein	5.81	1.60	-3.60	0.0003
AAEL005324		titin	32.44	9.60	-3.59	0.0000
AAEL013430		hypothetical protein	5.64	1.51	-3.58	0.0003
AAEL000204		hypothetical protein	33.82	10.12	-3.57	0.0000
AAEL007511		serine protease	2.45	0.59	-3.57	0.0114
AAEL011280		voltage-dependent p/q type calcium channel	29.61	8.61	-3.57	0.0000
AAEL011397		hypothetical protein	1.79	0.46	-3.57	0.0180
AAEL008534		hypothetical protein	71.58	21.11	-3.55	0.0000
AAEL013365		lysosomal acid lipase, putative	2.17	0.53	-3.55	0.0339
AAEL018150		hypothetical protein	1.06	0.27	-3.54	0.0295
AAEL012822		Misexpression suppressor of KSR, putative	4.19	1.24	-3.54	0.0000
AAEL013955		hypothetical protein	1.72	0.43	-3.53	0.0073
AAEL013732		mannosyltransferase 1, putative	4.66	1.30	-3.53	0.0016
AAEL006766		hypothetical protein	15.64	4.29	-3.51	0.0002
AAEL003674		hypothetical protein	44.95	12.43	-3.51	0.0024
AAEL007268			2.42	0.66	-3.50	0.0030
AAEL002554		anosmin, putative	21.65	6.52	-3.50	0.0000
AAEL011798		allergen, putative	77.12	22.87	-3.49	0.0000
AAEL004834			3.36	0.90	-3.49	0.0078
AAEL004369		alpha-glucosidase	12.15	3.22	-3.49	0.0148
AAEL005008		aquaporin	340.78	102.30	-3.49	0.0000
AAEL008336		snail protein, putative	1.04	0.30	-3.47	0.0136
AAEL004114		UNC93A protein, putative	40.95	12.37	-3.46	0.0000
AAEL014552		Glutamate receptor binding protein, putative	2.65	0.81	-3.46	0.0002
AAEL007604		Odorant-binding protein 56a, putative	52.04	15.42	-3.46	0.0000
AAEL003137		hypothetical protein	46.10	14.27	-3.44	0.0000
AAEL005530		hypothetical protein	57.75	17.74	-3.44	0.0000
AAEL008956		hypothetical protein	19.95	6.11	-3.44	0.0000
AAEL011612	CTLMA6	galactose-specific C-type lectin, putative	17.80	5.25	-3.42	0.0000
AAEL007156		hypothetical protein	25.17	7.73	-3.42	0.0000
AAEL015672		hypothetical protein	18.52	5.41	-3.41	0.0015
AAEL005503		hypothetical protein	1.56	0.40	-3.41	0.0385
AAEL005737		hypothetical protein	3.24	0.92	-3.40	0.0002
AAEL000268		lipase	75.66	22.98	-3.40	0.0000
AAEL010344		SEC14, putative	25.51	7.75	-3.40	0.0000

Table A10 Continued

Gene ID	Gene Name	Wiki Description	12h	4 days	Fold	*p* adj.
AAEL010326		hypothetical protein	6.60	1.98	-3.39	0.0000
AAEL009333		hypothetical protein	14.62	4.12	-3.39	0.0097
AAEL014114		mlck, drome	6.91	2.10	-3.38	0.0000
AAEL004731		hypothetical protein	3.63	0.96	-3.37	0.0119
AAEL007302		hypothetical protein	47.89	14.42	-3.37	0.0001
AAEL012046		flotillin-1	3.20	0.92	-3.36	0.0021
AAEL000691		hypothetical protein	4.32	1.04	-3.35	0.0424
AAEL011536		phosphoglucomutase	19.15	6.02	-3.35	0.0000
AAEL005112	CCEAE3A	alpha-esterase	6.62	2.02	-3.35	0.0002
AAEL009660		hypothetical protein	11.73	3.78	-3.31	0.0000
AAEL011818		hypothetical protein	8.09	2.54	-3.31	0.0023
AAEL007505		iroquois-class homeodomain protein irx	6.13	1.82	-3.30	0.0004
AAEL008929	CTLSE1	furrowed	32.99	10.44	-3.30	0.0000
AAEL010178		hypothetical protein	13.31	4.16	-3.30	0.0002
AAEL006582		calcium-transporting atpase	754.22	234.90	-3.30	0.0000
AAEL011364		hypothetical protein	1.13	0.32	-3.30	0.0047
AAEL007436		hypothetical protein	1.30	0.35	-3.29	0.0126
AAEL009906		hypothetical protein	19.07	5.98	-3.29	0.0001
AAEL012402		elongase, putative	43.17	13.37	-3.29	0.0002
AAEL018311		trichohyalin, putative	21.52	6.88	-3.27	0.0000
AAEL012616		nadp transhydrogenase	39.51	12.68	-3.27	0.0000
AAEL011132		metalloproteinase, putative	2.91	0.79	-3.26	0.0376
AAEL017430			37.67	12.23	-3.25	0.0000
AAEL003348		hypothetical protein	7.99	2.66	-3.23	0.0000
AAEL005181		aspartyl/asparaginyl beta-hydroxylase	80.04	26.21	-3.23	0.0000
AAEL004517		hypothetical protein	122.15	40.12	-3.22	0.0000
AAEL010370		aldehyde oxidase	12.53	4.07	-3.22	0.0000
AAEL001467		sdk-P1	4.06	1.32	-3.22	0.0000
AAEL003530		acidic ribosomal protein P1, putative	61.61	19.81	-3.22	0.0000
AAEL011457		hypothetical protein	87.74	28.90	-3.22	0.0000
AAEL008882		hypothetical protein	27.41	9.08	-3.21	0.0000
AAEL005643		guanine nucleotide exchange factor	3.30	1.01	-3.20	0.0010
AAEL002571		band 4.1-like protein 4A (NBL4 protein)	7.27	2.27	-3.20	0.0000
AAEL014144			2.35	0.77	-3.20	0.0007
AAEL015249		sulfate transporter	11.09	3.75	-3.18	0.0000
AAEL000700		cadherin	2.90	0.97	-3.17	0.0000
AAEL011787		hypothetical protein	1.27	0.38	-3.16	0.0068
AAEL013633		ubiquitin-conjugating enzyme h	4.69	1.31	-3.16	0.0249
AAEL012098		synaptic vesicle protein	14.95	4.89	-3.16	0.0004
AAEL006682		hypothetical protein	23.29	6.97	-3.15	0.0227
AAEL006740		hypothetical protein	32.85	10.70	-3.14	0.0000
AAEL008062		thrombospondin	10.20	3.39	-3.14	0.0000
AAEL004003		glucose dehydrogenase	5.21	1.64	-3.14	0.0003
AAEL008765		cuticle protein, putative	5.36	1.79	-3.14	0.0001
AAEL005779		CRAL/TRIO domain-containing protein	24.66	8.31	-3.13	0.0000
AAEL013807		hypothetical protein	8.66	2.60	-3.13	0.0106
AAEL005915		monocarboxylate transporter	3.95	1.19	-3.12	0.0108
AAEL007408		hypothetical protein	56.42	18.30	-3.11	0.0034
AAEL007447		hypothetical protein	1.61	0.48	-3.11	0.0092
AAEL005357		hypothetical protein	8.95	2.68	-3.11	0.0101
AAEL011797		venom allergen	75.06	25.16	-3.11	0.0000

Table A10 Continued

Gene ID	Gene Name	Wiki Description	12h	4 days	Fold	*p* adj.
AAEL012710		hypothetical protein	21.20	7.34	-3.11	0.0000
AAEL002092		cuticle protein, putative	1,903.85	640.51	-3.11	0.0000
AAEL013971		hypothetical protein	2.08	0.67	-3.10	0.0009
AAEL002848		tubulin beta chain	11.33	3.72	-3.07	0.0034
AAEL007667		hypothetical protein	1.73	0.54	-3.07	0.0081
AAEL011008		lipase	2.57	0.87	-3.07	0.0254
AAEL012612		serine/threonine protein kinase	15.23	5.18	-3.07	0.0000
AAEL010106		norepinephrine/norepinephrine transporter	6.97	2.27	-3.06	0.0009
AAEL016996			48.95	16.58	-3.06	0.0000
AAEL013229		tubulin alpha chain	297.85	103.76	-3.05	0.0000
AAEL009185		arginine or creatine kinase	1,910.12	664.86	-3.05	0.0000
AAEL011151		hypothetical protein	13.99	4.66	-3.05	0.0283
AAEL006777		hypothetical protein	39.53	13.39	-3.05	0.0000
AAEL010205		hypothetical protein	734.67	250.44	-3.04	0.0001
AAEL009354		hypothetical protein	2.15	0.68	-3.04	0.0017
AAEL012061		hypothetical protein	5.63	1.76	-3.04	0.0123
AAEL009426		hypothetical protein	5.33	1.69	-3.03	0.0042
AAEL002579		hypothetical protein	3.25	0.96	-3.03	0.0493
AAEL012131		cationic amino acid transporter	14.93	5.17	-3.02	0.0000
AAEL001527		hypothetical protein	5.34	1.69	-3.02	0.0043
AAEL008048		hypothetical protein	12.29	4.19	-3.01	0.0006
AAEL004979	CLIPD2	oviductin	1.68	0.54	-3.01	0.0184
AAEL006866		muscle lim protein	400.98	138.18	-3.00	0.0001
AAEL005327		hypothetical protein	6.01	2.04	-3.00	0.0000
AAEL007201		glutamyl aminopeptidase	58.52	20.81	-3.00	0.0000
AAEL006650		potassium channel beta	18.43	6.16	-2.99	0.0021
AAEL000519		hypothetical protein	847.32	301.57	-2.99	0.0000
AAEL005187		laminin gamma 1 chain	40.97	14.61	-2.99	0.0000
AAEL001842		zinc carboxypeptidase	2.50	0.81	-2.99	0.0274
AAEL014594	CYP301A1	cytochrome P450	8.17	2.85	-2.99	0.0000
AAEL004361		alpha-glucosidase	2.90	1.02	-2.99	0.0007
AAEL002268		hypothetical protein	8.18	2.47	-2.98	0.0340
AAEL006108	OBP24	hypothetical protein	36.36	12.89	-2.98	0.0000
AAEL002062	BETAFTZF1	nuclear hormone receptor ftz-f1 (ftz-f1 alpha)	3.44	1.11	-2.97	0.0046
AAEL012496		hypothetical protein	4.34	1.48	-2.97	0.0001
AAEL007990		hypothetical protein	28.13	10.16	-2.96	0.0000
AAEL005439		mical	2.02	0.67	-2.96	0.0062
AAEL015335		hypothetical protein	3.34	1.06	-2.95	0.0169
AAEL001504		tyrosine-phosphorylation-regulated kinase	12.15	4.31	-2.95	0.0000
AAEL002309	TPX4	peroxiredoxin 6, prx-6	278.14	99.14	-2.95	0.0000
AAEL003003		glutamate-gated chloride channel	3.14	1.02	-2.95	0.0069
AAEL000006		phosphoenolpyruvate carboxykinase	2.68	0.96	-2.94	0.0001
AAEL009949		homeotic antennapedia protein, putative	10.11	3.29	-2.94	0.0273
AAEL001582		kinesin	3.81	1.27	-2.93	0.0074
AAEL013575		hypothetical protein	1.82	0.60	-2.93	0.0172
AAEL012840		stathmin	16.07	5.40	-2.92	0.0035
AAEL008268		hypothetical protein	28.07	10.06	-2.92	0.0000
AAEL004244		hypothetical protein	10.74	3.77	-2.91	0.0000
AAEL011470		cis,cis-muconate transport protein MucK	414.63	151.65	-2.91	0.0000

Table A10 Continued

Gene ID	Gene Name	Wiki Description	12h	4 days	Fold	*p* adj.
AAEL008748			1.05	0.34	-2.91	0.0461
AAEL000695		hypothetical protein	6.06	2.02	-2.91	0.0044
AAEL010519		succinate dehydrogenase, putative	14.39	4.89	-2.90	0.0015
AAEL007582		granzyme A precursor, putative	37.18	13.49	-2.90	0.0000
AAEL011900		acetylglucosaminyltransferase	7.26	2.51	-2.89	0.0001
AAEL013343		lethal(2)essential for life protein, l2efl	58.16	21.39	-2.89	0.0000
AAEL008596	SPZ3A	Sptzle 3A (Spz3A)	13.84	5.01	-2.89	0.0000
AAEL011645		hypothetical protein	2.26	0.77	-2.89	0.0496
AAEL000281		hypothetical protein	56.21	20.69	-2.89	0.0000
AAEL001375		Y-box binding protein	185.03	69.00	-2.87	0.0000
AAEL013218		thiamine transporter	7.46	2.65	-2.86	0.0037
AAEL014419		hypothetical protein	63.41	23.23	-2.86	0.0000
AAEL006148		adamts-20	3.18	1.06	-2.85	0.0154
AAEL004197		hypothetical protein	2,881.38	1,030.13	-2.85	0.0025
AAEL010482		acidic membrane protein, putative	3.77	1.28	-2.84	0.0069
AAEL018137		hypothetical protein	13.02	4.79	-2.84	0.0000
AAEL003516		hypothetical protein	2.42	0.90	-2.84	0.0006
AAEL003307		receptor protein tyrosine phosphatase,	1.79	0.61	-2.83	0.0185
AAEL010210		neurogenic locus notch (notch)	8.80	3.29	-2.83	0.0000
AAEL013701		meiotic recombination protein spo11	1.09	0.36	-2.83	0.0403
AAEL014271		hypothetical protein	4.59	1.48	-2.83	0.0437
AAEL013319		hypothetical protein	4.59	1.69	-2.82	0.0012
AAEL012979		hypothetical protein	4.10	1.52	-2.82	0.0197
AAEL005256		hypothetical protein	6.53	2.33	-2.82	0.0003
AAEL013341		lethal(2)essential for life protein, l2efl	62.16	21.99	-2.81	0.0149
AAEL008001		hypothetical protein	5.22	1.97	-2.81	0.0103
AAEL005044		hypothetical protein	4.52	1.58	-2.81	0.0130
AAEL001490		acylphosphatase, putative	28.92	10.27	-2.80	0.0141
AAEL003609		neurobeachin	4.96	1.74	-2.80	0.0063
AAEL010757		hypothetical protein	2.26	0.81	-2.79	0.0057
AAEL007949		clk2	4.76	1.69	-2.79	0.0051
AAEL012168		zinc finger protein	1.34	0.47	-2.78	0.0078
AAEL008773		laminin A chain, putative	17.02	6.42	-2.78	0.0000
AAEL004666			12.64	4.82	-2.78	0.0000
AAEL000886		hypothetical protein	514.38	193.23	-2.77	0.0002
AAEL011094		hypothetical protein	63.52	24.41	-2.77	0.0000
AAEL010659		lethal(2)essential for life protein, l2efl	33.29	12.75	-2.76	0.0000
AAEL013057		serine/threonine-protein kinase wnk 1,3,4	2.45	0.87	-2.75	0.0059
AAEL012449		myosin x	3.17	1.20	-2.75	0.0000
AAEL012128		cationic amino acid transporter	3.08	1.10	-2.75	0.0387
AAEL004669		hypothetical protein	20.28	7.23	-2.74	0.0256
AAEL009337		adenylate kinase isoenzyme	454.24	177.25	-2.74	0.0000
AAEL011430		hypothetical protein	16.12	5.66	-2.74	0.0193
AAEL007463		5,10-methylenetetrahydrofolate reductase	5.34	2.04	-2.73	0.0019
AAEL001760		hypothetical protein	9.19	3.62	-2.73	0.0000
AAEL014226		hypothetical protein	90.99	35.22	-2.72	0.0000
AAEL012186			1.24	0.42	-2.72	0.0499
AAEL013174		hypothetical protein	2.38	0.92	-2.72	0.0007
AAEL014044		hypothetical protein	12.54	4.87	-2.71	0.0005
AAEL009492		hypothetical protein	69.51	27.36	-2.71	0.0000
AAEL001629			5.59	2.06	-2.70	0.0096
AAEL012561		hypothetical protein	6.66	2.53	-2.69	0.0000

Table A10 Continued

Gene ID	Gene Name	Wiki Description	12h	4 days	Fold	*p* adj.
AAEL006897		hypothetical protein	2.49	0.96	-2.69	0.0000
AAEL013956		ganglioside induced differentiation associated	12.21	4.50	-2.68	0.0071
AAEL002261		GTP cyclohydrolase i	338.05	134.07	-2.68	0.0000
AAEL011332		dopamine beta hydroxylase	108.96	42.29	-2.68	0.0006
AAEL002262		hypothetical protein	6.62	2.41	-2.67	0.0393
AAEL012013		hypothetical protein	1.46	0.51	-2.67	0.0472
AAEL012462		hypothetical protein	5.00	1.89	-2.67	0.0054
AAEL006496		steroid dehydrogenase	26.66	10.77	-2.67	0.0000
AAEL013452		hypothetical protein	15.11	5.99	-2.66	0.0003
AAEL005849		synaptic vesicle protein	101.93	40.49	-2.66	0.0000
AAEL006773		hypothetical protein	52.94	20.40	-2.66	0.0010
AAEL006558		n-acetylgalactosaminyltransferase	2.41	0.89	-2.66	0.0413
AAEL000994		hypothetical protein	53.85	21.58	-2.66	0.0000
AAEL007952			14.46	5.67	-2.66	0.0000
AAEL008078		clk2	31.10	12.30	-2.66	0.0001
AAEL009795		papilin	2.25	0.88	-2.65	0.0009
AAEL004363		hypothetical protein	13.86	5.24	-2.65	0.0116
AAEL006199		neurexin	10.52	4.08	-2.64	0.0010
AAEL010049		hypothetical protein	51.61	20.74	-2.64	0.0001
AAEL013656		bm-40 precursor	440.90	176.46	-2.63	0.0000
AAEL014217		nicotinate phosphoribosyltransferase	24.82	10.08	-2.63	0.0000
AAEL005519		synaptotagmin-14	3.28	1.18	-2.63	0.0283
AAEL001466		hypothetical protein	64.47	26.28	-2.63	0.0000
AAEL012344			4.93	1.81	-2.62	0.0194
AAEL011184		mitochondrial phosphate carrier protein	332.11	132.90	-2.62	0.0001
AAEL008340		cell adhesion molecule	58.70	23.86	-2.62	0.0000
AAEL017521			3.28	1.28	-2.61	0.0002
AAEL008315		calponin/transgelin	10.62	4.19	-2.61	0.0237
AAEL012613		hypothetical protein	10.47	4.19	-2.61	0.0000
AAEL003037		hypothetical protein	6.51	2.62	-2.61	0.0001
AAEL018324		regulating synaptic memb. exocytosis protein	1.64	0.61	-2.61	0.0284
AAEL005102		hypothetical protein	8.83	3.38	-2.60	0.0019
AAEL003129		neuroligin, putative	10.06	4.07	-2.60	0.0001
AAEL002879		heterogeneous nuclear ribonucleoprotein r	127.36	51.43	-2.60	0.0000
AAEL008915		Na-and Cl-activated ATP-sensitive K channel	3.25	1.25	-2.60	0.0011
AAEL014919		lipase 1 precursor	97.25	39.76	-2.60	0.0000
AAEL012665		glucose-6-phosphate isomerase	5.51	2.13	-2.60	0.0012
AAEL010802		hypothetical protein	15.93	6.35	-2.60	0.0001
AAEL006707		hypothetical protein	28.02	11.44	-2.59	0.0000
AAEL008390		guanylate cyclase	2.11	0.81	-2.59	0.0033
AAEL004102		aldo-keto reductase	111.63	45.94	-2.59	0.0000
AAEL015058		hypothetical protein	9.56	3.69	-2.59	0.0024
AAEL006899		DNA-J/hsp40	12.03	4.79	-2.59	0.0001
AAEL003407		hypothetical protein	13.83	5.76	-2.59	0.0049
AAEL004730		hypothetical protein	26.93	10.61	-2.58	0.0093
AAEL000609		hypothetical protein	135.06	55.70	-2.57	0.0000
AAEL002308		butyrate response factor 1 (TIS11B protein)	19.78	8.02	-2.57	0.0000
AAEL003734		aconitase, mitochondrial	25.48	10.57	-2.57	0.0000

Table A10 Continued

Gene ID	Gene Name	Wiki Description	12h	4 days	Fold	*p* adj.
AAEL014219		nicotinate phosphoribosyltransferase	26.58	11.01	-2.56	0.0000
AAEL001242		ribosomal pseudouridine synthase	6.82	2.57	-2.56	0.0359
AAEL011752	GSTI1	glutathione-s-transferase theta, gst	234.79	98.19	-2.55	0.0000
AAEL001045		hypothetical protein	12.49	5.06	-2.55	0.0417
AAEL003213		guanine deaminase	12.36	5.17	-2.54	0.0001
AAEL006774		hypothetical protein	9.77	3.92	-2.54	0.0151
AAEL005392		dihydropyridine-sensitive calcium channel	6.62	2.74	-2.54	0.0000
AAEL002043	CYP305A5	cytochrome P450	2.27	0.86	-2.54	0.0356
AAEL017444			10.29	4.38	-2.54	0.0003
AAEL001763		hypothetical protein	59.25	24.52	-2.54	0.0053
AAEL003391		tankyrase	3.76	1.48	-2.53	0.0041
AAEL011975		ubiquitin specific protease	7.77	3.21	-2.53	0.0001
AAEL001143		hypothetical protein	6.45	2.62	-2.53	0.0018
AAEL008354		gaba receptor invertebrate	8.07	3.19	-2.53	0.0060
AAEL006372		sulfate transporter	2.58	1.10	-2.52	0.0112
AAEL014343		hypothetical protein	5.44	2.11	-2.52	0.0139
AAEL003932		hypothetical protein	18.33	7.30	-2.51	0.0163
AAEL010294		membrane-associated guanylate kinase	35.34	14.91	-2.51	0.0000
AAEL005224		hypothetical protein	51.69	21.61	-2.51	0.0006
AAEL014279		glycosyltransferase	5.92	2.34	-2.51	0.0142
AAEL003560		pou domain/drifter/cf-1a	7.03	2.94	-2.50	0.0004
AAEL005264		hypothetical protein	23.54	9.36	-2.50	0.0097
AAEL009948		aldehyde dehydrogenase	2.20	0.89	-2.50	0.0196
AAEL012756		hypothetical protein	4.49	1.70	-2.49	0.0444
AAEL006695		hypothetical protein	222.87	93.43	-2.49	0.0010
AAEL007806		hypothetical protein	66.97	28.35	-2.49	0.0004
AAEL004089		hypothetical protein	5.27	2.15	-2.49	0.0100
AAEL002853		ccaat/enhancer binding protein	3.18	1.32	-2.48	0.0245
AAEL017529			24.35	10.44	-2.48	0.0000
AAEL010143		isocitrate dehydrogenase	55.30	23.58	-2.48	0.0000
AAEL009569		apolipoprotein D, putative	12.78	5.55	-2.47	0.0000
AAEL005319			50.66	21.52	-2.47	0.0004
AAEL010936		gamma glutamyl transpeptidases	17.70	7.56	-2.47	0.0000
AAEL008287	GPRDIH2	diuretic hormone receptor, putative	7.76	2.96	-2.47	0.0494
AAEL010479		sugar transporter	26.01	11.17	-2.47	0.0001
AAEL006955		cadherin	3.00	1.30	-2.47	0.0000
AAEL003658		laminin beta-2 chain	55.65	24.01	-2.47	0.0000
AAEL007643		molybdopterin synthase small subunit	31.26	13.54	-2.46	0.0057
AAEL009070		hypothetical protein	19.45	7.73	-2.46	0.0201
AAEL011766		hypothetical protein	4.60	2.00	-2.45	0.0132
AAEL008684		serrano protein	9.99	4.38	-2.45	0.0000
AAEL012519		actin binding protein, putative	3.17	1.24	-2.44	0.0424
AAEL017007			301.10	127.33	-2.44	0.0098
AAEL013872		hypothetical protein	51.41	22.22	-2.44	0.0000
AAEL001384		triple functional domain, trio	4.99	2.03	-2.44	0.0436
AAEL007105		hypothetical protein	7.31	3.10	-2.44	0.0010
AAEL007148		hypothetical protein	3.85	1.58	-2.43	0.0398
AAEL002583	TOLL7	toll	18.55	8.15	-2.43	0.0000
AAEL004812		kinesin-like protein KIF1A	30.04	12.46	-2.43	0.0356
AAEL012562		circadian locomoter output cycles kaput	2.67	1.12	-2.42	0.0043
AAEL007803		lamin b receptor	28.52	12.30	-2.42	0.0011

Table A10 Continued

Gene ID	Gene Name	Wiki Description	12h	4 days	Fold	*p* adj.
AAEL004600		hypothetical protein	6.62	2.92	-2.42	0.0000
AAEL000920		hypothetical protein	21.25	9.21	-2.41	0.0044
AAEL014367		hypothetical protein	29.91	13.22	-2.40	0.0000
AAEL012897		aconitase, mitochondrial	36.19	15.95	-2.40	0.0000
AAEL010399		1-acylglycerol-3-phosphate acyltransferase	33.42	14.78	-2.40	0.0002
AAEL012740		ATPase subunit, putative	354.46	157.37	-2.40	0.0000
AAEL010488		ets	15.04	6.73	-2.39	0.0000
AAEL003291		hypothetical protein	6.25	2.78	-2.38	0.0065
AAEL003733			3.17	1.36	-2.38	0.0024
AAEL010471		choline o-acyltransferase	2.86	1.29	-2.38	0.0437
AAEL004854		hypothetical protein	6.24	2.59	-2.38	0.0149
AAEL000539		hypothetical protein	58.19	26.03	-2.38	0.0005
AAEL000094		hypothetical protein	26.91	11.95	-2.38	0.0000
AAEL006012		factor for adipocyte differentiation	1.54	0.63	-2.36	0.0489
AAEL009114		hypothetical protein	13.08	5.65	-2.36	0.0092
AAEL002716		hypothetical protein	5.09	2.20	-2.36	0.0046
AAEL012421		cadherin	3.78	1.65	-2.36	0.0011
AAEL002230			13.90	6.15	-2.36	0.0016
AAEL001963		protein serine/threonine kinase, putative	131.56	59.65	-2.36	0.0000
AAEL003247			30.92	14.05	-2.36	0.0000
AAEL003618		sodium/shloride dependent aa transporter	33.82	15.19	-2.36	0.0007
AAEL014107		hypothetical protein	5.74	2.54	-2.35	0.0027
AAEL006768		hypothetical protein	69.59	31.39	-2.35	0.0000
AAEL013808		fascin	31.55	14.10	-2.35	0.0004
AAEL001356		RNA-binding protein	48.33	21.84	-2.35	0.0000
AAEL006264		glucose transporter (sugar transporter	75.68	34.16	-2.35	0.0000
AAEL013309		high-affinity copper uptake protein	104.28	47.55	-2.35	0.0000
AAEL011154		hypothetical protein	23.36	10.64	-2.35	0.0001
AAEL014347		hypothetical protein	1.32	0.57	-2.34	0.0028
AAEL002506	IRf	glutamate receptor, ionotropic kainate 1, 2, 3	21.25	9.59	-2.34	0.0004
AAEL007804		semaphorin	17.24	7.84	-2.33	0.0000
AAEL009175		slit protein	5.13	2.26	-2.33	0.0022
AAEL009659		heterogeneous nuclear ribonucleoprotein l	8.02	3.74	-2.32	0.0005
AAEL012349		lipase 1 precursor	36.85	16.76	-2.32	0.0000
AAEL009888		bumetanide-sensitive Na-K-Cl cotransport	7.99	3.60	-2.32	0.0001
AAEL011436		myosin xv	24.36	11.18	-2.32	0.0000
AAEL018218		A-kinase anchoring protein AKAP12	14.89	6.85	-2.32	0.0000
AAEL010379		ATP-binding cassette transporter	74.15	34.05	-2.31	0.0000
AAEL018234		hypothetical protein	5.52	2.47	-2.31	0.0052
AAEL013306		hypothetical protein	13.51	6.08	-2.30	0.0220
AAEL017518			4.53	2.10	-2.30	0.0076
AAEL005464		hypothetical protein	18.90	8.72	-2.30	0.0000
AAEL005822		hypothetical protein	23.08	10.75	-2.30	0.0000
AAEL000080		phosphoenolpyruvate carboxykinase	28.09	12.91	-2.29	0.0003
AAEL000102		hypothetical protein	10.82	4.99	-2.29	0.0033
AAEL005003		serine/threonine-protein kinase, putative	13.05	6.09	-2.29	0.0000
AAEL012890			3.41	1.55	-2.29	0.0005

Table A10 Continued

Gene ID	Gene Name	Wiki Description	12h	4 days	Fold	*p* adj.
AAEL000217		serine/threonine protein kinase	4.45	2.01	-2.29	0.0017
AAEL002530		hypothetical protein	9.91	4.35	-2.29	0.0241
AAEL013526		hypothetical protein	138.23	64.39	-2.28	0.0000
AAEL011792		potassium/chloride symporter, putative	2.59	1.20	-2.28	0.0117
AAEL004251			9.96	4.70	-2.27	0.0000
AAEL006680		hypothetical protein	2.15	0.97	-2.27	0.0038
AAEL018219			80.12	37.54	-2.27	0.0000
AAEL006649		tnf receptor associated factor	3.63	1.71	-2.26	0.0020
AAEL006664		hypothetical protein	5.96	2.76	-2.26	0.0084
AAEL013524		hypothetical protein	108.88	51.69	-2.26	0.0000
AAEL004661		beta-hexosaminidase	27.41	12.87	-2.26	0.0000
AAEL011265		abc transporter	15.17	7.08	-2.26	0.0001
AAEL006911		microtubule-associated protein	10.77	4.85	-2.25	0.0324
AAEL014391		map kinase phosphatase	6.28	2.86	-2.25	0.0020
AAEL014438		Juvenile hormone-inducible protein, putative	2.96	1.38	-2.25	0.0488
AAEL018268		disheveled associated activator	14.05	6.68	-2.25	0.0000
AAEL011065		hypothetical protein	6.33	2.90	-2.24	0.0048
AAEL011250		hypothetical protein	5.67	2.66	-2.24	0.0011
AAEL011256		cation efflux protein/ zinc transporter	5.23	2.44	-2.24	0.0106
AAEL000931		alkaline phosphatase	549.51	259.82	-2.24	0.0003
AAEL009619		voltage-gated potassium channel	3.60	1.60	-2.24	0.0205
AAEL008318		cadherin, putative	19.67	9.46	-2.23	0.0000
AAEL010952			1.66	0.75	-2.23	0.0312
AAEL013318		hypothetical protein	3.83	1.79	-2.22	0.0331
AAEL000121		dihydropyridine-sensitive l-type Ca channel	3.75	1.74	-2.22	0.0007
AAEL001969		protein serine/threonine kinase, putative	1,297.92	622.62	-2.22	0.0000
AAEL005369		zinc finger protein	18.81	8.65	-2.22	0.0422
AAEL010113		hypothetical protein	33.28	15.73	-2.22	0.0010
AAEL014428		hypothetical protein	20.37	9.71	-2.21	0.0000
AAEL013600		integrin alpha-ps	24.73	11.83	-2.20	0.0025
AAEL007191		amino acid transporter	45.98	21.98	-2.20	0.0011
AAEL008881		RHC18, putative	2.82	1.33	-2.20	0.0027
AAEL002684		dachshund, putative	6.50	3.13	-2.19	0.0165
AAEL004496		glutamate transporter	67.70	33.05	-2.19	0.0000
AAEL017309			6.95	3.16	-2.18	0.0412
AAEL008289		pupal cuticle protein 78E, putative	327.08	157.67	-2.18	0.0106
AAEL001283		hypothetical protein	6.33	3.13	-2.18	0.0119
AAEL017280			11.75	5.63	-2.17	0.0087
AAEL000540		fasciclin, putative	69.44	34.25	-2.17	0.0000
AAEL010189		hypothetical protein	42.52	20.14	-2.17	0.0362
AAEL017011			3.97	1.92	-2.17	0.0013
AAEL018036		hypothetical protein	8.95	4.31	-2.16	0.0045
AAEL004094		pou domain	14.77	7.13	-2.16	0.0046
AAEL000712		hypothetical protein	21.33	10.17	-2.15	0.0298
AAEL009684		hypothetical protein	14.52	6.94	-2.15	0.0178
AAEL000251		hypothetical protein	16.10	7.76	-2.15	0.0110
AAEL007029		tropomodulin	123.59	61.37	-2.15	0.0000
AAEL003688		hypothetical protein	11.74	5.69	-2.15	0.0046
AAEL000511		acetylcholinesterase	7.52	3.62	-2.15	0.0136
AAEL005634		harmonin, putative	21.98	10.66	-2.14	0.0257

Table A10 Continued

Gene ID	Gene Name	Wiki Description	12h	4 days	Fold	*p* adj.
AAEL002192		M12 mutant protein precursor, putative	5.76	2.79	-2.14	0.0106
AAEL004972		hypothetical protein	32.66	16.34	-2.14	0.0000
AAEL004222		voltage-dependent p/q type calcium channel	8.32	4.04	-2.14	0.0156
AAEL000288		hypothetical protein	25.23	12.29	-2.14	0.0023
AAEL011182		sex-determining protein fem-1	11.66	5.73	-2.13	0.0005
AAEL017572			10.74	5.07	-2.13	0.0373
AAEL011821		adenylyl cyclase-associated protein	5.46	2.65	-2.13	0.0419
AAEL014846		innexin	94.59	47.43	-2.13	0.0000
AAEL003594		kinectin, putative	8.25	4.17	-2.13	0.0017
AAEL004169		hypothetical protein	383.81	187.74	-2.13	0.0257
AAEL011349		serine protease	37.55	18.90	-2.12	0.0001
AAEL003772		hypothetical protein	10.69	5.36	-2.12	0.0001
AAEL002299		high affinity copper transporter, putative	119.58	60.49	-2.12	0.0000
AAEL011292		protease m1 zinc metalloprotease	303.60	152.29	-2.12	0.0001
AAEL010290		short-chain dehydrogenase	94.27	47.51	-2.12	0.0000
AAEL002972		brain chitinase and chia	5.39	2.61	-2.12	0.0250
AAEL010814		isocitrate dehydrogenase	60.35	30.28	-2.12	0.0003
AAEL000897		hypothetical protein	60.92	30.32	-2.12	0.0006
AAEL012913		hypothetical protein	4.82	2.38	-2.11	0.0259
AAEL002678		ras suppressor protein 1, rsu1	34.82	17.66	-2.11	0.0000
AAEL003044		Fasciclin-1 precursor	14.00	6.87	-2.11	0.0093
AAEL002820		hypothetical protein	2.95	1.49	-2.11	0.0017
AAEL009571		elongase, putative	60.42	30.01	-2.11	0.0007
AAEL010841		lupus la ribonucleoprotein	3.95	1.91	-2.11	0.0151
AAEL004221		glycogen synthase	13.36	6.76	-2.11	0.0001
AAEL002892		protein kinase c, mu	27.05	13.71	-2.11	0.0000
AAEL010037		phosphoglucomutase	29.21	14.68	-2.11	0.0000
AAEL006256		ATPase subunit, putative	158.56	79.93	-2.10	0.0011
AAEL002995		pyrazinamidase/nicotinamidase	24.30	12.25	-2.10	0.0015
AAEL018313		hypothetical protein	21.26	10.71	-2.10	0.0017
AAEL002542		triosephosphate isomerase	220.94	111.84	-2.10	0.0002
AAEL000577			22.84	11.60	-2.10	0.0001
AAEL006447		GATA transcription factor (GATAb)	2.06	1.00	-2.10	0.0230
AAEL002269		purine nucleoside phosphorylase	26.79	13.44	-2.10	0.0002
AAEL013461		parvin	79.83	40.50	-2.10	0.0000
AAEL008389		ankyrin repeat-rich membrane-spanning prot.	41.97	21.33	-2.10	0.0000
AAEL001876		decapentaplegic, deca	14.23	7.09	-2.10	0.0184
AAEL012404		transcription factor sp8,sp9	14.86	7.41	-2.09	0.0117
AAEL008102		actin binding protein, putative	27.07	13.79	-2.09	0.0000
AAEL010321		porphobilinogen deaminase	25.55	13.12	-2.08	0.0000
AAEL012363		hypothetical protein	3.55	1.85	-2.08	0.0150
AAEL011460		hypothetical protein	70.91	36.30	-2.08	0.0000
AAEL005218		hypothetical protein	225.53	116.39	-2.08	0.0000
AAEL012410	AGO1b	eukaryotic translation initiation factor 2c	6.06	3.14	-2.08	0.0011
AAEL007091		single-stranded DNA-binding protein mssp-1	12.30	6.14	-2.08	0.0077
AAEL014637		inositol 1,4,5-trisphosphate receptor	4.86	2.43	-2.08	0.0156
AAEL015320		striatin	18.96	9.57	-2.08	0.0033
AAEL012031		hypothetical protein	7.97	4.11	-2.08	0.0000

Table A10 Continued

Gene ID	Gene Name	Wiki Description	12h	4 days	Fold	*p* adj.
AAEL014950	SPZ3B	hypothetical protein	18.38	9.41	-2.07	0.0078
AAEL009362		cationic amino acid transporter	3.31	1.65	-2.07	0.0067
AAEL007320		hypothetical protein	5.61	2.84	-2.07	0.0468
AAEL018172		breast carcinoma amplified sequence	8.58	4.32	-2.07	0.0202
AAEL008478		hypothetical protein	61.85	31.61	-2.07	0.0002
AAEL016988			55.38	28.59	-2.07	0.0000
AAEL000233		membrane-associated guanylate kinase	16.95	8.62	-2.07	0.0038
AAEL007575		hypothetical protein	20.99	10.81	-2.07	0.0036
AAEL011248		innexin	72.08	37.30	-2.06	0.0000
AAEL004957		hypothetical protein	37.95	19.55	-2.06	0.0054
AAEL014018		hypothetical protein	10.65	5.51	-2.06	0.0043
AAEL007329		hypothetical protein	21.95	11.35	-2.06	0.0035
AAEL010469		hypothetical protein	5.10	2.50	-2.06	0.0404
AAEL005879		vinculin	28.76	14.99	-2.06	0.0000
AAEL001515	DEBCL	Bcl-2 associated protein, putative	57.37	29.95	-2.05	0.0000
AAEL004502		hypothetical protein	7.50	3.89	-2.05	0.0380
AAEL014394		growth factor receptor-bound protein	11.25	5.84	-2.05	0.0423
AAEL011789		citrate synthase	40.18	20.72	-2.05	0.0132
AAEL001005		calreticulin	88.43	46.27	-2.04	0.0000
AAEL008680		hypothetical protein	47.03	24.26	-2.04	0.0131
AAEL015219		hypothetical protein	10.81	5.36	-2.04	0.0357
AAEL011355		carnitine o-acetyltransferase	35.29	18.44	-2.04	0.0027
AAEL004515		hypothetical protein	28.79	15.11	-2.03	0.0003
AAEL006480		hypothetical protein	511.38	270.57	-2.03	0.0000
AAEL002457		hypothetical protein	152.04	80.08	-2.03	0.0000
AAEL017532			19.52	9.99	-2.03	0.0077
AAEL005565		hypothetical protein	39.27	20.60	-2.02	0.0000
AAEL012065		cytoplasmic polyadenyl. ele. binding protein	13.26	7.02	-2.02	0.0007
AAEL000967		tmc7 protein	16.72	8.73	-2.02	0.0001
AAEL006373		serine protease htra2	5.47	2.85	-2.02	0.0116
AAEL003623		hypothetical protein	17.03	8.94	-2.02	0.0006
AAEL005228		hypothetical protein	27.75	14.66	-2.02	0.0001
AAEL007132		dynein heavy chain	14.84	7.72	-2.02	0.0149
AAEL004434		transketolase	120.30	63.77	-2.02	0.0000
AAEL006783			7.36	3.78	-2.02	0.0382
AAEL008630		GTP-binding protein alpha subunit, gna	3.23	1.68	-2.01	0.0163
AAEL017064			59.88	31.74	-2.01	0.0002
AAEL002381		hypothetical protein	35.13	18.33	-2.01	0.0285
AAEL000855		mannosyltransferase 1, putative	17.88	9.40	-2.01	0.0004
AAEL008034		hypothetical protein	285.93	152.38	-2.01	0.0000
AAEL011193		steroid dehydrogenase	82.53	43.81	-2.01	0.0004
AAEL007773		hypothetical protein	24.65	13.00	-2.01	0.0007
AAEL001817		hypothetical protein	50.43	26.79	-2.01	0.0003
AAEL008277		WNT3 precursor, putative	22.74	12.01	-2.00	0.0005
AAEL000766		ubiquinol cytochrome C oxidoreductase	784.80	417.38	-2.00	0.0002
AAEL004803		hypothetical protein	6.00	3.22	-2.00	0.0447
AAEL006822		otopetrin	54.61	29.28	-2.00	0.0000
AAEL014422		syntrophin	15.22	8.13	-2.00	0.0003
AAEL006085		methylenetetrahydrofolate dehydrogenase	25.08	13.37	-2.00	0.0002

Table A10 Continued

Gene ID	Gene Name	Wiki Description	12h	4 days	Fold	*p* adj.
AAEL010764		aldehyde dehydrogenase	187.77	100.25	-2.00	0.0000
AAEL018309		lipase	42.06	22.39	-2.00	0.0001

Table A11 Differentially expressed gene in the antenna of males and females.

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
		Higher in Females				
AAEL002092		cuticle protein	24.80	640.22	22.15	0.0000
AAEL007098		4-nitrophenylphosphatase	0.18	4.45	19.82	0.0000
AAEL016981	Or36		0.53	12.23	19.46	0.0000
AAEL017065	Or92		0.21	4.28	18.55	0.0000
AAEL017316	Or107		0.16	3.53	17.63	0.0000
AAEL017014	Or105		1.82	33.69	17.44	0.0000
AAEL017537	Or123		0.64	11.63	16.64	0.0000
AAEL017377	Or117		0.64	11.72	16.24	0.0000
AAEL017043	Or84		24.49	367.48	14.65	0.0000
AAEL017505	Or103		4.77	72.29	14.46	0.0000
AAEL017000	Or97		0.42	6.69	14.15	0.0000
AAEL011036		hypothetical protein	0.07	1.68	14.03	0.0000
AAEL017201	Or94		1.72	24.91	13.98	0.0000
AAEL018070			2.08	28.55	13.06	0.0000
AAEL013789		hypothetical protein	0.57	9.25	12.97	0.0000
AAEL012198		adp,atp carrier protein	0.84	11.88	12.91	0.0000
AAEL017452			1.51	20.41	12.68	0.0000
AAEL017219	Or114		1.22	16.01	12.28	0.0000
AAEL001675	CLIPA10		0.69	8.29	11.70	0.0000
AAEL015474		hypothetical protein	0.02	1.42	11.63	0.0016
AAEL010779		pickpocket	1.09	13.51	11.63	0.0000
AAEL005682		protein serine/threonine kinase	0.07	1.92	11.22	0.0005
AAEL010242		hypothetical protein	49.49	560.93	11.14	0.0000
AAEL017123	Or113		9.04	102.03	11.00	0.0000
AAEL008984		hypothetical protein	0.97	12.88	10.59	0.0000
AAEL011796	Or62	Odorant receptor 7a	1.80	19.09	10.51	0.0000
AAEL013507	Or52	hypothetical protein	1.25	14.07	10.43	0.0000
AAEL003711		hypothetical protein	0.07	2.13	10.27	0.0017
AAEL014197	Or88	hypothetical protein	6.06	61.91	10.07	0.0000
AAEL009000		hypothetical protein	2.78	33.30	9.83	0.0000
AAEL005480		hairy protein	0.29	3.16	9.64	0.0000
AAEL014599		hypothetical protein	0.38	5.53	9.05	0.0003
AAEL018095			6.21	57.60	9.05	0.0000
AAEL017178	Or111		5.80	52.94	8.85	0.0000
AAEL017361	Or115		1.59	14.53	8.46	0.0000
AAEL016966	Or104		4.41	37.58	8.37	0.0000
AAEL017336			0.37	3.33	8.07	0.0000
AAEL017129	Or72		1.84	16.13	7.99	0.0000
AAEL011409	Or100	hypothetical protein	8.31	68.82	7.97	0.0000
AAEL012377	OBP55	Odorant-binding protein 56a	4,416.69	35,491.10	7.92	0.0000
AAEL016412			23.00	183.92	7.89	0.0000
AAEL014381		hypothetical protein	5.22	41.89	7.79	0.0000
AAEL002648		hypothetical protein	0.02	1.36	7.74	0.0162
AAEL000252		hypothetical protein	7.42	58.91	7.73	0.0000

Table A11 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL017974	HSP70Ab		0.51	4.01	7.49	0.0000
AAEL014615	CYP9J23	cytochrome P450	898.90	6,697.58	7.29	0.0000
AAEL006176	OBP27	Odorant-binding protein 56e	5,291.54	39,345.98	7.20	0.0000
AAEL017296	Or93		0.44	3.85	7.16	0.0000
AAEL013857		hypothetical protein	4.15	29.65	7.05	0.0000
AAEL017050	Or101		0.60	4.84	7.04	0.0000
AAEL014571		oviductin	0.18	1.41	6.97	0.0000
AAEL008904		coagulation factor X	0.50	3.87	6.92	0.0000
AAEL014764		acidic ribosomal protein P1	0.12	1.46	6.89	0.0071
AAEL003787		hypothetical protein	2.98	20.54	6.85	0.0000
AAEL018410	Sphinx_2		0.69	7.04	6.84	0.0009
AAEL001774		hypothetical protein	0.53	9.53	6.66	0.0187
AAEL005702		hypothetical protein	0.89	6.23	6.63	0.0000
AAEL017463	Or98		0.56	3.74	6.41	0.0000
AAEL013084			1.35	9.05	6.38	0.0000
AAEL011483		Odorant-binding protein 50c	0.95	7.13	6.33	0.0000
AAEL009774			0.91	5.86	6.25	0.0000
AAEL017347	Or87		12.04	77.99	6.24	0.0000
AAEL017104	Or121		1.94	12.64	6.18	0.0000
AAEL004301		hypothetical protein	6,104.67	38,504.43	6.14	0.0000
AAEL003848		hypothetical protein	0.15	2.02	6.08	0.0241
AAEL010910		retina aberrant in pattern	0.15	1.06	6.06	0.0001
AAEL007957		hypothetical protein	0.10	1.18	6.05	0.0122
AAEL016376			9.94	64.68	5.97	0.0000
AAEL006830		yellow protein precursor	10.06	60.69	5.96	0.0000
AAEL008946		acidic ribosomal protein P1	1.27	9.50	5.94	0.0006
AAEL011729		hypothetical protein	1.71	10.17	5.82	0.0000
AAEL017149	Or91		3.64	21.32	5.77	0.0000
AAEL014085	IR75k.2	ionotropic glutamate receptor-invertebrate	2.28	13.26	5.73	0.0000
AAEL002669		AMP dependent ligase	120.17	685.79	5.68	0.0000
AAEL011045		pupal cuticle protein	3.00	18.50	5.66	0.0000
AAEL011586		hypothetical protein	0.50	2.95	5.61	0.0000
AAEL006319		hypothetical protein	0.33	1.91	5.58	0.0000
AAEL009011		hypothetical protein	0.86	5.94	5.58	0.0016
AAEL000998		galactose-specific C-type lectin	0.37	2.42	5.55	0.0000
AAEL012431		AMP dependent ligase	1.18	6.67	5.53	0.0000
AAEL004944			0.39	2.78	5.48	0.0026
AAEL018091			119.48	651.40	5.46	0.0000
AAEL017495	Or95		0.96	5.38	5.44	0.0000
AAEL011583	Or11	Odorant receptor 56a	9.78	56.07	5.43	0.0000
AAEL004218	Or85	hypothetical protein	6.37	34.75	5.41	0.0000
AAEL000599			0.58	3.20	5.39	0.0000
AAEL010390		glucosyl/glucuronosyl transferases	0.78	4.40	5.35	0.0000
AAEL017370	Or126		2.06	12.74	5.34	0.0000
AAEL013563	Or122	hypothetical protein	0.76	4.27	5.31	0.0000
AAEL009197		hypothetical protein	0.64	3.78	5.29	0.0000
AAEL007714		hypothetical protein	0.14	1.13	5.27	0.0120
AAEL010130		Pupal cuticle protein	0.19	1.53	5.25	0.0189
AAEL007795	CYP4D37		3.42	19.60	5.20	0.0000
AAEL018086			1.89	9.93	5.19	0.0000
AAEL014627		short-chain dehydrogenase	1.24	6.62	5.16	0.0000
AAEL000882		hypothetical protein	0.56	3.10	5.13	0.0000
AAEL014811		hypothetical protein	0.50	2.75	5.12	0.0000
AAEL018107			0.79	4.21	5.08	0.0000

Table A11 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL013893	Or125	hypothetical protein	3.06	15.68	5.06	0.0000
AAEL017143	Or102		0.46	2.49	5.02	0.0000
AAEL002099		cuticle protein	2.29	14.73	5.02	0.0049
AAEL008023	CYP4C52	cytochrome P450	0.17	1.07	5.02	0.0005
AAEL007739		pupal cuticle protein	1.16	6.42	4.99	0.0000
AAEL001746		juvenile hormone resistance protein	13.56	67.37	4.97	0.0000
AAEL001617	Or124	hypothetical protein	0.27	1.61	4.97	0.0017
AAEL007145		hypothetical protein	0.25	1.41	4.95	0.0004
AAEL017018			27.82	137.90	4.95	0.0000
AAEL001553		hypothetical protein	4.48	23.71	4.95	0.0000
AAEL005782		hypothetical protein	0.54	2.85	4.93	0.0000
AAEL017009	Or119		1.08	5.47	4.93	0.0000
AAEL009127	CYP6M11	cytochrome P450	12.31	62.18	4.87	0.0000
AAEL009852		hypothetical protein	1.43	7.97	4.84	0.0004
AAEL014270	IR40a		0.48	2.48	4.80	0.0000
AAEL002167	Gr2	Gustatory receptor 21a	2.73	13.65	4.79	0.0000
AAEL006347		apyrase	3.01	14.29	4.76	0.0000
AAEL017841	U1		0.58	4.36	4.70	0.0336
AAEL001888		hypothetical protein	9.86	45.96	4.63	0.0000
AAEL000094		hypothetical protein	2.62	11.96	4.59	0.0000
AAEL017977	HSP70Ca		0.49	2.37	4.53	0.0001
AAEL007955	GSTE8	glutathione-s-transferase theta, gst	162.98	735.26	4.51	0.0000
AAEL009130	CYP6Z7		104.82	504.95	4.50	0.0000
AAEL013268		hypothetical protein	6.43	29.53	4.49	0.0000
AAEL007640		molybdopterin synthase large subunit	2.55	12.02	4.48	0.0000
AAEL005186		tmc3 protein	0.72	3.31	4.46	0.0000
AAEL007855		hypothetical protein	0.76	3.60	4.43	0.0000
AAEL006980		lipase	20.80	89.29	4.28	0.0000
AAEL011458		hypothetical protein	0.32	1.59	4.26	0.0049
AAEL008384		ATP-binding cassette sub-family A member 3	0.54	2.38	4.25	0.0000
AAEL005182	CCEJHE4F		5.10	23.65	4.25	0.0003
AAEL007113		selenophosphate synthase	38.65	164.66	4.25	0.0000
AAEL007954	GSTE1	glutathione-s-transferase theta, gst	200.15	867.53	4.22	0.0000
AAEL005374	SCRB1	sensory neuron membrane protein-1	444.03	1,932.02	4.20	0.0000
AAEL016161			2.06	11.02	4.18	0.0123
AAEL011423		sugar transporter	0.62	2.69	4.18	0.0000
AAEL012766	CYP325G2	cytochrome P450	363.41	1,545.36	4.17	0.0000
AAEL003967		calpain	0.42	1.80	4.16	0.0000
AAEL017976	HSP70Bb		0.34	1.51	4.09	0.0009
AAEL001855		zinc carboxypeptidase	6.26	25.50	4.07	0.0000
AAEL008219		elongase	8.17	33.28	4.07	0.0000
AAEL006635		hypothetical protein	0.59	2.78	4.07	0.0041
AAEL008799		hypothetical protein	0.88	3.74	4.05	0.0003
AAEL011027		hypothetical protein	23.58	95.44	4.01	0.0000
AAEL010386		glucosyl/glucuronosyl transferases	5.84	23.52	4.00	0.0000
AAEL017975	HSP70Ba		4.04	16.24	3.99	0.0000
AAEL002917		hypothetical protein	119.99	483.23	3.98	0.0000
AAEL006121		Trypsin	28.57	113.23	3.95	0.0000
AAEL007198		Osiris	1.35	5.38	3.92	0.0000
AAEL000066	IR41k	hypothetical protein	9.09	36.03	3.91	0.0000
AAEL008368	Or13	olfactory receptor	2.00	8.21	3.91	0.0000
AAEL010127		pupal cuticle protein 78E	1.36	5.80	3.91	0.0013
AAEL007147		hypothetical protein	4.38	17.70	3.90	0.0000

Table A11 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL013601		short-chain dehydrogenase	15.44	62.68	3.89	0.0000
AAEL001656		sodium-dependent phosphate transporter	22.07	86.85	3.86	0.0000
AAEL007643		molybdopterin synthase small subunit	3.09	13.53	3.86	0.0025
AAEL001342	Or59	hypothetical protein	6.12	24.51	3.86	0.0000
AAEL010255		hypothetical protein	1.42	5.65	3.86	0.0000
AAEL013323		hypothetical protein	2.10	8.49	3.85	0.0000
AAEL000614		Odorant receptor 83c	4.78	19.11	3.84	0.0000
AAEL005776	Or7	Odorant receptor 83b	604.69	2,323.57	3.84	0.0000
AAEL006318		short-chain dehydrogenase	2.37	9.18	3.83	0.0000
AAEL009131	CYP6Z8	cytochrome P450	1.31	5.36	3.81	0.0001
AAEL002617	OBP12	Odorant-binding protein 56e	869.08	3,478.15	3.80	0.0001
AAEL003622		delta(9)-desaturase	8.31	31.84	3.80	0.0000
AAEL002877			18.83	70.55	3.75	0.0000
AAEL004761		serine/threonine-protein kinase MAK	22.27	82.53	3.73	0.0000
AAEL005542		hypothetical protein	1.19	4.43	3.72	0.0000
AAEL001290		hypothetical protein	6.86	26.78	3.71	0.0001
AAEL007669		oxidoreductase	242.86	915.59	3.71	0.0000
AAEL001208		ubiquitin-conjugating enzyme variant	15.10	58.44	3.70	0.0001
AAEL000797		dimethylaniline monooxygenase	1.78	6.66	3.70	0.0000
AAEL010740		wingless	0.25	1.08	3.68	0.0091
AAEL008988		adult cuticle protein	0.44	1.86	3.67	0.0140
AAEL005489		olfactory receptor	4.36	16.81	3.67	0.0001
AAEL000039	IR41o	hypothetical protein	0.51	1.96	3.67	0.0006
AAEL011499	OBP47	Odorant-binding protein 58c	515.39	1,971.01	3.66	0.0000
AAEL000347		hypothetical protein	624.41	2,316.79	3.66	0.0000
AAEL007873		hypothetical protein	0.32	1.27	3.65	0.0162
AAEL004509		hypothetical protein	1.94	8.00	3.63	0.0103
AAEL000871		hypothetical protein	0.30	1.24	3.63	0.0042
AAEL014570		oviductin	13.94	50.69	3.62	0.0000
AAEL010551		hypothetical protein	1.66	6.17	3.61	0.0000
AAEL017981	HSP70Ca'		0.36	1.58	3.60	0.0257
AAEL017302			292.01	1,052.35	3.60	0.0000
AAEL008746		hypothetical protein	0.31	1.24	3.60	0.0018
AAEL009477		hypothetical protein	19.30	71.68	3.60	0.0000
AAEL015479	IR75k.4	glutamate receptor	1.63	5.88	3.60	0.0000
AAEL014412	CYP304B2	cytochrome P450	1.07	4.21	3.58	0.0020
AAEL002922	IR8a	glutamate receptor 7 (ampa)	13.09	47.25	3.58	0.0000
AAEL013947		hypothetical protein	0.95	3.49	3.58	0.0000
AAEL002146		hypothetical protein	19.83	70.98	3.57	0.0000
AAEL000560		hypothetical protein	0.70	2.64	3.57	0.0006
AAEL012688		hypothetical protein	0.35	1.32	3.57	0.0049
AAEL008269		hypothetical protein	23.89	89.94	3.56	0.0004
AAEL013345		alphaA-crystallin	1.09	4.11	3.55	0.0004
AAEL018303		hypothetical protein	10.50	37.33	3.54	0.0000
AAEL014978		adult cuticle protein	0.60	2.37	3.53	0.0120
AAEL011895	Or48	hypothetical protein	0.71	2.59	3.52	0.0000
AAEL009204		glucose dehydrogenase	1.49	5.30	3.51	0.0000
AAEL015181		hypothetical protein	0.44	1.71	3.51	0.0029
AAEL006341		hypothetical protein	23.14	80.90	3.51	0.0000
AAEL015276		hypothetical protein	1.85	6.89	3.50	0.0000
AAEL000954		hypothetical protein	167.18	580.50	3.49	0.0000
AAEL014579		Trypsin	2.92	10.62	3.49	0.0000
AAEL009044		amine oxidase	1.04	3.76	3.48	0.0002
AAEL017320			169.85	593.11	3.48	0.0000

Table A11 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL012654		triacylglycerol lipase, pancreatic	19.96	69.02	3.44	0.0000
AAEL002378		carboxylesterase	1.78	6.23	3.44	0.0000
AAEL017427	Or96		2.27	8.15	3.43	0.0005
AAEL018145		arginine or creatine kinase	29.22	99.61	3.42	0.0000
AAEL010775	IR75e.3	hypothetical protein	4.71	16.30	3.42	0.0000
AAEL010750		hypothetical protein	19.41	65.62	3.41	0.0000
AAEL014600		4-hydroxyphenylpyruvate dioxygenase	8.88	31.35	3.40	0.0002
AAEL013366	IR21a		0.73	2.54	3.39	0.0000
AAEL006672		hypothetical protein	7.20	24.29	3.38	0.0000
AAEL003617		alcohol dehydrogenase	0.33	1.17	3.38	0.0090
AAEL000705		steroid dehydrogenase	21.46	72.50	3.37	0.0000
AAEL007815	CYP4D24	cytochrome P450	140.93	487.73	3.35	0.0001
AAEL010951		glutamate decarboxylase	35.42	118.59	3.32	0.0000
AAEL005578		hypothetical protein	2.88	9.76	3.31	0.0000
AAEL008043	PNRLIKE	nuclear receptor	14.49	47.97	3.31	0.0000
AAEL000237		hypothetical protein	2.44	8.15	3.29	0.0000
AAEL006627		serine-type enodpeptidase	8.78	29.44	3.29	0.0000
AAEL013492	PPO5	prophenoloxidase	0.45	1.49	3.29	0.0015
AAEL002348		paired box protein pax-6	5.89	19.79	3.27	0.0000
AAEL003236		hypothetical protein	25.74	85.31	3.26	0.0000
AAEL000566		hypothetical protein	1.17	3.93	3.26	0.0000
AAEL007997		hypothetical protein	2.23	7.44	3.26	0.0000
AAEL006345	Or39	hypothetical protein	1.13	3.77	3.25	0.0004
AAEL011344		hypothetical protein	4.38	14.33	3.24	0.0000
AAEL003899		sugar transporter	10.48	33.78	3.24	0.0000
AAEL008895		hypothetical protein	1.74	6.13	3.23	0.0014
AAEL011014		hypothetical protein	22.44	72.53	3.23	0.0000
AAEL009982	Or12	Odorant receptor 56a	3.63	12.31	3.23	0.0009
AAEL014607		cytochrome P450	12.19	39.28	3.23	0.0000
AAEL002666		AMP dependent ligase	150.69	487.41	3.22	0.0000
AAEL002904		Juvenile hormone-inducible protein	126.00	409.95	3.21	0.0000
AAEL010381		glucosyl/glucuronosyl transferases	2.84	9.10	3.21	0.0000
AAEL007716		hypothetical protein	47.51	151.85	3.20	0.0000
AAEL018118		helicase	12.58	41.66	3.19	0.0004
AAEL002591	OBP13	Odorant-binding protein 56e	267.32	860.32	3.18	0.0000
AAEL010764		aldehyde dehydrogenase	31.44	100.24	3.17	0.0000
AAEL006207		hypothetical protein	19.95	62.93	3.16	0.0000
AAEL009115		hypothetical protein	62.96	200.64	3.16	0.0000
AAEL014083		hypothetical protein	9.54	30.14	3.14	0.0000
AAEL006961		lipase	0.57	1.91	3.14	0.0037
AAEL001107		hypothetical protein	90.38	289.56	3.13	0.0000
AAEL001320	CYP9M4	cytochrome P450	2.11	6.98	3.13	0.0004
AAEL012266	CYP4C38	cytochrome P450	86.90	272.76	3.13	0.0000
AAEL013295		hypothetical protein	0.88	2.81	3.11	0.0010
AAEL003891		ctl transporter	13.25	41.29	3.11	0.0000
AAEL010372		aldehyde oxidase	13.32	41.74	3.11	0.0000
AAEL004383		hypothetical protein	13.40	41.49	3.11	0.0000
AAEL000800		microsomal dipeptidase	7.86	24.81	3.11	0.0000
AAEL012144	CYP303A1	cytochrome P450	0.44	1.45	3.10	0.0015
AAEL009334			157.58	488.68	3.10	0.0000
AAEL000071	OBP2	Odorant-binding protein 56a	151.92	491.70	3.09	0.0016
AAEL001697		adenylate cyclase	1.25	3.93	3.09	0.0000
AAEL014959		heterogeneous nuclear ribonucleoprotein	370.27	1,137.38	3.09	0.0000
AAEL006617		hypothetical protein	6.02	18.36	3.08	0.0000

Table A11 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL002655		matrix metalloproteinase	1.83	5.65	3.07	0.0000
AAEL013423	Or78	hypothetical protein	3.68	11.25	3.07	0.0000
AAEL005777		hypothetical protein	3.19	9.81	3.04	0.0000
AAEL001444		hypothetical protein	5.36	16.33	3.04	0.0000
AAEL008558		tetratricopeptide repeat protein, tpr	20.95	63.29	3.04	0.0000
AAEL008182		hypothetical protein	1.25	3.84	3.03	0.0018
AAEL002292		glucose transport protein	0.44	1.50	3.03	0.0430
AAEL012037		sulfate transporter	3.65	10.98	3.02	0.0000
AAEL010405		alkyldihydroxyacetonephosphate synthase	9.05	27.30	3.02	0.0000
AAEL006606		hypothetical protein	2.15	7.38	3.02	0.0220
AAEL007393		hypothetical protein	10.04	30.40	2.99	0.0000
AAEL010938		l-asparaginase	0.70	2.30	2.99	0.0035
AAEL011599		ADP-ribosylation factor	2.40	7.11	2.99	0.0000
AAEL005706		triacylglycerol lipase	27.08	81.31	2.99	0.0000
AAEL002972		brain chitinase and chia	0.87	2.61	2.98	0.0004
AAEL014363		hypothetical protein	0.74	2.60	2.98	0.0371
AAEL004014		glucose dehydrogenase	72.54	215.67	2.98	0.0000
AAEL003076		glucosyl/glucuronosyl transferases	290.07	856.56	2.97	0.0000
AAEL001547		hypothetical protein	9.79	29.20	2.97	0.0000
AAEL002039		nadph oxidase	5.74	17.04	2.97	0.0000
AAEL002717	GPR5HT8		2.38	6.95	2.95	0.0000
AAEL014569			0.54	1.59	2.95	0.0001
AAEL005433		hypothetical protein	0.94	2.85	2.95	0.0000
AAEL014612		cytochrome P450	42.71	126.13	2.95	0.0000
AAEL009714		hypothetical protein	1.79	5.73	2.93	0.0042
AAEL018052		hypothetical protein	9.02	26.13	2.92	0.0000
AAEL008010		sidestep protein	0.69	2.22	2.92	0.0107
AAEL006758		hypothetical protein	0.65	2.06	2.91	0.0195
AAEL010382		aldehyde oxidase	106.72	309.90	2.91	0.0000
AAEL012659		protein serine/threonine kinase	4.97	15.13	2.90	0.0057
AAEL006760		bc8 orange interacting protein	1.78	5.17	2.90	0.0000
AAEL001345		hypothetical protein	1.96	5.76	2.90	0.0000
AAEL012698		ATP-binding cassette sub-family A member 3	5.22	14.97	2.89	0.0000
AAEL013242			0.39	1.15	2.89	0.0000
AAEL015663		cytochrome P450	1.01	3.04	2.88	0.0009
AAEL011028		hypothetical protein	0.37	1.12	2.88	0.0059
AAEL012303		hypothetical protein	1.36	4.10	2.87	0.0002
AAEL015566	OBP62	Odorant-binding protein 58c	442.54	1,268.24	2.86	0.0000
AAEL013153	IR31a	hypothetical protein	4.24	12.10	2.86	0.0000
AAEL014267		hypothetical protein	1.91	5.46	2.86	0.0001
AAEL018030			32.75	94.11	2.86	0.0000
AAEL003767		hypothetical protein	8.20	23.23	2.85	0.0000
AAEL013296		hypothetical protein	7.82	22.16	2.85	0.0000
AAEL002929		AMP dependent ligase	0.37	1.08	2.85	0.0187
AAEL004027		glucose dehydrogenase	7.25	20.80	2.85	0.0000
AAEL008624		abc transporter	52.40	147.71	2.85	0.0000
AAEL017973	HSP70Aa		0.71	2.13	2.84	0.0305
AAEL007285		hypothetical protein	9.73	27.61	2.84	0.0000
AAEL004048		UNC93A protein	217.71	613.79	2.83	0.0000
AAEL008660		fig-alpha	36.55	103.18	2.83	0.0000
AAEL000089	IR41n	hypothetical protein	22.41	63.15	2.82	0.0000
AAEL004031		hypothetical protein	0.96	2.73	2.82	0.0031
AAEL004402		alpha-l-iduronidase	4.00	11.26	2.81	0.0000

Table A11 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL009123	CYP6Z6	cytochrome P450	57.07	168.45	2.81	0.0090
AAEL000148		hypothetical protein	3.04	8.47	2.80	0.0000
AAEL005700	CYP325X4		0.97	2.76	2.80	0.0010
AAEL005364		adaptin, alpha/gamma/epsilon	11.14	31.00	2.80	0.0000
AAEL000195		hypothetical protein	32.27	89.80	2.80	0.0000
AAEL006326		deoxyribonuclease I	0.47	1.36	2.80	0.0103
AAEL011951		elongase	4.57	12.78	2.79	0.0000
AAEL012063		hypothetical protein	4.57	12.78	2.79	0.0000
AAEL004349		tetraspanin	40.78	113.77	2.78	0.0000
AAEL000011	IR41e	hypothetical protein	1.10	3.07	2.76	0.0000
AAEL008840		hypothetical protein	10.51	28.87	2.74	0.0000
AAEL006454	OBP1	Odorant-binding protein 56a	2,500.59	6,951.88	2.74	0.0001
AAEL006618		hypothetical protein	4.06	11.00	2.74	0.0000
AAEL012332		hypothetical protein	1.27	3.49	2.73	0.0000
AAEL010500	GSTX2	glutathione-s-transferase theta, gst	932.83	2,544.58	2.73	0.0000
AAEL011770	CYP325L1	cytochrome P450	41.90	113.14	2.72	0.0000
AAEL000007	IR41a.1	hypothetical protein	6.82	18.68	2.71	0.0000
AAEL008146			5.11	13.86	2.71	0.0000
AAEL010489		hypothetical protein	107.22	296.37	2.71	0.0005
AAEL009233		zinc metalloprotease	9.99	27.05	2.71	0.0000
AAEL004905		monocarboxylate transporter	37.26	99.80	2.71	0.0000
AAEL012162		aldehyde dehydrogenase	3.56	9.75	2.71	0.0000
AAEL012489		hypothetical protein	4.88	13.15	2.70	0.0000
AAEL004343	OBP19	hypothetical protein	2.04	5.94	2.70	0.0228
AAEL005032		hypothetical protein	90.33	250.24	2.70	0.0014
AAEL000773		kinesin heavy chain	47.55	127.60	2.70	0.0000
AAEL009149		kinectin	7.81	21.12	2.70	0.0000
AAEL005590		autotransporter adhesin precursor	1.01	2.73	2.69	0.0000
AAEL013155		hypothetical protein	1.21	3.45	2.69	0.0170
AAEL011869		hypothetical protein	5.10	13.66	2.68	0.0001
AAEL012014		l-lactate dehydrogenase	3.96	11.29	2.67	0.0180
AAEL001090	GSTD7	glutathione-s-transferase theta, gst	44.62	119.65	2.67	0.0000
AAEL001219		hypothetical protein	6.14	16.37	2.67	0.0000
AAEL001671		hypothetical protein	1.94	5.13	2.67	0.0000
AAEL004568		adp-ribosylation factor, arf	15.69	41.42	2.66	0.0000
AAEL011292		protease m1 zinc metalloprotease	57.59	152.30	2.66	0.0000
AAEL002752		anaphase-promoting complex, subunit-5	8.00	21.07	2.65	0.0000
AAEL007485		sodium-dependent phosphate transporter	217.66	570.74	2.65	0.0000
AAEL000051	OBP3	Odorant-binding protein 56e	2,322.94	6,299.41	2.65	0.0021
AAEL010662	OBP43	Odorant-binding protein 58c	1,256.80	3,335.18	2.64	0.0000
AAEL008442	Or14	hypothetical protein	11.71	31.07	2.64	0.0000
AAEL000962		hypothetical protein	20.46	53.55	2.64	0.0000
AAEL012694		Juvenile hormone-inducible protein	15.80	42.10	2.64	0.0000
AAEL003398		hypothetical protein	54.44	143.21	2.64	0.0000
AAEL003016		hypothetical protein	47.88	126.19	2.63	0.0000
AAEL005133		tetratricopeptide repeat protein, tpr	24.54	64.16	2.62	0.0000
AAEL007598		hypothetical protein	3.28	8.68	2.62	0.0006
AAEL003760		hypothetical protein	31.94	85.67	2.61	0.0047
AAEL012349		lipase 1 precursor	6.45	16.76	2.60	0.0000
AAEL009737		hypothetical protein	5.92	15.22	2.60	0.0000
AAEL007517		oviductin	5.89	15.19	2.60	0.0000
AAEL010853		AMP dependent ligase	1.69	4.44	2.60	0.0038
AAEL015567	OBP63	Odorant-binding protein 58c	1,446.10	3,769.70	2.60	0.0000
AAEL001513		wd-repeat protein	7.32	19.04	2.59	0.0000

Table A11 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL013637		homogentisate 1,2-dioxygenase	14.83	38.45	2.59	0.0000
AAEL008327		huntingtin-interacting protein	19.91	51.58	2.59	0.0000
AAEL014333		hypothetical protein	10.57	27.28	2.59	0.0000
AAEL013350		heat shock protein 26kD	3.83	10.20	2.58	0.0008
AAEL006886		hypothetical protein	25.11	65.28	2.58	0.0000
AAEL015553	GPR5HT6	5-hydroxytryptamine 2 receptor	3.02	7.68	2.58	0.0000
AAEL012731		adenylate kinase 1	31.20	80.24	2.58	0.0000
AAEL006080		DNA repair protein rad51	5.54	14.15	2.58	0.0000
AAEL017105	Or106		2.29	5.98	2.57	0.0012
AAEL006338		sulfotransferase (sult)	1.40	3.58	2.57	0.0007
AAEL007302		hypothetical protein	5.37	14.44	2.57	0.0233
AAEL010409	Or30	hypothetical protein	2.35	6.13	2.57	0.0001
AAEL014616	CYP9J27	cytochrome P450	5.45	13.93	2.56	0.0000
AAEL009813	IR25a	glutamate receptor 7 (ampa)	89.20	228.53	2.55	0.0000
AAEL002560		hypothetical protein	34.84	87.89	2.55	0.0000
AAEL008342		monocarboxylate transporter	11.20	28.32	2.54	0.0000
AAEL014419		hypothetical protein	8.80	23.23	2.54	0.0142
AAEL005095	GPRGPH	insl3/relaxin receptor	0.54	1.41	2.54	0.0348
AAEL002335		atbf1	11.63	29.30	2.54	0.0000
AAEL003320		hypothetical protein	7.19	18.37	2.53	0.0002
AAEL002209		hypothetical protein	17.28	43.53	2.53	0.0000
AAEL013294		hypothetical protein	9.95	25.16	2.52	0.0000
AAEL005694		hypothetical protein	0.51	1.32	2.52	0.0166
AAEL014993			3.35	8.34	2.52	0.0000
AAEL002940		AMP dependent ligase	33.51	85.02	2.51	0.0002
AAEL018048			0.56	1.52	2.51	0.0181
AAEL013648		hypothetical protein	111.34	275.90	2.50	0.0000
AAEL005791		hypothetical protein	0.38	1.01	2.50	0.0110
AAEL010944		hypothetical protein	79.83	207.71	2.50	0.0195
AAEL007730		tetratricopeptide repeat protein 10, tpr10	6.87	17.27	2.50	0.0000
AAEL000687		glucosyl/glucuronosyl transferases	5.91	14.71	2.50	0.0000
AAEL000312		hypothetical protein	10.51	26.47	2.50	0.0000
AAEL002786		hypothetical protein	21.90	54.20	2.50	0.0000
AAEL003698		hypothetical protein	77.00	191.72	2.49	0.0000
AAEL002522		adenosine deaminase acting on RNA (adar)-2	3.56	8.85	2.49	0.0000
AAEL012615		hypothetical protein	0.97	2.45	2.49	0.0000
AAEL000885		cytoplasmic dynein heavy chain	3.41	8.60	2.49	0.0014
AAEL008149		hypothetical protein	2.42	6.42	2.49	0.0491
AAEL010002		mitochondrial import inner membrane translocase subunit tim17	7.52	18.97	2.48	0.0015
AAEL004700		cdkl1/4	49.69	122.44	2.48	0.0000
AAEL006190		hypothetical protein	33.55	82.67	2.48	0.0000
AAEL001878		lipase	67.89	168.11	2.48	0.0000
AAEL000575		apyrase	2.80	7.32	2.48	0.0270
AAEL011080		intraflagellar transport 80	5.78	14.29	2.48	0.0000
AAEL000845			0.93	2.31	2.48	0.0002
AAEL009205		hypothetical protein	0.44	1.10	2.48	0.0005
AAEL005920		hypothetical protein	15.46	38.02	2.48	0.0000
AAEL010492		hypothetical protein	2.62	6.59	2.47	0.0004
AAEL013649		elongase	17.37	43.78	2.47	0.0040
AAEL001510	Or23	Odorant receptor 94b	5.41	13.49	2.47	0.0000
AAEL010943		hypothetical protein	634.68	1,555.60	2.46	0.0000
AAEL017340			420.70	1,034.20	2.46	0.0000

Table A11 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL015231		hypothetical protein	2.43	5.90	2.45	0.0000
AAEL009211		hypothetical protein	7.11	17.25	2.45	0.0000
AAEL005104		hypothetical protein	0.91	2.22	2.44	0.0000
AAEL010413		cak1	5.55	13.50	2.44	0.0000
AAEL008083		laminin receptor	7.15	17.95	2.44	0.0116
AAEL010687		hypothetical protein	1.55	3.89	2.43	0.0102
AAEL004932		tyrosine-protein kinase	1.63	3.90	2.43	0.0000
AAEL010384		aldehyde oxidase	1.48	3.64	2.43	0.0001
AAEL003121		hypothetical protein	2.98	7.21	2.43	0.0000
AAEL006574		nuclear transcription factor, x-box binding 1 (nfx1)	0.62	1.49	2.42	0.0038
AAEL000306		hypothetical protein	7.29	18.01	2.42	0.0002
AAEL007019		phosphate transporter	170.82	415.29	2.42	0.0001
AAEL013887		hypothetical protein	11.75	28.55	2.42	0.0002
AAEL006638		acetylglucosaminyltransferase	26.42	63.41	2.42	0.0000
AAEL011020		hypothetical protein	0.91	2.27	2.42	0.0074
AAEL002554		anosmin	2.72	6.52	2.41	0.0000
AAEL011957		elongase	92.29	228.15	2.41	0.0099
AAEL005806			4.15	10.09	2.41	0.0005
AAEL003002		hypothetical protein	7.28	17.36	2.41	0.0000
AAEL012905			18.67	44.55	2.41	0.0000
AAEL011898		1-acyl-sn-glycerol-3-phosphate acyltransferase	56.32	134.22	2.40	0.0000
AAEL007135		peroxiredoxin 5, prdx5	637.34	1,518.33	2.40	0.0000
AAEL011810		hypothetical protein	28.21	70.79	2.40	0.0408
AAEL001118		hypothetical protein	1.96	4.65	2.39	0.0000
AAEL003132		intraflagellar transport protein	1.84	4.46	2.38	0.0055
AAEL005520		carbonic anhydrase	86.38	205.89	2.38	0.0001
AAEL010410		Odorant receptor 9a	1.14	2.87	2.38	0.0256
AAEL012318		2-amino-3-ketobutyrate coenzyme a ligase	1.84	4.41	2.37	0.0030
AAEL005718	CLIPA3	serine protease	3.29	7.92	2.37	0.0053
AAEL012017		hypothetical protein	10.86	27.22	2.37	0.0166
AAEL000041		forkhead box protein (AaegFOXM2)	11.19	26.55	2.36	0.0000
AAEL010073		metalloendopeptidase	18.62	43.87	2.36	0.0000
AAEL008820		hypothetical protein	2.99	7.05	2.36	0.0013
AAEL010204		dihydropyrimidine dehydrogenase	8.21	19.31	2.36	0.0000
AAEL001463		hypothetical protein	11.43	26.69	2.36	0.0000
AAEL001466		hypothetical protein	11.18	26.28	2.35	0.0000
AAEL008878		diacylglycerol o-acyltransferase	38.73	91.06	2.35	0.0000
AAEL002951		forkhead protein/ forkhead protein domain	10.79	25.56	2.35	0.0001
AAEL004021		glucose dehydrogenase	2.23	5.19	2.35	0.0000
AAEL001106		hypothetical protein	12.43	29.31	2.35	0.0001
AAEL003831		fatty acid hydroxylase	12.19	28.58	2.35	0.0000
AAEL018198	IR75e.2	glutamate receptor	6.22	14.76	2.35	0.0017
AAEL015340		hypothetical protein	3.39	7.94	2.34	0.0004
AAEL014818		sil1	0.96	2.30	2.34	0.0157
AAEL006982		lipase	20.10	46.66	2.34	0.0000
AAEL008077		hypothetical protein	1.37	3.31	2.34	0.0016
AAEL006855		UDP-galactose transporter	108.52	251.51	2.34	0.0000
AAEL014172		protein kinase	6.50	15.59	2.33	0.0075
AAEL001374			58.23	134.75	2.33	0.0000
AAEL002658		AMP dependent ligase	26.55	61.65	2.33	0.0000
AAEL006340		hypothetical protein	4.81	11.20	2.33	0.0000
AAEL009664		aldehyde dehydrogenase	8.05	18.59	2.33	0.0000

Table A11 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL013198	IR75i		4.31	10.10	2.32	0.0013
AAEL018025			152.60	354.45	2.32	0.0000
AAEL006329		hypothetical protein	1.31	3.13	2.32	0.0107
AAEL014734		saccharopine dehydrogenase	0.58	1.40	2.32	0.0182
AAEL003203		fatty acid desaturase	129.02	300.59	2.32	0.0005
AAEL013194		hypothetical protein	10.18	23.60	2.32	0.0000
AAEL014609	CYP9J26	cytochrome P450	22.85	52.66	2.32	0.0000
AAEL002478		double-stranded binding protein	10.68	24.70	2.31	0.0000
AAEL010663		cleavage and polyadenylation specificity factor	11.78	27.01	2.31	0.0000
AAEL001491		hypothetical protein	2.75	6.45	2.31	0.0028
AAEL011416		hypothetical protein	2,119.81	4,880.15	2.31	0.0000
AAEL018001			31.71	72.75	2.31	0.0000
AAEL003153		hypothetical protein	0.65	1.51	2.31	0.0015
AAEL002909		lysosomal acid lipase	0.57	1.32	2.31	0.0441
AAEL002311		ADP-ribosylation factor	64.89	148.78	2.30	0.0000
AAEL009960		hypothetical protein	2.74	6.26	2.30	0.0000
AAEL010998		hypothetical protein	0.47	1.10	2.29	0.0132
AAEL005349		hypothetical protein	6.17	14.11	2.29	0.0002
AAEL004736			24.26	55.96	2.29	0.0006
AAEL008448	Or15	hypothetical protein	6.60	15.23	2.29	0.0006
AAEL005937			54.67	123.70	2.29	0.0000
AAEL015063		elongase	2.40	5.50	2.29	0.0091
AAEL012946		hypothetical protein	8.04	18.41	2.28	0.0001
AAEL005648	CLIPB16	serine carboxypeptidase	8.69	19.88	2.28	0.0002
AAEL008703		scaffold attachment factor B	69.42	157.47	2.28	0.0000
AAEL005021		hypothetical protein	1.26	2.84	2.27	0.0003
AAEL007111		hypothetical protein	0.95	2.16	2.27	0.0000
AAEL017407			5.46	12.60	2.27	0.0001
AAEL009690		hypothetical protein	6.04	13.68	2.27	0.0004
AAEL011263		phosphatidylethanolamine-binding proteir	321.27	730.71	2.27	0.0003
AAEL014087	IR75k.3		5.40	12.20	2.27	0.0000
AAEL006350		hypothetical protein	2.27	5.21	2.27	0.0163
AAEL018508	Sphinx_1		7.83	18.32	2.27	0.0407
AAEL006003	Or10	odorant receptor	10.25	23.55	2.26	0.0030
AAEL007353		cullin	16.80	37.85	2.26	0.0000
AAEL014813		viral IAP-associated factor	1.47	3.39	2.26	0.0368
AAEL010666	OBP42	Odorant-binding protein 58c	2,568.24	5,816.78	2.25	0.0008
AAEL013321			7.86	17.65	2.25	0.0000
AAEL007897	SPZ4		16.01	35.88	2.25	0.0001
AAEL006690			3.49	7.85	2.25	0.0002
AAEL000095	IR41d.3	hypothetical protein	12.66	28.23	2.25	0.0000
AAEL000047	IR41i	hypothetical protein	3.43	7.85	2.24	0.0168
AAEL018040		hypothetical protein	269.34	596.73	2.24	0.0000
AAEL010428	Or26		8.78	19.58	2.24	0.0000
AAEL014086	IR75o	hypothetical protein	4.05	9.31	2.24	0.0111
AAEL000127		AMP dependent coa ligase	1.51	3.42	2.24	0.0012
AAEL006042		arginine or creatine kinase	14.05	31.17	2.23	0.0000
AAEL001088			32.64	71.91	2.22	0.0000
AAEL014521		hypothetical protein	0.46	1.00	2.22	0.0090
AAEL003030		hypothetical protein	10.36	22.68	2.21	0.0000
AAEL011368		sugar transporter	17.35	37.82	2.20	0.0000
AAEL005465		hypothetical protein	12.90	28.65	2.20	0.0006
AAEL015339		hypothetical protein	1.35	2.93	2.20	0.0211

Table A11 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL005884		hypothetical protein	92.75	203.44	2.20	0.0000
AAEL001318		CRAL/TRIO domain-containing protein	1.88	4.31	2.20	0.0067
AAEL011843	Or5	Odorant receptor 85c	2.10	4.76	2.20	0.0197
AAEL007606		hypothetical protein	8.57	18.84	2.20	0.0000
AAEL007213		delta(9)-desaturase	255.16	563.06	2.19	0.0021
AAEL005507		inhibitory pou	4.19	9.34	2.19	0.0191
AAEL013662		anterior fat body protein	2.26	5.00	2.19	0.0002
AAEL012687		Juvenile hormone-inducible protein	2.50	5.39	2.19	0.0006
AAEL002573		hypothetical protein	1.98	4.58	2.19	0.0258
AAEL006143		hypothetical protein	273.15	590.61	2.19	0.0000
AAEL017256			62.43	135.54	2.18	0.0000
AAEL009876		hypothetical protein	67.31	145.81	2.18	0.0000
AAEL012299		protein phosphatase 2c	3.45	7.66	2.18	0.0095
AAEL014872		hypothetical protein	10.60	23.10	2.18	0.0002
AAEL005155		hypothetical protein	2.46	5.35	2.18	0.0001
AAEL006646		hypothetical protein	17.63	38.07	2.17	0.0000
AAEL011158		disulfide oxidoreductase	8.70	18.88	2.17	0.0000
AAEL000689		steroid dehydrogenase	23.79	51.18	2.17	0.0000
AAEL008647			16.53	35.56	2.17	0.0000
AAEL012054		Quiescin-sulfhydryl oxidase4	51.75	111.44	2.16	0.0000
AAEL012845		mitochondrial import inner membrane translocase	13.15	28.34	2.16	0.0000
AAEL014407		B-cell lymphoma/leukaemia 11A extra long form	1.03	2.20	2.16	0.0000
AAEL002919		hypothetical protein	150.67	323.64	2.16	0.0000
AAEL002479			2.77	6.07	2.15	0.0301
AAEL004217		hypothetical protein	7.24	15.50	2.15	0.0002
AAEL011173			0.69	1.52	2.15	0.0010
AAEL007373		ammonium transporter	52.09	112.03	2.15	0.0002
AAEL007276		hypothetical protein	1.13	2.42	2.14	0.0019
AAEL011512		hypothetical protein	1.13	2.41	2.14	0.0174
AAEL011685		hypothetical protein	9.27	20.04	2.14	0.0149
AAEL003069		hypothetical protein	15.64	33.00	2.14	0.0000
AAEL014089	IR75k.1		6.08	13.09	2.14	0.0022
AAEL011769	CYP325M4	cytochrome P450	1.81	3.90	2.13	0.0026
AAEL001985		protein serine/threonine kinase	297.58	632.13	2.13	0.0001
AAEL002153		hypothetical protein	2.55	5.32	2.13	0.0017
AAEL010162			14.23	30.00	2.13	0.0000
AAEL007952			2.67	5.67	2.12	0.0027
AAEL007386		hypothetical protein	4.69	9.80	2.12	0.0000
AAEL002553		hypothetical protein	1.40	2.97	2.12	0.0182
AAEL000628	Or63	Odorant receptor 83c	10.46	22.14	2.12	0.0018
AAEL010656	LRIM12	hypothetical protein	1.75	3.70	2.11	0.0094
AAEL017982	HSP70Cb'		1.14	2.39	2.11	0.0254
AAEL000520			2.80	5.92	2.10	0.0022
AAEL013420	Or79	olfactory receptor	11.00	23.11	2.10	0.0046
AAEL000048	Gr4	gustatory receptor for trehalose	2.83	5.94	2.10	0.0246
AAEL009246		glycoside hydrolases	2.11	4.45	2.10	0.0048
AAEL013470		hypothetical protein	1.43	3.09	2.10	0.0112
AAEL003889	GNBPB1	gram-negative bacteria binding protein	9.26	19.93	2.10	0.0474
AAEL005999	Or2	olfactory receptor	6.88	14.40	2.10	0.0004
AAEL010418	Or27	hypothetical protein	9.86	20.57	2.09	0.0050

Table A11 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL006811	CYP9J8	cytochrome P450	6.36	13.34	2.08	0.0071
AAEL004119		ribonuclease p/mrp subunit	104.78	215.80	2.08	0.0000
AAEL003997		hypothetical protein	5.01	10.59	2.08	0.0254
AAEL015293			2.64	5.49	2.08	0.0000
AAEL017001			3.30	6.92	2.08	0.0012
AAEL000519		hypothetical protein	145.83	301.55	2.08	0.0000
AAEL011513		hypothetical protein	53.96	111.91	2.07	0.0013
AAEL005558		hypothetical protein	273.81	564.84	2.07	0.0004
AAEL010043	GPRCAL1		12.04	24.47	2.06	0.0001
AAEL004332		hypothetical protein	13.91	28.42	2.06	0.0000
AAEL010109		hypothetical protein	72.22	148.13	2.06	0.0001
AAEL013008		intraflagellar transport 52	3.60	7.37	2.06	0.0004
AAEL015313	OBP59	hypothetical protein	239.29	491.79	2.06	0.0009
AAEL005769		glucose dehydrogenase	29.26	59.58	2.05	0.0000
AAEL007374		yellow protein precursor	91.45	187.38	2.05	0.0004
AAEL013023		hypothetical protein	17.24	35.24	2.05	0.0001
AAEL013545		hypothetical protein	125.51	256.73	2.05	0.0000
AAEL005674		hypothetical protein	52.16	105.93	2.05	0.0000
AAEL004041		flotillin-2	33.62	68.16	2.05	0.0000
AAEL005253		hypothetical protein	3.73	7.56	2.04	0.0348
AAEL008198		EGF repeat molecule	52.87	106.80	2.04	0.0000
AAEL002741	SCRB6	neither inactivation nor afterpotential D	2.57	5.38	2.04	0.0134
AAEL005234		hypothetical protein	5.47	11.20	2.04	0.0001
AAEL010223		phosphatidylserine decarboxylase	30.10	60.74	2.04	0.0000
AAEL005227		hypothetical protein	1.90	3.86	2.03	0.0116
AAEL001639		hypothetical protein	8.04	16.22	2.03	0.0000
AAEL015584		molybdopterin synthase large subunit	20.77	41.38	2.02	0.0000
AAEL014090		hypothetical protein	7.39	14.81	2.02	0.0000
AAEL006214		hypothetical protein	8.36	16.58	2.01	0.0000
AAEL009116		hypothetical protein	9.41	18.54	2.01	0.0001
AAEL004235		kinesin-like protein Klp10A	46.26	92.66	2.01	0.0005
AAEL000723		hypothetical protein	6.21	12.37	2.01	0.0000
AAEL003842		hypothetical protein	4.95	9.78	2.00	0.0007
		Higher in Males				
AAEL000873			533.71	1.69	-285.00	0.0000
AAEL006259	GPROP2	rhodopsin	28,541.71	59.68	-172.33	0.0000
AAEL004814		potassium-dependent sodium-calcium exchanger	356.08	2.04	-153.68	0.0000
AAEL003116		phosrestin i (arrestin b) (arrestin 2)	1,259.94	6.34	-130.09	0.0000
AAEL006498	GPROP1	rhodopsin	6,227.14	19.13	-128.71	0.0000
AAEL008756		hypothetical protein	13.59	0.03	-110.65	0.0000
AAEL015354		oxidase/peroxidase	25.46	0.21	-110.64	0.0000
AAEL000960		hypothetical protein	18.01	0.02	-104.36	0.0000
AAEL010950		hypothetical protein	31.93	0.08	-97.74	0.0000
AAEL007493		hypothetical protein	58.56	0.38	-90.64	0.0000
AAEL006014	HPX1	oxidase/peroxidase	58.15	0.54	-82.44	0.0000
AAEL001754		hypothetical protein	19.66	0.11	-81.38	0.0000
AAEL012248			11.92	0.08	-80.99	0.0000
AAEL000596		myosin	35.53	0.30	-74.66	0.0000
AAEL007294		hypothetical protein	17.52	0.13	-66.02	0.0000
AAEL009615	GPROP8	ultraviolet-sensitive opsin	434.40	1.99	-66.00	0.0000
AAEL013535		phosrestin ii (arrestin a) (arrestin 1)	1,113.81	3.57	-64.67	0.0000
AAEL009541		hypothetical protein	16.12	0.18	-62.33	0.0000
AAEL010712		low-density lipoprotein receptor (ldl)	19.15	0.21	-61.64	0.0000

Table A11 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL015659		hypothetical protein	3.79	0.00	-60.88	0.0000
AAEL003441		hypothetical protein	3.20	0.02	-55.17	0.0000
AAEL008383		hypothetical protein	39.25	0.49	-54.52	0.0000
AAEL005252	CRZ	hypothetical protein	14.41	0.14	-52.75	0.0000
AAEL002961		Osiris	9.87	0.07	-48.16	0.0000
AAEL014315		hypothetical protein	32.01	0.50	-48.07	0.0000
AAEL007502		iroquois-class homeodomain protein irx	8.27	0.09	-47.87	0.0000
AAEL013266		hypothetical protein	18.01	0.25	-46.24	0.0000
AAEL007989		hypothetical protein	1.49	0.01	-46.10	0.0000
AAEL012139		allatostatin, B-type	34.43	0.58	-45.04	0.0000
AAEL005575		transient receptor potential channel 4	231.60	1.30	-44.51	0.0000
AAEL003318		oligopeptide transporter	56.25	1.14	-44.38	0.0000
AAEL015658		hypothetical protein	4.22	0.00	-44.18	0.0000
AAEL005437		transient receptor potential channel	13.94	0.07	-43.44	0.0000
AAEL013215			1.56	0.02	-42.71	0.0000
AAEL006451		hypothetical protein	39.11	0.06	-42.35	0.0000
AAEL010393		ferritin subunit	13.55	0.16	-41.21	0.0000
AAEL005138		glucosyl/glucuronosyl transferases	3.14	0.03	-38.71	0.0000
AAEL017215	CYP325U1		4.60	0.07	-36.16	0.0000
AAEL013911		hypothetical protein	24.69	0.56	-35.93	0.0000
AAEL000630		cardioacceleratory peptide 2a	3.23	0.00	-35.89	0.0000
AAEL008722		hypothetical protein	1.59	0.02	-35.81	0.0000
AAEL010396		secreted ferritin G subunit precursor	2.22	0.04	-34.56	0.0000
AAEL000669		hypothetical protein	68.62	0.53	-32.59	0.0000
AAEL015251		hypothetical protein	17.82	0.29	-32.39	0.0000
AAEL013645		hypothetical protein	14.05	0.25	-32.14	0.0000
AAEL011981		glutamate decarboxylase	59.44	1.48	-30.12	0.0000
AAEL009835		hypothetical protein	5.16	0.07	-29.46	0.0000
AAEL009939		hypothetical protein	1.37	0.00	-29.41	0.0000
AAEL002424		hypothetical protein	19.21	0.44	-29.14	0.0000
AAEL012850			4.67	0.06	-28.56	0.0000
AAEL017100			11.28	0.21	-28.38	0.0000
AAEL007814		n-twist	4.75	0.07	-28.15	0.0000
AAEL002740		homeobox protein otx	2.04	0.00	-27.82	0.0000
AAEL006615		zinc finger protein	1.40	0.01	-26.65	0.0000
AAEL007221			1.17	0.00	-26.49	0.0000
AAEL003260		hypothetical protein	5.80	0.07	-26.42	0.0000
AAEL003551		hypothetical protein	71.88	2.41	-25.87	0.0000
AAEL006167			1.24	0.01	-24.95	0.0000
AAEL002633	CYP9J31	cytochrome P450	7.73	0.18	-24.68	0.0000
AAEL008108		guanine nucleotide-binding protein beta 2	78.69	2.58	-24.55	0.0000
AAEL004883		guanylate cyclase	1.75	0.02	-24.39	0.0000
AAEL002638	CYP9J6	cytochrome P450	24.37	0.78	-24.25	0.0000
AAEL005899		hypothetical protein	7.70	0.13	-23.75	0.0000
AAEL000457		hypothetical protein	25.40	0.85	-23.39	0.0000
AAEL009593		hypothetical protein	5.94	0.15	-23.05	0.0000
AAEL012109		sucrose transport protein	9.28	0.27	-22.58	0.0000
AAEL005770	OBP21	Odorant-binding protein 99c	14.84	0.50	-22.50	0.0000
AAEL018302		aromatic amino acid decarboxylase	2.75	0.06	-22.34	0.0000
AAEL002541		cystinosin	2.06	0.02	-21.43	0.0000
AAEL004890		hypothetical protein	9.86	0.40	-21.35	0.0000
AAEL000937		hypothetical protein	7.77	0.20	-21.13	0.0000
AAEL012491	CYP6P12	cytochrome P450	2.99	0.06	-20.79	0.0000
AAEL008111		hypothetical protein	50.12	1.72	-20.68	0.0000

Table A11 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL007224	LRIM22	hypothetical protein	13.22	0.42	-20.52	0.0000
AAEL007831		hypothetical protein	1.78	0.02	-20.44	0.0000
AAEL000021		hypothetical protein	2.59	0.06	-20.11	0.0000
AAEL012542		short neuropeptide F precursor	23.24	0.70	-19.98	0.0000
AAEL009544		hypothetical protein	40.90	1.54	-19.48	0.0000
AAEL008909		hypothetical protein	5.06	0.14	-18.71	0.0000
AAEL017120			3.01	0.07	-18.59	0.0000
AAEL001148		homeobox protein	2.24	0.02	-18.37	0.0000
AAEL002733		hypothetical protein	15.24	0.29	-18.32	0.0000
AAEL003794		homeobox protein nk-2	5.41	0.09	-18.00	0.0000
AAEL015657		hypothetical protein	2.49	0.03	-16.95	0.0000
AAEL014284		forkhead box protein (AaegFOXD)	1.60	0.03	-16.93	0.0000
AAEL011768		hypothetical protein	1.36	0.02	-16.70	0.0000
AAEL010886		carbonic anhydrase II	2.44	0.06	-16.59	0.0000
AAEL011716		tartan	1.25	0.03	-16.19	0.0000
AAEL001696		paired box protein	1.37	0.00	-16.18	0.0001
AAEL012998		hypothetical protein	7.15	0.31	-15.75	0.0000
AAEL006537		hypothetical protein	50.14	2.27	-15.51	0.0000
AAEL006602		hypothetical protein	44.55	2.52	-15.48	0.0000
AAEL009745		nitric oxide synthase	2.91	0.11	-15.48	0.0000
AAEL004676		(s)-2-hydroxy-acid oxidase	11.06	0.49	-15.46	0.0000
AAEL015583		molybdopterin synthase small subunit	5.33	0.11	-15.23	0.0000
AAEL017220			3.07	0.13	-15.01	0.0000
AAEL003035	GPROP9	ultraviolet-sensitive opsin	248.96	0.29	-14.90	0.0007
AAEL015148		hypothetical protein	1.21	0.00	-14.84	0.0002
AAEL011366		hypothetical protein	7.63	0.40	-14.73	0.0000
AAEL012492	CYP6AA5	cytochrome P450	25.74	1.50	-14.71	0.0000
AAEL000926			39.95	2.67	-14.33	0.0000
AAEL008485		hypothetical protein	124.21	6.73	-14.22	0.0000
AAEL004032		acetylcholine receptor protein alpha	6.71	0.29	-14.21	0.0000
AAEL001474		hypothetical protein	2.68	0.05	-14.17	0.0000
AAEL000780		amino acid transporter	7.33	0.33	-14.08	0.0000
AAEL013776		hypothetical protein	93.67	6.12	-14.03	0.0000
AAEL003291		hypothetical protein	49.98	2.78	-13.98	0.0000
AAEL013554	CYP4J14	cytochrome P450	3.22	0.13	-13.58	0.0000
AAEL010856		dopamine beta hydroxylase	6.70	0.28	-13.53	0.0000
AAEL000250			2.46	0.10	-13.36	0.0000
AAEL007010	CYP6AG4	cytochrome P450	10.00	0.67	-13.30	0.0000
AAEL013043		NADH dehydrogenase	3.93	0.00	-13.26	0.0006
AAEL006644		hypothetical protein	6.04	0.32	-13.13	0.0000
AAEL005444			14.37	0.89	-13.09	0.0000
AAEL005443		hypothetical protein	1.28	0.03	-12.92	0.0001
AAEL000538		hypothetical protein	2.66	0.00	-12.91	0.0010
AAEL002023		imaginal disc growth factor	5,269.21	374.87	-12.75	0.0000
AAEL000607		hypothetical protein	7.10	0.17	-12.72	0.0000
AAEL014610	CYP9J29	cytochrome P450	1.66	0.04	-12.72	0.0001
AAEL006484	GPROP3	rhodopsin	4.69	0.16	-12.70	0.0001
AAEL003894	GNBPB5	gram-negative bacteria binding protein	4.29	0.24	-12.69	0.0000
AAEL012060		hypothetical protein	21.86	1.23	-12.62	0.0000
AAEL010657		hypothetical protein	2.64	0.00	-12.55	0.0009
AAEL004418		hypothetical protein	1.16	0.03	-12.46	0.0002
AAEL003024		netrin	2.82	0.16	-12.35	0.0000
AAEL018228		monocarboxylate transporter	2.29	0.12	-12.33	0.0000
AAEL005296		hypothetical protein	12.68	0.96	-12.27	0.0000

Table A11 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL006092		tartan	2.13	0.09	-12.11	0.0000
AAEL012399		hypothetical protein	2.81	0.00	-12.10	0.0011
AAEL012881		hypothetical protein	1.27	0.03	-12.06	0.0001
AAEL008903		zinc finger protein	1.11	0.03	-12.06	0.0003
AAEL018308		acetylcholine receptor protein alpha	4.01	0.21	-12.01	0.0000
AAEL000863		SPASIC protein	1.06	0.02	-11.81	0.0005
AAEL011998		hypothetical protein	17.48	1.37	-11.68	0.0000
AAEL002509		glutamate receptor	3.67	0.12	-11.67	0.0001
AAEL004810		hypothetical protein	42.98	3.59	-11.65	0.0000
AAEL012596		sodium/chloride dependent transporter	60.64	3.83	-11.57	0.0000
AAEL002558		myomesin	5.70	0.47	-11.56	0.0000
AAEL000398		sidestep protein	3.19	0.19	-11.46	0.0000
AAEL012555		maltose phosphorylase	4.30	0.28	-11.45	0.0000
AAEL006366		hypothetical protein	2.47	0.07	-11.37	0.0002
AAEL006736		hypothetical protein	14.55	1.18	-11.34	0.0000
AAEL006323		hypothetical protein	21.60	1.67	-11.11	0.0000
AAEL002231		cuticle protein	8.02	0.32	-10.99	0.0002
AAEL002606	OBP35	Odorant-binding protein 56e	43,654.92	3,758.14	-10.89	0.0000
AAEL007978		angiotensin-converting-relatedenzyme	553.44	49.06	-10.78	0.0000
AAEL009421		cyclophilin-r	17.29	1.20	-10.69	0.0000
AAEL013763		arrowhead	1.30	0.00	-10.65	0.0026
AAEL007233		zinc finger protein	1.98	0.08	-10.64	0.0002
AAEL013959		hypothetical protein	2.67	0.13	-10.64	0.0000
AAEL009135		hypothetical protein	2.16	0.12	-10.43	0.0000
AAEL003003		glutamate-gated chloride channel	14.49	1.02	-10.40	0.0000
AAEL002676		angiotensin-converting enzyme	163.86	15.44	-10.22	0.0000
AAEL007024	CYP6AG3	cytochrome P450	11.26	0.86	-10.14	0.0000
AAEL005089		hypothetical protein	1.11	0.03	-10.12	0.0015
AAEL007072		hypothetical protein	5.93	0.56	-10.03	0.0000
AAEL001181		hypothetical protein	10.53	0.93	-9.99	0.0000
AAEL000236		hypothetical protein	1.07	0.02	-9.94	0.0015
AAEL012110		protease m1 zinc metalloprotease	78.90	7.09	-9.91	0.0000
AAEL008527			237.93	21.20	-9.91	0.0000
AAEL005966		hypothetical protein	15.31	1.34	-9.74	0.0000
AAEL007079		hypothetical protein	2.27	0.17	-9.51	0.0000
AAEL015305		sulfotransferase (sult)	10.50	1.02	-9.43	0.0000
AAEL006975		leucine aminopeptidase	3.27	0.14	-9.41	0.0016
AAEL001695		orthopedia homeobox protein	2.06	0.08	-9.37	0.0007
AAEL000254		nuclear factor i	11.82	0.85	-9.31	0.0000
AAEL005318		hypothetical protein	1.58	0.12	-9.22	0.0000
AAEL006630		hypothetical protein	1.01	0.06	-9.21	0.0003
AAEL008241		hypothetical protein	6.73	0.16	-9.20	0.0057
AAEL006109	OBP23	hypothetical protein	7.27	0.67	-9.20	0.0000
AAEL009266		c4b-binding protein beta chain	13.61	1.26	-9.19	0.0000
AAEL004572		hypothetical protein	2.83	0.18	-9.01	0.0001
AAEL001257		sugar transporter	6.24	0.57	-8.99	0.0000
AAEL012441		hypothetical protein	7.97	0.75	-8.95	0.0000
AAEL006470		hypothetical protein	1.00	0.00	-8.92	0.0065
AAEL004077		hypothetical protein	5.77	0.47	-8.86	0.0000
AAEL010631		hypothetical protein	1.33	0.06	-8.83	0.0005
AAEL018150		hypothetical protein	2.65	0.27	-8.71	0.0000
AAEL014370		hypothetical protein	3.03	0.19	-8.52	0.0011
AAEL002456		hypothetical protein	2.59	0.20	-8.44	0.0001
AAEL004359		hypothetical protein	17.74	1.83	-8.42	0.0000

Table A11 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL010934		hypothetical protein	4.52	0.39	-8.41	0.0000
AAEL002622		vitamin k-dependent gamma-carboxylase	3.56	0.35	-8.41	0.0000
AAEL011574		hypothetical protein	31.06	2.29	-8.40	0.0005
AAEL014520		follistatin	50.86	5.75	-8.39	0.0000
AAEL011931		hypothetical protein	1.04	0.00	-8.38	0.0099
AAEL002876		hypothetical protein	3.71	0.29	-8.36	0.0001
AAEL001517		carboxylesterase	9.65	0.91	-8.33	0.0000
AAEL008082		hypothetical protein	9.98	0.56	-8.27	0.0008
AAEL003319		hypothetical protein	5.99	0.51	-8.23	0.0000
AAEL010648		hypothetical protein	42.60	5.01	-8.19	0.0000
AAEL011740		hypothetical protein	5.26	0.58	-8.16	0.0000
AAEL017529			95.38	10.44	-8.15	0.0000
AAEL017422			1.92	0.08	-8.06	0.0025
AAEL012949		transferrin	90.81	10.81	-8.04	0.0000
AAEL000341		basic helix-loop-helix protein	5.88	0.14	-7.96	0.0121
AAEL004054	CYP4G36	cytochrome P450	178.93	21.16	-7.96	0.0000
AAEL009478		hypothetical protein	2.69	0.21	-7.95	0.0000
AAEL006535		neurotransmitter gated ion channel	9.78	1.10	-7.88	0.0000
AAEL004446		hypothetical protein	6.61	0.52	-7.86	0.0006
AAEL004898		hypothetical protein	27.06	3.12	-7.80	0.0000
AAEL003093		elongase	11.27	1.27	-7.74	0.0000
AAEL015598		hypothetical protein	2.10	0.15	-7.73	0.0001
AAEL012186			4.19	0.42	-7.71	0.0000
AAEL012704		hypothetical protein	27.72	3.22	-7.69	0.0000
AAEL006526		neurotransmitter gated ion channel	56.84	6.39	-7.68	0.0000
AAEL014553		triacylglycerol lipase, pancreatic	4.10	0.34	-7.68	0.0012
AAEL001676		defective proboscis extension response	1.79	0.14	-7.61	0.0001
AAEL012554		maltose phosphorylase	1.04	0.11	-7.61	0.0004
AAEL001969		protein serine/threonine kinase	4,905.92	622.35	-7.55	0.0000
AAEL000645		hypothetical protein	35.92	4.62	-7.53	0.0000
AAEL007584		hypothetical protein	3.65	0.38	-7.51	0.0002
AAEL009693		hypothetical protein	1.45	0.00	-7.44	0.0168
AAEL018521	Sphinx_2		2.97	0.00	-7.43	0.0163
AAEL009991		myosin iii	17.30	1.98	-7.42	0.0000
AAEL001504		tyrosine-phosphorylation-regulated kinase	38.05	4.31	-7.38	0.0000
AAEL010557		hypothetical protein	115.68	14.44	-7.32	0.0000
AAEL010039		hypothetical protein	1.04	0.05	-7.31	0.0058
AAEL018357			2.16	0.24	-7.26	0.0000
AAEL004876		guanylate cyclase	3.53	0.37	-7.23	0.0000
AAEL009792	LRIM25	hypothetical protein	14.13	1.34	-7.22	0.0004
AAEL015306		hypothetical protein	27.35	2.99	-7.19	0.0000
AAEL010646		hypothetical protein	13.08	1.55	-7.18	0.0000
AAEL007709	GPRGBB3		1.36	0.14	-7.12	0.0003
AAEL002518	IRg	glutamate receptor	5.31	0.64	-7.02	0.0000
AAEL005698		protein serine/threonine kinase	11.46	1.30	-6.90	0.0000
AAEL004233		hypothetical protein	2.36	0.23	-6.87	0.0026
AAEL012952		hypothetical protein	6.45	0.65	-6.83	0.0003
AAEL012481	HPX6	oxidase/peroxidase	4.67	0.62	-6.80	0.0000
AAEL007129		defective proboscis extension response	6.80	0.75	-6.78	0.0000
AAEL007789		alkyldihydroxyacetonephosphate synthase	1.78	0.24	-6.78	0.0000
AAEL004724		carboxylesterase	1.15	0.09	-6.77	0.0014
AAEL006019		voltage-gated sodium channel	78.39	6.20	-6.76	0.0076
AAEL011474		hypothetical protein	4.01	0.54	-6.73	0.0000

Table A11 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL000428		tryptophan 2,3-dioxygenase	3.93	0.50	-6.72	0.0000
AAEL006106	OBP26	hypothetical protein	22.45	2.89	-6.65	0.0000
AAEL000310		hypothetical protein	8.81	1.13	-6.62	0.0000
AAEL002254		hypothetical protein	4.31	0.56	-6.62	0.0000
AAEL009150		hypothetical protein	218.12	31.57	-6.61	0.0000
AAEL010924		ca-activated cl channel protein	2.45	0.31	-6.55	0.0000
AAEL007826		cgmp-dependent protein kinase	199.41	29.67	-6.52	0.0000
AAEL013259		hypothetical protein	1.20	0.09	-6.51	0.0076
AAEL006675			4.19	0.60	-6.45	0.0000
AAEL009330		carbonic anhydrase II	6.52	0.21	-6.43	0.0297
AAEL012494	CYP6BZ1	cytochrome P450	11.84	1.52	-6.41	0.0000
AAEL017270			2.00	0.18	-6.39	0.0032
AAEL004513		neurotransmitter gated ion channel	53.36	8.01	-6.37	0.0000
AAEL013424		hypothetical protein	11.78	1.34	-6.35	0.0004
AAEL000086	CLIPB32	clip-domain serine protease	2.16	0.22	-6.34	0.0002
AAEL011426		hypothetical protein	11.03	1.63	-6.32	0.0000
AAEL004428		salivary gland-expressed bHLH	2.05	0.14	-6.31	0.0109
AAEL013218		thiamine transporter	17.78	2.65	-6.30	0.0000
AAEL009630		cgmp-specific 3,5-cyclic phosphodiesterase	1.73	0.22	-6.28	0.0000
AAEL002500		hypothetical protein	3.05	0.19	-6.28	0.0145
AAEL002218		hypothetical protein	1.35	0.00	-6.28	0.0344
AAEL003183		oxidoreductase	7.03	0.76	-6.20	0.0020
AAEL001747		hypothetical protein	1.79	0.12	-6.18	0.0187
AAEL008750		hypothetical protein	3.83	0.35	-6.17	0.0073
AAEL001486		hypothetical protein	2.24	0.00	-6.14	0.0380
AAEL012437		hypothetical protein	1.81	0.21	-6.13	0.0003
AAEL017402			379.93	39.92	-6.08	0.0061
AAEL017262			426.24	12.65	-6.08	0.0386
AAEL009252		hypothetical protein	1.05	0.06	-6.05	0.0175
AAEL018199		hypothetical protein	474.09	71.57	-6.04	0.0000
AAEL012873		angiotensin-converting enzyme	1.88	0.26	-6.03	0.0014
AAEL007968		hypothetical protein	11.87	1.65	-6.02	0.0000
AAEL013651		hypothetical protein	3.21	0.36	-6.02	0.0001
AAEL010506		GTP-binding protein alpha subunit, gna	83.37	12.37	-5.99	0.0000
AAEL006556		hypothetical protein	3.23	0.38	-5.97	0.0000
AAEL008070		hypothetical protein	60.76	9.60	-5.97	0.0000
AAEL017500			156.35	24.17	-5.95	0.0000
AAEL012609		4-aminobutyrate aminotransferase	23.13	3.57	-5.90	0.0000
AAEL014765		hypothetical protein	9.18	1.44	-5.90	0.0000
AAEL006932		transcription factor ap-2	36.38	5.93	-5.87	0.0000
AAEL012975		hypothetical protein	6.90	1.00	-5.84	0.0000
AAEL009323		carbonic anhydrase precursor	26.75	4.20	-5.83	0.0000
AAEL005753		serine protease	283.32	46.46	-5.80	0.0000
AAEL018008			5.34	0.67	-5.80	0.0038
AAEL008331		hypothetical protein	69.59	11.46	-5.79	0.0000
AAEL002738		synaptic vesicle protein	1.18	0.14	-5.75	0.0014
AAEL002228		fatty acid synthase	5.76	0.40	-5.75	0.0331
AAEL008940		chaoptin	4.26	0.59	-5.74	0.0003
AAEL005432		hypothetical protein	1.65	0.19	-5.73	0.0087
AAEL009909		cln3/battenin	13.22	2.22	-5.72	0.0000
AAEL010681		Na/Cl dependent neurotransmitter transporter	52.39	8.32	-5.72	0.0000
AAEL000242		voltage-gated potassium channel	2.22	0.27	-5.71	0.0003

Table A11 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL003050		hypothetical protein	3.73	0.44	-5.69	0.0087
AAEL002665		matrix metalloproteinase	1.50	0.20	-5.69	0.0002
AAEL011139		hypothetical protein	53.38	8.46	-5.66	0.0000
AAEL000551		hypothetical protein	212.32	36.37	-5.66	0.0000
AAEL001628		hypothetical protein	3.88	0.47	-5.66	0.0012
AAEL000298		sodium/shloride dependent amino acid transporter	3.17	0.35	-5.66	0.0078
AAEL001031		hypothetical protein	13.66	2.11	-5.65	0.0000
AAEL011941		oxidase/peroxidase	1.75	0.18	-5.60	0.0122
AAEL009418		hypothetical protein	1.91	0.20	-5.59	0.0049
AAEL003934		hypothetical protein	2,909.59	480.34	-5.58	0.0000
AAEL005447		hypothetical protein	4.60	0.63	-5.58	0.0074
AAEL005282		hypothetical protein	6.54	1.03	-5.56	0.0000
AAEL003508		serine-pyruvate aminotransferase	1.57	0.18	-5.56	0.0051
AAEL002513		hypothetical protein	1.15	0.15	-5.55	0.0016
AAEL014893	CYP6BB2	cytochrome P450	6.68	0.97	-5.55	0.0015
AAEL013303		hypothetical protein	14.66	2.37	-5.54	0.0000
AAEL014541		maltose phosphorylase	3.57	0.60	-5.54	0.0000
AAEL005822		hypothetical protein	63.48	10.74	-5.52	0.0000
AAEL015611		hypothetical protein	3.06	0.30	-5.48	0.0215
AAEL014886		4-aminobutyrate aminotransferase	18.67	3.07	-5.46	0.0000
AAEL003114		hypothetical protein	4.37	0.60	-5.46	0.0029
AAEL008294		pupal cuticle protein 78E	1.72	0.13	-5.45	0.0255
AAEL001293		hypothetical protein	5.72	0.85	-5.40	0.0015
AAEL000576		lachesin	1.23	0.11	-5.39	0.0170
AAEL001075		hypothetical protein	2.39	0.29	-5.38	0.0030
AAEL008855		dynein heavy chain	10.32	1.35	-5.37	0.0069
AAEL004805		potassium-dependent sodium-calcium exchanger	10.98	1.53	-5.35	0.0034
AAEL004360		hypothetical protein	2.00	0.37	-5.35	0.0006
AAEL003491		proline synthetase associated protein	119.35	21.76	-5.34	0.0000
AAEL014231		hypothetical protein	28.06	4.97	-5.34	0.0000
AAEL004466	LRIM23	hypothetical protein	1.29	0.12	-5.33	0.0277
AAEL006058	CYP325Q2	cytochrome P450	3.59	0.61	-5.28	0.0000
AAEL010041		hypothetical protein	5.27	0.73	-5.27	0.0008
AAEL011125		hypothetical protein	2.01	0.30	-5.27	0.0005
AAEL003560		pou domain/drifter/cf-1a	16.13	2.94	-5.22	0.0000
AAEL015563		cytochrome P450	2.60	0.41	-5.21	0.0005
AAEL006161	CLIPB31	clip-domain serine protease	29.80	5.08	-5.20	0.0000
AAEL011809		glucose dehydrogenase	1.89	0.30	-5.20	0.0002
AAEL015592		structural maintenance of chromosomes smc1	3.92	0.69	-5.17	0.0000
AAEL005440		hypothetical protein	1.69	0.24	-5.16	0.0001
AAEL006336		hypothetical protein	1.64	0.26	-5.15	0.0011
AAEL006542		serine carboxypeptidase	3.70	0.66	-5.15	0.0000
AAEL004725		hypothetical protein	25.24	4.56	-5.13	0.0000
AAEL014125		nk homeobox protein	1.29	0.12	-5.13	0.0217
AAEL007770		voltage and ligand gated potassium channel	6.98	1.17	-5.13	0.0000
AAEL008031		carbonic anhydrase	7.16	1.19	-5.12	0.0001
AAEL003772		hypothetical protein	30.44	5.36	-5.11	0.0000
AAEL008129		hypothetical protein	22.41	4.16	-5.09	0.0000
AAEL010894		carbonic anhydrase II	1.61	0.15	-5.09	0.0424
AAEL001390		hypothetical protein	342.46	46.57	-5.08	0.0125

Table A11 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL010094		cyclin b	1.92	0.27	-5.08	0.0031
AAEL003970			50.48	9.44	-5.06	0.0000
AAEL014551		triacylglycerol lipase, pancreatic	1.05	0.14	-5.05	0.0015
AAEL015316		5'-3' exoribonuclease	1.71	0.19	-5.04	0.0142
AAEL002042		deoxyribonuclease I	9.75	1.64	-5.01	0.0000
AAEL006102		Gelsolin precursor	269.34	49.43	-4.99	0.0000
AAEL009881		dynein heavy chain	51.98	9.46	-4.98	0.0000
AAEL005772	OBP22	Odorant-binding protein 99c	153.87	28.24	-4.97	0.0000
AAEL016972			27.87	5.21	-4.94	0.0000
AAEL008501		hypothetical protein	5.24	1.01	-4.93	0.0000
AAEL008847		wingless	3.78	0.68	-4.91	0.0000
AAEL010634		hypothetical protein	3.55	0.56	-4.86	0.0042
AAEL005749		lysosomal alpha-mannosidase	6.02	1.21	-4.86	0.0000
AAEL013807		hypothetical protein	20.45	2.61	-4.85	0.0293
AAEL011702		hypothetical protein	3.28	0.59	-4.85	0.0001
AAEL001319		hypothetical protein	103.83	20.71	-4.85	0.0000
AAEL003270		hypothetical protein	1.29	0.19	-4.84	0.0028
AAEL008617		hypothetical protein	2.49	0.40	-4.84	0.0008
AAEL010097		hypothetical protein	2.39	0.31	-4.83	0.0274
AAEL011364		hypothetical protein	2.01	0.32	-4.82	0.0044
AAEL008222		lipase	3.90	0.51	-4.82	0.0253
AAEL000351		hypothetical protein	12.18	2.32	-4.81	0.0000
AAEL010263		hypothetical protein	57.64	11.73	-4.78	0.0000
AAEL004246		still life	10.47	1.93	-4.78	0.0001
AAEL005853		amino acid transporter	6.86	1.36	-4.73	0.0001
AAEL015520		protein-l-isoaspartate o-methyltransferase	3.39	0.64	-4.73	0.0001
AAEL010397		hypothetical protein	1.10	0.16	-4.73	0.0101
AAEL008843		hypothetical protein	1.80	0.23	-4.72	0.0315
AAEL018262		ORF-A short	1.81	0.34	-4.71	0.0000
AAEL005378		set domain protein	3.89	0.73	-4.69	0.0000
AAEL003082		kinectin	12.34	2.29	-4.68	0.0001
AAEL000612		hypothetical protein	4.76	0.82	-4.67	0.0405
AAEL000615		hypothetical protein	140.34	29.61	-4.64	0.0000
AAEL006096		Gelsolin precursor	461.63	92.61	-4.62	0.0000
AAEL009858		hypothetical protein	39.88	8.25	-4.61	0.0000
AAEL000288		hypothetical protein	62.80	12.30	-4.61	0.0000
AAEL006127		hypothetical protein	3.89	0.52	-4.58	0.0114
AAEL009024	GPRCAL3		3.88	0.72	-4.57	0.0015
AAEL006749		hypothetical protein	37.03	7.76	-4.56	0.0000
AAEL011671		hypothetical protein	4.70	0.90	-4.52	0.0002
AAEL012203		hypothetical protein	1.26	0.21	-4.52	0.0018
AAEL003047		netrin	4.98	0.94	-4.51	0.0006
AAEL010292		hypothetical protein	11.02	2.19	-4.51	0.0000
AAEL017329			1.95	0.35	-4.50	0.0013
AAEL011760		leucine-rich transmembrane protein	1.35	0.21	-4.50	0.0107
AAEL005442		guanylate cyclase beta 1 subunit	1.84	0.34	-4.49	0.0006
AAEL000200		hypothetical protein	1,100.92	232.83	-4.48	0.0000
AAEL015145		hypothetical protein	5.17	0.85	-4.48	0.0010
AAEL011787		hypothetical protein	1.99	0.38	-4.45	0.0003
AAEL007034		hypothetical protein	100.39	21.17	-4.43	0.0000
AAEL008885		hypothetical protein	8.11	1.56	-4.43	0.0012
AAEL002236		sodium/shloride dependent amino acid transporter	1.28	0.22	-4.43	0.0048
AAEL004447		hypothetical protein	2.84	0.34	-4.42	0.0344

Table A11 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL000019		hypothetical protein	513.31	108.73	-4.41	0.0000
AAEL009505		hypothetical protein	3.68	0.53	-4.41	0.0158
AAEL011153		hypothetical protein	12.14	2.02	-4.41	0.0008
AAEL008452		alpha-amylase	6.73	1.39	-4.40	0.0000
AAEL018123		receptor guanylate cyclase	45.46	10.09	-4.40	0.0000
AAEL012134		pur-alpha	4.52	0.84	-4.39	0.0007
AAEL008097		trypsin-eta	4.04	0.75	-4.39	0.0036
AAEL000079			1.86	0.34	-4.38	0.0063
AAEL006720		hypothetical protein	1.05	0.17	-4.36	0.0400
AAEL009352		hypothetical protein	3.46	0.68	-4.35	0.0000
AAEL014229		hypothetical protein	81.93	18.24	-4.34	0.0000
AAEL012829		hypothetical protein	8.78	2.06	-4.34	0.0000
AAEL001351		hypothetical protein	35.18	7.58	-4.33	0.0000
AAEL009124	CYP6N12	cytochrome P450	133.87	29.46	-4.31	0.0000
AAEL006921		calmodulin	29.32	6.27	-4.30	0.0000
AAEL002210		sodium/shloride dependent amino acid transporter	2.61	0.47	-4.30	0.0063
AAEL011166		cadherin	1.29	0.25	-4.28	0.0001
AAEL013574		apolipoprotein D	99.24	21.56	-4.28	0.0000
AAEL001127		defective proboscis extension response	7.85	1.52	-4.27	0.0009
AAEL006920	LRIM20	hypothetical protein	1.23	0.26	-4.26	0.0118
AAEL010172		hypothetical protein	3.30	0.71	-4.24	0.0006
AAEL004948		hypothetical protein	1.07	0.21	-4.24	0.0094
AAEL006250		insulin receptor tyrosine kinase substrate	1.22	0.23	-4.24	0.0025
AAEL004715		b-cell translocation protein	5.68	1.06	-4.24	0.0002
AAEL012689			12.93	2.75	-4.23	0.0002
AAEL013257		hypothetical protein	1.27	0.22	-4.22	0.0021
AAEL009260		hypothetical protein	2.20	0.37	-4.22	0.0036
AAEL006467		alcohol dehydrogenase	2.10	0.39	-4.21	0.0238
AAEL009596		sterol o-acyltransferase	1.89	0.34	-4.18	0.0137
AAEL012956		elastase	1.20	0.20	-4.18	0.0180
AAEL011508		hypothetical protein	32.52	6.80	-4.17	0.0010
AAEL005011		roundabout 1	1.35	0.25	-4.16	0.0021
AAEL005529		hypothetical protein	4.84	1.10	-4.15	0.0000
AAEL009955		hypothetical protein	25.74	5.73	-4.15	0.0000
AAEL010448		hypothetical protein	3,811.50	895.59	-4.12	0.0000
AAEL017507			5.59	0.95	-4.12	0.0076
AAEL008785		hypothetical protein	5,709.56	1,343.90	-4.12	0.0000
AAEL008032		hypothetical protein	16.04	3.76	-4.12	0.0000
AAEL014894		hypothetical protein	1.56	0.28	-4.11	0.0393
AAEL008726		hypothetical protein	2.93	0.59	-4.10	0.0002
AAEL004106		hairy protein	1.46	0.31	-4.10	0.0142
AAEL007533		hypothetical protein	6.27	1.32	-4.10	0.0106
AAEL009192	SCRASP1	serine protease	14.21	3.15	-4.10	0.0000
AAEL008033		hypothetical protein	3.74	0.79	-4.08	0.0210
AAEL006490	GPRCAL2		2.21	0.48	-4.07	0.0027
AAEL011275		organic cation transporter	13.15	3.05	-4.07	0.0000
AAEL009199		galactosy	1.21	0.24	-4.06	0.0351
AAEL013029		deoxyribonuclease I	5.55	1.27	-4.05	0.0000
AAEL006446		trehalose-6-phosphate synthase	20.35	3.67	-4.04	0.0383
AAEL000893		sex-determining region y protein, sry	3.74	0.90	-4.04	0.0000
AAEL012960		importin alpha	1.16	0.19	-4.04	0.0313
AAEL014427		hypothetical protein	2.02	0.30	-4.02	0.0438
AAEL004953		elongase	1.42	0.22	-4.01	0.0470

Table A11 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL011022		cysteine-rich protein	82.76	19.33	-4.00	0.0000
AAEL012039		zinc finger protein	2.36	0.50	-4.00	0.0002
AAEL008494		mitochondrial carrier protein ymc	10.50	2.35	-4.00	0.0012
AAEL012483		hypothetical protein	4.20	1.05	-3.99	0.0000
AAEL011359		NFAT	1.27	0.29	-3.99	0.0002
AAEL001929	SPZ5	hypothetical protein	1.28	0.22	-3.99	0.0113
AAEL014366		hypothetical protein	6.82	1.54	-3.98	0.0000
AAEL009907		hypothetical protein	1.30	0.26	-3.98	0.0039
AAEL017513			276.91	67.58	-3.97	0.0000
AAEL005741		forkhead protein/ forkhead protein domair	5.52	1.19	-3.94	0.0078
AAEL012138		24-dehydrocholesterol reductase	6.32	1.42	-3.94	0.0008
AAEL017479	GPRMGL1		1.92	0.30	-3.94	0.0422
AAEL005989		hypothetical protein	1.05	0.21	-3.93	0.0170
AAEL005634		harmonin	46.76	10.67	-3.92	0.0006
AAEL002506	IRf	glutamate receptor	38.95	9.59	-3.90	0.0000
AAEL014664		AMP dependent coa ligase	2.94	0.64	-3.89	0.0005
AAEL014200		hypothetical protein	1.20	0.22	-3.89	0.0092
AAEL003641		sodium/shloride dependent amino acid transporter	1.20	0.23	-3.88	0.0087
AAEL009625		short-chain dehydrogenase	5.24	1.15	-3.85	0.0152
AAEL011088		hypothetical protein	304.91	76.88	-3.85	0.0000
AAEL001920		hypothetical protein	19.83	4.99	-3.81	0.0000
AAEL001689		retinal homeobox protein	2.30	0.54	-3.81	0.0001
AAEL000910		hypothetical protein	1.54	0.30	-3.80	0.0235
AAEL013723		polypyrimidine tract binding protein	24.66	5.69	-3.79	0.0026
AAEL004361		alpha-glucosidase	3.91	1.02	-3.78	0.0000
AAEL002112		hypothetical protein	1.78	0.39	-3.77	0.0025
AAEL008354		gaba receptor invertebrate	13.70	3.19	-3.76	0.0015
AAEL009189		encore protein	7.62	1.84	-3.76	0.0002
AAEL004097		enhancer of split protein	85.44	22.33	-3.74	0.0000
AAEL014073		hypothetical protein	3.81	0.97	-3.74	0.0001
AAEL005112	CCEAE3A	alpha-esterase	8.30	2.02	-3.74	0.0005
AAEL011798		allergen	98.66	22.85	-3.74	0.0056
AAEL004502		hypothetical protein	14.70	3.89	-3.73	0.0000
AAEL001245		heterogeneous nuclear ribonucleoprotein	4.01	0.80	-3.73	0.0064
AAEL001552		hypothetical protein	2.36	0.62	-3.72	0.0001
AAEL009291		serine carboxypeptidase	18.99	4.90	-3.71	0.0000
AAEL008160		fatty acid synthase	3.13	0.69	-3.70	0.0239
AAEL000532		hypothetical protein	1.57	0.33	-3.67	0.0469
AAEL014202		wd-repeat protein	1.04	0.22	-3.65	0.0037
AAEL001877		fucosyltransferase 11 (fut11)	1.38	0.28	-3.65	0.0198
AAEL010034		hypothetical protein	54.86	13.68	-3.65	0.0003
AAEL012182		hypothetical protein	3.46	0.77	-3.65	0.0119
AAEL010481		sugar transporter	19.02	4.86	-3.64	0.0000
AAEL008039		hypothetical protein	9.94	2.27	-3.64	0.0205
AAEL004366		hypothetical protein	13.95	3.59	-3.64	0.0008
AAEL011129		alcohol dehydrogenase	27.58	6.94	-3.63	0.0006
AAEL003209		amalgam protein	2.90	0.67	-3.62	0.0013
AAEL009722		clip-domain serine protease	4.81	1.30	-3.61	0.0000
AAEL015308	SCRAL1	protein-lysine 6-oxidase	15.77	4.16	-3.61	0.0004
AAEL003920	GPRDOP1		79.30	21.41	-3.61	0.0000
AAEL012064		Niemann-Pick Type C-2	1,423.83	362.71	-3.60	0.0004
AAEL009947		homeotic antennapedia protein	1.22	0.29	-3.59	0.0284
AAEL010452		hypothetical protein	1,594.19	434.00	-3.59	0.0000

Table A11 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL012822		Misexpression suppressor of KSR	4.61	1.24	-3.59	0.0000
AAEL011042		hypothetical protein	3.58	0.81	-3.58	0.0232
AAEL002599		hypothetical protein	8.76	2.22	-3.56	0.0004
AAEL002624		serine protease	4.06	0.96	-3.56	0.0163
AAEL001500		insulinprotein enhancer protein isl	1.85	0.39	-3.54	0.0163
AAEL005014		transient receptor potential channel	3.41	0.83	-3.54	0.0047
AAEL017144			46.91	11.53	-3.54	0.0105
AAEL010781		ap endonuclease	4.03	1.08	-3.52	0.0000
AAEL006974			16.57	4.53	-3.52	0.0000
AAEL009554		hypothetical protein	2.06	0.52	-3.51	0.0038
AAEL003956		amino acid transporter	7.96	1.98	-3.51	0.0006
AAEL001503		sodium/hydrogen exchanger 3 (nhe3)	16.65	4.55	-3.51	0.0000
AAEL001868			1.24	0.29	-3.51	0.0169
AAEL008434		er lumen protein retaining receptor	3.65	0.80	-3.51	0.0067
AAEL006827	CYP12F8	cytochrome P450	3.35	0.76	-3.51	0.0168
AAEL017168			1.41	0.29	-3.50	0.0232
AAEL002587	OBP11	Odorant-binding protein 56e	809.73	225.52	-3.48	0.0000
AAEL014303			7.31	1.98	-3.48	0.0000
AAEL014663		AMP dependent coa ligase	3.23	0.76	-3.47	0.0033
AAEL001864		Eukaryotic translation initiation factor	194.07	53.21	-3.46	0.0000
AAEL006479		hypothetical protein	40.63	11.16	-3.46	0.0000
AAEL010747			1.44	0.33	-3.45	0.0118
AAEL007104		voltage-gated potassium channel	2.86	0.72	-3.44	0.0035
AAEL000342		peroxidasin	1.76	0.39	-3.44	0.0381
AAEL002256		collagen alpha 1(xviii) chain	10.65	2.81	-3.44	0.0012
AAEL004873		hypothetical protein	1,124.89	315.81	-3.42	0.0000
AAEL004547		hypothetical protein	9.42	2.50	-3.41	0.0117
AAEL004209		opioid-binding protein/cell adhesion molecule	6.07	1.65	-3.40	0.0000
AAEL007791		hypothetical protein	1.27	0.27	-3.40	0.0366
AAEL009461		histone H1	4.90	1.27	-3.39	0.0042
AAEL008566	GPRNNA11		2.07	0.50	-3.39	0.0066
AAEL003348		hypothetical protein	9.15	2.66	-3.39	0.0000
AAEL018333		colmedin	4.29	1.15	-3.39	0.0007
AAEL000105		beta-alanine synthase	8.96	2.50	-3.39	0.0027
AAEL003436		transcription factor coe3	1.48	0.38	-3.39	0.0298
AAEL012106		acetylcholine receptor protein	4.53	1.14	-3.38	0.0166
AAEL007391		hypothetical protein	6.80	1.88	-3.38	0.0006
AAEL011109		hypothetical protein	580.90	167.81	-3.38	0.0000
AAEL006254		beta-1,3-glucuronyltransferase s, p	39.55	11.21	-3.38	0.0000
AAEL012691		sodium/solute symporter	15.93	4.25	-3.37	0.0022
AAEL007436		hypothetical protein	1.41	0.35	-3.37	0.0004
AAEL003977		elongase	5.48	1.40	-3.36	0.0107
AAEL012711	CLIPC12	trypsin	2.03	0.49	-3.36	0.0308
AAEL005040		hypothetical protein	3.07	0.83	-3.36	0.0037
AAEL003407		hypothetical protein	19.42	5.76	-3.36	0.0000
AAEL002396		hypothetical protein	3.11	0.86	-3.35	0.0201
AAEL010936		gamma glutamyl transpeptidases	26.22	7.56	-3.34	0.0000
AAEL003279		clip-domain serine protease	6.91	2.05	-3.33	0.0000
AAEL009354		hypothetical protein	2.54	0.68	-3.33	0.0002
AAEL011905		myosin i	10.88	3.04	-3.32	0.0010
AAEL011191		protein phosphatase 1 binding protein	13.31	4.00	-3.31	0.0000
AAEL007587		hypothetical protein	171.17	50.14	-3.31	0.0000
AAEL006766		hypothetical protein	16.00	4.30	-3.31	0.0012

Table A11 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL008450		hypothetical protein	28.42	8.09	-3.31	0.0000
AAEL012401		short-chain dehydrogenase	82.22	23.89	-3.30	0.0000
AAEL013209		hypothetical protein	2.53	0.56	-3.29	0.0268
AAEL013894		hypothetical protein	10.67	3.09	-3.29	0.0000
AAEL008303		calponin/transgelin	84.45	24.51	-3.28	0.0001
AAEL009236			38.05	10.84	-3.28	0.0003
AAEL014885		hypothetical protein	2.32	0.56	-3.26	0.0197
AAEL006466		chondroitin synthase	28.90	8.34	-3.26	0.0000
AAEL003211		beta-carotene dioxygenase	38.44	10.88	-3.26	0.0010
AAEL007216		elongase	59.30	17.34	-3.26	0.0000
AAEL014830		cytochrome P450	1.67	0.49	-3.26	0.0411
AAEL004255		zinc finger protein	4.45	1.20	-3.25	0.0047
AAEL018149	IRc		8.96	2.57	-3.25	0.0003
AAEL003408		leucine-rich transmembrane protein	1.04	0.28	-3.25	0.0064
AAEL008579			2.88	0.79	-3.24	0.0075
AAEL015653		dehydrogenase	4.70	1.19	-3.23	0.0040
AAEL012773	CYP325M1	cytochrome P450	484.98	146.70	-3.23	0.0000
AAEL002397		hypothetical protein	195.31	57.19	-3.22	0.0001
AAEL003091		glucosyl/glucuronosyl transferases	13.76	3.81	-3.21	0.0076
AAEL010623		hypothetical protein	4.77	1.30	-3.21	0.0013
AAEL003299		hypothetical protein	14.16	4.16	-3.21	0.0029
AAEL013083		hypothetical protein	4.18	1.23	-3.19	0.0008
AAEL015296		septin	8.13	2.41	-3.18	0.0000
AAEL003782		hypothetical protein	4.15	1.18	-3.18	0.0115
AAEL009640		hypothetical protein	15.95	4.80	-3.17	0.0000
AAEL007046		mitochondrial brown fat uncoupling protein	9.94	2.81	-3.17	0.0112
AAEL014365		chromaffin granule amine transporter	2.31	0.71	-3.17	0.0042
AAEL006297		venom allergen	983.11	289.45	-3.17	0.0006
AAEL000311		hypothetical protein	3.54	1.05	-3.16	0.0018
AAEL000670		methionine sulfoxide reductase	247.88	73.61	-3.16	0.0004
AAEL003028		histamine-gated chloride channel subunit	7.65	2.13	-3.15	0.0116
AAEL018353		hypothetical protein	3.52	1.06	-3.15	0.0015
AAEL002579		hypothetical protein	3.70	0.96	-3.15	0.0469
AAEL005681	GPRHIS	hypothetical protein	6.52	1.72	-3.14	0.0415
AAEL002659		hypothetical protein	56.60	17.20	-3.14	0.0003
AAEL009126	CYP6N6	cytochrome P450	80.20	23.88	-3.14	0.0004
AAEL008194		protein phosphatase 2a, regulatory subuni	3.89	0.98	-3.13	0.0323
AAEL005357		hypothetical protein	9.58	2.69	-3.13	0.0024
AAEL007486	CCEAE20	alpha-esterase	1.44	0.36	-3.12	0.0421
AAEL003566		hypothetical protein	2.95	0.84	-3.12	0.0041
AAEL001626		zinc/iron transporter	79.77	24.68	-3.12	0.0000
AAEL012519		actin binding protein	4.41	1.24	-3.12	0.0023
AAEL010480		serine-pyruvate aminotransferase	1.76	0.48	-3.11	0.0213
AAEL010567		hypothetical protein	26.80	7.80	-3.11	0.0058
AAEL003599		hypothetical protein	18.07	5.37	-3.10	0.0001
AAEL008936		hypothetical protein	4.81	1.48	-3.09	0.0008
AAEL013239		bone morphogenetic protein	5.72	1.69	-3.09	0.0047
AAEL001546		protein phosphatase 1 regulatory	5.18	1.53	-3.09	0.0000
AAEL009112		hypothetical protein	3.93	1.18	-3.09	0.0013
AAEL006904		hypothetical protein	37.51	11.63	-3.08	0.0000
AAEL003215		heat shock factor binding protein	2.03	0.49	-3.08	0.0299
AAEL013555	CYP4J13	cytochrome P450	5.00	1.48	-3.08	0.0375
AAEL006046		hypothetical protein	11.77	3.06	-3.08	0.0215

Table A11 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL008412		mitochondrial import inner membrane translocase	8.03	2.53	-3.08	0.0000
AAEL003656		hypothetical protein	6.32	1.75	-3.08	0.0310
AAEL014719		inosine-uridine preferring nucleoside hydrolase	36.99	11.78	-3.07	0.0000
AAEL008055		nicotinic acetylcholine receptor subunit	1.64	0.45	-3.07	0.0434
AAEL007064	GNBPB6	gram-negative bacteria binding protein	36.16	11.67	-3.07	0.0000
AAEL009336			1.77	0.52	-3.06	0.0052
AAEL009261		hypothetical protein	1.70	0.57	-3.06	0.0072
AAEL007092		hypothetical protein	215.85	68.75	-3.06	0.0000
AAEL006899		DNA-J/hsp40	15.45	4.79	-3.06	0.0000
AAEL002305		hypothetical protein	5.71	1.62	-3.06	0.0491
AAEL000165		hypothetical protein	23.46	7.44	-3.06	0.0001
AAEL006825		hypothetical protein	33.36	10.36	-3.05	0.0001
AAEL009300		hypothetical protein	7.87	2.28	-3.05	0.0051
AAEL009663		hypothetical protein	2.86	0.89	-3.05	0.0040
AAEL001034			6.69	1.96	-3.05	0.0089
AAEL017391			11.38	3.48	-3.04	0.0013
AAEL015372		guanylate cyclase beta 1 subunit	2.69	0.75	-3.03	0.0232
AAEL013271		organic cation transporter	20.05	6.39	-3.03	0.0000
AAEL008859		adenylate cyclase	14.22	4.52	-3.03	0.0000
AAEL011890		hypothetical protein	525.84	168.58	-3.02	0.0000
AAEL014639		ubiquitin conjugating enzyme	8.26	2.54	-3.02	0.0222
AAEL011800		hypothetical protein	2.16	0.62	-3.02	0.0050
AAEL004834			3.04	0.90	-3.01	0.0101
AAEL010139		serine protease	26.63	7.61	-3.01	0.0490
AAEL008006		3-hydroxyacyl-coa dehyrogenase	83.27	26.15	-3.00	0.0004
AAEL006148		adamts-20	3.56	1.06	-2.99	0.0020
AAEL005980		hypothetical protein	5.04	1.47	-2.98	0.0102
AAEL000263		hypothetical protein	1.39	0.42	-2.97	0.0000
AAEL002301		serine protease	9.94	3.34	-2.97	0.0000
AAEL008657		midline fasciclin	420.50	136.05	-2.96	0.0000
AAEL005887		hypothetical protein	8.29	2.31	-2.96	0.0219
AAEL011884		hypothetical protein	17.27	5.25	-2.96	0.0059
AAEL006245		insulin receptor tyrosine kinase substrate	7.74	2.40	-2.96	0.0053
AAEL001108		protein kinase c	5.52	1.71	-2.96	0.0005
AAEL015314		camp-dependent protein kinase type ii	5.45	1.70	-2.96	0.0012
AAEL004632		hypothetical protein	6.00	1.69	-2.95	0.0174
AAEL007603	OBP10	Odorant-binding protein 56a	1,218.87	403.83	-2.95	0.0000
AAEL017576			35.52	11.20	-2.95	0.0069
AAEL008233		hypothetical protein	4.55	1.35	-2.94	0.0155
AAEL015454		hypothetical protein	6.92	2.22	-2.94	0.0045
AAEL003716		ribonuclease UK114	4.90	1.47	-2.93	0.0168
AAEL014839		sidestep protein	4.38	1.32	-2.93	0.0065
AAEL009889		hypothetical protein	2.31	0.70	-2.93	0.0091
AAEL004941	CYP6AK1	cytochrome P450	4.90	1.54	-2.92	0.0045
AAEL009072		ribonucleoprotein	12.59	3.76	-2.92	0.0322
AAEL001861		nuclear pore complex protein nup154	27.53	9.06	-2.92	0.0000
AAEL003457		hypothetical protein	3.69	1.25	-2.91	0.0175
AAEL003304		hypothetical protein	11.26	3.71	-2.91	0.0001
AAEL017136	CYP325V1		74.87	25.02	-2.90	0.0000
AAEL007447		hypothetical protein	1.59	0.48	-2.90	0.0027
AAEL006880		rab32	6.39	2.04	-2.89	0.0016
AAEL006555		hypothetical protein	5.79	1.86	-2.88	0.0015

Table A11 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL017146			322.07	107.58	-2.88	0.0002
AAEL012400		hydroxybutyrate dehydrogenase	16.65	5.52	-2.88	0.0000
AAEL014655		hypothetical protein	1.57	0.52	-2.87	0.0413
AAEL004000	TOLL10	toll	3.28	1.06	-2.87	0.0013
AAEL005978		hypothetical protein	11.44	3.59	-2.87	0.0078
AAEL011779		hypothetical protein	2.43	0.79	-2.87	0.0106
AAEL001629			6.40	2.07	-2.86	0.0025
AAEL011973		fumarylacetoacetate hydrolase	121.06	40.83	-2.86	0.0000
AAEL010210		neurogenic locus notch (notch)	9.68	3.29	-2.86	0.0000
AAEL012627		hypothetical protein	9.77	3.30	-2.85	0.0000
AAEL001987		protein serine/threonine kinase	23.57	7.64	-2.85	0.0006
AAEL012464			8.88	2.94	-2.85	0.0000
AAEL005323		kinesin motor protein	10.16	3.41	-2.85	0.0000
AAEL011004		hypothetical protein	8.89	3.06	-2.85	0.0000
AAEL017430			36.34	12.23	-2.84	0.0002
AAEL016982			87.96	30.26	-2.84	0.0000
AAEL013325		hypothetical protein	23.94	7.82	-2.83	0.0012
AAEL007667		hypothetical protein	1.68	0.54	-2.82	0.0011
AAEL008081		excision repair cross-complementing 1 ercc1	2.93	0.95	-2.81	0.0128
AAEL006710		nucleolysin tia-1	1.82	0.55	-2.81	0.0474
AAEL012311		vitellogenin	2,205.84	749.21	-2.81	0.0002
AAEL006834		glutamate semialdehyde dehydrogenase	29.68	9.42	-2.80	0.0451
AAEL013612		hypothetical protein	65.17	22.57	-2.80	0.0000
AAEL003104		tripartite motif protein trim2,3	29.66	10.28	-2.80	0.0000
AAEL010482		acidic membrane protein	3.97	1.28	-2.79	0.0011
AAEL000886		hypothetical protein	584.80	193.22	-2.79	0.0119
AAEL005464		hypothetical protein	25.11	8.73	-2.79	0.0000
AAEL007105		hypothetical protein	9.12	3.10	-2.78	0.0001
AAEL011928		hypothetical protein	19.61	6.61	-2.78	0.0023
AAEL004957		hypothetical protein	56.64	19.53	-2.78	0.0002
AAEL006968		hypothetical protein	9.68	3.33	-2.78	0.0039
AAEL009685		oxidoreductase	10.99	3.61	-2.78	0.0264
AAEL014454		hypothetical protein	45.18	15.79	-2.77	0.0000
AAEL014761		hypothetical protein	5.75	1.91	-2.77	0.0000
AAEL008534		hypothetical protein	59.87	21.11	-2.76	0.0000
AAEL001851		hypothetical protein	14.32	4.99	-2.76	0.0002
AAEL007633		dihydropyrimidinase	54.44	19.22	-2.75	0.0000
AAEL007719		rhombotin	5.87	2.01	-2.75	0.0003
AAEL000504		hypothetical protein	6.50	2.24	-2.74	0.0000
AAEL011151		hypothetical protein	13.18	4.65	-2.74	0.0295
AAEL018131		leucine-rich transmembrane protein	11.39	3.95	-2.74	0.0001
AAEL001435	SPZ2	Sptzle 2 (Spz2)	16.39	5.41	-2.74	0.0240
AAEL002018		hypothetical protein	289.90	102.88	-2.74	0.0000
AAEL008001		hypothetical protein	5.34	1.96	-2.74	0.0018
AAEL008156		hypothetical protein	6.88	2.27	-2.74	0.0060
AAEL013633		ubiquitin-conjugating enzyme h	4.22	1.31	-2.74	0.0175
AAEL004409		yellow protein	329.24	116.05	-2.74	0.0000
AAEL000657		hypothetical protein	1,165.26	415.31	-2.73	0.0000
AAEL009258		hypothetical protein	8.94	3.06	-2.73	0.0054
AAEL017521			3.73	1.28	-2.73	0.0000
AAEL005000		hypothetical protein	7.24	2.63	-2.72	0.0001
AAEL001763		hypothetical protein	68.05	24.50	-2.72	0.0001
AAEL007659		hypothetical protein	311.15	111.56	-2.72	0.0000

Table A11 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL009751		hypothetical protein	8.30	2.92	-2.72	0.0001
AAEL010479		sugar transporter	31.45	11.17	-2.71	0.0001
AAEL010102		tetraspanin	78.36	27.07	-2.71	0.0044
AAEL009906		hypothetical protein	17.30	5.97	-2.71	0.0098
AAEL004868		hemomucin	39.09	13.92	-2.71	0.0000
AAEL005915		monocarboxylate transporter	3.66	1.19	-2.70	0.0357
AAEL005338		novex-3 (titin isoform)	3.11	1.06	-2.70	0.0119
AAEL001128		AMP dependent coa ligase	13.90	4.78	-2.70	0.0297
AAEL009583		filamin	19.35	6.81	-2.70	0.0016
AAEL002317		insulin receptor	2.03	0.69	-2.69	0.0038
AAEL012326		calmodulin	1,357.29	473.92	-2.69	0.0057
AAEL001527		hypothetical protein	5.10	1.69	-2.68	0.0132
AAEL014945		hypothetical protein	2.99	1.04	-2.68	0.0254
AAEL013430		hypothetical protein	4.44	1.51	-2.67	0.0008
AAEL009629		endoU protein	413.33	149.78	-2.67	0.0000
AAEL004783		ornithine decarboxylase antizyme	1,195.57	430.02	-2.67	0.0001
AAEL001857		hypothetical protein	3.41	1.19	-2.67	0.0220
AAEL000809		hypothetical protein	3.02	1.02	-2.66	0.0166
AAEL001490		acylphosphatase	29.08	10.26	-2.66	0.0048
AAEL005581		norepinephrine/norepinephrine transporte	5.34	1.82	-2.66	0.0147
AAEL002063		cationic amino acid transporter	4.62	1.65	-2.65	0.0000
AAEL008455		hypothetical protein	6.50	2.40	-2.65	0.0000
AAEL017098			915.10	334.66	-2.64	0.0000
AAEL005149		liprin-beta1	29.10	10.85	-2.63	0.0000
AAEL007905		hypothetical protein	13.20	4.83	-2.63	0.0341
AAEL013770		zinc finger protein	3.74	1.27	-2.63	0.0272
AAEL006685		G-protein, gamma-subunit	88.85	33.28	-2.62	0.0008
AAEL010941		hypothetical protein	2.86	1.02	-2.62	0.0354
AAEL005815		vitellogenin	610.19	217.44	-2.61	0.0146
AAEL014456		hypothetical protein	19.03	6.95	-2.61	0.0109
AAEL009567		apolipoprotein D	54.14	19.86	-2.60	0.0003
AAEL014966		hypothetical protein	68.31	25.03	-2.59	0.0017
AAEL008236		sidestep protein	4.90	1.67	-2.59	0.0474
AAEL011676		AMP dependent coa ligase	1.77	0.63	-2.58	0.0017
AAEL015534		hypothetical protein	2.87	1.00	-2.58	0.0457
AAEL013184		hypothetical protein	57.18	21.72	-2.57	0.0000
AAEL001062		hypothetical protein	43.39	16.51	-2.57	0.0000
AAEL003914		guanylate kinase (cask)	30.94	11.46	-2.56	0.0027
AAEL006156		hypothetical protein	1.76	0.62	-2.56	0.0186
AAEL007407		hypothetical protein	11.35	4.15	-2.56	0.0225
AAEL004881		adam	1.15	0.38	-2.55	0.0413
AAEL005315		hypothetical protein	7.23	2.58	-2.55	0.0276
AAEL000715		zinc finger protein	55.08	21.00	-2.55	0.0000
AAEL010178		hypothetical protein	10.92	4.16	-2.55	0.0015
AAEL003237		protein-tyrosine-phosphatase	24.11	8.82	-2.54	0.0021
AAEL000735		acyl-CoA oxidase	3.50	1.25	-2.54	0.0212
AAEL006872		calponin/transgelin	80.54	30.15	-2.53	0.0070
AAEL011325		gonadotropin-releasing hormone receptor	2.65	1.02	-2.53	0.0009
AAEL009875		alanine aminotransferase	2.88	1.09	-2.52	0.0471
AAEL003131		hypothetical protein	4.02	1.51	-2.52	0.0449
AAEL012556		Ofd1 protein	21.14	7.83	-2.51	0.0261
AAEL006477		lachesin	5.69	2.20	-2.51	0.0038
AAEL007513		hypothetical protein	155.41	58.65	-2.51	0.0065
AAEL018185		hypothetical protein	1.12	0.45	-2.51	0.0219

Table A11 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL011730		Odorant-binding protein 99c	46.61	18.11	-2.51	0.0003
AAEL013971		hypothetical protein	1.80	0.67	-2.51	0.0015
AAEL007593	CLIPC2	lumbrokinase-3(1) precursor	40.83	15.60	-2.51	0.0005
AAEL005711		protein serine/threonine kinase	240.01	92.01	-2.51	0.0011
AAEL012509		carboxylesterase-6	3.60	1.40	-2.50	0.0121
AAEL014527		potassium-dependent sodium-calcium exchanger	30.33	11.60	-2.50	0.0011
AAEL010519		succinate dehydrogenase	13.30	4.90	-2.50	0.0006
AAEL004967		myo inositol monophosphatase	8.38	3.14	-2.50	0.0079
AAEL015040		multiple inositol polyphosphate phosphatase	24.51	9.41	-2.49	0.0015
AAEL015076		hypothetical protein	46.94	18.17	-2.48	0.0009
AAEL001207		hypothetical protein	15.03	5.84	-2.48	0.0004
AAEL002261		GTP cyclohydrolase i	345.86	134.06	-2.47	0.0010
AAEL008546		hypothetical protein	14.75	5.48	-2.47	0.0371
AAEL001757		iduronate 2-sulfatase precursor	7.75	2.86	-2.47	0.0233
AAEL007670			1.54	0.59	-2.47	0.0035
AAEL003015		protein phosphatase 2a, regulatory subuni	5.62	2.05	-2.46	0.0412
AAEL009480		hypothetical protein	29.83	11.95	-2.45	0.0000
AAEL002230			15.70	6.16	-2.45	0.0002
AAEL008513		hypothetical protein	17.15	6.71	-2.45	0.0010
AAEL013559		uncoordinated protein	22.22	8.65	-2.45	0.0039
AAEL012103		hypothetical protein	28.54	10.95	-2.45	0.0020
AAEL004351		casein kinase	27.70	11.01	-2.44	0.0001
AAEL005264		hypothetical protein	24.80	9.37	-2.44	0.0010
AAEL018266		autoimmune regulator	1.25	0.49	-2.43	0.0277
AAEL002661		matrix metalloproteinase	3.58	1.45	-2.43	0.0192
AAEL002309	TPX4	peroxiredoxin 6, prx-6	249.36	99.04	-2.43	0.0005
AAEL010205		hypothetical protein	635.93	250.10	-2.43	0.0029
AAEL000006		phosphoenolpyruvate carboxykinase	2.47	0.96	-2.43	0.0227
AAEL005959		phospholipase b, plb1	21.08	8.13	-2.43	0.0261
AAEL012086	LRIM1	hypothetical protein	23.81	9.48	-2.43	0.0003
AAEL007732		peptidyl-glycine alpha-amidating monooxygenase	48.83	19.38	-2.43	0.0007
AAEL002022		protein serine/threonine kinase	15.93	5.99	-2.42	0.0189
AAEL002781		galactokinase	7.14	2.87	-2.42	0.0007
AAEL012756		hypothetical protein	4.68	1.70	-2.42	0.0113
AAEL005137		tetraspanin	238.19	96.37	-2.42	0.0000
AAEL004664		hypothetical protein	10.77	4.24	-2.41	0.0119
AAEL007758		hypothetical protein	17.79	7.06	-2.41	0.0048
AAEL009380		phospholipase c beta	28.20	11.10	-2.41	0.0082
AAEL002516		hypothetical protein	2.65	1.07	-2.41	0.0147
AAEL002269		purine nucleoside phosphorylase	34.31	13.45	-2.41	0.0107
AAEL007500		hypothetical protein	5.00	1.91	-2.41	0.0109
AAEL011623		hypothetical protein	43.42	17.71	-2.41	0.0000
AAEL006777		hypothetical protein	33.80	13.40	-2.40	0.0012
AAEL010379		ATP-binding cassette transporter	84.01	34.06	-2.40	0.0000
AAEL013733		Psq-DNA binding domain protein	1.62	0.64	-2.40	0.0228
AAEL015458		transferrin	103.13	41.80	-2.40	0.0000
AAEL006171		n-myc downstream regulated	126.50	51.51	-2.40	0.0000
AAEL010867		serine protease	10.84	4.34	-2.39	0.0011
AAEL002055		neuroendocrine protein 7b2	211.37	84.06	-2.39	0.0091
AAEL013564		hypothetical protein	9.82	3.89	-2.39	0.0019
AAEL000640		alanine-glyoxylate aminotransferase	6.03	2.36	-2.39	0.0144

Table A11 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL004112	TPX2	peroxiredoxins, prx-1, prx-2, prx-3	1,255.12	509.14	-2.39	0.0001
AAEL011457		hypothetical protein	70.78	28.91	-2.38	0.0000
AAEL005643		guanine nucleotide exchange factor	2.60	1.01	-2.38	0.0051
AAEL012217		protease m1 zinc metalloprotease	5.29	2.08	-2.38	0.0380
AAEL007559		guanyl-nucleotide exchange factor	5.68	2.26	-2.38	0.0359
AAEL009216		camp-dependent protein	12.09	4.73	-2.37	0.0201
AAEL002892		protein kinase c, mu	33.56	13.71	-2.37	0.0001
AAEL009188		hypothetical protein	11.91	4.98	-2.37	0.0000
AAEL013457		RNA polymerase small Zn-binding subunit	17.46	6.95	-2.36	0.0161
AAEL007542		glutamate decarboxylase	58.52	24.25	-2.36	0.0000
AAEL003918		calcium-dependent protein kinase	6.47	2.50	-2.36	0.0089
AAEL008930		protein phosphatase-2b	50.59	20.61	-2.36	0.0013
AAEL005622		hypothetical protein	4.45	1.79	-2.36	0.0180
AAEL000334		villin	13.74	5.57	-2.36	0.0047
AAEL010536		alpha-amylase	1.49	0.60	-2.36	0.0021
AAEL002686		testisin precursor	9.04	3.57	-2.35	0.0473
AAEL002799		hypothetical protein	14.25	5.73	-2.35	0.0109
AAEL003017		hypothetical protein	11.12	4.36	-2.35	0.0032
AAEL010757		hypothetical protein	2.03	0.81	-2.35	0.0098
AAEL003609		neurobeachin	4.45	1.74	-2.35	0.0154
AAEL008928	Kir2A	inwardly rectifying k+ channel	150.17	62.34	-2.35	0.0000
AAEL004591		hypothetical protein	1.66	0.64	-2.34	0.0412
AAEL000309		hypothetical protein	3.90	1.56	-2.34	0.0077
AAEL002824		hypothetical protein	2.00	0.84	-2.34	0.0001
AAEL004363		hypothetical protein	13.12	5.25	-2.33	0.0205
AAEL017445			11.90	5.02	-2.33	0.0009
AAEL005200		juvenile hormone esterase	210.06	86.83	-2.33	0.0020
AAEL009684		hypothetical protein	16.97	6.95	-2.32	0.0002
AAEL014224	GPROAR1		1.64	0.65	-2.32	0.0428
AAEL018159		mannose-binding protein-assoc. serine protease	702.25	294.70	-2.32	0.0000
AAEL003581		amidophosphoribosyltransferase	7.80	3.37	-2.31	0.0000
AAEL012513		calcium-binding protein E63-1	10.57	4.51	-2.31	0.0022
AAEL004146	CRY1	DNA photolyase	42.58	17.97	-2.31	0.0000
AAEL008190		bhlh transcription factor	16.45	6.93	-2.30	0.0000
AAEL005319			51.17	21.50	-2.30	0.0009
AAEL012856		hypothetical protein	13.89	5.79	-2.30	0.0033
AAEL010111		leucine-rich transmembrane protein	23.09	9.83	-2.30	0.0000
AAEL007268			1.65	0.66	-2.30	0.0402
AAEL000101		AMP dependent coa ligase	2.64	1.09	-2.29	0.0025
AAEL003155		dynein heavy chain	1.28	0.53	-2.28	0.0031
AAEL005439		mical	1.66	0.67	-2.28	0.0235
AAEL009775			1.80	0.72	-2.28	0.0127
AAEL010147		hypothetical protein	5.93	2.51	-2.28	0.0035
AAEL004581		hypothetical protein	83.54	35.54	-2.27	0.0001
AAEL009185		arginine or creatine kinase	1,549.26	664.65	-2.27	0.0000
AAEL004741		aquaporin transporter	1.64	0.71	-2.26	0.0089
AAEL018021			91.20	38.53	-2.26	0.0135
AAEL005781		hypothetical protein	36.00	15.46	-2.26	0.0001
AAEL011154		hypothetical protein	24.58	10.64	-2.25	0.0004
AAEL007563	DUOX	dual oxidase 1	26.04	11.30	-2.25	0.0000
AAEL005951		lipid storage droplets surface binding protein	10.69	4.62	-2.25	0.0113

Table A11 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL010866		serine protease	50.41	21.78	-2.25	0.0000
AAEL014261		zinc finger protein	13.02	5.59	-2.24	0.0111
AAEL001294		hypothetical protein	1,431.77	623.92	-2.24	0.0000
AAEL014330		hypothetical protein	8.15	3.53	-2.24	0.0025
AAEL009948		aldehyde dehydrogenase	2.13	0.90	-2.24	0.0447
AAEL005640		hypothetical protein	6.49	2.75	-2.24	0.0179
AAEL001289		permease	3.17	1.40	-2.23	0.0388
AAEL000251		hypothetical protein	18.45	7.76	-2.23	0.0381
AAEL013319		hypothetical protein	3.86	1.69	-2.23	0.0029
AAEL015034		alcohol dehydrogenase	15.22	6.46	-2.23	0.0115
AAEL006012		factor for adipocyte differentiation	1.55	0.63	-2.23	0.0322
AAEL008620		D7 protein	3.72	1.62	-2.23	0.0076
AAEL011193		steroid dehydrogenase	99.96	43.81	-2.22	0.0000
AAEL004631		actin	312.96	133.01	-2.22	0.0402
AAEL002565		titin	25.12	10.80	-2.22	0.0133
AAEL012337			4.77	2.00	-2.22	0.0367
AAEL014413	CYP304C1	cytochrome P450	26.27	11.51	-2.22	0.0004
AAEL012168		zinc finger protein	1.14	0.47	-2.22	0.0180
AAEL002861		hypothetical protein	85.08	37.41	-2.22	0.0000
AAEL010694		5-formyltetrahydrofolate cyclo-ligase	2.98	1.24	-2.21	0.0229
AAEL009467		hypothetical protein	4.47	1.97	-2.21	0.0474
AAEL017575			1.62	0.68	-2.21	0.0305
AAEL007778		leucine-rich transmembrane protein	16.41	7.08	-2.21	0.0363
AAEL004114		UNC93A protein	28.75	12.38	-2.21	0.0238
AAEL018343		myosin light chain kinase	7.32	3.22	-2.20	0.0041
AAEL018236		crossveinless	3.12	1.34	-2.20	0.0003
AAEL001539		hypothetical protein	12.80	5.66	-2.20	0.0003
AAEL003642		serine protease	83.18	36.89	-2.20	0.0000
AAEL008046		rh antigen	34.03	14.94	-2.20	0.0013
AAEL011475	GPRGNR2	corazonin receptor	30.08	13.09	-2.20	0.0000
AAEL009895		neprilysin	261.04	115.90	-2.20	0.0000
AAEL004496		glutamate transporter	74.41	33.06	-2.19	0.0000
AAEL009560		apolipoprotein D	30.83	13.52	-2.19	0.0006
AAEL003933	DBLOX	oxidase/peroxidase	29.69	13.04	-2.19	0.0064
AAEL017293			98.97	43.05	-2.19	0.0264
AAEL012613		hypothetical protein	9.53	4.19	-2.19	0.0009
AAEL010793		f-box/leucine rich repeat protein	4.47	2.01	-2.19	0.0045
AAEL008876		deoxyribonuclease I	5.46	2.41	-2.18	0.0265
AAEL002946		hypothetical protein	17.99	8.02	-2.18	0.0009
AAEL000874	ARK	hypothetical protein	9.82	4.35	-2.18	0.0000
AAEL010269		venom allergen	834.63	366.46	-2.18	0.0166
AAEL002294			1.06	0.45	-2.18	0.0393
AAEL002244		hypothetical protein	11.20	4.99	-2.18	0.0047
AAEL018311		trichohyalin	15.52	6.88	-2.17	0.0077
AAEL012576		pyruvate kinase	154.95	69.68	-2.17	0.0000
AAEL008710		hypothetical protein	167.34	74.20	-2.17	0.0032
AAEL005983		hypothetical protein	3.54	1.56	-2.17	0.0425
AAEL007909		branched-chain amino acid aminotransferase	7.35	3.38	-2.17	0.0107
AAEL006447		GATA transcription factor (GATAb)	2.30	1.00	-2.16	0.0008
AAEL012273		hypothetical protein	17.34	7.75	-2.16	0.0006
AAEL004862		hypothetical protein	29.36	13.18	-2.16	0.0001
AAEL014736		hypothetical protein	3.98	1.76	-2.16	0.0166
AAEL003697	SRPN17	serine protease inhibitor, serpin	321.85	145.68	-2.15	0.0001

Table A11 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL011324		hypothetical protein	35.82	16.20	-2.15	0.0007
AAEL017229			2.78	1.24	-2.15	0.0003
AAEL004667		hypothetical protein	12.39	5.52	-2.15	0.0048
AAEL003419		hypothetical protein	31.17	14.01	-2.15	0.0048
AAEL014455		hypothetical protein	3.76	1.74	-2.15	0.0133
AAEL000644		hypothetical protein	31.53	14.21	-2.14	0.0009
AAEL002381		hypothetical protein	40.79	18.32	-2.14	0.0079
AAEL001582		kinesin	2.94	1.27	-2.14	0.0310
AAEL014950	SPZ3B	hypothetical protein	20.49	9.40	-2.14	0.0002
AAEL000320	CYP325T1		3.31	1.55	-2.14	0.0194
AAEL011821		adenylyl cyclase-associated protein	5.95	2.65	-2.14	0.0302
AAEL011347		hypothetical protein	23.79	10.87	-2.13	0.0000
AAEL017376			122.20	55.77	-2.13	0.0004
AAEL014079		serine protease inhibitor, serpin	9.30	4.32	-2.13	0.0095
AAEL012665		glucose-6-phosphate isomerase	4.88	2.13	-2.13	0.0039
AAEL007114		hypothetical protein	48.28	21.65	-2.13	0.0300
AAEL002663		kuzbanian	22.43	10.34	-2.13	0.0000
AAEL012612		serine/threonine protein kinase	11.44	5.19	-2.13	0.0002
AAEL001876		decapentaplegic, deca	15.63	7.10	-2.12	0.0035
AAEL005687		protein serine/threonine kinase	3,367.04	1,549.73	-2.12	0.0000
AAEL006768		hypothetical protein	69.04	31.38	-2.12	0.0077
AAEL016967			83.36	37.88	-2.12	0.0082
AAEL004244		hypothetical protein	8.45	3.78	-2.11	0.0226
AAEL018154		hypothetical protein	5.57	2.54	-2.11	0.0041
AAEL000652	GNBPA2		33.46	15.58	-2.11	0.0000
AAEL013318		hypothetical protein	3.89	1.79	-2.11	0.0102
AAEL017280			12.38	5.64	-2.11	0.0071
AAEL005369		zinc finger protein	19.21	8.66	-2.10	0.0390
AAEL006619		hypothetical protein	58.02	26.96	-2.10	0.0002
AAEL015639		transferrin	20.57	9.50	-2.10	0.0033
AAEL013343		lethal(2)essential for life protein, l2efl	45.85	21.38	-2.10	0.0001
AAEL007597	CLIPC3	serine protease	78.45	35.86	-2.10	0.0215
AAEL013395		hypothetical protein	74.03	34.11	-2.09	0.0013
AAEL001760		hypothetical protein	7.77	3.61	-2.09	0.0031
AAEL015022		glycoside hydrolases	39.38	18.14	-2.09	0.0150
AAEL004803		hypothetical protein	6.72	3.21	-2.09	0.0048
AAEL001946		four and a half lim domains	130.95	60.71	-2.09	0.0048
AAEL001959		hypothetical protein	21.54	10.01	-2.08	0.0000
AAEL011310		axonemal dynein intermediate chain polypeptide	7.28	3.37	-2.08	0.0061
AAEL000509		rho gtpase activating protein	4.82	2.28	-2.08	0.0006
AAEL006876		igf2 mRNA binding protein	2.25	1.04	-2.08	0.0028
AAEL003919		cationic amino acid transporter	61.09	28.76	-2.08	0.0000
AAEL000371		hypothetical protein	3.43	1.58	-2.08	0.0453
AAEL008484			10.16	4.74	-2.07	0.0020
AAEL004133		echinoid	8.47	4.04	-2.07	0.0000
AAEL004897		brain chitinase and chia	3.51	1.59	-2.07	0.0273
AAEL017401			19.96	8.85	-2.07	0.0326
AAEL003041		hypothetical protein	11.51	5.35	-2.07	0.0141
AAEL017012			99.94	46.98	-2.06	0.0028
AAEL017528			6.18	2.78	-2.06	0.0318
AAEL000074	CLIPB1	serine protease	38.81	18.42	-2.06	0.0002
AAEL012958		hypothetical protein	9.01	4.17	-2.06	0.0165
AAEL010488		ets	14.18	6.73	-2.06	0.0000

Table A11 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL004116		hypothetical protein	207.20	98.56	-2.06	0.0000
AAEL008684		serrano protein	9.17	4.38	-2.06	0.0006
AAEL013849		diacylglycerol kinase, zeta, iota	8.27	3.78	-2.06	0.0016
AAEL010933		hypothetical protein	11.62	5.40	-2.05	0.0102
AAEL000973		hypothetical protein	80.92	38.32	-2.05	0.0003
AAEL017078			51.75	24.32	-2.05	0.0049
AAEL003391		tankyrase	3.28	1.49	-2.05	0.0284
AAEL000729		hypothetical protein	55.63	26.06	-2.05	0.0090
AAEL003965		calpain	9.72	4.64	-2.05	0.0000
AAEL018059		RHO kinase	1.75	0.81	-2.05	0.0019
AAEL013956		ganglioside induced differentiation associated protein	9.95	4.50	-2.05	0.0241
AAEL009570		hypothetical protein	88.13	42.31	-2.05	0.0027
AAEL008413		serine/threonine protein kinase	9.90	4.62	-2.05	0.0087
AAEL017029			24.17	11.36	-2.04	0.0162
AAEL017472			16.28	7.85	-2.04	0.0357
AAEL007250		hypothetical protein	7.93	3.66	-2.04	0.0327
AAEL004479		organic cation transporter	19.65	9.42	-2.04	0.0000
AAEL002376		carboxylesterase	177.68	85.29	-2.04	0.0000
AAEL000695		hypothetical protein	4.50	2.02	-2.04	0.0400
AAEL000419		hypothetical protein	53.33	25.75	-2.03	0.0001
AAEL004569		hypothetical protein	16.99	8.21	-2.03	0.0000
AAEL011525		hypothetical protein	47.11	21.97	-2.03	0.0080
AAEL005670	SRPN1	serine protease inhibitor, serpin	12.74	6.08	-2.03	0.0001
AAEL015487		zinc finger protein	6.05	2.83	-2.03	0.0368
AAEL010000		ganglioside induced diff. associated protein	177.49	84.17	-2.02	0.0310
AAEL002879		heterogeneous nuclear ribonucleoprotein r	107.70	51.43	-2.02	0.0091
AAEL004871		hypothetical protein	21.64	10.50	-2.01	0.0020
AAEL010326		hypothetical protein	4.18	1.98	-2.01	0.0069
AAEL010783		sodium/potassium-dependent atpase	432.25	208.91	-2.01	0.0009
AAEL016962			32.33	15.63	-2.01	0.0000
AAEL015058		hypothetical protein	7.96	3.70	-2.01	0.0156
AAEL018215		dedicator of cytokinesis (dock)	5.23	2.53	-2.00	0.0014
AAEL006680		hypothetical protein	2.06	0.97	-2.00	0.0016

Table A12 Genes displaying dimorphic expression patterns in *A. aegypti*. Genes expressed almost exclusively in the antenna of males.

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL014520	GPROP9	ultraviolet-sensitive opsin	248.96	0.29	-14.90	0.0007
AAEL014765		hypothetical protein	68.62	0.53	-32.59	0.0000
AAEL015306		hypothetical protein	58.56	0.38	-90.64	0.0000
AAEL018008	HPX1	oxidase/peroxidase	58.15	0.54	-82.44	0.0000
AAEL008750		hypothetical protein	39.25	0.49	-54.52	0.0000
AAEL007814		hypothetical protein	39.11	0.06	-42.35	0.0000
AAEL008082		myosin	35.53	0.30	-74.66	0.0000
AAEL000551		allatostatin, B-type	34.43	0.58	-45.04	0.0000
AAEL017402		hypothetical protein	32.01	0.50	-48.07	0.0000
AAEL005770		hypothetical protein	31.93	0.08	-97.74	0.0000
AAEL004810		oxidase/peroxidase	25.46	0.21	-110.64	0.0000
AAEL015520		hypothetical protein	25.40	0.85	-23.39	0.0000
AAEL000242		hypothetical protein	24.69	0.56	-35.93	0.0000
AAEL008847	CYP9J6	cytochrome P450	24.37	0.78	-24.25	0.0000
AAEL014125		short neuropeptide F precursor	23.24	0.70	-19.98	0.0000
AAEL000021		hypothetical protein	19.66	0.11	-81.38	0.0000
AAEL013259		hypothetical protein	19.21	0.44	-29.14	0.0000
AAEL000398		low-density lipoprotein receptor (ldl)	19.15	0.21	-61.64	0.0000
AAEL005437		hypothetical protein	18.01	0.02	-104.36	0.0000
AAEL006975		hypothetical protein	18.01	0.25	-46.24	0.0000
AAEL001517		hypothetical protein	17.82	0.29	-32.39	0.0000
AAEL006602		hypothetical protein	17.52	0.13	-66.02	0.0000
AAEL000538		hypothetical protein	16.12	0.18	-62.33	0.0000
AAEL011574		hypothetical protein	15.24	0.29	-18.32	0.0000
AAEL018199	OBP21	Odorant-binding protein 99c	14.84	0.50	-22.50	0.0000
AAEL000926	CRZ	hypothetical protein	14.41	0.14	-52.75	0.0000
AAEL000612			14.37	0.89	-13.09	0.0000
AAEL015305		hypothetical protein	14.05	0.25	-32.14	0.0000
AAEL004883		transient receptor potential channel	13.94	0.07	-43.44	0.0000
AAEL005138		hypothetical protein	13.59	0.03	-110.65	0.0000
AAEL003291		ferritin subunit	13.55	0.16	-41.21	0.0000
AAEL010924	LRIM22	hypothetical protein	13.22	0.42	-20.52	0.0000
AAEL005442		hypothetical protein	12.68	0.96	-12.27	0.0000
AAEL012109			11.92	0.08	-80.99	0.0000
AAEL008843		nuclear factor i	11.82	0.85	-9.31	0.0000
AAEL006736			11.28	0.21	-28.38	0.0000
AAEL005378	CYP6AG3	cytochrome P450	11.26	0.86	-10.14	0.0000
AAEL003183		(s)-2-hydroxy-acid oxidase	11.06	0.49	-15.46	0.0000
AAEL006749		hypothetical protein	10.53	0.93	-9.99	0.0000
AAEL003560	CYP6AG4	cytochrome P450	10.00	0.67	-13.30	0.0000
AAEL002228		hypothetical protein	9.98	0.56	-8.27	0.0008
AAEL006167		Osiris	9.87	0.07	-48.16	0.0000
AAEL011474		hypothetical protein	9.86	0.40	-21.35	0.0000
AAEL009024		carboxylesterase	9.65	0.91	-8.33	0.0000
AAEL004572		sucrose transport protein	9.28	0.27	-22.58	0.0000
AAEL008111		iroquois-class homeodomain protein irx	8.27	0.09	-47.87	0.0000
AAEL004898		cuticle protein	8.02	0.32	-10.99	0.0002
AAEL014551		hypothetical protein	7.97	0.75	-8.95	0.0000
AAEL012399		hypothetical protein	7.77	0.20	-21.13	0.0000
AAEL002023	CYP9J31	cytochrome P450	7.73	0.18	-24.68	0.0000
AAEL001696		hypothetical protein	7.70	0.13	-23.75	0.0000
AAEL006106		hypothetical protein	7.63	0.40	-14.73	0.0000

Table A12 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL012186		amino acid transporter	7.33	0.33	-14.08	0.0000
AAEL011125	OBP23	hypothetical protein	7.27	0.67	-9.20	0.0000
AAEL009478		hypothetical protein	7.15	0.31	-15.75	0.0000
AAEL005444		hypothetical protein	7.10	0.17	-12.72	0.0000
AAEL005772		oxidoreductase	7.03	0.76	-6.20	0.0020
AAEL015316		defective proboscis extension response	6.80	0.75	-6.78	0.0000
AAEL000250		hypothetical protein	6.73	0.16	-9.20	0.0057
AAEL004359		acetylcholine receptor protein alpha	6.71	0.29	-14.21	0.0000
AAEL012441		dopamine beta hydroxylase	6.70	0.28	-13.53	0.0000
AAEL011787	CYP6BB2	cytochrome P450	6.68	0.97	-5.55	0.0015
AAEL008070		hypothetical protein	6.61	0.52	-7.86	0.0006
AAEL012555		carbonic anhydrase II	6.52	0.21	-6.43	0.0297
AAEL008855		hypothetical protein	6.45	0.65	-6.83	0.0003
AAEL002665		sugar transporter	6.24	0.57	-8.99	0.0000
AAEL003093		hypothetical protein	6.04	0.32	-13.13	0.0000
AAEL012873		hypothetical protein	5.99	0.51	-8.23	0.0000
AAEL000780		hypothetical protein	5.94	0.15	-23.05	0.0000
AAEL005432		hypothetical protein	5.93	0.56	-10.03	0.0000
AAEL003035		basic helix-loop-helix protein	5.88	0.14	-7.96	0.0121
AAEL003551		hypothetical protein	5.80	0.07	-26.42	0.0000
AAEL011426		hypothetical protein	5.77	0.47	-8.86	0.0000
AAEL000428		fatty acid synthase	5.76	0.40	-5.75	0.0331
AAEL010397		hypothetical protein	5.72	0.85	-5.40	0.0015
AAEL000086		myomesin	5.70	0.47	-11.56	0.0000
AAEL003047			5.59	0.95	-4.12	0.0076
AAEL000937		homeobox protein nk-2	5.41	0.09	-18.00	0.0000
AAEL014231			5.34	0.67	-5.80	0.0038
AAEL017120		molybdopterin synthase small subunit	5.33	0.11	-15.23	0.0000
AAEL001075	IRg	glutamate receptor	5.31	0.64	-7.02	0.0000
AAEL003970		hypothetical protein	5.27	0.73	-5.27	0.0008
AAEL011139		hypothetical protein	5.26	0.58	-8.16	0.0000
AAEL018262		hypothetical protein	5.17	0.85	-4.48	0.0010
AAEL000457		hypothetical protein	5.16	0.07	-29.46	0.0000
AAEL015148		hypothetical protein	5.06	0.14	-18.71	0.0000
AAEL011671		netrin	4.98	0.94	-4.51	0.0006
AAEL011364		hypothetical protein	4.76	0.82	-4.67	0.0405
AAEL008108		n-twist	4.75	0.07	-28.15	0.0000
AAEL000288		hypothetical protein	4.70	0.90	-4.52	0.0002
AAEL010856	GPROP3	rhodopsin	4.69	0.16	-12.70	0.0001
AAEL014541	HPX6	oxidase/peroxidase	4.67	0.62	-6.80	0.0000
AAEL012850			4.67	0.06	-28.56	0.0000
AAEL002638	CYP325U1		4.60	0.07	-36.16	0.0000
AAEL005822		hypothetical protein	4.60	0.63	-5.58	0.0074
AAEL004246		pur-alpha	4.52	0.84	-4.39	0.0007
AAEL012952		hypothetical protein	4.52	0.39	-8.41	0.0000
AAEL005447		hypothetical protein	4.37	0.60	-5.46	0.0029
AAEL009909		hypothetical protein	4.31	0.56	-6.62	0.0000
AAEL004077		maltose phosphorylase	4.30	0.28	-11.45	0.0000
AAEL008527	GNBPB5	gram-negative bacteria binding protein	4.29	0.24	-12.69	0.0000
AAEL011941		chaoptin	4.26	0.59	-5.74	0.0003
AAEL006259		hypothetical protein	4.22	0.00	-44.18	0.0000
AAEL005282			4.19	0.60	-6.45	0.0000
AAEL002254			4.19	0.42	-7.71	0.0000
AAEL014553		triacylglycerol lipase, pancreatic	4.10	0.34	-7.68	0.0012

Table A12 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL017329		serine protease	4.06	0.96	-3.56	0.0163
AAEL006102		trypsin-eta	4.04	0.75	-4.39	0.0036
AAEL002509		acetylcholine receptor protein alpha	4.01	0.21	-12.01	0.0000
AAEL011702		heterogeneous nuclear ribonucleoprotein	4.01	0.80	-3.73	0.0064
AAEL005753		hypothetical protein	4.01	0.54	-6.73	0.0000
AAEL009252		tryptophan 2,3-dioxygenase	3.93	0.50	-6.72	0.0000
AAEL010950		NADH dehydrogenase	3.93	0.00	-13.26	0.0006
AAEL005440		structural maintenance of chromosomes smc1	3.92	0.69	-5.17	0.0000
AAEL007968		lipase	3.90	0.51	-4.82	0.0253
AAEL010094		set domain protein	3.89	0.73	-4.69	0.0000
AAEL007034		protein phosphatase 2a, regulatory subunit	3.89	0.98	-3.13	0.0323
AAEL006556		hypothetical protein	3.89	0.52	-4.58	0.0114
AAEL013424		hypothetical protein	3.88	0.47	-5.66	0.0012
AAEL010894	GPRCAL3		3.88	0.72	-4.57	0.0015
AAEL009991		hypothetical protein	3.83	0.35	-6.17	0.0073
AAEL000200		hypothetical protein	3.81	0.97	-3.74	0.0001
AAEL000873		hypothetical protein	3.79	0.00	-60.88	0.0000
AAEL015563		wingless	3.78	0.68	-4.91	0.0000
AAEL006127		sex-determining region y protein, sry	3.74	0.90	-4.04	0.0000
AAEL013807		hypothetical protein	3.74	0.79	-4.08	0.0210
AAEL007826		hypothetical protein	3.73	0.44	-5.69	0.0087
AAEL010934		hypothetical protein	3.71	0.29	-8.36	0.0001
AAEL004360		serine carboxypeptidase	3.70	0.66	-5.15	0.0000
AAEL011760		hypothetical protein	3.70	0.96	-3.15	0.0469
AAEL012609		hypothetical protein	3.68	0.53	-4.41	0.0158
AAEL001148		glutamate receptor	3.67	0.12	-11.67	0.0001
AAEL002518		hypothetical protein	3.65	0.38	-7.51	0.0002
AAEL001319		er lumen protein retaining receptor	3.65	0.80	-3.51	0.0067
AAEL003508	CYP325Q2	cytochrome P450	3.59	0.61	-5.28	0.0000
AAEL008617		hypothetical protein	3.58	0.81	-3.58	0.0232
AAEL003934		maltose phosphorylase	3.57	0.60	-5.54	0.0000
AAEL018521		vitamin k-dependent gamma-carboxylase	3.56	0.35	-8.41	0.0000
AAEL008940		hypothetical protein	3.55	0.56	-4.86	0.0042
AAEL018357		guanylate cyclase	3.53	0.37	-7.23	0.0000
AAEL008501		hypothetical protein	3.46	0.77	-3.65	0.0119
AAEL015592		hypothetical protein	3.46	0.68	-4.35	0.0000
AAEL000351		transient receptor potential channel	3.41	0.83	-3.54	0.0047
AAEL008294		protein-l-isoaspartate o-methyltransferase	3.39	0.64	-4.73	0.0001
AAEL016972	CYP12F8	cytochrome P450	3.35	0.76	-3.51	0.0168
AAEL003772		hypothetical protein	3.30	0.71	-4.24	0.0006
AAEL001628		hypothetical protein	3.28	0.59	-4.85	0.0001
AAEL011366		leucine aminopeptidase	3.27	0.14	-9.41	0.0016
AAEL010646		hypothetical protein	3.23	0.38	-5.97	0.0000
AAEL009881		AMP dependent coa ligase	3.23	0.76	-3.47	0.0033
AAEL004814		cardioacceleratory peptide 2a	3.23	0.00	-35.89	0.0000
AAEL012998	CYP4J14	cytochrome P450	3.22	0.13	-13.58	0.0000
AAEL010039		hypothetical protein	3.21	0.36	-6.02	0.0001
AAEL014315		hypothetical protein	3.20	0.02	-55.17	0.0000
AAEL004418		sidestep protein	3.19	0.19	-11.46	0.0000
AAEL007584		sodium/shloride dependent amino acid transporter	3.17	0.35	-5.66	0.0078
AAEL000669		glucosyl/glucuronosyl transferases	3.14	0.03	-38.71	0.0000
AAEL006336		fatty acid synthase	3.13	0.69	-3.70	0.0239

Table A12 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL003082		hypothetical protein	3.11	0.86	-3.35	0.0201
AAEL011716			3.07	0.13	-15.01	0.0000
AAEL008222		hypothetical protein	3.07	0.83	-3.36	0.0037
AAEL012949		hypothetical protein	3.06	0.30	-5.48	0.0215
AAEL010657		hypothetical protein	3.05	0.19	-6.28	0.0145
AAEL009858			3.04	0.90	-3.01	0.0101
AAEL003894		hypothetical protein	3.03	0.19	-8.52	0.0011
AAEL002633			3.01	0.07	-18.59	0.0000
AAEL002740	CYP6P12	cytochrome P450	2.99	0.06	-20.79	0.0000
AAEL013535	Sphinx_2		2.97	0.00	-7.43	0.0163
AAEL005853		hypothetical protein	2.95	0.84	-3.12	0.0041
AAEL000576		AMP dependent coa ligase	2.94	0.64	-3.89	0.0005
AAEL012203		excision repair cross-complementing 1 ercc1	2.93	0.95	-2.81	0.0128
AAEL000298		hypothetical protein	2.93	0.59	-4.10	0.0002
AAEL012542		nitric oxide synthase	2.91	0.11	-15.48	0.0000
AAEL010041		amalgam protein	2.90	0.67	-3.62	0.0013
AAEL005749			2.88	0.79	-3.24	0.0075
AAEL008129		voltage-gated potassium channel	2.86	0.72	-3.44	0.0035
AAEL000615		hypothetical protein	2.86	0.89	-3.05	0.0040
AAEL001969		hypothetical protein	2.84	0.34	-4.42	0.0344
AAEL006484		hypothetical protein	2.83	0.18	-9.01	0.0001
AAEL007010		netrin	2.82	0.16	-12.35	0.0000
AAEL001754		hypothetical protein	2.81	0.00	-12.10	0.0011
AAEL009939		aromatic amino acid decarboxylase	2.75	0.06	-22.34	0.0000
AAEL002042		guanylate cyclase beta 1 subunit	2.69	0.75	-3.03	0.0232
AAEL012596		hypothetical protein	2.69	0.21	-7.95	0.0000
AAEL009835		hypothetical protein	2.68	0.05	-14.17	0.0000
AAEL006537		hypothetical protein	2.67	0.13	-10.64	0.0000
AAEL007493		hypothetical protein	2.66	0.00	-12.91	0.0010
AAEL008241		hypothetical protein	2.65	0.27	-8.71	0.0000
AAEL006014		hypothetical protein	2.64	0.00	-12.55	0.0009
AAEL004513		sodium/shloride dependent amino acid transporter	2.61	0.47	-4.30	0.0063
AAEL000310		cytochrome P450	2.60	0.41	-5.21	0.0005
AAEL018308		hypothetical protein	2.59	0.20	-8.44	0.0001
AAEL003260		hypothetical protein	2.59	0.06	-20.11	0.0000
AAEL006161		hypothetical protein	2.54	0.68	-3.33	0.0002
AAEL010681		hypothetical protein	2.53	0.56	-3.29	0.0268
AAEL008722		hypothetical protein	2.49	0.03	-16.95	0.0000
AAEL006019		hypothetical protein	2.49	0.40	-4.84	0.0008
AAEL005899		hypothetical protein	2.47	0.07	-11.37	0.0002
AAEL010292		phosphoenolpyruvate carboxykinase	2.47	0.96	-2.43	0.0227
AAEL007831			2.46	0.10	-13.36	0.0000
AAEL006535		ca-activated cl channel protein	2.45	0.31	-6.55	0.0000
AAEL006615		carbonic anhydrase II	2.44	0.06	-16.59	0.0000
AAEL010634		hypothetical protein	2.43	0.79	-2.87	0.0106
AAEL002622		hypothetical protein	2.39	0.29	-5.38	0.0030
AAEL000341		hypothetical protein	2.39	0.31	-4.83	0.0274
AAEL017262		zinc finger protein	2.36	0.50	-4.00	0.0002
AAEL013303		hypothetical protein	2.36	0.62	-3.72	0.0001
AAEL002676		hypothetical protein	2.36	0.23	-6.87	0.0026
AAEL002738		hypothetical protein	2.32	0.56	-3.26	0.0197
AAEL004725		hypothetical protein	2.31	0.70	-2.93	0.0091

Table A12 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL008031		chromaffin granule amine transporter	2.31	0.71	-3.17	0.0042
AAEL012975		retinal homeobox protein	2.30	0.54	-3.81	0.0001
AAEL002733		monocarboxylate transporter	2.29	0.12	-12.33	0.0000
AAEL013043		hypothetical protein	2.27	0.17	-9.51	0.0000
AAEL010712		hypothetical protein	2.24	0.00	-6.14	0.0380
AAEL007989		homeobox protein	2.24	0.02	-18.37	0.0000
AAEL013645		secreted ferritin G subunit precursor	2.22	0.04	-34.56	0.0000
AAEL006109		voltage-gated potassium channel	2.22	0.27	-5.71	0.0003
AAEL004428	GPRCAL2		2.21	0.48	-4.07	0.0027
AAEL009792		hypothetical protein	2.20	0.37	-4.22	0.0036
AAEL009421	CLIPB32	clip-domain serine protease	2.16	0.22	-6.34	0.0002
AAEL001181			2.16	0.24	-7.26	0.0000
AAEL010886		hypothetical protein	2.16	0.12	-10.43	0.0000
AAEL014893		hypothetical protein	2.16	0.62	-3.02	0.0050
AAEL007224		tartan	2.13	0.09	-12.11	0.0000
AAEL006096		aldehyde dehydrogenase	2.13	0.90	-2.24	0.0447
AAEL013776		hypothetical protein	2.10	0.15	-7.73	0.0001
AAEL012481		alcohol dehydrogenase	2.10	0.39	-4.21	0.0238
AAEL012437	GPRNNA11		2.07	0.50	-3.39	0.0066
AAEL017500		hypothetical protein	2.06	0.52	-3.51	0.0038
AAEL003318		cystinosin	2.06	0.02	-21.43	0.0000
AAEL015145		hypothetical protein	2.06	0.97	-2.00	0.0016
AAEL018302		orthopedia homeobox protein	2.06	0.08	-9.37	0.0007
AAEL015583		salivary gland-expressed bHLH	2.05	0.14	-6.31	0.0109
AAEL006498		homeobox protein otx	2.04	0.00	-27.82	0.0000
AAEL001486	CLIPC12	trypsin	2.03	0.49	-3.36	0.0308
AAEL006542		insulin receptor	2.03	0.69	-2.69	0.0038
AAEL002500		heat shock factor binding protein	2.03	0.49	-3.08	0.0299
AAEL003270		hypothetical protein	2.03	0.81	-2.35	0.0098
AAEL003319		hypothetical protein	2.02	0.30	-4.02	0.0438
AAEL017422		hypothetical protein	2.01	0.30	-5.27	0.0005
AAEL004446		hypothetical protein	2.01	0.32	-4.82	0.0044
AAEL005443			2.00	0.18	-6.39	0.0032
AAEL010263		hypothetical protein	2.00	0.84	-2.34	0.0001
AAEL004876		hypothetical protein	2.00	0.37	-5.35	0.0006
AAEL007709		hypothetical protein	1.99	0.38	-4.45	0.0003
AAEL002541		zinc finger protein	1.98	0.08	-10.64	0.0002
AAEL009693			1.95	0.35	-4.50	0.0013
AAEL009266		cyclin b	1.92	0.27	-5.08	0.0031
AAEL010648	GPRMGL1		1.92	0.30	-3.94	0.0422
AAEL009593			1.92	0.08	-8.06	0.0025
AAEL006092		hypothetical protein	1.91	0.20	-5.59	0.0049
AAEL011740		glucose dehydrogenase	1.89	0.30	-5.20	0.0002
AAEL006526		sterol o-acyltransferase	1.89	0.34	-4.18	0.0137
AAEL005318		angiotensin-converting enzyme	1.88	0.26	-6.03	0.0014
AAEL000645			1.86	0.34	-4.38	0.0063
AAEL004724		insulinprotein enhancer protein isl	1.85	0.39	-3.54	0.0163
AAEL001676		guanylate cyclase beta 1 subunit	1.84	0.34	-4.49	0.0006
AAEL008331		nucleolysin tia-1	1.82	0.55	-2.81	0.0474
AAEL012554		ORF-A short	1.81	0.34	-4.71	0.0000
AAEL000863		hypothetical protein	1.81	0.21	-6.13	0.0003
AAEL003003		hypothetical protein	1.80	0.23	-4.72	0.0315
AAEL004466		hypothetical protein	1.80	0.67	-2.51	0.0015
AAEL001390			1.80	0.72	-2.28	0.0127

Table A12 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL015657		hypothetical protein	1.79	0.12	-6.18	0.0187
AAEL012492		defective proboscis extension response	1.79	0.14	-7.61	0.0001
AAEL012110		alkyldihydroxyacetonephosphate synthase	1.78	0.24	-6.78	0.0000
AAEL005575		hypothetical protein	1.78	0.02	-20.44	0.0000
AAEL007129		hypothetical protein	1.78	0.39	-3.77	0.0025
AAEL010506			1.77	0.52	-3.06	0.0052
AAEL015611		AMP dependent coa ligase	1.77	0.63	-2.58	0.0017
AAEL009630		serine-pyruvate aminotransferase	1.76	0.48	-3.11	0.0213
AAEL007789		peroxidasin	1.76	0.39	-3.44	0.0381
AAEL002513		hypothetical protein	1.76	0.62	-2.56	0.0186
AAEL014610		oxidase/peroxidase	1.75	0.18	-5.60	0.0122
AAEL010097		RHO kinase	1.75	0.81	-2.05	0.0019
AAEL013266		guanylate cyclase	1.75	0.02	-24.39	0.0000
AAEL007233		cgmp-specific 3,5-cyclic phosphodiesterase	1.73	0.22	-6.28	0.0000
AAEL009745		pupal cuticle protein 78E	1.72	0.13	-5.45	0.0255
AAEL005296		5'-3' exoribonuclease	1.71	0.19	-5.04	0.0142
AAEL003050		hypothetical protein	1.70	0.57	-3.06	0.0072
AAEL000236		hypothetical protein	1.69	0.24	-5.16	0.0001
AAEL009323		hypothetical protein	1.68	0.54	-2.82	0.0011
AAEL001747		cytochrome P450	1.67	0.49	-3.26	0.0411
AAEL001293		hypothetical protein	1.66	0.64	-2.34	0.0412
AAEL015251	CYP9J29	cytochrome P450	1.66	0.04	-12.72	0.0001
AAEL006058		mical	1.66	0.67	-2.28	0.0235
AAEL003024		hypothetical protein	1.65	0.19	-5.73	0.0087
AAEL003491			1.65	0.66	-2.30	0.0402
AAEL006630		hypothetical protein	1.64	0.26	-5.15	0.0011
AAEL007770		aquaporin transporter	1.64	0.71	-2.26	0.0089
AAEL012494		nicotinic acetylcholine receptor subunit	1.64	0.45	-3.07	0.0434
AAEL004805	GPROAR1		1.64	0.65	-2.32	0.0428
AAEL011809			1.62	0.68	-2.21	0.0305
AAEL003114		Psq-DNA binding domain protein	1.62	0.64	-2.40	0.0228
AAEL004032		carbonic anhydrase II	1.61	0.15	-5.09	0.0424
AAEL013215		forkhead box protein (AaegFOXD)	1.60	0.03	-16.93	0.0000
AAEL013218		hypothetical protein	1.59	0.48	-2.90	0.0027
AAEL007502		hypothetical protein	1.59	0.02	-35.81	0.0000
AAEL014284		hypothetical protein	1.58	0.12	-9.22	0.0000
AAEL015598		hypothetical protein	1.57	0.33	-3.67	0.0469
AAEL013651		hypothetical protein	1.57	0.52	-2.87	0.0413
AAEL000607		serine-pyruvate aminotransferase	1.57	0.18	-5.56	0.0051
AAEL010631		hypothetical protein	1.56	0.28	-4.11	0.0393
AAEL005252			1.56	0.02	-42.71	0.0000
AAEL014886		factor for adipocyte differentiation	1.55	0.63	-2.23	0.0322
AAEL017529		hypothetical protein	1.54	0.30	-3.80	0.0235
AAEL001031			1.54	0.59	-2.47	0.0035
AAEL012881		matrix metalloproteinase	1.50	0.20	-5.69	0.0002
AAEL015659		hypothetical protein	1.49	0.01	-46.10	0.0000
AAEL009418		alpha-amylase	1.49	0.60	-2.36	0.0021
AAEL005698		transcription factor coe3	1.48	0.38	-3.39	0.0298
AAEL004054		hairy protein	1.46	0.31	-4.10	0.0142
AAEL009615		hypothetical protein	1.45	0.00	-7.44	0.0168
AAEL010557	CCEAE20	alpha-esterase	1.44	0.36	-3.12	0.0421
AAEL012704			1.44	0.33	-3.45	0.0118
AAEL002606		elongase	1.42	0.22	-4.01	0.0470
AAEL002876			1.41	0.29	-3.50	0.0232

Table A12 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL001504		hypothetical protein	1.41	0.35	-3.37	0.0004
AAEL008383		zinc finger protein	1.40	0.01	-26.65	0.0000
AAEL009150		hypothetical protein	1.39	0.42	-2.97	0.0000
AAEL018150		fucosyltransferase 11 (fut11)	1.38	0.28	-3.65	0.0198
AAEL003116		hypothetical protein	1.37	0.00	-29.41	0.0000
AAEL015354		paired box protein	1.37	0.00	-16.18	0.0001
AAEL017220	GPRGBB3		1.36	0.14	-7.12	0.0003
AAEL002961		hypothetical protein	1.36	0.02	-16.70	0.0000
AAEL005966		roundabout 1	1.35	0.25	-4.16	0.0021
AAEL011998		leucine-rich transmembrane protein	1.35	0.21	-4.50	0.0107
AAEL009541		hypothetical protein	1.35	0.00	-6.28	0.0344
AAEL007221		hypothetical protein	1.33	0.06	-8.83	0.0005
AAEL000254		hypothetical protein	1.30	0.26	-3.98	0.0039
AAEL012248		arrowhead	1.30	0.00	-10.65	0.0026
AAEL012060		hypothetical protein	1.29	0.19	-4.84	0.0028
AAEL007079		cadherin	1.29	0.25	-4.28	0.0001
AAEL011768	LRIM23	hypothetical protein	1.29	0.12	-5.33	0.0277
AAEL003794		nk homeobox protein	1.29	0.12	-5.13	0.0217
AAEL017215		hypothetical protein	1.28	0.03	-12.92	0.0001
AAEL013959	SPZ5	hypothetical protein	1.28	0.22	-3.99	0.0113
AAEL006932		dynein heavy chain	1.28	0.53	-2.28	0.0031
AAEL009135		sodium/shloride dependent amino acid transporter	1.28	0.22	-4.43	0.0048
AAEL002456		NFAT	1.27	0.29	-3.99	0.0002
AAEL010396		hypothetical protein	1.27	0.03	-12.06	0.0001
AAEL013763		hypothetical protein	1.27	0.22	-4.22	0.0021
AAEL001257		hypothetical protein	1.27	0.27	-3.40	0.0366
AAEL002558		hypothetical protein	1.26	0.21	-4.52	0.0018
AAEL002218		autoimmune regulator	1.25	0.49	-2.43	0.0277
AAEL000630		tartan	1.25	0.03	-16.19	0.0000
AAEL003441			1.24	0.01	-24.95	0.0000
AAEL011931			1.24	0.29	-3.51	0.0169
AAEL001695	LRIM20	hypothetical protein	1.23	0.26	-4.26	0.0118
AAEL009544		lachesin	1.23	0.11	-5.39	0.0170
AAEL007024		insulin receptor tyrosine kinase substrate	1.22	0.23	-4.24	0.0025
AAEL014370		homeotic antennapedia protein	1.22	0.29	-3.59	0.0284
AAEL000960		hypothetical protein	1.21	0.00	-14.84	0.0002
AAEL007072		galactosy	1.21	0.24	-4.06	0.0351
AAEL005089		sodium/shloride dependent amino acid transporter	1.20	0.23	-3.88	0.0087
AAEL002231		hypothetical protein	1.20	0.22	-3.89	0.0092
AAEL008903		elastase	1.20	0.20	-4.18	0.0180
AAEL004890		hypothetical protein	1.20	0.09	-6.51	0.0076
AAEL004676		synaptic vesicle protein	1.18	0.14	-5.75	0.0014
AAEL008756			1.17	0.00	-26.49	0.0000
AAEL013911		hypothetical protein	1.16	0.03	-12.46	0.0002
AAEL018228		importin alpha	1.16	0.19	-4.04	0.0313
AAEL012491		carboxylesterase	1.15	0.09	-6.77	0.0014
AAEL001474		hypothetical protein	1.15	0.15	-5.55	0.0016
AAEL004233		adam	1.15	0.38	-2.55	0.0413
AAEL017270		zinc finger protein	1.14	0.47	-2.22	0.0180
AAEL009330		hypothetical protein	1.12	0.45	-2.51	0.0219
AAEL006451		hypothetical protein	1.11	0.03	-10.12	0.0015
AAEL010393		zinc finger protein	1.11	0.03	-12.06	0.0003

Table A12 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL013554		hypothetical protein	1.10	0.16	-4.73	0.0101
AAEL006323		hypothetical protein	1.07	0.21	-4.24	0.0094
AAEL012139		hypothetical protein	1.07	0.02	-9.94	0.0015
AAEL015658		SPASIC protein	1.06	0.02	-11.81	0.0005
AAEL006675			1.06	0.45	-2.18	0.0393
AAEL002424		hypothetical protein	1.05	0.06	-6.05	0.0175
AAEL008485		triacylglycerol lipase, pancreatic	1.05	0.14	-5.05	0.0015
AAEL006644		hypothetical protein	1.05	0.17	-4.36	0.0400
AAEL006366		hypothetical protein	1.05	0.21	-3.93	0.0170
AAEL007978		wd-repeat protein	1.04	0.22	-3.65	0.0037
AAEL006470		leucine-rich transmembrane protein	1.04	0.28	-3.25	0.0064
AAEL008909		maltose phosphorylase	1.04	0.11	-7.61	0.0004
AAEL011981		hypothetical protein	1.04	0.05	-7.31	0.0058
AAEL007294		hypothetical protein	1.04	0.00	-8.38	0.0099
AAEL017100		hypothetical protein	1.01	0.06	-9.21	0.0003
AAEL000596		hypothetical protein	1.00	0.00	-8.92	0.0065

Table A13 Genes displaying dimorphic expression patterns in *A. aegypti*. Genes expressed almost exclusively in the antenna of females.

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL008984		hypothetical protein	0.97	12.88	10.59	0.0000
AAEL016981	Or36		0.53	12.23	19.46	0.0000
AAEL012198		adp,atp carrier protein	0.84	11.88	12.91	0.0000
AAEL017377	Or117		0.64	11.72	16.24	0.0000
AAEL017537	Or123		0.64	11.63	16.64	0.0000
AAEL001774		hypothetical protein	0.53	9.53	6.66	0.0187
AAEL013789		hypothetical protein	0.57	9.25	12.97	0.0000
AAEL001675	CLIPA10		0.69	8.29	11.70	0.0000
AAEL011483		Odorant-binding protein 50c	0.95	7.13	6.33	0.0000
AAEL018410	Sphinx_2		0.69	7.04	6.84	0.0009
AAEL017000	Or97		0.42	6.69	14.15	0.0000
AAEL005702		hypothetical protein	0.89	6.23	6.63	0.0000
AAEL009011		hypothetical protein	0.86	5.94	5.58	0.0016
AAEL009774			0.91	5.86	6.25	0.0000
AAEL014599		hypothetical protein	0.38	5.53	9.05	0.0003
AAEL017495	Or95		0.96	5.38	5.44	0.0000
AAEL017050	Or101		0.60	4.84	7.04	0.0000
AAEL007098		4-nitrophenylphosphatase	0.18	4.45	19.82	0.0000
AAEL010390		glucosyl/glucuronosyl transferases	0.78	4.40	5.35	0.0000
AAEL017841	U1		0.58	4.36	4.70	0.0336
AAEL017065	Or92		0.21	4.28	18.55	0.0000
AAEL013563	Or122	hypothetical protein	0.76	4.27	5.31	0.0000
AAEL018107			0.79	4.21	5.08	0.0000
AAEL017974	HSP70Ab		0.51	4.01	7.49	0.0000
AAEL008904		coagulation factor X	0.50	3.87	6.92	0.0000
AAEL017296	Or93		0.44	3.85	7.16	0.0000
AAEL009197		hypothetical protein	0.64	3.78	5.29	0.0000
AAEL017463	Or98		0.56	3.74	6.41	0.0000
AAEL008799		hypothetical protein	0.88	3.74	4.05	0.0003

Table A13 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL007855		hypothetical protein	0.76	3.60	4.43	0.0000
AAEL017316	Or107		0.16	3.53	17.63	0.0000
AAEL013947		hypothetical protein	0.95	3.49	3.58	0.0000
AAEL017336			0.37	3.33	8.07	0.0000
AAEL005186		tmc3 protein	0.72	3.31	4.46	0.0000
AAEL000599			0.58	3.20	5.39	0.0000
AAEL005480		hairy protein	0.29	3.16	9.64	0.0000
AAEL000882		hypothetical protein	0.56	3.10	5.13	0.0000
AAEL011586		hypothetical protein	0.50	2.95	5.61	0.0000
AAEL005782		hypothetical protein	0.54	2.85	4.93	0.0000
AAEL005433		hypothetical protein	0.94	2.85	2.95	0.0000
AAEL013295		hypothetical protein	0.88	2.81	3.11	0.0010
AAEL004944			0.39	2.78	5.48	0.0026
AAEL006635		hypothetical protein	0.59	2.78	4.07	0.0041
AAEL005700	CYP325X4		0.97	2.76	2.80	0.0010
AAEL014811		hypothetical protein	0.50	2.75	5.12	0.0000
AAEL004031		hypothetical protein	0.96	2.73	2.82	0.0031
AAEL011423		sugar transporter	0.62	2.69	4.18	0.0000
AAEL000560		hypothetical protein	0.70	2.64	3.57	0.0006
AAEL002972		brain chitinase and chia	0.87	2.61	2.98	0.0004
AAEL014363		hypothetical protein	0.74	2.60	2.98	0.0371
AAEL011895	Or48	hypothetical protein	0.71	2.59	3.52	0.0000
AAEL013366	IR21a		0.73	2.54	3.39	0.0000
AAEL017143	Or102		0.46	2.49	5.02	0.0000
AAEL014270	IR40a		0.48	2.48	4.80	0.0000
AAEL012615		hypothetical protein	0.97	2.45	2.49	0.0000
AAEL000998		galactose-specific C-type lectin	0.37	2.42	5.55	0.0000
AAEL008384		ATP-binding cassette sub-family A member 3	0.54	2.38	4.25	0.0000
AAEL017977	HSP70Ca		0.49	2.37	4.53	0.0001
AAEL014978		adult cuticle protein	0.60	2.37	3.53	0.0120
AAEL000845			0.93	2.31	2.48	0.0002
AAEL010938		l-asparaginase	0.70	2.30	2.99	0.0035
AAEL014818		sil1	0.96	2.30	2.34	0.0157
AAEL011020		hypothetical protein	0.91	2.27	2.42	0.0074
AAEL008010		sidestep protein	0.69	2.22	2.92	0.0107
AAEL005104		hypothetical protein	0.91	2.22	2.44	0.0000
AAEL007111		hypothetical protein	0.95	2.16	2.27	0.0000
AAEL003711		hypothetical protein	0.07	2.13	10.27	0.0017
AAEL017973	HSP70Aa		0.71	2.13	2.84	0.0305
AAEL006758		hypothetical protein	0.65	2.06	2.91	0.0195
AAEL003848		hypothetical protein	0.15	2.02	6.08	0.0241
AAEL000039	IR41o	hypothetical protein	0.51	1.96	3.67	0.0006
AAEL005682		protein serine/threonine kinase	0.07	1.92	11.22	0.0005
AAEL006319		hypothetical protein	0.33	1.91	5.58	0.0000
AAEL006961		lipase	0.57	1.91	3.14	0.0037
AAEL008988		adult cuticle protein	0.44	1.86	3.67	0.0140
AAEL003967		calpain	0.42	1.80	4.16	0.0000
AAEL015181		hypothetical protein	0.44	1.71	3.51	0.0029
AAEL011036		hypothetical protein	0.07	1.68	14.03	0.0000
AAEL001617	Or124	hypothetical protein	0.27	1.61	4.97	0.0017
AAEL011458		hypothetical protein	0.32	1.59	4.26	0.0049
AAEL014569			0.54	1.59	2.95	0.0001
AAEL017981	HSP70Ca'		0.36	1.58	3.60	0.0257

Table A13 Continued

Gene ID	Gene Name	Wiki Description	Male	Female	Fold	*p* adj.
AAEL010130		Pupal cuticle protein	0.19	1.53	5.25	0.0189
AAEL018048			0.56	1.52	2.51	0.0181
AAEL011173			0.69	1.52	2.15	0.0010
AAEL017976	HSP70Bb		0.34	1.51	4.09	0.0009
AAEL003153		hypothetical protein	0.65	1.51	2.31	0.0015
AAEL002292		glucose transport protein	0.44	1.50	3.03	0.0430
AAEL013492	PPO5	prophenoloxidase	0.45	1.49	3.29	0.0015
AAEL006574		nuclear transcription factor, x-box binding 1 (nfx1)	0.62	1.49	2.42	0.0038
AAEL014764		acidic ribosomal protein P1	0.12	1.46	6.89	0.0071
AAEL012144	CYP303A1	cytochrome P450	0.44	1.45	3.10	0.0015
AAEL015474		hypothetical protein	0.02	1.42	11.63	0.0016
AAEL014571		oviductin	0.18	1.41	6.97	0.0000
AAEL007145		hypothetical protein	0.25	1.41	4.95	0.0004
AAEL005095	GPRGPH	insl3/relaxin receptor	0.54	1.41	2.54	0.0348
AAEL014734		saccharopine dehydrogenase	0.58	1.40	2.32	0.0182
AAEL002648		hypothetical protein	0.02	1.36	7.74	0.0162
AAEL006326		deoxyribonuclease I	0.47	1.36	2.80	0.0103
AAEL012688		hypothetical protein	0.35	1.32	3.57	0.0049
AAEL005694		hypothetical protein	0.51	1.32	2.52	0.0166
AAEL002909		lysosomal acid lipase	0.57	1.32	2.31	0.0441
AAEL007873		hypothetical protein	0.32	1.27	3.65	0.0162
AAEL000871		hypothetical protein	0.30	1.24	3.63	0.0042
AAEL008746		hypothetical protein	0.31	1.24	3.60	0.0018
AAEL007957		hypothetical protein	0.10	1.18	6.05	0.0122
AAEL003617		alcohol dehydrogenase	0.33	1.17	3.38	0.0090
AAEL013242			0.39	1.15	2.89	0.0000
AAEL007714		hypothetical protein	0.14	1.13	5.27	0.0120
AAEL011028		hypothetical protein	0.37	1.12	2.88	0.0059
AAEL009205		hypothetical protein	0.44	1.10	2.48	0.0005
AAEL010998		hypothetical protein	0.47	1.10	2.29	0.0132
AAEL010740		wingless	0.25	1.08	3.68	0.0091
AAEL002929		AMP dependent ligase	0.37	1.08	2.85	0.0187
AAEL008023	CYP4C52	cytochrome P450	0.17	1.07	5.02	0.0005
AAEL010910		retina aberrant in pattern	0.15	1.06	6.06	0.0001
AAEL005791		hypothetical protein	0.38	1.01	2.50	0.0110
AAEL014521		hypothetical protein	0.46	1.00	2.22	0.0090

Table A14 Genes differentially expressed in the HT of males and females.

Gene ID	Gene Name	Wiki Description	Males	Females	Fold	*p* adj.
		Enriched in Females				
AAEL006138		hypothetical protein	0.00	4.95	389.20	0.0000
AAEL001414	LRIM9	hypothetical protein	3.47	311.78	100.96	0.0000
AAEL010434		hypothetical protein	0.08	6.27	82.54	0.0000
AAEL005672		adenosine deaminase	1.62	106.18	70.48	0.0000
AAEL010242		hypothetical protein	8.89	458.57	60.85	0.0000
AAEL001420	LRIM8	hypothetical protein	9.00	426.83	54.14	0.0000
AAEL003584		hypothetical protein	0.23	10.69	49.30	0.0000
AAEL000733		hydroxysteroid dehydrogenase	0.60	22.57	41.09	0.0000
AAEL014426		glycine dehydrogenase	0.10	3.02	30.76	0.0000
AAEL009852		hypothetical protein	2.61	115.46	29.47	0.0000
AAEL009459		hypothetical protein	5.62	269.39	28.81	0.0000
AAEL010228		hypothetical protein	14.20	641.38	27.56	0.0000
AAEL006424		D7 protein	14.47	842.64	26.45	0.0000
AAEL006406		hypothetical protein	7.28	558.11	25.55	0.0000
AAEL001402	LRIM10B	hypothetical protein	5.12	109.23	25.08	0.0000
AAEL003585		hypothetical protein	0.27	17.22	24.41	0.0000
AAEL006347		apyrase	5.43	367.08	24.27	0.0000
AAEL002675		arginase	4.42	91.52	23.74	0.0000
AAEL013492	PPO5	prophenoloxidase	0.42	8.29	22.26	0.0000
AAEL007599		cathepsin b	0.00	1.06	21.28	0.0000
AAEL003053		allergen	9.95	447.24	20.87	0.0000
AAEL006423		hypothetical protein	4.01	600.69	20.79	0.0000
AAEL013532		hypothetical protein	2.46	44.41	20.59	0.0000
AAEL011519		sucrose transport protein	0.10	2.72	20.45	0.0000
AAEL003600		hypothetical protein	10.02	609.38	20.33	0.0000
AAEL008619		hypothetical protein	26.24	439.18	20.15	0.0000
AAEL017484	CTLGA4		0.19	5.56	19.56	0.0000
AAEL006485		inosine-uridine preferring nucleoside hydrolase	5.51	252.04	19.43	0.0000
AAEL007818		trypsin	2.70	67.23	18.92	0.0000
AAEL010235		hypothetical protein	26.53	1,087.37	18.67	0.0000
AAEL007432		serine collagenase 1 precursor	1.07	32.87	18.59	0.0000
AAEL001703		serine-type enodpeptidase	0.08	2.71	18.09	0.0000
AAEL003182	SRPN26	SERPIN1 protein precursor	7.47	214.48	17.92	0.0000
AAEL003107		hypothetical protein	2.98	68.13	17.12	0.0000
AAEL007394		hypothetical protein	0.27	42.20	16.30	0.0000
AAEL001401	LRIM10A	hypothetical protein	7.23	98.99	16.21	0.0000
AAEL000229		hypothetical protein	5.79	248.65	15.96	0.0000
AAEL000748		hypothetical protein	1.28	49.79	14.90	0.0000
AAEL000732		hypothetical protein	2.46	105.99	14.84	0.0000
AAEL003881		anopheles stephensi ubiquitin	14.24	163.72	13.90	0.0000
AAEL002656		hypothetical protein	3.78	60.52	13.63	0.0000
AAEL007872		hypothetical protein	0.74	34.66	13.44	0.0000
AAEL008310		hypothetical protein	22.06	336.39	12.94	0.0000
AAEL003601		hypothetical protein	1.85	101.11	12.56	0.0000
AAEL017467			0.13	4.98	12.52	0.0000
AAEL000749		hypothetical protein	4.96	91.06	12.44	0.0000
AAEL010276		aminomethyltransferase	3.15	33.08	12.30	0.0000
AAEL000793		venom allergen	10.53	1,068.98	12.05	0.0000
AAEL000932		hypothetical protein	2.14	23.60	12.04	0.0000
AAEL012538	LRIM6	hypothetical protein	0.73	7.80	11.73	0.0000
AAEL008305		hypothetical protein	22.23	394.21	11.69	0.0000

Table A14 Continued

Gene ID	Gene Name	Wiki Description	Males	Females	Fold	*p* adj.
AAEL003057		allergen	4.09	39.29	11.37	0.0000
AAEL003100		hypothetical protein	2.07	45.63	11.34	0.0000
AAEL009669		hypothetical protein	1.47	13.90	11.01	0.0000
AAEL006417		D7 protein	10.77	534.84	10.94	0.0000
AAEL000650		hypothetical protein	3.35	30.62	10.68	0.0000
AAEL014412	CYP304B2	cytochrome P450	2.01	16.65	9.90	0.0000
AAEL006333		salivary apyrase	2.09	89.12	9.69	0.0000
AAEL000658		hypothetical protein	0.24	2.19	9.42	0.0000
AAEL008781		serine-type enodpeptidase	0.08	1.30	9.15	0.0000
AAEL006563		retinoid-inducible serine carboxypeptidase	0.35	3.10	9.14	0.0000
AAEL000786		hypothetical protein	5.62	40.04	8.27	0.0000
AAEL017022			28.01	188.41	8.21	0.0000
AAEL008083		laminin receptor	10.40	71.46	8.20	0.0000
AAEL000711		hypothetical protein	26.66	179.50	8.19	0.0000
AAEL006126		hypothetical protein	0.34	2.26	7.99	0.0000
AAEL004899		hypothetical protein	1.65	99.20	7.94	0.0002
AAEL011599		ADP-ribosylation factor	0.24	1.84	7.94	0.0000
AAEL000556	CTL25	galactose-specific C-type lectin	4.05	181.81	7.80	0.0002
AAEL003345		argininosuccinate lyase	34.07	222.22	7.64	0.0000
AAEL006617		hypothetical protein	3.77	23.94	7.36	0.0000
AAEL003352		ribosomal protein l7ae	14.96	88.08	7.02	0.0000
AAEL009992		hypothetical protein	0.88	26.63	6.99	0.0004
AAEL009993		hypothetical protein	1.32	36.53	6.43	0.0008
AAEL005295		hypothetical protein	0.53	3.23	6.28	0.0000
AAEL002704	SRPN23	serine protease inhibitor (serpin-4)	9.14	366.80	6.28	0.0010
AAEL000726		fibrinogen and fibronectin	8.50	122.19	6.22	0.0006
AAEL000909		histone H1	0.62	3.68	6.13	0.0000
AAEL007226		nidogen	0.45	2.37	6.13	0.0000
AAEL011926		brachyury	0.19	1.18	6.10	0.0000
AAEL006408		hypothetical protein	8.25	220.87	6.09	0.0012
AAEL015474		hypothetical protein	0.08	1.61	6.01	0.0010
AAEL004031		hypothetical protein	0.44	2.37	5.79	0.0000
AAEL003873		glycerol-3-phosphate dehydrogenase	195.27	938.77	5.75	0.0000
AAEL000533	CTL16	antifreeze protein	5.25	375.72	5.74	0.0020
AAEL013283		serine-type enodpeptidase	0.93	5.37	5.73	0.0000
AAEL008018	CYP4C51	cytochrome P450	0.10	2.58	5.71	0.0019
AAEL000087		macroglobulin/complement	1.25	7.51	5.62	0.0000
AAEL017409			0.48	2.64	5.60	0.0000
AAEL008045		hexamerin 2 beta	0.29	1.68	5.57	0.0000
AAEL001429		amino acid transporter	50.43	223.72	5.43	0.0000
AAEL014936		sarcosine dehydrogenase	0.24	1.29	5.42	0.0000
AAEL011756		aldehyde dehydrogenase	4.99	21.89	5.32	0.0000
AAEL013707		trypsin	0.56	2.85	5.27	0.0000
AAEL014128		hypothetical protein	10.94	49.57	5.24	0.0000
AAEL012578		phosphoserine aminotransferase	11.86	50.38	5.19	0.0000
AAEL006351		hypothetical protein	0.83	22.05	5.16	0.0041
AAEL010231		hypothetical protein	0.24	1.65	5.15	0.0004
AAEL007420	SRPN25	antithrombin	2.08	38.04	5.13	0.0040
AAEL010640		phosphoribosylamine-glycine ligase	1.99	8.40	5.11	0.0000
AAEL000575		apyrase	5.74	24.24	5.09	0.0000
AAEL007686		hypothetical protein	0.28	1.29	5.02	0.0000

Table A14 Continued

Gene ID	Gene Name	Wiki Description	Males	Females	Fold	*p* adj.
AAEL006486		hypothetical protein	1.01	4.36	4.94	0.0000
AAEL005429		2-oxoglutarate dehydrogenase	0.67	2.78	4.93	0.0000
AAEL000283	CTLMA16	galactose-specific C-type lectin	0.16	1.01	4.91	0.0007
AAEL000774		hypothetical protein	6.00	24.43	4.90	0.0000
AAEL000668		hypothetical protein	9.32	37.36	4.88	0.0000
AAEL009625		short-chain dehydrogenase	9.27	37.69	4.85	0.0000
AAEL007193		amino acid transporter	48.68	192.24	4.81	0.0000
AAEL005687		protein serine/threonine kinase	1.05	4.31	4.74	0.0000
AAEL006349		hypothetical protein	0.64	2.58	4.66	0.0000
AAEL008766		hypothetical protein	1.63	33.70	4.59	0.0084
AAEL002937		hypothetical protein	0.58	2.51	4.56	0.0000
AAEL009967		hypothetical protein	1.24	4.78	4.55	0.0000
AAEL009601		pyridoxine kinase	25.40	93.23	4.50	0.0000
AAEL017018			21.63	78.98	4.47	0.0000
AAEL002378		carboxylesterase	2.13	7.99	4.46	0.0000
AAEL010656	LRIM12	hypothetical protein	5.87	21.62	4.44	0.0000
AAEL014255		aquaporin	8.22	30.77	4.44	0.0000
AAEL009875		alanine aminotransferase	8.04	29.61	4.42	0.0000
AAEL003581		amidophosphoribosyltransferase	6.37	23.36	4.40	0.0000
AAEL011357		maintenance of killer 16 (mak16) protein	9.41	33.83	4.33	0.0000
AAEL002194		uricase	9.28	32.84	4.29	0.0000
AAEL013857		hypothetical protein	13.07	46.02	4.25	0.0000
AAEL009472		hypothetical protein	0.60	3.07	4.20	0.0020
AAEL018243		polypeptide of 976 aa	3.73	12.96	4.20	0.0000
AAEL013413		hypothetical protein	0.37	1.42	4.19	0.0000
AAEL004335		secreted ferritin G subunit precursor	0.75	2.86	4.18	0.0000
AAEL013498	PPO1	prophenoloxidase	0.55	2.00	4.17	0.0000
AAEL009313		elongation factor -1 beta,delta	197.86	669.37	4.15	0.0000
AAEL002588		hypothetical protein	6.13	20.89	4.14	0.0000
AAEL011763	PPO3	prophenoloxidase	1.91	6.61	4.14	0.0000
AAEL014811		hypothetical protein	0.28	1.21	4.13	0.0006
AAEL001953		hypothetical protein	35.09	141.69	4.13	0.0001
AAEL003655		hypothetical protein	0.22	8.62	4.13	0.0152
AAEL014108		aquaporin	2.30	8.11	4.07	0.0000
AAEL000099	CLIPB33	serine protease	7.58	25.52	4.06	0.0000
AAEL013517		pupal cuticle protein 78E	14.95	49.90	4.06	0.0000
AAEL014830		cytochrome P450	6.44	21.66	4.05	0.0000
AAEL011593	CLIPC11	elastase	0.48	1.82	4.04	0.0000
AAEL000364		glycine cleavage system h protein	6.75	23.61	4.04	0.0000
AAEL010028		sarcosine dehydrogenase	3.35	11.10	4.03	0.0000
AAEL002880		hypothetical protein	3.16	10.41	3.99	0.0000
AAEL008341		adenosylhomocysteinase	7.03	23.28	3.99	0.0000
AAEL010183		hypothetical protein	252.76	790.31	3.84	0.0000
AAEL011764	PPO10	prophenoloxidase	0.88	2.87	3.82	0.0000
AAEL006969		hypothetical protein	2.87	9.25	3.80	0.0000
AAEL006909		hypothetical protein	0.80	2.94	3.80	0.0003
AAEL013967		Methylmalonyl-CoA carboxyltransferase	6.75	21.21	3.78	0.0000
AAEL001252		rap1 gtpase-gdp dissociation stimulator	25.59	78.48	3.76	0.0000
AAEL003624		Na/Cl dependent amino acid transporter	2.71	8.43	3.76	0.0000

Table A14 Continued

Gene ID	Gene Name	Wiki Description	Males	Females	Fold	*p* adj.
AAEL014764		acidic ribosomal protein P1	1.09	3.99	3.75	0.0003
AAEL009888		bumetanide-sensitive Na-K-Cl cotransporter	1.00	3.12	3.75	0.0000
AAEL007113		selenophosphate synthase	25.32	77.30	3.74	0.0000
AAEL009045		amine oxidase	0.39	1.31	3.71	0.0000
AAEL000543	CTLMA11	galactose-specific C-type lectin	4.65	14.45	3.71	0.0000
AAEL002242		hypothetical protein	0.72	2.44	3.71	0.0000
AAEL006634		acetyl-coa acetyltransferase	12.92	39.18	3.71	0.0000
AAEL015249		sulfate transporter	18.81	57.14	3.70	0.0000
AAEL009766		lipoamide acyltransferase	4.69	14.23	3.70	0.0000
AAEL008516		RNA-binding protein	0.62	2.10	3.69	0.0000
AAEL012974		glycine cleavage system h protein	6.54	19.77	3.68	0.0000
AAEL006483		hypothetical protein	39.51	119.72	3.68	0.0000
AAEL010764		aldehyde dehydrogenase	21.90	65.93	3.66	0.0000
AAEL014600		4-hydroxyphenylpyruvate dioxygenase	5.46	16.39	3.65	0.0000
AAEL001656		sodium-dependent phosphate transporter	3.12	9.32	3.63	0.0000
AAEL012711	CLIPC12	trypsin	0.89	2.68	3.61	0.0000
AAEL012687		Juvenile hormone-inducible protein	3.40	10.14	3.60	0.0000
AAEL000530		hypothetical protein	1.75	5.24	3.59	0.0000
AAEL008844		calcium-binding protein	1,943.07	5,662.72	3.56	0.0000
AAEL007680		hypothetical protein	17.72	52.43	3.56	0.0000
AAEL004948		hypothetical protein	0.63	1.96	3.55	0.0000
AAEL008889	CYP6AL1	cytochrome P450	1.08	3.27	3.55	0.0000
AAEL001863		zinc carboxypeptidase	175.19	507.21	3.53	0.0000
AAEL011345		hypothetical protein	3.21	9.34	3.52	0.0000
AAEL010169		hypothetical protein	50.46	145.29	3.52	0.0000
AAEL010168		40S ribosomal protein S2	706.03	2,006.72	3.49	0.0000
AAEL005384		phosphoribosylformylglycinamidine synthase	4.42	12.75	3.49	0.0000
AAEL015086		hypothetical protein	0.50	5.35	3.49	0.0372
AAEL010540		alpha-amylase	1.30	3.96	3.48	0.0000
AAEL011985		hypothetical protein	18.43	52.67	3.48	0.0000
AAEL011476		hypothetical protein	28.35	80.99	3.47	0.0000
AAEL004493		ribosome biogenesis protein tsr1	12.53	35.61	3.47	0.0000
AAEL000436		hypothetical protein	7.68	21.76	3.46	0.0000
AAEL017072			3.27	9.77	3.46	0.0000
AAEL002875		hypothetical protein	9.31	26.81	3.43	0.0000
AAEL007986		hypothetical protein	613.87	1,759.14	3.41	0.0000
AAEL003514		centromere/microtubule binding protein cbf5	6.89	19.27	3.40	0.0000
AAEL005480		hairy protein	0.61	1.76	3.39	0.0000
AAEL002185		cuticle protein	245.47	673.85	3.38	0.0000
AAEL015645		RNA binding motif protein	0.40	1.26	3.35	0.0008
AAEL005694		hypothetical protein	0.47	1.45	3.35	0.0003
AAEL017096			994.73	2,722.63	3.34	0.0000
AAEL010296		carboxylase:pyruvate/acetyl-coa/propionyl-coa	2.75	7.67	3.34	0.0000
AAEL013533		hypothetical protein	313.13	852.48	3.33	0.0000
AAEL001091		malic enzyme	163.85	452.96	3.33	0.0000
AAEL005744		DEAD box ATP-dependent RNA helicase	23.35	63.30	3.31	0.0000
AAEL015114		hypothetical protein	4.20	11.69	3.29	0.0000

Table A14 Continued

Gene ID	Gene Name	Wiki Description	Males	Females	Fold	*p* adj.
AAEL002688		glucosyl/glucuronosyl transferases	14.26	38.39	3.28	0.0000
AAEL005638		hypothetical protein	38.24	101.77	3.26	0.0000
AAEL000252		hypothetical protein	13.41	36.28	3.25	0.0000
AAEL014300		hypothetical protein	2.16	6.32	3.24	0.0001
AAEL010782		carboxypeptidase	8.03	21.24	3.24	0.0000
AAEL008963		tyrosine aminotransferase	39.36	103.53	3.24	0.0000
AAEL006176	OBP27	Odorant-binding protein 56e	0.92	2.86	3.24	0.0017
AAEL018202		hypothetical protein	58.00	153.07	3.23	0.0000
AAEL003491		proline synthetase associated protein	19.77	51.77	3.22	0.0000
AAEL002686		testisin precursor	2.42	6.44	3.21	0.0000
AAEL000340		cytochrome P450	0.41	1.15	3.20	0.0000
AAEL005008		aquaporin	39.65	103.14	3.20	0.0000
AAEL012726		hypothetical protein	4.41	11.90	3.20	0.0000
AAEL017113			10.51	27.28	3.17	0.0000
AAEL003112		hypothetical protein	2.04	5.37	3.16	0.0000
AAEL013642		acyl-coa dehydrogenase	1.17	3.09	3.16	0.0000
AAEL008668	CLIPB22	MASP-2 protein	1.38	3.78	3.15	0.0000
AAEL012851		wd-repeat protein	6.42	16.63	3.15	0.0000
AAEL004997		U3 small nucleolar ribonucleoprotein protein	6.02	15.58	3.15	0.0000
AAEL012359		nucleoside-diphosphate kinase NBR-A	261.62	670.52	3.14	0.0000
AAEL011584		chaperonin-60kD, ch60	12.14	31.08	3.14	0.0000
AAEL006130		hypothetical protein	0.50	1.45	3.13	0.0012
AAEL011984		hypothetical protein	1.17	3.06	3.13	0.0000
AAEL011288		elongation factor 1 gamma	261.64	666.86	3.12	0.0000
AAEL012822		Misexpression suppressor of KSR	0.52	1.41	3.10	0.0001
AAEL001900		lactosylceramide 4-alpha-galactosyltransferase	0.59	1.57	3.08	0.0000
AAEL016994			1,148.65	2,876.92	3.07	0.0000
AAEL011624		granzyme A precursor	10.44	26.11	3.07	0.0000
AAEL008028		monocarboxylate transporter	14.94	37.46	3.07	0.0000
AAEL006355	SCRC1	hypothetical protein	0.53	1.42	3.06	0.0000
AAEL005335		hypothetical protein	0.41	1.13	3.05	0.0010
AAEL014904		DEAD box ATP-dependent RNA helicase	9.06	22.64	3.04	0.0000
AAEL010248		fibrillarin	1.70	4.28	3.03	0.0000
AAEL001052		heat shock protein	33.71	83.35	3.03	0.0000
AAEL015440		hypothetical protein	15.03	37.27	3.03	0.0000
AAEL000951		elongation factor 1-beta2	237.81	588.16	3.03	0.0000
AAEL001708		hypothetical protein	3.47	8.85	3.02	0.0000
AAEL000663		hypothetical protein	89.14	218.77	3.02	0.0000
AAEL007407		hypothetical protein	52.19	128.69	3.02	0.0000
AAEL010623		hypothetical protein	0.95	2.49	3.02	0.0000
AAEL002683		aldehyde oxidase	3.56	8.78	3.01	0.0000
AAEL012219		ubiquitin specific protease	25.39	62.45	3.01	0.0000
AAEL003631	CLIPB41	clip-domain serine protease	8.76	21.53	2.99	0.0000
AAEL013276		acid phosphatase	0.73	1.93	2.99	0.0002
AAEL002784		zinc finger protein	11.00	26.83	2.97	0.0000
AAEL017558			313.72	767.43	2.97	0.0000
AAEL004178		ribose-phosphate pyrophosphokinase 1	66.99	161.32	2.96	0.0000
AAEL003967		calpain	0.62	1.58	2.96	0.0000

Table A14 Continued

Gene ID	Gene Name	Wiki Description	Males	Females	Fold	*p* adj.
AAEL005628		hypothetical protein	16.42	39.69	2.95	0.0000
AAEL013880		MSF1 protein	230.62	563.64	2.95	0.0000
AAEL014234		hypothetical protein	6.99	17.76	2.94	0.0000
AAEL013990		hexamerin 2 beta	3.85	9.35	2.94	0.0000
AAEL018410	Sphinx_2		4.91	13.02	2.93	0.0012
AAEL009842	GALE12	keratinocyte lectin	3.79	9.68	2.93	0.0001
AAEL009115		hypothetical protein	52.03	124.72	2.93	0.0000
AAEL003235		hypothetical protein	19.69	47.04	2.93	0.0000
AAEL011255		GTP-binding protein-invertebrate	48.90	117.11	2.92	0.0000
AAEL012882		folylpolyglutamate synthase	13.21	31.72	2.92	0.0000
AAEL014664		AMP dependent coa ligase	2.23	5.44	2.92	0.0000
AAEL013438		LIM domain-binding protein 3	42.62	104.05	2.92	0.0000
AAEL006562		acid phosphatase	1.53	3.73	2.92	0.0000
AAEL013013		hypothetical protein	7.01	17.29	2.91	0.0000
AAEL005170		cytochrome c oxidase subunit iv	100.40	241.83	2.91	0.0000
AAEL013694		laminin receptor	108.40	257.21	2.90	0.0000
AAEL002617	OBP12	Odorant-binding protein 56e	1.98	5.05	2.90	0.0004
AAEL009170		six/sine homebox transcription factors	0.86	2.08	2.90	0.0000
AAEL009185		arginine or creatine kinase	1,380.53	3,300.70	2.90	0.0000
AAEL010035			1.10	2.70	2.89	0.0000
AAEL009843		serine-type enodpeptidase	2.88	7.11	2.88	0.0000
AAEL013884		synaptic vesicle protein	2.43	5.95	2.88	0.0000
AAEL017468			1,767.94	4,167.57	2.87	0.0000
AAEL008369		acylphosphatase	25.33	59.10	2.87	0.0000
AAEL012980		hypothetical protein	24.37	56.86	2.87	0.0000
AAEL018508	Sphinx_1		15.86	40.30	2.86	0.0006
AAEL006041		hypothetical protein	1.14	2.78	2.86	0.0000
AAEL013685		wd-repeat protein	1.76	4.21	2.85	0.0000
AAEL003071		tRNA pseudouridine synthase D	14.11	32.82	2.85	0.0000
AAEL013411		hypothetical protein	1.09	2.80	2.85	0.0018
AAEL018109		elastase	4.77	11.15	2.84	0.0000
AAEL012721		hypothetical protein	4.14	9.95	2.83	0.0000
AAEL013431		proline oxidase	204.46	473.29	2.83	0.0000
AAEL010627		hypothetical protein	0.41	1.09	2.83	0.0071
AAEL010288		carboxylase:pyruvate/acetyl-coa/propionyl-coa	0.88	2.09	2.82	0.0000
AAEL004455		hypothetical protein	6.83	15.78	2.82	0.0000
AAEL007880		ornithine decarboxylase	85.25	196.97	2.81	0.0000
AAEL007374		yellow protein precursor	41.38	94.34	2.81	0.0000
AAEL004135		sterol desaturase	1.47	3.50	2.81	0.0000
AAEL011738		hypothetical protein	1.85	4.28	2.81	0.0000
AAEL001490		acylphosphatase	353.10	814.85	2.80	0.0000
AAEL017851	U3		0.94	2.94	2.80	0.0452
AAEL000834		dimethylaniline monooxygenase	10.82	24.77	2.79	0.0000
AAEL001037		ribosomal RNA methyltransferase	5.89	13.44	2.79	0.0000
AAEL000638		hypothetical protein	201.29	455.10	2.78	0.0000
AAEL014551		triacylglycerol lipase, pancreatic	5.44	12.51	2.78	0.0000
AAEL002080		septin interacting protein	2.01	4.67	2.77	0.0000
AAEL008494		mitochondrial carrier protein ymc	45.35	102.50	2.76	0.0000
AAEL010821		60S acidic ribosomal protein P0	843.41	1,890.15	2.76	0.0000
AAEL017286			15.90	35.63	2.75	0.0000
AAEL006484	GPROP3	rhodopsin	1.46	3.61	2.75	0.0022
AAEL000879		cuticle protein	1.64	3.90	2.75	0.0002

Table A14 Continued

Gene ID	Gene Name	Wiki Description	Males	Females	Fold	*p* adj.
AAEL001888		hypothetical protein	10.23	22.92	2.75	0.0000
AAEL006448		hypothetical protein	0.77	1.75	2.74	0.0000
AAEL000269		hypothetical protein	183.69	409.60	2.74	0.0000
AAEL010630		xanthine dehydrogenase	0.53	1.23	2.74	0.0000
AAEL011676		AMP dependent coa ligase	1.34	3.03	2.72	0.0000
AAEL001082		hypothetical protein	1,222.98	3,380.04	2.72	0.0315
AAEL008141	PER		45.05	98.89	2.71	0.0000
AAEL007231	LRIM28	hypothetical protein	2.52	5.66	2.70	0.0000
AAEL002510		serine hydroxymethyltransferase	26.65	58.39	2.70	0.0000
AAEL008564		low-density lipoprotein receptor (ldl)	15.30	33.97	2.69	0.0000
AAEL004126		sterol desaturase	1.06	2.42	2.69	0.0000
AAEL001375		Y-box binding protein	118.35	257.72	2.68	0.0000
AAEL001068		myosin light chain 2V	17.55	38.44	2.68	0.0000
AAEL014583		60S acidic ribosomal protein P2	1,329.21	2,885.88	2.68	0.0000
AAEL003467		hypothetical protein	35.28	77.25	2.67	0.0000
AAEL013904		3-hydroxyisobutyrate dehydrogenase	46.96	101.82	2.66	0.0000
AAEL008490		NADH dehydrogenase	268.63	594.28	2.66	0.0000
AAEL011452		hypothetical protein	5.19	11.47	2.66	0.0000
AAEL010148		sodium/potassium-dependent atpase beta-2	134.55	290.71	2.64	0.0000
AAEL002814		hypothetical protein	9.58	20.59	2.63	0.0000
AAEL005032		hypothetical protein	31.33	66.85	2.63	0.0000
AAEL003125		acyl-coa dehydrogenase	8.50	18.22	2.63	0.0000
AAEL001795		orfY	16.78	35.94	2.62	0.0000
AAEL013069		receptor for activated protein kinas c (rack1)	971.74	2,067.73	2.62	0.0000
AAEL008077		hypothetical protein	2.29	4.91	2.61	0.0000
AAEL008886		hypothetical protein	9.38	20.11	2.61	0.0000
AAEL000024		dopachrome-conversion enzyme (DCE)	9.42	20.30	2.61	0.0000
AAEL001594		hypothetical protein	21.04	44.58	2.60	0.0000
AAEL003413		f-spondin	16.71	35.65	2.59	0.0000
AAEL009925		amidase	1.64	3.51	2.59	0.0000
AAEL017456			7.42	16.12	2.59	0.0000
AAEL001050		hypothetical protein	3.14	6.64	2.58	0.0000
AAEL004017		DNA polymerase v	4.26	8.96	2.58	0.0000
AAEL011184		mitochondrial phosphate carrier protein	1,444.91	3,614.75	2.58	0.0322
AAEL013417		fibrinogen and fibronectin	0.64	1.48	2.58	0.0066
AAEL013176		hypothetical protein	10.09	21.25	2.58	0.0000
AAEL001107		hypothetical protein	127.76	268.33	2.57	0.0000
AAEL010597		hypothetical protein	9.35	20.15	2.57	0.0000
AAEL012098		synaptic vesicle protein	104.93	219.74	2.57	0.0000
AAEL014418		hypothetical protein	1.31	3.09	2.57	0.0134
AAEL001865		NADH dehydrogenase	456.09	965.25	2.57	0.0000
AAEL003313		alkaline phosphatase	0.69	1.51	2.57	0.0004
AAEL002301		serine protease	11.72	25.09	2.56	0.0000
AAEL000115		hypothetical protein	2.14	4.61	2.56	0.0000
AAEL000563	CTLMA15	galactose-specific C-type lectin	2.42	5.25	2.56	0.0002
AAEL008757		juvenile hormone esterase	7.90	16.43	2.55	0.0000
AAEL013744		NADH:ubiquinone dehydrogenase	369.84	776.32	2.54	0.0000

Table A14 Continued

Gene ID	Gene Name	Wiki Description	Males	Females	Fold	*p* adj.
AAEL002867		phenylalanyl-tRNA synthetase alpha chain	14.89	30.95	2.54	0.0000
AAEL006200		hypothetical protein	95.22	198.79	2.54	0.0000
AAEL018590	Sphinx_1		12.66	28.45	2.54	0.0037
AAEL014318		hypothetical protein	118.42	244.89	2.54	0.0000
AAEL008876		deoxyribonuclease I	0.82	1.79	2.54	0.0015
AAEL004526		hypothetical protein	2.14	4.45	2.54	0.0000
AAEL008095		hypothetical protein	0.45	1.02	2.53	0.0055
AAEL009426		hypothetical protein	13.33	27.67	2.52	0.0000
AAEL014673		NADH:ubiquinone dehydrogenase	90.04	187.90	2.52	0.0000
AAEL011514		cytochrome c oxidase, subunit VIIC	468.71	955.88	2.51	0.0000
AAEL001367		type iv inositol 5-phosphatase	13.78	28.01	2.50	0.0000
AAEL001047		adenylate cyclase	30.55	62.49	2.50	0.0000
AAEL003676		myosin I	36.19	73.60	2.50	0.0000
AAEL005392		dihydropyridine-sensitive l-type calcium channel	2.71	5.56	2.50	0.0000
AAEL009682		serine collagenase 1 precursor	1.40	3.33	2.50	0.0321
AAEL015541		hypothetical protein	4.35	8.96	2.50	0.0000
AAEL005961		actin	837.85	1,719.96	2.50	0.0000
AAEL015663		cytochrome P450	0.48	1.10	2.50	0.0157
AAEL000897		hypothetical protein	5.60	11.51	2.49	0.0000
AAEL013032		hypothetical protein	11.32	23.31	2.49	0.0000
AAEL009309		lipid depleted protein	5.58	11.35	2.49	0.0000
AAEL014353		hypothetical protein	6.64	13.82	2.48	0.0000
AAEL001171		tRNA-dihydrouridine synthase	8.44	17.13	2.48	0.0000
AAEL017115			0.62	1.29	2.48	0.0000
AAEL012855		hypothetical protein	6.84	14.11	2.48	0.0000
AAEL001625		hypothetical protein	49.12	100.79	2.48	0.0000
AAEL014526		sideroflexin 1,2,3	36.78	74.42	2.47	0.0000
AAEL004851		hypothetical protein	5,045.16	10,100.90	2.47	0.0000
AAEL017265	CTLGA7	galactose-specific C-type lectin	14.07	28.62	2.47	0.0000
AAEL004063		wd-repeat protein	5.29	10.67	2.46	0.0000
AAEL002776		hypothetical protein	472.50	1,089.67	2.46	0.0325
AAEL002731	SRPN14	serine protease inhibitor, serpin	3.66	7.48	2.46	0.0000
AAEL002404		receptor protein tyrosine kinase	10.09	20.65	2.46	0.0000
AAEL013612		hypothetical protein	101.81	202.58	2.45	0.0000
AAEL018423	Sphinx_2		6.44	14.53	2.45	0.0214
AAEL004591		hypothetical protein	6.71	13.71	2.45	0.0000
AAEL003380	CYP4H28	cytochrome P450	1.94	4.08	2.45	0.0011
AAEL011282		ribosomal RNA small subunit methyltransferase	4.61	9.18	2.44	0.0000
AAEL002231		cuticle protein	15.55	31.12	2.44	0.0000
AAEL016995			1,244.55	2,463.95	2.44	0.0000
AAEL010776		carboxypeptidase	0.90	1.87	2.44	0.0007
AAEL005667		LIM domain-binding protein	91.20	181.24	2.43	0.0000
AAEL007537		hypothetical protein	0.74	1.64	2.43	0.0260
AAEL004342	OBP18	hypothetical protein	41.73	83.01	2.43	0.0000
AAEL009285		DEAD box ATP-dependent RNA helicase	8.59	16.96	2.42	0.0000
AAEL014599		hypothetical protein	1.44	3.06	2.42	0.0062
AAEL017898	RNaseP_nuc		0.69	1.57	2.42	0.0377
AAEL003606		purine biosynthesis protein 6, pur6	18.17	35.92	2.42	0.0000
AAEL017576			54.87	107.84	2.42	0.0000

Table A14 Continued

Gene ID	Gene Name	Wiki Description	Males	Females	Fold	*p* adj.
AAEL007887		ornithine decarboxylase	0.50	1.06	2.42	0.0076
AAEL009506		40S ribosomal protein S20	895.90	1,756.70	2.42	0.0000
AAEL010840		hypothetical protein	206.22	412.48	2.42	0.0000
AAEL018185		hypothetical protein	4.46	8.83	2.41	0.0000
AAEL006344		sulfotransferase (sult)	5.08	10.10	2.41	0.0000
AAEL013158		40S ribosomal protein S3a	372.61	729.68	2.41	0.0000
AAEL013968		hypothetical protein	7.06	13.90	2.41	0.0000
AAEL015136		Niemann-Pick Type C-2	10.23	20.23	2.41	0.0000
AAEL000987		60S ribosomal protein L8	1,130.68	2,216.42	2.41	0.0000
AAEL007593	CLIPC2	lumbrokinase-3(1) precursor	31.52	62.67	2.41	0.0000
AAEL014198		3-phosphatidyltransferase	14.48	28.49	2.41	0.0000
AAEL001343		hypothetical protein	7.49	14.93	2.41	0.0000
AAEL008463		DEAD box ATP-dependent RNA helicase	1.42	2.82	2.40	0.0000
AAEL010398		hypothetical protein	1.69	3.41	2.40	0.0003
AAEL000551		hypothetical protein	32.46	63.42	2.40	0.0000
AAEL004522	GAM1	hypothetical protein	2,051.80	4,000.53	2.40	0.0000
AAEL005819		l-allo-threonine aldolase	7.98	15.59	2.40	0.0000
AAEL012932		hypothetical protein	12.74	24.85	2.40	0.0000
AAEL002971		sarcalumenin	160.01	310.47	2.39	0.0000
AAEL015076		hypothetical protein	158.87	307.95	2.39	0.0000
AAEL004423		mitochondrial F0 ATP synthase D chain	877.78	1,740.34	2.39	0.0000
AAEL014903		40S ribosomal protein S24	317.70	615.95	2.39	0.0000
AAEL017451			10.23	19.95	2.39	0.0000
AAEL009859		nucleolar GTP-binding protein	194.39	376.48	2.39	0.0000
AAEL010823		ATP synthase delta chain	1,288.81	2,552.55	2.38	0.0000
AAEL006859		Myb-interacting protein	20.80	40.60	2.38	0.0000
AAEL010787		DEAD box ATP-dependent RNA helicase	314.17	607.81	2.38	0.0000
AAEL010280		hypothetical protein	1.22	2.40	2.38	0.0000
AAEL000766		ubiquinol cytochrome C oxidoreductase	2,564.50	5,023.67	2.38	0.0000
AAEL004301		hypothetical protein	1.08	2.37	2.38	0.0358
AAEL010591	GSTD6	glutathione-s-transferase theta, gst	2.18	4.41	2.38	0.0013
AAEL000988		hypothetical protein	4.26	8.26	2.37	0.0000
AAEL013221		60S ribosomal protein L10a	1,417.29	2,726.69	2.37	0.0000
AAEL012233		hypothetical protein	5.28	10.21	2.37	0.0000
AAEL001759		40S ribosomal protein S9	953.80	1,832.29	2.37	0.0000
AAEL008471		hypothetical protein	1.52	2.96	2.36	0.0000
AAEL012518		hypothetical protein	24.27	46.64	2.36	0.0000
AAEL010793		f-box/leucine rich repeat protein	11.33	21.75	2.36	0.0000
AAEL003661		translation initiation factor	27.98	53.57	2.36	0.0000
AAEL005890		hypothetical protein	23.07	44.29	2.36	0.0000
AAEL003293		GTP-binding protein	9.15	17.52	2.35	0.0000
AAEL001113		inorganic phosphate cotransporter	199.72	381.18	2.35	0.0000
AAEL008103		40S ribosomal protein S8	1,004.71	1,919.06	2.35	0.0000
AAEL003118		hypothetical protein	107.76	205.28	2.35	0.0000
AAEL010743		cysteine desulfurylase	74.67	142.57	2.35	0.0000
AAEL007495		phosphoglycerate mutase	79.87	152.95	2.34	0.0000
AAEL007674		hypothetical protein	1.95	3.82	2.34	0.0001
AAEL011194		hypothetical protein	2.01	3.97	2.34	0.0006
AAEL002504		ATP synthase delta chain, mitochondrial	915.04	1,909.00	2.34	0.0189

Table A14 Continued

Gene ID	Gene Name	Wiki Description	Males	Females	Fold	*p* adj.
AAEL006027		lipase	12.31	23.40	2.34	0.0000
AAEL006610		hypothetical protein	5.07	9.65	2.34	0.0000
AAEL003628	CLIPB38	clip-domain serine protease	1.65	3.25	2.34	0.0003
AAEL009513		adenylate cyclase	5.61	10.69	2.34	0.0000
AAEL008953		hypothetical protein	346.30	657.87	2.34	0.0000
AAEL003625	CLIPB8	clip-domain serine protease	46.76	88.85	2.34	0.0000
AAEL002160		GTP-binding protein	67.01	127.30	2.34	0.0000
AAEL008366		pyruvate dehydrogenase	7.13	13.57	2.34	0.0000
AAEL006704		fibrinogen and fibronectin	2,827.36	5,379.73	2.34	0.0000
AAEL013356		hypothetical protein	19.44	36.79	2.33	0.0000
AAEL000978		hypothetical protein	5.05	9.63	2.33	0.0000
AAEL010002		mitochondrial import inner membrane translocase	24.58	46.96	2.33	0.0000
AAEL013097		60S ribosomal protein L23	103.58	196.71	2.33	0.0000
AAEL001232		tubulointerstitial nephritis antigen	49.10	92.96	2.33	0.0000
AAEL004120		Niemann-Pick Type C-2	30.17	57.79	2.33	0.0000
AAEL012825		bifunctional purine biosynthesis protein	12.29	23.21	2.33	0.0000
AAEL004932		tyrosine-protein kinase	1.49	2.85	2.32	0.0000
AAEL002482		hypothetical protein	0.73	1.49	2.32	0.0151
AAEL010031		hypothetical protein	0.98	1.94	2.32	0.0025
AAEL003339		hypothetical protein	1.01	2.01	2.32	0.0031
AAEL002555		sodium/solute symporter	16.25	31.43	2.32	0.0001
AAEL009726		clip-domain serine protease	5.87	11.32	2.32	0.0001
AAEL003234		cytochrome c oxidase, subunit VIA	2,369.33	4,513.78	2.32	0.0000
AAEL002856		hypothetical protein	33.80	63.53	2.32	0.0000
AAEL013033		serine protease	17.88	34.36	2.32	0.0000
AAEL008124		RNA metheytransferase	2.85	5.45	2.32	0.0000
AAEL017195			210.55	395.53	2.32	0.0000
AAEL013134		DNA-directed RNA polymerase I largest subunit	2.76	5.21	2.31	0.0000
AAEL017421			21.07	39.49	2.31	0.0000
AAEL010621		hypothetical protein	1.00	1.97	2.31	0.0042
AAEL003039		nonsense-mediated mrna decay protein	66.66	124.59	2.30	0.0000
AAEL014630		cytochrome C1 heme lyase	130.54	246.67	2.30	0.0000
AAEL005451		hypothetical protein	1,468.73	2,733.66	2.29	0.0000
AAEL005629		ribosomal protein L35	1,090.21	2,025.78	2.29	0.0000
AAEL004060		hypothetical protein	1,117.05	2,114.05	2.29	0.0000
AAEL010975		paramyosin, long form	205.07	383.50	2.29	0.0000
AAEL004081		dj-1 protein (park7)	86.74	162.27	2.29	0.0000
AAEL009246		glycoside hydrolases	1.67	3.14	2.28	0.0000
AAEL011113		hypothetical protein	52.73	97.97	2.28	0.0000
AAEL012430		AMP dependent ligase	0.95	1.85	2.28	0.0035
AAEL001566		bone morphogenetic protein	1.43	2.69	2.28	0.0000
AAEL004728		5-methyltetrahydrofolate: methyltransferase	4.18	7.97	2.28	0.0002
AAEL005220		60S ribosomal protein L30	2.14	4.14	2.28	0.0029
AAEL018265		hypothetical protein	0.76	1.46	2.27	0.0023
AAEL014889		NADH:ubiquinone dehydrogenase	150.78	302.95	2.27	0.0219
AAEL012128		cationic amino acid transporter	27.42	50.50	2.27	0.0000
AAEL006719		alpha-amylase	330.58	611.28	2.27	0.0000
AAEL009363		ordml, arthropod	1.78	3.45	2.27	0.0045
AAEL012944		60S ribosomal protein L11	1,074.90	1,975.51	2.27	0.0000

Table A14 Continued

Gene ID	Gene Name	Wiki Description	Males	Females	Fold	*p* adj.
AAEL006582		Ca-transporting atpase sarcoplasmic	1,170.33	2,145.85	2.26	0.0000
AAEL013425		hypothetical protein	4.51	8.48	2.26	0.0001
AAEL008848		ATP synthase gamma subunit	1,197.39	2,387.16	2.26	0.0216
AAEL004941	CYP6AK1	cytochrome P450	5.93	10.96	2.26	0.0000
AAEL012377	OBP55	Odorant-binding protein 56a	1.01	2.06	2.25	0.0418
AAEL012100		hypothetical protein	5.93	10.92	2.25	0.0000
AAEL001887		glutamine synthetase 1, 2	34.20	62.65	2.25	0.0000
AAEL007158		nnp-1 protein (novel nuclear protein 1) (nop52)	5.89	10.79	2.25	0.0000
AAEL006511		anopheles stephensi ubiquitin	1,095.55	1,999.38	2.25	0.0000
AAEL003803		hypothetical protein	3.47	6.60	2.25	0.0023
AAEL000753		hypothetical protein	37.64	69.17	2.24	0.0000
AAEL003835		initiation factor 5a	236.20	430.33	2.24	0.0000
AAEL007784		hypothetical protein	4.91	9.11	2.24	0.0001
AAEL011746		succinyl-coa synthetase beta chain	372.39	688.97	2.24	0.0000
AAEL014067		hypothetical protein	0.98	1.96	2.24	0.0327
AAEL008002		mitochondrial NADH:ubiquin. oxidoreductase	479.75	884.22	2.24	0.0000
AAEL017325	CLIPB36		21.29	39.85	2.24	0.0005
AAEL000182		hypothetical protein	738.35	1,343.88	2.23	0.0000
AAEL000823		ribosomal protein L35A	1,361.15	2,465.96	2.23	0.0000
AAEL003530		acidic ribosomal protein P1	22.53	40.84	2.23	0.0000
AAEL003722		ribonuclease UK114	3.44	6.42	2.23	0.0009
AAEL005129		40S ribosomal protein S30	179.04	323.29	2.23	0.0000
AAEL014865		pyruvate dehydrogenase	0.95	1.79	2.22	0.0018
AAEL009912		hypothetical protein	6.19	11.24	2.22	0.0000
AAEL007839		beta-hexosaminidase	1.46	2.70	2.22	0.0001
AAEL001134		methylmalonate-semialdehyde dehydrogenase	57.44	103.57	2.22	0.0000
AAEL001281		hypothetical protein	505.66	911.79	2.22	0.0000
AAEL017513			42.66	76.91	2.22	0.0000
AAEL017007			874.86	1,573.49	2.22	0.0000
AAEL005085		60S ribosomal protein L30	209.85	378.33	2.22	0.0000
AAEL007868		ubiquinol-cytochrome c reductase complex	1,108.47	2,031.06	2.22	0.0000
AAEL014909		hypothetical protein	1.23	2.38	2.22	0.0181
AAEL004613		phenylalanyl-tRNA synthetase beta chain	22.10	39.75	2.22	0.0000
AAEL006239		glycerol kinase	18.18	33.14	2.22	0.0000
AAEL011696		hypothetical protein	1.35	2.51	2.22	0.0013
AAEL011597		hypothetical protein	5.67	10.37	2.22	0.0000
AAEL005307		aminoacyl-tRNA synthetase auxiliary protein,	25.10	45.20	2.21	0.0000
AAEL017177			2.14	3.92	2.21	0.0000
AAEL014838		ribosomal protein L27	56.38	101.37	2.21	0.0000
AAEL010756		40S ribosomal protein S19	585.92	1,052.34	2.21	0.0000
AAEL003949		hypothetical protein	3.80	6.86	2.21	0.0000
AAEL005269		ubiquinol-cytochrome c reductase complex core	630.03	1,233.64	2.21	0.0321
AAEL010359		ATP-dependent transporter	73.00	131.04	2.21	0.0000
AAEL007235		mitochondrial uncoupling protein	88.00	157.70	2.21	0.0000
AAEL000878		cuticle protein	0.82	1.63	2.21	0.0446
AAEL000227	SCRB8	epithelial membrane protein	13.88	25.05	2.20	0.0000

Table A14 Continued

Gene ID	Gene Name	Wiki Description	Males	Females	Fold	*p* adj.
AAEL008502		hypothetical protein	7.65	13.73	2.20	0.0000
AAEL005027		acidic ribosomal protein P1	189.90	338.63	2.20	0.0000
AAEL006147		brain chitinase and chia	1.21	2.28	2.20	0.0071
AAEL005336		d-3-phosphoglycerate dehydrogenase	14.80	26.54	2.20	0.0000
AAEL012864		hypothetical protein	1.92	3.52	2.20	0.0009
AAEL002534		60S ribosomal protein L10	2,143.15	3,819.21	2.19	0.0000
AAEL017075			103.48	183.71	2.19	0.0000
AAEL013484		hypothetical protein	48.62	86.47	2.19	0.0000
AAEL010988		cationic amino acid transporter	0.75	1.42	2.19	0.0148
AAEL002157		hypothetical protein	16.14	28.73	2.19	0.0000
AAEL007555		acyl-coa dehydrogenase	23.75	42.18	2.19	0.0000
AAEL001673		actin	149.55	266.32	2.19	0.0000
AAEL001847		hypothetical protein	27.42	48.65	2.19	0.0000
AAEL004022		carboxylesterase	3.55	6.39	2.19	0.0000
AAEL015006		60S ribosomal protein L23	129.49	229.50	2.18	0.0000
AAEL012260		wd-repeat protein	3.32	5.93	2.18	0.0000
AAEL008213		mitochondrial carrier protein	4.84	8.64	2.18	0.0000
AAEL004328		origin recognition complex subunit	1.07	1.95	2.17	0.0024
AAEL004151		hypothetical protein	755.94	1,331.27	2.17	0.0000
AAEL011070	CTLGA3	hypothetical protein	66.23	117.07	2.17	0.0000
AAEL003469		NHP2 protein	11.93	21.14	2.17	0.0000
AAEL009825		60S ribosomal protein L13a	481.38	849.45	2.17	0.0000
AAEL000279		N-formylmethionylaminoacyl-tRNA deformyl.	9.26	16.46	2.17	0.0000
AAEL006668		hypothetical protein	5.38	9.54	2.17	0.0000
AAEL007354		pseudouridylate synthase	6.79	12.06	2.17	0.0000
AAEL012235		hypothetical protein	17.97	31.55	2.16	0.0000
AAEL000311		hypothetical protein	20.50	36.35	2.16	0.0000
AAEL007352		hypothetical protein	1.17	2.23	2.16	0.0347
AAEL010801		hypothetical protein	1,058.82	1,875.10	2.16	0.0000
AAEL003018		hypothetical protein	39.20	68.41	2.15	0.0000
AAEL014629		hypothetical protein	36.95	66.05	2.15	0.0004
AAEL010754		hypothetical protein	955.47	1,697.02	2.15	0.0002
AAEL007408		hypothetical protein	147.13	255.54	2.14	0.0000
AAEL002825		NADH:ubiquinone dehydrogenase	171.44	302.58	2.14	0.0000
AAEL012131		cationic amino acid transporter	1.33	2.34	2.14	0.0000
AAEL007054		NADH dehydrogenase	111.98	196.84	2.14	0.0000
AAEL010485		sugar transporter	4.56	7.98	2.14	0.0000
AAEL005901		40S ribosomal protein S3a	386.96	670.24	2.14	0.0000
AAEL008882		hypothetical protein	7.26	12.60	2.14	0.0000
AAEL008932	Kir1	inwardly rectifying k+ channel	14.31	24.95	2.14	0.0000
AAEL011762		hypothetical protein	5.76	10.05	2.14	0.0000
AAEL001349			3.65	6.41	2.14	0.0000
AAEL014080		aldehyde dehydrogenase	5.50	9.56	2.13	0.0000
AAEL011824		gamma glutamyl transpeptidases	3.83	6.70	2.13	0.0000
AAEL013885		hypothetical protein	106.84	185.50	2.13	0.0000
AAEL004220		hypothetical protein	57.98	100.33	2.13	0.0000
AAEL007967		hypothetical protein	6.53	11.39	2.13	0.0000
AAEL017059			13.83	24.17	2.13	0.0000
AAEL011309		orotidine-5'-phosphate decarboxylase	23.18	40.30	2.13	0.0000
AAEL002993		39S ribosomal protein L43	78.02	136.43	2.13	0.0000

Table A14 Continued

Gene ID	Gene Name	Wiki Description	Males	Females	Fold	*p* adj.
AAEL005538		mitochondrial NADH:ubiquin. oxidoreductase	58.90	103.56	2.13	0.0000
AAEL012534		hypothetical protein	9.02	16.55	2.13	0.0166
AAEL011447		60S ribosomal protein L14	1,438.48	2,485.31	2.13	0.0000
AAEL000138		NADH dehydrogenase	327.73	571.49	2.13	0.0000
AAEL011055		chaperone protein dnaj	31.66	55.29	2.13	0.0000
AAEL008329		60S ribosomal protein L24	1,285.56	2,220.33	2.13	0.0000
AAEL004947		elongase	1.16	2.09	2.13	0.0040
AAEL014110		sulfite reductase	0.73	1.29	2.12	0.0021
AAEL002632		proacrosin	0.98	1.71	2.12	0.0001
AAEL003037		hypothetical protein	1.62	2.84	2.12	0.0001
AAEL010977		ATP-dependent transporter	394.66	677.89	2.12	0.0000
AAEL003630		hypothetical protein	42.24	72.51	2.12	0.0000
AAEL005567		nucleosome assembly protein	50.47	86.89	2.12	0.0000
AAEL010970		hypothetical protein	4.08	7.12	2.12	0.0001
AAEL018343		myosin light chain kinase	61.18	106.59	2.12	0.0000
AAEL008572		RNA-binding protein	3.28	5.70	2.12	0.0000
AAEL001316		hypothetical protein	14.58	25.05	2.11	0.0000
AAEL003654		hypothetical protein	4.55	7.85	2.11	0.0000
AAEL007270		hypothetical protein	1.38	2.37	2.11	0.0000
AAEL011157		NADH dehydrogenase	270.42	465.84	2.11	0.0000
AAEL005722		60S ribosomal protein L7a	1,613.86	2,759.58	2.11	0.0000
AAEL008389		ankyrin repeat-rich membrane-spanning protein	27.43	46.82	2.11	0.0000
AAEL009985		hypothetical protein	249.85	426.58	2.11	0.0000
AAEL012408		mitochondrial ribosomal protein, L53	32.60	56.42	2.11	0.0000
AAEL011289		hypothetical protein	6.59	11.26	2.11	0.0000
AAEL001261		hypothetical protein	17.22	29.63	2.11	0.0000
AAEL009080		importin 7	28.70	49.17	2.11	0.0000
AAEL010219		sugar transporter	9.19	15.70	2.11	0.0000
AAEL013223		hypothetical protein	3.47	6.21	2.11	0.0113
AAEL010763		hypothetical protein	6.49	11.42	2.11	0.0018
AAEL017010			4.87	8.32	2.10	0.0000
AAEL000952		hypothetical protein	3.41	5.86	2.10	0.0000
AAEL002813		coupling factor	1,141.75	1,983.57	2.10	0.0002
AAEL000068			664.03	1,130.48	2.10	0.0000
AAEL014039		hypothetical protein	1,094.24	1,893.67	2.10	0.0001
AAEL008852		hypothetical protein	9.51	16.22	2.10	0.0000
AAEL004445		DEAD box ATP-dependent RNA helicase	29.95	50.93	2.10	0.0000
AAEL002517		nucleoprotein	0.69	1.24	2.10	0.0299
AAEL010574		hypothetical protein	385.00	658.46	2.10	0.0000
AAEL011465		hypothetical protein	1.12	1.96	2.09	0.0019
AAEL010596		n-acetylgalactosaminyltransferase	9.20	15.62	2.09	0.0000
AAEL004284		mitochondrial ATPase inhibitor	33.29	56.49	2.09	0.0000
AAEL008192		40S ribosomal protein S3	784.50	1,328.19	2.09	0.0000
AAEL003755		BolA protein	20.79	35.35	2.09	0.0000
AAEL005498		hypothetical protein	2.34	4.20	2.09	0.0194
AAEL001479		protoheme ix farnesyltransferase	119.12	202.71	2.09	0.0000
AAEL014922		hypothetical protein	91.85	156.50	2.09	0.0000
AAEL013717		sphingomyelin phosphodiesterase	11.59	19.71	2.08	0.0000
AAEL014092		hypothetical protein	12.97	22.23	2.08	0.0001
AAEL010366		glucosyl/glucuronosyl transferases	64.00	107.69	2.08	0.0000

Table A14 Continued

Gene ID	Gene Name	Wiki Description	Males	Females	Fold	*p* adj.
AAEL005327		hypothetical protein	0.99	1.72	2.07	0.0018
AAEL005579		developmentally regulated GTP-binding protein 1	10.43	17.56	2.07	0.0000
AAEL010204		dihydropyrimidine dehydrogenase	4.05	6.92	2.07	0.0001
AAEL017303			1.99	3.53	2.07	0.0265
AAEL003942		60S ribosomal protein L44 L41	1,122.26	1,882.99	2.07	0.0000
AAEL003829		dynamin	55.59	93.40	2.07	0.0000
AAEL012736		ribosomal protein L15	464.77	781.70	2.07	0.0000
AAEL001488		ribosomal protein L15	373.95	627.88	2.07	0.0000
AAEL010230		NADH:ubiquinone dehydrogenase	418.29	713.21	2.07	0.0001
AAEL003423		NADH dehydrogenase	483.72	814.88	2.07	0.0000
AAEL011177		hypothetical protein	3.30	5.62	2.07	0.0001
AAEL011960		hypothetical protein	6.04	10.14	2.07	0.0000
AAEL011508		hypothetical protein	0.77	1.36	2.06	0.0121
AAEL014709		methionine-tRNA synthetase	1.92	3.25	2.06	0.0000
AAEL012731		adenylate kinase 1	30.75	51.25	2.06	0.0000
AAEL012585		60S ribosomal protein L7	1,181.20	1,970.63	2.06	0.0000
AAEL000037	CLIPB35	serine protease	20.01	34.25	2.06	0.0016
AAEL009662		hypothetical protein	2.66	4.44	2.06	0.0000
AAEL006164		hypothetical protein	81.93	138.50	2.06	0.0001
AAEL002176		inosine-uridine preferring nucleoside hydrolase	2.41	4.11	2.05	0.0007
AAEL011114		serine/threonine-protein kinase rio2 (rio kinase 2)	6.81	11.46	2.05	0.0000
AAEL009257		hypothetical protein	1,464.02	2,454.88	2.05	0.0000
AAEL006256		ATPase subunit	254.00	453.18	2.05	0.0419
AAEL013007		cytochrome c oxidase, subunit VB	41.70	69.62	2.05	0.0000
AAEL003604		hypothetical protein	0.95	1.60	2.05	0.0002
AAEL008887		cytochrome c oxidase,-subunit VIb	1,997.82	3,367.99	2.05	0.0001
AAEL010960		xaa-pro dipeptidase app(e.coli)	2.21	3.73	2.05	0.0002
AAEL000794		eukaryotic translation initiation factor 3 subunit	28.17	47.22	2.04	0.0000
AAEL010174		hypothetical protein	132.62	219.39	2.04	0.0000
AAEL011967		DNA photolyase	15.49	25.64	2.04	0.0000
AAEL000581		hypothetical protein	8.09	13.48	2.04	0.0000
AAEL000316		hypothetical protein	7.39	12.42	2.04	0.0002
AAEL012686		ribosomal protein S12	1,604.93	2,654.41	2.04	0.0000
AAEL008220		hypothetical protein	8.37	13.90	2.04	0.0000
AAEL005275		hypothetical protein	2.26	3.88	2.04	0.0117
AAEL005422		pyrroline-5-carboxylate dehydrogenase	127.62	212.66	2.04	0.0000
AAEL000936		hypothetical protein	7.11	11.85	2.04	0.0000
AAEL004188		hypothetical protein	43.61	72.95	2.04	0.0001
AAEL012185		ribosome biogenesis regulatory protein	8.09	13.40	2.04	0.0000
AAEL011627		ribose-5-phosphate isomerase	10.30	17.09	2.03	0.0000
AAEL000431		hypothetical protein	278.44	458.75	2.03	0.0000
AAEL006887		mrna turnover protein 4 mrt4	7.85	13.05	2.03	0.0000
AAEL013641		hypothetical protein	12.98	21.54	2.03	0.0000
AAEL004951		hypothetical protein	4.67	7.71	2.03	0.0000
AAEL003365		fumarylacetoacetate hydrolase	7.50	12.45	2.03	0.0000
AAEL001328		hypothetical protein	5.90	9.91	2.03	0.0005
AAEL014894		hypothetical protein	1.74	2.97	2.03	0.0102
AAEL008365		hypothetical protein	18.97	31.31	2.03	0.0000

Table A14 Continued

Gene ID	Gene Name	Wiki Description	Males	Females	Fold	*p* adj.
AAEL003691		hypothetical protein	0.80	1.36	2.03	0.0075
AAEL003019		hypothetical protein	19.30	31.75	2.03	0.0000
AAEL015275		hypothetical protein	1.39	2.33	2.02	0.0013
AAEL014797		acyl-coa dehydrogenase	3.66	6.05	2.02	0.0000
AAEL003396		60S ribosomal protein L32	1,361.13	2,229.70	2.02	0.0000
AAEL005236		hypothetical protein	342.02	560.04	2.02	0.0000
AAEL008450		hypothetical protein	4.05	6.80	2.02	0.0015
AAEL005753		serine protease	12.57	20.63	2.02	0.0000
AAEL015635		mitochondrial ribosomal protein, S10	3.40	5.70	2.02	0.0017
AAEL007597	CLIPC3	serine protease	18.59	30.53	2.02	0.0000
AAEL013224		hypothetical protein	3.95	6.82	2.01	0.0285
AAEL011852		hypothetical protein	5.58	9.29	2.01	0.0010
AAEL013555	CYP4J13	cytochrome P450	37.23	60.80	2.01	0.0000
AAEL014663		AMP dependent coa ligase	2.16	3.60	2.01	0.0027
AAEL005143		ubiquinone binding protein	395.64	655.09	2.01	0.0003
AAEL006721		2-oxoglutarate dehydrogenase	575.08	945.23	2.01	0.0000
AAEL017437			28.86	47.01	2.01	0.0000
AAEL017106			0.74	1.24	2.00	0.0089
AAEL002520		apolipoprotein D	2.38	4.02	2.00	0.0112
AAEL017064			37.16	60.27	2.00	0.0000
AAEL017516			1,186.72	1,928.43	2.00	0.0000
AAEL002797		hypothetical protein	212.62	348.82	2.00	0.0000
AAEL009647		hypothetical protein	7.01	11.44	2.00	0.0000
AAEL018115		hypothetical protein	11.70	19.01	2.00	0.0000
AAEL006836		dihydropteridine reductase	30.44	49.53	2.00	0.0000
AAEL008481		60S ribosomal protein L18	1,122.98	1,820.68	2.00	0.0000
AAEL014715		67 kDa polymerase-associated factor PAF67	13.53	22.08	2.00	0.0000
		Enriched in Males				
AAEL009451		actin	34.34	0.30	-77.46	0.0000
AAEL015658		hypothetical protein	2.89	0.00	-27.07	0.0000
AAEL013043		NADH dehydrogenase	11.25	0.06	-26.78	0.0000
AAEL015657		hypothetical protein	2.84	0.00	-22.60	0.0000
AAEL008567		serine-type enodpeptidase	6.41	0.13	-21.76	0.0000
AAEL008304		hypothetical protein	21.02	0.51	-18.98	0.0000
AAEL015659		hypothetical protein	9.52	0.37	-18.51	0.0000
AAEL000307		dynein heavy chain	1.27	0.06	-13.80	0.0000
AAEL010934		hypothetical protein	7.25	0.40	-12.94	0.0000
AAEL012829		hypothetical protein	7.05	0.38	-12.30	0.0000
AAEL012423		hypothetical protein	772.12	50.75	-11.91	0.0000
AAEL010941		hypothetical protein	3.86	0.21	-11.90	0.0000
AAEL002200		fatty acid synthase	3.83	0.20	-11.48	0.0000
AAEL006824		cytochrome P450	14.15	0.90	-11.21	0.0000
AAEL004341	CCEAE1O	alpha-esterase	3.63	0.22	-11.10	0.0000
AAEL008855		dynein heavy chain	12.04	0.89	-10.56	0.0000
AAEL014617	CYP9J28	cytochrome P450	36.12	2.64	-10.47	0.0000
AAEL009881		dynein heavy chain	68.67	5.23	-10.40	0.0000
AAEL013542		elongase	5.95	0.37	-10.33	0.0000
AAEL017220			1.62	0.09	-8.67	0.0000
AAEL003568			19.16	1.72	-8.57	0.0000
AAEL007072		hypothetical protein	2.23	0.15	-8.47	0.0000
AAEL003079		glucosyl/glucuronosyl transferases	38.03	3.41	-8.38	0.0000
AAEL014613	CYP9J24	cytochrome P450	1.78	0.12	-8.23	0.0000

Table A14 Continued

Gene ID	Gene Name	Wiki Description	Males	Females	Fold	*p* adj.
AAEL003888		ubiquitin	4,536.18	85.08	-8.15	0.0001
AAEL013322		hypothetical protein	7.30	0.69	-8.13	0.0000
AAEL006570		hypothetical protein	7.14	0.61	-7.93	0.0000
AAEL002227		fatty acid synthase	1.45	0.13	-7.80	0.0000
AAEL004466	LRIM23	hypothetical protein	6.27	0.56	-7.71	0.0000
AAEL010772		hypothetical protein	5.80	0.56	-7.68	0.0000
AAEL008754		hypothetical protein	3.24	0.25	-7.47	0.0000
AAEL009193		glucose dehydrogenase	1.34	0.05	-7.44	0.0001
AAEL002228		fatty acid synthase	8.90	0.66	-7.38	0.0000
AAEL011423		sugar transporter	2.03	0.21	-6.94	0.0000
AAEL001054	GSTD4	glutathione-s-transferase theta, gst	25.67	2.87	-6.84	0.0000
AAEL001951		actin	2,871.30	79.60	-6.60	0.0006
AAEL001747		hypothetical protein	1.88	0.16	-6.41	0.0000
AAEL004292		hypothetical protein	56.17	0.44	-6.37	0.0010
AAEL001737		hypothetical protein	2.52	0.22	-6.31	0.0000
AAEL000150		nitrilase	1.74	0.14	-6.31	0.0000
AAEL012420		pumilio	5.56	0.63	-6.23	0.0000
AAEL012441		hypothetical protein	4.58	0.55	-6.19	0.0000
AAEL008600		zinc carboxypeptidase	4.50	0.55	-6.03	0.0000
AAEL009889		hypothetical protein	2.52	0.30	-5.87	0.0000
AAEL004326		hypothetical protein	5.32	0.65	-5.85	0.0000
AAEL011126		alcohol dehydrogenase	19.85	2.70	-5.81	0.0000
AAEL002192		M12 mutant protein precursor	7.48	0.99	-5.75	0.0000
AAEL008036		dynein heavy chain	1.10	0.14	-5.62	0.0000
AAEL015583		molybdopterin synthase small subunit	1.51	0.00	-5.59	0.0023
AAEL010893		carbonic anhydrase	19.00	2.57	-5.52	0.0000
AAEL000021		hypothetical protein	1.79	0.21	-5.50	0.0000
AAEL008609		zinc carboxypeptidase	7.03	0.97	-5.43	0.0000
AAEL000627	CECA	antibacterial peptide	11.33	0.81	-5.41	0.0008
AAEL005625	GPROP5	rhodopsin	2.48	0.23	-5.40	0.0002
AAEL007543		hypothetical protein	5.20	0.61	-5.39	0.0000
AAEL010657		hypothetical protein	2.16	0.15	-5.36	0.0008
AAEL012416		hypothetical protein	1.91	0.22	-5.34	0.0000
AAEL010792		hypothetical protein	3.04	0.32	-5.30	0.0001
AAEL018349		antibacterial peptide	3.89	0.41	-5.25	0.0001
AAEL001552		hypothetical protein	1.62	0.21	-5.17	0.0000
AAEL008160		fatty acid synthase	5.45	0.62	-5.16	0.0000
AAEL005043		ATP-dependent bile acid permease	19.15	2.96	-5.14	0.0000
AAEL008345	CYP4G35	cytochrome P450	11.01	1.54	-5.13	0.0000
AAEL004446		hypothetical protein	5.85	0.85	-5.13	0.0000
AAEL017987			10.20	0.76	-5.01	0.0022
AAEL001130		alpha-amylase	1.11	0.13	-5.00	0.0001
AAEL004231		M12 mutant protein precursor	1.10	0.14	-4.99	0.0000
AAEL007283		acetyl-coa synthetase	4.57	0.69	-4.95	0.0000
AAEL009577		hypothetical protein	10.29	0.08	-4.88	0.0057
AAEL000678		alpha-amylase	8.98	1.43	-4.84	0.0000
AAEL009124	CYP6N12	cytochrome P450	30.84	5.11	-4.76	0.0000
AAEL008599		zinc carboxypeptidase	7.33	1.17	-4.75	0.0000
AAEL010157		microsomal glutathione s-transferase	58.75	9.85	-4.68	0.0000
AAEL014427		hypothetical protein	2.00	0.20	-4.59	0.0020
AAEL002549		hypothetical protein	32.72	5.64	-4.53	0.0000
AAEL007272		hypothetical protein	1.46	0.16	-4.48	0.0016

Table A14 Continued

Gene ID	Gene Name	Wiki Description	Males	Females	Fold	*p* adj.
AAEL011166		cadherin	1.05	0.15	-4.48	0.0000
AAEL011130		alcohol dehydrogenase	4.56	0.75	-4.47	0.0000
AAEL007057		retinoid-inducible serine carboxypeptidase	11.95	2.04	-4.44	0.0000
AAEL005091		hypothetical protein	2.70	0.43	-4.43	0.0000
AAEL007669		oxidoreductase	67.85	12.16	-4.42	0.0000
AAEL013770		zinc finger protein	2.31	0.40	-4.39	0.0000
AAEL006876		igf2 mRNA binding protein	1.65	0.28	-4.30	0.0000
AAEL015592		structural maintenance of chromosomes smc1	2.45	0.41	-4.29	0.0000
AAEL003424		zinc carboxypeptidase	8.68	1.56	-4.29	0.0000
AAEL003049		pupal cuticle protein 78E	6.95	0.30	-4.27	0.0126
AAEL017292			2.92	0.28	-4.24	0.0063
AAEL003741		hypothetical protein	1.50	0.24	-4.22	0.0000
AAEL012462		hypothetical protein	2.89	0.53	-4.21	0.0000
AAEL008745		hypothetical protein	4.31	0.79	-4.13	0.0000
AAEL002022		protein serine/threonine kinase	29.70	5.55	-4.13	0.0000
AAEL008617		hypothetical protein	1.12	0.19	-4.12	0.0000
AAEL002596	OBP9	Odorant-binding protein 56e	2.71	0.39	-4.11	0.0009
AAEL006137	SRPN19	hypothetical protein	1.12	0.17	-4.10	0.0004
AAEL002467		hypothetical protein	24.14	1.33	-4.05	0.0165
AAEL003098		glucosyl/glucuronosyl transferases	2.38	0.42	-4.03	0.0000
AAEL006738		breast cancer anti-estrogen resistance 1	1.82	0.32	-4.02	0.0000
AAEL000886		hypothetical protein	1,159.83	230.60	-3.96	0.0000
AAEL010462		vesamicol binding protein	5.68	1.07	-3.89	0.0000
AAEL014231		hypothetical protein	14.74	2.97	-3.88	0.0000
AAEL010369		phospholipase b, plb1	2.01	0.34	-3.87	0.0002
AAEL004044		hypothetical protein	2.17	0.43	-3.85	0.0000
AAEL001386		hypothetical protein	1.23	0.14	-3.85	0.0109
AAEL012491	CYP6P12	cytochrome P450	1.13	0.19	-3.82	0.0005
AAEL011183		hypothetical protein	30.93	6.34	-3.81	0.0000
AAEL011644		hypothetical protein	1.10	0.16	-3.81	0.0048
AAEL005437		transient receptor potential channel	26.95	5.59	-3.79	0.0000
AAEL004366		hypothetical protein	8.49	1.73	-3.79	0.0000
AAEL004255		zinc finger protein	2.51	0.50	-3.79	0.0000
AAEL017320			99.67	21.21	-3.75	0.0000
AAEL009127	CYP6M11	cytochrome P450	36.00	7.63	-3.75	0.0000
AAEL002305		hypothetical protein	3.95	0.80	-3.74	0.0000
AAEL011311		hypothetical protein	1.29	0.25	-3.72	0.0000
AAEL005643		guanine nucleotide exchange factor	1.70	0.35	-3.70	0.0000
AAEL009258		hypothetical protein	7.96	1.71	-3.69	0.0000
AAEL000259	CUSOD4	superoxide dismutase	85.65	5.83	-3.68	0.0277
AAEL005720		hypothetical protein	5.66	1.21	-3.66	0.0000
AAEL009072		ribonucleoprotein	9.53	1.95	-3.66	0.0000
AAEL003619		sodium/shloride dependent aa transporter	76.17	16.55	-3.60	0.0000
AAEL005369		zinc finger protein	13.78	2.97	-3.60	0.0000
AAEL011654		cationic amino acid transporter	1.90	0.39	-3.60	0.0000
AAEL001677		hypothetical protein	6.96	1.19	-3.59	0.0032
AAEL008746		hypothetical protein	3.47	0.32	-3.59	0.0279
AAEL006425		trypsin	110.05	24.11	-3.57	0.0000
AAEL001193		regulator of g protein signaling	5.90	1.19	-3.57	0.0000
AAEL004669		hypothetical protein	2.61	0.55	-3.57	0.0000

Table A14 Continued

Gene ID	Gene Name	Wiki Description	Males	Females	Fold	*p* adj.
AAEL009951		dimeric dihydrodiol dehydrogenase	74.76	16.17	-3.57	0.0000
AAEL007266		hypothetical protein	6.32	1.28	-3.57	0.0000
AAEL002294			1.19	0.25	-3.56	0.0000
AAEL010201		axonemal dynein intermediate chain	1.98	0.40	-3.56	0.0000
AAEL007265		hypothetical protein	13.13	2.72	-3.56	0.0000
AAEL003641		sodium/shloride dependent aa transporter	14.62	3.25	-3.55	0.0000
AAEL002919		hypothetical protein	5.24	1.08	-3.54	0.0000
AAEL009327		hypothetical protein	2.01	0.14	-3.52	0.0336
AAEL013487		RHO guanyl-nucleotide exchange factor	2.18	0.48	-3.52	0.0000
AAEL003099		glucosyl/glucuronosyl transferases	33.40	7.51	-3.51	0.0000
AAEL002317		insulin receptor	1.43	0.31	-3.50	0.0000
AAEL010381		glucosyl/glucuronosyl transferases	4.95	1.09	-3.49	0.0000
AAEL002640		discoidin domain receptor	1.80	0.38	-3.49	0.0000
AAEL000121		dihydropyridine-sensitive l-type calcium channel	2.43	0.53	-3.48	0.0000
AAEL005378		set domain protein	3.48	0.78	-3.45	0.0000
AAEL015457		hypothetical protein	2.69	0.47	-3.44	0.0049
AAEL004812		kinesin-like protein KIF1A	15.62	3.09	-3.43	0.0007
AAEL017302			225.11	52.25	-3.42	0.0000
AAEL006586		serine protease	22.36	5.06	-3.42	0.0000
AAEL009596		sterol o-acyltransferase	9.75	2.19	-3.41	0.0000
AAEL003674		hypothetical protein	202.81	15.72	-3.39	0.0418
AAEL008412		mitochondrial import inner memb. translocase	12.78	2.96	-3.39	0.0000
AAEL002425		ADP ribosylation factor	3.68	0.76	-3.39	0.0004
AAEL005960		hypothetical protein	2.30	0.43	-3.38	0.0037
AAEL006446		trehalose-6-phosphate synthase	209.11	49.11	-3.38	0.0000
AAEL011768		hypothetical protein	2.09	0.43	-3.38	0.0003
AAEL008014		ef hand protein	2.98	0.60	-3.37	0.0011
AAEL010757		hypothetical protein	1.26	0.29	-3.37	0.0000
AAEL001219		hypothetical protein	1.24	0.27	-3.37	0.0000
AAEL003211		beta-carotene dioxygenase	93.54	22.28	-3.35	0.0000
AAEL009418		hypothetical protein	1.73	0.31	-3.35	0.0077
AAEL008452		alpha-amylase	51.08	12.12	-3.33	0.0000
AAEL001034			1.34	0.28	-3.30	0.0010
AAEL000863		SPASIC protein	4.45	1.03	-3.30	0.0000
AAEL007200		amino acid transporter	2.10	0.47	-3.29	0.0000
AAEL006128		hypothetical protein	2.11	0.48	-3.27	0.0000
AAEL005357		hypothetical protein	5.05	0.58	-3.26	0.0435
AAEL000810		protein kinase c	5.39	1.20	-3.26	0.0001
AAEL018298		hypothetical protein	2.57	0.61	-3.26	0.0000
AAEL010606		down syndrome cell adhesion molecule	1.47	0.35	-3.25	0.0000
AAEL000621	CECN	antibacterial peptide	59.51	6.72	-3.24	0.0462
AAEL014893	CYP6BB2	cytochrome P450	535.37	131.87	-3.23	0.0000
AAEL012212		hypothetical protein	3.04	0.72	-3.22	0.0000
AAEL003041		hypothetical protein	4.08	0.90	-3.21	0.0005
AAEL003609		neurobeachin	3.71	0.89	-3.21	0.0000
AAEL013602		laminin gamma-3 chain	1.60	0.38	-3.20	0.0000
AAEL005621	GPROP4	rhodopsin	1.88	0.37	-3.20	0.0093
AAEL005089		hypothetical protein	2.42	0.55	-3.19	0.0002

Table A14 Continued

Gene ID	Gene Name	Wiki Description	Males	Females	Fold	*p* adj.
AAEL018324		regulating synaptic membrane exocytosis protein	2.16	0.52	-3.18	0.0000
AAEL006199		neurexin	3.75	0.93	-3.18	0.0000
AAEL004222		voltage-dependent p/q type calcium channel	7.76	1.94	-3.16	0.0000
AAEL008749		UDP-glucuronosyltransferase	2.04	0.47	-3.16	0.0001
AAEL002710		hypothetical protein	1.52	0.25	-3.15	0.0270
AAEL012840		stathmin	4.62	1.11	-3.14	0.0000
AAEL003014		hypothetical protein	2.55	0.62	-3.13	0.0000
AAEL001293		hypothetical protein	30.06	7.62	-3.12	0.0000
AAEL010292		hypothetical protein	6.98	1.74	-3.12	0.0000
AAEL007830	CYP4H29	cytochrome P450	23.70	6.02	-3.11	0.0000
AAEL009620		hypothetical protein	2.69	0.63	-3.10	0.0003
AAEL006019		voltage-gated sodium channel	1.53	0.38	-3.10	0.0000
AAEL011065		hypothetical protein	2.60	0.64	-3.10	0.0000
AAEL004681		hypothetical protein	3.17	0.73	-3.10	0.0008
AAEL013556	CYP4J15	cytochrome P450	1.14	0.25	-3.09	0.0035
AAEL002457		hypothetical protein	65.50	16.80	-3.09	0.0000
AAEL014235		calmodulin	1.18	0.26	-3.09	0.0022
AAEL011068		hypothetical protein	3.78	0.74	-3.08	0.0173
AAEL005284		receptor tyrosine phosphatase type r2a	6.83	1.76	-3.07	0.0000
AAEL012483		hypothetical protein	2.75	0.67	-3.07	0.0000
AAEL001384		triple functional domain, trio	3.33	0.84	-3.07	0.0000
AAEL005661		defective proboscis extension response	1.42	0.31	-3.06	0.0055
AAEL006327		sulfotransferase (sult)	7.80	1.98	-3.06	0.0000
AAEL004357		neuroligin	1.05	0.21	-3.06	0.0172
AAEL018241		hypothetical protein	1.69	0.43	-3.04	0.0000
AAEL015294		serine-type enodpeptidase	215.28	55.61	-3.04	0.0000
AAEL008354		gaba receptor invertebrate	17.04	4.37	-3.03	0.0000
AAEL013262		hypothetical protein	35.16	7.25	-3.01	0.0164
AAEL018317		hypothetical protein	1.33	0.34	-3.01	0.0000
AAEL008246		phospholipase c epsilon	8.51	2.20	-3.00	0.0000
AAEL005332		hypothetical protein	249.08	66.28	-3.00	0.0000
AAEL002786		hypothetical protein	1.01	0.26	-3.00	0.0000
AAEL000437		hypothetical protein	3.68	0.82	-2.99	0.0078
AAEL002732		nephrin	1.47	0.32	-2.98	0.0108
AAEL010106		norepinephrine/norepinephrine transporter	2.46	0.61	-2.98	0.0003
AAEL014005		clip-domain serine protease	8.77	2.28	-2.94	0.0000
AAEL002075		hypothetical protein	1.85	0.46	-2.94	0.0007
AAEL011310		axonemal dynein intermediate chain polypeptide	6.65	1.78	-2.93	0.0000
AAEL006995		sodium/solute symporter	1.26	0.31	-2.92	0.0008
AAEL005770	OBP21	Odorant-binding protein 99c	21.87	5.89	-2.92	0.0000
AAEL008055		nicotinic acetylcholine receptor subunit	4.23	1.14	-2.91	0.0000
AAEL004834			1.72	0.46	-2.90	0.0000
AAEL010386		glucosyl/glucuronosyl transferases	19.28	5.26	-2.90	0.0000
AAEL009619		voltage-gated potassium channel	2.48	0.66	-2.90	0.0000
AAEL013546		estrogen-related receptor (ERR)	3.87	1.04	-2.87	0.0000
AAEL005483		hypothetical protein	1.03	0.20	-2.85	0.0460
AAEL015598		hypothetical protein	2.87	0.74	-2.85	0.0005

Table A14 Continued

Gene ID	Gene Name	Wiki Description	Males	Females	Fold	*p* adj.
AAEL013529		synapsin	2.08	0.51	-2.85	0.0059
AAEL006451		hypothetical protein	72.34	20.19	-2.84	0.0000
AAEL017986			3.41	0.93	-2.84	0.0000
AAEL006191		hypothetical protein	3.72	1.02	-2.83	0.0000
AAEL009130	CYP6Z7		47.24	13.19	-2.83	0.0000
AAEL000174		retinal protein	2.47	0.63	-2.82	0.0022
AAEL018226		hypothetical protein	29.30	8.31	-2.81	0.0000
AAEL018039		tyrosine-phosphorylation-regulated kinase	15.07	4.16	-2.81	0.0000
AAEL008885		hypothetical protein	2.58	0.72	-2.81	0.0000
AAEL005686		hypothetical protein	1.49	0.36	-2.81	0.0102
AAEL010064		hypothetical protein	1.41	0.37	-2.80	0.0004
AAEL009873		hypothetical protein	1.57	0.39	-2.80	0.0057
AAEL004880		hypothetical protein	6.76	1.86	-2.79	0.0000
AAEL006651		dystrophin	5.71	1.60	-2.79	0.0000
AAEL012337			7.67	2.18	-2.78	0.0000
AAEL012492	CYP6AA5	cytochrome P450	7.22	1.94	-2.78	0.0002
AAEL012519		actin binding protein	1.43	0.39	-2.77	0.0004
AAEL003114		hypothetical protein	27.70	7.93	-2.77	0.0000
AAEL004258		hypothetical protein	3.63	1.01	-2.76	0.0000
AAEL003102		glucosyl/glucuronosyl transferases	2.17	0.59	-2.76	0.0003
AAEL014609	CYP9J26	cytochrome P450	388.28	112.70	-2.76	0.0000
AAEL011800		hypothetical protein	2.39	0.63	-2.75	0.0025
AAEL008789		apolipophorin-III	384.19	110.89	-2.75	0.0000
AAEL009965		hypothetical protein	1.38	0.33	-2.74	0.0220
AAEL003723	LYSC11	lysozyme P	59.23	16.71	-2.73	0.0000
AAEL015644		hypothetical protein	1.40	0.37	-2.73	0.0017
AAEL005599		defective proboscis extension response	1.65	0.40	-2.73	0.0197
AAEL017168			2.25	0.60	-2.73	0.0030
AAEL001531		hypothetical protein	4.88	1.21	-2.72	0.0164
AAEL006555		hypothetical protein	13.21	3.85	-2.71	0.0000
AAEL010682		armc4	2.45	0.70	-2.71	0.0000
AAEL008432		high-affinity choline transporter	6.41	1.83	-2.70	0.0000
AAEL008006		3-hydroxyacyl-coa dehyrogenase	206.51	62.14	-2.66	0.0000
AAEL001807	CYP9M9	cytochrome P450	2.58	0.74	-2.66	0.0001
AAEL000671	TOLL6	toll	3.36	0.99	-2.64	0.0000
AAEL001722		hypothetical protein	15.22	4.58	-2.64	0.0000
AAEL009948		aldehyde dehydrogenase	15.52	4.69	-2.63	0.0000
AAEL005188		acetylgalactosaminidase	2.36	0.63	-2.63	0.0128
AAEL000828		vitellogenin	4.74	1.37	-2.62	0.0001
AAEL011426		hypothetical protein	11.38	3.31	-2.62	0.0001
AAEL014278		hypothetical protein	15.69	4.69	-2.62	0.0000
AAEL015560		integrin alpha-ps	2.41	0.72	-2.62	0.0000
AAEL010780		carboxypeptidase	1.08	0.29	-2.61	0.0150
AAEL017069			1.14	0.28	-2.61	0.0412
AAEL005293	GALE8A	galectin	11.74	3.43	-2.60	0.0001
AAEL005128		hypothetical protein	1.19	0.32	-2.60	0.0140
AAEL018223		t-box transcription factor tbx2	1.79	0.54	-2.59	0.0000
AAEL004585		hypothetical protein	2,487.47	764.06	-2.58	0.0000
AAEL005130		zinc finger protein	1.83	0.53	-2.58	0.0021
AAEL005463		calbindin-32	17.98	5.53	-2.57	0.0000
AAEL006888			1.23	0.36	-2.57	0.0013
AAEL009775			2.59	0.79	-2.57	0.0000

Table A14 Continued

Gene ID	Gene Name	Wiki Description	Males	Females	Fold	*p* adj.
AAEL005026		ATP-dependent bile acid permease	1.26	0.38	-2.56	0.0000
AAEL000498		defective proboscis extension response	1.36	0.36	-2.56	0.0246
AAEL001307		SEC14	6.74	2.04	-2.55	0.0000
AAEL000381		syntrophin	3.41	0.99	-2.55	0.0027
AAEL018227		hypothetical protein	2.89	0.88	-2.55	0.0000
AAEL018232		hypothetical protein	3.09	0.95	-2.54	0.0000
AAEL002876		hypothetical protein	6.48	2.02	-2.54	0.0000
AAEL000371		hypothetical protein	2.23	0.61	-2.54	0.0193
AAEL005434		hypothetical protein	27.44	8.44	-2.54	0.0000
AAEL012463		hypothetical protein	7.27	2.22	-2.53	0.0000
AAEL009999		hypothetical protein	3.59	1.04	-2.53	0.0040
AAEL013505	GPRNPY7		2.37	0.70	-2.53	0.0016
AAEL001527		hypothetical protein	4.56	1.34	-2.52	0.0045
AAEL007557		asparagine synthetase	5.51	1.71	-2.52	0.0000
AAEL014343		hypothetical protein	4.22	1.27	-2.51	0.0011
AAEL008750		hypothetical protein	19.44	6.12	-2.51	0.0000
AAEL006800		sodium/chloride dependent transporter	2.91	0.91	-2.51	0.0000
AAEL014522		hypothetical protein	9.80	3.08	-2.50	0.0000
AAEL000604		hypothetical protein	5.23	1.63	-2.50	0.0000
AAEL007817		hypothetical protein	1.63	0.51	-2.50	0.0000
AAEL001108		protein kinase c	3.28	1.02	-2.49	0.0001
AAEL000405		odd Oz protein	10.71	3.43	-2.49	0.0000
AAEL013110		hypothetical protein	1.05	0.31	-2.48	0.0099
AAEL011900		acetylglucosaminyltransferase	1.58	0.44	-2.48	0.0330
AAEL006700		Trypsin	1.89	0.56	-2.48	0.0061
AAEL005752		lysosomal alpha-mannosidase	4.99	1.60	-2.46	0.0000
AAEL003615		nervy	1.92	0.58	-2.46	0.0053
AAEL018326		sodium/nucleoside cotransporter	5.24	1.69	-2.46	0.0000
AAEL017452			2.02	0.58	-2.45	0.0240
AAEL008226		hypothetical protein	1.02	0.32	-2.45	0.0005
AAEL007344		hypothetical protein	21.99	6.86	-2.45	0.0004
AAEL018236		crossveinless	1.03	0.33	-2.45	0.0001
AAEL014616	CYP9J27	cytochrome P450	23.79	7.76	-2.44	0.0000
AAEL014307		oligophrenin	2.08	0.65	-2.44	0.0003
AAEL004181			1.10	0.35	-2.44	0.0000
AAEL015093		triacylglycerol lipase, pancreatic	3.33	1.01	-2.44	0.0036
AAEL010265		hypothetical protein	7.61	2.45	-2.44	0.0000
AAEL009836		hypothetical protein	35.83	11.61	-2.44	0.0000
AAEL010950		hypothetical protein	58.39	19.19	-2.42	0.0000
AAEL010684		hypothetical protein	17.33	5.70	-2.42	0.0000
AAEL000723		hypothetical protein	1.19	0.38	-2.42	0.0006
AAEL009131	CYP6Z8	cytochrome P450	264.84	87.36	-2.42	0.0000
AAEL013174		hypothetical protein	1.71	0.54	-2.42	0.0019
AAEL013274		n-acetylgalactosaminyltransferase	1.23	0.39	-2.41	0.0017
AAEL005045		ATP-dependent bile acid permease	2.84	0.93	-2.40	0.0000
AAEL013077		hypothetical protein	17.27	5.64	-2.40	0.0000
AAEL007976		hypothetical protein	1.89	0.61	-2.40	0.0000
AAEL017479	GPRMGL1		4.35	1.36	-2.40	0.0040
AAEL002724		munc13-4	3.95	1.30	-2.40	0.0000
AAEL004281		short-chain dehydrogenase	1.34	0.40	-2.40	0.0171
AAEL002230			12.22	4.02	-2.39	0.0000
AAEL000747		hypothetical protein	3.49	1.12	-2.39	0.0009

Table A14 Continued

Gene ID	Gene Name	Wiki Description	Males	Females	Fold	*p* adj.
AAEL012457		alcohol dehydrogenase	31.26	10.43	-2.39	0.0000
AAEL008194		protein phosphatase 2a, regulatory subunit	1.97	0.60	-2.38	0.0209
AAEL014553		triacylglycerol lipase, pancreatic	11.03	3.57	-2.38	0.0002
AAEL018102			622.33	209.21	-2.38	0.0000
AAEL008424		sodium/shloride dependent aa transporter	2.26	0.72	-2.38	0.0015
AAEL013079		hypothetical protein	8.12	2.71	-2.38	0.0000
AAEL012850			10.24	3.38	-2.38	0.0000
AAEL011955		hypothetical protein	2.05	0.66	-2.37	0.0007
AAEL000566		hypothetical protein	5.23	1.68	-2.37	0.0011
AAEL002637		tripartite motif protein trim9	1.53	0.45	-2.37	0.0413
AAEL009684		hypothetical protein	7.84	2.46	-2.37	0.0096
AAEL014864		hypothetical protein	5.39	1.79	-2.36	0.0000
AAEL007046		mitochondrial brown fat uncoupling protein	4.86	1.62	-2.35	0.0000
AAEL005529		hypothetical protein	6.15	2.09	-2.35	0.0000
AAEL014972		hypothetical protein	1.49	0.47	-2.35	0.0072
AAEL003592		neurobeachin	2.04	0.69	-2.34	0.0000
AAEL006305		hypothetical protein	37.47	12.65	-2.34	0.0000
AAEL002943			1.32	0.44	-2.34	0.0002
AAEL007905		hypothetical protein	39.22	13.36	-2.33	0.0000
AAEL002868		myosin	3.75	1.26	-2.33	0.0000
AAEL017393			2.31	0.76	-2.33	0.0007
AAEL006288		hypothetical protein	8.66	2.90	-2.32	0.0001
AAEL000402		hypothetical protein	1.58	0.50	-2.32	0.0140
AAEL010082		hypothetical protein	3.23	1.09	-2.32	0.0001
AAEL001862		hypothetical protein	2.43	0.78	-2.31	0.0157
AAEL013596		phosphatidylinositol 3-kinase regulatory subunit	2.59	0.85	-2.31	0.0037
AAEL014607		cytochrome P450	67.42	23.40	-2.31	0.0000
AAEL005604		trypsin-epsilon	12.94	4.42	-2.31	0.0000
AAEL007791		hypothetical protein	1.61	0.53	-2.30	0.0100
AAEL002492		hypothetical protein	5.75	1.87	-2.30	0.0081
AAEL009755		hypothetical protein	2.81	0.94	-2.29	0.0014
AAEL009870		hypothetical protein	1.28	0.41	-2.29	0.0228
AAEL005560		sidestep protein	4.94	1.71	-2.28	0.0000
AAEL007002		calsenilin	4.61	1.55	-2.28	0.0016
AAEL009508		zinc finger protein	1.60	0.54	-2.27	0.0030
AAEL003391		tankyrase	3.77	1.28	-2.27	0.0011
AAEL003259		pupal cuticle protein 78E	73.47	25.95	-2.24	0.0000
AAEL015305		sulfotransferase (sult)	8.95	3.08	-2.24	0.0007
AAEL002642		tripartite motif protein trim9	2.57	0.83	-2.24	0.0382
AAEL007071		hypothetical protein	3.11	1.10	-2.24	0.0000
AAEL012186			1.40	0.47	-2.24	0.0076
AAEL006911		microtubule-associated protein	8.60	3.00	-2.24	0.0003
AAEL004273		short-chain dehydrogenase	15.09	5.37	-2.23	0.0000
AAEL017280			7.98	2.83	-2.23	0.0000
AAEL003026		regulator of g protein signaling	13.46	4.79	-2.22	0.0000
AAEL004854		hypothetical protein	5.75	2.02	-2.22	0.0007
AAEL009773		geminin	1.61	0.54	-2.22	0.0152
AAEL014285		growth hormone inducible	406.42	146.95	-2.21	0.0000
AAEL004054	CYP4G36	cytochrome P450	126.23	45.50	-2.21	0.0000
AAEL000578		hypothetical protein	1.59	0.55	-2.21	0.0052

Table A14 Continued

Gene ID	Gene Name	Wiki Description	Males	Females	Fold	*p* adj.
AAEL004067		mitochondrial benzodiazepine receptor	82.75	30.05	-2.20	0.0000
AAEL009269		hypothetical protein	5.48	1.98	-2.20	0.0000
AAEL002754		nephrin	2.88	1.03	-2.19	0.0002
AAEL000712		hypothetical protein	4.90	1.75	-2.17	0.0009
AAEL007213		delta(9)-desaturase	17.88	6.34	-2.17	0.0026
AAEL002576		sodium/solute symporter	6.07	2.21	-2.17	0.0000
AAEL017269			1.62	0.54	-2.17	0.0458
AAEL009847		microtubule-associated protein	15.22	5.60	-2.16	0.0000
AAEL015631		asparagine synthetase	5.25	1.91	-2.16	0.0000
AAEL008430		hypothetical protein	34.20	12.56	-2.16	0.0000
AAEL018329		potassium-dependent sodium-calcium exchanger	2.99	1.09	-2.15	0.0000
AAEL014718		shoc2	1.71	0.61	-2.15	0.0077
AAEL001734		bric-a-brac	3.72	1.34	-2.15	0.0024
AAEL000165		hypothetical protein	102.20	37.65	-2.15	0.0000
AAEL005808		alanyl aminopeptidase	3.59	1.32	-2.15	0.0000
AAEL004391			11.33	4.16	-2.15	0.0000
AAEL006783			4.22	1.55	-2.15	0.0000
AAEL012089		hypothetical protein	201.50	74.98	-2.14	0.0000
AAEL012057			3.22	1.19	-2.14	0.0000
AAEL004651		multiple ankyrin repeats single kh domain protein	6.30	2.28	-2.13	0.0047
AAEL006203		Juvenile hormone-inducible protein	3.73	1.36	-2.13	0.0024
AAEL005439		mical	2.79	1.02	-2.13	0.0017
AAEL017011			3.54	1.31	-2.13	0.0000
AAEL015432		Trypsin	1.90	0.66	-2.13	0.0401
AAEL001299		hypothetical protein	8.71	3.26	-2.13	0.0000
AAEL007384		activin receptor type ii	2.69	0.99	-2.13	0.0008
AAEL003197		hypothetical protein	20.01	7.27	-2.13	0.0042
AAEL018187		hypothetical protein	3.98	1.49	-2.12	0.0000
AAEL001582		kinesin	1.73	0.64	-2.12	0.0001
AAEL013350		heat shock protein 26kD	2.62	0.91	-2.12	0.0475
AAEL000520			10.01	3.77	-2.12	0.0000
AAEL011129		alcohol dehydrogenase	71.55	26.97	-2.11	0.0000
AAEL009760		Niemann-Pick Type C-2	1,071.28	405.31	-2.11	0.0000
AAEL006032		hypothetical protein	10.78	4.04	-2.11	0.0000
AAEL010034		hypothetical protein	13.63	4.83	-2.11	0.0352
AAEL010039		hypothetical protein	2.26	0.81	-2.10	0.0181
AAEL004597		hypothetical protein	1,411.84	534.76	-2.10	0.0000
AAEL012764		hypothetical protein	42.64	16.19	-2.10	0.0000
AAEL015296		septin	7.39	2.78	-2.10	0.0000
AAEL011641		transferrin	52.16	19.81	-2.10	0.0000
AAEL011392		hypothetical protein	10.74	4.08	-2.09	0.0000
AAEL005282		hypothetical protein	18.76	7.13	-2.09	0.0000
AAEL013305		bifunctional dihydrofolate reductase	13.55	5.16	-2.08	0.0000
AAEL002883		hypothetical protein	6.77	2.60	-2.08	0.0000
AAEL002234			2.45	0.94	-2.08	0.0000
AAEL017299			2.47	0.92	-2.07	0.0042
AAEL014370		hypothetical protein	3.82	1.42	-2.07	0.0073
AAEL013987		hypothetical protein	225.84	87.38	-2.07	0.0000
AAEL002711			2.63	1.00	-2.07	0.0004
AAEL010347		hypothetical protein	3.65	1.37	-2.07	0.0029

Table A14 Continued

Gene ID	Gene Name	Wiki Description	Males	Females	Fold	*p* adj.
AAEL002578		hypothetical protein	113.85	43.84	-2.07	0.0000
AAEL010933		hypothetical protein	6.07	2.32	-2.06	0.0001
AAEL008488		cysteine-rich secretory protein-2	2.18	0.82	-2.06	0.0038
AAEL011474		hypothetical protein	9.91	3.83	-2.06	0.0000
AAEL007132		dynein heavy chain	13.58	5.26	-2.05	0.0000
AAEL008532		carboxylesterase	4.59	1.74	-2.05	0.0016
AAEL007360		lethal(3)malignant brain tumor	4.42	1.71	-2.05	0.0000
AAEL009189		encore protein	4.22	1.63	-2.05	0.0001
AAEL005207		neprilysin	3.12	1.20	-2.05	0.0002
AAEL005511		hypothetical protein	5.02	1.95	-2.05	0.0000
AAEL006522		turtle protein, isoform	13.69	5.33	-2.04	0.0000
AAEL001643		hypothetical protein	1.82	0.67	-2.04	0.0276
AAEL015072		carboxylesterase	2.32	0.87	-2.04	0.0145
AAEL003603		transcription factor	6.63	2.55	-2.04	0.0005
AAEL012727		kek1	1.58	0.60	-2.04	0.0046
AAEL000948		hypothetical protein	70.37	27.55	-2.03	0.0000
AAEL011950		hypothetical protein	2.58	0.99	-2.03	0.0049
AAEL013939		erk1/2	5.03	1.95	-2.02	0.0007
AAEL018342		armadillo repeat protein	1.56	0.61	-2.02	0.0003
AAEL017445			1.76	0.66	-2.02	0.0163
AAEL006259	GPROP2	rhodopsin	81,600.97	32,309.19	-2.02	0.0000
AAEL008498		cohesin-subunit	1.48	0.56	-2.02	0.0086
AAEL014856		DNA mismatch repair protein spellchecker 1	1.29	0.48	-2.02	0.0373
AAEL001731		tyrosine-phosphorylation-regulated kinase	1.52	0.59	-2.02	0.0046
AAEL009858		hypothetical protein	72.32	28.74	-2.02	0.0000
AAEL011947		hypothetical protein	5.62	2.22	-2.02	0.0000
AAEL009024	GPRCAL3		10.18	4.01	-2.01	0.0000
AAEL004363		hypothetical protein	9.77	3.79	-2.01	0.0026
AAEL012494	CYP6BZ1	cytochrome P450	3.19	1.24	-2.01	0.0016
AAEL008630		GTP-binding protein alpha subunit, gna	1.34	0.52	-2.01	0.0100
AAEL017366			14.80	5.85	-2.01	0.0000
AAEL008413		serine/threonine protein kinase	5.42	2.15	-2.00	0.0000
AAEL010382		aldehyde oxidase	196.03	78.55	-2.00	0.0000
AAEL005318		hypothetical protein	3.55	1.40	-2.00	0.0001

Table A15 Genes enriched in the antenna of host seeking females. A multi-factor generalized model was used to take into consideration the effect of sex, age and preference.

Gene ID	Name	Length (bp)	Male	Female	Fold	HT	Antenna	Fold	Nectar	Host	Fold
AAEL006176	OBP27	812	2,902.61	12,532.45	2.04	1.26	21,392.75	8,422.31	4,535.90	19,835.26	2.68
AAEL010242	Unknown1	619	31.17	265.87	2.39	146.68	255.54	2.19	37.54	510.28	9.19
AAEL011409	Or100	1,236	4.57	22.90	3.51	0.05	38.55	439.59	8.70	34.77	2.25
AAEL011583	Or11	2,421	5.37	17.37	2.22	0.00	30.54	2,179.83	6.49	28.30	2.27
AAEL013507	Or52	3,010	0.69	4.51	5.21	0.00	7.45	955.43	1.49	7.10	2.11
AAEL013893	Or125	2,237	1.68	4.80	2.14	0.00	8.57	1,992.00	1.84	7.90	2.39
AAEL014197	Or88	1,227	3.32	19.23	4.50	0.00	32.08	3,691.52	6.06	31.23	2.28
AAEL014811	Unknown2	940	0.40	1.26	2.22	0.50	1.62	2.04	0.51	1.99	2.51
AAEL016412	ncRNA	73	12.61	55.76	3.16	0.00	94.98	803.41	17.77	92.76	2.55
AAEL016981	Or36	1,257	0.30	3.45	3.97	0.01	5.55	160.90	0.66	6.18	3.32
AAEL017000	Or97	1,209	0.23	1.90	4.29	0.00	3.10	415.87	0.41	3.37	3.43
AAEL017009	Or119	1,218	0.59	1.68	2.17	0.00	3.00	467.88	0.65	2.76	2.35
AAEL017014	Or105	1,260	1.00	10.82	8.46	0.01	17.47	903.89	3.31	16.99	2.04
AAEL017043	Or84	1,251	13.45	112.54	6.28	0.03	183.75	3,213.66	31.46	185.30	2.27
AAEL017065	Or92	1,263	0.11	1.23	5.98	0.00	1.99	294.07	0.26	2.16	3.25
AAEL017129	Or72	1,257	1.01	5.10	3.92	0.00	8.58	670.92	1.73	8.14	2.16
AAEL017149	Or91	1,167	2.00	6.63	2.60	0.00	11.62	1,468.37	2.47	10.75	2.25
AAEL017201	Or94	1,242	0.95	7.69	6.02	0.01	12.56	685.02	2.20	12.57	2.39
AAEL017219	Or114	1,233	0.67	5.06	5.98	0.00	8.30	1,067.48	1.57	8.07	2.13
AAEL017296	Or93	1,242	0.24	1.13	2.83	0.00	1.91	282.09	0.32	1.94	2.69
AAEL017537	Or123	1,137	0.36	3.43	5.06	0.01	5.55	188.71	0.82	5.87	2.89
AAEL018095	New_OR	1,257	3.42	17.45	3.32	0.01	29.36	781.44	5.30	29.08	2.57

Table A16. Effect of CO2 exposure on nectar-seeking females.

Gene	Olfaction genes with low expression with CO_2 exposure			
	12hManual-RPKMs	12hCO_2-RPKMs	Fold-Change	*p* adjusted
IR75k.1	21.41	8.60	-2.48	0.0000
IR75k.3	15.01	6.63	-2.25	0.0000
IR75l	16.21	4.35	-3.56	0.0000
IR76b	110.10	52.95	-2.08	0.0000
IR87a.1	14.65	6.17	-2.35	0.0000
IR87a.2	14.80	6.94	-2.13	0.0000
IR8a	61.51	28.72	-2.16	0.0000
IRc	2.82	1.06	-2.41	0.0021
OBP18	9.12	1.27	-3.81	0.0012
OBP2	1036.03	485.05	-2.17	0.0000
OBP36	489.65	203.00	-2.43	0.0000
OBP37	1204.17	535.08	-2.27	0.0000
OBP47	1173.97	472.74	-2.48	0.0000
Or10	25.44	12.44	-2.04	0.0000
Or12	20.57	5.60	-3.48	0.0000
Or17	6.13	2.49	-2.31	0.0015
Or24	6.89	2.55	-2.50	0.0005
Or36	4.54	1.92	-2.17	0.0104
Or43	5.10	1.10	-3.48	0.0003
Or96	13.24	6.35	-2.04	0.0010
	Olfaction genes with high expression with CO_2 exposure			
Gr19	0.51	2.89	4.79	0.0000
Gr20	0.45	2.19	4.35	0.0000
Gr60	0.13	1.95	5.46	0.0000
IR107.2	3.82	8.11	2.01	0.0000
IR40a	0.78	2.72	2.97	0.0001
IR68a	0.77	2.01	2.23	0.0105
IR93a	2.74	12.16	4.14	0.0000
OBP11	163.86	372.12	2.20	0.0000
OBP24	0.69	13.78	5.86	0.0000
OBP25	1.47	22.05	7.73	0.0000
OBP9	5.06	11.63	2.06	0.0113

Table A17 Trimming statistics from CLC genomics workbench of sequencing reads from small RNA sequencing libraries. Samples from female antenna (Ant, except 12hAnt) were sequenced at the University of Utah sequencing facility. The remaining samples were sequenced at Texas A&M sequencing facility.

Sample	# reads	Avg. Length	# reads after trim	Trimmed (%)	Avg. length after trim
12hAnt1	23,801,744	50.0	23,247,643	97.67	25.3
12hAnt2	30,317,440	50.0	29,400,181	96.97	24.4
4dAnt1	21,076,234	49.2	20,083,672	95.29	32.2
4dAnt2	39,461,138	47.6	33,125,703	83.95	27.0
4dAnt3	36,947,235	47.9	33,770,225	91.40	25.0
+3hAnt1	20,067,235	49.2	19,061,412	94.99	31.1
+3hAnt2	32,601,075	47.7	25,609,118	78.55	26.9
+3hAnt3	34,449,115	47.8	30,057,069	87.25	25.5
+24hAnt1	18,354,573	49.3	15,852,338	86.37	26.4
+24hAnt2	28,285,850	47.7	17,962,387	63.50	23.6
+24hAnt3	29,717,714	47.8	26,836,850	90.31	25.8
+48hAnt1	19,008,811	49.3	17,072,224	89.81	27.9
+48hAnt2	29,020,520	47.8	19,517,518	67.25	26.4
+48hAnt3	29,136,333	47.9	25,420,520	87.25	25.3
+72hAnt1	16,548,609	49.3	15,018,537	90.75	26.9
+72hAnt2	37,669,651	47.7	30,631,333	81.32	26.6
+72hAnt3	33,446,826	47.9	30,082,281	89.94	25.8
4dMaleAnt1	23,539,306	67.0	23,343,625	99.17	27.6
4dMaleAnt2	10,792,001	67.0	10,730,885	99.43	28.7
4dHT1	14,144,991	50.0	14,026,714	99.16	26.0
4dHT2	9,339,546	50.0	9,248,760	99.03	27.2
+3hHT1	16,527,989	50.0	16,443,963	99.49	26.3
+3hHT2	13,380,727	50.0	13,323,822	99.57	26.4
+24hHT1	15,368,913	50.0	15,295,608	99.52	26.5
+24hHT2	15,649,651	50.0	15,533,760	99.26	26.6
+48hHT1	7,218,521	50.0	7,195,585	99.68	26.2
+48hHT2	15,389,253	50.0	15,288,591	99.35	25.8
+72hHT1	14,155,779	50.0	14,037,034	99.16	26.1
+72hHT2	19,706,595	50.0	19,445,504	98.68	25.8
4dMaleHT1	19,708,353	50.0	19,433,863	98.61	24.1
4dMaleHT2	31,321,664	50.0	30,814,352	98.38	23.4
Total	706,153,392	50.3	636,911,077	92.29	26.4

Table A18 Filtering statistics of small RNA reads trimming and filtering using CLC genomics workbench.

	Input reads	No trim	Trimmed	Discarded
12hAnt1				
Ambiguity trim	23,801,744	23,790,937	10,807	0
Adapter trimming	23,801,744	10,011	23,789,655	2,078
Filter on length	23,799,666	23,247,643	0	552,023
12hAnt2				
Ambiguity trim	30,317,440	30,303,319	14,121	0
Adapter trimming	30,317,440	17,283	30,297,055	3,102
Filter on length	30,314,338	29,400,181	0	914,157
4dAnt1				
Ambiguity trim	21,076,234	21,073,892	2,342	0
Adapter trimming	21,076,234	4,266,876	16,023,152	786,206
Filter on length	20,290,028	20,083,672	0	206,356
4dAnt2				
Ambiguity trim	39,461,138	39,443,719	17,419	0
Adapter trimming	39,461,138	4,197,532	34,263,503	1,000,103
Filter on length	38,461,035	33,125,703	0	5,335,332
4dAnt3				
Ambiguity trim	36,947,235	36,942,471	4,764	0
Adapter trimming	36,947,235	1,428,146	35,077,807	441,282
Filter on length	36,505,953	33,770,225	0	2,735,728
+3hAnt1				
Ambiguity trim	20,067,235	20,065,006	2,229	0
Adapter trimming	20,067,235	3,891,343	15,555,711	620,181
Filter on length	19,447,054	19,061,412	0	385,642
+3hAnt2				
Ambiguity trim	32,601,075	32,586,801	14,274	0
Adapter trimming	32,601,075	3,261,219	26,182,420	3,157,436
Filter on length	29,443,639	25,609,118	0	3,834,521
+3hAnt3				
Ambiguity trim	34,449,115	34,444,622	4,493	0
Adapter trimming	34,449,115	2,043,673	32,047,990	357,452
Filter on length	34,091,663	30,057,069	0	4,034,594
+24hAnt1				
Ambiguity trim	18,354,573	18,352,581	1,992	0
Adapter trimming	18,354,573	1,687,116	15,913,745	753,712
Filter on length	17,600,861	15,852,338	0	1,748,523
+24hAnt2				
Ambiguity trim	28,285,850	28,273,094	12,756	0
Adapter trimming	28,285,850	419,676	23,050,770	4,815,404

Table A18 Continued

	Input reads	No trim	Trimmed	Discarded
Filter on length	23,470,446	17,962,387	0	5,508,059
+24hAnt3				
Ambiguity trim	29,717,714	29,713,837	3,877	0
Adapter trimming	29,717,714	1,784,334	27,410,236	523,144
Filter on length	29,194,570	26,836,850	0	2,357,720
+48hAnt1				
Ambiguity trim	19,008,811	19,006,731	2,080	0
Adapter trimming	19,008,811	2,441,825	16,020,527	546,459
Filter on length	18,462,352	17,072,224	0	1,390,128
+48hAnt2				
Ambiguity trim	29,020,520	29,007,558	12,962	0
Adapter trimming	29,020,520	1,842,803	21,455,750	5,721,967
Filter on length	23,298,553	19,517,518	0	3,781,035
+48hAnt3				
Ambiguity trim	29,136,333	29,132,536	3,797	0
Adapter trimming	29,136,333	1,782,453	26,479,191	874,689
Filter on length	28,261,644	25,420,520	0	2,841,124
+72hAnt1				
Ambiguity trim	16,548,609	16,546,752	1,857	0
Adapter trimming	16,548,609	1,428,706	14,699,747	420,156
Filter on length	16,128,453	15,018,537	0	1,109,916
+72hAnt2				
Ambiguity trim	37,669,651	37,652,649	17,002	0
Adapter trimming	37,669,651	3,821,826	30,737,507	3,110,318
Filter on length	34,559,333	30,631,333	0	3,928,000
+72hAnt3				
Ambiguity trim	33,446,826	33,442,441	4,385	0
Adapter trimming	33,446,826	2,417,728	30,543,480	485,618
Filter on length	32,961,208	30,082,281	0	2,878,927
4dMaleAnt1				
Ambiguity trim	23,539,306	23,523,379	15,927	0
Adapter trimming	23,539,306	11,016	23,522,823	5,467
Filter on length	23,533,839	23,343,625	0	190,214
4dMaleAnt2				
Ambiguity trim	10792001	10784613	7388	0
Adapter trimming	10792001	6268	10783849	1884
Filter on length	10790117	10730885	0	59232
4dHT1				
Ambiguity trim	14144991	14133706	11285	0
Adapter trimming	14144991	4053	14139147	1791

Table A18 Continued

	Input reads	No trim	Trimmed	Discarded
Filter on length	14143200	14026714	0	116486
4dHT2				
Ambiguity trim	9,339,546	9,332,181	7,365	0
Adapter trimming	9,339,546	3,160	9,334,753	1,633
Filter on length	9,337,913	9,248,760	0	89,153
+3hHT1				
Ambiguity trim	16527989	16514892	13097	0
Adapter trimming	16527989	6107	16520256	1626
Filter on length	16526363	16443963	0	82400
+3hHT2				
Ambiguity trim	13,380,727	13,370,229	10,498	0
Adapter trimming	13,380,727	5,839	13,373,252	1,636
Filter on length	13,379,091	13,323,822	0	55,269
+24hHT1				
Ambiguity trim	15,368,913	15,356,717	12,196	0
Adapter trimming	15,368,913	7,327	15,359,984	1,602
Filter on length	15,367,311	15,295,608	0	71,703
+24hHT2				
Ambiguity trim	15,649,651	15,640,833	8,818	0
Adapter trimming	15,649,651	9,567	15,638,101	1,983
Filter on length	15,647,668	15,533,760	0	113,908
+48hHT1				
Ambiguity trim	7,218,521	7,214,391	4,130	0
Adapter trimming	7,218,521	2,295	7,215,520	706
Filter on length	7,217,815	7,195,585	0	22,230
+48hHT2				
Ambiguity trim	15,389,253	15,380,528	8,725	0
Adapter trimming	15,389,253	4,652	15,381,996	2,605
Filter on length	15,386,648	15,288,591	0	98,057
+72hHT1				
Ambiguity trim	14,155,779	14,147,836	7,943	0
Adapter trimming	14,155,779	7,815	14,146,522	1,442
Filter on length	14,154,337	14,037,034	0	117,303
+72hHT2				
Ambiguity trim	19,706,595	19,695,082	11,513	0
Adapter trimming	19,706,595	8,221	19,696,915	1,459
Filter on length	19,705,136	19,445,504	0	259,632
4dMaleHT1				
Ambiguity trim	19,708,353	19,699,285	9,068	0
Adapter trimming	19,708,353	10,471	19,696,511	1,371

Table A18 Continued

	Input reads	No trim	Trimmed	Discarded
Filter on length	19,706,982	19,433,863	0	273,119
4dMaleHT2				
Ambiguity trim	31,321,664	31,307,459	14,205	0
Adapter trimming	31,321,664	24,303	31,294,794	2,567
Filter on length	31,319,097	30,814,352	0	504,745

Table A19 Annotation statistics of small RNA reads from antennal and head plus thorax samples.

Samples	Unannotated (reads)	Unannotated (%)	Annotated	Perfect matches	Mature 5' total	Mature 5' exact matches	Mature 5' variants (bp)	Mature 5' variants(n)	Non-mature total	Mature 3'	Precursor
12hAnt1	21,385,332	92.0	1,862,311	1,710,813	869,300	296,902	495,939	76,459	993,011	751,987	241,024
12hAnt2	28,039,569	91.6	1,360,612	1,246,124	666,455	227,804	380,128	58,523	694,157	517,673	176,484
4dAnt1	18,043,745	89.8	2,039,927	1,892,710	1,126,440	444,374	607,302	74,764	913,487	658,206	255,281
4dAnt2	27,268,058	82.3	5,857,645	5,391,413	2,999,507	673,640	2,115,103	210,764	2,858,138	606,734	2,251,404
4dAnt3	24,179,554	71.6	9,590,671	8,889,931	4,593,329	765,746	3,531,354	296,229	4,997,342	1,444,947	3,552,395
+3hAnt1	16,637,818	87.3	2,423,594	2,262,249	1,292,905	523,179	687,515	82,211	1,130,689	777,991	352,698
+3hAnt2	21,473,969	83.9	4,135,149	3,819,949	2,062,717	285,431	1,646,556	130,730	2,072,432	326,799	1,745,633
+3hAnt3	21,667,163	72.1	8,389,906	7,739,364	4,364,937	1,007,855	3,066,489	290,593	4,024,969	1,023,292	3,001,677
+24hAnt1	13,949,615	88.0	1,902,723	1,777,008	944,811	366,748	515,670	62,393	957,912	633,274	324,638
+24hAnt2	14,117,789	78.6	3,844,598	3,538,850	1,906,162	311,772	1,465,386	129,004	1,938,436	352,570	1,585,866
+24hAnt3	18,638,265	69.5	8,198,585	7,328,783	4,558,047	719,787	3,453,000	385,260	3,640,538	694,689	2,945,849
+48hAnt1	15,032,789	88.1	2,039,435	1,900,053	1,217,768	474,119	666,313	77,336	821,667	529,711	291,956
+48hAnt2	17,757,938	91.0	1,759,580	1,628,094	802,724	102,150	647,212	53,362	956,856	204,815	752,041
+48hAnt3	17,384,534	68.4	8,035,986	7,415,656	4,458,553	1,106,126	3,065,300	287,127	3,577,433	837,370	2,740,063
+72hAnt1	12,989,754	86.5	2,028,783	1,885,187	1,297,449	502,034	711,566	83,849	731,334	480,121	251,213
+72hAnt2	22,984,898	75.0	7,646,435	7,006,035	3,910,469	475,450	3,160,829	274,190	3,735,966	613,641	3,122,325
+72hAnt3	19,720,870	65.6	10,361,411	9,578,654	5,620,136	1,349,638	3,917,680	352,818	4,741,275	1,131,571	3,609,704
4dMaleAnt1	22,157,333	94.9	1,186,292	1,073,259	397,600	200,055	168,497	29,048	788,692	610,487	178,205
4dMaleAnt2	10,287,244	95.9	443,641	396,217	140,281	69,036	60,158	11,087	303,360	232,919	70,441
4dHT1	12,369,167	88.2	1,657,547	1,460,937	399,563	197,982	167,060	34,521	1,257,984	1,039,805	218,179
4dHT2	8,580,728	92.8	668,032	592,531	167,383	83,754	69,719	13,910	500,649	420,262	80,387
+3hHT1	14,981,922	91.1	1,462,041	1,288,584	405,500	206,559	164,496	34,445	1,056,541	865,489	191,052
+3hHT2	12,184,609	91.4	1,139,213	1,001,345	321,328	163,230	129,613	28,485	817,885	652,324	165,561
+24hHT1	14,224,810	93.0	1,070,798	939,381	277,404	135,566	117,845	23,993	793,394	666,560	126,834
+24hHT2	14,606,778	94	926,982	816,238	260,751	128,726	110,163	21,862	666,231	552,199	114,032
+48hHT1	6,615,595	91.9	579,990	507,921	190,258	90,196	84,420	15,642	389,732	306,116	83,616
+48hHT2	14,131,595	92.4	1,156,996	1,025,584	380,011	190,050	159,409	30,552	776,985	622,632	154,353
+72hHT1	12,904,493	91.9	1,132,541	998,095	286,887	139,170	123,757	23,960	845,654	695,944	149,710
+72hHT2	18,156,234	93.4	1,289,270	1,145,298	391,474	187,914	171,650	31,910	897,796	704,940	192,856
4dMaleHT1	18,404,251	94.7	1,029,612	921,728	569,928	187,667	324,656	57,605	459,684	349,141	110,543
4dMaleHT2	28,660,964	93.0	2,153,388	1,934,017	1,378,726	446,325	796,272	136,129	774,662	564,857	209,805
Total	539,537,383	86.45	97,373,694	89,112,008	48,258,803	12,058,985	32,781,057	3,418,761	49,114,891	19,869,066	29,245,825

Table A20 miRs with differential expression in the antenna of females of *A. aegypti*.

miRs	12h old	4 days old	Fold	p adj. value
mir-2940-5p	593.46	8371.89	13.27	0.0000
mir-317*	7483.48	54070.75	6.87	0.0000
mir-7	33253.59	228538.12	6.73	0.0000
mir-34-5p	7840.96	48314.48	6.06	0.0000
mir-263a-5p	418842.88	1906368.37	4.11	0.0002
mir-252-5p	4861.53	18829.31	3.68	0.0000
mir-307	12.13	45.45	3.39	0.0111
mir-1889-5p	8483.16	29644.49	3.23	0.0029
mir-980-3p	6.93	20.78	2.66	0.0453
mir-929*	47.68	127.55	2.57	0.0034
mir-11-5p	4034.41	9814.47	2.35	0.0049
mir-33	26.72	61.16	2.23	0.0168
mir-281-5p	4463.5	9761.5	2.17	0.0000
mir-184	9956.48	21803.48	2.17	0.0000
mir-252-3p	21.6	48.74	2.13	0.0477
mir-2765	35.26	73.8	2.03	0.0448
mir-9b	1401.93	653.98	-2.08	0.0264
mir-92b-3p	4907.65	2317.97	-2.10	0.0002
mir-981	1650.22	763.7	-2.16	0.0000
mir-306-5p	16276.8	6380.28	-2.51	0.0000
mir-9c-3p	423	163.76	-2.55	0.0000
mir-306-3p	30.63	10.52	-2.60	0.0463
mir-305-3p	769.12	254.86	-2.93	0.0000
mir-275-3p	22770.04	6545.01	-3.43	0.0000
mir-9c-5p	11757.25	3214.76	-3.61	0.0000
mir-8-5p	4720.16	1262.15	-3.63	0.0000
mir-375	498.89	123.03	-3.81	0.0000
mir-193	925.32	232.87	-3.84	0.0000
mir-285	493.4	43.12	-8.51	0.0000

Table A21 miRs with differential expression in the *A. aegypti* male tissues.

miR	HT	Antenna	Fold	*p* adj. value
mir-1891*	332.28	16788.14	49.82	0.0000
mir-7	217.23	5406.89	24.40	0.0000
mir-263a-5p	32447.42	566065.03	16.97	0.0000
mir-263a-3p	215.03	3543.91	16.39	0.0000
mir-1890	103.06	1669.91	16.23	0.0000
mir-263b-5p	602.57	5532.77	9.15	0.0000
mir-263b-3p	1.55	15.96	7.41	0.0000
mir-1889-3p	38.95	270.29	6.93	0.0000
mir-12-5p	627.76	4149.74	6.60	0.0000
mir-996	242.87	1576.31	6.48	0.0000
mir-279	1217.49	7982.86	6.48	0.0000
mir-12-3p	53.63	306.29	5.71	0.0000
mir-193	8.09	48.80	5.63	0.0000
mir-1889-5p	418.72	1788.45	4.26	0.0000
mir-9a*	918.56	3325.86	3.60	0.0000
mir-87	911.50	3087.86	3.37	0.0000
mir-2940-3p	3983.20	12582.05	3.15	0.0000
mir-276-1	122.92	391.46	3.14	0.0000
mir-2945-3p	240.27	676.86	2.80	0.0000
mir-14	22954.05	59702.20	2.59	0.0000
mir-276*	32496.56	82192.56	2.52	0.0000
mir-92a-3p	97.33	231.03	2.36	0.0000
mir-2940-5p	670.86	1587.88	2.36	0.0000
bantam-3p	32902.22	7879.04	2.18	0.0000
mir-92b-3p	1863.17	3988.56	2.14	0.0000
mir-317*	7742.66	15786.32	2.04	0.0000
mir-281-5p	6729.72	3343.65	-2.01	0.0000
mir-137*	557.22	238.08	-2.34	0.0000
mir-277-3p	55561.02	21264.44	-2.61	0.0000
mir-285	30051.60	11093.11	-2.70	0.0000
mir-932-5p	665.91	218.26	-3.04	0.0000
mir-133	1743.77	552.40	-3.15	0.0000
mir-8-3p	93741.99	29347.95	-3.19	0.0000
mir-124	141.83	43.81	-3.19	0.0000
mir-957	13666.42	4167.56	-3.28	0.0000
mir-281-3p	385.23	113.83	-3.36	0.0000
mir-31	580.24	166.05	-3.45	0.0000
mir-8-5p	11845.16	3414.94	-3.46	0.0000
mir-315-5p	1967.21	555.34	-3.53	0.0000
mir-277-5p	58.74	15.22	-3.58	0.0000
mir-184	91626.75	25480.10	-3.59	0.0000
mir-1	6103.93	1473.85	-4.12	0.0000
mir-283	346.84	72.44	-4.68	0.0000
mir-993	59.54	6.27	-8.76	0.0000
mir-2944b-3p	29.22	1.68	-10.61	0.0000
mir-2944a-5p	51.11	0.36	-40.18	0.0000
mir-1175-3p	41.67	0.36	-44.18	0.0000
mir-1175-5p	123.98	2.26	-45.00	0.0000

Table A21 Continued

miR	HT	Antenna	Fold	*p* adj. value
mir-2946	286.20	0.58	-64.83	0.0000
mir-309a*	275.50	0.58	-72.60	0.0000
mir-375	3596.29	45.47	-76.09	0.0000
mir-989	106.07	0.36	-81.82	0.0000
mir-1174	426.82	3.57	-102.81	0.0000
mir-2941-1	1259.44	0.73	-161.95	0.0000
mir-2944b-5p	131.78	0.00	-164.73	0.0000
mir-286b*	5823.75	0.58	-315.84	0.0000

Table A22 miRs with differential expression in the *A. aegypti* female tissues.

miR	HT	Antenna	Fold change	*p* adj. value
mir-7	365.92	196,155.44	528.00	0.0000
mir-263b-3p	0.00	45.81	157.26	0.0001
mir-263a-5p	19,895.10	1,589,486.30	76.58	0.0000
mir-1889-5p	702.35	24,976.35	34.28	0.0000
mir-1891*	531.96	11,124.04	20.48	0.0000
mir-12-5p	1,279.76	24,732.63	19.19	0.0000
mir-263b-5p	536.14	10,191.91	17.65	0.0000
mir-193	12.67	200.45	15.97	0.0000
mir-1890	203.36	3,146.31	15.31	0.0000
mir-263a-3p	199.88	2,761.26	13.59	0.0000
mir-12-3p	88.34	716.51	8.06	0.0000
mir-2940-5p	943.06	7,104.02	7.51	0.0000
mir-1889-3p	72.13	530.29	7.31	0.0000
mir-996	472.49	3,374.60	7.11	0.0000
mir-317*	7,665.05	46,189.37	5.98	0.0000
mir-279	2,404.53	11,470.39	4.75	0.0000
mir-87	1,377.38	6,134.21	4.42	0.0000
mir-965	19.76	85.12	4.22	0.0007
mir-33	14.31	53.16	3.87	0.0011
mir-14	48,601.35	182,461.47	3.74	0.0000
mir-276-1	222.99	828.41	3.70	0.0000
mir-92a-3p	130.34	470.41	3.55	0.0000
mir-276*	65,460.25	211,029.81	3.22	0.0000
mir-9a*	2,143.44	6,203.57	2.89	0.0000
mir-929*	38.51	109.53	2.77	0.0028
mir-79-3p	17.02	44.30	2.67	0.0292
mir-1000*	404.28	957.47	2.35	0.0011
mir-34-5p	19,543.13	41,627.29	2.13	0.0000
mir-13-5p	63.55	126.88	2.02	0.0022
mir-306-5p	11,423.95	5,481.26	-2.08	0.0002
mir-9c-3p	294.79	139.62	-2.09	0.0001
mir-11-3p	41,877.82	19,583.45	-2.13	0.0002
mir-278-3p	575.53	264.52	-2.17	0.0001
mir-31	1,117.81	418.96	-2.65	0.0030

Table A22 Continued

miR	HT	Antenna	Fold change	*p* adj. value
mir-981	1,777.99	654.76	-2.71	0.0000
mir-999	24,078.12	8,776.61	-2.72	0.0011
mir-10	53,592.28	17,899.61	-2.97	0.0004
mir-278-5p	533.00	153.42	-3.46	0.0000
mir-275-3p	21,116.47	5,593.51	-3.77	0.0000
mir-283	526.13	131.34	-3.97	0.0000
mir-277-5p	157.88	39.46	-3.99	0.0000
mir-305-3p	925.76	216.55	-4.27	0.0000
mir-308-5p	219.57	48.72	-4.44	0.0008
mir-277-3p	134,912.45	24,709.32	-5.42	0.0000
mir-184	111,921.53	18,761.09	-5.94	0.0000
mir-927	455.10	70.17	-6.45	0.0000
mir-190	1,998.38	303.21	-6.55	0.0000
mir-137*	868.42	122.44	-6.99	0.0000
mir-1	7,955.64	1,042.58	-7.57	0.0000
mir-8-3p	224,668.55	18,948.68	-11.75	0.0000
mir-957	21,632.17	1,710.95	-12.40	0.0000
mir-133	3,583.81	260.29	-13.40	0.0000
mir-316	746.73	53.48	-13.71	0.0000
mir-2942	5.00	0.16	-13.93	0.0382
mir-124	237.95	16.13	-14.29	0.0000
mir-8-5p	21,404.17	1,085.78	-19.51	0.0000
mir-315-5p	4,381.53	182.54	-23.02	0.0000
mir-932-3p	40.54	1.13	-25.95	0.0000
mir-1175-3p	87.40	1.77	-37.59	0.0000
mir-993	139.77	3.59	-39.86	0.0000
mir-315-3p	7.25	0.00	-53.21	0.0076
mir-1174	811.26	9.78	-74.45	0.0000
mir-375	8,403.74	107.20	-75.81	0.0000
mir-932-5p	1,168.68	13.20	-90.71	0.0000
mir-1175-5p	217.86	0.80	-159.53	0.0000
mir-285	30,929.04	35.75	-809.78	0.0000

Table A23 Differentially expressed miRs after blood feeding. Normalized reads counts are displayed. Values from the same sample may change according to the pairwise comparisons due to different library sizes.

	4d FemHT	3hHT	Fold	*p* adj. values
mir-275-5p	324.53	2203.93	5.60	0.0000
mir-305-3p	742.77	2189.64	2.69	0.0000
		24hHT		
mir-275-5p	300.66	1096.41	3.13	0.0000
mir-305-3p	688.16	1455.62	2.01	0.0000
		48hHT		
bantam-3p	36138.06	14053.98	-2.55	0.0000
mir-11-3p	22825.70	7628.31	-2.96	0.0000
mir-12-3p	48.22	15.73	-2.88	0.0010
mir-12-5p	699.19	244.88	-2.80	0.0000
mir-13-3p	1075.42	268.21	-3.95	0.0000
mir-137*	473.33	211.27	-2.25	0.0000
mir-1889-5p	382.70	100.61	-3.78	0.0000
mir-279	1309.97	594.99	-2.17	0.0000
mir-281-3p	400.83	184.16	-2.16	0.0000
mir-305-5p	998.37	403.81	-2.43	0.0000
mir-315-5p	2394.76	1100.25	-2.16	0.0000
mir-375	4588.86	1728.91	-2.63	0.0000
mir-79-3p	9.20	0.45	-3.79	0.0146
mir-8-3p	122689.03	43080.54	-2.82	0.0000
mir-965	10.82	0.89	-3.65	0.0150
mir-980-3p	15.53	2.23	-3.30	0.0158
mir-993	75.92	21.07	-3.21	0.0000
mir-996	257.35	81.67	-2.95	0.0000
mir-9a*	1170.08	303.14	-3.77	0.0000
mir-9b	283.29	117.06	-2.42	0.0000
mir-9c-5p	2662.50	997.07	-2.64	0.0000
mir-10	29233.84	59371.72	2.02	0.0000
mir-11-5p	2448.92	10540.81	4.24	0.0000
mir-125	4304.97	17319.30	3.96	0.0000
mir-133	1959.45	4819.86	2.43	0.0000
mir-184	61228.28	222926.63	3.59	0.0000
mir-252-3p	43.38	122.79	2.69	0.0000
mir-252-5p	5688.12	17045.40	2.96	0.0000
mir-263a-3p	109.54	291.62	2.57	0.0000
mir-263a-5p	10866.22	25442.75	2.32	0.0000
mir-278-5p	292.49	601.73	2.02	0.0000
mir-2940-3p	3684.93	9728.24	2.60	0.0000
mir-2941-1	7.64	30.80	3.41	0.0009
mir-306-3p	8.84	29.46	2.83	0.0048
mir-34-3p	2332.89	16354.17	6.86	0.0000
mir-34-5p	10677.25	27039.74	2.51	0.0000
mir-71-5p	166.16	360.28	2.13	0.0000
mir-8-5p	11671.79	24972.80	2.12	0.0000
mir-92a-3p	71.86	298.02	3.87	0.0000
mir-92a-5p	4.48	27.35	4.31	0.0003

Table A23 Continued

	4d FemHT	3hHT	Fold	*p* adj. values
mir-92b-3p	1492.72	7618.29	5.00	0.0000
mir-932-3p	22.17	46.92	2.00	0.0195
mir-970	3785.74	7654.52	2.00	0.0000
mir-988-3p	253.70	993.24	3.80	0.0000

Table A24 Polyadenylation sites (PAS) prediction of olfaction genes targeted by several miRs. The prediction was done on the webserver: www.imtech.res.in

PAS	Score	Start	Sequence
AAEL007110	*OR16*	3'UTR	1776 bp
1	0.94382	242	ACCATT
2	0.75499	636	AAAGGC
3	0.72787	644	TGAAAA
4	0.70724	169	GGAACC
5	0.70339	187	CAATTT
6	0.70284	226	CACAAA
7	0.676	156	ATAAGA
8	0.6671	677	TTCTTG
9	0.62839	664	TTTCGA
10	0.6141	102	AACATA
11	0.57359	700	AGGAGG
12	0.5496	208	CGTGGC
13	0.54053	655	CGCCAA
14	0.52466	1603	TCGATA
15	0.37798	142	CGCAGA
16	0.31939	613	AGGATT
17	0.24654	1629	AACTAT
18	0.2237	131	AAACAA
19	0.03282	281	CATCGT
20	0.00996	517	TCCATC
21	0.00457	529	GGCGAT
AAEL018149	*IRc*	3'UTR	1769 bp
1	0.62366	134	CCAACA
2	0.28364	587	TAGCAC
3	0.21754	542	ACGATT
4	0.21388	362	CAGTTA
5	0.20948	551	CAACAA
6	0.16321	567	ACATAG
7	0.0859	303	CAGCGA
8	0.0461	385	CAAACT
AAEL013507	*OR52*	3'UTR	1608 bp
1	1.33773	240	TATTAC
2	1.15986	273	ACTTTG
3	1.15593	205	GGGTCA
4	1.13602	224	AGCAAT
5	1.09633	261	GATGAA

Table A24 Continued

PAS	Score	Start	Sequence
6	1.02578	218	AAGAAA
7	1.01277	296	GGGTTG
8	0.91935	1341	GACGAT
9	0.88335	316	GACAGC
10	0.81471	290	AAAACA
11	0.80202	1091	GATGGA
12	0.69293	1450	CACGAA
13	0.69033	355	CATCCA
14	0.65501	334	AGGACC
15	0.62833	1344	GATAAA
16	0.61597	286	ACTAAA
17	0.39652	1126	AGGGAT
18	0.39022	1062	CAACTC
19	0.26514	1109	GGATTT
20	0.23969	547	AGTGCA
21	0.20812	1323	ACAGTA
22	0.20705	1444	TATAAA
23	0.17319	1050	ATGATT
24	0.08689	1213	AGAGAA
25	0.07541	1403	AAGATT
26	0.07001	1036	AGGAAT
27	0.05151	185	TAATGA
28	0.04802	1058	AATACA
29	0.02739	673	GCCAAG
30	0.00659	532	CCTTAC
AAEL000616	*OR42*	3'UTR	1395 bp
1	1.45781	881	TTGATG
2	1.22871	301	AATACG
3	1.16848	109	CTTCTT
4	1.16429	171	AGATTA
5	1.15629	308	AAAAGC
6	1.11955	862	ATTGTT
7	1.1118	165	TCATTC
8	1.09684	326	CACGCA
9	0.94826	845	GTGCGA
10	0.77602	190	TTCGTA
11	0.74523	350	GTGTTC
12	0.67956	365	TCTACG
13	0.64247	342	CTGAAA
14	0.58574	139	AATTTT
15	0.49189	905	TCGACA
16	0.19102	951	ACCAGC
17	0.11641	938	ATAAAA
18	0.0763	960	CCATTG
19	0.06477	423	GAAGGG
20	0.04842	285	CATAAA
21	0.04017	924	GAACTA
22	0.00679	1194	CGGAGG

Table A24 Continued

PAS	Score	Start	Sequence
AAEL002511	*IRd*	3'UTR	1363 bp
1	1.30607	928	GTGAAT
2	1.04742	945	TTTCCC
3	0.99568	1031	AGGAGG
4	0.97335	497	ATGAAT
5	0.89391	513	AGTCCG
6	0.85498	524	GTCCGT
7	0.8254	918	ACATTT
8	0.7841	300	TTCGAT
9	0.78203	736	GTTCTG
10	0.77649	180	TAAAAG
11	0.75772	474	AAACAA
12	0.75382	905	AGGTTG
13	0.73042	912	GCGGAA
14	0.67113	193	TATTTT
15	0.5937	484	TTGTAT
16	0.59209	303	GATAAA
17	0.57984	149	TAATTA
18	0.55715	996	AATTGA
19	0.53324	1051	TGCCAA
20	0.51064	1006	GGAAGA
21	0.49355	535	AGTAAA
22	0.48326	552	CGAGTA
23	0.44378	178	AATAAA
24	0.39406	710	GAGTGA
25	0.38559	129	GTGCGA
26	0.36729	123	TACAAG
27	0.35129	763	GGAGGA
28	0.34831	1103	GATCGG
29	0.25427	892	GACGTT
30	0.24908	141	ATTGCT
31	0.23265	415	ACAGTT
32	0.21223	283	CACCCA
33	0.21077	112	CACCTA
34	0.17243	1087	AACAAA
35	0.13471	877	CGAGGA
36	0.12842	554	AGTAAA
37	0.11761	461	AAGAAA
38	0.10851	855	GGACAG
39	0.08117	160	CGAATC
40	0.07253	439	AATATG
41	0.0262	270	GGGTAA

Table A25. The targets of known miRs of *A. aegypti*. Only targets with scores higher than 150 and energy requirements less than -20kcal are shown.

miR	Gene Name	Transcript	Total Score	Total Energy	3'UTR(bp)	Positions
aae-miR-79-5p	Or52	AAEL013507-RA	444	-55.99	1608	190 738 657
aae-miR-283	Or2	AAEL005999-RA	319	-47.47	1012	747 537
aae-miR-9b	Or125	AAEL013893-RA	453	-47.34	960	30 328 670
aae-miR-305-5p	OBP11	AAEL002587-RA	291	-44.23	1220	218 766
aae-miR-1889-3p	IR25a	AAEL009813-RA	426	-43.17	721	12 611 563
aae-miR-12-5p	Gr20	AAEL007935-RA	287	-42.83	179	114 152
aae-miR-12-5p	Gr20	AAEL007935-RF	287	-42.83	179	114 152
aae-miR-12-5p	Gr20	AAEL007935-RE	287	-42.83	179	114 152
aae-miR-12-5p	Gr20	AAEL007935-RC	287	-42.83	179	114 152
aae-miR-12-5p	Gr20	AAEL007935-RD	287	-42.83	179	114 152
aae-miR-12-5p	Gr20	AAEL007935-RG	287	-42.83	179	114 152
aae-miR-12-5p	Gr20	AAEL007935-RH	287	-42.83	179	114 152
aae-miR-12-5p	Gr20	AAEL007935-RB	287	-42.83	179	114 152
aae-miR-12-5p	Gr20	AAEL007935-RI	287	-42.83	179	114 152
aae-miR-309b-5p	IRc	AAEL018149-RA	285	-42.12	1769	42 1405
aae-miR-263a-3p	Or130	AAEL017285-RA	292	-38.91	200	45 30
aae-miR-133	IR76b	AAEL006360-RA	296	-38.03	471	398 340
aae-miR-315-5p	IRc	AAEL018149-RA	575	-36.94	1769	1569 816 839 876
aae-miR-2944a-3p	Or42	AAEL000616-RA	291	-36.21	1395	840 581
aae-miR-277-3p	Or16	AAEL007110-RA	430	-35.78	1776	853 1556 1335
aae-miR-315-5p	Forage2	AAEL007826-RA	446	-35.65	841	783 711 696
aae-miR-315-5p	IR25a	AAEL009813-RA	316	-35.65	721	404 125
aae-miR-2944a-5p	IR41e	AAEL000011-RA	293	-35.46	515	467 28
aae-miR-12-3p	Or18	AAEL017510-RA	282	-35.38	200	164 130
aae-miR-1890	Or16	AAEL007110-RA	286	-34.54	1776	1526 1593
aae-miR-9c-3p	Or16	AAEL007110-RA	302	-34.38	1776	1462 706
aae-miR-285	Or124	AAEL001617-RA	303	-34.17	200	122 145
aae-let-7	IRc	AAEL018149-RA	291	-34.08	1769	517 1032
aae-miR-307	IRd	AAEL002511-RA	290	-33.58	1363	894 172
aae-miR-980-3p	Or87	AAEL017347-RA	284	-33.33	200	49 1
aae-miR-190	OBP38	AAEL008013-RA	440	-33.29	643	53 388 83
aae-miR-71-3p	IRc	AAEL018149-RA	292	-32.99	1769	198 376
aae-miR-989	Or49	AAEL001303-RA	285	-32.99	1039	80 59
aae-miR-1000	Or42	AAEL000616-RA	292	-32.5	1395	235 260
aae-miR-133	Or98	AAEL017463-RA	155	-32.13	200	168
aae-miR-190	IR7v.3	AAEL018101-RA	300	-31.16	1110	895 650
aae-miR-219	OBP48	AAEL011494-RA	285	-31.14	355	182 229
aae-bantam-3p	Or16	AAEL007110-RA	292	-30.75	1776	1073 718
aae-miR-932-5p	IR7q.2	AAEL003341-RA	298	-30.7	200	118 167
aae-miR-33	Gr62	AAEL017040-RA	298	-30.14	200	87 37
aae-miR-283	Or125	AAEL013893-RA	283	-30.07	960	146 188
aae-miR-308-5p	Or16	AAEL007110-RA	290	-29.87	1776	125 1397
aae-miR-1	OBP11	AAEL002587-RA	312	-29.21	1220	1047 841

Table A25 Continued

miR	Gene Name	Transcript	Total Score	Total Energy	3'UTR(bp)	Positions
aae-miR-2941	Or21	AAEL017398-RA	150	-28.49	200	6
aae-miR-137	IR41n	AAEL000089-RA	294	-27.64	200	45 151
aae-miR-11-3p	OBP37	AAEL008009-RA	165	-27.47	200	144
aae-miR-278-3p	IR41j	AAEL000018-RA	156	-27.25	200	140
aae-miR-1890	IR76b	AAEL006360-RA	163	-27.12	471	255
aae-miR-33	Or52	AAEL013507-RA	293	-26.22	1608	1447 1506
aae-miR-2944b-5p	IR41e	AAEL000011-RA	302	-26.15	515	468 29
aae-miR-309b-3p	Or46	AAEL017174-RA	151	-25.87	200	132
aae-miR-317	OBP15	AAEL002598-RA	155	-25.48	190	62
aae-miR-11-3p	Or28	AAEL000391-RA	158	-25.45	200	13
aae-miR-2944b-5p	OBP15	AAEL002598-RA	160	-25.15	190	61
aae-miR-276-3p	Or30	AAEL010409-RA	153	-24.66	481	346
aae-miR-34-5p	Or2	AAEL005999-RA	162	-24.54	1012	769
aae-miR-193	IR41e	AAEL000011-RA	161	-24.48	515	322
aae-miR-309b-5p	Or26	AAEL010428-RA	152	-24.47	200	15
aae-miR-1175-5p	OBP58	AAEL014430-RA	152	-24.41	200	105
aae-miR-1000	IRh	AAEL013695-RA	150	-24.24	995	369
aae-miR-2940-5p	Or49	AAEL001303-RA	156	-24.16	1039	562
aae-miR-2945-5p	Gr66	AAEL017394-RA	153	-24.15	200	90
aae-miR-989	Or92	AAEL017065-RA	169	-24.08	200	89
aae-miR-981	Gr7	AAEL000060-RA	159	-23.97	200	21
aae-miR-375	Or87	AAEL017347-RA	155	-23.94	200	109
aae-miR-988-5p	Gr37	AAEL017235-RA	152	-23.91	200	22
aae-miR-309b-5p	OBP1	AAEL006454-RA	163	-23.74	237	1
aae-miR-92b-3p	Forage1	AAEL005754-RA	159	-23.68	200	5
aae-miR-13-5p	OBP17	AAEL004339-RA	299	-23.61	200	43 104
aae-miR-12-5p	Or41	AAEL003045-RA	169	-23.57	200	30
aae-miR-2942	Or103	AAEL017505-RA	290	-23.55	200	156 169
aae-miR-79-3p	IR7v.3	AAEL018101-RA	308	-23.38	1110	780 341
aae-bantam-5p	IRd	AAEL002511-RA	284	-23.34	1363	83 231
aae-miR-306-5p	Or119	AAEL017009-RA	156	-23.07	200	117
aae-miR-999	IR76b	AAEL006360-RA	299	-22.98	471	46 139
aae-miR-315-5p	Or48	AAEL011895-RA	177	-22.97	612	136
aae-miR-2944b-3p	OBP55	AAEL012377-RA	159	-22.9	137	18
aae-miR-283	Or20	AAEL004966-RA	150	-22.87	200	61
aae-miR-278-5p	Gr72	AAEL017216-RA	151	-22.84	200	124
aae-miR-315-5p	OBP29	AAEL006387-RA	308	-22.8	115	69 85
aae-miR-71-5p	Or56	AAEL017534-RA	151	-22.77	200	75
aae-miR-263a-5p	Gr14	AAEL011571-RA	163	-22.66	200	79
aae-miR-92b-3p	OBP11	AAEL002587-RA	158	-22.46	1220	769
aae-miR-iab-4-3p	IR7l	AAEL000462-RA	150	-22.31	200	59
aae-miR-79-3p	Or87	AAEL017347-RA	297	-22.25	200	48 1
aae-miR-92b-3p	IR41e	AAEL000011-RA	156	-22.21	515	334
aae-miR-309b-5p	Or8	AAEL012254-RA	150	-22.07	200	91

Table A25 Continued

miR	Gene Name	Transcript	Total Score	Total Energy	3'UTR(bp)	Positions
aae-miR-932-3p	Or14	AAEL008442-RA	161	-22.06	200	39
aae-bantam-5p	OBP39	AAEL009449-RA	170	-21.92	153	5
aae-miR-315-3p	OBP13	AAEL002591-RA	150	-21.9	469	38
aae-miR-92a-3p	IR41e	AAEL000011-RA	155	-21.88	515	335
aae-miR-998	Or124	AAEL001617-RA	164	-21.82	200	124
aae-miR-965	IR115	AAEL018097-RA	165	-21.77	200	87
aae-miR-92a-3p	Forage1	AAEL005754-RA	158	-21.77	200	7
aae-miR-1891	OBP9	AAEL002596-RA	158	-21.74	93	9
aae-miR-92a-3p	OBP11	AAEL002587-RA	158	-21.73	1220	770
aae-miR-11-5p	IR8a	AAEL002922-RA	154	-21.71	200	43
aae-miR-2940-5p	IR111.3	AAEL018094-RA	163	-21.66	138	17
aae-miR-996	Or14	AAEL008442-RA	163	-21.55	200	1
aae-miR-957	OBP57	AAEL000035-RA	151	-21.55	200	22
aae-miR-929	Forage2	AAEL007826-RA	175	-21.53	841	695
aae-miR-980-5p	OBP11	AAEL002587-RA	150	-21.43	1220	723
aae-bantam-5p	IR75l	AAEL005875-RA	174	-21.3	331	270
aae-miR-981	Forage2	AAEL007826-RA	157	-21.19	841	323
aae-miR-307	Or106	AAEL017105-RA	163	-21.18	200	131
aae-miR-306-5p	IR75k.3	AAEL014087-RA	167	-21.02	200	145
aae-miR-283	Or42	AAEL000616-RA	154	-21.01	1395	50
aae-miR-276-5p	OBP23	AAEL006109-RA	155	-20.96	320	220
aae-miR-980-3p	IR7r.1	AAEL014688-RB	156	-20.76	200	124
aae-miR-993	Or69	AAEL001221-RA	160	-20.75	200	65
aae-miR-1	Or74	AAEL006195-RA	150	-20.74	200	61
aae-miR-305-3p	IR31a	AAEL013153-RA	159	-20.63	200	23
aae-miR-989	Or97	AAEL017000-RA	151	-20.62	200	159
aae-miR-124	Gr3	AAEL010058-RA	156	-20.47	200	119
aae-miR-305-5p	Or11	AAEL011583-RA	154	-20.42	1116	27
aae-miR-9c-3p	Or110	AAEL016983-RA	151	-20.42	200	138
aae-miR-9c-3p	Or109	AAEL017028-RA	151	-20.42	200	138
aae-miR-2b	OBP37	AAEL008009-RA	150	-20.35	200	140
aae-miR-305-5p	OBP5	AAEL000139-RA	168	-20.33	356	96
aae-miR-2b	OBP35	AAEL002606-RA	155	-20.31	101	2
aae-miR-2a-5p	IR116	AAEL018098-RA	155	-20.15	223	197
aae-miR-137	OBP15	AAEL002598-RA	286	-20.12	190	1 6

Table A26. The targets of novel miRs of *A. aegypti*. Only targets with scores higher than 150 and energy requirements less than -20kcal are shown.

miR	Gene Name	Transcript	Total Score	Total Energy	3'UTR(bp)	Positions
Novel-miR11	IR75k.3	AAEL014087-RA	151	-26.83	200	87
Novel-miR15	Or125	AAEL013893-RA	151	-21.56	960	73
Novel-miR3	IR110	AAEL018090-RA	150	-22.81	280	86
Novel-miR4	IR7q.2	AAEL003341-RA	284	-23.44	200	119 170
Novel-miR7	OBP21	AAEL005770-RA	155	-25.88	565	258
Novel-miR9	OBP31	AAEL006396-RA	167	-24.13	200	117
Novel-miR9	Or103	AAEL017505-RA	314	-42.48	200	140 37