The Female Post-Mating Response Requires Genes Expressed in the Secondary Cells of the Male Accessory Gland in *Drosophila melanogaster*

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ABSTRACT Seminal proteins from the *Drosophila* male accessory gland induce post-mating responses (PMR) in females. The PMR comprise behavioral and physiological changes that include increased egg laying, decreased receptivity to courting males, and changes in the storage and use of sperm. Many of these changes are induced by a "sex peptide" (SP) and are maintained by SP's binding to, and slow release from, sperm. The accessory gland contains two secretory cell types with distinct morphological and developmental characteristics. Products of these "main" and "secondary" cells work interdependently to induce and maintain the PMR. To identify individual genes needed for the morphology and function of secondary cells, we studied *iab-6^{cocu}* males, whose secondary cells have abnormal morphology and fail to provide products to maintain the PMR. By RNA-seq, we identified 77 genes that are downregulated by a factor of >5× in *iab-6^{cocu}* males. By functional assays and microscopy, we tested 20 candidate genes and found that at least 9 are required for normal storage and release of SP in mated females. Knockdown of each of these 9 genes consequently leads to a reduction in egg laying and an increase in receptivity over time, confirming a role for the secondary cells in maintaining the long-term PMR. Interestingly, only 1 of the 9 genes, CG3349, encodes a previously reported seminal fluid protein (Sfp), suggesting that secondary cells may perform essential functions beyond the production and modification of known Sfps. At least 3 of the 9 genes also regulate the size and/or abundance of secondary cell vacuoles, suggesting that the vacuoles' contents may be important for the machinery used to maintain the PMR.

KEYWORDS reproduction; *Drosophila*; sex peptide; gene regulation; gene expression

SEMINAL fluid proteins (Sfps) play an essential role in reproduction. Sfps interact with the female, locally in the reproductive tract and more globally in the central nervous system, resulting in changes in female gene expression, behavior (in insects), and physiology (reviewed in Sirot *et al.* 2009). In *Drosophila*, these changes are collectively referred to as the female post-mating response (PMR). The male accessory gland (AG) is the source of many important Sfps that cause the PMR (Takemori and Yamamoto 2009). Each lobe of the accessory gland consists of a monolayer of secretory cells composed of two morphologically distinct cell types. Flat, polygonal "main cells" make up 96% of each lobe. The remaining 4% of the cells are large, spherical, vacuole-filled "secondary cells" (Bairati 1968; Bertram, *et al.* 1992) that are located only at the distal tip of each lobe. The multi-cell state of the AG is not unique. Other secretory organs, such as the pancreas (Brissova *et al.* 2005) and the epididymis (reviewed in Cornwall 2009), are also composed of multiple cell types, the products of which work together to regulate complex processes (Hermo 1995; Cheung *et al.* 2005; Pietrement *et al.* 2006; Kujala *et al.* 2007).

The two cell types of the *Drosophila melanogaster* male accessory gland make distinct products (Bertram *et al.* 1992; Gligorov *et al.* 2013) that act in a network (Ravi Ram and Wolfner 2009; Findlay *et al.* 2014) that allows for the seminal sex peptide (SP) to bind to sperm, enter the

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female sperm storage organs, and subsequently be cleaved from the sperm in storage (Liu and Kubli 2003; Peng *et al.* 2005a). The binding of SP to sperm and its gradual release by proteolytic cleavage allows its effects to persist long after mating has occurred (Chen and Buhler 1970; Chapman *et al.* 2003; Liu and Kubli 2003; Peng *et al.* 2005a). Through this mechanism, SP has been implicated in regulating long-term changes in female egg laying, receptivity, and various other post-mating responses (Chapman *et al.* 2003; Liu and Kubli 2003; Peng *et al.* 2005a,b; Avila *et al.* 2010; Apger-McGlaughon and Wolfner 2013). Collectively, the prolonged post-mating response that is mediated by SP is called the long-term response (LTR) (Peng *et al.* 2005a; Ravi Ram and Wolfner 2007). While main cells produce SP and other proteins necessary to initiate and maintain the LTR (Styger 1992; Liu and Kubli 2003), secondary cell products are essential to maintain the LTR (Leiblich *et al.* 2012; Minami *et al.* 2012; Gligorov *et al.* 2013). A few of these secondary cell products were identified by examining the cell type expression of known accessory gland proteins (Gligorov *et al.* 2013), but an unbiased search for other secondary cell products that mediate the PMR has not been done. Previously, we generated an enhancer deletion, *iab-6*^{cocu}, that removes the expression of the Hox gene, *Abdominal-B*, from the secondary cells of the male accessory gland. *iab-6*^{cocu} mutants display abnormal secondary cell morphology and are unable to maintain the LTR in their mates (Gligorov *et al.* 2013). The three secondary cell proteins known to be important for the long-term storage of SP (CG1652, CG1656, and CG17575) were still produced in *iab-6*^{cocu} males (Ravi Ram and Wolfner 2009; Gligorov *et al.* 2013) and transferred to females during mating. This suggests that the inability of *iab-6*^{cocu} mutants to maintain the LTR in their mates is caused by as-yet-unidentified protein(s) and that the mutant may provide a way to identify new secondary cell products necessary for the regulation of the LTR.

To identify secondary cell genes whose function is needed for the LTR, we used RNA-seq to compare transcripts from *iab-6*^{cocu} and wild-type accessory glands. Using both unbiased screening methods via secondary cell-specific RNA interference (RNAi) and more targeted bioinformatics approaches to narrow down targets, we selected 20 transcripts that were downregulated in *iab-6*^{cocu} for further study. Of these, 18 were efficiently knocked down by RNAi, and we characterized their effects on the regulation of the PMR. Nine of these genes are necessary for the normal long-term increase in egg laying and long-term reduction in female receptivity. Furthermore, knockdown of several of these genes impacted the number and size of the secondary cell's characteristic vacuoles, suggesting that these vacuoles may be essential for the regulation of the PMR. Surprisingly, only one of the nine genes encodes a protein that was previously known to be transferred to females, CG3349. One explanation for this finding is that the *iab-6*^{cocu} mutant may not primarily affect Sfps directly but instead might work through disrupting other, intracellular, functions such as vacuole-associated secretion.

Materials and Methods

Fly stocks and media

Flies were raised at room temperature (23° ± 1°) in bottles on standard yeast–glucose media (8.2% w/w yeast, 8.2% w/w glucose, 1% w/w agar, 1.2% v/w acid mix). Virgin females were aged 3–5 days from eclosion in groups of 5–12 in vials with added yeast. Male flies were aged 3–5 days from eclosion in groups of 10–20 in vials on standard yeast–glucose media. Fly lines containing a UAS-hairpin construct specific to each gene of interest were obtained from the Vienna *Drosophila* RNAi Center (VDRC) (Dietzl *et al.* 2007); line numbers for candidate genes discussed in this article are given in Supporting Information, Table S1 and Table S2. To generate knockdown males, each UAS-hairpin line was crossed to the secondary cell driver *iab-6*^{D1}*-Gal4/CyO* (Gligorov *et al.* 2013); control flies were generated by crossing the driver to the appropriate background line [*w[1118];P{attP,y[+],w[3′]* (*Attp*^{60100})] for KK insertion lines and *w*^{1118} for GD insertion lines. The level of knockdown of the targeted gene's expression, relative to controls, was confirmed by RT-PCR as described in Findlay *et al.* (2014) except that messenger RNA (mRNA) samples were extracted from dissected accessory glands rather than from whole flies (Table S1). In cases where knockdown was not detected with the *iab-6*^{D1}*-Gal4* driver, which might occur for a gene that is normally expressed in both main and secondary cell types, we also used *tubulin-Gal4* to check for the function of the RNAi construct (Table S1). If both drivers suggested that knockdown did not occur, the line was excluded from analysis. To generate GFP expression in the secondary cells, the *iab-6*^{D1}*-Gal4* driver was recombined with a *UAS-GFP* transgene on the second chromosome (generating *w*; *iab-6*^{D1}*-Gal4, UAS-GFP*) and crossed to RNAi lines as previously described.

mRNA-seq

To control for genetic background and for the PhiC31 insertion that was used to make the *iab-6*^{cocu} mutant (Gligorov *et al.* 2013) the *iab-5,6*^{rescue} line, which integrates a wild-type copy of the *iab-6* cis-regulatory region instead of the *iab-6*^{cocu} mutation, was used as the source of control accessory glands. Total RNA was isolated from 100 pairs of accessory glands per genotype from *iab5,6*^{rescue} and *iab-6*^{cocu} (*iab-5,6*$^{\Delta 5}$) males using the miRNeasy Mini Kit (catalog no. 217004, Qiagen). Approximately 10 μg of total RNA was obtained per genotype and was sent to Fasteris (Fasteris SA, Geneva) for sequencing on an Illumina sequencer and for bioinformatic analysis. For these experiments only a single round of "paired-end" mRNA sequencing was performed per genotype (Table S3). HiSeq was performed on a Hi-Sequation 2000 using 100-bp reads ($1 \times 100 + 7$). Samples were prepared using the TruSeq SBS v5 kit, and the data analysis pipeline was carried out using HiSeq Control Software V. 1.1.37.8, RTA 1.7.48, CASAVA 1.7. Sequences were aligned to the *D. melanogaster* genome sequence revision 5.30. Counts were normalized as reads per million by dividing by the total number of reads and multiplying by 1 million. Changes in the expression of candidate genes were verified through *in situ* hybridization to wild-type and mutant glands.

RNAi screening for genes affecting cellular morphology

For the 61 genes of the 77 downregulated genes for which UAS-short hairpin RNA (shRNA) lines were available, male flies carrying the UAS-shRNA constructs were crossed to *iab-6*^{DI}*-Gal4* and *iab-6*^{DI}*-Gal4*, *UAS-GFP* driver line females (all lines tested are shown in Table S4). The GFP marker, which is excluded from the secondary cell vacuoles, was used as an aid to visualize the cellular phenotype. Driver lines with and without a GFP marker were used separately to eliminate the effect, if any, of the *UAS-GFP* on the phenotype. For each cross, we analyzed the accessory glands of three, 3-day-old males using Nomarski microscopy for male progeny of *iab-6*^{D1}*-Gal4* mothers and a further three, 3-day-old males using fluorescence microscopy for male progeny from *iab-6*^{D1}*-Gal4, UAS-GFP* mothers. Based on our examinations under fluorescence and Nomarski microscopy, we did not observe any effect stemming from the *UAS-GFP* marker.

Vacuole size was measured using ImageJ v1.48 software (Wayne Rasband, National Institutes of Health) using images taken on a Zeiss Axioplan fluorescent microscope. Statistical significance was determined by ANOVA. The average vacuole diameters in the knockdown flies reported all are statistically different from wild-type controls (*iab-6*^{DI}*-Gal4*, *UAS-GFP*) ($P < 0.0005$) (Figure S1).

Data analysis for candidate selection

We used publicly available database information such as predicted function, the presence of a predicted signal sequence, and expression pattern to select additional candidates for functional analysis that did not impact cellular morphology. For each gene, the presence or absence of a predicted signal sequence was determined using SignalP (Petersen *et al.* 2011), and expression patterns outside the accessory gland were obtained from data reported by FlyBase (1999), Fly Atlas (Chintapalli *et al.* 2007), and ModENCODE (Roy *et al.* 2010; McQuilton *et al.* 2012; Young *et al.* 2012). Genes were counted as being expressed in a given location if at least one of these three sources reported expression there. However, preference was given to genes whose expression in the accessory gland was reported by multiple sources. For genes with no listed function in FlyBase, Pfam (Punta *et al.* 2012) was used to identify conserved domains where possible and function was proposed accordingly. For Gene Ontology (GO) Enrichment Analysis, the 77 genes that were downregulated in *iab-6*^{cocu} were run through the Database for Visualization and Integrated Discovery (DAVID) at high stringency using the complete list of genes detected by our RNA-seq run as background (Huang da *et al.* 2007, 2009).

Fertility/fecundity assays

Fertility/fecundity assays were performed as described in Gligorov *et al.* (2013) and Findlay *et al.* (2014). Briefly, 3- to 5-day-old virgin knockdown or control males were singly mated with Canton-S virgin females; males were then removed. Females, kept singly in vials, were transferred to fresh vials daily. The number of eggs laid each day was counted (fecundity) through day 10, and the number of progeny from each vial was also counted (fertility). Wilcoxon nonparametric tests were used to compare results for mates of RNAi and control males in total and on individual days. The overall 10-day trends were analyzed by repeated measures ANOVA (rmANOVA). All statistical analysis was performed with the JMP9 software (SAS Institute, 2010). For confirmation with additional RNAi lines, the same protocol was used except that egg counts were carried out for only 5 days since reduced egg laying was readily detectable in all of the initially tested lines for these genes by day 3.

Receptivity assays

Receptivity assays were performed as described in Gligorov *et al.* (2013) and Findlay *et al.* (2014). Briefly, 3- to 5-day-old virgin knockdown and control males were singly mated to Canton-S virgin females. Males were then removed and the females were aged individually in vials. Four days after the mating, a virgin Canton S male was introduced into each vial, and the vial was scored for whether or not the female remated within an hour of male introduction. Comparisons of remating frequency between females mated to either control or RNAi males were conducted using a Wilcoxon ranked-sums test using JMP9 software (SAS Institute, 2010).

Western blots

Females were frozen at 30 min after the start of mating (ASM) in liquid nitrogen or held in vials with yeast–glucose food for 4 days prior to being frozen. Virgin flies were flash-frozen at 3–5 days old in groups of 10–20 in liquid nitrogen. After flash freezing, all samples were stored at $-80°$ prior to dissection. Protein sample preparation and Western blot analyses were performed as in Ravi Ram *et al.* (2005), Ravi Ram and Wolfner (2009), and Gligorov *et al.* (2013). Primary antibodies for each of the LTR proteins (Liu and Kubli 2003; Ravi Ram and Wolfner 2009, 2007) were used at the following dilutions: SP (1:2000), CG1656 (1:1000), CG1652 (1:500), and CG9997 (1:2000).

Results

RNA-seq reveals 77 candidate genes downregulated by more than fivefold in the accessory glands of iab-6^{cocu} males

Previously, we discovered that the homeotic gene, *Abdominal-B*, is specifically expressed in the secondary cells of the accessory gland and that removal of its secondary cell-specific enhancer resulted in morphological defects in the secondary cells and a reduction of the LTR in the mated female (Gligorov *et al.* 2013). To identify additional secondary cell genes needed for the LTR, we attempted to identify mRNAs whose abundance differed in *iab-6*^{cocu} males relative to controls using RNAseq. Although RNAseq is generally used to characterize transcriptomes, we decided to use it here strictly as a tool to find new genes for functional testing of phenotypes in the accessory gland. Hence, we performed only RNAseq single runs on wild-type or *iab-6*^{cocu} accessory glands.

Our HiSeq run yielded 66,943,897 reads: 36,740,061 for *iab-5,6*^{rescue} (a wild-type line generated by the same genetic manipulation techniques that were used to create *iab-6*^{cocu}) and 30,203,836 for *iab-6*^{cocu}, mapping to 8764 genes. Fold differences were calculated by dividing the normalized number of reads per gene of each genotype: *iab-5,6*^{rescue}/*iab-6*^{cocu} for "downregulated genes" (which may require *Abd-B* for high expression in the accessory gland) and the inverse for upregulated genes (which might normally be repressed by *Abd-B*). Using a cutoff value of 5×, we found that 77 genes were downregulated in *iab-6*^{cocu} relative to controls and 115 genes were upregulated (for a complete list of detected RNAs, see Table S5; for downregulated genes, see Table S6; and for upregulated genes, see Table S7). For this study, we focused primarily on the downregulated genes, as described below.

Eight Sfps had previously been shown to be necessary to bind SP to sperm, allowing for the LTR. Previously, we showed that five of these "SP network" Sfps, and the SP itself, are present at wild-type levels in the accessory glands of *iab-6*^{cocu} males (Gligorov *et al.* 2013). Recently, three additional Sfps were found to be part of the network (Findlay *et al.* 2014). Because antibodies for these proteins (Intrepid, Antares, and Aquarius) are not available, we examined the abundance of their RNAs in our Hiseq database. We detected no differences in expression between *iab-6*^{cocu} and control accessory glands for any of these new SP network genes or for the five genes previously analyzed by Western blot (Table S8). These results agree with our previous conclusion that the loss of known LTR Sfps does not underlie the PMR phenotypes observed in mates of *iab-6*^{cocu} males (Gligorov *et al.* 2013).

We reasoned that since *iab-6*^{cocu} flies are defective in SP's ability to bind to sperm and enter into storage, products necessary for this process to occur are probably depleted or missing from the accessory glands of these males. This is consistent with the kinds of phenotypes seen in males knocked down or null for SP network genes upstream of SP storage (Ravi Ram and Wolfner 2009, 2007; Findlay *et al.* 2014). Therefore, we focused on the 77 genes that we found to be downregulated in *iab-6*^{cocu} (Table S6), as those genes might be most expected to include ones encoding proteins needed for the LTR. DAVID analysis for enriched GO terms within the 77 downregulated genes did not identify any significant classes or functions for the proteins encoded by these genes, perhaps in part because the most common predicted function of the genes that we detected was "unknown." Based on archived experimental and prediction data in FlyBase and conserved protein domains (determined using Pfam), the most common predicted functions for these genes, after unknown (32.5% or 25 genes), were serine-type endopeptidase activity (7.7% or 6 genes), transferase activity (7.7% or 6 genes), sodium:iodide symporter activity (7.7% or 6 genes), and transmembrane transporter function (5.2% or 4 genes). These particular classes of protein are interesting for several reasons. Proteases are a common constituent of seminal fluid in all animals (LaFlamme and Wolfner 2013) and are implicated in the regulation of the PMR in *D. melanogaster* (Findlay *et al.* 2014). The predicted transferases that we identified are primarily glycosyltransferases, which can catalyze reactions to generate O-linked or N-linked glycosylation. Glycosylation is often essential for the structure, function, and transport of glycoproteins and glycolipids. Furthermore, the glycosylation state of several essential PMR proteins is abnormal in *iab-6*^{cocu} males (Gligorov *et al.* 2013). The presence of sodium:iodide symporters might suggest a role for iodine in secondary cell function or secretions. While only 5 of the 77 genes encode proteins previously known to be transferred in seminal fluid (Table S9), 38 of the 77 predicted proteins (49.4%) have a predicted signal sequence, suggesting that these proteins could be secreted and thus may be previously undetected Sfps (Table S6). The even split between proteins with and without predicted signal sequences suggests that both intra- and extracellular functions of the secondary cells are likely impacted by the *iab-6*^{cocu} mutation.

Interestingly, very few of the 77 genes that are downregulated in *iab-6*^{cocu} accessory glands are primarily or exclusively expressed in these glands. This suggests that these genes may be important for general cellular functions or that they may have additional functions outside of reproduction. The most common sites of highest expression of these genes were the Malpighian tubules (32.5% or 25 genes), the testis (15.6% or 12 genes), and the midgut (11.7% or 9 genes) with only 2 genes (2.6%) expressed primarily in the AG. These two AG-specific genes are CG11598 and CG3349. They encode two previously identified Sfps (Ravi Ram *et al.* 2005) that have not yet been characterized. The high level of Malpighian tubule expression was initially surprising; however, other known Sfps also show expression in this organ. For example, the candidate gene CG13309 (Ravi Ram and Wolfner 2007) is most highly expressed in the Malpighian tubules (Chintapalli *et al.* 2007). However, CG13309 also has male-biased expression (Roy *et al.* 2010; McQuilton *et al.* 2012), is expressed at very low (Chintapalli *et al.* 2007) to moderate (Celniker *et al.* 2009) levels in the accessory gland, and encodes a protein known to be transferred to females during mating (Ravi Ram *et al.* 2005). Thus, we believe that the majority of the genes that we identified were detected based on accessory gland expression differences and were not due to contaminating tissues. The large overlap in expression of candidate genes between the accessory glands and the Malphigian tubule may instead suggest that these organs share some functions, the most likely of which is related to their roles as secretory tissues. A detailed account of the molecular characteristics and mRNA-seq results for the 77 genes can be found in Table S6.

Finally, it is interesting to note that a few of the genes cluster at a specific genetic locus. *CG12809*, *CG33783*, *CG33784*, *CG33631*, *CG5361*, and *CG33630* are all located next to each other within a 13-kb region of chromosome 3. The genomic colocalization of the genes, together with the RNA-seq results, suggests that these genes may be co-regulated as a gene neighborhood.

Prioritizing candidates for functional screening

Genes that regulate secondary cell morphology: The *iab-6^{cocu}* mutation was first identified based on its impact on secondary cell morphology. Males homozygous for this mutation have secondary cells that have a hexagonal shape, much like that of main cells, rather than being spherical. These cells also lack the large vacuoles that are characteristic of normal secondary cells (Gligorov *et al.* 2013). The cause of these morphology differences and whether they are related to the LTR phenotypes observed in mates of *iab-6^{cocu}* males is unclear. To begin to investigate this, we screened via knockdown all of the available candidates for cellular morphology phenotypes similar to those seen in *iab-6^{cocu}* mutants. For each gene for which an shRNA line was available (61 of the 77 genes), knockdown was performed using the *iab-6^{D1}-Gal4*, *UAS-GFP* driver line (Gligorov *et al.* 2013). The *iab-6^{D1}-Gal4* driver is a secondary cell-specific driver similar to the previously described *iab-6*^{D5}*-Gal4* driver except that the putative enhancer region controlling GAL4 expression in the secondary cells is 1.1 kb rather than the 2.8-kb region used in the *iab-6*^{D5} driver.

Of the 61 RNAi lines tested, knockdown of five genes—CG7882, CG9509, CG10514, CG14069, and CG31034—resulted in a detectable secondary cell morphology phenotype. For each case, the phenotypes were consistent between individual males but varied slightly between individual cells in a single gland (both more and less severe than the *iab-6^{cocu}* phenotype) (Figure 1). CG14069 knockdown resulted in the most *iab-6^{cocu}*-like vacuolar phenotype, where the large vacuoles in the secondary cells were completely absent (Figure 1B). However, CG14069 knockdown also displayed phenotypes not seen in *iab6^{cocu}* mutants, as the cells within a single gland varied in size and they appeared to partially lose their binucleate character. Knockdown of CG31034 and CG7882 resulted in weaker vacuole phenotypes (Figure 1, C and D) where some large vacuoles were present but were reduced in size [vacuole size: 2.42 ± 1.69 μm (n = 246) (CG31034); 2.40 ± 1.80 μm (n = 178) (CG7882)] and number relative to wild-type AGs [vacuole size: 4.74 ± 1.11 μm (n = 173)]. Knockdown of CG10514 showed an even weaker vacuole phenotype: the number of vacuoles was only slightly reduced, but the general size of the vacuoles was notably smaller [vacuole size 2.87 ± 1.54 μm (n = 243)] (Figure 1F). Finally, knockdown of CG9509 showed a unique secondary cell morphological phenotype characterized by what looked like multiple small vacuoles, which appeared to be interconnected, giving the cells a "grainy" appearance [vacuole size 2.36 ± 2.26 μm (n = 288)] (Figure 1E).

Another cell morphological characteristic of the secondary cells is their round shape; the cells became notably more hexagonal in *iab-6^{cocu}* mutants (Figure 1). Knockdown of a number of genes affected the cell shape and positioning of the secondary cells within the AG. The clearest examples of this are CG10514 and CG31034: in knockdowns of each of these genes, the secondary cells adopted more angular forms. In other knockdown lines, the cell shape changes were more subtle and might simply be linked to the loss of cell size from the loss of vacuoles. It is interesting to note, however, that many of the knockdown lines also displayed visible secondary cell-to-secondary cell contacts that are not normally seen in wild-type glands, but are seen in *iab-6^{cocu}* mutants (Figure 1, marked by an asterisk).

Ten more genes—CG5106, CG31198, CG33630, CG9294, CG15406, CG6602, CG12809, CG13538, CG18088, and CG14681—showed less penetrant knockdown phenotypes where morphological defects were seen in only one or two of the three accessory glands dissected (Figure S2). In the glands that had secondary cell phenotypes, most showed a reduction of the size of the vacuoles present compared to wild type. The vacuole sizes within the cells were variable, ranging from barely visible to close to the size of wild-type vacuoles. The remaining candidates screened did not display any secondary cell morphological phenotype upon knockdown, suggesting either insufficient knockdown, functional redundancy, or that the gene is not involved in regulating secondary cell morphology.

To test whether the genes that affected secondary cell morphology also affected the PMR, we performed 5-day egg-laying tests on the 15 genes that displayed some effect on cellular morphology. Four of the knockdown lines tested (CG7882, CG9509, CG14069, and CG15406) showed egg-laying phenotypes (see below). These results suggest that some but not all changes in vacuole number and/or size correlate with LTR defects. Consistent with these conclusions, independent results show that there are different types of vacuoles in secondary cells, with different functions (F. Karch laboratory, unpublished results; Bairati 1968). Based on these initial screens, we selected CG7882, CG9509, CG14069, and CG15406 for further analysis.

Other genes prioritized for functional screening: The lack of complete congruence between genes affecting secondary cell morphology and ones affecting the PMR led us to hypothesize that some genes needed for the PMR might not have been detected in our cellular morphology screen. Therefore, we also selected several other candidates from the initial 77 most-downregulated genes for functionality testing. We selected these additional candidates based on (1) their predicted function, (2) the presence of a predicted signal sequence in their encoded protein, and (3) confirmed expression in the accessory gland based on FlyAtlas and modENCODE (Chintapalli *et al.* 2007; Roy *et al.* 2010; McQuilton *et al.* 2012). We focused on candidate genes with predicted functions related to post-translational modification of proteins; with

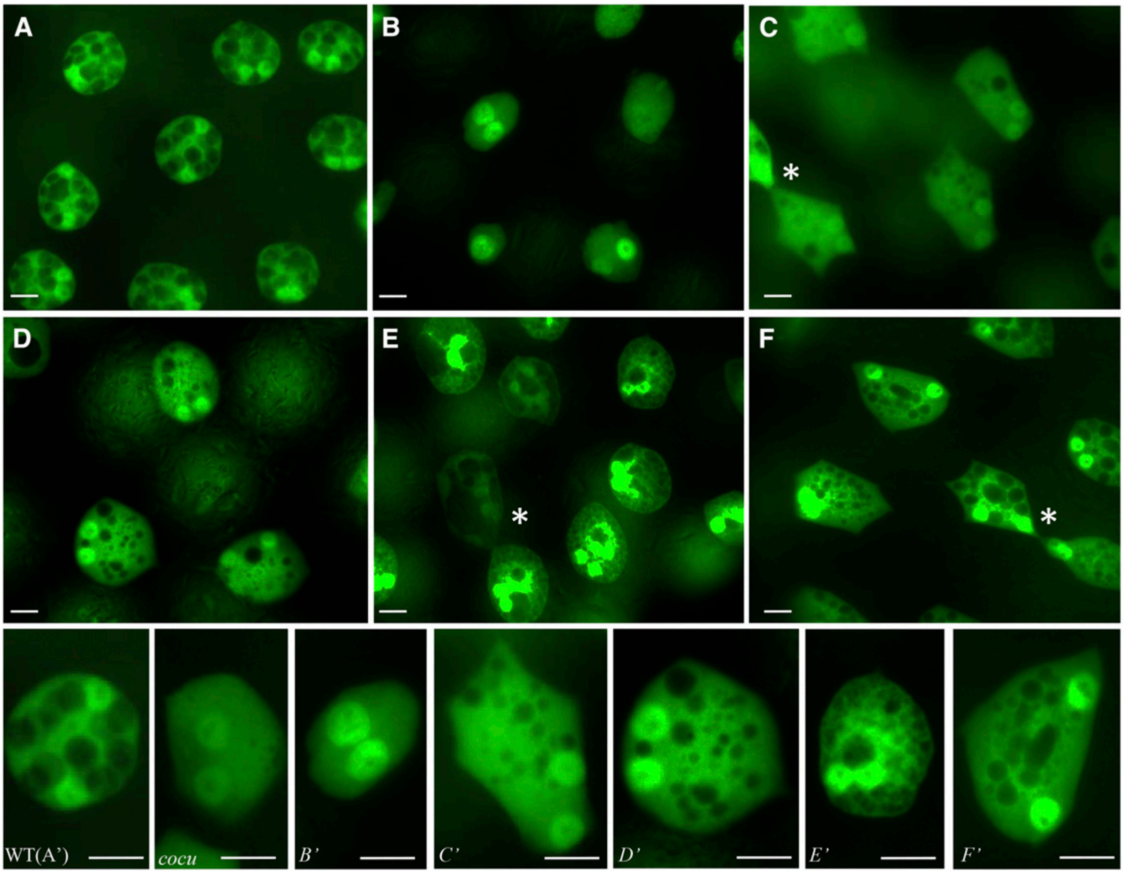

Figure 1 Knockdown of five genes showed consistent secondary cell morphological phenotypes. (A) GFP fluorescence in an accessory gland expressing *UAS-GFP* under the control of the *iab6^{DI}-Gal4* driver. The GFP signal can be seen exclusively in the secondary cells both in the nuclei and in the cytoplasm. Note that GFP signal is excluded from the vacuoles, which appear as black holes in the secondary cells. (B–F) Accessory glands expressing GFP and RNAi hairpins demonstrating the severity and variability of observed secondary cell morphology phenotypes between lines. The genes knocked down are as follows: (B) CG14069, (C) CG31034, (D) CG7889, (E) CG9509, and (F) CG10514. (A′–F′) Individual cells from A through F that are typical of each knockdown line (C′–F′) have been placed next to each other alongside a wild-type cell (A′) and an example of a secondary cell from the *iab-6^{cocu}* mutant for ease of comparison. In C, E, and F the asterisk (*) indicates visible cell contacts between secondary cells. Bars, 10 μm for all panels. Average vacuole diameters: control (*iab-6^{DI}-Gal4*, *UAS-GFP*) 4.74 ± 1.11 μm; CG31034 2.42 ± 1.69 μm; CG7889 2.40 ± 1.80 μm; CG9509 2.36 ± 2.26 μm; and CG10514 2.87 ± 1.54 μm (all values from these knockdown lines are significantly different from the controls (ANOVA $P < 0.0005$).

predicted roles in sugar transport, binding, or transfer; or with predicted roles in vacuole function (regardless of signal sequence). These functions were selected because our previous study suggested that the accessory glands of *iab-6^{cocu}* males were abnormal in these processes (Gligorov *et al.* 2013). We also included a few candidates that did not fall into these categories but encoded proteins with a putative signal sequence that thus might be Sfps, were members of a group of genes that were candidates to be regulated as part of a gene neighborhood, or encoded proteins in functional classes already known to be important for reproduction in flies or other organisms. Based on these selection criteria, we finished with a list of 20 candidate genes for further functional testing via secondary cell-specific RNAi (Table 1). This group included the four genes that were identified in our cellular morphology screen, all of which also met the functional criteria used to select the remaining candidates. Of these 20 candidate genes, we were able to confirm knockdown in the secondary cells via RT-PCR for 18 (Table S1). The remaining 2 candidates were excluded from further analysis.

Receptivity suppression is compromised in mates of males knocked down for nine candidate genes

Mates of *iab-6^{cocu}* males do not exhibit the extended post-mating responses associated with the LTR. In contrast to mates of control males, which remain unreceptive to remating for up to 10 days following an initial mating, mates of *iab-6^{cocu}* males return to virgin levels of receptivity by 4 days ASM. To test whether any of our candidate genes were needed for the LTR, we crossed virgin Canton-S females to either RNAi or control males and then removed the males. We tested the females individually for re-mating 4 days later, by presenting them with a wild-type male for 1 hr. Nine of the 18 candidate genes tested were needed to maintain decreased female receptivity; mates of males knocked down for CG15902, CG14292, CG3349, CG15406, CG43161, CG3285, CG7882, CG9509, or CG14069 were significantly

Table 1 Candidate genes

CG no.	Chromosome	ID	Fold decrease	Signal sequence	Function	Highest expression
CG14069	2L	CG14069	—	Yes	Unknown	Testis
CG15406	2L	CG15406	—	No	General/sugar transporter	Malpighian tubules
CG3285	2L	CG3285	—	No	General/sugar transporter	Malpighian tubules
CG33783	3R	CG33783	1043.24	No	Unknown	Unknown
CG33784	3R	CG33784	578.00	Yes	Unknown	Eye
CG33631	3R	CG33631	160.31	Yes	Unknown	Broad
CG11598	3R	CG11598	66.11	Yes	Lipase	Accessory gland
CG15902	3R	Ugt86Dj	46.04	Yes	UDP-glucosyl transferase	Midgut
CG14376	3R	CG14376	41.93	Yes	Solute-binding protein	Broad
CG7882	2R	CG7882	30.01	No	Transporter, general sugar	Malpighian tubules
CG43161	3R	Skeletor	28.02	Yes	Spindle assembly	—
CG9509	X	CG9509	26.31	No	Glucose-methanol-choline oxidoreductase	Malpighian tubules
CG13309	3L	CG13309	26.31	Yes	Unknown	Malpighian tubules
CG5361	3R	CG5361	22.20	No	Alkaline phosphatase	Malpighian tubules
CG1112	3R	α-Est7	21.92	No	Carboxyl-esterase	Broad
CG14292	3R	CG14292	18.09	Yes	Unknown	Malpighian tubules
CG33630	3R	CG33630	16.44	Yes	Unknown	Broad
CG14715	3R	CG14715	7.35	Yes	*cis*-transisomerase	Broad
CG3349	3L	CG3349	5.77	Yes	Unknown	Accessory gland
CG18088	2L	CG18088	5.49	Yes	Alkaline phosphatase	Salivary gland
CG31326	3R	CG31326	0.38	Yes	Serine protease	Spermathecae

We selected candidate genes based on a conglomeration of criteria including fold change, signal sequence, predicted function, expression pattern, and sex-biased expression. Particular preference was given to candidate genes that might be involved with glycosylation, sugar transport, or other post-translational modification to try to determine if these phenotypes in the *iab-6*^{cocu} mutant relate directly to the LTR. Fold decrease could not be calculated for CG14069, CG15406, and CG3285 since these transcripts were not detectable in *iab-6*^{cocu} males. Expression data were obtained from Fly Atlas (Chintapalli *et al.* 2007) or, in the case of male-biased data, from modENCODE (Roy *et al.* 2010; McQuilton *et al.* 2012). Tissue-specific expression data were not available for CG43161. The italicized gene, CG31326, is an off-target for the CG15406 RNAi line.

more receptive to remating at 4 days ASM than mates of control males (Figure 2). Of these positive candidates, only CG3349 was previously known to encode a transferred Sfp (Findlay *et al.* 2009). These results suggest that the *iab-6*^{cocu} mutation impacts the expression of multiple genes that encode proteins necessary for males to maintain the suppression of receptivity normally observed in mated females and may play a role in regulating the long-term post-mating response. Alternate lines for eight of the positive candidates confirmed these results; the second available line for CG15902 did not cause knockdown (Figure S3).

Mates of candidate males lay fewer eggs than mates of control males

To test if the genes uncovered in our receptivity screen also contribute to the ability of males to induce and maintain normal egg laying in their mates, another aspect of the LTR, RNAi or control males were crossed to Canton-S virgin females. Mates of knockdown males for each of the nine candidate genes identified in the receptivity screen showed the normal post-mating increase in egg laying in the first day after mating. However, this increase was significantly lower in mates of CG15406 knockdown males than in controls. Consistent with our receptivity results, mates of knockdowns of each of the candidate genes laid fewer eggs than mates of control males at post-day 1 time points. Thus, the same nine genes that are needed to maintain the reduced receptivity that is characteristic of mated females also play a role in maintaining long term egg laying (Figure 3). The available alternate lines for each of the positive candidates confirmed these results (Figure S3). The necessity of all nine genes in the accessory glands of males for the maintenance of the PMR in their mates suggests that each of these genes is important for the maintenance of long-term post-mating responses in mated females.

Sex peptide storage is abnormal in mates of males knocked down for each of the nine candidate genes

The LTR is due to the binding of SP to, and slow release of SP from, sperm (Peng *et al.* 2005a). In mates of *iab-6*^{cocu} males, SP fails to enter storage in the female seminal receptacle and as such is unable to maintain the LTR. Thus, a possible explanation for why knockdown of CG15902, CG14292, CG3349, CG3285, CG14069, CG7882, CG15406, CG9509, and CG43161 in the male impaired the LTR could be impairment of SP storage in mates of knockdown males. To test this hypothesis, we performed Western blots using SP antibodies to detect differences in SP levels in mates of control or knockdown males at 30 min ASM (to detect SP transfer levels) and 4 days ASM, when egg laying and receptivity differences between mates of knockdown and control males are readily apparent and SP levels reflect stored, sperm-bound SP (Ravi Ram and Wolfner 2009; Gligorov *et al.* 2013; Findlay *et al.* 2014).

In all cases, equivalent amounts of SP were produced by control and knockdown males and transferred to females. However, mates of males knocked down for any of the nine candidate genes tested show little or no SP retention in storage at the 4-day time point compared to controls (Figure 4). These data indicate that knockdown of any of these nine genes results in a defect in SP retention, thus explaining the defects in the LTR observed in mates of their knockdown males. Protein products of those genes that contain signal sequences could potentially function in the LTR network within the mated female. However, the predicted proteins encoded by CG9509, CG15406, CG7882, and CG3285 either do not contain predicted signal sequences or also contain predicted transmembrane domains. If these proteins are not secreted, they could indirectly influence the LTR by being necessary for proper post-translational modification, secretion, or function of LTR network proteins.

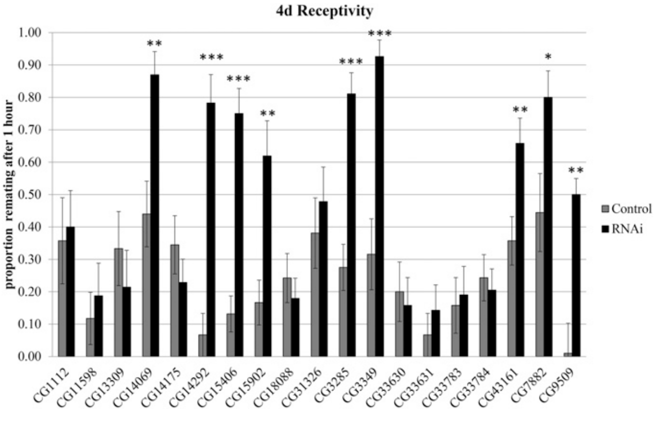

Figure 2 Mates of males knocked down for each of nine secondary-cell-expressed genes have an increased remating rate. The percentage of previously mated females that were willing to remate 4 days ASM to a wild-type male within 1 hr of exposure. At 4 days ASM females initially mated to males knocked down for CG14069, CG14292, CG15406, CG15902, CG3285, CG3349, CG43161, CG7882, and CG9509 are significantly more receptive to courting males compared to mates of control males (Wilcoxon ranked-sums test: *$P < 0.05$, **$P < 0.01$, and ***$P < 0.0001$; control—$n = 14$–42, average 25; RNAi—$n = 14$–39, average 25; specific values can be found in Table S2). Knockdown of CG31326, the potential off-target for CG15406, did not show a phenotype, confirming that the phenotype seen with knockdown of CG15406 is not the consequence of off-target effects. These results were confirmed using additional lines for all significant genes where available (Figure S3).

Discussion

Using RNA-seq we identified 77 transcripts that are downregulated by at least fivefold in the absence of *Abd-B* expression in the secondary cells of the male accessory gland. We chose a subset of these genes for further study based on expression pattern, predicted function, the presence of a signal sequence, or modifications in cellular morphology upon knockdown. We found that at least nine genes (CG14292, CG3349, CG14069, CG7882, CG15406, CG15902, CG43161, CG9509, and CG3285) are required for the secondary cell's function in maintaining the post-mating response. Knockdown of each of these nine gene candidates in the secondary cells resulted in a reduction in stored SP, consistent with their effect on the LTR. Four of our candidates were also necessary for the characteristic vacuoles and/or outward cellular morphology of the secondary cells.

Although we concentrated on the verification of the downregulated genes from our RNA-seq screen, we actually found more genes upregulated by $>5\times$ in our experiment than downregulated by $>5\times$ (115 *vs.* 73 genes). Among upregulated genes are a few genes previously identified as encoding constituents of the seminal fluid, such as Acp24A4 (Findlay *et al.* 2008), PEBme (Lung and Wolfner 2001), and PEBII (Bretman *et al.* 2010). Interestingly, *PEBme* (also known as Ejaculatory bulb protein of *melanogaster* or Ebp) and *PEBII* (also known as Ejaculatory bulb protein II or EbpII) are genes known be expressed in the ejaculatory bulb, but are 301 and 438× overexpressed, respectively, in *iab-6*^{cocu} mutants. Thus, we hypothesize that the *iab-6*^{cocu} mutation may cause secondary cell expression of genes whose transcription is normally repressed in those cells. Given that *iab-6*^{cocu} mutants disrupt *Abd-B* expression in the secondary cells and that *Abd-B* is a Hox gene that may contribute to the determination of secondary cell identity, our result may indicate that the *iab-6*^{cocu} phenotype could due to a failure to completely differentiate from a precursor cell type. Alternatively, it is also possible that secondary cells might influence the expression of genes in other cells through intercellular signaling. This latter hypothesis is supported by our RNAseq data for genes like CG11598. In wild-type accessory glands, CG11598 is expressed at high levels in both main cells and secondary cells (verified by *in situ* hybridization; data not shown) but is 66× downregulated in the *iab-6*^{cocu} flies. As secondary cells represent only 4% of the cells in the gland, this extremely large downregulation can be accounted for only by a change in CG11598 expression in the main cells.

Proteins important for multiple processes underlie the LTR defects in mates of iab-6^{cocu} *males*

Based on our results, it is clear that the *iab-6*^{cocu} mutation impacts a wide array of systems in the secondary cell that have consequences for the LTR. Of the nine candidates, five encode predicted secreted proteins, and only CG3349 is known to be transferred to females during mating (Findlay *et al.* 2008). However, the other four proteins may not have been detectable given that the secondary cells make up ~4% of the accessory gland, and as such these proteins may be present in low abundance. These proteins are potential candidates for being members of the network that binds SP to sperm.

Two of these proteins, encoded by *CG3349* and *CG14292*, have no domains predictive of their function, but the other three predicted proteins do (Drysdale 2008; Punta *et al.* 2012). CG14069 is predicted to have cytokine activity based on its similarity to the *Drosophila* growth-blocking peptide, a cytokine that regulates stressor-induced antimicrobial peptide expression in insects (Tsuzuki *et al.* 2012, 2014). While cytokines have not been previously described as transferred seminal fluid proteins in *Drosophila*, cytokines are present in the seminal fluid of most mammals (Gruschwitz *et al.* 1996;

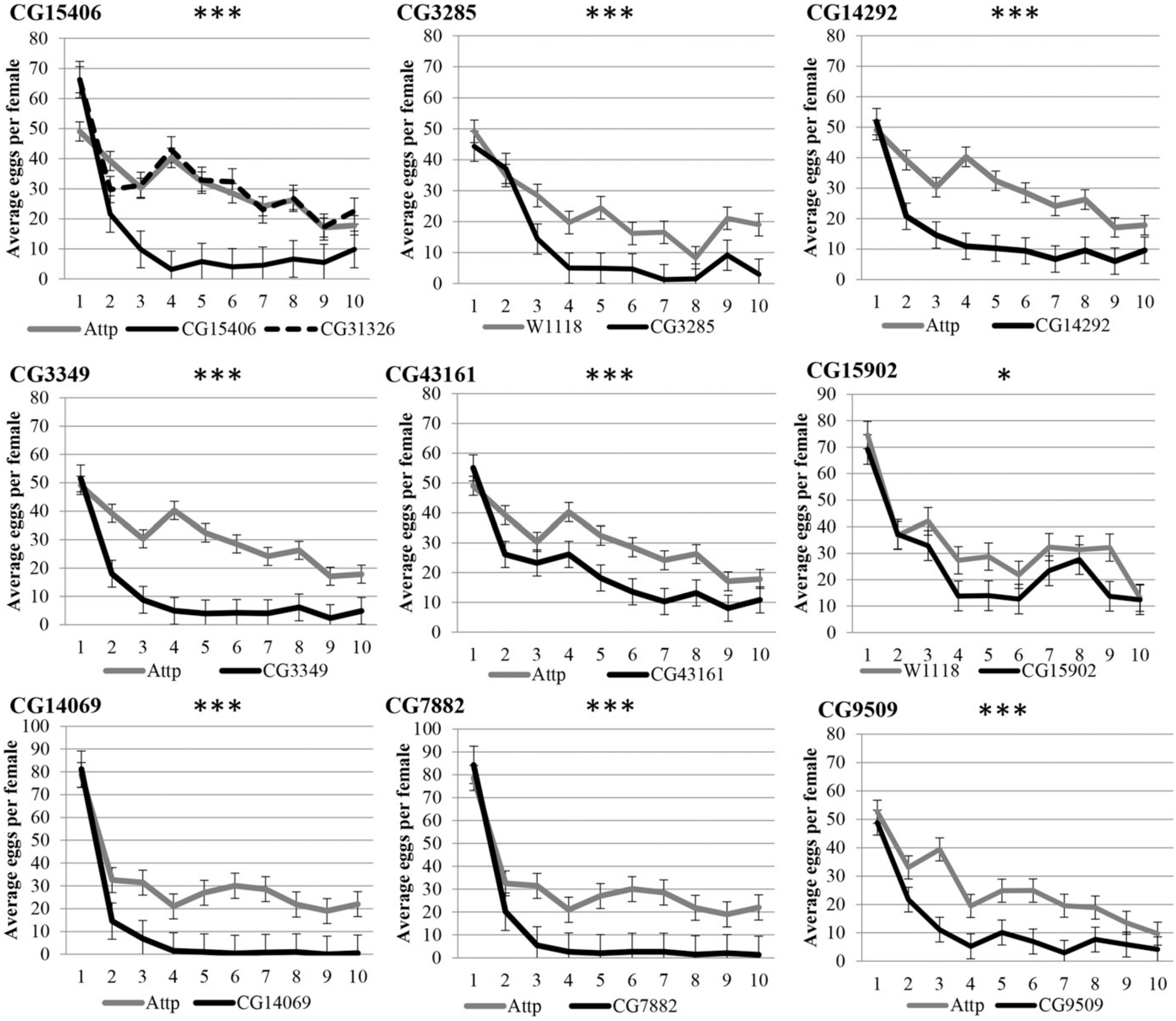

Figure 3 Mates of males knocked down for each of nine secondary-cell-expressed genes also show reduced long-term egg laying. The mean number of eggs laid per female mated to either control males (gray), knockdown males (black), or off-target knockdown males (black dashed line) over a 10-day period. Knockdown of CG15406 in males resulted in a difference in egg laying at 24 hr ASM (Wilcoxon ranked-sums test: $P = 0.0042$). However, the increase in egg laying observed in mates of CG15406 knockdown males appears to be an off-target effect of CG31326 (dashed line, Wilcoxon ranked-sums test: $P = 0.0008$) since mates of males knocked down for both genes (CG15406 and the off-target CG31326) or just CG31326 share this effect. There were no other differences at the 24 hr ASM time point across mates of knockdown males compared to controls. Mates of males knocked down for each of the nine candidates lay significantly fewer eggs over 10 days when compared to mates of control males (rmANOVA: $*P = <0.05$, $**P = <0.01$, $***P = <0.0001$; control: $n = 18–27$, average 22; knockdown: $n = 14–23$, average 19; see Table S2 for specific n and P-values). The number of progeny that were produced by each female were also counted so that hatchability (no. of progeny/no. of eggs) could be calculated. No significant differences in hatchability from controls were detected for mates of knockdown males of any of these candidate genes (data not shown). These results were confirmed using additional UAS-RNAi lines and a shorter 5-day egg-laying assay (Figure S4).

Dousset *et al.* 1997; Vera *et al.* 2003). In mammals, seminal cytokines, particularly TGF-β in human and mouse (Sharkey *et al.* 2012a), are activated in the seminal fluid and have been shown to interact with uterine and cervical epithelial cells to initiate pro-inflammatory cytokine synthesis and leukocyte recruitment in the female (Sharkey *et al.* 2007, 2012a,b). Sfps, including the sex peptide, also elicit an immune response in *Drosophila* (Peng *et al.* 2005b), suggesting a possible role for CG14069 in regulating this process. How CG14069 functions in SP storage and dynamics will require future study.

CG43161 (*skeletor*) encodes four alternative splice products, at least one of which is a component of the intracellular mitotic spindle matrix. The Skeletor-associated spindle is composed of filaments that do not contain actin or tubulin (Bairati 1968; Walker *et al.* 2000; Zheng 2010). Since there is

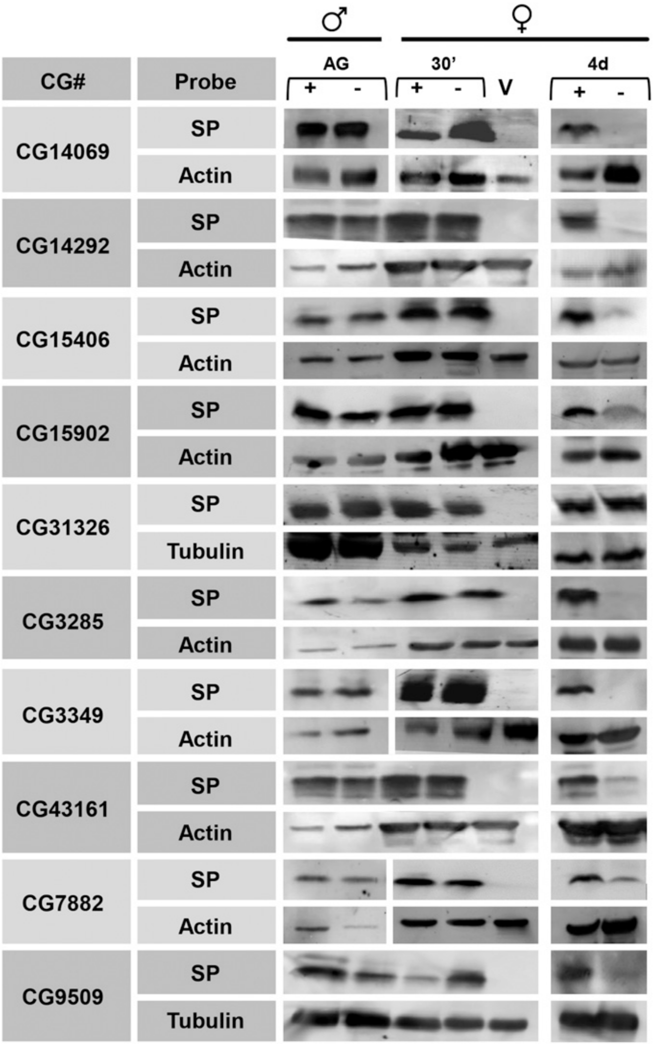

Figure 4 Sex peptide storage is impaired in mates of males knocked down for each of nine candidate genes. Mates of each of our nine knockdown males have less SP, as detected by antibodies to SP, in their reproductive tract at 4 days ASM. Tubulin or Actin was used as a loading control. Accessory gland extracts from a single male [Control (+) or RNAi (−)] were used as a positive control, and reproductive tract extracts from four virgin females were used as a negative control (V). Reproductive tract (RT) extracts were obtained from females mated to either control (+) or RNAi (−) males at 30 min ASM (2 RTs per) and 4 days ASM (18 RTs per). CG31326, an off-target for the CG15406 VDRC line, was included as a control. All mates of RNAi males have at least as much SP present in their reproductive tracts at 30 min ASM as do mates of control males, indicating normal SP transfer by knockdown males. However, significantly less SP is present in the female reproductive tract at 4 days ASM to any of the RNAi males, except for the off-target control CG31326, as expected, than is present in mates of control males, suggesting that SP storage is impaired.

no apparent difference in accessory gland size or secondary cell number in *iab-6*^{cocu} males (Gligorov *et al.* 2013), it seems unlikely that the reduction in CG43161 seen in these males leads to defects in cellular division. Non-tubulin-containing filaments were previously reported inside the vacuoles of the secondary cell as well as in the lumen of the accessory gland (Bairati 1966, 1968; Chen 1984) and appear to be transferred to females during mating (Bairati 1966). It will be intriguing to test whether Skeletor comprises these filaments and thus contributes to the PMR. Alternatively, three secreted splice variants of CG43161 contain DMB and DOMON domains, which are associated with modifying cell-surface proteins (Aravind 2001; Iyer *et al.* 2007) and could potentially thereby contribute to the function of the LTR network.

CG15902 encodes a protein predicted to have glycosyltransferase activity. At least two Sfps that are part of the SP pathway are known to be glycosylated: the lectins CG1656 and CG1652 (Gligorov *et al.* 2013; Ravi Ram and Wolfner 2007, 2009). The substrates for these proteins and the importance of their glycosylation state are currently unknown. CG15902 may play a role in regulating the sugars necessary for these seminal lectins to bind their targets or may suggest a regulatory role for glycosylation in the accessory gland. Further work looking into the substrates of CG15902 is needed to determine how it may help regulate the LTR.

The four other new genes needed for the LTR (CG9509, CG15406, CG7882, and CG3285) encode predicted intracellular or transmembrane proteins. Thus their likely function is in the production, secretion, or modification of secreted LTR proteins needed for the storage of SP. CG9509 is a member of the GMC oxidoreductase family of enzymes and has predicted choline dehydrogenase activity (Takeuchi *et al.* 2005). Other members of this family in mammals are important for reproduction, including the canonical choline dehydrogenase, which is essential for normal sperm motility and male fertility (Johnson *et al.* 2010, 2012).

The remaining three genes are predicted to encode members of the major facilitator superfamily, the largest known superfamily of secondary transport carriers (reviewed in Pao *et al.* 1998 and Reddy *et al.* 2012); CG15406, a predicted fructose transporter; CG7882, a glucose transporter; and CG3285, a general sugar transporter (FlyBase). The role of such sugar transporters in the LTR is unclear. One possibility is that they, potentially along with the glycosyltransferase CG15902, may facilitate the glycosylation of Sfps. Consistent with this idea, *iab-6*^{cocu} males impact the stability and glycosylation of some LTR network proteins (Gligorov *et al.* 2013). Whether these differences are directly related to the SP retention defect seen in mates of *iab-6*^{cocu} males is unclear. Accordingly, we tested mates of males knocked down for all 4 genes, as well as the 14 other candidate genes, by Western blot using antibodies to the proteins known to be abnormally glycosylated (CG1656/CG1652) in *iab-6*^{cocu} males or processed (CG9997) in their mates. No differences in CG9997 processing or in CG1656/CG1652 apparent molecular weight (Figure S5 and Figure S6) were detected in the mates of males knocked down for any of our candidate genes. Based on these results, we cannot draw any definitive conclusions about the relationship between the glycosylation of CG1656/CG1652 or the processing of CG9997 and SP storage. However, these results suggest that none of our candidate genes are involved in either process. Alternatively, these sugar transport proteins could affect the level of sugars in the ejaculate, promoting sperm motility, as occurs in mammals and honey bees (Poole and Edwards 1970; Caballero Peregrin *et al.* 1979; Hinton and Howards 1982; Hinton *et al.* 1983; Gonzales 2001; Gonzales and Villena 2001; Collins *et al.* 2006; King *et al.* 2011; Vivas-Acevedo *et al.* 2011), or possibly affecting the activity of SPR-expressing neurons, which express the fructose-responsive gustatory receptor 43a (Yapici *et al.* 2008; Miyamoto and Amrein 2014).

When changes in cellular morphology correlate with LTR differences, vacuole number is reduced

The original phenotype that led to the identification of *iab-6^{cocu}* as a secondary cell mutant was a dramatic change in cellular morphology from large, spherical-shaped cells filled with large vacuoles to the more main-cell-like small, hexagonal, vacuole-less cells. We were able to identify multiple genes whose products are required for the normal overall cell morphology. Knockdown of five genes (CG9509, CG14069, CG7882, CG31034, and CG10514) consistently affects vacuole number/size and alters the external cellular shape. We found that three of these genes, CG9509, CG14069, and CG7882, also affected the male's ability to induce the LTR. The lack of perfect correlation between these morphological phenotypes and changes in the LTR cannot be explained simply by the severity of the morphological changes. While the knockdown of CG10514 was much milder than the three lines that displayed LTR defects, knockdown of CG31034 gave a quite strong phenotype, affecting both the vacuole number/size and the external cellular shape. One possible way to explain part of this discrepancy could be that there are multiple types of vacuoles. Indeed, electron microscopy work performed in the 1960s (Bairati 1968) showed at least two distinct types of vacuoles in the secondary cells: one containing electron dense “filaments” and the other containing less dense material. Thus it is possible that knockdown of some of these gene products affects a class of vacuole that is important for the LTR, while the others affect a different class of vacuoles that do not play a definable role in the LTR pathway. CG31034 knockdown has a few vacuoles of close-to-normal size, but lacks most of the vacuoles seen in a normal secondary cell. Perhaps the remaining vacuoles are the ones important for the PMR.

How each of these five genes influences vacuole formation is less clear. One probable hypothesis is that the loss of vacuoles is only a readout of a more major change in the biology of the cells. This can perhaps be evidenced by the general changes in cell shape seen with the knockdown of some candidates. Normally, secondary cells are large, “pear-like” cells (Bairati 1968) sticking out of the main cell monolayer into the lumen. Although some of the effect on cell shape can be attributed simply to a loss of cytoplasmic volume from vacuole loss, knockdown of CG31034 and CG10514 creates prominent changes in cell shape that cannot be attributed solely to a reduction in vacuole numbers, which are less affected than in other knockdown lines. In particular, the connections often seen between secondary cells after knockdown of these genes, something that is not observed in wild-type glands, seem to indicate that the adherence properties (and maybe the cellular polarity) of these cells may be different. Given the predicted functions of CG31034 (endopeptidase) and CG10514 (phosphotransferase), cell adhesion or polarity might be modulated by protein modifications predicted to be mediated by these candidates. In the case of the predicted cytokine, CG14069, there is some evidence that cytokines can influence the vacuole formation that leads to endothelial tubes in human endothelial cells *in vitro* (Bayless 2000; Senger 1996) and also play a role in regulating the formation of autophagic vacuoles in macrophages (Harris 2007). However, given the multifaceted effect of the knockdown of this gene on cell size, vacuole number and nuclei number, a specific effect on vacuole formation seems less likely. It is possible, for example, that CG14069 instead might be important simply to preserve the secondary cell identity. That this effect is not seen in *iab-6^{cocu}* mutants could be attributed the complexity of the *iab-6^{cocu}* phenotype, which may somehow compensate for the effects of CG14069 knockdown through the regulation of other genes. More work is needed to determine the specific function of these vacuoles beyond that they have some important role in regulating the PMR.

Conclusion

Previously, we observed that the *iab-6^{cocu}* mutation influences post-translational modification of some Sfps, cellular morphology, and the maintenance of the LTR. We have demonstrated that at least nine individual genes that are down-regulated in the accessory gland of *iab-6^{cocu}* males encode proteins that are necessary for maintenance of SP in the mated female, and thus for the LTR. Knockdown of three of these genes also severely impacts the number of vacuoles present in the secondary cells and one mildly impacts both the vacuole number and the shape of these cells. Our results suggest that these phenotypes are interrelated but genetically separable and may argue for the importance of some secondary cell vacuoles in the maintenance of the LTR. Furthermore, we conclude that the *iab-6^{cocu}* mutation impacts the expression of genes required for multiple secondary cell functions, beyond simply the expression and secretion of transferred seminal fluid proteins, that are essential for the maintenance of the long-term response.

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GENETICS

Supporting Information
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The Female Post-Mating Response Requires Genes Expressed in the Secondary Cells of the Male Accessory Gland in *Drosophila melanogaster*

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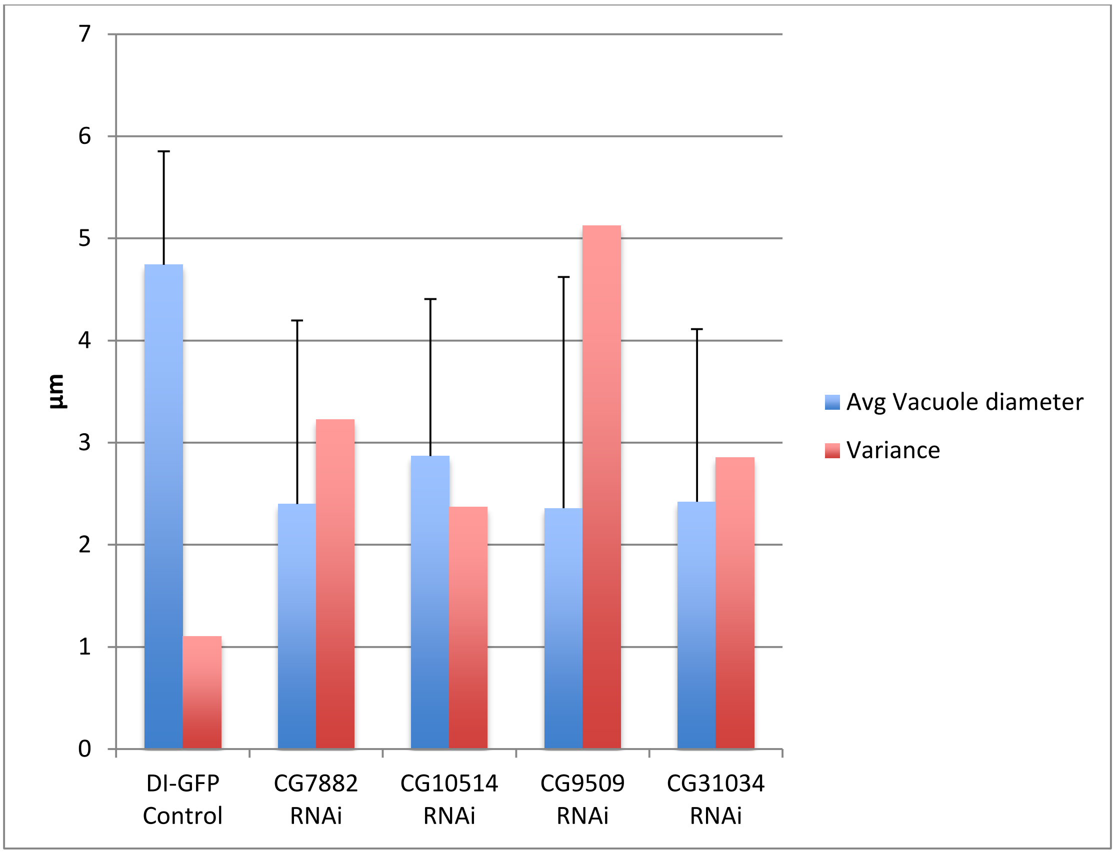

	DI-GFP Control	CG7882 RNAi	CG10514 RNAi	CG9509 RNAi	CG31034 RNAi
Avg Vacuole size	4.74	2.40	2.87	2.36	2.42
STD Dev	1.11	1.80	1.54	2.26	1.69
Variance	1.10	3.22	2.37	5.12	2.85
n	172	177	252	287	245

P values determined by ANOVA vs wt controls all <0.0005

Figure S1
Average secondary-cell vacuole diameter for knockdowns of selected genes. Vacuole size was measured using ImageJ v1.48 software (Wayne Rasband, NIH, USA) using images taken on a Zeiss Axioplan fluorescent microscope. Statistical significance was determined by ANOVA. In blue, are the averages of vacuole diameters in microns for each RNAi line (indicated below the graph, with error bars representing standard deviations. In red are the variance determinations from ANOVA. The average vacuole diameters of the knocked down lines reported all are statistically different from wild-type controls (iab6DI-Gal4, UAS-GFP) (p<0.0005).

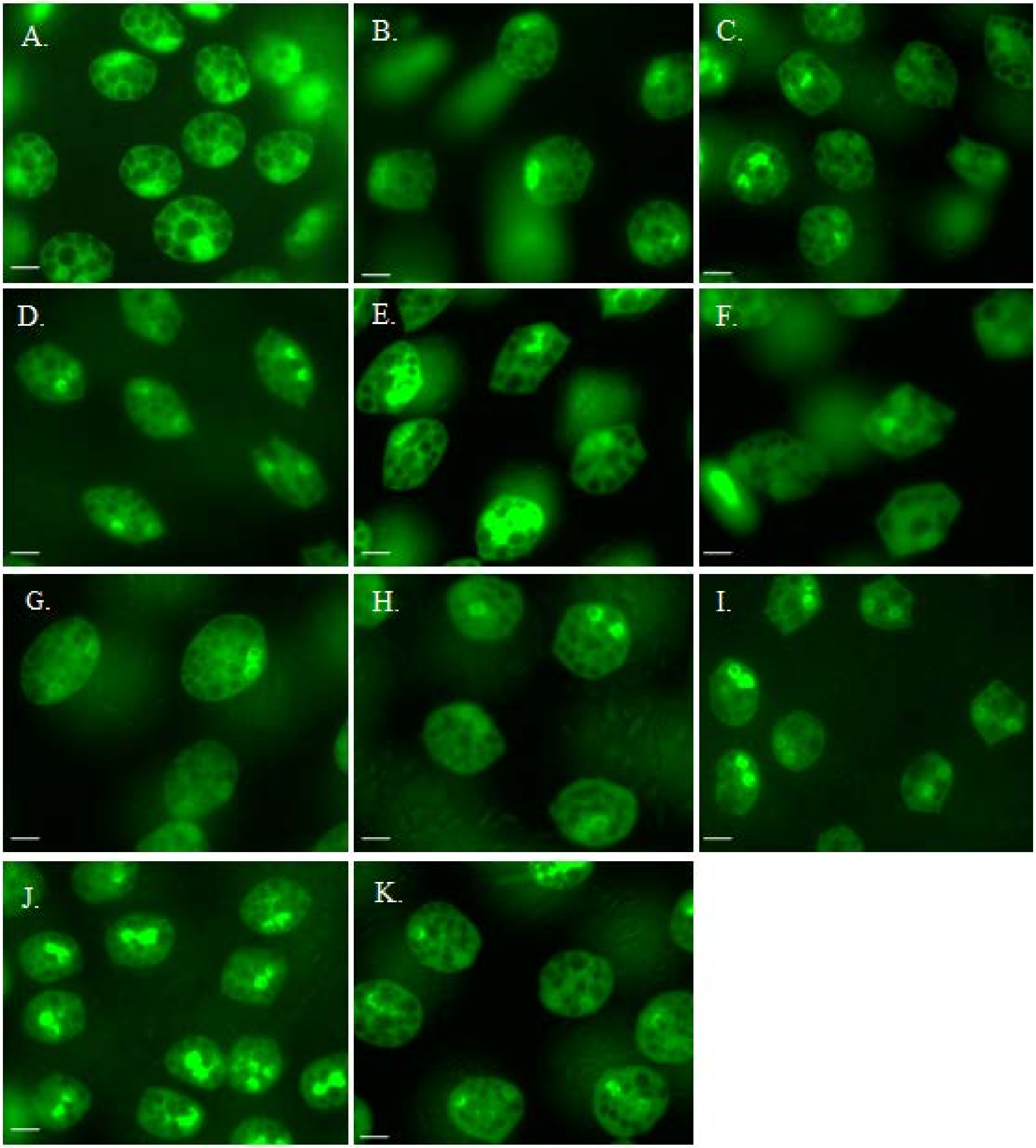

Figure S2: Knockdown of 10 genes showing partially penetrant secondary cell morphological phenotypes. For these genes, defects were seen in only one or two out of the three dissected accessory glands, A. wild type control, B. CG31198, C. CG33630, D. CG9294, E. CG15406, F. CG6602, G. CG12809, H. CG13538, I. CG18088, J. CG14681 and K. CG5106. The included scale bars are 10um for all panels.

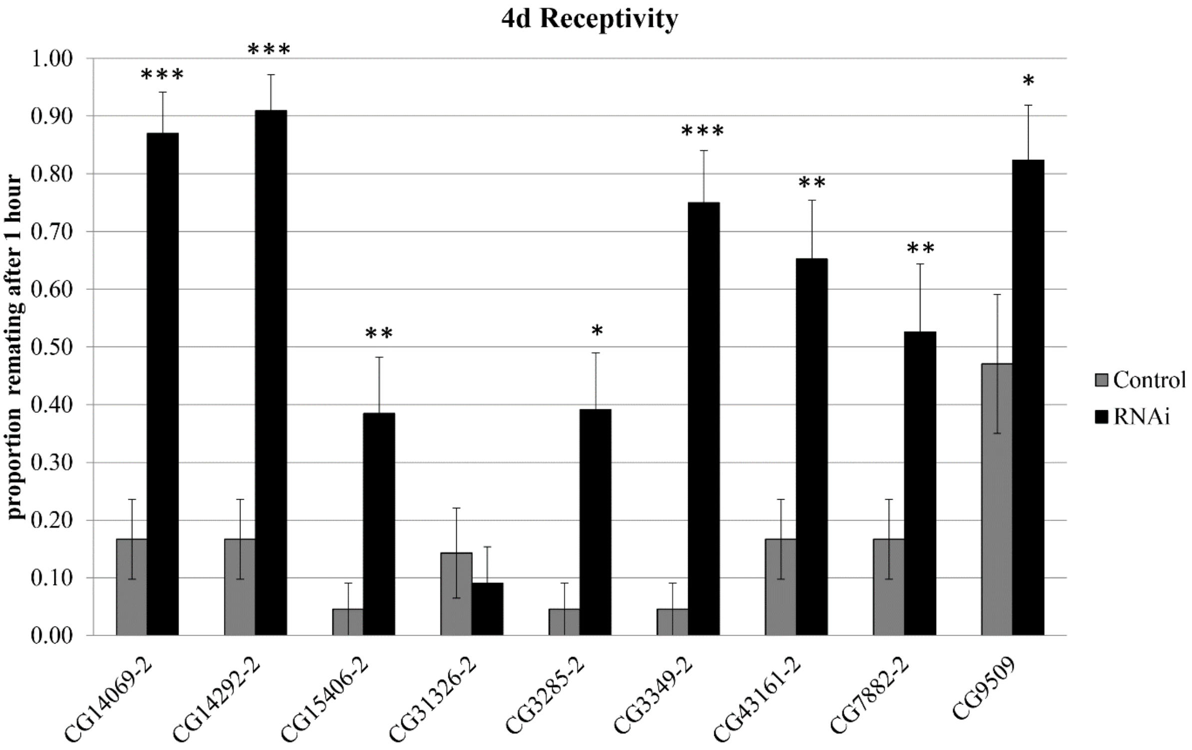

Figure S3: Increased receptivity in mates of males knocked-down using alternative lines confirm the importance of secondary cell expressed genes in remating rate. The percentage of previously mated females that were willing to remate 4 days after the start of mating (ASM) to a wild type male within 1 hour of exposure. At 4d ASM females initially mated to males knocked down for CG14069, CG14292, CG15406, CG3285, CG3349, CG43161, CG7882, and CG9509 are significantly more receptive to courting males compared to mates of control males (WRST *p=<0.05, **p=<0.01, *** p=<0.0001, specific values can be found in Table S2). The alternate line for CG15902 did not knock down and is not shown here.

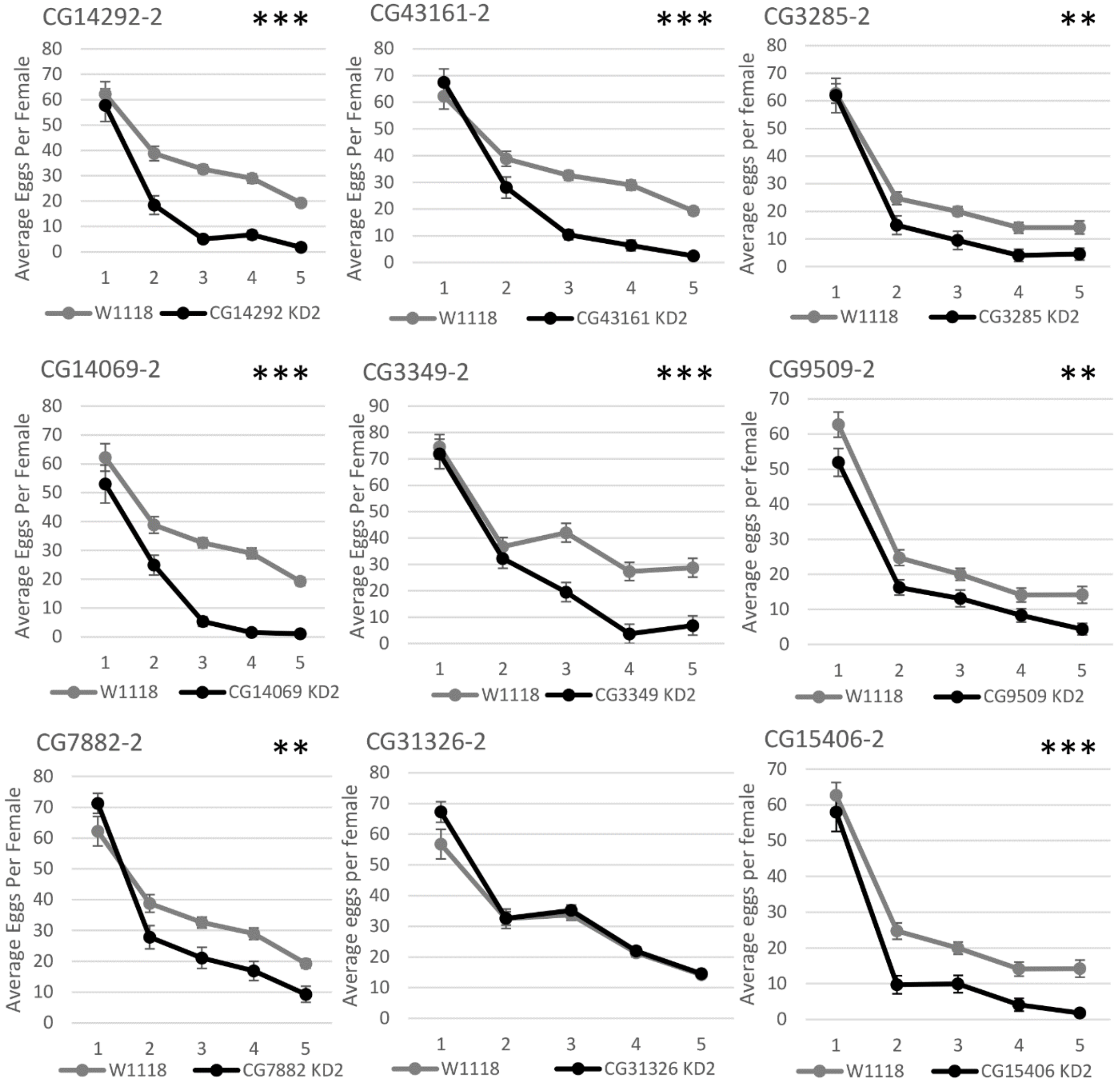

Figure S4: Reduced long term egg-laying in mates of males knocked-down using alternative lines confirm the importance of secondary cell expressed genes in long-term egg-laying. The mean number of eggs laid per female mated to either control males (grey) or knockdown males (black) over a 5 day period. Knockdown of CG15406 and CG31326 did not result in a significant difference at 24h (although CG31326 is trending at p=0.07), suggesting that at least for CG15406 the 24h phenotype may be a background effect. Mates of males knocked down for each of the alternate lines showed similar differences in egg-laying to those in Figure 3 (rmANOVA p= <0.05*, p=<0.01**, p=<0.0001***, specific values can be found in Table S2). The number of progeny that were produced by each female were also counted so that hatchability (#progeny/#eggs) could be calculated. No significant differences in hatchability were detected for any of these candidate genes (data not shown). The alternate line for CG15902 did not knock down and is not shown here. Unlike in Figure 3, the results for CG15406 and CG31326 were run on separate days and thus are reported individually.

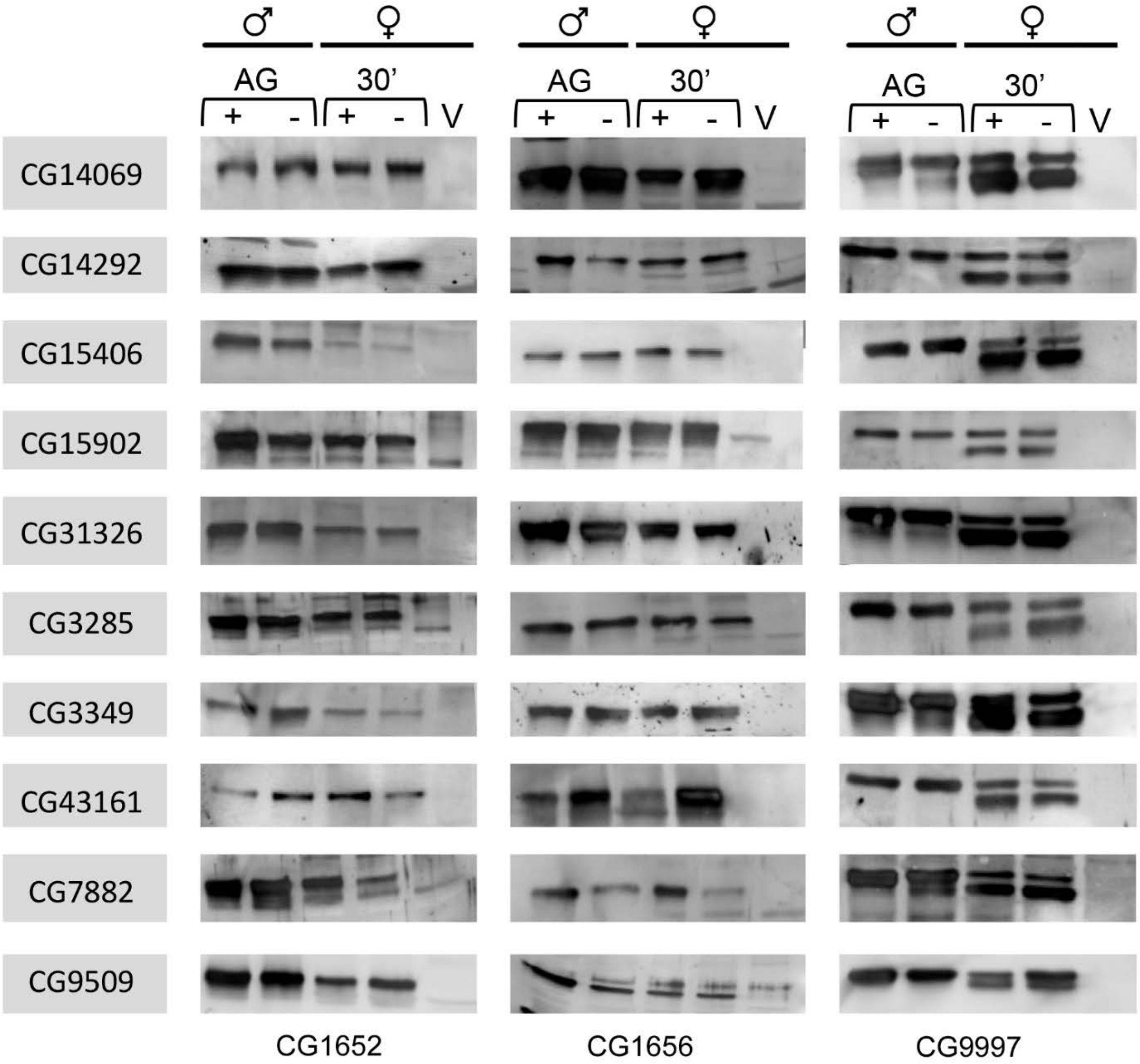

Figure S5: CG1656, CG1652, and CG9997 glycosylation and processing are normal in mates of males knocked down for our 9 LTR candidates. Accessory gland extracts from a single male (Control (+) or RNAi (-)) were used as a positive control and reproductive tract extracts from 4 virgin females were used as a negative control (V). Reproductive tract extracts were obtained from females mated to either control (+) or RNAi (-) males at 30' ASM (2 RTs per). CG31326, an off-target for the CG15406 VDRC line, as included as a control. All mates of RNAi males show no differences in CG1656/CG1652 apparent molecular weight or in CG9997 processing, suggesting that none of the knocked down genes is important for these processes.

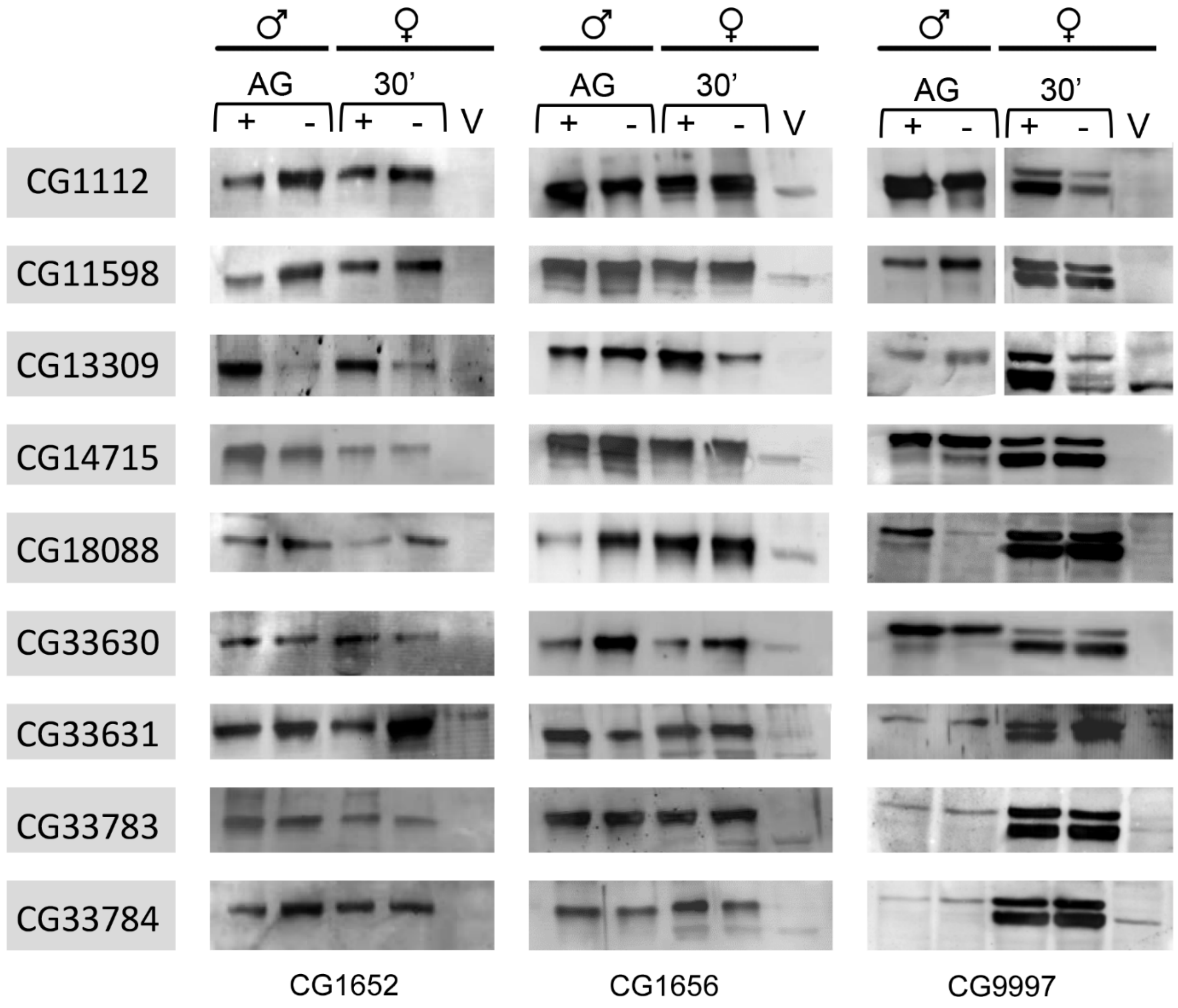

Figure S6: CG1656, CG1652, and CG9997 glycosylation and processing are normal in mates of males knocked down for the remaining 8 candidates. Accessory gland extracts from a single male (Control (+) or RNAi (-)) were used as a positive control and reproductive tract extracts from 4 virgin females were used as a negative control (V). Reproductive tract extracts were obtained from females mated to either control (+) or RNAi (-) males at 30' ASM (2 RTs per). All mates of RNAi males show no differences in CG1656/CG1652 apparent molecular weight or in CG9997 processing suggesting that none of these genes is important for these processes.

Table S1: Level of knockdown in RNAi lines used for post response mating assays

Gene	Line	VDRC ID	Library	nIOD Control	nIOD RNAi	% Expression of WT	Knocked Down	Driver
CG1112	1	105273	KK	0.513	0.240	46.8%	Yes	D1
CG11598	1	103262	KK	0.434	0.050	11.5%	Yes	D1
CG13309	1	101094	KK	0.059	0.013	22.1%	Yes	D1
CG14069	1	9519	GD	0.209	0.006	2.8%	Yes	D1
CG14069	2	9517	GD	0.196	0.081	41.3%	Yes	D1
CG14715	1	104124	KK	0.854	0.047	5.5%	Yes	D1
CG14292	1	102225	KK	0.996	0.138	13.8%	Yes	D1
CG14292	2	17261	GD	0.875	0.069	7.8%	Yes	D1
CG15406	1	105077	KK	0.507	0.028	5.5%	Yes	D1
CG15406	2	45887	GD	0.588	0.031	5.3%	Yes	D1
CG15902	1	104008	KK	0.153	0.185	121.2%	No	Tubulin
CG15902	2	8577	GD	3.309	0.312	9.4%	Yes	D1
CG18088	1	100340	KK	0.382	0.290	75.8%	Yes	D1
CG31326	1	108815	KK	0.025	0.048	194.2%	No	D1
CG31326	1	108815	KK	0.543	0.003	0.6%	Yes	Tubulin
CG31326	2	51890	GD	0.320	0.192	59.9%	Yes	Tubulin
CG3285	1	52669	GD	1.287	0.291	22.6%	Yes	D1
CG3285	2	51059	GD	0.839	0.032	3.9%	Yes	D1
CG3349	1	109764	KK	1.138	0.548	48.2%	Yes	D1
CG3349	2	26822	GD	1.138	0.672	59.1%	Yes	D1
CG33630	1	104105	KK	1.066	1.670	156.6%	No	D1
CG33630	1	104105	KK	0.154	0.098	63.6%	Yes	Tubulin
CG33631	1	101627	KK	0.284	0.032	11.3%	Yes	D1
CG33783	1	106535	KK	6.900	0.717	10.4%	Yes	D1
CG33784	1	104931	KK	1.502	0.053	3.5%	Yes	D1
CG43161	1	109085	KK	0.464	0.066	14.2%	Yes	D1
CG43161	2	52283	GD	0.086	0.042	49.2%	Yes	D1
CG5361	1	51984	GD	0.624	0.643	103.2%	No	Tubulin
CG7882	1	109918	KK	0.513	0.071	13.8%	Yes	D1
CG7882	2	8101	GD	0.579	0.147	25.3%	Yes	D1
CG9509	1	107089	KK	0.633	0.043	6.8%	Yes	D1
CG9509	2	6336	GD	14.741	1.536	10.4%	Yes	D1

Table S1: Knockdown in RNA lines for candidate Genes. For each of the candidates chosen, line numbers, VDRC transformant IDs, and their corresponding knockdown efficiency are reported. The level of expression is reported as normalized integrated optical density (nIOD) from RT-PCR results using the secondary cell specific *iab-6*^{D1}-GAL4 driver, or in cases where knockdown was not observed using this driver line, the ubiquitous tubulin-GAL4 line. RT-PCR signals were normalized and knockdown (KD) as % of wild type expression was calculated as described in (SITNIK *et al.* 2014). Failure to knock down using *iab-6*^{D1}-GAL4 with successful knockdown using *tubulin*-GAL4 suggests that these genes are likely to be expressed in the main cells or in both main and secondary cells. For the off-target gene CG31326, only *tubulin*-GAL4 knockdown results are reported for line 2, since the results from line 1 suggests that this gene is highly expressed in cells other than secondary cells. For CG15902 line 1 and CG5361 line1, only the tubulin-GAL4 driven knockdown result is reported, since knockdown was not observed using either driver. CG14376 was not detectable in the accessory gland by RT-PCR so knockdown could not be ascertained and is thus not included in this table. These lines (CG15902 line 1, CG14376 line 1, and CG5361 line 1) were removed from further analysis.

Table S2: Summary information and statistics

Stock Information				4d Receptivity			Egg-Laying rmANOVA			Day-1	Total Eggs
Gene	Line	VDRC ID	Library	p-value	N Control	N RNAi	p-value	N Control	N RNAi	p-value	p-value
CG1112	1	105273	KK	0.8031	14	20	n.d.	n.d.	n.d.	n.d.	n.d.
CG11598	1	103262	KK	0.5818	17	16	n.d.	n.d.	n.d.	n.d.	n.d.
CG13309	1	101094	KK	0.4646	18	14	n.d.	n.d.	n.d.	n.d.	n.d.
CG14069	1	9519	GD	**0.0021**	25	23	**<0.0001**	20	15	0.6053	**<0.0001**
CG14069	2	9517	GD	**<0.0001**	30	23	**<0.0001**	27	22	0.2819	**<0.0001**
CG14715	1	104124	KK	0.3069	29	35	n.d.	n.d.	n.d.	n.d.	n.d.
CG14292	1	102225	KK	**<0.0001**	15	23	**<0.0001**	19	19	0.0615	**<0.0001**
CG14292	2	17261	GD	**<0.0001**	30	22	**<0.0001**	27	22	0.7552	**<0.0001**
CG15406	1	105077	KK	**<0.0001**	38	32	**<0.0001**	19	19	**0.0042**	**<0.0001**
CG15406	2	45887	GD	**0.0058**	22	26	**<0.0001**	26	15	0.6068	**0.0002**
CG15902	2	8577	GD	**0.001**	30	21	**0.0124**	21	18	0.4218	**0.0201**
CG18088	1	100340	KK	0.5153	29	39	n.d.	n.d.	n.d.	n.d.	n.d.
CG31326	1	108815	KK	0.5199	21	23	0.2406	19	19	**0.0008**	0.2201
CG31326	2	51890	GD	0.5996	21	22	0.3012	21	22	0.0664	0.2795
CG3285	1	52669	GD	**<0.0001**	40	37	**<0.0001**	19	14	0.8553	**<0.0001**
CG3285	2	51059	GD	**0.0247**	22	23	**0.0054**	26	16	0.9072	**0.0058**
CG3349	1	109764	KK	**<0.0001**	19	27	**<0.0001**	19	19	0.161	**<0.0001**
CG3349	2	26822	GD	**<0.0001**	22	24	**0.0001**	21	19	0.8389	**0.0005**
CG33630	1	104105	KK	0.7353	20	19	n.d.	n.d.	n.d.	n.d.	n.d.
CG33631	1	101627	KK	0.4795	15	21	n.d.	n.d.	n.d.	n.d.	n.d.
CG33783	1	106535	KK	0.7892	19	21	n.d.	n.d.	n.d.	n.d.	n.d.
CG33784	1	104931	KK	0.6922	37	39	n.d.	n.d.	n.d.	n.d.	n.d.
CG43161	1	109085	KK	**0.0076**	42	38	**<0.0001**	19	22	0.0993	**0.0006**
CG43161	2	52283	GD	**0.0003**	30	23	**<0.0001**	27	20	0.5183	**<0.0001**
CG7882	1	109918	KK	**0.0171**	18	25	**<0.0001**	20	18	0.7256	**<0.0001**
CG7882	2	8101	GD	**0.0084**	30	19	**0.0093**	27	17	0.3169	**0.0099**
CG9509	1	107089	KK	**0.0004**	28	30	**<0.0001**	18	23	0.2694	**<0.0001**
CG9509	2	6336	GD	**0.0222**	18	17	**0.0006**	26	18	0.0675	**0.0023**

Table S2: Summary information and statistics. A summary of the receptivity and egg-laying findings presented in this paper. Experimental results are reported as raw p-values. Genes whose expression was not required for normal female receptivity were not included in the egg-laying assays and are listed as n.d. (not done). **Boldface** p-values indicate a significant change. Lines that were found to not knock down are excluded from this table and from our analysis.

Paired-end RNAseq:

Number of reads:

	Total No reads	Mapped	% all reads
CTRL	36740061	26069791	71.0%
Iab-6cocu	30203836	21318494	70.6%

Genes and exons (mapped to Drosophila melanogaster r5.30 fb2010_07 reference genome):

	Genes	Exons
Raw	84158	11982
Candidates	29617	8764

RNAseq Quality Control:

Read % Pass Filter	Read % Attributed	Read % Maximum	Read % Minimum	Error Rate (PhiX)	Average Q30
0.85	0.93	0.54	0.45	0.55%	83.3%

The quality of the RNAseq reads was evaluated using spiked PhiX genome controls to determine sequencing error rates. Furthermore, all reads were evaluated using Q30 criteria (the percentage of bases having a base quality greater than or equal to 30). The calculated error rates andQ30 results are presented below and were determined by Fasteris, SA (Geneva, CH) to be within normal specifications.

Table S3: Fly lines for the initial cell morphology screen. Gene names and VDRC transformant IDs for the UAS-RNAi lines used in the initial cell morphology screen.

Table S4: Fly lines for initial cellular morphology screen		
#	**Gene name:**	**VDRC trasformant ID**
1	alpha-Est5 (CG1089)	100526
2	alpha-Est7	105273
3	alphaTry	103292
4	beat-Ic	105066
5	beat-IV	110257
6	betaTry	102898
7	CG10514	107169
8	CG10560	104272
9	CG11598	103262
10	CG12374	101566
11	CG12506	109086
12	CG13309	101094
13	CG13538	102614
14	CG13793	50167
15	CG14069	9519
16	CG14245	17839
17	CG14292	102225
18	CG14376	100667
19	CG14681	109085
20	CG14715	104124
21	CG15155	104046
22	CG15406	105077
23	CG15614	100503
24	CG17752	106787
25	CG2187	101065
26	CG2196	108782
27	CG3106	42699
28	CG31090	108499
29	CG31198	107738
30	CG3285	52669
31	CG33630	104105
32	CG33631	101627
33	CG33783	106535
34	CG33784	104931
35	CG5361	51985
36	CG6602	106152
37	CG6628	49368
38	CG6733	102774
39	CG7882	109918
40	CG8157	18585
41	CG8934	103285
42	CG9259	103953
43	CG9294	102143
44	CG9509	107089
45	Cpr56F	16856
46	Jon65Aiv	15299
47	Jon74E	105316

Table S4: Fly lines for initial cellular morphology screen		
#	**Gene name:**	**VDRC trasformant ID**
48	Jon99Cii	109902
49	NaPi-T	106729
50	nerfin-2	101434
51	obst-A	102591
52	phr	35499
53	ple	108879
54	scpr-A	43220
55	scpr-C	16610
56	Traf1	110766
57	Ugt86Dj	101244
58	yellow-e	100926
59	gsb	107940
60	CG3349	109764
61	CG18088	100340

Table S4: Fly lines for the initial cell morphology screen. Gene names and VDRC transformant IDs for the UAS-RNAi lines used in the initial cell morphology screen.

Table S5: RNAseq results. The complete list of RNAs detected in our RNAseq analysis comparing accessory glands from control males to those of iab-6cocu males. Expression has been normalized (see materials and methods) and is reported as reads per million (RPM). Relative expression between the two samples is presented as fold changes (either up or down). This dataset includes RNAs that mapped to non-protein coding RNAs (such as miRNA precursors) and pseudo-genes in addition to RNAs that mapped to known protein coding genes. A (-) indicates that an accurate fold-change could not be calculated because the RNA was only detected in one of the two samples.

Probe	Feature	RPM		Fold increase	Fold Decrease
		Control	*iab-6* ^{cocu}		
CBP_gene	CBP	0	1.15879	-	0.00
CG13618_gene	CG13618	0	0.728384	-	0.00
CG14880_gene	CG14880	0	0.662168	-	0.00
CG15649_gene	CG15649	0	1.62231	-	0.00
CG2663_gene	CG2663	0	17.7461	-	0.00
CG2736_gene	CG2736	0	0.695276	-	0.00
CG32750_gene	CG32750	0	2.91354	-	0.00
CG3397_gene	CG3397	0	1.29123	-	0.00
CG41465_gene	CG41465	0	0.827709	-	0.00
en_gene	en	0	0.960143	-	0.00
GstE8_gene	GstE8	0	0.761493	-	0.00
lbl_gene	lbl	0	0.927035	-	0.00
v_gene	v	0	0.695276	-	0.00
PebII_gene	PebII	1.08873	476.827	437.97	0.00
CG31157_gene	CG31157	0.0272182	10.9589	402.63	0.00
Elo68alpha_gene	Elo68beta	0.0544365	19.3022	354.58	0.00
Cyp312a1_gene	Cyp312a1	0.136091	47.7092	350.57	0.00
Peb_gene	Peb	5.17147	1556.82	301.04	0.00
CG30427_gene	CG30427	0.108873	31.0225	284.94	0.00
svp_gene	svp	2.31355	551.718	238.47	0.00
CG34340_gene	CG34340	0.843766	172.726	204.71	0.00
CG18301_gene	CG18301	0.0544365	9.00548	165.43	0.01
CG34166_gene	CG34166	0.0816547	9.23724	113.13	0.01
CG16820_gene	CG16820	0.163309	18.0441	110.49	0.01
CG12268_gene	CG12268	0.163309	15.4947	94.88	0.01
CG34301_gene	CG34301	0.108873	9.60143	88.19	0.01
CG14410_gene	CG14410	0.517147	42.9416	83.04	0.01
CG10096_gene	CG34402	0.734893	60.8201	82.76	0.01
CG10097_gene	CG34402	0.734893	60.8201	82.76	0.01
Obp56g_gene	Obp56g	2.2319	161.933	72.55	0.01
inv_gene	inv	0.0272182	1.95339	71.77	0.01
Cpr23B_gene	Cpr23B	0.0272182	1.72164	63.25	0.02
Acp24A4_gene	Acp24A4	3.15732	170.309	53.94	0.02
CG13359_gene	CG13359	0.0544365	2.748	50.48	0.02
Cyp6t3_gene	Cyp6t3	0.0272182	1.1919	43.79	0.02
CG9503_gene	Flo-2	0.0816547	3.44327	42.17	0.02
CG11289_gene	CG11289	0.0272182	1.12568	41.36	0.02
Elo68beta_gene	Elo68beta	0.0272182	1.12568	41.36	0.02
CG9514_gene	Flo-2	0.163309	6.55546	40.14	0.02
CG3119_gene	CG3119	0.0544365	1.9865	36.49	0.03
CG7675_gene	CG7675	0.217746	6.38992	29.35	0.03
CG12224_gene	CG12224	0.0816547	2.31759	28.38	0.04
CG15234_gene	jing	0.0272182	0.728384	26.76	0.04
Prosalpha6T_gene	Prosalpha6T	0.326619	7.74736	23.72	0.04
CG33470_gene	CG33470	0.108873	2.54935	23.42	0.04
CG3513_gene	CG3513	0.0816547	1.82096	22.30	0.04
CG3568_gene	CG3568	0.163309	3.11219	19.06	0.05
IM10_gene	IM10	0.108873	2.01961	18.55	0.05
Tsp_gene	CG11327	0.108873	1.82096	16.73	0.06
Cyp6g2_gene	Cyp6g2	0.0816547	1.35744	16.62	0.06
igl_gene	igl	0.381055	6.3237	16.60	0.06
alphagamma-element:CR32865_gene	ma-elemen	0.0544365	0.794601	14.60	0.07

CG13215_gene	CG13215	0.0544365	0.794601	14.60	0.07
GNBP3_gene	GNBP3	0.0544365	0.761493	13.99	0.07
CG30194_gene	CG30194	0.680456	9.33656	13.72	0.07
unc-115_gene	CG18542	10.0163	136.87	13.66	0.07
Ance-4_gene	Ance-4	0.0544365	0.695276	12.77	0.08
CG7214_gene	CG7214	0.0816547	1.02636	12.57	0.08
CR33471_gene	CR33471	0.108873	1.35744	12.47	0.08
CG11315_gene	CG11315	0.0544365	0.662168	12.16	0.08
NtR_gene	NtR	0.0544365	0.662168	12.16	0.08
CG3884_gene	CG3884	0.244964	2.97975	12.16	0.08
CG17321_gene	CG17321	0.163309	1.92029	11.76	0.09
CG31087_gene	CG31087	0.163309	1.88718	11.56	0.09
CG9265_gene	betaInt-nu	0.244964	2.748	11.22	0.09
CG1468_gene	CG1468	0.136091	1.52299	11.19	0.09
CG31760_gene	CG31760	0.353837	3.90679	11.04	0.09
CG6188_gene	CG6188	0.435492	4.7345	10.87	0.09
CG9782_gene	CG9782	0.0816547	0.860818	10.54	0.09
CG10657_gene	CG10657	2.25911	23.1759	10.26	0.10
CG41326_gene	CG17684	0.0816547	0.794601	9.73	0.10
Phk-3_gene	Jhebp29	0.843766	8.01223	9.50	0.11
CG30158_gene	CG30158	0.108873	0.993251	9.12	0.11
pgant2_gene	pgant2	0.46271	4.13855	8.94	0.11
unc-4_gene	unc-4	0.163309	1.42366	8.72	0.11
CG1213_gene	CG1213	0.163309	1.39055	8.51	0.12
CG31871_gene	CG31871	0.0816547	0.695276	8.51	0.12
Lip2_gene	Lip2	0.0816547	0.695276	8.51	0.12
Sodh-1_gene	Sodh-1	0.381055	3.21151	8.43	0.12
Cyt-b5-r_gene	Cyt-b5-r	1.25204	10.3298	8.25	0.12
CG6908_gene	CG6908	0.217746	1.78785	8.21	0.12
Cyp311a1_gene	Cyp311a1	0.190528	1.55609	8.17	0.12
uta_gene	Mms19	0.898202	7.31695	8.15	0.12
CG15283_gene	CG15283	0.0816547	0.662168	8.11	0.12
CG8051_gene	CG8051	0.136091	1.09258	8.03	0.12
klu_gene	klu	0.108873	0.860818	7.91	0.13
CG6067_gene	CG6067	0.136091	1.05947	7.79	0.13
CG31974_gene	CG31974	2.17746	16.8522	7.74	0.13
CG14439_gene	CG14439	0.244964	1.88718	7.70	0.13
CG11147_gene	CG11030	2.61295	19.6333	7.51	0.13
CG30279_gene	CG11170	0.46271	3.44327	7.44	0.13
CG17322_gene	CG17322	0.979857	7.25073	7.40	0.14
CG15615_gene	CG15615	0.870984	6.38992	7.34	0.14
CG10680_gene	CG10680	0.408274	2.94665	7.22	0.14
CG1124_gene	CG1124	0.163309	1.15879	7.10	0.14
CG12643_gene	CG12643	0.244964	1.72164	7.03	0.14
Galpha73B_gene	Galpha73B	0.244964	1.68853	6.89	0.15
CG3244_gene	CG3244	0.136091	0.927035	6.81	0.15
tor_gene	CG30493	0.244964	1.65542	6.76	0.15
CG15546_gene	CG15546	0.108873	0.728384	6.69	0.15
CG11314_gene	CG11314	0.299401	1.9865	6.63	0.15
CG4666_gene	CG4666	0.870984	5.72775	6.58	0.15
CG17108_gene	CG17108	4.81763	31.6516	6.57	0.15
CG11034_gene	CG11034	6.80456	44.6963	6.57	0.15
CG12990_gene	beta-Spec	1.90528	12.3825	6.50	0.15
CG15368_gene	CG15368	0.517147	3.34395	6.47	0.15
CG4741_gene	CG4741	2.04137	13.144	6.44	0.16
CG41353_gene	CG41353	0.789329	5.06558	6.42	0.16
CG34393_gene	CG34393	1.17038	7.48249	6.39	0.16
Ptr_gene	Ptr	1.22482	7.81358	6.38	0.16
CG41336_gene	Parp	0.190528	1.1919	6.26	0.16
CG6426_gene	CG6426	0.272182	1.68853	6.20	0.16

Cyp4p1_gene	hig	2.06859	12.7798	6.18	0.16
Cyp6w1_gene	Cyp6w1	0.408274	2.51624	6.16	0.16
CG31839_gene	CG33119	0.381055	2.28448	6.00	0.17
CG3608_gene	CG4741	1.9325	11.4886	5.94	0.17
NepYr_gene	NepYr	5.00816	29.4002	5.87	0.17
CG15369_gene	CG15369	0.136091	0.794601	5.84	0.17
Glt_gene	Glt	0.707674	4.10544	5.80	0.17
CG8942_gene	CG8942	0.244964	1.39055	5.68	0.18
Cpr67B_gene	Cpr67B	0.843766	4.76761	5.65	0.18
CG13427_gene	CG13427	0.190528	1.05947	5.56	0.18
CG31352_gene	CG31352	27.436	151.14	5.51	0.18
RfaBp_gene	RfaBp	6.34185	34.6314	5.46	0.18
CG15293_gene	CG15293	0.598801	3.24462	5.42	0.18
CG41482_gene	CG41482	0.136091	0.728384	5.35	0.19
Cpr66D_gene	Cpr66D	0.163309	0.860818	5.27	0.19
Jheh3_gene	Jheh3	5.33478	27.9766	5.24	0.19
spdo_gene	H4alphaEF	0.489928	2.54935	5.20	0.19
GstE9_gene	GstE9	0.843766	4.27098	5.06	0.20
CG11951_gene	CG11951	0.217746	1.09258	5.02	0.20
CG10927_gene	CG10927	3.86499	19.0042	4.92	0.20
CG31786_gene	CG31786	0.163309	0.794601	4.87	0.21
CG6106_gene	CG6106	0.244964	1.1919	4.87	0.21
Hn_gene	Hn	0.244964	1.1919	4.87	0.21
CG34177_gene	CG34177	1.00708	4.80071	4.77	0.21
CG34178_gene	CG34177	1.00708	4.80071	4.77	0.21
CG1673_gene	CG1673	0.326619	1.55609	4.76	0.21
CG12681_gene	CG12681	0.381055	1.78785	4.69	0.21
CG9511_gene	CG9511	0.381055	1.78785	4.69	0.21
Idgf2_gene	CG5888	1.41535	6.62168	4.68	0.21
CG16756_gene	CG16756	0.163309	0.761493	4.66	0.21
CG14762_gene	CG14762	0.299401	1.39055	4.64	0.22
Hsp27_gene	Hsp27	3.10288	14.2035	4.58	0.22
rtet_gene	rtet	0.544365	2.48313	4.56	0.22
CG4250_gene	CG4250	0.299401	1.35744	4.53	0.22
CG1688_gene	CG1688	0.979857	4.37031	4.46	0.22
mRpS28_gene	CG10927	3.07566	13.7069	4.46	0.22
CG1698_gene	CG1688	0.979857	4.3372	4.43	0.23
Cyp28a5_gene	Cyp28a5	0.272182	1.1919	4.38	0.23
CG14695_gene	CG14695	1.25204	5.46288	4.36	0.23
CG5778_gene	CG5778	0.190528	0.827709	4.34	0.23
Cyt-c-d_gene	CG31782	0.62602	2.71489	4.34	0.23
CG4267_gene	CG4267	5.25312	22.7455	4.33	0.23
CG32801_gene	CG32801	0.244964	1.05947	4.33	0.23
CG9444_gene	CG9444	1.06151	4.56896	4.30	0.23
CG4716_gene	CG4716	2.69461	11.5217	4.28	0.23
CG3246_gene	sec5	0.435492	1.82096	4.18	0.24
Gprk1_gene	Gprk1	27.0005	110.516	4.09	0.24
CG34402_gene	CG34402	19.2705	78.4337	4.07	0.25
tRNA:CR30232_gene	NA:CR3023	0.163309	0.662168	4.05	0.25
CG7330_gene	CG7330	0.326619	1.32434	4.05	0.25
su(rdgB)69_gene	ycbeta100	3.70168	14.965	4.04	0.25
CG13539_gene	CG34371	4.00108	16.1569	4.04	0.25
CanB_gene	CanB	0.272182	1.09258	4.01	0.25
CG6503_gene	CG6503	0.46271	1.85407	4.01	0.25
CG34314_gene	Rad1	0.190528	0.761493	4.00	0.25
Rad1_gene	Rad1	0.190528	0.761493	4.00	0.25
CG12063_gene	CG12063	0.299401	1.1919	3.98	0.25
PIP82_gene	Nrg	0.517147	2.05272	3.97	0.25
CG5323_gene	CG5323	2.85792	11.2237	3.93	0.25
CG2989_gene	CG2989	1.17038	4.53585	3.88	0.26

Nplp2_gene	Nplp2	1.63309	6.25748	3.83	0.26
CG13300_gene	CG13300	0.190528	0.728384	3.82	0.26
CG12001_gene	CG12001	2.31355	8.83994	3.82	0.26
PH4alphaSG1_gene	H4alphaSG	17.338	65.9519	3.80	0.26
CG12253_gene	CG12253	0.217746	0.827709	3.80	0.26
nAcRalpha-7E_gene	AcRalpha-7	2.31355	8.77372	3.79	0.26
CG9813_gene	CG34309	0.952639	3.5757	3.75	0.27
CG7900_gene	CG7900	6.77734	25.0299	3.69	0.27
Gr47a_gene	CG34363	0.353837	1.29123	3.65	0.27
CG12402_gene	CG12402	0.299401	1.09258	3.65	0.27
CG13707_gene	CG13707	0.571583	2.08583	3.65	0.27
n-syb_gene	n-syb	0.244964	0.893926	3.65	0.27
cv-2_gene	cv-2	0.217746	0.794601	3.65	0.27
Cyp6a8_gene	Cyp6a8	0.598801	2.18515	3.65	0.27
CG16815_gene	CG16815	0.190528	0.695276	3.65	0.27
CG30502_gene	CG30502	0.544365	1.9865	3.65	0.27
Obp8a_gene	Obp8a	11.2684	40.922	3.63	0.28
CG11550_gene	CG11550	1.03429	3.74125	3.62	0.28
CG2065_gene	CG2065	0.680456	2.45002	3.60	0.28
CG14629_gene	CG14629	0.979857	3.50949	3.58	0.28
dream_gene	dream	0.870984	3.11219	3.57	0.28
CR40469_gene	CR40469	104.845	372.105	3.55	0.28
CG17761_gene	CG17761	0.598801	2.11894	3.54	0.28
Hsp22_gene	Hsp22	5.14425	18.1765	3.53	0.28
Hsp67Bb_gene	Hsp22	5.14425	18.1765	3.53	0.28
CG9812_gene	CG9812	1.14317	4.03922	3.53	0.28
CG14990_gene	CG14990	0.244964	0.860818	3.51	0.28
CG6704_gene	CG6704	0.244964	0.860818	3.51	0.28
Tig_gene	Tig	0.653238	2.28448	3.50	0.29
Nox_gene	Nox	0.408274	1.42366	3.49	0.29
CG40211_gene	CG40211	0.190528	0.662168	3.48	0.29
GRHR_gene	GRHR	0.190528	0.662168	3.48	0.29
CG1941_gene	CG1941	10.5335	36.4523	3.46	0.29
CG12116_gene	CG33223	1.00708	3.47638	3.45	0.29
CG10031_gene	CG10031	1.46979	5.06558	3.45	0.29
CG15828_gene	CG15828	2.20468	7.58182	3.44	0.29
CG5080_gene	CG5080	1.11595	3.80746	3.41	0.29
CG31431_gene	CG31431	0.272182	0.927035	3.41	0.29
CG12112_gene	CG12112	2.58573	8.80683	3.41	0.29
CG7966_gene	CG7966	4.76319	16.2231	3.41	0.29
CG33223_gene	CG33223	1.08873	3.67503	3.38	0.30
CG11125_gene	CG30502	0.46271	1.55609	3.36	0.30
Fs_gene	CG8079	2.85792	9.56832	3.35	0.30
fon_gene	CG17350	1.17038	3.90679	3.34	0.30
Gycbeta100B_gene	ycbeta100	4.98094	16.6204	3.34	0.30
Adh_gene	osp	43.6308	145.18	3.33	0.30
Adhr_gene	osp	43.6308	145.18	3.33	0.30
CG4950_gene	CG4950	0.299401	0.993251	3.32	0.30
CG9518_gene	Flo-2	0.381055	1.25812	3.30	0.30
CG8046_gene	CG8046	0.272182	0.893926	3.28	0.30
CG4398_gene	CG4398	0.244964	0.794601	3.24	0.31
CG34371_gene	CG34371	6.77734	21.9509	3.24	0.31
Hsp68_gene	CG6000	1.68753	5.46288	3.24	0.31
Hsp70Bbb_gene	Hsp70Bbb	7.78442	25.1624	3.23	0.31
Sodh-2_gene	Sodh-2	8.19269	26.3212	3.21	0.31
CG16965_gene	CG16965	0.217746	0.695276	3.19	0.31
CG12947_gene	CG12947	1.22482	3.90679	3.19	0.31
Hsp70Ab_gene	Hsp70Ab	34.8394	110.383	3.17	0.32
CG1494_gene	CG1494	0.272182	0.860818	3.16	0.32
Dsp1_gene	Dsp1	11.0234	34.6976	3.15	0.32

CG8791_gene	CG8791	0.707674	2.21826	3.13	0.32
Hsc70-2_gene	Hsc70-2	4.54545	14.1704	3.12	0.32
CG1492_gene	CG1806	0.435492	1.35744	3.12	0.32
CG32791_gene	CG32791	0.244964	0.761493	3.11	0.32
CG3597_gene	CG3597	0.299401	0.927035	3.10	0.32
nord_gene	nord	0.408274	1.25812	3.08	0.32
CG5958_gene	CG5958	0.62602	1.92029	3.07	0.33
CG8907_gene	CG8907	2.50408	7.68114	3.07	0.33
PebIII_gene	PebIII	29.7223	90.717	3.05	0.33
CG13607_gene	CG13607	0.489928	1.48988	3.04	0.33
CG11019_gene	CG11019	0.217746	0.662168	3.04	0.33
CG14132_gene	CG14132	0.217746	0.662168	3.04	0.33
CG34370_gene	CG34370	0.598801	1.82096	3.04	0.33
CG31176_gene	CG31176	0.92542	2.81421	3.04	0.33
CG11656_gene	CG8031	0.571583	1.72164	3.01	0.33
Hsp70Ba_gene	Hsp70Ba	7.43058	22.3482	3.01	0.33
CG13908_gene	CG13908	0.408274	1.22501	3.00	0.33
Ppn_gene	Ppn	4.08274	12.217	2.99	0.33
CS-2_gene	CS-2	0.244964	0.728384	2.97	0.34
Cht2_gene	Cht2	0.680456	2.01961	2.97	0.34
CG1961_gene	CG1961	0.435492	1.29123	2.96	0.34
Oseg5_gene	Oseg5	0.272182	0.794601	2.92	0.34
CG6234_gene	CG6234	0.952639	2.7811	2.92	0.34
CG9990_gene	CG9990	4.3277	12.6143	2.91	0.34
Hsp70Aa_gene	Hsp70Aa	37.3434	108.827	2.91	0.34
CG33696_gene	fry	3.78334	11.0251	2.91	0.34
Tequila_gene	Tequila	1.87806	5.46288	2.91	0.34
Hsp70Bb_gene	Hsp70Bb	10.8329	30.9894	2.86	0.35
Hsp70Bc_gene	Hsp70Bc	8.46487	24.2022	2.86	0.35
CG13676_gene	CG13676	0.244964	0.695276	2.84	0.35
Lsd-1_gene	Lsd-1	0.979857	2.7811	2.84	0.35
CG9510_gene	CG9510	1.87806	5.29734	2.82	0.35
CG9515_gene	CG9510	1.87806	5.29734	2.82	0.35
CG13293_gene	CG13293	0.353837	0.993251	2.81	0.36
king-tubby_gene	king-tubby	22.7817	63.7005	2.80	0.36
CG13157_gene	CG13157	0.653238	1.82096	2.79	0.36
CG13728_gene	CG13728	0.653238	1.82096	2.79	0.36
NC2beta_gene	NC2beta	4.98094	13.8724	2.79	0.36
Hex-C_gene	CG8079	1.22482	3.41016	2.78	0.36
pinta_gene	pinta	0.571583	1.5892	2.78	0.36
CG1441_gene	CG1441	0.299401	0.827709	2.76	0.36
CG3984_gene	CG3984	0.299401	0.827709	2.76	0.36
ana_gene	ana	13.2553	36.5516	2.76	0.36
CG32046_gene	CG32046	18.6173	50.9869	2.74	0.37
CG8517_gene	CG8517	1.25204	3.41016	2.72	0.37
CG31347_gene	Arp87C	0.353837	0.960143	2.71	0.37
CG14304_gene	CG14304	0.353837	0.960143	2.71	0.37
CG8399_gene	CG8399	3.94665	10.694	2.71	0.37
CG14905_gene	CG14905	0.489928	1.32434	2.70	0.37
sofe_gene	sofe	0.489928	1.32434	2.70	0.37
CG12768_gene	CG12768	0.244964	0.662168	2.70	0.37
Ela_gene	Ela	0.244964	0.662168	2.70	0.37
CG8317_gene	CG8317	0.381055	1.02636	2.69	0.37
CG34251_gene	CG34251	0.517147	1.39055	2.69	0.37
CG18547_gene	CG18547	1.85084	4.96626	2.68	0.37
CG18375_gene	CG18375	32.4986	87.0088	2.68	0.37
CG3581_gene	Ino80	0.272182	0.728384	2.68	0.37
CG8145_gene	CG8145	0.544365	1.45677	2.68	0.37
dve_gene	dve	31.6548	84.0953	2.66	0.38
CG8193_gene	CG8193	0.46271	1.22501	2.65	0.38

CG31326_gene	CG31326	0.489928	1.29123	2.64	0.38
CG9928_gene	CG9928	0.489928	1.29123	2.64	0.38
Nhe3_gene	Nhe3	8.11104	21.2887	2.62	0.38
qua_gene	qua	1.06151	2.7811	2.62	0.38
lwf_gene	lwf	1.14317	2.97975	2.61	0.38
CG9752_gene	RpL29	1.74197	4.53585	2.60	0.38
squ_gene	grp	0.408274	1.05947	2.59	0.39
CG31714_gene	CG31714	1.55144	4.00611	2.58	0.39
CG17118_gene	CG6443	1.17038	3.01286	2.57	0.39
stan_gene	stan	5.79749	14.8988	2.57	0.39
CG7860_gene	CG32584	1.25204	3.21151	2.57	0.39
CG13791_gene	CG13791	0.272182	0.695276	2.55	0.39
CG30178_gene	Phm	0.272182	0.695276	2.55	0.39
CG5204_gene	CG5204	0.571583	1.45677	2.55	0.39
Fsh_gene	Fsh	1.68753	4.27098	2.53	0.40
CG32333_gene	CG32333	0.680456	1.72164	2.53	0.40
CG18208_gene	CG18208	0.353837	0.893926	2.53	0.40
CG30411_gene	CG9812	0.898202	2.25137	2.51	0.40
Hsp26_gene	Hsp26	7.32171	18.342	2.51	0.40
vis_gene	vis	0.46271	1.15879	2.50	0.40
CG1909_gene	CG1909	0.62602	1.55609	2.49	0.40
ImpL2_gene	ImpL2	0.816547	2.01961	2.47	0.40
spn-E_gene	spn-E	0.979857	2.41691	2.47	0.41
lin-28_gene	lin-28	1.71475	4.20476	2.45	0.41
CG10650_gene	CG10650	3.81055	9.30345	2.44	0.41
CG13717_gene	CG13717	0.326619	0.794601	2.43	0.41
ppk_gene	ppk	0.326619	0.794601	2.43	0.41
santa-maria_gene	santa-maria	0.326619	0.794601	2.43	0.41
snoRNA:Psi28S-291_gene	RpL3	0.571583	1.39055	2.43	0.41
CG10469_gene	CG10469	0.408274	0.993251	2.43	0.41
CG3823_gene	CG3823	0.898202	2.18515	2.43	0.41
CG7526_gene	CG7526	1.60588	3.90679	2.43	0.41
CG4629_gene	Atg4	14.2351	34.5651	2.43	0.41
Hsp23_gene	Hsp23	1.38813	3.34395	2.41	0.42
CG3571_gene	CG3571	2.61295	6.29059	2.41	0.42
CG9394_gene	king-tubby	9.47195	22.7786	2.40	0.42
Prx2540-2_gene	Prx2540-2	1.17038	2.81421	2.40	0.42
CG32108_gene	CG32108	1.11595	2.68178	2.40	0.42
stai_gene	stai	1.33369	3.1453	2.36	0.42
CG15653_gene	CG15653	0.435492	1.02636	2.36	0.42
CG9123_gene	HDAC6	0.435492	1.02636	2.36	0.42
CG18210_gene	CG18210	0.381055	0.893926	2.35	0.43
dmrt11E_gene	dmrt11E	0.381055	0.893926	2.35	0.43
CG5237_gene	CG3773	1.08873	2.54935	2.34	0.43
CG16857_gene	CG16857	1.7964	4.20476	2.34	0.43
alpha-Est10_gene	alpha-Est10	2.58573	6.02572	2.33	0.43
CG40006_gene	CG40006	0.598801	1.39055	2.32	0.43
CR31808_gene	CG31782	8.08382	18.7724	2.32	0.43
CG5613_gene	CG12994	1.46979	3.41016	2.32	0.43
Jhe_gene	Jhe	2.15024	4.96626	2.31	0.43
Tps1_gene	Tps1	8.84593	20.4279	2.31	0.43
CG6891_gene	CG6891	7.43058	17.0839	2.30	0.43
CG10026_gene	CG10026	2.93957	6.75411	2.30	0.44
ChLD3_gene	ChLD3	0.489928	1.12568	2.30	0.44
fat-spondin_gene	fat-spondin	1.46979	3.37705	2.30	0.44
CG10617_gene	CG10617	0.707674	1.62231	2.29	0.44
sns_gene	sns	0.707674	1.62231	2.29	0.44
Gadd45_gene	Gadd45	2.61295	5.95951	2.28	0.44
Rfx_gene	Rfx	3.70168	8.40953	2.27	0.44
CG7724_gene	CG7724	0.408274	0.927035	2.27	0.44

DNApol-eta_gene	CG7442	0.598801	1.35744	2.27	0.44
obst-E_gene	obst-E	0.789329	1.78785	2.27	0.44
olf186-M_gene	olf186-F	1.55144	3.50949	2.26	0.44
CG8620_gene	CG8620	0.571583	1.29123	2.26	0.44
CG2919_gene	CG2919	0.381055	0.860818	2.26	0.44
CG17560_gene	CG17560	2.47686	5.56221	2.25	0.45
CG13731_gene	CG13731	0.870984	1.95339	2.24	0.45
CG9267_gene	CG9267	2.77626	6.22437	2.24	0.45
lectin-28C_gene	lectin-28C	2.2319	4.99936	2.24	0.45
Appl_gene	Appl	1.1976	2.68178	2.24	0.45
Karl_gene	Karl	0.489928	1.09258	2.23	0.45
CG5819_gene	CG5819	0.326619	0.728384	2.23	0.45
Cpr50Ca_gene	Cpr50Ca	2.25911	5.03247	2.23	0.45
tutl_gene	tutl	2.72182	6.05883	2.23	0.45
CG30108_gene	CG30108	1.41535	3.1453	2.22	0.45
CG31826_gene	Ku80	1.41535	3.1453	2.22	0.45
CG32044_gene	CG32044	3.04844	6.75411	2.22	0.45
CG15529_gene	CG15529	0.299401	0.662168	2.21	0.45
CG6441_gene	CG15819	0.299401	0.662168	2.21	0.45
Gr94a_gene	p53	0.299401	0.662168	2.21	0.45
CG11353_gene	CG11353	2.39521	5.29734	2.21	0.45
CG16743_gene	CG16743	0.734893	1.62231	2.21	0.45
argos_gene	CG33158	0.435492	0.960143	2.20	0.45
CG11030_gene	CG11030	12.9559	28.4732	2.20	0.46
Hml_gene	Hml	2.2319	4.90004	2.20	0.46
CG4726_gene	CG4726	0.408274	0.893926	2.19	0.46
CG6113_gene	CG6113	0.408274	0.893926	2.19	0.46
CG12994_gene	CG12994	1.60588	3.50949	2.19	0.46
CG14688_gene	CG14688	21.2574	46.12	2.17	0.46
CG9162_gene	CG9162	0.62602	1.35744	2.17	0.46
Rh7_gene	Rh7	1.08873	2.35069	2.16	0.46
PH4alphaEFB_gene	H4alphaEF	32.9069	71.0175	2.16	0.46
snoRNA:Or-aca5_gene	oRNA:Or-ac	0.353837	0.761493	2.15	0.46
CG34406_gene	CG34406	0.816547	1.75474	2.15	0.47
CG4596_gene	CG4596	0.46271	0.993251	2.15	0.47
CG4511_gene	CG4511	4.54545	9.73386	2.14	0.47
CG18170_gene	CG18170	0.789329	1.68853	2.14	0.47
CG33791_gene	CG18170	0.789329	1.68853	2.14	0.47
Acox57D-p_gene	Acox57D-p	1.66031	3.5426	2.13	0.47
CG32206_gene	CG32206	0.326619	0.695276	2.13	0.47
CG12105_gene	CG18170	0.762111	1.62231	2.13	0.47
CG4865_gene	CG4865	0.653238	1.39055	2.13	0.47
dpr8_gene	dpr8	2.06859	4.40341	2.13	0.47
CG14935_gene	CG31757	2.36799	5.03247	2.13	0.47
CG31278_gene	CG14684	0.734893	1.55609	2.12	0.47
CG6293_gene	CG6293	4.05552	8.57507	2.11	0.47
CG11170_gene	CG11170	52.5584	110.814	2.11	0.47
CG11473_gene	CG11473	4.05552	8.54196	2.11	0.47
MtnA_gene	MtnA	81.6547	171.899	2.11	0.48
CG32581_gene	CG32581	13.3642	28.0097	2.10	0.48
Sr-CI_gene	Sr-CI	0.489928	1.02636	2.09	0.48
CG10621_gene	CG10621	0.680456	1.42366	2.09	0.48
Uhg2_gene	Uhg2	0.870984	1.82096	2.09	0.48
Hf_gene	Hf	1.74197	3.64192	2.09	0.48
CG13875_gene	CG13875	0.381055	0.794601	2.09	0.48
CG16959_gene	CG17081	0.381055	0.794601	2.09	0.48
CG17352_gene	CG17352	0.571583	1.1919	2.09	0.48
CG9134_gene	CG9134	2.74904	5.72775	2.08	0.48
CG3505_gene	CG3505	1.22482	2.54935	2.08	0.48
Prat2_gene	Prat2	1.27926	2.64867	2.07	0.48

CG31772_gene	CG31772	39.3576	81.4466	2.07	0.48
CG13001_gene	CG13001	0.544365	1.12568	2.07	0.48
RluA-1_gene	RluA-1	0.544365	1.12568	2.07	0.48
CG2493_gene	cdc23	4.43657	9.17102	2.07	0.48
CG7713_gene	CG7713	1.33369	2.748	2.06	0.49
CG14471_gene	Src42A	2.91235	5.99262	2.06	0.49
TyrR_gene	TyrR	2.17746	4.46963	2.05	0.49
grh_gene	grh	0.517147	1.05947	2.05	0.49
Lhr_gene	Lhr	1.27926	2.61556	2.04	0.49
Spn27A_gene	cup	1.68753	3.44327	2.04	0.49
CG15307_gene	CG15307	1.41535	2.88043	2.04	0.49
zfh1_gene	zfh1	0.653238	1.32434	2.03	0.49
CG32776_gene	CG32776	0.326619	0.662168	2.03	0.49
CG15831_gene	CG40368	0.326619	0.662168	2.03	0.49
CG13745_gene	CG13745	4.65432	9.43589	2.03	0.49
yellow-b_gene	yellow-b	0.408274	0.827709	2.03	0.49
CG7296_gene	CG7296	0.571583	1.15879	2.03	0.49
CG32572_gene	CG34325	1.76919	3.5757	2.02	0.49
CG15087_gene	CG15073	10.3974	20.9907	2.02	0.50
Marcal1_gene	Marcal1	1.27926	2.58245	2.02	0.50
tok_gene	tok	1.98693	4.00611	2.02	0.50
CG34016_gene	CG4629	0.789329	1.5892	2.01	0.50
CG9597_gene	spn-E	0.789329	1.5892	2.01	0.50
CG12641_gene	CG12641	0.62602	1.25812	2.01	0.50
CG15067_gene	CG18107	0.62602	1.25812	2.01	0.50
CG41462_gene	CG41462	0.46271	0.927035	2.00	0.50
CG15601_gene	CG15601	0.762111	1.52299	2.00	0.50
Ndg_gene	Ndg	0.381055	0.761493	2.00	0.50
timeout_gene	timeout	2.42242	4.83382	2.00	0.50
CG11899_gene	CG11899	1.36091	2.71489	1.99	0.50
Shaw_gene	Shaw	1.95971	3.90679	1.99	0.50
CG8062_gene	CG8062	2.2319	4.43652	1.99	0.50
CG3239_gene	CG3239	0.816547	1.62231	1.99	0.50
CG9360_gene	m	1.03429	2.05272	1.98	0.50
CG1239_gene	CG1239	0.952639	1.88718	1.98	0.50
CG3038_gene	CG3038	0.653238	1.29123	1.98	0.51
CG3829_gene	CG3829	1.08873	2.15204	1.98	0.51
CG32444_gene	CG32444	7.24005	14.3028	1.98	0.51
CG6206_gene	CG6206	21.3119	41.9483	1.97	0.51
CG3056_gene	CG3056	30.9744	60.8863	1.97	0.51
Idh_gene	Idh	225.775	443.718	1.97	0.51
amd_gene	amd	0.353837	0.695276	1.96	0.51
CG11281_gene	CG11281	0.489928	0.960143	1.96	0.51
CG9780_gene	cpx	0.489928	0.960143	1.96	0.51
CG16898_gene	CG16898	9.93466	19.4677	1.96	0.51
Glut1_gene	Glut1	16.712	32.7442	1.96	0.51
CG31607_gene	CG8552	0.62602	1.22501	1.96	0.51
osp_gene	osp	101.252	197.988	1.96	0.51
RluA-2_gene	RluA-2	2.06859	4.03922	1.95	0.51
CG3294_gene	CG3294	0.952639	1.85407	1.95	0.51
CG17574_gene	CG17574	10.2341	19.8981	1.94	0.51
CG34325_gene	CG34325	19.9238	38.7368	1.94	0.51
CG2765_gene	CG2765	14.9973	29.036	1.94	0.52
Sema-1a_gene	Sema-1a	5.06259	9.80008	1.94	0.52
CG8630_gene	CG8630	42.9776	83.1682	1.94	0.52
snoRNA:Psi28S-1837a_gene	CG10576	0.46271	0.893926	1.93	0.52
CG14625_gene	CG14625	0.46271	0.893926	1.93	0.52
CG9344_gene	CG9344	1.74197	3.34395	1.92	0.52
CG31886_gene	CG31886	5.00816	9.60143	1.92	0.52
Takr99D_gene	Takr99D	1.7964	3.44327	1.92	0.52

CG6495_gene	CG6495	0.381055	0.728384	1.91	0.52
CG5065_gene	CG5065	1.14317	2.18515	1.91	0.52
Sox100B_gene	Sox100B	1.68753	3.21151	1.90	0.53
CG14303_gene	CG14303	0.435492	0.827709	1.90	0.53
CG34041_gene	CG34041	87.3978	166.005	1.90	0.53
CG32169_gene	CG32169	9.96188	18.9049	1.90	0.53
CG5390_gene	CG5390	1.85084	3.50949	1.90	0.53
UK114_gene	UK114	1.17038	2.21826	1.90	0.53
Pif1A_gene	Pif1B	72.5911	137.334	1.89	0.53
Pif1B_gene	Pif1B	72.5911	137.334	1.89	0.53
CG3699_gene	CG3699	0.544365	1.02636	1.89	0.53
CG15784_gene	CG15784	29.9945	56.5491	1.89	0.53
Hsp83_gene	Hsp83	369.542	696.071	1.88	0.53
Fps85D_gene	CG8129	14.6162	27.48	1.88	0.53
CG6484_gene	CG6484	32.1447	60.3897	1.88	0.53
CR41602_gene	CR41602	7.51224	14.1042	1.88	0.53
CG34451_gene	CG34451	0.653238	1.22501	1.88	0.53
CG3775_gene	Pde9	0.653238	1.22501	1.88	0.53
CG11776_gene	CG11776	13.9085	26.0563	1.87	0.53
CG31857_gene	bun	0.707674	1.32434	1.87	0.53
CG6094_gene	CG6094	1.9325	3.60881	1.87	0.54
kal-1_gene	kal-1	0.816547	1.52299	1.87	0.54
mia_gene	mia	0.816547	1.52299	1.87	0.54
yellow-f2_gene	yellow-f2	0.408274	0.761493	1.87	0.54
CG17081_gene	CG17081	0.870984	1.62231	1.86	0.54
CG8490_gene	CG8490	0.870984	1.62231	1.86	0.54
Toll-7_gene	Toll-7	0.870984	1.62231	1.86	0.54
Rep1_gene	Rep1	3.1301	5.82707	1.86	0.54
CG17224_gene	CG17224	1.7964	3.34395	1.86	0.54
CG11275_gene	CG11170	49.9999	93.0345	1.86	0.54
CG40486_gene	CG40486	6.28741	11.6873	1.86	0.54
ade5_gene	ade5	11.6222	21.5867	1.86	0.54
alpha-Est9_gene	alpha-Est9	2.04137	3.77436	1.85	0.54
CG31016_gene	CG31016	48.4213	89.4257	1.85	0.54
GstE3_gene	GstE3	0.898202	1.65542	1.84	0.54
CR30066_gene	Ih	0.952639	1.75474	1.84	0.54
pb_gene	pb	1.00708	1.85407	1.84	0.54
grk_gene	grk	2.66739	4.90004	1.84	0.54
Cyp4d2_gene	Cyp4d2	7.1584	13.144	1.84	0.54
CG34430_gene	CG14764	1.497	2.748	1.84	0.54
Lsd-2_gene	Lsd-2	55.3075	101.08	1.83	0.55
InR_gene	InR	29.2868	53.47	1.83	0.55
CG11378_gene	CG11378	0.598801	1.09258	1.82	0.55
cpx_gene	cpx	0.816547	1.48988	1.82	0.55
CG14888_gene	CG14888	0.381055	0.695276	1.82	0.55
CG9203_gene	CG9203	0.381055	0.695276	1.82	0.55
AR-2_gene	AR-2	5.38921	9.83319	1.82	0.55
CG9572_gene	CG9572	0.544365	0.993251	1.82	0.55
CG17803_gene	CG17803	0.653238	1.1919	1.82	0.55
CG3655_gene	CG3655	21.8018	39.6638	1.82	0.55
DopR2_gene	DopR2	2.36799	4.30409	1.82	0.55
CG6921_gene	CG6921	37.4523	68.0046	1.82	0.55
CG31689_gene	CG31689	9.60804	17.415	1.81	0.55
CG1360_gene	CG1360	1.22482	2.21826	1.81	0.55
yuri_gene	yuri	4.84485	8.77372	1.81	0.55
Spn43Ab_gene	pk	2.34077	4.23787	1.81	0.55
gol_gene	gol	1.00708	1.82096	1.81	0.55
phl_gene	phl	12.4932	22.5799	1.81	0.55
CG13966_gene	CG13966	0.843766	1.52299	1.80	0.55
CG33171_gene	CG33171	1.57866	2.84732	1.80	0.55

clt_gene	clt	2.31355	4.17166	1.80	0.55
CG7470_gene	CG7470	2.77626	4.99936	1.80	0.56
CR33655_gene	CG9485	5.44365	9.80008	1.80	0.56
DNApol-alpha180_gene	Apol-alpha	0.62602	1.12568	1.80	0.56
Reg-2_gene	Reg-2	15.841	28.3739	1.79	0.56
CG8219_gene	CG8219	0.979857	1.75474	1.79	0.56
lds_gene	lds	0.979857	1.75474	1.79	0.56
CG14358_gene	CG14358	0.46271	0.827709	1.79	0.56
CG33099_gene	CG33099	0.46271	0.827709	1.79	0.56
CG34398_gene	CG34398	0.46271	0.827709	1.79	0.56
CG4036_gene	CG4036	3.64724	6.52235	1.79	0.56
CG10265_gene	CG10265	0.870984	1.55609	1.79	0.56
CG15628_gene	CG15628	0.870984	1.55609	1.79	0.56
Ten-a_gene	Ten-a	2.0958	3.74125	1.79	0.56
CG34272_gene	CG34272	0.816547	1.45677	1.78	0.56
CG15432_gene	CG15432	13.3642	23.838	1.78	0.56
CG8326_gene	CG8326	1.98693	3.5426	1.78	0.56
Dip2_gene	Dip2	1.9325	3.44327	1.78	0.56
CG3430_gene	CG3430	0.762111	1.35744	1.78	0.56
CG8668_gene	CG8668	2.93957	5.23112	1.78	0.56
CG13654_gene	Cad96Ca	0.707674	1.25812	1.78	0.56
CG6630_gene	CG6441	16.1949	28.7712	1.78	0.56
CG10175_gene	CG10175	54.1099	96.0805	1.78	0.56
nrv2_gene	nrv2	11.0778	19.6664	1.78	0.56
CG4984_gene	CG4984	2.31355	4.10544	1.77	0.56
CG41138_gene	CG41138	0.653238	1.15879	1.77	0.56
CG4577_gene	CG4577	0.653238	1.15879	1.77	0.56
DopR_gene	DopR	0.653238	1.15879	1.77	0.56
Cct2_gene	Cct2	9.6897	17.1832	1.77	0.56
CG33970_gene	CG33970	5.49809	9.73386	1.77	0.56
CG13893_gene	MED14	9.39029	16.6204	1.77	0.56
CG6785_gene	CG6785	3.78334	6.68789	1.77	0.57
CG13868_gene	CG8920	162.357	286.983	1.77	0.57
CG32711_gene	CG32711	6.36907	11.2568	1.77	0.57
CG10237_gene	CG10237	9.30864	16.4218	1.76	0.57
CG32944_gene	CG32944	0.544365	0.960143	1.76	0.57
CG12119_gene	CG12119	11.7583	20.7258	1.76	0.57
CG5707_gene	CG5707	0.789329	1.39055	1.76	0.57
CG3523_gene	CG3523	32.9069	57.9397	1.76	0.57
Wnt5_gene	Wnt5	4.13717	7.28384	1.76	0.57
CG3488_gene	CG3488	20.0871	35.3597	1.76	0.57
CG15536_gene	CG15536	1.71475	3.01286	1.76	0.57
cpsf_gene	cpsf	24.7686	43.4382	1.75	0.57
CG1806_gene	CG1806	2.5313	4.43652	1.75	0.57
CG1628_gene	CG2124	1.60588	2.81421	1.75	0.57
CG7990_gene	CG7990	3.15732	5.5291	1.75	0.57
CG31453_gene	CG31453	0.435492	0.761493	1.75	0.57
CG34020_gene	CG34020	0.435492	0.761493	1.75	0.57
CG13876_gene	CG13876	2.55852	4.46963	1.75	0.57
CG15345_gene	CG15345	0.62602	1.09258	1.75	0.57
CG40244_gene	CG40244	0.62602	1.09258	1.75	0.57
CG8129_gene	CG8129	0.62602	1.09258	1.75	0.57
Cbp80_gene	Cbp80	25.8573	45.1267	1.75	0.57
CG9460_gene	CG9460	17.3108	30.1617	1.74	0.57
laza_gene	laza	17.2291	29.9962	1.74	0.57
CG9640_gene	CG9640	1.33369	2.31759	1.74	0.58
Mt2_gene	Mt2	0.571583	0.993251	1.74	0.58
CG32687_gene	CG32687	5.85192	10.1643	1.74	0.58
Pfrx_gene	Pfrx	26.6194	46.1531	1.73	0.58
CG6023_gene	CG6023	1.60588	2.7811	1.73	0.58

CG40467_gene	CG40467	1.03429	1.78785	1.73	0.58
CG6038_gene	mtTFB1	2.58573	4.46963	1.73	0.58
APC7_gene	APC7	0.517147	0.893926	1.73	0.58
wun_gene	wun	10.9417	18.9049	1.73	0.58
CG8112_gene	CG8112	4.08274	7.05208	1.73	0.58
CG14534_gene	CG14534	1.17038	2.01961	1.73	0.58
CG17575_gene	CG17575	1147.66	1979.58	1.72	0.58
CG33138_gene	CG33138	11.4044	19.6664	1.72	0.58
Act87E_gene	Act87E	122.645	210.9	1.72	0.58
CG30154_gene	CG30154	2.17746	3.74125	1.72	0.58
CG14947_gene	CG14947	0.46271	0.794601	1.72	0.58
ths_gene	ths	1.98693	3.41016	1.72	0.58
CG7384_gene	CG6094	9.28142	15.892	1.71	0.58
CG5945_gene	CG5945	0.734893	1.25812	1.71	0.58
CG6981_gene	CG32223	3.48394	5.95951	1.71	0.58
baf_gene	baf	5.36199	9.17102	1.71	0.58
emp_gene	emp	22.9994	39.2334	1.71	0.59
CG32193_gene	Eip75B	0.408274	0.695276	1.70	0.59
unc-5_gene	unc-5	0.408274	0.695276	1.70	0.59
CG6685_gene	CG6685	0.952639	1.62231	1.70	0.59
CG6357_gene	CG6357	55.6885	94.8224	1.70	0.59
CG2976_gene	CG2976	9.90744	16.8522	1.70	0.59
cnn_gene	cnn	5.63418	9.56832	1.70	0.59
Dhpr_gene	Dhpr	3.37506	5.72775	1.70	0.59
Cyp9c1_gene	CG13594	25.5579	43.3389	1.70	0.59
CG17218_gene	CG17218	4.08274	6.91965	1.69	0.59
Sirt6_gene	Sirt6	1.38813	2.35069	1.69	0.59
Rep4_gene	CG6043	5.49809	9.30345	1.69	0.59
CG8121_gene	CG8121	5.08981	8.60818	1.69	0.59
CG31759_gene	aret	1.60588	2.71489	1.69	0.59
CG32143_gene	CG32143	0.489928	0.827709	1.69	0.59
CG10102_gene	CG10102	30.2395	51.0862	1.69	0.59
CG14247_gene	CG14247	3.02123	5.09869	1.69	0.59
CG9338_gene	CG9338	8.08382	13.6407	1.69	0.59
Kua_gene	Kua	0.843766	1.42366	1.69	0.59
cni_gene	cni	1.98693	3.34395	1.68	0.59
CG32407_gene	CG32407	1.85084	3.11219	1.68	0.59
CG9485_gene	CG9485	13.3914	22.5137	1.68	0.59
CG12911_gene	CG12911	3.4295	5.76086	1.68	0.60
CG6171_gene	Trax	1.71475	2.88043	1.68	0.60
CG14782_gene	CG14782	26.81	44.9943	1.68	0.60
CycH_gene	CycH	1.57866	2.64867	1.68	0.60
Cyp4g1_gene	Cyp4g1	2.58573	4.3372	1.68	0.60
Ada_gene	Ada	2.0958	3.50949	1.67	0.60
cdc23_gene	cdc23	5.36199	8.97237	1.67	0.60
CG34138_gene	CG6231	0.870984	1.45677	1.67	0.60
CG13894_gene	CG13894	0.435492	0.728384	1.67	0.60
CG3842_gene	CG3842	0.435492	0.728384	1.67	0.60
CG5984_gene	CG5984	0.435492	0.728384	1.67	0.60
CG31184_gene	CG33108	2.04137	3.41016	1.67	0.60
CG11241_gene	CG11241	6.72291	11.2237	1.67	0.60
CG9029_gene	CG9029	3936.71	6570.89	1.67	0.60
CG3831_gene	CG9849	1.17038	1.95339	1.67	0.60
7SLRNA_gene	7SLRNA	17.1203	28.5725	1.67	0.60
CG1299_gene	CG1299	65.5143	109.324	1.67	0.60
CG15186_gene	CG15186	14.7251	24.5664	1.67	0.60
Lcch3_gene	Lcch3	0.734893	1.22501	1.67	0.60
CG11710_gene	CG11710	8.16547	13.6075	1.67	0.60
Acox57D-d_gene	Acox57D-d	1.25204	2.08583	1.67	0.60
CG7341_gene	CG7341	2.50408	4.17166	1.67	0.60

CG31169_gene	CG31169	23.9521	39.8956	1.67	0.60
CG9586_gene	CG13108	8.11104	13.5082	1.67	0.60
Grip84_gene	Grip84	4.57267	7.61493	1.67	0.60
Rya-r44F_gene	Rya-r44F	25.8301	43.0078	1.67	0.60
CG32406_gene	CG32406	3.18453	5.29734	1.66	0.60
Jheh1_gene	Jheh1	38.541	63.8992	1.66	0.60
Ggamma30A_gene	Ggamma30	13.7997	22.8779	1.66	0.60
HdacX_gene	HdacX	1.57866	2.61556	1.66	0.60
CG11321_gene	CG11321	11.6222	19.236	1.66	0.60
CG8925_gene	CG8925	7.32171	12.1177	1.66	0.60
gsb_gene	gsb	0.762111	1.25812	1.65	0.61
CG42227_gene	CG42227	3.21175	5.29734	1.65	0.61
RfC38_gene	CG4738	1.60588	2.64867	1.65	0.61
CG13248_gene	CG13248	0.843766	1.39055	1.65	0.61
CG34017_gene	CG34017	0.843766	1.39055	1.65	0.61
CG31523_gene	CG31523	20.9036	34.4327	1.65	0.61
CG11073_gene	CG11073	0.46271	0.761493	1.65	0.61
CG11841_gene	CG11841	0.46271	0.761493	1.65	0.61
Ste:CG33236_gene	te:CG3323	0.46271	0.761493	1.65	0.61
Caps_gene	Caps	16.3309	26.8509	1.64	0.61
sle_gene	sle	10.2341	16.8191	1.64	0.61
Sans_gene	Sans	4.81763	7.9129	1.64	0.61
Cg25C_gene	Cg25C	25.7485	42.2794	1.64	0.61
CG8273_gene	CG8273	5.30756	8.7075	1.64	0.61
CG14853_gene	CG14853	1.25204	2.05272	1.64	0.61
PGRP-LB_gene	CG17230	4.46379	7.31695	1.64	0.61
dos_gene	dos	4.95372	8.11155	1.64	0.61
CG31812_gene	CG31812	1.497	2.45002	1.64	0.61
FucTC_gene	FucTC	1.497	2.45002	1.64	0.61
Mcr_gene	Mcr	33.0974	54.1653	1.64	0.61
Pk61C_gene	Pk61C	66.467	108.496	1.63	0.61
CG10550_gene	CG10550	4.38214	7.15141	1.63	0.61
CG5224_gene	CG5224	3.4295	5.59532	1.63	0.61
ds_gene	ds	1.27926	2.08583	1.63	0.61
Ef1beta_gene	Ef1beta	90.8817	147.994	1.63	0.61
Mob1_gene	Mob1	18.6173	30.2942	1.63	0.61
CG32021_gene	CG32021	2.0958	3.41016	1.63	0.61
bmm_gene	bmm	4.51823	7.35006	1.63	0.61
inaD_gene	RpL23	1.06151	1.72164	1.62	0.62
CG2321_gene	Ptp99A	0.653238	1.05947	1.62	0.62
CG3339_gene	CG3339	0.898202	1.45677	1.62	0.62
yellow-h_gene	yellow-h	0.489928	0.794601	1.62	0.62
CG14481_gene	CG4966	0.571583	0.927035	1.62	0.62
Sld5_gene	Sld5	0.571583	0.927035	1.62	0.62
rdgB_gene	rdgB	4.81763	7.81358	1.62	0.62
Cad96Cb_gene	Cad96Cb	0.408274	0.662168	1.62	0.62
CG14823_gene	CG14823	0.408274	0.662168	1.62	0.62
CG17189_gene	CG17189	0.408274	0.662168	1.62	0.62
CG7702_gene	CG7702	0.408274	0.662168	1.62	0.62
CG5783_gene	CG5783	2.69461	4.37031	1.62	0.62
CG10133_gene	CG10133	1.87806	3.04597	1.62	0.62
Ast_gene	Ast	0.734893	1.1919	1.62	0.62
aret_gene	aret	2.20468	3.5757	1.62	0.62
mthl3_gene	mthl3	6.47794	10.4954	1.62	0.62
Arc1_gene	Arc1	332.525	538.342	1.62	0.62
CG4975_gene	CG4975	3.62003	5.86018	1.62	0.62
Spt3_gene	Spt3	3.04844	4.93315	1.62	0.62
CG34365_gene	CG34365	2.2319	3.60881	1.62	0.62
CG1681_gene	CG1681	6.80456	10.992	1.62	0.62
stck_gene	stck	15.9499	25.7583	1.61	0.62

CG34195_gene	CG34195	2.91235	4.70139	1.61	0.62
Obp99d_gene	Obp99d	9.58082	15.4616	1.61	0.62
CG11409_gene	CG11409	1.17038	1.88718	1.61	0.62
Gcn2_gene	Gcn2	9.41751	15.1636	1.61	0.62
tsh_gene	tsh	0.762111	1.22501	1.61	0.62
CG5646_gene	CG5646	1.36091	2.18515	1.61	0.62
CG3097_gene	CG3097	56.1512	90.1541	1.61	0.62
CG11035_gene	CG10903	3.75612	6.02572	1.60	0.62
tmod_gene	tmod	111.159	178.256	1.60	0.62
CG16718_gene	CG34138	2.91235	4.66828	1.60	0.62
CG1890_gene	CG1890	2.06859	3.31084	1.60	0.62
snoRNA:Psi28S-1837b_gene	CG10576	0.517147	0.827709	1.60	0.62
CG17129_gene	CG17129	0.517147	0.827709	1.60	0.62
CG3630_gene	CG3630	2.93957	4.70139	1.60	0.63
CG3624_gene	CG3624	2.42242	3.87368	1.60	0.63
CG12592_gene	CG12592	2.34077	3.74125	1.60	0.63
side_gene	side	1.38813	2.21826	1.60	0.63
CG30285_gene	CG30285	1.82362	2.91354	1.60	0.63
mthl2_gene	mthl2	0.435492	0.695276	1.60	0.63
CG14821_gene	CG14821	0.870984	1.39055	1.60	0.63
Hk_gene	Hk	4.6271	7.38317	1.60	0.63
CG1939_gene	CG1939	5.41643	8.64129	1.60	0.63
CG1298_gene	CG1298	18.6173	29.6982	1.60	0.63
CG7095_gene	CG7095	1.22482	1.95339	1.59	0.63
CG4080_gene	CG4080	11.8672	18.9049	1.59	0.63
Ntf-2r_gene	Ntf-2r	1.14317	1.82096	1.59	0.63
CG11594_gene	CG1134	10.2068	16.2562	1.59	0.63
CG12375_gene	CG8673	6.72291	10.694	1.59	0.63
Cad87A_gene	Cad87A	10.479	16.6535	1.59	0.63
CG15170_gene	CG15170	0.979857	1.55609	1.59	0.63
CG8398_gene	CG8398	15.5416	24.6657	1.59	0.63
glu_gene	CG17904	4.57267	7.25073	1.59	0.63
CG9238_gene	CG9238	4.57267	7.25073	1.59	0.63
Dif_gene	CG15141	48.5301	76.9108	1.58	0.63
CG4495_gene	CG4495	14.8067	23.4076	1.58	0.63
CG1518_gene	CG1518	29.6679	46.8484	1.58	0.63
CG8012_gene	CG8012	4.30048	6.78722	1.58	0.63
CG8795_gene	CG8795	3.02123	4.76761	1.58	0.63
CG8204_gene	CG30466	1.00708	1.5892	1.58	0.63
CG1801_gene	CG1801	0.734893	1.15879	1.58	0.63
CG13594_gene	CG13594	29.5862	46.5504	1.57	0.64
CG3085_gene	CG3085	0.653238	1.02636	1.57	0.64
pio_gene	pio	23.6527	37.1145	1.57	0.64
CG13822_gene	CG13822	1.03429	1.62231	1.57	0.64
RfC40_gene	RfC40	2.36799	3.70814	1.57	0.64
l(1)G0148_gene	l(1)G0148	21.0125	32.8766	1.56	0.64
B-H2_gene	B-H2	0.571583	0.893926	1.56	0.64
CG32554_gene	CG6506	1.14317	1.78785	1.56	0.64
CG10581_gene	Sin	1.14317	1.78785	1.56	0.64
CG16753_gene	CG16753	2.58573	4.03922	1.56	0.64
Grip_gene	Grip	3.45672	5.39667	1.56	0.64
CG3348_gene	Hmu	1.63309	2.54935	1.56	0.64
CG9336_gene	CG9336	103.919	162.198	1.56	0.64
Bruce_gene	Bruce	118.808	185.407	1.56	0.64
mRpS14_gene	mRpS14	3.75612	5.86018	1.56	0.64
snoRNA:Or-CD2_gene	CG8078	2.12302	3.31084	1.56	0.64
CG3703_gene	mus81	1.06151	1.65542	1.56	0.64
CG3603_gene	CG3603	7.24005	11.29	1.56	0.64
CG14463_gene	CG14463	1.9325	3.01286	1.56	0.64
CG17802_gene	CG17802	1.85084	2.88043	1.56	0.64

CG31288_gene	CG31288	0.489928	0.761493	1.55	0.64
CG6813_gene	CG6813	0.489928	0.761493	1.55	0.64
CG30152_gene	CG30152	5.19868	8.07844	1.55	0.64
t_gene	t	1.76919	2.748	1.55	0.64
CG6179_gene	CG6179	1.27926	1.9865	1.55	0.64
CG10623_gene	CG10623	22.945	35.6246	1.55	0.64
Fbxl4_gene	Fbxl4	4.13717	6.42303	1.55	0.64
CG8641_gene	CG8641	0.789329	1.22501	1.55	0.64
Tsf1_gene	Tsf1	3.45672	5.36356	1.55	0.64
CG5599_gene	CG5599	1.68753	2.61556	1.55	0.65
CRMP_gene	CRMP	3.97386	6.15816	1.55	0.65
CG2617_gene	CG2617	2.88513	4.46963	1.55	0.65
CG14523_gene	CG33203	1.497	2.31759	1.55	0.65
CG34362_gene	CG34362	7.62111	11.7866	1.55	0.65
CG30259_gene	CG30259	3.21175	4.96626	1.55	0.65
CG6055_gene	CG6055	21.5841	33.3732	1.55	0.65
CG8920_gene	CG11200	244.284	377.667	1.55	0.65
az2_gene	az2	1.30648	2.01961	1.55	0.65
CG12267_gene	CG12267	3.7289	5.76086	1.54	0.65
CG34318_gene	CG34365	1.11595	1.72164	1.54	0.65
CG8179_gene	CG34365	1.11595	1.72164	1.54	0.65
CG11739_gene	CG11739	1.63309	2.51624	1.54	0.65
CG6912_gene	CG6912	0.816547	1.25812	1.54	0.65
Pi3K59F_gene	Pi3K59F	11.8672	18.2758	1.54	0.65
CG5639_gene	raps	2.55852	3.9399	1.54	0.65
CG18317_gene	CG18317	7.26727	11.1906	1.54	0.65
CG11737_gene	CG11737	8.70984	13.4089	1.54	0.65
Spn2_gene	Spn2	4943.95	7604.99	1.54	0.65
CG32397_gene	CG18769	72.836	112.006	1.54	0.65
CG15819_gene	CG15819	5.57974	8.57507	1.54	0.65
CG33464_gene	CG33464	0.517147	0.794601	1.54	0.65
dgo_gene	dgo	2.17746	3.34395	1.54	0.65
shrb_gene	shrb	37.2346	57.1782	1.54	0.65
wun2_gene	wun2	2.80348	4.30409	1.54	0.65
so_gene	so	1.14317	1.75474	1.53	0.65
Mst33A_gene	Mst33A	0.62602	0.960143	1.53	0.65
mRpL13_gene	CG10602	1.98693	3.04597	1.53	0.65
olf413_gene	olf413	2.0958	3.21151	1.53	0.65
CG18005_gene	CG11033	7.34893	11.2568	1.53	0.65
CG10383_gene	CG10336	11.2411	17.2164	1.53	0.65
CG30015_gene	CG30015	18.5356	28.3739	1.53	0.65
TpnC73F_gene	TpnC73F	22.945	35.0949	1.53	0.65
CG13511_gene	CG13511	0.952639	1.45677	1.53	0.65
FKBP59_gene	FKBP59	13.5547	20.7258	1.53	0.65
CG30496_gene	CG30493	3.18453	4.86693	1.53	0.65
CG5704_gene	CG5704	1.06151	1.62231	1.53	0.65
CG9626_gene	CG9626	11.105	16.9515	1.53	0.66
CG16771_gene	CG13085	1.38813	2.11894	1.53	0.66
CG4786_gene	CG4786	3.64724	5.56221	1.53	0.66
CG34394_gene	CG34394	36.8807	56.1849	1.52	0.66
CG14964_gene	CG14964	3.02123	4.60206	1.52	0.66
CG14234_gene	CG14234	43.7397	66.6141	1.52	0.66
betaggt-II_gene	betaggt-II	10.8056	16.4549	1.52	0.66
CG10990_gene	CG10990	85.2203	129.652	1.52	0.66
CG8801_gene	CG8801	371.774	565.491	1.52	0.66
CG34150_gene	CG34150	0.870984	1.32434	1.52	0.66
CG32109_gene	CG32109	2.28633	3.47638	1.52	0.66
CG6583_gene	CG17217	5.55252	8.44264	1.52	0.66
CG5861_gene	c(2)M	1.95971	2.97975	1.52	0.66
CG34239_gene	CG6327	1.08873	1.65542	1.52	0.66

CG7841_gene	CG7841	0.435492	0.662168	1.52	0.66
dnt_gene	dnt	5.98801	9.1048	1.52	0.66
amn_gene	CG32529	0.653238	0.993251	1.52	0.66
CG15674_gene	CG15674	0.544365	0.827709	1.52	0.66
Cyp28d2_gene	Cyp28d2	0.544365	0.827709	1.52	0.66
CG31612_gene	CG31612	0.762111	1.15879	1.52	0.66
luna_gene	luna	8.84593	13.442	1.52	0.66
CG4685_gene	CG4685	25.8846	39.2996	1.52	0.66
Ku80_gene	Ku80	2.20468	3.34395	1.52	0.66
Rh50_gene	Rh50	1.98693	3.01286	1.52	0.66
cl_gene	cl	5.85192	8.87305	1.52	0.66
Pde9_gene	Pde9	1.66031	2.51624	1.52	0.66
CG31323_gene	CG31323	4.54545	6.88654	1.52	0.66
CG6287_gene	CG6287	42.0522	63.7005	1.51	0.66
Mms19_gene	Mms19	13.1192	19.865	1.51	0.66
fax_gene	fax	35.6559	53.9667	1.51	0.66
Cng_gene	Cng	1.11595	1.68853	1.51	0.66
CG5569_gene	CG5569	1.00708	1.52299	1.51	0.66
Thor_gene	Thor	45.1006	68.2033	1.51	0.66
CG14526_gene	CG33203	2.58573	3.90679	1.51	0.66
CG33082_gene	CG33082	1.57866	2.3838	1.51	0.66
CG2791_gene	CG2791	46.9515	70.885	1.51	0.66
Wnt2_gene	Wnt2	1.46979	2.21826	1.51	0.66
CG18769_gene	CG18769	77.4087	116.806	1.51	0.66
CG11971_gene	CG11971	5.55252	8.37642	1.51	0.66
CG15321_gene	CG15321	2.04137	3.07908	1.51	0.66
CG17361_gene	CG17361	1.25204	1.88718	1.51	0.66
CG13890_gene	CG13890	6.72291	10.1312	1.51	0.66
srp_gene	srp	25.6396	38.6375	1.51	0.66
CG6199_gene	CG6199	5.8247	8.77372	1.51	0.66
CG10440_gene	CG10440	1.71475	2.58245	1.51	0.66
CG1764_gene	CG1764	1.71475	2.58245	1.51	0.66
l(1)G0289_gene	l(1)G0289	29.7495	44.7625	1.50	0.66
Oscillin_gene	Oscillin	2.42242	3.64192	1.50	0.67
skpB_gene	skpB	0.46271	0.695276	1.50	0.67
Sema-2a_gene	Sema-2a	4.05552	6.09194	1.50	0.67
CG14407_gene	CG14407	4.65432	6.98587	1.50	0.67
CG14516_gene	CG14516	5.00816	7.5156	1.50	0.67
CG3754_gene	CG3754	0.816547	1.22501	1.50	0.67
beat-Ib_gene	beat-Ib	3.64724	5.46288	1.50	0.67
CG5715_gene	CG5715	1.06151	1.5892	1.50	0.67
Fpps_gene	CG7741	8.38322	12.5481	1.50	0.67
LamC_gene	ttv	20.1959	30.2279	1.50	0.67
CG8503_gene	CG8503	2.85792	4.27098	1.49	0.67
CG15539_gene	CG15539	150.354	224.475	1.49	0.67
CG30085_gene	CG30085	1.1976	1.78785	1.49	0.67
mRpL55_gene	mRpL55	0.598801	0.893926	1.49	0.67
Pvf3_gene	Pvf3	6.83178	10.1974	1.49	0.67
CG13085_gene	Pax	2.64017	3.9399	1.49	0.67
Tkr_gene	Tkr	4.08274	6.09194	1.49	0.67
Rgk1_gene	Rgk1	0.843766	1.25812	1.49	0.67
CG15816_gene	CG32560	4.10996	6.12505	1.49	0.67
CG33334_gene	CG33334	6.91343	10.2967	1.49	0.67
bon_gene	bon	13.473	20.0637	1.49	0.67
CG11753_gene	Dhod	9.47195	14.1042	1.49	0.67
AdoR_gene	AdoR	0.734893	1.09258	1.49	0.67
CG1136_gene	CG1136	0.734893	1.09258	1.49	0.67
CG14610_gene	CG14610	2.93957	4.37031	1.49	0.67
CG9918_gene	CG9918	0.979857	1.45677	1.49	0.67
CG6329_gene	CG6329	2.44964	3.64192	1.49	0.67

CG1702_gene	CG1702	1.46979	2.18515	1.49	0.67
CG4851_gene	CG4851	3.32063	4.93315	1.49	0.67
CG5467_gene	CG5467	78.824	117.071	1.49	0.67
CG9747_gene	CG9747	66.0315	98.0339	1.48	0.67
Syn1_gene	Syn1	4.81763	7.15141	1.48	0.67
W_gene	W	4.08274	6.05883	1.48	0.67
CG6403_gene	CG6403	2.85792	4.23787	1.48	0.67
CG15247_gene	CG15247	2.74904	4.07233	1.48	0.68
fus_gene	fus	29.9945	44.4314	1.48	0.68
CG12379_gene	CG8191	0.62602	0.927035	1.48	0.68
CG5740_gene	CG33334	9.14533	13.5413	1.48	0.68
CG6434_gene	CG6434	80.6204	119.356	1.48	0.68
CG31145_gene	CG31145	90.8273	134.387	1.48	0.68
CkIIalpha-i1_gene	CkIIalpha-i1	1.00708	1.48988	1.48	0.68
sn_gene	sws	10.9962	16.2562	1.48	0.68
CG18135_gene	CG18135	63.4729	93.8291	1.48	0.68
mthl5_gene	CG31368	2.5313	3.74125	1.48	0.68
CG10639_gene	Tango6	9.2542	13.6738	1.48	0.68
CG5888_gene	CG5888	3.04844	4.50274	1.48	0.68
CG30109_gene	CG30109	0.762111	1.12568	1.48	0.68
CG32534_gene	CoRest	0.762111	1.12568	1.48	0.68
kek1_gene	kek1	3.56559	5.26423	1.48	0.68
fry_gene	fry	42.3788	62.5417	1.48	0.68
Sur_gene	Sur	4.35492	6.42303	1.47	0.68
CG18747_gene	CG18747	0.898202	1.32434	1.47	0.68
CG6693_gene	CG6693	10.0163	14.7663	1.47	0.68
Mcm6_gene	Mcm6	4.51823	6.65478	1.47	0.68
CG7149_gene	CG7149	0.517147	0.761493	1.47	0.68
bol_gene	bol	60.5062	89.0946	1.47	0.68
CG13760_gene	CG13760	2.06859	3.04597	1.47	0.68
Est-P_gene	Est-P	3.64724	5.36356	1.47	0.68
pck_gene	pck	12.0032	17.6468	1.47	0.68
CG16892_gene	CG16892	2.61295	3.84057	1.47	0.68
CG13116_gene	Nckx30C	0.653238	0.960143	1.47	0.68
CG8589_gene	CG8589	1.44257	2.11894	1.47	0.68
hdc_gene	hdc	9.9891	14.667	1.47	0.68
gcl_gene	gcl	6.31463	9.27035	1.47	0.68
CG33182_gene	CG17724	9.47195	13.9055	1.47	0.68
CG30492_gene	CG30492	109.363	160.509	1.47	0.68
bnl_gene	bnl	2.64017	3.87368	1.47	0.68
mam_gene	mam	22.7272	33.3401	1.47	0.68
CG40354_gene	CG40354	2.25911	3.31084	1.47	0.68
CG11852_gene	CG11852	4.51823	6.62168	1.47	0.68
CG32786_gene	CG32786	1.1976	1.75474	1.47	0.68
Tl_gene	Tl	12.3843	18.1434	1.47	0.68
CG33785_gene	CG33785	3.89221	5.69464	1.46	0.68
CG33786_gene	CG33785	3.89221	5.69464	1.46	0.68
Snm1_gene	Snm1	2.15024	3.1453	1.46	0.68
CG7368_gene	CG7368	15.8138	23.1096	1.46	0.68
CG2781_gene	CG2781	15.9499	23.3083	1.46	0.68
CG40050_gene	CG40050	4.05552	5.9264	1.46	0.68
p24-2_gene	p24-2	57.1311	83.4662	1.46	0.68
CG7023_gene	CG7029	63.3913	92.5379	1.46	0.69
CG32649_gene	CG32649	14.0174	20.461	1.46	0.69
CG1868_gene	CG1814	3.26619	4.76761	1.46	0.69
frtz_gene	mRpL48	4.35492	6.35681	1.46	0.69
CG5966_gene	CG5966	0.680456	0.993251	1.46	0.69
CG7381_gene	CG7381	0.680456	0.993251	1.46	0.69
CG14401_gene	CG14401	5.30756	7.74736	1.46	0.69
cort_gene	cup	1.22482	1.78785	1.46	0.69

CG3511_gene	CG3511	2.31355	3.37705	1.46	0.69
CG14351_gene	CG14351	7.89329	11.5217	1.46	0.69
CG8159_gene	CG8159	0.952639	1.39055	1.46	0.69
CG10075_gene	CG9948	2.04137	2.97975	1.46	0.69
CG6972_gene	Ccap	1.76919	2.58245	1.46	0.69
CG1943_gene	CG1943	33.7234	49.1659	1.46	0.69
Cont_gene	Cont	75.3129	109.754	1.46	0.69
Tsp42Ed_gene	Tsp42Ed	18.454	26.884	1.46	0.69
CG4449_gene	CG4449	1.7964	2.61556	1.46	0.69
CG14322_gene	CG14322	10.9417	15.9251	1.46	0.69
CG10399_gene	CG10399	1.52422	2.21826	1.46	0.69
CG5339_gene	CG17658	5.41643	7.87979	1.45	0.69
CG41511_gene	CG41511	5.41643	7.87979	1.45	0.69
CG11679_gene	CG11679	8.21991	11.9521	1.45	0.69
Zw_gene	Zw	9.33586	13.5744	1.45	0.69
CG4004_gene	CG4004	4.05552	5.89329	1.45	0.69
CG6782_gene	CG6782	13.1464	19.1035	1.45	0.69
CG6783_gene	CG6782	13.1464	19.1035	1.45	0.69
CG14817_gene	CG14817	6.99509	10.1643	1.45	0.69
CG9948_gene	CG9948	2.93957	4.27098	1.45	0.69
CG34112_gene	CR41470	2.93957	4.27098	1.45	0.69
Cad99C_gene	Cad99C	0.979857	1.42366	1.45	0.69
dnk_gene	dnk	0.979857	1.42366	1.45	0.69
CG17739_gene	CG17739	4.49101	6.52235	1.45	0.69
HmgD_gene	HmgD	9.41751	13.6738	1.45	0.69
para_gene	para	3.23897	4.70139	1.45	0.69
mst_gene	mst	2.96679	4.30409	1.45	0.69
Hr46_gene	Hr46	0.707674	1.02636	1.45	0.69
CG14630_gene	CG33082	1.27926	1.85407	1.45	0.69
CG33671_gene	spt4	14.1263	20.461	1.45	0.69
CG33672_gene	spt4	14.1263	20.461	1.45	0.69
CG1332_gene	CG1332	13.2825	19.236	1.45	0.69
CG9815_gene	CG9815	2.28633	3.31084	1.45	0.69
ImpE3_gene	CG2747	0.571583	0.827709	1.45	0.69
Ste:CG33244_gene	te:CG3324	0.571583	0.827709	1.45	0.69
CG11875_gene	CG11875	1.57866	2.28448	1.45	0.69
CG30493_gene	CG30493	5.47087	7.9129	1.45	0.69
SK_gene	SK	12.2482	17.713	1.45	0.69
CG4872_gene	CG4872	12.1393	17.5474	1.45	0.69
CG17086_gene	CG17086	0.870984	1.25812	1.44	0.69
Octbeta2R_gene	Octbeta2R	3.48394	5.03247	1.44	0.69
stumps_gene	stumps	9.44473	13.6407	1.44	0.69
G-ialpha65A_gene	G-ialpha65A	5.9608	8.60818	1.44	0.69
CG13004_gene	CG13004	2.47686	3.5757	1.44	0.69
CG4611_gene	CG4611	2.47686	3.5757	1.44	0.69
pyx_gene	Kaz1-ORFB	4.51823	6.52235	1.44	0.69
lbm_gene	lbm	1.60588	2.31759	1.44	0.69
CG11198_gene	CG11198	32.2264	46.4842	1.44	0.69
snoRNA:Psi28S-2179_gene	RpL22	0.734893	1.05947	1.44	0.69
CG14985_gene	CG14985	4.27326	6.15816	1.44	0.69
CG14518_gene	CG14518	1.03429	1.48988	1.44	0.69
Ntf-2_gene	Ntf-2	9.30864	13.4089	1.44	0.69
CG14973_gene	CG14973	1.33369	1.92029	1.44	0.69
5PtaseI_gene	CG31110	1.63309	2.35069	1.44	0.69
CG13360_gene	CG13360	0.898202	1.29123	1.44	0.70
CG15210_gene	sbr	1.7964	2.58245	1.44	0.70
Tsp42Eb_gene	Tsp42Ea	0.598801	0.860818	1.44	0.70
CG7059_gene	CG7059	28.4975	40.9551	1.44	0.70
CG1621_gene	CG1621	72.3461	103.96	1.44	0.70
CG1575_gene	CG1575	7.21284	10.3629	1.44	0.70

Acer_gene	Acer	7.67555	11.0251	1.44	0.70
CG10721_gene	CG10721	6.77734	9.73386	1.44	0.70
dsx_gene	lds	19.8965	28.5725	1.44	0.70
CG12106_gene	CG12106	3.02123	4.3372	1.44	0.70
swi2_gene	CG4966	2.72182	3.90679	1.44	0.70
CG9154_gene	CG13993	4.87207	6.98587	1.43	0.70
CG5004_gene	CG5004	7.92051	11.3562	1.43	0.70
CG13084_gene	CG13084	1.52422	2.18515	1.43	0.70
Tsf2_gene	Tsf2	16.6848	23.9042	1.43	0.70
ref(2)P_gene	ref(2)P	82.0358	117.402	1.43	0.70
Glu-RIB_gene	Glu-RIB	0.46271	0.662168	1.43	0.70
Lsm11_gene	Lsm11	0.46271	0.662168	1.43	0.70
CG7081_gene	CG7081	2.31355	3.31084	1.43	0.70
csul_gene	csul	4.3277	6.19127	1.43	0.70
CG3975_gene	CG15267	2.93957	4.20476	1.43	0.70
CG10147_gene	CG10147	1.08873	1.55609	1.43	0.70
GstD10_gene	GstD10	6.39629	9.13791	1.43	0.70
Oatp26F_gene	CG34345	3.75612	5.36356	1.43	0.70
CG2083_gene	CG2083	3.1301	4.46963	1.43	0.70
Mst36Fb_gene	Mst36Fb	0.62602	0.893926	1.43	0.70
rdgBbeta_gene	rdgBbeta	2.04137	2.91354	1.43	0.70
CG8116_gene	CG8116	1.74197	2.48313	1.43	0.70
Rrp1_gene	Rrp1	3.81055	5.42977	1.42	0.70
unc-13_gene	unc-13	23.5166	33.5057	1.42	0.70
CG8441_gene	CG8441	4.9265	7.01898	1.42	0.70
Bx42_gene	Bx42	20.7131	29.4996	1.42	0.70
mus210_gene	mus210	12.6293	17.9778	1.42	0.70
CG11915_gene	Lmpt	6.72291	9.56832	1.42	0.70
CG13090_gene	CG13090	5.44365	7.74736	1.42	0.70
CG12972_gene	CG32436	4.16439	5.9264	1.42	0.70
CG5326_gene	CG5326	60.2884	85.7507	1.42	0.70
mthl1_gene	mthl1	6.91343	9.83319	1.42	0.70
Aats-met_gene	Aats-met	1.76919	2.51624	1.42	0.70
CG4749_gene	CG4749	4.19161	5.95951	1.42	0.70
CG34038_gene	CG34038	4.84485	6.88654	1.42	0.70
pncr012:2L_gene	pncr012:2L	2.58573	3.67503	1.42	0.70
Ance_gene	Ance	10.9962	15.6272	1.42	0.70
Ipp_gene	Ipp	9.22699	13.1109	1.42	0.70
shg_gene	shg	10.8601	15.4285	1.42	0.70
CG31004_gene	CG31004	6.17854	8.77372	1.42	0.70
CG9650_gene	CG9650	0.489928	0.695276	1.42	0.70
Scgdelta_gene	Scgdelta	0.653238	0.927035	1.42	0.70
CG11048_gene	CG11048	0.979857	1.39055	1.42	0.70
CG4594_gene	CG4594	1.14317	1.62231	1.42	0.70
CG6631_gene	CG6631	12.466	17.6799	1.42	0.71
CG18336_gene	CG18336	3.62003	5.1318	1.42	0.71
CG14411_gene	CG14411	19.8149	28.0759	1.42	0.71
CG15027_gene	CG15027	4.79041	6.78722	1.42	0.71
scb_gene	scb	46.7609	66.2168	1.42	0.71
CG14277_gene	CG14277	32.3625	45.7889	1.41	0.71
CG11110_gene	CG11110	3.83777	5.42977	1.41	0.71
hoe1_gene	hoe1	17.5286	24.7982	1.41	0.71
l(1)G0193_gene	CG1530	27.7354	39.2334	1.41	0.71
CG34330_gene	CG34330	5.5253	7.81358	1.41	0.71
Cas_gene	mdy	10.0708	14.2366	1.41	0.71
ras_gene	CG32676	33.9684	48.0071	1.41	0.71
CG6444_gene	CG6444	3.37506	4.76761	1.41	0.71
CG32252_gene	CG1332	0.843766	1.1919	1.41	0.71
rpr_gene	rpr	0.843766	1.1919	1.41	0.71
CG17159_gene	CG17162	16.086	22.7123	1.41	0.71

CG17162_gene	CG17162	16.086	22.7123	1.41	0.71
p53_gene	p53	3.04844	4.30409	1.41	0.71
l(1)G0237_gene	CG11699	1.52422	2.15204	1.41	0.71
CG12765_gene	CG12765	1.52422	2.15204	1.41	0.71
Shc_gene	Shc	6.96787	9.83319	1.41	0.71
sli_gene	CG33464	1.1976	1.68853	1.41	0.71
Asator_gene	Asator	12.5204	17.6468	1.41	0.71
Rala_gene	Rala	109.417	154.153	1.41	0.71
CG32698_gene	CG32698	1.03429	1.45677	1.41	0.71
CG4313_gene	CG4313	3.10288	4.37031	1.41	0.71
CG1750_gene	mRpL32	0.517147	0.728384	1.41	0.71
snoRNA:Psi18S-920_gene	RpL10Ab	0.517147	0.728384	1.41	0.71
mdy_gene	CG13280	10.6968	15.0643	1.41	0.71
ade2_gene	CG31643	19.3522	27.2482	1.41	0.71
Cad74A_gene	Cad74A	52.3679	73.7324	1.41	0.71
CG7985_gene	CG7985	1.38813	1.95339	1.41	0.71
Grip75_gene	Grip75	8.68262	12.217	1.41	0.71
CG9801_gene	CG9801	15.46	21.7522	1.41	0.71
CG4957_gene	CG4957	3.1301	4.40341	1.41	0.71
MP1_gene	MP1	2.61295	3.67503	1.41	0.71
CG13516_gene	CG13516	0.870984	1.22501	1.41	0.71
CG33087_gene	CG33087	6.45072	9.0717	1.41	0.71
ppl_gene	ppl	3.83777	5.39667	1.41	0.71
CSN5_gene	CSN5	9.2542	13.0116	1.41	0.71
CG3409_gene	CG3409	39.7386	55.8538	1.41	0.71
CG14945_gene	CG14945	3.51115	4.93315	1.40	0.71
CG18542_gene	CG18542	3.51115	4.93315	1.40	0.71
CG4558_gene	CG4558	6.69569	9.40278	1.40	0.71
CG33203_gene	CG33203	5.30756	7.44938	1.40	0.71
ave_gene	Rpn6	1.76919	2.48313	1.40	0.71
LanB2_gene	LanB2	62.8197	88.1676	1.40	0.71
CG12703_gene	CG12703	32.8524	46.0869	1.40	0.71
Indy_gene	Indy	20.822	29.2016	1.40	0.71
mir-283_gene	l(1)G0168	3.56559	4.99936	1.40	0.71
Rrp46_gene	Rrp46	3.21175	4.50274	1.40	0.71
rho-4_gene	rho-4	12.1393	17.0177	1.40	0.71
CG32543_gene	CG32543	1.25204	1.75474	1.40	0.71
CG41265_gene	CG41265	3.40228	4.76761	1.40	0.71
Pi4KIIalpha_gene	Snm1	20.2504	28.3408	1.40	0.71
CG8066_gene	CG8066	10.6968	14.965	1.40	0.71
CG32706_gene	CG32706	0.544365	0.761493	1.40	0.71
CG6356_gene	CG6356	0.544365	0.761493	1.40	0.71
CG8351_gene	CG8351	23.5982	33.0091	1.40	0.71
CG6805_gene	CG6805	9.44473	13.2102	1.40	0.71
CG13211_gene	CG18336	22.3462	31.2543	1.40	0.71
cib_gene	cib	27.4904	38.4388	1.40	0.72
pnut_gene	pnut	13.3642	18.6731	1.40	0.72
CG10083_gene	CG10083	4.05552	5.66153	1.40	0.72
OdsH_gene	OdsH	4.98094	6.95276	1.40	0.72
CG3371_gene	CG3371	7.02231	9.80008	1.40	0.72
SP71_gene	SP71	0.92542	1.29123	1.40	0.72
serp_gene	serp	1.85084	2.58245	1.40	0.72
CG14440_gene	CG32741	5.38921	7.5156	1.39	0.72
CG14400_gene	CG9335	1.11595	1.55609	1.39	0.72
Cctgamma_gene	Cctgamma	22.9178	31.9496	1.39	0.72
CG12883_gene	CG12883	3.7289	5.19802	1.39	0.72
CG4279_gene	CG9437	5.2259	7.28384	1.39	0.72
CG14963_gene	CG32278	1.30648	1.82096	1.39	0.72
Vha68-1_gene	Vha68-1	13.473	18.7724	1.39	0.72
CG14005_gene	CG14005	3.18453	4.43652	1.39	0.72

CG15266_gene	CG15266	1.87806	2.61556	1.39	0.72
endoB_gene	endoB	2.25911	3.1453	1.39	0.72
N_gene	N	1.33369	1.85407	1.39	0.72
Dhap-at_gene	CG5116	1.52422	2.11894	1.39	0.72
CG14183_gene	CG14183	0.762111	1.05947	1.39	0.72
mus209_gene	mus209	0.762111	1.05947	1.39	0.72
CG1792_gene	CG1792	1.71475	2.3838	1.39	0.72
CG8008_gene	CG8008	19.4883	27.0827	1.39	0.72
Art4_gene	CG34360	4.40936	6.12505	1.39	0.72
CG10000_gene	CG10000	4.21883	5.86018	1.39	0.72
CG33332_gene	CG33331	3.83777	5.33045	1.39	0.72
Amy-d_gene	Amy-d	10.7784	14.965	1.39	0.72
l(3)neo43_gene	l(3)neo43	1.9325	2.68178	1.39	0.72
CG13014_gene	CG13014	6.77734	9.40278	1.39	0.72
GluRIIE_gene	GluRIIE	1.55144	2.15204	1.39	0.72
Spx_gene	Spx	5.06259	7.01898	1.39	0.72
Got1_gene	Got1	38.1872	52.9403	1.39	0.72
CG3566_gene	Spt6	10.724	14.8657	1.39	0.72
CG31638_gene	CG31638	7.24005	10.0318	1.39	0.72
Rae1_gene	CG10320	7.86607	10.8927	1.38	0.72
amx_gene	mxc	7.10396	9.83319	1.38	0.72
CG13796_gene	CG13796	1.57866	2.18515	1.38	0.72
sas_gene	sas	18.3723	25.4272	1.38	0.72
HDAC4_gene	HDAC4	11.2956	15.6272	1.38	0.72
Pld_gene	Pld	11.1595	15.4285	1.38	0.72
Obp99c_gene	Gycalpha99	6.80456	9.40278	1.38	0.72
Gli_gene	Gli	12.466	17.2164	1.38	0.72
CG33155_gene	AGO1	19.7877	27.3144	1.38	0.72
mRpL53_gene	AGO1	19.7877	27.3144	1.38	0.72
CG3036_gene	CG3036	3.83777	5.29734	1.38	0.72
Pdp_gene	Pdp	21.2302	29.3009	1.38	0.72
Dip-B_gene	Dip-B	65.9226	90.9487	1.38	0.72
CG10710_gene	CG10743	0.816547	1.12568	1.38	0.73
LanA_gene	LanA	87.18	120.15	1.38	0.73
CG13623_gene	CG6607	3.07566	4.23787	1.38	0.73
SP2637_gene	SP2637	10.8873	14.9981	1.38	0.73
CG32852_gene	Csk	1.85084	2.54935	1.38	0.73
Dgk_gene	Dgk	41.8072	57.5755	1.38	0.73
seq_gene	CG17724	10.724	14.7663	1.38	0.73
CR41509_gene	CR41509	1.03429	1.42366	1.38	0.73
Mgstl_gene	Mgstl	5.17147	7.1183	1.38	0.73
Mst36Fa_gene	Mst36Fa	1.66031	2.28448	1.38	0.73
kappaB-Ras_gene	kappaB-Ras	5.60696	7.71425	1.38	0.73
homer_gene	homer	6.45072	8.87305	1.38	0.73
CG31195_gene	CG17838	25.4491	34.9956	1.38	0.73
CG18643_gene	CG18643	0.62602	0.860818	1.38	0.73
CG5096_gene	CG5091	0.62602	0.860818	1.38	0.73
CG12118_gene	CG12106	6.91343	9.5021	1.37	0.73
CG32756_gene	CG32756	3.56559	4.90004	1.37	0.73
CG31082_gene	scrib	26.7011	36.6841	1.37	0.73
Nrg_gene	Nrg	70.2503	96.5109	1.37	0.73
CG31223_gene	CG31223	3.18453	4.37031	1.37	0.73
CG14450_gene	mael	2.34077	3.21151	1.37	0.73
icln_gene	icln	1.71475	2.35069	1.37	0.73
Iris_gene	CG4552	1.9325	2.64867	1.37	0.73
ncd_gene	CG7789	1.9325	2.64867	1.37	0.73
sinu_gene	sinu	12.2482	16.7859	1.37	0.73
CG11652_gene	CG11652	6.66847	9.13791	1.37	0.73
Ugt58Fa_gene	Ugt58Fa	6.66847	9.13791	1.37	0.73
CG15561_gene	CG15561	4.10996	5.62842	1.37	0.73

ine_gene	CG17840	8.21991	11.2568	1.37	0.73
wus_gene	wus	27.3271	37.4125	1.37	0.73
Updo_gene	Updo	27.8443	38.1077	1.37	0.73
Ote_gene	Ote	0.870984	1.1919	1.37	0.73
CR12628_gene	CR12628	1.30648	1.78785	1.37	0.73
Atg9_gene	Atg9	18.6173	25.4603	1.37	0.73
CG9547_gene	CG31638	4.16439	5.69464	1.37	0.73
CG11309_gene	CG11309	5.71583	7.81358	1.37	0.73
CG9617_gene	CG9617	8.13826	11.1244	1.37	0.73
gammaTub23C_gene	mmaTub2	1.33369	1.82096	1.37	0.73
l(2)06496_gene	CG30194	10.2613	14.0048	1.36	0.73
GlcAT-I_gene	GlcAT-I	2.01415	2.748	1.36	0.73
CG10053_gene	CG10053	3.59281	4.90004	1.36	0.73
CG32584_gene	CG32584	7.18562	9.80008	1.36	0.73
CG14721_gene	CG14721	8.11104	11.0582	1.36	0.73
CG4738_gene	Csl4	11.9488	16.2893	1.36	0.73
CG3961_gene	CG3961	3.15732	4.30409	1.36	0.73
drongo_gene	drongo	14.6706	19.9975	1.36	0.73
Gapdh2_gene	Gapdh2	111.595	152.1	1.36	0.73
shu_gene	shu	2.25911	3.07908	1.36	0.73
CG13185_gene	CG13185	40.6913	55.4565	1.36	0.73
CG13604_gene	CG13604	1.36091	1.85407	1.36	0.73
CG4627_gene	CG4627	1.36091	1.85407	1.36	0.73
RfC3_gene	RfC3	1.36091	1.85407	1.36	0.73
snoRNA:Me28S-G2596_gene	dom	2.50408	3.41016	1.36	0.73
CG34315_gene	lat	1.82362	2.48313	1.36	0.73
Mpk2_gene	Mpk2	3.64724	4.96626	1.36	0.73
CG31100_gene	CG31100	116.167	158.126	1.36	0.73
CG17163_gene	CG17163	2.74904	3.74125	1.36	0.73
CG6153_gene	CG6153	2.5313	3.44327	1.36	0.74
CG34396_gene	CG34396	25.8301	35.128	1.36	0.74
CG4239_gene	CG4239	9.22699	12.5481	1.36	0.74
CG12418_gene	CG34360	1.85084	2.51624	1.36	0.74
CG6638_gene	rhea	3.70168	5.03247	1.36	0.74
not_gene	not	3.23897	4.40341	1.36	0.74
CG31156_gene	CG31156	4.87207	6.62168	1.36	0.74
AGO3_gene	AGO3	8.356	11.3562	1.36	0.74
CG31793_gene	CG31793	2.0958	2.84732	1.36	0.74
Bka_gene	Bka	5.36199	7.28384	1.36	0.74
Trxr-1_gene	sni	69.6787	94.6237	1.36	0.74
CG34404_gene	CG6171	1.17038	1.5892	1.36	0.74
CG15877_gene	CG15877	4.68154	6.35681	1.36	0.74
CG13344_gene	CG13344	2.58573	3.50949	1.36	0.74
heph_gene	heph	42.3788	57.5093	1.36	0.74
CG32436_gene	CG32436	6.12411	8.3102	1.36	0.74
morgue_gene	morgue	11.35	15.3954	1.36	0.74
CG12863_gene	CG12863	2.36799	3.21151	1.36	0.74
CG15072_gene	CG15072	5.47087	7.41628	1.36	0.74
CG6746_gene	CG12264	10.724	14.5346	1.36	0.74
CG33229_gene	CG16971	26.0751	35.3266	1.35	0.74
CG10431_gene	CG10431	5.28034	7.15141	1.35	0.74
Mdr49_gene	Sans	214.698	290.758	1.35	0.74
CG7593_gene	Pcd	1.44257	1.95339	1.35	0.74
Flo_gene	Flo	8.19269	11.0913	1.35	0.74
mtSSB_gene	CG31287	1.68753	2.28448	1.35	0.74
CG9249_gene	Mpp6	5.79749	7.84669	1.35	0.74
CR41470_gene	CG14646	16.7937	22.7123	1.35	0.74
Cct1_gene	Cct1	93.5491	126.441	1.35	0.74
Rrp42_gene	Rrp42	2.44964	3.31084	1.35	0.74
CG16719_gene	CG6767	0.734893	0.993251	1.35	0.74

Ets96B_gene	Ets96B	1.25204	1.68853	1.35	0.74
ifc_gene	ifc	26.7555	36.055	1.35	0.74
CG32017_gene	CG32017	6.31463	8.50885	1.35	0.74
CG11077_gene	CG11077	6.58682	8.87305	1.35	0.74
rig_gene	rig	9.74413	13.1109	1.35	0.74
CG8600_gene	CG8600	16.9297	22.7786	1.35	0.74
Tpr2_gene	Tpr2	83.2878	112.006	1.34	0.74
CG10681_gene	CG10681	1.55144	2.08583	1.34	0.74
CG6231_gene	CG6231	7.7572	10.4291	1.34	0.74
ast_gene	ast	5.9608	8.01223	1.34	0.74
CG5516_gene	CG5516	4.40936	5.9264	1.34	0.74
CG17059_gene	CG17059	10.3974	13.9717	1.34	0.74
Klp31E_gene	Klp31E	4.16439	5.59532	1.34	0.74
ida_gene	ida	1.82362	2.45002	1.34	0.74
CG30127_gene	CG30127	1.30648	1.75474	1.34	0.74
CG13857_gene	CG7059	5.49809	7.38317	1.34	0.74
CG2121_gene	CG2121	3.67446	4.93315	1.34	0.74
CG14291_gene	CG14291	1.57866	2.11894	1.34	0.75
CG18262_gene	CG18262	2.36799	3.1784	1.34	0.75
CG1140_gene	CG1140	9.22699	12.3825	1.34	0.75
CG11919_gene	CG18003	2.64017	3.5426	1.34	0.75
CG18003_gene	CG18003	2.64017	3.5426	1.34	0.75
CG5934_gene	CG5934	3.70168	4.96626	1.34	0.75
CG3570_gene	CG3570	5.55252	7.44938	1.34	0.75
CG6404_gene	CG6404	3.97386	5.33045	1.34	0.75
CG11597_gene	CG5946	4.51823	6.05883	1.34	0.75
CG31183_gene	CG31183	3.45672	4.63517	1.34	0.75
CG7627_gene	CG7627	10.4518	14.0048	1.34	0.75
lat_gene	lat	1.87806	2.51624	1.34	0.75
wge_gene	wge	19.325	25.8908	1.34	0.75
CG40040_gene	CG40040	4.30048	5.76086	1.34	0.75
pea_gene	pea	11.0506	14.7994	1.34	0.75
Nup75_gene	Nup75	6.77734	9.0717	1.34	0.75
CG5009_gene	CG5009	8.16547	10.9258	1.34	0.75
CG34001_gene	CG34001	1.36091	1.82096	1.34	0.75
CG7759_gene	CG7759	1.36091	1.82096	1.34	0.75
snoRNA:Psi18S-531_gene	RpL22	1.36091	1.82096	1.34	0.75
CG31961_gene	CG31961	3.81055	5.09869	1.34	0.75
CG3191_gene	CG3191	2.44964	3.27773	1.34	0.75
CG14100_gene	CG9330	2.44964	3.27773	1.34	0.75
CG33557_gene	CG33557	0.544365	0.728384	1.34	0.75
CG4587_gene	CG4587	0.544365	0.728384	1.34	0.75
cutlet_gene	cutlet	0.544365	0.728384	1.34	0.75
CG32343_gene	CG32343	2.99401	4.00611	1.34	0.75
DnaJ-1_gene	DnaJ-1	99.401	132.996	1.34	0.75
Pep_gene	Pep	92.161	123.229	1.34	0.75
Wwox_gene	CG7224	5.49809	7.35006	1.34	0.75
CG8079_gene	CG8079	5.2259	6.98587	1.34	0.75
CG11604_gene	CG11604	9.63526	12.8792	1.34	0.75
CG13994_gene	CG13994	4.13717	5.5291	1.34	0.75
KH1_gene	KH1	3.04844	4.07233	1.34	0.75
CG33305_gene	CG33305	1.38813	1.85407	1.34	0.75
CG8436_gene	CG8436	2.77626	3.70814	1.34	0.75
dm_gene	dm	69.842	93.2663	1.34	0.75
mira_gene	Hs6st	1.11595	1.48988	1.34	0.75
CG7970_gene	CG7970	6.69569	8.93926	1.34	0.75
CG31538_gene	l(3)82Fd	1.68753	2.25137	1.33	0.75
CG14757_gene	CG14757	0.843766	1.12568	1.33	0.75
Cyp313b1_gene	Cyp313b1	0.843766	1.12568	1.33	0.75
PHDP_gene	PHDP	0.843766	1.12568	1.33	0.75

Bsg_gene	Bsg	62.7653	83.7311	1.33	0.75
CG13277_gene	ChLD3	7.32171	9.76697	1.33	0.75
rumi_gene	CG31139	4.79041	6.38992	1.33	0.75
CG32549_gene	CG32549	9.58082	12.7798	1.33	0.75
CG13741_gene	CG8080	1.41535	1.88718	1.33	0.75
CG6663_gene	CG6663	4031.57	5372.5	1.33	0.75
CG18549_gene	CG18549	15.1606	20.1961	1.33	0.75
su(r)_gene	su(r)	36.9352	49.199	1.33	0.75
Kif3C_gene	Kif3C	21.2302	28.2746	1.33	0.75
Df31_gene	Df31	12.3571	16.4549	1.33	0.75
CG14211_gene	CG14211	4.0283	5.36356	1.33	0.75
CG7110_gene	CG7110	6.91343	9.20413	1.33	0.75
CG7891_gene	CG7891	8.08382	10.7602	1.33	0.75
CG13601_gene	CG5857	2.61295	3.47638	1.33	0.75
CG3074_gene	CG5625	74.7957	99.4907	1.33	0.75
CG11242_gene	CG11242	3.78334	5.03247	1.33	0.75
SmD3_gene	Oda	26.565	35.3266	1.33	0.75
CG13229_gene	CG13229	1.17038	1.55609	1.33	0.75
scrib_gene	scrib	115.65	153.755	1.33	0.75
scu_gene	scu	14.3712	19.1035	1.33	0.75
raw_gene	raw	14.6706	19.5008	1.33	0.75
CG15923_gene	bon	4.40936	5.86018	1.33	0.75
CAP-D2_gene	CAP-D2	1.46979	1.95339	1.33	0.75
Gal_gene	Gal	2.06859	2.748	1.33	0.75
klar_gene	klar	30.4844	40.4915	1.33	0.75
SerT_gene	SerT	6.23298	8.27709	1.33	0.75
Irbp_gene	Irbp	3.26619	4.3372	1.33	0.75
Alp23B_gene	Alp23B	0.598801	0.794601	1.33	0.75
CG17855_gene	CG17855	0.598801	0.794601	1.33	0.75
CG14220_gene	CG14220	5.68861	7.54871	1.33	0.75
pyr_gene	pyr	24.6869	32.7442	1.33	0.75
Nak_gene	Nak	49.3739	65.4884	1.33	0.75
mus308_gene	CG12279	3.62003	4.80071	1.33	0.75
CG4334_gene	CG4334	2.42242	3.21151	1.33	0.75
CG6579_gene	CG6579	56.0424	74.2952	1.33	0.75
CG7943_gene	CG7943	3.94665	5.23112	1.33	0.75
CG14984_gene	CG14984	1.52422	2.01961	1.33	0.75
Nufip_gene	MED11	1.52422	2.01961	1.33	0.75
Ets97D_gene	T48	4.57267	6.05883	1.33	0.75
CG4272_gene	Rab5	9.77135	12.9454	1.32	0.75
CG10512_gene	CG33056	3.97386	5.26423	1.32	0.75
CG12164_gene	CG12164	1.22482	1.62231	1.32	0.75
CG3911_gene	CG3911	12.5748	16.6535	1.32	0.76
CG9527_gene	CG9527	4.30048	5.69464	1.32	0.76
CG33116_gene	CG33116	1.85084	2.45002	1.32	0.76
Trf2_gene	Trf2	23.1627	30.6584	1.32	0.76
chn_gene	chn	2.47686	3.27773	1.32	0.76
CG6459_gene	CG6459	8.0566	10.6609	1.32	0.76
CG10158_gene	CG10158	4.65432	6.15816	1.32	0.76
CG3044_gene	CG3044	3.7289	4.93315	1.32	0.76
Rpb4_gene	Rpb4	4.98094	6.58857	1.32	0.76
CG11206_gene	CG34208	3.75612	4.96626	1.32	0.76
CG6432_gene	Dis3	0.62602	0.827709	1.32	0.76
sei_gene	sei	0.62602	0.827709	1.32	0.76
CG33181_gene	otu	79.0146	104.457	1.32	0.76
Aats-tyr_gene	Aats-tyr	34.8938	46.12	1.32	0.76
CG41133_gene	CG15831	2.20468	2.91354	1.32	0.76
CG31534_gene	CG31534	25.8301	34.1347	1.32	0.76
CG2862_gene	CG2862	17.964	23.7387	1.32	0.76
CG9319_gene	CG9319	9.47195	12.515	1.32	0.76

Fer1_gene	Fer1	25.2585	33.3732	1.32	0.76
Paip2_gene	Paip2	15.8138	20.8914	1.32	0.76
CG4068_gene	CG4068	16.1949	21.388	1.32	0.76
CG34455_gene	CG34455	3.18453	4.20476	1.32	0.76
CG5190_gene	CG5190	4.79041	6.3237	1.32	0.76
CG17264_gene	CG17264	1.27926	1.68853	1.32	0.76
Ipk2_gene	Ipk2	1.27926	1.68853	1.32	0.76
CG5676_gene	Ror	12.5476	16.5542	1.32	0.76
lectin-46Cb_gene	CG1648	919.895	1213.52	1.32	0.76
CG13430_gene	CG13430	2.25911	2.97975	1.32	0.76
CG18065_gene	CG13430	2.25911	2.97975	1.32	0.76
CG34438_gene	CG34438	10.3429	13.6407	1.32	0.76
CG4619_gene	CG4619	8.73706	11.5217	1.32	0.76
CG5454_gene	CG5454	6.17854	8.14466	1.32	0.76
pncr016:2R_gene	pncr016:2R	1.63309	2.15204	1.32	0.76
CG13139_gene	CG13139	0.653238	0.860818	1.32	0.76
CG14898_gene	Dhfr	0.653238	0.860818	1.32	0.76
trsn_gene	trsn	4.24605	5.59532	1.32	0.76
Nf1_gene	Nf1	13.7724	18.1434	1.32	0.76
bsk_gene	bsk	10.9962	14.4684	1.32	0.76
CG8080_gene	Dbp45A	3.67446	4.83382	1.32	0.76
Act42A_gene	PNGase	26.0751	34.3003	1.32	0.76
CG3225_gene	CG15629	1.00708	1.32434	1.32	0.76
Cp1_gene	Cp1	177.517	233.381	1.31	0.76
CG6904_gene	CG6904	15.5416	20.4279	1.31	0.76
CG15678_gene	CG15678	0.680456	0.893926	1.31	0.76
Bc_gene	elk	0.680456	0.893926	1.31	0.76
CG10479_gene	CG10479	4.08274	5.36356	1.31	0.76
gsb-n_gene	gsb-n	2.04137	2.68178	1.31	0.76
CG14184_gene	CG14184	3.75612	4.93315	1.31	0.76
CG6770_gene	CG6770	1588.46	2086.13	1.31	0.76
CG17646_gene	CG17646	5.47087	7.18452	1.31	0.76
glo_gene	glo	44.2296	58.0721	1.31	0.76
stau_gene	stau	18.5356	24.3347	1.31	0.76
CG11008_gene	CG11008	6.20576	8.14466	1.31	0.76
CG9339_gene	CG9339	31.1105	40.8226	1.31	0.76
CG12134_gene	CG12134	4.84485	6.35681	1.31	0.76
CG7516_gene	CG7516	7.62111	9.99873	1.31	0.76
mei-9_gene	mei-9	9.36308	12.2832	1.31	0.76
CG13550_gene	CG13550	3.83777	5.03247	1.31	0.76
Arc42_gene	Arc42	6.99509	9.17102	1.31	0.76
CG32418_gene	CG32418	6.99509	9.17102	1.31	0.76
CG18343_gene	CG18343	61.6221	80.7844	1.31	0.76
Myt1_gene	Myt1	2.80348	3.67503	1.31	0.76
ctp_gene	ctp	167.147	218.979	1.31	0.76
CG12237_gene	CG12237	14.5073	19.0042	1.31	0.76
dpr19_gene	dpr19	0.707674	0.927035	1.31	0.76
pont_gene	pont	12.7926	16.7528	1.31	0.76
CG6878_gene	CG7011	4.6271	6.05883	1.31	0.76
CG11880_gene	CG11880	11.0506	14.4684	1.31	0.76
Ptp4E_gene	Ptp4E	9.9891	13.0778	1.31	0.76
CG15098_gene	CG15098	109.254	142.995	1.31	0.76
mip40_gene	mip40	7.18562	9.40278	1.31	0.76
Syx8_gene	Syx8	7.56667	9.8994	1.31	0.76
CG14965_gene	CG14958	1.44257	1.88718	1.31	0.76
CG3756_gene	CG3756	5.47087	7.15141	1.31	0.77
bt_gene	bt	212.602	277.879	1.31	0.77
5-HT1A_gene	5-HT1A	36.9079	48.2389	1.31	0.77
CG14122_gene	CG14122	0.734893	0.960143	1.31	0.77
CG14881_gene	CG14881	0.734893	0.960143	1.31	0.77

sqz_gene	sqz	0.734893	0.960143	1.31	0.77
Psc_gene	Psc	5.17147	6.75411	1.31	0.77
d4_gene	d4	13.3097	17.3819	1.31	0.77
CG11977_gene	CG31100	99.1289	129.421	1.31	0.77
l(2)37Cg_gene	l(2)37Cg	4.10996	5.36356	1.31	0.77
Yippee_gene	Yippee	7.53945	9.83319	1.30	0.77
CG3437_gene	CG3437	3.02123	3.9399	1.30	0.77
CG8435_gene	CG8435	3.02123	3.9399	1.30	0.77
CG7029_gene	CG7029	163.799	213.582	1.30	0.77
CG4159_gene	CG4159	3.78334	4.93315	1.30	0.77
CG31451_gene	CG31451	8.70984	11.3562	1.30	0.77
CG11970_gene	CG11970	7.97495	10.396	1.30	0.77
CG12576_gene	CG14618	48.9928	63.8661	1.30	0.77
CG2614_gene	CG2614	7.62111	9.93251	1.30	0.77
Faa_gene	Faa	6.88622	8.97237	1.30	0.77
bl_gene	bl	24.5236	31.9496	1.30	0.77
CG7460_gene	Ccn	14.5618	18.9711	1.30	0.77
CG4797_gene	CG4797	10.3974	13.5413	1.30	0.77
CG31460_gene	CG31460	4.6271	6.02572	1.30	0.77
Tsp39D_gene	Tsp39D	10.9145	14.2035	1.30	0.77
CG31637_gene	CG31637	14.5073	18.8718	1.30	0.77
l(2)05510_gene	l(2)05510	10.5879	13.7731	1.30	0.77
CG6608_gene	CG6608	8.62818	11.2237	1.30	0.77
Clp_gene	Clp	3.15732	4.10544	1.30	0.77
nito_gene	nito	25.6668	33.3732	1.30	0.77
CG31146_gene	CG31146	17.4197	22.6461	1.30	0.77
Rev1_gene	Rev1	5.55252	7.21763	1.30	0.77
pum_gene	pum	25.3946	33.0091	1.30	0.77
CG2051_gene	CG2051	6.75012	8.77372	1.30	0.77
O-fut1_gene	O-fut1	1.98693	2.58245	1.30	0.77
CG5147_gene	CG5147	10.3429	13.442	1.30	0.77
kel_gene	CG5758	10.3429	13.442	1.30	0.77
mri_gene	mri	10.3702	13.4751	1.30	0.77
CG1957_gene	CG1957	8.38322	10.8927	1.30	0.77
CG8557_gene	CG8557	36.3636	47.2457	1.30	0.77
CG16791_gene	CG16791	89.1398	115.813	1.30	0.77
CG10932_gene	CG10932	6.80456	8.83994	1.30	0.77
hep_gene	hep	32.6619	42.4118	1.30	0.77
Dcr-1_gene	Dcr-1	9.6897	12.5812	1.30	0.77
aru_gene	aru	59.8257	77.6723	1.30	0.77
CG18596_gene	CG18596	12.6293	16.3886	1.30	0.77
lok_gene	lok	1.63309	2.11894	1.30	0.77
CG41278_gene	CG41278	0.816547	1.05947	1.30	0.77
CG12534_gene	CG12534	2.44964	3.1784	1.30	0.77
CG4933_gene	CG4933	4.49101	5.82707	1.30	0.77
CG7357_gene	CG7357	7.81164	10.1312	1.30	0.77
thoc5_gene	thoc5	4.54545	5.89329	1.30	0.77
htl_gene	htl	10.7512	13.9386	1.30	0.77
tra_gene	l(3)73Ah	2.50408	3.24462	1.30	0.77
Set_gene	Set	23.8704	30.9232	1.30	0.77
Dyrk3_gene	Dyrk3	19.7604	25.5928	1.30	0.77
Aldh-III_gene	Aldh-III	26.5378	34.3665	1.30	0.77
Dip1_gene	Dip1	0.843766	1.09258	1.29	0.77
DNApol-iota_gene	NApol-iot	3.37506	4.37031	1.29	0.77
CG1648_gene	CG1648	2320.6	3004.45	1.29	0.77
fs(1)h_gene	fs(1)h	68.1001	88.1676	1.29	0.77
CG32195_gene	CG7341	2.12302	2.748	1.29	0.77
CG7231_gene	Snoo	4.68154	6.05883	1.29	0.77
CG31044_gene	CG31044	1.71475	2.21826	1.29	0.77
CG16912_gene	Eap	3.02123	3.90679	1.29	0.77

CG34229_gene	CG34229	3.89221	5.03247	1.29	0.77
JhI-21_gene	CG14945	13.8541	17.9116	1.29	0.77
Dhc64C_gene	CG18808	59.7985	77.3081	1.29	0.77
CG3837_gene	CG3837	16.6303	21.4873	1.29	0.77
ptc_gene	ptc	8.81871	11.3893	1.29	0.77
CG2975_gene	CG2975	60.9144	78.6655	1.29	0.77
Act5C_gene	Act5C	520.222	671.504	1.29	0.77
CG9004_gene	CG9004	8.02938	10.3629	1.29	0.77
kraken_gene	kraken	17.4469	22.5137	1.29	0.77
sif_gene	sif	4.49101	5.79397	1.29	0.78
escl_gene	escl	0.898202	1.15879	1.29	0.78
snoRNA:Psi18S-301_gene	RNA:Psi18S	0.898202	1.15879	1.29	0.78
ade3_gene	ade3	45.2095	58.3039	1.29	0.78
CG7744_gene	CG7744	1.36091	1.75474	1.29	0.78
PDCD-5_gene	CG5027	9.09089	11.7204	1.29	0.78
CG14341_gene	CG14341	10.0435	12.9454	1.29	0.78
CG9577_gene	CG9577	9.63526	12.4156	1.29	0.78
Bem46_gene	Bem46	15.6505	20.163	1.29	0.78
CG6232_gene	CG6232	10.5879	13.6407	1.29	0.78
XRCC1_gene	XRCC1	5.5253	7.1183	1.29	0.78
Nmdar1_gene	Nmdar1	6.01523	7.74736	1.29	0.78
CG11456_gene	CG11456	2.31355	2.97975	1.29	0.78
CG4841_gene	CG4841	19.706	25.361	1.29	0.78
LysP_gene	LysP	1.87806	2.41691	1.29	0.78
CG14512_gene	Vha100-1	1.87806	2.41691	1.29	0.78
CG1753_gene	CG1753	10.8056	13.9055	1.29	0.78
Cdc37_gene	Cdc37	20.8764	26.8509	1.29	0.78
CG31630_gene	milt	3.34784	4.30409	1.29	0.78
CG10217_gene	CG10217	41.2356	53.0065	1.29	0.78
CG18445_gene	CG18445	34.1045	43.8355	1.29	0.78
CG14483_gene	CG14483	22.1829	28.5063	1.29	0.78
mys_gene	mys	64.7522	83.2014	1.28	0.78
CG7378_gene	CG7378	13.0648	16.7859	1.28	0.78
CG6568_gene	CG6568	5.85192	7.5156	1.28	0.78
Asph_gene	Asph	12.1938	15.6603	1.28	0.78
CG10435_gene	CG3223	10.7512	13.8062	1.28	0.78
nvy_gene	nvy	1.95971	2.51624	1.28	0.78
l(2)35Bd_gene	l(2)35Bd	2.93957	3.77436	1.28	0.78
CG6984_gene	CG6984	0.979857	1.25812	1.28	0.78
pie_gene	pie	0.979857	1.25812	1.28	0.78
MED9_gene	MED9	8.84593	11.3562	1.28	0.78
FK506-bp2_gene	FK506-bp2	38.1328	48.9342	1.28	0.78
CG2924_gene	CG2924	20.9036	26.8178	1.28	0.78
Sin_gene	Sin	5.49809	7.05208	1.28	0.78
dlp_gene	dlp	7.02231	9.00548	1.28	0.78
Ssrp_gene	Ssrp	13.5819	17.415	1.28	0.78
CG10883_gene	CG5060	1.00708	1.29123	1.28	0.78
Syn2_gene	Syn2	24.823	31.8172	1.28	0.78
CG10419_gene	CG10419	1.52422	1.95339	1.28	0.78
snmRNA:184_gene	dom	1.52422	1.95339	1.28	0.78
Hsromega_gene	Hsromega	83.0156	106.377	1.28	0.78
CG2813_gene	CG2813	8.16547	10.4622	1.28	0.78
CG9125_gene	CG9132	4.59988	5.89329	1.28	0.78
GstS1_gene	GstS1	13.3369	17.0839	1.28	0.78
CG13365_gene	CG13365	3.59281	4.60206	1.28	0.78
Dox-A2_gene	Dox-A2	31.4099	40.2267	1.28	0.78
CG2694_gene	CG2694	3.10288	3.97301	1.28	0.78
CG10336_gene	CG10336	0.517147	0.662168	1.28	0.78
CG31922_gene	CG31922	0.517147	0.662168	1.28	0.78
Shal_gene	Shal	0.517147	0.662168	1.28	0.78

ara_gene	ara	6.72291	8.60818	1.28	0.78
CG31216_gene	CG31216	1.55144	1.9865	1.28	0.78
CG4424_gene	CG4424	2.06859	2.64867	1.28	0.78
Ac13E_gene	Ac13E	10.8601	13.9055	1.28	0.78
CG5938_gene	CG5938	9.33586	11.9521	1.28	0.78
Baldspot_gene	Baldspot	8.84593	11.3231	1.28	0.78
bru-3_gene	bru-3	7.81164	9.99873	1.28	0.78
CG31241_gene	CG31241	9.44473	12.0846	1.28	0.78
CG30494_gene	CG30492	14.2896	18.2758	1.28	0.78
lectin-21Ca_gene	lectin-21Ca	118.073	151.007	1.28	0.78
CG10483_gene	CG10483	2.12302	2.71489	1.28	0.78
Mlh1_gene	CG2183	1.06151	1.35744	1.28	0.78
PGRP-LE_gene	PGRP-LE	9.09089	11.621	1.28	0.78
Trf_gene	Trf	1.60588	2.05272	1.28	0.78
CG30118_gene	CG30118	102.994	131.639	1.28	0.78
CG17807_gene	CG33143	5.9608	7.61493	1.28	0.78
Synd_gene	Synd	24.9591	31.8834	1.28	0.78
twf_gene	twf	10.3157	13.1771	1.28	0.78
CG17230_gene	CG31374	28.2525	36.0881	1.28	0.78
CG14550_gene	CG14543	2.72182	3.47638	1.28	0.78
CG30377_gene	CG30377	1.08873	1.39055	1.28	0.78
CG1665_gene	CG1665	3.83777	4.90004	1.28	0.78
Sc2_gene	Sc2	17.0386	21.7522	1.28	0.78
CG1516_gene	CG1671	43.9847	56.1518	1.28	0.78
Rpp30_gene	Rpp30	2.20468	2.81421	1.28	0.78
CR41503_gene	CR41503	5.57974	7.1183	1.28	0.78
Hil_gene	Hil	1.11595	1.42366	1.28	0.78
CG8965_gene	CG8965	2.80348	3.5757	1.28	0.78
CG10732_gene	CG10732	17.4197	22.2157	1.28	0.78
CG9698_gene	CG9698	7.89329	10.0649	1.28	0.78
CG2258_gene	CG2258	2.25911	2.88043	1.28	0.78
CG2254_gene	CG2254	7.34893	9.36967	1.27	0.78
Cralbp_gene	PGRP-LD	0.571583	0.728384	1.27	0.78
CG7601_gene	CG7601	2.85792	3.64192	1.27	0.78
Fmr1_gene	Fmr1	22.9994	29.3009	1.27	0.78
Tsp96F_gene	Tsp96F	12.1121	15.4285	1.27	0.79
CG8191_gene	CG8191	2.31355	2.94665	1.27	0.79
sec15_gene	sec15	10.4246	13.2765	1.27	0.79
Klp61F_gene	CG9194	1.17038	1.48988	1.27	0.79
Ptp52F_gene	Ptp52F	1.17038	1.48988	1.27	0.79
CG18316_gene	CG18316	4.68154	5.95951	1.27	0.79
Amy-p_gene	Amy-p	14.6979	18.7062	1.27	0.79
nonA-l_gene	nonA-l	16.5487	21.0569	1.27	0.79
pcs_gene	pcs	27.7898	35.3597	1.27	0.79
CG10103_gene	CG8549	21.9107	27.8773	1.27	0.79
CG11837_gene	CG11837	2.96679	3.77436	1.27	0.79
dyn-p25_gene	dyn-p25	3.56559	4.53585	1.27	0.79
cyp33_gene	CG34194	4.16439	5.29734	1.27	0.79
CG9839_gene	CG8351	4.16439	5.29734	1.27	0.79
CG6607_gene	CG6607	7.1584	9.1048	1.27	0.79
CG12344_gene	CG12325	0.598801	0.761493	1.27	0.79
CG41105_gene	CG41105	2.39521	3.04597	1.27	0.79
CG1135_gene	CG1135	16.2221	20.6265	1.27	0.79
Jupiter_gene	Jupiter	6.01523	7.64804	1.27	0.79
Fur2_gene	Fur2	6.66847	8.47574	1.27	0.79
lolal_gene	lolal	34.5672	43.9348	1.27	0.79
CG14145_gene	CG14145	4.27326	5.42977	1.27	0.79
CG14968_gene	CG14968	2.44964	3.11219	1.27	0.79
CG4707_gene	CG3570	2.44964	3.11219	1.27	0.79
CG18166_gene	CG32817	1.22482	1.55609	1.27	0.79

CG7429_gene	CG7429	4.30048	5.46288	1.27	0.79
CG7194_gene	CG7194	4.3277	5.49599	1.27	0.79
Nup44A_gene	Nup44A	6.20576	7.87979	1.27	0.79
CG33469_gene	CG33469	0.62602	0.794601	1.27	0.79
CG5098_gene	CG5098	9.39029	11.919	1.27	0.79
CG7785_gene	CG7785	1.25204	1.5892	1.27	0.79
lectin-46Ca_gene	CG1648	1306.78	1658.66	1.27	0.79
Fkbp13_gene	Fkbp13	355.089	450.638	1.27	0.79
TppII_gene	TppII	70.087	88.9291	1.27	0.79
CG7888_gene	CG7888	6.31463	8.01223	1.27	0.79
Dbi_gene	Dbi	41.154	52.2119	1.27	0.79
CG17689_gene	CG17689	8.24713	10.4622	1.27	0.79
CG10958_gene	CG15335	1.90528	2.41691	1.27	0.79
RhoGAP18B_gene	RhoGAP18	11.4589	14.5346	1.27	0.79
Obp58b_gene	Obp58b	3.18453	4.03922	1.27	0.79
CG8708_gene	CG8708	571.855	725.305	1.27	0.79
okr_gene	Bem46	6.39629	8.11155	1.27	0.79
CG6000_gene	CG6000	1.27926	1.62231	1.27	0.79
Shawn_gene	Tyler	2.55852	3.24462	1.27	0.79
Tyler_gene	Tyler	2.55852	3.24462	1.27	0.79
Arc-p20_gene	Arc-p20	22.4278	28.4401	1.27	0.79
CG8366_gene	Strn-Mlck	5.77027	7.31695	1.27	0.79
CG7175_gene	CG7175	4.49101	5.69464	1.27	0.79
Su(H)_gene	Su(H)	3.21175	4.07233	1.27	0.79
ia2_gene	ia2	95.7266	121.375	1.27	0.79
CG3815_gene	CG3815	4.51823	5.72775	1.27	0.79
CG31648_gene	Cap-D3	3.23897	4.10544	1.27	0.79
Socs16D_gene	Socs16D	11.6766	14.7994	1.27	0.79
CG10267_gene	CG10267	5.85192	7.41628	1.27	0.79
CG14667_gene	CG14667	2.61295	3.31084	1.27	0.79
CG14543_gene	CG14543	6.53238	8.27709	1.27	0.79
CG13117_gene	Nckx30C	0.653238	0.827709	1.27	0.79
CG14464_gene	CG14464	9.88022	12.515	1.27	0.79
Atac1_gene	CG3430	3.29341	4.17166	1.27	0.79
CG13018_gene	pea	1.98693	2.51624	1.27	0.79
Rpl135_gene	Rpl135	9.96188	12.6143	1.27	0.79
ect_gene	ect	1.33369	1.68853	1.27	0.79
CG3287_gene	CG3287	18.0185	22.8117	1.27	0.79
CG10904_gene	CG10904	6.01523	7.61493	1.27	0.79
CG12026_gene	CG12026	4.68154	5.9264	1.27	0.79
mRpL15_gene	Psn	4.68154	5.9264	1.27	0.79
CG1707_gene	CG1707	14.7251	18.64	1.27	0.79
CG17565_gene	CG17565	4.73597	5.99262	1.27	0.79
mRpL12_gene	mRpL12	6.88622	8.7075	1.26	0.79
CG5270_gene	CG5270	13.092	16.5542	1.26	0.79
CG13124_gene	CG13124	59.5535	75.2885	1.26	0.79
Nmt_gene	Nmt	7.70276	9.73386	1.26	0.79
Tsp42El_gene	Tsp42El	2.80348	3.5426	1.26	0.79
Bmcp_gene	Bmcp	11.9216	15.0643	1.26	0.79
CG2930_gene	CG2930	33.0974	41.8159	1.26	0.79
CG17265_gene	CG17265	0.707674	0.893926	1.26	0.79
CG34244_gene	CG34244	0.707674	0.893926	1.26	0.79
CG14855_gene	CG14855	1.41535	1.78785	1.26	0.79
CG3651_gene	CG3651	9.96188	12.5812	1.26	0.79
Idgf3_gene	Idgf3	41.4806	52.3775	1.26	0.79
CG5991_gene	Atg6	9.30864	11.7535	1.26	0.79
CG5853_gene	CG4619	2.15024	2.71489	1.26	0.79
CG6574_gene	CG6574	8.60097	10.8595	1.26	0.79
Pak3_gene	Pak3	35.2204	44.4646	1.26	0.79
CG9850_gene	CG9850	2.88513	3.64192	1.26	0.79

CG17286_gene	tra	1.44257	1.82096	1.26	0.79
bs_gene	bs	3.62003	4.56896	1.26	0.79
Dlc90F_gene	Dlc90F	39.1671	49.4308	1.26	0.79
CG8026_gene	CG8026	37.8061	47.7092	1.26	0.79
tacc_gene	tacc	28.4158	35.8564	1.26	0.79
CG9699_gene	CG9699	8.79149	11.0913	1.26	0.79
CG10073_gene	CG10073	0.734893	0.927035	1.26	0.79
CG3918_gene	CG3918	11.0234	13.9055	1.26	0.79
CG3313_gene	CG3532	2.20468	2.7811	1.26	0.79
tex_gene	tex	4.43657	5.59532	1.26	0.79
CG6299_gene	CG6299	47.5503	59.9593	1.26	0.79
CG8142_gene	e(y)1	2.2319	2.81421	1.26	0.79
CG5532_gene	CG5532	11.2139	14.1373	1.26	0.79
nocturnin_gene	nocturnin	9.74413	12.2832	1.26	0.79
CG9418_gene	CG9418	3.02123	3.80746	1.26	0.79
CG15309_gene	CG15309	12.1121	15.263	1.26	0.79
CG8635_gene	CG8635	37.1529	46.8152	1.26	0.79
comt_gene	comt	0.762111	0.960143	1.26	0.79
scaf6_gene	CG7842	13.7724	17.3488	1.26	0.79
CG9917_gene	CG9917	32.2264	40.5909	1.26	0.79
CG7275_gene	CG7275	10.0708	12.6805	1.26	0.79
CG10641_gene	CG10431	22.5911	28.4401	1.26	0.79
CG3732_gene	bonsai	11.7855	14.8326	1.26	0.79
GalNAc-T1_gene	GalNAc-T1	20.4409	25.7252	1.26	0.79
CG13773_gene	CG13773	3.15732	3.97301	1.26	0.79
CG4259_gene	CG4259	0.789329	0.993251	1.26	0.79
CG15727_gene	CG15727	1.57866	1.9865	1.26	0.79
koi_gene	koi	2.36799	2.97975	1.26	0.79
CG3368_gene	CG3368	14.2624	17.9447	1.26	0.79
skpA_gene	skpA	60.4789	76.0831	1.26	0.79
CYLD_gene	CYLD	8.76428	11.0251	1.26	0.79
sty_gene	sty	11.976	15.0643	1.26	0.79
Smg6_gene	Smg6	30.675	38.5713	1.26	0.80
Sdic3_gene	Sdic3	2.42242	3.04597	1.26	0.80
CG14578_gene	eIF-4B	0.816547	1.02636	1.26	0.80
CG34345_gene	CG34345	42.6238	53.5694	1.26	0.80
CG31746_gene	CG31746	8.21991	10.3298	1.26	0.80
Shab_gene	Shab	1.66031	2.08583	1.26	0.80
CG1632_gene	CG1632	3.32063	4.17166	1.26	0.80
CG5973_gene	CG5973	3.32063	4.17166	1.26	0.80
CG5321_gene	CG5321	4.16439	5.23112	1.26	0.80
CG14318_gene	CG14318	3.34784	4.20476	1.26	0.80
CG14741_gene	CG14741	7.53945	9.469	1.26	0.80
capu_gene	capu	16.7937	21.09	1.26	0.80
CG10638_gene	CG10638	10.9417	13.74	1.26	0.80
CG31374_gene	CG31374	21.0941	26.4867	1.26	0.80
CG8359_gene	CG8359	0.843766	1.05947	1.26	0.80
CG9531_gene	CG9531	0.843766	1.05947	1.26	0.80
CG13252_gene	CG13252	19.461	24.434	1.26	0.80
CG8885_gene	CG8885	5.98801	7.5156	1.26	0.80
zormin_gene	zormin	86.9623	109.125	1.25	0.80
nudC_gene	nudC	9.47195	11.8859	1.25	0.80
ACXD_gene	ACXD	6.04245	7.58182	1.25	0.80
CG4278_gene	CG4278	9.49917	11.919	1.25	0.80
ttv_gene	ttv	31.1105	39.0348	1.25	0.80
CG30035_gene	Roc2	31.3554	39.3328	1.25	0.80
Akap200_gene	Akap200	106.668	133.791	1.25	0.80
CG1971_gene	CG1971	3.51115	4.40341	1.25	0.80
CG34117_gene	CG34117	5.28034	6.62168	1.25	0.80
htt_gene	htt	47.9858	60.1579	1.25	0.80

CG9362_gene	CG9362	3.59281	4.50274	1.25	0.80
jog_gene	jog	9.88022	12.3825	1.25	0.80
CG11105_gene	CG11105	0.898202	1.12568	1.25	0.80
casp_gene	CG8399	13.5002	16.9184	1.25	0.80
CG3919_gene	CG3919	1.82362	2.28448	1.25	0.80
CG17612_gene	Traf1	1.82362	2.28448	1.25	0.80
synj_gene	synj	18.3179	22.9441	1.25	0.80
dock_gene	dock	12.8742	16.1238	1.25	0.80
CG14812_gene	CG14812	6.45072	8.07844	1.25	0.80
und_gene	und	38.9221	48.7355	1.25	0.80
CG34316_gene	mRpS10	2.80348	3.50949	1.25	0.80
mRpS10_gene	mRpS10	2.80348	3.50949	1.25	0.80
mRpL39_gene	mRpL39	7.48502	9.36967	1.25	0.80
CG31159_gene	CG31159	1.87806	2.35069	1.25	0.80
CG8034_gene	CG8034	21.6929	27.1489	1.25	0.80
CG5808_gene	CG5808	5.6614	7.08519	1.25	0.80
Gapdh1_gene	Gapdh1	146.924	183.851	1.25	0.80
CG31687_gene	CG31687	3.81055	4.76761	1.25	0.80
CG13339_gene	CG13339	2.85792	3.5757	1.25	0.80
CG5933_gene	CG5933	2.85792	3.5757	1.25	0.80
Ipk1_gene	Ipk1	2.85792	3.5757	1.25	0.80
CG6900_gene	CG6900	1.90528	2.3838	1.25	0.80
sws_gene	sws	30.6477	38.3395	1.25	0.80
bw_gene	CG5360	1.9325	2.41691	1.25	0.80
CG12821_gene	CG12822	38.8949	48.6362	1.25	0.80
yip2_gene	yip2	15.6233	19.5339	1.25	0.80
CG4291_gene	CG4291	1.95971	2.45002	1.25	0.80
CG18530_gene	CG18530	31.3554	39.2003	1.25	0.80
CG12923_gene	CG1513	0.979857	1.22501	1.25	0.80
sls_gene	sls	166.957	208.715	1.25	0.80
CG18067_gene	CG18067	506.368	632.834	1.25	0.80
Cyp6a13_gene	Cyp6a13	19.8693	24.8313	1.25	0.80
rictor_gene	rictor	21.9107	27.3806	1.25	0.80
CAP_gene	CG12910	85.8191	107.238	1.25	0.80
vn_gene	vn	2.99401	3.74125	1.25	0.80
Cap-H2_gene	Cap-H2	9.03646	11.29	1.25	0.80
sip1_gene	sip1	4.0283	5.03247	1.25	0.80
CG12299_gene	CG12299	1.00708	1.25812	1.25	0.80
CG9682_gene	CG9682	1.00708	1.25812	1.25	0.80
Wsck_gene	atl	4.05552	5.06558	1.25	0.80
CG17838_gene	CG17838	122.727	153.292	1.25	0.80
fs(1)K10_gene	fs(1)K10	13.2008	16.488	1.25	0.80
CG15092_gene	CG15092	2.04137	2.54935	1.25	0.80
Alas_gene	Alas	18.454	23.0434	1.25	0.80
MBD-like_gene	MBD-like	4.10996	5.1318	1.25	0.80
CG33277_gene	CG33277	1.03429	1.29123	1.25	0.80
CG7800_gene	CG7800	5.17147	6.45613	1.25	0.80
Ncc69_gene	Ncc69	35.4382	44.2328	1.25	0.80
Cdk9_gene	Cdk9	7.32171	9.13791	1.25	0.80
Ggamma1_gene	Ggamma1	67.1474	83.7973	1.25	0.80
Dg_gene	Dg	36.8263	45.9544	1.25	0.80
CG30054_gene	CG30054	2.12302	2.64867	1.25	0.80
janA_gene	janB	5.30756	6.62168	1.25	0.80
ex_gene	ex	23.5166	29.334	1.25	0.80
CG3631_gene	CG3631	3.21175	4.00611	1.25	0.80
CG18081_gene	CG12713	18.3995	22.9441	1.25	0.80
CG8964_gene	CG8964	1.08873	1.35744	1.25	0.80
CG31920_gene	Plc21C	1.08873	1.35744	1.25	0.80
arr_gene	arr	13.1192	16.3555	1.25	0.80
kek5_gene	kek5	14.2351	17.7461	1.25	0.80

SelG_gene	SelG	18.6445	23.2421	1.25	0.80
CG33205_gene	CG33205	99.1289	123.56	1.25	0.80
CG6836_gene	CG6836	2.20468	2.748	1.25	0.80
CG7466_gene	CG7466	12.3843	15.4285	1.25	0.80
CG32210_gene	CG32210	54.7631	68.2033	1.25	0.80
spt4_gene	spt4	20.5498	25.5928	1.25	0.80
Rca1_gene	Rca1	1.14317	1.42366	1.25	0.80
Ho_gene	Ho	9.28142	11.5548	1.24	0.80
CG16952_gene	CG16952	13.9357	17.3488	1.24	0.80
CG4064_gene	CG4064	1.17038	1.45677	1.24	0.80
CG31763_gene	bru-2	12.9559	16.1238	1.24	0.80
Sop2_gene	Sop2	15.4872	19.2691	1.24	0.80
CG18410_gene	Ets96B	5.9608	7.41628	1.24	0.80
CG5970_gene	CG5970	3.59281	4.46963	1.24	0.80
trol_gene	trol	137.207	170.674	1.24	0.80
CG17746_gene	CG17746	7.24005	9.00548	1.24	0.80
CG14030_gene	CG14030	8.51931	10.5947	1.24	0.80
CG6550_gene	l(2)k01209	12.221	15.1967	1.24	0.80
CG13005_gene	CG13005	1.22482	1.52299	1.24	0.80
SIFR_gene	SIFR	3.70168	4.60206	1.24	0.80
CG7866_gene	CG7866	11.2411	13.9717	1.24	0.80
CG10898_gene	CG10898	2.50408	3.11219	1.24	0.80
CG14897_gene	CG14897	3.81055	4.7345	1.24	0.80
CG7747_gene	CG7747	5.08981	6.3237	1.24	0.80
pes_gene	pes	8.9548	11.1244	1.24	0.80
Ate1_gene	CG9864	7.72998	9.60143	1.24	0.81
poe_gene	CG7466	169.325	210.304	1.24	0.81
l(3)j2D3_gene	l(3)j2D3	3.89221	4.83382	1.24	0.81
CG2093_gene	CG2093	74.5508	92.571	1.24	0.81
Atg12_gene	Atg12	1.33369	1.65542	1.24	0.81
CG11095_gene	CG11095	1.33369	1.65542	1.24	0.81
CG6830_gene	Ho	2.66739	3.31084	1.24	0.81
CG31163_gene	CG31163	32.0359	39.7632	1.24	0.81
CG11985_gene	CG11985	6.72291	8.34331	1.24	0.81
CG32226_gene	CG32226	9.44473	11.7204	1.24	0.81
CG31643_gene	CG31643	4.05552	5.03247	1.24	0.81
lqf_gene	lqf	51.7963	64.2634	1.24	0.81
CG1443_gene	CG1443	28.7152	35.6246	1.24	0.81
CG7351_gene	CG7351	5.5253	6.85343	1.24	0.81
CG7323_gene	CG7323	8.30156	10.2967	1.24	0.81
CG33967_gene	CG33967	24.9863	30.9894	1.24	0.81
CG10824_gene	NF4Agamm	1.41535	1.75474	1.24	0.81
CG7639_gene	pcs	24.0881	29.8638	1.24	0.81
Egfr_gene	Egfr	22.6728	28.109	1.24	0.81
lp259_gene	RpS27A	118.318	146.67	1.24	0.81
cul-4_gene	cul-4	20.0054	24.7982	1.24	0.81
CG5376_gene	CG7048	1.44257	1.78785	1.24	0.81
CR32477_gene	CG16971	742.35	919.949	1.24	0.81
D1_gene	D1	52.2318	64.7269	1.24	0.81
CG7288_gene	CG7288	2.93957	3.64192	1.24	0.81
CG31150_gene	CG31150	1.497	1.85407	1.24	0.81
ATP7_gene	ATP7	25.4491	31.5192	1.24	0.81
BCL7-like_gene	BCL7-like	6.06967	7.5156	1.24	0.81
disco-r_gene	disco-r	6.12411	7.58182	1.24	0.81
CG15835_gene	CG15835	7.70276	9.53521	1.24	0.81
CG11638_gene	CG11638	1.55144	1.92029	1.24	0.81
CG3683_gene	CG3683	6.20576	7.68114	1.24	0.81
Pepck_gene	Pepck	32.798	40.5909	1.24	0.81
CG16971_gene	CG16971	163.092	201.829	1.24	0.81
mus312_gene	mus312	9.47195	11.7204	1.24	0.81

CG1275_gene	CG1275	72.6727	89.9224	1.24	0.81
CG11334_gene	CG11334	15.8682	19.6333	1.24	0.81
CG13288_gene	CG13288	3.18453	3.9399	1.24	0.81
tou_gene	tou	17.5558	21.7191	1.24	0.81
CG6523_gene	CG6523	14.4529	17.8785	1.24	0.81
CG7502_gene	RhoGAP18	6.45072	7.97912	1.24	0.81
CG6294_gene	CG6299	4.89928	6.05883	1.24	0.81
CG17202_gene	CG17202	16.3582	20.2292	1.24	0.81
CG5146_gene	CG5146	13.1464	16.2562	1.24	0.81
Nup133_gene	Nup133	5.00816	6.19127	1.24	0.81
mRpL52_gene	mRpL52	3.34784	4.13855	1.24	0.81
CG4857_gene	CG4857	33.6418	41.5841	1.24	0.81
puc_gene	puc	25.2858	31.2543	1.24	0.81
CG15602_gene	CG15602	3.37506	4.17166	1.24	0.81
CG9941_gene	CG9941	18.7806	23.209	1.24	0.81
bc10_gene	bc10	13.6636	16.8853	1.24	0.81
MESK2_gene	MESK2	42.9232	53.0396	1.24	0.81
cup_gene	cup	17.2019	21.2556	1.24	0.81
l(2)k05713_gene	l(2)k05713	12.0577	14.8988	1.24	0.81
CG32048_gene	CG32048	29.4501	36.3861	1.24	0.81
Ih_gene	Ih	43.3314	53.5362	1.24	0.81
CG10137_gene	CG10137	27.7898	34.3334	1.24	0.81
CG34104_gene	CG34104	5.30756	6.55546	1.24	0.81
CG11180_gene	CG9945	14.2351	17.5805	1.24	0.81
CG12814_gene	CG12814	12.466	15.3954	1.23	0.81
CG10702_gene	CG10702	48.1763	59.4958	1.23	0.81
imd_gene	GstE9	12.5748	15.5278	1.23	0.81
CG15134_gene	CG15134	9.03646	11.1575	1.23	0.81
CG5525_gene	CG5525	22.2917	27.5131	1.23	0.81
Upf3_gene	CG5602	9.44473	11.6541	1.23	0.81
CG12194_gene	CG12194	22.9178	28.2746	1.23	0.81
CG10165_gene	CG10137	27.1094	33.4395	1.23	0.81
Acp32CD_gene	Samuel	2585.16	3188.7	1.23	0.81
Gr43a_gene	CG11107	1.95971	2.41691	1.23	0.81
CG8202_gene	CG8202	3.94665	4.86693	1.23	0.81
csw_gene	csw	84.8393	104.622	1.23	0.81
CG9914_gene	CG9914	7.92051	9.76697	1.23	0.81
CG31676_gene	CG31676	26.6194	32.8104	1.23	0.81
Cyp6d5_gene	rdx	51.2247	63.1377	1.23	0.81
pyd_gene	pyd	68.0456	83.8635	1.23	0.81
dwg_gene	dwg	4.21883	5.19802	1.23	0.81
CG9743_gene	CG9743	8.68262	10.694	1.23	0.81
CG12370_gene	CG12370	4.35492	5.36356	1.23	0.81
CG7255_gene	CG7255	44.3113	54.5626	1.23	0.81
Mlc2_gene	Mlc2	235.465	289.831	1.23	0.81
tra2_gene	tra2	6.859	8.44264	1.23	0.81
CG15105_gene	CG15105	27.5449	33.903	1.23	0.81
CG11851_gene	CG11851	13.7997	16.9846	1.23	0.81
CG34240_gene	CG34240	6.94065	8.54196	1.23	0.81
Cyp6g1_gene	Cyp6g1	11.7583	14.4684	1.23	0.81
l(3)87Df_gene	l(3)87Df	2.36799	2.91354	1.23	0.81
Sdic1_gene	Sdic1	2.36799	2.91354	1.23	0.81
CG7611_gene	CG7611	45.9444	56.516	1.23	0.81
drl_gene	drl	2.42242	2.97975	1.23	0.81
fbp_gene	fbp	16.957	20.8583	1.23	0.81
SF1_gene	SF1	42.3516	52.0795	1.23	0.81
I-2_gene	I-2	14.97	18.4083	1.23	0.81
CG12107_gene	CG12107	15.0517	18.5076	1.23	0.81
CG13667_gene	CG13667	5.28034	6.48924	1.23	0.81
Drp1_gene	Drp1	37.2618	45.7889	1.23	0.81

awd_gene	CG1896	208.41	256.06	1.23	0.81
CG31705_gene	CG31705	27.191	33.4064	1.23	0.81
CG33502_gene	CG33502	5.44365	6.68789	1.23	0.81
CG3639_gene	CG3639	2.74904	3.37705	1.23	0.81
CG5191_gene	CG5191	8.27435	10.1643	1.23	0.81
pug_gene	pug	13.9902	17.1832	1.23	0.81
CG15347_gene	CG15347	11.3228	13.9055	1.23	0.81
CG6812_gene	CG6812	5.68861	6.98587	1.23	0.81
Rac2_gene	Rac2	14.2624	17.5143	1.23	0.81
312_gene	Ptp61F	2.88513	3.5426	1.23	0.81
CG32741_gene	CG32741	8.6554	10.6278	1.23	0.81
CG4019_gene	CG4019	2.91235	3.5757	1.23	0.81
CG8675_gene	CG8675	5.90636	7.25073	1.23	0.81
chico_gene	chico	20.6859	25.3941	1.23	0.81
Hmr_gene	Hmr	2.96679	3.64192	1.23	0.81
SAK_gene	SAK	2.96679	3.64192	1.23	0.81
CG8031_gene	CG7518	8.92758	10.9589	1.23	0.81
CG14801_gene	CG14801	30.0489	36.8827	1.23	0.81
Slbp_gene	Slbp	3.02123	3.70814	1.23	0.81
Frq2_gene	Frq2	3.07566	3.77436	1.23	0.81
Vps16A_gene	Vps16A	9.58082	11.7535	1.23	0.82
CG2604_gene	CG2604	29.0963	35.6908	1.23	0.82
Meics_gene	Meics	6.5596	8.04534	1.23	0.82
CG34133_gene	CG34133	13.2553	16.2562	1.23	0.82
CG10414_gene	CG10414	3.32063	4.07233	1.23	0.82
defl_gene	nbs	6.75012	8.27709	1.23	0.82
mRpS29_gene	mRpS29	10.2885	12.6143	1.23	0.82
CG32104_gene	CG32104	10.3429	12.6805	1.23	0.82
CG40130_gene	Gprk1	14.0718	17.2495	1.23	0.82
CG5254_gene	CG5254	10.6696	13.0778	1.23	0.82
Samuel_gene	Samuel	2630.29	3223.37	1.23	0.82
mle_gene	mle	26.1295	32.0158	1.23	0.82
CG1896_gene	CG1896	7.53945	9.23724	1.23	0.82
CG11723_gene	CG11723	7.64833	9.36967	1.23	0.82
CG12769_gene	CG12769	3.83777	4.70139	1.23	0.82
CG11489_gene	CG11489	3.89221	4.76761	1.22	0.82
Map205_gene	Map205	23.4077	28.6719	1.22	0.82
CG1882_gene	CG1882	19.6244	24.0367	1.22	0.82
mRpS30_gene	mRpS30	7.86607	9.63454	1.22	0.82
CG8235_gene	CG8235	8.0566	9.8663	1.22	0.82
Dref_gene	Dref	12.3571	15.1305	1.22	0.82
asparagine-synthetase_gene	chb	4.46379	5.46288	1.22	0.82
FK506-bp1_gene	mRpL9	32.6347	39.9287	1.22	0.82
Arp5_gene	Arp5	9.6897	11.8528	1.22	0.82
CG34317_gene	Arp5	9.6897	11.8528	1.22	0.82
hh_gene	CG31457	4.87207	5.95951	1.22	0.82
Mgat2_gene	Mgat2	5.30756	6.48924	1.22	0.82
CG12016_gene	CG12016	11.2139	13.7069	1.22	0.82
Nat1_gene	Nat1	28.307	34.5983	1.22	0.82
CG33204_gene	Doa	5.71583	6.98587	1.22	0.82
DebB_gene	CG13175	5.90636	7.21763	1.22	0.82
CG10249_gene	CG10249	12.0305	14.7001	1.22	0.82
Cortactin_gene	Cortactin	6.09689	7.44938	1.22	0.82
CG14232_gene	CG14232	12.5748	15.3623	1.22	0.82
CG32147_gene	CG32147	6.45072	7.87979	1.22	0.82
CG13213_gene	CG13213	13.1192	16.0245	1.22	0.82
mRpL16_gene	mRpL16	6.859	8.37642	1.22	0.82
CG9305_gene	CG9305	6.94065	8.47574	1.22	0.82
CG4733_gene	CG4733	14.2896	17.4481	1.22	0.82
Hexo1_gene	Hexo1	14.6706	17.9116	1.22	0.82

ear_gene	ear	7.72998	9.43589	1.22	0.82
Tsp42Ei_gene	Tsp42Ei	8.90037	10.8595	1.22	0.82
Tm1_gene	Tm1	144.121	175.839	1.22	0.82
vkg_gene	vkg	20.1959	24.6326	1.22	0.82
CG2107_gene	CG2107	10.098	12.3163	1.22	0.82
CG10188_gene	CG10188	11.595	14.1373	1.22	0.82
CG3704_gene	CG3704	11.7583	14.3359	1.22	0.82
CG6412_gene	CG6412	11.9216	14.5346	1.22	0.82
Pink1_gene	Pink1	74.8774	91.2136	1.22	0.82
Vps25_gene	Vps25	8.62818	10.4954	1.22	0.82
CG7849_gene	CG7849	1.33369	1.62231	1.22	0.82
mRpS6_gene	mRpS6	2.72182	3.31084	1.22	0.82
CR41437_gene	CG12567	2.91235	3.5426	1.22	0.82
CG3774_gene	CG3774	12.7381	15.4947	1.22	0.82
CG17262_gene	CG17262	0.870984	1.05947	1.22	0.82
CG14655_gene	CG14655	1.66031	2.01961	1.22	0.82
CG32736_gene	CG32736	1.66031	2.01961	1.22	0.82
CG4103_gene	CG4103	1.7964	2.18515	1.22	0.82
CG7544_gene	CG7544	0.707674	0.860818	1.22	0.82
v(2)k05816_gene	v(2)k05816	0.707674	0.860818	1.22	0.82
CG13088_gene	CG13088	1.71475	2.08583	1.22	0.82
mus304_gene	mus304	1.71475	2.08583	1.22	0.82
CG13631_gene	CG13631	42.5421	51.7484	1.22	0.82
CG32219_gene	Ac76E	1.85084	2.25137	1.22	0.82
Pms2_gene	unc-5	1.85084	2.25137	1.22	0.82
CG14966_gene	CG14966	1.74197	2.11894	1.22	0.82
CG18335_gene	CG13213	0.571583	0.695276	1.22	0.82
CG13335_gene	CG13335	1.87806	2.28448	1.22	0.82
CG6345_gene	Rrp46	1.87806	2.28448	1.22	0.82
CG10361_gene	CG10361	0.598801	0.728384	1.22	0.82
Ubx_gene	Ubx	0.598801	0.728384	1.22	0.82
CG11796_gene	CG5872	0.789329	0.960143	1.22	0.82
mRpL4_gene	CG4278	5.90636	7.18452	1.22	0.82
CG10669_gene	CG10669	2.12302	2.58245	1.22	0.82
CG2100_gene	CG2100	8.19269	9.96562	1.22	0.82
gogo_gene	gogo	1.90528	2.31759	1.22	0.82
CG31342_gene	CG31342	10.7512	13.0778	1.22	0.82
ld14_gene	ld14	2.04137	2.48313	1.22	0.82
jigr1_gene	jigr1	6.47794	7.87979	1.22	0.82
CG33267_gene	CG33267	0.62602	0.761493	1.22	0.82
CR41501_gene	CR41501	0.843766	1.02636	1.22	0.82
CG17333_gene	CG17333	6.5596	7.97912	1.22	0.82
CG30290_gene	CG30290	4.38214	5.33045	1.22	0.82
CG7272_gene	CG7272	4.40936	5.36356	1.22	0.82
YL-1_gene	YL-1	4.79041	5.82707	1.22	0.82
Pgant35A_gene	Pgant35A	7.13118	8.67439	1.22	0.82
CG11870_gene	CG11870	14.3168	17.415	1.22	0.82
CG17510_gene	CG17510	12.6565	15.3954	1.22	0.82
Gpi1_gene	Gpi1	2.66739	3.24462	1.22	0.82
Ras85D_gene	Ras85D	14.2896	17.3819	1.22	0.82
CG1103_gene	CG9772	2.99401	3.64192	1.22	0.82
mRpL21_gene	mRpL21	3.15732	3.84057	1.22	0.82
CG6353_gene	CG6353	9.2542	11.2568	1.22	0.82
CG10903_gene	CG10903	8.24713	10.0318	1.22	0.82
Lrr47_gene	Lrr47	1.11595	1.35744	1.22	0.82
CG13896_gene	CG13896	1.44257	1.75474	1.22	0.82
CG31133_gene	kal-1	1.76919	2.15204	1.22	0.82
CG5602_gene	CG5602	1.9325	2.35069	1.22	0.82
Oseg6_gene	Oseg6	1.00708	1.22501	1.22	0.82
sd_gene	sd	42.9776	52.245	1.22	0.82

CG14299_gene	CG14299	48.4213	58.8336	1.22	0.82
CG31224_gene	CG14303	24.0065	29.1685	1.22	0.82
CG5288_gene	CG5288	41.5623	50.4903	1.21	0.82
CG3825_gene	CG3825	18.3995	22.3482	1.21	0.82
Src42A_gene	Src42A	36.4724	44.299	1.21	0.82
CG1774_gene	CG1774	16.6848	20.2623	1.21	0.82
foxo_gene	foxo	48.0674	58.3701	1.21	0.82
bun_gene	bun	93.032	112.966	1.21	0.82
tth_gene	BthD	48.9928	59.4626	1.21	0.82
CG15012_gene	Hexo1	12.1121	14.7001	1.21	0.82
Mnf_gene	Mnf	23.8704	28.9698	1.21	0.82
CG8547_gene	CG8547	35.7648	43.4051	1.21	0.82
CG4849_gene	CG4849	11.0778	13.442	1.21	0.82
sgg_gene	sgg	107.022	129.851	1.21	0.82
jing_gene	jing	17.583	21.3218	1.21	0.82
CG1745_gene	CG1745	8.46487	10.2636	1.21	0.82
CG7180_gene	CG31746	8.00216	9.70075	1.21	0.82
CG32473_gene	CG32473	22.7545	27.5793	1.21	0.83
CG8678_gene	CG8678	7.26727	8.80683	1.21	0.83
M6_gene	M6	7.24005	8.77372	1.21	0.83
chic_gene	chic	114.698	138.923	1.21	0.83
CG2943_gene	CG2943	67.6646	81.9432	1.21	0.83
CG7967_gene	CG13920	17.4741	21.1563	1.21	0.83
Rlip_gene	Rlip	5.63418	6.82033	1.21	0.83
MICAL_gene	MICAL	27.5449	33.3401	1.21	0.83
Coprox_gene	Coprox	16.4943	19.9644	1.21	0.83
Art1_gene	Art1	21.6657	26.2218	1.21	0.83
Got2_gene	CG7289	56.4234	68.2695	1.21	0.83
CG7033_gene	CG7033	29.3141	35.4591	1.21	0.83
Sk1_gene	CG11727	4.84485	5.86018	1.21	0.83
CG7791_gene	CG34200	9.52639	11.5217	1.21	0.83
PNGase_gene	PNGase	57.0767	69.031	1.21	0.83
CG14714_gene	CG14714	4.65432	5.62842	1.21	0.83
pen_gene	dod	18.5628	22.4475	1.21	0.83
CG17209_gene	CG17209	8.13826	9.83319	1.21	0.83
CG33506_gene	HPS	4.05552	4.90004	1.21	0.83
l(3)neo38_gene	l(3)neo38	8.08382	9.76697	1.21	0.83
key_gene	CG3589	11.7038	14.1373	1.21	0.83
Ard1_gene	Ard1	15.46	18.6731	1.21	0.83
Mp20_gene	Mp20	49.4828	59.7606	1.21	0.83
CG18659_gene	CG11784	29.8584	36.055	1.21	0.83
CG18048_gene	CG18048	3.64724	4.40341	1.21	0.83
l(1)G0155_gene	l(1)G0155	32.1447	38.803	1.21	0.83
CG2021_gene	CG12018	3.56559	4.30409	1.21	0.83
flw_gene	flw	63.4185	76.5466	1.21	0.83
ppa_gene	ppa	24.5781	29.6651	1.21	0.83
Rbp9_gene	Rbp9	28.062	33.8699	1.21	0.83
CG4966_gene	CG4966	17.3652	20.9576	1.21	0.83
fz2_gene	fz2	20.6314	24.8975	1.21	0.83
CG14435_gene	CG14435	6.61403	7.97912	1.21	0.83
ari-2_gene	ari-2	9.63526	11.621	1.21	0.83
CG17294_gene	CG17294	3.18453	3.84057	1.21	0.83
Pde11_gene	Pde11	31.6548	38.174	1.21	0.83
DIP1_gene	DIP1	56.6956	68.3688	1.21	0.83
CG11727_gene	CG11727	37.6428	45.3916	1.21	0.83
CG2063_gene	CG2063	9.30864	11.2237	1.21	0.83
Pop2_gene	Pop2	27.7082	33.4064	1.21	0.83
su(f)_gene	CG17162	18.209	21.9509	1.21	0.83
CoRest_gene	CoRest	18.1818	21.9177	1.21	0.83
Mhc_gene	Mhc	535.111	644.984	1.21	0.83

spn-A_gene	CG7946	2.93957	3.5426	1.21	0.83
CG4645_gene	CG4645	37.9422	45.7227	1.21	0.83
Ufd1-like_gene	mRpL2	20.4137	24.5995	1.21	0.83
Nup98_gene	Nup98	28.6064	34.4658	1.20	0.83
RnrS_gene	RnrS	8.49209	10.2305	1.20	0.83
CG11367_gene	CG11367	36.1186	43.5044	1.20	0.83
gb_gene	gb	8.30156	9.99873	1.20	0.83
HmgZ_gene	HmgZ	80.2122	96.6102	1.20	0.83
CG4709_gene	CG4709	2.72182	3.27773	1.20	0.83
CSN6_gene	CSN6	8.00216	9.63454	1.20	0.83
ph-p_gene	ph-p	15.9227	19.1698	1.20	0.83
CG41466_gene	CG31523	2.61295	3.1453	1.20	0.83
Uba2_gene	Uba2	18.1546	21.8515	1.20	0.83
vig_gene	vas	15.5416	18.7062	1.20	0.83
CG3921_gene	CG3921	10.3157	12.4156	1.20	0.83
CG18177_gene	CG18177	5.11703	6.15816	1.20	0.83
dpr13_gene	dpr13	5.06259	6.09194	1.20	0.83
CG8206_gene	CG8206	12.5476	15.0974	1.20	0.83
CG9996_gene	CG9996	2.47686	2.97975	1.20	0.83
qkr54B_gene	qkr54B	7.40336	8.90615	1.20	0.83
CG31531_gene	CG31531	39.4665	47.4774	1.20	0.83
CG33121_gene	CG33121	58.8186	70.7526	1.20	0.83
Gyc76C_gene	Gyc76C	63.6907	76.6128	1.20	0.83
Gbeta5_gene	Gbeta5	2.42242	2.91354	1.20	0.83
Sps2_gene	Sps2	14.5073	17.4481	1.20	0.83
cher_gene	CG5148	197.768	237.851	1.20	0.83
CG17724_gene	CG17724	19.2705	23.1759	1.20	0.83
CG7420_gene	CG7420	4.73597	5.69464	1.20	0.83
CG5377_gene	CG5377	6.96787	8.37642	1.20	0.83
Gclc_gene	Gclc	13.7452	16.5211	1.20	0.83
CG13067_gene	CG13067	2.28633	2.748	1.20	0.83
CG5110_gene	CG5110	9.11811	10.9589	1.20	0.83
Cdk5_gene	Cdk5	4.54545	5.46288	1.20	0.83
CG30349_gene	CG30349	11.35	13.6407	1.20	0.83
CG10947_gene	CG10947	2.25911	2.71489	1.20	0.83
CG8300_gene	CG8300	2.25911	2.71489	1.20	0.83
hoip_gene	hoip	6.72291	8.07844	1.20	0.83
CG4945_gene	CG4945	4.43657	5.33045	1.20	0.83
Marf_gene	Marf	105.035	126.176	1.20	0.83
CG10038_gene	CG10038	4.35492	5.23112	1.20	0.83
CG4752_gene	CG4752	10.8873	13.0778	1.20	0.83
CG8180_gene	CG8180	2.15024	2.58245	1.20	0.83
CG9619_gene	CG9619	2.15024	2.58245	1.20	0.83
CG4573_gene	TMS1	2.15024	2.58245	1.20	0.83
CG3262_gene	CG3262	15.0245	18.0441	1.20	0.83
mRpL44_gene	CG12162	6.42351	7.71425	1.20	0.83
CG11092_gene	CG11092	8.49209	10.1974	1.20	0.83
bcn92_gene	Pgd	4.24605	5.09869	1.20	0.83
CG8461_gene	mRpL11	4.21883	5.06558	1.20	0.83
CG6443_gene	CG6443	4.19161	5.03247	1.20	0.83
CG7650_gene	CG7650	2.06859	2.48313	1.20	0.83
Or59b_gene	CG34372	22.6184	27.1489	1.20	0.83
Spn_gene	Spn	18.454	22.1495	1.20	0.83
CG11255_gene	CG11255	26.6194	31.9496	1.20	0.83
CG7600_gene	CG7600	61.3227	73.5999	1.20	0.83
CG9904_gene	CG9904	2.04137	2.45002	1.20	0.83
isopeptidase-T-3_gene	peptidase-	1.98693	2.3838	1.20	0.83
CG16865_gene	CG16865	1.95971	2.35069	1.20	0.83
CG32521_gene	CG32521	15.6505	18.7724	1.20	0.83
CG31906_gene	CG31906	5.77027	6.91965	1.20	0.83

CG7441_gene	CG7441	5.74305	6.88654	1.20	0.83
CG8044_gene	CG8044	3.78334	4.53585	1.20	0.83
LpR1_gene	LpR1	3.78334	4.53585	1.20	0.83
CanA1_gene	CanA1	5.63418	6.75411	1.20	0.83
Pvf2_gene	Pvf2	1.87806	2.25137	1.20	0.83
CG32559_gene	CG32560	1.85084	2.21826	1.20	0.83
Tsp86D_gene	Tsp86D	1.85084	2.21826	1.20	0.83
dap_gene	dap	5.5253	6.62168	1.20	0.83
PTP-ER_gene	PTP-ER	16.5759	19.865	1.20	0.83
Start1_gene	Start1	9.17255	10.992	1.20	0.83
opa1-like_gene	CG8468	25.5035	30.559	1.20	0.83
COQ7_gene	COQ7	7.26727	8.7075	1.20	0.83
CG1671_gene	CG1671	14.0991	16.8853	1.20	0.83
CG13897_gene	CG13897	22.8633	27.3806	1.20	0.84
axo_gene	axo	8.73706	10.4622	1.20	0.84
CG2124_gene	CG2124	1.74197	2.08583	1.20	0.84
CG34411_gene	CG34411	13.6363	16.3224	1.20	0.84
Ugt86Da_gene	Ugt86Da	22.0468	26.3874	1.20	0.84
CG7787_gene	CG7787	6.75012	8.07844	1.20	0.84
NijA_gene	NijA	1.68753	2.01961	1.20	0.84
CG34360_gene	CG34360	33.6418	40.2598	1.20	0.84
Hel25E_gene	Hel25E	26.8644	32.1482	1.20	0.84
up_gene	up	163.609	195.77	1.20	0.84
san_gene	san	13.2008	15.7927	1.20	0.84
veli_gene	veli	3.29341	3.9399	1.20	0.84
ham_gene	ham	32.8796	39.3328	1.20	0.84
Nc_gene	Nc	1.63309	1.95339	1.20	0.84
CG17715_gene	CG17715	8.08382	9.66765	1.20	0.84
CG16817_gene	CG16817	81.2737	97.1731	1.20	0.84
CG31864_gene	CG31864	1.57866	1.88718	1.20	0.84
CG14711_gene	CG6808	3.15732	3.77436	1.20	0.84
fra_gene	fra	11.0506	13.2102	1.20	0.84
CG12948_gene	CG12948	4.70876	5.62842	1.20	0.84
CG31367_gene	CG31367	21.9651	26.2549	1.20	0.84
CG7097_gene	CG7097	17.2019	20.5603	1.20	0.84
CG10082_gene	CG10082	25.0136	29.8969	1.20	0.84
CG14995_gene	CG14990	27.6265	33.0091	1.19	0.84
arg_gene	arg	12.2754	14.667	1.19	0.84
MED23_gene	MED23	4.59988	5.49599	1.19	0.84
CG9902_gene	CG9902	1.52422	1.82096	1.19	0.84
CG32640_gene	CG34411	6.01523	7.18452	1.19	0.84
T-cp1_gene	T-cp1	22.1284	26.4205	1.19	0.84
Nup214_gene	Nup214	17.6646	21.09	1.19	0.84
CG33691_gene	CG33692	20.6042	24.5995	1.19	0.84
CG33692_gene	CG33692	20.6042	24.5995	1.19	0.84
CG32783_gene	CG32783	1.46979	1.75474	1.19	0.84
CG5924_gene	CG4537	1.46979	1.75474	1.19	0.84
Arc2_gene	CG10102	8.79149	10.4954	1.19	0.84
Pp4-19C_gene	Pp4-19C	10.2341	12.217	1.19	0.84
mnb_gene	CG6769	21.8563	26.0894	1.19	0.84
Nrx-1_gene	Nrx-1	2.91235	3.47638	1.19	0.84
CG5316_gene	CG5316	21.6929	25.8908	1.19	0.84
Alg10_gene	Alg10	8.62818	10.2967	1.19	0.84
rab3-GAP_gene	rab3-GAP	25.6668	30.6252	1.19	0.84
CG14034_gene	CG14034	659.416	786.655	1.19	0.84
NitFhit_gene	Gyk	22.3462	26.6522	1.19	0.84
Hpr1_gene	CG10999	8.356	9.96562	1.19	0.84
perd_gene	perd	13.9085	16.5873	1.19	0.84
CG4615_gene	CG4615	22.2373	26.5198	1.19	0.84
CG33108_gene	CG33108	4.16439	4.96626	1.19	0.84

Rbf_gene	Rbf	13.8813	16.5542	1.19	0.84
CG32442_gene	CG32442	1.38813	1.65542	1.19	0.84
Tdc1_gene	CG9422	1.38813	1.65542	1.19	0.84
dsh_gene	dsh	13.718	16.3555	1.19	0.84
CG8892_gene	CG8892	10.9145	13.0116	1.19	0.84
CG40470_gene	CG40470	1.36091	1.62231	1.19	0.84
CG13933_gene	CG13933	13.5819	16.19	1.19	0.84
Cct5_gene	Cct5	28.4431	33.903	1.19	0.84
CG4679_gene	CG4679	5.41643	6.45613	1.19	0.84
CG17836_gene	CG17836	228.715	272.614	1.19	0.84
CG8038_gene	CG8209	4.05552	4.83382	1.19	0.84
spel1_gene	spel1	2.69461	3.21151	1.19	0.84
Tfb2_gene	Tfb2	6.72291	8.01223	1.19	0.84
CG30077_gene	CG30077	5.30756	6.3237	1.19	0.84
CG10555_gene	CG10555	11.8399	14.1042	1.19	0.84
CG10343_gene	CG10343	10.479	12.4819	1.19	0.84
ligatin_gene	Pglym78	19.5699	23.3083	1.19	0.84
CG1105_gene	CG1988	11.6766	13.9055	1.19	0.84
CG5435_gene	CG6388	1.27926	1.52299	1.19	0.84
btl_gene	l(3)70Da	1.27926	1.52299	1.19	0.84
CG9906_gene	para	2.5313	3.01286	1.19	0.84
Cpr92A_gene	Cpr92A	1.25204	1.48988	1.19	0.84
CG5056_gene	CG5056	7.40336	8.80683	1.19	0.84
Gs1_gene	Gs1	9.79857	11.6541	1.19	0.84
l(2)37Cc_gene	l(2)37Cc	36.6358	43.5706	1.19	0.84
Sox14_gene	Sox14	12.1938	14.5015	1.19	0.84
dei_gene	dei	1.1976	1.42366	1.19	0.84
CG11504_gene	CG15525	4.79041	5.69464	1.19	0.84
CSN3_gene	CSN3	4.79041	5.69464	1.19	0.84
CG34039_gene	CG34039	2.39521	2.84732	1.19	0.84
CG1814_gene	Not1	21.3391	25.361	1.19	0.84
CG13163_gene	CG13163	2.36799	2.81421	1.19	0.84
CG3770_gene	CG3770	4.70876	5.59532	1.19	0.84
CG11146_gene	CG11146	1.17038	1.39055	1.19	0.84
CG10899_gene	CG10899	8.19269	9.73386	1.19	0.84
CG5491_gene	CG5491	5.8247	6.91965	1.19	0.84
CG7339_gene	CG7339	4.65432	5.5291	1.19	0.84
CG4496_gene	CG4495	10.3429	12.2832	1.19	0.84
Irc_gene	Irc	6.83178	8.11155	1.19	0.84
CG4618_gene	CG4618	10.1524	12.0514	1.19	0.84
Rpt4_gene	wuho	21.3935	25.3941	1.19	0.84
CG12104_gene	CG12104	7.86607	9.33656	1.19	0.84
CG6845_gene	CG6845	4.49101	5.33045	1.19	0.84
CG9107_gene	CG9107	5.60696	6.65478	1.19	0.84
tsr_gene	tsr	43.522	51.6491	1.19	0.84
CG3714_gene	CG3714	13.3914	15.892	1.19	0.84
CG4853_gene	CG4853	16.6576	19.7657	1.19	0.84
CG7830_gene	CG7840	164.943	195.704	1.19	0.84
CG10585_gene	CG10585	3.32063	3.9399	1.19	0.84
Arf84F_gene	Arf84F	2.20468	2.61556	1.19	0.84
Pten_gene	Pten	8.81871	10.4622	1.19	0.84
CG4133_gene	CG4133	3.29341	3.90679	1.19	0.84
CG31935_gene	CG14351	13.092	15.5278	1.19	0.84
noe_gene	blot	4.35492	5.16491	1.19	0.84
CG13826_gene	CG13826	3.26619	3.87368	1.19	0.84
CG3434_gene	CG3552	6.53238	7.74736	1.19	0.84
Lerp_gene	Lerp	53.2661	63.1708	1.19	0.84
Rsf1_gene	Rsf1	24.823	29.4333	1.19	0.84
CG7333_gene	CG7333	7.48502	8.87305	1.19	0.84
CG34237_gene	CG34237	38.3777	45.4909	1.19	0.84

Klp98A_gene	Klp98A	20.2504	24.0036	1.19	0.84
CG17124_gene	CG17124	6.36907	7.54871	1.19	0.84
CG10069_gene	CG10069	54.0282	64.0316	1.19	0.84
CG9296_gene	CG9296	9.52639	11.29	1.19	0.84
sda_gene	sda	51.8235	61.416	1.19	0.84
CG34056_gene	CG34056	12.6837	15.0312	1.19	0.84
CG34310_gene	cup	5.28034	6.25748	1.19	0.84
Aly_gene	Aly	22.1012	26.1887	1.18	0.84
CG32062_gene	CG32062	15.7866	18.7062	1.18	0.84
CG31973_gene	CG31973	83.1245	98.4974	1.18	0.84
CG13364_gene	CG13369	63.0647	74.7256	1.18	0.84
CG15445_gene	CG15445	23.1083	27.3806	1.18	0.84
GstE7_gene	GstE7	2.0958	2.48313	1.18	0.84
Lar_gene	Lar	19.8693	23.5401	1.18	0.84
Unc-89_gene	Unc-89	33.1518	39.2665	1.18	0.84
Nlp_gene	Nlp	49.7005	58.8667	1.18	0.84
mTTF_gene	mTTF	5.17147	6.12505	1.18	0.84
rad50_gene	rad50	15.46	18.3089	1.18	0.84
CG17144_gene	CG17144	11.2684	13.3427	1.18	0.84
CG11396_gene	CG11396	18.4268	21.8184	1.18	0.84
CG6808_gene	CG14710	4.08274	4.83382	1.18	0.84
CG7263_gene	CG7261	12.221	14.4684	1.18	0.84
CG5641_gene	Sas	8.13826	9.63454	1.18	0.84
twi_gene	twi	5.06259	5.99262	1.18	0.84
gp210_gene	gp210	34.2406	40.5247	1.18	0.84
CG17667_gene	Atg1	7.04953	8.34331	1.18	0.84
CG15914_gene	CG15914	1.00708	1.1919	1.18	0.84
CG17572_gene	CG17572	1.00708	1.1919	1.18	0.84
CG32613_gene	CG34346	1.00708	1.1919	1.18	0.84
nod_gene	nod	1.00708	1.1919	1.18	0.84
CG2003_gene	heph	24.1426	28.5725	1.18	0.84
eIF2B-gamma_gene	IF2B-gamm	14.0174	16.5873	1.18	0.85
CG10139_gene	CG10139	6.96787	8.24399	1.18	0.85
CG11808_gene	CG11808	3.97386	4.70139	1.18	0.85
CG5059_gene	CG5059	45.5089	53.8342	1.18	0.85
CG10466_gene	CG10466	1.95971	2.31759	1.18	0.85
CG12702_gene	CG12703	0.979857	1.15879	1.18	0.85
LysS_gene	LysS	0.979857	1.15879	1.18	0.85
CG8974_gene	Rhp	38.9493	46.0538	1.18	0.85
PNUTS_gene	PNUTS	106.042	125.381	1.18	0.85
NFAT_gene	NFAT	26.2384	31.0225	1.18	0.85
CG7456_gene	Grip75	64.0173	75.6858	1.18	0.85
Chmp1_gene	Chmp1	28.062	33.1746	1.18	0.85
CG8257_gene	CG13016	5.79749	6.85343	1.18	0.85
px_gene	px	39.412	46.5835	1.18	0.85
Snx6_gene	Snx6	33.424	39.4983	1.18	0.85
CG13920_gene	CG13920	2.85792	3.37705	1.18	0.85
Aats-ser_gene	CG6218	2.85792	3.37705	1.18	0.85
ca_gene	ca	16.1949	19.1366	1.18	0.85
olf186-F_gene	olf186-F	15.215	17.9778	1.18	0.85
smt3_gene	smt3	56.0151	66.1836	1.18	0.85
CG2247_gene	CG2247	36.9896	43.7031	1.18	0.85
CG7182_gene	CG7182	15.9227	18.8056	1.18	0.85
CG6983_gene	CG6983	9.36308	11.0582	1.18	0.85
Rab10_gene	CG17068	56.9134	67.21	1.18	0.85
CG10741_gene	CG10741	38.16	45.0605	1.18	0.85
CR34262_gene	CR34262	0.92542	1.09258	1.18	0.85
CG5886_gene	CG5886	7.37614	8.7075	1.18	0.85
egh_gene	egh	84.7032	99.9873	1.18	0.85
CG3308_gene	CG5919	41.4262	48.9011	1.18	0.85

CG1885_gene	CG1885	3.67446	4.3372	1.18	0.85
Cyp303a1_gene	Cyp303a1	3.67446	4.3372	1.18	0.85
CG13369_gene	CG13369	32.1447	37.9422	1.18	0.85
sbr_gene	sbr	34.8121	41.0875	1.18	0.85
gek_gene	gek	17.3652	20.4941	1.18	0.85
thoc6_gene	Est-P	3.64724	4.30409	1.18	0.85
CG31751_gene	CG31751	54.5998	64.4289	1.18	0.85
CG7145_gene	CG7145	60.9144	71.8783	1.18	0.85
yps_gene	yps	91.2628	107.668	1.18	0.85
CG7839_gene	CG7839	27.0822	31.9496	1.18	0.85
crb_gene	crb	22.4823	26.5198	1.18	0.85
CG30357_gene	CG14767	0.898202	1.05947	1.18	0.85
CG31414_gene	CG31414	0.898202	1.05947	1.18	0.85
CG16812_gene	CG16812	9.88022	11.6541	1.18	0.85
CG11089_gene	CG11089	13.3369	15.7265	1.18	0.85
Tao-1_gene	Tao-1	29.2868	34.532	1.18	0.85
Spn1_gene	CG9455	262.112	309.034	1.18	0.85
dUTPase_gene	dUTPase	3.53837	4.17166	1.18	0.85
trio_gene	trio	14.1263	16.6535	1.18	0.85
Ptpa_gene	Ptpa	4.40936	5.19802	1.18	0.85
Nipsnap_gene	Nipsnap	18.4268	21.7191	1.18	0.85
CG13567_gene	CG13567	4.38214	5.16491	1.18	0.85
Cirl_gene	Cirl	98.9111	116.575	1.18	0.85
CG6843_gene	CG6843	11.35	13.3758	1.18	0.85
CG31855_gene	CG31855	6.96787	8.21088	1.18	0.85
CG33156_gene	CG33156	13.0375	15.3623	1.18	0.85
CG12065_gene	CG12065	10.4246	12.2832	1.18	0.85
CG14333_gene	Brf	3.45672	4.07233	1.18	0.85
CG6764_gene	CG6764	44.774	52.7416	1.18	0.85
CG9426_gene	CG9426	22.3734	26.3543	1.18	0.85
CG17996_gene	CG31812	6.859	8.07844	1.18	0.85
CG6236_gene	CG6236	8.54653	10.0649	1.18	0.85
CG34246_gene	CG34246	2.55852	3.01286	1.18	0.85
CG4497_gene	CG4497	2.55852	3.01286	1.18	0.85
Idgf1_gene	CG5888	2.55852	3.01286	1.18	0.85
CG9875_gene	CG9875	6.80456	8.01223	1.18	0.85
CG4610_gene	CG4610	7.64833	9.00548	1.18	0.85
fau_gene	fau	137.098	161.403	1.18	0.85
Ercc1_gene	Ercc1	1.68753	1.9865	1.18	0.85
CG33293_gene	CG12163	0.843766	0.993251	1.18	0.85
Hrb98DE_gene	Hrb98DE	93.0592	109.523	1.18	0.85
CG5068_gene	CG5068	4.19161	4.93315	1.18	0.85
CG5537_gene	CG5537	22.6184	26.6191	1.18	0.85
CG3184_gene	CG3184	3.34784	3.9399	1.18	0.85
CG33110_gene	CG33110	16.7392	19.6995	1.18	0.85
ebi_gene	ebi	16.7392	19.6995	1.18	0.85
CG11412_gene	CG11412	23.4077	27.5462	1.18	0.85
Roc2_gene	Roc2	38.4322	45.226	1.18	0.85
CG13901_gene	CG13901	2.50408	2.94665	1.18	0.85
CG8839_gene	CG8839	48.394	56.9464	1.18	0.85
Art8_gene	Nup154	10.8056	12.7136	1.18	0.85
CG8111_gene	CG8111	9.96188	11.7204	1.18	0.85
Mcm3_gene	Mcm3	1.66031	1.95339	1.18	0.85
CG15771_gene	CG15771	19.08	22.4475	1.18	0.85
CG6359_gene	CG6359	34.8121	40.9551	1.18	0.85
CG14869_gene	CG14869	37.289	43.8686	1.18	0.85
elav_gene	arg	4.89928	5.76086	1.18	0.85
Cdc6_gene	CG6416	4.89928	5.76086	1.18	0.85
140up_gene	twf	4.89928	5.76086	1.18	0.85
CG13260_gene	CG13260	0.816547	0.960143	1.18	0.85

Pmm45A_gene	Pmm45A	35.9281	42.2463	1.18	0.85
CG9311_gene	CG9311	56.5595	66.4816	1.18	0.85
p47_gene	p47	14.5345	17.0839	1.18	0.85
CG2543_gene	CG2543	2.42242	2.84732	1.18	0.85
ALiX_gene	ALiX	62.5747	73.5337	1.18	0.85
CG4721_gene	CG7029	4.00108	4.70139	1.18	0.85
CG40005_gene	CG40005	2.39521	2.81421	1.17	0.85
CG17141_gene	HP1c	3.18453	3.74125	1.17	0.85
CG1998_gene	CG1998	6.36907	7.48249	1.17	0.85
per_gene	per	4.76319	5.59532	1.17	0.85
CG11033_gene	CG11033	29.3685	34.4989	1.17	0.85
CG6066_gene	CG6066	3.94665	4.63517	1.17	0.85
mRpL30_gene	mRpL30	11.8127	13.8724	1.17	0.85
R_gene	R	81.8725	96.1467	1.17	0.85
CG11814_gene	CG11814	25.9662	30.4928	1.17	0.85
CG2519_gene	CG2519	28.2525	33.1746	1.17	0.85
gce_gene	gce	9.41751	11.0582	1.17	0.85
Aps_gene	Aps	95.6721	112.337	1.17	0.85
spen_gene	spen	124.632	146.339	1.17	0.85
CG11155_gene	CG11155	11.7583	13.8062	1.17	0.85
CG8888_gene	CG8888	13.2553	15.5609	1.17	0.85
CG5292_gene	CG5292	5.44365	6.38992	1.17	0.85
CG7802_gene	CG7802	5.44365	6.38992	1.17	0.85
CG31229_gene	CG31229	3.07566	3.60881	1.17	0.85
CG6767_gene	CG6767	41.5078	48.7024	1.17	0.85
CG12321_gene	CG7940	9.96188	11.6873	1.17	0.85
CG5694_gene	CG5694	9.93466	11.6541	1.17	0.85
RhoGAP19D_gene	RhoGAP19D	16.7937	19.6995	1.17	0.85
msl-3_gene	form3	6.859	8.04534	1.17	0.85
CG10562_gene	CG10562	1.52422	1.78785	1.17	0.85
Srp54_gene	Srp54	15.2422	17.8785	1.17	0.85
Gr32a_gene	Gr32a	0.762111	0.893926	1.17	0.85
CG17257_gene	CG17219	9.90744	11.621	1.17	0.85
CG34417_gene	CG34417	137.724	161.536	1.17	0.85
CG1675_gene	cbx	13.6908	16.0576	1.17	0.85
wdp_gene	wdp	15.9227	18.6731	1.17	0.85
Osi13_gene	Osi13	3.02123	3.5426	1.17	0.85
CG4973_gene	CG4390	2.25911	2.64867	1.17	0.85
mRpL2_gene	mRpL2	8.98202	10.5285	1.17	0.85
CG6178_gene	CG6178	6.69569	7.84669	1.17	0.85
CG6340_gene	CG6340	12.6293	14.7994	1.17	0.85
CG32485_gene	CG32485	11.8672	13.9055	1.17	0.85
cana_gene	cana	50.9798	59.7275	1.17	0.85
CG33695_gene	cana	50.9798	59.7275	1.17	0.85
tsu_gene	tsu	16.2493	19.0373	1.17	0.85
CG16926_gene	CG15120	4.40936	5.16491	1.17	0.85
CG13377_gene	cin	5.14425	6.02572	1.17	0.85
prel_gene	prel	21.9379	25.6921	1.17	0.85
CG8632_gene	CG8632	10.2341	11.9852	1.17	0.85
elk_gene	elk	4.38214	5.1318	1.17	0.85
btn_gene	CG6937	3.64724	4.27098	1.17	0.85
snRNP69D_gene	snRNP69D	3.64724	4.27098	1.17	0.85
CG33169_gene	CG33169	70.6313	82.7047	1.17	0.85
CG3793_gene	CG3793	5.08981	5.95951	1.17	0.85
CG31547_gene	CG31547	135.166	158.258	1.17	0.85
CG3045_gene	a	1.44257	1.68853	1.17	0.85
Ca-alpha1T_gene	Ca-alpha1T	12.2482	14.3359	1.17	0.85
shi_gene	shi	28.062	32.8435	1.17	0.85
mbc_gene	mbc	29.4774	34.4989	1.17	0.85
CG31324_gene	CG31324	17.9368	20.9907	1.17	0.85

CG32662_gene	CG32663	46.4071	54.2977	1.17	0.85
if_gene	if	36.3636	42.5443	1.17	0.85
CG32281_gene	CG32278	4.27326	4.99936	1.17	0.85
Myo95E_gene	CG6178	12.0849	14.1373	1.17	0.85
CG11601_gene	smo	15.5961	18.2427	1.17	0.85
Cdc27_gene	Cdc27	17.7191	20.7258	1.17	0.85
CG1695_gene	CG1695	0.707674	0.827709	1.17	0.85
CG6959_gene	CG6959	14.1535	16.5542	1.17	0.85
CG14570_gene	Rpb8	1.41535	1.65542	1.17	0.85
smid_gene	smid	23.2172	27.1489	1.17	0.86
msl-2_gene	msl-2	13.3369	15.594	1.17	0.86
Cyp6u1_gene	Cyp6u1	6.31463	7.38317	1.17	0.86
CG9143_gene	CG11788	13.2825	15.5278	1.17	0.86
CG12123_gene	CG12123	2.0958	2.45002	1.17	0.86
CG12991_gene	CG12991	12.5204	14.6339	1.17	0.86
shot_gene	shot	198.067	231.494	1.17	0.86
MYPT-75D_gene	MYPT-75D	25.0136	29.2347	1.17	0.86
CaMKI_gene	CaMKI	21.5024	25.1293	1.17	0.86
Cog7_gene	Cog7	15.215	17.7792	1.17	0.86
CG17922_gene	CG30290	2.06859	2.41691	1.17	0.86
CG5274_gene	CG5274	4.81763	5.62842	1.17	0.86
CG9298_gene	CG9298	6.17854	7.21763	1.17	0.86
Tango14_gene	Tango14	9.60804	11.2237	1.17	0.86
CG11791_gene	CG11791	46.6521	54.4964	1.17	0.86
MED22_gene	MED22	4.10996	4.80071	1.17	0.86
a_gene	a	10.9145	12.7467	1.17	0.86
Ulp1_gene	Ulp1	23.1899	27.0827	1.17	0.86
CG9056_gene	CG9056	34.7577	40.5909	1.17	0.86
CG17440_gene	CG17440	0.680456	0.794601	1.17	0.86
CG7912_gene	Nlp	0.680456	0.794601	1.17	0.86
l(3)05822_gene	l(3)05822	40.1197	46.8484	1.17	0.86
IP3K1_gene	IP3K1	100.571	117.402	1.17	0.86
Bx_gene	Bx	10.7784	12.5812	1.17	0.86
CG15645_gene	CG15645	3.34784	3.90679	1.17	0.86
CG5789_gene	CG6631	18.7262	21.8515	1.17	0.86
CG11221_gene	CG11221	1.33369	1.55609	1.17	0.86
CG5800_gene	CG5800	13.9902	16.3224	1.17	0.86
sdk_gene	sdk	62.8741	73.3351	1.17	0.86
Lap1_gene	Lap1	2.64017	3.07908	1.17	0.86
CG14562_gene	CG14562	5.93358	6.91965	1.17	0.86
Syb_gene	CG12913	79.6406	92.869	1.17	0.86
Nrt_gene	Nrt	7.21284	8.40953	1.17	0.86
CG9896_gene	CG9896	58.2198	67.8722	1.17	0.86
GstD3_gene	GstD3	1.30648	1.52299	1.17	0.86
Irp-1B_gene	Irp-1B	24.1426	28.1421	1.17	0.86
CG3777_gene	CG3777	45.019	52.4768	1.17	0.86
14-3-3zeta_gene	14-3-3zeta	305.28	355.816	1.17	0.86
CG14200_gene	CG14200	20.1687	23.5069	1.17	0.86
CG12012_gene	CG12012	7.13118	8.3102	1.17	0.86
CG8152_gene	CG8152	2.58573	3.01286	1.17	0.86
mRpL43_gene	mRpL43	2.58573	3.01286	1.17	0.86
CG8818_gene	CG13151	38.1055	44.3983	1.17	0.86
CG4953_gene	CG4953	4.51823	5.26423	1.17	0.86
CG11964_gene	CG11963	12.9014	15.0312	1.17	0.86
CG5188_gene	CG5188	3.86499	4.50274	1.17	0.86
CG12974_gene	CG12974	1.9325	2.25137	1.17	0.86
CG32939_gene	CG32939	1.9325	2.25137	1.17	0.86
CG13096_gene	CG13096	18.0185	20.9907	1.16	0.86
CG7137_gene	CG7137	5.14425	5.99262	1.16	0.86
Cyp12c1_gene	Cyp12c1	3.21175	3.74125	1.16	0.86

Chi_gene	Chi	16.6848	19.4346	1.16	0.86
Aats-lys_gene	Aats-lys	43.5492	50.722	1.16	0.86
CG30195_gene	CG30195	1.27926	1.48988	1.16	0.86
CG30081_gene	CG8092	1.27926	1.48988	1.16	0.86
Pcd_gene	Pcd	2.55852	2.97975	1.16	0.86
E2f2_gene	E2f2	7.02231	8.17777	1.16	0.86
MED28_gene	MED28	4.46379	5.19802	1.16	0.86
CG11426_gene	CG11426	1.90528	2.21826	1.16	0.86
CG1907_gene	CG1907	25.3946	29.5658	1.16	0.86
CG41463_gene	CG31522	15.841	18.4414	1.16	0.86
CG12880_gene	CG31055	2.5313	2.94665	1.16	0.86
CG34363_gene	CG34363	96.0804	111.84	1.16	0.86
CG9779_gene	MP1	18.3179	21.3218	1.16	0.86
CG11419_gene	CG4853	6.31463	7.35006	1.16	0.86
CG4656_gene	CG4656	15.7594	18.342	1.16	0.86
CG18854_gene	IP3K1	189.493	220.502	1.16	0.86
CG34372_gene	CG34372	242.596	282.282	1.16	0.86
yellow-d_gene	CG13551	0.62602	0.728384	1.16	0.86
CG32103_gene	CG32103	33.0157	38.4057	1.16	0.86
CG30342_gene	CG30342	9.33586	10.8595	1.16	0.86
CG15335_gene	CG15335	17.338	20.163	1.16	0.86
CG8726_gene	nito	19.8149	23.0434	1.16	0.86
CG11168_gene	CG11168	91.8888	106.808	1.16	0.86
snoRNA:660_gene	Act57B	100.435	116.74	1.16	0.86
Las_gene	Las	6.12411	7.1183	1.16	0.86
Rep_gene	Rep	6.12411	7.1183	1.16	0.86
wuho_gene	wuho	7.94773	9.23724	1.16	0.86
CG7277_gene	Cap-D3	20.1687	23.4407	1.16	0.86
CG4210_gene	CG4210	5.49809	6.38992	1.16	0.86
CG2911_gene	Spec2	3.04844	3.5426	1.16	0.86
CG11593_gene	CG11593	7.92051	9.20413	1.16	0.86
Aos1_gene	Pros25	10.3429	12.0183	1.16	0.86
porin_gene	porin	191.562	222.588	1.16	0.86
CG6689_gene	CG4820	5.47087	6.35681	1.16	0.86
CG9215_gene	CG9215	5.47087	6.35681	1.16	0.86
CG5112_gene	CG5112	258.737	300.624	1.16	0.86
Hsc70-5_gene	Hsc70-5	52.8306	61.3829	1.16	0.86
cno_gene	cno	24.8503	28.8705	1.16	0.86
CG3894_gene	CG3894	7.26727	8.44264	1.16	0.86
beta-Spec_gene	beta-Spec	196.733	228.547	1.16	0.86
CG2972_gene	CG2972	18.1546	21.09	1.16	0.86
kermit_gene	kermit	8.46487	9.83319	1.16	0.86
CG11337_gene	Gcn2	6.64125	7.71425	1.16	0.86
CG7974_gene	CG7974	4.21883	4.90004	1.16	0.86
Bj1_gene	Bj1	7.21284	8.37642	1.16	0.86
CG31142_gene	CG31142	15.5688	18.0772	1.16	0.86
CG31370_gene	CG31370	1.1976	1.39055	1.16	0.86
CG10098_gene	CG10098	5.98801	6.95276	1.16	0.86
PGRP-LD_gene	PGRP-LD	5.98801	6.95276	1.16	0.86
Pmi_gene	PGRP-LD	5.98801	6.95276	1.16	0.86
CG13436_gene	rig	0.598801	0.695276	1.16	0.86
Tgt_gene	Tgt	4.19161	4.86693	1.16	0.86
CG7156_gene	repo	2.99401	3.47638	1.16	0.86
CG3508_gene	CG3508	2.39521	2.7811	1.16	0.86
CG1311_gene	CG1311	19.7332	22.911	1.16	0.86
Ranbp9_gene	Ranbp9	22.074	25.6259	1.16	0.86
B52_gene	B52	49.4011	57.3437	1.16	0.86
CG10602_gene	CG10602	26.1567	30.3604	1.16	0.86
CG34164_gene	CG5317	24.3603	28.2746	1.16	0.86
CG5317_gene	CG5317	24.3603	28.2746	1.16	0.86

crp_gene	crp	58.7642	68.2033	1.16	0.86
CG14803_gene	CG14815	5.33478	6.19127	1.16	0.86
CG33936_gene	CG33936	109.064	126.573	1.16	0.86
Su(P)_gene	Su(P)	11.8399	13.74	1.16	0.86
eap_gene	Nrx-IV	5.90636	6.85343	1.16	0.86
muskelin_gene	muskelin	3.53837	4.10544	1.16	0.86
CG7598_gene	CG7598	11.1867	12.9785	1.16	0.86
CG12913_gene	CG12913	80.5388	93.4318	1.16	0.86
Es2_gene	Es2	4.10996	4.76761	1.16	0.86
CG13012_gene	r	10.5607	12.2501	1.16	0.86
CG32278_gene	CG32278	21.6929	25.1624	1.16	0.86
CG8549_gene	CG8549	9.96188	11.5548	1.16	0.86
CG12484_gene	CG12484	1.17038	1.35744	1.16	0.86
CG33095_gene	CG33096	25.6124	29.6982	1.16	0.86
CG17097_gene	CG17097	27995.5	32459	1.16	0.86
CG11967_gene	CG11967	1.74197	2.01961	1.16	0.86
CG33969_gene	fbl	21.4752	24.8975	1.16	0.86
pncr003:2L_gene	pncr003:2L	61.9487	71.8121	1.16	0.86
CG41283_gene	CG40178	2.31355	2.68178	1.16	0.86
CG17029_gene	brm	14.97	17.3488	1.16	0.86
CG30456_gene	CG30456	12.0849	14.0048	1.16	0.86
CG4643_gene	CG17059	12.602	14.6008	1.16	0.86
trk_gene	CG31873	0.571583	0.662168	1.16	0.86
CG31904_gene	CG31904	0.571583	0.662168	1.16	0.86
CG34149_gene	CG34149	0.571583	0.662168	1.16	0.86
CG6560_gene	CG6560	0.571583	0.662168	1.16	0.86
CG9542_gene	DLP	1.14317	1.32434	1.16	0.86
CG13877_gene	Kaz1-ORFB	1.14317	1.32434	1.16	0.86
CG33260_gene	Trl	1.14317	1.32434	1.16	0.86
CG30000_gene	CG30000	4.00108	4.63517	1.16	0.86
CG32344_gene	CG32344	18.2907	21.1894	1.16	0.86
CG14967_gene	gry	21.1486	24.5002	1.16	0.86
CG17788_gene	CG17788	1.71475	1.9865	1.16	0.86
CG1078_gene	CG1078	17.1203	19.8319	1.16	0.86
CG2991_gene	CG2991	39.9019	46.2193	1.16	0.86
CG2202_gene	CG2202	9.66248	11.1906	1.16	0.86
achi_gene	achi	3.97386	4.60206	1.16	0.86
CG11562_gene	CG11562	2.25911	2.61556	1.16	0.86
CG32594_gene	hiw	12.3843	14.3359	1.16	0.86
CG14511_gene	CG14511	5.06259	5.86018	1.16	0.86
CG9715_gene	CG9715	47.7952	55.3241	1.16	0.86
SNF1A_gene	SNF1A	42.1611	48.8017	1.16	0.86
poly_gene	poly	61.8126	71.5472	1.16	0.86
CG1640_gene	CG1640	76.8643	88.9622	1.16	0.86
CG7656_gene	CG7656	11.7583	13.6075	1.16	0.86
CG5241_gene	CG5241	5.03538	5.82707	1.16	0.86
Pka-R2_gene	Pka-R2	73.7887	85.3865	1.16	0.86
mRpL14_gene	mRpL14	3.34784	3.87368	1.16	0.86
CG13952_gene	CG13952	1.11595	1.29123	1.16	0.86
CG7183_gene	CG7183	5.57974	6.45613	1.16	0.86
e(y)2_gene	CG11696	7.78442	9.00548	1.16	0.86
norpA_gene	norpA	17.2019	19.8981	1.16	0.86
CG9372_gene	CG9372	4.43657	5.1318	1.16	0.86
veg_gene	veg	8.30156	9.60143	1.16	0.86
Oda_gene	Oda	713.336	824.995	1.16	0.86
CG15814_gene	CG15814	22.6456	26.1887	1.16	0.86
c12.2_gene	c12.2	15.9771	18.4745	1.16	0.86
CG9194_gene	CG9194	9.30864	10.7602	1.16	0.87
Deaf1_gene	Deaf1	12.0305	13.9055	1.16	0.87
CG5919_gene	CG5919	12.5476	14.5015	1.16	0.87

CG14882_gene	CG14882	1.63309	1.88718	1.16	0.87
CG14933_gene	CG31757	7.07674	8.17777	1.16	0.87
Dbp45A_gene	Dbp45A	9.2542	10.694	1.16	0.87
CG30403_gene	CG30403	0.544365	0.629059	1.16	0.87
CG5053_gene	CG5053	17.3652	20.0637	1.16	0.87
CG32627_gene	CG9940	8.68262	10.0318	1.16	0.87
Mlf_gene	CG8297	33.6145	38.8361	1.16	0.87
CG5018_gene	CG5018	5.9608	6.88654	1.16	0.87
ric8a_gene	ric8a	5.9608	6.88654	1.16	0.87
CG33978_gene	CG33978	3.78334	4.37031	1.16	0.87
Sara_gene	Sara	17.828	20.5934	1.16	0.87
Uev1A_gene	Uev1A	44.2841	51.1524	1.16	0.87
ab_gene	ab	3.23897	3.74125	1.16	0.87
CG14102_gene	HLH106	3.23897	3.74125	1.16	0.87
CG4433_gene	CG4433	5.93358	6.85343	1.16	0.87
Atg8a_gene	Atg8a	361.676	417.695	1.15	0.87
CG13255_gene	CG13255	64.48	74.4607	1.15	0.87
S6k_gene	S6k	46.1621	53.3045	1.15	0.87
CG33230_gene	CG7955	7.48502	8.64129	1.15	0.87
VhaSFD_gene	CG31782	101.034	116.641	1.15	0.87
betaTub60D_gene	betaTub60D	13.8813	16.0245	1.15	0.87
Jra_gene	Jra	19.2161	22.1826	1.15	0.87
CG17680_gene	CG17680	16.0043	18.4745	1.15	0.87
CG7949_gene	CG7949	6.91343	7.97912	1.15	0.87
Stat92E_gene	Stat92E	50.9526	58.8005	1.15	0.87
Aut1_gene	Aut1	11.6494	13.442	1.15	0.87
kuk_gene	kuk	25.3946	29.3009	1.15	0.87
CG5913_gene	CG5913	16.9025	19.5008	1.15	0.87
CG6745_gene	CG6745	7.37614	8.50885	1.15	0.87
Aats-ala-m_gene	CG10671	8.41044	9.70075	1.15	0.87
CG11660_gene	CG11660	10.5062	12.1177	1.15	0.87
CG17337_gene	CG17337	27.2727	31.453	1.15	0.87
CG10262_gene	CG10262	2.0958	2.41691	1.15	0.87
CG17325_gene	CG17325	2.0958	2.41691	1.15	0.87
CG3835_gene	CG3835	38.2144	44.0673	1.15	0.87
SRPK_gene	dup	43.4403	50.093	1.15	0.87
Galpha49B_gene	Galpha49B	63.7996	73.5668	1.15	0.87
CG2129_gene	CG2129	2.61295	3.01286	1.15	0.87
Hrs_gene	Hrs	16.1949	18.6731	1.15	0.87
Picot_gene	Picot	28.6064	32.9759	1.15	0.87
szar_gene	Pomp	33.669	38.803	1.15	0.87
CG15744_gene	CG15744	4.13717	4.76761	1.15	0.87
Apc2_gene	Apc2	5.17147	5.95951	1.15	0.87
Dsor1_gene	Dsor1	12.9287	14.8988	1.15	0.87
MED6_gene	CG8478	14.9973	17.2826	1.15	0.87
CG5091_gene	CG5091	10.3157	11.8859	1.15	0.87
CG18507_gene	CG18507	59.8257	68.9316	1.15	0.87
CG15609_gene	CG15609	13.9085	16.0245	1.15	0.87
CG6719_gene	CG6719	10.2885	11.8528	1.15	0.87
CG33713_gene	CG33713	46.7065	53.8011	1.15	0.87
CG33714_gene	CG33713	46.7065	53.8011	1.15	0.87
bin3_gene	bin3	31.301	36.055	1.15	0.87
dsd_gene	dsd	41.4262	47.7092	1.15	0.87
CG10428_gene	CG10428	4.59988	5.29734	1.15	0.87
CG7519_gene	CG7519	4.08274	4.70139	1.15	0.87
kst_gene	kst	108.084	124.454	1.15	0.87
CG12006_gene	CG12006	3.56559	4.10544	1.15	0.87
CG6181_gene	CG6181	22.9178	26.3874	1.15	0.87
CG14647_gene	CG9853	8.62818	9.93251	1.15	0.87
CG5787_gene	CG5787	39.031	44.9281	1.15	0.87

CG8258_gene	CG8258	30.4028	34.9956	1.15	0.87
Ca-beta_gene	Ca-beta	2.5313	2.91354	1.15	0.87
CG12698_gene	CG12698	16.6848	19.2029	1.15	0.87
CG7828_gene	pncr011:3L	3.53837	4.07233	1.15	0.87
CG8223_gene	CG8223	23.7343	27.3144	1.15	0.87
CG5620_gene	CG5620	11.105	12.7798	1.15	0.87
CG5362_gene	CG5362	100.463	115.614	1.15	0.87
Rab35_gene	Rab35	29.7223	34.201	1.15	0.87
CG7818_gene	CG7818	3.02123	3.47638	1.15	0.87
HLHmbeta_gene	HLHmbeta	1.00708	1.15879	1.15	0.87
fs(2)ltoPP43_gene	fs(2)ltoPP43	8.54653	9.83319	1.15	0.87
Doa_gene	CG33203	32.6619	37.578	1.15	0.87
Dhfr_gene	Dhfr	5.5253	6.35681	1.15	0.87
zf30C_gene	zf30C	35.6559	41.0213	1.15	0.87
DDB1_gene	DDB1	51.1159	58.8005	1.15	0.87
CG4325_gene	CG4325	2.50408	2.88043	1.15	0.87
Nacalpha_gene	Dgkepsilon	228.034	262.218	1.15	0.87
CG12125_gene	CG12125	3.48394	4.00611	1.15	0.87
CG11454_gene	CG11454	7.4578	8.57507	1.15	0.87
fray_gene	CG7694	77.8714	89.5251	1.15	0.87
NHP2_gene	NHP2	13.8813	15.9582	1.15	0.87
wgn_gene	wgn	9.41751	10.8264	1.15	0.87
Vps16B_gene	ca	4.95372	5.69464	1.15	0.87
Itp-r83A_gene	Nmdar1	53.3205	61.2836	1.15	0.87
CG3016_gene	CG3016	9.36308	10.7602	1.15	0.87
CG10189_gene	CG18094	4.9265	5.66153	1.15	0.87
CG14438_gene	CG14438	34.4583	39.5976	1.15	0.87
CG1354_gene	CG1354	65.351	75.0898	1.15	0.87
smg_gene	smg	11.2956	12.9785	1.15	0.87
lkb1_gene	CG9588	13.2553	15.2299	1.15	0.87
CG5445_gene	CG5445	13.7452	15.7927	1.15	0.87
CG14109_gene	CG14109	1.95971	2.25137	1.15	0.87
lin-52_gene	lin-52	1.95971	2.25137	1.15	0.87
Nmnat_gene	Nmnat	5.38921	6.19127	1.15	0.87
CG2116_gene	CG15335	15.1878	17.4481	1.15	0.87
MED24_gene	MED24	13.6908	15.7265	1.15	0.87
unk_gene	unk	21.5024	24.6988	1.15	0.87
RhoGAP5A_gene	RhoGAP5A	4.38214	5.03247	1.15	0.87
CG15141_gene	CG15141	3.89221	4.46963	1.15	0.87
CG17219_gene	CG17219	3.89221	4.46963	1.15	0.87
drosha_gene	drosha	22.2917	25.5928	1.15	0.87
pod1_gene	pod1	36.2547	41.6172	1.15	0.87
Gbp_gene	CG5189	14.0174	16.0907	1.15	0.87
CG13506_gene	CG13506	32.3625	37.1476	1.15	0.87
CG13097_gene	CG13097	13.0375	14.965	1.15	0.87
CG32641_gene	CG34411	7.24005	8.3102	1.15	0.87
l(1)G0230_gene	l(1)G0230	26.5106	30.4266	1.15	0.87
CG6448_gene	CG6448	67.4196	77.3743	1.15	0.87
CG31650_gene	SP555	12.9831	14.8988	1.15	0.87
CG10496_gene	CG10496	17.3108	19.865	1.15	0.87
CG7956_gene	CG7956	13.9357	15.9913	1.15	0.87
CG4069_gene	CG10688	9.60804	11.0251	1.15	0.87
CR32028_gene	CR32028	63.6907	73.0702	1.15	0.87
fbl_gene	fbl	18.6717	21.4211	1.15	0.87
CG15747_gene	CG15747	5.74305	6.58857	1.15	0.87
blp_gene	blp	5.25312	6.02572	1.15	0.87
CG4098_gene	CG32164	4.76319	5.46288	1.15	0.87
CG7903_gene	CG7903	14.7523	16.9184	1.15	0.87
Mtr3_gene	CG7757	7.13118	8.17777	1.15	0.87
CG8149_gene	CG8149	18.5356	21.2556	1.15	0.87

CG9866_gene	CG9866	6.17854	7.08519	1.15	0.87
l(2)05714_gene	CG3756	5.2259	5.99262	1.15	0.87
CG15822_gene	CG15822	3.32063	3.80746	1.15	0.87
CG10543_gene	CG10543	15.6505	17.9447	1.15	0.87
CG12343_gene	RpS15Ab	17.0658	19.5671	1.15	0.87
CG1845_gene	CG1845	20.3592	23.3414	1.15	0.87
CG1240_gene	CG1240	53.9466	61.8464	1.15	0.87
Pkc98E_gene	Pkc98E	19.8693	22.7786	1.15	0.87
Pax_gene	Pax	52.504	60.191	1.15	0.87
DppIII_gene	DppIII	110.615	126.805	1.15	0.87
CG5148_gene	CG5148	20.7947	23.838	1.15	0.87
CG10907_gene	CG10907	124.251	142.432	1.15	0.87
CG8863_gene	CG8863	154.355	176.931	1.15	0.87
CG15912_gene	Usf	1.41535	1.62231	1.15	0.87
CG17034_gene	CG17034	174.006	199.445	1.15	0.87
CG9135_gene	CG9135	4.70876	5.39667	1.15	0.87
CG18041_gene	Cad99C	8.00216	9.17102	1.15	0.87
CG12567_gene	CG12567	25.8846	29.6651	1.15	0.87
CG12128_gene	CG12128	76.5921	87.7703	1.15	0.87
bor_gene	bor	13.1192	15.0312	1.15	0.87
CG7694_gene	CG7694	83.3967	95.5508	1.15	0.87
Pak_gene	Pak	14.5073	16.6204	1.15	0.87
l(2)gl_gene	l(2)gl	55.6613	63.7667	1.15	0.87
rept_gene	rept	7.92051	9.0717	1.15	0.87
CG3008_gene	CG3008	8.84593	10.1312	1.15	0.87
Dek_gene	Dek	70.2775	80.4865	1.15	0.87
Sbf_gene	HisCl1	14.4257	16.5211	1.15	0.87
lark_gene	lark	16.2493	18.6069	1.15	0.87
CG9922_gene	CG3061	8.356	9.56832	1.15	0.87
snf_gene	snf	21.8018	24.9637	1.15	0.87
Pka-C3_gene	Pka-C3	20.3865	23.3414	1.14	0.87
drpr_gene	drpr	25.939	29.6982	1.14	0.87
vas_gene	vas	26.4017	30.2279	1.14	0.87
pgant3_gene	pgant3	8.32878	9.53521	1.14	0.87
Rpb10_gene	Rpb10	6.01523	6.88654	1.14	0.87
CG8315_gene	CG8315	5.06259	5.79397	1.14	0.87
CG17295_gene	CG17295	3.21175	3.67503	1.14	0.87
CG9257_gene	CG9257	32.0359	36.651	1.14	0.87
Rga_gene	Rga	46.6793	53.4038	1.14	0.87
mei-S332_gene	Vrp1	2.28633	2.61556	1.14	0.87
rtGEF_gene	rtGEF	11.4044	13.0447	1.14	0.87
Pfk_gene	Pfk	33.2879	38.0746	1.14	0.87
Cap-D3_gene	Cap-D3	31.0016	35.4591	1.14	0.87
CG7987_gene	CG7987	25.0408	28.6387	1.14	0.87
CG6729_gene	CG6729	11.7855	13.4751	1.14	0.87
meso18E_gene	meso18E	3.62003	4.13855	1.14	0.87
put_gene	put	17.1747	19.6333	1.14	0.87
CG13630_gene	Rpb10	8.57375	9.80008	1.14	0.87
CG12213_gene	CG12213	4.05552	4.63517	1.14	0.87
POSH_gene	POSH	4.05552	4.63517	1.14	0.87
l(1)G0232_gene	l(1)G0232	20.7131	23.6725	1.14	0.87
CG3160_gene	CG3160	5.85192	6.68789	1.14	0.88
mRpL10_gene	mRpL10	5.38921	6.15816	1.14	0.88
CG32721_gene	CG32721	8.08382	9.23724	1.14	0.88
yellow-c_gene	yellow-c	5.8247	6.65478	1.14	0.88
gukh_gene	gukh	10.2885	11.7535	1.14	0.88
Hel89B_gene	Hel89B	30.8655	35.2604	1.14	0.88
EDTP_gene	Lhr	20.1143	22.9772	1.14	0.88
CG13603_gene	CG13603	16.9842	19.4015	1.14	0.88
26-29-p_gene	26-29-p	20.9853	23.9705	1.14	0.88

CG6659_gene	CG6659	17.3925	19.865	1.14	0.88
CG1623_gene	CG1623	118.889	135.777	1.14	0.88
CG6879_gene	CG6879	1.33369	1.52299	1.14	0.88
CG12818_gene	CG12818	2.66739	3.04597	1.14	0.88
babo_gene	babo	27.9804	31.9496	1.14	0.88
ferrochelatase_gene	rrochelatas	8.43766	9.63454	1.14	0.88
U2af50_gene	U2af50	30.5933	34.9293	1.14	0.88
CG4822_gene	CG4822	3.10288	3.5426	1.14	0.88
CG8445_gene	CG8443	3.10288	3.5426	1.14	0.88
cos_gene	cos	3.10288	3.5426	1.14	0.88
cora_gene	cora	96.5976	110.284	1.14	0.88
CG14748_gene	CG14748	7.97495	9.1048	1.14	0.88
CG31673_gene	CG31673	11.5133	13.144	1.14	0.88
Treh_gene	Treh	248.72	283.937	1.14	0.88
CG12091_gene	CG12091	20.7947	23.7387	1.14	0.88
l(1)G0004_gene	l(1)G0004	14.589	16.6535	1.14	0.88
blue_gene	blue	11.4861	13.1109	1.14	0.88
Mekk1_gene	CG14302	37.0985	42.3456	1.14	0.88
CG8321_gene	CG8321	6.17854	7.05208	1.14	0.88
l(1)G0020_gene	CG1785	8.81871	10.0649	1.14	0.88
CG34228_gene	CG34228	3.07566	3.50949	1.14	0.88
EcR_gene	EcR	15.7866	18.011	1.14	0.88
Gdh_gene	CG5854	55.4708	63.2701	1.14	0.88
CG17508_gene	CG17508	71.5023	81.5459	1.14	0.88
Aats-thr_gene	Aats-thr	58.8458	67.1107	1.14	0.88
CG1244_gene	CG1244	80.1577	91.4122	1.14	0.88
CG7889_gene	CG7889	6.96787	7.94601	1.14	0.88
CG4557_gene	CG4557	24.7958	28.2746	1.14	0.88
CG11208_gene	CG11048	13.9085	15.8589	1.14	0.88
CG3925_gene	CG3925	11.2956	12.8792	1.14	0.88
hyd_gene	dmt	81.192	92.571	1.14	0.88
faf_gene	faf	81.818	93.2663	1.14	0.88
r-l_gene	AnnIX	16.4126	18.7062	1.14	0.88
CG6259_gene	CG6259	15.5144	17.6799	1.14	0.88
shep_gene	shep	106.233	121.044	1.14	0.88
CG32000_gene	CG32000	67.4468	76.8445	1.14	0.88
CG30084_gene	CG30084	60.86	69.3289	1.14	0.88
LIMK1_gene	LIMK1	11.1323	12.6805	1.14	0.88
Hr38_gene	CG2617	78.2525	89.1278	1.14	0.88
CG5608_gene	CG5608	6.83178	7.78047	1.14	0.88
CG8788_gene	CG8788	20.9036	23.8049	1.14	0.88
CG12129_gene	CG12129	8.9548	10.1974	1.14	0.88
CG6020_gene	CG5130	106.587	121.375	1.14	0.88
dbo_gene	dbo	16.1949	18.4414	1.14	0.88
CG32694_gene	CG32694	69.4065	79.0297	1.14	0.88
CG7220_gene	CG7220	15.2967	17.415	1.14	0.88
CG31344_gene	CG31344	2.12302	2.41691	1.14	0.88
CG15642_gene	CG15642	7.62111	8.67439	1.14	0.88
CG10214_gene	Lsd-1	8.46487	9.63454	1.14	0.88
CG34126_gene	CG34126	42.3244	48.1727	1.14	0.88
CG9391_gene	CG9391	22.4278	25.5266	1.14	0.88
Gug_gene	Gug	28.3342	32.2476	1.14	0.88
pll_gene	TfIIA-L	7.18562	8.17777	1.14	0.88
Hnf4_gene	Hnf4	13.5002	15.3623	1.14	0.88
Bub3_gene	ppk19	6.75012	7.68114	1.14	0.88
CG13611_gene	CG13611	0.843766	0.960143	1.14	0.88
CG9009_gene	CG9009	19.8149	22.5468	1.14	0.88
RhoGAP68F_gene	RhoGAP68	17.6919	20.1299	1.14	0.88
CG10731_gene	Aats-cys	14.3168	16.2893	1.14	0.88
Ext2_gene	Aats-cys	14.3168	16.2893	1.14	0.88

CG11265_gene	CG11265	21.0397	23.9374	1.14	0.88
mew_gene	mew	26.0206	29.5989	1.14	0.88
CG5589_gene	CG5589	5.03538	5.72775	1.14	0.88
Tsp42Ej_gene	Tsp42Ej	5.03538	5.72775	1.14	0.88
CG7988_gene	CG7183	3.34784	3.80746	1.14	0.88
CG6145_gene	CG6145	52.2046	59.3633	1.14	0.88
CG14998_gene	CG14998	75.5578	85.9162	1.14	0.88
CG3288_gene	CG3288	3.75612	4.27098	1.14	0.88
CG4030_gene	CG4030	11.6766	13.2765	1.14	0.88
Gp150_gene	Gp150	83.3695	94.7893	1.14	0.88
RpS9_gene	RpS9	279.776	318.072	1.14	0.88
CG7356_gene	CG7356	37.4523	42.5774	1.14	0.88
CG7332_gene	CG7332	18.7262	21.2887	1.14	0.88
Pgm_gene	Pgm	45.7539	52.0133	1.14	0.88
CG1142_gene	CG1142	8.30156	9.43589	1.14	0.88
CG32448_gene	CG7414	3.32063	3.77436	1.14	0.88
CG8596_gene	lark	10.3702	11.7866	1.14	0.88
CG11920_gene	CG11920	4.13717	4.70139	1.14	0.88
TH1_gene	TH1	21.7746	24.732	1.14	0.88
CG5645_gene	CG11534	11.4861	13.0447	1.14	0.88
msl-1_gene	msl-1	16.7664	19.0373	1.14	0.88
CG7686_gene	CG7686	142.705	162.032	1.14	0.88
mRpL33_gene	mRpL33	1.63309	1.85407	1.14	0.88
CG14502_gene	sbb	0.816547	0.927035	1.14	0.88
CG33090_gene	CG33090	1.22482	1.39055	1.14	0.88
Nup62_gene	Nup62	9.79857	11.1244	1.14	0.88
CG31530_gene	CG31530	2.85792	3.24462	1.14	0.88
CG6115_gene	CG6115	45.2912	51.4173	1.14	0.88
Chd64_gene	Chd64	157.022	178.256	1.14	0.88
CG1550_gene	CG1550	16.712	18.9711	1.14	0.88
CG3530_gene	eIF2B-delta	14.2624	16.19	1.14	0.88
l(2)05070_gene	CG8389	26.8644	30.4928	1.14	0.88
Txl_gene	Txl	29.2868	33.2408	1.14	0.88
CG32536_gene	CG32537	5.28034	5.99262	1.13	0.88
sima_gene	sima	80.7838	91.6771	1.13	0.88
Eap_gene	Eap	8.51931	9.66765	1.13	0.88
wupA_gene	wupA	131.764	149.517	1.13	0.88
CSN7_gene	CSN7	14.9973	17.0177	1.13	0.88
CycC_gene	CG33332	3.64724	4.13855	1.13	0.88
CG4866_gene	CG4866	3.64724	4.13855	1.13	0.88
CG10107_gene	CG10107	28.3614	32.1813	1.13	0.88
mura_gene	mura	37.2346	42.2463	1.13	0.88
CG10527_gene	CG10527	29.9401	33.9692	1.13	0.88
Vang_gene	Vang	15.3511	17.415	1.13	0.88
CG18619_gene	CG18619	12.5204	14.2035	1.13	0.88
CG2656_gene	CG2656	18.9439	21.4873	1.13	0.88
CG17186_gene	CG17186	2.01415	2.28448	1.13	0.88
CG7928_gene	Axn	5.63418	6.38992	1.13	0.88
CG6163_gene	CG6163	5.2259	5.9264	1.13	0.88
CG7638_gene	CG7638	6.83178	7.74736	1.13	0.88
hay_gene	hay	8.43766	9.56832	1.13	0.88
CG4804_gene	CG4804	1.60588	1.82096	1.13	0.88
Top2_gene	Top2	38.8677	44.0673	1.13	0.88
CG9149_gene	CG9149	14.8067	16.7859	1.13	0.88
CG31102_gene	CG31102	1.1976	1.35744	1.13	0.88
MESR4_gene	MESR4	29.8856	33.8699	1.13	0.88
Atg1_gene	Atg1	23.4893	26.6191	1.13	0.88
l(1)G0431_gene	l(1)G0431	15.4872	17.5474	1.13	0.88
CG4662_gene	CG4662	19.0528	21.5867	1.13	0.88
CG1677_gene	CG1677	28.5792	32.38	1.13	0.88

CG31688_gene	CG31688	13.092	14.8326	1.13	0.88
CG32816_gene	CG3777	40.0653	45.3916	1.13	0.88
CG33324_gene	CG33324	3.56559	4.03922	1.13	0.88
CG9890_gene	CG9890	3.56559	4.03922	1.13	0.88
Axn_gene	Axn	15.4327	17.4812	1.13	0.88
cpo_gene	cpo	228.143	258.411	1.13	0.88
CG9581_gene	CG9577	9.09089	10.2967	1.13	0.88
CG8211_gene	CG8211	14.2079	16.0907	1.13	0.88
CG12428_gene	btz	2.36799	2.68178	1.13	0.88
mRpS18C_gene	mRpS18C	1.57866	1.78785	1.13	0.88
atl_gene	atl	97.6591	110.582	1.13	0.88
Pp2B-14D_gene	Pp2B-14D	34.6488	39.2334	1.13	0.88
Ect4_gene	Ect4	131.872	149.319	1.13	0.88
CG4140_gene	dyn-p25	4.3277	4.90004	1.13	0.88
pr_gene	bwa	24.3875	27.6124	1.13	0.88
l(2)efl_gene	CG5431	23.5982	26.7185	1.13	0.88
CG8778_gene	CG8778	7.86607	8.90615	1.13	0.88
CG33977_gene	CG33977	3.53837	4.00611	1.13	0.88
CG31739_gene	CG31739	16.086	18.2096	1.13	0.88
CG17111_gene	CG17111	25.0952	28.407	1.13	0.88
Syx13_gene	Syx13	7.83885	8.87305	1.13	0.88
Snap24_gene	Snap24	5.87914	6.65478	1.13	0.88
Mkk4_gene	Mkk4	39.1943	44.3652	1.13	0.88
CG3803_gene	CG3803	3.91943	4.43652	1.13	0.88
psq_gene	psq	42.7054	48.3382	1.13	0.88
snama_gene	snama	16.0588	18.1765	1.13	0.88
CG5325_gene	CG5325	14.4801	16.3886	1.13	0.88
Sulf1_gene	Sulf1	19.951	22.5799	1.13	0.88
CG6225_gene	CG6225	8.19269	9.27035	1.13	0.88
aPKC_gene	CG10257	13.2553	14.9981	1.13	0.88
CG17177_gene	CG17177	29.2324	33.0753	1.13	0.88
uzip_gene	uzip	19.4883	22.0502	1.13	0.88
Hlc_gene	Hlc	59.118	66.8789	1.13	0.88
CG14194_gene	CG14194	37.534	42.4449	1.13	0.88
bsf_gene	bsf	23.2172	26.2549	1.13	0.88
CG13220_gene	CG13220	23.9521	27.0827	1.13	0.88
CG3353_gene	CG3353	4.24605	4.80071	1.13	0.88
l(1)G0003_gene	l(1)G0003	21.6113	24.434	1.13	0.88
CG1416_gene	CG1416	29.6951	33.5719	1.13	0.88
CG18622_gene	CG18622	18.8895	21.3549	1.13	0.88
l(2)09851_gene	l(2)09851	10.0163	11.3231	1.13	0.88
CG8314_gene	CG8314	7.70276	8.7075	1.13	0.88
CG6841_gene	CG6841	11.5405	13.0447	1.13	0.88
inx3_gene	CG31048	8.84593	9.99873	1.13	0.88
Act57B_gene	Act57B	822.29	929.418	1.13	0.88
CG3719_gene	SNF1A	14.2079	16.0576	1.13	0.88
kin17_gene	kin17	11.5133	13.0116	1.13	0.88
l(3)01239_gene	l(3)01239	31.056	35.0949	1.13	0.88
CG12304_gene	CG12304	15.7049	17.7461	1.13	0.88
CG12264_gene	CG12264	16.8481	19.0373	1.13	0.89
JIL-1_gene	JIL-1	58.9547	66.6141	1.13	0.89
chrb_gene	chrb	21.8018	24.6326	1.13	0.89
CG30415_gene	CG30415	30.2123	34.1347	1.13	0.89
CG17153_gene	CG17153	10.3157	11.6541	1.13	0.89
MED14_gene	MED14	23.6799	26.7516	1.13	0.89
AGO1_gene	AGO1	98.0673	110.781	1.13	0.89
CG16779_gene	CG16779	0.762111	0.860818	1.13	0.89
CG6108_gene	CG6043	7.62111	8.60818	1.13	0.89
Reg-5_gene	Reg-5	11.4044	12.8792	1.13	0.89
Eip93F_gene	Eip93F	133.968	151.272	1.13	0.89

CG3552_gene	CG3437	11.7583	13.2765	1.13	0.89
TfIIEbeta_gene	TfIIEbeta	4.54545	5.1318	1.13	0.89
CG5510_gene	Apc2	12.4932	14.1042	1.13	0.89
Trap1_gene	Trap1	24.197	27.3144	1.13	0.89
CG7172_gene	CG7172	12.0849	13.6407	1.13	0.89
CG8334_gene	CG8334	15.1061	17.0508	1.13	0.89
CG11583_gene	CG1311	10.9417	12.3494	1.13	0.89
CG9740_gene	CG9740	2.25911	2.54935	1.13	0.89
CG7430_gene	CG7430	57.2128	64.5613	1.13	0.89
CG33170_gene	CG33170	6.39629	7.21763	1.13	0.89
ics_gene	ics	18.0185	20.3285	1.13	0.89
betaTub97EF_gene	etaTub97E	26.6194	30.0293	1.13	0.89
UGP_gene	PGRP-LF	61.7854	69.6931	1.13	0.89
Prosbeta3_gene	CG11980	37.0713	41.8159	1.13	0.89
CG33331_gene	CG33331	1.497	1.68853	1.13	0.89
Uhg1_gene	Uhg1	1.497	1.68853	1.13	0.89
oaf_gene	oaf	4.49101	5.06558	1.13	0.89
Rho1_gene	Rho1	240.364	271.091	1.13	0.89
CG13512_gene	CG13512	5.60696	6.3237	1.13	0.89
ced-6_gene	ced-6	30.6205	34.532	1.13	0.89
shakB_gene	shakB	3.7289	4.20476	1.13	0.89
Dcr-2_gene	Rab4	42.4877	47.9078	1.13	0.89
A3-3_gene	A3-3	42.0522	47.4112	1.13	0.89
CG6751_gene	CG6751	31.6276	35.6577	1.13	0.89
gk_gene	gk	3.34784	3.77436	1.13	0.89
tub_gene	tub	4.46379	5.03247	1.13	0.89
CG13162_gene	CG13162	1.11595	1.25812	1.13	0.89
CG30491_gene	CG17985	2.2319	2.51624	1.13	0.89
mtTFB2_gene	mtTFB2	2.2319	2.51624	1.13	0.89
CG10948_gene	CG10948	18.209	20.5272	1.13	0.89
Hsp60_gene	Hsp60	43.4403	48.9673	1.13	0.89
ben_gene	ben	61.8671	69.7262	1.13	0.89
Mys45A_gene	tsu	34.0772	38.4057	1.13	0.89
Psf1_gene	Psf1	8.51931	9.60143	1.13	0.89
l(1)G0136_gene	l(1)G0136	3.70168	4.17166	1.13	0.89
Fib_gene	Fib	19.9782	22.5137	1.13	0.89
CG41284_gene	CG41284	4.43657	4.99936	1.13	0.89
CG2698_gene	CG2698	25.8573	29.1354	1.13	0.89
e(y)1_gene	e(y)1	9.22699	10.396	1.13	0.89
CG9320_gene	CG9320	13.2825	14.965	1.13	0.89
nct_gene	nct	25.4491	28.6719	1.13	0.89
CG13671_gene	CG7197	11.4317	12.8792	1.13	0.89
CG1530_gene	CG1530	12.1666	13.7069	1.13	0.89
CG30440_gene	CG30440	0.734893	0.827709	1.13	0.89
CG7993_gene	CG7993	9.17255	10.3298	1.13	0.89
sec10_gene	sec10	14.6706	16.5211	1.13	0.89
tun_gene	tun	4.76319	5.36356	1.13	0.89
Tango2_gene	Tango2	3.29341	3.70814	1.13	0.89
CG2233_gene	CG2233	23.0539	25.957	1.13	0.89
CG32085_gene	CG32085	245.372	276.256	1.13	0.89
CG9003_gene	CG9003	8.41044	9.469	1.13	0.89
CG2931_gene	CG2931	6.94065	7.81358	1.13	0.89
MED17_gene	MED17	6.20576	6.98587	1.13	0.89
hop_gene	CG11750	18.6173	20.9576	1.13	0.89
mRpL32_gene	mRpL32	2.91235	3.27773	1.13	0.89
Nipped-A_gene	Nipped-A	58.247	65.5546	1.13	0.89
CG4390_gene	CG4390	31.301	35.2273	1.13	0.89
Actr13E_gene	l(1)G0136	10.5335	11.8528	1.13	0.89
CG8306_gene	CG8306	39.9292	44.9281	1.13	0.89
CG5558_gene	nos	9.79857	11.0251	1.13	0.89

CG7047_gene	CG7047	2.17746	2.45002	1.13	0.89
cln3_gene	cln3	12.3299	13.8724	1.13	0.89
CG9247_gene	CG9248	37.3434	42.0145	1.13	0.89
jar_gene	jar	89.9019	101.146	1.13	0.89
PGRP-LC_gene	PGRP-LC	14.8612	16.7197	1.13	0.89
Cat_gene	Cat	36.5813	41.1537	1.12	0.89
CG4199_gene	CG4199	16.6576	18.7393	1.12	0.89
CG15084_gene	CG15084	2.5313	2.84732	1.12	0.89
Nedd4_gene	Nedd4	46.271	52.0464	1.12	0.89
Ranbp11_gene	Ranbp11	13.718	15.4285	1.12	0.89
128up_gene	128up	26.7011	30.0293	1.12	0.89
CG8679_gene	CG8678	2.88513	3.24462	1.12	0.89
CG31999_gene	CG31999	30.5933	34.3996	1.12	0.89
CG18858_gene	CG18858	24.4692	27.5131	1.12	0.89
CG9117_gene	CG9117	1.7964	2.01961	1.12	0.89
IM4_gene	IM4	3.59281	4.03922	1.12	0.89
CG1407_gene	CG12128	39.8475	44.7956	1.12	0.89
CG15160_gene	CG15160	8.24713	9.27035	1.12	0.89
wit_gene	dib	10.3974	11.6873	1.12	0.89
CG12090_gene	CG12090	27.2455	30.6252	1.12	0.89
CG5360_gene	CG5360	6.80456	7.64804	1.12	0.89
CG6665_gene	CG6665	16.1132	18.1103	1.12	0.89
CG32528_gene	CG32528	16.0588	18.0441	1.12	0.89
Pros28.1_gene	Pros28.1	36.7446	41.2861	1.12	0.89
CG1233_gene	CG1233	14.2624	16.0245	1.12	0.89
CG8449_gene	Su(var)3-7	7.83885	8.80683	1.12	0.89
CG3967_gene	CG3689	67.964	76.3479	1.12	0.89
CG2263_gene	CG2263	35.9009	40.326	1.12	0.89
CG10803_gene	CG10803	7.81164	8.77372	1.12	0.89
CG18812_gene	CG18812	97.904	109.953	1.12	0.89
CG11319_gene	CG11319	23.4077	26.2881	1.12	0.89
CG1236_gene	CG1236	26.2384	29.4665	1.12	0.89
CG7995_gene	CG7995	12.7654	14.3359	1.12	0.89
CG15352_gene	CG15352	0.707674	0.794601	1.12	0.89
CG16787_gene	thoc5	2.12302	2.3838	1.12	0.89
CG32082_gene	CG32082	6.36907	7.15141	1.12	0.89
CG33228_gene	CG33228	2.47686	2.7811	1.12	0.89
CG9870_gene	CG9870	1.41535	1.5892	1.12	0.89
CG11586_gene	CG1309	10.2613	11.5217	1.12	0.89
CG5142_gene	CG5142	60.0707	67.4418	1.12	0.89
mei-P26_gene	mei-P26	11.6494	13.0778	1.12	0.89
CG8297_gene	CG8297	17.2836	19.4015	1.12	0.89
CG13850_gene	CG13855	4.9265	5.5291	1.12	0.89
Rheb_gene	Rheb	35.5198	39.8625	1.12	0.89
CG17904_gene	CG17904	13.0103	14.6008	1.12	0.89
Cyp4aa1_gene	Cyp4aa1	17.9096	20.0968	1.12	0.89
CG11555_gene	CG11604	10.5335	11.8197	1.12	0.89
mRpL42_gene	mRpL42	8.41044	9.43589	1.12	0.89
br_gene	br	5.25312	5.89329	1.12	0.89
Tm2_gene	Tm2	137.561	154.318	1.12	0.89
wls_gene	Alg10	7.67555	8.60818	1.12	0.89
CG18268_gene	CG18268	7.67555	8.60818	1.12	0.89
Klp64D_gene	Klp64D	9.41751	10.5616	1.12	0.89
CG9776_gene	CG9776	85.057	95.3852	1.12	0.89
RhoGEF2_gene	RhoGEF2	53.3205	59.7937	1.12	0.89
CG32163_gene	CG32163	6.96787	7.81358	1.12	0.89
CG11877_gene	CG11877	3.48394	3.90679	1.12	0.89
dpld_gene	dpld	28.9058	32.4131	1.12	0.89
CG5591_gene	CG5591	49.7822	55.8207	1.12	0.89
bru-2_gene	bru-2	127.953	143.459	1.12	0.89

Ark_gene	Ark	7.64833	8.57507	1.12	0.89
CG14618_gene	CG14618	7.64833	8.57507	1.12	0.89
Ance-3_gene	Ance-3	1.38813	1.55609	1.12	0.89
CG11769_gene	CG11769	1.38813	1.55609	1.12	0.89
CG6791_gene	wkd	15.5961	17.4812	1.12	0.89
fu2_gene	fu2	3.81055	4.27098	1.12	0.89
CG7878_gene	CG7878	48.1491	53.9667	1.12	0.89
CG3626_gene	CG3626	20.0871	22.5137	1.12	0.89
CG15547_gene	CG15547	6.23298	6.98587	1.12	0.89
CG32789_gene	CG32789	18.3451	20.5603	1.12	0.89
Gas41_gene	Gas41	2.42242	2.71489	1.12	0.89
CG14896_gene	CG14896	9.33586	10.4622	1.12	0.89
CG3663_gene	CG3663	3.45672	3.87368	1.12	0.89
CG13379_gene	CG13379	4.49101	5.03247	1.12	0.89
aop_gene	CG15382	18.9983	21.2887	1.12	0.89
CG12391_gene	CG12391	15.1878	17.0177	1.12	0.89
Not1_gene	Not1	190.664	213.615	1.12	0.89
CG32409_gene	CG32409	7.24005	8.11155	1.12	0.89
CG11357_gene	CG11357	5.17147	5.79397	1.12	0.89
Ric_gene	Ric	17.583	19.6995	1.12	0.89
CG6005_gene	CG6005	2.06859	2.31759	1.12	0.89
U2af38_gene	U2af38	12.7381	14.2697	1.12	0.89
sage_gene	sage	2.74904	3.07908	1.12	0.89
Spec2_gene	Spec2	10.9962	12.3163	1.12	0.89
CG31012_gene	CG31012	42.5966	47.7092	1.12	0.89
fh_gene	fh	1.71475	1.92029	1.12	0.89
GATAd_gene	GATAd	9.2542	10.3629	1.12	0.89
GlyP_gene	GlyP	52.0957	58.337	1.12	0.89
CG11943_gene	CG11943	13.3642	14.965	1.12	0.89
gdl_gene	Z600	2.39521	2.68178	1.12	0.89
gdl-ORF39_gene	Z600	2.39521	2.68178	1.12	0.89
cdc14_gene	cdc14	25.9662	29.0692	1.12	0.89
CG7955_gene	CG7955	25.9662	29.0692	1.12	0.89
CG32413_gene	CG32413	27.6265	30.9232	1.12	0.89
CG17331_gene	CG17331	20.0871	22.4806	1.12	0.89
CG14367_gene	CG14367	3.40228	3.80746	1.12	0.89
CG10376_gene	CG10341	24.823	27.7779	1.12	0.89
Mov34_gene	Mov34	37.8878	42.3787	1.12	0.89
14-3-3epsilon_gene	4-3-3epsilo	299.265	334.726	1.12	0.89
Dys_gene	Dys	78.0619	87.3068	1.12	0.89
enok_gene	enok	32.7435	36.6179	1.12	0.89
CG3734_gene	Ino80	6.06967	6.78722	1.12	0.89
sec24_gene	CG12744	48.1763	53.8673	1.12	0.89
CG14709_gene	CG14709	28.2798	31.6185	1.12	0.89
Pi3K92E_gene	Pi3K92E	19.4883	21.7853	1.12	0.89
CG11574_gene	CG11574	1.00708	1.12568	1.12	0.89
futsch_gene	futsch	1.00708	1.12568	1.12	0.89
hiw_gene	hiw	65.106	72.7722	1.12	0.89
Smr_gene	Smr	39.9292	44.6301	1.12	0.89
Dp_gene	CG4643	36.2003	40.4584	1.12	0.89
CG6928_gene	CG6928	69.3521	77.5067	1.12	0.89
MED15_gene	MED15	13.718	15.3292	1.12	0.89
c12.1_gene	c12.1	10.6968	11.9521	1.12	0.89
CG11982_gene	CG11982	12.3571	13.8062	1.12	0.90
CG14375_gene	CG14375	1.33369	1.48988	1.12	0.90
CG8032_gene	CG8032	4.00108	4.46963	1.12	0.90
slo_gene	slo	4.00108	4.46963	1.12	0.90
eIF2B-alpha_gene	CG7866	6.66847	7.44938	1.12	0.90
Paf-AHalpha_gene	Paf-AHalpha	9.33586	10.4291	1.12	0.90
Tim8_gene	Tim8	12.3299	13.7731	1.12	0.90

CG12400_gene	CG12400	9.66248	10.7933	1.12	0.90
CG7671_gene	CG7671	4.3277	4.83382	1.12	0.90
CG11050_gene	CG11050	76.1294	85.0223	1.12	0.90
BRWD3_gene	BRWD3	35.9009	40.0942	1.12	0.90
CG12909_gene	CG12909	4.98094	5.56221	1.12	0.90
Unr_gene	Unr	69.0255	77.0763	1.12	0.90
CG6511_gene	CG6511	5.30756	5.9264	1.12	0.90
CG8915_gene	CG8915	5.30756	5.9264	1.12	0.90
CG13016_gene	CG13016	3.97386	4.43652	1.12	0.90
melt_gene	melt	3.97386	4.43652	1.12	0.90
rhea_gene	rhea	96.1893	107.37	1.12	0.90
CG3156_gene	CG3156	2.31355	2.58245	1.12	0.90
HERC2_gene	HERC2	18.835	21.0238	1.12	0.90
CG1674_gene	CG1674	29.0691	32.4462	1.12	0.90
CG34449_gene	CG34449	5.28034	5.89329	1.12	0.90
Ras64B_gene	Rop	47.4686	52.9734	1.12	0.90
CG3887_gene	CG3887	34.921	38.9686	1.12	0.90
alpha-Spec_gene	alpha-Spec	138.595	154.649	1.12	0.90
CG6393_gene	CG6393	19.08	21.2887	1.12	0.90
mRpL18_gene	tafazzin	3.94665	4.40341	1.12	0.90
wdb_gene	wdb	41.7256	46.5504	1.12	0.90
Grip128_gene	Grip128	9.82579	10.9589	1.12	0.90
Fcp3C_gene	Fcp3C	14.7251	16.4218	1.12	0.90
lace_gene	lace	16.0315	17.8785	1.12	0.90
Kap-alpha3_gene	Kap-alpha3	90.8273	101.279	1.12	0.90
CG5844_gene	CG5844	9.79857	10.9258	1.12	0.90
CG32772_gene	CG32772	21.2302	23.6725	1.12	0.90
Myo61F_gene	Myo61F	5.55252	6.19127	1.12	0.90
mRpS16_gene	mRpS16	5.2259	5.82707	1.12	0.90
ik2_gene	ik2	13.3914	14.9319	1.12	0.90
CG10600_gene	CG10600	29.9673	33.4064	1.11	0.90
eco_gene	eco	28.3342	31.5854	1.11	0.90
CG6405_gene	CG6405	44.9373	50.093	1.11	0.90
CG30499_gene	CG30499	7.1584	7.97912	1.11	0.90
l(3)73Ah_gene	CG32163	13.3369	14.8657	1.11	0.90
Phax_gene	Phax	6.50516	7.25073	1.11	0.90
l(2)03709_gene	l(2)03709	25.694	28.6387	1.11	0.90
CG9821_gene	CG9821	87.4522	97.4711	1.11	0.90
Syx7_gene	Syx7	17.2291	19.2029	1.11	0.90
CG16935_gene	CG13343	10.0435	11.1906	1.11	0.90
CG9934_gene	CG9934	27.5176	30.6584	1.11	0.90
Nckx30C_gene	Nckx30C	2.58573	2.88043	1.11	0.90
CG8707_gene	CG8707	14.5345	16.19	1.11	0.90
sec71_gene	sec71	70.087	78.0696	1.11	0.90
CG12413_gene	CG12413	2.25911	2.51624	1.11	0.90
or_gene	or	6.77734	7.54871	1.11	0.90
CG16953_gene	CG16953	64.2078	71.5141	1.11	0.90
mRpL24_gene	CG14044	12.9014	14.369	1.11	0.90
vap_gene	vap	31.6004	35.1942	1.11	0.90
CG8289_gene	CG8289	15.7866	17.5805	1.11	0.90
CG13923_gene	CG12022	3.53837	3.9399	1.11	0.90
CG13319_gene	CG13319	1.60588	1.78785	1.11	0.90
lack_gene	lack	19.2433	21.4211	1.11	0.90
CG17768_gene	CG17768	8.6554	9.63454	1.11	0.90
LSm-4_gene	CG17768	8.6554	9.63454	1.11	0.90
CG32560_gene	CG32560	36.4724	40.5909	1.11	0.90
crm_gene	CG2712	5.11703	5.69464	1.11	0.90
CG12084_gene	CG12084	11.1867	12.4487	1.11	0.90
CG5794_gene	CG5794	29.3957	32.7111	1.11	0.90
CG11107_gene	CG11107	27.4632	30.559	1.11	0.90

RhoGAP93B_gene	RhoGAP93B	3.51115	3.90679	1.11	0.90
CG32663_gene	CG32663	111.078	123.594	1.11	0.90
CG1972_gene	CG1972	18.4812	20.5603	1.11	0.90
RhoGAPp190_gene	hoGAPp19	33.7234	37.5118	1.11	0.90
Pli_gene	Pli	37.534	41.7497	1.11	0.90
CG14253_gene	CG14253	6.99509	7.78047	1.11	0.90
spin_gene	spin	37.1801	41.3524	1.11	0.90
CG3328_gene	CG3328	1.90528	2.11894	1.11	0.90
CG17221_gene	CG17221	10.7784	11.9852	1.11	0.90
PP2A-B'_gene	PP2A-B'	46.2166	51.3842	1.11	0.90
Zpr1_gene	Zpr1	12.6565	14.0711	1.11	0.90
CG10809_gene	CG10809	4.73597	5.26423	1.11	0.90
CG18476_gene	CG14715	4.73597	5.26423	1.11	0.90
CG11268_gene	CG11268	1.57866	1.75474	1.11	0.90
Or59c_gene	CG34372	31.5459	35.0618	1.11	0.90
Med_gene	CycG	18.5901	20.6596	1.11	0.90
LpR2_gene	LpR2	14.8067	16.4549	1.11	0.90
CG11138_gene	CG11138	22.9178	25.4603	1.11	0.90
metl_gene	metl	5.9608	6.62168	1.11	0.90
ran_gene	ran	93.1681	103.497	1.11	0.90
CG4991_gene	CG4991	64.2078	71.3154	1.11	0.90
CG10306_gene	CG10306	76.1022	84.5257	1.11	0.90
CG32234_gene	CG32234	1.87806	2.08583	1.11	0.90
CG10949_gene	CG10949	3.1301	3.47638	1.11	0.90
mRpL3_gene	mRpL3	6.2602	6.95276	1.11	0.90
mad2_gene	CG5537	1.25204	1.39055	1.11	0.90
MED19_gene	MED19	8.43766	9.36967	1.11	0.90
PR2_gene	PR2	7.81164	8.67439	1.11	0.90
Gga_gene	Gga	17.7735	19.7326	1.11	0.90
Mmp1_gene	Pof	6.23298	6.91965	1.11	0.90
CG1815_gene	CG1815	71.0396	78.8642	1.11	0.90
CG7718_gene	CG7718	2.80348	3.11219	1.11	0.90
CG6014_gene	CG6014	136.989	152.067	1.11	0.90
CG12042_gene	CG2064	13.6908	15.1967	1.11	0.90
CG6479_gene	CG6479	2.17746	2.41691	1.11	0.90
mRpS7_gene	mRpS7	17.4197	19.3353	1.11	0.90
CG33275_gene	CG33275	38.5683	42.8091	1.11	0.90
Tal_gene	Tal	30.4572	33.8037	1.11	0.90
CG11055_gene	CG11055	14.9156	16.5542	1.11	0.90
CG31522_gene	CG31522	63.9629	70.9844	1.11	0.90
lectin-30A_gene	lectin-30A	2049.97	2274.81	1.11	0.90
LanB1_gene	LanB1	83.1245	92.2399	1.11	0.90
Nup107_gene	Nup107	15.8138	17.5474	1.11	0.90
CG5381_gene	CG4972	22.319	24.7651	1.11	0.90
SNF4Agamma_gene	NF4Agamm	66.3309	73.5999	1.11	0.90
CG8494_gene	CG8494	18.5901	20.6265	1.11	0.90
l(1)G0156_gene	l(1)G0156	38.0783	42.2463	1.11	0.90
Src64B_gene	Src64B	16.712	18.5407	1.11	0.90
pncr013:4_gene	pncr013:4	4.3277	4.80071	1.11	0.90
Sas_gene	Sas	0.92542	1.02636	1.11	0.90
dlg1_gene	dlg1	68.7261	76.2155	1.11	0.90
Taf5_gene	CG6751	10.7784	11.9521	1.11	0.90
CG11122_gene	CG11122	10.1524	11.2568	1.11	0.90
CG11151_gene	l(1)dd4	40.283	44.6632	1.11	0.90
Rab7_gene	Rab7	129.423	143.492	1.11	0.90
CG31381_gene	CG11089	4.30048	4.76761	1.11	0.90
CG10825_gene	CG10825	2.15024	2.3838	1.11	0.90
Smc5_gene	Smc5	2.15024	2.3838	1.11	0.90
Rad23_gene	Rad23	66.0042	73.1695	1.11	0.90
CG12054_gene	CG12054	19.325	21.4211	1.11	0.90

Khc_gene	Khc	92.2699	102.272	1.11	0.90
CG8072_gene	dpr10	25.7212	28.5063	1.11	0.90
PQBP-1_gene	PQBP-1	1.22482	1.35744	1.11	0.90
l(1)G0222_gene	l(1)G0222	38.2144	42.3456	1.11	0.90
CG14023_gene	CG14023	22.2917	24.6988	1.11	0.90
TpnC47D_gene	TpnC47D	12.8198	14.2035	1.11	0.90
msk_gene	msk	85.7375	94.9879	1.11	0.90
CG14231_gene	CG14231	1.52422	1.68853	1.11	0.90
ftz-f1_gene	ftz-f1	13.092	14.5015	1.11	0.90
Aats-leu_gene	Aats-leu	8.51931	9.43589	1.11	0.90
Ubc-E2H_gene	Ubc-E2H	69.0527	76.4804	1.11	0.90
CG8086_gene	CG8086	6.99509	7.74736	1.11	0.90
CG2970_gene	CG2970	8.81871	9.76697	1.11	0.90
CkIIbeta_gene	CkIIbeta	44.6651	49.4639	1.11	0.90
CG2950_gene	CG2950	20.6586	22.8779	1.11	0.90
CG2540_gene	CG2540	9.41751	10.4291	1.11	0.90
Nmda1_gene	Nmda1	112.33	124.388	1.11	0.90
eyg_gene	eyg	30.9471	34.2672	1.11	0.90
p120ctn_gene	p120ctn	21.5296	23.838	1.11	0.90
sun_gene	CG8578	6.66847	7.38317	1.11	0.90
CG8004_gene	CG8004	4.54545	5.03247	1.11	0.90
CG7048_gene	CG7048	16.0315	17.7461	1.11	0.90
CG14889_gene	CG14889	2.72182	3.01286	1.11	0.90
CG7971_gene	CG7971	27.2182	30.1286	1.11	0.90
CG14446_gene	CG14446	5.74305	6.35681	1.11	0.90
CG18259_gene	CG6891	6.04245	6.68789	1.11	0.90
CG9232_gene	cup	9.66248	10.694	1.11	0.90
Keap1_gene	Keap1	3.32063	3.67503	1.11	0.90
sktl_gene	insc	33.5057	37.0814	1.11	0.90
kay_gene	kay	41.3445	45.7558	1.11	0.90
pn_gene	pn	7.53945	8.34331	1.11	0.90
pgc_gene	T3dh	3.91943	4.3372	1.11	0.90
CG7338_gene	CG7338	46.1077	51.02	1.11	0.90
CG7770_gene	CG7770	11.1323	12.3163	1.11	0.90
CG4406_gene	CG4406	18.9167	20.9245	1.11	0.90
mbo_gene	mbo	11.7038	12.9454	1.11	0.90
CG2790_gene	CG3770	15.2967	16.9184	1.11	0.90
CG32529_gene	CG32529	26.3745	29.1685	1.11	0.90
Bgb_gene	Bgb	1.1976	1.32434	1.11	0.90
yellow-d2_gene	CG13551	0.598801	0.662168	1.11	0.90
CG2898_gene	CG17841	0.598801	0.662168	1.11	0.90
CG5757_gene	CG5757	0.598801	0.662168	1.11	0.90
CG9634_gene	CG9634	0.598801	0.662168	1.11	0.90
CG16742_gene	CG16742	4.79041	5.29734	1.11	0.90
Stim_gene	Stim	73.2443	80.9831	1.11	0.90
CG4552_gene	CG4552	61.5405	68.0377	1.11	0.90
CG2875_gene	CG32792	9.2542	10.2305	1.11	0.90
Taf12_gene	Taf12	8.0566	8.90615	1.11	0.90
l(2)k05819_gene	l(2)k05819	36.6902	40.5578	1.11	0.90
CG5902_gene	CG5902	13.718	15.1636	1.11	0.90
CG5346_gene	CG5346	30.3756	33.5719	1.11	0.90
CG40439_gene	CG40439	8.92758	9.8663	1.11	0.90
CG3883_gene	KH1	3.86499	4.27098	1.11	0.90
CG14130_gene	CG14130	7.43058	8.21088	1.11	0.90
CG9437_gene	CG9437	6.83178	7.54871	1.10	0.91
CG5776_gene	CG5776	3.26619	3.60881	1.10	0.91
CG5867_gene	CG5867	6.23298	6.88654	1.10	0.91
CG10724_gene	CG10724	21.0669	23.2752	1.10	0.91
His2Av_gene	His2Av	17.5013	19.3353	1.10	0.91
Oatp74D_gene	Oatp74D	2.66739	2.94665	1.10	0.91

CG10209_gene	CG10209	5.03538	5.56221	1.10	0.91
Sod_gene	Sod	66.0042	72.9046	1.10	0.91
rdx_gene	rdx	131.709	145.478	1.10	0.91
CG10144_gene	CG10144	6.80456	7.5156	1.10	0.91
CG17121_gene	CG17121	15.3783	16.9846	1.10	0.91
mRpS34_gene	mRpS34	6.20576	6.85343	1.10	0.91
CG10340_gene	CG10340	12.1121	13.3758	1.10	0.91
CG8036_gene	CG8036	141.916	156.702	1.10	0.91
CG10286_gene	CG10286	16.5215	18.2427	1.10	0.91
Imp_gene	Imp	16.5215	18.2427	1.10	0.91
hts_gene	hts	88.1871	97.3717	1.10	0.91
mRpS18B_gene	mRpS18B	3.53837	3.90679	1.10	0.91
prp8_gene	prp8	56.614	62.5086	1.10	0.91
CG8814_gene	CG8814	17.9368	19.7988	1.10	0.91
CG9226_gene	Arc-p20	2.93957	3.24462	1.10	0.91
CG17568_gene	CG17568	1.46979	1.62231	1.10	0.91
CG12753_gene	CG12753	8.51931	9.40278	1.10	0.91
Cyp6a17_gene	Cyp6a17	44.6379	49.2653	1.10	0.91
fl(2)d_gene	fl(2)d	31.9814	35.2935	1.10	0.91
CG15673_gene	CG15673	7.92051	8.74061	1.10	0.91
CG1017_gene	CG1017	12.602	13.9055	1.10	0.91
CG8481_gene	MED6	21.3935	23.6063	1.10	0.91
Art7_gene	CG3085	7.89329	8.7075	1.10	0.91
CG14650_gene	CG14650	35.3293	38.9686	1.10	0.91
CG32165_gene	CG32165	22.1829	24.4671	1.10	0.91
btsz_gene	CG14857	27.7082	30.559	1.10	0.91
CG6506_gene	CG6506	12.2482	13.5082	1.10	0.91
PH4alphaNE3_gene	H4alphaNE	441.807	487.256	1.10	0.91
CG3520_gene	CG3520	4.95372	5.46288	1.10	0.91
CG3638_gene	CG3638	14.8612	16.3886	1.10	0.91
CG31301_gene	CG31301	10.7784	11.8859	1.10	0.91
CG5541_gene	hiw	50.6804	55.8869	1.10	0.91
CG9243_gene	CG9246	11.35	12.515	1.10	0.91
CG5830_gene	CG5830	43.6036	48.0734	1.10	0.91
Cbl_gene	Cbl	15.4055	16.9846	1.10	0.91
th_gene	th	52.2862	57.6417	1.10	0.91
scyl_gene	scyl	163.827	180.606	1.10	0.91
CG5728_gene	BRWD3	46.4615	51.2187	1.10	0.91
CG16985_gene	CG12182	1.74197	1.92029	1.10	0.91
CG34174_gene	CG34174	1.74197	1.92029	1.10	0.91
CG33498_gene	CG33498	0.870984	0.960143	1.10	0.91
hyx_gene	hyx	15.0789	16.6204	1.10	0.91
CG3532_gene	CG3532	35.6559	39.2996	1.10	0.91
CG8290_gene	CG8290	11.595	12.7798	1.10	0.91
RN-tre_gene	CG8067	13.9085	15.3292	1.10	0.91
CG2983_gene	CG2983	107.185	118.131	1.10	0.91
CG14210_gene	CG14210	4.05552	4.46963	1.10	0.91
Nmd3_gene	pn	23.1627	25.5266	1.10	0.91
toe_gene	toe	237.887	262.152	1.10	0.91
CG13557_gene	CG34372	15.0245	16.5542	1.10	0.91
CG31441_gene	CG31441	1.44257	1.5892	1.10	0.91
CR40190_gene	CR40190	12.6837	13.9717	1.10	0.91
Stam_gene	Stam	29.6679	32.678	1.10	0.91
CG40500_gene	CG40500	23.326	25.6921	1.10	0.91
CG17360_gene	CG17360	5.47087	6.02572	1.10	0.91
CG32111_gene	CG32111	2.01415	2.21826	1.10	0.91
CG2774_gene	CG2774	68.1545	75.0567	1.10	0.91
CG7206_gene	CG7206	11.2139	12.3494	1.10	0.91
dco_gene	dco	52.0413	57.3106	1.10	0.91
Atg4_gene	Atg4	18.1001	19.9312	1.10	0.91

CG7222_gene	CG7222	8.90037	9.80008	1.10	0.91
CG10326_gene	CG10326	12.3299	13.5744	1.10	0.91
car_gene	car	9.44473	10.396	1.10	0.91
CG3585_gene	CG3585	107.322	118.131	1.10	0.91
milt_gene	milt	39.4937	43.4713	1.10	0.91
CG5732_gene	CG31163	1.71475	1.88718	1.10	0.91
b_gene	b	0.571583	0.629059	1.10	0.91
CG1295_gene	CG1295	0.571583	0.629059	1.10	0.91
CG17707_gene	CG17707	0.571583	0.629059	1.10	0.91
CG5869_gene	CG17328	5.71583	6.29059	1.10	0.91
CG2082_gene	CG2082	23.4349	25.7914	1.10	0.91
CG11249_gene	CG11249	1.14317	1.25812	1.10	0.91
Tap42_gene	Tap42	9.14533	10.0649	1.10	0.91
sec8_gene	sec8	19.706	21.686	1.10	0.91
CG7382_gene	CG7382	9.41751	10.3629	1.10	0.91
cathD_gene	cathD	66.7664	73.4675	1.10	0.91
r_gene	r	31.9542	35.1611	1.10	0.91
CG12340_gene	CG12340	24.7958	27.2813	1.10	0.91
CG4554_gene	CG4554	19.3794	21.3218	1.10	0.91
CG11299_gene	CG11299	9.96188	10.9589	1.10	0.91
CG33057_gene	CG33057	13.092	14.4021	1.10	0.91
CG3386_gene	CG3386	3.1301	3.44327	1.10	0.91
dom_gene	CG30394	90.419	99.4576	1.10	0.91
caup_gene	caup	12.221	13.442	1.10	0.91
CG8386_gene	CG8370	8.51931	9.36967	1.10	0.91
CG17090_gene	CG17090	35.4654	39.0017	1.10	0.91
CG5548_gene	CG5548	14.1807	15.594	1.10	0.91
Ptp69D_gene	Ptp69D	13.6091	14.965	1.10	0.91
stv_gene	stv	39.9292	43.9017	1.10	0.91
CG5660_gene	CG5660	1.41535	1.55609	1.10	0.91
Hus1-like_gene	Hus1-like	1.41535	1.55609	1.10	0.91
Neu3_gene	Neu3	8.76428	9.63454	1.10	0.91
galectin_gene	galectin	22.5911	24.8313	1.10	0.91
S6kII_gene	CG17600	9.03646	9.93251	1.10	0.91
gry_gene	CG32276	26.81	29.4665	1.10	0.91
Syn_gene	Syn	34.9754	38.4388	1.10	0.91
trbl_gene	trbl	11.8399	13.0116	1.10	0.91
rno_gene	rno	24.4964	26.9171	1.10	0.91
lap_gene	lap	31.5187	34.6314	1.10	0.91
Syx17_gene	Syx17	10.969	12.0514	1.10	0.91
NPC1_gene	NPC1	92.4059	101.51	1.10	0.91
Atg6_gene	Atg6	11.7855	12.9454	1.10	0.91
Cip4_gene	Cip4	17.9368	19.6995	1.10	0.91
AnnX_gene	CG9578	43.9847	48.3051	1.10	0.91
Abi_gene	Abi	22.1284	24.3015	1.10	0.91
l(2)08717_gene	l(2)08717	19.325	21.2225	1.10	0.91
CG2076_gene	CG2076	21.2847	23.3745	1.10	0.91
Lac_gene	Lac	48.7207	53.5031	1.10	0.91
CG5414_gene	CG5414	1.95971	2.15204	1.10	0.91
CG3947_gene	Pitslre	14.8339	16.2893	1.10	0.91
CG4781_gene	CG4781	10.9145	11.9852	1.10	0.91
Pp1-87B_gene	Pp1-87B	101.823	111.807	1.10	0.91
CG32068_gene	CG32068	15.3783	16.8853	1.10	0.91
Mdh_gene	Mdh	32.1447	35.2935	1.10	0.91
CG31005_gene	CG31005	4.19161	4.60206	1.10	0.91
Taf2_gene	CG34382	12.847	14.1042	1.10	0.91
Fdh_gene	Fdh	54.7087	60.0586	1.10	0.91
CG3077_gene	CG3077	3.34784	3.67503	1.10	0.91
CG9053_gene	CG9053	6.96787	7.64804	1.10	0.91
CG4877_gene	CG4877	8.356	9.17102	1.10	0.91

CG8816_gene	Cyp301a1	2.50408	2.748	1.10	0.91
Hr39_gene	Hr39	7.51224	8.24399	1.10	0.91
CG8446_gene	CG8446	88.677	97.3055	1.10	0.91
shn_gene	shn	48.3668	53.0727	1.10	0.91
Tsc1_gene	Tsc1	35.8464	39.3328	1.10	0.91
CG10672_gene	CG4618	11.9488	13.1109	1.10	0.91
GstD1_gene	GstD9	262.574	288.109	1.10	0.91
slgA_gene	slgA	33.043	36.2537	1.10	0.91
Sobp_gene	Sobp	1.38813	1.52299	1.10	0.91
ago_gene	ago	28.0348	30.7577	1.10	0.91
CG16708_gene	CG16708	33.8595	37.1476	1.10	0.91
hpo_gene	hpo	13.0375	14.3028	1.10	0.91
cbx_gene	CG30010	20.2232	22.1826	1.10	0.91
zfh2_gene	zfh2	20.2232	22.1826	1.10	0.91
CG8734_gene	CG8734	1.66031	1.82096	1.10	0.91
snmRNA:128_gene	Msp-300	1.66031	1.82096	1.10	0.91
Neos_gene	Neos	3.32063	3.64192	1.10	0.91
Tak1_gene	Tak1	19.8965	21.8184	1.10	0.91
grp_gene	grp	5.5253	6.05883	1.10	0.91
Roe1_gene	Roe1	7.4578	8.17777	1.10	0.91
CG31149_gene	CG31149	166.821	182.924	1.10	0.91
Trc8_gene	CG2010	54.6542	59.9262	1.10	0.91
pAbp_gene	pAbp	2210.64	2423.76	1.10	0.91
CG14614_gene	CG14614	60.6967	66.5478	1.10	0.91
Kul_gene	Kul	6.61403	7.25073	1.10	0.91
Aats-pro_gene	CG1246	2.20468	2.41691	1.10	0.91
msps_gene	msps	38.0239	41.6834	1.10	0.91
CG15019_gene	Syx17	44.8829	49.199	1.10	0.91
CG18397_gene	CG18397	7.43058	8.14466	1.10	0.91
CG4090_gene	CG4090	3.02123	3.31084	1.10	0.91
sec6_gene	sec6	18.1274	19.865	1.10	0.91
msn_gene	msn	34.3222	37.6111	1.10	0.91
ppan_gene	ppan	6.31463	6.91965	1.10	0.91
CG14671_gene	CG14671	10.4246	11.4224	1.10	0.91
iHog_gene	iHog	3.56559	3.90679	1.10	0.91
CG9005_gene	CG9005	50.7348	55.589	1.10	0.91
CG4404_gene	CG4404	30.7022	33.6381	1.10	0.91
CG8735_gene	CG8735	18.6173	20.3948	1.10	0.91
crn_gene	crn	19.4338	21.2887	1.10	0.91
CG15817_gene	CG15817	15.5961	17.0839	1.10	0.91
CG10462_gene	CG10462	15.8682	17.3819	1.10	0.91
CG2046_gene	CG1218	7.92051	8.67439	1.10	0.91
CG6567_gene	CG6567	19.9238	21.8184	1.10	0.91
Dpit47_gene	Dpit47	11.1867	12.2501	1.10	0.91
dnc_gene	dnc	41.399	45.3254	1.09	0.91
CG30409_gene	CG30409	1.36091	1.48988	1.09	0.91
CG8783_gene	CG8783	2.44964	2.68178	1.09	0.91
CG30060_gene	CG17034	0.816547	0.893926	1.09	0.91
DmsR-1_gene	DmsR-1	0.544365	0.595951	1.09	0.91
CG1893_gene	Jafrac2	15.2422	16.6866	1.09	0.91
mal_gene	mal	7.62111	8.34331	1.09	0.91
Elongin-C_gene	Elongin-C	44.9101	49.1659	1.09	0.91
CG33971_gene	CG12090	4.08274	4.46963	1.09	0.91
CG34131_gene	CG7071	14.6979	16.0907	1.09	0.91
CG12177_gene	CG12177	2.17746	2.3838	1.09	0.91
CG7016_gene	CG7016	1.08873	1.1919	1.09	0.91
park_gene	park	1.08873	1.1919	1.09	0.91
CG9611_gene	CG14367	12.7926	14.0048	1.09	0.91
Gs2_gene	Gs2	87.2617	95.5177	1.09	0.91
CG11961_gene	CG11961	35.6015	38.9686	1.09	0.91

Mkp3_gene	Mkp3	7.86607	8.60818	1.09	0.91
l(2)44DEa_gene	l(2)44DEa	187.643	205.338	1.09	0.91
CG12082_gene	CG12082	31.4371	34.3996	1.09	0.91
CG14804_gene	CG14804	51.7419	56.6153	1.09	0.91
CG3542_gene	CG3542	11.3772	12.4487	1.09	0.91
nAcRalpha-96Aa_gene	cRalpha-96	20.0326	21.9177	1.09	0.91
CG17293_gene	CG17293	15.6777	17.1501	1.09	0.91
CG6833_gene	CG6833	3.78334	4.13855	1.09	0.91
CG34413_gene	CG34413	18.1001	19.7988	1.09	0.91
CG8291_gene	CG8291	14.0446	15.3623	1.09	0.91
CG6995_gene	CG6995	34.0228	37.2138	1.09	0.91
mnd_gene	mnd	9.9891	10.9258	1.09	0.91
alpha-Adaptin_gene	Rpl135	45.6178	49.8943	1.09	0.91
Karybeta3_gene	Karybeta3	276.51	302.412	1.09	0.91
RpS27A_gene	RpS27A	635.982	695.475	1.09	0.91
CG12081_gene	CG12081	23.7071	25.9239	1.09	0.91
CG2201_gene	CG2201	43.6308	47.7092	1.09	0.91
Nup358_gene	Nup358	88.051	96.2792	1.09	0.91
bbg_gene	bbg	12.3843	13.5413	1.09	0.91
Atf-2_gene	Atf-2	32.8252	35.8895	1.09	0.91
CG9062_gene	Vhl	18.5628	20.2954	1.09	0.91
wal_gene	wal	37.915	41.4517	1.09	0.91
cic_gene	cic	14.5073	15.8589	1.09	0.91
Gfr_gene	mRpL1	10.2068	11.1575	1.09	0.91
CG15896_gene	CG15896	1.87806	2.05272	1.09	0.91
Vhl_gene	Vhl	11.2684	12.3163	1.09	0.91
CG5691_gene	CG5691	7.24005	7.9129	1.09	0.91
CG2097_gene	CG1236	15.5416	16.9846	1.09	0.92
CG34132_gene	CG7102	6.69569	7.31695	1.09	0.92
CG11820_gene	CG11820	3.21175	3.50949	1.09	0.92
dre4_gene	dre4	25.1497	27.48	1.09	0.92
Tip60_gene	CG4865	7.7572	8.47574	1.09	0.92
CG3071_gene	CG3071	10.4246	11.3893	1.09	0.92
CG32856_gene	CG5516	2.93957	3.21151	1.09	0.92
CG16941_gene	CG3534	12.5476	13.7069	1.09	0.92
p16-ARC_gene	p16-ARC	19.4883	21.2887	1.09	0.92
XNP_gene	XNP	31.7637	34.6976	1.09	0.92
Eno_gene	Eno	276.211	301.717	1.09	0.92
sfl_gene	sfl	11.7311	12.8129	1.09	0.92
Klc_gene	Klc	28.5247	31.155	1.09	0.92
CG6637_gene	CG6637	14.1263	15.4285	1.09	0.92
CG30463_gene	CG30463	309.172	337.672	1.09	0.92
l(1)G0022_gene	l(1)G0022	32.7708	35.7902	1.09	0.92
Arpc3A_gene	Arpc3A	3.7289	4.07233	1.09	0.92
mRpL51_gene	CG13089	6.12411	6.68789	1.09	0.92
blot_gene	blot	132.798	145.015	1.09	0.92
PSR_gene	PSR	6.91343	7.54871	1.09	0.92
CG4592_gene	CG4592	3.97386	4.3372	1.09	0.92
CG5612_gene	CG5612	380.429	415.212	1.09	0.92
polybromo_gene	polybromo	33.043	36.055	1.09	0.92
CG14098_gene	CG32210	2.64017	2.88043	1.09	0.92
Lnk_gene	Lnk	13.9902	15.263	1.09	0.92
lin_gene	lin	12.9287	14.1042	1.09	0.92
RhoGAP15B_gene	RhoGAP15E	13.1736	14.369	1.09	0.92
CG9144_gene	CG13994	6.58682	7.18452	1.09	0.92
CG7071_gene	CG7071	14.7523	16.0907	1.09	0.92
CG7054_gene	CG7054	17.1203	18.6731	1.09	0.92
CalpB_gene	CalpB	22.1012	24.1029	1.09	0.92
Cyp4ac3_gene	tkv	0.789329	0.860818	1.09	0.92
alien_gene	CG17906	18.6717	20.3617	1.09	0.92

Taf4_gene	Taf4	56.0151	61.085	1.09	0.92
Dbp73D_gene	Dbp73D	6.04245	6.58857	1.09	0.92
CG9205_gene	trio	17.8552	19.4677	1.09	0.92
CG3040_gene	CG3040	9.44473	10.2967	1.09	0.92
CG5969_gene	CG5969	7.07674	7.71425	1.09	0.92
AnnIX_gene	AnnIX	94.8556	103.397	1.09	0.92
CG1109_gene	CG1109	25.939	28.2746	1.09	0.92
Hop_gene	Hop	37.6973	41.0875	1.09	0.92
Ing3_gene	Ing3	3.40228	3.70814	1.09	0.92
hrg_gene	hrg	41.3173	45.0274	1.09	0.92
CG9422_gene	CG9422	5.2259	5.69464	1.09	0.92
CG3983_gene	CG3983	24.823	27.0495	1.09	0.92
Mlc-c_gene	Mlc-c	47.4958	51.7484	1.09	0.92
Cam_gene	Cam	314.398	342.539	1.09	0.92
CG3362_gene	CG3362	4.95372	5.39667	1.09	0.92
CG17765_gene	CG17765	14.8612	16.19	1.09	0.92
hkl_gene	hkl	41.4534	45.1598	1.09	0.92
CG4365_gene	CG4365	31.2738	34.0685	1.09	0.92
CG11267_gene	CG11267	10.9417	11.919	1.09	0.92
CG1667_gene	CG1667	6.50516	7.08519	1.09	0.92
Int6_gene	CG9706	143.848	156.669	1.09	0.92
CG30394_gene	CG30394	21.0669	22.9441	1.09	0.92
Graf_gene	Graf	18.9711	20.6596	1.09	0.92
sqd_gene	sqd	443.821	483.316	1.09	0.92
CG9293_gene	CG9293	6.23298	6.78722	1.09	0.92
Rs1_gene	Rs1	19.7332	21.4873	1.09	0.92
Dad_gene	Dad	30.3756	33.0753	1.09	0.92
CG8232_gene	CG8232	26.7011	29.0692	1.09	0.92
MED30_gene	MED30	6.47794	7.05208	1.09	0.92
CG14213_gene	CG14213	21.2302	23.1096	1.09	0.92
CG31304_gene	CG31304	11.6494	12.6805	1.09	0.92
CG12096_gene	CG12096	12.1666	13.2434	1.09	0.92
ERp60_gene	CG13190	935.301	1018.05	1.09	0.92
IP3K2_gene	IP3K2	17.338	18.8718	1.09	0.92
vav_gene	vav	34.676	37.7436	1.09	0.92
CG34423_gene	CG34423	1.03429	1.12568	1.09	0.92
Ddc_gene	CG10561	3.10288	3.37705	1.09	0.92
Cyp6a22_gene	Cyp6a22	3.10288	3.37705	1.09	0.92
stmA_gene	CG30356	21.6929	23.6063	1.09	0.92
CG9393_gene	CG9393	6.45072	7.01898	1.09	0.92
CG4607_gene	CG4607	9.79857	10.6609	1.09	0.92
numb_gene	numb	17.2564	18.7724	1.09	0.92
MED20_gene	MED20	3.34784	3.64192	1.09	0.92
CG13025_gene	Nrt	3.34784	3.64192	1.09	0.92
CG31122_gene	CG31122	9.52639	10.3629	1.09	0.92
CG30190_gene	CG30190	11.8399	12.8792	1.09	0.92
CG30193_gene	CG30190	11.8399	12.8792	1.09	0.92
FucTB_gene	FucTB	2.8307	3.07908	1.09	0.92
Atg2_gene	Atg2	66.3853	72.2094	1.09	0.92
gig_gene	gig	23.4077	25.4603	1.09	0.92
CG1599_gene	CG1665	21.3119	23.1759	1.09	0.92
CG33256_gene	Lmpt	1.7964	1.95339	1.09	0.92
CG3735_gene	CG3735	8.98202	9.76697	1.09	0.92
spi_gene	spi	8.98202	9.76697	1.09	0.92
CG33330_gene	CG33330	10.5062	11.4224	1.09	0.92
CG32676_gene	CG32676	32.2536	35.0618	1.09	0.92
emb_gene	emb	71.6384	77.8709	1.09	0.92
Cpr_gene	Cpr	155.008	168.489	1.09	0.92
Pi3K21B_gene	Pi3K21B	29.6407	32.2145	1.09	0.92
CG7565_gene	Ect4	31.8998	34.6645	1.09	0.92

CG30327_gene	CG6393	2.04137	2.21826	1.09	0.92
CG6509_gene	CG6509	34.9482	37.9753	1.09	0.92
CG7510_gene	CG7510	110.37	119.919	1.09	0.92
RanGap_gene	RanGap	18.3451	19.9312	1.09	0.92
CG7408_gene	CG7408	34.6488	37.6442	1.09	0.92
CG7632_gene	CG7632	3.56559	3.87368	1.09	0.92
Rpl1_gene	CG12869	29.7768	32.3469	1.09	0.92
CG4785_gene	CG4785	6.61403	7.18452	1.09	0.92
Pcl_gene	Pcl	6.61403	7.18452	1.09	0.92
EloA_gene	EloA	61.2955	66.5809	1.09	0.92
CG31221_gene	CG31221	0.762111	0.827709	1.09	0.92
CG6040_gene	CG6040	32.7163	35.5253	1.09	0.92
Fs(2)Ket_gene	Fs(2)Ket	21.0397	22.8448	1.09	0.92
Cdc42_gene	Cdc42	29.3685	31.8834	1.09	0.92
Eaf6_gene	mthl2	2.5313	2.748	1.09	0.92
Sce_gene	Sce	5.30756	5.76086	1.09	0.92
CG7523_gene	CG7523	14.3985	15.6272	1.09	0.92
Gbeta13F_gene	Gbeta13F	50.136	54.3971	1.08	0.92
CG31782_gene	grp	184.621	200.306	1.08	0.92
CG1607_gene	CG1607	1.00708	1.09258	1.08	0.92
CG32297_gene	CG32297	1.00708	1.09258	1.08	0.92
CG1970_gene	CG1970	75.7484	82.175	1.08	0.92
chif_gene	chif	31.4371	34.1016	1.08	0.92
CG3107_gene	CG3107	56.0696	60.8201	1.08	0.92
primo-1_gene	primo-2	12.0577	13.0778	1.08	0.92
primo-2_gene	primo-2	12.0577	13.0778	1.08	0.92
CalpC_gene	CalpC	13.3097	14.4353	1.08	0.92
Pez_gene	Pez	7.78442	8.44264	1.08	0.92
CG10671_gene	CG4623	35.9009	38.9355	1.08	0.92
CG12219_gene	CG12219	3.51115	3.80746	1.08	0.92
CG4294_gene	CG4294	51.6602	56.0194	1.08	0.92
Tom40_gene	Tom40	13.0375	14.1373	1.08	0.92
CG9643_gene	CG9643	7.26727	7.87979	1.08	0.92
CG2938_gene	CG2938	17.0386	18.4745	1.08	0.92
pit_gene	CG6015	29.3141	31.784	1.08	0.92
CG4089_gene	CG4089	1.25204	1.35744	1.08	0.92
CG9449_gene	CG9449	1.25204	1.35744	1.08	0.92
tankyrase_gene	tankyrase	22.5095	24.4009	1.08	0.92
cv-c_gene	cv-c	26.5106	28.7381	1.08	0.92
CG31712_gene	CG31712	36.4997	39.5645	1.08	0.92
Ef1gamma_gene	Ef1gamma	465.704	504.77	1.08	0.92
Hsc70-4_gene	Hsc70-4	1137.99	1233.35	1.08	0.92
CG11247_gene	CG11247	14.97	16.2231	1.08	0.92
Sp7_gene	Sp7	1.497	1.62231	1.08	0.92
CG12203_gene	CG12203	18.454	19.9975	1.08	0.92
ari-1_gene	ari-1	23.1899	25.1293	1.08	0.92
CG7394_gene	CG7394	7.72998	8.37642	1.08	0.92
CG8005_gene	CG8005	4.73597	5.1318	1.08	0.92
CG7655_gene	CG7655	3.23897	3.50949	1.08	0.92
CG8578_gene	CG8578	8.21991	8.90615	1.08	0.92
nej_gene	nej	29.8856	32.38	1.08	0.92
CG10195_gene	CG10195	6.72291	7.28384	1.08	0.92
CG11844_gene	CG11844	114.507	124.057	1.08	0.92
CG4119_gene	CG4119	18.9167	20.4941	1.08	0.92
eIF2B-beta_gene	eIF2B-beta	15.6777	16.9846	1.08	0.92
mkg-p_gene	CG33057	12.6837	13.74	1.08	0.92
CG33932_gene	CG33932	5.47087	5.9264	1.08	0.92
Rpp20_gene	CG33932	5.47087	5.9264	1.08	0.92
HP1b_gene	HP1b	9.19977	9.96562	1.08	0.92
MAPk-Ak2_gene	MAPk-Ak2	46.7065	50.5896	1.08	0.92

CG11418_gene	CG11418	3.97386	4.30409	1.08	0.92
CG14749_gene	CG14749	5.9608	6.45613	1.08	0.92
lrrk_gene	lrrk	5.9608	6.45613	1.08	0.92
l(3)s1921_gene	CG1910	14.6434	15.8589	1.08	0.92
CG17896_gene	CG17896	57.8116	62.6079	1.08	0.92
ed_gene	ed	75.9117	82.2081	1.08	0.92
CG2059_gene	CG2059	6.94065	7.5156	1.08	0.92
Lag1_gene	Lag1	38.8677	42.0807	1.08	0.92
mRpL19_gene	mRpL19	5.44365	5.89329	1.08	0.92
eff_gene	eff	152.585	165.178	1.08	0.92
CG32066_gene	CG32066	14.589	15.7927	1.08	0.92
Patr-1_gene	Patr-1	14.8339	16.0576	1.08	0.92
Fmo-2_gene	Fmo-2	5.93358	6.42303	1.08	0.92
ssh_gene	ssh	18.5356	20.0637	1.08	0.92
CaMKII_gene	CaMKII	38.2961	41.4517	1.08	0.92
CG10575_gene	CG10575	10.3702	11.2237	1.08	0.92
ph-d_gene	ph-d	7.40336	8.01223	1.08	0.92
qm_gene	qm	11.105	12.0183	1.08	0.92
Chrac-14_gene	mus201	3.70168	4.00611	1.08	0.92
mus201_gene	mus201	3.70168	4.00611	1.08	0.92
E(Pc)_gene	E(Pc)	48.5846	52.5761	1.08	0.92
lama_gene	lama	39.1943	42.4118	1.08	0.92
CG13197_gene	CG13197	4.43657	4.80071	1.08	0.92
PPP4R2r_gene	PPP4R2r	40.1741	43.4713	1.08	0.92
CG18591_gene	CG7102	18.9711	20.5272	1.08	0.92
CG4360_gene	CG4360	90.6368	98.067	1.08	0.92
fru_gene	fru	5.41643	5.86018	1.08	0.92
CG4925_gene	mRpS34	5.41643	5.86018	1.08	0.92
CG10283_gene	CG10283	8.60097	9.30345	1.08	0.92
CG4364_gene	CG4364	138.813	150.146	1.08	0.92
l(2)k09022_gene	l(2)k09022	18.9167	20.461	1.08	0.92
Cyp4e1_gene	Cyp4e1	86.2274	93.2663	1.08	0.92
CG9000_gene	CG9000	36.3364	39.2996	1.08	0.92
CG8594_gene	CG8594	75.0135	81.1155	1.08	0.92
CG5742_gene	CG5742	12.0032	12.9785	1.08	0.92
sog_gene	sog	16.1676	17.4812	1.08	0.92
CG13392_gene	CG13392	3.4295	3.70814	1.08	0.92
CG10337_gene	ref(2)P	5.63418	6.09194	1.08	0.92
mrj_gene	mrj	18.1001	19.5671	1.08	0.93
Myo31DF_gene	Myo31DF	14.1807	15.3292	1.08	0.93
CG8498_gene	Rbsn	16.6031	17.9447	1.08	0.93
eIF3-S8_gene	eIF3-S8	565.895	611.611	1.08	0.93
CG5871_gene	CG5871	15.6233	16.8853	1.08	0.93
Pros45_gene	Pros45	61.9487	66.9451	1.08	0.93
CG5720_gene	CG5720	18.2907	19.7657	1.08	0.93
dl_gene	dl	11.9488	12.9123	1.08	0.93
CG31148_gene	CG31148	5.60696	6.05883	1.08	0.93
Gfat1_gene	Gfat1	51.4153	55.5559	1.08	0.93
Su(var)2-HP2_gene	u(var)2-HP	27.5176	29.7313	1.08	0.93
CG3403_gene	CG3270	22.1557	23.9374	1.08	0.93
pk_gene	pk	16.0315	17.3157	1.08	0.93
ire-1_gene	ire-1	95.4544	103.099	1.08	0.93
CG5205_gene	CG5205	24.2787	26.2218	1.08	0.93
Rm62_gene	Rm62	424.931	458.915	1.08	0.93
CG12730_gene	CG12730	11.1595	12.0514	1.08	0.93
Mhcl_gene	Mhcl	84.8665	91.644	1.08	0.93
CG11980_gene	CG11980	31.7637	34.3003	1.08	0.93
crol_gene	crol	104.981	113.363	1.08	0.93
Pxn_gene	Pxn	51.3608	55.4565	1.08	0.93
CG7324_gene	CG7338	177.027	191.135	1.08	0.93

Pgi_gene	Pgi	59.0364	63.7336	1.08	0.93
CG6610_gene	CG6610	2.17746	2.35069	1.08	0.93
mtTFB1_gene	mtTFB1	23.9521	25.8576	1.08	0.93
l(1)dd4_gene	l(1)dd4	54.627	58.966	1.08	0.93
Syx16_gene	l(1)G0004	7.97495	8.60818	1.08	0.93
CoVa_gene	glo	89.167	96.2461	1.08	0.93
CG30157_gene	Cyp6u1	1.9325	2.08583	1.08	0.93
Pgd_gene	Pgd	34.05	36.7503	1.08	0.93
Mtor_gene	Mtor	71.9106	77.606	1.08	0.93
CG11696_gene	CG11696	6.75012	7.28384	1.08	0.93
CG12453_gene	CG12453	1.68753	1.82096	1.08	0.93
CG18094_gene	CG18094	1.68753	1.82096	1.08	0.93
Atx2_gene	Atx2	65.0788	70.2229	1.08	0.93
tho2_gene	tho2	27.2182	29.3671	1.08	0.93
snRNP70K_gene	snRNP70K	18.0457	19.4677	1.08	0.93
CG5543_gene	CG5543	5.77027	6.22437	1.08	0.93
CG3295_gene	CG9346	32.6891	35.2604	1.08	0.93
CG2158_gene	CG2158	16.8209	18.1434	1.08	0.93
su(Hw)_gene	su(Hw)	15.841	17.0839	1.08	0.93
CG9603_gene	CG9603	66.1676	71.3486	1.08	0.93
CG32176_gene	CG32176	16.7664	18.0772	1.08	0.93
Cyp12a5_gene	Cyp12a5	4.79041	5.16491	1.08	0.93
CG12785_gene	Mst89B	10.7784	11.621	1.08	0.93
CG8636_gene	CG8636	94.5562	101.941	1.08	0.93
CG3499_gene	CG3499	33.5057	36.1212	1.08	0.93
CG9630_gene	CG9630	10.2885	11.0913	1.08	0.93
Nap1_gene	Nap1	82.7707	89.2271	1.08	0.93
Alh_gene	Alh	138.976	149.815	1.08	0.93
CG9240_gene	CG9240	11.2411	12.1177	1.08	0.93
mbf1_gene	mbf1	39.2215	42.2794	1.08	0.93
CG1371_gene	CG12920	28.933	31.1881	1.08	0.93
gft_gene	gft	34.4311	37.1145	1.08	0.93
nes_gene	nes	14.344	15.4616	1.08	0.93
CG6712_gene	CG5325	10.9962	11.8528	1.08	0.93
Sh3beta_gene	Sh3beta	84.3766	90.9487	1.08	0.93
slmo_gene	slmo	37.7517	40.6902	1.08	0.93
CG6769_gene	CG6769	23.1355	24.9306	1.08	0.93
CG31549_gene	CG31549	19.08	20.5603	1.08	0.93
CG15617_gene	CG15617	11.9216	12.8461	1.08	0.93
CG10153_gene	CG12859	6.91343	7.44938	1.08	0.93
desat1_gene	desat1	292.868	315.556	1.08	0.93
Pp2A-29B_gene	Pp2A-29B	92.6781	99.8549	1.08	0.93
CG3995_gene	CG5220	3.81055	4.10544	1.08	0.93
CG34257_gene	CG14102	0.952639	1.02636	1.08	0.93
CG5840_gene	CG5840	0.952639	1.02636	1.08	0.93
CG7730_gene	CG7730	0.952639	1.02636	1.08	0.93
CG4042_gene	CG4042	7.13118	7.68114	1.08	0.93
CG1789_gene	CG1789	7.34893	7.9129	1.08	0.93
CTCF_gene	qm	13.0375	14.038	1.08	0.93
Smg5_gene	Smg5	48.1219	51.8146	1.08	0.93
T3dh_gene	T3dh	4.0283	4.3372	1.08	0.93
skd_gene	skd	30.7838	33.1415	1.08	0.93
CG4617_gene	CG4617	15.6233	16.8191	1.08	0.93
CG10737_gene	CG10737	80.185	86.3135	1.08	0.93
enc_gene	enc	56.9678	61.3167	1.08	0.93
CG10077_gene	CG10077	358.791	386.176	1.08	0.93
CG5611_gene	CG5611	5.90636	6.35681	1.08	0.93
CG7304_gene	CG7304	154.246	166.005	1.08	0.93
cpa_gene	cpa	55.0081	59.1978	1.08	0.93
CG5706_gene	CG5706	38.9493	41.9152	1.08	0.93

CG5642_gene	CG5642	191.399	205.967	1.08	0.93
CG30187_gene	CG30187	0.707674	0.761493	1.08	0.93
slmb_gene	slmb	43.6308	46.9477	1.08	0.93
CG3415_gene	kat80	45.0462	48.4707	1.08	0.93
CG8184_gene	CG8184	96.4342	103.762	1.08	0.93
h_gene	h	50.9253	54.7944	1.08	0.93
CG30392_gene	CG30392	36.7718	39.5645	1.08	0.93
CG2225_gene	CG2225	8.24713	8.87305	1.08	0.93
CG40451_gene	Parp	90.2013	97.0407	1.08	0.93
vir_gene	CG34424	12.9287	13.9055	1.08	0.93
loco_gene	mRpL45	73.7887	79.3608	1.08	0.93
l(3)02640_gene	CG2211	6.34185	6.82033	1.08	0.93
Hex-A_gene	Hex-A	177.653	191.035	1.08	0.93
Su(var)3-9_gene	Su(var)3-9	121.938	131.109	1.08	0.93
CG11859_gene	CG11859	16.4126	17.6468	1.08	0.93
CstF-50_gene	CstF-50	3.51115	3.77436	1.07	0.93
CG13472_gene	CG13472	16.3854	17.6137	1.07	0.93
CG10341_gene	CG10341	10.2885	11.0582	1.07	0.93
barr_gene	barr	3.97386	4.27098	1.07	0.93
Klp68D_gene	Klp68D	6.77734	7.28384	1.07	0.93
CG5077_gene	CG5077	37.3707	40.1605	1.07	0.93
CG6175_gene	CG6175	24.9863	26.8509	1.07	0.93
Fem-1_gene	Fem-1	17.0386	18.3089	1.07	0.93
CG41339_gene	Parp	104.055	111.807	1.07	0.93
shf_gene	COQ7	9.79857	10.5285	1.07	0.93
HP1c_gene	HP1c	11.8944	12.7798	1.07	0.93
CG32394_gene	CG32394	20.5226	22.0502	1.07	0.93
brk_gene	brk	9.5536	10.2636	1.07	0.93
CG13322_gene	CG13322	7.21284	7.74736	1.07	0.93
nmd_gene	nmd	26.7555	28.7381	1.07	0.93
CG10092_gene	CG10092	2.55852	2.748	1.07	0.93
CG11760_gene	CG11760	8.60097	9.23724	1.07	0.93
CG9034_gene	CG9034	9.28142	9.96562	1.07	0.93
CG9300_gene	CG9300	11.35	12.1839	1.07	0.93
CG14352_gene	CG14352	1.38813	1.48988	1.07	0.93
Cyp6a2_gene	Epac	2.31355	2.48313	1.07	0.93
ix_gene	ix	4.16439	4.46963	1.07	0.93
Grip71_gene	Grip71	0.92542	0.993251	1.07	0.93
CG6617_gene	CG6540	12.0305	12.9123	1.07	0.93
CG15099_gene	CG15083	65.8409	70.6533	1.07	0.93
Smn_gene	Smn	9.00924	9.66765	1.07	0.93
CR33328_gene	sqd	219.787	235.831	1.07	0.93
CG6191_gene	CG6191	30.4572	32.678	1.07	0.93
eIF-2beta_gene	eIF-2beta	81.6547	87.6048	1.07	0.93
CG12325_gene	CG12325	6.91343	7.41628	1.07	0.93
Jafrac2_gene	Jafrac2	35.6831	38.2733	1.07	0.93
Dmn_gene	Dmn	29.6951	31.8503	1.07	0.93
CG17556_gene	CG31274	13.1192	14.0711	1.07	0.93
UbcD6_gene	UbcD6	22.319	23.9374	1.07	0.93
CG6842_gene	CG6842	51.0614	54.7613	1.07	0.93
Sdic2_gene	Sdic2	4.59988	4.93315	1.07	0.93
itp_gene	CG4622	12.4115	13.3096	1.07	0.93
Fer1HCH_gene	Fer1HCH	76.4561	81.9763	1.07	0.93
l(2)35Df_gene	l(2)35Df	15.3783	16.488	1.07	0.93
CG3891_gene	CG3911	3.21175	3.44327	1.07	0.93
CG7218_gene	CG7218	13.5275	14.5015	1.07	0.93
SMC1_gene	SMC1	25.2041	27.0164	1.07	0.93
CG3563_gene	CG3563	48.7751	52.2781	1.07	0.93
Tsp97E_gene	Tsp97E	4.57267	4.90004	1.07	0.93
RpLP2_gene	RpLP2	467.092	500.499	1.07	0.93

CG6623_gene	CG4210	8.68262	9.30345	1.07	0.93
Moe_gene	Moe	230.294	246.757	1.07	0.93
CSN8_gene	CSN8	5.25312	5.62842	1.07	0.93
CG17618_gene	CG6982	23.5166	25.1955	1.07	0.93
CG6982_gene	CG6982	23.5166	25.1955	1.07	0.93
CG14670_gene	CG14670	23.0266	24.6657	1.07	0.93
CG1738_gene	CG1738	2.50408	2.68178	1.07	0.93
CG4225_gene	CG4225	18.8895	20.2292	1.07	0.93
CG7375_gene	MED24	17.0386	18.2427	1.07	0.93
CG33056_gene	CG33054	5.90636	6.3237	1.07	0.93
CG34349_gene	CG34349	13.8541	14.8326	1.07	0.93
nbs_gene	CG14174	8.62818	9.23724	1.07	0.93
Nep4_gene	Nep4	1.36091	1.45677	1.07	0.93
sbb_gene	sbb	23.816	25.4935	1.07	0.93
mtm_gene	mtm	19.7332	21.1231	1.07	0.93
beta4GalT7_gene	beta4GalT7	5.44365	5.82707	1.07	0.93
CG5899_gene	CG5899	17.6919	18.938	1.07	0.93
cta_gene	cta	21.7474	23.2752	1.07	0.93
CG32164_gene	CG32164	48.1763	51.5497	1.07	0.93
Prm_gene	Prm	198.802	212.721	1.07	0.93
CG14805_gene	CG14805	16.957	18.1434	1.07	0.93
Dbp80_gene	CG41274	16.2765	17.415	1.07	0.93
mor_gene	Rbf2	40.0108	42.8091	1.07	0.93
CG12190_gene	CG12190	17.8552	19.1035	1.07	0.93
kat80_gene	kat80	53.3205	57.0457	1.07	0.93
CLIP-190_gene	CLIP-190	252.286	269.899	1.07	0.93
cactin_gene	Pp4-19C	8.356	8.93926	1.07	0.93
CG3224_gene	CG3224	19.1889	20.5272	1.07	0.93
Sep1_gene	01-Sep	22.5639	24.136	1.07	0.93
TfIIFalpha_gene	TfIIFalpha	38.1328	40.7895	1.07	0.93
CG14816_gene	CG14816	8.57375	9.17102	1.07	0.93
KaiRIA_gene	GluRIIE	1.57866	1.68853	1.07	0.93
CG31274_gene	CG31274	3.15732	3.37705	1.07	0.93
caz_gene	caz	24.0881	25.7583	1.07	0.94
CG15735_gene	CG15735	24.0881	25.7583	1.07	0.94
cnc_gene	cnc	134.349	143.657	1.07	0.94
Chd1_gene	Chd1	36.4452	38.9686	1.07	0.94
Spn7_gene	Spn7	253.81	271.356	1.07	0.94
TfIIA-S_gene	TfIIA-S	18.209	19.4677	1.07	0.94
CG15701_gene	CG15706	1.7964	1.92029	1.07	0.94
CG34179_gene	slmo	1.7964	1.92029	1.07	0.94
dalao_gene	dalao	27.3816	29.2678	1.07	0.94
sni_gene	sni	10.098	10.7933	1.07	0.94
CG10277_gene	CG10277	38.3505	40.9882	1.07	0.94
CG9987_gene	CG9987	20.1687	21.5536	1.07	0.94
CG7185_gene	CG7185	19.4883	20.8252	1.07	0.94
CG2691_gene	CG2691	30.2395	32.3138	1.07	0.94
CG16896_gene	Atf-2	4.9265	5.26423	1.07	0.94
eIF-1A_gene	eIF-1A	241.263	257.782	1.07	0.94
CG10492_gene	CG10492	18.7806	20.0637	1.07	0.94
mRpS25_gene	mRpS25	3.1301	3.34395	1.07	0.94
CG1218_gene	CG1218	6.2602	6.68789	1.07	0.94
par-1_gene	par-1	136.363	145.677	1.07	0.94
Rpn9_gene	CG10365	36.2003	38.6706	1.07	0.94
CCS_gene	CCS	5.36199	5.72775	1.07	0.94
Fur1_gene	Fur1	22.1012	23.6063	1.07	0.94
Jafrac1_gene	Jafrac1	89.3847	95.4515	1.07	0.94
CG11508_gene	Socs44A	32.9885	35.2273	1.07	0.94
TORC_gene	TORC	27.6265	29.4996	1.07	0.94
ApepP_gene	ApepP	21.6113	23.0765	1.07	0.94

CG7099_gene	CG7099	7.56667	8.07844	1.07	0.94
CG31108_gene	CG31108	19.3522	20.6596	1.07	0.94
CG4806_gene	CG4806	24.6869	26.3543	1.07	0.94
CG14713_gene	CG14713	10.4518	11.1575	1.07	0.94
CG13827_gene	CG13827	1.33369	1.42366	1.07	0.94
CG12301_gene	CG12301	10.6696	11.3893	1.07	0.94
CG31248_gene	CG31248	126.891	135.446	1.07	0.94
Parg_gene	Parg	8.21991	8.77372	1.07	0.94
Usp36_gene	Usp36	38.4322	41.0213	1.07	0.94
CG4290_gene	CG4290	4.21883	4.50274	1.07	0.94
CG9139_gene	CG9139	8.6554	9.23724	1.07	0.94
CG40045_gene	CG40045	55.4436	59.1647	1.07	0.94
bves_gene	CG1518	69.6243	74.2952	1.07	0.94
CG17343_gene	CG17343	1.55144	1.65542	1.07	0.94
CG31633_gene	CG31633	3.10288	3.31084	1.07	0.94
Sdic4_gene	Sdic4	4.65432	4.96626	1.07	0.94
CG10627_gene	CG10627	7.7572	8.27709	1.07	0.94
Su(var)2-10_gene	Su(var)2-1	14.1807	15.1305	1.07	0.94
Nrx-IV_gene	Nrx-IV	50.7076	54.0991	1.07	0.94
Kap3_gene	Kap3	11.9488	12.7467	1.07	0.94
Roc1a_gene	Roc1a	46.4615	49.5632	1.07	0.94
Lmpt_gene	Lmpt	61.9487	66.0843	1.07	0.94
CG1636_gene	CG1636	19.461	20.759	1.07	0.94
RpII15_gene	RpII15	13.0375	13.9055	1.07	0.94
sol_gene	sol	18.1001	19.3022	1.07	0.94
Tor_gene	Tor	22.7272	24.2353	1.07	0.94
SelR_gene	SelR	16.9842	18.1103	1.07	0.94
Sas-4_gene	Sas-4	2.20468	2.35069	1.07	0.94
Ranbp16_gene	Ranbp16	10.1252	10.7933	1.07	0.94
tgo_gene	CG11986	23.1083	24.6326	1.07	0.94
rux_gene	rux	2.64017	2.81421	1.07	0.94
mRpS22_gene	mRpS22	13.4186	14.3028	1.07	0.94
CG31683_gene	CG31683	19.5699	20.8583	1.07	0.94
CG11893_gene	CG11893	2.85792	3.04597	1.07	0.94
CG3773_gene	CG3773	3.07566	3.27773	1.07	0.94
Cyp313a4_gene	Cyp313a4	3.07566	3.27773	1.07	0.94
mRpL54_gene	mRpL54	3.07566	3.27773	1.07	0.94
Spt5_gene	Spt5	34.05	36.2868	1.07	0.94
CG32512_gene	bves	49.6461	52.9072	1.07	0.94
Caf1_gene	Caf1	9.44473	10.0649	1.07	0.94
CG2812_gene	CG2812	19.1072	20.3617	1.07	0.94
Rel_gene	Nmdmc	57.5394	61.3167	1.07	0.94
CG31158_gene	btn	29.6135	31.5523	1.07	0.94
VhaM9.7-1_gene	CG18675	7.4578	7.94601	1.07	0.94
CG6758_gene	CG6758	8.11104	8.64129	1.07	0.94
CG34125_gene	CG34125	16.4398	17.5143	1.07	0.94
StIP_gene	StIP	12.7109	13.5413	1.07	0.94
CG14408_gene	CG14408	21.4752	22.8779	1.07	0.94
CG10222_gene	CG10222	4.38214	4.66828	1.07	0.94
Spat_gene	Spat	8.98202	9.56832	1.07	0.94
su(s)_gene	su(s)	75.7484	80.6851	1.07	0.94
Tango7_gene	Tango7	179.232	190.903	1.07	0.94
CG10971_gene	CG32113	12.0305	12.8129	1.07	0.94
S2P_gene	S2P	25.7757	27.4468	1.06	0.94
CG7102_gene	CG7102	26.6194	28.3408	1.06	0.94
Eip75B_gene	Eip75B	47.3325	50.391	1.06	0.94
ORMDL_gene	ORMDL	18.5084	19.6995	1.06	0.94
CG9629_gene	CG9666	1.52422	1.62231	1.06	0.94
CG9853_gene	CG9853	32.2264	34.3003	1.06	0.94
CG30423_gene	Atf-2	23.9521	25.4935	1.06	0.94

CG10194_gene	CG10194	2.39521	2.54935	1.06	0.94
ap_gene	ap	0.653238	0.695276	1.06	0.94
snoRNA:Psi28S-1837c_gene	CG10576	0.653238	0.695276	1.06	0.94
botv_gene	botv	4.13717	4.40341	1.06	0.94
Mst85C_gene	Mst85C	4.35492	4.63517	1.06	0.94
CG2702_gene	CG2702	5.6614	6.02572	1.06	0.94
CG5335_gene	Atg7	15.0245	15.9913	1.06	0.94
Rpn1_gene	Rpn1	77.9258	82.9365	1.06	0.94
Irp-1A_gene	Irp-1A	35.8464	38.1409	1.06	0.94
CG18811_gene	CG18811	141.861	150.941	1.06	0.94
hk_gene	hk	17.3652	18.4745	1.06	0.94
elB_gene	elB	41.1812	43.8024	1.06	0.94
qkr58E-3_gene	qkr58E-3	17.5558	18.6731	1.06	0.94
Aldh_gene	Aldh	154.491	164.317	1.06	0.94
loqs_gene	loqs	10.3974	11.0582	1.06	0.94
ptr_gene	ptr	30.1034	32.0158	1.06	0.94
CG13993_gene	CG13993	4.98094	5.29734	1.06	0.94
CG31075_gene	CG14253	51.5241	54.7944	1.06	0.94
CG4452_gene	CG4452	17.0931	18.1765	1.06	0.94
CG2147_gene	CG2147	12.7654	13.5744	1.06	0.94
eIF4G_gene	eIF4G	359.308	382.071	1.06	0.94
CG3165_gene	CG3165	4.10996	4.37031	1.06	0.94
CG6512_gene	CG6512	46.7065	49.6626	1.06	0.94
lig_gene	lig	142.488	151.504	1.06	0.94
mus309_gene	CG14721	7.56667	8.04534	1.06	0.94
CG13551_gene	CG13551	32.8524	34.9293	1.06	0.94
Vinc_gene	Vinc	41.4806	44.1004	1.06	0.94
CG4658_gene	CG5846	78.824	83.7973	1.06	0.94
Rpn5_gene	Rpn5	68.0184	72.3087	1.06	0.94
twin_gene	twin	39.4937	41.9814	1.06	0.94
l(1)G0144_gene	l(1)G0144	3.02123	3.21151	1.06	0.94
pcm_gene	pcm	10.9962	11.6873	1.06	0.94
Zfrp8_gene	Zfrp8	5.38921	5.72775	1.06	0.94
CG30296_gene	CG30296	5.17147	5.49599	1.06	0.94
Ca-alpha1D_gene	Ca-alpha1D	133.043	141.373	1.06	0.94
CG9666_gene	Max	4.73597	5.03247	1.06	0.94
CG14222_gene	CG14222	9.47195	10.0649	1.06	0.94
CG10238_gene	CG10238	9.2542	9.83319	1.06	0.94
CG11563_gene	CG11563	4.51823	4.80071	1.06	0.94
eIF5B_gene	eIF5B	115.95	123.196	1.06	0.94
CG10535_gene	CG10535	19.7877	21.0238	1.06	0.94
gro_gene	gro	60.6423	64.4289	1.06	0.94
beta4GalNAcTA_gene	ta4GalNAc	2.15024	2.28448	1.06	0.94
CG3652_gene	Tps1	14.8339	15.7596	1.06	0.94
dod_gene	dod	12.6837	13.4751	1.06	0.94
Sdc_gene	Sdc	65.351	69.4283	1.06	0.94
trx_gene	CG14839	44.2841	47.047	1.06	0.94
CG6006_gene	CG6006	18.4812	19.6333	1.06	0.94
CG9674_gene	CG9674	299.129	317.774	1.06	0.94
mRpL20_gene	mRpL20	3.86499	4.10544	1.06	0.94
CG34446_gene	CG34446	1.9325	2.05272	1.06	0.94
CG4572_gene	CG11447	26.8372	28.5063	1.06	0.94
Tango10_gene	Tango10	29.3957	31.2212	1.06	0.94
CG5290_gene	CG5290	5.36199	5.69464	1.06	0.94
Ada2b_gene	Ada2b	10.724	11.3893	1.06	0.94
CG5168_gene	CG5168	42.025	44.6301	1.06	0.94
Cdk4_gene	Cdk4	1.71475	1.82096	1.06	0.94
Cyp6d4_gene	Cyp6d4	1.71475	1.82096	1.06	0.94
CG5604_gene	CG5604	182.553	193.85	1.06	0.94
cdm_gene	cdm	18.4268	19.5671	1.06	0.94

CG6859_gene	CG6859	21.203	22.5137	1.06	0.94
CG31086_gene	CG31086	3.21175	3.41016	1.06	0.94
CG4713_gene	CG4713	14.1263	14.9981	1.06	0.94
As_gene	As	19.8965	21.1231	1.06	0.94
CG14977_gene	CG14977	11.976	12.7136	1.06	0.94
Faf_gene	Faf	35.7103	37.9091	1.06	0.94
CG32223_gene	CG32223	14.7523	15.6603	1.06	0.94
CG5535_gene	CG5535	27.5721	29.2678	1.06	0.94
CG11436_gene	CG11436	4.27326	4.53585	1.06	0.94
jagn_gene	CG2082	23.4893	24.9306	1.06	0.94
Eip63F-1_gene	Eip63F-1	4.05552	4.30409	1.06	0.94
l(2)01289_gene	l(2)01289	22.6184	24.0036	1.06	0.94
Hmgs_gene	Vha44	491.97	522.086	1.06	0.94
CG13800_gene	CG13800	48.639	51.616	1.06	0.94
Dnr1_gene	Dnr1	34.1317	36.2206	1.06	0.94
CG10673_gene	CG10673	9.17255	9.73386	1.06	0.94
CG31048_gene	CG31048	24.7414	26.2549	1.06	0.94
CG3402_gene	CG3402	5.11703	5.42977	1.06	0.94
CG2662_gene	CG2662	1.27926	1.35744	1.06	0.94
CG1969_gene	CG1969	13.8541	14.7001	1.06	0.94
CG5792_gene	CG5792	18.5356	19.6664	1.06	0.94
CG30373_gene	CG30373	6.17854	6.55546	1.06	0.94
CG13126_gene	CG13126	3.62003	3.84057	1.06	0.94
nop5_gene	xl6	31.2738	33.1746	1.06	0.94
CG11902_gene	CG11902	5.74305	6.09194	1.06	0.94
DIP2_gene	mthl14	36.3636	38.5713	1.06	0.94
CG6688_gene	CG6688	4.46379	4.7345	1.06	0.94
CG6945_gene	CG6945	4.46379	4.7345	1.06	0.94
mof_gene	mof	6.58682	6.98587	1.06	0.94
CG10494_gene	MESK2	9.77135	10.3629	1.06	0.94
MED16_gene	MED16	6.15132	6.52235	1.06	0.94
CG33199_gene	CG8229	24.6053	26.0894	1.06	0.94
CG8417_gene	CG8417	22.2645	23.6063	1.06	0.94
CG5451_gene	CG5451	4.0283	4.27098	1.06	0.94
CG3407_gene	CG3407	2.96679	3.1453	1.06	0.94
mav_gene	mav	163.446	173.256	1.06	0.94
Hdm_gene	Hdm	8.46487	8.97237	1.06	0.94
CG9836_gene	CG9836	23.2716	24.6657	1.06	0.94
l(2)k09913_gene	l(2)k09913	22.8089	24.1691	1.06	0.94
CG3605_gene	CG3605	27.0277	28.6387	1.06	0.94
CG8949_gene	CG8949	32.9341	34.8962	1.06	0.94
CG10664_gene	CG10664	154.001	163.158	1.06	0.94
CG4293_gene	arg	56.9134	60.2904	1.06	0.94
CG4448_gene	EloA	6.53238	6.91965	1.06	0.94
CG30486_gene	CG30486	73.2987	77.6391	1.06	0.94
CG7498_gene	CG7498	6.31463	6.68789	1.06	0.94
Lk6_gene	Lk6	911.185	964.911	1.06	0.94
l(2)k10201_gene	l(2)k10201	6.09689	6.45613	1.06	0.94
wee_gene	CG10354	5.25312	5.56221	1.06	0.94
CG17912_gene	CG17912	11.976	12.6805	1.06	0.94
CG18600_gene	CG18600	8.19269	8.67439	1.06	0.94
CG15382_gene	CG15382	1.46979	1.55609	1.06	0.94
xl6_gene	xl6	33.3696	35.3266	1.06	0.94
CG9044_gene	CG9044	32.5258	34.4327	1.06	0.94
Hrb87F_gene	Hrb87F	73.4348	77.7385	1.06	0.94
CG6678_gene	CG6560	2.0958	2.21826	1.06	0.94
Dcp2_gene	Dcp2	61.4044	64.9917	1.06	0.94
CG5931_gene	CG5931	54.8992	58.1052	1.06	0.94
wds_gene	wds	11.105	11.7535	1.06	0.94
CG17078_gene	CG17078	8.16547	8.64129	1.06	0.94

CG31445_gene	CG31445	43.3314	45.8551	1.06	0.94
Adgf-D_gene	ninaB	6.69569	7.08519	1.06	0.95
CG31368_gene	CG31368	20.0871	21.2556	1.06	0.95
CG6276_gene	CG14866	6.47794	6.85343	1.06	0.95
CG6180_gene	CG6180	53.4839	56.5822	1.06	0.95
CG1116_gene	CG1116	8.98202	9.5021	1.06	0.95
Mlp84B_gene	Alh	93.3041	98.6961	1.06	0.95
CG10080_gene	CG10080	29.4229	31.1219	1.06	0.95
CG10418_gene	CG10418	3.75612	3.97301	1.06	0.95
CG5226_gene	CG5226	3.75612	3.97301	1.06	0.95
CG12314_gene	CG34163	0.62602	0.662168	1.06	0.95
CG6762_gene	CG6762	3.1301	3.31084	1.06	0.95
Dhc62B_gene	CG8001	0.62602	0.662168	1.06	0.95
CG8319_gene	CG8319	3.1301	3.31084	1.06	0.95
CG3939_gene	Fcp3C	17.5286	18.5407	1.06	0.95
slik_gene	slik	85.7103	90.6507	1.06	0.95
Tango11_gene	Tango11	31.2738	33.0753	1.06	0.95
CG11802_gene	CG11802	4.79041	5.06558	1.06	0.95
CG1234_gene	CG1234	16.0315	16.9515	1.06	0.95
CG8108_gene	CG8108	58.4376	61.7802	1.06	0.95
Elongin-B_gene	CG5412	33.8867	35.8233	1.06	0.95
CG31140_gene	CG31140	26.81	28.3408	1.06	0.95
CG2478_gene	CG2611	19.1072	20.1961	1.06	0.95
Adam_gene	Adam	68.5083	72.408	1.06	0.95
CG3358_gene	CG3358	12.6565	13.3758	1.06	0.95
rost_gene	rost	21.9923	23.2421	1.06	0.95
zip_gene	zip	156.532	165.409	1.06	0.95
pr-set7_gene	pr-set7	9.11811	9.63454	1.06	0.95
CG2926_gene	CG2926	62.3298	65.8526	1.06	0.95
CG10274_gene	CG7376	11.595	12.2501	1.06	0.95
CG41099_gene	CG41099	57.1039	60.3235	1.06	0.95
swm_gene	swm	36.8263	38.9023	1.06	0.95
kirre_gene	kirre	1.03429	1.09258	1.06	0.95
sno_gene	sno	13.4458	14.2035	1.06	0.95
CG3534_gene	CG3534	25.2313	26.6522	1.06	0.95
Nsf2_gene	Nsf2	37.4251	39.5314	1.06	0.95
CG14894_gene	CG14894	10.1252	10.694	1.06	0.95
CG11876_gene	CG11876	33.424	35.2935	1.06	0.95
CG1785_gene	CG1785	33.8323	35.7239	1.06	0.95
Pde8_gene	Pde8	117.583	124.156	1.06	0.95
Tis11_gene	Tis11	18.5628	19.6002	1.06	0.95
CG6792_gene	CG6792	2.88513	3.04597	1.06	0.95
CG8939_gene	CG8939	27.5993	29.1354	1.06	0.95
Rab14_gene	Rab14	24.7142	26.0894	1.06	0.95
Unc-76_gene	Unc-76	22.0196	23.2421	1.06	0.95
Nc73EF_gene	Nc73EF	132.662	140.015	1.06	0.95
jim_gene	jim	42.3244	44.6632	1.06	0.95
CG6151_gene	CG6151	40.4735	42.7098	1.06	0.95
adp_gene	adp	23.6254	24.9306	1.06	0.95
nahoda_gene	nahoda	36.7718	38.803	1.06	0.95
CG3907_gene	CG3907	25.8573	27.2813	1.06	0.95
CG6776_gene	CG6776	20.4953	21.6198	1.05	0.95
Adk3_gene	CG4674	11.2684	11.8859	1.05	0.95
CG10289_gene	CG10289	24.5781	25.9239	1.05	0.95
Best1_gene	Best1	22.319	23.5401	1.05	0.95
CG33981_gene	CG6355	210.288	221.793	1.05	0.95
CG6355_gene	CG6355	210.288	221.793	1.05	0.95
Eph_gene	Eph	71.8289	75.752	1.05	0.95
nrv1_gene	nrv1	61.5677	64.9255	1.05	0.95
Pvr_gene	Pvr	37.0168	39.0348	1.05	0.95

CG5625_gene	CG5625	41.2901	43.5375	1.05	0.95
CG15684_gene	CG15684	1.22482	1.29123	1.05	0.95
CG14280_gene	CG14280	0.816547	0.860818	1.05	0.95
CG6196_gene	CG6196	4.49101	4.7345	1.05	0.95
CG12024_gene	CG12024	9.39029	9.8994	1.05	0.95
CG32681_gene	CG17841	2.44964	2.58245	1.05	0.95
CG10889_gene	CG4936	3.26619	3.44327	1.05	0.95
CG33096_gene	CG33096	12.4387	13.1109	1.05	0.95
Nop56_gene	Nop56	32.8252	34.5983	1.05	0.95
CG33774_gene	l(2)k10201	7.53945	7.94601	1.05	0.95
how_gene	how	44.4202	46.8152	1.05	0.95
CG7484_gene	CG7484	32.3897	34.1347	1.05	0.95
CG18624_gene	CG18624	38.7043	40.7895	1.05	0.95
CkIalpha_gene	CkIalpha	134.404	141.638	1.05	0.95
CG13349_gene	CG13349	32.5802	34.3334	1.05	0.95
CG2947_gene	CG2947	26.4561	27.8773	1.05	0.95
CG12608_gene	CG12608	19.1072	20.1299	1.05	0.95
CG32486_gene	CG32486	78.0347	82.2081	1.05	0.95
eIF-3p66_gene	eIF-3p66	144.012	151.703	1.05	0.95
CG9090_gene	CG9090	7.51224	7.9129	1.05	0.95
CG11318_gene	CG11318	7.10396	7.48249	1.05	0.95
Rpn2_gene	Rpn2	86.2546	90.8494	1.05	0.95
CG11539_gene	Med	6.69569	7.05208	1.05	0.95
CG15525_gene	CG15524	28.9874	30.5259	1.05	0.95
CG7911_gene	CG15524	28.9874	30.5259	1.05	0.95
CG1172_gene	CG1172	7.29449	7.68114	1.05	0.95
l(3)neo18_gene	l(3)neo18	28.5519	30.0624	1.05	0.95
CG32446_gene	CG32446	27.7354	29.2016	1.05	0.95
CG30122_gene	CG30122	67.5829	71.1499	1.05	0.95
C3G_gene	C3G	8.90037	9.36967	1.05	0.95
CG14764_gene	CG14764	40.8546	43.0078	1.05	0.95
CG6388_gene	CG6388	12.7381	13.4089	1.05	0.95
CG14478_gene	CG14478	31.3282	32.9759	1.05	0.95
rl_gene	rl	36.5813	38.505	1.05	0.95
CG14613_gene	CG14613	5.25312	5.5291	1.05	0.95
CG30069_gene	CG30069	53.3205	56.1187	1.05	0.95
CG2118_gene	CG2118	6.2602	6.58857	1.05	0.95
Herp_gene	Herp	96.9242	102.007	1.05	0.95
CG7009_gene	CG7009	7.26727	7.64804	1.05	0.95
TMS1_gene	TMS1	25.2313	26.5529	1.05	0.95
CG11526_gene	CG12016	80.7021	84.923	1.05	0.95
Mat1_gene	Mat1	10.2885	10.8264	1.05	0.95
CG8370_gene	ATPCL	10.8873	11.4555	1.05	0.95
Smox_gene	Smox	43.7397	46.0206	1.05	0.95
Patj_gene	Patj	32.8524	34.5651	1.05	0.95
TfIIB_gene	TfIIB	8.46487	8.90615	1.05	0.95
nudE_gene	nudE	20.958	22.0502	1.05	0.95
D19B_gene	D19B	9.06368	9.53521	1.05	0.95
Pk17E_gene	Pk17E	23.7615	24.9968	1.05	0.95
CG7158_gene	CG11249	27.5721	29.0029	1.05	0.95
CG12050_gene	CG12050	17.0931	17.9778	1.05	0.95
CG31063_gene	CG31063	43.8214	46.0869	1.05	0.95
CG4045_gene	CG4061	5.2259	5.49599	1.05	0.95
CG10841_gene	CG10841	9.44473	9.93251	1.05	0.95
Kr-h1_gene	Kr-h1	94.4473	99.3251	1.05	0.95
CG14182_gene	CG14182	1.60588	1.68853	1.05	0.95
CG5721_gene	nopo	16.8481	17.713	1.05	0.95
MTA1-like_gene	MTA1-like	37.8878	39.8294	1.05	0.95
CG30387_gene	CG30387	184.812	194.28	1.05	0.95
nAcRalpha-96Ab_gene	cRalpha-96	2.20468	2.31759	1.05	0.95

CG5116_gene	CG5116	4.40936	4.63517	1.05	0.95
CG9335_gene	CG9335	4.40936	4.63517	1.05	0.95
CG2982_gene	CG2982	16.0315	16.8522	1.05	0.95
CG2135_gene	pncr017:3R	16.6303	17.4812	1.05	0.95
CG18672_gene	CG18672	53.2933	56.0194	1.05	0.95
Oseg1_gene	CG13667	5.60696	5.89329	1.05	0.95
CG16903_gene	CG4025	19.6244	20.6265	1.05	0.95
CG9425_gene	CG9425	43.8486	46.0869	1.05	0.95
smi35A_gene	smi35A	12.4115	13.0447	1.05	0.95
CG5877_gene	CG5877	6.80456	7.15141	1.05	0.95
CG7942_gene	msk	3.40228	3.5757	1.05	0.95
snmRNA:357_gene	Msr-110	91.8071	96.4778	1.05	0.95
blw_gene	blw	357.757	375.946	1.05	0.95
Atg7_gene	Atg7	19.5971	20.5934	1.05	0.95
CG3301_gene	CG3301	5.19868	5.46288	1.05	0.95
Adf1_gene	Adf1	10.9962	11.5548	1.05	0.95
Rab4_gene	Rab4	38.9765	40.9551	1.05	0.95
CG31902_gene	CG31902	115.732	121.607	1.05	0.95
CG9588_gene	CG9588	9.39029	9.8663	1.05	0.95
UBL3_gene	UBL3	17.1747	18.0441	1.05	0.95
ppk19_gene	ppk19	0.598801	0.629059	1.05	0.95
CG8414_gene	mRpL34	8.38322	8.80683	1.05	0.95
CG7692_gene	CG7692	4.19161	4.40341	1.05	0.95
AGO2_gene	AGO2	136.717	143.624	1.05	0.95
AP-47_gene	CG8199	47.6864	50.093	1.05	0.95
Mad_gene	Mad	20.7403	21.7853	1.05	0.95
Rapgap1_gene	Rapgap1	53.8377	56.5491	1.05	0.95
Ptpmeg_gene	Ptpmeg	62.7653	65.9188	1.05	0.95
CG41378_gene	CG41378	11.35	11.919	1.05	0.95
CG32177_gene	CG32177	150.326	157.861	1.05	0.95
CG10011_gene	CG9986	17.7191	18.6069	1.05	0.95
fat2_gene	fat2	24.8775	26.1225	1.05	0.95
ECSIT_gene	ECSIT	5.77027	6.05883	1.05	0.95
Ady43A_gene	Ady43A	2.58573	2.71489	1.05	0.95
CG10632_gene	CG10632	94.4473	99.1596	1.05	0.95
Mpp6_gene	Mpp6	3.97386	4.17166	1.05	0.95
CG12811_gene	CG12811	11.9216	12.515	1.05	0.95
CG7492_gene	CG32373	35.1388	36.8827	1.05	0.95
lectin-29Ca_gene	lectin-29Ca	1234.05	1295.17	1.05	0.95
Vps20_gene	Vps20	22.8089	23.9374	1.05	0.95
nuf_gene	nuf	41.8072	43.8686	1.05	0.95
CG18766_gene	CG17991	8.51931	8.93926	1.05	0.95
CG8134_gene	CG8134	8.51931	8.93926	1.05	0.95
Ptp10D_gene	Ptp10D	31.4915	33.0422	1.05	0.95
tlk_gene	tlk	36.037	37.8098	1.05	0.95
CG14230_gene	CG14230	8.70984	9.13791	1.05	0.95
ND42_gene	ND42	49.4828	51.9139	1.05	0.95
CG5515_gene	CHORD	16.4126	17.2164	1.05	0.95
Pkcdelta_gene	Pkcdelta	8.30156	8.7075	1.05	0.95
Rab1_gene	Rab1	205.525	215.569	1.05	0.95
Pros26.4_gene	CG31142	87.3433	91.6109	1.05	0.95
Madm_gene	Madm	29.2324	30.6584	1.05	0.95
CG14786_gene	CG14786	17.7735	18.64	1.05	0.95
Ack_gene	Ack	15.5961	16.3555	1.05	0.95
eIF3-S10_gene	eIF3-S10	319.216	334.759	1.05	0.95
CG4287_gene	CG4287	7.10396	7.44938	1.05	0.95
tRNA:CR31577_gene	CG14322	0.789329	0.827709	1.05	0.95
stwl_gene	stwl	8.68262	9.1048	1.05	0.95
Acp53C14a_gene	Acp53C14a	6278.51	6583.7	1.05	0.95
CG10321_gene	CG10321	26.2384	27.5131	1.05	0.95

A16_gene	A16	11.4317	11.9852	1.05	0.95
CG8605_gene	CG8605	30.3211	31.784	1.05	0.95
CG5384_gene	CG5384	29.5318	30.9563	1.05	0.95
Vap-33-1_gene	Vap-33-1	125.803	131.871	1.05	0.95
CG10703_gene	CG10703	26.7555	28.0428	1.05	0.95
CG4165_gene	CG4165	16.712	17.5143	1.05	0.95
CG4041_gene	CG4041	8.84593	9.27035	1.05	0.95
CG8060_gene	CG8060	8.84593	9.27035	1.05	0.95
Tim10_gene	CG10307	23.571	24.6988	1.05	0.95
CG5860_gene	CG5860	25.5307	26.7516	1.05	0.95
bwa_gene	bwa	409.526	429.051	1.05	0.95
CG15881_gene	CG15881	4.89928	5.1318	1.05	0.95
CG6680_gene	CG6680	4.89928	5.1318	1.05	0.95
CG11755_gene	CG11755	0.979857	1.02636	1.05	0.95
CG7177_gene	CG7177	43.1137	45.1598	1.05	0.95
CG10588_gene	CG10588	14.8884	15.594	1.05	0.95
CG14906_gene	CG14907	12.3299	12.9123	1.05	0.95
CG14907_gene	CG14907	12.3299	12.9123	1.05	0.95
mib2_gene	CG31800	15.46	16.19	1.05	0.95
DnaJ-H_gene	DnaJ-H	26.4017	27.6455	1.05	0.96
bif_gene	bif	95.6177	100.12	1.05	0.96
X11Lbeta_gene	X11Lbeta	81.3281	85.1547	1.05	0.96
APC4_gene	APC4	4.30048	4.50274	1.05	0.96
ck_gene	ck	47.3053	49.5301	1.05	0.96
CG6860_gene	CG6860	9.77135	10.2305	1.05	0.96
Brf_gene	Brf	106.886	111.906	1.05	0.96
CG6461_gene	CG6461	663.526	694.647	1.05	0.96
RpS29_gene	RpS29	444.283	465.106	1.05	0.96
Gprk2_gene	CG11337	51.3608	53.768	1.05	0.96
eEF1delta_gene	eEF1delta	141.943	148.59	1.05	0.96
Mnn1_gene	Mnn1	27.8987	29.2016	1.05	0.96
Cog3_gene	Cog3	33.7506	35.3266	1.05	0.96
CG4022_gene	CG4022	2.34077	2.45002	1.05	0.96
ft_gene	ft	2.34077	2.45002	1.05	0.96
CG7766_gene	CG7766	48.3668	50.6227	1.05	0.96
Msp-300_gene	Msp-300	252.694	264.47	1.05	0.96
CG7603_gene	CG7603	23.1899	24.2684	1.05	0.96
mRpL46_gene	mRpL46	12.2754	12.8461	1.05	0.96
CG32038_gene	CG32038	11.105	11.621	1.05	0.96
Taf6_gene	Taf6	17.338	18.1434	1.05	0.96
Rpb8_gene	Rpb8	18.8895	19.7657	1.05	0.96
Ssl1_gene	Ssl1	7.59389	7.94601	1.05	0.96
CG4963_gene	CG4963	7.78442	8.14466	1.05	0.96
Ten-m_gene	Ten-m	15.7594	16.488	1.05	0.96
Thd1_gene	Thd1	40.6096	42.478	1.05	0.96
CG32767_gene	CG32767	18.2634	19.1035	1.05	0.96
Pcmt_gene	Pcmt	15.5416	16.2562	1.05	0.96
flfl_gene	omd	58.0565	60.7208	1.05	0.96
CG12499_gene	CG12499	19.0256	19.8981	1.05	0.96
CG10347_gene	CG10347	10.479	10.9589	1.05	0.96
GLaz_gene	GLaz	17.0658	17.8454	1.05	0.96
CG41262_gene	CG41262	37.2346	38.9355	1.05	0.96
Plap_gene	CG14341	24.6053	25.7252	1.05	0.96
PEK_gene	PEK	28.8513	30.1617	1.05	0.96
eIF-2alpha_gene	eIF-2alpha	102.232	106.874	1.05	0.96
RhoBTB_gene	RhoBTB	19.1616	20.0306	1.05	0.96
CG10916_gene	CG10916	8.90037	9.30345	1.05	0.96
CG3164_gene	CG3164	95.1822	99.4907	1.05	0.96
CG9248_gene	CG9248	32.6891	34.1678	1.05	0.96
CG11872_gene	CG11872	3.67446	3.84057	1.05	0.96

CG34299_gene	CG34299	297.196	310.623	1.05	0.96
pHCl_gene	pHCl	107.077	111.906	1.05	0.96
mRpS17_gene	mRpS17	5.79749	6.05883	1.05	0.96
CG3420_gene	CG3420	1.9325	2.01961	1.05	0.96
CG30488_gene	CG30488	324.169	338.765	1.05	0.96
debcl_gene	debcl	14.0991	14.7332	1.04	0.96
Obp56i_gene	Obp56i	76.2383	79.6588	1.04	0.96
dpr10_gene	dpr10	36.4724	38.1077	1.04	0.96
TXBP181-like_gene	CG1968	12.9287	13.5082	1.04	0.96
CG8531_gene	CG8531	17.3652	18.1434	1.04	0.96
CG7362_gene	CG3563	8.68262	9.0717	1.04	0.96
sra_gene	sra	16.0043	16.7197	1.04	0.96
SoxN_gene	SoxN	9.2542	9.66765	1.04	0.96
Mtl_gene	Mtl	6.94065	7.25073	1.04	0.96
CG9067_gene	CG9067	2.31355	2.41691	1.04	0.96
CG5126_gene	CG4896	21.3935	22.3482	1.04	0.96
CG7806_gene	CG7806	32.7435	34.201	1.04	0.96
Gap1_gene	Gap1	12.7109	13.2765	1.04	0.96
Scamp_gene	Scamp	60.8328	63.535	1.04	0.96
CG8229_gene	CG8229	32.7163	34.1678	1.04	0.96
z_gene	boi	8.46487	8.83994	1.04	0.96
Prosap_gene	Prosap	176.973	184.811	1.04	0.96
Hmu_gene	Hmu	83.2606	86.9426	1.04	0.96
hang_gene	hang	32.0903	33.5057	1.04	0.96
SMC2_gene	SMC2	3.26619	3.41016	1.04	0.96
Rpn6_gene	Rpn6	88.9492	92.869	1.04	0.96
CG9940_gene	CG11158	14.3985	15.0312	1.04	0.96
Dab_gene	Dab	32.6347	34.0685	1.04	0.96
Trx-2_gene	Trx-2	76.2111	79.5594	1.04	0.96
CG13919_gene	CG13919	3.83777	4.00611	1.04	0.96
CG32365_gene	CG32365	24.5509	25.6259	1.04	0.96
Ank_gene	Ank	133.642	139.486	1.04	0.96
CG6565_gene	CG6565	9.19977	9.60143	1.04	0.96
CG7028_gene	CG7028	13.7997	14.4021	1.04	0.96
pyd3_gene	pyd3	14.1807	14.7994	1.04	0.96
Arp8_gene	Arp8	4.79041	4.99936	1.04	0.96
CG17737_gene	CG17737	62.6564	65.389	1.04	0.96
l(1)1Bi_gene	l(1)1Bi	9.77135	10.1974	1.04	0.96
cpb_gene	cpb	44.8285	46.7821	1.04	0.96
CG12004_gene	CG12004	25.2858	26.3874	1.04	0.96
CG15440_gene	CG15440	10.5335	10.992	1.04	0.96
Pka-R1_gene	Pka-R1	73.5165	76.7121	1.04	0.96
CG1635_gene	CG1635	6.50516	6.78722	1.04	0.96
CG18604_gene	CG18604	6.88622	7.18452	1.04	0.96
CG4845_gene	CG4845	14.344	14.965	1.04	0.96
CG31371_gene	CG31371	7.4578	7.78047	1.04	0.96
Sry-delta_gene	Sry-delta	10.5062	10.9589	1.04	0.96
GlcAT-P_gene	GlcAT-P	54.627	56.9795	1.04	0.96
CG6498_gene	CG6498	30.3483	31.6516	1.04	0.96
CG10417_gene	CG10417	32.8252	34.2341	1.04	0.96
Rad21_gene	CG41262	36.9896	38.5713	1.04	0.96
CDC45L_gene	CG3021	3.81055	3.97301	1.04	0.96
CG6569_gene	CG6637	0.571583	0.595951	1.04	0.96
CG32415_gene	S6k	0.571583	0.595951	1.04	0.96
CG16863_gene	CG16863	0.762111	0.794601	1.04	0.96
CG8646_gene	CG8646	0.952639	0.993251	1.04	0.96
Coq2_gene	eIF4AIII	3.23897	3.37705	1.04	0.96
CG14117_gene	CG14117	2.47686	2.58245	1.04	0.96
CG31869_gene	CG31869	1.71475	1.78785	1.04	0.96
Fdxh_gene	CG4452	1.90528	1.9865	1.04	0.96

CG11417_gene	CG11417	18.835	19.6333	1.04	0.96
CG17664_gene	CG17664	12.7381	13.2765	1.04	0.96
Tom7_gene	Tom7	34.7849	36.2537	1.04	0.96
coro_gene	coro	50.136	52.245	1.04	0.96
nmo_gene	nmo	7.21284	7.5156	1.04	0.96
CG1420_gene	CG1957	13.092	13.6407	1.04	0.96
CG5044_gene	CG5044	10.9962	11.4555	1.04	0.96
CG16908_gene	CG16908	5.30756	5.5291	1.04	0.96
Hsf_gene	Hsf	20.6586	21.5204	1.04	0.96
Fit1_gene	Fit1	92.4332	96.2461	1.04	0.96
Psn_gene	Psn	13.4186	13.9717	1.04	0.96
thoc7_gene	thoc7	21.5296	22.4144	1.04	0.96
CG5278_gene	CG5278	48.1491	50.1261	1.04	0.96
insc_gene	insc	38.1328	39.6969	1.04	0.96
CG4663_gene	CG4663	14.344	14.9319	1.04	0.96
NfI_gene	NfI	2.8307	2.94665	1.04	0.96
CG33521_gene	CG33521	21.6929	22.5799	1.04	0.96
CG15211_gene	CG15211	10.7512	11.1906	1.04	0.96
CG34256_gene	CG34256	58.0837	60.4559	1.04	0.96
bic_gene	bic	307.757	320.324	1.04	0.96
CG4049_gene	CG4049	7.72998	8.04534	1.04	0.96
CG4300_gene	CG4300	136.5	142.068	1.04	0.96
atms_gene	atms	9.9891	10.396	1.04	0.96
Ced-12_gene	Ced-12	4.89928	5.09869	1.04	0.96
mge_gene	ida	24.3059	25.2948	1.04	0.96
CG7369_gene	CG7369	14.3168	14.8988	1.04	0.96
CG6455_gene	CG6455	40.1197	41.7497	1.04	0.96
Lasp_gene	Lasp	35.0299	36.4523	1.04	0.96
CG11968_gene	CG11967	11.2956	11.7535	1.04	0.96
DNApol-delta_gene	Arf72A	4.3277	4.50274	1.04	0.96
CG6744_gene	CG5276	6.20576	6.45613	1.04	0.96
CG17597_gene	CG17322	12.0305	12.515	1.04	0.96
spas_gene	spas	9.96188	10.3629	1.04	0.96
CG2316_gene	CG2316	57.3216	59.6282	1.04	0.96
CG33144_gene	CG33144	35.6831	37.1145	1.04	0.96
CG11395_gene	CG11395	9.19977	9.56832	1.04	0.96
CG10486_gene	CG10486	7.13118	7.41628	1.04	0.96
CG7053_gene	Pk17E	14.8067	15.3954	1.04	0.96
CG14767_gene	CG14767	128.361	133.46	1.04	0.96
CG3192_gene	CG3192	27.3543	28.4401	1.04	0.96
4EHP_gene	4EHP	45.1279	46.9146	1.04	0.96
CG8878_gene	CG12367	16.6576	17.3157	1.04	0.96
CG1359_gene	CG1359	4.49101	4.66828	1.04	0.96
Usp7_gene	Usp7	98.3667	102.239	1.04	0.96
CG15073_gene	CG15073	4.30048	4.46963	1.04	0.96
CG33722_gene	CG18749	155.171	161.271	1.04	0.96
CG18749_gene	CG18749	155.171	161.271	1.04	0.96
CG3011_gene	CG12236	74.9318	77.8709	1.04	0.96
CG1458_gene	CG1458	34.5672	35.9226	1.04	0.96
CG13484_gene	CG13484	4.10996	4.27098	1.04	0.96
CG14073_gene	CG14073	19.7877	20.5603	1.04	0.96
step_gene	step	22.4006	23.2752	1.04	0.96
CG2111_gene	X11Lbeta	80.4299	83.5655	1.04	0.96
CSN1b_gene	CSN1b	14.1807	14.7332	1.04	0.96
TfIIFbeta_gene	Cap-H2	10.2613	10.6609	1.04	0.96
Pros54_gene	Pros54	36.9352	38.3726	1.04	0.96
Cyp6v1_gene	Cyp6v1	16.2221	16.8522	1.04	0.96
par-6_gene	par-6	21.0669	21.8846	1.04	0.96
Snap_gene	Snap	59.2813	61.5816	1.04	0.96
eIF4AIII_gene	eIF4AIII	21.5841	22.4144	1.04	0.96

CG9797_gene	CG9797	14.5073	15.0643	1.04	0.96
Tpi_gene	Tpi	39.0582	40.5578	1.04	0.96
CG31105_gene	CG31105	350.734	364.192	1.04	0.96
da_gene	da	29.7495	30.8901	1.04	0.96
mtacp1_gene	mtacp1	14.3168	14.8657	1.04	0.96
tud_gene	tud	192.814	200.206	1.04	0.96
CG1962_gene	ik2	18.9439	19.6664	1.04	0.96
shtd_gene	CG11655	15.7866	16.3886	1.04	0.96
l(2)NC136_gene	l(2)NC136	52.5584	54.5626	1.04	0.96
CG3640_gene	CG3640	507.43	526.754	1.04	0.96
CG13588_gene	CG13588	4.08274	4.23787	1.04	0.96
CG3764_gene	CG3764	171.829	178.355	1.04	0.96
CG3500_gene	CG3500	45.8083	47.5436	1.04	0.96
Rab2_gene	Rab2	59.5263	61.7802	1.04	0.96
CG7834_gene	CG7834	46.3527	48.1065	1.04	0.96
bonsai_gene	bonsai	4.81763	4.99936	1.04	0.96
CG15199_gene	CG15199	11.2956	11.7204	1.04	0.96
Mer_gene	Mer	17.7735	18.4414	1.04	0.96
CG30355_gene	l(2)44DEa	0.92542	0.960143	1.04	0.96
betaTub56D_gene	etaTub56	158.056	163.986	1.04	0.96
Dak1_gene	Dak1	54.7631	56.814	1.04	0.96
CG7564_gene	CG7564	21.829	22.6461	1.04	0.96
Gmer_gene	asrij	8.13826	8.44264	1.04	0.96
Sra-1_gene	Sra-1	62.3298	64.6607	1.04	0.96
l(1)G0060_gene	l(1)G0060	27.5449	28.5725	1.04	0.96
Ciao1_gene	Ercc1	25.694	26.6522	1.04	0.96
CG1021_gene	CG1021	25.313	26.2549	1.04	0.96
torp4a_gene	mRpL30	25.8573	26.8178	1.04	0.96
abs_gene	abs	7.7572	8.04534	1.04	0.96
CG7879_gene	CG7864	12.9287	13.4089	1.04	0.96
CG14480_gene	CG14480	28.9874	30.0624	1.04	0.96
l(2)37Ce_gene	l(2)37Ce	14.3985	14.9319	1.04	0.96
CG14722_gene	CG14722	39.1126	40.5578	1.04	0.96
CG34186_gene	CG34186	3.32063	3.44327	1.04	0.96
CG13779_gene	CG13779	26.3745	27.3475	1.04	0.96
exd_gene	exd	75.6123	78.4006	1.04	0.96
CanA-14F_gene	CanA-14F	50.8709	52.7416	1.04	0.96
CG4646_gene	CG4646	6.45072	6.68789	1.04	0.96
CG4673_gene	CG4673	23.2172	24.0698	1.04	0.96
CG14806_gene	CG14806	6.2602	6.48924	1.04	0.96
CG8950_gene	CG8950	3.1301	3.24462	1.04	0.96
CG18490_gene	CG18490	21.9107	22.7123	1.04	0.96
Ephrin_gene	Ephrin	25.7757	26.7185	1.04	0.96
CG5708_gene	CG5708	7.72998	8.01223	1.04	0.96
CG17233_gene	CG17233	15.46	16.0245	1.04	0.96
mld_gene	mld	30.8927	32.0158	1.04	0.96
boca_gene	boca	12.6837	13.144	1.04	0.96
SrpRbeta_gene	SrpRbeta	25.7212	26.6522	1.04	0.97
m_gene	m	2.93957	3.04597	1.04	0.97
CG12159_gene	CG12159	15.2422	15.7927	1.04	0.97
CG4400_gene	CG4400	10.8329	11.2237	1.04	0.97
Hcf_gene	Hcf	43.8758	45.4578	1.04	0.97
CG11210_gene	CG11210	22.7545	23.5732	1.04	0.97
CG6961_gene	CG6961	4.95372	5.1318	1.04	0.97
CG33217_gene	CG33217	7.70276	7.97912	1.04	0.97
CG1146_gene	CG33232	32.6347	33.8037	1.04	0.97
Clic_gene	Clic	38.8677	40.2598	1.04	0.97
CG17652_gene	CG17652	2.74904	2.84732	1.04	0.97
Klp10A_gene	Klp10A	17.0386	17.6468	1.04	0.97
CG18284_gene	CG18284	6745.82	6984.84	1.04	0.97

CG15675_gene	CG15675	3.83777	3.97301	1.04	0.97
mip120_gene	mip120	56.2873	58.2707	1.04	0.97
stc_gene	stc	92.0793	95.319	1.04	0.97
CG1983_gene	CG1983	4.38214	4.53585	1.04	0.97
Cys_gene	Cys	54.4093	56.3173	1.04	0.97
caps_gene	caps	128.089	132.566	1.03	0.97
RpIII128_gene	RpIII128	15.3239	15.8589	1.03	0.97
CG41274_gene	CG41274	8.57375	8.87305	1.03	0.97
CG3198_gene	CG3198	22.4006	23.1759	1.03	0.97
CG6272_gene	pncr011:3L	5.8247	6.02572	1.03	0.97
Parp_gene	Parp	173.544	179.514	1.03	0.97
kar_gene	kar	18.7262	19.3684	1.03	0.97
G9a_gene	G9a	14.1807	14.667	1.03	0.97
CG3281_gene	Hsp70Ab	5.08981	5.26423	1.03	0.97
phol_gene	phol	15.0789	15.594	1.03	0.97
CG9951_gene	CG9951	15.9771	16.5211	1.03	0.97
Ddx1_gene	Ddx1	16.3309	16.8853	1.03	0.97
CG13886_gene	CG13886	8.16547	8.44264	1.03	0.97
CG31217_gene	CG31217	7.07674	7.31695	1.03	0.97
beat-IIb_gene	beat-IIb	0.544365	0.562842	1.03	0.97
CG5428_gene	CG5428	0.544365	0.562842	1.03	0.97
CG32184_gene	Nedd4	0.544365	0.562842	1.03	0.97
H_gene	H	19.2161	19.865	1.03	0.97
CG4901_gene	CG4901	12.1393	12.5481	1.03	0.97
RhoGDI_gene	RhoGDI	59.744	61.7471	1.03	0.97
CG7628_gene	CG7628	7.24005	7.48249	1.03	0.97
CG17260_gene	CG17260	3.62003	3.74125	1.03	0.97
CG8042_gene	RNaseX25	43.2498	44.6963	1.03	0.97
CG13759_gene	CG13759	287.397	296.982	1.03	0.97
CG3800_gene	CG3800	590.663	610.353	1.03	0.97
CG7280_gene	CG34422	5.06259	5.23112	1.03	0.97
CG12182_gene	CG16984	2.5313	2.61556	1.03	0.97
CG3573_gene	CG3573	13.0103	13.442	1.03	0.97
l(2)35Di_gene	l(2)35Di	36.4997	37.7104	1.03	0.97
mRpL36_gene	mRpL36	1.98693	2.05272	1.03	0.97
CG8831_gene	CG8831	7.94773	8.21088	1.03	0.97
CG31550_gene	CG31550	35.9281	37.1145	1.03	0.97
ProsMA5_gene	ProsMA5	35.3837	36.5516	1.03	0.97
CG7397_gene	CG7397	3.4295	3.5426	1.03	0.97
CG9065_gene	CG9065	3.4295	3.5426	1.03	0.97
Plc21C_gene	Plc21C	35.1932	36.353	1.03	0.97
unc-13-4A_gene	unc-13-4A	6.31463	6.52235	1.03	0.97
Pcf11_gene	Pcf11	60.9689	62.9721	1.03	0.97
Ssdp_gene	Ssdp	26.5106	27.3806	1.03	0.97
Spt6_gene	Spt6	148.775	153.656	1.03	0.97
CG3075_gene	CG3075	7.21284	7.44938	1.03	0.97
CG14430_gene	CG14430	40.2013	41.5179	1.03	0.97
Gel_gene	Gel	47.5775	49.1328	1.03	0.97
CG9601_gene	Arf84F	5.2259	5.39667	1.03	0.97
CR41056_gene	CR41056	10.4518	10.7933	1.03	0.97
CG3335_gene	CG3335	17.828	18.4083	1.03	0.97
Sug_gene	Sug	7.02231	7.25073	1.03	0.97
ksr_gene	CG14670	14.9428	15.4285	1.03	0.97
CG8569_gene	CG8569	3.23897	3.34395	1.03	0.97
CG31357_gene	CG31357	13.3097	13.74	1.03	0.97
Nurf-38_gene	Nurf-38	49.9999	51.616	1.03	0.97
CG5343_gene	CG5188	7.72998	7.97912	1.03	0.97
CG31120_gene	CG31120	16.3582	16.8853	1.03	0.97
Fen1_gene	CG5859	1.7964	1.85407	1.03	0.97
CG4893_gene	CG4893	13.473	13.9055	1.03	0.97

mRpL48_gene	mRpL48	0.898202	0.927035	1.03	0.97
CG9153_gene	CG9153	29.6407	30.5921	1.03	0.97
Bap55_gene	Bap55	11.1323	11.4886	1.03	0.97
ko_gene	ko	212.928	219.707	1.03	0.97
shark_gene	shark	6.99509	7.21763	1.03	0.97
CG1600_gene	CG1600	25.0952	25.8908	1.03	0.97
CG1440_gene	CG1440	194.937	201.1	1.03	0.97
CG7824_gene	CG7824	7.70276	7.94601	1.03	0.97
CG4729_gene	CG4729	29.9129	30.857	1.03	0.97
CG33249_gene	CG33249	22.5639	23.2752	1.03	0.97
CG31191_gene	CG31191	11.4589	11.8197	1.03	0.97
HisCl1_gene	HisCl1	8.0566	8.3102	1.03	0.97
Mbs_gene	Mbs	47.0059	48.4707	1.03	0.97
RpL39_gene	RpL39	48.4213	49.9274	1.03	0.97
PhKgamma_gene	PhKgamma	20.9036	21.5536	1.03	0.97
CG6834_gene	CG6834	113.446	116.972	1.03	0.97
CG32708_gene	CG32708	5.71583	5.89329	1.03	0.97
Arf79F_gene	Arf79F	408.464	421.139	1.03	0.97
CG3740_gene	dor	18.7534	19.3353	1.03	0.97
CG5447_gene	CG5447	7.67555	7.9129	1.03	0.97
Atpalpha_gene	Atpalpha	305.389	314.828	1.03	0.97
Nup153_gene	Nup153	46.9243	48.3713	1.03	0.97
Gl_gene	Gl	36.3908	37.5118	1.03	0.97
CG4266_gene	CG4266	25.1497	25.9239	1.03	0.97
CG10333_gene	CG10333	20.332	20.9576	1.03	0.97
Syx1A_gene	4EHP	16.2221	16.7197	1.03	0.97
CrebB-17A_gene	CrebB-17A	16.9297	17.4481	1.03	0.97
Prosalpha7_gene	Prosalpha7	44.529	45.8882	1.03	0.97
CG6686_gene	CG6686	36.8535	37.9753	1.03	0.97
exba_gene	exba	171.257	176.468	1.03	0.97
CG3860_gene	CG3860	8.90037	9.17102	1.03	0.97
CG13917_gene	CG13917	30.7838	31.7178	1.03	0.97
CG6672_gene	CG6672	54.0827	55.7214	1.03	0.97
CG1347_gene	CG1347	49.4556	50.9538	1.03	0.97
Ngp_gene	CG14480	73.8159	76.0499	1.03	0.97
Chc_gene	Chc	241.344	248.644	1.03	0.97
CG5037_gene	CG5037	13.3369	13.74	1.03	0.97
l(2)35Bg_gene	yellow-c	19.0256	19.6002	1.03	0.97
CG3394_gene	CG3394	9.06368	9.33656	1.03	0.97
CG11127_gene	CG11141	6.39629	6.58857	1.03	0.97
CG32580_gene	CG32580	133.887	137.896	1.03	0.97
qtc_gene	qtc	37.9967	39.1341	1.03	0.97
CG12163_gene	CG12163	515.459	530.86	1.03	0.97
CG2713_gene	CG2713	8.51931	8.77372	1.03	0.97
micr_gene	micr	66.1676	68.137	1.03	0.97
CG32667_gene	CG32667	107.131	110.317	1.03	0.97
CG5261_gene	CG5261	31.0288	31.9496	1.03	0.97
l(2)k07824_gene	Nup62	8.32878	8.57507	1.03	0.97
Sac1_gene	Sac1	44.2841	45.5902	1.03	0.97
CG2218_gene	CG2218	16.1132	16.5873	1.03	0.97
CG7728_gene	CG7728	36.1186	37.1807	1.03	0.97
brm_gene	brm	73.2987	75.454	1.03	0.97
MRP_gene	CG5792	41.9433	43.1733	1.03	0.97
CG5013_gene	CG5013	2.47686	2.54935	1.03	0.97
CG15168_gene	CG15168	6.01523	6.19127	1.03	0.97
CG1812_gene	CG1812	9.5536	9.83319	1.03	0.97
CG10914_gene	CG10914	2.8307	2.91354	1.03	0.97
CG12367_gene	CG12367	20.5226	21.1231	1.03	0.97
Zn72D_gene	Zn72D	31.6548	32.5786	1.03	0.97
NAT1_gene	NAT1	215.16	221.429	1.03	0.97

CG5554_gene	CG5554	65.5688	67.4749	1.03	0.97
CG8828_gene	CG8828	30.2123	31.0888	1.03	0.97
CG12467_gene	CG12467	7.59389	7.81358	1.03	0.97
Drip_gene	Drip	85.7647	88.2338	1.03	0.97
CG1646_gene	CG1646	47.8225	49.199	1.03	0.97
GckIII_gene	GckIII	25.939	26.6854	1.03	0.97
angel_gene	CG30183	4.05552	4.17166	1.03	0.97
l(1)G0045_gene	Mlc-c	4.05552	4.17166	1.03	0.97
TpnC25D_gene	TpnC25D	18.8622	19.4015	1.03	0.97
Csp_gene	Csp	86.2002	88.6642	1.03	0.97
mRpL22_gene	mRpL22	7.40336	7.61493	1.03	0.97
CG4502_gene	CG4502	13.7452	14.1373	1.03	0.97
CG11486_gene	CG11486	16.7392	17.2164	1.03	0.97
fz4_gene	CG8300	12.6837	13.0447	1.03	0.97
bchs_gene	bchs	18.6717	19.2029	1.03	0.97
Gpdh_gene	Gpdh	82.4168	84.7574	1.03	0.97
CG12859_gene	CG12859	13.5547	13.9386	1.03	0.97
CG11900_gene	CG11899	2.64017	2.71489	1.03	0.97
CG31285_gene	epsin-like	2.64017	2.71489	1.03	0.97
tral_gene	tral	66.1676	68.0377	1.03	0.97
CG4169_gene	CG4169	73.2987	75.3547	1.03	0.97
rho-7_gene	CG34231	8.9548	9.20413	1.03	0.97
CG31033_gene	CG31033	7.02231	7.21763	1.03	0.97
CG5171_gene	CG5160	6.66847	6.85343	1.03	0.97
CG7998_gene	CG7998	105.062	107.966	1.03	0.97
bft_gene	bft	7.53945	7.74736	1.03	0.97
Snoo_gene	Snoo	13.5002	13.8724	1.03	0.97
CG5189_gene	CG5189	5.9608	6.12505	1.03	0.97
KCNQ_gene	CG18011	13.1464	13.5082	1.03	0.97
REG_gene	REG	57.4849	59.0653	1.03	0.97
CG14636_gene	CG12582	2.80348	2.88043	1.03	0.97
CG11137_gene	CG33170	13.3097	13.6738	1.03	0.97
CG5630_gene	CG31191	11.3772	11.6873	1.03	0.97
CG11248_gene	CG11248	59.1452	60.7539	1.03	0.97
CG6903_gene	CG6903	32.3353	33.2077	1.03	0.97
drk_gene	drk	82.0902	84.2939	1.03	0.97
CG2843_gene	CG2843	12.5748	12.9123	1.03	0.97
CG9399_gene	CG9399	20.958	21.5204	1.03	0.97
CG8545_gene	CG8828	30.2123	31.0225	1.03	0.97
PRL-1_gene	PRL-1	123.598	126.904	1.03	0.97
CG9596_gene	CG11043	8.02938	8.24399	1.03	0.97
CG31729_gene	CG31729	198.802	204.113	1.03	0.97
CG9266_gene	CG9266	3.83777	3.9399	1.03	0.97
CG2658_gene	CG2658	13.2553	13.6075	1.03	0.97
CG32685_gene	CG32685	47.9585	49.2322	1.03	0.97
mRpL9_gene	mRpL9	12.9014	13.2434	1.03	0.97
CG5874_gene	CG5874	18.1274	18.6069	1.03	0.97
SCAR_gene	l(2)06225	28.933	29.6982	1.03	0.97
CG8607_gene	CG8607	2.61295	2.68178	1.03	0.97
hb_gene	hb	2.61295	2.68178	1.03	0.97
CG17181_gene	CG17181	1.74197	1.78785	1.03	0.97
CG34452_gene	CG34452	3.48394	3.5757	1.03	0.97
CG4074_gene	CG4074	3.48394	3.5757	1.03	0.97
CG7945_gene	CG7945	22.2917	22.8779	1.03	0.97
CG3149_gene	cv	14.0991	14.4684	1.03	0.97
CG3621_gene	CG3621	15.4872	15.892	1.03	0.97
CG10424_gene	CG10424	12.5204	12.8461	1.03	0.97
EfTuM_gene	mip120	47.4686	48.7024	1.03	0.97
Mo25_gene	Mo25	68.8349	70.6202	1.03	0.97
CG5687_gene	CG5687	49.5372	50.8214	1.03	0.97

CG1837_gene	CG1837	85.8191	88.0352	1.03	0.97
Dhod_gene	CG8021	52.4496	53.8011	1.03	0.97
alph_gene	alph	83.9955	86.148	1.03	0.98
Spn3_gene	Spn3	7604.23	7798.91	1.03	0.98
Pc_gene	CG7632	5.55252	5.69464	1.03	0.98
rev7_gene	rev7	4.16439	4.27098	1.03	0.98
CycT_gene	CycT	44.0663	45.1929	1.03	0.98
CG14683_gene	pug	11.6222	11.919	1.03	0.98
kz_gene	pcx	7.4578	7.64804	1.03	0.98
RhoGEF3_gene	RhoGEF3	4.68154	4.80071	1.03	0.98
mRpL45_gene	mRpL45	17.8552	18.3089	1.03	0.98
CG5815_gene	CG5815	13.1736	13.5082	1.03	0.98
snmRNA:649_gene	Dip-C	3.29341	3.37705	1.03	0.98
CG14286_gene	CG14286	3.81055	3.90679	1.03	0.98
CG4289_gene	CG4289	9.52639	9.76697	1.03	0.98
CG7148_gene	CG7148	6.23298	6.38992	1.03	0.98
U2A_gene	CG12107	4.3277	4.43652	1.03	0.98
mit(1)15_gene	mit(1)15	37.5612	38.505	1.03	0.98
CG6954_gene	CG6954	17.828	18.2758	1.03	0.98
Bap170_gene	Bap170	15.0517	15.4285	1.03	0.98
alc_gene	CG8058	51.878	53.1721	1.02	0.98
CG17549_gene	CG17549	146.625	150.279	1.02	0.98
CG31548_gene	CG31548	10.8873	11.1575	1.02	0.98
CG32556_gene	CG32556	25.7485	26.3874	1.02	0.98
CG9636_gene	CG9636	15.8955	16.2893	1.02	0.98
Aats-trp_gene	Aats-trp	17.964	18.4083	1.02	0.98
l(2)37Bb_gene	CG10470	9.49917	9.73386	1.02	0.98
CG3744_gene	CG3744	14.5073	14.8657	1.02	0.98
Mctp_gene	Mctp	5.00816	5.1318	1.02	0.98
CG10802_gene	CG10802	17.6102	18.0441	1.02	0.98
CG13900_gene	CG13900	42.9776	44.0341	1.02	0.98
Acp53C14b_gene	Acp53C14b	5416.27	5549.36	1.02	0.98
Spf45_gene	Spf45	14.8339	15.1967	1.02	0.98
CG15629_gene	CG15629	1.03429	1.05947	1.02	0.98
Ser7_gene	Ser7	1.03429	1.05947	1.02	0.98
CG5846_gene	CG4709	23.7887	24.3678	1.02	0.98
lic_gene	lic	18.1001	18.5407	1.02	0.98
CG9986_gene	CG9986	7.24005	7.41628	1.02	0.98
Cyp4e3_gene	Cyp4e3	3.62003	3.70814	1.02	0.98
CG11576_gene	CG11576	5.17147	5.29734	1.02	0.98
yki_gene	yki	14.6434	14.9981	1.02	0.98
Mnt_gene	Mnt	26.184	26.8178	1.02	0.98
sll_gene	sll	12.7381	13.0447	1.02	0.98
Rop_gene	Rop	49.4011	50.5896	1.02	0.98
chb_gene	chb	88.1055	90.2203	1.02	0.98
RpS13_gene	RpS13	355.47	363.994	1.02	0.98
Exp6_gene	Exp6	17.2019	17.6137	1.02	0.98
CG11444_gene	CG11444	45.4	46.4842	1.02	0.98
CG2789_gene	CG2789	52.259	53.5031	1.02	0.98
CG8455_gene	CG8455	8.24713	8.44264	1.02	0.98
CG18675_gene	CG18675	8.57375	8.77372	1.02	0.98
CG8738_gene	CG8738	1.71475	1.75474	1.02	0.98
tws_gene	tws	39.6025	40.5247	1.02	0.98
Rab11_gene	Rab11	99.9454	102.272	1.02	0.98
Hrb27C_gene	Hrb27C	220.549	225.667	1.02	0.98
gish_gene	gish	25.5307	26.1225	1.02	0.98
Apc_gene	Apc	22.1012	22.613	1.02	0.98
CG2199_gene	CG2199	14.5618	14.8988	1.02	0.98
Sply_gene	Sply	56.0151	57.3106	1.02	0.98
CG4389_gene	CG3838	95.9171	98.1332	1.02	0.98

Psf3_gene	Psf3	31.6548	32.38	1.02	0.98
fu12_gene	fu12	2.39521	2.45002	1.02	0.98
CG17840_gene	CG17840	95.1005	97.2724	1.02	0.98
CG5946_gene	CG5946	44.6379	45.6565	1.02	0.98
CG5161_gene	CG5161	9.74413	9.96562	1.02	0.98
Ent1_gene	Ent1	9.74413	9.96562	1.02	0.98
ScpX_gene	ScpX	22.8905	23.4076	1.02	0.98
CG10055_gene	CG10055	20.9853	21.4542	1.02	0.98
armi_gene	armi	2.55852	2.61556	1.02	0.98
Adar_gene	Adar	23.1627	23.6725	1.02	0.98
CG5033_gene	CG5033	21.0941	21.5536	1.02	0.98
mRpL40_gene	mRpL40	2.72182	2.7811	1.02	0.98
cdc2rk_gene	mRpL42	4.76319	4.86693	1.02	0.98
tipE_gene	CG18675	0.680456	0.695276	1.02	0.98
snoRNA:Psi28S-3385b_gene	exba	0.680456	0.695276	1.02	0.98
CG18731_gene	CG18731	16.4943	16.8522	1.02	0.98
MRG15_gene	CG4338	7.64833	7.81358	1.02	0.98
CG7215_gene	CG7217	39.7659	40.624	1.02	0.98
CG7217_gene	CG7217	39.7659	40.624	1.02	0.98
btz_gene	btz	19.0256	19.4346	1.02	0.98
AP-2sigma_gene	AP-2sigma	7.13118	7.28384	1.02	0.98
CHOp24_gene	CHOp24	207.457	211.894	1.02	0.98
CG16890_gene	p38b	5.08981	5.19802	1.02	0.98
CG5028_gene	CG5028	42.2427	43.1402	1.02	0.98
CG17698_gene	CG17698	26.2928	26.8509	1.02	0.98
CG2217_gene	CG2217	2.20468	2.25137	1.02	0.98
CG5597_gene	CG5597	4.40936	4.50274	1.02	0.98
viaf_gene	CG6931	13.2281	13.5082	1.02	0.98
bur_gene	bur	33.3968	34.1016	1.02	0.98
CG4996_gene	CG4996	9.66248	9.8663	1.02	0.98
CG8207_gene	CG8207	26.7828	27.3475	1.02	0.98
UbcD4_gene	UbcD4	35.2476	35.9888	1.02	0.98
Nhe2_gene	Nhe2	185.547	189.446	1.02	0.98
mRpL1_gene	mRpL1	6.77734	6.91965	1.02	0.98
RpII215_gene	PGRP-SA	59.6352	60.8863	1.02	0.98
CG6543_gene	CG30485	11.35	11.5879	1.02	0.98
CG5805_gene	CG5805	9.14533	9.33656	1.02	0.98
CG9932_gene	CG9932	256.069	261.391	1.02	0.98
PHGPx_gene	CG11526	46.5432	47.5105	1.02	0.98
CG10754_gene	CG11006	10.9962	11.2237	1.02	0.98
CG10962_gene	rdgA	65.106	66.4485	1.02	0.98
CG6424_gene	CG6424	53.0756	54.1653	1.02	0.98
RpL3_gene	RpL3	626.156	638.992	1.02	0.98
Rpb5_gene	Rpb5	16.0315	16.3555	1.02	0.98
AttC_gene	AttC	0.843766	0.860818	1.02	0.98
CG12279_gene	CG12279	5.90636	6.02572	1.02	0.98
Mi-2_gene	Mi-2	248.394	253.378	1.02	0.98
CG5319_gene	Brf	89.0309	90.8163	1.02	0.98
trc_gene	trc	21.0669	21.4873	1.02	0.98
TSG101_gene	TSG101	21.0669	21.4873	1.02	0.98
Vrp1_gene	Vrp1	14.9973	15.2961	1.02	0.98
CG17754_gene	CG17754	23.9248	24.4009	1.02	0.98
CG3226_gene	CG3226	20.5498	20.9576	1.02	0.98
mts_gene	mts	155.634	158.722	1.02	0.98
fidipidine_gene	fidipidine	14.3168	14.6008	1.02	0.98
Ccn_gene	Ccn	28.2798	28.8374	1.02	0.98
e(r)_gene	e(r)	34.8394	35.5253	1.02	0.98
dpr7_gene	dpr7	3.70168	3.77436	1.02	0.98
Rme-8_gene	Rme-8	38.8677	39.6307	1.02	0.98
CG5114_gene	CG5114	14.97	15.263	1.02	0.98

CG8270_gene	CG8270	5.87914	5.99262	1.02	0.98
CG5045_gene	CG5045	21.6657	22.0833	1.02	0.98
RpL37A_gene	RpL37A	105.471	107.503	1.02	0.98
CG6133_gene	CG6133	17.964	18.3089	1.02	0.98
rb_gene	rb	23.1627	23.6063	1.02	0.98
CG14057_gene	CG14057	1.00708	1.02636	1.02	0.98
CG1249_gene	CG17919	37.5884	38.3064	1.02	0.98
CG2017_gene	CG2017	17.2836	17.6137	1.02	0.98
CG11113_gene	CG11166	94.9645	96.7758	1.02	0.98
CG31064_gene	CG31064	8.54653	8.7075	1.02	0.98
Fim_gene	Fim	58.9819	60.0917	1.02	0.98
Aats-gln_gene	CG11858	47.7408	48.6362	1.02	0.98
CG3654_gene	CG3654	49.9183	50.8545	1.02	0.98
CG15803_gene	CG15803	2.17746	2.21826	1.02	0.98
CG2091_gene	CG2091	4.51823	4.60206	1.02	0.98
CG6084_gene	CG6084	53.8649	54.8606	1.02	0.98
rogdi_gene	rogdi	5.85192	5.95951	1.02	0.98
Sap-r_gene	CG15547	628.252	639.786	1.02	0.98
CG3634_gene	CG3634	18.0457	18.3751	1.02	0.98
sqh_gene	sqh	55.6069	56.6153	1.02	0.98
CG3493_gene	CG13550	61.9215	63.0384	1.02	0.98
Uch-L3_gene	Uch-L3	12.6837	12.9123	1.02	0.98
CG14270_gene	CG14270	5.17147	5.26423	1.02	0.98
CG3980_gene	CG3980	1.33369	1.35744	1.02	0.98
CG34183_gene	FKBP59	1.33369	1.35744	1.02	0.98
CG7371_gene	cl	20.1687	20.5272	1.02	0.98
CG2246_gene	CG2246	17.6646	17.9778	1.02	0.98
CG8043_gene	CG8043	6.83178	6.95276	1.02	0.98
Bin1_gene	CG8927	6.83178	6.95276	1.02	0.98
CG1427_gene	CG1427	10.9962	11.1906	1.02	0.98
CG34293_gene	CG31065	4.16439	4.23787	1.02	0.98
DLP_gene	DLP	26.6467	27.1158	1.02	0.98
Trip1_gene	CG34125	148.503	151.107	1.02	0.98
Arf72A_gene	Arf72A	41.4534	42.1801	1.02	0.98
CG8320_gene	CG8320	22.9722	23.3745	1.02	0.98
Kap-alpha1_gene	Kap-alpha1	22.2917	22.6792	1.02	0.98
CG10311_gene	CG10311	11.976	12.1839	1.02	0.98
roX1_gene	roX1	436.445	444.016	1.02	0.98
Ald_gene	Ald	258.138	262.583	1.02	0.98
CG34036_gene	CG2165	45.3728	46.1531	1.02	0.98
CG7146_gene	CG7146	4.81763	4.90004	1.02	0.98
Fer2LCH_gene	Fer1HCH	125.912	128.063	1.02	0.98
CG5127_gene	CG5127	4.98094	5.06558	1.02	0.98
Fatp_gene	Fatp	97.7679	99.4245	1.02	0.98
Pros29_gene	Pros29	39.4937	40.1605	1.02	0.98
CG15641_gene	CG15641	86.3907	87.8365	1.02	0.98
Pros26_gene	Pros26	34.4855	35.0618	1.02	0.98
ec_gene	ec	3.64724	3.70814	1.02	0.98
rnh1_gene	rnh1	5.47087	5.56221	1.02	0.98
Ac76E_gene	Ac76E	22.3734	22.7455	1.02	0.98
CG4751_gene	CG4751	11.4317	11.621	1.02	0.98
CG30437_gene	CG30437	21.0397	21.388	1.02	0.98
CG16868_gene	CG16868	9.60804	9.76697	1.02	0.98
CG1529_gene	CG1529	8.27435	8.40953	1.02	0.98
xmas-1_gene	xmas-1	2.15024	2.18515	1.02	0.98
CG6091_gene	CG6091	26.2928	26.7185	1.02	0.98
CG15100_gene	CG15100	27.2727	27.7117	1.02	0.98
Zeelin1_gene	Zeelin1	94.3657	95.8819	1.02	0.98
CG2701_gene	CG2694	31.056	31.5523	1.02	0.98
tai_gene	tai	67.2291	68.3026	1.02	0.98

pncr011:3L_gene	pncr011:3L	7.26727	7.38317	1.02	0.98
CG1514_gene	CG1514	7.43058	7.54871	1.02	0.98
CG5590_gene	CG5590	25.7485	26.1556	1.02	0.98
CG9213_gene	CG32584	5.28034	5.36356	1.02	0.98
Miro_gene	Miro	26.565	26.9833	1.02	0.98
CG5027_gene	CG5027	10.724	10.8927	1.02	0.98
CG32056_gene	CG32056	61.8126	62.7735	1.02	0.98
MESR6_gene	MESR6	9.71691	9.8663	1.02	0.98
Cyp9f3Psi_gene	CG34402	3.29341	3.34395	1.02	0.98
CG4699_gene	CG4699	43.6308	44.299	1.02	0.98
CG17472_gene	CG17472	1847.68	1875.89	1.02	0.98
CG16974_gene	CG16974	67.3107	68.3357	1.02	0.99
growl_gene	growl	150.408	152.696	1.02	0.99
CG14687_gene	CG14687	7.24005	7.35006	1.02	0.99
CG1381_gene	Jra	14.4801	14.7001	1.02	0.99
CG10777_gene	CG10777	62.6836	63.6343	1.02	0.99
CG7845_gene	CG7845	11.5133	11.6873	1.02	0.99
pall_gene	CG3654	7.72998	7.84669	1.02	0.99
CG4038_gene	CG34396	20.7131	21.0238	1.02	0.99
Myb_gene	Myb	29.2596	29.6982	1.01	0.99
CG3356_gene	CG3356	21.3663	21.686	1.01	0.99
Xe7_gene	Xe7	32.5258	33.0091	1.01	0.99
CG10635_gene	CG4780	13.963	14.1704	1.01	0.99
mask_gene	mask	139.085	141.141	1.01	0.99
Hmgcr_gene	Rpn9	154.681	156.967	1.01	0.99
CG7518_gene	CG7518	29.6951	30.1286	1.01	0.99
JhI-26_gene	JhI-26	36.0914	36.6179	1.01	0.99
CG4764_gene	CG4764	20.4953	20.7921	1.01	0.99
gammaSnap_gene	gammaSnap	7.04953	7.15141	1.01	0.99
CG5174_gene	CG5174	78.3341	79.4601	1.01	0.99
CG11858_gene	CG11858	8.02938	8.14466	1.01	0.99
CR41111_gene	CR41111	27.681	28.0759	1.01	0.99
Nle_gene	CG2794	9.33586	9.469	1.01	0.99
CG8931_gene	CG8931	9.33586	9.469	1.01	0.99
CG1598_gene	CG2137	32.7435	33.2077	1.01	0.99
Cyp49a1_gene	G-oalpha47A	11.4589	11.621	1.01	0.99
E(bx)_gene	E(bx)	59.1725	59.9924	1.01	0.99
CG32155_gene	CG32155	1.63309	1.65542	1.01	0.99
CG17026_gene	brm	10.9417	11.0913	1.01	0.99
CG10495_gene	CG10495	2.44964	2.48313	1.01	0.99
D12_gene	D12	2.44964	2.48313	1.01	0.99
CG5524_gene	CG5524	3.10288	3.1453	1.01	0.99
l(1)10Bb_gene	l(1)10Bb	5.71583	5.79397	1.01	0.99
Tbp-1_gene	Tbp-1	35.1115	35.5915	1.01	0.99
CG12034_gene	CG12034	13.5547	13.74	1.01	0.99
Rab5_gene	Rab5	78.3885	79.4601	1.01	0.99
CG3267_gene	CG3267	5.87914	5.95951	1.01	0.99
CG18004_gene	CG18004	3.91943	3.97301	1.01	0.99
nopo_gene	nopo	1.30648	1.32434	1.01	0.99
Ilk_gene	Ilk	37.7245	38.2402	1.01	0.99
CG13640_gene	CG13640	0.816547	0.827709	1.01	0.99
CG14632_gene	CG14632	0.816547	0.827709	1.01	0.99
CG5859_gene	CG5859	6.20576	6.29059	1.01	0.99
CG2224_gene	CG2224	3.59281	3.64192	1.01	0.99
CG13807_gene	CG13807	2.93957	2.97975	1.01	0.99
dmt_gene	dmt	13.2281	13.4089	1.01	0.99
RpII18_gene	RpII18	11.2684	11.4224	1.01	0.99
Nup154_gene	Nup154	14.0174	14.2035	1.01	0.99
CG9467_gene	CG9467	212.166	214.973	1.01	0.99
Trax_gene	Trax	12.221	12.3825	1.01	0.99

unc-119_gene	unc-119	21.829	22.1164	1.01	0.99
CG9216_gene	CG9216	156.178	158.225	1.01	0.99
CG10730_gene	bwa	278.089	281.719	1.01	0.99
Khc-73_gene	Khc-73	43.6308	44.1997	1.01	0.99
msopa_gene	msopa	2112.52	2140.03	1.01	0.99
RpL23_gene	RpL23	380.593	385.547	1.01	0.99
ewg_gene	ewg	18.6989	18.938	1.01	0.99
for_gene	for	119.924	121.442	1.01	0.99
retn_gene	retn	146.897	148.756	1.01	0.99
CG3558_gene	CG3558	16.2493	16.4549	1.01	0.99
l(3)L1231_gene	l(3)L1231	26.32	26.6522	1.01	0.99
CG3760_gene	CG3760	35.7376	36.1875	1.01	0.99
jp_gene	jp	43.6853	44.2328	1.01	0.99
CG33111_gene	CG33111	156.505	158.457	1.01	0.99
CG3560_gene	CG32576	58.2743	58.9991	1.01	0.99
CG3033_gene	CG3033	38.6227	39.101	1.01	0.99
CG12868_gene	CG12868	4.21883	4.27098	1.01	0.99
CG3194_gene	CG3194	8.43766	8.54196	1.01	0.99
CG8228_gene	CG8228	8.43766	8.54196	1.01	0.99
CG12581_gene	CG12581	65.2149	66.0181	1.01	0.99
CG6051_gene	CG6051	59.8529	60.5883	1.01	0.99
brn_gene	brn	3.89221	3.9399	1.01	0.99
capt_gene	CG4764	38.1055	38.5713	1.01	0.99
Nmdmc_gene	Nmdmc	68.2089	69.031	1.01	0.99
l(2)s5379_gene	CG15387	178.361	180.507	1.01	0.99
CG13913_gene	CG13913	15.215	15.3954	1.01	0.99
CG10631_gene	CG10631	17.8007	18.011	1.01	0.99
rin_gene	rin	148.993	150.742	1.01	0.99
woc_gene	woc	48.2035	48.7686	1.01	0.99
CG14980_gene	CG14977	10.3429	10.4622	1.01	0.99
Pp1alpha-96A_gene	p1alpha-96	127.817	129.288	1.01	0.99
CG11771_gene	CG11771	27.9531	28.2746	1.01	0.99
RpL15_gene	RpL15	515.214	521.126	1.01	0.99
CG9132_gene	CG9132	64.6161	65.3559	1.01	0.99
CG14482_gene	CG14482	12.2754	12.4156	1.01	0.99
katanin-60_gene	CG1115	17.1203	17.3157	1.01	0.99
CG5741_gene	CG5741	19.5427	19.7657	1.01	0.99
CG14442_gene	CG14442	43.277	43.7693	1.01	0.99
kis_gene	kis	130.348	131.804	1.01	0.99
CG32138_gene	CG32138	61.4588	62.1444	1.01	0.99
CG7239_gene	CG7239	4.35492	4.40341	1.01	0.99
CG41623_gene	CR41111	27.4088	27.7117	1.01	0.99
Frq1_gene	Frq1	2.0958	2.11894	1.01	0.99
mRpL11_gene	mRpL11	2.0958	2.11894	1.01	0.99
Ptp99A_gene	Ptp99A	37.7245	38.1409	1.01	0.99
Tsp42Eg_gene	Tsp42Eg	12.2482	12.3825	1.01	0.99
p38b_gene	p38b	25.939	26.2218	1.01	0.99
Rac1_gene	Rac1	145.618	147.2	1.01	0.99
CG3501_gene	PIP5K59B	17.7191	17.9116	1.01	0.99
CG15439_gene	CG15439	5.79749	5.86018	1.01	0.99
CG6796_gene	CG6796	1.9325	1.95339	1.01	0.99
MED11_gene	MED11	5.63418	5.69464	1.01	0.99
CG10225_gene	Hmgcr	20.4409	20.6596	1.01	0.99
CG8209_gene	CG8209	25.7485	26.0232	1.01	0.99
moody_gene	moody	12.5476	12.6805	1.01	0.99
Mapmodulin_gene	Mapmoduli	51.4697	52.0133	1.01	0.99
rap_gene	rap	14.1535	14.3028	1.01	0.99
Pitslre_gene	Pitslre	86.3091	87.2075	1.01	0.99
CG10743_gene	CG10743	26.6739	26.9502	1.01	0.99
CG12252_gene	ori	4.98094	5.03247	1.01	0.99

RpS18_gene	RpS18	392.841	396.903	1.01	0.99
CG8602_gene	CG8602	92.7053	93.6636	1.01	0.99
GNBP1_gene	GNBP1	1.60588	1.62231	1.01	0.99
CG4589_gene	CG4589	93.7396	94.69	1.01	0.99
Tfb1_gene	Tfb1	17.0114	17.1832	1.01	0.99
CG34013_gene	dpr7	3.04844	3.07908	1.01	0.99
Sras_gene	Sucb	3.04844	3.07908	1.01	0.99
CG4936_gene	CG4936	9.14533	9.23724	1.01	0.99
Acp53Ea_gene	Acp53Ea	3649.34	3685.26	1.01	0.99
CG3279_gene	RabX6	7.04953	7.1183	1.01	0.99
CG10855_gene	CG10855	4.16439	4.20476	1.01	0.99
CG5872_gene	CG5872	4.16439	4.20476	1.01	0.99
trus_gene	trus	4.16439	4.20476	1.01	0.99
CG16721_gene	CG16721	31.8726	32.1813	1.01	0.99
Nxt1_gene	CG5543	2.72182	2.748	1.01	0.99
SF2_gene	SF2	39.6842	40.0611	1.01	0.99
CG31680_gene	CG31680	386.363	389.984	1.01	0.99
EfSec_gene	EfSec	2.55852	2.58245	1.01	0.99
pita_gene	CG17280	13.9085	14.038	1.01	0.99
CG7065_gene	CG7065	15.1878	15.3292	1.01	0.99
CG7453_gene	CG7453	24.6053	24.8313	1.01	0.99
Dr_gene	Dr	15.3239	15.4616	1.01	0.99
CG8993_gene	CG8993	16.2765	16.4218	1.01	0.99
CG7265_gene	CG3731	18.5084	18.6731	1.01	0.99
CG7246_gene	CG7246	4.46379	4.50274	1.01	0.99
CG34383_gene	CG34383	26.7828	27.0164	1.01	0.99
CG16969_gene	CG16969	1.11595	1.12568	1.01	0.99
CG7366_gene	CG7366	1.11595	1.12568	1.01	0.99
CG33214_gene	CG33214	79.2051	79.8905	1.01	0.99
Rgl_gene	Rgl	39.3576	39.6969	1.01	0.99
att-ORFA_gene	att-ORFA	7.64833	7.71425	1.01	0.99
CG34439_gene	TppII	8.60097	8.67439	1.01	0.99
Gap69C_gene	Gap69C	99.3466	100.186	1.01	0.99
CG33129_gene	CG33129	45.0462	45.4247	1.01	0.99
CG5130_gene	CG5130	79.5861	80.2547	1.01	0.99
Rlb1_gene	Rlb1	7.32171	7.38317	1.01	0.99
CG2310_gene	CG2310	2.06859	2.08583	1.01	0.99
Trn-SR_gene	Trn-SR	8.11104	8.17777	1.01	0.99
boi_gene	boi	10.0163	10.0981	1.01	0.99
CG32039_gene	CG32039	12.8742	12.9785	1.01	0.99
CG17280_gene	CG17280	45.1279	45.4909	1.01	0.99
CG17184_gene	CG17184	12.7109	12.8129	1.01	0.99
CG5177_gene	CG5177	53.375	53.8011	1.01	0.99
Mkrn1_gene	Mkrn1	24.1426	24.3347	1.01	0.99
Ppox_gene	CG31126	12.3843	12.4819	1.01	0.99
Pur-alpha_gene	Pur-alpha	25.7212	25.9239	1.01	0.99
CG34140_gene	CG13875	15.2422	15.3623	1.01	0.99
Mkp_gene	CG13875	15.2422	15.3623	1.01	0.99
CG7154_gene	CG7154	16.0315	16.1569	1.01	0.99
TfIIEalpha_gene	TfIIEalpha	9.36308	9.43589	1.01	0.99
Taf13_gene	CG10721	5.55252	5.59532	1.01	0.99
CG10463_gene	CG10463	4.59988	4.63517	1.01	0.99
Sir2_gene	DnaJ-H	56.124	56.5491	1.01	0.99
Tab2_gene	Tab2	16.1676	16.2893	1.01	0.99
maf-S_gene	maf-S	75.4218	75.9837	1.01	0.99
CG1553_gene	mus205	64.6433	65.1242	1.01	0.99
l(2)k07433_gene	l(2)k07433	35.166	35.426	1.01	0.99
por_gene	por	12.1938	12.2832	1.01	0.99
CG8009_gene	CG8009	6.80456	6.85343	1.01	0.99
wfs1_gene	wfs1	6.80456	6.85343	1.01	0.99

Timp_gene	Syn	31.3282	31.5523	1.01	0.99
CG5828_gene	CG5828	2.5313	2.54935	1.01	0.99
CG2794_gene	CG2794	10.9145	10.992	1.01	0.99
CG14656_gene	CG14656	21.5024	21.6529	1.01	0.99
CG16758_gene	CG33232	67.8279	68.3026	1.01	0.99
CG3678_gene	CG3678	16.4398	16.5542	1.01	0.99
CG18178_gene	CG18178	12.1666	12.2501	1.01	0.99
CG2469_gene	CG2277	55.7702	56.1518	1.01	0.99
CG10354_gene	CG10354	23.2172	23.3745	1.01	0.99
eas_gene	eas	100.898	101.577	1.01	0.99
CG5498_gene	CG5498	5.5253	5.56221	1.01	0.99
CG15107_gene	CG15107	1.57866	1.5892	1.01	0.99
NPFR76F_gene	NPFR76F	3.15732	3.1784	1.01	0.99
CG5555_gene	CG5555	9.30864	9.36967	1.01	0.99
CG9953_gene	CG9953	29.0146	29.2016	1.01	0.99
kto_gene	kto	19.706	19.8319	1.01	0.99
Rb97D_gene	Rb97D	19.706	19.8319	1.01	0.99
CG8963_gene	CG8963	104.79	105.45	1.01	0.99
Pat1_gene	Pat1	31.9542	32.1482	1.01	0.99
Su(var)3-7_gene	Su(var)3-7	19.5155	19.6333	1.01	0.99
CG9018_gene	CG9018	6.45072	6.48924	1.01	0.99
CG3436_gene	CG3436	25.0136	25.1624	1.01	0.99
Nopp140_gene	Nopp140	36.9624	37.1807	1.01	0.99
CG6700_gene	Nos	83.0429	83.5324	1.01	0.99
CG1542_gene	CG1542	15.5688	15.6603	1.01	0.99
beta4GalNAcTB_gene	ta4GalNAc	7.07674	7.1183	1.01	0.99
fal_gene	fal	2.8307	2.84732	1.01	0.99
mRpL34_gene	mRpL34	1.41535	1.42366	1.01	0.99
CG4332_gene	CG4332	28.933	29.1023	1.01	0.99
CG4538_gene	CG4538	69.1616	69.5607	1.01	0.99
CG34051_gene	CG34051	941.397	946.8	1.01	0.99
Neb-cGP_gene	Neb-cGP	16.6576	16.7528	1.01	0.99
alphaTub84B_gene	lphaTub84	226.265	227.554	1.01	0.99
CG6204_gene	CG6204	24.6597	24.7982	1.01	0.99
ldlCp_gene	CG5044	39.5753	39.7963	1.01	0.99
Obp22a_gene	Obp22a	378.551	380.647	1.01	0.99
RpL23A_gene	RpL23A	504.572	507.353	1.01	0.99
Calx_gene	Calx	33.424	33.605	1.01	0.99
Crag_gene	CG12659	26.184	26.3212	1.01	0.99
CG10660_gene	CG10660	11.595	11.6541	1.01	0.99
CycK_gene	CycK	33.2063	33.3732	1.01	0.99
CG7140_gene	CG7140	19.7332	19.8319	1.01	1.00
noi_gene	noi	17.6919	17.7792	1.00	1.00
RpL13A_gene	RpL13A	464.098	466.365	1.00	1.00
Atet_gene	Atet	9.39029	9.43589	1.00	1.00
CG6379_gene	CG6379	12.5204	12.5812	1.00	1.00
dpr_gene	dpr	15.6505	15.7265	1.00	1.00
mRpL27_gene	mRpL27	3.75612	3.77436	1.00	1.00
Rbf2_gene	Rbf2	1.25204	1.25812	1.00	1.00
CG8777_gene	CG8777	8.76428	8.80683	1.00	1.00
CG11534_gene	CG11534	6.2602	6.29059	1.00	1.00
CG2010_gene	CG2010	11.2684	11.3231	1.00	1.00
raps_gene	raps	11.2684	11.3231	1.00	1.00
S1P_gene	S1P	4.38214	4.40341	1.00	1.00
CG13343_gene	CG13343	7.18562	7.21763	1.00	1.00
CG5986_gene	Rox8	10.7784	10.8264	1.00	1.00
prd_gene	prd	204.79	205.702	1.00	1.00
CG15014_gene	CG32250	9.52639	9.56832	1.00	1.00
CG3061_gene	CG3061	110.207	110.681	1.00	1.00
CG2162_gene	CG2162	12.9559	13.0116	1.00	1.00

CG14040_gene	eIF-3p40	61.0233	61.2836	1.00	1.00
CG11131_gene	CG11131	18.7262	18.8056	1.00	1.00
CG13284_gene	CG13284	41.9705	42.147	1.00	1.00
RFeSP_gene	RFeSP	67.8551	68.137	1.00	1.00
CG7006_gene	CG7006	4.05552	4.07233	1.00	1.00
pbl_gene	pbl	11.5405	11.5879	1.00	1.00
Eip55E_gene	Eip55E	59.7168	59.9593	1.00	1.00
Poxm_gene	Poxm	14.344	14.4021	1.00	1.00
Glycogenin_gene	Glycogenin	140.909	141.472	1.00	1.00
gw_gene	gw	119.624	120.084	1.00	1.00
CG5446_gene	CG5446	35.3565	35.4922	1.00	1.00
yemalpha_gene	CG11877	5.60696	5.62842	1.00	1.00
Sema-1b_gene	Sema-1b	35.1932	35.3266	1.00	1.00
prominin-like_gene	rominin-lik	6.69569	6.721	1.00	1.00
CG6422_gene	CG6422	26.1567	26.2549	1.00	1.00
CG7864_gene	CG12099	8.87315	8.90615	1.00	1.00
Top3beta_gene	Top3beta	22.1012	22.1826	1.00	1.00
CG3280_gene	CG3280	1.08873	1.09258	1.00	1.00
CG17493_gene	CG17493	20.0598	20.1299	1.00	1.00
CG32113_gene	CG32113	17.2564	17.3157	1.00	1.00
CG13965_gene	CG13965	182.117	182.725	1.00	1.00
l(1)G0084_gene	l(1)G0084	23.9248	24.0036	1.00	1.00
jdp_gene	jdp	10.098	10.1312	1.00	1.00
CG3058_gene	CG3058	6.36907	6.38992	1.00	1.00
Pp2C1_gene	Pp2C1	18.9439	19.0042	1.00	1.00
CG14164_gene	CalpB	16.1404	16.19	1.00	1.00
CG6709_gene	CalpB	16.1404	16.19	1.00	1.00
CG6168_gene	CG6168	885.165	887.867	1.00	1.00
ytr_gene	ytr	77.572	77.8047	1.00	1.00
Dok_gene	Dok	4.65432	4.66828	1.00	1.00
CG32243_gene	CG32243	6.20576	6.22437	1.00	1.00
CG40120_gene	CG40120	21.5569	21.6198	1.00	1.00
Atg5_gene	Atg5	7.13118	7.15141	1.00	1.00
Ski6_gene	CG5705	3.56559	3.5757	1.00	1.00
ATPCL_gene	CG8320	126.02	126.375	1.00	1.00
CG8538_gene	CG8538	13.6363	13.6738	1.00	1.00
CG11836_gene	CG11836	4.0283	4.03922	1.00	1.00
CG14153_gene	CG32066	4.0283	4.03922	1.00	1.00
CG7358_gene	CG7358	25.0952	25.1624	1.00	1.00
asf1_gene	asf1	6.50516	6.52235	1.00	1.00
CG14641_gene	CG14641	22.4551	22.5137	1.00	1.00
CG9448_gene	CG9448	31.7365	31.8172	1.00	1.00
Eb1_gene	Eb1	34.676	34.7638	1.00	1.00
Dot_gene	Dot	2.47686	2.48313	1.00	1.00
CG14425_gene	Sxl	35.7376	35.8233	1.00	1.00
Sxl_gene	Sxl	35.7376	35.8233	1.00	1.00
CG40084_gene	CG40084	42.8415	42.9416	1.00	1.00
CG13625_gene	CG13625	13.1464	13.1771	1.00	1.00
CG3305_gene	CG3305	271.039	271.588	1.00	1.00
NP15.6_gene	gatA	43.0865	43.1733	1.00	1.00
alpha-Cat_gene	alpha-Cat	55.2258	55.3241	1.00	1.00
CG31303_gene	CG4196	0.92542	0.927035	1.00	1.00
dikar_gene	dikar	1.85084	1.85407	1.00	1.00
brp_gene	brp	1.38813	1.39055	1.00	1.00
CG30269_gene	CG30269	1.38813	1.39055	1.00	1.00
RhoGAP16F_gene	RhoGAP16F	1.38813	1.39055	1.00	1.00
CG9318_gene	CG9318	253.075	253.511	1.00	1.00
CG5521_gene	CG5521	46.2438	46.3186	1.00	1.00
ash2_gene	ash2	12.7926	12.8129	1.00	1.00
CG5087_gene	CG5087	21.4208	21.4542	1.00	1.00

CG12162_gene	CG12162	9.5536	9.56832	1.00	1.00
Su(Tpl)_gene	Mi-2	113.255	113.429	1.00	1.00
cdi_gene	cdi	77.1909	77.3081	1.00	1.00
CG6116_gene	CG6116	8.16547	8.17777	1.00	1.00
Ahcy13_gene	Ahcy13	32.6619	32.7111	1.00	1.00
Uba1_gene	Uba1	170.087	170.343	1.00	1.00
CG17471_gene	CG33521	18.9439	18.9711	1.00	1.00
CG6192_gene	CG6192	44.0391	44.1004	1.00	1.00
CG12424_gene	CG12424	34.4855	34.532	1.00	1.00
Top1_gene	Top1	90.9634	91.0811	1.00	1.00
Sk2_gene	Sk2	26.6194	26.6522	1.00	1.00
CG4330_gene	CG4330	237.234	237.519	1.00	1.00
CalpA_gene	CalpA	7.07674	7.08519	1.00	1.00
CG9253_gene	CG9253	29.9945	30.0293	1.00	1.00
CG6695_gene	CG6695	15.841	15.8589	1.00	1.00
Cdep_gene	Cdep	53.2117	53.2714	1.00	1.00
tna_gene	tna	49.6733	49.7288	1.00	1.00
CG11619_gene	CG11619	21.6657	21.686	1.00	1.00
CG31392_gene	CG31392	2.15024	2.15204	1.00	1.00
Traf2_gene	Traf2	12.4387	12.4487	1.00	1.00
CREG_gene	CREG	8.13826	8.14466	1.00	1.00
Egm_gene	Egm	9.82579	9.83319	1.00	1.00
CG14196_gene	CG14196	5.5253	5.5291	1.00	1.00
nkd_gene	nkd	11.0506	11.0582	1.00	1.00
RpL22_gene	RpL22	386.771	387.037	1.00	1.00
CG12272_gene	CG12272	13.5002	13.5082	1.00	1.00
CG9772_gene	CG14645	4.59988	4.60206	1.00	1.00
bab2_gene	bab2	4.13717	4.13855	1.00	1.00
CG31938_gene	Eno	6.58682	6.58857	1.00	1.00
eIF6_gene	ytr	24.197	24.2022	1.00	1.00
Ice_gene	Ice	2.44964	2.45002	1.00	1.00
CG14043_gene	CG14043	11.0234	11.0251	1.00	1.00
Xbp1_gene	Xbp1	495.59	495.632	1.00	1.00
Zyx102EF_gene	Zyx102EF	18.209	18.2096	1.00	1.00
CG4747_gene	CG4747	40.3919	40.3922	1.00	1.00
CG7530_gene	CG7530	10.8601	10.8595	1.00	1.00
ND75_gene	ND75	89.4664	89.4588	1.00	1.00
vsg_gene	vsg	328.905	328.866	1.00	1.00
aralar1_gene	aralar1	25.9934	25.9901	1.00	1.00
slpr_gene	slpr	24.1426	24.136	1.00	1.00
CG2446_gene	CG2446	77.4359	77.4074	1.00	1.00
nompB_gene	nompB	213.364	213.284	1.00	1.00
omd_gene	lkb1	16.4943	16.488	1.00	1.00
X11L_gene	X11L	7.02231	7.01898	1.00	1.00
RpL7_gene	RpL7	654.435	654.089	1.00	1.00
Neurochondrin_gene	eurochondr	26.4017	26.3874	1.00	1.00
AP-50_gene	AP-50	14.344	14.3359	1.00	1.00
CG12000_gene	CG12000	50.1904	50.1592	1.00	1.00
CG5366_gene	CG5366	44.393	44.3652	1.00	1.00
Abl_gene	Abl	25.4763	25.4603	1.00	1.00
BG642312_gene	BG642312	7227.86	7223.06	1.00	1.00
CG31917_gene	CG31917	14.1807	14.1704	1.00	1.00
TFAM_gene	TFAM	14.9428	14.9319	1.00	1.00
CG15589_gene	CG15589	0.762111	0.761493	1.00	1.00
CG30105_gene	icln	0.762111	0.761493	1.00	1.00
CG8360_gene	CG8360	9.14533	9.13791	1.00	1.00
CG10565_gene	CG10566	55.1442	55.0923	1.00	1.00
CG9784_gene	CG9784	13.8541	13.8393	1.00	1.00
CG8765_gene	CG8765	6.99509	6.98587	1.00	1.00
fws_gene	fws	59.1452	59.0653	1.00	1.00

orb2_gene	orb2	27.817	27.7779	1.00	1.00
D19A_gene	D19A	13.5275	13.5082	1.00	1.00
CG4420_gene	CG4420	17.7735	17.7461	1.00	1.00
CG10226_gene	CG10226	4.70876	4.70139	1.00	1.00
gatA_gene	CG14285	45.2639	45.1929	1.00	1.00
CG9086_gene	CG9086	70.9307	70.8188	1.00	1.00
robo_gene	robo	8.6554	8.64129	1.00	1.00
Taf1_gene	Taf1	30.5117	30.4597	1.00	1.00
CG8312_gene	CG8312	84.2405	84.0953	1.00	1.00
Hrp59_gene	CG8149	33.5329	33.4726	1.00	1.00
CG7940_gene	CG7208	7.13118	7.1183	1.00	1.00
vls_gene	lok	2.12302	2.11894	1.00	1.00
CG12393_gene	slmo	9.5536	9.53521	1.00	1.00
mRpL35_gene	mRpL35	5.30756	5.29734	1.00	1.00
CG4930_gene	CG4930	25.7485	25.6921	1.00	1.00
RpS15Ab_gene	RpS15Ab	67.093	66.9451	1.00	1.00
CG17660_gene	CG17660	36.037	35.9557	1.00	1.00
CG7698_gene	CstF-64	6.20576	6.19127	1.00	1.00
RpS6_gene	RpS6	621.284	619.822	1.00	1.00
CG12746_gene	CG12746	24.3603	24.3015	1.00	1.00
Stlk_gene	Stlk	19.8149	19.7657	1.00	1.00
CG14567_gene	CG14567	15.8682	15.8258	1.00	1.00
Gint3_gene	Gint3	36.8535	36.7503	1.00	1.00
CG4788_gene	CG4788	1.66031	1.65542	1.00	1.00
CG11695_gene	CG11695	6.64125	6.62168	1.00	1.00
RabX6_gene	RabX6	4.98094	4.96626	1.00	1.00
CG3321_gene	CG3321	45.2367	45.0936	1.00	1.00
CG30372_gene	CG30372	18.835	18.7724	1.00	1.00
MCPH1_gene	CG30038	36.6085	36.4854	1.00	1.00
CG4061_gene	CG4199	4.51823	4.50274	1.00	1.00
CG9104_gene	CG4872	9.03646	9.00548	1.00	1.00
CG12848_gene	CG12848	7.07674	7.05208	1.00	1.00
bhr_gene	bhr	45.019	44.8619	1.00	1.00
CG11847_gene	CG11847	88.677	88.3663	1.00	1.00
CG12079_gene	CG12079	33.2607	33.1415	1.00	1.00
5-HT2_gene	5-HT2	28.5792	28.4732	1.00	1.00
mub_gene	mub	63.7723	63.535	1.00	1.00
wdn_gene	wdn	9.77135	9.73386	1.00	1.00
RpS20_gene	RpS20	94.8556	94.4913	1.00	1.00
l(3)07882_gene	CG5840	20.1415	20.0637	1.00	1.00
spag_gene	spag	3.45672	3.44327	1.00	1.00
lgs_gene	lgs	41.78	41.6172	1.00	1.00
CG1603_gene	CG1603	3.75612	3.74125	1.00	1.00
CG6144_gene	CG6144	8.11104	8.07844	1.00	1.00
CG2182_gene	MED27	45.7811	45.5902	1.00	1.00
CG17726_gene	CG17726	5.25312	5.23112	1.00	1.00
CG14830_gene	CG14830	48.013	47.8085	1.00	1.00
CG7181_gene	CG7181	26.4017	26.2881	1.00	1.00
CG3252_gene	CG3252	28.4975	28.3739	1.00	1.00
CG6428_gene	CG6428	9.74413	9.70075	1.00	1.00
RpL12_gene	RpL12	261.268	260.066	1.00	1.00
CG5734_gene	CG5734	11.3772	11.3231	1.00	1.00
CG9967_gene	CG9967	1.1976	1.1919	1.00	1.00
CG4271_gene	CG4271	156.859	156.106	1.00	1.00
bip2_gene	bip2	98.4756	98.0008	1.00	1.00
CG7536_gene	CG7536	20.1959	20.0968	1.00	1.00
CG31678_gene	CG2614	98.2579	97.769	1.00	1.01
CG7630_gene	CG7630	27.6537	27.5131	0.99	1.01
pps_gene	pps	19.8693	19.7657	0.99	1.01
CG5514_gene	CG5514	58.7098	58.4032	0.99	1.01

CG10973_gene	CG10984	6.42351	6.38992	0.99	1.01
CG14815_gene	MED18	16.8753	16.7859	0.99	1.01
CG40160_gene	CG40160	61.5132	61.1843	0.99	1.01
Lig4_gene	Lig4	4.9265	4.90004	0.99	1.01
CG32638_gene	rad	34.1861	34.0023	0.99	1.01
CG12895_gene	CG12895	4.3277	4.30409	0.99	1.01
CG9867_gene	CG9867	4.3277	4.30409	0.99	1.01
cin_gene	cin	24.7686	24.6326	0.99	1.01
CG3590_gene	Pxd	24.4692	24.3347	0.99	1.01
CR41598_gene	CG40178	10.5879	10.5285	0.99	1.01
CG7789_gene	CG7789	10.5879	10.5285	0.99	1.01
CG4858_gene	CG4858	12.8198	12.7467	0.99	1.01
dbr_gene	dbr	25.1769	25.0299	0.99	1.01
MED26_gene	MED26	49.755	49.4639	0.99	1.01
CG8064_gene	CG8064	13.5547	13.4751	0.99	1.01
CG17168_gene	CG17168	12.3571	12.2832	0.99	1.01
Srp9_gene	Srp9	23.2172	23.0765	0.99	1.01
CG9702_gene	CG9702	393.249	390.844	0.99	1.01
CG12935_gene	CG12935	6.09689	6.05883	0.99	1.01
CG6650_gene	endos	18.2907	18.1765	0.99	1.01
MED1_gene	MED1	15.46	15.3623	0.99	1.01
His3.3B_gene	His3.3B	199.864	198.584	0.99	1.01
CG3847_gene	CG3847	28.9602	28.7712	0.99	1.01
CG6931_gene	CG6931	1.63309	1.62231	0.99	1.01
CG18347_gene	CG18347	2.96679	2.94665	0.99	1.01
CG17723_gene	CG17723	61.105	60.6877	0.99	1.01
CdGAPr_gene	CdGAPr	28.7697	28.5725	0.99	1.01
CG11042_gene	His3.3B	87.18	86.5784	0.99	1.01
CG6016_gene	CG6016	33.5057	33.2739	0.99	1.01
CG17272_gene	RpS20	29.2052	29.0029	0.99	1.01
CG6951_gene	CG17233	150.871	149.815	0.99	1.01
Sucb_gene	Sucb	8.00216	7.94601	0.99	1.01
CG32719_gene	CG32719	2.66739	2.64867	0.99	1.01
CG7039_gene	CG7039	11.4044	11.3231	0.99	1.01
HPS_gene	HPS	5.03538	4.99936	0.99	1.01
CG14229_gene	CG14229	3.70168	3.67503	0.99	1.01
CG12262_gene	CG32373	46.9243	46.5835	0.99	1.01
MED18_gene	MED18	5.77027	5.72775	0.99	1.01
CG7712_gene	CG12942	21.5841	21.4211	0.99	1.01
CG11266_gene	CG11266	67.8551	67.3424	0.99	1.01
ATPsyn-gamma_gene	TPsyn-gamr	121.938	121.011	0.99	1.01
CG12828_gene	CG12828	119.57	118.66	0.99	1.01
CG17841_gene	CG17841	153.701	152.53	0.99	1.01
CG8230_gene	CG8230	152.068	150.908	0.99	1.01
CG11403_gene	CG11403	1.03429	1.02636	0.99	1.01
mus205_gene	Gapdh1	7.24005	7.18452	0.99	1.01
CG8389_gene	CG8389	7.97495	7.9129	0.99	1.01
CG6028_gene	mRpL35	12.847	12.7467	0.99	1.01
eIF2B-delta_gene	eIF2B-delta	23.6254	23.4407	0.99	1.01
aay_gene	CG3967	51.9596	51.5497	0.99	1.01
MED21_gene	CG40351	3.83777	3.80746	0.99	1.01
edl_gene	edl	11.2139	11.1244	0.99	1.01
TfIIA-L_gene	TfIIA-L	49.4283	49.0335	0.99	1.01
CG5857_gene	CG5857	11.9488	11.8528	0.99	1.01
SytIV_gene	SytIV	7.07674	7.01898	0.99	1.01
mei-W68_gene	par-1	12.3843	12.2832	0.99	1.01
Oamb_gene	Oamb	35.2204	34.9293	0.99	1.01
CG11984_gene	CG11984	33.4512	33.1746	0.99	1.01
CG13176_gene	CG13176	12.5204	12.4156	0.99	1.01
Mipp2_gene	Mipp2	42.2699	41.9152	0.99	1.01

RpS23_gene	RpS23	498.91	494.705	0.99	1.01
Magi_gene	mago	17.964	17.8123	0.99	1.01
Aats-phe_gene	Aats-phe	13.6908	13.5744	0.99	1.01
RpS24_gene	RpS24	429.722	426.005	0.99	1.01
CG6905_gene	CG6905	12.3571	12.2501	0.99	1.01
CG13964_gene	sick	12.3571	12.2501	0.99	1.01
CG3838_gene	CG3838	20.0054	19.8319	0.99	1.01
CG12734_gene	CG12734	15.4327	15.2961	0.99	1.01
CG14207_gene	CG14207	27.191	26.9502	0.99	1.01
CG33965_gene	CG33965	0.734893	0.728384	0.99	1.01
Mcm2_gene	Mcm2	0.734893	0.728384	0.99	1.01
CG30156_gene	vimar	1.46979	1.45677	0.99	1.01
CG17282_gene	CG17282	11.7583	11.6541	0.99	1.01
CG17839_gene	CG17839	21.0125	20.8252	0.99	1.01
Nep1_gene	Nep1	9.9891	9.8994	0.99	1.01
CG4911_gene	CG4911	24.5236	24.3015	0.99	1.01
CG1291_gene	CG1291	80.2666	79.5263	0.99	1.01
CG12384_gene	CG12384	32.7163	32.4131	0.99	1.01
Akt1_gene	Akt1	58.3831	57.8403	0.99	1.01
sec5_gene	sec5	22.2917	22.0833	0.99	1.01
Pk92B_gene	Pk92B	24.9319	24.6988	0.99	1.01
Rpn11_gene	Rpn11	24.9319	24.6988	0.99	1.01
CG7364_gene	CG7364	96.1893	95.2859	0.99	1.01
CG11245_gene	Pkcdelta	4.54545	4.50274	0.99	1.01
CHIP_gene	CHIP	13.7724	13.6407	0.99	1.01
myoglianin_gene	myoglianin	54.7903	54.2646	0.99	1.01
Rack1_gene	Rack1	446.025	441.732	0.99	1.01
Pabp2_gene	Pabp2	29.5862	29.3009	0.99	1.01
Ank2_gene	CG32373	3.07566	3.04597	0.99	1.01
CG10132_gene	CG10132	29.2868	29.0029	0.99	1.01
fwd_gene	fwd	50.5171	50.0268	0.99	1.01
CG2811_gene	CG3760	9.66248	9.56832	0.99	1.01
Trl_gene	Trl	40.9907	40.5909	0.99	1.01
Hdac3_gene	Hdac3	5.85192	5.79397	0.99	1.01
JTBR_gene	Patj	4.68154	4.63517	0.99	1.01
Sep2_gene	02-Sep	29.6951	29.4002	0.99	1.01
CG5640_gene	CG5640	10.2341	10.1312	0.99	1.01
Mio_gene	Mio	58.3287	57.741	0.99	1.01
ttk_gene	ttk	80.1033	79.2946	0.99	1.01
nrm_gene	nrm	17.0931	16.9184	0.99	1.01
lilli_gene	lilli	29.9401	29.632	0.99	1.01
Ucp4A_gene	Ucp4A	7.59389	7.5156	0.99	1.01
CG12201_gene	CG12201	6.42351	6.35681	0.99	1.01
pnt_gene	pnt	8.46487	8.37642	0.99	1.01
CG17684_gene	CG17684	25.8301	25.5597	0.99	1.01
CG31495_gene	CG31495	3.64724	3.60881	0.99	1.01
CG15387_gene	CG7082	34.8666	34.4989	0.99	1.01
CG7066_gene	CG7066	5.68861	5.62842	0.99	1.01
glec_gene	glec	28.8786	28.5725	0.99	1.01
CG5726_gene	CG5726	19.6788	19.4677	0.99	1.01
MED8_gene	CG8920	6.99509	6.91965	0.99	1.01
CG16940_gene	thoc7	27.9804	27.6786	0.99	1.01
CG31493_gene	CG31493	225.993	223.548	0.99	1.01
sprt_gene	sprt	12.3843	12.2501	0.99	1.01
CG8616_gene	CG8616	13.8269	13.6738	0.99	1.01
Prosbeta5_gene	Prosbeta5	62.2753	61.5816	0.99	1.01
CG9330_gene	CG9330	63.5818	62.8728	0.99	1.01
CG17100_gene	CG17100	99.5099	98.3981	0.99	1.01
alpha4GT2_gene	alpha4GT2	71.8562	71.0506	0.99	1.01
CG7427_gene	CG7427	10.6151	10.4954	0.99	1.01

gpp_gene	gpp	28.933	28.6056	0.99	1.01
CG34200_gene	CG34200	7.26727	7.18452	0.99	1.01
rasp_gene	rasp	18.8895	18.6731	0.99	1.01
CG17278_gene	CG17278	11.1867	11.0582	0.99	1.01
Arp66B_gene	Arp66B	33.6962	33.307	0.99	1.01
Ino80_gene	Ino80	96.1076	94.9879	0.99	1.01
CG15880_gene	CG15880	0.870984	0.860818	0.99	1.01
CG30010_gene	CG30010	1.30648	1.29123	0.99	1.01
CG41454_gene	CG41454	2.61295	2.58245	0.99	1.01
CG32280_gene	CG14962	21.3391	21.09	0.99	1.01
CG15216_gene	CG15216	2.17746	2.15204	0.99	1.01
CG4692_gene	CG13587	52.0957	51.4835	0.99	1.01
CG8001_gene	CG8001	13.2008	13.0447	0.99	1.01
CG2467_gene	CG2467	11.4589	11.3231	0.99	1.01
CG1316_gene	CG1316	131.845	130.281	0.99	1.01
Rgk3_gene	Rgk3	5.79749	5.72775	0.99	1.01
Asx_gene	Asx	16.957	16.7528	0.99	1.01
lola_gene	lola	229.395	226.627	0.99	1.01
ltd_gene	ltd	19.706	19.4677	0.99	1.01
CG11752_gene	CG11752	14.344	14.1704	0.99	1.01
RpII140_gene	RpII140	59.2541	58.5356	0.99	1.01
CG9705_gene	CG9705	22.0196	21.7522	0.99	1.01
CG11490_gene	CG11490	21.5841	21.3218	0.99	1.01
Rab8_gene	Rab8	63.8812	63.1046	0.99	1.01
CG8323_gene	CG8323	3.62003	3.5757	0.99	1.01
CG1832_gene	CG1832	26.3473	26.0232	0.99	1.01
Oscp_gene	Oscp	44.4202	43.8686	0.99	1.01
Pxd_gene	Pxd	27.4904	27.1489	0.99	1.01
CG31211_gene	CG31211	51.9324	51.2849	0.99	1.01
Eip71CD_gene	Eip71CD	12.8742	12.7136	0.99	1.01
CG13175_gene	CG13175	12.4387	12.2832	0.99	1.01
CG33964_gene	CG13175	12.4387	12.2832	0.99	1.01
CG11873_gene	CG11873	11.5678	11.4224	0.99	1.01
CG31475_gene	CG31475	10.6968	10.5616	0.99	1.01
CG7414_gene	CG7414	217.664	214.906	0.99	1.01
CG33248_gene	CG33248	10.5335	10.396	0.99	1.01
RpL30_gene	RpL30	195.971	193.386	0.99	1.01
CG5863_gene	CG5863	3.89221	3.84057	0.99	1.01
CG7979_gene	CG7979	14.1263	13.9386	0.99	1.01
CG17528_gene	CG17528	22.9178	22.613	0.99	1.01
CG3876_gene	CG15880	4.89928	4.83382	0.99	1.01
Rpn7_gene	CG34376	47.6864	47.047	0.99	1.01
CG9804_gene	CG9804	7.92051	7.81358	0.99	1.01
CG11505_gene	CG11505	40.1741	39.6307	0.99	1.01
mRpS26_gene	mRpS26	5.47087	5.39667	0.99	1.01
CG9461_gene	CG9461	18.9983	18.7393	0.99	1.01
BG4_gene	pit	4.0283	3.97301	0.99	1.01
Clc_gene	CG6951	148.476	146.438	0.99	1.01
CG5705_gene	CG5705	3.02123	2.97975	0.99	1.01
CG14814_gene	CG14814	1.00708	0.993251	0.99	1.01
CG3223_gene	CG3223	6.61403	6.52235	0.99	1.01
Gef26_gene	Gef26	12.221	12.0514	0.99	1.01
CHORD_gene	CHORD	5.60696	5.5291	0.99	1.01
Smg1_gene	Smg1	34.2133	33.7374	0.99	1.01
wnd_gene	wnd	7.18562	7.08519	0.99	1.01
CG4593_gene	CG4593	9.77135	9.63454	0.99	1.01
Sip1_gene	Sip1	231.192	227.951	0.99	1.01
CG12214_gene	CG12214	80.5932	79.4601	0.99	1.01
CG11537_gene	CG11537	43.522	42.9085	0.99	1.01
TBPH_gene	TBPH	16.6576	16.4218	0.99	1.01

CG5026_gene	CG5026	8.90037	8.77372	0.99	1.01
cact_gene	fzy	51.388	50.6558	0.99	1.01
CG9147_gene	CG9147	1.57866	1.55609	0.99	1.01
CG32441_gene	CG32441	21.6657	21.3549	0.99	1.01
Use1_gene	Dhpr	14.344	14.1373	0.99	1.01
kuz_gene	kuz	82.3352	81.1486	0.99	1.01
CG8889_gene	CG8889	5.87914	5.79397	0.99	1.01
Fak56D_gene	Fak56D	15.0517	14.8326	0.99	1.01
CG31873_gene	CG31873	6.45072	6.35681	0.99	1.01
Fas1_gene	Fas1	76.1567	75.0236	0.99	1.02
Srp19_gene	Srp19	32.6347	32.1482	0.99	1.02
CG34376_gene	CG34376	12.1666	11.9852	0.99	1.02
MAN1_gene	MAN1	10.0163	9.8663	0.99	1.02
CG31472_gene	CG31472	35.6287	35.0949	0.99	1.02
xmas-2_gene	xmas-2	6.15132	6.05883	0.98	1.02
Dyb_gene	Dyb	18.454	18.1765	0.98	1.02
CG9063_gene	CG9063	26.32	25.9239	0.98	1.02
pri_gene	pri	22.5911	22.2488	0.98	1.02
Ide_gene	CG13247	26.7283	26.3212	0.98	1.02
CG5758_gene	CG5758	14.2896	14.0711	0.98	1.02
CG6876_gene	CG6876	21.1486	20.8252	0.98	1.02
CG8311_gene	CG8311	5.71583	5.62842	0.98	1.02
dpr2_gene	dpr2	0.571583	0.562842	0.98	1.02
CG7168_gene	CG7993	3.4295	3.37705	0.98	1.02
CG1701_gene	CG1701	242.841	239.042	0.98	1.02
CG3342_gene	CG3918	4.27326	4.20476	0.98	1.02
CG34415_gene	CG15614	30.0489	29.5658	0.98	1.02
snmRNA:359_gene	Pax	3.70168	3.64192	0.98	1.02
CG14956_gene	CG14956	6.83178	6.721	0.98	1.02
east_gene	east	64.6161	63.5681	0.98	1.02
CG11414_gene	CG11414	60.4789	59.4958	0.98	1.02
Vha100-1_gene	Vha100-1	128.198	126.11	0.98	1.02
eRF1_gene	eRF1	126.048	123.991	0.98	1.02
Rpn12_gene	Rpn12	45.8083	45.0605	0.98	1.02
CG6643_gene	CG6643	65.2966	64.2303	0.98	1.02
CG9186_gene	CG2469	60.5878	59.5951	0.98	1.02
Arc-p34_gene	Arc-p34	34.1317	33.5719	0.98	1.02
CG9769_gene	CG9769	168.345	165.575	0.98	1.02
CG6045_gene	CG6045	81.4642	80.1223	0.98	1.02
Rbp1-like_gene	Rbp1-like	100.762	99.0934	0.98	1.02
l(2)k14505_gene	l(2)k14505	5.25312	5.16491	0.98	1.02
CG9536_gene	CG9536	40.1741	39.4983	0.98	1.02
CG15514_gene	CG15514	9.22699	9.0717	0.98	1.02
CG14712_gene	CG14712	18.454	18.1434	0.98	1.02
CG7120_gene	CG7120	5.9608	5.86018	0.98	1.02
CG11788_gene	CG11788	1.98693	1.95339	0.98	1.02
La_gene	spir	31.3554	30.8239	0.98	1.02
Rtf1_gene	Rtf1	16.0315	15.7596	0.98	1.02
CG8368_gene	CG8368	21.4208	21.0569	0.98	1.02
Dms_gene	Dms	63.8268	62.7404	0.98	1.02
CG31126_gene	CG31126	2.69461	2.64867	0.98	1.02
CG32857_gene	CG32857	6.09689	5.99262	0.98	1.02
l(1)G0334_gene	l(1)G0334	58.2743	57.2775	0.98	1.02
CG15173_gene	Catsup	7.51224	7.38317	0.98	1.02
gus_gene	gus	35.5742	34.9624	0.98	1.02
Prosbeta2_gene	Prosbeta2	38.541	37.876	0.98	1.02
sim_gene	sim	26.9188	26.4536	0.98	1.02
CG34420_gene	CG34420	11.0506	10.8595	0.98	1.02
Gld_gene	Gld	1047.28	1029.14	0.98	1.02
l(2)06225_gene	l(2)06225	39.7931	39.101	0.98	1.02

Chro_gene	CG11109	21.0941	20.7258	0.98	1.02
CG2712_gene	CG2712	2.12302	2.08583	0.98	1.02
CG15643_gene	CG32584	0.707674	0.695276	0.98	1.02
CG9793_gene	CG9793	0.707674	0.695276	0.98	1.02
CG7757_gene	CG7757	10.6151	10.4291	0.98	1.02
CG9796_gene	CG9796	45.6994	44.895	0.98	1.02
RpL19_gene	RpL19	618.371	607.34	0.98	1.02
CG30020_gene	CG30020	12.5748	12.3494	0.98	1.02
gem_gene	gem	62.9558	61.8133	0.98	1.02
CG14893_gene	CG14893	21.448	21.0569	0.98	1.02
Rpt3_gene	Rpt3	34.1317	33.5057	0.98	1.02
CG9172_gene	CG9172	31.301	30.7246	0.98	1.02
CG7207_gene	CG7207	36.0914	35.426	0.98	1.02
Pomp_gene	Pomp	21.9923	21.5867	0.98	1.02
lwr_gene	lwr	70.9035	69.5938	0.98	1.02
CG11148_gene	CG11148	75.1224	73.7324	0.98	1.02
CG9455_gene	CG9455	4.79041	4.70139	0.98	1.02
CG3700_gene	CG3700	2.39521	2.35069	0.98	1.02
RpL9_gene	RpL9	445.917	437.627	0.98	1.02
CG6370_gene	CG6370	405.878	398.327	0.98	1.02
CG6674_gene	CG6674	4.08274	4.00611	0.98	1.02
cg_gene	cg	55.2803	54.2315	0.98	1.02
SP1173_gene	SP1173	16.0315	15.7265	0.98	1.02
CG4612_gene	CG4612	14.344	14.0711	0.98	1.02
CG13089_gene	CG13089	5.90636	5.79397	0.98	1.02
CG4329_gene	Vps20	0.843766	0.827709	0.98	1.02
lid_gene	lid	61.8671	60.6877	0.98	1.02
CG5850_gene	CG5850	43.4131	42.5774	0.98	1.02
JhI-1_gene	JhI-1	8.84593	8.67439	0.98	1.02
GlcT-1_gene	GlcT-1	5.33478	5.23112	0.98	1.02
Arp14D_gene	Arp14D	52.504	51.4835	0.98	1.02
KrT95D_gene	KrT95D	62.7381	61.5154	0.98	1.02
CG1578_gene	CG1578	26.9461	26.4205	0.98	1.02
CG4598_gene	CG4598	10.8056	10.5947	0.98	1.02
CG14619_gene	CG14619	15.2967	14.9981	0.98	1.02
CG40351_gene	CG40351	40.9362	40.1274	0.98	1.02
CG32576_gene	CG32576	71.8834	70.4546	0.98	1.02
CG2165_gene	CG2165	211.622	207.391	0.98	1.02
CG41335_gene	Parp	36.6902	35.9557	0.98	1.02
btv_gene	btv	10.6423	10.4291	0.98	1.02
mRpS9_gene	CG10092	22.5367	22.0833	0.98	1.02
CG8165_gene	Rlc1	2.93957	2.88043	0.98	1.02
CG6015_gene	CG6015	13.718	13.442	0.98	1.02
CG5073_gene	CG6136	35.792	35.0618	0.98	1.02
CG30007_gene	CG30007	6.15132	6.02572	0.98	1.02
eIF-4a_gene	eIF-4a	854.462	836.98	0.98	1.02
Hexo2_gene	Hexo2	203.429	199.246	0.98	1.02
Hsc70Cb_gene	Hsc70Cb	97.0875	95.0873	0.98	1.02
Rbp2_gene	Rbp2	138.84	135.976	0.98	1.02
CG10395_gene	CG10395	5.30756	5.19802	0.98	1.02
CG4542_gene	CG4542	13.963	13.6738	0.98	1.02
RpL10Ab_gene	RpL10Ab	457.648	448.155	0.98	1.02
Spn6_gene	Spn6	6.5596	6.42303	0.98	1.02
ecd_gene	ecd	11.0234	10.7933	0.98	1.02
CG31716_gene	CG31716	65.1605	63.7998	0.98	1.02
CG5199_gene	CG5910	4.46379	4.37031	0.98	1.02
CG6420_gene	CG6420	7.81164	7.64804	0.98	1.02
CG4946_gene	CG4946	5.57974	5.46288	0.98	1.02
CG10365_gene	CG10365	24.5509	24.0367	0.98	1.02
CG7668_gene	CG7668	41.4262	40.5578	0.98	1.02

CG32264_gene	CG32264	43.2226	42.3125	0.98	1.02
CG5508_gene	CG5508	30.9471	30.2942	0.98	1.02
CG7997_gene	Hmgs	17.2836	16.9184	0.98	1.02
Eip74EF_gene	Eip74EF	28.9874	28.3739	0.98	1.02
CG6416_gene	CG6416	66.3309	64.9255	0.98	1.02
UbcD10_gene	aft	36.2275	35.4591	0.98	1.02
CG34191_gene	CG34415	21.1758	20.7258	0.98	1.02
CG1134_gene	CG1134	2.36799	2.31759	0.98	1.02
CG4769_gene	CG4769	53.6199	52.4768	0.98	1.02
Blimp-1_gene	Blimp-1	16.712	16.3555	0.98	1.02
CG41128_gene	Parp	13.3642	13.0778	0.98	1.02
ird5_gene	ird5	8.62818	8.44264	0.98	1.02
Moca-cyp_gene	Moca-cyp	24.9047	24.3678	0.98	1.02
CG34008_gene	Srp14	1.25204	1.22501	0.98	1.02
Spn43Aa_gene	Spn43Aa	56.614	55.3903	0.98	1.02
CG4802_gene	CG4802	15.2967	14.965	0.98	1.02
CG2839_gene	CG2839	688.594	673.656	0.98	1.02
CG7442_gene	CG7442	23.0811	22.5799	0.98	1.02
CG9140_gene	CG9140	75.7756	74.1297	0.98	1.02
CG7379_gene	CG7379	14.4529	14.1373	0.98	1.02
Rnp4F_gene	Sas10	16.5215	16.1569	0.98	1.02
CG8078_gene	CG8078	9.853	9.63454	0.98	1.02
CG11376_gene	CG11376	29.9673	29.3009	0.98	1.02
CG15523_gene	CG15523	66.1676	64.6938	0.98	1.02
CG8552_gene	CG8552	130.348	127.434	0.98	1.02
CG14224_gene	CG14224	119.787	117.104	0.98	1.02
CG31524_gene	CG31524	180.647	176.6	0.98	1.02
CG6597_gene	CG6597	19.4066	18.9711	0.98	1.02
bip1_gene	bip1	6.09689	5.95951	0.98	1.02
CG7376_gene	CG7376	3.04844	2.97975	0.98	1.02
Sec61gamma_gene	ec61gamm	110.261	107.768	0.98	1.02
Krn_gene	CG32177	63.2824	61.8464	0.98	1.02
RpL37a_gene	RpL37a	320.522	313.238	0.98	1.02
CG1041_gene	CG10286	57.5938	56.2842	0.98	1.02
CG11655_gene	CG11655	8.02938	7.84669	0.98	1.02
CG30185_gene	CG30185	22.9722	22.4475	0.98	1.02
SMSr_gene	SMSr	14.8067	14.4684	0.98	1.02
CG18870_gene	CG18870	1.66031	1.62231	0.98	1.02
CG32479_gene	CG32479	88.2688	86.2473	0.98	1.02
Trn_gene	Trn	25.8573	25.2617	0.98	1.02
CG33143_gene	CG33143	5.25312	5.1318	0.98	1.02
CG12010_gene	CG12010	3.59281	3.50949	0.98	1.02
CG9323_gene	CG9320	8.98202	8.77372	0.98	1.02
Cpr73D_gene	Cpr73D	1.7964	1.75474	0.98	1.02
Cp190_gene	CG4334	50.9798	49.795	0.98	1.02
fdl_gene	CG12370	18.9167	18.4745	0.98	1.02
CG14939_gene	CG14939	17.1203	16.7197	0.98	1.02
CG1115_gene	CG1115	21.3935	20.8914	0.98	1.02
CG18273_gene	CG18273	17.6646	17.2495	0.98	1.02
mip130_gene	Edem1	73.2715	71.5472	0.98	1.02
eIF-3p40_gene	eIF-3p40	175.639	171.501	0.98	1.02
CG10465_gene	CG10465	30.2123	29.4996	0.98	1.02
CG10320_gene	CG10320	22.3462	21.8184	0.98	1.02
CG9007_gene	CG9007	73.3804	71.6465	0.98	1.02
Map60_gene	Map60	2.06859	2.01961	0.98	1.02
cyc_gene	cyc	23.1627	22.613	0.98	1.02
RpL36_gene	RpL36	302.585	295.393	0.98	1.02
CG4230_gene	CG4230	4.27326	4.17166	0.98	1.02
CG7579_gene	CG7579	132.988	129.818	0.98	1.02
MED31_gene	MED31	13.5002	13.1771	0.98	1.02

CG5198_gene	CG5198	4.54545	4.43652	0.98	1.02
CG11897_gene	CG11897	11.5678	11.29	0.98	1.02
ash1_gene	ash1	13.9085	13.5744	0.98	1.02
CG6364_gene	CG6364	20.9308	20.4279	0.98	1.02
CG31019_gene	CG2246	2.34077	2.28448	0.98	1.02
CG8027_gene	CG8027	2.34077	2.28448	0.98	1.02
CG7130_gene	CG7130	11.8399	11.5548	0.98	1.02
fog_gene	fog	11.8399	11.5548	0.98	1.02
RpL17_gene	RpL17	313.881	306.286	0.98	1.02
fng_gene	fng	2.47686	2.41691	0.98	1.02
ps_gene	ps	189.221	184.612	0.98	1.02
Hs2st_gene	RanGap	7.97495	7.78047	0.98	1.02
Nnp-1_gene	Nnp-1	16.3582	15.9582	0.98	1.03
CG6480_gene	CG6480	5.77027	5.62842	0.98	1.03
rok_gene	rok	49.1834	47.974	0.98	1.03
CG4972_gene	CG4972	44.2296	43.1402	0.98	1.03
CG1308_gene	CG1308	11.9488	11.6541	0.98	1.03
CG32199_gene	CG4174	407.757	397.698	0.98	1.03
Rpt1_gene	CG17985	63.4457	61.8796	0.98	1.03
CG31457_gene	CG31457	3.02123	2.94665	0.98	1.03
CG30421_gene	CG30421	36.6085	35.6908	0.97	1.03
CG10373_gene	CG10373	121.475	118.429	0.97	1.03
Actn_gene	Actn	94.8556	92.4717	0.97	1.03
ATPsyn-Cf6_gene	ATPsyn-Cf6	59.1997	57.7079	0.97	1.03
CG11006_gene	CG11006	28.3614	27.6455	0.97	1.03
CG4288_gene	CG4288	36.5813	35.6577	0.97	1.03
CG14290_gene	CG14290	20.4137	19.8981	0.97	1.03
CG2144_gene	CG2144	30.2667	29.4996	0.97	1.03
Aprt_gene	Aprt	4.38214	4.27098	0.97	1.03
didum_gene	didum	40.528	39.4983	0.97	1.03
gfzf_gene	CG2656	13.5547	13.2102	0.97	1.03
CG3363_gene	CG3363	9.71691	9.469	0.97	1.03
CG8671_gene	CG8671	15.3239	14.9319	0.97	1.03
DMAP1_gene	DMAP1	10.5335	10.2636	0.97	1.03
RpS15_gene	CG4945	250.734	244.307	0.97	1.03
CG10992_gene	CG10992	302.776	294.963	0.97	1.03
Uch_gene	Uch	18.8622	18.3751	0.97	1.03
Vps36_gene	Vps36	6.42351	6.25748	0.97	1.03
CG10616_gene	CG10616	19.8149	19.3022	0.97	1.03
r2d2_gene	r2d2	27.7354	27.0164	0.97	1.03
CG8790_gene	poly	105.988	103.232	0.97	1.03
Sirt2_gene	Sirt2	7.78442	7.58182	0.97	1.03
CG1344_gene	CG1344	29.3413	28.5725	0.97	1.03
inx7_gene	inx7	42.4332	41.3193	0.97	1.03
CG8858_gene	CG8858	31.7637	30.9232	0.97	1.03
CG7115_gene	CG7115	18.8078	18.3089	0.97	1.03
CG4281_gene	CG4281	25.7485	25.063	0.97	1.03
CG9281_gene	CG9281	147.931	143.988	0.97	1.03
CG1532_gene	CG1532	31.056	30.2279	0.97	1.03
PyK_gene	PyK	159.608	155.345	0.97	1.03
Sh_gene	Sh	1.36091	1.32434	0.97	1.03
Taf11_gene	zf30C	4.89928	4.76761	0.97	1.03
CG12179_gene	CG12179	3.81055	3.70814	0.97	1.03
CG8067_gene	CG8067	1.63309	1.5892	0.97	1.03
CG12029_gene	CG12029	0.680456	0.662168	0.97	1.03
CG15904_gene	CG15904	2.31355	2.25137	0.97	1.03
CG30273_gene	CG30273	0.816547	0.794601	0.97	1.03
CG3808_gene	CG18135	8.84593	8.60818	0.97	1.03
CG11451_gene	CG11451	0.952639	0.927035	0.97	1.03
CR41506_gene	CR41506	0.952639	0.927035	0.97	1.03

CG3746_gene	CG3746	2.99401	2.91354	0.97	1.03
CG30160_gene	CG30160	0.544365	0.529734	0.97	1.03
CG3817_gene	CG3817	5.44365	5.29734	0.97	1.03
mthl9_gene	Ptpmeg	0.544365	0.529734	0.97	1.03
CG18764_gene	CG18764	1.22482	1.1919	0.97	1.03
CG4630_gene	CG4630	2.44964	2.3838	0.97	1.03
Roc1b_gene	CG6905	2.44964	2.3838	0.97	1.03
CG32032_gene	CG32032	1.90528	1.85407	0.97	1.03
CG6847_gene	CG6847	3.94665	3.84057	0.97	1.03
CG6962_gene	sad	3.94665	3.84057	0.97	1.03
HBS1_gene	HBS1	20.4137	19.865	0.97	1.03
mei-41_gene	mei-41	2.85792	2.7811	0.97	1.03
Pde6_gene	Pde6	56.4234	54.8937	0.97	1.03
CG9795_gene	CG9795	26.2384	25.5266	0.97	1.03
slim_gene	slim	42.406	41.253	0.97	1.03
CG9662_gene	CG9662	17.3925	16.9184	0.97	1.03
CG3792_gene	CG3792	35.3021	34.3334	0.97	1.03
Cyp9f2_gene	Cyp9f2	22.4006	21.7853	0.97	1.03
CG5674_gene	btv	10.5879	10.2967	0.97	1.03
CG7922_gene	CG7922	8.13826	7.9129	0.97	1.03
Rrp6_gene	CG3631	23.8704	23.209	0.97	1.03
stg_gene	stg	7.59389	7.38317	0.97	1.03
emc_gene	emc	28.6064	27.811	0.97	1.03
l(1)G0095_gene	l(1)G0095	14.0991	13.7069	0.97	1.03
RpS11_gene	RpS11	237.37	230.765	0.97	1.03
CG32500_gene	CG32500	6.23298	6.05883	0.97	1.03
ogre_gene	ogre	82.7707	80.4534	0.97	1.03
Grip163_gene	Grip163	5.8247	5.66153	0.97	1.03
l(1)G0168_gene	l(1)G0168	609.444	592.309	0.97	1.03
CG3711_gene	CG3711	20.0326	19.4677	0.97	1.03
CG11141_gene	CG11141	4.05552	3.9399	0.97	1.03
CG17735_gene	CG17735	93.0047	90.3528	0.97	1.03
CG30022_gene	sprt	7.97495	7.74736	0.97	1.03
CtBP_gene	CtBP	100.272	97.4048	0.97	1.03
CG11963_gene	CG11963	53.2389	51.7153	0.97	1.03
CG4025_gene	CG4025	11.35	11.0251	0.97	1.03
Gclm_gene	Gclm	18.3723	17.8454	0.97	1.03
Scm_gene	SpdS	29.178	28.3408	0.97	1.03
CG4674_gene	CG4674	29.0419	28.2083	0.97	1.03
CG3609_gene	CG3609	21.6113	20.9907	0.97	1.03
Ac78C_gene	Ac78C	41.4534	40.2598	0.97	1.03
Mlp60A_gene	Mlp60A	16.3309	15.8589	0.97	1.03
Nup58_gene	Nup58	3.23897	3.1453	0.97	1.03
cul-2_gene	cul-2	24.6869	23.9705	0.97	1.03
AcCoAS_gene	AcCoAS	219.08	212.721	0.97	1.03
CG31510_gene	CG31108	11.8672	11.5217	0.97	1.03
CG17766_gene	mip130	49.4828	48.0403	0.97	1.03
l(2)not_gene	l(2)not	31.8181	30.8901	0.97	1.03
CG8841_gene	CG13163	13.0648	12.6805	0.97	1.03
CG5023_gene	CG5023	7.81164	7.58182	0.97	1.03
mbt_gene	mbt	15.6233	15.1636	0.97	1.03
rdgA_gene	rdgA	38.6499	37.5118	0.97	1.03
Suv4-20_gene	Roc1a	53.7288	52.1457	0.97	1.03
tst_gene	CG10375	17.7735	17.2495	0.97	1.03
su(w[a])_gene	CG33082	1134.7	1101.22	0.97	1.03
CG7843_gene	CG7843	89.6569	87.0088	0.97	1.03
CG12488_gene	CG12488	23.1355	22.4475	0.97	1.03
osa_gene	osa	79.3412	76.977	0.97	1.03
prod_gene	prod	11.2956	10.9589	0.97	1.03
CG9809_gene	CG9809	19.7604	19.1698	0.97	1.03

ofs_gene	CG33111	102.967	99.888	0.97	1.03
CG4774_gene	CG4774	4.30048	4.17166	0.97	1.03
Usf_gene	Usf	8.60097	8.34331	0.97	1.03
CG12736_gene	didum	8.46487	8.21088	0.97	1.03
CG6453_gene	CG6453	141.208	136.969	0.97	1.03
Tctp_gene	Tctp	454.109	440.474	0.97	1.03
CG31690_gene	CG31690	2.01415	1.95339	0.97	1.03
CG13189_gene	MCPH1	26.184	25.3941	0.97	1.03
CG7781_gene	CG7787	3.89221	3.77436	0.97	1.03
CG3338_gene	CG3338	15.4327	14.965	0.97	1.03
CG4301_gene	CG4301	1.87806	1.82096	0.97	1.03
CG5567_gene	CG5567	14.344	13.9055	0.97	1.03
CG8944_gene	CG8944	10.5879	10.2636	0.97	1.03
Cnx99A_gene	Cnx99A	296.271	287.182	0.97	1.03
CG11455_gene	CG11455	24.9047	24.136	0.97	1.03
CG32732_gene	CG32732	4.95372	4.80071	0.97	1.03
CG16989_gene	CG16989	41.0996	39.8294	0.97	1.03
jbug_gene	jbug	81.9269	79.3939	0.97	1.03
Tudor-SN_gene	Tudor-SN	260.206	252.153	0.97	1.03
CG12241_gene	CG12241	73.081	70.8188	0.97	1.03
CG18217_gene	CG18217	4.81763	4.66828	0.97	1.03
CG4968_gene	CG4968	14.3168	13.8724	0.97	1.03
RpS8_gene	RpS8	648.883	628.695	0.97	1.03
asrij_gene	asrij	10.6968	10.3629	0.97	1.03
Scs-fp_gene	Scs-fp	83.4239	80.8175	0.97	1.03
RNaseX25_gene	RNaseX25	22.7272	22.0171	0.97	1.03
CG9386_gene	RnpS1	4.54545	4.40341	0.97	1.03
CG7920_gene	CG7920	134.621	130.414	0.97	1.03
CPTI_gene	CG11777	35.4109	34.3003	0.97	1.03
CG17734_gene	CG17734	16.1676	15.6603	0.97	1.03
msta_gene	msta	1.46979	1.42366	0.97	1.03
CG5577_gene	CG5577	21.9107	21.2225	0.97	1.03
CG6071_gene	CG6071	900.407	872.042	0.97	1.03
Psa_gene	Psa	321.992	311.848	0.97	1.03
Kr-h2_gene	Kr-h2	59.0092	57.1451	0.97	1.03
CG6726_gene	CG13830	9.60804	9.30345	0.97	1.03
disp_gene	disp	13.6091	13.1771	0.97	1.03
CG4282_gene	CG4282	4.00108	3.87368	0.97	1.03
pcx_gene	pcx	39.7386	38.4719	0.97	1.03
alphaTub84D_gene	lphaTub84	33.5873	32.5124	0.97	1.03
CR34285_gene	Ino80	66.9024	64.76	0.97	1.03
l(1)G0269_gene	l(1)G0269	17.9913	17.415	0.97	1.03
CG9175_gene	CG9175	26.9188	26.0563	0.97	1.03
Nedd8_gene	Nedd8	6.2602	6.05883	0.97	1.03
CG9286_gene	CG9286	9.58082	9.27035	0.97	1.03
CG2112_gene	CG2112	2.39521	2.31759	0.97	1.03
CG40001_gene	CG40001	1.1976	1.15879	0.97	1.03
CG33232_gene	CG33232	101.633	98.3319	0.97	1.03
CG15118_gene	botv	59.7168	57.7741	0.97	1.03
CG31116_gene	CG31116	139.875	135.314	0.97	1.03
Srp68_gene	Srp68	99.1833	95.9481	0.97	1.03
CG30428_gene	CG30428	6.91343	6.68789	0.97	1.03
CG13384_gene	CG13384	10.3702	10.0318	0.97	1.03
mRpS31_gene	mRpS31	5.71583	5.5291	0.97	1.03
Adk1_gene	Adk1	18.9983	18.3751	0.97	1.03
CG11523_gene	Ddx1	13.0103	12.5812	0.97	1.03
Mst57Da_gene	Mst57Da	6810.63	6585.12	0.97	1.03
Cdk8_gene	Cdk8	3.18453	3.07908	0.97	1.03
CG16789_gene	CG16789	1.06151	1.02636	0.97	1.03
LBR_gene	LBR	3.18453	3.07908	0.97	1.03

CG9757_gene	CG9757	6.36907	6.15816	0.97	1.03
CG32666_gene	CG32666	33.424	32.3138	0.97	1.03
CG5522_gene	CG5522	5.17147	4.99936	0.97	1.03
CG9806_gene	CG9806	81.682	78.9635	0.97	1.03
CG12404_gene	CG12404	33.3968	32.2807	0.97	1.03
CG14777_gene	CG14777	6.88622	6.65478	0.97	1.03
CG6697_gene	CG6697	10.724	10.3629	0.97	1.03
cav_gene	twin	2.91235	2.81421	0.97	1.03
CG14061_gene	CG14061	1777.57	1717.6	0.97	1.03
CG17323_gene	CG17323	9.39029	9.0717	0.97	1.04
Elf_gene	SC35	185.411	179.116	0.97	1.04
CG11388_gene	CG11388	5.55252	5.36356	0.97	1.04
Dcp-1_gene	pita	0.92542	0.893926	0.97	1.04
CG10984_gene	CG10984	14.5345	14.038	0.97	1.04
CG17985_gene	CG30492	76.8643	74.229	0.97	1.04
CG9727_gene	CG9727	15.0517	14.5346	0.97	1.04
endos_gene	endos	19.4066	18.7393	0.97	1.04
SC35_gene	SC35	20.1959	19.5008	0.97	1.04
CycD_gene	CycD	9.36308	9.03859	0.97	1.04
CG2260_gene	CG1575	7.64833	7.38317	0.97	1.04
CG7870_gene	CG7870	39.031	37.6773	0.97	1.04
CG9380_gene	CG9380	4.21883	4.07233	0.97	1.04
CG32626_gene	CG32626	66.8208	64.4951	0.97	1.04
CG31950_gene	CG31950	2.50408	2.41691	0.97	1.04
CG6311_gene	CG6311	17.5286	16.9184	0.97	1.04
CrebA_gene	CrebA	329.695	318.205	0.97	1.04
Aats-ile_gene	Aats-ile	99.6188	96.1467	0.97	1.04
CG13907_gene	CG32479	58.9003	56.8471	0.97	1.04
CG9350_gene	CG9350	25.694	24.7982	0.97	1.04
ATPsyn-d_gene	ATPsyn-d	60.4789	58.3701	0.97	1.04
CG13362_gene	sdk	9.74413	9.40278	0.96	1.04
CG4813_gene	CG4813	4.87207	4.70139	0.96	1.04
oho23B_gene	oho23B	74.6324	72.0107	0.96	1.04
Crk_gene	Crk	26.4561	25.5266	0.96	1.04
CG11699_gene	CG11699	11.8399	11.4224	0.96	1.04
CG32373_gene	CG32373	103.729	100.054	0.96	1.04
Pnn_gene	Pnn	6.83178	6.58857	0.96	1.04
CG1161_gene	CG1161	23.5166	22.6792	0.96	1.04
CG11158_gene	CG11158	15.8955	15.3292	0.96	1.04
CG3548_gene	CG3548	3.02123	2.91354	0.96	1.04
CG9865_gene	CG15675	19.4338	18.7393	0.96	1.04
trn_gene	trn	4.46379	4.30409	0.96	1.04
CG30497_gene	CG30497	144.284	139.121	0.96	1.04
g_gene	g	20.7403	19.9975	0.96	1.04
CG17002_gene	CG17002	7.34893	7.08519	0.96	1.04
Pvf1_gene	Pvf1	62.4659	60.2241	0.96	1.04
Ef2b_gene	Ef2b	3455.33	3331.1	0.96	1.04
CG9945_gene	CG9945	10.7512	10.3629	0.96	1.04
CG13650_gene	CG13650	6.42351	6.19127	0.96	1.04
tafazzin_gene	tafazzin	26.3473	25.3941	0.96	1.04
Ork1_gene	Ork1	14.1535	13.6407	0.96	1.04
CG6654_gene	CG4203	3.53837	3.41016	0.96	1.04
Gyk_gene	mri	88.1599	84.9561	0.96	1.04
l(2)37Cd_gene	l(2)37Cd	2.0958	2.01961	0.96	1.04
P5cr_gene	P5cr	11.1323	10.7271	0.96	1.04
CG1572_gene	CG1572	34.295	33.0422	0.96	1.04
me31B_gene	me31B	59.6624	57.4761	0.96	1.04
CG34422_gene	CG34422	35.8464	34.532	0.96	1.04
CG8336_gene	Or67b	10.0708	9.70075	0.96	1.04
CG32573_gene	CG32573	10.724	10.3298	0.96	1.04

Obp18a_gene	Obp18a	1.95971	1.88718	0.96	1.04
CG6664_gene	CG6664	14.3712	13.8393	0.96	1.04
CG9384_gene	CG9384	12.4115	11.9521	0.96	1.04
CG7342_gene	CG7342	136.608	131.54	0.96	1.04
sds22_gene	sds22	17.3652	16.7197	0.96	1.04
CG8833_gene	CG8833	5.74305	5.5291	0.96	1.04
CG4091_gene	mRpL43	5.08981	4.90004	0.96	1.04
Xpac_gene	Xpac	4.43657	4.27098	0.96	1.04
BtbVII_gene	BtbVII	27.0005	25.9901	0.96	1.04
CG31937_gene	CG31937	23.4621	22.5799	0.96	1.04
CG14879_gene	CG14879	69.7331	67.1107	0.96	1.04
CG5482_gene	CG5482	38.0511	36.6179	0.96	1.04
CG9066_gene	CG9066	119.733	115.217	0.96	1.04
Tollo_gene	Tollo	29.3141	28.2083	0.96	1.04
mod(r)_gene	mod(r)	11.595	11.1575	0.96	1.04
CG31496_gene	CG31496	140.038	134.751	0.96	1.04
RpL14_gene	RpL14	214.915	206.795	0.96	1.04
ball_gene	ball	4.16439	4.00611	0.96	1.04
CG16986_gene	CG16986	4.16439	4.00611	0.96	1.04
Aats-asn_gene	Aats-asn	63.4729	61.0518	0.96	1.04
Amph_gene	Amph	49.8094	47.9078	0.96	1.04
granny-smith_gene	ranny-smit	22.1012	21.2556	0.96	1.04
Abd-B_gene	Abd-B	81.7636	78.6324	0.96	1.04
CG7637_gene	CG12935	5.19868	4.99936	0.96	1.04
CG9997_gene	CG9997	892.132	857.904	0.96	1.04
RhoGAP1A_gene	RhoGAP1A	58.0837	55.8538	0.96	1.04
CG30159_gene	Tsp42Ea	14.9428	14.369	0.96	1.04
CG3065_gene	CG3065	20.6586	19.865	0.96	1.04
odd_gene	odd	8.57375	8.24399	0.96	1.04
Cyp4d8_gene	Cyp4d8	1.68753	1.62231	0.96	1.04
CG8852_gene	CG8852	5.57974	5.36356	0.96	1.04
CG4407_gene	CG4407	19.9782	19.2029	0.96	1.04
sw_gene	sw	19.1889	18.4414	0.96	1.04
CG7261_gene	CG7261	13.092	12.5812	0.96	1.04
CG34129_gene	CG34129	733.477	704.844	0.96	1.04
CG8862_gene	Cct5	2.72182	2.61556	0.96	1.04
MED27_gene	MED27	3.23897	3.11219	0.96	1.04
aft_gene	aft	10.2341	9.83319	0.96	1.04
Pkn_gene	Pkn	44.6924	42.9416	0.96	1.04
CG31635_gene	CG31635	41.8344	40.1936	0.96	1.04
Pdsw_gene	Pdsw	20.332	19.5339	0.96	1.04
ND23_gene	ND23	30.43	29.2347	0.96	1.04
CG8378_gene	CG8378	31.4643	30.2279	0.96	1.04
CG6230_gene	Gr32a	120.795	116.012	0.96	1.04
cals_gene	cals	193.576	185.904	0.96	1.04
CG14076_gene	CG6841	1.03429	0.993251	0.96	1.04
CG15738_gene	CG15738	3.62003	3.47638	0.96	1.04
CG34250_gene	CG34250	3.10288	2.97975	0.96	1.04
CG32758_gene	CG32758	25.9662	24.9306	0.96	1.04
RpL6_gene	RpL6	697.304	669.484	0.96	1.04
PKD_gene	PKD	39.657	38.0746	0.96	1.04
wts_gene	wts	26.2112	25.1624	0.96	1.04
CG8155_gene	CG8155	10.0708	9.66765	0.96	1.04
Dap160_gene	Dap160	22.5911	21.686	0.96	1.04
CG33123_gene	CG33123	75.3673	72.3418	0.96	1.04
ATPsyn-b_gene	ATPsyn-b	99.2377	95.2528	0.96	1.04
mats_gene	mats	10.969	10.5285	0.96	1.04
CG14084_gene	CG14084	42.2972	40.5909	0.96	1.04
CG9288_gene	CG9288	7.86607	7.54871	0.96	1.04
egr_gene	egr	2.44964	2.35069	0.96	1.04

CG3781_gene	Lag1	22.8089	21.8846	0.96	1.04
CG16833_gene	CG16833	15.9771	15.3292	0.96	1.04
CG13298_gene	CG13298	21.7746	20.8914	0.96	1.04
Mtch_gene	Mtch	48.6934	46.7159	0.96	1.04
RpS17_gene	RpS17	223.843	214.741	0.96	1.04
pUf68_gene	pUf68	62.0576	59.5289	0.96	1.04
CG40263_gene	CG40263	69.3793	66.5478	0.96	1.04
Psi_gene	Psi	37.9695	36.4192	0.96	1.04
CG32703_gene	CG32703	1.41535	1.35744	0.96	1.04
CR32078_gene	CR32078	1.41535	1.35744	0.96	1.04
CG34339_gene	CG34339	30.1034	28.8705	0.96	1.04
CG6966_gene	CG6966	90.6912	86.9757	0.96	1.04
Vha14_gene	Vha14	63.6635	61.0518	0.96	1.04
Pis_gene	Pis	23.1355	22.1826	0.96	1.04
CG5003_gene	CG5017	10.1524	9.73386	0.96	1.04
baz_gene	baz	17.9913	17.2495	0.96	1.04
Socs44A_gene	Socs44A	5.5253	5.29734	0.96	1.04
cer_gene	cer	20.0326	19.2029	0.96	1.04
CG2556_gene	CG2556	43.522	41.7166	0.96	1.04
MED10_gene	PDCD-5	24.0065	23.0103	0.96	1.04
Cyt-b5_gene	Cyt-b5	157.349	150.809	0.96	1.04
CG7044_gene	CG7044	9.88022	9.469	0.96	1.04
CG32306_gene	CG32306	82.1174	78.6986	0.96	1.04
kdn_gene	kdn	186.418	178.653	0.96	1.04
Rab40_gene	Rab40	6.66847	6.38992	0.96	1.04
CG7741_gene	CG7741	5.77027	5.5291	0.96	1.04
Brd8_gene	Brd8	7.04953	6.75411	0.96	1.04
Z4_gene	Z4	52.9123	50.6889	0.96	1.04
Nos_gene	Nos	17.0386	16.3224	0.96	1.04
Snr1_gene	Snr1	14.7251	14.1042	0.96	1.04
exo70_gene	exo70	10.7512	10.2967	0.96	1.04
CG6049_gene	CG6014	250.843	240.201	0.96	1.04
CG17494_gene	CG17494	57.2944	54.8606	0.96	1.04
bbx_gene	waw	67.7734	64.8924	0.96	1.04
waw_gene	waw	67.7734	64.8924	0.96	1.04
CG17190_gene	CG17190	5.87914	5.62842	0.96	1.04
att-ORFB_gene	att-ORFA	4.59988	4.40341	0.96	1.04
CG6937_gene	CG33107	10.8601	10.396	0.96	1.04
dor_gene	dor	30.4028	29.1023	0.96	1.04
CG12316_gene	CG12316	3.70168	3.5426	0.96	1.04
CG8743_gene	CG8743	13.9085	13.3096	0.96	1.04
CG9376_gene	CG9376	12.2482	11.7204	0.96	1.05
CG2061_gene	CG2061	2.04137	1.95339	0.96	1.05
sop_gene	sop	542.541	519.073	0.96	1.05
CG31957_gene	CG31957	2.42242	2.31759	0.96	1.05
sob_gene	sob	9.6897	9.27035	0.96	1.05
CG7580_gene	CG7580	24.9863	23.9042	0.96	1.05
CG3004_gene	Gga	10.0708	9.63454	0.96	1.05
Apf_gene	Apf	8.41044	8.04534	0.96	1.05
Bre1_gene	Bre1	25.6124	24.5002	0.96	1.05
Odc1_gene	Odc1	6.36907	6.09194	0.96	1.05
CG12140_gene	CG12140	21.3935	20.461	0.96	1.05
RpL4_gene	RpL4	685.682	655.711	0.96	1.05
CG6017_gene	CG6017	9.79857	9.36967	0.96	1.05
Aats-val_gene	Aats-val	41.0996	39.2996	0.96	1.05
CG12582_gene	CG12582	29.6407	28.3408	0.96	1.05
CG4585_gene	CG4585	13.6091	13.0116	0.96	1.05
Atf6_gene	Atf6	88.1327	84.2608	0.96	1.05
tara_gene	tara	9.66248	9.23724	0.96	1.05
BEAF-32_gene	CR30478	10.0435	9.60143	0.96	1.05

lbk_gene	lbk	25.0408	23.9374	0.96	1.05
koko_gene	Vha100-2	13.092	12.515	0.96	1.05
CG31919_gene	CG31650	109.281	104.457	0.96	1.05
CG33995_gene	CG31650	109.281	104.457	0.96	1.05
Csk_gene	CG14712	63.5274	60.7208	0.96	1.05
Pect_gene	Pect	195.373	186.731	0.96	1.05
mus101_gene	mus101	1.52422	1.45677	0.96	1.05
CG33281_gene	CG33281	11.4317	10.9258	0.96	1.05
CG12355_gene	CG12355	1.14317	1.09258	0.96	1.05
NiPp1_gene	CG6796	1.14317	1.09258	0.96	1.05
CG6724_gene	CG6724	9.14533	8.74061	0.96	1.05
CG31849_gene	CG5287	0.762111	0.728384	0.96	1.05
CG8353_gene	CG8353	0.762111	0.728384	0.96	1.05
bab1_gene	bab1	4.19161	4.00611	0.96	1.05
CG6185_gene	CG6185	1.90528	1.82096	0.96	1.05
l(3)04053_gene	l(3)04053	10.6696	10.1974	0.96	1.05
CG7852_gene	CG7852	12.1938	11.6541	0.96	1.05
CG12558_gene	CG12558	184.757	176.567	0.96	1.05
CG6854_gene	CG6854	25.8846	24.732	0.96	1.05
Rab23_gene	Rab23	2.91235	2.7811	0.95	1.05
CG6043_gene	CG6043	38.8677	37.1145	0.95	1.05
slif_gene	slif	13.0375	12.4487	0.95	1.05
CG12263_gene	CG12263	7.59389	7.25073	0.95	1.05
Bap60_gene	Bap60	33.5329	32.0158	0.95	1.05
arm_gene	arm	128.307	122.501	0.95	1.05
Rpd3_gene	Rpd3	19.7332	18.8387	0.95	1.05
CG1908_gene	CG1908	8.60097	8.21088	0.95	1.05
CG3173_gene	CG3173	24.2787	23.1759	0.95	1.05
Est-6_gene	Est-6	6907.09	6592.94	0.95	1.05
CG12877_gene	CG12877	5.68861	5.42977	0.95	1.05
Mvl_gene	Mvl	49.0473	46.8152	0.95	1.05
CG12822_gene	CG12822	18.454	17.6137	0.95	1.05
CG9915_gene	CG9915	10.9962	10.4954	0.95	1.05
Sur-8_gene	Sur-8	7.07674	6.75411	0.95	1.05
B4_gene	B4	11.6222	11.0913	0.95	1.05
CG8928_gene	CG8928	5.55252	5.29734	0.95	1.05
Mpcp_gene	Mpcp	349.999	333.898	0.95	1.05
SelD_gene	SelD	10.724	10.2305	0.95	1.05
CG6673_gene	se	33.424	31.8834	0.95	1.05
dally_gene	dally	15.2422	14.5346	0.95	1.05
Rab6_gene	Rab6	93.8213	89.4588	0.95	1.05
sphinx1_gene	sphinx1	104.273	99.4245	0.95	1.05
CG14285_gene	CG14285	1.00708	0.960143	0.95	1.05
plexB_gene	plexB	40.909	39.0017	0.95	1.05
CG31908_gene	CG31908	26.81	25.5597	0.95	1.05
CG1597_gene	CG34348	35.1115	33.4726	0.95	1.05
CG12547_gene	CG12547	26.0479	24.8313	0.95	1.05
Idgf4_gene	Idgf4	66.4397	63.3363	0.95	1.05
cry_gene	cry	77.9258	74.2621	0.95	1.05
CSN4_gene	CSN4	27.2455	25.957	0.95	1.05
mRpL37_gene	mRpL37	4.51823	4.30409	0.95	1.05
Tre1_gene	Tre1	4.51823	4.30409	0.95	1.05
M(2)21AB_gene	M(2)21AB	379.368	361.378	0.95	1.05
CG8135_gene	CG8135	72.1284	68.6999	0.95	1.05
CG1746_gene	CG1746	360.451	343.301	0.95	1.05
grau_gene	grau	13.4186	12.7798	0.95	1.05
CG34295_gene	CG34295	24.5781	23.4076	0.95	1.05
NPC2_gene	NPC2	52.6401	50.1261	0.95	1.05
RpS16_gene	RpS16	186.962	178.024	0.95	1.05
Ef1alpha48D_gene	f1alpha48	7145.01	6802.71	0.95	1.05

CG10260_gene	CG10260	47.2237	44.9612	0.95	1.05
CG11665_gene	CG11665	31.4371	29.93	0.95	1.05
CG6490_gene	CG6490	18.5356	17.6468	0.95	1.05
tamo_gene	tamo	22.2917	21.2225	0.95	1.05
CG14476_gene	CG14476	437.424	416.437	0.95	1.05
Dhh1_gene	Dhh1	4.38214	4.17166	0.95	1.05
Rlc1_gene	Rlb1	5.63418	5.36356	0.95	1.05
Gas8_gene	Gas8	0.62602	0.595951	0.95	1.05
CG32170_gene	Lmpt	7.51224	7.15141	0.95	1.05
CG7322_gene	CG7322	1.87806	1.78785	0.95	1.05
Rtc1_gene	Rtc1	3.75612	3.5757	0.95	1.05
CG40228_gene	CG40228	11.2684	10.7271	0.95	1.05
path_gene	path	162.112	154.318	0.95	1.05
CG3645_gene	CG3645	16.5215	15.7265	0.95	1.05
CG34380_gene	CG34380	4.6271	4.40341	0.95	1.05
lva_gene	lva	450.843	429.018	0.95	1.05
Ca-P60A_gene	Ca-P60A	368.508	350.651	0.95	1.05
E2f_gene	E2f	114.589	109.026	0.95	1.05
Haspin_gene	Haspin	13.1192	12.4819	0.95	1.05
CG7000_gene	NF4Agamm	4.87207	4.63517	0.95	1.05
Aats-his_gene	Aats-his	53.8377	51.2187	0.95	1.05
CG5745_gene	CG5745	9.9891	9.5021	0.95	1.05
CG33558_gene	CG33558	33.8323	32.1813	0.95	1.05
trpl_gene	trpl	3.62003	3.44327	0.95	1.05
CG12378_gene	RhoGAP92E	5.11703	4.86693	0.95	1.05
Sas10_gene	Sas10	11.7311	11.1575	0.95	1.05
L_gene	L	50.8981	48.4044	0.95	1.05
Arp11_gene	Arp11	7.72998	7.35006	0.95	1.05
Lim1_gene	Lim1	13.3369	12.6805	0.95	1.05
CG13367_gene	CG13367	5.60696	5.33045	0.95	1.05
CG10576_gene	CG10576	176.565	167.793	0.95	1.05
CG15130_gene	CG15130	1.74197	1.65542	0.95	1.05
CG12333_gene	koko	4.59988	4.37031	0.95	1.05
CG6750_gene	CG6750	24.1154	22.911	0.95	1.05
CG11874_gene	CG11874	25.4763	24.2022	0.95	1.05
CG32267_gene	CG32267	5.9608	5.66153	0.95	1.05
CkIIalpha_gene	CkIIalpha	82.8251	78.6655	0.95	1.05
CG6766_gene	CG6766	111.241	105.649	0.95	1.05
CG11015_gene	CG11015	31.6548	30.0624	0.95	1.05
CG2211_gene	CG2211	11.2956	10.7271	0.95	1.05
CG7262_gene	CG7262	6.45072	6.12505	0.95	1.05
eIF-4B_gene	eIF-4B	278.96	264.834	0.95	1.05
CG8516_gene	CG8516	22.6728	21.5204	0.95	1.05
CG4644_gene	CG4644	6.31463	5.99262	0.95	1.05
p_gene	p	18.9439	17.9778	0.95	1.05
Acyp2_gene	Acyp2	5.19868	4.93315	0.95	1.05
CG4238_gene	CG4238	41.2084	39.101	0.95	1.05
Upf2_gene	Upf2	23.1355	21.9509	0.95	1.05
CG34401_gene	CG34401	8.41044	7.97912	0.95	1.05
CG1657_gene	CG1657	45.7539	43.4051	0.95	1.05
Sos_gene	Sos	16.1949	15.3623	0.95	1.05
CG9028_gene	CG9028	22.1284	20.9907	0.95	1.05
CG31110_gene	bai	15.3239	14.5346	0.95	1.05
RpLP0_gene	RpLP0	840.091	796.819	0.95	1.05
CDase_gene	CDase	1.60588	1.52299	0.95	1.05
CG9773_gene	CG9773	13.092	12.4156	0.95	1.05
CG5385_gene	CG5385	23.571	22.3482	0.95	1.05
crq_gene	ex	33.0702	31.3536	0.95	1.05
CG2865_gene	CG2865	26.8916	25.4935	0.95	1.05
CG18815_gene	CG18815	19.4883	18.4745	0.95	1.05

RpL28_gene	CG12034	130.702	123.892	0.95	1.05
CG13424_gene	CG13424	184.703	175.077	0.95	1.05
alpha-Est3_gene	alpha-Est3	17.9913	17.0508	0.95	1.06
CG5798_gene	CG5798	23.0266	21.8184	0.95	1.06
sta_gene	sta	563.69	534.104	0.95	1.06
l(3)82Fd_gene	l(3)82Fd	297.822	282.183	0.95	1.06
CG10467_gene	CG10467	10.8329	10.2636	0.95	1.06
CG9346_gene	CG9346	10.8329	10.2636	0.95	1.06
GluRIIA_gene	CG14017	8.24713	7.81358	0.95	1.06
Hem_gene	Hem	32.1175	30.4266	0.95	1.06
MBD-R2_gene	MBD-R2	28.4158	26.9171	0.95	1.06
Anxb11_gene	Traf3	144.393	136.771	0.95	1.06
snmRNA:641_gene	nmRNA:64	3.32063	3.1453	0.95	1.06
CG31436_gene	CG31436	6.64125	6.29059	0.95	1.06
CG17187_gene	CG17187	17.828	16.8853	0.95	1.06
gbb_gene	gbb	66.9297	63.3694	0.95	1.06
regucalcin_gene	regucalcin	521.992	494.109	0.95	1.06
Best2_gene	Best2	172.863	163.622	0.95	1.06
CG15133_gene	CG15133	8.9548	8.47574	0.95	1.06
sdt_gene	sdt	60.8328	57.5755	0.95	1.06
CG14657_gene	CG14657	55.9063	52.9072	0.95	1.06
CG11448_gene	CG11448	52.0957	49.2984	0.95	1.06
CG32833_gene	CG32834	321.856	304.564	0.95	1.06
CG34015_gene	CG34015	2.44964	2.31759	0.95	1.06
CG6656_gene	CG6656	3.67446	3.47638	0.95	1.06
CG10999_gene	CG10999	6.61403	6.25748	0.95	1.06
Art3_gene	Art3	8.32878	7.87979	0.95	1.06
CG30179_gene	CG30179	0.734893	0.695276	0.95	1.06
CG32647_gene	CG32647	0.734893	0.695276	0.95	1.06
snoRNA:Psi28S-1153_gene	NA:Psi28S-	0.734893	0.695276	0.95	1.06
CG17359_gene	CG17361	1.71475	1.62231	0.95	1.06
CG7946_gene	CG7946	19.8421	18.7724	0.95	1.06
Btk29A_gene	Btk29A	171.393	162.132	0.95	1.06
lin19_gene	lin19	48.2307	45.6233	0.95	1.06
CG12788_gene	CG14210	8.92758	8.44264	0.95	1.06
Tim9b_gene	CG14210	8.92758	8.44264	0.95	1.06
CG1826_gene	CG1826	8.92758	8.44264	0.95	1.06
CG5703_gene	CG5703	20.1687	19.0704	0.95	1.06
Mat89Bb_gene	Mat89Bb	6.47794	6.12505	0.95	1.06
bys_gene	bys	10.5062	9.93251	0.95	1.06
CG4065_gene	Zfrp8	10.5062	9.93251	0.95	1.06
NetA_gene	NetA	9.52639	9.00548	0.95	1.06
sec13_gene	sec13	171.72	162.33	0.95	1.06
CG31380_gene	CG31380	18.0729	17.0839	0.95	1.06
Hr78_gene	Hr78	63.9629	60.4559	0.95	1.06
RpS25_gene	RpS25	387.425	366.179	0.95	1.06
CG11076_gene	CG11076	34.54	32.6449	0.95	1.06
CG17033_gene	CG17033	7.32171	6.91965	0.95	1.06
skf_gene	CG7737	3.29341	3.11219	0.94	1.06
CG7609_gene	CG7609	6.58682	6.22437	0.94	1.06
Cka_gene	Cka	32.4441	30.6584	0.94	1.06
CG5585_gene	CG5585	6.34185	5.99262	0.94	1.06
Strn-Mlck_gene	Cyp4aa1	206.723	195.339	0.94	1.06
CG3625_gene	CG3625	178.661	168.82	0.94	1.06
CG8793_gene	CG8793	218.971	206.894	0.94	1.06
Pros35_gene	Pros35	28.7697	27.182	0.94	1.06
TfIIS_gene	TfIIS	16.5759	15.6603	0.94	1.06
CG2006_gene	CG2006	103.593	97.8684	0.94	1.06
CG31419_gene	CG31419	154.981	146.372	0.94	1.06
CG12207_gene	CG12207	19.8421	18.7393	0.94	1.06

CG9578_gene	CG9578	12.4115	11.7204	0.94	1.06
CG15926_gene	CG15926	27.9804	26.4205	0.94	1.06
CG8929_gene	CG8929	40.6096	38.3395	0.94	1.06
Hr96_gene	Hr96	19.5699	18.4745	0.94	1.06
Nipped-B_gene	Nipped-B	48.1219	45.4247	0.94	1.06
Ubi-p63E_gene	Ubi-p63E	492.786	465.106	0.94	1.06
CG1824_gene	CG1824	17.6102	16.6204	0.94	1.06
SCAP_gene	SCAP	41.4806	39.1341	0.94	1.06
Mipp1_gene	Mipp1	24.4964	23.1096	0.94	1.06
CG14174_gene	CG14174	2.66739	2.51624	0.94	1.06
Pglym78_gene	Pglym78	44.7196	42.1801	0.94	1.06
Exn_gene	Exn	22.7817	21.4873	0.94	1.06
CG5746_gene	CG5746	22.2917	21.0238	0.94	1.06
Upf1_gene	Upf1	51.9596	49.0004	0.94	1.06
TepIII_gene	TepIII	13.2008	12.4487	0.94	1.06
CG6289_gene	CG6289	5798.06	5466.86	0.94	1.06
CG6073_gene	CG6073	11.1323	10.4954	0.94	1.06
frc_gene	CG32174	12.221	11.5217	0.94	1.06
CG14899_gene	CG14899	59.0364	55.6552	0.94	1.06
CG15412_gene	CG15412	1.08873	1.02636	0.94	1.06
RNaseP:RNA_gene	CG1746	1.08873	1.02636	0.94	1.06
CG5262_gene	CG5262	5.19868	4.90004	0.94	1.06
mRpL23_gene	CG8993	4.10996	3.87368	0.94	1.06
RpL27A_gene	RpL27A	495.481	466.994	0.94	1.06
CG7337_gene	CG7337	122.918	115.846	0.94	1.06
CG33052_gene	CG33052	19.2161	18.1103	0.94	1.06
ATPsyn-beta_gene	ATPsyn-bet	324.224	305.491	0.94	1.06
CG32174_gene	CG32174	13.2825	12.515	0.94	1.06
CG17249_gene	CG13919	4.70876	4.43652	0.94	1.06
Xpd_gene	Xpd	4.70876	4.43652	0.94	1.06
CG32537_gene	CG32537	5.55252	5.23112	0.94	1.06
Myd88_gene	Myd88	40.5552	38.2071	0.94	1.06
Spase12_gene	CG2006	100.027	94.2264	0.94	1.06
CG6327_gene	CG6327	141.29	133.096	0.94	1.06
CG32201_gene	CG4174	200.109	188.486	0.94	1.06
mRpS21_gene	CG8870	6.99509	6.58857	0.94	1.06
CG4949_gene	CG4949	1.68753	1.5892	0.94	1.06
l(3)03670_gene	l(3)03670	29.5318	27.811	0.94	1.06
CanB2_gene	CanB2	49.0473	46.1862	0.94	1.06
CG33097_gene	CG33097	23.7343	22.3482	0.94	1.06
Bap_gene	Bap	83.9411	79.0297	0.94	1.06
dpa_gene	dpa	3.97386	3.74125	0.94	1.06
CG12259_gene	CG12259	11.9216	11.2237	0.94	1.06
Rh4_gene	Rh4	22.7545	21.4211	0.94	1.06
Ravus_gene	Ravus	3.1301	2.94665	0.94	1.06
mr_gene	mr	8.54653	8.04534	0.94	1.06
CG34440_gene	CG34440	13.1192	12.3494	0.94	1.06
CG34441_gene	CG34440	13.1192	12.3494	0.94	1.06
Thiolase_gene	CG5569	28.1437	26.4867	0.94	1.06
CG1074_gene	CG1074	13.2281	12.4487	0.94	1.06
HDAC6_gene	CG9114	12.3843	11.6541	0.94	1.06
CG13204_gene	CG13204	1.44257	1.35744	0.94	1.06
CG4887_gene	CG4887	29.4501	27.7117	0.94	1.06
CG9684_gene	stck	13.5819	12.7798	0.94	1.06
CG30338_gene	CG34364	4.9265	4.63517	0.94	1.06
CG7326_gene	CG7326	5.5253	5.19802	0.94	1.06
Mlc1_gene	Mlc1	68.4539	64.3958	0.94	1.06
CG7842_gene	CG7842	4.43657	4.17166	0.94	1.06
RnpS1_gene	RnpS1	6.23298	5.86018	0.94	1.06
CG1317_gene	CG1317	86.173	81.0162	0.94	1.06

CG30359_gene	CG30359	1.7964	1.68853	0.94	1.06
snoRNA:Me28S-G764_gene	Arf79F	0.598801	0.562842	0.94	1.06
CG41320_gene	CG41320	0.598801	0.562842	0.94	1.06
Crg-1_gene	Crg-1	0.598801	0.562842	0.94	1.06
simj_gene	simj	10.8873	10.2305	0.94	1.06
CG8379_gene	CG8379	23.1899	21.7853	0.94	1.06
CG12341_gene	CG12936	8.60097	8.07844	0.94	1.06
CG17255_gene	CG17255	100.68	94.5575	0.94	1.06
Topors_gene	Topors	5.85192	5.49599	0.94	1.06
CG6488_gene	CG6488	15.4055	14.4684	0.94	1.06
CG7200_gene	CG5783	3.70168	3.47638	0.94	1.06
CG9410_gene	CG9410	3.10288	2.91354	0.94	1.06
CG1523_gene	CG1646	14.7795	13.8724	0.94	1.07
CG6856_gene	CG6856	6.31463	5.9264	0.94	1.07
CG5273_gene	CG5273	27.5176	25.8245	0.94	1.07
CG3249_gene	CG3249	81.7092	76.679	0.94	1.07
trr_gene	CG14806	16.7937	15.7596	0.94	1.07
Rab21_gene	Rab21	5.71583	5.36356	0.94	1.07
CG5727_gene	CG5727	3.81055	3.5757	0.94	1.07
RpS27_gene	RpS27	192.977	181.07	0.94	1.07
RpL38_gene	RpL38	138.759	130.182	0.94	1.07
CG31872_gene	CG31872	24648.2	23123.7	0.94	1.07
fu_gene	fu	3.21175	3.01286	0.94	1.07
CG5284_gene	CG5284	54.4637	51.0862	0.94	1.07
CG8199_gene	CG8199	4.51823	4.23787	0.94	1.07
Aats-cys_gene	Aats-cys	12.9559	12.1508	0.94	1.07
CG12171_gene	CG12171	16.5215	15.4947	0.94	1.07
CG8740_gene	CG8740	31.1377	29.2016	0.94	1.07
CHKov2_gene	CHKov2	108.955	102.172	0.94	1.07
Iswi_gene	Iswi	10.098	9.469	0.94	1.07
CG4730_gene	Lgr3	1.30648	1.22501	0.94	1.07
CG32810_gene	CG32810	38.5955	36.1875	0.94	1.07
CG33158_gene	CG33158	32.172	30.1617	0.94	1.07
CG9099_gene	CG4875	14.1263	13.2434	0.94	1.07
Sin3A_gene	CG8594	137.806	129.189	0.94	1.07
CG17082_gene	CG17082	30.9744	29.036	0.94	1.07
NTPase_gene	betaggt-II	94.5834	88.6642	0.94	1.07
Slh_gene	Slh	86.2546	80.8507	0.94	1.07
CG10344_gene	CG10344	1.66031	1.55609	0.94	1.07
CG10426_gene	CG10426	1.66031	1.55609	0.94	1.07
CG11377_gene	CG11377	71.965	67.4418	0.94	1.07
Su(z)2_gene	Su(z)2	20.7403	19.4346	0.94	1.07
CG5484_gene	CG5484	38.2689	35.8564	0.94	1.07
Acf1_gene	Acf1	14.8067	13.8724	0.94	1.07
CG32350_gene	CG32350	14.2079	13.3096	0.94	1.07
RpL7A_gene	RpL7A	516.085	483.382	0.94	1.07
mRpS35_gene	mRpS35	5.79749	5.42977	0.94	1.07
CG11896_gene	CG11896	6.15132	5.76086	0.94	1.07
CG5903_gene	CG5903	35.0027	32.7773	0.94	1.07
MED4_gene	MED4	3.78334	3.5426	0.94	1.07
CG6125_gene	CG6125	85.0026	79.5925	0.94	1.07
CG6439_gene	CG6439	33.0974	30.9894	0.94	1.07
CG17273_gene	CG17273	139.575	130.646	0.94	1.07
CG10375_gene	CG10375	9.44473	8.83994	0.94	1.07
CG7331_gene	CG7331	24.5509	22.9772	0.94	1.07
CG1091_gene	CG1939	24.3059	22.7455	0.94	1.07
egl_gene	egl	33.8595	31.6847	0.94	1.07
CG41343_gene	CG41343	1.41535	1.32434	0.94	1.07
CG8089_gene	CG8089	3.53837	3.31084	0.94	1.07
CG17681_gene	CG17681	1.06151	0.993251	0.94	1.07

lea_gene	lea	1.06151	0.993251	0.94	1.07
CG5835_gene	CG11779	4.59988	4.30409	0.94	1.07
CG3448_gene	CG3529	4.59988	4.30409	0.94	1.07
mth_gene	Ptpmeg	7.43058	6.95276	0.94	1.07
Oseg4_gene	drpr	2.12302	1.9865	0.94	1.07
CG9992_gene	CG9992	6.01523	5.62842	0.94	1.07
l(3)mbt_gene	CG14260	19.5699	18.3089	0.94	1.07
CG11608_gene	CG11608	287.969	269.403	0.94	1.07
CG5823_gene	CG5823	34.1589	31.9496	0.94	1.07
CycG_gene	CycG	411.703	385.05	0.94	1.07
CG34057_gene	CG34057	46.271	43.2726	0.94	1.07
RpL34b_gene	RpL34b	131.165	122.633	0.93	1.07
CG15917_gene	CG15917	45.8627	42.8753	0.93	1.07
RpS4_gene	RpS4	556.94	520.662	0.93	1.07
CG18012_gene	CG18012	48.0946	44.9612	0.93	1.07
mRpL41_gene	CG11808	2.93957	2.748	0.93	1.07
CG31883_gene	Oatp30B	4696.45	4390.04	0.93	1.07
RpL26_gene	RpL26	457.076	427.231	0.93	1.07
CG8507_gene	CG8507	21.8563	20.4279	0.93	1.07
WASp_gene	WASp	9.28142	8.67439	0.93	1.07
CycE_gene	CycE	5.98801	5.59532	0.93	1.07
CG4882_gene	TM4SF	17.964	16.7859	0.93	1.07
CG5664_gene	CG5664	3.75612	3.50949	0.93	1.07
CG40042_gene	Gpb5	39.9019	37.28	0.93	1.07
CG14441_gene	CG14441	6.80456	6.35681	0.93	1.07
CG3209_gene	CG3209	49.1562	45.9213	0.93	1.07
Acph-1_gene	Acph-1	24.9863	23.3414	0.93	1.07
CG14868_gene	CG14868	2.69461	2.51624	0.93	1.07
sina_gene	Rh4	22.7272	21.2225	0.93	1.07
CG16979_gene	CG16979	32.0903	29.9631	0.93	1.07
cul-5_gene	cul-5	7.37614	6.88654	0.93	1.07
CG17490_gene	CG17490	15.5688	14.5346	0.93	1.07
Cyp317a1_gene	Cyp317a1	8.19269	7.64804	0.93	1.07
Clk_gene	Clk	17.2019	16.0576	0.93	1.07
CG6227_gene	CG6227	16.8481	15.7265	0.93	1.07
Mgat1_gene	CG13424	384.376	358.762	0.93	1.07
Cyp28d1_gene	Cyp28d1	3.15732	2.94665	0.93	1.07
CG4622_gene	CG13585	13.092	12.217	0.93	1.07
CG33054_gene	CG34261	12.7381	11.8859	0.93	1.07
CG13887_gene	CG13887	152.341	142.134	0.93	1.07
CG15745_gene	CG15745	44.8557	41.849	0.93	1.07
CG30169_gene	CG30169	3.62003	3.37705	0.93	1.07
CG3726_gene	CG3726	25.8029	24.0698	0.93	1.07
CG11063_gene	CG11063	6.88622	6.42303	0.93	1.07
CG5315_gene	CG5315	112.275	104.722	0.93	1.07
BG642163_gene	BG642163	3739.9	3488.2	0.93	1.07
CG15770_gene	CG15770	1.63309	1.52299	0.93	1.07
CG8192_gene	IF2B-gamm	1.63309	1.52299	0.93	1.07
CG34171_gene	Fas3	2.44964	2.28448	0.93	1.07
Ste:CG33245_gene	te:CG3324	0.816547	0.761493	0.93	1.07
CG9921_gene	CG9921	9.79857	9.13791	0.93	1.07
Caki_gene	Caki	14.6979	13.7069	0.93	1.07
CG3731_gene	CycC	69.5154	64.8262	0.93	1.07
CG9855_gene	CG9855	32.7708	30.559	0.93	1.07
CG17385_gene	CG17385	18.9983	17.713	0.93	1.07
CG10263_gene	CG10263	4.54545	4.23787	0.93	1.07
CG4768_gene	CG4768	15.841	14.7663	0.93	1.07
CG14223_gene	CG14223	2.0958	1.95339	0.93	1.07
mod(mdg4)_gene	mod(mdg4	118.073	110.019	0.93	1.07
CG5731_gene	CG5731	66.7391	62.1775	0.93	1.07

pix_gene	pix	434.267	404.518	0.93	1.07
Rhp_gene	Rhp	3.02123	2.81421	0.93	1.07
CG8798_gene	CG9372	26.3745	24.5664	0.93	1.07
CG12728_gene	CG12728	7.78442	7.25073	0.93	1.07
Pgk_gene	CG2843	101.987	94.9879	0.93	1.07
CR41597_gene	CR41597	8.24713	7.68114	0.93	1.07
CG15435_gene	CG15435	9.17255	8.54196	0.93	1.07
CG30038_gene	CG30038	5.68861	5.29734	0.93	1.07
CG15922_gene	CG5180	5.68861	5.29734	0.93	1.07
Tif-IA_gene	Tif-IA	29.3685	27.3475	0.93	1.07
CG15535_gene	CG15535	3.94665	3.67503	0.93	1.07
CG14969_gene	CG14969	28.6608	26.6854	0.93	1.07
CG15696_gene	CG15696	9.28142	8.64129	0.93	1.07
vvl_gene	vvl	126.075	117.336	0.93	1.07
RpL5_gene	RpL5	993.167	924.253	0.93	1.07
CG15083_gene	CG15083	14.9428	13.9055	0.93	1.07
HLH106_gene	HLH106	115.786	107.735	0.93	1.07
Jheh2_gene	Jheh2	97.2236	90.4521	0.93	1.07
RhoGAP92B_gene	RhoGAP92B	62.2481	57.9066	0.93	1.07
VhaPPA1-1_gene	VhaPPA1-1	75.7756	70.4877	0.93	1.08
syd_gene	syd	122.509	113.959	0.93	1.08
ena_gene	CG15118	6.01523	5.59532	0.93	1.08
Rab-RP4_gene	Rab-RP4	16.7664	15.594	0.93	1.08
CG4848_gene	CG4848	44.393	41.2861	0.93	1.08
Aph-4_gene	Aph-4	435.465	404.982	0.93	1.08
Pros25_gene	Pros25	27.6265	25.6921	0.93	1.08
Rab39_gene	Rab39	7.97495	7.41628	0.93	1.08
CG1910_gene	CG1910	81.3553	75.6526	0.93	1.08
CG13282_gene	CG13282	11.7855	10.9589	0.93	1.08
CG13609_gene	CG5669	14.2079	13.2102	0.93	1.08
CG7549_gene	CG7549	26.2112	24.3678	0.93	1.08
CG12360_gene	CG12360	38.8949	36.1543	0.93	1.08
CG8010_gene	vav	8.19269	7.61493	0.93	1.08
roq_gene	roq	38.0783	35.3929	0.93	1.08
Vha36_gene	Vha36	87.4522	81.2811	0.93	1.08
Adk2_gene	Adk2	32.5258	30.2279	0.93	1.08
CG18292_gene	CG18292	14.6434	13.6075	0.93	1.08
CG14883_gene	CG14883	3.91943	3.64192	0.93	1.08
CG2453_gene	CG2453	3.91943	3.64192	0.93	1.08
CG2200_gene	CG2200	17.2836	16.0576	0.93	1.08
CG18789_gene	CG18789	1.497	1.39055	0.93	1.08
RnrL_gene	RnrL	1.497	1.39055	0.93	1.08
mRpS11_gene	CG3983	2.99401	2.7811	0.93	1.08
CG13605_gene	CG18428	33.043	30.6915	0.93	1.08
pain_gene	pain	14.0446	13.0447	0.93	1.08
CG13895_gene	CG13895	5.5253	5.1318	0.93	1.08
msi_gene	msi	5.06259	4.70139	0.93	1.08
CG10960_gene	CG10960	48.0946	44.6632	0.93	1.08
CG9646_gene	CG9646	22.319	20.7258	0.93	1.08
CG5618_gene	CG5618	18.2907	16.9846	0.93	1.08
CG10584_gene	CG10584	8.16547	7.58182	0.93	1.08
yrt_gene	yrt	18.3995	17.0839	0.93	1.08
RpS3_gene	RpS3	517.582	480.568	0.93	1.08
Ranbp21_gene	Ranbp21	27.817	25.8245	0.93	1.08
Hs3st-A_gene	Hs3st-A	1.03429	0.960143	0.93	1.08
pad_gene	pad	3.10288	2.88043	0.93	1.08
fz3_gene	fz3	38.5955	35.8233	0.93	1.08
cdc16_gene	cdc16	3.67446	3.41016	0.93	1.08
ergic53_gene	ergic53	452.449	419.88	0.93	1.08
ox_gene	mRpL18	33.5057	31.0888	0.93	1.08

CG32112_gene	CG32112	3.21175	2.97975	0.93	1.08
Ubi-p5E_gene	Ubi-p5E	417.746	387.567	0.93	1.08
Flo-2_gene	Flo-2	209.444	194.313	0.93	1.08
cype_gene	cype	26.3745	24.4671	0.93	1.08
betaggt-I_gene	betaggt-I	39.3304	36.4854	0.93	1.08
lig3_gene	CG34402	15.2422	14.1373	0.93	1.08
CG18428_gene	CG18428	6.53238	6.05883	0.93	1.08
SdhB_gene	SdhB	60.7239	56.3173	0.93	1.08
CG5978_gene	CG32351	5.49809	5.09869	0.93	1.08
CG4297_gene	CG4297	268.644	249.107	0.93	1.08
RpL34a_gene	RpL34a	73.952	68.5674	0.93	1.08
Csl4_gene	Csl4	5.03538	4.66828	0.93	1.08
CG2186_gene	CG2186	16.0043	14.8326	0.93	1.08
CG31300_gene	CG31300	6.859	6.35681	0.93	1.08
snmRNA:765_gene	Msp-300	1.14317	1.05947	0.93	1.08
CG2608_gene	CG2608	3.4295	3.1784	0.93	1.08
cue_gene	Psa	150.435	139.419	0.93	1.08
mod_gene	mod	188.922	175.077	0.93	1.08
CG14646_gene	CG14646	16.1132	14.9319	0.93	1.08
CG8728_gene	CG8728	13.2553	12.2832	0.93	1.08
Osbp_gene	CG11771	148.775	137.863	0.93	1.08
CG5021_gene	CG5021	60.3156	55.8869	0.93	1.08
CG31418_gene	CG31418	543.902	503.943	0.93	1.08
CG33649_gene	Orc5	8.79149	8.14466	0.93	1.08
DNApol-gamma35_gene	Orc5	8.79149	8.14466	0.93	1.08
Past1_gene	CG14394	30.1306	27.9104	0.93	1.08
Ptp61F_gene	Ptp61F	160.56	148.723	0.93	1.08
LysE_gene	LysE	173.407	160.609	0.93	1.08
retm_gene	retm	55.4436	51.3511	0.93	1.08
CG1951_gene	CG1951	10.9417	10.1312	0.93	1.08
Gos28_gene	Gos28	10.9417	10.1312	0.93	1.08
CG11790_gene	CG11790	56.0696	51.9139	0.93	1.08
CG7372_gene	comm3	4.89928	4.53585	0.93	1.08
Vps28_gene	Vps28	20.8492	19.3022	0.93	1.08
CG1309_gene	CG1309	24.0337	22.2488	0.93	1.08
dpp_gene	dpp	41.9161	38.803	0.93	1.08
mRpL38_gene	mRpL38	4.3277	4.00611	0.93	1.08
CG13585_gene	CG13585	237.996	220.303	0.93	1.08
Pi3K68D_gene	Pi3K68D	57.7299	53.4369	0.93	1.08
AlstR_gene	AlstR	1.25204	1.15879	0.93	1.08
CG31111_gene	CG31111	1.25204	1.15879	0.93	1.08
CG4757_gene	CG4757	1.25204	1.15879	0.93	1.08
CG13775_gene	SA	1.25204	1.15879	0.93	1.08
snmRNA:204_gene	CG32638	5.68861	5.26423	0.93	1.08
RpL40_gene	RpL40	458.682	424.449	0.93	1.08
CG8188_gene	CG8188	70.6313	65.3559	0.93	1.08
CG11447_gene	CG11447	6.36907	5.89329	0.93	1.08
CG3709_gene	CG3709	5.11703	4.7345	0.93	1.08
CG34431_gene	CG14764	1.9325	1.78785	0.93	1.08
sec3_gene	sec3	16.8209	15.5609	0.93	1.08
Prp18_gene	P5cr	7.1584	6.62168	0.93	1.08
CG14060_gene	CG14060	31.2465	28.9036	0.93	1.08
CG10987_gene	bves	7.83885	7.25073	0.92	1.08
CG10470_gene	CG10470	17.7191	16.3886	0.92	1.08
CG3214_gene	CG3214	11.2411	10.396	0.92	1.08
CG17019_gene	CG17019	8.62818	7.97912	0.92	1.08
svr_gene	svr	134.295	124.19	0.92	1.08
Mmp2_gene	Mmp2	11.35	10.4954	0.92	1.08
Acp26Aa_gene	Acp26Aa	7681.72	7102.97	0.92	1.08
sax_gene	sax	12.8198	11.8528	0.92	1.08

sphinx2_gene	sphinx2	333.805	308.603	0.92	1.08
CG33231_gene	CG33231	1.36091	1.25812	0.92	1.08
CG4194_gene	CG4199	0.680456	0.629059	0.92	1.08
MED25_gene	MED25	6.80456	6.29059	0.92	1.08
Sgt_gene	Sgt	76.6466	70.8519	0.92	1.08
CG4040_gene	CG4040	11.7855	10.8927	0.92	1.08
CG31121_gene	CG11089	18.0185	16.6535	0.92	1.08
dx_gene	dx	11.3228	10.4622	0.92	1.08
CG7556_gene	CG7556	102.803	94.9879	0.92	1.08
CG15658_gene	CG15658	2.15024	1.9865	0.92	1.08
CG31710_gene	pelo	2.15024	1.9865	0.92	1.08
CG13698_gene	CG13698	13.3369	12.3163	0.92	1.08
pfk_gene	pfk	5.19868	4.80071	0.92	1.08
AP-1gamma_gene	P-1gamm	70.958	65.5215	0.92	1.08
drm_gene	drm	77.7353	71.779	0.92	1.08
betaCop_gene	betaCop	312.329	288.374	0.92	1.08
CG3408_gene	CG3408	4.51823	4.17166	0.92	1.08
CG7011_gene	CG6876	57.3761	52.9734	0.92	1.08
Acp70A_gene	Acp70A	358.655	331.084	0.92	1.08
heix_gene	heix	177.844	164.151	0.92	1.08
mfas_gene	mfas	3019.89	2787.23	0.92	1.08
CR32009_gene	CR32009	6.99509	6.45613	0.92	1.08
Oatp30B_gene	Oatp30B	4793.6	4423.97	0.92	1.08
CG1531_gene	CG1531	22.1012	20.3948	0.92	1.08
CG8097_gene	CG8097	1.57866	1.45677	0.92	1.08
CG10447_gene	CG10447	2.36799	2.18515	0.92	1.08
CG14710_gene	CG14710	2.36799	2.18515	0.92	1.08
CG34130_gene	CG34130	458.301	422.761	0.92	1.08
CG7457_gene	CG32373	4.95372	4.56896	0.92	1.08
CG10284_gene	CG10284	1246.3	1149.39	0.92	1.08
rad_gene	rad	8.32878	7.68114	0.92	1.08
eIF-4E_gene	eIF-4E	83.5056	77.0101	0.92	1.08
jumu_gene	jumu	3.37506	3.11219	0.92	1.08
CG15717_gene	CG15717	5.06259	4.66828	0.92	1.08
CG2183_gene	CG2183	1.68753	1.55609	0.92	1.08
CG7506_gene	CG7506	7.64833	7.05208	0.92	1.08
CG32795_gene	CG32795	16.1949	14.9319	0.92	1.08
CG6254_gene	Invadolysi	4.27326	3.9399	0.92	1.08
geminin_gene	geminin	11.1323	10.2636	0.92	1.08
CG5690_gene	mu2	2.58573	2.3838	0.92	1.08
CG33174_gene	CG33174	17.5286	16.1569	0.92	1.08
scat_gene	scat	65.3782	60.2572	0.92	1.08
CG17514_gene	CG17514	141.861	130.745	0.92	1.09
CG16972_gene	Edem2	10.6696	9.83319	0.92	1.09
sm_gene	sm	414.752	382.236	0.92	1.09
CG13188_gene	CG13188	0.898202	0.827709	0.92	1.09
CG9306_gene	CG9306	28.9602	26.6854	0.92	1.09
Aats-glupro_gene	Aats-glupr	83.7233	77.1425	0.92	1.09
alpha-Man-II_gene	lpha-Man-	125.803	115.912	0.92	1.09
mrt_gene	CG5938	38.3777	35.3597	0.92	1.09
eca_gene	eca	136.554	125.812	0.92	1.09
Dcp1_gene	Dcp1	12.1121	11.1575	0.92	1.09
ImpL3_gene	ImpL3	73.8975	68.0708	0.92	1.09
Atg18_gene	Atg18	27.2455	25.0962	0.92	1.09
sba_gene	sba	26.3473	24.2684	0.92	1.09
CG17486_gene	CG17486	41.3445	38.0746	0.92	1.09
cp309_gene	cp309	35.6287	32.8104	0.92	1.09
CG6540_gene	CG6540	2.91235	2.68178	0.92	1.09
Slip1_gene	Slip1	22.4006	20.6265	0.92	1.09
CG30438_gene	CG30438	2438.07	2244.88	0.92	1.09

HtrA2_gene	HtrA2	3.91943	3.60881	0.92	1.09
CG6734_gene	CG6734	13.7724	12.6805	0.92	1.09
RpL18A_gene	cyp33	370.658	341.248	0.92	1.09
CG18557_gene	CG18557	2.01415	1.85407	0.92	1.09
zetaCOP_gene	zetaCOP	86.1457	79.2946	0.92	1.09
Acon_gene	Acon	130.321	119.952	0.92	1.09
Tie_gene	Tie	62.1665	57.2113	0.92	1.09
Prx5037_gene	Prx5037	7.26727	6.68789	0.92	1.09
CG4393_gene	CG4393	17.6646	16.2562	0.92	1.09
vlc_gene	vlc	26.1567	24.0698	0.92	1.09
RpL35_gene	RpL35	425.503	391.54	0.92	1.09
CG6409_gene	CG6409	58.111	53.47	0.92	1.09
CG7289_gene	CG7289	56.0968	51.616	0.92	1.09
CG2177_gene	CG2177	65.7048	60.4559	0.92	1.09
NetB_gene	NetB	4.24605	3.90679	0.92	1.09
pgant8_gene	pgant8	45.8355	42.147	0.92	1.09
CG7810_gene	CG7818	5.90636	5.42977	0.92	1.09
GXIVsPLA2_gene	GXIVsPLA2	41.5623	38.2071	0.92	1.09
Scr_gene	Scr	60.7239	55.8207	0.92	1.09
CG5267_gene	unc-104	138.568	127.368	0.92	1.09
CG12124_gene	CG12124	4.89928	4.50274	0.92	1.09
CG12229_gene	CG32176	2.44964	2.25137	0.92	1.09
CG34355_gene	CG34355	1.22482	1.12568	0.92	1.09
CG7101_gene	CG7101	1.22482	1.12568	0.92	1.09
endoA_gene	endoA	17.2564	15.8589	0.92	1.09
CdsA_gene	CdsA	19.2433	17.6799	0.92	1.09
CG10874_gene	CG10874	10.3429	9.5021	0.92	1.09
CG13531_gene	CG3649	24.6869	22.6792	0.92	1.09
CG14074_gene	CG14074	1.33369	1.22501	0.92	1.09
CG6707_gene	CG6707	37.4523	34.3996	0.92	1.09
CG17600_gene	CG17600	60.234	55.3241	0.92	1.09
RpS26_gene	RpS26	334.431	307.146	0.92	1.09
mago_gene	mago	12.221	11.2237	0.92	1.09
CG4847_gene	CG4847	2799.59	2571.06	0.92	1.09
eIF3-S9_gene	eIF3-S9	547.141	502.42	0.92	1.09
CG8677_gene	CG8677	47.0603	43.2064	0.92	1.09
CG6241_gene	CG6241	2.88513	2.64867	0.92	1.09
CG11828_gene	CG11828	227.136	208.517	0.92	1.09
Mes-4_gene	CG5508	13.092	12.0183	0.92	1.09
RpL13_gene	Dref	361.458	331.779	0.92	1.09
CG31998_gene	CG31998	52.3407	48.0403	0.92	1.09
CG2846_gene	CG2846	31.8181	29.2016	0.92	1.09
CG14542_gene	CG14542	24.2787	22.2819	0.92	1.09
l(2)k14710_gene	l(2)k14710	10.7512	9.8663	0.92	1.09
Gdi_gene	Gdi	272.074	249.67	0.92	1.09
CG34213_gene	CG34213	3.10288	2.84732	0.92	1.09
Dlic2_gene	Dlic2	26.7011	24.5002	0.92	1.09
phtf_gene	phtf	9.74413	8.93926	0.92	1.09
CG12204_gene	CG12203	4.87207	4.46963	0.92	1.09
CG11866_gene	CG11866	16.3854	15.0312	0.92	1.09
CG1307_gene	CG1307	20.4681	18.7724	0.92	1.09
CG5910_gene	CG5910	3.4295	3.1453	0.92	1.09
CG13689_gene	CG13689	1.76919	1.62231	0.92	1.09
rho_gene	rho	5.41643	4.96626	0.92	1.09
CG12338_gene	CG12338	5.5253	5.06558	0.92	1.09
CG15011_gene	CG1265	14.8067	13.5744	0.92	1.09
fy_gene	CG31898	1.98693	1.82096	0.92	1.09
spict_gene	spict	8.0566	7.38317	0.92	1.09
CG14615_gene	CG14615	4.08274	3.74125	0.92	1.09
Lis-1_gene	Lis-1	32.8796	30.1286	0.92	1.09

YT521-B_gene	YT521-B	36.6085	33.5388	0.92	1.09
CG1718_gene	CG1718	45.9716	42.1139	0.92	1.09
Hph_gene	Hph	36.5813	33.5057	0.92	1.09
l(2)k01209_gene	l(2)k01209	16.086	14.7332	0.92	1.09
Aats-ala_gene	Aats-ala	67.964	62.2437	0.92	1.09
CG30291_gene	CG30291	51.0886	46.7821	0.92	1.09
CG34197_gene	hts	4.95372	4.53585	0.92	1.09
CG6398_gene	CG6398	96.407	88.2669	0.92	1.09
toc_gene	toc	95.4	87.3399	0.92	1.09
CG6690_gene	CG6690	569.406	521.225	0.92	1.09
CG13802_gene	DmsR-2	8.68262	7.94601	0.92	1.09
DmsR-2_gene	DmsR-2	8.68262	7.94601	0.92	1.09
cbt_gene	cbt	11.7583	10.7602	0.92	1.09
CG7597_gene	CG7597	42.1883	38.6044	0.92	1.09
Tim9a_gene	Tim9a	3.18453	2.91354	0.91	1.09
CG9590_gene	CG9590	31.9542	29.2347	0.91	1.09
CG10956_gene	CG10956	167.991	153.689	0.91	1.09
Aef1_gene	Aef1	35.5742	32.5455	0.91	1.09
Hs6st_gene	Hs6st	150.735	137.896	0.91	1.09
CG9897_gene	CG9897	6.58682	6.02572	0.91	1.09
p130CAS_gene	p130CAS	6.69569	6.12505	0.91	1.09
CG6126_gene	CG6126	3.62003	3.31084	0.91	1.09
Obp56f_gene	Obp56f	520.984	476.463	0.91	1.09
Mef2_gene	Mef2	20.2776	18.5407	0.91	1.09
CG32191_gene	CG32191	4.16439	3.80746	0.91	1.09
CG5118_gene	CG31922	12.4932	11.4224	0.91	1.09
Prat_gene	Taf7	12.4932	11.4224	0.91	1.09
CG7407_gene	CG7407	8.43766	7.71425	0.91	1.09
CG4705_gene	CG4705	9.52639	8.7075	0.91	1.09
CG8444_gene	CG8444	70.2775	64.2303	0.91	1.09
TER94_gene	TER94	186.527	170.475	0.91	1.09
alt_gene	alt	307.103	280.66	0.91	1.09
Arf51F_gene	Arf51F	22.2101	20.2954	0.91	1.09
CG15706_gene	CG15706	5.90636	5.39667	0.91	1.09
pgant6_gene	pgant6	42.4332	38.7699	0.91	1.09
CG9960_gene	CG9960	6.66847	6.09194	0.91	1.09
snapin_gene	CG9960	6.66847	6.09194	0.91	1.09
Qm_gene	Qm	800.625	731.265	0.91	1.09
CG10171_gene	CG10171	9.06368	8.27709	0.91	1.10
CG2219_gene	CG2219	10.479	9.56832	0.91	1.10
UbcD2_gene	UbcD2	13.5275	12.3494	0.91	1.10
Nop60B_gene	Nop60B	32.2808	29.4665	0.91	1.10
alpha-Est8_gene	alpha-Est8	26.2656	23.9705	0.91	1.10
Ogt_gene	Ogt	77.3543	70.5871	0.91	1.10
smo_gene	smo	10.7784	9.83319	0.91	1.10
CG5180_gene	CG5180	5.44365	4.96626	0.91	1.10
Cks85A_gene	CG8112	0.544365	0.496626	0.91	1.10
CG9317_gene	CG9317	0.544365	0.496626	0.91	1.10
Mes2_gene	Mes2	0.544365	0.496626	0.91	1.10
mir-281b_gene	Oda	0.544365	0.496626	0.91	1.10
tko_gene	tko	5.00816	4.56896	0.91	1.10
mir-304_gene	l(1)G0168	0.653238	0.595951	0.91	1.10
CG8239_gene	CG8239	1.52422	1.39055	0.91	1.10
CG14763_gene	nito	1.52422	1.39055	0.91	1.10
CG2611_gene	CG2611	2.06859	1.88718	0.91	1.10
CG41293_gene	CG17163	0.979857	0.893926	0.91	1.10
CG33937_gene	CG33936	0.979857	0.893926	0.91	1.10
Or43b_gene	lin19	3.15732	2.88043	0.91	1.10
CG8388_gene	CG8389	3.91943	3.5757	0.91	1.10
CG11307_gene	CG11307	1.74197	1.5892	0.91	1.10

qkr58E-1_gene	qkr58E-1	97.6591	89.0615	0.91	1.10
mthl10_gene	Ptpmeg	12.7109	11.5879	0.91	1.10
Iap2_gene	Iap2	37.2618	33.9692	0.91	1.10
Pde1c_gene	Pde1c	11.2956	10.2967	0.91	1.10
MTF-1_gene	MTF-1	21.2847	19.4015	0.91	1.10
CG8443_gene	CG8443	31.7093	28.9036	0.91	1.10
CG10166_gene	CG10166	49.8094	45.3916	0.91	1.10
CG7328_gene	gig	8.13826	7.41628	0.91	1.10
bocksbeutel_gene	P58IPK	20.7131	18.8718	0.91	1.10
CG4567_gene	CG4567	6.50516	5.9264	0.91	1.10
sl_gene	sl	12.2482	11.1575	0.91	1.10
Tsp42Ea_gene	Tsp42Ea	44.8285	40.8226	0.91	1.10
Tango5_gene	Tango5	50.5443	46.0206	0.91	1.10
scra_gene	scra	8.87315	8.07844	0.91	1.10
Ost48_gene	Ost48	382.199	347.936	0.91	1.10
beta'Cop_gene	beta'Cop	326.701	297.379	0.91	1.10
Tom20_gene	Tom20	23.2444	21.1563	0.91	1.10
mthl4_gene	mthl4	3.78334	3.44327	0.91	1.10
comm_gene	comm	44.529	40.5247	0.91	1.10
RpL8_gene	RpL8	558.845	508.545	0.91	1.10
CG7857_gene	CG7272	3.56559	3.24462	0.91	1.10
Sap47_gene	Sap47	79.069	71.9445	0.91	1.10
CG10586_gene	CG10586	475.476	432.627	0.91	1.10
beat-VII_gene	beat-VII	3.23897	2.94665	0.91	1.10
CG17683_gene	CG17683	18.9983	17.2826	0.91	1.10
CG8533_gene	CG8533	5.60696	5.09869	0.91	1.10
CG11306_gene	CG11306	68.9438	62.6742	0.91	1.10
GalNAc-T2_gene	GalNAc-T2	73.7887	67.0776	0.91	1.10
CG14962_gene	rasp	2.47686	2.25137	0.91	1.10
CG5357_gene	CG5357	4.84485	4.40341	0.91	1.10
dj-1beta_gene	dj-1beta	16.7937	15.263	0.91	1.10
CG8475_gene	CG8475	32.2808	29.334	0.91	1.10
Bsg25D_gene	Bsg25D	77.4631	70.3884	0.91	1.10
CG40298_gene	CG40298	2.25911	2.05272	0.91	1.10
CG9598_gene	CG9598	25.8029	23.4407	0.91	1.10
CG12586_gene	CG34357	168.835	153.358	0.91	1.10
CG6136_gene	CG6136	6.12411	5.56221	0.91	1.10
mRpS18A_gene	mRpS18A	2.04137	1.85407	0.91	1.10
CaBP1_gene	CaBP1	467.256	424.383	0.91	1.10
CG14662_gene	CG14662	3.86499	3.50949	0.91	1.10
CG8132_gene	CG8132	7.62111	6.91965	0.91	1.10
CG11037_gene	CG11037	1261.62	1145.48	0.91	1.10
Cchl_gene	Cchl	25.8573	23.4738	0.91	1.10
CG6666_gene	CG6666	62.5475	56.7809	0.91	1.10
Surf1_gene	Surf1	1.82362	1.65542	0.91	1.10
CG17806_gene	CG17806	3.4295	3.11219	0.91	1.10
Mrtf_gene	Mrtf	2980.75	2704.82	0.91	1.10
CG8485_gene	CG8485	14.8884	13.5082	0.91	1.10
LysD_gene	LysC	205.117	186.102	0.91	1.10
CG7082_gene	CG7082	27.8443	25.2617	0.91	1.10
CG8613_gene	CG8613	36.7174	33.307	0.91	1.10
Fas3_gene	Fas3	39627.2	35943.3	0.91	1.10
CG17665_gene	CG17665	25.0408	22.7123	0.91	1.10
RpII33_gene	RpII33	9.09089	8.24399	0.91	1.10
Acp36DE_gene	Fas3	39522.7	35839.3	0.91	1.10
CG5976_gene	CG5969	19.0256	17.2495	0.91	1.10
aph-1_gene	aph-1	7.1584	6.48924	0.91	1.10
CG7329_gene	CG7329	45.6178	41.3524	0.91	1.10
CG4980_gene	CG4980	5.6614	5.1318	0.91	1.10
T48_gene	T48	5.55252	5.03247	0.91	1.10

CG34357_gene	CG34357	180.266	163.357	0.91	1.10
Mitf_gene	Mitf	53.2389	48.2389	0.91	1.10
CG6194_gene	CG5038	15.8955	14.4021	0.91	1.10
Acp62F_gene	Mrtf	2961.73	2683.47	0.91	1.10
Tsp29Fb_gene	Tsp29Fb	149.102	135.082	0.91	1.10
PpD3_gene	PpD3	10.2341	9.27035	0.91	1.10
epsin-like_gene	epsin-like	41.2356	37.3462	0.91	1.10
robl_gene	robl	9.6897	8.77372	0.91	1.10
Taf10b_gene	Taf10b	19.3794	17.5474	0.91	1.10
Gfat2_gene	Gfat2	86.7173	78.5	0.91	1.10
CG34136_gene	CG12050	1.17038	1.05947	0.91	1.10
MESR3_gene	MESR3	52.8578	47.8416	0.91	1.10
CG4780_gene	CG4780	19.3522	17.5143	0.91	1.10
epsilonCOP_gene	epsilonCOP	142.896	129.321	0.91	1.10
CG12717_gene	CG12717	5.63418	5.09869	0.90	1.11
LysC_gene	LysC	164.317	148.69	0.90	1.11
CG1602_gene	CG1602	2.2319	2.01961	0.90	1.11
CG17982_gene	CG17982	3.29341	2.97975	0.90	1.11
dpr18_gene	dpr18	14.2351	12.8792	0.90	1.11
CG7837_gene	CG12068	5.41643	4.90004	0.90	1.11
CG18143_gene	aux	14.97	13.5413	0.90	1.11
CG15312_gene	CG15312	3.18453	2.88043	0.90	1.11
Scgbeta_gene	Scgbeta	1.06151	0.960143	0.90	1.11
CG4196_gene	CG4196	35.9825	32.5455	0.90	1.11
CG17712_gene	CG17712	9.44473	8.54196	0.90	1.11
NK7.1_gene	NK7.1	8.38322	7.58182	0.90	1.11
CG9864_gene	CG9864	28.0076	25.3279	0.90	1.11
CG1120_gene	CG1120	4.13717	3.74125	0.90	1.11
CG8272_gene	CG8272	4.13717	3.74125	0.90	1.11
CG3163_gene	CG3163	5.08981	4.60206	0.90	1.11
RpS7_gene	RpS7	418.072	377.998	0.90	1.11
CG10508_gene	CG10508	9.11811	8.24399	0.90	1.11
CG9027_gene	CG9027	25.1224	22.7123	0.90	1.11
CG13784_gene	CG13784	65.8137	59.4958	0.90	1.11
Taf7_gene	CG2943	4.87207	4.40341	0.90	1.11
CG1463_gene	CG32654	29.0146	26.2218	0.90	1.11
Psf2_gene	Psf2	1.90528	1.72164	0.90	1.11
RpLP1_gene	RpLP1	447.441	404.286	0.90	1.11
CG6149_gene	CG6149	410.642	370.979	0.90	1.11
CG34242_gene	CG34242	3.70168	3.34395	0.90	1.11
CG3909_gene	CG3909	10.0435	9.0717	0.90	1.11
mRpL28_gene	mRpL28	30.1306	27.2151	0.90	1.11
CG5629_gene	CG5629	42.8143	38.6706	0.90	1.11
CG3446_gene	CG3446	60.7783	54.8937	0.90	1.11
CG32016_gene	CG32016	33.3968	30.1617	0.90	1.11
CG10359_gene	CG10359	3.59281	3.24462	0.90	1.11
CG11178_gene	CG11178	9.82579	8.87305	0.90	1.11
CG9246_gene	CG9246	34.4311	31.0888	0.90	1.11
CG31222_gene	CG31222	17.6374	15.9251	0.90	1.11
raptor_gene	Mipp2	19.2161	17.3488	0.90	1.11
CG5807_gene	CG5807	6.96787	6.29059	0.90	1.11
CG1271_gene	CG1271	1.68753	1.52299	0.90	1.11
CG31865_gene	CG31865	1.68753	1.52299	0.90	1.11
CG10176_gene	CG10176	15.1878	13.7069	0.90	1.11
CG31388_gene	CG31388	0.843766	0.761493	0.90	1.11
Su(fu)_gene	Su(fu)	14.97	13.5082	0.90	1.11
RpL24_gene	RpL24	351.034	316.748	0.90	1.11
CG3419_gene	CG3419	9.90744	8.93926	0.90	1.11
CG8768_gene	CG8776	4.95372	4.46963	0.90	1.11
ken_gene	ken	13.1736	11.8859	0.90	1.11

Cyp4g15_gene	Cyp4g15	7.37614	6.65478	0.90	1.11
CG2747_gene	CG2747	46.2438	41.7166	0.90	1.11
CG3680_gene	CG3680	27.4904	24.7982	0.90	1.11
CG4820_gene	CG4820	1.57866	1.42366	0.90	1.11
CG4884_gene	CG4884	1.57866	1.42366	0.90	1.11
alphaCop_gene	alphaCop	476.21	429.416	0.90	1.11
NaCP60E_gene	NaCP60E	246.053	221.859	0.90	1.11
E23_gene	E23	8.51931	7.68114	0.90	1.11
CG2921_gene	CG2921	15.46	13.9386	0.90	1.11
CG33523_gene	CG33523	63.3096	57.0788	0.90	1.11
CG4753_gene	CG4753	24.4964	22.0833	0.90	1.11
CG31731_gene	CG31731	102.803	92.6703	0.90	1.11
CG32091_gene	CG32091	26.3745	23.7718	0.90	1.11
CG32985_gene	CG32985	571.855	515.398	0.90	1.11
pho_gene	pho	19.325	17.415	0.90	1.11
cm_gene	inx7	14.0718	12.6805	0.90	1.11
snoRNA:Me18S-A425_gene	RpL3	1.46979	1.32434	0.90	1.11
ncm_gene	ncm	307.185	276.786	0.90	1.11
CG3032_gene	CG3032	0.734893	0.662168	0.90	1.11
CG7131_gene	CG8064	0.734893	0.662168	0.90	1.11
BM-40-SPARC_gene	M-40-SPAR	38.1055	34.3334	0.90	1.11
Ahcy89E_gene	Ahcy89E	11.6494	10.4954	0.90	1.11
Gtp-bp_gene	Gtp-bp	173.516	156.305	0.90	1.11
CG4221_gene	CG4221	4.30048	3.87368	0.90	1.11
CG16936_gene	CG3894	49.4011	44.4977	0.90	1.11
CG5862_gene	CG5862	84.1044	75.752	0.90	1.11
Alg-2_gene	Parp	28.933	26.0563	0.90	1.11
CG11807_gene	CG11807	11.2139	10.0981	0.90	1.11
Rap2l_gene	Rap2l	10.479	9.43589	0.90	1.11
CG8771_gene	CG8776	25.1497	22.6461	0.90	1.11
CG13380_gene	CG4174	2045.26	1841.62	0.90	1.11
CG4174_gene	CG4174	2045.26	1841.62	0.90	1.11
CG11596_gene	CG11596	13.2008	11.8859	0.90	1.11
hig_gene	hig	224.414	202.06	0.90	1.11
CG34347_gene	CG34347	33.9412	30.559	0.90	1.11
CG11839_gene	CG11839	3.45672	3.11219	0.90	1.11
RpS12_gene	RpS12	268.072	241.327	0.90	1.11
Esp_gene	Esp	10.0435	9.03859	0.90	1.11
CG5222_gene	CG5414	6.69569	6.02572	0.90	1.11
CG16700_gene	CG16700	13.9085	12.515	0.90	1.11
CG9436_gene	CG9436	9.93466	8.93926	0.90	1.11
Eip63E_gene	Eip63E	38.2689	34.4327	0.90	1.11
CG13559_gene	CG13559	19.5427	17.5805	0.90	1.11
CG8003_gene	CG8003	14.9428	13.442	0.90	1.11
CG6463_gene	CG6463	10.7512	9.66765	0.90	1.11
CG13366_gene	CG13366	35.3837	31.8172	0.90	1.11
CG8397_gene	Rrp42	25.8846	23.2752	0.90	1.11
Rpb7_gene	CG12241	5.00816	4.50274	0.90	1.11
CG33960_gene	CG33960	0.62602	0.562842	0.90	1.11
CG6418_gene	CG6418	14.9156	13.4089	0.90	1.11
CG1418_gene	CG12130	65.1877	58.6018	0.90	1.11
crc_gene	crc	411.975	370.317	0.90	1.11
dp_gene	dp	28.1437	25.2948	0.90	1.11
Nep3_gene	Nep3	4.27326	3.84057	0.90	1.11
sar1_gene	sar1	244.257	219.509	0.90	1.11
CG9799_gene	CG9799	21.6657	19.4677	0.90	1.11
CG34123_gene	alphaPS4	40.8274	36.6841	0.90	1.11
Aac11_gene	Aac11	53.5111	48.0734	0.90	1.11
sick_gene	sick	113.5	101.941	0.90	1.11
CG8128_gene	CG8128	9.36308	8.40953	0.90	1.11

NC2alpha_gene	NC2alpha	4.68154	4.20476	0.90	1.11
CG14065_gene	CG14065	17.4741	15.6934	0.90	1.11
RpL11_gene	RpL11	250.353	224.806	0.90	1.11
eIF-5A_gene	eIF-5A	362.656	325.621	0.90	1.11
trem_gene	CG4854	2.28633	2.05272	0.90	1.11
CG8712_gene	CG8713	3.4295	3.07908	0.90	1.11
bowl_gene	bowl	28.9874	26.0232	0.90	1.11
Msr-110_gene	Msr-110	2189.46	1965.45	0.90	1.11
SmB_gene	CG5168	9.5536	8.57507	0.90	1.11
CG30080_gene	CG30080	2.80348	2.51624	0.90	1.11
CG9947_gene	CG9947	19.6244	17.6137	0.90	1.11
CG15531_gene	CG15531	11.2139	10.0649	0.90	1.11
CG17032_gene	CG17032	18.4812	16.5873	0.90	1.11
Rbp1_gene	Rbp1	20.6586	18.5407	0.90	1.11
Dredd_gene	l(1)1Bi	17.2291	15.4616	0.90	1.11
CG8021_gene	CG8021	9.44473	8.47574	0.90	1.11
CG14216_gene	CG14216	6.64125	5.95951	0.90	1.11
nonA_gene	nonA	28.2253	25.3279	0.90	1.11
CG8237_gene	CG8237	61.731	55.3903	0.90	1.11
CG18233_gene	CG4174	429.341	385.216	0.90	1.11
CG10915_gene	CG10915	14.2079	12.7467	0.90	1.11
CG7386_gene	CG7386	3.21175	2.88043	0.90	1.12
RpS14a_gene	RpS14a	370.876	332.541	0.90	1.12
CG8891_gene	CG3792	6.83178	6.12505	0.90	1.12
CG1513_gene	CG1513	30.9471	27.7448	0.90	1.12
CG1737_gene	CG1737	25.5579	22.911	0.90	1.12
Zip3_gene	Zip3	3.10288	2.7811	0.90	1.12
CG31284_gene	mRpS9	11.2684	10.0981	0.90	1.12
l(2)37Cb_gene	l(2)37Cb	7.64833	6.85343	0.90	1.12
CG11009_gene	CG11009	77.4087	69.3621	0.90	1.12
rgr_gene	rgr	6.61403	5.9264	0.90	1.12
RpS28b_gene	RpS28b	526.727	471.927	0.90	1.12
CG31365_gene	cenB1A	12.602	11.29	0.90	1.12
CG14997_gene	CG14997	15.5961	13.9717	0.90	1.12
RhoGAP71E_gene	RhoGAP71E	10.0163	8.97237	0.90	1.12
CG11123_gene	CG11123	13.0103	11.6541	0.90	1.12
CG11279_gene	CG11279	5.98801	5.36356	0.90	1.12
rut_gene	rut	36.8535	33.0091	0.90	1.12
Rbsn_gene	Rbsn	8.46487	7.58182	0.90	1.12
Rrp45_gene	CG4756	5.47087	4.90004	0.90	1.12
CG5669_gene	cav	6.91343	6.19127	0.90	1.12
spn-F_gene	spn-F	10.3157	9.23724	0.90	1.12
CG6195_gene	CG6195	15.6777	14.038	0.90	1.12
Tom34_gene	Tom34	15.6777	14.038	0.90	1.12
CG4756_gene	CG4756	15.1606	13.5744	0.90	1.12
CG17180_gene	CG17180	1.44257	1.29123	0.90	1.12
CR30478_gene	CR30478	2.88513	2.58245	0.90	1.12
CG18616_gene	CG18616	10.098	9.03859	0.90	1.12
CG33303_gene	CG33303	224.659	201.067	0.89	1.12
CG8176_gene	Rlc1	30.5933	27.3806	0.89	1.12
spri_gene	spri	28.5247	25.5266	0.89	1.12
Tsp42Ee_gene	Tsp42Ee	189.602	169.647	0.89	1.12
CG8029_gene	CG8029	128.633	115.085	0.89	1.12
CG17883_gene	CG17883	60.8872	54.4633	0.89	1.12
CG13151_gene	CG13151	4.10996	3.67503	0.89	1.12
CG3618_gene	CG3618	3.18453	2.84732	0.89	1.12
CHES-1-like_gene	CHES-1-like	36.663	32.7773	0.89	1.12
Srp72_gene	Srp72	59.6624	53.3376	0.89	1.12
dik_gene	CG7536	7.18562	6.42303	0.89	1.12
DnaJ-60_gene	Dat	7.18562	6.42303	0.89	1.12

CG3797_gene	CG3797	25.9662	23.209	0.89	1.12
sav_gene	sav	7.59389	6.78722	0.89	1.12
CG5001_gene	CG5001	13.3369	11.919	0.89	1.12
CG3587_gene	CG3587	4.00108	3.5757	0.89	1.12
l(2)tid_gene	l(2)not	20.6042	18.4083	0.89	1.12
CG8331_gene	CG8331	155.933	139.287	0.89	1.12
CG12093_gene	CG12093	37.1801	33.2077	0.89	1.12
CG17266_gene	CG17266	2.15024	1.92029	0.89	1.12
CG7049_gene	CG7049	31.7365	28.3408	0.89	1.12
CG10068_gene	CG10098	14.5345	12.9785	0.89	1.12
MICAL-like_gene	MICAL-like	20.6586	18.4414	0.89	1.12
CG5953_gene	CG5953	53.2389	47.5105	0.89	1.12
CG8187_gene	CG30467	6.64125	5.9264	0.89	1.12
CG2807_gene	CG2807	35.1388	31.3536	0.89	1.12
SA_gene	SA	9.49917	8.47574	0.89	1.12
CG11007_gene	CG11007	9.90744	8.83994	0.89	1.12
CG6950_gene	CG6950	47.7952	42.6436	0.89	1.12
CG11347_gene	CG11347	70.7674	63.1377	0.89	1.12
CG12075_gene	CG12075	28.2798	25.2286	0.89	1.12
RpL41_gene	NaCP60E	241.317	215.271	0.89	1.12
SP1029_gene	SP1029	1.22482	1.09258	0.89	1.12
CG30503_gene	sPLA2	1.63309	1.45677	0.89	1.12
CG34141_gene	Pkn	3.26619	2.91354	0.89	1.12
CG30386_gene	CG30387	2.85792	2.54935	0.89	1.12
egg_gene	egg	6.12411	5.46288	0.89	1.12
Ctr1A_gene	Ctr1A	12.847	11.4555	0.89	1.12
CG7739_gene	AGO2	67.0658	59.7937	0.89	1.12
CG1399_gene	CG1399	62.8469	56.0194	0.89	1.12
Opbp_gene	Opbp	6.31463	5.62842	0.89	1.12
CG3702_gene	CG3702	47.5503	42.3787	0.89	1.12
CG10324_gene	CG10326	7.83885	6.98587	0.89	1.12
Cap_gene	Cap	11.2956	10.0649	0.89	1.12
GS_gene	GS	9.2542	8.24399	0.89	1.12
CG1924_gene	CG1924	7.32171	6.52235	0.89	1.12
Cyp4p2_gene	hig	14.8339	13.2102	0.89	1.12
CG7816_gene	CG7816	71.1213	63.3363	0.89	1.12
CG8243_gene	CG8243	37.5884	33.4726	0.89	1.12
CG32221_gene	CG32221	4.16439	3.70814	0.89	1.12
vib_gene	vib	38.5955	34.3665	0.89	1.12
CG1620_gene	CG1620	36.1458	32.1813	0.89	1.12
CG9270_gene	CR33319	22.8361	20.3285	0.89	1.12
RpS14b_gene	RpS14b	117.093	104.225	0.89	1.12
CG13142_gene	CG13142	1.11595	0.993251	0.89	1.12
CG4825_gene	CG5104	12.5748	11.1906	0.89	1.12
RpL35A_gene	RpL35A	188.976	168.157	0.89	1.12
Rab9_gene	Rab9	2.93957	2.61556	0.89	1.12
CG10353_gene	CG10353	32.6347	29.036	0.89	1.12
Pdk_gene	Pdk	78.3341	69.6931	0.89	1.12
CG34306_gene	Cdep	1.82362	1.62231	0.89	1.12
CG11071_gene	CG11071	1.82362	1.62231	0.89	1.12
CG1663_gene	CG1663	1.82362	1.62231	0.89	1.12
CG6934_gene	CG6934	3.64724	3.24462	0.89	1.12
CG14854_gene	CG14854	9.11811	8.11155	0.89	1.12
RecQ5_gene	CG9628	26.8372	23.8711	0.89	1.12
hfw_gene	hfw	40.909	36.3861	0.89	1.12
CG14903_gene	CG14903	2.5313	2.25137	0.89	1.12
RpS5a_gene	RpS5a	283.179	251.822	0.89	1.12
CG15096_gene	CG15096	85.5197	76.0499	0.89	1.12
mRNA-capping-enzyme_gene	-capping-e	30.8655	27.4468	0.89	1.12
CG11070_gene	CG11070	25.8029	22.9441	0.89	1.12

CG40191_gene	CG40191	43.3859	38.5713	0.89	1.12
Sfmbt_gene	Sfmbt	22.7545	20.2292	0.89	1.12
CG9471_gene	CG9471	29.4229	26.1556	0.89	1.12
CG18011_gene	CG18011	2.8307	2.51624	0.89	1.12
CG12173_gene	CG12173	7.78442	6.91965	0.89	1.12
CG13624_gene	CG13624	51.4425	45.7227	0.89	1.13
CG30116_gene	CG30116	41.3173	36.7172	0.89	1.13
RpL31_gene	RpL31	282.525	250.995	0.89	1.13
CG4896_gene	CG4896	142.977	127.004	0.89	1.13
O-fut2_gene	O-fut2	24.1154	21.4211	0.89	1.13
CG13295_gene	CG13295	5.85192	5.19802	0.89	1.13
plexA_gene	plexA	71.4207	63.4357	0.89	1.13
ush_gene	ush	12.0032	10.6609	0.89	1.13
Camta_gene	Camta	8.57375	7.61493	0.89	1.13
gammaCop_gene	gammaCop	195.454	173.587	0.89	1.13
Atu_gene	Atu	13.3097	11.8197	0.89	1.13
CG17259_gene	CG17259	103.048	91.5116	0.89	1.13
CG15695_gene	CG15695	144.366	128.196	0.89	1.13
Myo10A_gene	Myo10A	8.16547	7.25073	0.89	1.13
Ogg1_gene	Ogg1	3.7289	3.31084	0.89	1.13
CR32010_gene	CR32010	8.46487	7.5156	0.89	1.13
Fancd2_gene	Fancd2	1.00708	0.893926	0.89	1.13
l(1)G0255_gene	CG3192	66.0587	58.6349	0.89	1.13
CG14235_gene	CG14235	97.4141	86.446	0.89	1.13
Vha44_gene	Vha44	72.455	64.2965	0.89	1.13
CG2185_gene	CG2185	49.1017	43.5706	0.89	1.13
crl_gene	crl	30.7838	27.3144	0.89	1.13
CG9894_gene	CG9894	109.118	96.8089	0.89	1.13
blow_gene	CG2093	121.475	107.768	0.89	1.13
CG17242_gene	CG17242	2113.55	1874.99	0.89	1.13
CG5355_gene	CG5355	80.2122	71.1499	0.89	1.13
CG15202_gene	CG15202	3.91943	3.47638	0.89	1.13
brat_gene	brat	58.4648	51.8477	0.89	1.13
CG4875_gene	CG4875	7.13118	6.3237	0.89	1.13
CG9328_gene	CG9328	15.7594	13.9717	0.89	1.13
Sod2_gene	Sod2	39.8475	35.3266	0.89	1.13
CG12130_gene	CG15863	77.3815	68.6006	0.89	1.13
CG11134_gene	l(1)dd4	9.93466	8.80683	0.89	1.13
CG4603_gene	CG4603	12.7381	11.29	0.89	1.13
wmd_gene	CG30185	27.5721	24.434	0.89	1.13
CG6907_gene	CG6907	21.8563	19.3684	0.89	1.13
CG5439_gene	CG5439	6.01523	5.33045	0.89	1.13
5-HT7_gene	5-HT7	8.81871	7.81358	0.89	1.13
Paps_gene	Paps	16.0315	14.2035	0.89	1.13
CG13902_gene	CG13902	8.11104	7.18452	0.89	1.13
Adgf-C_gene	Adgf-C	51.633	45.7227	0.89	1.13
Tim17a2_gene	Hph	7.10396	6.29059	0.89	1.13
comm2_gene	comm2	18.5084	16.3886	0.89	1.13
CG32095_gene	RpL10Ab	4.30048	3.80746	0.89	1.13
Men_gene	Men	109.036	96.4778	0.88	1.13
larp_gene	larp	499.781	442.162	0.88	1.13
RpS10b_gene	RpS10b	435.846	385.58	0.88	1.13
CG1227_gene	CG1227	5.38921	4.76761	0.88	1.13
CG34353_gene	CG34353	0.598801	0.529734	0.88	1.13
CG17829_gene	CG17829	8.98202	7.94601	0.88	1.13
CG33635_gene	CG33635	8.68262	7.68114	0.88	1.13
CG4670_gene	CG4670	352.531	311.848	0.88	1.13
CG12773_gene	CG12773	48.2852	42.7098	0.88	1.13
l(2)34Fa_gene	bgm	21.3391	18.8718	0.88	1.13
CG5802_gene	CG5802	109.172	96.544	0.88	1.13

Acp26Ab_gene	Acp26Ab	880.347	778.51	0.88	1.13
CG18234_gene	CG4174	452.313	399.982	0.88	1.13
sut1_gene	sut1	12.9559	11.4555	0.88	1.13
CG1104_gene	CG1965	87.9966	77.8047	0.88	1.13
CG15443_gene	CG15435	21.4208	18.938	0.88	1.13
KdelR_gene	KdelR	385.9	341.149	0.88	1.13
CG15715_gene	CG15715	8.76428	7.74736	0.88	1.13
CG12099_gene	CG12099	60.9417	53.8673	0.88	1.13
CG16777_gene	ps	3.48394	3.07908	0.88	1.13
CG17776_gene	CG17776	8.356	7.38317	0.88	1.13
CG6967_gene	CG6967	2.58573	2.28448	0.88	1.13
a6_gene	CG14798	7.4578	6.58857	0.88	1.13
CG2277_gene	CG2277	7.4578	6.58857	0.88	1.13
CG33259_gene	CG33259	93.7669	82.8372	0.88	1.13
Mtp_gene	Mtp	2.28633	2.01961	0.88	1.13
CG6454_gene	CG6454	43.6308	38.5382	0.88	1.13
Spp_gene	Spp	591.997	522.814	0.88	1.13
CG10413_gene	CG10413	79.7495	70.4215	0.88	1.13
CG12250_gene	msi	5.36199	4.7345	0.88	1.13
CG14103_gene	CG14103	29.8584	26.3543	0.88	1.13
CG5151_gene	CG5151	15.2694	13.4751	0.88	1.13
Dis3_gene	Dis3	17.1475	15.1305	0.88	1.13
CG13663_gene	CG13663	17.9368	15.8258	0.88	1.13
CG32276_gene	CG32276	545.318	481.098	0.88	1.13
CG9520_gene	CG9520	2.47686	2.18515	0.88	1.13
His3.3A_gene	His3.3A	31.1921	27.5131	0.88	1.13
CG7083_gene	Apol-alpha	20.4953	18.0772	0.88	1.13
Tapdelta_gene	Tapdelta	98.7206	87.0419	0.88	1.13
CG32196_gene	CG32196	4.05552	3.5757	0.88	1.13
sev_gene	sev	8.79149	7.74736	0.88	1.13
Tbp_gene	CG10306	7.70276	6.78722	0.88	1.13
CG5941_gene	CG5941	8.49209	7.48249	0.88	1.13
CG11906_gene	CG11906	5.03538	4.43652	0.88	1.13
CG3662_gene	CG3662	545.944	480.999	0.88	1.14
CG5047_gene	CG5047	23.4893	20.6927	0.88	1.14
CG33092_gene	CG33092	2.36799	2.08583	0.88	1.14
CG31320_gene	NK7.1	1.57866	1.39055	0.88	1.14
Su(dx)_gene	Su(dx)	59.5807	52.4768	0.88	1.14
CG32262_gene	CG32262	7.29449	6.42303	0.88	1.14
unc-104_gene	unc-104	210.207	185.076	0.88	1.14
Dip-C_gene	Dip-C	35.2748	31.0557	0.88	1.14
CG33051_gene	CG33051	4.9265	4.3372	0.88	1.14
CG8090_gene	CG8090	18.0185	15.8589	0.88	1.14
Su(var)205_gene	CG8419	27.3543	24.0698	0.88	1.14
CG6852_gene	CG6852	20.1687	17.7461	0.88	1.14
CG8866_gene	CG8866	6.88622	6.05883	0.88	1.14
hoe2_gene	hoe2	5.60696	4.93315	0.88	1.14
RpL36A_gene	CG7429	251.034	220.866	0.88	1.14
l(2)dtl_gene	l(2)dtl	1.76919	1.55609	0.88	1.14
CG9669_gene	TSG101	44.4202	39.0679	0.88	1.14
CG2034_gene	CG2034	28.4975	25.063	0.88	1.14
CG13830_gene	CG13830	11.595	10.1974	0.88	1.14
Fit2_gene	Fit2	4.51823	3.97301	0.88	1.14
CG9498_gene	CG9498	56.8589	49.9936	0.88	1.14
Buffy_gene	Buffy	92.1065	80.9831	0.88	1.14
CG10688_gene	CG10688	69.0255	60.6877	0.88	1.14
CG3337_gene	CG3337	5.49809	4.83382	0.88	1.14
CG11163_gene	CG11163	12.466	10.9589	0.88	1.14
MAGE_gene	MAGE	4.21883	3.70814	0.88	1.14
CG6197_gene	CG6197	23.7343	20.8583	0.88	1.14

CG4050_gene	CG4050	16.467	14.4684	0.88	1.14
CG9723_gene	CG32573	18.9167	16.6204	0.88	1.14
CG40127_gene	CG40127	41.4534	36.4192	0.88	1.14
CG1840_gene	CG1840	4.89928	4.30409	0.88	1.14
CG32533_gene	CG32533	4.89928	4.30409	0.88	1.14
CG4095_gene	l(1)G0255	4.89928	4.30409	0.88	1.14
CG8927_gene	CG8927	0.979857	0.860818	0.88	1.14
CG6218_gene	Sra-1	16.5487	14.5346	0.88	1.14
CG8979_gene	CG13188	22.1284	19.4346	0.88	1.14
Dat_gene	Dat	84.3766	74.0965	0.88	1.14
Acp53C14c_gene	Acp53C14c	385.655	338.666	0.88	1.14
RpL32_gene	RpL32	228.552	200.703	0.88	1.14
CG32654_gene	CG32654	192.324	168.886	0.88	1.14
CG7745_gene	CG7745	4.59988	4.03922	0.88	1.14
pan_gene	pan	21.2302	18.64	0.88	1.14
Cht4_gene	Cht4	9.88022	8.67439	0.88	1.14
Surf4_gene	Surf4	263.445	231.262	0.88	1.14
CG11811_gene	CG11811	6.94065	6.09194	0.88	1.14
CG31738_gene	CG31738	278.633	244.538	0.88	1.14
Scsalpha_gene	Scsalpha	1064.86	934.517	0.88	1.14
His4r_gene	His4r	177.245	155.543	0.88	1.14
CG8526_gene	CG8526	3.81055	3.34395	0.88	1.14
Rox8_gene	Rox8	48.7207	42.7429	0.88	1.14
inx2_gene	inx7	23.326	20.461	0.88	1.14
CG16717_gene	CG16717	4.19161	3.67503	0.88	1.14
nec_gene	pk	8.38322	7.35006	0.88	1.14
Tango6_gene	Tango6	9.06368	7.94601	0.88	1.14
Pcaf_gene	Pcaf	19.6788	17.2495	0.88	1.14
BG642167_gene	BG642167	954.19	836.384	0.88	1.14
wkd_gene	wkd	45.9716	40.2929	0.88	1.14
CG12007_gene	CG12007	12.466	10.9258	0.88	1.14
CG34002_gene	CG34002	556.668	487.885	0.88	1.14
qkr58E-2_gene	qkr58E-2	119.978	105.152	0.88	1.14
CG8680_gene	CG8680	17.5286	15.3623	0.88	1.14
sec23_gene	sec23	221.203	193.85	0.88	1.14
CG15626_gene	CG15626	15.3783	13.4751	0.88	1.14
CG8092_gene	CG8092	35.7103	31.2874	0.88	1.14
CG2249_gene	CG2249	43.4948	38.1077	0.88	1.14
CG34033_gene	CG34033	242.923	212.821	0.88	1.14
Ir_gene	Ir	15.0789	13.2102	0.88	1.14
CG6282_gene	CG6282	0.680456	0.595951	0.88	1.14
pncr014:3L_gene	CG6650	0.680456	0.595951	0.88	1.14
bgm_gene	CG33681	52.1774	45.6896	0.88	1.14
CG2371_gene	CG2371	8.356	7.31695	0.88	1.14
CG5036_gene	CG5036	2.91235	2.54935	0.88	1.14
OstStt3_gene	CG11820	763.363	668.16	0.88	1.14
CG6662_gene	CG6662	11.35	9.93251	0.88	1.14
CG5196_gene	CG5196	11.5405	10.0981	0.88	1.14
CG10561_gene	CG10561	4.65432	4.07233	0.87	1.14
Acp29AB_gene	Acp29AB	590.772	516.888	0.87	1.14
CG16711_gene	CG16711	42.7871	37.4125	0.87	1.14
Nca_gene	CG7646	13.7452	12.0183	0.87	1.14
Eaat1_gene	Eaat1	2.61295	2.28448	0.87	1.14
DNApol-alpha50_gene	IApol-alpha	23.8976	20.8914	0.87	1.14
CG9302_gene	CG9302	32.172	28.109	0.87	1.14
CG31515_gene	CG31515	73.9792	64.6276	0.87	1.14
CG4686_gene	CG4686	7.24005	6.3237	0.87	1.14
mus301_gene	mus301	1.06151	0.927035	0.87	1.15
RpS30_gene	RpS30	191.344	167.098	0.87	1.15
CG32158_gene	CG33158	19.8693	17.3488	0.87	1.15

CG34148_gene	CG33092	2.31355	2.01961	0.87	1.15
CG4455_gene	CG4455	8.19269	7.15141	0.87	1.15
CG4338_gene	CG4338	10.3974	9.0717	0.87	1.15
CG11658_gene	CG11658	111.758	97.5042	0.87	1.15
Max_gene	Max	11.8399	10.3298	0.87	1.15
Gef64C_gene	Gef64C	45.0462	39.2996	0.87	1.15
CG10219_gene	Plip	32.1447	28.0428	0.87	1.15
Eps-15_gene	Eps-15	20.8764	18.2096	0.87	1.15
corto_gene	corto	46.0805	40.1936	0.87	1.15
Orct_gene	Orct	95.8627	83.5987	0.87	1.15
l(2)k16918_gene	l(2)k16918	7.59389	6.62168	0.87	1.15
Orc4_gene	Orc4	3.26619	2.84732	0.87	1.15
CG6613_gene	CG6613	6.91343	6.02572	0.87	1.15
CG33505_gene	CG33505	3.45672	3.01286	0.87	1.15
Surf6_gene	CG4538	15.6505	13.6407	0.87	1.15
abo_gene	abo	8.0566	7.01898	0.87	1.15
CG2025_gene	CG2025	63.7723	55.5559	0.87	1.15
CG9746_gene	CG9746	39.1126	34.0685	0.87	1.15
CG3091_gene	CG3091	4.59988	4.00611	0.87	1.15
RpL27_gene	RpL27	570.222	496.593	0.87	1.15
CG31109_gene	CG31109	2.39521	2.08583	0.87	1.15
SH3PX1_gene	SH3PX1	17.338	15.0974	0.87	1.15
CG10648_gene	CG10648	18.2907	15.9251	0.87	1.15
CG30106_gene	CG30106	3.53837	3.07908	0.87	1.15
CG17598_gene	CG17600	38.6227	33.605	0.87	1.15
Dph5_gene	CSN6	11.9488	10.396	0.87	1.15
Su(z)12_gene	Su(z)12	18.3451	15.9582	0.87	1.15
CG1358_gene	CG1358	102.64	89.2602	0.87	1.15
CG6321_gene	CG7888	17.9368	15.594	0.87	1.15
aux_gene	CG14636	49.4828	43.0078	0.87	1.15
CG8412_gene	CG8412	31.5459	27.4137	0.87	1.15
CG17271_gene	CG17271	120.169	104.424	0.87	1.15
nAcRalpha-80B_gene	AcRalpha-8	0.762111	0.662168	0.87	1.15
net_gene	net	1.90528	1.65542	0.87	1.15
CG14059_gene	CG14059	0.952639	0.827709	0.87	1.15
CG1965_gene	CG1965	19.6244	17.0508	0.87	1.15
Aats-gly_gene	Aats-gly	44.9373	39.0348	0.87	1.15
eIF5_gene	eIF5	238.323	206.96	0.87	1.15
CG8617_gene	CG8617	6.75012	5.86018	0.87	1.15
CG17446_gene	CG17446	5.98801	5.19802	0.87	1.15
CG11777_gene	CG11777	4.46379	3.87368	0.87	1.15
plx_gene	plx	20.7947	18.0441	0.87	1.15
snmRNA:838_gene	vsg	33.043	28.6719	0.87	1.15
dia_gene	dia	35.9553	31.1881	0.87	1.15
CG7720_gene	CG7720	98.149	85.1216	0.87	1.15
Phm_gene	Phm	139.847	121.276	0.87	1.15
CG1968_gene	CG1968	33.0702	28.6719	0.87	1.15
CG10516_gene	CG10516	4.9265	4.27098	0.87	1.15
CG33528_gene	CG33528	2.17746	1.88718	0.87	1.15
Grasp65_gene	Grasp65	157.43	136.44	0.87	1.15
Tango1_gene	Tango1	268.263	232.421	0.87	1.15
CG5380_gene	CG5380	3.78334	3.27773	0.87	1.15
CG11779_gene	CG11779	13.1464	11.3893	0.87	1.15
CG3902_gene	CG3902	36.6902	31.784	0.87	1.15
pgant4_gene	pgant4	92.7326	80.3209	0.87	1.15
CG12025_gene	CG12025	14.6434	12.6805	0.87	1.15
alpha-Est1_gene	alpha-Est1	1.60588	1.39055	0.87	1.15
CG7927_gene	CG7927	98.9655	85.6845	0.87	1.15
bel_gene	bel	134.05	116.045	0.87	1.16
CG3862_gene	CG3662	7.07674	6.12505	0.87	1.16

GIIIspla2_gene	GIIIspla2	2.8307	2.45002	0.87	1.16
CG1703_gene	CG1703	91.2356	78.9635	0.87	1.16
CG12395_gene	CG12395	5.28034	4.56896	0.87	1.16
CG3589_gene	CG3589	5.08981	4.40341	0.87	1.16
CG34346_gene	CG34346	34.0228	29.4333	0.87	1.16
CG8902_gene	CG13779	2.44964	2.11894	0.87	1.16
CG15431_gene	CG15431	6.12411	5.29734	0.86	1.16
CG1888_gene	CG1888	10.8329	9.36967	0.86	1.16
CG31021_gene	CG31021	239.167	206.861	0.86	1.16
CG41254_gene	CR41510	5.93358	5.1318	0.86	1.16
CG13446_gene	CG13446	4.70876	4.07233	0.86	1.16
coilin_gene	CG2158	6.58682	5.69464	0.86	1.16
CG17593_gene	CG17593	69.1343	59.7606	0.86	1.16
snmRNA:438_gene	klar	1.03429	0.893926	0.86	1.16
Gnf1_gene	Gnf1	21.2302	18.342	0.86	1.16
Crc_gene	Crc	2293.3	1980.84	0.86	1.16
CG31866_gene	CG31866	2.72182	2.35069	0.86	1.16
RpS15Aa_gene	RpS15Aa	620.494	535.727	0.86	1.16
CG8493_gene	CG8493	5.06259	4.37031	0.86	1.16
CG18787_gene	CG31865	2.5313	2.18515	0.86	1.16
Pdh_gene	CG4933	2.5313	2.18515	0.86	1.16
CG9095_gene	CG9095	4.87207	4.20476	0.86	1.16
CG15618_gene	CG15618	5.5253	4.76761	0.86	1.16
NUCB1_gene	NUCB1	701.033	604.89	0.86	1.16
l(1)G0007_gene	l(1)G0007	101.878	87.9027	0.86	1.16
CG10221_gene	Tbp-1	55.4708	47.8416	0.86	1.16
Edem2_gene	Edem2	77.6264	66.9451	0.86	1.16
CG31413_gene	CG31413	410.751	354.227	0.86	1.16
Pdp1_gene	Pdp1	176.374	152.1	0.86	1.16
CG10444_gene	CG10444	10.098	8.7075	0.86	1.16
CG11160_gene	CG11160	2.15024	1.85407	0.86	1.16
Acp63F_gene	Scsalpha	941.506	811.817	0.86	1.16
CG34159_gene	CG34159	15.7049	13.5413	0.86	1.16
SpdS_gene	SpdS	4.95372	4.27098	0.86	1.16
CG6410_gene	CG6410	11.2139	9.66765	0.86	1.16
CG17931_gene	CG17931	47.4686	40.922	0.86	1.16
CG11190_gene	CG11190	44.4746	38.3395	0.86	1.16
Sirt4_gene	Sirt4	1.95971	1.68853	0.86	1.16
CG13758_gene	CG13758	2.61295	2.25137	0.86	1.16
CG7616_gene	CG7616	5.2259	4.50274	0.86	1.16
CG6621_gene	CG4674	12.8742	11.0913	0.86	1.16
CstF-64_gene	CstF-64	6.99509	6.02572	0.86	1.16
Cbp53E_gene	Cbp53E	2.42242	2.08583	0.86	1.16
Cyp4p3_gene	hig	202.449	174.316	0.86	1.16
Ant2_gene	CG15211	454.109	390.944	0.86	1.16
CG32230_gene	CG32230	33.8051	29.1023	0.86	1.16
CG9911_gene	CG9911	241.644	207.987	0.86	1.16
CG16728_gene	CG16728	5.77027	4.96626	0.86	1.16
sesB_gene	Ant2	452.041	389.023	0.86	1.16
Pdi_gene	Pdi	3860.01	3321.63	0.86	1.16
CG11885_gene	CG11885	6.69569	5.76086	0.86	1.16
Met_gene	Met	6.69569	5.76086	0.86	1.16
CG5989_gene	CG5989	13.8541	11.919	0.86	1.16
CG14598_gene	CG14598	3.81055	3.27773	0.86	1.16
mRpS5_gene	mRpS5	45.5361	39.1672	0.86	1.16
CG30183_gene	CG30183	11.0506	9.5021	0.86	1.16
Taf8_gene	Taf8	3.62003	3.11219	0.86	1.16
CG2852_gene	CG2852	523.461	449.976	0.86	1.16
Acp76A_gene	Acp76A	5802.66	4987.15	0.86	1.16
CG17065_gene	Rab10	6.39629	5.49599	0.86	1.16

CG31704_gene	CG31757	238.241	204.676	0.86	1.16
CG1973_gene	CG1973	162.792	139.85	0.86	1.16
CG12030_gene	CG12030	68.8349	59.1316	0.86	1.16
CG3527_gene	CG3527	5.55252	4.76761	0.86	1.16
pigeon_gene	pigeon	3.70168	3.1784	0.86	1.16
CG12170_gene	CG12170	8.13826	6.98587	0.86	1.16
c11.1_gene	c11.1	46.0533	39.5314	0.86	1.16
CG14971_gene	CycJ	34.4855	29.5989	0.86	1.17
CG11664_gene	CG11664	153.919	132.102	0.86	1.17
G-salpha60A_gene	G-salpha60	39.657	34.0354	0.86	1.17
CG8611_gene	CG8611	9.79857	8.40953	0.86	1.17
CG34163_gene	CG34163	4.89928	4.20476	0.86	1.17
CG30343_gene	CG30343	4.43657	3.80746	0.86	1.17
CG11999_gene	CG11999	84.5671	72.5736	0.86	1.17
CG5131_gene	CG5131	3.97386	3.41016	0.86	1.17
dup_gene	dup	3.97386	3.41016	0.86	1.17
eIF2B-epsilon_gene	IF2B-epsilo	22.9178	19.6664	0.86	1.17
SRm160_gene	SRm160	32.5258	27.9104	0.86	1.17
CG18809_gene	CG14235	13.5819	11.6541	0.86	1.17
CG18231_gene	CG4174	263.854	226.395	0.86	1.17
FucTA_gene	FucTA	121.856	104.556	0.86	1.17
CG17068_gene	CG17068	9.88022	8.47574	0.86	1.17
CG10590_gene	CG10590	180.212	154.583	0.86	1.17
CG34445_gene	CG34445	3.32063	2.84732	0.86	1.17
CG12290_gene	CG12290	23.2444	19.9312	0.86	1.17
Dnz1_gene	CG17086	41.0451	35.1942	0.86	1.17
CG11781_gene	beta4GalT7	15.6777	13.442	0.86	1.17
Aats-asp_gene	Aats-asp	37.0713	31.784	0.86	1.17
Ugt_gene	Ugt	365.922	313.702	0.86	1.17
Drs_gene	Drs	2.85792	2.45002	0.86	1.17
CG4789_gene	CG9132	23.5982	20.2292	0.86	1.17
CG6330_gene	CG6330	31.4099	26.9171	0.86	1.17
CG17834_gene	CG17834	18.5901	15.9251	0.86	1.17
CG8709_gene	CG8709	30.185	25.8576	0.86	1.17
Golgin84_gene	CG6454	28.7969	24.6657	0.86	1.17
cnk_gene	cnk	20.1415	17.2495	0.86	1.17
Syx18_gene	mld	52.9667	45.3585	0.86	1.17
CG13510_gene	CG13510	65.977	56.4829	0.86	1.17
CG11498_gene	CG15529	2.20468	1.88718	0.86	1.17
CG32075_gene	CG32075	8.08382	6.91965	0.86	1.17
CG2023_gene	CG2023	11.0234	9.43589	0.86	1.17
CG7861_gene	CG7861	11.0234	9.43589	0.86	1.17
CG15456_gene	CG15456	0.734893	0.629059	0.86	1.17
CG8405_gene	CG8405	40.7729	34.8962	0.86	1.17
CG33298_gene	CG33298	27.2455	23.3083	0.86	1.17
CG17637_gene	CG32425	850.325	727.391	0.86	1.17
CG10587_gene	CG10587	135.002	115.482	0.86	1.17
CG3271_gene	CG3271	8.43766	7.21763	0.86	1.17
CG10674_gene	CG10674	12.9287	11.0582	0.86	1.17
mRpS33_gene	CG14881	3.48394	2.97975	0.86	1.17
RpL29_gene	RpL29	29.8856	25.5597	0.86	1.17
S_gene	S	26.0206	22.2488	0.86	1.17
CG7443_gene	Poxm	7.51224	6.42303	0.86	1.17
SsRbeta_gene	SsRbeta	75.8028	64.7931	0.85	1.17
RpL18_gene	CG8616	238.105	203.517	0.85	1.17
pds5_gene	pds5	24.7142	21.1231	0.85	1.17
CG2137_gene	Cyt-b5	8.32878	7.1183	0.85	1.17
CG4815_gene	CG4815	71.2029	60.8532	0.85	1.17
CG10338_gene	CG10338	16.0043	13.6738	0.85	1.17
Syx5_gene	Syx5	162.085	138.459	0.85	1.17

CG34034_gene	CG34034	1453.21	1241.17	0.85	1.17
CG34053_gene	CG34053	124.36	106.179	0.85	1.17
CG32369_gene	CG32369	22.4551	19.1698	0.85	1.17
Bzd_gene	mit(1)15	7.7572	6.62168	0.85	1.17
CG7589_gene	CG7589	46.8154	39.9618	0.85	1.17
CG34381_gene	CG34381	8.02938	6.85343	0.85	1.17
RpL21_gene	RpL21	643.303	548.904	0.85	1.17
CG1622_gene	CG1622	6.01523	5.1318	0.85	1.17
CG32069_gene	CG32069	4.19161	3.5757	0.85	1.17
Pkc53E_gene	Pkc53E	486.009	414.55	0.85	1.17
CG1129_gene	CG1129	51.5514	43.9679	0.85	1.17
CG17370_gene	CG17370	7.10396	6.05883	0.85	1.17
beat-IIIc_gene	beat-IIIc	126.048	107.503	0.85	1.17
Teh1_gene	Teh1	22.4823	19.1698	0.85	1.17
CG15743_gene	CG15743	65.2421	55.6221	0.85	1.17
CG7359_gene	CG7359	188.051	160.311	0.85	1.17
CG11577_gene	CG11577	44.1752	37.6442	0.85	1.17
CG12236_gene	CG12236	6.45072	5.49599	0.85	1.17
CG3529_gene	CG3529	20.1687	17.1832	0.85	1.17
CG8298_gene	CG8298	2.72182	2.31759	0.85	1.17
Srp54k_gene	Srp54k	204.953	174.514	0.85	1.17
CG30089_gene	CG30089	2.17746	1.85407	0.85	1.17
snoRNA:Psi28S-3571_gene	exba	1.36091	1.15879	0.85	1.17
CG10628_gene	CG10628	3.26619	2.7811	0.85	1.17
Dp1_gene	imd	1050.43	893.893	0.85	1.18
CG6406_gene	CG34195	68.9983	58.7012	0.85	1.18
CG6013_gene	CG6013	11.1323	9.469	0.85	1.18
CG18522_gene	CG18522	91.9432	78.202	0.85	1.18
siz_gene	siz	43.7669	37.2138	0.85	1.18
CG10029_gene	CG10029	456.014	387.699	0.85	1.18
CG31800_gene	CG31800	5.06259	4.30409	0.85	1.18
Tob_gene	Tob	9.853	8.37642	0.85	1.18
Gp93_gene	Gp93	2138.89	1818.28	0.85	1.18
CG31915_gene	Cap-D3	4.24605	3.60881	0.85	1.18
CG2264_gene	CG2264	14.5345	12.3494	0.85	1.18
bigmax_gene	CG3368	8.84593	7.5156	0.85	1.18
CG14747_gene	CG14747	3.4295	2.91354	0.85	1.18
CG14199_gene	CG14199	6.58682	5.59532	0.85	1.18
Arf102F_gene	Arf102F	87.9966	74.7256	0.85	1.18
krz_gene	krz	18.4812	15.6934	0.85	1.18
CG15864_gene	CG15864	261.513	222.058	0.85	1.18
CG15116_gene	CG15116	447.005	379.488	0.85	1.18
CG10366_gene	CG10366	3.78334	3.21151	0.85	1.18
CG7188_gene	CG7188	149.074	126.54	0.85	1.18
glob1_gene	glob1	16.6576	14.1373	0.85	1.18
Ndae1_gene	Ndae1	34.2133	29.036	0.85	1.18
mthl14_gene	mthl14	1.17038	0.993251	0.85	1.18
cag_gene	CG30020	3.51115	2.97975	0.85	1.18
CG33172_gene	CG33172	2.34077	1.9865	0.85	1.18
Spase18-21_gene	Spase18-21	395.835	335.918	0.85	1.18
CG5382_gene	CG7071	39.0582	33.1415	0.85	1.18
CG6140_gene	CG6140	137.126	116.343	0.85	1.18
mRpL17_gene	mRpL17	8.00216	6.78722	0.85	1.18
rec_gene	pha-Man-I	119.515	101.345	0.85	1.18
Vha13_gene	Vha13	129.396	109.721	0.85	1.18
Cenp-C_gene	Cenp-C	1.7964	1.52299	0.85	1.18
CG11986_gene	CG11986	0.898202	0.761493	0.85	1.18
CG10981_gene	CG10981	3.59281	3.04597	0.85	1.18
CG8195_gene	CG8195	18.5901	15.7596	0.85	1.18
comm3_gene	comm3	27.2999	23.1428	0.85	1.18

CG14131_gene	Pi3K68D	30.0762	25.4935	0.85	1.18
CG6701_gene	CG6701	80.8382	68.4681	0.85	1.18
Cyp12a4_gene	Cyp12a4	22.8361	19.3353	0.85	1.18
CG7840_gene	CG7840	17.6374	14.9319	0.85	1.18
CG41347_gene	CG41347	22.9178	19.4015	0.85	1.18
Cyt-c-p_gene	CG31782	70.6313	59.7937	0.85	1.18
CG2818_gene	CG2818	16.1132	13.6407	0.85	1.18
Oat_gene	Oat	5.28034	4.46963	0.85	1.18
Obp56e_gene	Obp56e	192.324	162.794	0.85	1.18
PH4alphaNE2_gene	CG34041	428.987	363.033	0.85	1.18
Rab30_gene	Rab30	12.5204	10.5947	0.85	1.18
sano_gene	sano	16.9025	14.3028	0.85	1.18
cdc2c_gene	cdc2c	0.62602	0.529734	0.85	1.18
CG9663_gene	CG9663	2.85792	2.41691	0.85	1.18
CG18258_gene	CG18258	1290.31	1091.12	0.85	1.18
PIP5K59B_gene	PIP5K59B	3.21175	2.71489	0.85	1.18
Corp_gene	CG1632	1.60588	1.35744	0.85	1.18
Spred_gene	Spred	10.4246	8.80683	0.84	1.18
CG11175_gene	CG16742	0.979857	0.827709	0.84	1.18
Pkd2_gene	Pkd2	0.979857	0.827709	0.84	1.18
piwi_gene	SCAR	0.979857	0.827709	0.84	1.18
CG31694_gene	CG31694	100.054	84.4926	0.84	1.18
RpS3A_gene	RpS3A	1191.26	1005.96	0.84	1.18
CG6308_gene	CG6308	5.60696	4.7345	0.84	1.18
chrw_gene	chrw	19.8421	16.7528	0.84	1.18
CG8408_gene	CG8408	48.4757	40.922	0.84	1.18
Liprin-alpha_gene	iprin-alpha	16.6303	14.038	0.84	1.18
Prx6005_gene	CG8814	4.00108	3.37705	0.84	1.18
CG17018_gene	CG17018	93.9029	79.2283	0.84	1.19
CG14541_gene	CG14541	44.8557	37.8429	0.84	1.19
CG14142_gene	CG14142	1.68753	1.42366	0.84	1.19
Hira_gene	Hira	5.06259	4.27098	0.84	1.19
dare_gene	CG18335	4.79041	4.03922	0.84	1.19
Peritrophin-15b_gene	ritrophin-1	63.8812	53.8342	0.84	1.19
Traf3_gene	Traf3	32.8524	27.6786	0.84	1.19
mib1_gene	mRpS31	41.3445	34.83	0.84	1.19
CG9849_gene	CG9849	18.5901	15.6603	0.84	1.19
CG14434_gene	CG14434	4.95372	4.17166	0.84	1.19
CG14778_gene	CG14778	0.707674	0.595951	0.84	1.19
CG15524_gene	CG15524	0.707674	0.595951	0.84	1.19
RabX4_gene	RabX4	0.707674	0.595951	0.84	1.19
CG15661_gene	CG15661	2.12302	1.78785	0.84	1.19
DNApol-epsilon_gene	NApol-epsil	2.12302	1.78785	0.84	1.19
CG1927_gene	CG1140	70.9035	59.6944	0.84	1.19
Invadolysin_gene	Invadolysi	19.9782	16.8191	0.84	1.19
pygo_gene	pygo	6.80456	5.72775	0.84	1.19
CG8372_gene	CG8372	18.1001	15.2299	0.84	1.19
CG4269_gene	CG4269	7.24005	6.09194	0.84	1.19
CG6986_gene	CG6986	2.91235	2.45002	0.84	1.19
CG5885_gene	yip2	85.9552	72.3087	0.84	1.19
Syx6_gene	Syx6	22.2373	18.7062	0.84	1.19
CG32635_gene	CG32635	2.55852	2.15204	0.84	1.19
CG2292_gene	CG2264	5.55252	4.66828	0.84	1.19
CG33080_gene	CG33080	23.3533	19.6333	0.84	1.19
CG8776_gene	CG8776	38.4866	32.3469	0.84	1.19
Taf10_gene	Taf10b	12.7654	10.7271	0.84	1.19
CG7546_gene	CG7546	163.663	137.499	0.84	1.19
CG32452_gene	CG32452	3.78334	3.1784	0.84	1.19
CG15117_gene	CG15117	609.852	512.319	0.84	1.19
CG17027_gene	brm	1.14317	0.960143	0.84	1.19

CG11975_gene	CG11975	11.1595	9.36967	0.84	1.19
dome_gene	dome	57.866	48.57	0.84	1.19
CG12541_gene	CG12541	0.789329	0.662168	0.84	1.19
loj_gene	loj	49.7822	41.7497	0.84	1.19
VhaM9.7-2_gene	VhaM9.7-2	49.0745	41.1537	0.84	1.19
Epac_gene	Epac	46.516	39.0017	0.84	1.19
CG5287_gene	CG5287	25.7485	21.5867	0.84	1.19
CG14617_gene	CG14617	23.816	19.9644	0.84	1.19
CR40472_gene	CG41347	21.8835	18.342	0.84	1.19
Top3alpha_gene	Top3alpha	4.46379	3.74125	0.84	1.19
CG5038_gene	CG5038	6.91343	5.79397	0.84	1.19
LysB_gene	LysB	53.375	44.7294	0.84	1.19
CG5793_gene	CG5793	6.12411	5.1318	0.84	1.19
deltaCOP_gene	deltaCOP	181.274	151.901	0.84	1.19
Aats-arg_gene	Aats-arg	23.1627	19.4015	0.84	1.19
CG7488_gene	CG7488	5.41643	4.53585	0.84	1.19
Tom70_gene	CG18788	23.4077	19.6002	0.84	1.19
CG10157_gene	CG10157	5.85192	4.90004	0.84	1.19
CG11857_gene	CG11857	222.863	186.533	0.84	1.19
CG12926_gene	CG30005	62.983	52.7085	0.84	1.19
CG5854_gene	CG5854	29.3957	24.5995	0.84	1.19
CG30410_gene	CG30409	78.4974	65.687	0.84	1.20
CG30004_gene	CG30004	4.70876	3.9399	0.84	1.20
Spase22-23_gene	CG13609	8622.39	7214.15	0.84	1.20
BicD_gene	BicD	63.9084	53.47	0.84	1.20
CG15482_gene	Pect	11.595	9.70075	0.84	1.20
alpha-Man-IIb_gene	pha-Man-I	503.646	421.238	0.84	1.20
CG13587_gene	CG13587	1.30648	1.09258	0.84	1.20
Ppt1_gene	CG11284	6.53238	5.46288	0.84	1.20
CG17843_gene	CG17843	1075.75	899.522	0.84	1.20
Noa36_gene	Noa36	14.6162	12.217	0.84	1.20
CG40169_gene	CG40169	4.87207	4.07233	0.84	1.20
pgant5_gene	pgant5	112.112	93.6967	0.84	1.20
mxc_gene	mxc	8.51931	7.1183	0.84	1.20
Acp95EF_gene	Spase22-23	8403.77	7020.76	0.84	1.20
CG1126_gene	CG1126	2.25911	1.88718	0.84	1.20
Sry-beta_gene	Sry-beta	2.25911	1.88718	0.84	1.20
Antp_gene	Antp	4.51823	3.77436	0.84	1.20
Mst57Dc_gene	Mst57Dc	4379.12	3657.58	0.84	1.20
CG9754_gene	CG30387	5.90636	4.93315	0.84	1.20
wapl_gene	wapl	24.2242	20.2292	0.84	1.20
CG9886_gene	CG9886	9.63526	8.04534	0.83	1.20
mRpL50_gene	Neos	2.77626	2.31759	0.83	1.20
CG3021_gene	CG3021	13.8813	11.5879	0.83	1.20
CG5500_gene	CG5500	3.7289	3.11219	0.83	1.20
ro_gene	CG5500	3.7289	3.11219	0.83	1.20
CG7550_gene	CG7942	3.7289	3.11219	0.83	1.20
Eip78C_gene	Eip78C	3.7289	3.11219	0.83	1.20
spir_gene	spir	3.7289	3.11219	0.83	1.20
CG14701_gene	CG14701	9.79857	8.17777	0.83	1.20
CG13937_gene	CG13937	0.952639	0.794601	0.83	1.20
CG30217_gene	CG30217	1.46979	1.22501	0.83	1.20
CG9977_gene	CG9977	272.319	226.925	0.83	1.20
CG31161_gene	CG31161	82.8523	69.031	0.83	1.20
CG5104_gene	CG5104	29.804	24.8313	0.83	1.20
CG13865_gene	CG13865	7.1584	5.95951	0.83	1.20
CG13196_gene	Buffy	10.3429	8.60818	0.83	1.20
CG17119_gene	CG17119	1.55144	1.29123	0.83	1.20
her_gene	her	8.43766	7.01898	0.83	1.20
CG10979_gene	CG10979	10.7512	8.93926	0.83	1.20

CG5463_gene	CG6129	1.63309	1.35744	0.83	1.20
mei-217_gene	mei-218	1.63309	1.35744	0.83	1.20
mei-218_gene	mei-218	1.63309	1.35744	0.83	1.20
CG7133_gene	CG7133	16.9297	14.0711	0.83	1.20
CG30345_gene	CG30345	8.76428	7.28384	0.83	1.20
CG5392_gene	Prosbeta2	3.86499	3.21151	0.83	1.20
CG5078_gene	CG32425	62.7108	52.0795	0.83	1.20
CG8520_gene	CG8520	12.847	10.6609	0.83	1.21
vri_gene	vri	43.9302	36.4523	0.83	1.21
CG9231_gene	CG9231	11.7311	9.73386	0.83	1.21
CG8233_gene	CG8233	28.5792	23.7056	0.83	1.21
Tfb4_gene	CG4749	1.1976	0.993251	0.83	1.21
Cyp318a1_gene	Cyp318a1	1.1976	0.993251	0.83	1.21
CG13350_gene	CG13350	4.79041	3.97301	0.83	1.21
CG4562_gene	CG4562	0.598801	0.496626	0.83	1.21
CR41507_gene	CR41507	0.598801	0.496626	0.83	1.21
IFa_gene	Start1	0.598801	0.496626	0.83	1.21
Ste:CG33247_gene	te:CG3324	0.598801	0.496626	0.83	1.21
Cypl_gene	CG17180	4.19161	3.47638	0.83	1.21
Cyp6d2_gene	Cyp6d2	6.06967	5.03247	0.83	1.21
sip3_gene	sip3	90.7728	75.2553	0.83	1.21
CG6322_gene	CG6322	4.27326	3.5426	0.83	1.21
CG4203_gene	CG4203	3.07566	2.54935	0.83	1.21
CG32813_gene	CG32813	35.6559	29.5327	0.83	1.21
Dgp-1_gene	Dgp-1	67.6373	56.0194	0.83	1.21
CG14275_gene	CG14275	6.5596	5.42977	0.83	1.21
Spase25_gene	Spase25	371.175	307.213	0.83	1.21
CG1024_gene	CG1024	3.32063	2.748	0.83	1.21
CG1092_gene	CG1092	0.680456	0.562842	0.83	1.21
CG33492_gene	CG33492	0.680456	0.562842	0.83	1.21
CG9492_gene	CG9492	0.680456	0.562842	0.83	1.21
CG7139_gene	CG7139	30.675	25.361	0.83	1.21
CG14104_gene	CG14104	2.12302	1.75474	0.83	1.21
G-oalpha47A_gene	-oalpha47	42.6238	35.2273	0.83	1.21
CG41475_gene	fog	2.88513	2.3838	0.83	1.21
CG34116_gene	CG15881	1.44257	1.1919	0.83	1.21
CG9519_gene	Flo-2	191.154	157.894	0.83	1.21
CG10651_gene	CG10651	163.691	135.182	0.83	1.21
CG32137_gene	CG32137	44.5018	36.7503	0.83	1.21
CG1444_gene	CG1444	13.5547	11.1906	0.83	1.21
Jhebp29_gene	Jhebp29	11.35	9.36967	0.83	1.21
CG12963_gene	CG12963	0.762111	0.629059	0.83	1.21
CG2278_gene	CG2278	0.762111	0.629059	0.83	1.21
CG9331_gene	CG9331	3.89221	3.21151	0.83	1.21
mRpL49_gene	mRpL49	7.51224	6.19127	0.82	1.21
CG5160_gene	CG5160	0.843766	0.695276	0.82	1.21
esc_gene	esc	0.843766	0.695276	0.82	1.21
Vha68-2_gene	Vha68-2	249.782	205.802	0.82	1.21
Vha100-2_gene	Vha100-2	54.872	45.1929	0.82	1.21
CG10184_gene	CG10184	92.542	76.1824	0.82	1.21
Sclp_gene	Sclp	4.54545	3.74125	0.82	1.21
Trp1_gene	Trp1	654.98	539.037	0.82	1.22
ARP-like_gene	ARP-like	209.771	172.627	0.82	1.22
CG32372_gene	CG32372	16.9842	13.9717	0.82	1.22
Hsp67Bc_gene	Hsp67Bc	2.85792	2.35069	0.82	1.22
l(3)70Da_gene	l(3)70Da	3.86499	3.1784	0.82	1.22
CG11560_gene	CG11560	5.9608	4.90004	0.82	1.22
CG9396_gene	CG9396	1.00708	0.827709	0.82	1.22
PpV_gene	PpV	14.1807	11.6541	0.82	1.22
CG14621_gene	CG14621	33.5601	27.5793	0.82	1.22

CG13373_gene	CG13373	3.10288	2.54935	0.82	1.22
RhoGAP102A_gene	hoGAP102	1.08873	0.893926	0.82	1.22
Cdk7_gene	Cdk7	7.62111	6.25748	0.82	1.22
CG9168_gene	Ptp61F	104.736	85.9493	0.82	1.22
CG7197_gene	Rab-RP3	15.0517	12.3494	0.82	1.22
CG30005_gene	CG30005	12.0305	9.8663	0.82	1.22
snoRNA:Me28S-A982a_gene	NA:Me28S-	4.9265	4.03922	0.82	1.22
CG9119_gene	CG9119	8.68262	7.1183	0.82	1.22
Gip_gene	CG2909	21.0941	17.2826	0.82	1.22
CG4624_gene	CG4624	1.33369	1.09258	0.82	1.22
CG5039_gene	CG5039	8.00216	6.55546	0.82	1.22
CG30395_gene	CG30395	314.806	257.881	0.82	1.22
CG9356_gene	CG8132	30.4028	24.8975	0.82	1.22
SPoCk_gene	SPoCk	156.342	127.997	0.82	1.22
CG12942_gene	CG12942	2.99401	2.45002	0.82	1.22
CG31106_gene	CG31106	4.57267	3.74125	0.82	1.22
CG5214_gene	CG5214	58.5737	47.9078	0.82	1.22
Rrp4_gene	Rrp4	12.7109	10.396	0.82	1.22
l(1)G0469_gene	l(1)G0007	27.3271	22.3482	0.82	1.22
MrgBP_gene	CG13751	13.0375	10.6609	0.82	1.22
CG6694_gene	CG6694	9.96188	8.14466	0.82	1.22
CG9416_gene	CG10051	16.6031	13.5744	0.82	1.22
CG30026_gene	CG30026	10.2068	8.34331	0.82	1.22
CG11927_gene	CG11927	12.0305	9.83319	0.82	1.22
CG32133_gene	CG32133	26.9461	22.0171	0.82	1.22
CG31659_gene	CG31659	326.619	266.854	0.82	1.22
CG4783_gene	Hs6st	10.9417	8.93926	0.82	1.22
colt_gene	Taf10	50.381	41.1537	0.82	1.22
mRpS23_gene	RpII33	3.89221	3.1784	0.82	1.22
Rpb11_gene	CLIP-190	1.98693	1.62231	0.82	1.22
CG2816_gene	CG2816	2.06859	1.68853	0.82	1.23
CG30094_gene	CG30094	2.06859	1.68853	0.82	1.23
CG1732_gene	CG1732	6.45072	5.26423	0.82	1.23
ome_gene	ome	64.48	52.6092	0.82	1.23
CG32100_gene	CG32100	2.2319	1.82096	0.82	1.23
CG3476_gene	CG3476	6.77734	5.5291	0.82	1.23
CG30460_gene	CG6967	30.3211	24.732	0.82	1.23
Tsp66E_gene	Tsp66E	9.33586	7.61493	0.82	1.23
CG30390_gene	CG30390	2.64017	2.15204	0.82	1.23
CG31038_gene	CG31038	40.0108	32.6118	0.82	1.23
oxt_gene	CG2034	8.24713	6.721	0.81	1.23
tim_gene	tim	100.435	81.8439	0.81	1.23
CG17292_gene	CG17292	5.77027	4.70139	0.81	1.23
Cbp20_gene	Cbp20	9.14533	7.44938	0.81	1.23
cenB1A_gene	cenB1A	37.8061	30.7908	0.81	1.23
18w_gene	18w	9.63526	7.84669	0.81	1.23
CG13398_gene	CG13398	13.0103	10.5947	0.81	1.23
CG15032_gene	CG15032	11.0234	8.97237	0.81	1.23
CG5961_gene	CG5961	12.4932	10.1643	0.81	1.23
chm_gene	chm	4.27326	3.47638	0.81	1.23
CG1776_gene	CG1776	4.35492	3.5426	0.81	1.23
CG9667_gene	CG9667	4.76319	3.87368	0.81	1.23
CG30344_gene	CG30344	128.77	104.722	0.81	1.23
sNPF_gene	sNPF	4.84485	3.9399	0.81	1.23
CG3104_gene	CG3104	10.2613	8.34331	0.81	1.23
neb_gene	neb	36.7991	29.8969	0.81	1.23
SuUR_gene	SuUR	7.70276	6.25748	0.81	1.23
CG12155_gene	CG12155	15.215	12.3494	0.81	1.23
garz_gene	garz	220.577	179.017	0.81	1.23
CG15635_gene	CG15635	3637.85	2952.27	0.81	1.23

CG40178_gene	CG40178	63.7723	51.7484	0.81	1.23
rg_gene	rg	213.908	173.488	0.81	1.23
CG15122_gene	CG15122	1.55144	1.25812	0.81	1.23
CG34172_gene	CG34172	0.816547	0.662168	0.81	1.23
CG5431_gene	CG5431	0.816547	0.662168	0.81	1.23
snoRNA:Me28S-C2645c_gene	pncr012:2L	0.816547	0.662168	0.81	1.23
tRNA:CR31494_gene	CG31248	2.36799	1.92029	0.81	1.23
CG32499_gene	CG32499	2.36799	1.92029	0.81	1.23
CG2909_gene	CG2909	4.3277	3.50949	0.81	1.23
Rad17_gene	CG3508	2.77626	2.25137	0.81	1.23
CG17270_gene	CG17270	0.734893	0.595951	0.81	1.23
CG10472_gene	CG6592	0.734893	0.595951	0.81	1.23
Mct1_gene	Mct1	0.734893	0.595951	0.81	1.23
Tsp2A_gene	CG11418	0.653238	0.529734	0.81	1.23
CG16947_gene	CG16947	0.898202	0.728384	0.81	1.23
Ance-5_gene	Ance-5	0.571583	0.463517	0.81	1.23
Caf1-180_gene	Caf1-180	7.02231	5.69464	0.81	1.23
MESK4_gene	MESK4	2.5313	2.05272	0.81	1.23
jet_gene	betaggt-I	11.0234	8.93926	0.81	1.23
Orc1_gene	CG2144	2.20468	1.78785	0.81	1.23
Cyp4ae1_gene	Cyp4ae1	1.38813	1.12568	0.81	1.23
CG13462_gene	CG13462	1.46979	1.1919	0.81	1.23
CG12121_gene	Gr8a	156.587	126.938	0.81	1.23
cbs_gene	cbs	22.1829	17.9778	0.81	1.23
Acp54A1_gene	Acp54A1	3719.67	3014.05	0.81	1.23
agt_gene	Spase18-21	21.6657	17.5474	0.81	1.23
E(z)_gene	CG34001	15.6233	12.6474	0.81	1.24
vih_gene	vih	6.50516	5.26423	0.81	1.24
CG17544_gene	CG17544	19.0256	15.3954	0.81	1.24
ERR_gene	CG7979	11.4589	9.27035	0.81	1.24
CG10646_gene	CG10681	5.60696	4.53585	0.81	1.24
CG10863_gene	CG10863	47.3597	38.3064	0.81	1.24
CG5167_gene	CG5167	61.3227	49.5963	0.81	1.24
Cyp12d1-d_gene	Cyp12d1-d	4.87207	3.9399	0.81	1.24
CG1749_gene	CG1749	51.9596	42.0145	0.81	1.24
CG10795_gene	CG10795	7.29449	5.89329	0.81	1.24
Hsc70-3_gene	Hsc70-3	4163.63	3363.81	0.81	1.24
ci_gene	ci	14.2624	11.5217	0.81	1.24
CG12659_gene	CG12081	3.48394	2.81421	0.81	1.24
CG7772_gene	CG7772	2.99401	2.41691	0.81	1.24
CG14521_gene	CG14521	2.91235	2.35069	0.81	1.24
CG7685_gene	CG7685	5.41643	4.37031	0.81	1.24
Papst2_gene	Papst2	37.8334	30.5259	0.81	1.24
Sin1_gene	Sin1	5.00816	4.03922	0.81	1.24
CG11109_gene	CG11109	18.3995	14.8326	0.81	1.24
CG34352_gene	CG34352	380.729	306.915	0.81	1.24
fok_gene	neb	26.3473	21.2225	0.81	1.24
Nhe1_gene	CG11377	175.449	141.307	0.81	1.24
beat-Vb_gene	beat-Vb	19.4066	15.6272	0.81	1.24
wg_gene	wg	1.9325	1.55609	0.81	1.24
Cf2_gene	Cf2	37.915	30.5259	0.81	1.24
Cyp12e1_gene	Cyp12e1	3.78334	3.04597	0.81	1.24
bai_gene	bai	230.103	185.241	0.81	1.24
l(1)G0196_gene	CG14617	84.3221	67.8722	0.80	1.24
CG14215_gene	CG14215	23.816	19.1698	0.80	1.24
fz_gene	fz	30.7838	24.7651	0.80	1.24
noc_gene	noc	11.4044	9.17102	0.80	1.24
mus81_gene	mus81	1.60588	1.29123	0.80	1.24
CG3168_gene	CG3168	8.6554	6.95276	0.80	1.24
Vha55_gene	Vha55	297.196	238.48	0.80	1.25

SIP1_gene	SIP1	9.66248	7.74736	0.80	1.25
Gs1l_gene	Gs1l	15.1606	12.1508	0.80	1.25
wibg_gene	bgcn	4.6271	3.70814	0.80	1.25
CG7778_gene	CG7778	20.1687	16.1569	0.80	1.25
CG13762_gene	CG13762	1.11595	0.893926	0.80	1.25
CG4935_gene	CG4935	1.11595	0.893926	0.80	1.25
mu2_gene	CG1017	2.2319	1.78785	0.80	1.25
CG10747_gene	neb	11.3772	9.1048	0.80	1.25
mspo_gene	mspo	3.10288	2.48313	0.80	1.25
CG40002_gene	CG40002	37.7789	30.2279	0.80	1.25
form3_gene	form3	6.99509	5.59532	0.80	1.25
CG6310_gene	CG6310	1.98693	1.5892	0.80	1.25
tefu_gene	tefu	7.86607	6.29059	0.80	1.25
CG8525_gene	CG8520	2.93957	2.35069	0.80	1.25
CG18788_gene	CG18788	0.952639	0.761493	0.80	1.25
CG5181_gene	CG5181	6.58682	5.26423	0.80	1.25
exo84_gene	gro	17.6102	14.0711	0.80	1.25
CG6923_gene	CG6923	10.9417	8.74061	0.80	1.25
pasha_gene	pasha	4.51823	3.60881	0.80	1.25
Arp87C_gene	Arp87C	40.8002	32.5786	0.80	1.25
l(1)G0320_gene	l(1)G0320	195.781	156.305	0.80	1.25
clumsy_gene	clumsy	1.74197	1.39055	0.80	1.25
Pbgs_gene	Pbgs	14.3985	11.4886	0.80	1.25
CG13836_gene	CG13836	2.5313	2.01961	0.80	1.25
sec31_gene	sec31	199.727	159.351	0.80	1.25
CG10882_gene	CG10882	258.219	206	0.80	1.25
CG14785_gene	CG14785	1.66031	1.32434	0.80	1.25
CG2941_gene	CG2941	3.23897	2.58245	0.80	1.25
CG9791_gene	CG9791	3.23897	2.58245	0.80	1.25
CG8310_gene	CG8310	7.26727	5.79397	0.80	1.25
CG12560_gene	CG12560	4.0283	3.21151	0.80	1.25
CG7872_gene	CG7872	52.9123	42.1801	0.80	1.25
CG8177_gene	CG8177	117.066	93.2994	0.80	1.25
CG30008_gene	CG1513	0.789329	0.629059	0.80	1.25
Gr8a_gene	Gr8a	0.789329	0.629059	0.80	1.25
CG15506_gene	CG15506	3.86499	3.07908	0.80	1.26
CG8083_gene	CG8083	6.94065	5.5291	0.80	1.26
MED7_gene	MED7	8.43766	6.721	0.80	1.26
CG5220_gene	CG5220	10.724	8.54196	0.80	1.26
CG34294_gene	CG34294	2.28633	1.82096	0.80	1.26
Axs_gene	Axs	15.215	12.1177	0.80	1.26
CG33145_gene	CG33145	3.78334	3.01286	0.80	1.26
CG31757_gene	CG31757	3299.97	2627.65	0.80	1.26
CG30263_gene	CG30263	5.19868	4.13855	0.80	1.26
CG17919_gene	CG17919	59.9346	47.7092	0.80	1.26
NLaz_gene	NLaz	59.4719	47.3119	0.80	1.26
Os-C_gene	Os-C	65.5143	52.1126	0.80	1.26
CG1756_gene	CG1756	0.707674	0.562842	0.80	1.26
GluRIIC_gene	GluRIIC	9.90744	7.87979	0.80	1.26
Tina-1_gene	Tina-1	37.6428	29.93	0.80	1.26
tos_gene	CG31751	3.37506	2.68178	0.79	1.26
CG7646_gene	CG7646	2.66739	2.11894	0.79	1.26
CG2004_gene	Hexo2	71.2301	56.5822	0.79	1.26
p115_gene	p115	73.7614	58.5687	0.79	1.26
CG32808_gene	CG32808	0.62602	0.496626	0.79	1.26
CG41516_gene	CG34357	3.75612	2.97975	0.79	1.26
CG6838_gene	CG6838	142.488	113.032	0.79	1.26
Elp3_gene	Elp3	11.1867	8.87305	0.79	1.26
CG7458_gene	CG7458	9.853	7.81358	0.79	1.26
sec63_gene	sec63	679.776	539.071	0.79	1.26

CG18281_gene	CG32425	505.035	400.247	0.79	1.26
CG34379_gene	CG34379	33.5601	26.586	0.79	1.26
sphinx_gene	sphinx	19.1072	15.1305	0.79	1.26
CG2685_gene	CG2685	10.1252	8.01223	0.79	1.26
Vha26_gene	Vha26	393.222	311.153	0.79	1.26
CG7582_gene	CAP-D2	2.80348	2.21826	0.79	1.26
CG1079_gene	CG1079	2.80348	2.21826	0.79	1.26
Sirt7_gene	Sirt7	2.80348	2.21826	0.79	1.26
pelo_gene	pelo	28.7152	22.7123	0.79	1.26
Set2_gene	Set2	30.8111	24.3678	0.79	1.26
Chrac-16_gene	Chrac-16	9.33586	7.38317	0.79	1.26
Orct2_gene	Orct2	71.1757	56.2842	0.79	1.26
CG33491_gene	CG33491	1.63309	1.29123	0.79	1.26
CG32250_gene	CG32250	22.8633	18.0772	0.79	1.26
CG11600_gene	CG11600	52.8034	41.7497	0.79	1.26
CG8830_gene	CG8830	28.307	22.3813	0.79	1.26
CG31093_gene	CG31093	3.81055	3.01286	0.79	1.26
CG14892_gene	CG14892	0.544365	0.430409	0.79	1.26
CG30174_gene	CG30174	0.544365	0.430409	0.79	1.26
CG6332_gene	CG6332	0.544365	0.430409	0.79	1.26
Argk_gene	Argk	310.832	245.631	0.79	1.27
roX2_gene	roX2	7.4578	5.89329	0.79	1.27
Vha16_gene	Vha16	370.086	292.446	0.79	1.27
CG9526_gene	CG9526	18.9439	14.965	0.79	1.27
CG8451_gene	CG8455	131.6	103.927	0.79	1.27
disco_gene	disco	6.75012	5.33045	0.79	1.27
CG15611_gene	CG15611	32.1175	25.361	0.79	1.27
CG12920_gene	CG12920	1.55144	1.22501	0.79	1.27
CG15356_gene	CG15356	4.65432	3.67503	0.79	1.27
CG7497_gene	CG7497	7.67555	6.05883	0.79	1.27
CG33288_gene	CG6049	101.715	80.2878	0.79	1.27
Ent2_gene	Ent2	83.6145	65.985	0.79	1.27
CG12928_gene	RpL31	8.60097	6.78722	0.79	1.27
beat-IIIb_gene	beat-IIIb	1.00708	0.794601	0.79	1.27
CG1265_gene	CG1265	1.00708	0.794601	0.79	1.27
CG12795_gene	CG12795	6.96787	5.49599	0.79	1.27
CG17816_gene	CG17816	5.41643	4.27098	0.79	1.27
CG15385_gene	CG15385	48.1219	37.9422	0.79	1.27
CG8813_gene	CG31694	1.46979	1.15879	0.79	1.27
CG17721_gene	CG17721	6.80456	5.36356	0.79	1.27
CG4553_gene	CG4553	3.40228	2.68178	0.79	1.27
CG12688_gene	CG12688	1.9325	1.52299	0.79	1.27
usnp_gene	usnp	11.6494	9.17102	0.79	1.27
CG11566_gene	CG11566	1.38813	1.09258	0.79	1.27
stg1_gene	CG11566	1.38813	1.09258	0.79	1.27
CG11882_gene	CG11882	1.38813	1.09258	0.79	1.27
ct_gene	ct	1.38813	1.09258	0.79	1.27
CG5644_gene	Srp68	1.38813	1.09258	0.79	1.27
CG14353_gene	CG14353	3.23897	2.54935	0.79	1.27
CG31715_gene	CG31715	5.55252	4.37031	0.79	1.27
Rpl12_gene	CG6800	2.77626	2.18515	0.79	1.27
slv_gene	slv	87.3706	68.7661	0.79	1.27
CG16838_gene	CG16838	5.47087	4.30409	0.79	1.27
CG7461_gene	CG7461	78.8785	62.0451	0.79	1.27
CG13390_gene	CG17293	3.62003	2.84732	0.79	1.27
CG11864_gene	CG11864	204.845	161.105	0.79	1.27
Syx4_gene	Syx4	3.15732	2.48313	0.79	1.27
CG11590_gene	CG11590	160.56	126.275	0.79	1.27
CG3632_gene	CG9911	22.2373	17.4812	0.79	1.27
Ero1L_gene	Ero1L	179.069	140.711	0.79	1.27

dlt_gene	alpha-Spec	3.45672	2.71489	0.79	1.27
CG10866_gene	CG10866	1.68753	1.32434	0.78	1.27
CG5849_gene	CG5849	0.843766	0.662168	0.78	1.27
insv_gene	insv	0.843766	0.662168	0.78	1.27
CG11399_gene	CG4289	14.7251	11.5548	0.78	1.27
CG14752_gene	CG14752	7.89329	6.19127	0.78	1.27
Sema-5c_gene	Sema-5c	32.798	25.7252	0.78	1.27
Pka-C1_gene	Pka-C1	115.46	90.5514	0.78	1.28
CG14252_gene	CG14252	1.22482	0.960143	0.78	1.28
CG18356_gene	CG18356	1.22482	0.960143	0.78	1.28
CG5880_gene	CG5880	1.22482	0.960143	0.78	1.28
c(3)G_gene	CG9589	1.60588	1.25812	0.78	1.28
CG5276_gene	CG5276	39.6842	31.0888	0.78	1.28
CG32850_gene	CG32850	9.17255	7.18452	0.78	1.28
CG32043_gene	CG32043	11.2956	8.83994	0.78	1.28
CG33679_gene	CG33679	1.90528	1.48988	0.78	1.28
CG1847_gene	CG1847	5.33478	4.17166	0.78	1.28
CG12938_gene	CG12938	1.52422	1.1919	0.78	1.28
dbe_gene	dbe	14.3985	11.2568	0.78	1.28
CG15438_gene	Elp3	26.8644	20.9907	0.78	1.28
CG4951_gene	Gp93	42.5966	33.2739	0.78	1.28
lt_gene	lt	36.0642	28.1421	0.78	1.28
CG18324_gene	CG18324	8.27435	6.45613	0.78	1.28
CG6325_gene	CG6325	5.68861	4.43652	0.78	1.28
Cyp12b2_gene	Cyp12b2	7.43058	5.79397	0.78	1.28
smi21F_gene	smi21F	67.6646	52.7416	0.78	1.28
CG31918_gene	His3.3A	2.80348	2.18515	0.78	1.28
CG30100_gene	CG30100	4.54545	3.5426	0.78	1.28
CG12918_gene	CG2249	236.472	184.281	0.78	1.28
CG30389_gene	CG30389	27.4904	21.4211	0.78	1.28
CG8713_gene	CG8713	4.16439	3.24462	0.78	1.28
Lam_gene	Lam	26.184	20.3948	0.78	1.28
tkv_gene	TpnC25D	424.033	330.256	0.78	1.28
CG14796_gene	CG14796	17.4741	13.6075	0.78	1.28
CG14135_gene	CG14135	2.72182	2.11894	0.78	1.28
CG14943_gene	CG31757	0.680456	0.529734	0.78	1.28
AP-1sigma_gene	AP-1sigma	87.7244	68.2695	0.78	1.28
CG5060_gene	CG5060	8.76428	6.82033	0.78	1.29
Nep5_gene	NepYr	37.3979	29.1023	0.78	1.29
tomosyn_gene	tomosyn	74.7685	58.1714	0.78	1.29
tau_gene	CG34294	20.9036	16.2562	0.78	1.29
Spt-I_gene	Spt-I	24.1426	18.7724	0.78	1.29
CG9706_gene	CG9706	121.094	94.1271	0.78	1.29
CG31128_gene	CG31128	0.979857	0.761493	0.78	1.29
CG7722_gene	CG7722	0.979857	0.761493	0.78	1.29
trh_gene	trh	0.979857	0.761493	0.78	1.29
CG11103_gene	CG11103	6.859	5.33045	0.78	1.29
Prestin_gene	Prestin	7.1584	5.56221	0.78	1.29
CG32970_gene	wb	6.09689	4.7345	0.78	1.29
CG9304_gene	CG9304	36.8807	28.6387	0.78	1.29
usp_gene	Actn	48.013	37.28	0.78	1.29
CG10880_gene	CG34174	7.29449	5.66153	0.78	1.29
CG11188_gene	CG11188	14.7251	11.4224	0.78	1.29
CG12879_gene	CG12879	620.195	480.502	0.77	1.29
CG30055_gene	Sin3A	14.3168	11.0913	0.77	1.29
by_gene	by	76.8099	59.4958	0.77	1.29
CG7091_gene	CG7091	17.9096	13.8724	0.77	1.29
CG8860_gene	CG8860	45.7539	35.426	0.77	1.29
CG31053_gene	CG5508	1.7964	1.39055	0.77	1.29
CG4680_gene	CG4680	0.598801	0.463517	0.77	1.29

Notum_gene	Notum	0.598801	0.463517	0.77	1.29
CG34408_gene	CG34408	69.6787	53.9335	0.77	1.29
CG32700_gene	CG32700	17.2564	13.3427	0.77	1.29
CG15556_gene	CG15556	19.7877	15.2961	0.77	1.29
CG10254_gene	CG10254	54.001	41.7166	0.77	1.29
CG9920_gene	CG9920	1.71475	1.32434	0.77	1.29
VhaAC39_gene	VhaAC39	137.806	106.311	0.77	1.30
CG31781_gene	CG31781	33.6145	25.9239	0.77	1.30
CG2767_gene	CG2767	47.2237	36.4192	0.77	1.30
CG13192_gene	CG13192	8.98202	6.91965	0.77	1.30
CG5010_gene	CG5010	52.4768	40.4253	0.77	1.30
tan_gene	tan	4.59988	3.5426	0.77	1.30
CG14798_gene	CG14798	2.15024	1.65542	0.77	1.30
wbl_gene	wbl	268.835	206.96	0.77	1.30
CG14072_gene	CG14072	194.583	149.584	0.77	1.30
CG1486_gene	CG1486	215.514	165.608	0.77	1.30
CG12699_gene	CG12699	4.13717	3.1784	0.77	1.30
CG33325_gene	CG33325	87.425	67.1438	0.77	1.30
CG9641_gene	mmaTub2	8.19269	6.29059	0.77	1.30
Dgkepsilon_gene	Dgkepsilon	28.2525	21.686	0.77	1.30
grass_gene	grass	5.00816	3.84057	0.77	1.30
CG11750_gene	CG11750	6.09689	4.66828	0.77	1.31
CG15386_gene	CG15386	21.1486	16.19	0.77	1.31
Plip_gene	Plip	10.4246	7.97912	0.77	1.31
CG12975_gene	CG10508	4.84485	3.70814	0.77	1.31
CG14818_gene	CG14805	23.0266	17.6137	0.76	1.31
CG8786_gene	CG8786	10.6968	8.17777	0.76	1.31
CG2918_gene	CG2918	1724.63	1316.92	0.76	1.31
cv_gene	cv	11.1867	8.54196	0.76	1.31
CG12512_gene	CG12512	23.2444	17.7461	0.76	1.31
CG33487_gene	CG33487	1.38813	1.05947	0.76	1.31
CG5455_gene	CG5455	64.4256	49.1659	0.76	1.31
CG32454_gene	CG11367	1.82362	1.39055	0.76	1.31
CG32803_gene	CG32803	3.64724	2.7811	0.76	1.31
CG10924_gene	CG10924	2.25911	1.72164	0.76	1.31
alpha-Man-I_gene	lpha-Man-	105.443	80.3209	0.76	1.31
rols_gene	rols	739.356	563.173	0.76	1.31
CG6718_gene	CG6718	72.8632	55.4896	0.76	1.31
CG13393_gene	CG17295	84.3493	64.2303	0.76	1.31
CG3814_gene	CG3814	12.4387	9.469	0.76	1.31
CG1662_gene	CG1662	9.52639	7.25073	0.76	1.31
CG9171_gene	CG9171	45.5906	34.6976	0.76	1.31
CG3153_gene	CG3153	87.0984	66.2499	0.76	1.31
CG13283_gene	CG13283	0.653238	0.496626	0.76	1.32
CG31537_gene	cno	0.870984	0.662168	0.76	1.32
bnb_gene	Pk17E	0.870984	0.662168	0.76	1.32
Srp14_gene	Srp14	7.62111	5.79397	0.76	1.32
Tango9_gene	Tango9	31.1649	23.6394	0.76	1.32
CG31360_gene	CG31360	6.72291	5.09869	0.76	1.32
CG10050_gene	CG10050	1.66031	1.25812	0.76	1.32
CG31249_gene	CG31360	16.7392	12.6805	0.76	1.32
CG12929_gene	Updo	4.3277	3.27773	0.76	1.32
CG14507_gene	Brd8	33.8867	25.659	0.76	1.32
CG7777_gene	CG7777	34.0228	25.7583	0.76	1.32
CG4565_gene	CG6567	2.44964	1.85407	0.76	1.32
mbl_gene	mbl	279.586	211.529	0.76	1.32
CG11400_gene	CG11400	27.6265	20.8914	0.76	1.32
CG12983_gene	CG12983	3.37506	2.54935	0.76	1.32
Rtnl1_gene	Rtnl1	94.284	71.2161	0.76	1.32
foi_gene	foi	102.504	77.4074	0.76	1.32

CG15528_gene	CG15528	0.789329	0.595951	0.76	1.32
GluRIIB_gene	GluRIIB	0.789329	0.595951	0.76	1.32
snoRNA:Me28S-A2634b_gene	A:Me28S-A	0.789329	0.595951	0.76	1.32
CG15841_gene	CG6555	1609.63	1214.98	0.75	1.32
CG6555_gene	CG6555	1609.63	1214.98	0.75	1.32
CG32495_gene	CG32495	9.60804	7.25073	0.75	1.33
CG10425_gene	CG10425	23.2988	17.5805	0.75	1.33
Ubp64E_gene	Ubp64E	158.682	119.72	0.75	1.33
Nelf-E_gene	CG32355	4.87207	3.67503	0.75	1.33
CG12018_gene	CG12018	1.36091	1.02636	0.75	1.33
CG34233_gene	CG34233	1.36091	1.02636	0.75	1.33
ETHR_gene	ETHR	2.72182	2.05272	0.75	1.33
pen-2_gene	pen-2	2.72182	2.05272	0.75	1.33
CG14694_gene	CG4570	3.86499	2.91354	0.75	1.33
p24-1_gene	p24-1	295.672	222.72	0.75	1.33
CG5412_gene	TFAM	6.859	5.16491	0.75	1.33
CG32425_gene	CG32425	3234.15	2435.35	0.75	1.33
Pof_gene	CG33228	3.4295	2.58245	0.75	1.33
CG33251_gene	CG9915	3.4295	2.58245	0.75	1.33
CHKov1_gene	CHKov1	73.1626	55.0592	0.75	1.33
Grd_gene	Grd	3.21175	2.41691	0.75	1.33
FucT6_gene	FucT6	189.874	142.863	0.75	1.33
CG3309_gene	CG3309	3.34784	2.51624	0.75	1.33
CheB42c_gene	CG33558	0.92542	0.695276	0.75	1.33
CG8460_gene	CG8460	53.5927	40.2598	0.75	1.33
CG12772_gene	CG12772	19.2161	14.4353	0.75	1.33
Tango13_gene	Tango13	142.27	106.808	0.75	1.33
toy_gene	toy	6.39629	4.80071	0.75	1.33
CG18508_gene	CG18508	25.4763	19.1035	0.75	1.33
CG32686_gene	CG17841	1.98693	1.48988	0.75	1.33
fliI_gene	fliI	33.3968	25.0299	0.75	1.33
Ctr1B_gene	Ctr1B	6.45072	4.83382	0.75	1.33
CG7504_gene	CG7504	1.76919	1.32434	0.75	1.34
CG7003_gene	FucTA	5.6614	4.23787	0.75	1.34
CG1582_gene	CG1582	26.81	20.0637	0.75	1.34
CG10570_gene	CG10570	137.479	102.835	0.75	1.34
CG10041_gene	CG10041	124.714	93.2663	0.75	1.34
CG1647_gene	CG1647	5.93358	4.43652	0.75	1.34
Spn4_gene	Spn4	11.1595	8.34331	0.75	1.34
CG10778_gene	CG10778	11.0778	8.27709	0.75	1.34
CR32011_gene	CR32011	10.0163	7.48249	0.75	1.34
Tango4_gene	Tango4	6.20576	4.63517	0.75	1.34
CG6683_gene	CG6765	1.55144	1.15879	0.75	1.34
Cyp28c1_gene	Cyp28c1	113.636	84.8568	0.75	1.34
CG7742_gene	Cyp28d1	90.3646	67.4749	0.75	1.34
TRAM_gene	TRAM	279.613	208.715	0.75	1.34
Spn5_gene	Spn5	72.1011	53.8011	0.75	1.34
CG32699_gene	CG32699	19.08	14.2366	0.75	1.34
CG31717_gene	CG31717	15.841	11.8197	0.75	1.34
CR33963_gene	Tis11	2.04137	1.52299	0.75	1.34
CG7737_gene	CG7737	14.0718	10.4954	0.75	1.34
corn_gene	corn	9.63526	7.18452	0.75	1.34
ATbp_gene	ATbp	2.5313	1.88718	0.75	1.34
CG33007_gene	PR2	0.843766	0.629059	0.75	1.34
Acp98AB_gene	CG12879	170.713	127.269	0.75	1.34
CG32368_gene	CG32368	8.08382	6.02572	0.75	1.34
ubl_gene	ubl	3.02123	2.25137	0.75	1.34
CG6201_gene	CG4713	1.33369	0.993251	0.74	1.34
CG5594_gene	CG5594	42.7326	31.8172	0.74	1.34
CG31743_gene	CG31743	6.31463	4.70139	0.74	1.34

CG34313_gene	CG31743	6.31463	4.70139	0.74	1.34
CG11284_gene	CG11284	119.624	89.0284	0.74	1.34
rad201_gene	Rad51C	2.80348	2.08583	0.74	1.34
Ssb-c31a_gene	Ssb-c31a	10.0163	7.44938	0.74	1.34
CG33224_gene	CG33224	8.32878	6.19127	0.74	1.35
Hsc70-1_gene	Hsc70-1	0.979857	0.728384	0.74	1.35
CG30467_gene	CG30467	5.03538	3.74125	0.74	1.35
CG34424_gene	CG34423	2.58573	1.92029	0.74	1.35
CecA1_gene	CecA1	46.1894	34.2672	0.74	1.35
CG32154_gene	CG32154	11.7855	8.74061	0.74	1.35
mRpS24_gene	CG6182	2.85792	2.11894	0.74	1.35
CG13101_gene	CG13101	13.4458	9.96562	0.74	1.35
CG15436_gene	CG15436	17.6102	13.0447	0.74	1.35
snoRNA:Psi28S-3186_gene	exba	0.62602	0.463517	0.74	1.35
ori_gene	ori	8.90037	6.58857	0.74	1.35
AlkB_gene	AlkB	3.53837	2.61556	0.74	1.35
Snap25_gene	Snap25	26.9733	19.9312	0.74	1.35
CG3940_gene	CG3940	4.84485	3.5757	0.74	1.35
Sptr_gene	Es2	11.7583	8.67439	0.74	1.36
CG8486_gene	CG8486	35.8192	26.4205	0.74	1.36
CG16772_gene	CG16772	14.589	10.7602	0.74	1.36
CG11069_gene	CG11069	5.25312	3.87368	0.74	1.36
CR33294_gene	CR33294	3.59281	2.64867	0.74	1.36
pst_gene	pst	32.1447	23.6725	0.74	1.36
CG15739_gene	CG15739	1.03429	0.761493	0.74	1.36
CG32186_gene	CG32186	1.03429	0.761493	0.74	1.36
CG10307_gene	CG10307	2.20468	1.62231	0.74	1.36
CG4854_gene	CG4854	1.17038	0.860818	0.74	1.36
CG32159_gene	CG33158	3.64724	2.68178	0.74	1.36
CG11360_gene	CG11360	8.60097	6.3237	0.74	1.36
spz_gene	spz	6.2602	4.60206	0.74	1.36
CG3099_gene	CG3099	2.61295	1.92029	0.73	1.36
CG32590_gene	CG32590	1.30648	0.960143	0.73	1.36
nAcRbeta-21C_gene	AcRbeta-21	1.30648	0.960143	0.73	1.36
CG1902_gene	CG34364	173.734	127.666	0.73	1.36
pkaap_gene	pkaap	9.41751	6.91965	0.73	1.36
mio_gene	mio	21.7746	15.9913	0.73	1.36
Nek2_gene	Nek2	16.3854	12.0183	0.73	1.36
CG10208_gene	CG10208	1.98693	1.45677	0.73	1.36
CG30051_gene	CG8830	2.80348	2.05272	0.73	1.37
CG4616_gene	CG4616	6.28741	4.60206	0.73	1.37
CG15863_gene	CG15863	3.34784	2.45002	0.73	1.37
CG10019_gene	CG10019	3.48394	2.54935	0.73	1.37
CG33253_gene	CG33253	3.62003	2.64867	0.73	1.37
Cyp6a9_gene	Cyp6a19	12.7654	9.33656	0.73	1.37
vimar_gene	vimar	18.1546	13.2765	0.73	1.37
apt_gene	apt	42.4332	31.0225	0.73	1.37
CG3689_gene	CG3689	29.5318	21.5867	0.73	1.37
CG12455_gene	CG12455	168.073	122.766	0.73	1.37
Awh_gene	Awh	24.6597	18.011	0.73	1.37
CG13766_gene	CG13766	1.497	1.09258	0.73	1.37
GlcAT-S_gene	GlcAT-S	1.36091	0.993251	0.73	1.37
CG17258_gene	CG17257	0.544365	0.397301	0.73	1.37
CG34253_gene	CG34253	0.544365	0.397301	0.73	1.37
Mst89B_gene	Mst89B	0.544365	0.397301	0.73	1.37
CG31068_gene	CG31064	0.680456	0.496626	0.73	1.37
CG18171_gene	drpr	0.680456	0.496626	0.73	1.37
Pal_gene	Pal	1.22482	0.893926	0.73	1.37
CG32022_gene	CG32022	9.17255	6.68789	0.73	1.37
Tsp42Ef_gene	Tsp42Ef	17.7191	12.9123	0.73	1.37

Socs36E_gene	Socs36E	10.4518	7.61493	0.73	1.37
CG7112_gene	CG7112	54.9809	40.028	0.73	1.37
CkIIalpha-i3_gene	CkIIalpha-i3	3.18453	2.31759	0.73	1.37
Wnt6_gene	Wnt6	9.88022	7.18452	0.73	1.38
CG1319_gene	CG1319	19.4883	14.1704	0.73	1.38
CG10433_gene	CG10433	95.6721	69.5607	0.73	1.38
CG31098_gene	CG31098	8.92758	6.48924	0.73	1.38
CG8683_gene	CG8683	97.523	70.885	0.73	1.38
mars_gene	drk	2.0958	1.52299	0.73	1.38
CG8281_gene	CG8281	4.05552	2.94665	0.73	1.38
CG9523_gene	CG9523	48.6662	35.3597	0.73	1.38
Cyp4e2_gene	Cyp4e2	54.7903	39.7963	0.73	1.38
Cpr51A_gene	Cpr51A	7.43058	5.39667	0.73	1.38
CG15353_gene	CG15353	1.68753	1.22501	0.73	1.38
CG11166_gene	CG11166	1203.07	873.3	0.73	1.38
Csat_gene	Csat	95.0461	68.7992	0.72	1.38
CG4623_gene	CG4623	68.6172	49.6626	0.72	1.38
CG32412_gene	CG32409	9.33586	6.75411	0.72	1.38
CG9220_gene	CG9220	18.6717	13.5082	0.72	1.38
Catsup_gene	Catsup	183.342	132.434	0.72	1.38
CG12320_gene	CG18598	1.74197	1.25812	0.72	1.38
CG32428_gene	CG32428	8.43766	6.09194	0.72	1.39
Gr39a_gene	Mio	3.34784	2.41691	0.72	1.39
CG3857_gene	CG3857	4.54545	3.27773	0.72	1.39
Fibp_gene	Fibp	3.67446	2.64867	0.72	1.39
CG10959_gene	CG10959	1.46979	1.05947	0.72	1.39
CG31708_gene	CG31708	11.2139	8.07844	0.72	1.39
CG8303_gene	CG8303	97.3052	70.0242	0.72	1.39
Fas2_gene	Fas2	32.4441	23.3414	0.72	1.39
Cyp12d1-p_gene	Cyp12d1-p	7.92051	5.69464	0.72	1.39
CG13606_gene	CG13606	0.598801	0.430409	0.72	1.39
snoRNA:Me28S-G1083a_gene	Nop60B	0.598801	0.430409	0.72	1.39
RecQ4_gene	RecQ4	0.598801	0.430409	0.72	1.39
Gasp_gene	Gasp	2.39521	1.72164	0.72	1.39
Alk_gene	Alk	8.84593	6.35681	0.72	1.39
CG15093_gene	CG15093	22.2101	15.9251	0.72	1.39
CG4743_gene	CG5039	7.48502	5.36356	0.72	1.40
CG32202_gene	CG32202	4.76319	3.41016	0.72	1.40
wek_gene	wek	4.76319	3.41016	0.72	1.40
nemy_gene	CG8776	1.85084	1.32434	0.72	1.40
CG33290_gene	CG33290	395.073	282.679	0.72	1.40
CG11686_gene	CG11686	4.49101	3.21151	0.72	1.40
CG15343_gene	CG15343	5.74305	4.10544	0.71	1.40
GM130_gene	GM130	102.096	72.9709	0.71	1.40
CG4213_gene	CG4213	3.4295	2.45002	0.71	1.40
Irk2_gene	Irk2	1.71475	1.22501	0.71	1.40
alpha4GT1_gene	CG17264	3.75612	2.68178	0.71	1.40
CG14669_gene	CG14669	6.91343	4.93315	0.71	1.40
CG34288_gene	CG34288	0.789329	0.562842	0.71	1.40
CG10178_gene	CG10178	11.8944	8.47574	0.71	1.40
CG13926_gene	CG13926	3.34784	2.3838	0.71	1.40
CG11926_gene	CG11926	15.9499	11.3562	0.71	1.40
CG13315_gene	CG13315	12.3299	8.77372	0.71	1.41
CG3303_gene	CG3303	3.86499	2.748	0.71	1.41
CG7192_gene	CG7192	31.301	22.2488	0.71	1.41
CG5089_gene	CG8303	15.6505	11.1244	0.71	1.41
Anp_gene	Anp	629.558	447.261	0.71	1.41
Sec61beta_gene	Sec61beta	124.986	88.7636	0.71	1.41
CG41329_gene	CG17429	0.653238	0.463517	0.71	1.41
CG30381_gene	CG8791	1.30648	0.927035	0.71	1.41

CG15237_gene	SdhB	12.2754	8.7075	0.71	1.41
CG6793_gene	rols	24.5509	17.415	0.71	1.41
Prx2540-1_gene	Prx2540-1	5.28034	3.74125	0.71	1.41
CG32682_gene	lpha-Man-	2.47686	1.75474	0.71	1.41
CG15891_gene	CG15896	9.11811	6.45613	0.71	1.41
CG15892_gene	CG15896	9.11811	6.45613	0.71	1.41
CG15916_gene	CG15916	7.81164	5.5291	0.71	1.41
bgcn_gene	bgcn	5.6614	4.00611	0.71	1.41
P58IPK_gene	P58IPK	297.849	210.602	0.71	1.41
kni_gene	kni	4.73597	3.34395	0.71	1.42
CG10908_gene	CG10908	46.2438	32.6449	0.71	1.42
CG2906_gene	CG2906	4.40936	3.11219	0.71	1.42
CG9114_gene	dah	2.72182	1.92029	0.71	1.42
CG8654_gene	CG8654	45.7539	32.2476	0.70	1.42
CG41242_gene	CG41242	5.17147	3.64192	0.70	1.42
Cyp1_gene	Cyp1	334.458	235.235	0.70	1.42
CG5402_gene	CG5402	682.307	479.707	0.70	1.42
CG12945_gene	CG8500	14.1807	9.96562	0.70	1.42
CG8369_gene	CG8369	11.0778	7.78047	0.70	1.42
CG10420_gene	CG10420	25.4218	17.8454	0.70	1.42
CG12854_gene	CG12854	0.707674	0.496626	0.70	1.42
Mes4_gene	Mes4	6.36907	4.46963	0.70	1.42
CG32579_gene	CG32579	1.41535	0.993251	0.70	1.42
CG5162_gene	CG5162	3793.27	2659.43	0.70	1.43
CG3669_gene	CG3669	3.45672	2.41691	0.70	1.43
CG5458_gene	CG5287	3.45672	2.41691	0.70	1.43
CG18581_gene	CG18581	3.64724	2.54935	0.70	1.43
CG30340_gene	CG1902	22.6456	15.8258	0.70	1.43
CG14414_gene	CG14414	3.51115	2.45002	0.70	1.43
skpF_gene	CG5357	1.85084	1.29123	0.70	1.43
Klp3A_gene	Klp3A	3.89221	2.71489	0.70	1.43
CG6765_gene	CG6745	2.80348	1.95339	0.70	1.44
CG15021_gene	CG15021	28.8513	20.0968	0.70	1.44
Klp67A_gene	CG34456	6.04245	4.20476	0.70	1.44
CG5916_gene	CG5916	1.33369	0.927035	0.70	1.44
CG31313_gene	CG31313	1.90528	1.32434	0.70	1.44
CG18673_gene	CG18673	0.571583	0.397301	0.70	1.44
CG30222_gene	CG30222	0.952639	0.662168	0.70	1.44
CG11674_gene	l(1)G0007	0.952639	0.662168	0.70	1.44
alpha-Est4_gene	alpha-Est4	0.762111	0.529734	0.70	1.44
CG41268_gene	CG41268	0.762111	0.529734	0.70	1.44
snoRNA:Psi28S-3327b_gene	RpS4	0.762111	0.529734	0.70	1.44
Kaz1-ORFA_gene	CG16940	4.38214	3.04597	0.70	1.44
Kaz1-ORFB_gene	CG16940	4.38214	3.04597	0.70	1.44
CG11136_gene	CG11136	1.71475	1.1919	0.70	1.44
CG6614_gene	CG6614	13.3097	9.23724	0.69	1.44
CG3579_gene	CG3579	2.5313	1.75474	0.69	1.44
CG11889_gene	CG11889	4.68154	3.24462	0.69	1.44
CG11891_gene	CG11889	4.68154	3.24462	0.69	1.44
CG15111_gene	CG15118	30.9471	21.4211	0.69	1.44
CG13123_gene	CG13123	1.57866	1.09258	0.69	1.44
CG10633_gene	CG10633	3.97386	2.748	0.69	1.45
RhoL_gene	RhoL	45.2095	31.2543	0.69	1.45
CG16799_gene	CG16799	23.816	16.4218	0.69	1.45
CG34263_gene	mRpL17	5.08981	3.50949	0.69	1.45
l(2)01810_gene	l(2)01810	6.72291	4.63517	0.69	1.45
PGRP-SA_gene	PGRP-SA	2.44964	1.68853	0.69	1.45
prom_gene	prom	0.816547	0.562842	0.69	1.45
Ste:CG33238_gene	te:CG3323	0.816547	0.562842	0.69	1.45
Dscam_gene	Dscam	40.3647	27.811	0.69	1.45

ald_gene	ald	5.14425	3.5426	0.69	1.45
CG10663_gene	CG10663	0.62602	0.430409	0.69	1.45
LCBP1_gene	LCBP1	0.62602	0.430409	0.69	1.45
mir-281aS_gene	Oda	0.62602	0.430409	0.69	1.45
CG5285_gene	CG5285	1.06151	0.728384	0.69	1.46
CG11093_gene	CG11093	14.0446	9.63454	0.69	1.46
CG4447_gene	Klp67A	6.04245	4.13855	0.68	1.46
Chit_gene	CG30463	18.6717	12.7798	0.68	1.46
cas_gene	cas	2.17746	1.48988	0.68	1.46
CG33213_gene	mRpS22	2.17746	1.48988	0.68	1.46
CG9691_gene	CG9691	6.58682	4.50274	0.68	1.46
CG3238_gene	CG3238	1.55144	1.05947	0.68	1.46
CG2889_gene	CG2889	13.5819	9.27035	0.68	1.47
CG32809_gene	CG32809	6.5596	4.46963	0.68	1.47
Tsp74F_gene	Tsp74F	0.680456	0.463517	0.68	1.47
Met75Ca_gene	Met75Ca	3110.61	2112.68	0.68	1.47
CG9008_gene	CG9008	1.17038	0.794601	0.68	1.47
CG4101_gene	CG4101	3.51115	2.3838	0.68	1.47
CG6182_gene	CG6182	4.73597	3.21151	0.68	1.47
CG14180_gene	CG14180	1.90528	1.29123	0.68	1.48
sgl_gene	Surf1	11.5405	7.81358	0.68	1.48
vir-1_gene	vir-1	39.6298	26.8178	0.68	1.48
Mst57Db_gene	Mst57Db	2574.55	1740.34	0.68	1.48
CG31065_gene	CG31065	0.979857	0.662168	0.68	1.48
CG12003_gene	CG7879	0.734893	0.496626	0.68	1.48
Met75Cb_gene	Met75Cb	3136.36	2117.64	0.68	1.48
CG31675_gene	CG31675	3.97386	2.68178	0.67	1.48
Sox102F_gene	Sox102F	3.7289	2.51624	0.67	1.48
CG12056_gene	CG12056	14.6706	9.8994	0.67	1.48
CG11474_gene	CG11474	2.74904	1.85407	0.67	1.48
BG642378_gene	BG642378	71.339	47.974	0.67	1.49
Caf1-105_gene	Caf1-105	1.03429	0.695276	0.67	1.49
CG32628_gene	CG9940	1.03429	0.695276	0.67	1.49
Rad51C_gene	Rad51C	1.03429	0.695276	0.67	1.49
CG13957_gene	CG13957	12.3299	8.27709	0.67	1.49
CG6999_gene	CG6999	0.789329	0.529734	0.67	1.49
CG3014_gene	CG3014	4.73597	3.1784	0.67	1.49
snmRNA:158_gene	nmRNA:15	3.70168	2.48313	0.67	1.49
CG1637_gene	CG2157	196.57	131.804	0.67	1.49
CG34189_gene	unc-104	19.8693	13.3096	0.67	1.49
CG8500_gene	CG8500	4.05552	2.71489	0.67	1.49
CG34364_gene	Map60	1.63309	1.09258	0.67	1.49
Or59a_gene	Or59a	3.81055	2.54935	0.67	1.49
CG16734_gene	CG16734	1.08873	0.728384	0.67	1.49
CG10063_gene	CG9953	0.544365	0.364192	0.67	1.49
stj_gene	stj	0.544365	0.364192	0.67	1.49
Ugt86Dc_gene	Ugt86Dc	0.544365	0.364192	0.67	1.49
CG4829_gene	CG4829	20.8492	13.9386	0.67	1.50
CG30165_gene	CG30165	1.9325	1.29123	0.67	1.50
Sec61alpha_gene	Sec61alpha	392.596	260.728	0.66	1.51
CG2641_gene	CG2641	1.1976	0.794601	0.66	1.51
stet_gene	stet	0.598801	0.397301	0.66	1.51
CG9512_gene	Flo-2	2.0958	1.39055	0.66	1.51
CG10006_gene	CG10006	2.15024	1.42366	0.66	1.51
CG3003_gene	CG3003	2.15024	1.42366	0.66	1.51
CG9272_gene	CG9272	2.15024	1.42366	0.66	1.51
SamDC_gene	SamDC	70.6041	46.6828	0.66	1.51
scf_gene	scf	311.567	205.868	0.66	1.51
pxb_gene	pxb	1.90528	1.25812	0.66	1.51
CG14544_gene	CG14544	0.952639	0.629059	0.66	1.51

CG14022_gene	cype	68.0728	44.7956	0.66	1.52
CG7267_gene	CG7267	2.66739	1.75474	0.66	1.52
Pbprp4_gene	CG10050	1.00708	0.662168	0.66	1.52
CG9737_gene	CG9737	1.36091	0.893926	0.66	1.52
CG34348_gene	CG34348	2.72182	1.78785	0.66	1.52
CG8419_gene	CG8419	1.71475	1.12568	0.66	1.52
CG14149_gene	CG14149	7.21284	4.7345	0.66	1.52
CG12022_gene	CG12022	2.06859	1.35744	0.66	1.52
CG4928_gene	CG4928	22.1557	14.5346	0.66	1.52
CG31997_gene	CG31997	22.2373	14.5677	0.66	1.53
Ste:CG33237_gene	te:CG3323	1.06151	0.695276	0.65	1.53
ovo_gene	ovo	4.24605	2.7811	0.65	1.53
CG4827_gene	CG4827	399.373	261.159	0.65	1.53
Edem1_gene	Edem1	133.505	87.2737	0.65	1.53
CG7914_gene	CG7914	1.87806	1.22501	0.65	1.53
CG14033_gene	tkv	1.87806	1.22501	0.65	1.53
CG15094_gene	CG15094	83.7505	54.5626	0.65	1.53
CG30339_gene	CG1902	18.4812	12.0183	0.65	1.54
CG12288_gene	CG12288	2.39521	1.55609	0.65	1.54
Tsp26A_gene	Tsp26A	2.39521	1.55609	0.65	1.54
TepIV_gene	TepIV	95.5633	62.012	0.65	1.54
jhamt_gene	jhamt	16.2765	10.5616	0.65	1.54
CG15236_gene	CG15236	49.755	32.2807	0.65	1.54
CG34273_gene	Pde6	0.816547	0.529734	0.65	1.54
CG5149_gene	CG5149	8.79149	5.69464	0.65	1.54
CG7219_gene	CG7219	4.19161	2.71489	0.65	1.54
CecA2_gene	CecA2	0.870984	0.562842	0.65	1.55
CG6522_gene	CG6522	7.48502	4.83382	0.65	1.55
CG4908_gene	CG4908	1.33369	0.860818	0.65	1.55
Cyp6a23_gene	Cyp6a23	5.79749	3.74125	0.65	1.55
otk_gene	otk	2.88513	1.85407	0.64	1.56
CG18331_gene	CG18331	1.44257	0.927035	0.64	1.56
CG15220_gene	CG15220	1.95971	1.25812	0.64	1.56
CG12713_gene	CG12713	0.979857	0.629059	0.64	1.56
Fhos_gene	Fhos	62.3026	39.9618	0.64	1.56
Cht3_gene	Cht3	1.497	0.960143	0.64	1.56
CG7529_gene	CG33214	5.90636	3.77436	0.64	1.56
CG2126_gene	CG2126	5.49809	3.50949	0.64	1.57
CG30090_gene	CG30090	4.46379	2.84732	0.64	1.57
Tsp42Ek_gene	Tsp42Ek	1.71475	1.09258	0.64	1.57
GstE5_gene	GstE5	0.571583	0.364192	0.64	1.57
Ugt86Dd_gene	Ugt86Dd	0.571583	0.364192	0.64	1.57
CG31251_gene	CG31251	1.14317	0.728384	0.64	1.57
mmy_gene	mmy	194.529	123.858	0.64	1.57
CG34120_gene	CG34120	226.81	144.386	0.64	1.57
CG32982_gene	CG32982	7.02231	4.46963	0.64	1.57
desert_gene	desert	14.0991	8.97237	0.64	1.57
CG11226_gene	CG11226	13.5275	8.60818	0.64	1.57
CG31758_gene	CG31757	35.3837	22.5137	0.64	1.57
stnA_gene	stnB	4.16439	2.64867	0.64	1.57
stnB_gene	stnB	4.16439	2.64867	0.64	1.57
CG34035_gene	CG34035	14.8884	9.469	0.64	1.57
CG30382_gene	CG30382	27.0822	17.2164	0.64	1.57
CG15399_gene	CG15399	0.62602	0.397301	0.63	1.58
Tehao_gene	Tehao	0.62602	0.397301	0.63	1.58
CG16716_gene	sm	1.87806	1.1919	0.63	1.58
neur_gene	neur	5.79749	3.67503	0.63	1.58
CG32541_gene	CG32541	16.1676	10.2305	0.63	1.58
Ets21C_gene	Ets21C	0.680456	0.430409	0.63	1.58
pros_gene	pros	0.680456	0.430409	0.63	1.58

PGRP-LA_gene	PGRP-LA	11.105	7.01898	0.63	1.58
CG3376_gene	CG3376	5.6614	3.5757	0.63	1.58
CG15394_gene	CG15394	267.256	168.522	0.63	1.59
CG11784_gene	CG11784	5.19868	3.27773	0.63	1.59
wb_gene	wb	49.7822	31.3867	0.63	1.59
Mdr65_gene	Mdr65	10.098	6.35681	0.63	1.59
Syt7_gene	Syt7	7.04953	4.43652	0.63	1.59
CG41248_gene	CG41248	0.789329	0.496626	0.63	1.59
CG7025_gene	CG7025	6.58682	4.13855	0.63	1.59
Mocs1_gene	Mocs1	3.48394	2.18515	0.63	1.59
RpA-70_gene	RpA-70	17.9913	11.2237	0.62	1.60
CG1827_gene	CG12928	35.0843	21.8515	0.62	1.61
CG17350_gene	CG17350	10.969	6.82033	0.62	1.61
fzy_gene	fzy	1.22482	0.761493	0.62	1.61
CG3332_gene	CG3332	14.2351	8.83994	0.62	1.61
tgy_gene	tgy	1.33369	0.827709	0.62	1.61
CG17328_gene	CG17328	1.44257	0.893926	0.62	1.61
CG9775_gene	CG9775	44.9645	27.8441	0.62	1.61
CG13299_gene	CG13299	1.66031	1.02636	0.62	1.62
CG3973_gene	CG3973	67.3652	41.6172	0.62	1.62
Dup99B_gene	Dup99B	361.132	222.886	0.62	1.62
Ef1alpha100E_gene	f1alpha100	5.60696	3.44327	0.61	1.63
Adgf-A_gene	Adgf-A	8.62818	5.29734	0.61	1.63
CG4164_gene	CG4164	222.836	136.671	0.61	1.63
GstE1_gene	GstE1	8.62818	5.26423	0.61	1.64
Trim9_gene	Trim9	11.7038	7.1183	0.61	1.64
Fili_gene	Fili	1.52422	0.927035	0.61	1.64
Ste:CG33243_gene	te:CG3324	0.816547	0.496626	0.61	1.64
CG11044_gene	CG11044	0.653238	0.397301	0.61	1.64
sca_gene	sca	0.653238	0.397301	0.61	1.64
Wnt4_gene	Wnt4	0.653238	0.397301	0.61	1.64
CG33307_gene	cenG1A	0.92542	0.562842	0.61	1.64
CG13332_gene	CG33528	0.92542	0.562842	0.61	1.64
se_gene	se	1.41535	0.860818	0.61	1.64
Or65c_gene	Or65c	1.30648	0.794601	0.61	1.64
CG30001_gene	CG30001	30.8655	18.7062	0.61	1.65
CG31516_gene	aux	20.2776	12.2832	0.61	1.65
CG7144_gene	CG7144	6.61403	4.00611	0.61	1.65
CG6910_gene	CG6910	64.0173	38.7699	0.61	1.65
CG9427_gene	CG9427	143.876	87.0088	0.60	1.65
CG31619_gene	CG31619	4.05552	2.45002	0.60	1.66
PH4alphaNE1_gene	H4alphaNE	7.24005	4.37031	0.60	1.66
CG8785_gene	CG8785	22.319	13.442	0.60	1.66
mirr_gene	mirr	2.69461	1.62231	0.60	1.66
CG32645_gene	CG32645	2.42242	1.45677	0.60	1.66
CG11342_gene	CG11342	1.71475	1.02636	0.60	1.67
fas_gene	fas	4.81763	2.88043	0.60	1.67
CG9664_gene	CG9664	17.2291	10.2967	0.60	1.67
Prosalpha6_gene	phr	26.5922	15.892	0.60	1.67
CG17327_gene	CG7488	5.6614	3.37705	0.60	1.68
Nep2_gene	Nep2	29.3141	17.4812	0.60	1.68
SP1070_gene	SP1070	43.032	25.659	0.60	1.68
CG30115_gene	CG30115	25.2858	15.0643	0.60	1.68
CG12674_gene	dpr3	2.61295	1.55609	0.60	1.68
CG31777_gene	CG31777	1.27926	0.761493	0.60	1.68
CG9413_gene	CG9413	32.1175	19.0704	0.59	1.68
Orc5_gene	Sop2	2.2319	1.32434	0.59	1.69
Gycalpha99B_gene	ycalpha99	2.01415	1.1919	0.59	1.69
CG10864_gene	CG31122	1.00708	0.595951	0.59	1.69
snoRNA:Me28S-A1322_gene	f1alpha48	1.00708	0.595951	0.59	1.69

CG16790_gene	CG16790	2.69461	1.5892	0.59	1.70
GstD9_gene	GstD9	27.1638	15.9582	0.59	1.70
scarface_gene	scarface	3.89221	2.28448	0.59	1.70
CG15121_gene	CG15121	1.52422	0.893926	0.59	1.71
CG30033_gene	dare	1.52422	0.893926	0.59	1.71
CG7069_gene	CG7069	0.734893	0.430409	0.59	1.71
CG9548_gene	epsilonCOP	2.88513	1.68853	0.59	1.71
CG5084_gene	CG5084	0.680456	0.397301	0.58	1.71
dpr3_gene	dpr3	39.2759	22.911	0.58	1.71
Gmd_gene	Gmd	111.649	64.8593	0.58	1.72
CG32792_gene	CG32792	1.1976	0.695276	0.58	1.72
CG18367_gene	CG18367	0.571583	0.331084	0.58	1.73
rst_gene	rst	0.571583	0.331084	0.58	1.73
nompA_gene	nompA	22.319	12.9123	0.58	1.73
Fmo-1_gene	Fmo-1	3.32063	1.92029	0.58	1.73
CG2145_gene	CG2145	15.9771	9.23724	0.58	1.73
CG18628_gene	CG18628	1202.77	694.879	0.58	1.73
CG4839_gene	CG4839	115.024	66.3823	0.58	1.73
CG4983_gene	CG4983	2.12302	1.22501	0.58	1.73
CG18661_gene	CG18661	3.10288	1.78785	0.58	1.74
CG14021_gene	CG14021	179.994	103.431	0.57	1.74
yin_gene	yin	69.8965	40.1274	0.57	1.74
cenG1A_gene	cenG1A	29.3957	16.8522	0.57	1.74
CG11398_gene	CG11398	1.38813	0.794601	0.57	1.75
U26_gene	U26	8.21991	4.70139	0.57	1.75
GstE6_gene	GstE6	14.344	8.17777	0.57	1.75
CG4537_gene	CG4537	2.85792	1.62231	0.57	1.76
CG32702_gene	CG32702	18.6717	10.5947	0.57	1.76
CG13190_gene	CG13190	10.9145	6.19127	0.57	1.76
CG15097_gene	l(2)03709	11.8672	6.721	0.57	1.77
CG15365_gene	CG15365	0.762111	0.430409	0.56	1.77
CG7573_gene	CG7573	0.762111	0.430409	0.56	1.77
CG9297_gene	CG9297	20.6586	11.6541	0.56	1.77
CG32152_gene	CG5151	2.2319	1.25812	0.56	1.77
CG8093_gene	CG8093	1.11595	0.629059	0.56	1.77
adat_gene	CAH1	63.1191	35.4922	0.56	1.78
CG7409_gene	CG32373	11.4861	6.45613	0.56	1.78
CG7433_gene	CG7433	1.41535	0.794601	0.56	1.78
CG8420_gene	CG8420	692.432	387.633	0.56	1.79
CG10407_gene	CG10407	227.681	127.335	0.56	1.79
CG9935_gene	CG9935	5.38921	3.01286	0.56	1.79
CG10126_gene	CG10126	128.606	71.8452	0.56	1.79
CG32352_gene	CG32352	47.6047	26.586	0.56	1.79
CadN_gene	CadN	36.6085	20.4279	0.56	1.79
lectin-21Cb_gene	lectin-21Cb	56.995	31.784	0.56	1.79
Irk3_gene	Grip71	0.653238	0.364192	0.56	1.79
Tango12_gene	Tango12	0.653238	0.364192	0.56	1.79
CG5337_gene	TfIIB	3.91943	2.18515	0.56	1.79
CG9525_gene	CG9525	93.1953	51.8808	0.56	1.80
CG31846_gene	CG31846	17.583	9.76697	0.56	1.80
CG30197_gene	Cpr51A	2.80348	1.55609	0.56	1.80
CG34255_gene	Rad9	1.1976	0.662168	0.55	1.81
CG34220_gene	CG18445	0.898202	0.496626	0.55	1.81
CG6696_gene	fu	0.898202	0.496626	0.55	1.81
CG14301_gene	CG14301	1.74197	0.960143	0.55	1.81
e_gene	e	1.14317	0.629059	0.55	1.82
CG2064_gene	CG2064	9.09089	4.99936	0.55	1.82
CAH1_gene	CAH1	76.4016	42.0145	0.55	1.82
CG30104_gene	CG30104	175.667	96.4116	0.55	1.82
CG14212_gene	CG14212	1.08873	0.595951	0.55	1.83

CG14248_gene	CG14248	2.36799	1.29123	0.55	1.83
CG13397_gene	CG13397	26.5378	14.4353	0.54	1.84
CG1434_gene	CG1434	6.39629	3.47638	0.54	1.84
CG11112_gene	CG11166	518.671	280.891	0.54	1.85
CG10553_gene	CG10553	20.1143	10.8927	0.54	1.85
CG31953_gene	CG31953	0.734893	0.397301	0.54	1.85
CG9628_gene	CG9628	108.982	58.6018	0.54	1.86
Rab-RP3_gene	Rab-RP3	32.2264	17.2495	0.54	1.87
CG13077_gene	CG13077	2.42242	1.29123	0.53	1.88
CG11722_gene	CG3909	2.42242	1.29123	0.53	1.88
PGRP-LF_gene	PGRP-LF	2.42242	1.29123	0.53	1.88
Tsp3A_gene	Tsp3A	2.61295	1.39055	0.53	1.88
CG6867_gene	Sh	0.62602	0.331084	0.53	1.89
CG31525_gene	CG9809	0.816547	0.430409	0.53	1.90
tsl_gene	tsl	0.816547	0.430409	0.53	1.90
Ugt36Bc_gene	Ugt36Bc	6.50516	3.41016	0.52	1.91
CG11842_gene	CG11842	0.762111	0.397301	0.52	1.92
CG11253_gene	RpS12	0.571583	0.297975	0.52	1.92
gkt_gene	gkt	2.04137	1.05947	0.52	1.93
CG18304_gene	CG18304	105.008	54.4302	0.52	1.93
CG30151_gene	CG30151	79.9944	41.4517	0.52	1.93
CG11261_gene	CG14117	2.93957	1.52299	0.52	1.93
CG8774_gene	CG8774	387.942	200.902	0.52	1.93
CG31847_gene	CG31847	16.1404	8.3102	0.51	1.94
CG14372_gene	CG14372	2.12302	1.09258	0.51	1.94
CG18853_gene	CG18853	6.61403	3.37705	0.51	1.96
cac_gene	cac	0.843766	0.430409	0.51	1.96
hbs_gene	hbs	3065.84	1557.82	0.51	1.97
Cyp4ac1_gene	tkv	129.94	66.0181	0.51	1.97
knrl_gene	knrl	2.61295	1.32434	0.51	1.97
CG10936_gene	CG10936	4.05552	2.05272	0.51	1.98
CG7224_gene	CG7224	31.7637	16.0576	0.51	1.98
CG31473_gene	CG31472	2.0958	1.05947	0.51	1.98
CG8262_gene	sec31	2.55852	1.29123	0.50	1.98
CG17387_gene	CG17387	9.90744	4.99936	0.50	1.98
CG34447_gene	CG34447	206.423	104.159	0.50	1.98
Leucokinin_gene	Leucokinin	1.11595	0.562842	0.50	1.98
CG11257_gene	CG11257	7.7572	3.90679	0.50	1.99
CG15362_gene	CG15362	3.94665	1.9865	0.50	1.99
CAH2_gene	CAH2	21.448	10.7933	0.50	1.99
CG2915_gene	CG2906	60.7511	30.559	0.50	1.99
CG4078_gene	CG4078	4.35492	2.18515	0.50	1.99
CG15317_gene	CG15317	3.10288	1.55609	0.50	1.99
CG33279_gene	CG33279	1.38813	0.695276	0.50	2.00
CG14044_gene	CG14044	0.92542	0.463517	0.50	2.00
CG14934_gene	CG31757	0.92542	0.463517	0.50	2.00
CG5527_gene	CG5527	4.43657	2.21826	0.50	2.00
CG41439_gene	CG41439	4.05552	2.01961	0.50	2.01
bxd_gene	bxd	1.1976	0.595951	0.50	2.01
CG13912_gene	CG13912	1.7964	0.893926	0.50	2.01
Gr97a_gene	Gr97a	1.7964	0.893926	0.50	2.01
CG32355_gene	CG32355	35.4926	17.6137	0.50	2.02
TotM_gene	TotM	4.13717	2.05272	0.50	2.02
CG32683_gene	CG32683	89.6841	44.4977	0.50	2.02
CG11200_gene	CG11200	0.734893	0.364192	0.50	2.02
CR41508_gene	CR41508	0.734893	0.364192	0.50	2.02
DAT_gene	DAT	0.734893	0.364192	0.50	2.02
CG8468_gene	CG8468	1.46979	0.728384	0.50	2.02
AQP_gene	AQP	9.82579	4.86693	0.50	2.02
CG5397_gene	CG5397	12.5748	6.22437	0.49	2.02

CG13449_gene	CG13449	0.870984	0.430409	0.49	2.02
CG15414_gene	CG15414	2.01415	0.993251	0.49	2.03
CG6114_gene	CG6114	1.00708	0.496626	0.49	2.03
Tsp29Fa_gene	Tsp29Fa	3.04844	1.48988	0.49	2.05
CG33681_gene	CG33681	5.36199	2.61556	0.49	2.05
Ste:CG33241_gene	te:CG3324	1.22482	0.595951	0.49	2.06
CG10970_gene	CG10970	0.680456	0.331084	0.49	2.06
mir-281a_gene	Oda	0.680456	0.331084	0.49	2.06
CG13879_gene	CG13879	0.544365	0.264867	0.49	2.06
Ste:CG33239_gene	te:CG3323	0.952639	0.463517	0.49	2.06
CG5948_gene	CG5948	1.57866	0.761493	0.48	2.07
CG31817_gene	CG31817	1.30648	0.629059	0.48	2.08
CG3604_gene	CG3604	37.8606	18.2096	0.48	2.08
CG4942_gene	CG4942	2.20468	1.05947	0.48	2.08
CG16712_gene	CG16712	42.5966	20.461	0.48	2.08
CG34261_gene	park	2.06859	0.993251	0.48	2.08
CG15753_gene	CG15753	0.898202	0.430409	0.48	2.09
CG6465_gene	CG6465	2.01415	0.960143	0.48	2.10
betaInt-nu_gene	betaInt-nu	42.2972	20.163	0.48	2.10
mre11_gene	mre11	6.39629	3.04597	0.48	2.10
CG3270_gene	CG3270	2.50408	1.1919	0.48	2.10
CG4880_gene	CG4880	5.00816	2.3838	0.48	2.10
Ugt86De_gene	Ugt86De	2.99401	1.42366	0.48	2.10
CG13950_gene	CG13950	22.4551	10.6609	0.47	2.11
mol_gene	mol	4.68154	2.21826	0.47	2.11
CG6470_gene	CG6470	76.32	36.1212	0.47	2.11
CG31821_gene	CG31821	28.1437	13.3096	0.47	2.11
CG13708_gene	CG13708	0.843766	0.397301	0.47	2.12
CG12310_gene	CG12310	42.8687	20.0968	0.47	2.13
CG5773_gene	CG5773	7.21284	3.34395	0.46	2.16
CG15786_gene	CG15786	0.571583	0.264867	0.46	2.16
CG32259_gene	wit	1.14317	0.529734	0.46	2.16
CG12307_gene	CG12307	1.36091	0.629059	0.46	2.16
Rad9_gene	CG6852	2.15024	0.993251	0.46	2.16
GNBP2_gene	GNBP2	4.54545	2.08583	0.46	2.18
Ace_gene	Ace	14.5618	6.65478	0.46	2.19
Tsf3_gene	CG15706	0.870984	0.397301	0.46	2.19
CG13460_gene	CG13460	0.653238	0.297975	0.46	2.19
CG4509_gene	CG4509	0.653238	0.297975	0.46	2.19
CG11475_gene	CG6393	2.47686	1.12568	0.45	2.20
CG13704_gene	CG13704	1.38813	0.629059	0.45	2.21
CG34215_gene	CG15236	37.8878	17.0177	0.45	2.23
CG6401_gene	CG6401	1.76919	0.794601	0.45	2.23
pncr009:3L_gene	pncr009:3L	6.06967	2.71489	0.45	2.24
CG8058_gene	CG8058	37.6156	16.7528	0.45	2.25
del_gene	CG9253	1.41535	0.629059	0.44	2.25
CG10005_gene	CG10005	0.898202	0.397301	0.44	2.26
stl_gene	stl	0.898202	0.397301	0.44	2.26
Msi_gene	Adgf-A	0.598801	0.264867	0.44	2.26
CG13792_gene	CG13792	0.680456	0.297975	0.44	2.28
CG16850_gene	CG31846	2.50408	1.09258	0.44	2.29
CG9766_gene	CG9766	5.85192	2.54935	0.44	2.30
CG13285_gene	CG13285	0.762111	0.331084	0.43	2.30
CG17751_gene	CG17751	0.92542	0.397301	0.43	2.33
CG3323_gene	CG3323	3.10288	1.32434	0.43	2.34
mRpS2_gene	CG11927	21.2302	9.03859	0.43	2.35
CG7406_gene	CG7406	0.544365	0.231759	0.43	2.35
CG8539_gene	CG8539	0.544365	0.231759	0.43	2.35
CG33472_gene	CG33472	1.08873	0.463517	0.43	2.35
sced_gene	sced	1.08873	0.463517	0.43	2.35

CG33922_gene	CG33922	0.62602	0.264867	0.42	2.36
CG31058_gene	tau	1.25204	0.529734	0.42	2.36
CG13542_gene	CG13542	0.707674	0.297975	0.42	2.37
CG32245_gene	CG32245	1.57866	0.662168	0.42	2.38
CG2157_gene	CG2157	1.11595	0.463517	0.42	2.41
Cyp6a20_gene	Cyp6a20	6.31463	2.61556	0.41	2.41
CG32212_gene	pncr009:3L	3.91943	1.62231	0.41	2.42
Cyp4ac2_gene	tkv	7.78442	3.21151	0.41	2.42
CG8105_gene	CG9220	11.5133	4.70139	0.41	2.45
CG4302_gene	Glycogenin	13.963	5.69464	0.41	2.45
CG18249_gene	CG18249	0.571583	0.231759	0.41	2.47
CG18228_gene	CG18228	15.6777	6.35681	0.41	2.47
CG17025_gene	CG14372	2.31355	0.927035	0.40	2.50
CG10513_gene	CG10513	3.07566	1.22501	0.40	2.51
Spindly_gene	CG8852	1.25204	0.496626	0.40	2.52
Ripalpha_gene	Ripalpha	1.76919	0.695276	0.39	2.54
tnc_gene	tnc	14.6162	5.72775	0.39	2.55
CG31778_gene	CG31778	1.52422	0.595951	0.39	2.56
Ugt36Ba_gene	Ugt36Ba	1.36091	0.529734	0.39	2.57
snmRNA:400_gene	nmRNA:40	0.680456	0.264867	0.39	2.57
Cyp6a21_gene	Cyp6a21	33.0974	12.8461	0.39	2.58
rk_gene	rk	1.11595	0.430409	0.39	2.59
Ugt35b_gene	Ugt35b	1094.45	421.238	0.38	2.60
Cyp6a19_gene	Cyp6a19	1.55144	0.595951	0.38	2.60
CG8837_gene	CG8837	1.38813	0.529734	0.38	2.62
CG11883_gene	CG11883	31.0016	11.8197	0.38	2.62
DNaseII_gene	DNaseII	6.09689	2.31759	0.38	2.63
CG16713_gene	CG16713	5.71583	2.15204	0.38	2.66
Ste:CG33242_gene	te:CG3324	1.06151	0.397301	0.37	2.67
CG14395_gene	CG14395	1.25204	0.463517	0.37	2.70
NPFR1_gene	NPFR1	14.8612	5.49599	0.37	2.70
CG9030_gene	CG9030	0.816547	0.297975	0.36	2.74
CG18213_gene	CG18213	0.544365	0.19865	0.36	2.74
Cpr49Ah_gene	Cpr49Ah	0.544365	0.19865	0.36	2.74
CG9522_gene	Flo-2	0.544365	0.19865	0.36	2.74
CG34335_gene	CG34335	707.974	256.491	0.36	2.76
chp_gene	chp	41.5078	14.9981	0.36	2.77
Rpt3R_gene	Rpt3R	3.21175	1.15879	0.36	2.77
Inos_gene	Inos	45.8627	16.5211	0.36	2.78
pdm3_gene	pdm3	1.1976	0.430409	0.36	2.78
ppk28_gene	ppk28	1.1976	0.430409	0.36	2.78
Cyp9b2_gene	Cyp9b2	0.653238	0.231759	0.35	2.82
CG17386_gene	CG17386	1.497	0.529734	0.35	2.83
CG2680_gene	CG2680	0.843766	0.297975	0.35	2.83
CG31788_gene	CG31788	78.3613	27.6124	0.35	2.84
CG6784_gene	CG6784	9.30864	3.24462	0.35	2.87
zwilch_gene	zwilch	0.762111	0.264867	0.35	2.88
CG18180_gene	fry	0.571583	0.19865	0.35	2.88
CG17928_gene	CG17928	4.3277	1.48988	0.34	2.90
CG10445_gene	CG10445	1.9325	0.662168	0.34	2.92
CG13751_gene	CG13751	57.7027	19.6995	0.34	2.93
CG3117_gene	CG3117	0.680456	0.231759	0.34	2.94
CG9609_gene	CG9609	28.5792	9.70075	0.34	2.95
Ugt35a_gene	Ugt35a	84.5399	28.6719	0.34	2.95
CG14913_gene	Samuel	22.3462	7.48249	0.33	2.99
CG6361_gene	CG6361	1.08873	0.364192	0.33	2.99
CG8834_gene	CG8834	14.3168	4.76761	0.33	3.00
CG18558_gene	CG18558	2.88513	0.960143	0.33	3.00
CG5873_gene	CG5873	2.12302	0.695276	0.33	3.05
CG11592_gene	CG3625	1.11595	0.364192	0.33	3.06

CG12766_gene	CG12766	2.34077	0.761493	0.33	3.07
CG32984_gene	CG32984	1.74197	0.562842	0.32	3.09
CG15152_gene	CG15152	0.92542	0.297975	0.32	3.11
TepII_gene	TepII	98.0401	31.1881	0.32	3.14
lectin-22C_gene	lectin-22C	0.62602	0.19865	0.32	3.15
CG6018_gene	px	5.57974	1.75474	0.31	3.18
CG16752_gene	CG16752	4.3277	1.35744	0.31	3.19
CG34354_gene	CG34354	9.33586	2.88043	0.31	3.24
CG32354_gene	exo70	2.64017	0.794601	0.30	3.32
CG12896_gene	CG12896	4.40936	1.32434	0.30	3.33
Ugt86Dg_gene	Ugt86Dg	1.22482	0.364192	0.30	3.36
GRHRII_gene	GRHRII	1.46979	0.430409	0.29	3.41
pncr015:3L_gene	pncr015:3L	0.680456	0.19865	0.29	3.43
sisA_gene	sisA	15.1878	4.40341	0.29	3.45
CG13245_gene	beat-Ic	2.85792	0.827709	0.29	3.45
Lsp1beta_gene	Lsp1beta	0.707674	0.19865	0.28	3.56
Peritrophin-A_gene	eritrophin-	12.4115	3.47638	0.28	3.57
nAcRalpha-30D_gene	cRalpha-3	16.7937	4.70139	0.28	3.57
CG4484_gene	CG4484	0.952639	0.264867	0.28	3.60
Oatp58Dc_gene	Oatp58Dc	0.952639	0.264867	0.28	3.60
CG2974_gene	CG2972	3.10288	0.860818	0.28	3.60
CG33988_gene	CG33988	8.356	2.28448	0.27	3.66
tam_gene	tam	2.42242	0.662168	0.27	3.66
Ste12DOR_gene	Ste12DOR	1.36091	0.364192	0.27	3.74
CG16733_gene	CG16733	0.870984	0.231759	0.27	3.76
CG14838_gene	CG14838	0.62602	0.165542	0.26	3.78
CG6789_gene	rg	1.14317	0.297975	0.26	3.84
CG8586_gene	CG8586	16.9025	4.40341	0.26	3.84
CG31955_gene	CG31955	7.86607	1.9865	0.25	3.96
CG34235_gene	CG34235	0.789329	0.19865	0.25	3.97
CG30058_gene	CG4616	7.07674	1.75474	0.25	4.03
CG34312_gene	CG4616	7.07674	1.75474	0.25	4.03
CG9021_gene	CG9021	1.60588	0.397301	0.25	4.04
CG13394_gene	CG13384	1.76919	0.430409	0.24	4.11
CG15140_gene	CG15140	11.4589	2.748	0.24	4.17
CG30076_gene	ttv	2.77626	0.662168	0.24	4.19
CG8908_gene	CG8908	11.8399	2.7811	0.23	4.26
Obp44a_gene	Pabp2	0.707674	0.165542	0.23	4.27
Obp51a_gene	hbs	1368.42	315.556	0.23	4.34
Obp99b_gene	Obp99b	11.5133	2.64867	0.23	4.35
abd-A_gene	abd-A	18.6989	4.10544	0.22	4.55
LvpH_gene	Cyp4e1	2.28633	0.496626	0.22	4.60
dsf_gene	dsf	1.52422	0.331084	0.22	4.60
GstD5_gene	GstD5	9.49917	2.05272	0.22	4.63
CG8560_gene	CG8560	0.62602	0.132434	0.21	4.73
CG9406_gene	Magi	0.62602	0.132434	0.21	4.73
Obp49a_gene	CG8776	0.952639	0.19865	0.21	4.80
CG5002_gene	CG5002	4.30048	0.893926	0.21	4.81
CG7084_gene	CG7084	2.74904	0.562842	0.20	4.88
CG3690_gene	CG3690	3.04844	0.595951	0.20	5.12
Cdlc2_gene	Cdlc2	0.680456	0.132434	0.19	5.14
beat-IIIa_gene	beat-IIIa	3.59281	0.695276	0.19	5.17
snoRNA:Me28S-A1705_gene	CG32683	0.898202	0.165542	0.18	5.43
ry_gene	ry	0.544365	0.0993251	0.18	5.48
CG18088_gene	CG18088	4.00108	0.728384	0.18	5.49
CG34366_gene	CG34366	0.952639	0.165542	0.17	5.75
CG3759_gene	CG3759	0.571583	0.0993251	0.17	5.75
yip7_gene	yip7	0.571583	0.0993251	0.17	5.75
CG3349_gene	CG3349	24.0881	4.17166	0.17	5.77
beat-Ic_gene	beat-Ic	62.7925	10.4954	0.17	5.98

CG10764_gene	CG10764	0.653238	0.0993251	0.15	6.58
ple_gene	ple	0.680456	0.0993251	0.15	6.85
CG8157_gene	CG8157	2.55852	0.364192	0.14	7.03
CG14715_gene	CG14715	8.27435	1.12568	0.14	7.35
NaPi-T_gene	NaPi-T	2.12302	0.264867	0.12	8.02
CG6602_gene	CG6602	1.68753	0.19865	0.12	8.49
CG14245_gene	CG14245	0.598801	0.0662168	0.11	9.04
CG14246_gene	CG14245	0.598801	0.0662168	0.11	9.04
Uro_gene	Uro	0.62602	0.0662168	0.11	9.45
CG3106_gene	CG3106	1.03429	0.0993251	0.10	10.41
phr_gene	phr	12.2482	1.09258	0.09	11.21
CG12506_gene	CG12506	1.497	0.132434	0.09	11.30
CG11892_gene	CG11892	1.52422	0.132434	0.09	11.51
CG15614_gene	CG15614	1.22482	0.0993251	0.08	12.33
scpr-A_gene	scpr-A	7.56667	0.529734	0.07	14.28
Traf1_gene	Traf1	11.2956	0.761493	0.07	14.83
CG33630_gene	CG33630	0.544365	0.0331084	0.06	16.44
CG31198_gene	CG31198	0.571583	0.0331084	0.06	17.26
CG14292_gene	CG14292	2.39521	0.132434	0.06	18.09
CG2187_gene	CG2187	0.598801	0.0331084	0.06	18.09
yellow-e_gene	yellow-e	1.82362	0.0993251	0.05	18.36
CG41443_gene	CG41443	0.653238	0.0331084	0.05	19.73
scpr-B_gene	CG31388	1.98693	0.0993251	0.05	20.00
CG15155_gene	CG15155	0.680456	0.0331084	0.05	20.55
CG6628_gene	dpr10	2.04137	0.0993251	0.05	20.55
CG34167_gene	beat-Ic	13.3369	0.629059	0.05	21.20
Jon65Aiv_gene	Jon65Aiv	0.707674	0.0331084	0.05	21.37
alpha-Est7_gene	alpha-Est7	2.17746	0.0993251	0.05	21.92
CG5361_gene	CG5361	1.46979	0.0662168	0.05	22.20
obst-A_gene	obst-A	0.762111	0.0331084	0.04	23.02
CG10514_gene	CG10514	0.843766	0.0331084	0.04	25.48
alpha-Est5_gene	alpha-Est5	2.5313	0.0993251	0.04	25.48
CG31090_gene	CG31090	2.5313	0.0993251	0.04	25.48
scpr-C_gene	scpr-C	4.27326	0.165542	0.04	25.81
CG13309_gene	CG13309	0.870984	0.0331084	0.04	26.31
CG9509_gene	Flo-2	1.74197	0.0662168	0.04	26.31
CG14681_gene	Skeletor	22.2645	0.794601	0.04	28.02
Skeletor_gene	Skeletor	22.2645	0.794601	0.04	28.02
CG8934_gene	CG31090	0.979857	0.0331084	0.03	29.60
CG7882_gene	CG7882	1.98693	0.0662168	0.03	30.01
CG13793_gene	CG13793	40.528	1.25812	0.03	32.21
CG9294_gene	CG9294	2.28633	0.0662168	0.03	34.53
Cyp6a14_gene	Cyp6a14	5.90636	0.165542	0.03	35.68
CG7874_gene	CG7874	24.6325	0.629059	0.03	39.16
CG13538_gene	CG13538	1.36091	0.0331084	0.02	41.10
CG14376_gene	CG14376	12.4932	0.297975	0.02	41.93
Ugt86Dj_gene	Ugt86Dj	1.52422	0.0331084	0.02	46.04
Cpr56F_gene	Cpr56F	1.74197	0.0331084	0.02	52.61
CG9259_gene	CG9259	3.53837	0.0662168	0.02	53.44
CG11598_gene	CG11598	941.234	14.2366	0.02	66.11
CR11700_gene	CR11700	13.963	0.19865	0.01	70.29
CG33631_gene	CG33631	5.30756	0.0331084	0.01	160.31
CG33784_gene	CG33784	18.9711	0.0331084	0.00	573.00
CG33783_gene	CG33783	34.54	0.0331084	0.00	1043.24
alphaTry_gene	alphaTry	0.653238	0	0.00	-
beat-IV_gene	beat-IV	0.62602	0	0.00	-
betaTry_gene	betaTry	1.14317	0	0.00	-
CG10560_gene	CG10560	1.11595	0	0.00	-
CG12374_gene	CG12374	0.653238	0	0.00	-
CG13656_gene	CG13656	0.653238	0	0.00	-

CG6733_gene	CG13830	0.62602	0	0.00	-
CG14069_gene	CG14069	0.680456	0	0.00	-
CG15406_gene	CG15406	1.52422	0	0.00	-
CG17752_gene	CG17752	3.78334	0	0.00	-
CG2196_gene	CG2196	1.27926	0	0.00	-
CG31272_gene	CG31272	0.544365	0	0.00	-
CG3285_gene	CG3285	1.27926	0	0.00	-
CG33775_gene	CG33775	1.9325	0	0.00	-
CG8197_gene	CG8197	0.789329	0	0.00	-
Jon74E_gene	Jon74E	0.979857	0	0.00	-
Jon99Cii_gene	Jon99Cii	0.680456	0	0.00	-
nerfin-2_gene	nerfin-2	0.62602	0	0.00	-

Table S6: Genes with down-regulated expression in *iab-6*^{cocu} males

Gene ID	CG #	Fold	Signal	Predicted Function	Reported AG	Highest Expression
alpha-Est5	CG1089	25.48	No	Carboxylesterase	very low	Midgut
alpha-Est7	CG1112	21.92	No	Carboxylesterase	moderate	Broad
alphaTry	CG18444	-	Yes	trypsin, serine protease	high	Midgut
beat-Ic	CG4838	5.98	No	Cell Adhesion	very low	CNS
beat-IIIa	CG12621	5.17	No	immunoglobulin-like	very low	Broad
beat-IV	CG18211	-	Yes	immunoglobulin-like	very low	CNS
betaTry	CG10152	-	Yes	trypsin, serine protease	high	Midgut
Cdlc2	CG5450	5.14	No	Dynein light chain	very high	Testis
CG10514	CG10514	25.48	No	CHK-kinase like	moderately high	Malpighian Tubules
CG10560	CG10560	-	No	CHK-kinase like	moderate	Malpighian Tubules
CG10764	CG10764	6.58	Yes	Peptidase S1A	none	Testis
CG11598	CG11598	66.11	Yes	Lipase	moderate	Accessory Gland
CG11892	CG11892	11.51	No	CHK kinase-like, DUF227	moderate	Malpighian Tubules
CG12374	CG12374	-	Yes	M14 Protease inhibitor	moderate	Midgut
CG12506	CG12506	11.3	Yes	Unknown	moderately high	Testis
CG13309	CG13309	26.31	Yes	chitin binding	moderate	Malpighian Tubules
CG13538	CG13538	41.1	No	Unknown	moderate	Testis
CG13793	CG13793	32.21	No	Neurotransmitter	very low	Heart
CG14069	CG14069	-	Yes	cytokine activity	low	Testis
CG14245	CG14245	9.04	Yes	chitin binding	moderately high	-
CG14246	CG14246	9.04	Yes	Unknown	none	Malpighian Tubules
CG14292	CG14292	18.09	Yes	Unknown	moderately high	Malpighian Tubules
CG14376	CG14376	41.93	Yes	solute-binding protein	none	Broad
CG14715	CG14715	7.35	Yes	peptidyl-prolyl cis-trans	low	Broad
CG15155	CG15155	20.55	No	Acyl-CoA N-Acyltransferase	low	Malpighian Tubules
CG15406	CG15406	-	Yes	fructose/general transporter	moderate	Malpighian Tubules
CG15614	CG15614	12.33	No	G-coupled protein receptor	none	Broad
CG17210	CG17210	20	Yes	CAP domain protein, allergen	very low	Testis
CG17752	CG17752	-	Yes	transmembrane transport	low	Malpighian Tubules
CG18088	CG18088	5.49	Yes	Alkaline Phosphatase	very low	salivary gland
CG2187	CG2187	18.09	No	sodium symporter	very low	Malpighian Tubules
CG2196	CG2196	-	No	transmembrane transport	low	Malpighian Tubules
CG3106	CG3106	10.41	Yes	Acyl-CoA N-Acyltransferase	low	Midgut
CG31090	CG42235	29.6	No	sodium symporter	low	Malpighian Tubules
CG31198	CG31198	17.26	Yes	Peptidase M1	very high	Midgut
CG31272	CG31272	-	No	Lipid Transport	low	Malpighian Tubules
CG3285	CG3285	-	Yes	general/sugar transporter	very low	Malpighian Tubules
CG3349	CG3349	5.77	Yes	Unknown	moderate	Accessory Gland
CG33630	CG33630	16.44	Yes	Unknown	very low	Broad
CG33631	CG33631	160.31	Yes	Unknown	very low	Broad
CG33775	CG33775	-	No	Unknown	none	Broad

Table S6: Genes with down-regulated expression in *iab-6*^{cocu} males

Gene ID	CG #	Fold	Signal	Predicted Function	Reported AG	Highest Expression
CG33783	CG33783	1043.24	No	Unknown	-	-
CG33784	CG33784	578	Yes	Unknown	none	Eye
CG34167	CG34167	21.2	No	Unknown	low	Testis
CG34366	CG34366	5.75	No	voltage dependant potassium	none	Broad
CG3690	CG3690	5.12	No	general/sugar transporter	very low	Malpighian Tubules
CG41443	CG41443	19.78	No	non-protein coding	none	Testis
CG5361	CG5361	22.2	No	Alkaline Phosphatase	very low	Malpighian Tubules
CG6602	CG6602	8.49	Yes	Unknown	low	Malpighian Tubules
CG6628	CG6628	20.55	Yes	CAP domain protein	very low	Testis
CG6783	CG6783	-	No	serine protease inhibitor	low	Malpighian Tubules
CG7874	CG7874	39.16	Yes	chitin binding peritrophin-A,	very high	Malpighian Tubules
CG7882	CG7882	30.01	No	transporter, general sugar	low	Malpighian Tubules
CG8157	CG8157	7.03	Yes	Unknown	low	Broad
CG8197	CG8197	-	No	Unknown	low	Testis
CG9259	CG9259	53.44	No	CHK-kinase like/Duff227	moderate	Malpighian Tubules
CG9294	CG9294	34.53	No	peptidase S1/S6	none	Broad
CG9509	CG9509	26.31	No	glucose-methanol-choline	moderate	Malpighian Tubules
Cpr56F	CG9036	52.61	Yes	insect cuticle protein	low	Testis
CR11700	CG11700	70.29	no	ubiquitin family related	low	Testis
Cyp6a14	CG8687	35.68	Yes	cytochrome P450	very low	Crop
Jon65Aiv	CG6467	21.37	Yes	peptidase S1/S6	very high	midgut
Jon74E	CG6298	-	No	Peptidase S1A	moderate	Midgut
Jon99Cii	CG31034	-	Yes	Peptidase S1A	very high	-
NaPi-T	CG10207	8.02	No	Phosphate transport	low	Malpighian Tubules
nerfin-2	CG12809	-	No	zinc/nucleic acid binding	none	CNS
obst-A	CG17052	23.02	Yes	chitin-binding	very low	Broad
phr	CG11205	11.21	No	DNA photolase, DNA repair	low	Broad
ple	CG10118	6.85	No	Tyrosine-3 monohydroxilase	very low	CNS
scpr-A	CG5207	14.28	Yes	CAP domain protein	very high	Testis
scpr-C	CG5106	25.81	Yes	unknown, CAP allergen	very high	Testis
Skeletor	CG43161	28.02	Yes	Spindle Assembly	very low	-
Traf1	CG3048	14.83	No	JNK, Cell Death, Apoptosis, Cell	very low	CNS
Ugt86Dj	CG15902	46.04	Yes	UDP-glucosyltransferase	very low	Midgut
Uro	CG7171	9.45	No	Uricase	moderate	Malpighian Tubules
yellow-e	CG9792	18.36	yes	isomerase activity	none	Carcass
yip7	CG6457	5.75	Yes	serine protease	very high	Midgut

Table S6: Genes with down-regulated expression in *iab-6*^{cocu} males. Data in this table are compiled from signal sequence predictions obtained from SignalP 4.0 (Petersen *et al.* 2011), annotated functions from FlyBase (1994), previously reported organ expression from Fly Atlas (Chintapalli *et al.* 2007) and accessory gland (AG) expression levels from modENCODE (McQuilton *et al.* 2012; Roy *et al.* 2010) except for phr, where modENCODE reports no expression and Fly Atlas reports low expression. Accessory gland expression is reported as listed in the modENCODE Development RNA-seq report for each gene (none, very low, low, moderate, moderately high, high, very high, and extremely high). No fold differences were able to be calculated for entries with (-) since the gene was not detected in *iab-6*^{cocu} males. Expression data delineated with a (-) was not available from any currently available sources. The shaded cells are adjacent genes that are part of a putative regulatory cluster. Only unique entries for predicted protein coding genes are included in this list.

Table S7: Genes with up-regulated expression in *iab-6*^{cocu} males. (.xlsx, 1 MB)

Available for download as a .xlsx file at:

http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.115.181644/-/DC1/TableS7.xlsx

Table S8: Expression of known LTR genes

Gene	Fold Change	Direction of Change	Chromosome	Feature	Cellular Origin
CG1656[12]	1.27	+	2R	Lectin	Secondary[11]
CG1652[12]	1.32	+	2R	Lectin	Secondary[11]
CG9997[12]	1.04	-	3R	Protease	Main[11]
CG17575[12]	1.72	+	2R	CRISP	Secondary[11]
Seminase[73]	1.10	-	3L	Protease	Main[11]
Sex Peptide[22]	1.08	-	3L	peptide/prohormone	Main[22]
Intrepid	1.05	-	3R	Protease	unknown
Antares	1.05	+	2R	CRISP	unknown
Aquarius	1.03	-	3R	Protease	unknown

Table S8: Expression of known LTR genes. The expression differences for known Long-term response genes (CHAPMAN *et al.* 2001; GLIGOROV *et al.* 2013; LAFLAMME *et al.* 2012; RAM and WOLFNER 2009; STYGER 1992). None of these genes show >2-fold differences in RNA levels between *iab-6*^{cocu} and controls, suggesting that their expression is not impacted by the *iab-6*^{cocu} mutation.

Table S9: Expression differences in known accessory gland protein genes				
Gene	**Fold Change**	**Direction of Change**	**Chromosome**	**Feature**
CG11598	66.1	-	3R	Lipase
CG13309	26.3	-	3L	Unknown
scpr-A	14.3	-	3R	CRISP
CG3349	5.8	-	3L	Unknown
Cdlc2	5.1	-	2L	Dynein light chain
CG14913	3.0	-	2L	Unknown
Obp56g	72.6	+	2R	Odorant Binding
Acp24A4	53.9	+	2L	Protease Inhibitor
CG6426	6.2	+	2R	Destabilase
Glt	5.8	+	2L	Carboxylesterase
Cpr67B	5.7	+	3L	Cuticle Protein

Table S9: Expression differences in known accessory gland protein genes. The expression differences (- = down-regulated, + = up-regulated), location, and predicted function for known accessory gland proteins. Annotated functions were obtained from FlyBase (1994) if available.